Biophysical Journal, Volume 97

Supporting Material

An Energetic Representation of Protein Architecture that is Independent of Primary and Secondary Structure

Jason Vertrees, James O Wrabl, and Vincent J Hilser

Supporting Material: Methods Details for Vertrees, *et al*. "An Energetic Representation of Protein Architecture that is Independent of Primary and Secondary Structure"

Thermodynamic environment space of proteins defined from native state ensembles

Previously, we described the COREX/BEST algorithm (1-3), which generates a conformational ensemble for a protein using the high-resolution structure as a template. COREX/BEST requires as input the three-dimensional structural coordinates of a protein and, after processing a large number of conformational microstates varying from fully folded to fully unfolded, outputs a thermodynamic (*i.e.* energetic) model of the protein's native state ensemble. This algorithm has been vetted in both retrospective validation (4-7) and prediction (1), and thus provides a reasonable representation of the ensemble. For this work, a COREX/BEST analysis was performed on each member of a database of 120 diverse human proteins (8, 9) (Table S1 in the Supporting Material) using the default parameters: window size, 5; minimum window size, 4; temperature T, 25.0 ˚C; and entropy weighting, W, 0.5. For shorter proteins, those with lengths less than approximately 100 residues, the full ensemble was enumerated. For longer proteins, where calculation of a full ensemble would be prohibitive, a Monte Carlo ensemble was enumerated with a fixed sample size of 250,000 microstates. This sample size had been previously determined to accurately represent the thermodynamic information contained in the full ensemble while requiring fewer computational resources (8). All proteins in this set were between 50–250 residues in length, devoid of missing coordinates, and with resolution ≤ 2.5 Å. Secondary structure was assigned using STRIDE (10).

In Eqs. 1 — 4 of the main text, $[\Delta G]_j$, $[\Delta H_{ap}]_j$, $[\Delta H_{pol}]_j$, and $[T\Delta S_{conf}]_j$ were the residue specific thermodynamic descriptors for the native state ensemble at position j, P_i was the Boltzmann weighted probability of a particular microstate i in the entire ensemble, and P_{i,F_j} or P_{k,NF_j} were the respective probabilities in the folded (Q_{F_j}) or unfolded (Q_{NF_j}) subensembles of a microstate i or k containing residue j in either a folded or unfolded conformation. Symbolically, these probabilities were:

$$P_i = \frac{\exp\left(\frac{-\Delta G_i}{RT}\right)}{\sum_k \exp\left(\frac{-\Delta G_k}{RT}\right)} = \frac{\exp\left(\frac{-\Delta G_i}{RT}\right)}{Q}, \tag{S1}$$

$$P_{i,F_j} = \frac{\exp\left(\frac{-\Delta G_i}{RT}\right)}{\sum_{k\in F_j} \exp\left(\frac{-\Delta G_k}{RT}\right)} = \frac{\exp\left(\frac{-\Delta G_i}{RT}\right)}{Q_{F_j}}, \tag{S2}$$

$$P_{i,NF_j} = \frac{\exp\left(\frac{-\Delta G_i}{RT}\right)}{\sum_{k\in NF_j} \exp\left(\frac{-\Delta G_k}{RT}\right)} = \frac{\exp\left(\frac{-\Delta G_i}{RT}\right)}{Q_{NF_j}}, \tag{S3}$$

where i was the index for all N states in the complete ensemble or the folded (N_{F_j}) or unfolded (N_{NF_j}) subensembles, R was the gas constant, and T was the temperature of the ensemble. ΔG_i was the Gibbs free energy of folding of microstate i, estimated from a surface area-based parameterization of a variant of the Gibbs—Helmholtz equation (1, 2),

$$\Delta G_i = \Delta H_i(T_{0,H}) - T\Delta S_i(T_{0,S}) - W \cdot T\Delta S_{i,conf} + \Delta C_{p,i}\left[(T - T_{0,H}) - T\ln\frac{T}{T_{0,S}}\right], \tag{S4}$$

where $W\cdot T\Delta S_{i,conf}$ was an empirical conformational entropy term (11), and $\Delta C_{p,i}$ was the heat capacity. The heat capacity was related to the change in solvent accessible surface area of unfolding, ΔASA, by the linear function (12, 13)

$$\Delta C_{p,i} = \Delta C_{p,ap} + \Delta C_{p,pol} = 0.45 \cdot \Delta ASA_{ap} - 0.26 \cdot \Delta ASA_{pol} . \tag{S5}$$

The enthalpy and entropy of the same unfolding reaction were also parameterized as linear functions of surface area (11, 14, 15):

$$\Delta H_i(T_{0,H}) = -8.44 \cdot \Delta ASA_{ap} + 31.4 \cdot \Delta ASA_{pol} , \tag{S6}$$

$$\Delta S_i(T_{0,S}) = \Delta C_{p,ap} \ln\left(\frac{T}{385}\right) - \Delta C_{p,pol} \ln\left(\frac{T}{335}\right) , \tag{S7}$$

where the 385 and 335 referred to the temperatures in Kelvin at which the apolar and polar solvation entropies are zero, respectively.

Finally, for each residue j two partitions (mutually exclusive subsets) were created, the union of which was the complete set S of N microstates; one consisted of all the N_{F_j} microstates where residue j was folded (F_j) and the other consisted of all other N_{NF_j} microstates where residue j was not folded (NF_j). Formally, for each residue j it was written:

$$F_j = \{\forall\ microstates\ s \in S \mid residue\ j\ is\ folded\ in\ microstate\ s\ \} , \tag{S8}$$

$$NF_j = \{\forall\ microstates\ t \in S \mid residue\ j\ is\ not\ folded\ in\ microstate\ t\ \} . \tag{S9}$$

Principal components analysis of thermodynamic environment space

Principal components analysis (PCA) is a commonly used linear method for subspace decomposition (16, 17). In favorable cases, PCA can reveal latent organization in multidimensional data. Briefly, given a p x n data matrix A in row-observation form (each of the n columns is a "dimension" and each of the p rows is an "observation" from an experiment, *e.g.* a four dimensional thermodynamic vector from COREX/BEST), the data are first centered by removing the mean value of each dimension from the original data, giving a new matrix $\hat{A}$. Second, the sample covariance matrix for $\hat{A}$ is created by the formula,

$$\mathrm{cov}\left(\hat{A}\right) = \frac{1}{n-1}\hat{A}^T\hat{A} \ . \tag{S10}$$

This sample covariance matrix is square, symmetric and positive semi-definite. Each entry a_{ij} in the matrix contains the statistically defined notion of variance of a dimension when i equals j, and covariance of two dimensions when i is not equal to j. Thus, if any two axes are correlated their corresponding a_{ij} entries in the sample covariance matrix will be non-zero, and zero otherwise. PCA maps the original data onto new coordinates, through a rotation matrix, such that the sample covariance matrix of the new points is diagonal. Hence, the new axes are uncorrelated (in fact they are an orthogonal subspace of $\Re^n$). This data transformation allowed us to invoke the orthogonal decomposition theorem (17) to dissect the difference of two coordinates in terms of the orthogonal parts of their difference vector. Or, in other words one could "move" from point to point in the new coordinate space and explain the difference between the two points as sums of vectors that were all at right angles (uncorrelated). Furthermore, because the rotation matrix allowed a mapping from TE space to PCA space and back, elucidation of the biophysical changes underlying changes in TE space was made possible. This last point is emphasized because it allowed interpretation of protein thermodynamics in terms of the physical quantities of solvent exposed surface area and conformational entropy embodied in the COREX/BEST energy function (Eq. S4, above).

PCA was performed using the *R* function princomp (http://www.r-project.org) on the four-dimensional energetic data computed from the 120 native state ensembles of the protein database mentioned above. This function performed the following tasks: the energetic data was put into mean deviation form (*i.e.* centered in the original coordinate system), the eigenvector decomposition for its covariance matrix was calculated, and the data were projected onto the new orthonormal basis by multiplying the original data by the eigenvectors of the original sample covariance matrix.

References

1. Hilser, V. J., and E. Freire. 1996. Structure-based calculation of the equilibrium folding pathway of proteins. Correlation with hydrogen exchange protection factors. Journal of molecular biology 262:756-772.
2. Hilser, V. J., E. B. Garcia-Moreno, T. G. Oas, G. Kapp, and S. T. Whitten. 2006. A statistical thermodynamic model of the protein ensemble. Chemical reviews 106:1545-1558.
3. Vertrees, J., P. Barritt, S. Whitten, and V. J. Hilser. 2005. COREX/BEST server: a web browser-based program that calculates regional stability variations within protein structures. Bioinformatics (Oxford, England) 21:3318-3319.
4. Babu, C. R., V. J. Hilser, and A. J. Wand. 2004. Direct access to the cooperative substructure of proteins and the protein ensemble via cold denaturation. Nature structural & molecular biology 11:352-357.
5. Pan, H., J. C. Lee, and V. J. Hilser. 2000. Binding sites in Escherichia coli dihydrofolate reductase communicate by modulating the conformational ensemble. Proceedings of the National Academy of Sciences of the United States of America 97:12020-12025.
6. Whitten, S. T., E. B. Garcia-Moreno, and V. J. Hilser. 2005. Local conformational fluctuations can modulate the coupling between proton binding and global structural transitions in proteins. Proceedings of the National Academy of Sciences of the United States of America 102:4282-4287.
7. Wooll, J. O., J. O. Wrabl, and V. J. Hilser. 2000. Ensemble modulation as an origin of denaturant-independent hydrogen exchange in proteins. Journal of molecular biology 301:247-256.
8. Larson, S. A., and V. J. Hilser. 2004. Analysis of the "thermodynamic information content" of a Homo sapiens structural database reveals hierarchical thermodynamic organization. Protein Sci 13:1787-1801.
9. Vertrees, J. 2008. A thermodynamic definition of protein folds. In Department of Biochemistry and Molecular Biology. University of Texas Medical Branch, Galveston.
10. Frishman, D., and P. Argos. 1995. Knowledge-based protein secondary structure assignment. Proteins 23:566-579.
11. D'Aquino, J. A., J. Gomez, V. J. Hilser, K. H. Lee, L. M. Amzel, and E. Freire. 1996. The magnitude of the backbone conformational entropy change in protein folding. Proteins 25:143-156.
12. Murphy, K. P., and S. J. Gill. 1991. Solid model compounds and the thermodynamics of protein unfolding. Journal of molecular biology 222:699-709.
13. Murphy, K. P., P. L. Privalov, and S. J. Gill. 1990. Common features of protein unfolding and dissolution of hydrophobic compounds. Science (New York, N.Y 247:559-561.
14. Xie, D., and E. Freire. 1994. Structure based prediction of protein folding intermediates. Journal of molecular biology 242:62-80.
15. Murphy, K. P., and E. Freire. 1992. Thermodynamics of structural stability and cooperative folding behavior in proteins. Advances in protein chemistry 43:313-361.
16. Manly, B. F. J. 1986. Multivariate statistical methods: a primer. Chapman and Hall, New York.
17. Lay, D. C. 2003. Linear Algebra and its Applications, Third Edition. Pearson, Addison-Wesley.

Table S1. Native state thermodynamic descriptors for 120 human proteins, computed by COREX / BEST. Values are in kcal / mol at 25.0 ˚C.

pdb_id	chain_id	residue_name	residue_number	secondary_structure	ΔG	ΔH_{ap}	ΔH_{pol}	$T\Delta S_{conf}$
1A17	A	PRO	19	C	-4.088234	4.229515	-4.258223	-0.638051
1A17	A	PRO	20	C	-4.088234	4.229515	-4.258223	-0.638051
1A17	A	ALA	21	C	-4.088234	4.229515	-4.258223	-0.638051
1A17	A	ASP	22	H	-4.088234	4.229515	-4.258223	-0.638051
1A17	A	GLY	23	H	-4.395059	4.491100	-5.243721	-1.389826
1A17	A	ALA	24	H	-4.930556	6.148327	-8.159145	-3.874544
1A17	A	LEU	25	H	-5.552081	6.798558	-9.171590	-4.644301
1A17	A	LYS	26	H	-6.610406	6.526865	-9.689133	-4.016628
1A17	A	ARG	27	H	-10.027918	8.392879	-13.102609	-3.592472
1A17	A	ALA	28	H	-11.547228	8.870021	-15.155323	-3.819945
1A17	A	GLU	29	H	-11.993160	7.697427	-17.671230	-4.980113
1A17	A	GLU	30	H	-12.011963	7.615513	-17.562346	-4.923039
1A17	A	LEU	31	H	-13.139681	11.366618	-16.369216	-4.036027
1A17	A	LYS	32	H	-13.065989	11.154140	-16.482125	-4.050610
1A17	A	THR	33	H	-12.474828	8.330376	-15.708499	-2.938021
1A17	A	GLN	34	H	-12.520082	8.240084	-15.716579	-2.939194
1A17	A	ALA	35	H	-12.529733	8.194302	-15.650048	-2.894527
1A17	A	ASN	36	H	-12.321728	9.443244	-15.752733	-3.655399
1A17	A	ASP	37	H	-11.488114	11.147777	-13.235503	-3.364622
1A17	A	TYR	38	H	-11.360736	11.688554	-12.606813	-3.100844
1A17	A	PHE	39	H	-10.876461	9.348967	-12.322829	-2.266623
1A17	A	LYS	40	H	-10.486195	8.822022	-13.471065	-3.218164
1A17	A	ALA	41	H	-10.184868	8.470210	-14.085092	-3.860546
1A17	A	LYS	42	C	-10.185516	8.233633	-14.301024	-3.929296
1A17	A	ASP	43	C	-10.201176	8.133810	-14.393417	-3.984509
1A17	A	TYR	44	H	-10.316673	8.281318	-14.884580	-4.494765
1A17	A	GLU	45	H	-10.338378	8.593204	-14.698058	-4.459103
1A17	A	ASN	46	H	-10.677223	9.913595	-14.192282	-4.176209
1A17	A	ALA	47	H	-10.803762	10.161601	-13.986717	-4.195451
1A17	A	ILE	48	H	-10.827877	10.138555	-14.007947	-4.264436
1A17	A	LYS	49	H	-10.831987	10.124365	-14.018560	-4.284319
1A17	A	PHE	50	H	-11.727084	13.469695	-13.614216	-4.915525
1A17	A	TYR	51	H	-14.821048	17.123920	-15.372153	-3.949987
1A17	A	SER	52	H	-12.833865	9.081237	-15.253298	-3.117168
1A17	A	GLN	53	H	-11.541239	10.556718	-11.257822	-1.702637
1A17	A	ALA	54	H	-11.367847	10.695685	-10.998516	-1.468322
1A17	A	ILE	55	H	-10.939290	10.498511	-12.351790	-2.674115
1A17	A	GLU	56	H	-9.983440	9.274290	-12.959182	-3.973646
1A17	A	LEU	57	H	-9.969631	9.274998	-12.954372	-3.941211
1A17	A	ASN	58	T	-9.959467	9.096937	-13.023144	-3.911031
1A17	A	PRO	59	T	-9.892907	8.865811	-12.699751	-3.511876
1A17	A	SER	60	T	-9.945343	8.739812	-12.620518	-3.485597
1A17	A	ASN	61	T	-10.768209	8.057163	-11.148776	-1.044528
1A17	A	ALA	62	H	-10.842748	7.907113	-10.850633	-0.823343
1A17	A	ILE	63	H	-11.096568	7.773438	-10.180317	-0.374679
1A17	A	TYR	64	H	-13.193237	13.100452	-15.448571	-4.271119
1A17	A	TYR	65	H	-14.443991	17.585250	-15.599794	-4.954800
1A17	A	GLY	66	H	-15.006748	17.026488	-15.653388	-4.189998
1A17	A	ASN	67	H	-15.815305	13.332556	-20.208326	-5.163681
1A17	A	ARG	68	H	-15.937090	12.742439	-21.058928	-5.581323
1A17	A	SER	69	H	-15.326597	15.289824	-15.583607	-2.931261
1A17	A	LEU	70	H	-13.837566	18.141365	-13.326423	-4.071611
1A17	A	ALA	71	H	-12.695262	18.296939	-12.651233	-4.877062
1A17	A	TYR	72	H	-11.953098	16.959377	-11.776407	-4.145421
1A17	A	LEU	73	H	-9.214913	10.962293	-7.693840	-1.661507
1A17	A	ARG	74	H	-9.167536	10.942407	-7.786291	-1.616574
1A17	A	THR	75	H	-7.714858	9.226388	-9.836964	-3.878166
1A17	A	GLU	76	C	-7.267304	9.699423	-9.820404	-4.312219
1A17	A	CYS	77	C	-7.256069	9.734204	-9.816781	-4.289060
1A17	A	TYR	78	H	-7.277666	9.692001	-9.898401	-4.387673
1A17	A	GLY	79	H	-7.208081	9.310570	-9.803963	-4.065870
1A17	A	TYR	80	H	-7.498347	9.466380	-9.669469	-4.049918
1A17	A	ALA	81	H	-8.399012	7.121575	-9.223916	-1.737536
1A17	A	LEU	82	H	-8.480046	6.448983	-9.178047	-1.539171
1A17	A	GLY	83	H	-8.482279	6.422613	-9.175348	-1.537788
1A17	A	ASP	84	H	-10.693062	8.969510	-14.594901	-4.155851
1A17	A	ALA	85	H	-11.027437	8.701850	-14.745479	-4.142139
1A17	A	THR	86	H	-11.018802	10.800450	-13.563478	-4.101301
1A17	A	ARG	87	H	-10.967835	12.418411	-12.615887	-3.999479
1A17	A	ALA	88	H	-10.777298	12.347342	-11.978758	-3.423974
1A17	A	ILE	89	H	-10.268371	10.566458	-11.187145	-2.473943
1A17	A	GLU	90	H	-8.777502	8.420470	-11.778830	-3.959060
1A17	A	LEU	91	H	-8.674386	9.106660	-11.649479	-4.079680
1A17	A	ASP	92	T	-8.595617	9.468046	-11.402458	-3.960660
1A17	A	LYS	93	T	-8.593483	9.484269	-11.396306	-3.956006
1A17	A	LYS	94	T	-8.582116	9.632852	-11.239636	-3.887955
1A17	A	TYR	95	T	-9.222765	12.368581	-10.088223	-3.495899

```
1A17        A          ILE             96                   H -9.563242 12.149004 -9.266223 -2.560799
1A17        A          LYS             97                   H -10.216843 12.287275 -8.324252 -1.439083
1A17        A          GLY             98                   H -10.324378 12.208146 -7.949149 -1.293446
1A17        A          TYR             99                   H -13.307592 17.929504 -14.195065 -5.121068
1A17        A          TYR            100                   H -14.182042 18.191242 -15.371451 -5.726600
1A17        A          ARG            101                   H -16.105558 15.368904 -19.131676 -5.162957
1A17        A          ARG            102                   H -15.126754 11.482142 -18.126516 -3.871202
1A17        A          ALA            103                   H -14.210495 10.671313 -15.886021 -2.536827
1A17        A          ALA            104                   H -13.478539  9.879416 -14.329275 -1.681489
1A17        A          SER            105                   H -12.834209 11.504410 -15.336116 -3.637266
1A17        A          ASN            106                   H -10.538561 11.226804 -13.533015 -5.071582
1A17        A          MET            107                   H -8.503859  8.964730 -9.914900 -3.201073
1A17        A          ALA            108                   H -8.475762  9.026136 -9.912745 -3.141613
1A17        A          LEU            109                   H -8.472710  9.030683 -9.919199 -3.133458
1A17        A          GLY            110                   C -8.471014  9.033100 -9.932383 -3.135943
1A17        A          LYS            111                   C -8.486033  8.985380 -9.839158 -3.082180
1A17        A          PHE            112                   H -10.142534 10.474122 -10.535181 -2.211954
1A17        A          ARG            113                   H -10.708664 10.032674 -11.697195 -2.101353
1A17        A          ALA            114                   H -10.861416 10.065637 -11.846479 -2.263008
1A17        A          ALA            115                   H -10.982799 10.037453 -11.197960 -1.849092
1A17        A          LEU            116                   H -11.225646  8.576422 -10.213330 -0.535815
1A17        A          ARG            117                   H -11.233886  8.495207 -10.170934 -0.502801
1A17        A          ASP            118                   H -13.998629  9.712871 -15.086479 -1.656285
1A17        A          TYR            119                   H -14.056722 16.874018 -12.001393 -2.017949
1A17        A          GLU            120                   H -9.633674 10.734616 -10.640854 -3.367415
1A17        A          THR            121                   H -8.044326 11.531850 -8.588353 -3.754356
1A17        A          VAL            122                   H -7.981076 11.689777 -8.531135 -3.646410
1A17        A          VAL            123                   H -7.909530 11.359240 -8.525362 -3.387969
1A17        A          LYS            124                   H -7.555027  9.003771 -7.427987 -1.801218
1A17        A          VAL            125                   H -7.400753  8.621166 -8.228149 -2.251249
1A17        A          LYS            126                   T -7.035974  7.106397 -9.722675 -3.353395
1A17        A          PRO            127                   T -6.771894  6.145401 -9.888315 -3.184543
1A17        A          HIS            128                   T -6.742624  6.098909 -9.865969 -3.114525
1A17        A          ASP            129                   T -6.814410  6.095149 -10.353882 -3.533458
1A17        A          LYS            130                   H -6.871767  5.936146 -10.305348 -3.513788
1A17        A          ASP            131                   H -7.254937  4.959021 -9.991842 -2.695443
1A17        A          ALA            132                   H -8.349766  6.131887 -9.376701 -1.725121
1A17        A          LYS            133                   H -10.342388  7.769047 -14.569345 -4.007043
1A17        A          MET            134                   H -10.387548  7.900142 -14.716187 -4.241077
1A17        A          LYS            135                   H -10.978646  9.804288 -14.847609 -4.998946
1A17        A          TYR            136                   H -13.084335 11.359802 -16.460652 -3.999669
1A17        A          GLN            137                   H -12.416113  8.191144 -17.294264 -4.207934
1A17        A          GLU            138                   H -11.761653  8.120215 -15.107181 -3.154286
1A17        A          CYS            139                   H -11.631948  8.491237 -14.667195 -2.953270
1A17        A          ASN            140                   H -10.077681  8.986479 -12.947792 -3.804641
1A17        A          LYS            141                   H -8.814791  8.654974 -11.703792 -4.125861
1A17        A          ILE            142                   H -8.805188  8.695829 -11.709409 -4.111938
1A17        A          VAL            143                   H -8.801239  8.691315 -11.712977 -4.097353
1A17        A          LYS            144                   H -8.796854  8.672249 -11.716137 -4.074780
1A17        A          GLN            145                   H -8.817476  8.597309 -11.785016 -4.115137
1A17        A          LYS            146                   H -8.267341  7.550998 -11.228885 -3.890239
1A17        A          ALA            147                   H -7.974329  6.935334 -10.650817 -3.136471
1A17        A          PHE            148                   H -7.913402  6.797584 -10.505852 -2.883232
1A17        A          GLU            149                   H -7.840064  6.573380 -10.220699 -2.506056
1A17        A          ARG            150                   H -7.628817  6.161862 -10.468006 -2.593128
1A17        A          ALA            151                   H -7.237597  4.874735 -11.076848 -3.224339
1A17        A          ILE            152                   H -7.303786  4.723560 -11.275055 -3.384789
1A17        A          ALA            153                   H -7.314895  4.663271 -11.378499 -3.461871
1A17        A          GLY            154                   H -7.335843  4.636940 -11.550649 -3.621428
1A17        A          ASP            155                   H -7.454216  4.494339 -11.676130 -3.802321
1A17        A          GLU            156                   H -7.880585  5.428160 -18.392861 -8.967991
1A17        A          HIS            157                   H -7.277396  5.157786 -18.168969 -9.273007
1A17        A          LYS            158                   H -7.103023  5.192358 -18.072566 -9.227468
1A17        A          ARG            159                   H -7.106515  5.206398 -18.116572 -9.279044
1A17        A          SER            160                   H -5.151071  4.353920 -12.920383 -7.461410
1A17        A          VAL            161                   H -4.034144  4.074604 -10.938041 -6.681879
1A17        A          VAL            162                   H -3.456483  3.815106 -10.125767 -6.344303
1A17        A          ASP            163                   H -3.450138  3.794814 -10.103499 -6.293541
1A17        A          SER            164                   H -2.769826  2.900624 -8.288102 -5.199539
1A17        A          LEU            165                   C -2.036441  2.478622 -6.661099 -4.491124
1A17        A          ASP            166                   T -1.280662  1.605998 -5.777555 -4.111708
1A17        A          ILE            167                   T -1.185602  1.596833 -5.812112 -4.025543
1A17        A          GLU            168                   T -1.145099  1.576089 -5.850256 -3.970007
1A17        A          SER            169                   T -1.103814  1.553536 -5.823486 -3.868669
1A17        A          MET            170                   T -0.752962  1.115471 -4.664708 -2.946069
1A17        A          THR            171                   C  0.719721  0.776795 -1.669004 -2.386563
1A17        A          ILE            172                   C  1.288819  1.099277 -2.555069 -3.547982
1A17        A          GLU            173                   C  1.594454  1.932941 -3.734511 -4.769777
1A17        A          ASP            174                   C  1.709211  2.374302 -4.386279 -5.289300
1A17        A          GLU            175                   C  1.709211  2.374302 -4.386279 -5.289300
1A17        A          TYR            176                   C  1.709211  2.374302 -4.386279 -5.289300
```

1A17	A	SER	177	C	1.709211	2.374302	-4.386279	-5.289300
1A3K	A	LEU	114	C	-3.795896	5.319212	-5.095889	-2.303290
1A3K	A	ILE	115	T	-3.795896	5.319212	-5.095889	-2.303290
1A3K	A	VAL	116	T	-3.795896	5.319212	-5.095889	-2.303290
1A3K	A	PRO	117	T	-3.795896	5.319212	-5.095889	-2.303290
1A3K	A	TYR	118	E	-6.491379	9.279862	-8.171481	-3.449300
1A3K	A	ASN	119	E	-7.804469	10.865694	-10.604788	-4.533642
1A3K	A	LEU	120	E	-7.444147	11.334876	-9.071765	-4.023622
1A3K	A	PRO	121	E	-5.095300	8.203109	-7.644930	-4.147609
1A3K	A	LEU	122	T	-4.959394	8.623210	-7.635319	-4.158951
1A3K	A	PRO	123	T	-4.781427	8.320754	-7.782229	-4.076167
1A3K	A	GLY	124	T	-4.718671	8.391703	-7.807964	-4.056232
1A3K	A	GLY	125	T	-4.722423	8.370757	-7.803621	-4.055320
1A3K	A	VAL	126	C	-5.160953	8.617991	-8.004681	-3.949571
1A3K	A	VAL	127	T	-5.362237	7.956907	-8.169204	-3.847171
1A3K	A	PRO	128	T	-6.059217	9.074551	-8.100711	-3.866274
1A3K	A	ARG	129	T	-8.137297	10.174868	-9.854334	-3.518732
1A3K	A	MET	130	E	-9.705483	13.757996	-10.687737	-3.947508
1A3K	A	LEU	131	E	-10.460622	16.937303	-11.601635	-4.819429
1A3K	A	ILE	132	E	-9.229132	14.632217	-10.418945	-4.655457
1A3K	A	THR	133	E	-8.608347	13.312379	-10.798529	-4.775957
1A3K	A	ILE	134	E	-8.383501	13.465199	-10.511994	-4.615287
1A3K	A	LEU	135	E	-8.322775	13.325541	-10.662215	-4.616365
1A3K	A	GLY	136	E	-8.070298	12.118381	-10.907501	-4.488873
1A3K	A	THR	137	E	-7.037423	9.296349	-9.958427	-4.139565
1A3K	A	VAL	138	E	-6.029658	8.811935	-8.672984	-3.986773
1A3K	A	LYS	139	T	-5.224603	7.600741	-8.939818	-4.416015
1A3K	A	PRO	140	T	-5.212891	7.597870	-8.987810	-4.416322
1A3K	A	ASN	141	T	-5.214509	7.591341	-8.981618	-4.416791
1A3K	A	ALA	142	T	-5.238136	7.540083	-8.949327	-4.430398
1A3K	A	ASN	143	C	-5.383201	7.205857	-9.097714	-4.560165
1A3K	A	ARG	144	B	-7.523562	7.603966	-11.420932	-4.436856
1A3K	A	ILE	145	E	-10.402238	11.696306	-13.284884	-4.596369
1A3K	A	ALA	146	E	-12.378804	13.709511	-15.201659	-4.524811
1A3K	A	LEU	147	E	-13.040688	15.310277	-15.250658	-4.643413
1A3K	A	ASP	148	E	-13.865018	18.357578	-15.155261	-4.839122
1A3K	A	PHE	149	E	-12.945424	14.304555	-16.966773	-5.738621
1A3K	A	GLN	150	E	-10.471578	7.692527	-17.040152	-5.870469
1A3K	A	ARG	151	E	-8.978925	8.154080	-14.475898	-5.366944
1A3K	A	GLY	152	T	-8.692327	8.121797	-14.215129	-5.122898
1A3K	A	ASN	153	T	-8.691957	8.125920	-14.215705	-5.122671
1A3K	A	ASP	154	E	-8.692315	8.122874	-14.213729	-5.122160
1A3K	A	VAL	155	E	-8.722046	8.149532	-14.068452	-5.083639
1A3K	A	ALA	156	E	-9.259059	8.083038	-13.798547	-4.730723
1A3K	A	PHE	157	E	-12.987831	15.241604	-15.221014	-4.800110
1A3K	A	HIS	158	E	-14.324500	19.808475	-15.276576	-4.946153
1A3K	A	PHE	159	E	-14.514966	20.883996	-14.739979	-4.956236
1A3K	A	ASN	160	E	-15.133180	18.100939	-18.258242	-5.572586
1A3K	A	PRO	161	E	-14.903597	16.101901	-19.281625	-5.789644
1A3K	A	ARG	162	E	-13.352425	11.806010	-18.930910	-5.983399
1A3K	A	PHE	163	E	-8.027973	9.199743	-12.768528	-5.648470
1A3K	A	ASN	164	E	-4.872219	3.937081	-10.255917	-4.690588
1A3K	A	GLU	165	E	-4.861927	3.969055	-10.287212	-4.687010
1A3K	A	ASN	166	T	-4.844667	4.053957	-10.284126	-4.661402
1A3K	A	ASN	167	T	-4.844386	4.057044	-10.284562	-4.660921
1A3K	A	ARG	168	E	-4.847131	4.033229	-10.272991	-4.656284
1A3K	A	ARG	169	E	-6.670051	6.553817	-10.875676	-4.041486
1A3K	A	VAL	170	E	-6.938089	6.991697	-10.194263	-3.790508
1A3K	A	ILE	171	E	-9.326159	10.815131	-11.368334	-3.696593
1A3K	A	VAL	172	E	-10.783823	13.658498	-13.237979	-4.270838
1A3K	A	CYS	173	E	-11.073199	13.834241	-14.327704	-4.922213
1A3K	A	ASN	174	E	-11.112991	12.252412	-16.203557	-5.614167
1A3K	A	THR	175	E	-9.223704	8.462186	-14.326496	-5.261566
1A3K	A	LYS	176	E	-5.947568	6.089437	-10.773120	-4.900806
1A3K	A	LEU	177	E	-4.808787	7.429394	-8.978748	-4.961091
1A3K	A	ASP	178	T	-4.602625	7.012629	-9.386190	-5.024554
1A3K	A	ASN	179	T	-4.599811	7.007397	-9.405616	-5.025025
1A3K	A	ASN	180	E	-4.599828	7.006780	-9.405923	-5.025117
1A3K	A	TRP	181	E	-4.663885	7.111992	-9.250788	-5.039061
1A3K	A	GLY	182	C	-5.318191	6.006352	-10.416996	-5.173756
1A3K	A	ARG	183	C	-7.721742	5.979381	-13.657783	-5.153497
1A3K	A	GLU	184	C	-9.228349	6.805896	-15.725519	-5.536398
1A3K	A	GLU	185	E	-10.587760	6.956597	-18.006447	-5.728005
1A3K	A	ARG	186	E	-10.921053	7.379002	-17.661877	-5.302393
1A3K	A	GLN	187	E	-10.236674	12.714909	-12.378165	-4.339998
1A3K	A	SER	188	C	-9.775184	15.078949	-10.783096	-4.250115
1A3K	A	VAL	189	C	-9.599902	15.916924	-10.591015	-4.417619
1A3K	A	PHE	190	C	-9.587350	16.109135	-10.541851	-4.436518
1A3K	A	PRO	191	C	-9.259085	15.658638	-10.720220	-4.675207
1A3K	A	PHE	192	C	-8.445221	13.057083	-10.907011	-4.932673
1A3K	A	GLU	193	T	-5.790282	6.045689	-10.147009	-4.521299

1A3K	A	SER	194	T	-5.787793	6.065120	-10.153986	-4.522088
1A3K	A	GLY	195	T	-5.787277	6.070454	-10.156554	-4.522800
1A3K	A	LYS	196	E	-5.788003	6.059590	-10.155482	-4.522228
1A3K	A	PRO	197	E	-5.793308	6.004231	-10.147653	-4.518115
1A3K	A	PHE	198	E	-8.864590	11.599154	-11.888104	-4.829246
1A3K	A	LYS	199	E	-9.907095	12.749619	-13.026775	-5.324384
1A3K	A	ILE	200	E	-11.786423	16.804482	-13.431727	-5.040319
1A3K	A	GLN	201	E	-12.300214	17.828127	-13.806363	-4.944489
1A3K	A	VAL	202	E	-10.422328	14.883655	-10.908762	-4.019919
1A3K	A	LEU	203	E	-8.505736	12.132166	-10.255587	-4.318028
1A3K	A	VAL	204	E	-7.843078	11.142445	-10.588409	-4.533973
1A3K	A	GLU	205	T	-7.818789	11.251597	-10.637287	-4.558065
1A3K	A	PRO	206	T	-7.817914	11.256406	-10.642573	-4.559551
1A3K	A	ASP	207	T	-7.824948	11.214587	-10.640984	-4.566497
1A3K	A	HIS	208	E	-8.040055	10.862322	-10.821478	-4.669914
1A3K	A	PHE	209	E	-9.695423	13.923700	-11.913256	-5.145617
1A3K	A	LYS	210	E	-11.496415	14.717343	-14.398392	-5.355826
1A3K	A	VAL	211	E	-11.351782	10.658113	-14.788710	-4.200284
1A3K	A	ALA	212	E	-9.030805	7.008153	-13.335198	-4.135472
1A3K	A	VAL	213	E	-8.068458	7.288640	-12.672077	-4.447780
1A3K	A	ASN	214	T	-8.002931	7.362083	-12.816997	-4.490130
1A3K	A	ASP	215	T	-7.986694	7.447820	-12.834947	-4.495566
1A3K	A	ALA	216	E	-7.977272	7.520291	-12.841981	-4.505343
1A3K	A	HIS	217	E	-8.084513	7.636861	-12.750031	-4.579048
1A3K	A	LEU	218	E	-9.117249	8.953139	-13.884652	-4.836566
1A3K	A	LEU	219	E	-9.805716	11.052814	-13.508839	-4.802857
1A3K	A	GLN	220	E	-10.331180	11.771593	-13.515318	-4.965322
1A3K	A	TYR	221	E	-13.469401	16.767908	-16.222402	-5.749358
1A3K	A	ASN	222	E	-12.057633	10.680221	-16.818629	-5.338660
1A3K	A	HIS	223	T	-11.372993	10.935191	-16.356324	-5.429649
1A3K	A	ARG	224	T	-10.961308	11.651024	-15.576112	-5.307277
1A3K	A	VAL	225	T	-9.104039	10.857888	-12.224301	-4.705969
1A3K	A	LYS	226	T	-8.596855	9.046226	-13.174583	-4.880217
1A3K	A	LYS	227	T	-8.518600	9.367329	-13.130958	-4.896755
1A3K	A	LEU	228	G	-8.516867	9.383313	-13.123798	-4.892268
1A3K	A	ASN	229	G	-8.464065	9.446648	-13.164100	-4.898148
1A3K	A	GLU	230	G	-8.690437	8.838958	-13.689960	-5.003279
1A3K	A	ILE	231	C	-9.315271	11.260021	-13.312826	-4.968137
1A3K	A	SER	232	C	-9.665116	11.040376	-13.709397	-4.902751
1A3K	A	LYS	233	E	-9.682535	11.026360	-13.701926	-4.914190
1A3K	A	LEU	234	E	-9.963717	12.554488	-13.299914	-4.759341
1A3K	A	GLY	235	E	-9.517620	11.023741	-13.605241	-4.891670
1A3K	A	ILE	236	E	-9.115786	12.466566	-12.256870	-4.848455
1A3K	A	SER	237	E	-9.046809	12.264708	-12.482357	-4.914281
1A3K	A	GLY	238	E	-8.772710	12.710938	-12.206021	-5.023337
1A3K	A	ASP	239	T	-8.664907	12.982828	-11.957829	-5.007397
1A3K	A	ILE	240	E	-8.416435	13.208289	-11.112321	-4.760294
1A3K	A	ASP	241	E	-8.213262	12.434012	-10.994498	-4.593551
1A3K	A	LEU	242	E	-8.074475	12.133326	-10.826763	-4.395902
1A3K	A	THR	243	E	-8.146152	11.972668	-10.709245	-4.295427
1A3K	A	SER	244	E	-8.202436	11.807516	-10.658546	-4.241991
1A3K	A	ALA	245	E	-8.298841	11.983412	-10.778320	-4.341635
1A3K	A	SER	246	E	-7.845493	12.248374	-9.909749	-4.427681
1A3K	A	TYR	247	E	-5.697419	11.682764	-6.116196	-3.770879
1A3K	A	THR	248	E	-5.697419	11.682764	-6.116196	-3.770879
1A3K	A	MET	249	E	-5.697419	11.682764	-6.116196	-3.770879
1A3K	A	ILE	250	C	-5.697419	11.682764	-6.116196	-3.770879
1AD6	A	VAL	378	C	1.194471	0.859040	-2.650295	-3.187195
1AD6	A	MET	379	C	1.194471	0.859040	-2.650295	-3.187195
1AD6	A	ASN	380	C	1.194471	0.859040	-2.650295	-3.187195
1AD6	A	THR	381	C	1.194471	0.859040	-2.650295	-3.187195
1AD6	A	ILE	382	C	0.211472	1.482354	-0.477322	-1.475847
1AD6	A	GLN	383	C	-2.555068	2.500004	-4.291126	-2.162391
1AD6	A	GLN	384	H	-3.991119	3.410535	-6.696200	-3.124966
1AD6	A	LEU	385	H	-6.330467	7.840476	-8.652000	-4.119013
1AD6	A	MET	386	H	-8.701192	10.504525	-12.385157	-5.496427
1AD6	A	MET	387	H	-9.679638	10.202929	-14.407501	-5.747898
1AD6	A	ILE	388	H	-9.968234	9.415297	-14.059323	-4.579315
1AD6	A	LEU	389	H	-10.010147	9.069834	-13.822149	-4.278017
1AD6	A	ASN	390	H	-9.995935	8.827133	-13.856487	-4.185787
1AD6	A	SER	391	H	-9.517083	6.136914	-12.759684	-2.740752
1AD6	A	ALA	392	C	-8.539395	7.151731	-11.649819	-3.362270
1AD6	A	SER	393	C	-8.465358	7.166073	-11.879194	-3.506481
1AD6	A	ASP	394	C	-8.430820	7.160005	-11.876772	-3.446497
1AD6	A	GLN	395	C	-8.347535	7.118754	-11.736394	-3.288158
1AD6	A	PRO	396	C	-8.380019	7.430579	-11.692305	-3.394664
1AD6	A	SER	397	C	-8.907982	7.490609	-12.300187	-3.277248
1AD6	A	GLU	398	H	-9.072637	7.563931	-11.898719	-2.858028
1AD6	A	ASN	399	H	-9.185908	7.665471	-11.891571	-2.943751
1AD6	A	LEU	400	H	-9.657270	8.716641	-13.119937	-3.801117
1AD6	A	ILE	401	H	-9.803068	8.522491	-13.853782	-4.298633

1AD6	A	SER	402	H	-10.229875	9.301877	-13.838746	-4.631641
1AD6	A	TYR	403	H	-14.685681	15.112654	-18.016381	-5.170195
1AD6	A	PHE	404	H	-11.349080	10.482240	-12.622767	-3.119108
1AD6	A	ASN	405	H	-8.761384	3.951817	-11.728284	-2.468792
1AD6	A	ASN	406	H	-8.638099	4.040715	-11.904034	-2.492751
1AD6	A	CYS	407	T	-8.309801	4.587352	-12.526201	-3.121107
1AD6	A	THR	408	T	-7.858763	6.987220	-12.058364	-4.039776
1AD6	A	VAL	409	T	-7.805268	7.108960	-11.870010	-3.891594
1AD6	A	ASN	410	T	-7.923571	7.911233	-11.885037	-4.199817
1AD6	A	PRO	411	H	-7.940116	8.183623	-11.749608	-4.216488
1AD6	A	LYS	412	H	-8.062581	9.015725	-11.329247	-4.255606
1AD6	A	GLU	413	H	-8.819241	8.726868	-10.738462	-2.666358
1AD6	A	SER	414	H	-9.220426	8.989234	-11.498263	-2.976815
1AD6	A	ILE	415	H	-9.330926	9.114484	-11.655986	-3.169416
1AD6	A	LEU	416	H	-9.549591	8.581533	-12.921590	-3.859844
1AD6	A	LYS	417	H	-10.125907	8.225017	-13.804491	-4.249540
1AD6	A	ARG	418	H	-13.189879	9.521675	-17.545652	-4.066770
1AD6	A	VAL	419	H	-11.060791	10.078400	-11.378174	-2.204154
1AD6	A	LYS	420	H	-10.344565	9.240360	-11.093720	-2.165416
1AD6	A	ASP	421	H	-10.275647	9.290021	-11.147770	-2.144733
1AD6	A	ILE	422	H	-10.256541	9.515076	-11.163724	-2.201861
1AD6	A	GLY	423	H	-10.223671	9.806022	-11.298952	-2.360151
1AD6	A	TYR	424	H	-10.372511	9.804576	-11.334010	-2.428536
1AD6	A	ILE	425	H	-11.125266	12.497975	-12.262579	-3.155032
1AD6	A	PHE	426	H	-11.489139	14.949332	-12.817561	-4.160563
1AD6	A	LYS	427	H	-11.153960	14.125634	-12.873524	-4.262017
1AD6	A	GLU	428	H	-9.378578	12.246799	-11.172973	-4.466103
1AD6	A	LYS	429	H	-9.335072	12.214276	-11.086957	-4.294872
1AD6	A	PHE	430	H	-9.308165	12.163094	-11.049486	-4.182460
1AD6	A	ALA	431	H	-8.138150	6.236444	-8.882959	-1.544588
1AD6	A	LYS	432	H	-7.150249	4.024206	-10.831905	-2.838807
1AD6	A	ALA	433	H	-5.583151	4.592074	-9.708619	-3.971321
1AD6	A	VAL	434	H	-5.348127	4.141785	-9.152819	-3.301860
1AD6	A	GLY	435	C	-5.166428	3.401891	-8.941102	-2.860172
1AD6	A	GLN	436	C	-5.145250	3.322049	-8.963012	-2.816337
1AD6	A	GLY	437	C	-5.134289	3.347416	-9.007572	-2.846883
1AD6	A	CYS	438	H	-5.448300	2.526628	-8.653663	-2.023523
1AD6	A	VAL	439	H	-5.737402	2.099992	-9.065586	-2.084979
1AD6	A	GLU	440	H	-6.435683	3.807706	-10.676630	-3.111282
1AD6	A	ILE	441	H	-6.698773	4.991016	-11.377465	-3.987272
1AD6	A	GLY	442	H	-7.297375	6.725829	-11.462271	-4.519190
1AD6	A	SER	443	H	-9.208106	6.301246	-10.847473	-2.089756
1AD6	A	GLN	444	H	-12.090039	7.349220	-16.058487	-3.564032
1AD6	A	ARG	445	H	-15.134867	10.845633	-17.615520	-3.318478
1AD6	A	TYR	446	H	-14.321518	14.743688	-13.217263	-2.515765
1AD6	A	LYS	447	H	-14.297120	14.648674	-13.478217	-2.597405
1AD6	A	LEU	448	H	-14.087742	15.236421	-14.333102	-3.320043
1AD6	A	GLY	449	H	-14.078592	15.270088	-14.347780	-3.313076
1AD6	A	VAL	450	H	-14.079305	15.267838	-14.343047	-3.312490
1AD6	A	ARG	451	H	-14.716457	16.291487	-16.652793	-4.899895
1AD6	A	LEU	452	H	-14.755853	16.754338	-16.345350	-4.915963
1AD6	A	TYR	453	H	-16.244790	18.845051	-15.936073	-3.637579
1AD6	A	TYR	454	H	-16.597035	20.267170	-16.873398	-4.490719
1AD6	A	ARG	455	H	-15.803084	14.897545	-16.972510	-3.456924
1AD6	A	VAL	456	H	-15.224301	15.159731	-15.991678	-3.358132
1AD6	A	MET	457	H	-14.550221	15.695575	-16.997207	-4.887348
1AD6	A	GLU	458	H	-14.128564	15.157913	-17.721625	-5.499750
1AD6	A	SER	459	H	-13.709230	13.628599	-16.363617	-4.204859
1AD6	A	MET	460	H	-13.490615	13.374667	-15.772373	-3.808826
1AD6	A	LEU	461	H	-13.476506	13.266556	-15.851410	-3.804019
1AD6	A	LYS	462	H	-12.326916	7.590747	-17.964750	-4.580659
1AD6	A	SER	463	H	-10.593393	7.315863	-15.656458	-4.719214
1AD6	A	GLU	464	H	-9.805456	7.410839	-12.658734	-3.051179
1AD6	A	GLU	465	H	-9.017302	5.693071	-11.015539	-1.926755
1AD6	A	GLU	466	H	-8.106780	4.815242	-8.956388	-0.980260
1AD6	A	ARG	467	H	-8.054515	4.928168	-9.274515	-1.161993
1AD6	A	LEU	468	H	-7.986812	5.272274	-9.667263	-1.529051
1AD6	A	SER	469	C	-8.006345	5.205963	-9.603657	-1.498142
1AD6	A	ILE	470	C	-8.091221	5.226500	-9.477410	-1.494441
1AD6	A	GLN	471	C	-8.948002	7.344403	-13.002430	-4.006214
1AD6	A	ASN	472	C	-9.211239	8.213170	-13.157131	-4.525388
1AD6	A	PHE	473	C	-10.175764	14.239502	-11.499843	-4.414607
1AD6	A	SER	474	H	-10.129105	13.953887	-11.463284	-4.257493
1AD6	A	LYS	475	H	-9.790356	12.003398	-10.767223	-3.195797
1AD6	A	LEU	476	H	-9.786787	11.995964	-10.779232	-3.191246
1AD6	A	LEU	477	H	-9.792796	11.682498	-10.957088	-3.203567
1AD6	A	ASN	478	H	-9.958272	9.652230	-11.715136	-2.845466
1AD6	A	ASP	479	C	-10.010729	9.576370	-11.775011	-2.903032
1AD6	A	ASN	480	H	-10.603995	9.760226	-15.052114	-4.770306
1AD6	A	ILE	481	H	-10.621556	9.730960	-15.111055	-4.839524
1AD6	A	PHE	482	H	-10.915345	10.871672	-14.898484	-5.188470

1AD6	A	HIS	483	H	-12.179784	12.256564	-13.061448	-3.140792
1AD6	A	MET	484	H	-13.348115	15.437370	-13.585541	-3.325213
1AD6	A	SER	485	H	-13.230323	15.683531	-12.187682	-2.537361
1AD6	A	LEU	486	H	-12.213937	15.051444	-9.616443	-1.602136
1AD6	A	LEU	487	H	-11.275342	14.665771	-10.698606	-2.953674
1AD6	A	ALA	488	H	-11.215931	14.577541	-11.065275	-3.121783
1AD6	A	CYS	489	H	-11.206793	14.544711	-11.092516	-3.109359
1AD6	A	ALA	490	H	-11.201445	14.540228	-11.075354	-3.087106
1AD6	A	LEU	491	H	-11.292736	14.482529	-11.431287	-3.373702
1AD6	A	GLU	492	H	-12.224352	14.075007	-13.653196	-3.740901
1AD6	A	VAL	493	H	-11.596461	15.552044	-12.525678	-4.441697
1AD6	A	VAL	494	H	-11.608683	15.631303	-12.547764	-4.509760
1AD6	A	MET	495	H	-11.638835	15.679885	-12.684275	-4.682349
1AD6	A	ALA	496	H	-11.540607	14.992126	-12.661031	-4.331130
1AD6	A	THR	497	H	-11.472993	14.284732	-13.092886	-4.323134
1AD6	A	TYR	498	T	-11.476187	11.068288	-14.855146	-4.368111
1AD6	A	SER	499	T	-11.041980	9.102694	-13.952993	-3.230573
1AD6	A	ARG	500	T	-9.777626	6.231506	-11.047437	-1.576823
1AD6	A	SER	501	T	-7.763543	4.028756	-9.180141	-1.498680
1AD6	A	THR	502	C	-6.608358	4.297432	-10.434748	-3.276242
1AD6	A	SER	503	T	-6.081057	4.247429	-11.034730	-4.018402
1AD6	A	GLN	504	T	-6.078555	4.252136	-11.040545	-4.014049
1AD6	A	ASN	505	T	-6.079172	4.250560	-11.042750	-4.017869
1AD6	A	LEU	506	T	-6.113513	4.268265	-11.157768	-4.168357
1AD6	A	ASP	507	T	-6.388405	4.227604	-11.467910	-4.522193
1AD6	A	SER	508	T	-8.879088	7.111629	-13.065936	-3.852722
1AD6	A	GLY	509	T	-9.042243	9.045872	-12.565714	-4.033288
1AD6	A	THR	510	C	-9.101938	9.414626	-12.470364	-4.150141
1AD6	A	ASP	511	C	-9.102689	9.428050	-12.459416	-4.150391
1AD6	A	LEU	512	C	-9.188320	9.869545	-11.997952	-4.081705
1AD6	A	SER	513	C	-9.691229	9.804991	-10.313326	-2.656519
1AD6	A	PHE	514	C	-11.984993	15.171953	-11.148292	-2.824421
1AD6	A	PRO	515	H	-11.487311	15.599644	-8.628840	-1.791281
1AD6	A	TRP	516	H	-11.429219	15.962928	-8.357805	-1.713647
1AD6	A	ILE	517	H	-11.007304	16.231989	-9.236269	-2.583299
1AD6	A	LEU	518	H	-8.660900	13.400719	-9.276262	-4.272700
1AD6	A	ASN	519	H	-8.524609	13.198641	-8.960831	-3.811163
1AD6	A	VAL	520	H	-8.458714	13.045298	-8.806581	-3.567527
1AD6	A	LEU	521	H	-8.208497	11.932490	-8.279684	-2.827093
1AD6	A	ASN	522	C	-7.889584	11.279226	-8.859282	-3.145620
1AD6	A	LEU	523	C	-8.039338	10.639948	-8.870971	-2.836165
1AD6	A	LYS	524	C	-8.095269	10.465133	-8.984867	-2.916685
1AD6	A	ALA	525	H	-8.131769	10.372956	-9.078109	-3.006873
1AD6	A	PHE	526	H	-8.345856	10.609495	-9.861289	-3.698320
1AD6	A	ASP	527	H	-9.737885	12.595416	-11.637553	-4.716199
1AD6	A	PHE	528	H	-11.699276	18.465451	-11.420574	-4.495950
1AD6	A	TYR	529	H	-11.164571	16.678258	-10.328715	-3.594438
1AD6	A	LYS	530	H	-10.273182	12.350013	-9.634350	-2.357008
1AD6	A	VAL	531	H	-10.263233	12.388255	-9.636578	-2.346680
1AD6	A	ILE	532	H	-10.238687	12.518484	-9.720208	-2.405940
1AD6	A	GLU	533	H	-10.043013	12.456593	-10.465860	-2.968404
1AD6	A	SER	534	H	-10.100989	12.138636	-10.548727	-2.960805
1AD6	A	PHE	535	H	-10.612569	13.568316	-12.093599	-4.275463
1AD6	A	ILE	536	H	-9.608036	8.811732	-10.762717	-2.558999
1AD6	A	LYS	537	H	-9.525282	8.272687	-11.599758	-2.871770
1AD6	A	ALA	538	H	-9.341771	8.615166	-12.421836	-3.697252
1AD6	A	GLU	539	T	-9.275414	8.758044	-12.521704	-3.749453
1AD6	A	GLY	540	T	-9.107236	8.993477	-12.291979	-3.658013
1AD6	A	ASN	541	T	-9.314518	9.658875	-13.125937	-4.307737
1AD6	A	LEU	542	T	-9.218668	10.239468	-12.623814	-4.204866
1AD6	A	THR	543	C	-8.950635	10.275865	-12.112472	-4.232620
1AD6	A	ARG	544	H	-8.966796	10.216791	-12.032017	-4.164783
1AD6	A	GLU	545	H	-9.093076	10.336350	-12.143321	-4.349010
1AD6	A	MET	546	H	-9.127697	10.368822	-12.196091	-4.460424
1AD6	A	ILE	547	H	-9.260939	10.286029	-12.175044	-4.558629
1AD6	A	LYS	548	H	-10.855063	8.557498	-12.197229	-2.303043
1AD6	A	HIS	549	H	-12.216654	10.638471	-13.747201	-2.988265
1AD6	A	LEU	550	H	-13.362314	12.513938	-17.300959	-4.780515
1AD6	A	GLU	551	H	-13.103422	11.297628	-16.792646	-4.173179
1AD6	A	ARG	552	H	-13.123344	10.132902	-17.218361	-4.003753
1AD6	A	CYS	553	H	-13.041990	10.957689	-17.018668	-4.218706
1AD6	A	GLU	554	H	-12.834988	12.138798	-16.571088	-4.460579
1AD6	A	HIS	555	H	-11.280186	12.318965	-12.806776	-4.023870
1AD6	A	ARG	556	H	-9.868730	12.291692	-9.687195	-3.063585
1AD6	A	ILE	557	H	-7.426660	10.044566	-9.180531	-3.994072
1AD6	A	MET	558	H	-5.908862	7.956620	-8.612678	-4.176656
1AD6	A	GLU	559	H	-5.509622	6.732974	-7.043632	-2.572618
1AD6	A	SER	560	H	-5.509622	6.732974	-7.043632	-2.572618
1AD6	A	LEU	561	C	-5.509622	6.732974	-7.043632	-2.572618
1AD6	A	ALA	562	C	-5.509622	6.732974	-7.043632	-2.572618
1ALY	A	GLY	116	T	-2.433419	0.795202	-8.342820	-4.015216

```
1ALY          A          ASP             117                    T -2.433419  0.795202 -8.342820 -4.015216
1ALY          A          GLN             118                    T -2.433419  0.795202 -8.342820 -4.015216
1ALY          A          ASN             119                    T -2.433419  0.795202 -8.342820 -4.015216
1ALY          A          PRO             120                    T -3.109821  0.942349 -9.321871 -4.460460
1ALY          A          GLN             121                    T -4.861659  2.013606 -12.488736 -5.538398
1ALY          A          ILE             122                    C -6.028418  5.293124 -13.199148 -6.365626
1ALY          A          ALA             123                    E -7.615020  7.375118 -14.917271 -6.825568
1ALY          A          ALA             124                    E -8.770932 10.046372 -12.500244 -4.726522
1ALY          A          HIS             125                    E -10.558858 13.289023 -12.806951 -4.189826
1ALY          A          VAL             126                    E -10.477797 13.183995 -13.111338 -4.407161
1ALY          A          ILE             127                    E -10.392140 11.879791 -14.956346 -5.302788
1ALY          A          SER             128                    E -9.366368  8.553688 -14.714549 -5.281906
1ALY          A          GLU             129                    C -6.174876  5.603950 -10.558250 -4.438151
1ALY          A          ALA             130                    C -2.905714  3.944419 -6.300631 -3.672515
1ALY          A          SER             131                    C -2.154112  4.939659 -5.510054 -3.836649
1ALY          A          SER             132                    C -2.102016  4.992909 -5.630116 -3.857380
1ALY          A          LYS             133                    C -2.099304  5.004726 -5.642757 -3.859435
1ALY          A          THR             134                    C -2.099919  5.004080 -5.637292 -3.858594
1ALY          A          THR             135                    C -2.283624  5.311186 -5.321704 -3.868669
1ALY          A          SER             136                    C -3.567429  5.424804 -6.730061 -3.897102
1ALY          A          VAL             137                    B -5.319125  7.339545 -8.103538 -4.091987
1ALY          A          LEU             138                    C -8.043423 11.111847 -9.578771 -4.060010
1ALY          A          GLN             139                    C -11.354099 13.578373 -16.400770 -6.495113
1ALY          A          TRP             140                    E -9.100812 14.368437 -10.987302 -5.386923
1ALY          A          ALA             141                    E -6.367838  8.855744 -9.898251 -4.986208
1ALY          A          GLU             142                    C -5.488784 10.393332 -8.495570 -5.161690
1ALY          A          LYS             143                    T -5.206195 10.377915 -8.342518 -5.057245
1ALY          A          GLY             144                    T -5.140168 10.478806 -8.366293 -5.047375
1ALY          A          TYR             145                    T -5.140712 10.474524 -8.364492 -5.046976
1ALY          A          TYR             146                    T -5.219708 10.712844 -8.146979 -5.056004
1ALY          A          THR             147                    E -5.619794 10.584606 -8.207549 -4.903918
1ALY          A          MET             148                    E -6.470128 11.329805 -8.592326 -4.963610
1ALY          A          SER             149                    C -9.289103 10.476218 -13.798944 -5.119838
1ALY          A          ASN             150                    T -8.995461  9.321434 -13.710047 -4.978374
1ALY          A          ASN             151                    T -8.879455  9.906032 -13.415247 -4.934122
1ALY          A          LEU             152                    T -8.879127  9.996990 -13.351112 -4.921493
1ALY          A          VAL             153                    E -8.637283 10.306318 -12.891983 -4.923839
1ALY          A          THR             154                    E -5.903875  8.822223 -9.758647 -5.397095
1ALY          A          LEU             155                    E -5.886506  8.827535 -9.849363 -5.414825
1ALY          A          GLU             156                    E -5.877446  8.810489 -9.924069 -5.431297
1ALY          A          ASN             157                    T -5.876355  8.815729 -9.930962 -5.432478
1ALY          A          GLY             158                    T -5.878551  8.809087 -9.921544 -5.434077
1ALY          A          LYS             159                    T -7.653037  8.817406 -13.506584 -6.058278
1ALY          A          GLN             160                    E -8.247149  8.456718 -14.489864 -6.334845
1ALY          A          LEU             161                    E -9.538082 11.883129 -13.686443 -5.951261
1ALY          A          THR             162                    E -11.126130 14.013601 -14.349779 -5.126392
1ALY          A          VAL             163                    E -10.571903 11.358685 -14.413527 -4.872361
1ALY          A          LYS             164                    C -9.864485 10.617703 -14.158874 -5.100488
1ALY          A          ARG             165                    C -9.848396 10.712399 -14.167404 -5.107592
1ALY          A          GLN             166                    C -9.875456 10.512375 -14.232751 -5.133388
1ALY          A          GLY             167                    E -9.892691 10.533810 -14.184944 -5.139131
1ALY          A          LEU             168                    E -10.040743 10.612401 -14.063757 -5.205706
1ALY          A          TYR             169                    E -11.715579 15.376494 -14.235731 -5.271908
1ALY          A          TYR             170                    E -12.447876 17.941195 -13.329755 -5.023260
1ALY          A          ILE             171                    E -12.555920 18.399719 -12.753226 -4.875753
1ALY          A          TYR             172                    E -14.105536 17.702211 -16.134365 -4.956532
1ALY          A          ALA             173                    E -13.608544 16.480467 -15.915476 -4.973588
1ALY          A          GLN             174                    E -13.400643 15.898007 -16.372873 -5.180875
1ALY          A          VAL             175                    E -12.773407 15.275194 -16.012781 -5.386617
1ALY          A          THR             176                    E -12.726579 14.978754 -16.341703 -5.489325
1ALY          A          PHE             177                    E -12.750993 14.955964 -16.318013 -5.507341
1ALY          A          CYS             178                    E -12.837812 14.686120 -16.516354 -5.604884
1ALY          A          SER             179                    E -12.375240 11.272593 -17.712020 -5.580024
1ALY          A          ASN             180                    T -11.698372  8.700625 -18.095314 -5.644163
1ALY          A          ARG             181                    T -11.007795  8.447083 -17.288873 -5.493075
1ALY          A          GLU             182                    T -9.044914  6.391838 -14.805410 -5.093900
1ALY          A          ALA             183                    T -8.152775  5.632253 -13.841097 -4.706626
1ALY          A          SER             184                    T -7.938071  5.763612 -13.771759 -4.662320
1ALY          A          SER             185                    T -7.854637  6.455688 -13.474087 -4.641548
1ALY          A          GLN             186                    T -7.828065  6.771694 -13.348906 -4.630535
1ALY          A          ALA             187                    T -7.897306  6.947181 -13.117905 -4.555545
1ALY          A          PRO             188                    E -8.313221  8.530434 -12.658802 -4.513363
1ALY          A          PHE             189                    E -8.817217 11.843079 -11.371270 -4.448145
1ALY          A          ILE             190                    E -9.469471 13.562479 -11.024496 -4.317643
1ALY          A          ALA             191                    E -10.282012 14.380055 -11.009723 -3.900871
1ALY          A          SER             192                    E -11.347930 14.939403 -13.354027 -4.530267
1ALY          A          LEU             193                    E -11.646546 14.490182 -14.057718 -4.716309
1ALY          A          CYS             194                    E -11.678357 14.048675 -14.426964 -4.824888
1ALY          A          LEU             195                    E -10.140073  9.365881 -15.254561 -5.391349
1ALY          A          LYS             196                    E -8.819859  6.634069 -14.642531 -5.108684
1ALY          A          SER             197                    T -6.464208  5.431775 -11.335563 -4.639390
```

1ALY	A	PRO	198	T	-4.727457	5.940937	-8.698451	-4.479965
1ALY	A	GLY	199	T	-4.706851	5.951707	-8.779656	-4.483947
1ALY	A	ARG	200	T	-4.703934	5.964483	-8.792022	-4.484287
1ALY	A	PHE	201	C	-4.685575	6.151896	-8.763107	-4.482930
1ALY	A	GLU	202	C	-4.714948	6.193581	-8.634607	-4.475191
1ALY	A	ARG	203	E	-6.249259	9.173762	-9.666960	-4.513455
1ALY	A	ILE	204	E	-6.314603	12.571143	-7.485881	-4.127455
1ALY	A	LEU	205	E	-6.221651	13.397655	-6.931498	-4.046835
1ALY	A	LEU	206	E	-6.479894	14.108867	-6.497958	-3.804661
1ALY	A	ARG	207	E	-6.109276	11.802517	-7.612981	-4.017221
1ALY	A	ALA	208	E	-6.121026	11.742246	-7.608617	-4.018771
1ALY	A	ALA	209	E	-6.321114	10.859324	-8.263926	-4.169086
1ALY	A	ASN	210	E	-6.490311	9.401712	-8.998034	-4.264956
1ALY	A	THR	211	E	-6.544323	9.178245	-9.008084	-4.276037
1ALY	A	HIS	212	C	-8.348581	8.589765	-13.250071	-4.993979
1ALY	A	SER	213	T	-6.354891	5.495204	-10.724788	-4.266533
1ALY	A	SER	214	T	-6.090091	5.131227	-11.084876	-4.315659
1ALY	A	ALA	215	T	-5.891040	4.757851	-11.441959	-4.394984
1ALY	A	LYS	216	T	-5.876321	4.729525	-11.528766	-4.421049
1ALY	A	PRO	217	C	-5.880998	4.691890	-11.521963	-4.415930
1ALY	A	CYS	218	C	-6.218548	4.156223	-12.201434	-4.550396
1ALY	A	GLY	219	E	-6.571335	3.882211	-12.584261	-4.669691
1ALY	A	GLN	220	E	-7.933085	4.418434	-14.807804	-5.353027
1ALY	A	GLN	221	E	-9.977446	5.100538	-17.830102	-5.571656
1ALY	A	SER	222	E	-8.576252	12.291312	-10.257502	-4.464199
1ALY	A	ILE	223	E	-7.559416	11.865189	-9.386752	-4.448911
1ALY	A	HIS	224	E	-6.383328	11.275696	-8.070456	-4.370135
1ALY	A	LEU	225	E	-6.339535	11.437853	-8.104934	-4.370068
1ALY	A	GLY	226	E	-6.168997	11.262541	-8.413132	-4.460226
1ALY	A	GLY	227	E	-6.175917	11.253441	-8.396586	-4.460881
1ALY	A	VAL	228	E	-6.225088	11.211550	-8.324290	-4.461748
1ALY	A	PHE	229	E	-6.865179	11.269911	-9.223440	-4.663997
1ALY	A	GLU	230	E	-6.976561	10.792308	-9.373417	-4.726529
1ALY	A	LEU	231	E	-9.156804	13.023797	-11.216817	-4.581483
1ALY	A	GLN	232	B	-9.984793	11.140916	-14.215193	-4.969681
1ALY	A	PRO	233	T	-9.438720	10.567525	-12.860913	-4.380924
1ALY	A	GLY	234	T	-9.430468	10.621535	-12.866926	-4.385169
1ALY	A	ALA	235	B	-9.515361	10.633906	-12.589227	-4.259259
1ALY	A	SER	236	E	-9.642050	10.447034	-12.373579	-4.141607
1ALY	A	VAL	237	E	-9.683346	10.662496	-12.063573	-4.065415
1ALY	A	PHE	238	E	-11.316819	15.550618	-13.150146	-4.632082
1ALY	A	VAL	239	E	-10.988781	13.267494	-13.815529	-4.711276
1ALY	A	ASN	240	E	-10.597480	11.814682	-14.422584	-4.863099
1ALY	A	VAL	241	E	-9.311590	9.834756	-12.799387	-4.401767
1ALY	A	THR	242	T	-9.146146	9.393584	-13.223041	-4.494700
1ALY	A	ASP	243	T	-8.875936	9.519721	-12.937636	-4.447100
1ALY	A	PRO	244	G	-8.827638	9.553378	-12.941462	-4.434085
1ALY	A	SER	245	G	-8.835278	9.534797	-12.924783	-4.425638
1ALY	A	GLN	246	G	-9.117441	9.530020	-13.223447	-4.509619
1ALY	A	VAL	247	B	-7.352362	7.973461	-10.843215	-4.354409
1ALY	A	SER	248	C	-5.785527	5.149177	-10.748484	-4.664171
1ALY	A	HIS	249	C	-4.465024	5.256609	-8.999811	-4.604333
1ALY	A	GLY	250	T	-3.786000	5.767682	-8.401814	-4.759773
1ALY	A	THR	251	T	-3.782381	5.786665	-8.414172	-4.761203
1ALY	A	GLY	252	T	-3.783762	5.781709	-8.408628	-4.762124
1ALY	A	PHE	253	T	-3.802937	5.808653	-8.330893	-4.764080
1ALY	A	THR	254	E	-4.007986	6.025935	-8.134155	-4.828748
1ALY	A	SER	255	E	-6.806125	8.867872	-10.407060	-4.979119
1ALY	A	PHE	256	E	-11.573553	15.077970	-14.260007	-5.434141
1ALY	A	GLY	257	E	-9.792790	14.286287	-10.985420	-4.681875
1ALY	A	LEU	258	E	-8.680709	13.409774	-9.179427	-3.824486
1ALY	A	LEU	259	E	-8.680709	13.409774	-9.179427	-3.824486
1ALY	A	LYS	260	E	-8.680709	13.409774	-9.179427	-3.824486
1ALY	A	LEU	261	C	-8.680709	13.409774	-9.179427	-3.824486
1B56	A	THR	3	C	-6.257161	7.033560	-9.185410	-3.650927
1B56	A	VAL	4	G	-6.257161	7.033560	-9.185410	-3.650927
1B56	A	GLN	5	G	-6.257161	7.033560	-9.185410	-3.650927
1B56	A	GLN	6	G	-6.257161	7.033560	-9.185410	-3.650927
1B56	A	LEU	7	G	-7.974457	11.132250	-10.258627	-4.500509
1B56	A	GLU	8	C	-10.002533	12.929662	-13.821722	-5.855770
1B56	A	GLY	9	E	-11.343829	13.427250	-16.460869	-6.884542
1B56	A	ARG	10	E	-14.010194	17.122186	-17.558180	-5.811340
1B56	A	TRP	11	E	-12.533935	15.564286	-14.596612	-4.989684
1B56	A	ARG	12	E	-9.885829	10.294696	-13.493313	-4.783853
1B56	A	LEU	13	E	-7.976517	8.228102	-11.948320	-4.613237
1B56	A	VAL	14	E	-6.906384	5.814092	-12.038576	-4.585173
1B56	A	ASP	15	E	-6.903316	5.828409	-12.054613	-4.588840
1B56	A	SER	16	E	-6.902651	5.831745	-12.059696	-4.590090
1B56	A	LYS	17	E	-6.905677	5.807952	-12.056368	-4.590437
1B56	A	GLY	18	T	-7.007221	5.371857	-12.088780	-4.587570
1B56	A	PHE	19	H	-9.783243	8.840753	-15.577199	-5.438557

1B56	A	ASP	20	H	-10.432977	9.363372	-16.452316	-5.727943
1B56	A	GLU	21	H	-10.791462	9.581428	-16.449629	-5.790555
1B56	A	TYR	22	H	-12.532879	14.887521	-17.152102	-6.232692
1B56	A	MET	23	H	-10.048008	11.581072	-14.319338	-5.821663
1B56	A	LYS	24	H	-9.213858	10.329813	-13.750069	-5.397369
1B56	A	GLU	25	H	-7.370449	9.079475	-11.313025	-5.051804
1B56	A	LEU	26	H	-6.364584	8.067015	-10.221022	-4.584120
1B56	A	GLY	27	C	-4.903725	5.331480	-9.095095	-4.181372
1B56	A	VAL	28	C	-4.875479	5.407939	-9.132392	-4.168463
1B56	A	GLY	29	C	-4.871186	5.424958	-9.147078	-4.169042
1B56	A	ILE	30	H	-4.878683	5.379876	-9.121331	-4.156610
1B56	A	ALA	31	H	-4.919487	5.204332	-9.060110	-4.133472
1B56	A	LEU	32	H	-6.583344	7.184379	-10.148170	-3.971977
1B56	A	ARG	33	H	-7.646515	8.179088	-11.363822	-4.291435
1B56	A	LYS	34	H	-8.382833	9.335905	-12.140532	-4.459509
1B56	A	MET	35	H	-8.428061	9.479552	-12.546080	-4.782647
1B56	A	GLY	36	H	-6.088716	7.655849	-9.308107	-4.217214
1B56	A	ALA	37	H	-5.946690	7.982208	-9.248654	-4.160271
1B56	A	MET	38	H	-5.940889	7.993692	-9.275478	-4.163064
1B56	A	ALA	39	C	-5.944747	7.987242	-9.252812	-4.158726
1B56	A	LYS	40	C	-5.949361	7.973271	-9.230580	-4.154544
1B56	A	PRO	41	C	-6.833678	9.190518	-9.181313	-3.976248
1B56	A	ASP	42	E	-8.638044	9.259836	-12.205736	-4.479215
1B56	A	CYS	43	E	-10.019839	11.098145	-14.296811	-4.883357
1B56	A	ILE	44	E	-8.765600	11.396080	-11.607135	-4.751893
1B56	A	ILE	45	E	-6.362778	8.698495	-9.916604	-4.890056
1B56	A	THR	46	E	-4.527615	5.687599	-9.332034	-4.946157
1B56	A	CYS	47	E	-3.981996	5.024500	-9.498827	-5.033394
1B56	A	ASP	48	E	-3.952181	5.148053	-9.511721	-5.029934
1B56	A	GLY	49	T	-3.952243	5.147137	-9.511871	-5.030077
1B56	A	LYS	50	T	-3.962315	5.086833	-9.505005	-5.032222
1B56	A	ASN	51	E	-4.234485	4.815379	-9.613409	-5.076323
1B56	A	LEU	52	E	-5.737373	7.539197	-9.752672	-4.952389
1B56	A	THR	53	E	-9.075757	9.867426	-13.516911	-5.407701
1B56	A	ILE	54	E	-11.247452	14.596478	-15.695392	-6.010526
1B56	A	LYS	55	E	-10.165981	10.293418	-15.311344	-5.632886
1B56	A	THR	56	E	-9.072890	8.580533	-14.136236	-5.122804
1B56	A	GLU	57	E	-9.023521	8.500834	-14.313974	-5.151444
1B56	A	SER	58	T	-6.689522	8.054922	-10.588308	-4.810957
1B56	A	THR	59	T	-6.653318	8.104692	-10.688168	-4.815769
1B56	A	LEU	60	T	-6.653779	8.105937	-10.684186	-4.815470
1B56	A	LYS	61	T	-6.662060	8.105344	-10.639058	-4.812751
1B56	A	THR	62	E	-6.660121	8.128447	-10.641458	-4.815270
1B56	A	THR	63	E	-8.262369	9.272275	-12.413843	-4.968885
1B56	A	GLN	64	E	-9.584659	12.543792	-13.677914	-5.637862
1B56	A	PHE	65	E	-9.727479	12.899881	-13.316691	-5.596998
1B56	A	SER	66	E	-9.613118	12.223444	-13.635784	-5.527552
1B56	A	CYS	67	E	-8.866077	9.083453	-13.910264	-5.357541
1B56	A	THR	68	E	-6.920937	10.738514	-9.895434	-5.086193
1B56	A	LEU	69	T	-6.917135	10.751717	-9.911336	-5.086502
1B56	A	GLY	70	T	-6.842393	10.766854	-10.132325	-5.139658
1B56	A	GLU	71	E	-6.843268	10.769797	-10.125088	-5.139780
1B56	A	LYS	72	E	-6.860965	10.828764	-10.015018	-5.134093
1B56	A	PHE	73	E	-8.069013	11.001521	-11.859665	-5.525218
1B56	A	GLU	74	E	-8.079200	10.871301	-11.932653	-5.548716
1B56	A	GLU	75	E	-9.822762	10.501164	-15.480664	-5.822401
1B56	A	THR	76	E	-7.343313	7.856815	-12.279833	-5.364646
1B56	A	THR	77	E	-7.312813	7.902895	-12.365128	-5.370728
1B56	A	ALA	78	T	-7.308307	7.909758	-12.389767	-5.373328
1B56	A	ASP	79	T	-7.311103	7.902055	-12.379604	-5.372786
1B56	A	GLY	80	T	-7.312381	7.898586	-12.371640	-5.372201
1B56	A	ARG	81	E	-8.941750	8.997423	-14.370978	-5.570657
1B56	A	LYS	82	E	-9.875388	9.497308	-15.871140	-5.820196
1B56	A	THR	83	E	-10.403862	10.285428	-16.249574	-5.942501
1B56	A	GLN	84	E	-11.049273	11.347997	-16.315931	-5.652702
1B56	A	THR	85	E	-11.033113	11.886597	-15.855491	-5.515070
1B56	A	VAL	86	E	-10.745818	12.248443	-15.089847	-5.203223
1B56	A	CYS	87	E	-10.177188	10.439219	-14.522063	-4.917285
1B56	A	ASN	88	E	-6.595147	7.527309	-10.402423	-4.599472
1B56	A	PHE	89	E	-5.325200	7.937085	-8.466579	-4.329514
1B56	A	THR	90	E	-5.219571	8.231659	-8.504197	-4.355648
1B56	A	ASP	91	T	-5.218640	8.235396	-8.509492	-4.356005
1B56	A	GLY	92	T	-5.218738	8.235172	-8.508521	-4.355919
1B56	A	ALA	93	E	-5.279697	8.312350	-8.304044	-4.329472
1B56	A	LEU	94	E	-6.287557	9.748388	-8.726928	-4.489491
1B56	A	VAL	95	E	-9.027636	10.670636	-11.940330	-4.589277
1B56	A	GLN	96	E	-12.024761	12.990980	-15.556648	-5.348977
1B56	A	HIS	97	E	-13.166810	13.381326	-18.641936	-6.515769
1B56	A	GLN	98	E	-9.407466	10.503049	-14.781298	-6.405870
1B56	A	GLU	99	E	-5.052506	9.093129	-8.794625	-5.541829
1B56	A	TRP	100	E	-4.611166	8.967075	-8.753854	-5.490013

```
1B56        A          ASP            101                   T -4.534885  8.593687 -9.060061 -5.477597
1B56        A          GLY            102                   T -4.534524  8.593511 -9.063188 -5.477628
1B56        A          LYS            103                   E -4.534680  8.593014 -9.061686 -5.477378
1B56        A          GLU            104                   E -4.854610  8.232355 -9.252035 -5.429482
1B56        A          SER            105                   E -5.784620  5.881385 -11.296213 -5.383376
1B56        A          THR            106                   E -8.912067  8.353335 -14.201977 -5.522154
1B56        A          ILE            107                   E -11.467683 12.365598 -15.868666 -5.435320
1B56        A          THR            108                   E -11.830895 12.978656 -15.956740 -5.488004
1B56        A          ARG            109                   E -10.202230 13.271910 -13.304827 -5.544415
1B56        A          LYS            110                   E -4.861151  7.969654 -8.351928 -4.931378
1B56        A          LEU            111                   E -2.627902  7.702969 -5.687926 -4.884994
1B56        A          LYS            112                   E -2.597872  7.829781 -5.743985 -4.894835
1B56        A          ASP            113                   T -2.596448  7.839099 -5.749648 -4.894800
1B56        A          GLY            114                   T -2.596443  7.839165 -5.749683 -4.894798
1B56        A          LYS            115                   E -2.609872  7.831858 -5.686898 -4.891255
1B56        A          LEU            116                   E -4.365336 10.156360 -6.749272 -4.960127
1B56        A          VAL            117                   E -6.182197 11.537241 -7.977299 -4.760225
1B56        A          VAL            118                   E -9.295232 14.708832 -10.738478 -4.867085
1B56        A          GLU            119                   E -10.752949 15.295815 -14.850011 -6.172433
1B56        A          CYS            120                   E -8.953876  8.078909 -14.306104 -5.390310
1B56        A          VAL            121                   E -6.938639  8.327326 -10.993320 -4.923864
1B56        A          MET            122                   E -5.655915  8.477108 -9.348416 -4.887917
1B56        A          ASN            123                   T -5.040681  6.970536 -9.399499 -4.690917
1B56        A          ASN            124                   T -4.968592  7.132335 -9.391067 -4.664949
1B56        A          VAL            125                   E -4.969276  7.131442 -9.385401 -4.664097
1B56        A          THR            126                   E -4.990282  7.087820 -9.331335 -4.655227
1B56        A          CYS            127                   E -5.191495  6.517237 -9.409354 -4.562466
1B56        A          THR            128                   E -6.252463  8.380432 -9.322845 -4.462465
1B56        A          ARG            129                   E -11.824254 12.474640 -15.874864 -5.193526
1B56        A          ILE            130                   E -11.412526 16.230865 -14.239698 -5.981592
1B56        A          TYR            131                   E -9.430974 13.415238 -12.268033 -5.508186
1B56        A          GLU            132                   E -5.786313  6.824197 -8.990081 -4.018113
1B56        A          LYS            133                   E -5.786313  6.824197 -8.990081 -4.018113
1B56        A          VAL            134                   C -5.786313  6.824197 -8.990081 -4.018113
1B56        A          GLU            135                   C -5.786313  6.824197 -8.990081 -4.018113
1B90        A          LYS              1                   C -10.640866  9.379202 -14.619421 -4.553443
1B90        A          GLN              2                   B -10.640866  9.379202 -14.619421 -4.553443
1B90        A          PHE              3                   C -10.640866  9.379202 -14.619421 -4.553443
1B90        A          THR              4                   C -10.640866  9.379202 -14.619421 -4.553443
1B90        A          LYS              5                   H -13.681732 12.807432 -19.958785 -6.440011
1B90        A          CYS              6                   H -11.660715 11.872784 -16.228765 -5.761778
1B90        A          GLU              7                   H -10.787838 12.813063 -14.381355 -5.310937
1B90        A          LEU              8                   H -10.192411 14.439890 -12.600528 -4.994977
1B90        A          SER              9                   H -9.845820 13.278363 -12.833354 -4.876410
1B90        A          GLN             10                   H -7.535867  9.709440 -10.255031 -4.345441
1B90        A          LEU             11                   H -7.391280 10.365479 -10.105963 -4.352142
1B90        A          LEU             12                   H -7.038152 10.985544 -9.776164 -4.462306
1B90        A          LYS             13                   G -6.268350  8.483318 -10.168246 -4.604229
1B90        A          ASP             14                   G -6.264123  8.499082 -10.188764 -4.610230
1B90        A          ILE             15                   G -6.327625  8.398384 -10.212700 -4.653557
1B90        A          ASP             16                   T -5.965326  7.465784 -10.795668 -4.915131
1B90        A          GLY             17                   T -5.361198  7.866143 -9.757807 -4.929047
1B90        A          TYR             18                   G -5.413221  8.083610 -9.658931 -4.957466
1B90        A          GLY             19                   G -5.325934  8.378258 -9.497432 -4.872398
1B90        A          GLY             20                   G -5.324282  8.390542 -9.491251 -4.866887
1B90        A          ILE             21                   C -5.428741  8.732065 -9.121235 -4.804237
1B90        A          ALA             22                   C -6.240801 10.189984 -8.948482 -4.454238
1B90        A          LEU             23                   H -6.472787 10.326152 -8.576151 -4.335231
1B90        A          PRO             24                   H -8.386114 12.431243 -9.626011 -4.033854
1B90        A          GLU             25                   H -10.158636 17.019723 -11.012573 -4.627640
1B90        A          LEU             26                   H -10.293357 17.561723 -10.847552 -4.722149
1B90        A          ILE             27                   H -10.924757 18.081848 -12.201035 -5.084264
1B90        A          CYS             28                   H -10.983517 15.975012 -13.915497 -5.465462
1B90        A          THR             29                   H -10.537301 15.251326 -13.475333 -5.518113
1B90        A          MET             30                   H -10.540731 15.011996 -13.594715 -5.514110
1B90        A          PHE             31                   H -8.584734 10.157621 -12.526064 -5.215674
1B90        A          HIS             32                   H -8.582187 10.167294 -12.538511 -5.218026
1B90        A          THR             33                   H -8.584770 10.149479 -12.530249 -5.215968
1B90        A          SER             34                   H -8.598500 10.032083 -12.522108 -5.210143
1B90        A          GLY             35                   T -8.600239 10.020241 -12.514850 -5.209210
1B90        A          TYR             36                   T -11.378503 13.350059 -15.644059 -5.649609
1B90        A          ASP             37                   B -8.699312  9.823452 -11.801147 -4.471428
1B90        A          THR             38                   T -8.312157  9.733694 -12.028985 -4.532804
1B90        A          GLN             39                   T -5.885608  7.983983 -8.641083 -4.051386
1B90        A          ALA             40                   T -5.776763  7.749802 -9.031566 -4.101624
1B90        A          ILE             41                   E -4.148982  6.013891 -8.047542 -4.426746
1B90        A          VAL             42                   E -3.676333  4.695895 -8.635689 -4.495099
1B90        A          GLU             43                   E -3.099790  5.144590 -8.275558 -4.868668
1B90        A          ASN             44                   T -3.096881  5.142104 -8.306459 -4.884232
1B90        A          ASP             45                   T -3.097672  5.141553 -8.303687 -4.885740
1B90        A          GLU             46                   T -3.201063  4.989561 -8.351306 -4.960621
```

1B9O	A	SER	47	T	-3.369741	5.432681	-8.085412	-5.086836
1B9O	A	THR	48	E	-5.616255	6.860581	-10.745625	-5.460628
1B9O	A	GLU	49	E	-7.596640	9.486249	-12.772138	-6.071475
1B9O	A	TYR	50	E	-10.797453	15.971403	-18.550445	-9.821615
1B9O	A	GLY	51	T	-12.210458	15.655272	-19.143379	-8.330927
1B9O	A	LEU	52	T	-12.956843	16.559422	-16.275054	-5.963925
1B9O	A	PHE	53	T	-13.639310	18.340820	-15.874840	-5.788859
1B9O	A	GLN	54	T	-13.494926	16.204007	-17.149807	-5.954713
1B9O	A	ILE	55	E	-10.850774	13.119877	-14.448410	-5.714398
1B9O	A	SER	56	E	-10.790907	13.258959	-14.585121	-5.768189
1B9O	A	ASN	57	T	-10.714956	13.428583	-14.743313	-5.845485
1B9O	A	LYS	58	T	-10.241376	14.210664	-14.058031	-5.920853
1B9O	A	LEU	59	T	-10.236606	14.216347	-14.075545	-5.920885
1B9O	A	TRP	60	T	-10.375405	14.234293	-14.197405	-5.929730
1B9O	A	CYS	61	C	-9.616436	7.791916	-15.989532	-5.518818
1B9O	A	LYS	62	B	-8.964184	7.458709	-14.797044	-5.066017
1B9O	A	SER	63	B	-8.000940	5.812958	-13.391270	-4.410292
1B9O	A	SER	64	T	-6.919582	4.592687	-11.953997	-3.943251
1B9O	A	GLN	65	T	-6.867064	4.649701	-12.089086	-3.980868
1B9O	A	VAL	66	B	-5.329772	6.332089	-8.182313	-3.453963
1B9O	A	PRO	67	T	-5.135852	6.400507	-8.511010	-3.636789
1B9O	A	GLN	68	T	-5.126923	6.447654	-8.528737	-3.647727
1B9O	A	SER	69	T	-5.151445	6.536677	-8.396103	-3.639170
1B9O	A	ARG	70	C	-5.148681	6.554020	-8.406252	-3.645162
1B9O	A	ASN	71	T	-5.823448	6.757100	-9.574933	-4.150637
1B9O	A	ILE	72	T	-7.128996	8.315852	-11.322314	-4.506664
1B9O	A	CYS	73	T	-7.618464	8.098137	-12.630024	-4.848835
1B9O	A	ASP	74	T	-7.490555	7.904911	-12.736614	-4.844307
1B9O	A	ILE	75	C	-7.837782	8.049111	-13.418487	-5.014664
1B9O	A	SER	76	B	-7.976038	7.723733	-13.543421	-4.976288
1B9O	A	CYS	77	G	-8.083196	7.369378	-13.655973	-4.971935
1B9O	A	ASP	78	G	-8.309064	7.460661	-13.417432	-4.858194
1B9O	A	LYS	79	G	-9.292790	8.634181	-14.126379	-4.981129
1B9O	A	PHE	80	G	-10.463290	12.277932	-14.902647	-5.336196
1B9O	A	LEU	81	C	-8.164442	10.503530	-11.326664	-4.903459
1B9O	A	ASP	82	C	-6.873870	8.010608	-10.802952	-4.607239
1B9O	A	ASP	83	C	-6.629874	8.198703	-10.848804	-4.655180
1B9O	A	ASP	84	C	-6.626141	8.205032	-10.866077	-4.655735
1B9O	A	ILE	85	H	-6.626062	8.205670	-10.865905	-4.655421
1B9O	A	THR	86	H	-6.671225	8.025904	-10.833940	-4.636235
1B9O	A	ASP	87	H	-7.260667	8.589313	-10.997183	-4.749215
1B9O	A	ASP	88	H	-9.557362	9.519207	-13.684354	-4.737048
1B9O	A	ILE	89	H	-10.314964	12.066340	-13.811030	-4.801471
1B9O	A	MET	90	H	-10.475561	11.892086	-14.140894	-4.945234
1B9O	A	CYS	91	H	-10.391238	12.469980	-13.936698	-5.011813
1B9O	A	ALA	92	H	-10.345253	12.960518	-13.747431	-5.004953
1B9O	A	LYS	93	H	-10.287839	13.363227	-13.618011	-5.028547
1B9O	A	LYS	94	H	-9.132120	14.009385	-10.284502	-4.430213
1B9O	A	ILE	95	H	-7.695819	14.677764	-7.916503	-4.290170
1B9O	A	LEU	96	H	-6.311654	10.620112	-8.477396	-4.437801
1B9O	A	ASP	97	H	-5.793980	9.884598	-8.551805	-4.429151
1B9O	A	ILE	98	H	-5.683685	10.024303	-8.605959	-4.450725
1B9O	A	LYS	99	H	-5.683543	10.024049	-8.610256	-4.453404
1B9O	A	GLY	100	C	-5.701910	9.875677	-8.639280	-4.458988
1B9O	A	ILE	101	H	-5.932909	9.727149	-8.686950	-4.461328
1B9O	A	ASP	102	H	-6.723310	10.759790	-8.915919	-4.568884
1B9O	A	TYR	103	H	-9.098527	13.742878	-11.422242	-5.292310
1B9O	A	TRP	104	H	-8.386737	14.406379	-9.431739	-4.800161
1B9O	A	LEU	105	H	-5.723211	7.774631	-8.514258	-4.044027
1B9O	A	ALA	106	T	-4.770755	6.370211	-8.179134	-3.906527
1B9O	A	HIS	107	T	-4.742464	6.417155	-8.286322	-3.939206
1B9O	A	LYS	108	T	-4.699524	6.502751	-8.400178	-3.982968
1B9O	A	ALA	109	T	-4.678620	6.523980	-8.481637	-4.009317
1B9O	A	LEU	110	T	-4.783026	6.301490	-8.513368	-4.015830
1B9O	A	CYS	111	T	-5.732353	7.498680	-10.515379	-4.679539
1B9O	A	THR	112	T	-5.563423	7.381225	-10.135072	-4.559367
1B9O	A	GLU	113	T	-5.742518	7.281060	-10.310794	-4.564445
1B9O	A	LYS	114	T	-5.889381	7.226405	-10.210246	-4.514439
1B9O	A	LEU	115	G	-5.927829	7.160893	-10.069001	-4.463411
1B9O	A	GLU	116	G	-6.005445	7.203634	-9.799445	-4.397479
1B9O	A	GLN	117	G	-7.471478	7.528107	-11.745169	-4.691659
1B9O	A	TRP	118	G	-8.908107	11.635303	-14.022504	-6.479697
1B9O	A	LEU	119	C	-4.930608	5.718054	-9.822473	-5.063939
1B9O	A	CYS	120	C	-3.454516	4.017423	-8.092946	-4.327044
1B9O	A	GLU	121	C	-3.454516	4.017423	-8.092946	-4.327044
1B9O	A	LYS	122	C	-3.454516	4.017423	-8.092946	-4.327044
1B9O	A	LEU	123	C	-3.454516	4.017423	-8.092946	-4.327044
1BD8	A	ARG	7	H	-7.414095	5.512327	-11.455609	-3.708748
1BD8	A	ALA	8	H	-7.414095	5.512327	-11.455609	-3.708748
1BD8	A	GLY	9	H	-7.414095	5.512327	-11.455609	-3.708748
1BD8	A	ASP	10	H	-7.414095	5.512327	-11.455609	-3.708748

1BD8	A	ARG	11	H	-10.363962	6.658240	-15.899881	-4.608222
1BD8	A	LEU	12	H	-11.349741	11.550752	-14.698634	-4.472762
1BD8	A	SER	13	H	-10.558554	8.933440	-14.656840	-4.148912
1BD8	A	GLY	14	H	-9.560564	7.808998	-13.508397	-3.774216
1BD8	A	ALA	15	H	-9.288291	8.213187	-13.310774	-3.795946
1BD8	A	ALA	16	H	-8.917036	7.777213	-13.479567	-3.994522
1BD8	A	ALA	17	H	-8.359811	7.529941	-13.055930	-4.190844
1BD8	A	ARG	18	H	-7.659383	6.816766	-12.594081	-4.357107
1BD8	A	GLY	19	C	-7.028369	7.020608	-12.312750	-4.864587
1BD8	A	ASP	20	C	-7.005157	7.154642	-12.296266	-4.866388
1BD8	A	VAL	21	H	-7.010805	7.191908	-12.270026	-4.874286
1BD8	A	GLN	22	H	-7.046210	7.201415	-12.235905	-4.908599
1BD8	A	GLU	23	H	-7.215182	7.430878	-12.178837	-5.067259
1BD8	A	VAL	24	H	-8.666709	10.566253	-12.134064	-4.646445
1BD8	A	ARG	25	H	-9.520698	11.629584	-12.352506	-4.379573
1BD8	A	ARG	26	H	-9.999366	12.014017	-12.560968	-4.277758
1BD8	A	LEU	27	H	-10.641661	13.506229	-13.106407	-4.426153
1BD8	A	LEU	28	H	-8.075101	9.009895	-11.357713	-4.384957
1BD8	A	HIS	29	H	-7.767297	8.598130	-11.485422	-4.240788
1BD8	A	ARG	30	H	-7.191736	8.318652	-10.626653	-3.906915
1BD8	A	GLU	31	C	-7.185300	8.333187	-10.644607	-3.906470
1BD8	A	LEU	32	C	-7.174217	8.377299	-10.656313	-3.903229
1BD8	A	VAL	33	C	-7.299201	8.340837	-10.474452	-3.774016
1BD8	A	HIS	34	T	-7.277703	8.960056	-10.136315	-3.768684
1BD8	A	PRO	35	T	-8.014234	11.056467	-10.282998	-3.952779
1BD8	A	ASP	36	T	-8.034215	11.090858	-10.247473	-3.970572
1BD8	A	ALA	37	T	-8.024164	10.842464	-10.442048	-4.014419
1BD8	A	LEU	38	C	-6.316597	6.258561	-10.917369	-4.585135
1BD8	A	ASN	39	B	-5.714296	6.883539	-10.627827	-4.958128
1BD8	A	ARG	40	T	-5.683041	7.004537	-10.662374	-4.967458
1BD8	A	PHE	41	T	-5.677554	7.041537	-10.673517	-4.971038
1BD8	A	GLY	42	T	-5.678509	7.041022	-10.669332	-4.972424
1BD8	A	LYS	43	B	-5.910187	7.526656	-10.537618	-5.143585
1BD8	A	THR	44	C	-7.332582	9.558044	-11.419445	-5.166375
1BD8	A	ALA	45	G	-8.415314	11.101702	-11.977200	-5.331337
1BD8	A	LEU	46	G	-10.463185	14.705881	-12.724037	-5.163345
1BD8	A	GLN	47	G	-11.782266	16.747814	-13.991928	-5.225965
1BD8	A	VAL	48	C	-10.864982	14.545899	-13.284217	-5.047642
1BD8	A	MET	49	C	-10.613058	14.013070	-13.582358	-5.168600
1BD8	A	MET	50	T	-10.021966	12.774527	-13.477584	-5.122054
1BD8	A	PHE	51	T	-9.678928	12.654320	-13.216088	-5.048139
1BD8	A	GLY	52	T	-8.028373	10.394692	-10.943547	-4.538809
1BD8	A	SER	53	T	-8.011764	10.421470	-10.967958	-4.525477
1BD8	A	THR	54	H	-7.957326	10.687519	-10.882455	-4.478266
1BD8	A	ALA	55	H	-7.966978	10.669785	-10.840219	-4.466542
1BD8	A	ILE	56	H	-7.981437	10.626105	-10.789841	-4.454414
1BD8	A	ALA	57	H	-9.175998	13.101204	-10.761316	-4.122702
1BD8	A	LEU	58	H	-9.339944	13.502728	-10.347873	-4.087110
1BD8	A	GLU	59	H	-11.066504	14.697200	-13.525673	-4.833681
1BD8	A	LEU	60	H	-8.739122	13.622506	-10.511632	-4.964682
1BD8	A	LEU	61	H	-7.563497	11.877562	-10.004788	-4.821116
1BD8	A	LYS	62	H	-7.386356	11.039923	-10.541565	-4.796167
1BD8	A	GLN	63	H	-7.380311	11.022590	-10.572044	-4.790971
1BD8	A	GLY	64	C	-7.367760	10.955060	-10.635971	-4.777599
1BD8	A	ALA	65	C	-7.409127	10.629448	-10.698582	-4.726974
1BD8	A	SER	66	T	-8.008248	8.765246	-12.302362	-4.582284
1BD8	A	PRO	67	T	-8.795081	9.136088	-12.964974	-4.193940
1BD8	A	ASN	68	T	-8.255763	7.513808	-13.647192	-4.782564
1BD8	A	VAL	69	T	-8.084678	6.886263	-13.863790	-4.789950
1BD8	A	GLN	70	C	-6.970053	4.234248	-13.410951	-4.859368
1BD8	A	ASP	71	T	-5.590219	4.401458	-11.006009	-4.540473
1BD8	A	THR	72	T	-5.575637	4.436664	-11.053257	-4.543779
1BD8	A	SER	73	T	-5.579741	4.421581	-11.032411	-4.539760
1BD8	A	GLY	74	T	-5.582351	4.417958	-11.017538	-4.539146
1BD8	A	THR	75	C	-5.633667	4.468404	-10.810316	-4.510686
1BD8	A	SER	76	C	-7.766884	5.947443	-12.966191	-4.675527
1BD8	A	PRO	77	H	-10.201474	11.409226	-13.640253	-4.587821
1BD8	A	VAL	78	H	-10.318360	11.907659	-13.199104	-4.561205
1BD8	A	HIS	79	H	-11.688857	14.189375	-14.283710	-4.598177
1BD8	A	ASP	80	H	-11.169240	12.228584	-14.105126	-4.455355
1BD8	A	ALA	81	H	-10.110190	11.098940	-13.236631	-4.406116
1BD8	A	ALA	82	H	-9.893052	11.142001	-13.336737	-4.462367
1BD8	A	ARG	83	H	-9.603276	11.759217	-13.015878	-4.579629
1BD8	A	THR	84	H	-7.732025	11.014757	-10.505709	-4.793374
1BD8	A	GLY	85	T	-7.635571	11.259069	-10.574453	-4.819675
1BD8	A	PHE	86	T	-7.639972	11.291110	-10.546483	-4.824822
1BD8	A	LEU	87	H	-7.579499	11.568271	-10.483658	-4.808287
1BD8	A	ASP	88	H	-7.568235	11.640326	-10.472403	-4.806342
1BD8	A	THR	89	H	-8.330780	13.427867	-10.679638	-4.813628
1BD8	A	LEU	90	H	-8.729538	14.228609	-10.364455	-4.667636
1BD8	A	LYS	91	H	-8.620870	14.175683	-10.295959	-4.560400

1BD8	A	VAL	92	H	-8.853120	14.290623	-10.280927	-4.260869
1BD8	A	LEU	93	H	-7.966895	11.522031	-10.155124	-4.284926
1BD8	A	VAL	94	H	-6.789788	9.303382	-9.534504	-4.136001
1BD8	A	GLU	95	H	-6.725480	9.150464	-9.813427	-4.187787
1BD8	A	HIS	96	H	-6.722148	9.136951	-9.838307	-4.192329
1BD8	A	GLY	97	C	-6.726656	9.081936	-9.852854	-4.195529
1BD8	A	ALA	98	C	-6.783706	8.882578	-9.842545	-4.180964
1BD8	A	ASP	99	T	-7.811593	8.665495	-12.125831	-4.510030
1BD8	A	VAL	100	T	-8.420577	10.171700	-11.930848	-4.278811
1BD8	A	ASN	101	T	-8.469387	9.436557	-12.401451	-4.312887
1BD8	A	VAL	102	T	-7.754570	7.401704	-12.161217	-4.196619
1BD8	A	PRO	103	C	-6.510296	5.632672	-11.329726	-4.332861
1BD8	A	ASP	104	T	-6.088611	6.017239	-11.017706	-4.417510
1BD8	A	GLY	105	T	-6.014018	6.398895	-10.920680	-4.417003
1BD8	A	THR	106	T	-6.014625	6.407014	-10.911055	-4.415278
1BD8	A	GLY	107	T	-6.036804	6.413467	-10.861381	-4.424893
1BD8	A	ALA	108	C	-6.337474	7.067345	-10.623293	-4.473868
1BD8	A	LEU	109	C	-7.260541	9.396663	-10.207792	-4.402345
1BD8	A	PRO	110	H	-9.328640	14.528574	-10.443109	-4.052206
1BD8	A	ILE	111	H	-9.671206	16.162811	-9.932876	-4.084691
1BD8	A	HIS	112	H	-10.408968	17.630672	-10.647086	-4.211274
1BD8	A	LEU	113	H	-9.977065	14.592159	-11.786993	-4.558258
1BD8	A	ALA	114	H	-8.351909	10.763380	-11.591321	-4.890690
1BD8	A	VAL	115	H	-8.207691	10.585014	-11.916646	-4.954709
1BD8	A	GLN	116	H	-7.697313	9.150071	-12.423591	-5.115671
1BD8	A	GLU	117	H	-6.505127	7.903966	-10.686228	-4.714860
1BD8	A	GLY	118	C	-6.225421	8.485632	-10.049265	-4.467036
1BD8	A	HIS	119	C	-6.226814	8.525878	-9.985215	-4.436184
1BD8	A	THR	120	H	-6.210810	8.619154	-9.922959	-4.395303
1BD8	A	ALA	121	H	-6.238769	8.650337	-9.781675	-4.353398
1BD8	A	VAL	122	H	-6.715181	9.812054	-8.995484	-3.983154
1BD8	A	VAL	123	H	-7.890668	12.027967	-8.950833	-3.512564
1BD8	A	SER	124	H	-8.184069	11.757474	-8.924782	-3.425257
1BD8	A	PHE	125	H	-9.966277	15.069412	-11.018911	-3.999762
1BD8	A	LEU	126	H	-9.904234	13.055669	-12.595965	-4.506264
1BD8	A	ALA	127	H	-9.821543	11.840589	-13.403029	-4.657966
1BD8	A	ALA	128	T	-9.840450	11.408276	-13.716320	-4.733432
1BD8	A	GLU	129	T	-9.672525	10.916275	-14.101498	-4.935162
1BD8	A	SER	130	T	-7.916702	10.282638	-10.933966	-4.628864
1BD8	A	ASP	131	T	-6.314398	10.792399	-8.014208	-4.171128
1BD8	A	LEU	132	T	-6.298684	10.821989	-8.069883	-4.175239
1BD8	A	HIS	133	T	-6.221824	10.525607	-8.348575	-4.154677
1BD8	A	ARG	134	T	-6.205300	10.470090	-8.413189	-4.137490
1BD8	A	ARG	135	C	-5.394115	6.872945	-8.829071	-3.855506
1BD8	A	ASP	136	T	-5.079059	6.582993	-8.872595	-4.020286
1BD8	A	ALA	137	T	-4.993108	6.741973	-8.947701	-4.068242
1BD8	A	ARG	138	T	-5.001059	6.725232	-8.929695	-4.069793
1BD8	A	GLY	139	T	-5.003233	6.718792	-8.922828	-4.071643
1BD8	A	LEU	140	C	-5.298569	7.358327	-8.869978	-4.263123
1BD8	A	THR	141	C	-6.157664	7.900387	-9.467694	-4.373807
1BD8	A	PRO	142	H	-8.625854	11.501815	-11.050303	-4.409992
1BD8	A	LEU	143	H	-9.984064	15.047563	-12.060969	-4.674593
1BD8	A	GLU	144	H	-9.827969	14.234529	-12.212948	-4.668123
1BD8	A	LEU	145	H	-9.818163	14.105407	-12.258648	-4.650331
1BD8	A	ALA	146	H	-9.082682	9.976768	-13.019953	-4.679468
1BD8	A	LEU	147	H	-8.153530	8.640761	-12.536514	-4.741391
1BD8	A	GLN	148	H	-8.112471	8.490694	-12.717153	-4.751746
1BD8	A	ARG	149	H	-8.002168	7.860430	-13.077021	-4.732421
1BD8	A	GLY	150	T	-7.579035	7.782142	-12.461732	-4.564768
1BD8	A	ALA	151	T	-7.600729	7.774110	-12.411793	-4.543021
1BD8	A	GLN	152	H	-7.792091	7.625080	-12.437032	-4.441891
1BD8	A	ASP	153	H	-7.762420	7.980123	-12.234865	-4.405061
1BD8	A	LEU	154	H	-7.841159	8.342564	-11.891032	-4.370289
1BD8	A	VAL	155	H	-8.760813	10.960747	-12.052275	-4.347136
1BD8	A	ASP	156	H	-8.745474	11.488573	-12.369438	-4.819719
1BD8	A	ILE	157	H	-8.186375	12.522806	-11.352962	-5.239289
1BD8	A	LEU	158	H	-7.029907	10.128511	-10.103495	-4.711212
1BD8	A	GLN	159	H	-5.108958	5.327847	-8.798574	-3.793715
1BD8	A	GLY	160	H	-5.108958	5.327847	-8.798574	-3.793715
1BD8	A	HIS	161	C	-5.108958	5.327847	-8.798574	-3.793715
1BD8	A	MET	162	C	-5.108958	5.327847	-8.798574	-3.793715
1BIK	A	SER	25	T	-7.357268	4.211299	-13.271993	-4.301518
1BIK	A	CYS	26	T	-7.357268	4.211299	-13.271993	-4.301518
1BIK	A	GLN	27	T	-7.357268	4.211299	-13.271993	-4.301518
1BIK	A	LEU	28	T	-7.357268	4.211299	-13.271993	-4.301518
1BIK	A	GLY	29	C	-7.176017	7.351022	-11.783184	-4.647991
1BIK	A	TYR	30	C	-7.034551	9.493371	-10.124009	-4.353832
1BIK	A	SER	31	C	-6.814262	8.402637	-10.602094	-4.297340
1BIK	A	ALA	32	C	-4.300721	4.969411	-8.354024	-4.142457
1BIK	A	GLY	33	C	-3.064680	3.253709	-7.952193	-4.276010
1BIK	A	PRO	34	C	-2.952657	3.288406	-8.061181	-4.256355

```
1BIK        A          CYS             35                    C -2.946623  3.282633 -8.094311 -4.257996
1BIK        A          MET             36                    C -2.944441  3.284239 -8.107570 -4.259264
1BIK        A          GLY             37                    C -3.007615  3.095981 -8.072346 -4.266719
1BIK        A          MET             38                    C -3.950390  3.423508 -8.723963 -4.137973
1BIK        A          THR             39                    E -5.451612  3.275954 -11.278609 -4.394913
1BIK        A          SER             40                    E -6.200491  3.961157 -11.623869 -4.511182
1BIK        A          ARG             41                    E -9.799862  7.474591 -15.312219 -5.114269
1BIK        A          TYR             42                    E -12.664001 13.685185 -16.880992 -5.757443
1BIK        A          PHE             43                    E -10.314982 12.573491 -13.454829 -5.354861
1BIK        A          TYR             44                    E -9.186164  9.426594 -13.813176 -5.250783
1BIK        A          ASN             45                    E -6.914333  5.507167 -12.166292 -4.833495
1BIK        A          GLY             46                    T -6.686855  5.714355 -12.053750 -4.696072
1BIK        A          THR             47                    T -6.685744  5.718591 -12.059565 -4.696078
1BIK        A          SER             48                    T -6.687015  5.703739 -12.056766 -4.694655
1BIK        A          MET             49                    T -6.693981  5.667921 -12.036181 -4.688354
1BIK        A          ALA             50                    E -7.356572  6.209311 -11.847988 -4.410173
1BIK        A          CYS             51                    E -9.912666 10.401803 -14.629141 -5.056859
1BIK        A          GLU             52                    E -10.250068 12.270061 -14.226457 -5.332161
1BIK        A          THR             53                    E -10.249435 12.377410 -14.182819 -5.340911
1BIK        A          PHE             54                    E -10.496708 13.167629 -13.796979 -5.363217
1BIK        A          GLN             55                    E -11.172960 11.005575 -17.249949 -6.052641
1BIK        A          TYR             56                    E -8.810700  7.717965 -13.960771 -5.207136
1BIK        A          GLY             57                    C -4.696891  4.795439 -10.343633 -5.207451
1BIK        A          GLY             58                    C -4.615770  4.830418 -10.668125 -5.316627
1BIK        A          CYS             59                    C -4.552649  4.786288 -10.825725 -5.328348
1BIK        A          MET             60                    C -4.546597  4.803307 -10.850896 -5.333335
1BIK        A          GLY             61                    C -4.546624  4.802745 -10.851995 -5.334108
1BIK        A          ASN             62                    T -5.431446  4.834281 -12.610055 -5.767223
1BIK        A          GLY             63                    T -5.850032  4.596507 -12.339709 -5.469164
1BIK        A          ASN             64                    T -7.226180  6.498654 -13.450961 -5.845479
1BIK        A          ASN             65                    T -8.850779  7.096903 -15.705586 -6.296705
1BIK        A          PHE             66                    B -11.674761 11.493277 -17.672070 -6.028193
1BIK        A          VAL             67                    C -9.134860  8.478098 -14.110005 -5.320513
1BIK        A          THR             68                    C -9.101708  8.492829 -14.232657 -5.341686
1BIK        A          GLU             69                    H -9.101918  8.491939 -14.231095 -5.341579
1BIK        A          LYS             70                    H -9.101700  8.491558 -14.233236 -5.341810
1BIK        A          GLU             71                    H -9.102599  8.476078 -14.236073 -5.341605
1BIK        A          CYS             72                    H -10.706942  8.960090 -16.740322 -5.752365
1BIK        A          LEU             73                    H -11.955331  9.599764 -18.632648 -5.876541
1BIK        A          GLN             74                    H -11.929346  9.572854 -18.691797 -5.877888
1BIK        A          THR             75                    H -11.226737  8.673649 -17.202480 -5.283699
1BIK        A          CYS             76                    H -10.818743  7.858288 -16.903344 -5.049409
1BIK        A          ARG             77                    C -10.718497  7.859108 -16.642584 -4.853057
1BIK        A          THR             78                    C -9.139941  6.111283 -14.031433 -4.145926
1BIK        A          VAL             79                    G -8.284655  5.913925 -13.066322 -4.014627
1BIK        A          ALA             80                    G -8.131071  6.602560 -12.861936 -4.071331
1BIK        A          ALA             81                    G -7.899751  7.120375 -12.591839 -4.113427
1BIK        A          CYS             82                    G -7.393961  7.993385 -11.471024 -4.114844
1BIK        A          ASN             83                    G -6.772806  8.677387 -9.653314 -3.757474
1BIK        A          LEU             84                    C -6.787782  8.937346 -9.461645 -3.729914
1BIK        A          PRO             85                    C -5.893860  9.433258 -7.462773 -3.447033
1BIK        A          ILE             86                    C -5.713846  9.630155 -7.417042 -3.455027
1BIK        A          VAL             87                    C -5.663683  9.461437 -7.596300 -3.496904
1BIK        A          ARG             88                    C -5.308603  8.357648 -7.824098 -3.583080
1BIK        A          GLY             89                    C -4.599716  5.698924 -8.163187 -3.605225
1BIK        A          PRO             90                    C -4.507411  5.712401 -8.125829 -3.596706
1BIK        A          CYS             91                    C -4.498795  5.631469 -8.171527 -3.589373
1BIK        A          ARG             92                    C -4.356307  6.386026 -7.708440 -3.536285
1BIK        A          ALA             93                    C -4.412667  6.357763 -7.654833 -3.524756
1BIK        A          PHE             94                    C -4.834777  8.230100 -6.970450 -3.430622
1BIK        A          ILE             95                    E -5.119656  8.935027 -6.602154 -3.396619
1BIK        A          GLN             96                    E -5.209205  9.220292 -6.282069 -3.399499
1BIK        A          LEU             97                    E -7.020733 11.968440 -7.725510 -3.909906
1BIK        A          TRP             98                    E -9.579359 16.804473 -9.549437 -4.372860
1BIK        A          ALA             99                    E -8.941126 10.351956 -12.647315 -4.722728
1BIK        A          PHE            100                    E -6.815151  7.804462 -10.074194 -4.217024
1BIK        A          ASP            101                    E -2.573685  3.894548 -6.538526 -4.171997
1BIK        A          ALA            102                    T -2.177028  3.835425 -6.587750 -4.133311
1BIK        A          VAL            103                    T -2.128523  3.905645 -6.736331 -4.186989
1BIK        A          LYS            104                    T -2.127672  3.910197 -6.741552 -4.188011
1BIK        A          GLY            105                    T -2.127708  3.910521 -6.741296 -4.188166
1BIK        A          LYS            106                    E -2.520033  3.826570 -6.754428 -4.094276
1BIK        A          CYS            107                    E -3.651908  4.601861 -8.193061 -4.613450
1BIK        A          VAL            108                    E -5.914788  7.393242 -10.014439 -4.692188
1BIK        A          LEU            109                    E -6.920767  9.669368 -9.937724 -4.768021
1BIK        A          PHE            110                    E -9.252856 15.314337 -12.768469 -6.313698
1BIK        A          PRO            111                    E -9.856864 13.354950 -12.909955 -5.051103
1BIK        A          TYR            112                    E -9.797754 10.142939 -14.813323 -5.356527
1BIK        A          GLY            113                    C -6.470288  5.338812 -12.138316 -5.182087
1BIK        A          GLY            114                    C -6.453564  5.351091 -12.216988 -5.190666
1BIK        A          CYS            115                    C -6.450710  5.353593 -12.235115 -5.191477
```

1BIK	A	GLN	116	C	-6.451229	5.347910	-12.234333	-5.191672
1BIK	A	GLY	117	C	-6.452397	5.340440	-12.228615	-5.191112
1BIK	A	ASN	118	T	-8.469181	5.885702	-15.138259	-5.472528
1BIK	A	GLY	119	T	-9.550331	6.213387	-16.092739	-5.393047
1BIK	A	ASN	120	T	-11.007441	8.103614	-17.612551	-5.806178
1BIK	A	LYS	121	T	-12.181829	10.276163	-18.368287	-6.229667
1BIK	A	PHE	122	B	-13.711235	16.220584	-18.181982	-6.410142
1BIK	A	TYR	123	C	-13.352761	14.535040	-18.603977	-6.555435
1BIK	A	SER	124	C	-12.661087	9.972396	-19.716619	-6.313179
1BIK	A	GLU	125	H	-12.535313	9.933685	-19.827477	-6.321148
1BIK	A	LYS	126	H	-12.229601	9.304591	-19.750572	-6.198248
1BIK	A	GLU	127	H	-12.233371	9.127160	-19.929688	-6.268681
1BIK	A	CYS	128	H	-11.237894	10.536051	-18.357543	-7.029112
1BIK	A	ARG	129	H	-9.721049	10.166396	-15.019677	-6.033217
1BIK	A	GLU	130	H	-7.643024	8.796681	-11.721943	-5.087511
1BIK	A	TYR	131	H	-6.816722	8.147039	-10.459141	-4.370228
1BIK	A	CYS	132	H	-6.816722	8.147039	-10.459141	-4.370228
1BIK	A	GLY	133	C	-6.816722	8.147039	-10.459141	-4.370228
1BIK	A	VAL	134	C	-6.816722	8.147039	-10.459141	-4.370228
1BKF	A	GLY	1	C	-6.733960	7.495679	-9.443404	-3.589599
1BKF	A	VAL	2	E	-6.733960	7.495679	-9.443404	-3.589599
1BKF	A	GLN	3	E	-6.733960	7.495679	-9.443404	-3.589599
1BKF	A	VAL	4	E	-6.733960	7.495679	-9.443404	-3.589599
1BKF	A	GLU	5	E	-5.713607	6.564558	-8.994867	-4.086456
1BKF	A	THR	6	E	-3.409409	6.383341	-5.890205	-3.905698
1BKF	A	ILE	7	E	-3.402172	6.374687	-5.940157	-3.909889
1BKF	A	SER	8	E	-3.383398	6.283145	-6.087053	-3.927833
1BKF	A	PRO	9	T	-3.310238	5.922805	-6.454388	-3.951981
1BKF	A	GLY	10	C	-3.184368	5.450192	-6.881360	-4.027853
1BKF	A	ASP	11	T	-3.819236	3.653129	-9.008781	-4.270164
1BKF	A	GLY	12	T	-3.832598	3.616604	-8.984263	-4.270132
1BKF	A	ARG	13	T	-3.873286	3.630932	-8.866521	-4.255509
1BKF	A	THR	14	T	-4.083682	3.839235	-8.713270	-4.313942
1BKF	A	PHE	15	C	-5.614857	6.962314	-9.388667	-4.420044
1BKF	A	PRO	16	C	-6.456830	9.041902	-9.338409	-4.003730
1BKF	A	LYS	17	T	-6.319371	8.610377	-9.742050	-4.266616
1BKF	A	ARG	18	T	-6.268609	8.630091	-9.866995	-4.328341
1BKF	A	GLY	19	T	-6.273566	8.599877	-9.863322	-4.329178
1BKF	A	GLN	20	E	-6.403492	8.211600	-10.156861	-4.445054
1BKF	A	THR	21	E	-6.764838	8.341961	-10.662418	-4.789075
1BKF	A	CYS	22	E	-7.695609	9.000417	-11.356990	-4.967874
1BKF	A	VAL	23	E	-9.712266	11.022684	-13.611948	-5.214035
1BKF	A	VAL	24	E	-10.668615	13.007939	-13.243543	-4.666812
1BKF	A	HIS	25	E	-10.875725	13.132436	-13.007397	-4.602506
1BKF	A	TYR	26	E	-12.346858	15.640762	-15.406358	-5.399106
1BKF	A	THR	27	E	-10.840487	13.856632	-14.250211	-5.679841
1BKF	A	GLY	28	E	-9.660864	10.630542	-13.679061	-5.197120
1BKF	A	MET	29	E	-8.394441	8.811870	-12.708113	-5.072811
1BKF	A	LEU	30	T	-6.175028	5.271889	-10.758465	-4.489116
1BKF	A	GLU	31	T	-4.614835	4.302583	-9.758862	-4.754812
1BKF	A	ASP	32	T	-4.581961	4.599511	-9.746261	-4.774767
1BKF	A	GLY	33	T	-4.581120	4.606042	-9.749187	-4.774954
1BKF	A	LYS	34	C	-4.581891	4.601177	-9.745553	-4.774583
1BKF	A	LYS	35	E	-4.622589	4.559452	-9.676389	-4.795625
1BKF	A	PHE	36	E	-6.293229	9.791484	-9.598558	-5.115245
1BKF	A	ASP	37	E	-8.354017	9.458024	-12.090358	-4.939743
1BKF	A	SER	38	E	-9.835872	11.172503	-13.538894	-5.119935
1BKF	A	SER	39	G	-9.966362	6.178503	-16.530051	-5.234935
1BKF	A	ARG	40	G	-7.787088	3.746497	-14.026187	-4.800044
1BKF	A	ASP	41	G	-5.386600	3.783428	-10.060013	-4.107783
1BKF	A	LYS	42	G	-5.377192	3.844349	-10.076907	-4.107721
1BKF	A	ASN	43	T	-5.346341	4.101813	-10.038653	-4.104282
1BKF	A	LYS	44	T	-5.345760	4.115071	-10.035737	-4.104120
1BKF	A	PRO	45	C	-5.355219	4.122193	-9.972338	-4.093050
1BKF	A	PHE	46	E	-6.947326	8.749377	-9.731913	-4.058491
1BKF	A	LYS	47	E	-7.096685	9.066661	-9.331094	-4.046001
1BKF	A	PHE	48	E	-9.240517	14.618831	-9.658303	-4.307047
1BKF	A	MET	49	E	-8.038045	9.192463	-11.511378	-4.885982
1BKF	A	LEU	50	E	-6.866151	8.067930	-10.884844	-4.878873
1BKF	A	GLY	51	T	-5.144417	6.013777	-9.274312	-4.568201
1BKF	A	LYS	52	T	-5.111446	6.190202	-9.271257	-4.552428
1BKF	A	GLN	53	C	-5.104020	6.245439	-9.270005	-4.545960
1BKF	A	GLU	54	C	-5.107162	6.233955	-9.256706	-4.543199
1BKF	A	VAL	55	C	-5.133996	6.157125	-9.185795	-4.527609
1BKF	A	ILE	56	C	-6.699722	9.577891	-9.246445	-4.232288
1BKF	A	ARG	57	H	-7.623978	10.726756	-9.363203	-4.069996
1BKF	A	GLY	58	H	-8.866052	11.429969	-10.713783	-4.330246
1BKF	A	TRP	59	H	-11.217662	15.576733	-11.798833	-4.338825
1BKF	A	GLU	60	H	-12.311017	13.252736	-16.195996	-5.154505
1BKF	A	GLU	61	H	-10.364523	10.149008	-13.634786	-4.460101
1BKF	A	GLY	62	H	-9.630764	11.435265	-12.392522	-4.461722

1BKF	A	VAL	63	H	-9.623655	11.448100	-12.415758	-4.461659
1BKF	A	ALA	64	H	-9.616025	11.444878	-12.453577	-4.463783
1BKF	A	GLN	65	C	-9.594901	11.393130	-12.567003	-4.487654
1BKF	A	MET	66	C	-9.771682	11.860088	-12.258081	-4.512908
1BKF	A	SER	67	T	-11.137242	10.855446	-15.714237	-4.981992
1BKF	A	VAL	68	T	-11.220588	10.481762	-16.016290	-5.066313
1BKF	A	GLY	69	T	-11.348702	10.285672	-16.173729	-5.170438
1BKF	A	GLN	70	E	-12.271878	10.717354	-17.614447	-5.365728
1BKF	A	ARG	71	E	-12.753884	10.571094	-18.094426	-5.308899
1BKF	A	ALA	72	E	-12.347818	14.122366	-14.890567	-4.753406
1BKF	A	LYS	73	E	-12.259142	15.540786	-13.935553	-4.662150
1BKF	A	LEU	74	E	-11.426259	14.855419	-12.403601	-4.092708
1BKF	A	THR	75	E	-9.136135	11.304576	-10.763063	-4.000299
1BKF	A	ILE	76	E	-8.835259	11.688157	-10.618918	-3.958081
1BKF	A	SER	77	C	-7.882403	11.379066	-9.584048	-3.970312
1BKF	A	PRO	78	G	-7.832646	11.850282	-9.640972	-4.097417
1BKF	A	ASP	79	G	-7.693077	12.417674	-9.794963	-4.369725
1BKF	A	TYR	80	G	-7.707621	12.995285	-9.928177	-4.678259
1BKF	A	ALA	81	C	-6.455432	14.404261	-10.461352	-6.945347
1BKF	A	TYR	82	T	-5.192376	12.329196	-8.796822	-6.176683
1BKF	A	GLY	83	T	-4.413025	9.747580	-7.914416	-5.152812
1BKF	A	ALA	84	T	-3.310730	9.731882	-6.341001	-5.141016
1BKF	A	THR	85	T	-2.361704	5.480443	-5.542427	-3.888477
1BKF	A	GLY	86	T	-1.803394	4.815335	-5.117192	-3.673793
1BKF	A	VAL	87	B	-1.363317	6.328634	-3.834011	-3.527515
1BKF	A	PRO	88	T	-1.338282	6.466337	-3.825013	-3.525533
1BKF	A	GLY	89	T	-1.343354	6.482052	-3.794818	-3.522807
1BKF	A	ILE	90	T	-1.448126	6.743121	-3.411257	-3.432473
1BKF	A	ILE	91	B	-1.712237	7.719332	-2.566643	-3.258646
1BKF	A	PRO	92	T	-2.932304	9.963557	-4.624940	-4.245524
1BKF	A	PRO	93	T	-3.428666	11.742786	-6.159733	-5.774341
1BKF	A	HIS	94	T	-4.355553	12.181573	-7.267461	-5.963798
1BKF	A	ALA	95	T	-5.275705	12.125693	-7.958070	-5.153283
1BKF	A	THR	96	C	-5.595765	11.753405	-7.643465	-4.816575
1BKF	A	LEU	97	E	-7.734209	15.324607	-9.428082	-5.563268
1BKF	A	VAL	98	E	-9.478475	15.169305	-9.985637	-4.470925
1BKF	A	PHE	99	E	-12.032695	17.672555	-11.407226	-4.128457
1BKF	A	ASP	100	E	-13.949320	17.207982	-15.804253	-4.800605
1BKF	A	VAL	101	E	-13.747364	19.384996	-15.464542	-5.704734
1BKF	A	GLU	102	E	-12.017735	18.441742	-13.349790	-5.936717
1BKF	A	LEU	103	E	-9.196810	15.891697	-8.926452	-4.467118
1BKF	A	LEU	104	E	-6.361744	11.363841	-6.549443	-3.607401
1BKF	A	LYS	105	E	-6.361744	11.363841	-6.549443	-3.607401
1BKF	A	LEU	106	E	-6.361744	11.363841	-6.549443	-3.607401
1BKF	A	GLU	107	C	-6.361744	11.363841	-6.549443	-3.607401
1BKR	A	LYS	2	H	-5.514301	3.770435	-10.989812	-3.909980
1BKR	A	SER	3	H	-5.514301	3.770435	-10.989812	-3.909980
1BKR	A	ALA	4	H	-5.514301	3.770435	-10.989812	-3.909980
1BKR	A	LYS	5	H	-5.514301	3.770435	-10.989812	-3.909980
1BKR	A	ASP	6	H	-5.803708	3.899597	-11.497926	-4.302168
1BKR	A	ALA	7	H	-6.514523	4.268917	-12.529867	-4.785684
1BKR	A	LEU	8	H	-8.033162	8.265476	-13.372612	-5.578265
1BKR	A	LEU	9	H	-9.771626	11.200963	-14.835012	-5.822385
1BKR	A	LEU	10	H	-10.374128	11.448987	-13.997521	-4.802139
1BKR	A	TRP	11	H	-12.246690	15.181467	-15.743459	-5.390116
1BKR	A	CYS	12	H	-11.237676	13.030161	-15.582673	-5.906248
1BKR	A	GLN	13	H	-9.909491	11.669871	-13.972823	-5.478910
1BKR	A	MET	14	H	-6.640385	9.510213	-10.091580	-5.065316
1BKR	A	LYS	15	H	-6.600234	9.717640	-10.138187	-5.083451
1BKR	A	THR	16	H	-6.390205	9.650537	-10.083975	-4.903734
1BKR	A	ALA	17	T	-6.172597	9.221723	-10.211060	-4.827432
1BKR	A	GLY	18	T	-6.068051	9.612854	-10.041360	-4.815587
1BKR	A	TYR	19	T	-6.316687	9.846621	-10.013431	-4.673062
1BKR	A	PRO	20	T	-5.728719	10.926794	-8.334021	-4.560790
1BKR	A	ASN	21	T	-5.243072	11.130662	-7.798286	-4.761318
1BKR	A	VAL	22	T	-5.266096	11.277316	-7.702940	-4.773584
1BKR	A	ASN	23	C	-5.291408	11.262171	-7.638738	-4.774416
1BKR	A	ILE	24	C	-5.297188	11.248513	-7.616837	-4.773962
1BKR	A	HIS	25	C	-5.517742	11.094729	-7.704904	-4.891059
1BKR	A	ASN	26	T	-7.391510	9.584298	-10.990150	-4.972382
1BKR	A	PHE	27	T	-9.576480	13.724182	-13.093121	-5.541550
1BKR	A	THR	28	T	-9.953289	13.670193	-13.337741	-5.518202
1BKR	A	THR	29	G	-10.129300	13.039516	-13.476946	-5.482537
1BKR	A	SER	30	G	-11.588311	13.957181	-14.914102	-5.577426
1BKR	A	TRP	31	G	-13.627792	16.294615	-17.172451	-5.590990
1BKR	A	ARG	32	T	-13.121298	12.889421	-17.623447	-5.288946
1BKR	A	ASP	33	T	-12.442231	14.940971	-15.601846	-5.368251
1BKR	A	GLY	34	T	-12.169245	15.397770	-15.370689	-5.425407
1BKR	A	MET	35	H	-12.145761	15.546996	-15.315713	-5.411041
1BKR	A	ALA	36	H	-12.046121	16.024467	-15.001436	-5.321166
1BKR	A	PHE	37	H	-11.944983	17.360270	-14.084706	-5.228676

1BKR	A	ASN	38	H	-11.696266	17.224822	-13.402947	-5.025323
1BKR	A	ALA	39	H	-11.161819	17.211139	-12.246580	-4.818419
1BKR	A	LEU	40	H	-10.857952	17.456895	-12.156467	-4.997965
1BKR	A	ILE	41	H	-10.781344	17.203635	-12.378983	-5.043098
1BKR	A	HIS	42	H	-10.722671	16.375626	-12.829264	-5.047164
1BKR	A	LYS	43	H	-9.697274	10.182300	-13.928025	-4.898860
1BKR	A	HIS	44	H	-8.950632	10.197327	-12.667498	-4.637457
1BKR	A	ARG	45	C	-8.591604	10.784815	-11.895643	-4.444152
1BKR	A	PRO	46	G	-8.062252	10.168037	-11.760823	-4.580843
1BKR	A	ASP	47	G	-8.061276	10.181413	-11.760788	-4.582341
1BKR	A	LEU	48	G	-8.083436	10.331421	-11.634708	-4.575404
1BKR	A	ILE	49	C	-7.815437	10.411096	-11.373868	-4.652906
1BKR	A	ASP	50	C	-7.104624	10.793298	-10.357990	-4.889174
1BKR	A	PHE	51	G	-7.168845	10.926936	-10.233483	-4.919353
1BKR	A	ASP	52	G	-7.164032	10.893512	-10.279149	-4.922103
1BKR	A	LYS	53	G	-7.164861	10.870597	-10.286200	-4.921732
1BKR	A	LEU	54	C	-7.255234	10.877706	-10.201643	-4.957745
1BKR	A	LYS	55	T	-8.250715	6.547940	-14.003903	-4.755428
1BKR	A	LYS	56	T	-8.145312	6.687295	-13.958372	-4.802321
1BKR	A	SER	57	T	-8.027370	7.122300	-13.690587	-4.782315
1BKR	A	ASN	58	T	-8.025252	7.149498	-13.690396	-4.788545
1BKR	A	ALA	59	H	-8.065816	7.124967	-13.612046	-4.775089
1BKR	A	HIS	60	H	-8.517280	8.719913	-13.364592	-4.928226
1BKR	A	TYR	61	H	-8.890010	8.890286	-13.197405	-4.831092
1BKR	A	ASN	62	H	-10.513268	10.059677	-15.588923	-5.430703
1BKR	A	LEU	63	H	-11.736824	13.443567	-15.389092	-5.308098
1BKR	A	GLN	64	H	-12.605718	13.299828	-17.075627	-5.599836
1BKR	A	ASN	65	H	-13.441441	13.032465	-18.845934	-5.699802
1BKR	A	ALA	66	H	-13.671647	13.989524	-18.309486	-5.344261
1BKR	A	PHE	67	H	-13.730024	14.604564	-17.983045	-5.304754
1BKR	A	ASN	68	H	-11.720260	10.065614	-16.699148	-5.204776
1BKR	A	LEU	69	H	-9.841205	11.004373	-13.134134	-4.733856
1BKR	A	ALA	70	H	-9.177219	11.763342	-12.445831	-4.844129
1BKR	A	GLU	71	H	-6.934264	9.565822	-10.615248	-5.142741
1BKR	A	GLN	72	H	-6.815442	10.018792	-10.491830	-5.083793
1BKR	A	HIS	73	H	-6.579972	10.753270	-9.950378	-4.937807
1BKR	A	LEU	74	H	-6.541213	10.877407	-9.961254	-4.942553
1BKR	A	GLY	75	C	-6.142650	10.615621	-9.630168	-4.921072
1BKR	A	LEU	76	C	-6.293444	11.151775	-9.294144	-4.843604
1BKR	A	THR	77	T	-6.191675	11.208763	-9.285305	-4.882575
1BKR	A	LYS	78	T	-6.282085	11.079225	-9.392652	-4.931994
1BKR	A	LEU	79	T	-6.257269	11.137294	-9.344888	-4.900394
1BKR	A	LEU	80	C	-6.541448	11.825464	-9.380984	-4.780394
1BKR	A	ASP	81	C	-6.052494	11.071822	-8.668946	-4.508218
1BKR	A	PRO	82	H	-6.149192	10.972847	-8.552088	-4.402098
1BKR	A	GLU	83	H	-6.132517	10.810451	-8.640157	-4.383431
1BKR	A	ASP	84	H	-6.152277	10.623222	-8.692473	-4.366990
1BKR	A	ILE	85	H	-5.967927	9.880984	-8.755311	-4.257190
1BKR	A	SER	86	H	-5.824770	8.039537	-9.244826	-4.086162
1BKR	A	VAL	87	T	-5.322010	7.232909	-9.108888	-4.087804
1BKR	A	ASP	88	T	-5.299176	7.292984	-9.169408	-4.127375
1BKR	A	HIS	89	T	-5.290761	7.306362	-9.200035	-4.139423
1BKR	A	PRO	90	T	-5.368057	7.079833	-9.240791	-4.139777
1BKR	A	ASP	91	C	-5.563204	6.956163	-9.292434	-4.189412
1BKR	A	GLU	92	H	-6.769768	8.723131	-11.120663	-4.834589
1BKR	A	LYS	93	H	-7.182342	8.857395	-11.337098	-4.531904
1BKR	A	SER	94	H	-7.646544	9.298601	-11.334444	-4.294190
1BKR	A	ILE	95	H	-7.857572	9.957764	-10.806733	-4.168804
1BKR	A	ILE	96	H	-8.062790	10.531802	-10.072718	-3.944721
1BKR	A	THR	97	H	-8.076490	10.534020	-9.993356	-3.925685
1BKR	A	TYR	98	H	-10.582002	16.621314	-11.540817	-4.394533
1BKR	A	VAL	99	H	-10.611112	16.734789	-11.474007	-4.397965
1BKR	A	VAL	100	H	-10.630973	16.314895	-11.943980	-4.575518
1BKR	A	THR	101	H	-10.804873	16.355549	-12.045180	-4.689188
1BKR	A	TYR	102	H	-11.380578	17.588900	-12.480692	-5.089315
1BKR	A	TYR	103	H	-11.086775	18.106217	-13.056796	-5.851046
1BKR	A	HIS	104	H	-9.978845	15.643166	-12.636860	-5.935852
1BKR	A	TYR	105	H	-9.097903	14.241294	-11.480958	-5.302113
1BKR	A	PHE	106	H	-6.994520	10.328563	-8.967819	-4.103921
1BKR	A	SER	107	H	-6.994520	10.328563	-8.967819	-4.103921
1BKR	A	LYS	108	C	-6.994520	10.328563	-8.967819	-4.103921
1BKR	A	MET	109	C	-6.994520	10.328563	-8.967819	-4.103921
1BR9	A	CYS	1	C	-5.938481	3.111527	-10.461754	-3.281209
1BR9	A	SER	2	C	-5.938481	3.111527	-10.461754	-3.281209
1BR9	A	CYS	3	C	-5.938481	3.111527	-10.461754	-3.281209
1BR9	A	SER	4	C	-5.938481	3.111527	-10.461754	-3.281209
1BR9	A	PRO	5	C	-6.436815	4.402745	-10.696872	-3.739011
1BR9	A	VAL	6	C	-7.371480	6.146912	-11.348364	-4.262803
1BR9	A	HIS	7	C	-9.508811	9.972824	-13.839186	-5.554031
1BR9	A	PRO	8	H	-11.453417	14.018759	-15.288100	-5.931355
1BR9	A	GLN	9	H	-12.110104	15.645530	-12.785464	-4.536957

1BR9	A	GLN	10	H	-13.603561	12.209934	-17.302186	-5.024257
1BR9	A	ALA	11	H	-11.577100	10.903608	-14.427185	-4.384196
1BR9	A	PHE	12	H	-11.163896	10.291144	-14.948917	-4.586529
1BR9	A	CYS	13	H	-9.473067	7.151781	-13.590235	-4.207117
1BR9	A	ASN	14	H	-8.954742	8.852394	-12.488599	-4.091302
1BR9	A	ALA	15	T	-8.882301	9.307438	-12.199361	-3.986509
1BR9	A	ASP	16	T	-8.885127	9.325198	-12.174633	-3.981698
1BR9	A	VAL	17	E	-8.887907	9.362295	-12.131149	-3.969995
1BR9	A	VAL	18	E	-9.141492	10.688246	-11.389723	-3.855883
1BR9	A	ILE	19	E	-10.079004	13.235362	-10.217427	-3.282762
1BR9	A	ARG	20	E	-11.085833	15.774896	-11.891308	-4.017877
1BR9	A	ALA	21	E	-10.383459	12.705726	-11.710474	-3.767501
1BR9	A	LYS	22	E	-9.824187	12.749685	-11.581246	-4.183113
1BR9	A	ALA	23	E	-8.866753	10.047368	-11.195697	-3.895011
1BR9	A	VAL	24	E	-7.021077	9.597673	-10.215026	-4.801277
1BR9	A	SER	25	E	-6.944143	9.420455	-10.365363	-4.750728
1BR9	A	GLU	26	E	-6.478042	8.585546	-10.186244	-4.656314
1BR9	A	LYS	27	E	-6.463492	8.539975	-10.254911	-4.658116
1BR9	A	GLU	28	E	-6.364040	8.182703	-10.597836	-4.733165
1BR9	A	VAL	29	E	-6.150759	6.959281	-11.905387	-5.356037
1BR9	A	ASP	30	E	-5.494962	6.739466	-13.471676	-7.346892
1BR9	A	SER	31	E	-4.670279	6.001756	-12.921264	-7.589202
1BR9	A	GLY	32	E	-4.084110	5.448690	-10.659263	-5.970056
1BR9	A	ASN	33	E	-2.845993	4.238580	-6.736997	-4.155855
1BR9	A	ASP	34	T	-1.583094	4.051756	-5.614043	-4.248640
1BR9	A	ILE	35	T	-1.529780	4.102553	-5.697390	-4.233878
1BR9	A	TYR	36	T	-1.529434	4.105079	-5.698416	-4.233797
1BR9	A	GLY	37	T	-1.533547	4.098557	-5.677323	-4.232231
1BR9	A	ASN	38	C	-1.601764	4.041166	-5.532456	-4.209280
1BR9	A	PRO	39	E	-3.004326	4.326891	-6.474341	-3.895344
1BR9	A	ILE	40	E	-4.484663	6.296652	-12.226039	-7.349907
1BR9	A	LYS	41	E	-5.093758	6.714233	-12.699378	-7.798030
1BR9	A	ARG	42	E	-9.179998	11.503048	-18.453877	-9.713707
1BR9	A	ILE	43	E	-11.811520	12.959703	-16.705824	-6.181006
1BR9	A	GLN	44	E	-14.160802	16.859021	-17.189227	-5.681383
1BR9	A	TYR	45	E	-13.684847	16.870061	-16.069282	-5.506413
1BR9	A	GLU	46	E	-9.893860	13.074154	-11.666183	-4.890917
1BR9	A	ILE	47	E	-9.276840	12.533765	-11.584996	-4.845280
1BR9	A	LYS	48	E	-8.973999	12.431671	-11.850042	-5.056589
1BR9	A	GLN	49	E	-8.964926	12.488034	-11.880014	-5.070920
1BR9	A	ILE	50	E	-8.963129	12.495920	-11.888011	-5.072355
1BR9	A	LYS	51	E	-9.090768	12.351476	-11.993703	-5.125240
1BR9	A	MET	52	E	-9.358820	12.684025	-12.290817	-5.289827
1BR9	A	PHE	53	E	-8.663033	10.901708	-10.839219	-4.380606
1BR9	A	LYS	54	E	-8.132581	8.030153	-12.564204	-4.642968
1BR9	A	GLY	55	C	-5.393783	4.654934	-9.319915	-4.057224
1BR9	A	PRO	56	C	-5.363626	4.845980	-9.311084	-4.045507
1BR9	A	GLU	57	C	-5.346000	4.955610	-9.331306	-4.051512
1BR9	A	LYS	58	C	-5.348022	4.936140	-9.326663	-4.050561
1BR9	A	ASP	59	C	-5.351192	4.930529	-9.302802	-4.046376
1BR9	A	ILE	60	C	-6.858967	8.557101	-9.477699	-3.986370
1BR9	A	GLU	61	C	-7.431288	8.639840	-10.021827	-4.255110
1BR9	A	PHE	62	E	-10.734607	14.012404	-13.026338	-4.859973
1BR9	A	ILE	63	E	-10.798156	15.086396	-12.443779	-4.816816
1BR9	A	TYR	64	E	-11.063749	14.958875	-12.557632	-4.505535
1BR9	A	THR	65	E	-9.044171	9.464984	-10.713671	-3.354754
1BR9	A	ALA	66	C	-7.436610	6.823635	-9.250124	-2.758048
1BR9	A	PRO	67	C	-5.536617	4.420561	-7.778998	-2.595242
1BR9	A	SER	68	C	-5.420105	4.283149	-8.168237	-2.693345
1BR9	A	SER	69	G	-5.312508	4.464829	-8.567828	-2.931344
1BR9	A	ALA	70	G	-5.285406	4.549108	-8.628241	-2.961927
1BR9	A	VAL	71	G	-5.279134	4.593172	-8.643292	-2.983372
1BR9	A	CYS	72	C	-5.845055	5.127019	-10.151877	-3.632508
1BR9	A	GLY	73	C	-6.104983	6.045979	-10.262665	-3.913164
1BR9	A	VAL	74	C	-6.648651	7.626307	-9.652653	-3.575814
1BR9	A	SER	75	C	-6.697160	9.256757	-8.999387	-3.666718
1BR9	A	LEU	76	C	-6.291428	9.794087	-8.551931	-4.173020
1BR9	A	ASP	77	C	-5.535997	6.497471	-9.196975	-4.171069
1BR9	A	VAL	78	T	-5.364068	6.520013	-9.279182	-4.208891
1BR9	A	GLY	79	T	-5.326509	6.535402	-9.480876	-4.310957
1BR9	A	GLY	80	T	-5.351487	6.380941	-9.525824	-4.331786
1BR9	A	LYS	81	T	-5.441569	5.872138	-9.699235	-4.332396
1BR9	A	LYS	82	C	-6.018749	6.838750	-10.112685	-4.608966
1BR9	A	GLU	83	E	-6.901381	7.483689	-12.097604	-5.627913
1BR9	A	TYR	84	E	-11.483378	14.384321	-14.245824	-5.262887
1BR9	A	LEU	85	E	-9.814813	13.751241	-9.919273	-3.804296
1BR9	A	ILE	86	E	-8.946400	12.484480	-9.609063	-3.666642
1BR9	A	ALA	87	E	-8.827021	11.899498	-10.187285	-3.777269
1BR9	A	GLY	88	E	-8.118932	8.179069	-12.008498	-4.384954
1BR9	A	LYS	89	E	-7.315854	7.865927	-12.300898	-5.129925
1BR9	A	ALA	90	E	-6.764277	7.113598	-11.937501	-5.110617

```
1BR9        A          GLU             91                   C -6.282119  6.728054 -11.667397 -5.228705
1BR9        A          GLY             92                   T -6.251741  6.853480 -11.672042 -5.236484
1BR9        A          ASP             93                   T -6.269589  6.863319 -11.637938 -5.254633
1BR9        A          GLY             94                   T -6.349997  6.733596 -11.526922 -5.235189
1BR9        A          LYS             95                   E -6.564619  6.753001 -11.458360 -5.300344
1BR9        A          MET             96                   E -7.995769  9.269354 -11.822760 -5.335166
1BR9        A          HIS             97                   E -10.557372 12.690932 -13.901827 -5.014663
1BR9        A          ILE             98                   C -9.226301 10.871051 -11.710596 -4.458158
1BR9        A          THR             99                   T -9.189213 11.028139 -11.774315 -4.485974
1BR9        A          LEU            100                   T -9.178070 11.095961 -11.768406 -4.477927
1BR9        A          CYS            101                   T -9.139353 11.244086 -11.706107 -4.431128
1BR9        A          ASP            102                   T -9.089553 11.774981 -11.317977 -4.319293
1BR9        A          PHE            103                   E -9.854396 14.769064 -10.680917 -4.029096
1BR9        A          ILE            104                   E -9.396026 15.543855 -10.020628 -4.341259
1BR9        A          VAL            105                   E -8.574419 12.414884 -10.036246 -4.152234
1BR9        A          PRO            106                   E -8.248564 13.006827 -9.718928 -4.335686
1BR9        A          TRP            107                   G -8.249010 12.929341 -9.819601 -4.382748
1BR9        A          ASP            108                   G -6.927995  8.052917 -10.000511 -4.219662
1BR9        A          THR            109                   G -6.862596  8.163701 -10.198457 -4.296646
1BR9        A          LEU            110                   C -6.888000  8.021226 -10.205649 -4.305812
1BR9        A          SER            111                   C -6.914752  7.753845 -10.245408 -4.294112
1BR9        A          THR            112                   H -6.916417  7.737604 -10.239963 -4.291623
1BR9        A          THR            113                   H -8.149797  9.636800 -11.767635 -4.934582
1BR9        A          GLN            114                   H -11.353170  9.205797 -16.422004 -4.962271
1BR9        A          LYS            115                   H -11.356751  9.328148 -16.317633 -4.927680
1BR9        A          LYS            116                   H -9.298168  8.199866 -12.832459 -4.317705
1BR9        A          SER            117                   H -9.306312  8.206397 -12.779269 -4.309540
1BR9        A          LEU            118                   H -9.306295  8.207261 -12.778984 -4.309551
1BR9        A          ASN            119                   T -9.306367  8.206704 -12.778240 -4.309385
1BR9        A          HIS            120                   T -9.313854  8.176582 -12.743724 -4.302416
1BR9        A          ARG            121                   T -12.873117 11.842687 -16.867904 -5.043777
1BR9        A          TYR            122                   G -12.125272 11.946963 -16.032318 -5.440098
1BR9        A          GLN            123                   G -8.655710  5.935388 -14.066159 -5.040221
1BR9        A          MET            124                   G -7.987618  6.102795 -14.370698 -5.469378
1BR9        A          GLY            125                   G -7.551369  5.039200 -14.302095 -5.291678
1BR9        A          CYS            126                   T -7.515688  5.193898 -14.276480 -5.280263
1BR9        A          GLU            127                   T -7.508654  5.234258 -14.275580 -5.275581
1BR9        A          CYS            128                   T -7.600348  5.122501 -14.312575 -5.315160
1BR9        A          LYS            129                   E -7.854906  4.578374 -14.205743 -5.122440
1BR9        A          ILE            130                   E -9.008266  8.382816 -13.974174 -5.102747
1BR9        A          THR            131                   E -9.472895  9.651544 -14.188646 -4.941139
1BR9        A          ARG            132                   E -8.289665  9.474916 -11.073444 -4.174578
1BR9        A          CYS            133                   C -3.942592  4.761012 -6.051212 -3.058698
1BR9        A          PRO            134                   C -2.663495  4.333418 -5.643750 -3.379913
1BR9        A          MET            135                   T -2.433789  4.309877 -5.644068 -3.354189
1BR9        A          ILE            136                   T -2.390050  4.445481 -5.644328 -3.346933
1BR9        A          PRO            137                   T -2.374257  4.480899 -5.673922 -3.347618
1BR9        A          CYS            138                   T -2.418934  4.449292 -5.632341 -3.362139
1BR9        A          TYR            139                   C -2.945274  4.643926 -5.631690 -3.229048
1BR9        A          ILE            140                   C -3.759804  6.006678 -5.916007 -3.209704
1BR9        A          SER            141                   C -4.464874  5.835008 -6.935168 -3.353563
1BR9        A          SER            142                   T -5.659774  7.076125 -9.241811 -3.973604
1BR9        A          PRO            143                   T -5.753071  7.027546 -9.155826 -3.975788
1BR9        A          ASP            144                   T -7.184153  6.743254 -10.621855 -3.844658
1BR9        A          GLU            145                   E -8.804834  7.275343 -13.264756 -4.566468
1BR9        A          CYS            146                   E -11.092977  7.549580 -16.932615 -5.176212
1BR9        A          LEU            147                   E -12.795567 10.176924 -18.040643 -5.501439
1BR9        A          TRP            148                   E -15.754764 14.955592 -21.022574 -6.107242
1BR9        A          MET            149                   H -11.536128 11.401031 -15.827503 -5.372416
1BR9        A          ASP            150                   H -11.134739 11.068489 -15.431225 -5.088137
1BR9        A          TRP            151                   H -7.640935  8.744863 -9.887033 -3.984825
1BR9        A          VAL            152                   H -6.667483  7.472191 -9.683318 -4.002160
1BR9        A          THR            153                   H -6.421332  7.248583 -9.873850 -4.014806
1BR9        A          GLU            154                   H -6.370776  7.222367 -10.095643 -4.082074
1BR9        A          LYS            155                   C -6.007527  6.863126 -10.076852 -4.191826
1BR9        A          ASN            156                   T -6.037465  6.753230 -10.124536 -4.213138
1BR9        A          ILE            157                   T -6.230726  6.594317 -10.314879 -4.293146
1BR9        A          ASN            158                   T -6.398339  6.522487 -10.338432 -4.376172
1BR9        A          GLY            159                   T -6.451514  6.483645 -10.126906 -4.332793
1BR9        A          HIS            160                   H -8.525281  7.915604 -12.431533 -4.696959
1BR9        A          GLN            161                   H -10.979895 10.098351 -15.473883 -5.220466
1BR9        A          ALA            162                   H -12.039184 10.611975 -17.129107 -5.436594
1BR9        A          LYS            163                   H -12.621459 12.877890 -17.252955 -5.576385
1BR9        A          PHE            164                   H -12.738174 15.062916 -15.880086 -5.267122
1BR9        A          PHE            165                   C -12.430200 14.486336 -15.678650 -5.141252
1BR9        A          ALA            166                   E -12.402695 14.280278 -15.814112 -5.126993
1BR9        A          CYS            167                   E -12.117484 11.813661 -16.366853 -4.928471
1BR9        A          ILE            168                   E -10.926291  8.478812 -15.447916 -4.592573
1BR9        A          LYS            169                   E -8.883263  5.098090 -15.433911 -5.180493
1BR9        A          ARG            170                   T -7.232291  4.515987 -11.913179 -4.055705
1BR9        A          SER            171                   T -6.830906  4.093666 -12.191695 -4.187270
```

```
1BR9        A          ASP             172                   T -6.826150  4.096297 -12.218852 -4.190878
1BR9        A          GLY             173                   T -6.826616  4.093332 -12.216536 -4.190642
1BR9        A          SER             174                   C -6.844728  4.065404 -12.116689 -4.159311
1BR9        A          CYS             175                   E -7.241032  3.675067 -12.532133 -4.329293
1BR9        A          ALA             176                   E -9.231989  8.796155 -14.314742 -5.411053
1BR9        A          TRP             177                   E -7.917848 12.086192 -10.384142 -5.340353
1BR9        A          TYR             178                   E -4.908857  6.070038 -7.806319 -3.972696
1BR9        A          ARG             179                   C -1.520901  3.690475 -4.006491 -3.173629
1BR9        A          GLY             180                   C -1.520901  3.690475 -4.006491 -3.173629
1BR9        A          ALA             181                   C -1.520901  3.690475 -4.006491 -3.173629
1BR9        A          ALA             182                   C -1.520901  3.690475 -4.006491 -3.173629
1BUO        A          MET               6                   C  3.310986  0.918831 -3.614749 -5.455660
1BUO        A          GLY               7                   C  3.310986  0.918831 -3.614749 -5.455660
1BUO        A          MET               8                   C  3.310986  0.918831 -3.614749 -5.455660
1BUO        A          ILE               9                   C  3.310986  0.918831 -3.614749 -5.455660
1BUO        A          GLN              10                   C  1.223035  1.189859 -3.261444 -3.248465
1BUO        A          LEU              11                   C  1.062922  1.041999 -2.881404 -3.070814
1BUO        A          GLN              12                   C  0.640941  1.246653 -2.352065 -2.674995
1BUO        A          ASN              13                   C -0.045878  1.409598 -2.689587 -2.526321
1BUO        A          PRO              14                   C -0.482544  1.023018 -2.933970 -2.417411
1BUO        A          SER              15                   H -1.267975  1.983884 -4.123352 -2.899855
1BUO        A          HIS              16                   H -1.745247  3.000191 -5.263650 -3.731990
1BUO        A          PRO              17                   H -2.082748  3.086599 -6.419903 -4.407382
1BUO        A          THR              18                   H -2.213202  3.214707 -6.641387 -4.675529
1BUO        A          GLY              19                   H -2.454056  3.219391 -7.182211 -5.088691
1BUO        A          LEU              20                   H -2.950475  3.144618 -7.854431 -5.405378
1BUO        A          LEU              21                   H -4.514589  5.574574 -10.056731 -6.280865
1BUO        A          CYS              22                   H -5.108332  5.706381 -11.051598 -6.798710
1BUO        A          LYS              23                   H -6.740067  6.973850 -13.719181 -7.917629
1BUO        A          ALA              24                   H -10.154769  9.879638 -18.735113 -8.476839
1BUO        A          ASN              25                   H -10.312890  9.663973 -19.577373 -9.230394
1BUO        A          GLN              26                   H -10.785146  9.285373 -19.314227 -8.365107
1BUO        A          MET              27                   H -11.313866  9.689334 -17.861604 -6.858364
1BUO        A          ARG              28                   H -9.025864  6.007459 -12.778566 -4.359544
1BUO        A          LEU              29                   H -6.017799  5.358192 -9.829957 -4.801864
1BUO        A          ALA              30                   H -5.132125  4.881556 -9.171153 -4.431144
1BUO        A          GLY              31                   T -5.125342  4.885557 -9.221527 -4.443409
1BUO        A          THR              32                   T -5.125045  4.886617 -9.223187 -4.443129
1BUO        A          LEU              33                   T -5.125802  4.885403 -9.218724 -4.443201
1BUO        A          CYS              34                   T -5.273446  4.752435 -9.050321 -4.340583
1BUO        A          ASP              35                   C -7.746281  5.333297 -13.549609 -5.426107
1BUO        A          VAL              36                   E -9.508636  7.230153 -12.728757 -3.920292
1BUO        A          VAL              37                   E -10.604155  8.255282 -13.294425 -3.987331
1BUO        A          ILE              38                   E -11.734435 11.155105 -14.008102 -4.195901
1BUO        A          MET              39                   E -10.906051  9.306053 -14.586020 -4.940279
1BUO        A          VAL              40                   E -8.717376  8.381466 -11.380753 -4.231765
1BUO        A          ASP              41                   T -8.714772  8.390161 -11.399523 -4.236156
1BUO        A          SER              42                   T -8.708827  8.414681 -11.417105 -4.234738
1BUO        A          GLN              43                   T -8.706434  8.441384 -11.419052 -4.238843
1BUO        A          GLU              44                   E -8.718249  8.434769 -11.351101 -4.220653
1BUO        A          PHE              45                   E -10.944771 11.636141 -13.509375 -4.511474
1BUO        A          HIS              46                   E -11.071795 11.912973 -13.002923 -4.344507
1BUO        A          ALA              47                   E -11.533184 13.127795 -12.832831 -4.644807
1BUO        A          HIS              48                   C -12.710474 14.480182 -14.810979 -5.167859
1BUO        A          ARG              49                   H -12.450083 13.002131 -14.576687 -4.747553
1BUO        A          THR              50                   H -7.508361  9.945659 -7.665537 -3.266129
1BUO        A          VAL              51                   H -7.464802 10.122437 -7.789165 -3.322752
1BUO        A          LEU              52                   H -7.419440 10.180892 -7.906734 -3.345516
1BUO        A          ALA              53                   H -7.267417  9.670245 -8.438105 -3.517079
1BUO        A          CYS              54                   H -7.252235  9.709754 -8.536731 -3.574189
1BUO        A          THR              55                   H -7.872083  9.277925 -10.150900 -4.144531
1BUO        A          SER              56                   C -7.962062  8.759638 -10.272889 -4.157712
1BUO        A          LYS              57                   H -8.081411  8.285999 -10.477187 -4.276890
1BUO        A          MET              58                   H -9.397226 11.420895 -12.328772 -5.706573
1BUO        A          PHE              59                   H -11.154671 14.819120 -12.040188 -4.522273
1BUO        A          GLU              60                   H -10.587706 12.866152 -12.218702 -4.378385
1BUO        A          ILE              61                   H -10.148778 12.003237 -12.035092 -4.176480
1BUO        A          LEU              62                   H -8.985515 10.809241 -9.818700 -3.578090
1BUO        A          PHE              63                   H -8.471232  8.560677 -10.495265 -3.619099
1BUO        A          HIS              64                   T -7.338578  4.639710 -11.817251 -4.417828
1BUO        A          ARG              65                   T -6.989261  4.375009 -11.693549 -4.165421
1BUO        A          ASN              66                   T -6.990503  4.359759 -11.695232 -4.166533
1BUO        A          SER              67                   C -7.008081  4.169846 -11.764766 -4.187459
1BUO        A          GLN              68                   C -7.037588  4.032438 -11.804872 -4.215646
1BUO        A          HIS              69                   E -7.462504  4.128686 -11.552546 -3.860652
1BUO        A          TYR              70                   E -10.278199 13.718358 -12.497152 -4.976455
1BUO        A          THR              71                   E -8.645154 15.242496 -9.055007 -5.056386
1BUO        A          LEU              72                   E -8.631860 15.288531 -9.032412 -5.029833
1BUO        A          ASP              73                   T -8.622021 15.256679 -9.040074 -5.006428
1BUO        A          PHE              74                   T -8.629519 15.259090 -8.993583 -4.995430
1BUO        A          LEU              75                   T -8.635007 15.212038 -9.000444 -4.997778
```

1BUO	A	SER	76	C	-10.186290	14.096760	-10.568930	-4.122257
1BUO	A	PRO	77	H	-10.564365	13.430735	-11.123048	-4.230173
1BUO	A	LYS	78	H	-11.601395	11.829348	-14.445675	-4.861550
1BUO	A	THR	79	H	-11.622725	11.678824	-14.427473	-4.835432
1BUO	A	PHE	80	H	-12.938680	15.023411	-15.019546	-5.485305
1BUO	A	GLN	81	H	-14.989311	15.774165	-18.060359	-5.654440
1BUO	A	GLN	82	H	-15.591645	16.880275	-19.262908	-6.196746
1BUO	A	ILE	83	H	-14.375799	18.432033	-13.986809	-4.767450
1BUO	A	LEU	84	H	-14.372173	18.502574	-13.966579	-4.770202
1BUO	A	GLU	85	H	-14.272575	18.783461	-14.494901	-5.107356
1BUO	A	TYR	86	H	-13.698873	18.062859	-14.571803	-5.240872
1BUO	A	ALA	87	H	-10.601340	12.463852	-11.166839	-3.947874
1BUO	A	TYR	88	H	-9.148706	14.168961	-8.829213	-4.323078
1BUO	A	THR	89	H	-5.929192	9.454101	-7.595894	-4.835736
1BUO	A	ALA	90	C	-4.813948	8.791523	-5.875520	-3.885646
1BUO	A	THR	91	C	-4.735644	8.789661	-6.139015	-3.966172
1BUO	A	LEU	92	C	-4.629839	8.710528	-6.187221	-3.894336
1BUO	A	GLN	93	C	-4.519874	8.073309	-6.519354	-3.883975
1BUO	A	ALA	94	C	-4.571788	7.916554	-6.459152	-3.800038
1BUO	A	LYS	95	C	-5.062241	6.937990	-7.614916	-3.909129
1BUO	A	ALA	96	G	-5.205481	6.436063	-7.509128	-3.738015
1BUO	A	GLU	97	G	-5.540587	5.017202	-8.328240	-3.900020
1BUO	A	ASP	98	G	-7.314584	6.059683	-11.822429	-5.205079
1BUO	A	LEU	99	H	-9.034595	6.825883	-13.084805	-4.569516
1BUO	A	ASP	100	H	-11.108735	9.307489	-16.593877	-5.574798
1BUO	A	ASP	101	H	-11.741920	10.200360	-16.265992	-5.107217
1BUO	A	LEU	102	H	-12.216870	12.664520	-15.361437	-4.908125
1BUO	A	LEU	103	H	-11.471325	13.195713	-12.359167	-4.072113
1BUO	A	TYR	104	H	-10.435154	12.916264	-11.747686	-4.647366
1BUO	A	ALA	105	H	-10.210885	13.236739	-10.433616	-3.736113
1BUO	A	ALA	106	H	-10.159140	13.415872	-10.669548	-3.891074
1BUO	A	GLU	107	H	-10.119484	13.586399	-10.708886	-3.932788
1BUO	A	ILE	108	H	-10.155676	13.643086	-10.675674	-3.952362
1BUO	A	LEU	109	H	-10.579922	14.500908	-9.713231	-3.114175
1BUO	A	GLU	110	C	-10.843527	15.141766	-12.766894	-5.203534
1BUO	A	ILE	111	C	-10.991000	15.115362	-12.677248	-5.103059
1BUO	A	GLU	112	H	-10.988743	14.133969	-13.348646	-5.224757
1BUO	A	TYR	113	H	-11.020634	14.066478	-13.459217	-5.287405
1BUO	A	LEU	114	H	-11.019316	14.033911	-13.514105	-5.311741
1BUO	A	GLU	115	H	-11.427403	13.599135	-14.618638	-5.575594
1BUO	A	GLU	116	H	-11.122173	13.197144	-16.506977	-6.954578
1BUO	A	GLN	117	H	-10.108726	12.993154	-15.214809	-7.318593
1BUO	A	CYS	118	H	-8.632142	11.536769	-12.825125	-6.865386
1BUO	A	LEU	119	H	-7.174637	10.697490	-11.361122	-6.849027
1BUO	A	LYS	120	H	-6.162090	8.840150	-9.775081	-5.531998
1BUO	A	MET	121	H	-5.834639	8.774708	-9.437271	-5.259348
1BUO	A	LEU	122	H	-5.018252	7.068797	-6.946727	-3.606067
1BUO	A	GLU	123	H	-3.589038	4.183244	-4.729628	-2.617708
1BUO	A	THR	124	H	-3.589038	4.183244	-4.729628	-2.617708
1BUO	A	ILE	125	H	-3.589038	4.183244	-4.729628	-2.617708
1BUO	A	GLN	126	C	-3.589038	4.183244	-4.729628	-2.617708
1BY2	A	ALA	0	C	-2.992142	4.050994	-6.756895	-3.523535
1BY2	A	VAL	1	C	-2.992142	4.050994	-6.756895	-3.523535
1BY2	A	ASN	2	T	-2.992142	4.050994	-6.756895	-3.523535
1BY2	A	ASP	3	T	-2.992142	4.050994	-6.756895	-3.523535
1BY2	A	GLY	4	T	-3.826432	4.848553	-8.481377	-4.440204
1BY2	A	ASP	5	E	-4.707937	5.777443	-9.798260	-5.218956
1BY2	A	MET	6	E	-6.799727	9.891707	-11.977118	-6.583349
1BY2	A	ARG	7	E	-9.803853	10.752762	-14.997387	-5.657525
1BY2	A	LEU	8	E	-6.288626	6.960494	-10.308498	-4.604429
1BY2	A	ALA	9	E	-5.463053	4.514304	-10.876614	-4.532418
1BY2	A	ASP	10	C	-3.490063	2.893654	-8.666698	-4.353873
1BY2	A	GLY	11	T	-3.415997	2.978420	-8.848394	-4.394012
1BY2	A	GLY	12	T	-3.414098	2.988190	-8.857647	-4.395322
1BY2	A	ALA	13	T	-3.418650	2.957607	-8.846637	-4.393551
1BY2	A	THR	14	T	-3.433042	2.938742	-8.790804	-4.390069
1BY2	A	ASN	15	T	-4.670912	3.670510	-10.210769	-4.674594
1BY2	A	GLN	16	E	-6.783962	6.123044	-11.773027	-4.779818
1BY2	A	GLY	17	E	-8.473906	7.732209	-13.073993	-4.856907
1BY2	A	ARG	18	E	-13.104275	12.815124	-18.304783	-5.735938
1BY2	A	VAL	19	E	-13.482003	14.274607	-17.002900	-5.292626
1BY2	A	GLU	20	E	-13.429552	14.768218	-16.746264	-5.236568
1BY2	A	ILE	21	E	-10.433191	16.219794	-11.490597	-4.969633
1BY2	A	PHE	22	E	-9.233492	13.863062	-11.082120	-4.829088
1BY2	A	TYR	23	E	-8.647330	14.615999	-10.530519	-5.068742
1BY2	A	ARG	24	T	-7.577338	11.445599	-10.605491	-5.005999
1BY2	A	GLY	25	T	-7.542794	11.492239	-10.718387	-5.038959
1BY2	A	GLN	26	E	-7.546605	11.460594	-10.715972	-5.039717
1BY2	A	TRP	27	E	-7.576778	11.354829	-10.702311	-5.052212
1BY2	A	GLY	28	E	-7.640488	10.927867	-10.766444	-5.034133
1BY2	A	THR	29	E	-9.213220	12.324443	-12.700201	-5.569178

1BY2	A	VAL	30	E	-10.973333	13.294856	-14.689007	-5.221020
1BY2	A	CYS	31	B	-11.244341	12.088362	-15.449682	-5.227389
1BY2	A	ASP	32	T	-11.510321	10.420304	-16.313443	-5.195643
1BY2	A	ASN	33	T	-12.563827	11.444834	-18.309896	-5.538705
1BY2	A	LEU	34	T	-10.378626	13.226023	-12.452562	-4.645670
1BY2	A	TRP	35	T	-10.340769	13.195560	-12.583766	-4.652972
1BY2	A	ASP	36	C	-9.678720	10.017727	-13.455751	-4.461544
1BY2	A	LEU	37	H	-9.635686	9.984508	-13.561303	-4.458068
1BY2	A	THR	38	H	-9.631950	9.988995	-13.572354	-4.456517
1BY2	A	ASP	39	H	-9.818246	8.762218	-14.068142	-4.390620
1BY2	A	ALA	40	H	-9.796046	8.818558	-14.045639	-4.363069
1BY2	A	SER	41	H	-10.786620	10.372517	-14.833612	-4.311308
1BY2	A	VAL	42	H	-10.722587	10.782520	-13.926122	-3.871992
1BY2	A	VAL	43	H	-10.200952	10.699408	-13.166637	-3.824354
1BY2	A	CYS	44	H	-8.882449	7.725449	-12.943262	-4.099550
1BY2	A	ARG	45	H	-8.734689	8.537542	-12.639196	-4.111950
1BY2	A	ALA	46	H	-8.608499	9.392489	-12.877511	-4.504753
1BY2	A	LEU	47	H	-8.581161	9.532374	-12.927825	-4.574303
1BY2	A	GLY	48	C	-8.546066	9.742950	-12.976256	-4.688169
1BY2	A	PHE	49	C	-8.700725	12.690312	-12.604906	-5.340223
1BY2	A	GLU	50	C	-7.521250	10.442587	-11.353898	-5.302449
1BY2	A	ASN	51	C	-6.865559	10.745283	-9.909062	-4.816138
1BY2	A	ALA	52	E	-6.665791	11.015590	-9.471577	-4.571380
1BY2	A	THR	53	E	-5.900875	10.615469	-8.253719	-4.372631
1BY2	A	GLN	54	E	-5.899712	10.601624	-8.261246	-4.368600
1BY2	A	ALA	55	E	-5.928175	10.619083	-8.115985	-4.309736
1BY2	A	LEU	56	E	-6.013922	10.555778	-7.954448	-4.260652
1BY2	A	GLY	57	T	-6.073104	10.435078	-7.909734	-4.291065
1BY2	A	ARG	58	T	-8.144933	9.417984	-11.653238	-4.036657
1BY2	A	ALA	59	T	-7.627380	10.143885	-10.775574	-4.367258
1BY2	A	ALA	60	T	-7.319730	10.428396	-10.815958	-4.809327
1BY2	A	PHE	61	T	-7.318048	10.532258	-10.845065	-4.872790
1BY2	A	GLY	62	T	-5.184602	5.077988	-10.372379	-4.908443
1BY2	A	GLN	63	C	-5.090562	5.355797	-10.341669	-4.859123
1BY2	A	GLY	64	C	-5.065549	5.429963	-10.330475	-4.830239
1BY2	A	SER	65	C	-5.071625	5.378241	-10.325101	-4.826461
1BY2	A	GLY	66	C	-5.072236	5.374103	-10.322274	-4.826100
1BY2	A	PRO	67	C	-6.040542	7.220004	-10.165041	-4.481764
1BY2	A	ILE	68	E	-6.817256	7.885787	-10.165213	-4.241773
1BY2	A	MET	69	E	-8.842964	11.817551	-11.327989	-4.593281
1BY2	A	LEU	70	E	-10.106064	14.916450	-11.582953	-4.895334
1BY2	A	ASP	71	T	-11.846705	15.890168	-15.364520	-5.688133
1BY2	A	GLU	72	T	-9.908436	11.231621	-14.017583	-5.511792
1BY2	A	VAL	73	T	-8.723225	9.193223	-13.619090	-5.415480
1BY2	A	GLN	74	B	-6.567087	5.706964	-12.370978	-5.327817
1BY2	A	CYS	75	C	-5.066306	5.382078	-10.375026	-5.054521
1BY2	A	THR	76	T	-4.058232	4.889653	-8.859764	-4.541270
1BY2	A	GLY	77	T	-4.056702	4.891973	-8.870229	-4.542208
1BY2	A	THR	78	T	-4.056845	4.891043	-8.869084	-4.541938
1BY2	A	GLU	79	T	-4.065260	4.880577	-8.819215	-4.530594
1BY2	A	ALA	80	C	-4.174711	4.791365	-8.535894	-4.426079
1BY2	A	SER	81	C	-7.221958	7.762886	-11.999225	-4.700729
1BY2	A	LEU	82	G	-7.258770	9.664756	-10.939378	-4.603161
1BY2	A	ALA	83	G	-6.859155	8.380474	-11.355929	-4.731218
1BY2	A	ASP	84	G	-6.815541	8.347460	-11.485381	-4.759534
1BY2	A	CYS	85	C	-6.778596	7.741642	-11.958246	-4.904000
1BY2	A	LYS	86	B	-6.728037	8.229914	-11.734726	-4.932918
1BY2	A	SER	87	C	-6.853956	8.105663	-11.900026	-4.987545
1BY2	A	LEU	88	C	-7.141754	9.619341	-11.633539	-5.021057
1BY2	A	GLY	89	T	-7.146907	10.128050	-11.339823	-4.999964
1BY2	A	TRP	90	T	-6.850984	12.213357	-9.392499	-4.817271
1BY2	A	LEU	91	T	-5.987581	7.735052	-10.310998	-4.832051
1BY2	A	LYS	92	T	-5.711431	6.875239	-10.613025	-4.761404
1BY2	A	SER	93	C	-5.707919	6.789052	-10.677382	-4.769468
1BY2	A	ASN	94	C	-5.704919	6.736155	-10.717826	-4.772246
1BY2	A	CYS	95	C	-5.761701	6.197521	-10.904318	-4.775498
1BY2	A	ARG	96	C	-6.234308	5.629430	-11.309075	-4.682679
1BY2	A	HIS	97	G	-7.656614	6.772275	-13.250012	-5.041054
1BY2	A	GLU	98	G	-8.184784	6.919600	-13.400127	-5.076402
1BY2	A	ARG	99	G	-12.233742	9.486290	-18.562680	-5.380280
1BY2	A	ASP	100	B	-11.443284	10.500581	-15.110797	-4.318824
1BY2	A	ALA	101	C	-10.022086	10.113861	-13.201045	-4.209047
1BY2	A	GLY	102	E	-9.997349	10.252327	-13.400349	-4.352114
1BY2	A	VAL	103	E	-9.777669	10.949911	-14.048057	-5.092012
1BY2	A	VAL	104	E	-8.301269	9.336818	-13.742627	-6.006711
1BY2	A	CYS	105	E	-5.755776	7.195567	-10.408487	-5.257684
1BY2	A	THR	106	C	-3.545855	5.982054	-6.632380	-4.009157
1BY2	A	ASN	107	C	-3.545855	5.982054	-6.632380	-4.009157
1BY2	A	GLU	108	C	-3.545855	5.982054	-6.632380	-4.009157
1BY2	A	THR	109	C	-3.545855	5.982054	-6.632380	-4.009157
1BYQ	A	PRO	11	C	-0.056100	0.187493	-4.294811	-3.123981

```
1BYQ        A          MET             12                 C -0.056100  0.187493 -4.294811 -3.123981
1BYQ        A          GLU             13                 C -0.056100  0.187493 -4.294811 -3.123981
1BYQ        A          GLU             14                 C -0.056100  0.187493 -4.294811 -3.123981
1BYQ        A          GLU             15                 C -1.781001  1.958661 -5.478957 -3.290630
1BYQ        A          GLU             16                 C -2.757012  3.480464 -7.416471 -4.455605
1BYQ        A          VAL             17                 E -3.061886  4.196861 -7.372348 -4.775751
1BYQ        A          GLU             18                 E -5.044427  6.880942 -11.189301 -6.367031
1BYQ        A          THR             19                 E -5.351408  7.920586 -11.049010 -6.640556
1BYQ        A          PHE             20                 E -7.239395 11.185089 -9.934168 -4.822908
1BYQ        A          ALA             21                 E -7.676076 11.241978 -8.918781 -4.106907
1BYQ        A          PHE             22                 C -10.707378 15.679589 -10.714764 -4.104094
1BYQ        A          GLN             23                 C -11.498306 12.283530 -13.667766 -3.889952
1BYQ        A          ALA             24                 H -10.242851 10.527854 -11.926392 -3.598748
1BYQ        A          GLU             25                 H -10.233306 10.597486 -11.970608 -3.627580
1BYQ        A          ILE             26                 H -10.243188 10.595735 -11.919171 -3.617287
1BYQ        A          ALA             27                 H -10.241807 10.596625 -11.923615 -3.615270
1BYQ        A          GLN             28                 H -10.282313 10.574303 -11.798423 -3.605594
1BYQ        A          LEU             29                 H -12.225987 14.882542 -14.422280 -4.676220
1BYQ        A          MET             30                 H -12.737399 15.148875 -13.801433 -3.806244
1BYQ        A          SER             31                 H -11.041165 11.064081 -11.793717 -2.915034
1BYQ        A          LEU             32                 H -9.577173 11.537959 -9.532236 -2.858914
1BYQ        A          ILE             33                 H -8.558315 10.815677 -8.958753 -3.004020
1BYQ        A          ILE             34                 H -8.504692 10.846720 -9.111968 -3.044824
1BYQ        A          ASN             35                 H -8.423895 10.723554 -9.640644 -3.269309
1BYQ        A          THR             36                 C -8.422095 10.720742 -9.668292 -3.285345
1BYQ        A          PHE             37                 C -8.502665 10.599898 -9.732737 -3.353676
1BYQ        A          TYR             38                 T -9.317613 10.427883 -12.391369 -4.294000
1BYQ        A          SER             39                 T -9.563926 10.042783 -13.257783 -4.718281
1BYQ        A          ASN             40                 T -10.788023 11.164444 -13.249884 -4.121993
1BYQ        A          LYS             41                 T -11.726532 12.917722 -13.591478 -4.362042
1BYQ        A          GLU             42                 H -13.069890 13.444906 -16.029472 -4.901706
1BYQ        A          ILE             43                 H -13.083215 13.435187 -15.984213 -4.895384
1BYQ        A          PHE             44                 H -14.010655 18.432887 -16.361064 -6.040335
1BYQ        A          LEU             45                 H -14.881653 20.339498 -15.152934 -4.951490
1BYQ        A          ARG             46                 H -15.244282 17.467713 -17.265479 -4.836159
1BYQ        A          GLU             47                 H -13.782820 13.656896 -15.278127 -3.928314
1BYQ        A          LEU             48                 H -13.193203 13.150255 -14.800074 -3.714022
1BYQ        A          ILE             49                 H -13.122458 12.912690 -15.038986 -3.722035
1BYQ        A          SER             50                 H -12.791140 10.288317 -17.174648 -4.348231
1BYQ        A          ASN             51                 H -12.656292  9.777319 -17.353916 -4.286063
1BYQ        A          SER             52                 H -12.601272  9.607506 -17.243930 -4.186040
1BYQ        A          SER             53                 H -12.358666  9.252696 -16.568922 -3.906376
1BYQ        A          ASP             54                 H -10.975292  9.199587 -13.065143 -3.191951
1BYQ        A          ALA             55                 H -10.893747  9.808100 -13.110729 -3.343033
1BYQ        A          LEU             56                 H -10.890068  9.895430 -13.077034 -3.342069
1BYQ        A          ASP             57                 H -10.774165 10.045427 -13.110312 -3.363508
1BYQ        A          LYS             58                 H -10.766617 10.231915 -13.125423 -3.427990
1BYQ        A          ILE             59                 H -11.202107 12.482139 -13.759019 -4.054499
1BYQ        A          ARG             60                 H -10.889584 11.422553 -15.205013 -4.916764
1BYQ        A          TYR             61                 H -9.430690  9.815192 -12.810483 -4.404743
1BYQ        A          GLU             62                 H -8.087326  8.801647 -10.375600 -3.730808
1BYQ        A          THR             63                 H -5.849905  5.536489 -7.335344 -2.528624
1BYQ        A          LEU             64                 T -5.246171  4.930218 -7.000509 -2.305018
1BYQ        A          THR             65                 T -5.172683  4.978003 -7.404086 -2.499466
1BYQ        A          ASP             66                 T -5.118264  5.182875 -7.466356 -2.554765
1BYQ        A          PRO             67                 T -5.102798  5.225833 -7.486584 -2.560417
1BYQ        A          SER             68                 T -5.293404  5.142950 -7.581577 -2.586225
1BYQ        A          LYS             69                 T -5.985732  6.410200 -9.335473 -3.508732
1BYQ        A          LEU             70                 T -6.040825  7.032579 -9.417392 -3.772490
1BYQ        A          ASP             71                 C -6.019646  5.650259 -10.430315 -4.025744
1BYQ        A          SER             72                 C -5.753571  6.282323 -9.489159 -3.884711
1BYQ        A          GLY             73                 C -5.686104  6.445050 -9.415070 -3.857140
1BYQ        A          LYS             74                 C -5.688019  6.445619 -9.401956 -3.853926
1BYQ        A          GLU             75                 C -5.838741  6.398109 -8.959302 -3.600154
1BYQ        A          LEU             76                 C -6.070732  7.470547 -8.197231 -3.521387
1BYQ        A          HIS             77                 C -6.967024  7.884338 -8.942760 -3.631028
1BYQ        A          ILE             78                 E -9.239554 11.676099 -9.684556 -3.451518
1BYQ        A          ASN             79                 E -11.139860 15.173445 -13.087440 -4.865034
1BYQ        A          LEU             80                 E -11.819052 17.549262 -11.890614 -3.960122
1BYQ        A          ILE             81                 E -11.759447 15.409885 -12.914028 -3.955340
1BYQ        A          PRO             82                 E -10.772204  9.093119 -14.252287 -4.084802
1BYQ        A          ASN             83                 E -10.503987  7.790836 -15.086479 -4.304367
1BYQ        A          LYS             84                 G -10.293843  7.871319 -15.037023 -4.358143
1BYQ        A          GLN             85                 G -10.268622  7.953900 -15.103096 -4.401779
1BYQ        A          ASP             86                 G -10.262975  8.090679 -15.041774 -4.401968
1BYQ        A          ARG             87                 C -10.521197  8.195950 -15.355466 -4.567168
1BYQ        A          THR             88                 E -10.719473 10.747054 -13.952544 -4.341732
1BYQ        A          LEU             89                 E -11.301021 14.993134 -12.406892 -4.129093
1BYQ        A          THR             90                 E -11.464534 16.469514 -11.130468 -3.722028
1BYQ        A          ILE             91                 E -11.253978 15.150384 -11.538891 -3.701331
1BYQ        A          VAL             92                 E -11.047809 14.374391 -11.841333 -3.691317
```

1BYQ	A	ASP	93	E	-10.258716	11.642470	-12.083386	-3.971122
1BYQ	A	THR	94	C	-9.507555	12.173606	-10.993901	-4.061090
1BYQ	A	GLY	95	C	-8.679673	12.322445	-11.568988	-5.112383
1BYQ	A	ILE	96	C	-8.678856	12.341607	-11.569609	-5.118277
1BYQ	A	GLY	97	C	-8.664347	12.320970	-11.595653	-5.103173
1BYQ	A	MET	98	C	-8.695216	12.372250	-11.590677	-5.163938
1BYQ	A	THR	99	C	-8.791042	12.338329	-11.821479	-5.339101
1BYQ	A	LYS	100	H	-10.159840	12.018612	-12.600835	-4.213451
1BYQ	A	ALA	101	H	-9.762515	11.570787	-11.785714	-3.822087
1BYQ	A	ASP	102	H	-9.867743	11.576186	-11.629071	-3.702516
1BYQ	A	LEU	103	H	-9.873470	11.666990	-11.537067	-3.675886
1BYQ	A	ILE	104	H	-9.875528	11.635270	-11.501069	-3.633731
1BYQ	A	ASN	105	H	-9.605179	10.958878	-12.479758	-4.172703
1BYQ	A	ASN	106	H	-9.790123	10.412423	-13.366922	-4.425933
1BYQ	A	LEU	107	H	-9.036063	10.009355	-10.819772	-3.373828
1BYQ	A	GLY	108	C	-8.394717	8.435128	-10.701444	-3.287359
1BYQ	A	THR	109	C	-7.800779	7.391097	-9.929999	-2.871001
1BYQ	A	ILE	110	C	-6.588077	5.849528	-10.460347	-3.802722
1BYQ	A	ALA	111	C	-6.524345	5.988481	-10.427674	-3.756746
1BYQ	A	LYS	112	C	-6.509013	6.027971	-10.429938	-3.751715
1BYQ	A	SER	113	C	-6.271265	6.572737	-9.563148	-3.469176
1BYQ	A	GLY	114	H	-6.299482	6.574502	-9.565189	-3.511263
1BYQ	A	THR	115	H	-6.754677	7.671772	-8.428452	-3.011880
1BYQ	A	LYS	116	H	-6.851202	7.760525	-8.122871	-2.952207
1BYQ	A	ALA	117	H	-6.889998	7.733275	-7.973896	-2.922616
1BYQ	A	PHE	118	H	-9.710042	14.583140	-9.974393	-3.808658
1BYQ	A	MET	119	H	-10.116677	14.772861	-11.336387	-4.191896
1BYQ	A	GLU	120	H	-7.851098	8.761952	-10.315299	-3.791829
1BYQ	A	ALA	121	H	-7.054126	8.150109	-8.837053	-3.104509
1BYQ	A	LEU	122	H	-6.177011	7.814838	-7.324361	-2.767572
1BYQ	A	GLN	123	H	-5.514214	5.577672	-7.931956	-2.903809
1BYQ	A	ALA	124	C	-5.365192	6.066607	-7.668526	-2.856590
1BYQ	A	GLY	125	C	-5.365322	6.065447	-7.681348	-2.866493
1BYQ	A	ALA	126	C	-5.391144	5.982059	-7.653527	-2.866702
1BYQ	A	ASP	127	C	-5.527037	5.535545	-7.853400	-2.917836
1BYQ	A	ILE	128	G	-6.216876	7.839479	-7.031812	-2.803382
1BYQ	A	SER	129	G	-7.783489	8.807024	-11.162417	-4.354291
1BYQ	A	MET	130	G	-8.041875	11.954521	-9.886834	-4.324621
1BYQ	A	ILE	131	G	-7.641357	11.699288	-9.257241	-4.038076
1BYQ	A	GLY	132	G	-7.276086	10.973511	-8.778402	-3.702621
1BYQ	A	GLN	133	G	-7.193718	11.006931	-8.737302	-3.651812
1BYQ	A	PHE	134	G	-7.216792	11.084602	-8.657731	-3.657468
1BYQ	A	GLY	135	C	-7.344987	10.754288	-8.423556	-3.446762
1BYQ	A	VAL	136	C	-7.560377	10.461935	-8.313238	-3.318852
1BYQ	A	GLY	137	G	-8.379059	11.400772	-8.553408	-3.342389
1BYQ	A	PHE	138	G	-10.666374	17.083848	-10.730240	-4.466900
1BYQ	A	TYR	139	G	-10.942604	17.026311	-11.623031	-5.062190
1BYQ	A	SER	140	G	-12.760507	19.127857	-12.157337	-4.228553
1BYQ	A	ALA	141	G	-12.471848	19.493723	-10.620321	-3.597988
1BYQ	A	TYR	142	G	-12.563956	19.671844	-10.440792	-3.527348
1BYQ	A	LEU	143	G	-11.323864	15.964644	-10.883957	-3.859670
1BYQ	A	VAL	144	C	-10.681242	14.518059	-10.628914	-3.546458
1BYQ	A	ALA	145	E	-10.460619	14.135402	-11.679776	-4.093449
1BYQ	A	GLU	146	E	-10.396940	14.082915	-11.779632	-4.119094
1BYQ	A	LYS	147	E	-10.310057	14.282286	-11.560365	-4.007914
1BYQ	A	VAL	148	E	-10.177754	14.226545	-10.934902	-3.663052
1BYQ	A	THR	149	E	-10.363920	14.394527	-11.141164	-3.768494
1BYQ	A	VAL	150	E	-10.545759	14.770077	-10.124296	-3.218037
1BYQ	A	ILE	151	E	-10.646670	14.794083	-9.746214	-3.041645
1BYQ	A	THR	152	E	-10.800159	14.460247	-9.741594	-2.989160
1BYQ	A	LYS	153	E	-11.521898	10.071843	-15.317979	-4.541212
1BYQ	A	HIS	154	T	-10.809421	8.739300	-15.222159	-4.693600
1BYQ	A	ASN	155	T	-10.690843	8.688713	-15.877957	-5.033042
1BYQ	A	ASP	156	T	-10.641926	8.986564	-15.839263	-5.052771
1BYQ	A	ASP	157	T	-10.649285	8.978303	-15.827177	-5.058297
1BYQ	A	GLU	158	C	-10.765733	8.922625	-15.886410	-5.141415
1BYQ	A	GLN	159	E	-11.451943	9.907544	-17.681082	-6.113203
1BYQ	A	TYR	160	E	-12.120475	12.524250	-15.429184	-5.265675
1BYQ	A	ALA	161	E	-13.831252	14.401443	-16.194554	-4.634255
1BYQ	A	TRP	162	E	-13.901239	14.147211	-15.650506	-4.018066
1BYQ	A	GLU	163	E	-9.642839	7.411929	-12.614879	-3.671158
1BYQ	A	SER	164	E	-7.079415	5.501552	-9.619127	-3.123434
1BYQ	A	SER	165	C	-4.948548	5.791521	-8.566198	-4.119389
1BYQ	A	ALA	166	T	-4.941366	5.849106	-8.559768	-4.110466
1BYQ	A	GLY	167	T	-4.941092	5.851397	-8.560637	-4.110197
1BYQ	A	GLY	168	T	-4.941303	5.850857	-8.559193	-4.110352
1BYQ	A	SER	169	E	-4.957362	5.861083	-8.531064	-4.137617
1BYQ	A	PHE	170	E	-7.537273	10.577563	-8.118449	-3.382429
1BYQ	A	THR	171	E	-9.486930	10.819270	-10.451509	-3.528878
1BYQ	A	VAL	172	E	-12.058712	14.084177	-16.532342	-6.274594
1BYQ	A	ARG	173	E	-9.329738	10.151052	-17.877326	-9.174426

1BYQ	A	THR	174	E	-7.739734	7.660142	-12.624399	-5.318473
1BYQ	A	ASP	175	C	-3.962245	3.938367	-10.005712	-5.692564
1BYQ	A	THR	176	C	-3.865016	4.245947	-10.139912	-5.746227
1BYQ	A	GLY	177	C	-3.758122	4.266151	-9.770212	-5.389073
1BYQ	A	GLU	178	C	-3.758133	4.265963	-9.769706	-5.388687
1BYQ	A	PRO	179	C	-3.758787	4.262443	-9.766957	-5.389037
1BYQ	A	MET	180	C	-4.489902	5.054480	-9.173765	-4.636925
1BYQ	A	GLY	181	C	-4.826806	4.358421	-7.873142	-3.566196
1BYQ	A	ARG	182	C	-9.288491	9.046714	-12.519686	-4.243521
1BYQ	A	GLY	183	E	-9.568257	11.829707	-11.134337	-3.957892
1BYQ	A	THR	184	E	-9.874600	14.133787	-9.682401	-3.676649
1BYQ	A	LYS	185	E	-9.842915	14.437163	-9.681038	-3.724885
1BYQ	A	VAL	186	E	-9.838707	14.516818	-9.631485	-3.706601
1BYQ	A	ILE	187	E	-9.838854	14.521244	-9.627531	-3.706070
1BYQ	A	LEU	188	E	-10.961068	17.865064	-10.408342	-4.117997
1BYQ	A	HIS	189	E	-11.114206	16.440082	-12.040762	-4.591209
1BYQ	A	LEU	190	E	-11.004999	11.526188	-15.280885	-5.234713
1BYQ	A	LYS	191	T	-9.381403	8.261146	-13.701900	-4.852334
1BYQ	A	GLU	192	T	-8.578710	8.020267	-12.651883	-4.613557
1BYQ	A	ASP	193	T	-8.577872	8.026942	-12.655112	-4.614324
1BYQ	A	GLN	194	T	-8.579898	8.016020	-12.649025	-4.614950
1BYQ	A	THR	195	G	-8.585989	7.998555	-12.607674	-4.602256
1BYQ	A	GLU	196	G	-8.753358	7.961119	-12.295895	-4.532950
1BYQ	A	TYR	197	G	-12.072830	14.647045	-14.827104	-5.181948
1BYQ	A	LEU	198	G	-12.569369	16.283531	-15.097931	-5.293003
1BYQ	A	GLU	199	C	-12.547616	15.753014	-15.215819	-5.171030
1BYQ	A	GLU	200	H	-12.757861	13.914097	-15.511069	-4.416026
1BYQ	A	ARG	201	H	-12.596343	12.126319	-15.715785	-4.066265
1BYQ	A	ARG	202	H	-12.691578	11.317267	-16.201670	-4.071396
1BYQ	A	ILE	203	H	-11.215263	14.218813	-11.008762	-3.430682
1BYQ	A	LYS	204	H	-9.698046	10.911517	-10.601458	-3.345126
1BYQ	A	GLU	205	H	-9.572712	10.710106	-11.375863	-3.659158
1BYQ	A	ILE	206	H	-9.549059	10.747179	-11.444652	-3.672074
1BYQ	A	VAL	207	H	-9.539683	10.738086	-11.494733	-3.678089
1BYQ	A	LYS	208	H	-9.568272	10.506119	-11.586266	-3.700514
1BYQ	A	LYS	209	H	-10.355437	10.115965	-14.546373	-4.734346
1BYQ	A	HIS	210	H	-10.254569	10.957322	-14.367867	-5.083479
1BYQ	A	SER	211	H	-8.036436	8.003039	-10.833928	-3.958744
1BYQ	A	GLN	212	T	-7.926960	8.601816	-10.677575	-3.958524
1BYQ	A	PHE	213	T	-7.392128	10.339329	-8.835184	-3.621797
1BYQ	A	ILE	214	T	-6.892531	11.991070	-7.041215	-3.341741
1BYQ	A	GLY	215	C	-6.690771	11.764294	-7.614114	-3.616207
1BYQ	A	TYR	216	C	-6.753851	12.194702	-7.261182	-3.580960
1BYQ	A	PRO	217	C	-6.717846	12.479471	-7.214898	-3.639429
1BYQ	A	ILE	218	E	-6.513182	13.582935	-6.477748	-3.769026
1BYQ	A	THR	219	E	-6.187754	12.119509	-6.231801	-3.464993
1BYQ	A	LEU	220	E	-4.986245	10.690853	-5.676388	-3.690144
1BYQ	A	PHE	221	C	-4.986245	10.690853	-5.676388	-3.690144
1BYQ	A	VAL	222	C	-4.986245	10.690853	-5.676388	-3.690144
1BYQ	A	GLU	223	C	-4.986245	10.690853	-5.676388	-3.690144
1CBS	A	PRO	1	C	-10.672284	10.526783	-14.211039	-4.410769
1CBS	A	ASN	2	C	-10.672284	10.526783	-14.211039	-4.410769
1CBS	A	PHE	3	C	-10.672284	10.526783	-14.211039	-4.410769
1CBS	A	SER	4	C	-10.672284	10.526783	-14.211039	-4.410769
1CBS	A	GLY	5	E	-11.031583	13.582464	-14.490604	-5.414432
1CBS	A	ASN	6	E	-10.696065	15.799087	-12.617229	-5.181321
1CBS	A	TRP	7	E	-10.251650	16.144012	-11.575005	-4.794798
1CBS	A	LYS	8	E	-8.038348	11.442182	-9.830272	-4.255928
1CBS	A	ILE	9	E	-7.598485	10.598483	-10.139812	-4.216802
1CBS	A	ILE	10	E	-7.405162	10.035219	-10.657659	-4.350376
1CBS	A	ARG	11	E	-7.405846	10.022991	-10.659834	-4.349968
1CBS	A	SER	12	E	-7.408309	9.995643	-10.660981	-4.349859
1CBS	A	GLU	13	E	-7.651385	9.321601	-11.108880	-4.405564
1CBS	A	ASN	14	T	-8.154402	8.652313	-12.035022	-4.708441
1CBS	A	PHE	15	H	-10.938840	14.068665	-14.865748	-5.583996
1CBS	A	GLU	16	H	-11.170720	15.198804	-14.912743	-5.781319
1CBS	A	GLU	17	H	-10.880173	15.307864	-13.708203	-5.256871
1CBS	A	LEU	18	H	-10.927924	16.008572	-13.076178	-5.025038
1CBS	A	LEU	19	H	-9.829520	13.386911	-11.932393	-4.650146
1CBS	A	LYS	20	H	-8.535570	11.108705	-11.204132	-4.489032
1CBS	A	VAL	21	H	-8.097841	10.631448	-11.053784	-4.350428
1CBS	A	LEU	22	H	-7.795669	9.526042	-11.566875	-4.422355
1CBS	A	GLY	23	C	-5.683063	4.027794	-10.657628	-4.201723
1CBS	A	VAL	24	C	-5.426597	4.254814	-10.506310	-4.083361
1CBS	A	ASN	25	C	-5.423726	4.246231	-10.526191	-4.085674
1CBS	A	VAL	26	H	-5.425252	4.219357	-10.532591	-4.085249
1CBS	A	MET	27	H	-5.429340	4.193823	-10.520939	-4.081999
1CBS	A	LEU	28	H	-6.022497	4.765646	-10.342011	-3.891949
1CBS	A	ARG	29	H	-7.954229	6.813681	-13.245110	-4.573086
1CBS	A	LYS	30	H	-7.677176	6.704522	-11.337692	-3.469374
1CBS	A	ILE	31	H	-7.708151	6.893951	-11.048600	-3.335486

1CBS	A	ALA	32	H	-7.708412	6.924622	-11.007125	-3.319251
1CBS	A	VAL	33	H	-7.713676	6.854236	-10.866460	-3.200454
1CBS	A	ALA	34	H	-7.696001	6.831035	-10.942026	-3.209234
1CBS	A	ALA	35	H	-8.712345	8.205691	-12.252530	-3.452116
1CBS	A	ALA	36	H	-9.092350	7.922913	-13.362858	-3.733378
1CBS	A	SER	37	T	-9.130219	7.835286	-13.561997	-3.819659
1CBS	A	LYS	38	T	-9.312939	7.958593	-13.754899	-3.932665
1CBS	A	PRO	39	T	-9.713855	9.499386	-13.633511	-4.038971
1CBS	A	ALA	40	E	-9.723302	9.833367	-13.544664	-4.105773
1CBS	A	VAL	41	E	-9.906278	10.465992	-13.243228	-4.133293
1CBS	A	GLU	42	E	-10.524878	12.617217	-13.798459	-4.673020
1CBS	A	ILE	43	E	-9.018623	9.583428	-13.728750	-5.456736
1CBS	A	LYS	44	E	-7.908683	6.572015	-14.295466	-5.663092
1CBS	A	GLN	45	E	-6.606661	5.297190	-12.856218	-5.329817
1CBS	A	GLU	46	E	-6.368055	6.680519	-11.977731	-5.164331
1CBS	A	GLY	47	T	-6.368081	6.680328	-11.977516	-5.164304
1CBS	A	ASP	48	T	-6.374472	6.651293	-11.958358	-5.160602
1CBS	A	THR	49	E	-6.413477	6.692274	-11.792594	-5.124095
1CBS	A	PHE	50	E	-7.022218	9.470218	-10.206151	-4.830502
1CBS	A	TYR	51	E	-12.889380	14.800310	-16.683436	-5.647200
1CBS	A	ILE	52	E	-12.004477	14.606277	-15.353790	-5.611756
1CBS	A	LYS	53	E	-10.363871	11.058774	-15.078284	-5.593963
1CBS	A	THR	54	E	-8.468865	9.381300	-11.950149	-4.578239
1CBS	A	SER	55	E	-8.210501	9.146677	-12.242664	-4.611219
1CBS	A	THR	56	E	-6.299972	9.126920	-9.371919	-4.650720
1CBS	A	THR	57	T	-6.249348	8.984724	-9.570649	-4.639963
1CBS	A	VAL	58	T	-6.218650	8.979835	-9.679854	-4.651432
1CBS	A	ARG	59	E	-6.229971	8.976241	-9.643482	-4.655191
1CBS	A	THR	60	E	-5.944727	9.646419	-9.495094	-4.838988
1CBS	A	THR	61	E	-6.386077	10.245925	-9.769769	-5.046953
1CBS	A	GLU	62	E	-6.450354	10.576487	-9.537439	-5.107747
1CBS	A	ILE	63	E	-6.497099	10.712992	-9.352697	-5.126512
1CBS	A	ASN	64	E	-6.497507	10.726656	-9.342619	-5.126288
1CBS	A	PHE	65	E	-8.548899	13.353736	-10.822454	-4.834043
1CBS	A	LYS	66	E	-5.804215	9.489272	-8.661046	-4.829889
1CBS	A	VAL	67	T	-5.786608	9.583067	-8.691180	-4.832529
1CBS	A	GLY	68	T	-5.750823	9.724742	-8.783893	-4.872626
1CBS	A	GLU	69	E	-5.751128	9.722037	-8.783498	-4.873007
1CBS	A	GLU	70	E	-5.754840	9.702851	-8.772363	-4.873994
1CBS	A	PHE	71	E	-7.198529	12.235984	-10.115705	-5.330274
1CBS	A	GLU	72	E	-7.425931	12.014615	-10.310255	-5.521550
1CBS	A	GLU	73	E	-10.191408	13.461801	-14.299508	-6.120313
1CBS	A	GLN	74	E	-10.281154	10.340246	-15.890843	-5.953056
1CBS	A	THR	75	T	-9.951123	10.118914	-15.320396	-5.628877
1CBS	A	VAL	76	T	-9.848819	9.970942	-15.357730	-5.519838
1CBS	A	ASP	77	T	-9.810993	9.784047	-15.465997	-5.493906
1CBS	A	GLY	78	T	-9.809787	9.781498	-15.471816	-5.493415
1CBS	A	ARG	79	C	-10.074376	9.882965	-15.276594	-5.293454
1CBS	A	PRO	80	E	-10.666868	8.805683	-16.236329	-5.099993
1CBS	A	CYS	81	E	-11.163091	8.843911	-17.163910	-5.382144
1CBS	A	LYS	82	E	-11.282747	12.356557	-15.297229	-5.188403
1CBS	A	SER	83	E	-10.993552	13.056889	-14.277571	-4.854517
1CBS	A	LEU	84	E	-10.035506	13.635930	-12.044299	-4.526914
1CBS	A	VAL	85	E	-9.672463	12.968926	-12.198473	-4.511741
1CBS	A	LYS	86	E	-8.438292	10.280592	-11.870617	-4.744761
1CBS	A	TRP	87	E	-8.132542	9.851866	-12.109949	-4.795409
1CBS	A	GLU	88	E	-7.375560	9.196578	-11.762855	-5.074163
1CBS	A	SER	89	E	-7.377075	9.169892	-11.783637	-5.083958
1CBS	A	GLU	90	T	-7.381621	9.150555	-11.783036	-5.091456
1CBS	A	ASN	91	T	-7.476031	9.020892	-11.775258	-5.145557
1CBS	A	LYS	92	E	-7.561005	8.989332	-11.668862	-5.188752
1CBS	A	MET	93	E	-10.163892	12.169623	-14.739791	-5.820093
1CBS	A	VAL	94	E	-10.888269	13.793130	-15.201038	-6.082207
1CBS	A	CYS	95	E	-11.534794	12.628021	-17.400656	-6.433860
1CBS	A	GLU	96	E	-11.266143	12.698317	-17.398146	-6.593857
1CBS	A	GLN	97	E	-10.898021	11.399126	-16.484650	-5.941800
1CBS	A	LYS	98	E	-6.074752	8.007962	-9.361185	-4.529959
1CBS	A	LEU	99	E	-4.613055	7.082388	-7.965300	-4.351167
1CBS	A	LEU	100	T	-2.446813	5.605535	-6.092094	-4.517046
1CBS	A	LYS	101	T	-2.396499	5.560656	-6.252934	-4.508390
1CBS	A	GLY	102	T	-2.393095	5.558674	-6.276585	-4.509471
1CBS	A	GLU	103	C	-2.394272	5.553344	-6.270296	-4.509139
1CBS	A	GLY	104	C	-2.407683	5.516051	-6.229660	-4.509654
1CBS	A	PRO	105	C	-3.860368	4.889481	-8.031992	-4.286904
1CBS	A	LYS	106	C	-5.463229	5.055440	-10.203165	-4.545067
1CBS	A	THR	107	E	-7.950258	7.138508	-12.590497	-4.748525
1CBS	A	SER	108	E	-10.437538	8.445396	-15.574633	-5.078673
1CBS	A	TRP	109	E	-14.753535	14.708552	-19.941570	-6.019047
1CBS	A	THR	110	E	-13.908947	16.655689	-17.491873	-6.201016
1CBS	A	ARG	111	E	-10.852820	13.785768	-13.995276	-5.664817
1CBS	A	GLU	112	E	-7.240501	9.152017	-11.032730	-5.123629

1CBS	A	LEU	113	E	-4.632910	5.972280	-8.874473	-4.724758
1CBS	A	THR	114	T	-3.505886	5.313102	-8.274062	-4.888870
1CBS	A	ASN	115	T	-3.503250	5.326547	-8.285509	-4.889896
1CBS	A	ASP	116	T	-3.503237	5.326680	-8.285604	-4.889898
1CBS	A	GLY	117	T	-3.504321	5.319650	-8.280510	-4.889425
1CBS	A	GLU	118	C	-3.599007	5.209269	-8.175737	-4.914916
1CBS	A	LEU	119	E	-6.712567	8.336079	-10.821200	-5.093950
1CBS	A	ILE	120	E	-9.729806	12.035627	-12.922307	-5.106821
1CBS	A	LEU	121	E	-11.315856	16.684729	-14.532219	-5.808772
1CBS	A	THR	122	E	-11.310551	14.907666	-14.629984	-5.273758
1CBS	A	MET	123	E	-9.266159	10.626521	-12.526972	-4.765986
1CBS	A	THR	124	E	-6.583606	8.627996	-9.096666	-4.026382
1CBS	A	ALA	125	E	-5.385912	7.657620	-8.170096	-3.876421
1CBS	A	ASP	126	T	-5.365190	7.627293	-8.285172	-3.894708
1CBS	A	ASP	127	T	-5.334426	7.679237	-8.380484	-3.920178
1CBS	A	VAL	128	E	-5.335179	7.675642	-8.375294	-3.919119
1CBS	A	VAL	129	E	-5.411120	7.548146	-8.281557	-3.905443
1CBS	A	CYS	130	E	-6.807313	7.917882	-10.697959	-4.401608
1CBS	A	THR	131	E	-7.102127	8.654149	-10.169604	-4.397564
1CBS	A	ARG	132	E	-12.138979	12.631722	-16.151359	-5.281170
1CBS	A	VAL	133	E	-11.384813	16.523033	-12.620862	-4.921105
1CBS	A	TYR	134	E	-9.387726	14.006207	-10.025330	-4.077563
1CBS	A	VAL	135	E	-9.387726	14.006207	-10.025330	-4.077563
1CBS	A	ARG	136	E	-9.387726	14.006207	-10.025330	-4.077563
1CBS	A	GLU	137	C	-9.387726	14.006207	-10.025330	-4.077563
1CDY	A	LYS	1	C	-7.884606	9.358869	-10.628142	-4.126544
1CDY	A	LYS	2	E	-7.884606	9.358869	-10.628142	-4.126544
1CDY	A	VAL	3	E	-7.884606	9.358869	-10.628142	-4.126544
1CDY	A	VAL	4	E	-7.884606	9.358869	-10.628142	-4.126544
1CDY	A	LEU	5	E	-8.562825	12.915777	-11.183035	-5.229599
1CDY	A	GLY	6	E	-7.056685	8.293800	-11.610262	-5.192609
1CDY	A	LYS	7	E	-5.762918	8.940705	-9.626952	-5.146646
1CDY	A	LYS	8	T	-5.596097	9.023222	-9.577503	-5.034512
1CDY	A	GLY	9	T	-5.483445	9.035916	-9.636404	-5.011796
1CDY	A	ASP	10	b	-5.479517	9.057641	-9.632338	-5.007172
1CDY	A	THR	11	C	-5.514191	9.165584	-9.497401	-4.991986
1CDY	A	VAL	12	E	-6.032424	9.365022	-9.669312	-4.783258
1CDY	A	GLU	13	E	-6.457837	9.458574	-9.928651	-4.882225
1CDY	A	LEU	14	E	-7.799732	12.601186	-10.056967	-4.706427
1CDY	A	THR	15	C	-8.298821	12.446082	-10.481756	-4.697707
1CDY	A	CYS	16	C	-9.713673	8.662159	-15.225176	-4.841033
1CDY	A	THR	17	B	-8.807008	5.828587	-14.765764	-4.692088
1CDY	A	ALA	18	C	-7.506683	6.136478	-12.792535	-4.703878
1CDY	A	SER	19	C	-7.409352	6.217758	-12.923248	-4.726655
1CDY	A	GLN	20	C	-7.347524	6.383785	-12.940723	-4.739560
1CDY	A	LYS	21	C	-7.281967	6.516593	-12.932581	-4.718143
1CDY	A	LYS	22	C	-7.321410	6.585608	-12.820040	-4.721425
1CDY	A	SER	23	C	-7.946066	7.335375	-13.319047	-4.748477
1CDY	A	ILE	24	C	-8.229544	7.707306	-13.102642	-4.684137
1CDY	A	GLN	25	C	-8.611097	7.642172	-12.925073	-4.542771
1CDY	A	PHE	26	E	-12.460905	13.945335	-15.728899	-5.148366
1CDY	A	HIS	27	E	-13.403813	14.687489	-16.545156	-5.391506
1CDY	A	TRP	28	E	-14.878332	14.579991	-20.170740	-6.322320
1CDY	A	LYS	29	E	-11.693966	7.373599	-18.880635	-5.967306
1CDY	A	ASN	30	E	-8.286641	4.970541	-14.615096	-5.084807
1CDY	A	SER	31	T	-8.156727	5.207572	-14.811564	-5.171924
1CDY	A	ASN	32	T	-8.100881	5.643792	-14.753114	-5.208966
1CDY	A	GLN	33	T	-8.097768	5.689596	-14.748616	-5.210352
1CDY	A	ILE	34	E	-8.079308	5.945161	-14.667765	-5.208742
1CDY	A	LYS	35	E	-8.797049	8.269706	-14.826007	-5.508311
1CDY	A	ILE	36	E	-9.302662	11.187013	-13.762997	-5.479889
1CDY	A	LEU	37	E	-9.360537	10.226948	-14.240398	-5.375067
1CDY	A	GLY	38	E	-7.833343	5.227529	-14.283773	-5.215531
1CDY	A	ASN	39	E	-6.805949	5.194179	-12.976266	-5.104608
1CDY	A	GLN	40	E	-6.663162	5.701518	-12.786079	-5.062412
1CDY	A	GLY	41	T	-6.652419	5.739748	-12.803258	-5.058932
1CDY	A	SER	42	T	-6.655903	5.726105	-12.790567	-5.056481
1CDY	A	PHE	43	E	-6.736412	5.853865	-12.573099	-5.035116
1CDY	A	LEU	44	E	-7.514169	7.619692	-12.279120	-4.910644
1CDY	A	THR	45	E	-8.829390	8.076606	-14.190177	-4.972241
1CDY	A	LYS	46	E	-8.204503	6.233355	-13.948113	-4.925079
1CDY	A	SER	47	T	-7.338185	6.410011	-12.397487	-4.544671
1CDY	A	PRO	48	T	-6.788134	6.596930	-11.864297	-4.584169
1CDY	A	SER	49	T	-6.705762	6.673927	-11.971085	-4.634371
1CDY	A	LYS	50	T	-6.703771	6.679095	-11.979345	-4.636185
1CDY	A	LEU	51	T	-6.747595	6.734577	-11.840062	-4.616680
1CDY	A	ASN	52	G	-6.945984	6.836328	-11.800170	-4.689854
1CDY	A	ASP	53	G	-7.869308	7.274465	-12.864459	-4.989109
1CDY	A	ARG	54	G	-9.735511	8.075768	-15.208880	-5.255966
1CDY	A	ALA	55	E	-11.551166	11.007435	-16.735881	-5.569775
1CDY	A	ASP	56	E	-12.429967	9.704562	-18.802727	-5.349264

1CDY	A	SER	57	C	-12.012853	9.958633	-17.158725	-4.815990
1CDY	A	ARG	58	C	-12.033787	10.051360	-16.978725	-4.734638
1CDY	A	ARG	59	H	-11.592254	11.351178	-16.006586	-4.821967
1CDY	A	SER	60	H	-11.031822	11.654605	-15.501559	-5.159245
1CDY	A	LEU	61	H	-10.851505	11.974172	-15.485405	-5.326393
1CDY	A	TRP	62	H	-10.824604	12.168431	-15.588171	-5.488736
1CDY	A	ASP	63	H	-10.631666	12.046627	-15.605179	-5.522241
1CDY	A	GLN	64	C	-10.616988	12.239771	-15.530559	-5.548473
1CDY	A	GLY	65	C	-10.819033	12.546758	-15.617436	-5.609513
1CDY	A	ASN	66	B	-10.998661	12.630087	-15.566783	-5.558090
1CDY	A	PHE	67	C	-11.088981	13.196081	-15.041864	-5.391538
1CDY	A	PRO	68	C	-11.295191	16.788953	-12.768205	-4.793597
1CDY	A	LEU	69	E	-11.180404	17.312467	-12.275968	-4.778385
1CDY	A	ILE	70	E	-11.061949	16.917219	-12.534624	-4.841302
1CDY	A	ILE	71	E	-10.987128	16.444359	-12.944856	-4.939495
1CDY	A	LYS	72	T	-10.911917	15.754491	-13.486725	-5.080769
1CDY	A	ASN	73	T	-9.901909	11.395916	-13.801322	-5.128949
1CDY	A	LEU	74	b	-9.816382	11.002437	-14.061294	-5.132621
1CDY	A	LYS	75	C	-9.538298	10.176278	-14.485146	-5.228361
1CDY	A	ILE	76	G	-9.490708	10.028560	-14.636854	-5.240777
1CDY	A	GLU	77	G	-9.436246	9.749389	-14.901376	-5.298106
1CDY	A	ASP	78	G	-9.730655	9.060958	-15.655665	-5.423221
1CDY	A	SER	79	C	-9.832723	8.794692	-15.784613	-5.480138
1CDY	A	ASP	80	E	-10.443810	8.271485	-16.969076	-5.670799
1CDY	A	THR	81	E	-10.783480	7.810042	-17.439180	-5.872061
1CDY	A	TYR	82	E	-13.017982	14.579762	-17.731174	-5.894204
1CDY	A	ILE	83	E	-12.379073	14.257846	-16.398063	-5.705994
1CDY	A	CYS	84	E	-10.613403	9.669613	-16.019064	-5.662895
1CDY	A	GLU	85	E	-10.461015	9.621713	-16.304951	-5.733536
1CDY	A	VAL	86	E	-9.823605	9.112429	-16.100869	-5.890365
1CDY	A	GLU	87	T	-9.808273	9.085872	-16.197459	-5.912969
1CDY	A	ASP	88	T	-9.801948	9.028363	-16.270176	-5.931853
1CDY	A	GLN	89	E	-9.966104	8.894083	-16.359216	-6.019365
1CDY	A	LYS	90	E	-10.025927	8.844227	-16.264589	-6.026069
1CDY	A	GLU	91	E	-11.582909	8.720592	-19.721998	-6.727331
1CDY	A	GLU	92	E	-11.896827	10.656444	-18.723021	-6.456220
1CDY	A	VAL	93	E	-12.150665	16.142912	-14.615685	-5.112107
1CDY	A	GLN	94	E	-12.148020	16.538246	-14.304893	-5.030598
1CDY	A	LEU	95	E	-11.761750	18.094566	-12.709720	-4.855229
1CDY	A	LEU	96	E	-11.349000	19.035051	-11.789211	-4.867268
1CDY	A	VAL	97	E	-10.075105	16.945016	-10.242075	-4.540747
1CDY	A	PHE	98	E	-9.310760	17.080092	-9.495905	-4.646003
1CDY	A	GLY	99	E	-7.680062	10.364060	-10.619780	-4.643421
1CDY	A	LEU	100	E	-7.589592	10.356896	-10.795782	-4.651195
1CDY	A	THR	101	E	-7.400069	9.340135	-11.445747	-4.687725
1CDY	A	ALA	102	E	-7.176648	8.467709	-11.863499	-4.724805
1CDY	A	ASN	103	T	-6.987985	7.770717	-12.161997	-4.759246
1CDY	A	SER	104	T	-7.182033	6.927400	-12.778379	-4.804226
1CDY	A	ASP	105	T	-7.221179	6.694183	-12.855140	-4.810834
1CDY	A	THR	106	T	-7.355461	6.700031	-12.776703	-4.817426
1CDY	A	HIS	107	E	-7.686708	6.679748	-12.835151	-4.831889
1CDY	A	LEU	108	E	-8.557928	9.492901	-12.702741	-4.661965
1CDY	A	LEU	109	T	-7.828924	7.874558	-12.582979	-4.761393
1CDY	A	GLN	110	T	-7.820511	7.923742	-12.595816	-4.778586
1CDY	A	GLY	111	T	-7.809194	7.990559	-12.626153	-4.794001
1CDY	A	GLN	112	b	-7.815521	7.971349	-12.608458	-4.793658
1CDY	A	SER	113	C	-7.949492	7.597634	-12.694897	-4.829782
1CDY	A	LEU	114	E	-9.502786	11.173471	-13.841925	-5.308905
1CDY	A	THR	115	E	-10.064562	11.882224	-14.277398	-5.551864
1CDY	A	LEU	116	E	-11.232455	14.461859	-14.679420	-5.364571
1CDY	A	THR	117	E	-11.338098	13.808873	-14.948741	-5.158211
1CDY	A	LEU	118	E	-9.649086	12.019549	-12.214106	-4.647191
1CDY	A	GLU	119	E	-6.775196	8.030542	-10.606352	-4.721958
1CDY	A	SER	120	C	-5.429283	7.245281	-9.348986	-4.598445
1CDY	A	PRO	121	T	-3.913145	5.872635	-7.363079	-4.029984
1CDY	A	PRO	122	T	-3.779771	5.850133	-7.561005	-4.043962
1CDY	A	GLY	123	T	-3.777788	5.851978	-7.573684	-4.044867
1CDY	A	SER	124	T	-3.781527	5.838323	-7.554475	-4.040465
1CDY	A	SER	125	C	-3.815513	5.759529	-7.455701	-4.007608
1CDY	A	PRO	126	C	-4.720266	5.757965	-8.376185	-4.092067
1CDY	A	SER	127	E	-7.142235	6.504734	-11.362388	-4.302260
1CDY	A	VAL	128	E	-9.749250	9.931289	-12.947722	-3.989856
1CDY	A	GLN	129	C	-10.705394	10.313768	-14.233525	-4.168475
1CDY	A	CYS	130	C	-11.427057	11.147210	-14.920739	-4.593066
1CDY	A	ARG	131	B	-12.711465	8.534857	-19.466875	-5.293657
1CDY	A	SER	132	T	-9.351895	5.930346	-15.104507	-4.788997
1CDY	A	PRO	133	T	-8.245005	5.374188	-14.511498	-4.967997
1CDY	A	ARG	134	T	-8.170176	5.482816	-14.636030	-4.998424
1CDY	A	GLY	135	T	-7.178284	6.055304	-12.936422	-4.977966
1CDY	A	LYS	136	C	-7.024351	5.960518	-13.046609	-4.943674
1CDY	A	ASN	137	B	-6.671628	6.080909	-12.570550	-4.868820

1CDY	A	ILE	138	C	-6.652288	6.129285	-12.505695	-4.830977
1CDY	A	GLN	139	C	-5.862526	5.259092	-11.607804	-4.779546
1CDY	A	GLY	140	B	-5.848000	5.401434	-11.508236	-4.754436
1CDY	A	GLY	141	T	-5.862261	5.425842	-11.453697	-4.752263
1CDY	A	LYS	142	T	-5.935964	5.321738	-11.373939	-4.748843
1CDY	A	THR	143	E	-5.950903	5.311782	-11.330112	-4.754151
1CDY	A	LEU	144	E	-7.102825	7.490884	-11.520591	-4.702210
1CDY	A	SER	145	E	-8.538556	9.866408	-12.529915	-4.676034
1CDY	A	VAL	146	E	-9.149144	10.560122	-13.033812	-4.438948
1CDY	A	SER	147	T	-9.081564	10.387422	-13.127609	-4.460873
1CDY	A	GLN	148	T	-9.319571	9.798919	-13.834387	-4.525972
1CDY	A	LEU	149	b	-9.430524	9.727167	-13.941867	-4.566897
1CDY	A	GLU	150	C	-9.589675	9.624858	-14.206062	-4.662686
1CDY	A	LEU	151	G	-9.730495	8.882408	-15.084838	-4.870023
1CDY	A	GLN	152	G	-10.023282	8.077743	-16.416430	-5.212724
1CDY	A	ASP	153	G	-10.158603	7.719547	-16.696986	-5.281088
1CDY	A	SER	154	C	-10.057811	8.565609	-16.200193	-5.269242
1CDY	A	GLY	155	E	-9.742858	10.722256	-14.879546	-5.458991
1CDY	A	THR	156	E	-9.927479	12.245554	-14.297778	-5.583348
1CDY	A	TRP	157	E	-10.004087	12.982295	-13.845576	-5.587010
1CDY	A	THR	158	E	-9.958127	12.897571	-13.932739	-5.563140
1CDY	A	CYS	159	E	-10.075114	13.024168	-13.852604	-5.633009
1CDY	A	THR	160	E	-10.951104	13.134023	-15.303006	-5.510795
1CDY	A	VAL	161	E	-9.029081	10.321461	-12.862755	-5.058480
1CDY	A	LEU	162	E	-8.288875	9.291402	-13.276696	-5.422511
1CDY	A	GLN	163	E	-7.474104	9.265111	-12.537451	-5.623774
1CDY	A	ASN	164	T	-6.582122	9.512920	-10.582557	-5.121753
1CDY	A	GLN	165	T	-6.483998	9.775138	-10.579034	-5.134092
1CDY	A	LYS	166	E	-6.491507	9.772845	-10.550951	-5.135605
1CDY	A	LYS	167	E	-6.496795	9.964761	-10.435893	-5.133762
1CDY	A	VAL	168	E	-6.587683	10.094147	-10.126697	-5.040488
1CDY	A	GLU	169	E	-7.481291	12.043297	-10.533905	-5.273663
1CDY	A	PHE	170	E	-8.476578	15.807154	-10.432766	-5.570501
1CDY	A	LYS	171	E	-8.485251	15.806403	-10.402024	-5.571264
1CDY	A	ILE	172	E	-9.247264	15.203571	-11.633667	-5.352638
1CDY	A	ASP	173	E	-8.768483	14.204709	-10.882501	-4.931651
1CDY	A	ILE	174	E	-7.111312	12.412122	-7.501468	-3.674392
1CDY	A	VAL	175	E	-5.098687	8.523099	-5.889639	-2.876250
1CDY	A	VAL	176	E	-5.098687	8.523099	-5.889639	-2.876250
1CDY	A	LEU	177	C	-5.098687	8.523099	-5.889639	-2.876250
1CDY	A	ALA	178	C	-5.098687	8.523099	-5.889639	-2.876250
1CLL	A	LEU	4	C	-2.878702	4.676041	-6.017969	-3.420758
1CLL	A	THR	5	H	-2.878702	4.676041	-6.017969	-3.420758
1CLL	A	GLU	6	H	-2.878702	4.676041	-6.017969	-3.420758
1CLL	A	GLU	7	H	-2.878702	4.676041	-6.017969	-3.420758
1CLL	A	GLN	8	H	-4.014652	5.807220	-8.236287	-4.350606
1CLL	A	ILE	9	H	-4.855012	6.667741	-9.781458	-5.023528
1CLL	A	ALA	10	H	-5.583595	7.565019	-11.305899	-5.853877
1CLL	A	GLU	11	H	-6.098819	8.356684	-11.942629	-6.427459
1CLL	A	PHE	12	H	-7.624002	12.936596	-13.752923	-7.650716
1CLL	A	LYS	13	H	-8.167589	13.508384	-14.858688	-8.038912
1CLL	A	GLU	14	H	-8.418063	13.184976	-15.037092	-7.871570
1CLL	A	ALA	15	H	-8.943464	13.297681	-14.785821	-7.356209
1CLL	A	PHE	16	H	-10.022938	10.841047	-13.210616	-4.140176
1CLL	A	SER	17	H	-10.036138	10.542229	-13.175497	-4.024545
1CLL	A	LEU	18	H	-10.292706	10.490317	-13.197633	-3.985446
1CLL	A	PHE	19	H	-10.081259	10.762113	-14.571501	-5.447481
1CLL	A	ASP	20	T	-8.119267	4.098493	-15.312358	-5.403933
1CLL	A	LYS	21	T	-5.676193	2.731416	-12.726768	-5.327990
1CLL	A	ASP	22	T	-4.698920	3.094098	-11.281003	-5.078796
1CLL	A	GLY	23	T	-4.614528	3.616178	-11.106305	-5.045831
1CLL	A	ASP	24	C	-4.607249	3.695614	-11.098398	-5.046502
1CLL	A	GLY	25	C	-4.608436	3.700395	-11.087877	-5.045806
1CLL	A	THR	26	E	-4.713367	3.892814	-10.777195	-4.990693
1CLL	A	ILE	27	E	-5.755348	7.315779	-10.012370	-4.853020
1CLL	A	THR	28	C	-7.180569	10.258055	-10.575380	-5.117475
1CLL	A	THR	29	H	-8.903529	12.626935	-12.281564	-5.433358
1CLL	A	LYS	30	H	-9.847446	11.927245	-14.220740	-5.414447
1CLL	A	GLU	31	H	-10.160846	11.939511	-14.847156	-5.506582
1CLL	A	LEU	32	H	-9.996848	12.855170	-13.786899	-5.319757
1CLL	A	GLY	33	H	-9.963182	12.834780	-14.521630	-5.839521
1CLL	A	THR	34	H	-9.890881	12.894385	-14.921695	-6.130433
1CLL	A	VAL	35	H	-9.862950	12.798307	-14.964521	-6.088155
1CLL	A	MET	36	H	-9.388640	9.306524	-14.966459	-5.348852
1CLL	A	ARG	37	H	-8.362333	5.342887	-14.251579	-4.619600
1CLL	A	SER	38	H	-5.790051	4.216522	-11.167581	-4.593700
1CLL	A	LEU	39	C	-5.322268	6.041116	-10.230031	-4.700678
1CLL	A	GLY	40	C	-5.199925	6.208143	-10.297686	-4.742310
1CLL	A	GLN	41	C	-5.197106	6.219686	-10.308163	-4.744184
1CLL	A	ASN	42	C	-5.159536	6.291687	-10.322425	-4.734501
1CLL	A	PRO	43	C	-5.367025	7.350768	-9.963414	-4.775490

```
1CLL        A         THR           44                 C -5.874186  7.062075 -10.739543 -4.745343
1CLL        A         GLU           45                 H -6.391137  7.238425 -10.946879 -4.498082
1CLL        A         ALA           46                 H -6.414816  7.187890 -10.874948 -4.473451
1CLL        A         GLU           47                 H -6.879084  7.124271 -11.030078 -4.347072
1CLL        A         LEU           48                 H -7.905275  7.379376 -12.039180 -4.467487
1CLL        A         GLN           49                 H -10.740546  9.341791 -16.776832 -5.335331
1CLL        A         ASP           50                 H -9.171665  9.821146 -13.130074 -4.941056
1CLL        A         MET           51                 H -9.010567 10.269170 -12.949947 -4.899742
1CLL        A         ILE           52                 H -8.892577 10.213303 -13.083703 -4.883442
1CLL        A         ASN           53                 H -8.196167  7.945579 -13.272835 -4.796431
1CLL        A         GLU           54                 H -8.068798  7.745704 -13.433968 -4.787456
1CLL        A         VAL           55                 H -7.622188  6.493228 -13.236312 -4.708431
1CLL        A         ASP           56                 T -6.503546  3.058140 -13.467504 -4.922591
1CLL        A         ALA           57                 T -4.481154  1.662840 -11.283490 -4.916402
1CLL        A         ASP           58                 T -4.339538  1.967318 -11.398298 -4.984264
1CLL        A         GLY           59                 T -4.302721  2.235696 -11.350526 -4.982104
1CLL        A         ASN           60                 C -4.303622  2.232023 -11.347969 -4.982905
1CLL        A         GLY           61                 C -4.316086  2.226714 -11.301771 -4.983248
1CLL        A         THR           62                 C -5.096719  3.893680 -11.544114 -5.161874
1CLL        A         ILE           63                 E -5.957359  6.453697 -10.640420 -4.943156
1CLL        A         ASP           64                 E -8.570454  9.020896 -13.085766 -5.134854
1CLL        A         PHE           65                 H -10.130863 13.946703 -12.677700 -4.807589
1CLL        A         PRO           66                 H -10.248148 13.825637 -12.593296 -4.715546
1CLL        A         GLU           67                 H -10.952451 14.160331 -13.324661 -4.804868
1CLL        A         PHE           68                 H -11.705449 15.958975 -14.070515 -5.017885
1CLL        A         LEU           69                 H -11.188399 13.819669 -14.208903 -4.927056
1CLL        A         THR           70                 H -10.154816 10.571705 -13.718396 -4.508098
1CLL        A         MET           71                 H -10.117882 10.433553 -13.887853 -4.532894
1CLL        A         MET           72                 H -9.899070 10.397074 -14.023177 -4.607763
1CLL        A         ALA           73                 H -9.357005  8.739944 -14.007876 -4.477979
1CLL        A         ARG           74                 H -8.866200  7.670423 -14.093845 -4.596253
1CLL        A         LYS           75                 H -8.202701  7.437079 -13.527137 -4.876695
1CLL        A         MET           76                 H -7.470065  6.620879 -12.998527 -4.881012
1CLL        A         LYS           77                 H -7.394188  6.459923 -13.129654 -4.846717
1CLL        A         ASP           78                 H -7.405651  6.429921 -13.122943 -4.857587
1CLL        A         THR           79                 H -7.428884  6.403281 -13.101896 -4.868034
1CLL        A         ASP           80                 H -7.548302  6.161785 -13.097750 -4.843680
1CLL        A         SER           81                 H -8.516301  5.701609 -14.472190 -4.691215
1CLL        A         GLU           82                 H -9.539734  6.970432 -16.272343 -5.118748
1CLL        A         GLU           83                 H -9.475628  7.691208 -15.795271 -5.082313
1CLL        A         GLU           84                 H -9.540887  8.947977 -15.092040 -4.967173
1CLL        A         ILE           85                 H -9.743528 10.018363 -14.497146 -4.869187
1CLL        A         ARG           86                 H -9.874137 10.549682 -14.054742 -4.724163
1CLL        A         GLU           87                 H -9.452109 10.450061 -12.815758 -4.153039
1CLL        A         ALA           88                 H -9.561883 10.676356 -12.410912 -3.965046
1CLL        A         PHE           89                 H -9.753910 10.696452 -11.977185 -3.720060
1CLL        A         ARG           90                 H -9.665077 10.907096 -12.098390 -3.798929
1CLL        A         VAL           91                 H -9.640273 10.933616 -12.215940 -3.877168
1CLL        A         PHE           92                 H -9.412064 10.863566 -13.483038 -5.172152
1CLL        A         ASP           93                 T -7.472598  4.255733 -14.319921 -5.314155
1CLL        A         LYS           94                 T -5.062771  3.028969 -11.658594 -5.216981
1CLL        A         ASP           95                 T -5.027410  3.155770 -11.731210 -5.233572
1CLL        A         GLY           96                 T -5.019614  3.236094 -11.729474 -5.234233
1CLL        A         ASN           97                 C -5.019846  3.233284 -11.728884 -5.234197
1CLL        A         GLY           98                 C -5.028998  3.221366 -11.687998 -5.232844
1CLL        A         TYR           99                 C -6.591457  5.993131 -12.667559 -5.458953
1CLL        A         ILE          100                 B -7.581012  9.323021 -11.637438 -5.278988
1CLL        A         SER          101                 C -10.145451 10.670866 -14.796394 -5.083805
1CLL        A         ALA          102                 H -10.684492 10.769969 -15.072937 -4.666526
1CLL        A         ALA          103                 H -10.783907 10.468545 -15.205012 -4.639894
1CLL        A         GLU          104                 H -10.832328 10.325177 -15.212949 -4.643489
1CLL        A         LEU          105                 H -11.165616 12.539886 -15.875935 -5.598071
1CLL        A         ARG          106                 H -9.945806 13.705779 -16.872621 -8.625816
1CLL        A         HIS          107                 H -8.028387 12.772708 -14.525243 -8.166522
1CLL        A         VAL          108                 H -7.758472 11.891560 -13.713304 -7.095846
1CLL        A         MET          109                 H -6.803008  8.334729 -11.923614 -5.465195
1CLL        A         THR          110                 H -4.788990  6.043095 -9.273832 -4.838162
1CLL        A         ASN          111                 H -3.961396  5.014208 -8.832643 -4.645136
1CLL        A         LEU          112                 H -3.627813  6.055823 -8.143912 -4.613469
1CLL        A         GLY          113                 C -3.557974  6.111079 -8.235949 -4.635238
1CLL        A         GLU          114                 C -3.558462  6.111125 -8.233013 -4.634736
1CLL        A         LYS          115                 C -3.633588  6.130946 -8.107229 -4.607756
1CLL        A         LEU          116                 C -3.969581  7.233844 -7.659939 -4.621818
1CLL        A         THR          117                 C -4.823031  6.594375 -9.113615 -4.798049
1CLL        A         ASP          118                 H -6.471829  7.499224 -11.744854 -4.928756
1CLL        A         GLU          119                 H -6.720464  7.287766 -11.948577 -4.890220
1CLL        A         GLU          120                 H -7.169470  7.436745 -12.270614 -4.870046
1CLL        A         VAL          121                 H -7.388839  7.502749 -11.979227 -4.770073
1CLL        A         ASP          122                 H -8.855449  9.003462 -14.886154 -5.816767
1CLL        A         GLU          123                 H -9.482857  9.129326 -14.536516 -4.935840
1CLL        A         MET          124                 H -9.692418 10.000725 -13.498132 -4.375089
```

1CLL	A	ILE	125	H	-9.573704	10.038366	-13.318369	-4.243192
1CLL	A	ARG	126	H	-8.872695	9.123885	-12.678497	-4.188296
1CLL	A	GLU	127	H	-8.739351	8.856945	-13.002781	-4.295977
1CLL	A	ALA	128	H	-7.269370	6.343631	-12.217088	-4.650611
1CLL	A	ASP	129	T	-6.823979	4.698176	-13.121029	-4.829228
1CLL	A	ILE	130	T	-5.131564	2.805492	-11.674819	-4.979222
1CLL	A	ASP	131	T	-5.110619	2.842389	-11.765716	-5.004988
1CLL	A	GLY	132	T	-5.105529	2.879433	-11.776403	-5.007394
1CLL	A	ASP	133	C	-5.119953	2.798810	-11.766945	-5.015491
1CLL	A	GLY	134	C	-5.137938	2.784563	-11.700358	-5.016359
1CLL	A	GLN	135	C	-6.947453	4.674266	-13.994457	-5.584111
1CLL	A	VAL	136	B	-7.894750	7.214480	-13.088524	-5.257525
1CLL	A	ASN	137	C	-11.369691	9.869616	-17.115805	-5.714343
1CLL	A	TYR	138	H	-12.559448	15.280027	-17.127699	-6.146547
1CLL	A	GLU	139	H	-11.209912	18.783223	-15.564819	-8.188517
1CLL	A	GLU	140	H	-10.679874	18.723605	-14.719833	-7.902855
1CLL	A	PHE	141	H	-7.760057	15.834976	-9.667045	-6.249743
1CLL	A	VAL	142	H	-5.638081	10.863355	-8.364590	-5.276486
1CLL	A	GLN	143	H	-4.842505	9.574858	-7.837688	-4.837871
1CLL	A	MET	144	H	-3.310712	7.733027	-4.942055	-3.544662
1CLL	A	MET	145	H	-3.310712	7.733027	-4.942055	-3.544662
1CLL	A	THR	146	H	-3.310712	7.733027	-4.942055	-3.544662
1CLL	A	ALA	147	C	-3.310712	7.733027	-4.942055	-3.544662
1CTQ	A	MET	1	C	-8.723944	11.670208	-11.609516	-5.019133
1CTQ	A	THR	2	C	-8.723944	11.670208	-11.609516	-5.019133
1CTQ	A	GLU	3	E	-8.723944	11.670208	-11.609516	-5.019133
1CTQ	A	TYR	4	E	-8.723944	11.670208	-11.609516	-5.019133
1CTQ	A	LYS	5	E	-10.842209	14.631651	-13.936805	-5.692956
1CTQ	A	LEU	6	E	-10.016992	16.412137	-9.330808	-3.875495
1CTQ	A	VAL	7	E	-9.772801	15.542110	-9.842184	-3.830394
1CTQ	A	VAL	8	E	-8.585284	11.538955	-10.518517	-4.074373
1CTQ	A	VAL	9	E	-7.047449	7.258359	-11.112210	-4.428914
1CTQ	A	GLY	10	E	-6.206878	5.856025	-11.132239	-4.489899
1CTQ	A	ALA	11	T	-5.479303	5.711843	-10.339357	-4.474226
1CTQ	A	GLY	12	T	-5.468524	5.734734	-10.384484	-4.485284
1CTQ	A	GLY	13	T	-5.471135	5.711610	-10.383964	-4.487030
1CTQ	A	VAL	14	T	-5.510753	5.628549	-10.330285	-4.489024
1CTQ	A	GLY	15	C	-5.668789	5.695520	-10.082927	-4.482664
1CTQ	A	LYS	16	H	-7.835396	7.090074	-12.839770	-5.069396
1CTQ	A	SER	17	H	-10.631197	10.098980	-15.621141	-5.007412
1CTQ	A	ALA	18	H	-11.156636	12.506064	-14.773058	-4.770146
1CTQ	A	LEU	19	H	-11.446063	13.654111	-14.331237	-4.793611
1CTQ	A	THR	20	H	-11.875321	15.772435	-13.511385	-4.635640
1CTQ	A	ILE	21	H	-11.879963	15.795843	-13.513517	-4.653166
1CTQ	A	GLN	22	H	-11.636471	14.522600	-15.364642	-5.931606
1CTQ	A	LEU	23	H	-8.801751	12.493077	-11.271877	-5.095083
1CTQ	A	ILE	24	H	-8.685116	12.765534	-11.633907	-5.279191
1CTQ	A	GLN	25	H	-8.451767	13.027439	-12.904048	-6.260135
1CTQ	A	ASN	26	C	-7.990354	12.242359	-13.017190	-6.255288
1CTQ	A	HIS	27	C	-7.109847	10.283200	-10.782725	-4.947164
1CTQ	A	PHE	28	C	-5.220798	10.154159	-6.921666	-4.244796
1CTQ	A	VAL	29	C	-3.369465	6.670305	-6.049942	-4.002000
1CTQ	A	ASP	30	C	-2.285495	4.323665	-6.176027	-4.003669
1CTQ	A	GLU	31	C	-2.244830	4.416452	-6.277800	-4.030746
1CTQ	A	TYR	32	C	-2.230731	4.464379	-6.312655	-4.033995
1CTQ	A	ASP	33	C	-2.233738	4.432445	-6.312435	-4.032739
1CTQ	A	PRO	34	C	-2.327311	4.050862	-6.323170	-4.013676
1CTQ	A	THR	35	T	-3.681763	5.803452	-7.512541	-4.193078
1CTQ	A	ILE	36	T	-4.436683	6.447491	-7.633226	-4.042478
1CTQ	A	GLU	37	T	-6.098037	8.881710	-9.600016	-4.764251
1CTQ	A	ASP	38	E	-7.581812	10.267250	-13.364357	-6.174434
1CTQ	A	SER	39	E	-8.005209	10.509809	-13.571243	-6.317269
1CTQ	A	TYR	40	E	-9.496214	12.240532	-13.077541	-5.118228
1CTQ	A	ARG	41	E	-7.721215	10.570799	-9.986993	-4.353341
1CTQ	A	LYS	42	E	-7.562829	10.650939	-10.099579	-4.351005
1CTQ	A	GLN	43	E	-7.488292	10.442461	-10.356569	-4.372769
1CTQ	A	VAL	44	E	-6.368916	7.093753	-10.328530	-4.282565
1CTQ	A	VAL	45	E	-5.988907	6.542672	-10.928602	-4.629954
1CTQ	A	ILE	46	E	-5.897422	6.417903	-11.145034	-4.743381
1CTQ	A	ASP	47	T	-5.857462	6.200489	-11.378087	-4.800154
1CTQ	A	GLY	48	T	-5.859608	6.185487	-11.383211	-4.804089
1CTQ	A	GLU	49	E	-6.123463	6.009724	-11.977103	-5.105435
1CTQ	A	THR	50	E	-6.657752	6.126486	-12.535147	-5.235943
1CTQ	A	CYS	51	E	-7.331181	4.629330	-14.016176	-5.392566
1CTQ	A	LEU	52	E	-9.108031	7.874065	-14.386912	-5.279268
1CTQ	A	LEU	53	E	-11.431625	14.912767	-14.528655	-5.106191
1CTQ	A	ASP	54	E	-11.420649	15.408875	-14.306735	-5.152183
1CTQ	A	ILE	55	E	-11.319805	15.769725	-13.805164	-5.036231
1CTQ	A	LEU	56	E	-11.142822	14.594237	-14.259010	-5.090554
1CTQ	A	ASP	57	E	-11.214423	13.579341	-15.003922	-5.213192
1CTQ	A	THR	58	C	-10.147243	9.504115	-15.297280	-5.304250

1CTQ	A	ALA	59	C	-8.191017	5.773468	-13.935150	-4.944833
1CTQ	A	GLY	60	C	-7.774881	6.551167	-13.749612	-5.143224
1CTQ	A	GLN	61	C	-7.692459	6.656707	-13.759422	-5.115185
1CTQ	A	GLU	62	G	-7.326847	6.591554	-13.173387	-4.896745
1CTQ	A	GLU	63	G	-7.327753	6.589094	-13.168931	-4.894765
1CTQ	A	TYR	64	G	-7.478410	6.864308	-12.962042	-4.884111
1CTQ	A	SER	65	H	-7.695231	6.659013	-12.694598	-4.683860
1CTQ	A	ALA	66	H	-7.778725	6.546674	-12.522178	-4.646732
1CTQ	A	MET	67	H	-10.379205	8.949185	-15.213697	-5.092708
1CTQ	A	ARG	68	H	-12.760864	10.555718	-18.562969	-5.394854
1CTQ	A	ASP	69	H	-13.090615	9.887816	-19.313203	-5.490459
1CTQ	A	GLN	70	H	-12.817542	12.027521	-17.693949	-5.375203
1CTQ	A	TYR	71	H	-12.512667	13.965576	-16.170696	-5.356043
1CTQ	A	MET	72	H	-11.300034	10.611276	-16.199197	-5.397057
1CTQ	A	ARG	73	H	-9.588439	7.231403	-14.923646	-4.882161
1CTQ	A	THR	74	H	-9.309683	8.909727	-14.291975	-5.014790
1CTQ	A	GLY	75	C	-9.294606	9.058845	-14.270668	-5.018999
1CTQ	A	GLU	76	C	-9.294132	9.070633	-14.266782	-5.018981
1CTQ	A	GLY	77	E	-9.300647	9.187685	-14.164276	-4.999240
1CTQ	A	PHE	78	E	-9.815377	12.188392	-13.213860	-5.202984
1CTQ	A	LEU	79	E	-11.030015	16.021708	-12.903486	-4.907954
1CTQ	A	CYS	80	E	-11.280395	17.248990	-12.186848	-4.565964
1CTQ	A	VAL	81	E	-11.122752	17.462410	-11.767530	-4.439736
1CTQ	A	PHE	82	E	-11.143830	16.663932	-12.463812	-4.624026
1CTQ	A	ALA	83	E	-10.366288	12.319568	-13.908204	-4.992492
1CTQ	A	ILE	84	T	-9.962241	10.643962	-14.600388	-5.138543
1CTQ	A	ASN	85	T	-9.673444	9.329620	-15.318808	-5.324989
1CTQ	A	ASN	86	T	-9.663273	9.212274	-15.426007	-5.349747
1CTQ	A	THR	87	H	-9.558368	9.340705	-15.271344	-5.299461
1CTQ	A	LYS	88	H	-9.661874	9.083185	-15.481316	-5.339622
1CTQ	A	SER	89	H	-9.874381	9.079942	-15.596479	-5.374413
1CTQ	A	PHE	90	H	-10.361137	10.989679	-14.705191	-5.122048
1CTQ	A	GLU	91	H	-10.336085	10.844475	-14.794019	-5.132011
1CTQ	A	ASP	92	H	-11.050473	11.230767	-15.809606	-5.339167
1CTQ	A	ILE	93	H	-11.296089	11.240293	-15.739914	-5.336785
1CTQ	A	HIS	94	H	-11.336820	10.922329	-15.765981	-5.324025
1CTQ	A	GLN	95	H	-11.358021	10.766647	-15.746380	-5.315077
1CTQ	A	TYR	96	H	-14.501985	14.031792	-18.299541	-5.487246
1CTQ	A	ARG	97	H	-16.365564	13.168210	-22.727080	-6.450292
1CTQ	A	GLU	98	H	-14.013611	10.966954	-19.497086	-5.613944
1CTQ	A	GLN	99	H	-13.767515	11.450251	-19.271871	-5.524997
1CTQ	A	ILE	100	H	-12.576530	13.948146	-16.142764	-5.361229
1CTQ	A	LYS	101	H	-10.166990	10.203273	-14.418210	-5.206333
1CTQ	A	ARG	102	H	-9.571786	8.626893	-14.462818	-4.841712
1CTQ	A	VAL	103	H	-8.760398	7.748342	-14.033239	-4.933650
1CTQ	A	LYS	104	H	-8.023892	5.712376	-14.471062	-5.126248
1CTQ	A	ASP	105	C	-7.178001	5.434547	-13.111765	-4.812457
1CTQ	A	SER	106	T	-7.157188	5.539618	-13.091140	-4.798200
1CTQ	A	ASP	107	T	-7.156356	5.589902	-13.075017	-4.804126
1CTQ	A	ASP	108	T	-7.185265	5.511660	-13.030968	-4.795273
1CTQ	A	VAL	109	T	-7.297115	5.653520	-12.691215	-4.709527
1CTQ	A	PRO	110	C	-8.864021	9.747670	-12.783076	-4.653418
1CTQ	A	MET	111	E	-9.496344	13.013629	-12.405353	-4.894193
1CTQ	A	VAL	112	E	-9.917445	14.919039	-11.618678	-4.449409
1CTQ	A	LEU	113	E	-10.052179	15.128042	-11.502580	-4.419778
1CTQ	A	VAL	114	E	-10.087467	14.623202	-11.796741	-4.462926
1CTQ	A	GLY	115	E	-10.108822	14.266482	-12.038535	-4.529462
1CTQ	A	ASN	116	E	-10.506283	12.408043	-13.937166	-4.822623
1CTQ	A	LYS	117	T	-8.451810	8.044896	-13.568761	-5.399633
1CTQ	A	CYS	118	T	-6.575309	5.514596	-11.708205	-4.736345
1CTQ	A	ASP	119	T	-6.548764	5.589125	-11.771374	-4.740273
1CTQ	A	LEU	120	T	-6.517584	5.610747	-11.848740	-4.728786
1CTQ	A	ALA	121	T	-6.509804	5.641564	-11.860838	-4.721926
1CTQ	A	ALA	122	T	-6.531212	5.554727	-11.801516	-4.695655
1CTQ	A	ARG	123	T	-7.834099	6.767751	-13.210075	-4.603162
1CTQ	A	THR	124	C	-8.086043	6.570133	-13.280788	-4.455947
1CTQ	A	VAL	125	C	-8.699034	8.185942	-13.310315	-4.329947
1CTQ	A	GLU	126	C	-8.718799	8.325649	-13.378380	-4.408809
1CTQ	A	SER	127	H	-8.763983	8.322028	-13.285593	-4.391399
1CTQ	A	ARG	128	H	-8.766711	8.318051	-13.273406	-4.389447
1CTQ	A	GLN	129	H	-8.886488	8.396735	-13.134129	-4.401475
1CTQ	A	ALA	130	H	-9.104205	8.253662	-12.989800	-4.375910
1CTQ	A	GLN	131	H	-11.601568	8.608313	-17.335760	-4.660289
1CTQ	A	ASP	132	H	-11.138283	8.263248	-15.939464	-4.164365
1CTQ	A	LEU	133	H	-11.154840	8.736293	-15.589543	-4.090436
1CTQ	A	ALA	134	H	-10.395135	8.450497	-15.124643	-4.386306
1CTQ	A	ARG	135	H	-9.732912	9.106813	-14.298107	-4.605789
1CTQ	A	SER	136	H	-9.303801	9.919370	-13.490366	-4.628248
1CTQ	A	TYR	137	H	-9.317724	10.041775	-13.432149	-4.658033
1CTQ	A	GLY	138	C	-9.014282	11.753500	-12.217014	-4.582101
1CTQ	A	ILE	139	C	-9.052200	12.052173	-12.016209	-4.591014

1CTQ	A	PRO	140	C	-9.174042	12.866582	-11.548732	-4.583002
1CTQ	A	TYR	141	E	-9.490259	14.440938	-10.709761	-4.544771
1CTQ	A	ILE	142	E	-9.484131	14.353765	-10.779672	-4.547772
1CTQ	A	GLU	143	E	-10.618803	14.016484	-14.174172	-5.328295
1CTQ	A	THR	144	C	-9.017755	10.963632	-12.612487	-5.141310
1CTQ	A	SER	145	T	-9.019302	10.825209	-12.679690	-5.140475
1CTQ	A	ALA	146	T	-9.001520	10.759971	-12.779812	-5.141223
1CTQ	A	LYS	147	T	-8.680284	9.343275	-13.636812	-5.268432
1CTQ	A	THR	148	T	-8.608262	9.186274	-13.751321	-5.234126
1CTQ	A	ARG	149	T	-8.970021	7.781926	-14.897629	-5.323789
1CTQ	A	GLN	150	T	-8.858799	7.837049	-14.883014	-5.292193
1CTQ	A	GLY	151	T	-8.126702	9.231590	-12.351986	-4.775074
1CTQ	A	VAL	152	H	-8.232334	9.618021	-11.856123	-4.641810
1CTQ	A	GLU	153	H	-8.272287	9.716027	-11.656852	-4.615649
1CTQ	A	ASP	154	H	-8.277232	9.722799	-11.620029	-4.611817
1CTQ	A	ALA	155	H	-8.320898	9.829604	-11.368964	-4.570528
1CTQ	A	PHE	156	H	-11.425937	16.259548	-12.362292	-4.683603
1CTQ	A	TYR	157	H	-12.842465	18.253734	-14.397623	-5.180449
1CTQ	A	THR	158	H	-12.680935	16.429604	-14.655267	-4.900092
1CTQ	A	LEU	159	H	-12.730806	16.172717	-14.652777	-4.865121
1CTQ	A	VAL	160	H	-12.666778	15.970754	-15.127181	-5.100699
1CTQ	A	ARG	161	H	-12.010616	13.349352	-16.391795	-5.733126
1CTQ	A	GLU	162	H	-8.859219	10.916236	-12.123372	-5.066698
1CTQ	A	ILE	163	H	-7.191113	8.005964	-10.255710	-3.981675
1CTQ	A	ARG	164	H	-7.191113	8.005964	-10.255710	-3.981675
1CTQ	A	GLN	165	H	-7.191113	8.005964	-10.255710	-3.981675
1CTQ	A	HIS	166	C	-7.191113	8.005964	-10.255710	-3.981675
1CY5	A	MET	1	C	-10.634385	6.860637	-16.055233	-4.480675
1CY5	A	ASP	2	C	-10.634385	6.860637	-16.055233	-4.480675
1CY5	A	ALA	3	H	-10.634385	6.860637	-16.055233	-4.480675
1CY5	A	LYS	4	H	-10.634385	6.860637	-16.055233	-4.480675
1CY5	A	ALA	5	H	-12.121625	9.439992	-17.593826	-5.067311
1CY5	A	ARG	6	H	-12.494705	13.141717	-16.194059	-4.986383
1CY5	A	ASN	7	H	-10.930613	11.669280	-14.996411	-5.301188
1CY5	A	CYS	8	H	-10.627517	12.428184	-14.545034	-5.238954
1CY5	A	LEU	9	H	-10.553813	12.640528	-14.495618	-5.206510
1CY5	A	LEU	10	H	-10.393587	12.097554	-14.735180	-5.185476
1CY5	A	GLN	11	H	-10.239881	11.660897	-14.870365	-5.163314
1CY5	A	HIS	12	H	-10.425021	11.781774	-14.863749	-5.099011
1CY5	A	ARG	13	H	-10.603137	11.179569	-15.260712	-5.082025
1CY5	A	GLU	14	H	-10.287052	11.638196	-14.677064	-5.156377
1CY5	A	ALA	15	H	-10.387836	12.024525	-14.520635	-5.186288
1CY5	A	LEU	16	H	-10.560147	13.028024	-14.156106	-5.261806
1CY5	A	GLU	17	H	-10.529142	12.968379	-14.293524	-5.315277
1CY5	A	LYS	18	H	-9.972306	13.202634	-13.638019	-5.433380
1CY5	A	ASP	19	H	-9.968363	13.581938	-13.492559	-5.478471
1CY5	A	ILE	20	C	-9.206470	13.315555	-12.148750	-5.184002
1CY5	A	LYS	21	C	-8.609148	12.967725	-11.516314	-5.077595
1CY5	A	THR	22	H	-8.569686	13.099288	-11.535837	-5.087643
1CY5	A	SER	23	H	-8.602548	13.079240	-11.446977	-5.062413
1CY5	A	TYR	24	H	-8.619756	13.055632	-11.391266	-5.053413
1CY5	A	ILE	25	H	-8.807552	12.996691	-11.285100	-5.045225
1CY5	A	MET	26	H	-10.124896	14.763925	-12.257921	-5.261120
1CY5	A	ASP	27	H	-11.343627	12.061259	-15.634753	-5.164073
1CY5	A	HIS	28	H	-11.063278	11.753554	-15.360479	-5.190869
1CY5	A	MET	29	H	-8.811135	9.382541	-12.845163	-4.923567
1CY5	A	ILE	30	H	-8.061442	8.696712	-12.366557	-4.720306
1CY5	A	SER	31	H	-8.002917	8.875322	-12.425779	-4.748245
1CY5	A	ASP	32	H	-7.972392	8.964131	-12.490783	-4.777989
1CY5	A	GLY	33	C	-7.849166	9.309283	-12.341501	-4.763666
1CY5	A	PHE	34	C	-7.954124	9.394043	-12.231877	-4.712769
1CY5	A	LEU	35	C	-7.725405	9.157590	-11.574717	-4.472762
1CY5	A	THR	36	C	-7.563519	8.521798	-11.892509	-4.494836
1CY5	A	ILE	37	H	-7.560341	8.425852	-11.940634	-4.488265
1CY5	A	SER	38	H	-7.632776	8.112446	-11.977573	-4.462132
1CY5	A	GLU	39	H	-7.645102	8.035503	-11.976490	-4.465618
1CY5	A	GLU	40	H	-8.228082	7.293251	-13.173458	-4.692874
1CY5	A	GLU	41	H	-7.748916	9.254288	-11.353992	-4.691416
1CY5	A	LYS	42	H	-7.542669	10.409048	-11.059276	-4.887712
1CY5	A	VAL	43	H	-7.016205	10.397560	-10.515780	-4.830917
1CY5	A	ARG	44	H	-6.582829	9.028247	-10.962367	-4.934782
1CY5	A	ASN	45	H	-6.574121	9.003795	-11.019404	-4.945515
1CY5	A	GLU	46	C	-6.656288	8.957629	-11.003921	-4.987182
1CY5	A	PRO	47	C	-6.698579	8.664756	-11.039819	-4.961788
1CY5	A	THR	48	C	-6.949191	7.757093	-11.510760	-5.050800
1CY5	A	GLN	49	H	-8.902402	7.711427	-14.976990	-5.559985
1CY5	A	GLN	50	H	-9.910975	7.421089	-15.873174	-5.257463
1CY5	A	GLN	51	H	-9.964133	7.307017	-15.710155	-5.201420
1CY5	A	ARG	52	H	-13.221298	12.089405	-19.021848	-5.703637
1CY5	A	ALA	53	H	-11.557423	17.568283	-12.167886	-4.974395
1CY5	A	ALA	54	H	-11.393151	17.183389	-12.665794	-5.067138

1CY5	A	MET	55	H	-11.316566	17.384082	-12.815006	-5.180771
1CY5	A	LEU	56	H	-11.198289	17.694785	-12.794527	-5.244315
1CY5	A	ILE	57	H	-11.114033	17.954465	-12.799934	-5.316656
1CY5	A	LYS	58	H	-10.095893	15.578059	-12.250842	-5.515343
1CY5	A	MET	59	H	-9.974809	15.742660	-12.377985	-5.609876
1CY5	A	ILE	60	H	-9.914268	15.544012	-12.582129	-5.625430
1CY5	A	LEU	61	H	-9.904535	15.303211	-12.752796	-5.644428
1CY5	A	LYS	62	C	-9.859748	14.628285	-13.198442	-5.674141
1CY5	A	LYS	63	C	-10.401620	13.527128	-14.933847	-5.934515
1CY5	A	ASP	64	C	-10.722290	11.413870	-16.322992	-5.917239
1CY5	A	ASN	65	H	-11.048610	9.347441	-17.723621	-6.007465
1CY5	A	ASP	66	H	-11.223912	8.780645	-17.864451	-5.979823
1CY5	A	SER	67	H	-12.552416	10.788074	-18.597545	-5.796054
1CY5	A	TYR	68	H	-13.183597	13.536522	-17.689172	-5.741954
1CY5	A	VAL	69	H	-13.934421	16.053371	-17.353314	-5.479607
1CY5	A	SER	70	H	-14.280949	18.267342	-16.583830	-5.474715
1CY5	A	PHE	71	H	-13.906897	20.473945	-14.762772	-5.331942
1CY5	A	TYR	72	H	-12.765627	17.931623	-13.670648	-4.859798
1CY5	A	ASN	73	H	-9.984563	13.314302	-11.752562	-4.546910
1CY5	A	ALA	74	H	-9.732819	13.642218	-11.783911	-4.588005
1CY5	A	LEU	75	H	-8.310830	12.104765	-10.994960	-4.955615
1CY5	A	LEU	76	H	-8.225156	12.076538	-11.227568	-5.005534
1CY5	A	HIS	77	H	-8.199385	12.003633	-11.356840	-5.016775
1CY5	A	GLU	78	H	-8.220034	11.899831	-11.402546	-5.044585
1CY5	A	GLY	79	C	-8.228876	11.824056	-11.427270	-5.052372
1CY5	A	TYR	80	C	-9.156616	11.348288	-13.375615	-5.278324
1CY5	A	LYS	81	H	-9.060682	9.890129	-12.775890	-4.365611
1CY5	A	ASP	82	H	-8.994356	10.156423	-12.281355	-4.120510
1CY5	A	LEU	83	H	-8.989990	10.488184	-12.021457	-4.050600
1CY5	A	ALA	84	H	-8.997029	10.515753	-11.953236	-4.016601
1CY5	A	ALA	85	H	-8.995819	10.538761	-11.962223	-4.028587
1CY5	A	LEU	86	H	-9.567059	12.082164	-11.948871	-4.109203
1CY5	A	LEU	87	H	-8.560205	14.073438	-10.559548	-5.234298
1CY5	A	HIS	88	G	-6.490398	10.034855	-8.802943	-4.364028
1CY5	A	ASP	89	G	-5.974633	9.542221	-8.287428	-3.923429
1CY5	A	GLY	90	G	-5.974633	9.542221	-8.287428	-3.923429
1CY5	A	ILE	91	C	-5.974633	9.542221	-8.287428	-3.923429
1CY5	A	PRO	92	C	-5.974633	9.542221	-8.287428	-3.923429
1CZT	A	GLY	0	C	-4.279772	3.174064	-8.897417	-3.672832
1CZT	A	CYS	1	C	-4.279772	3.174064	-8.897417	-3.672832
1CZT	A	SER	2	C	-4.279772	3.174064	-8.897417	-3.672832
1CZT	A	THR	3	E	-4.279772	3.174064	-8.897417	-3.672832
1CZT	A	PRO	4	E	-5.392495	4.600458	-10.040855	-4.225982
1CZT	A	LEU	5	C	-7.421162	8.786829	-12.335441	-5.433340
1CZT	A	GLY	6	T	-8.068595	9.224711	-13.872398	-6.191359
1CZT	A	MET	7	T	-7.975675	7.756839	-14.013046	-5.823657
1CZT	A	GLU	8	T	-7.217022	7.323078	-12.759081	-5.303300
1CZT	A	ASN	9	T	-6.841845	7.264912	-12.552752	-5.271387
1CZT	A	GLY	10	T	-6.822694	7.271791	-12.612578	-5.277996
1CZT	A	LYS	11	T	-6.829634	7.269489	-12.572480	-5.258949
1CZT	A	ILE	12	T	-6.904055	7.210538	-12.424072	-5.190637
1CZT	A	GLU	13	T	-7.222566	7.299540	-12.557482	-5.259469
1CZT	A	ASN	14	G	-8.527088	8.130448	-14.553014	-5.457084
1CZT	A	LYS	15	G	-8.890951	9.449005	-14.291350	-5.296015
1CZT	A	GLN	16	G	-9.159555	10.582781	-13.947874	-5.298192
1CZT	A	ILE	17	E	-8.821069	10.332021	-13.049602	-4.843217
1CZT	A	THR	18	E	-8.902058	10.506316	-12.736708	-4.617384
1CZT	A	ALA	19	E	-8.922210	10.606453	-12.627992	-4.590937
1CZT	A	SER	20	C	-9.039168	10.493136	-12.675834	-4.582721
1CZT	A	SER	21	C	-9.048378	10.473322	-12.667222	-4.586907
1CZT	A	PHE	22	C	-8.289383	12.393197	-11.050297	-5.188945
1CZT	A	LYS	23	C	-5.919575	7.204477	-10.105835	-4.870222
1CZT	A	LYS	24	E	-2.856897	5.522416	-6.794405	-4.667724
1CZT	A	SER	25	E	-2.825698	5.454774	-6.952270	-4.673835
1CZT	A	TRP	26	T	-2.819924	5.477883	-6.981792	-4.680753
1CZT	A	TRP	27	T	-2.819977	5.477255	-6.981445	-4.680702
1CZT	A	GLY	28	T	-2.823151	5.467980	-6.964111	-4.679292
1CZT	A	ASP	29	E	-4.491413	4.698619	-9.783610	-4.808576
1CZT	A	TYR	30	E	-5.576431	7.747467	-9.880586	-5.308793
1CZT	A	TRP	31	C	-10.520137	14.335585	-14.561273	-6.353547
1CZT	A	GLU	32	C	-11.292601	16.569064	-14.295162	-5.974145
1CZT	A	PRO	33	G	-11.574310	16.036680	-12.725135	-4.727115
1CZT	A	PHE	34	G	-11.603454	15.764458	-12.443820	-4.491015
1CZT	A	ARG	35	G	-11.608955	15.711934	-12.424334	-4.479664
1CZT	A	ALA	36	T	-11.611112	15.676921	-12.427990	-4.477226
1CZT	A	ARG	37	B	-14.137119	10.869604	-20.079316	-5.389786
1CZT	A	LEU	38	T	-9.112383	6.986288	-14.675895	-5.186722
1CZT	A	ASN	39	T	-8.351926	4.452757	-15.119728	-4.874826
1CZT	A	ALA	40	T	-6.802223	5.616276	-11.232280	-4.057345
1CZT	A	GLN	41	C	-6.703136	5.686642	-11.474339	-4.148655
1CZT	A	GLY	42	T	-6.676362	5.825611	-11.504615	-4.167594

1CZT	A	ARG	43	T	-6.686143	5.806361	-11.451847	-4.150626
1CZT	A	VAL	44	T	-6.712468	5.911978	-11.277467	-4.123151
1CZT	A	ASN	45	T	-7.656000	6.710403	-12.655288	-4.633352
1CZT	A	ALA	46	C	-8.524186	8.836048	-12.161716	-4.577657
1CZT	A	TRP	47	E	-12.313765	14.624162	-15.770598	-5.416331
1CZT	A	GLN	48	E	-9.528073	8.585392	-14.870773	-5.545576
1CZT	A	ALA	49	T	-7.785953	6.989995	-13.139170	-5.161939
1CZT	A	LYS	50	T	-7.514219	6.637550	-13.555344	-5.279892
1CZT	A	ALA	51	T	-7.332473	6.157867	-13.837067	-5.272043
1CZT	A	ASN	52	T	-7.302572	6.191136	-13.932806	-5.308917
1CZT	A	ASN	53	T	-7.312125	6.161631	-13.926379	-5.310270
1CZT	A	ASN	54	T	-7.640557	5.615864	-14.582065	-5.436307
1CZT	A	LYS	55	T	-8.000484	5.268170	-14.842474	-5.397631
1CZT	A	GLN	56	T	-9.003052	7.236221	-15.819884	-6.050997
1CZT	A	TRP	57	C	-10.213864	9.810855	-16.070534	-6.260442
1CZT	A	LEU	58	E	-12.387464	14.565454	-16.566613	-6.153259
1CZT	A	GLU	59	E	-12.473552	14.995819	-15.655424	-5.509715
1CZT	A	ILE	60	E	-10.644923	13.690270	-13.490948	-5.345227
1CZT	A	ASP	61	E	-8.845755	12.845221	-11.674563	-5.385177
1CZT	A	LEU	62	E	-8.098769	13.298428	-10.675747	-5.286602
1CZT	A	LEU	63	E	-8.060392	13.295161	-10.813170	-5.316451
1CZT	A	LYS	64	E	-8.052637	13.321639	-10.836989	-5.319537
1CZT	A	ILE	65	E	-8.055676	13.342100	-10.817129	-5.320878
1CZT	A	LYS	66	E	-8.224781	13.530663	-10.570572	-5.298843
1CZT	A	LYS	67	E	-9.463114	14.134275	-12.721818	-5.614861
1CZT	A	ILE	68	E	-9.767950	16.398918	-11.086371	-4.764376
1CZT	A	THR	69	E	-9.782171	16.601297	-10.661530	-4.506489
1CZT	A	ALA	70	E	-9.857345	16.563809	-10.443981	-4.362163
1CZT	A	ILE	71	E	-9.876967	16.563234	-10.378102	-4.333216
1CZT	A	ILE	72	E	-9.977166	16.575627	-10.235826	-4.284628
1CZT	A	THR	73	E	-10.550701	15.597421	-11.967012	-4.720637
1CZT	A	GLN	74	E	-11.415829	12.234434	-17.007408	-5.912115
1CZT	A	GLY	75	C	-8.240697	5.914756	-14.025128	-5.091376
1CZT	A	CYS	76	E	-6.845311	5.121989	-12.215241	-4.592750
1CZT	A	LYS	77	E	-5.521640	4.621271	-10.465920	-4.321953
1CZT	A	SER	78	E	-5.398644	4.772208	-10.592760	-4.360849
1CZT	A	LEU	79	T	-5.397024	4.779165	-10.602882	-4.363202
1CZT	A	SER	80	T	-5.401900	4.770001	-10.574711	-4.357212
1CZT	A	SER	81	E	-5.450799	4.746664	-10.449675	-4.341357
1CZT	A	GLU	82	E	-6.382007	5.453467	-11.187002	-4.538850
1CZT	A	MET	83	E	-8.891235	7.335477	-14.319065	-5.226533
1CZT	A	TYR	84	E	-12.542060	13.232688	-17.075096	-5.881401
1CZT	A	VAL	85	E	-13.688716	17.006289	-17.236088	-5.994299
1CZT	A	LYS	86	E	-13.640268	17.548367	-16.822338	-5.934878
1CZT	A	SER	87	E	-13.830748	18.140395	-16.548896	-5.701522
1CZT	A	TYR	88	E	-13.817398	18.803279	-16.186401	-5.692419
1CZT	A	THR	89	E	-13.177154	18.515275	-15.489564	-5.781493
1CZT	A	ILE	90	E	-12.971489	18.457725	-15.520046	-5.877060
1CZT	A	HIS	91	E	-11.784761	16.992689	-16.456014	-7.335325
1CZT	A	TYR	92	E	-9.440802	13.490525	-13.239187	-6.154569
1CZT	A	SER	93	E	-5.999160	6.738427	-10.416040	-4.881435
1CZT	A	GLU	94	T	-3.608322	5.212792	-7.952744	-4.657275
1CZT	A	GLN	95	T	-3.533491	5.590708	-7.974028	-4.695251
1CZT	A	GLY	96	T	-3.491094	5.768677	-8.004185	-4.703938
1CZT	A	VAL	97	T	-3.486558	5.795387	-8.011291	-4.701611
1CZT	A	GLU	98	T	-3.495171	5.781416	-7.975565	-4.698658
1CZT	A	TRP	99	C	-4.486391	8.326516	-8.233115	-4.875176
1CZT	A	LYS	100	E	-5.014882	8.252666	-8.425204	-4.755490
1CZT	A	PRO	101	E	-6.375539	9.263281	-8.916285	-4.382818
1CZT	A	TYR	102	C	-11.405762	14.295576	-14.954767	-5.258756
1CZT	A	ARG	103	C	-8.176832	8.326168	-11.999526	-4.440413
1CZT	A	LEU	104	T	-5.383267	5.163429	-9.455574	-4.049733
1CZT	A	LYS	105	T	-4.388130	3.424555	-9.085452	-3.812908
1CZT	A	SER	106	T	-4.312628	3.431562	-9.268301	-3.851477
1CZT	A	SER	107	T	-4.311576	3.436610	-9.275599	-3.853410
1CZT	A	MET	108	C	-4.299395	3.508197	-9.305404	-3.871985
1CZT	A	VAL	109	C	-4.402093	3.200658	-9.279719	-3.838318
1CZT	A	ASP	110	C	-5.461916	4.078133	-10.672292	-4.236561
1CZT	A	LYS	111	C	-6.499748	7.185718	-11.012226	-4.766227
1CZT	A	ILE	112	E	-6.543105	7.259592	-10.833914	-4.753830
1CZT	A	PHE	113	E	-8.438379	12.497671	-11.444870	-5.095398
1CZT	A	GLU	114	E	-8.316098	10.634838	-12.349281	-5.077290
1CZT	A	GLY	115	C	-8.136227	9.648427	-12.847036	-5.135208
1CZT	A	ASN	116	C	-8.072424	7.089391	-14.075286	-5.132644
1CZT	A	THR	117	C	-5.314435	4.962529	-10.253485	-4.688489
1CZT	A	ASN	118	T	-5.265107	5.060223	-10.398184	-4.728338
1CZT	A	THR	119	T	-5.250843	5.108898	-10.434274	-4.731308
1CZT	A	LYS	120	T	-5.217323	5.268928	-10.458064	-4.741981
1CZT	A	GLY	121	T	-5.218814	5.268281	-10.449545	-4.741519
1CZT	A	HIS	122	C	-6.313192	7.033640	-11.698236	-5.047582
1CZT	A	VAL	123	E	-6.687963	7.780392	-11.374651	-4.925145

1CZT	A	LYS	124	E	-6.883272	8.148317	-11.078580	-4.952533
1CZT	A	ASN	125	E	-8.682141	10.932801	-12.930238	-5.224104
1CZT	A	PHE	126	E	-8.467034	13.701883	-10.218979	-4.578699
1CZT	A	PHE	127	E	-8.331658	14.381927	-9.475851	-4.359683
1CZT	A	ASN	128	E	-6.743201	11.744592	-7.631799	-3.847995
1CZT	A	PRO	129	E	-6.590178	12.086821	-7.649292	-3.884652
1CZT	A	PRO	130	E	-6.589972	12.088799	-7.649744	-3.884673
1CZT	A	ILE	131	E	-6.607204	12.035903	-7.599109	-3.872356
1CZT	A	ILE	132	E	-6.618141	11.982149	-7.574128	-3.867814
1CZT	A	SER	133	E	-7.449929	13.305128	-7.810673	-4.043623
1CZT	A	ARG	134	E	-10.776056	15.521958	-11.507435	-4.506578
1CZT	A	PHE	135	E	-13.348912	18.134570	-14.515055	-4.874272
1CZT	A	ILE	136	E	-13.078034	19.478494	-12.632254	-4.355888
1CZT	A	ARG	137	E	-12.127804	18.389318	-12.302138	-4.690797
1CZT	A	VAL	138	E	-9.714378	15.479214	-10.125212	-4.471412
1CZT	A	ILE	139	E	-9.474182	15.776089	-10.343367	-4.630771
1CZT	A	PRO	140	E	-9.334521	15.664773	-10.719955	-4.801584
1CZT	A	LYS	141	E	-9.290756	15.409158	-11.060236	-4.902284
1CZT	A	THR	142	E	-9.291302	15.363297	-11.091278	-4.909146
1CZT	A	TRP	143	E	-9.676889	15.292251	-12.048695	-5.321203
1CZT	A	ASN	144	E	-9.972894	13.977089	-13.510595	-5.671170
1CZT	A	GLN	145	T	-10.485490	12.200133	-15.610965	-5.987590
1CZT	A	SER	146	T	-10.951316	12.190262	-15.822314	-5.758265
1CZT	A	ILE	147	C	-11.011731	12.346070	-15.617273	-5.741071
1CZT	A	THR	148	E	-11.044319	12.282204	-15.560418	-5.741559
1CZT	A	LEU	149	E	-11.900985	14.987713	-14.510945	-5.486314
1CZT	A	ARG	150	E	-14.440287	18.221018	-16.838488	-5.540007
1CZT	A	LEU	151	E	-12.807523	19.468020	-13.298821	-5.415725
1CZT	A	GLU	152	E	-12.820686	19.490441	-13.289153	-5.452968
1CZT	A	LEU	153	E	-11.896681	18.070340	-14.760021	-6.687913
1CZT	A	PHE	154	E	-9.371877	12.624249	-13.467412	-6.160619
1CZT	A	GLY	155	E	-5.598660	6.479413	-10.107458	-4.926530
1CZT	A	CYS	156	E	-4.449117	5.770116	-8.109003	-4.006914
1CZT	A	ASP	157	E	-4.449117	5.770116	-8.109003	-4.006914
1CZT	A	ILE	158	C	-4.449117	5.770116	-8.109003	-4.006914
1CZT	A	TYR	159	C	-4.449117	5.770116	-8.109003	-4.006914
1D7P	M	LEU	1	C	-3.643243	0.818293	-8.881493	-3.541802
1D7P	M	ASN	2	T	-3.643243	0.818293	-8.881493	-3.541802
1D7P	M	SER	3	T	-3.643243	0.818293	-8.881493	-3.541802
1D7P	M	CYS	4	T	-3.643243	0.818293	-8.881493	-3.541802
1D7P	M	SER	5	T	-5.519317	2.623546	-12.025043	-4.495284
1D7P	M	MET	6	E	-6.371953	4.984567	-12.863038	-4.992660
1D7P	M	PRO	7	E	-6.707349	6.658537	-12.300146	-4.991777
1D7P	M	LEU	8	C	-7.143306	9.449320	-10.389582	-4.347492
1D7P	M	GLY	9	T	-7.122614	9.450511	-10.439373	-4.361678
1D7P	M	MET	10	T	-7.506713	9.772541	-11.854985	-5.031325
1D7P	M	GLU	11	T	-6.954737	8.479914	-10.969897	-4.603744
1D7P	M	SER	12	T	-6.945568	8.240363	-11.048474	-4.555334
1D7P	M	LYS	13	T	-6.934671	8.206561	-11.104720	-4.556247
1D7P	M	ALA	14	T	-6.947534	8.106427	-11.061820	-4.500782
1D7P	M	ILE	15	T	-7.069366	8.024945	-10.798053	-4.363437
1D7P	M	SER	16	T	-8.228675	6.903826	-13.588408	-4.425637
1D7P	M	ASP	17	G	-8.498670	6.989862	-14.384169	-4.756645
1D7P	M	ALA	18	G	-8.632510	7.346488	-14.338281	-4.759165
1D7P	M	GLN	19	G	-8.993708	8.744359	-14.355362	-5.055671
1D7P	M	ILE	20	E	-8.839744	9.194646	-13.796778	-4.881307
1D7P	M	THR	21	E	-8.841595	10.093312	-13.210690	-4.791717
1D7P	M	ALA	22	E	-9.002532	10.680668	-12.753819	-4.666374
1D7P	M	SER	23	T	-9.132453	10.770564	-12.697902	-4.697729
1D7P	M	SER	24	T	-9.132161	10.772667	-12.704566	-4.702665
1D7P	M	TYR	25	T	-9.033516	11.224511	-12.685381	-4.981992
1D7P	M	PHE	26	C	-7.386032	6.305558	-12.101192	-4.565942
1D7P	M	THR	27	E	-4.424343	4.213749	-8.865337	-4.236822
1D7P	M	ASN	28	E	-4.212306	4.323505	-9.068843	-4.294979
1D7P	M	MET	29	T	-4.211965	4.327212	-9.070523	-4.295453
1D7P	M	PHE	30	T	-4.212055	4.326187	-9.069992	-4.295344
1D7P	M	ALA	31	E	-4.214761	4.317912	-9.056161	-4.294153
1D7P	M	THR	32	E	-4.923498	4.585940	-9.536579	-4.426654
1D7P	M	TRP	33	C	-8.624034	10.806264	-12.031063	-5.118123
1D7P	M	SER	34	C	-10.375434	11.940720	-13.777529	-4.805169
1D7P	M	PRO	35	G	-10.455598	11.780405	-13.577349	-4.695914
1D7P	M	SER	36	G	-10.484124	11.612750	-13.538394	-4.674158
1D7P	M	LYS	37	G	-10.506625	11.475245	-13.499914	-4.656211
1D7P	M	ALA	38	T	-10.508756	11.458760	-13.493222	-4.653471
1D7P	M	ARG	39	B	-12.810290	12.015939	-17.839119	-5.436120
1D7P	M	LEU	40	T	-7.930145	8.820460	-11.902627	-4.985552
1D7P	M	HIS	41	T	-6.138490	5.631907	-10.482082	-4.260718
1D7P	M	LEU	42	T	-5.950168	5.667591	-10.611890	-4.250390
1D7P	M	GLN	43	C	-5.869032	5.544007	-10.826651	-4.276324
1D7P	M	GLY	44	T	-5.759963	5.809512	-10.803388	-4.296142
1D7P	M	ARG	45	T	-5.775342	5.730514	-10.774548	-4.277987

```
1D7P         M          SER              46                T -6.204627  6.008377 -11.162245 -4.335508
1D7P         M          ASN              47                T -6.525682  6.185005 -11.308771 -4.416671
1D7P         M          ALA              48                C -6.816269  7.124125 -10.688050 -4.393829
1D7P         M          TRP              49                B -11.744956 14.344932 -13.881514 -4.636064
1D7P         M          ARG              50                C -10.478368 11.529504 -14.274990 -5.322250
1D7P         M          PRO              51                T -7.988017  9.370255 -11.972899 -5.165242
1D7P         M          GLN              52                T -7.766647  8.915530 -12.400573 -5.181410
1D7P         M          VAL              53                T -7.592462  8.035093 -12.750652 -5.034012
1D7P         M          ASN              54                T -7.538592  8.041480 -12.868487 -5.058369
1D7P         M          ASN              55                T -7.530923  8.076253 -12.878229 -5.064230
1D7P         M          PRO              56                T -7.890423  7.028286 -13.665768 -4.982184
1D7P         M          LYS              57                T -8.177673  6.477189 -13.866179 -4.835646
1D7P         M          GLU              58                T -8.860228  8.678868 -14.063559 -5.339757
1D7P         M          TRP              59                C -9.843851 11.061564 -13.877723 -5.449232
1D7P         M          LEU              60                E -11.993435 14.078074 -15.045875 -5.458481
1D7P         M          GLN              61                E -14.173011 15.574115 -18.745723 -6.125017
1D7P         M          VAL              62                E -12.665105 14.180008 -16.309478 -5.742565
1D7P         M          ASP              63                E -11.628078 14.072062 -15.923740 -6.271406
1D7P         M          PHE              64                E -10.733732 15.249476 -14.306953 -6.269257
1D7P         M          GLN              65                E -10.451934 14.641684 -14.783837 -6.396694
1D7P         M          LYS              66                E -10.419646 14.717534 -14.866434 -6.418899
1D7P         M          THR              67                E -10.412528 14.777138 -14.827855 -6.404470
1D7P         M          MET              68                E -10.347925 14.698784 -14.549527 -6.188614
1D7P         M          LYS              69                E -9.937666 14.093654 -12.671409 -5.130184
1D7P         M          VAL              70                E -9.096349 13.667604 -10.674134 -4.468869
1D7P         M          THR              71                E -8.987155 13.578362 -10.910312 -4.534807
1D7P         M          GLY              72                E -8.984779 13.564475 -10.932361 -4.538299
1D7P         M          VAL              73                E -8.992149 13.548304 -10.908294 -4.530412
1D7P         M          THR              74                E -9.080091 13.451391 -10.811483 -4.507506
1D7P         M          THR              75                E -9.938802 13.142697 -12.701723 -5.013252
1D7P         M          GLN              76                E -10.856986 12.326247 -15.915108 -5.667715
1D7P         M          GLY              77                C -6.372803  8.758299 -9.143434 -4.384381
1D7P         M          VAL              78                E -4.813704  7.438885 -7.458802 -3.945269
1D7P         M          LYS              79                E -2.331948  6.170434 -5.141658 -4.161517
1D7P         M          SER              80                E -2.307760  6.165463 -5.256540 -4.172523
1D7P         M          LEU              81                T -2.307260  6.167222 -5.260967 -4.173207
1D7P         M          LEU              82                T -2.307906  6.164134 -5.256512 -4.172796
1D7P         M          THR              83                E -2.316296  6.143972 -5.224041 -4.174188
1D7P         M          SER              84                E -4.225406  5.855331 -7.868047 -4.288432
1D7P         M          MET              85                E -6.524223  8.009841 -10.299253 -4.817406
1D7P         M          TYR              86                E -10.831410 13.792775 -13.634570 -5.367832
1D7P         M          VAL              87                E -12.809162 18.338191 -14.988133 -5.585040
1D7P         M          LYS              88                E -12.261083 19.676494 -13.104638 -5.517513
1D7P         M          GLU              89                E -12.167911 19.691023 -13.136168 -5.506901
1D7P         M          PHE              90                E -12.105244 19.717008 -13.058367 -5.434147
1D7P         M          LEU              91                E -11.957646 18.512299 -13.571832 -5.362166
1D7P         M          ILE              92                E -12.019625 18.299752 -13.666820 -5.365989
1D7P         M          SER              93                E -12.293624 15.185397 -15.712032 -5.318182
1D7P         M          SER              94                E -11.003419  7.431795 -17.903645 -5.688118
1D7P         M          SER              95                E -8.697334  4.281391 -15.564945 -5.142833
1D7P         M          GLN              96                T -6.898277  3.149618 -13.575565 -4.885148
1D7P         M          ASP              97                T -6.123827  6.545122 -11.526445 -5.201262
1D7P         M          GLY              98                T -5.986179  6.952486 -11.411281 -5.192219
1D7P         M          HIS              99                T -5.963033  7.150657 -11.360698 -5.182615
1D7P         M          GLN             100                T -5.968789  7.179740 -11.320024 -5.183111
1D7P         M          TRP             101                C -6.099685  8.191850 -10.786719 -5.259932
1D7P         M          THR             102                E -6.813301  9.099665 -10.837337 -5.124624
1D7P         M          LEU             103                E -7.883999 12.189430 -10.197822 -4.987053
1D7P         M          PHE             104                C -9.182825 12.471569 -13.106642 -5.771529
1D7P         M          PHE             105                E -5.623987  5.426035 -10.624984 -4.902553
1D7P         M          GLN             106                E -3.899218  4.709876 -8.507400 -4.577872
1D7P         M          ASN             107                T -3.871450  4.784975 -8.576266 -4.585194
1D7P         M          GLY             108                T -3.853176  4.883356 -8.590426 -4.580923
1D7P         M          LYS             109                E -3.853221  4.882904 -8.590072 -4.580830
1D7P         M          VAL             110                E -3.883842  4.854297 -8.481193 -4.563192
1D7P         M          LYS             111                C -5.390939  7.022310 -9.596877 -4.606790
1D7P         M          VAL             112                C -5.924195  8.020394 -9.024176 -4.433083
1D7P         M          PHE             113                E -9.848156 13.164567 -12.504543 -4.832340
1D7P         M          GLN             114                E -10.615393 10.926564 -15.969377 -5.474516
1D7P         M          GLY             115                C -9.791074  8.006264 -15.873148 -5.462729
1D7P         M          ASN             116                C -9.820234  7.588667 -16.018247 -5.447415
1D7P         M          GLN             117                C -8.221636  8.327320 -12.669271 -4.930858
1D7P         M          ASP             118                T -8.005152  8.715354 -12.552395 -4.902388
1D7P         M          SER             119                T -7.973015  8.809184 -12.568076 -4.889277
1D7P         M          PHE             120                T -7.605646  9.442067 -11.382803 -4.498178
1D7P         M          THR             121                T -7.478745  9.181635 -11.432851 -4.397946
1D7P         M          PRO             122                C -7.003311  8.868373 -10.088620 -3.940170
1D7P         M          VAL             123                E -7.007354  8.903728 -9.998200 -3.888047
1D7P         M          VAL             124                E -6.659229  9.396671 -9.648237 -4.016137
1D7P         M          ASN             125                E -6.629914  9.378104 -9.646503 -4.010676
1D7P         M          CYS             126                E -4.747784  8.957257 -5.881594 -3.425315
```

1D7P	M	LEU	127	E	-4.725419	9.093887	-5.881812	-3.432828
1D7P	M	ASP	128	E	-4.520166	8.993632	-6.112711	-3.480755
1D7P	M	PRO	129	E	-4.517052	9.017812	-6.112491	-3.482821
1D7P	M	PRO	130	E	-4.519363	9.015467	-6.097332	-3.480710
1D7P	M	LEU	131	E	-5.146858	9.157474	-6.786116	-3.628737
1D7P	M	LEU	132	E	-5.212365	8.882934	-6.769724	-3.623120
1D7P	M	THR	133	E	-6.915465	11.110665	-8.318241	-4.092101
1D7P	M	ARG	134	E	-9.954417	13.375704	-11.582747	-4.566576
1D7P	M	TYR	135	E	-13.555459	16.892635	-15.751344	-5.225938
1D7P	M	LEU	136	E	-13.862561	18.451334	-15.196665	-5.105266
1D7P	M	ARG	137	E	-14.120808	18.796670	-15.464734	-5.167983
1D7P	M	ILE	138	E	-12.870330	16.507713	-14.732713	-5.121581
1D7P	M	HIS	139	E	-12.740667	16.746332	-14.861970	-5.199986
1D7P	M	PRO	140	E	-12.462386	16.738578	-14.659687	-5.124502
1D7P	M	GLN	141	E	-11.635674	14.451639	-14.906628	-5.439145
1D7P	M	SER	142	E	-11.495150	14.045200	-15.216879	-5.464634
1D7P	M	TRP	143	E	-11.023049	14.379669	-14.191429	-5.325049
1D7P	M	VAL	144	E	-10.209836	12.848941	-13.320141	-4.938850
1D7P	M	HIS	145	T	-10.132153	13.147546	-13.240304	-4.935311
1D7P	M	GLN	146	T	-10.168761	13.108988	-13.129767	-4.896966
1D7P	M	ILE	147	C	-10.182163	13.123483	-13.054947	-4.881609
1D7P	M	ALA	148	C	-10.273058	12.852921	-12.992258	-4.828154
1D7P	M	LEU	149	B	-11.335486	15.380068	-12.791058	-4.918013
1D7P	M	ARG	150	E	-14.231604	17.865957	-16.510951	-5.318250
1D7P	M	MET	151	E	-11.851031	15.274141	-14.014056	-5.299829
1D7P	M	GLU	152	E	-11.851064	15.256708	-14.061579	-5.329680
1D7P	M	VAL	153	E	-11.100512	14.466103	-14.947864	-6.129884
1D7P	M	LEU	154	E	-9.342166	11.202243	-13.929621	-5.943240
1D7P	M	GLY	155	E	-6.287801	6.626622	-10.902363	-4.931816
1D7P	M	CYS	156	E	-5.070002	5.712923	-8.882365	-4.005424
1D7P	M	GLU	157	E	-5.070002	5.712923	-8.882365	-4.005424
1D7P	M	ALA	158	C	-5.070002	5.712923	-8.882365	-4.005424
1D7P	M	GLN	159	C	-5.070002	5.712923	-8.882365	-4.005424
1DV8	A	CYS	153	C	-3.716559	2.645865	-8.031519	-3.452165
1DV8	A	PRO	154	T	-3.716559	2.645865	-8.031519	-3.452165
1DV8	A	VAL	155	T	-3.716559	2.645865	-8.031519	-3.452165
1DV8	A	ASN	156	T	-3.716559	2.645865	-8.031519	-3.452165
1DV8	A	TRP	157	T	-5.237491	7.859362	-8.530734	-4.528046
1DV8	A	VAL	158	E	-6.841740	9.384370	-11.190125	-5.315207
1DV8	A	GLU	159	E	-7.450403	10.168219	-12.170093	-5.737104
1DV8	A	HIS	160	E	-8.178293	8.524976	-12.864079	-4.713683
1DV8	A	GLU	161	T	-8.195443	8.386184	-12.785690	-4.637819
1DV8	A	ARG	162	T	-8.217649	8.178625	-12.741351	-4.584752
1DV8	A	SER	163	E	-8.535913	8.363934	-12.929698	-4.806418
1DV8	A	CYS	164	E	-9.838455	7.670636	-14.824333	-4.878428
1DV8	A	TYR	165	E	-13.255549	11.566594	-17.577049	-5.151455
1DV8	A	TRP	166	E	-14.486836	15.011632	-17.685455	-5.211376
1DV8	A	PHE	167	E	-9.930222	11.840803	-13.179312	-5.158806
1DV8	A	SER	168	C	-9.120701	9.597554	-13.692871	-5.170729
1DV8	A	ARG	169	C	-8.642463	9.263553	-13.087393	-4.833132
1DV8	A	SER	170	C	-8.611209	9.459308	-13.062432	-4.833706
1DV8	A	GLY	171	C	-8.588357	9.607432	-13.051461	-4.837863
1DV8	A	LYS	172	B	-8.640522	9.406984	-13.056781	-4.802396
1DV8	A	ALA	173	C	-8.834453	9.851161	-12.652249	-4.599231
1DV8	A	TRP	174	H	-9.690119	12.649582	-12.848297	-4.725188
1DV8	A	ALA	175	H	-9.796558	11.641285	-13.487605	-4.702849
1DV8	A	ASP	176	H	-9.995608	10.946476	-13.803073	-4.611887
1DV8	A	ALA	177	H	-10.133854	10.651116	-13.770169	-4.543492
1DV8	A	ASP	178	H	-10.750028	8.397108	-15.895795	-4.884388
1DV8	A	ASN	179	H	-10.754106	8.224589	-15.974447	-4.882111
1DV8	A	TYR	180	H	-12.140438	10.396334	-17.825613	-5.223352
1DV8	A	CYS	181	H	-10.378258	5.795457	-16.312975	-4.623202
1DV8	A	ARG	182	H	-8.275437	6.702807	-12.686089	-4.255148
1DV8	A	LEU	183	H	-8.074948	7.186550	-12.672434	-4.331148
1DV8	A	GLU	184	H	-8.050246	7.387675	-12.657033	-4.345393
1DV8	A	ASP	185	C	-8.036704	7.498031	-12.638220	-4.338248
1DV8	A	ALA	186	C	-8.045521	7.562032	-12.566463	-4.331789
1DV8	A	HIS	187	E	-8.675850	9.259064	-12.522769	-4.495748
1DV8	A	LEU	188	E	-8.827097	15.204626	-9.095872	-4.038879
1DV8	A	VAL	189	C	-8.443522	14.400053	-8.917870	-3.923043
1DV8	A	VAL	190	C	-8.427837	14.446632	-8.962505	-3.962051
1DV8	A	VAL	191	C	-8.413874	14.363413	-9.085751	-3.994913
1DV8	A	THR	192	C	-8.414511	14.319290	-9.120198	-4.005547
1DV8	A	SER	193	C	-8.682967	13.255804	-9.763362	-4.063364
1DV8	A	TRP	194	H	-9.746569	12.987227	-12.370132	-4.766833
1DV8	A	GLU	195	H	-10.368910	11.638609	-14.151864	-5.168794
1DV8	A	GLU	196	H	-11.396146	10.436358	-16.591551	-5.746836
1DV8	A	GLN	197	H	-14.181762	13.053367	-20.068422	-5.997068
1DV8	A	LYS	198	H	-11.170970	13.942267	-12.948120	-4.647634
1DV8	A	PHE	199	H	-10.748884	14.218363	-12.756501	-4.641727
1DV8	A	VAL	200	H	-10.459445	13.762269	-12.851068	-4.575755

1DV8	A	GLN	201	H	-8.765765	10.065077	-12.307726	-4.820003
1DV8	A	HIS	202	H	-6.895715	8.713503	-9.768191	-4.161876
1DV8	A	HIS	203	H	-6.849007	8.765406	-9.863430	-4.160815
1DV8	A	ILE	204	H	-6.598270	8.546791	-10.021654	-4.177923
1DV8	A	GLY	205	T	-6.443732	8.512588	-10.198762	-4.272808
1DV8	A	PRO	206	T	-6.453725	8.500438	-10.161520	-4.263330
1DV8	A	VAL	207	T	-6.812319	8.373426	-10.582586	-4.372040
1DV8	A	ASN	208	C	-6.856329	8.293647	-10.548063	-4.389542
1DV8	A	THR	209	E	-7.308572	8.474253	-10.804586	-4.594670
1DV8	A	TRP	210	E	-10.044330	15.305977	-11.577361	-4.980129
1DV8	A	MET	211	E	-11.157397	16.915441	-13.560605	-5.633586
1DV8	A	GLY	212	E	-11.116880	16.484258	-13.985050	-5.741294
1DV8	A	LEU	213	E	-11.166025	14.537631	-14.980425	-5.642185
1DV8	A	HIS	214	E	-8.218164	8.027343	-13.658346	-5.740525
1DV8	A	ASP	215	T	-6.275153	5.818793	-11.879818	-5.316990
1DV8	A	GLN	216	T	-6.053559	7.632070	-11.142498	-5.368980
1DV8	A	ASN	217	T	-5.694294	9.009604	-9.974599	-5.143975
1DV8	A	GLY	218	T	-5.694173	9.011422	-9.974647	-5.143931
1DV8	A	PRO	219	C	-5.702552	9.025907	-9.922303	-5.135409
1DV8	A	TRP	220	C	-5.972685	10.927833	-8.831332	-5.039853
1DV8	A	LYS	221	E	-6.160595	10.665952	-8.577867	-4.873959
1DV8	A	TRP	222	E	-8.041643	12.361098	-10.274115	-4.908271
1DV8	A	VAL	223	T	-5.718697	6.581521	-9.863531	-4.663864
1DV8	A	ASP	224	T	-5.716333	6.594012	-9.877837	-4.667085
1DV8	A	GLY	225	T	-5.698544	6.671793	-9.931621	-4.681384
1DV8	A	THR	226	C	-5.676117	6.773655	-9.966280	-4.684490
1DV8	A	ASP	227	T	-5.562775	6.818430	-10.124828	-4.724655
1DV8	A	TYR	228	T	-6.391981	7.897366	-10.949940	-4.925092
1DV8	A	GLU	229	T	-6.127457	8.372486	-10.453237	-4.816334
1DV8	A	THR	230	T	-6.162078	8.329268	-10.384511	-4.797018
1DV8	A	GLY	231	T	-6.214673	8.226926	-10.338304	-4.799862
1DV8	A	PHE	232	C	-6.711476	9.256266	-9.701038	-4.650201
1DV8	A	LYS	233	C	-6.712693	9.249403	-9.693890	-4.649241
1DV8	A	ASN	234	C	-9.271685	11.285082	-13.156911	-5.353786
1DV8	A	TRP	235	B	-9.584604	12.377190	-13.098996	-5.351317
1DV8	A	ARG	236	T	-7.635069	8.612647	-11.349223	-4.674219
1DV8	A	PRO	237	T	-6.469026	7.086353	-10.820591	-4.603087
1DV8	A	GLU	238	T	-6.461675	7.083344	-10.863211	-4.607019
1DV8	A	GLN	239	T	-6.462328	7.076997	-10.860164	-4.606010
1DV8	A	PRO	240	T	-6.464457	7.057883	-10.854238	-4.603646
1DV8	A	ASP	241	T	-6.544361	6.845192	-10.839524	-4.612717
1DV8	A	ASP	242	C	-7.930046	8.647179	-17.221412	-8.545623
1DV8	A	TRP	243	C	-7.066287	7.976659	-13.626284	-6.322838
1DV8	A	TYR	244	T	-6.016448	7.589067	-10.517645	-4.981270
1DV8	A	GLY	245	T	-3.652825	4.750226	-8.283783	-4.745644
1DV8	A	HIS	246	T	-3.138542	4.617875	-8.182141	-4.747963
1DV8	A	GLY	247	T	-2.082073	3.865830	-7.284950	-4.809806
1DV8	A	LEU	248	C	-2.081552	3.868417	-7.288336	-4.810326
1DV8	A	GLY	249	C	-2.082209	3.864078	-7.285167	-4.810168
1DV8	A	GLY	250	C	-2.127218	3.782345	-7.179259	-4.795278
1DV8	A	GLY	251	C	-2.196293	3.671492	-7.026823	-4.774996
1DV8	A	GLU	252	C	-6.146958	6.768682	-11.174660	-5.224168
1DV8	A	ASP	253	C	-8.085228	6.320708	-14.394181	-5.588824
1DV8	A	CYS	254	E	-9.885312	7.043428	-16.702859	-5.778857
1DV8	A	ALA	255	E	-11.338382	8.867048	-16.916475	-5.309610
1DV8	A	HIS	256	E	-12.986171	13.430296	-17.514135	-5.396769
1DV8	A	PHE	257	E	-11.735797	11.205116	-16.795639	-5.689464
1DV8	A	THR	258	T	-10.896610	8.988634	-16.989268	-5.687174
1DV8	A	ASP	259	T	-10.887459	8.987724	-17.023590	-5.691677
1DV8	A	ASP	260	T	-10.887247	8.984216	-17.028686	-5.693243
1DV8	A	GLY	261	T	-10.887309	8.984273	-17.028262	-5.693329
1DV8	A	ARG	262	C	-11.033623	8.449834	-17.091584	-5.683280
1DV8	A	TRP	263	E	-12.989028	11.583357	-18.221090	-5.731254
1DV8	A	ASN	264	E	-13.771050	10.765671	-20.444184	-5.991644
1DV8	A	ASP	265	E	-12.627103	8.578983	-18.777908	-5.302437
1DV8	A	ASP	266	E	-11.387071	10.090312	-16.159517	-5.071951
1DV8	A	VAL	267	T	-9.208261	10.060653	-12.926687	-4.750384
1DV8	A	CYS	268	T	-9.192862	10.109761	-12.965015	-4.752362
1DV8	A	GLN	269	T	-9.192094	10.117005	-12.966421	-4.752185
1DV8	A	ARG	270	T	-9.193693	10.121826	-12.951287	-4.750907
1DV8	A	PRO	271	C	-9.206591	10.118955	-12.888553	-4.744544
1DV8	A	TYR	272	B	-11.324333	12.168134	-14.474669	-4.831389
1DV8	A	ARG	273	E	-12.971105	15.032899	-15.180557	-4.865328
1DV8	A	TRP	274	E	-14.469208	20.153039	-14.972963	-5.187317
1DV8	A	VAL	275	E	-14.121282	16.750592	-17.425102	-5.885053
1DV8	A	CYS	276	E	-12.157450	10.348301	-17.909307	-6.001432
1DV8	A	GLU	277	E	-9.706773	8.856766	-14.213291	-4.916424
1DV8	A	THR	278	E	-9.706773	8.856766	-14.213291	-4.916424
1DV8	A	GLU	279	E	-9.706773	8.856766	-14.213291	-4.916424
1DV8	A	LEU	280	C	-9.706773	8.856766	-14.213291	-4.916424
1E21	A	ALA	7	H	-10.836289	10.309875	-13.978746	-4.194534

1E21	A	PHE	8	H	-10.836289	10.309875	-13.978746	-4.194534
1E21	A	GLN	9	H	-10.836289	10.309875	-13.978746	-4.194534
1E21	A	ARG	10	H	-10.836289	10.309875	-13.978746	-4.194534
1E21	A	GLN	11	H	-13.124200	11.653016	-17.841742	-5.476791
1E21	A	HIS	12	H	-12.964146	9.813369	-19.066562	-5.839089
1E21	A	MET	13	B	-9.771129	7.752438	-15.486128	-5.439370
1E21	A	ASP	14	T	-6.588137	5.915030	-11.243009	-4.578149
1E21	A	SER	15	T	-5.240783	6.817686	-8.572905	-4.039071
1E21	A	ASP	16	T	-4.796556	6.819030	-8.309105	-3.967982
1E21	A	SER	17	T	-4.784557	6.844024	-8.336506	-3.962994
1E21	A	SER	18	C	-4.773996	6.857349	-8.360522	-3.955549
1E21	A	PRO	19	C	-4.801802	6.903855	-8.223880	-3.925075
1E21	A	SER	20	T	-5.128049	6.874009	-8.225337	-3.885976
1E21	A	SER	21	T	-6.642868	7.547669	-10.094173	-3.685683
1E21	A	SER	22	T	-7.008433	7.111409	-10.464956	-3.661868
1E21	A	SER	23	T	-7.895220	5.433957	-12.912809	-4.009532
1E21	A	THR	24	H	-7.978063	5.229801	-12.994875	-4.078254
1E21	A	TYR	25	H	-9.508400	9.698670	-14.500927	-5.163935
1E21	A	CYS	26	H	-10.052534	10.094059	-15.431862	-5.543647
1E21	A	ASN	27	H	-10.235393	10.279001	-15.263385	-5.561990
1E21	A	GLN	28	H	-9.813512	10.170323	-14.482749	-5.122109
1E21	A	MET	29	H	-10.140986	10.210032	-14.148059	-4.836932
1E21	A	MET	30	H	-10.108129	10.121416	-14.279588	-4.838356
1E21	A	ARG	31	H	-10.102680	9.955788	-14.314575	-4.789687
1E21	A	ARG	32	H	-10.095324	9.977700	-14.351585	-4.805878
1E21	A	ARG	33	H	-11.224562	9.454298	-17.097277	-5.202933
1E21	A	ASN	34	T	-9.582824	7.687879	-16.343891	-6.121002
1E21	A	MET	35	T	-9.529982	7.811484	-16.339880	-6.096106
1E21	A	THR	36	T	-9.096701	7.654451	-15.830144	-5.798732
1E21	A	GLN	37	T	-9.063016	7.594998	-15.914895	-5.784006
1E21	A	GLY	38	T	-8.491688	6.936572	-14.637543	-5.101438
1E21	A	ARG	39	T	-8.468948	6.991027	-14.240038	-4.822044
1E21	A	CYS	40	T	-8.476001	6.959282	-14.222340	-4.811818
1E21	A	LYS	41	C	-8.581913	6.887358	-14.010970	-4.672670
1E21	A	PRO	42	C	-8.595154	6.911624	-13.926603	-4.651443
1E21	A	VAL	43	E	-9.384864	7.991433	-14.141531	-4.569946
1E21	A	ASN	44	E	-10.517595	9.339944	-16.326075	-5.473712
1E21	A	THR	45	E	-10.651106	9.622991	-15.988161	-5.431496
1E21	A	PHE	46	E	-11.772647	13.101343	-15.382417	-5.222819
1E21	A	VAL	47	E	-12.141046	13.890319	-15.495298	-5.115118
1E21	A	HIS	48	C	-10.837961	10.991261	-15.095723	-5.220617
1E21	A	GLU	49	C	-8.735737	8.243551	-13.377162	-4.973658
1E21	A	PRO	50	C	-8.158981	9.155512	-12.046334	-4.547500
1E21	A	LEU	51	H	-8.138057	9.215353	-12.081557	-4.545539
1E21	A	VAL	52	H	-8.071765	9.336409	-12.128674	-4.550776
1E21	A	ASP	53	H	-8.075143	9.334447	-12.109527	-4.545656
1E21	A	VAL	54	H	-8.300372	9.891206	-11.551229	-4.350815
1E21	A	GLN	55	H	-9.210036	10.588661	-12.794392	-4.598121
1E21	A	ASN	56	H	-9.322061	10.463146	-12.877224	-4.654794
1E21	A	VAL	57	G	-10.560184	11.064354	-15.353492	-5.077104
1E21	A	CYS	58	G	-10.462834	10.417768	-15.947163	-5.375998
1E21	A	PHE	59	G	-10.251014	10.348646	-15.759398	-5.427421
1E21	A	GLN	60	C	-8.917889	8.838676	-13.780860	-5.187762
1E21	A	GLU	61	E	-5.576301	7.572357	-9.373774	-4.807985
1E21	A	LYS	62	E	-5.433267	7.388377	-9.634902	-4.770506
1E21	A	VAL	63	E	-5.429891	7.372004	-9.662959	-4.770142
1E21	A	THR	64	C	-5.405625	7.163786	-9.860498	-4.777403
1E21	A	CYS	65	T	-5.403310	7.123777	-9.894272	-4.778631
1E21	A	LYS	66	T	-6.139179	5.353236	-11.894091	-4.750716
1E21	A	ASN	67	T	-6.425494	2.345899	-14.721639	-5.261836
1E21	A	GLY	68	T	-6.358343	2.456876	-14.745729	-5.310416
1E21	A	GLN	69	C	-6.491128	2.520930	-14.786334	-5.400685
1E21	A	GLY	70	C	-6.515045	2.566801	-14.710344	-5.412365
1E21	A	ASN	71	C	-6.659045	2.815854	-14.541865	-5.478553
1E21	A	CYS	72	E	-7.545687	3.628973	-14.876777	-5.511667
1E21	A	TYR	73	E	-11.685971	10.112352	-17.893914	-5.871305
1E21	A	LYS	74	E	-9.765842	9.663303	-14.828271	-5.694002
1E21	A	SER	75	T	-9.388322	9.427057	-14.843193	-5.604356
1E21	A	ASN	76	T	-8.747366	9.971928	-13.806782	-5.555076
1E21	A	SER	77	T	-8.700370	10.190682	-13.745297	-5.523636
1E21	A	SER	78	T	-8.679914	10.340204	-13.723899	-5.524240
1E21	A	MET	79	E	-8.781434	10.477907	-13.525514	-5.493763
1E21	A	HIS	80	E	-8.889326	10.747141	-13.264324	-5.492076
1E21	A	ILE	81	E	-9.972065	13.341694	-13.227149	-5.294379
1E21	A	THR	82	E	-10.594334	14.253623	-13.678186	-5.574502
1E21	A	ASP	83	E	-11.705801	11.942334	-17.136955	-5.710613
1E21	A	CYS	84	E	-8.120652	10.212539	-11.249240	-4.813174
1E21	A	ARG	85	E	-4.766405	8.681660	-7.472773	-4.604861
1E21	A	LEU	86	E	-3.466850	6.786760	-7.184115	-4.698981
1E21	A	THR	87	T	-2.778875	4.787958	-7.200743	-4.333954
1E21	A	ASN	88	T	-2.775141	4.800118	-7.216110	-4.334537

1E21	A	GLY	89	T	-2.774912	4.800115	-7.217821	-4.334395
1E21	A	SER	90	T	-2.795753	4.656727	-7.207002	-4.321607
1E21	A	ARG	91	T	-2.995940	3.876988	-7.209180	-4.143071
1E21	A	TYR	92	T	-5.466326	6.527239	-10.133567	-4.392152
1E21	A	PRO	93	T	-5.975115	6.401932	-10.996690	-4.457991
1E21	A	ASN	94	T	-6.044625	6.448208	-10.940924	-4.501265
1E21	A	CYS	95	T	-6.143293	6.510076	-10.901625	-4.592767
1E21	A	ALA	96	C	-7.212814	8.461313	-14.139194	-6.737552
1E21	A	TYR	97	E	-8.895095	10.117353	-13.000666	-5.241742
1E21	A	ARG	98	E	-10.422352	11.576576	-15.072770	-5.349978
1E21	A	THR	99	E	-9.593064	10.779832	-14.288394	-5.519178
1E21	A	SER	100	E	-9.558304	10.723778	-14.375522	-5.516100
1E21	A	PRO	101	E	-9.526345	10.775432	-14.424417	-5.534344
1E21	A	LYS	102	E	-9.531941	10.741892	-14.445022	-5.547456
1E21	A	GLU	103	E	-9.608752	10.893393	-14.361784	-5.603941
1E21	A	ARG	104	E	-10.578162	12.281596	-15.378891	-5.704091
1E21	A	HIS	105	E	-10.687716	14.058075	-14.049182	-5.271354
1E21	A	ILE	106	E	-10.802228	15.378742	-12.540044	-4.475308
1E21	A	ILE	107	E	-10.785292	15.188737	-12.359384	-4.269589
1E21	A	VAL	108	E	-9.908072	11.226583	-13.079875	-4.458260
1E21	A	ALA	109	E	-8.276830	7.936968	-12.326836	-4.407993
1E21	A	CYS	110	E	-5.617363	5.086727	-9.922107	-4.161810
1E21	A	GLU	111	E	-5.460259	5.671076	-9.814807	-4.159714
1E21	A	GLY	112	T	-5.262703	6.072144	-9.569613	-4.071569
1E21	A	SER	113	T	-5.261074	6.085417	-9.569754	-4.069804
1E21	A	PRO	114	T	-5.264366	6.077413	-9.554460	-4.067778
1E21	A	TYR	115	T	-5.730917	7.301770	-9.145634	-3.957961
1E21	A	VAL	116	E	-6.002309	7.134875	-8.962731	-3.844853
1E21	A	PRO	117	E	-8.607789	11.261564	-10.157015	-3.596236
1E21	A	VAL	118	E	-9.811020	14.014070	-11.204783	-3.943724
1E21	A	HIS	119	E	-10.203922	15.520206	-11.084555	-4.179428
1E21	A	PHE	120	E	-10.171179	15.549243	-11.409516	-4.489009
1E21	A	ASP	121	E	-8.345418	9.388258	-12.206559	-4.933933
1E21	A	ALA	122	E	-5.245665	7.442609	-7.460487	-3.583916
1E21	A	SER	123	E	-5.245665	7.442609	-7.460487	-3.583916
1E21	A	VAL	124	E	-5.245665	7.442609	-7.460487	-3.583916
1E21	A	GLU	125	C	-5.245665	7.442609	-7.460487	-3.583916
1E87	A	SER	83	T	-5.427984	3.583447	-11.868958	-4.681266
1E87	A	SER	84	T	-5.427984	3.583447	-11.868958	-4.681266
1E87	A	CYS	85	T	-5.427984	3.583447	-11.868958	-4.681266
1E87	A	SER	86	T	-5.427984	3.583447	-11.868958	-4.681266
1E87	A	GLU	87	T	-4.620155	8.369559	-8.244406	-4.808143
1E87	A	ASP	88	T	-4.645249	8.606345	-8.081534	-4.840110
1E87	A	TRP	89	T	-4.761952	9.777182	-7.268510	-4.835604
1E87	A	VAL	90	E	-4.772151	9.798516	-7.177693	-4.813843
1E87	A	GLY	91	E	-4.772867	9.798555	-7.168686	-4.811552
1E87	A	TYR	92	E	-8.678480	14.186010	-11.130663	-5.417521
1E87	A	GLN	93	T	-9.796716	11.667950	-13.886148	-5.339345
1E87	A	ARG	94	T	-9.849367	11.268630	-13.907040	-5.289142
1E87	A	LYS	95	E	-10.808937	12.632343	-14.926882	-5.941941
1E87	A	CYS	96	E	-13.426745	13.332922	-18.489279	-6.129051
1E87	A	TYR	97	E	-12.273382	14.689533	-14.457952	-4.919181
1E87	A	PHE	98	E	-8.203737	9.306552	-11.022950	-4.165200
1E87	A	ILE	99	E	-5.561106	9.052356	-8.096986	-4.425407
1E87	A	SER	100	C	-5.496752	9.105767	-8.285477	-4.465423
1E87	A	THR	101	C	-5.479767	9.125344	-8.357671	-4.476701
1E87	A	VAL	102	C	-5.479765	9.125365	-8.357695	-4.476712
1E87	A	LYS	103	C	-5.485760	9.123565	-8.330614	-4.479880
1E87	A	ARG	104	B	-6.696490	9.620412	-10.128349	-4.824619
1E87	A	SER	105	C	-7.592354	9.800089	-10.842168	-4.864151
1E87	A	TRP	106	H	-11.832041	13.997291	-15.632687	-5.538949
1E87	A	THR	107	H	-11.394978	8.506459	-17.585936	-5.415227
1E87	A	SER	108	H	-11.331374	8.524472	-17.672662	-5.413448
1E87	A	ALA	109	H	-11.196913	8.647097	-17.718578	-5.437262
1E87	A	GLN	110	H	-11.188613	8.097393	-18.053879	-5.459561
1E87	A	ASN	111	H	-8.576767	5.683532	-13.908006	-4.532303
1E87	A	ALA	112	H	-8.260298	6.020092	-13.723744	-4.471810
1E87	A	CYS	113	H	-7.151634	4.832429	-13.073380	-4.669491
1E87	A	SER	114	H	-5.845552	5.968087	-10.249480	-4.344963
1E87	A	GLU	115	H	-5.741978	6.185819	-10.351116	-4.394793
1E87	A	HIS	116	H	-5.745064	6.203794	-10.328411	-4.395129
1E87	A	GLY	117	C	-5.745288	6.225686	-10.316173	-4.395349
1E87	A	ALA	118	C	-5.793861	6.364069	-10.090572	-4.368756
1E87	A	THR	119	E	-6.794460	7.495333	-10.934575	-4.651061
1E87	A	LEU	120	E	-8.538243	10.601903	-11.877187	-4.574928
1E87	A	ALA	121	C	-8.784655	10.611634	-11.603396	-4.434409
1E87	A	VAL	122	C	-10.520192	13.910536	-12.961830	-4.442282
1E87	A	ILE	123	C	-10.671461	13.559355	-13.625213	-4.668661
1E87	A	ASP	124	C	-11.027924	12.103015	-15.158723	-4.915606
1E87	A	SER	125	C	-11.314854	10.202711	-16.782471	-5.168121
1E87	A	GLU	126	H	-11.379510	9.489544	-17.822961	-5.619659

1E87	A	LYS	127	H	-11.492556	9.192994	-18.047180	-5.726904
1E87	A	ASP	128	H	-12.052354	9.426052	-19.020498	-6.146181
1E87	A	MET	129	H	-12.115204	9.974452	-18.681936	-6.167223
1E87	A	ASN	130	H	-11.919301	11.907393	-16.912752	-5.647964
1E87	A	PHE	131	H	-12.430155	15.508930	-14.349926	-4.812660
1E87	A	LEU	132	H	-12.316788	15.883567	-14.195609	-4.751539
1E87	A	LYS	133	H	-11.168183	13.767607	-13.653037	-4.763725
1E87	A	ARG	134	H	-10.423585	11.725467	-13.248893	-4.249668
1E87	A	TYR	135	H	-9.853938	11.747257	-12.979196	-4.533068
1E87	A	ALA	136	H	-7.778019	8.659911	-11.644179	-4.743471
1E87	A	GLY	137	T	-7.739174	8.740021	-11.766470	-4.775888
1E87	A	ARG	138	T	-7.740307	8.733003	-11.763324	-4.776369
1E87	A	GLU	139	T	-7.744858	8.716775	-11.753156	-4.782111
1E87	A	GLU	140	C	-7.755353	8.663178	-11.734082	-4.783619
1E87	A	HIS	141	E	-9.356218	10.124691	-13.564976	-5.251744
1E87	A	TRP	142	E	-11.488654	17.254527	-13.367674	-5.197074
1E87	A	VAL	143	E	-11.541685	17.604096	-14.287074	-5.852150
1E87	A	GLY	144	E	-10.845929	14.947360	-14.707317	-6.020545
1E87	A	LEU	145	E	-10.243670	13.918857	-14.531620	-6.036592
1E87	A	LYS	146	E	-7.268391	7.800921	-12.504495	-5.638399
1E87	A	LYS	147	E	-3.866899	6.154312	-8.071965	-4.934101
1E87	A	GLU	148	T	-2.760249	3.775898	-7.385131	-4.263886
1E87	A	PRO	149	T	-2.748151	3.888005	-7.387030	-4.269221
1E87	A	GLY	150	T	-2.747640	3.893801	-7.388921	-4.269702
1E87	A	HIS	151	T	-2.747932	3.891862	-7.386341	-4.268990
1E87	A	PRO	152	C	-2.846511	3.473033	-7.243485	-4.136816
1E87	A	TRP	153	E	-5.046030	9.304882	-7.427486	-4.460240
1E87	A	LYS	154	E	-6.937122	10.549807	-9.464052	-4.750121
1E87	A	TRP	155	E	-9.907806	11.397845	-14.680561	-5.743750
1E87	A	SER	156	T	-6.678249	5.858374	-12.553284	-5.481476
1E87	A	ASN	157	T	-6.541143	6.735212	-12.249704	-5.441936
1E87	A	GLY	158	T	-6.500878	6.908511	-12.254044	-5.431783
1E87	A	LYS	159	C	-6.471285	7.016606	-12.249857	-5.410904
1E87	A	GLU	160	B	-6.444825	7.218167	-12.179893	-5.386439
1E87	A	PHE	161	C	-7.102170	10.067599	-11.435779	-5.194371
1E87	A	ASN	162	C	-7.478665	10.305544	-11.780502	-5.094679
1E87	A	ASN	163	T	-7.702038	10.969732	-11.468705	-4.990516
1E87	A	TRP	164	T	-7.953422	12.291129	-10.955552	-4.944145
1E87	A	PHE	165	T	-5.830264	10.001890	-8.034793	-4.490426
1E87	A	ASN	166	T	-4.736373	5.308099	-8.958400	-4.160606
1E87	A	VAL	167	C	-4.732840	5.303779	-8.983217	-4.163443
1E87	A	THR	168	B	-4.728025	5.295321	-9.024980	-4.172066
1E87	A	GLY	169	C	-4.723306	5.296381	-9.062640	-4.182236
1E87	A	SER	170	C	-4.821409	4.455375	-9.253958	-4.127461
1E87	A	ASP	171	C	-6.943033	5.393924	-13.543700	-5.138442
1E87	A	LYS	172	C	-7.150283	5.208910	-13.837414	-5.313491
1E87	A	CYS	173	E	-7.559175	5.807840	-13.650940	-5.411054
1E87	A	VAL	174	E	-10.294491	9.719397	-14.592486	-4.895141
1E87	A	PHE	175	E	-10.710845	15.340706	-13.017494	-5.448870
1E87	A	LEU	176	E	-8.164933	11.521518	-11.573643	-5.522690
1E87	A	LYS	177	E	-6.913606	10.628045	-10.537531	-5.420136
1E87	A	ASN	178	T	-6.831178	10.481954	-10.747189	-5.403436
1E87	A	THR	179	T	-6.827361	10.477590	-10.768231	-5.401649
1E87	A	GLU	180	E	-6.827986	10.472127	-10.766597	-5.401593
1E87	A	VAL	181	E	-6.892123	10.358708	-10.679108	-5.387532
1E87	A	SER	182	E	-8.003099	9.544402	-12.289132	-5.288408
1E87	A	SER	183	E	-8.393367	8.443133	-13.812188	-5.525724
1E87	A	MET	184	E	-6.369628	7.680580	-10.971911	-5.241004
1E87	A	GLU	185	T	-5.742841	7.120728	-11.020958	-5.350226
1E87	A	CYS	186	T	-5.653943	7.375340	-10.985521	-5.334176
1E87	A	GLU	187	T	-5.649122	7.427286	-10.982740	-5.335324
1E87	A	LYS	188	T	-5.654230	7.420525	-10.958907	-5.333345
1E87	A	ASN	189	C	-5.857193	7.321883	-10.988625	-5.374936
1E87	A	LEU	190	B	-6.787007	9.218701	-10.766400	-5.248386
1E87	A	TYR	191	E	-8.491709	13.729933	-10.737072	-5.481181
1E87	A	TRP	192	E	-12.379194	19.970975	-13.777704	-5.983638
1E87	A	ILE	193	E	-13.074260	21.724957	-13.608985	-5.886616
1E87	A	CYS	194	E	-13.316811	17.405307	-16.891551	-6.346266
1E87	A	ASN	195	E	-11.430905	11.888988	-15.919021	-5.748264
1E87	A	LYS	196	E	-8.466050	9.937029	-11.181377	-4.290160
1E87	A	PRO	197	E	-8.466050	9.937029	-11.181377	-4.290160
1E87	A	TYR	198	C	-8.466050	9.937029	-11.181377	-4.290160
1E87	A	LYS	199	C	-8.466050	9.937029	-11.181377	-4.290160
1EAZ	A	SER	190	C	-3.746533	5.238372	-5.551265	-2.692166
1EAZ	A	ALA	191	C	-3.746533	5.238372	-5.551265	-2.692166
1EAZ	A	VAL	192	E	-3.746533	5.238372	-5.551265	-2.692166
1EAZ	A	ILE	193	E	-3.746533	5.238372	-5.551265	-2.692166
1EAZ	A	LYS	194	E	-6.199465	8.589348	-9.944019	-4.560136
1EAZ	A	ALA	195	E	-6.746556	9.752077	-10.499722	-5.119934
1EAZ	A	GLY	196	E	-7.652303	10.134660	-12.151168	-5.918491
1EAZ	A	TYR	197	E	-10.351415	11.833569	-14.666002	-5.477827

1EAZ	A	CYS	198	E	-10.387039	11.576161	-14.558146	-5.344727
1EAZ	A	VAL	199	E	-10.493567	11.491566	-14.365690	-5.248721
1EAZ	A	LYS	200	E	-9.998189	9.085200	-16.100537	-6.076304
1EAZ	A	GLN	201	E	-7.012727	5.112442	-12.819790	-5.053068
1EAZ	A	GLY	202	T	-3.193683	1.810695	-8.399402	-4.093831
1EAZ	A	ALA	203	T	-2.659530	2.040823	-8.042703	-4.025950
1EAZ	A	VAL	204	T	-2.657461	2.060840	-8.049479	-4.028953
1EAZ	A	MET	205	T	-2.657447	2.061040	-8.049591	-4.028986
1EAZ	A	LYS	206	T	-2.657833	2.059043	-8.046380	-4.028265
1EAZ	A	ASN	207	C	-2.969983	2.214612	-7.735289	-3.947544
1EAZ	A	TRP	208	E	-6.018681	7.760197	-9.836508	-4.803894
1EAZ	A	LYS	209	E	-8.853148	10.299426	-13.192841	-5.492657
1EAZ	A	ARG	210	E	-10.740872	14.290605	-16.377287	-7.081824
1EAZ	A	ARG	211	E	-11.263024	15.743235	-16.272917	-7.432818
1EAZ	A	TYR	212	E	-14.475010	21.951695	-15.770168	-6.107614
1EAZ	A	PHE	213	E	-14.150638	18.623080	-16.126684	-5.602295
1EAZ	A	GLN	214	E	-12.018674	12.162078	-17.416262	-6.141632
1EAZ	A	LEU	215	E	-9.694056	10.682523	-13.703660	-5.273344
1EAZ	A	ASP	216	E	-9.311489	11.047327	-13.447068	-5.236250
1EAZ	A	GLU	217	T	-9.024116	10.950601	-13.372280	-5.200730
1EAZ	A	ASN	218	T	-9.020210	10.980297	-13.378761	-5.203110
1EAZ	A	THR	219	E	-9.023509	10.979598	-13.353598	-5.197286
1EAZ	A	ILE	220	E	-9.248495	11.132279	-13.226905	-5.170355
1EAZ	A	GLY	221	E	-9.579075	10.896259	-13.274715	-5.151931
1EAZ	A	TYR	222	E	-11.905221	16.009544	-14.492373	-5.610303
1EAZ	A	PHE	223	E	-10.546888	13.402282	-17.235281	-7.974378
1EAZ	A	LYS	224	T	-8.161696	6.040730	-13.829881	-5.006854
1EAZ	A	SER	225	T	-6.825221	4.879818	-12.482289	-4.693396
1EAZ	A	GLU	226	T	-4.663923	4.282877	-9.738738	-4.619512
1EAZ	A	LEU	227	T	-4.363919	4.868483	-9.273925	-4.422829
1EAZ	A	GLU	228	T	-4.318220	5.115485	-9.227504	-4.408388
1EAZ	A	LYS	229	C	-4.240584	5.639316	-8.942953	-4.332291
1EAZ	A	GLU	230	C	-4.207485	5.959302	-8.772555	-4.295288
1EAZ	A	PRO	231	T	-4.545555	7.535323	-7.973901	-4.018961
1EAZ	A	LEU	232	T	-4.993032	9.709349	-7.276221	-3.897839
1EAZ	A	ARG	233	E	-5.148459	10.173845	-6.865959	-3.799251
1EAZ	A	VAL	234	E	-5.649363	11.323628	-6.738431	-3.807175
1EAZ	A	ILE	235	E	-6.426215	13.919855	-6.476749	-3.812526
1EAZ	A	PRO	236	E	-6.670667	13.163004	-7.699589	-4.091619
1EAZ	A	LEU	237	G	-6.843381	12.676335	-8.258927	-4.233678
1EAZ	A	LYS	238	G	-6.707501	11.936021	-8.808910	-4.341955
1EAZ	A	GLU	239	G	-6.662423	11.882121	-8.859706	-4.346278
1EAZ	A	VAL	240	E	-6.683070	11.839793	-8.865564	-4.351266
1EAZ	A	HIS	241	E	-7.136652	11.102154	-10.181962	-4.580962
1EAZ	A	LYS	242	E	-7.267292	10.752601	-10.328783	-4.586109
1EAZ	A	VAL	243	E	-7.705276	12.111889	-10.152160	-4.568516
1EAZ	A	GLN	244	E	-8.297460	11.125861	-12.429592	-5.140343
1EAZ	A	GLU	245	E	-8.551278	10.550575	-13.748272	-5.652469
1EAZ	A	CYS	246	T	-8.509470	8.899825	-14.516216	-5.615328
1EAZ	A	LYS	247	T	-7.848432	5.621009	-14.149515	-4.866045
1EAZ	A	GLN	248	T	-7.897256	4.846177	-14.381472	-4.748366
1EAZ	A	SER	249	T	-7.304331	4.685330	-13.376587	-4.498669
1EAZ	A	ASP	250	G	-6.974905	5.346662	-12.823702	-4.521661
1EAZ	A	ILE	251	G	-6.962078	5.390999	-12.816341	-4.518255
1EAZ	A	MET	252	G	-7.059885	5.612674	-12.614096	-4.518950
1EAZ	A	MET	253	C	-7.067614	5.618271	-12.575817	-4.515067
1EAZ	A	ARG	254	T	-7.407362	6.332973	-12.341327	-4.602911
1EAZ	A	ASP	255	T	-8.776862	6.875126	-14.154262	-4.878074
1EAZ	A	ASN	256	T	-10.352697	8.246470	-16.695537	-5.524075
1EAZ	A	LEU	257	E	-10.786523	9.080697	-16.216902	-5.399403
1EAZ	A	PHE	258	E	-12.509426	16.763902	-15.616272	-5.744807
1EAZ	A	GLU	259	E	-11.130833	13.992575	-13.706148	-5.098165
1EAZ	A	ILE	260	E	-7.948436	10.928747	-9.670284	-4.061198
1EAZ	A	VAL	261	E	-7.904916	10.793885	-9.921725	-4.094351
1EAZ	A	THR	262	E	-7.225088	9.610993	-10.613952	-4.538467
1EAZ	A	THR	263	T	-7.223236	9.616943	-10.624545	-4.539792
1EAZ	A	SER	264	T	-7.223981	9.611782	-10.620867	-4.539154
1EAZ	A	ARG	265	E	-7.429485	9.071462	-11.022424	-4.739211
1EAZ	A	THR	266	E	-7.448570	9.073504	-10.950506	-4.746148
1EAZ	A	PHE	267	E	-10.622498	11.736545	-14.035872	-4.985086
1EAZ	A	TYR	268	E	-12.434081	16.461283	-15.516210	-5.596772
1EAZ	A	VAL	269	E	-10.626216	10.099057	-14.865851	-4.968699
1EAZ	A	GLN	270	E	-10.432716	9.197115	-15.527525	-4.999818
1EAZ	A	ALA	271	C	-8.263392	5.219460	-13.667637	-4.449411
1EAZ	A	ASP	272	C	-7.809274	4.867813	-14.037256	-4.671764
1EAZ	A	SER	273	C	-7.806237	4.884745	-14.050396	-4.675602
1EAZ	A	PRO	274	H	-7.798615	4.926268	-14.071331	-4.690141
1EAZ	A	GLU	275	H	-7.799716	4.925927	-14.065715	-4.690305
1EAZ	A	GLU	276	H	-8.149162	4.771920	-14.424961	-4.895315
1EAZ	A	MET	277	H	-9.924837	8.764044	-15.699899	-5.477289
1EAZ	A	HIS	278	H	-10.012924	9.083015	-15.427169	-5.444703

```
1EAZ        A          SER            279                   H -11.079444 11.683657 -15.444338 -5.049760
1EAZ        A          TRP            280                   H -11.118647 13.924169 -13.586949 -4.481611
1EAZ        A          ILE            281                   H -9.956347 11.089613 -11.864282 -3.497536
1EAZ        A          LYS            282                   H -8.766458  8.282576 -11.937254 -3.638257
1EAZ        A          ALA            283                   H -8.708980  8.486459 -11.950056 -3.642909
1EAZ        A          VAL            284                   H -8.677567  8.634279 -12.017984 -3.681242
1EAZ        A          SER            285                   H -8.601400  8.626036 -12.455764 -3.953965
1EAZ        A          GLY            286                   H -8.090116  8.226558 -12.832595 -4.672514
1EAZ        A          ALA            287                   H -7.880938  8.433806 -12.362639 -4.613596
1EAZ        A          ILE            288                   H -6.828437  6.512940 -10.534604 -3.688639
1EAZ        A          VAL            289                   H -5.948508  4.634896 -9.670745 -3.099316
1EAZ        A          ALA            290                   H -5.948508  4.634896 -9.670745 -3.099316
1EAZ        A          GLN            291                   H -5.948508  4.634896 -9.670745 -3.099316
1EAZ        A          ARG            292                   C -5.948508  4.634896 -9.670745 -3.099316
1ESR        A          PRO              2                   T -1.260548  1.763084 -8.070143 -4.740687
1ESR        A          ASP              3                   T -1.260548  1.763084 -8.070143 -4.740687
1ESR        A          SER              4                   T -1.260548  1.763084 -8.070143 -4.740687
1ESR        A          VAL              5                   T -1.260548  1.763084 -8.070143 -4.740687
1ESR        A          SER              6                   T -1.294114  1.890081 -8.099896 -4.841106
1ESR        A          ILE              7                   T -1.286829  2.132359 -8.042130 -4.877643
1ESR        A          PRO              8                   C -1.354133  2.249293 -8.046224 -4.989884
1ESR        A          ILE              9                   C -1.564295  2.990233 -8.062693 -5.282393
1ESR        A          THR             10                   C -1.762284  3.362821 -8.039802 -5.430938
1ESR        A          CYS             11                   C -2.496724  4.990119 -8.675539 -5.918483
1ESR        A          CYS             12                   T -4.615738  6.277408 -11.492532 -6.385744
1ESR        A          PHE             13                   T -5.225794  8.621624 -9.435864 -5.023172
1ESR        A          ASN             14                   T -4.950316  8.321986 -7.982103 -4.125474
1ESR        A          VAL             15                   T -4.519583  8.543383 -6.019507 -3.337082
1ESR        A          ILE             16                   C -4.310820  8.994063 -5.594619 -3.261256
1ESR        A          ASN             17                   C -4.079890  8.978807 -5.498125 -3.284510
1ESR        A          ARG             18                   C -4.100674  9.028206 -5.409563 -3.246291
1ESR        A          LYS             19                   C -4.161301  9.180413 -5.281580 -3.249963
1ESR        A          ILE             20                   C -4.400681  9.506873 -5.270903 -3.316562
1ESR        A          PRO             21                   C -4.675223  9.208332 -5.401747 -3.336581
1ESR        A          ILE             22                   G -5.968121 11.247953 -6.019937 -3.322402
1ESR        A          GLN             23                   G -7.027361 11.011346 -8.212241 -4.021479
1ESR        A          ARG             24                   G -8.924211 11.733156 -11.346538 -4.427998
1ESR        A          LEU             25                   E -9.301776 12.456215 -11.457581 -4.585140
1ESR        A          GLU             26                   E -9.684665 11.707196 -12.692711 -4.677244
1ESR        A          SER             27                   E -9.767588 11.345666 -12.819092 -4.634990
1ESR        A          TYR             28                   E -8.069517 11.265553 -9.217729 -3.813825
1ESR        A          THR             29                   E -6.919801  8.095125 -9.497151 -3.777254
1ESR        A          ARG             30                   E -5.557517  6.897416 -8.119362 -3.617882
1ESR        A          ILE             31                   E -3.860050  6.072742 -6.956269 -4.033508
1ESR        A          THR             32                   C -2.762751  5.125467 -7.861389 -5.095172
1ESR        A          ASN             33                   T -2.731245  5.143323 -7.864708 -5.044124
1ESR        A          ILE             34                   T -2.728709  5.143798 -7.870977 -5.039466
1ESR        A          GLN             35                   T -2.732364  5.134104 -7.872941 -5.049284
1ESR        A          CYS             36                   T -2.822950  4.978046 -8.018648 -5.199884
1ESR        A          PRO             37                   C -4.406674  5.581293 -8.020335 -4.032901
1ESR        A          LYS             38                   C -5.577412  6.780601 -9.497954 -4.148763
1ESR        A          GLU             39                   C -6.122848  8.701209 -9.899249 -4.612121
1ESR        A          ALA             40                   E -6.512361  9.947657 -9.666479 -4.670540
1ESR        A          VAL             41                   E -7.204721 11.445224 -8.049591 -3.834914
1ESR        A          ILE             42                   E -10.128110 13.212813 -10.938016 -3.902781
1ESR        A          PHE             43                   E -11.750610 16.788588 -11.488991 -3.990627
1ESR        A          LYS             44                   E -10.107247  8.042935 -15.686377 -5.635843
1ESR        A          THR             45                   E -9.301247  7.570495 -15.031983 -5.445572
1ESR        A          GLN             46                   T -8.484937  7.296835 -14.528633 -5.629945
1ESR        A          ARG             47                   T -7.976495  8.173850 -13.103117 -5.239303
1ESR        A          GLY             48                   T -7.396979  8.129760 -11.913594 -4.879158
1ESR        A          LYS             49                   C -7.367113  8.229321 -11.853770 -4.832607
1ESR        A          GLU             50                   E -7.378422  8.285786 -11.771751 -4.812928
1ESR        A          VAL             51                   E -7.448218  8.444619 -11.437044 -4.694469
1ESR        A          CYS             52                   E -7.603585  8.333523 -11.264127 -4.611260
1ESR        A          ALA             53                   E -8.846639 10.013344 -11.899528 -4.216678
1ESR        A          ASP             54                   T -9.569585 10.458469 -12.964673 -4.227488
1ESR        A          PRO             55                   T -9.863288  9.716472 -13.455944 -4.094516
1ESR        A          LYS             56                   T -10.066544  8.777337 -14.033163 -4.147104
1ESR        A          GLU             57                   T -10.429258  8.585010 -14.279854 -4.176921
1ESR        A          ARG             58                   H -11.434697  8.325199 -16.131470 -4.394681
1ESR        A          TRP             59                   H -12.457535 11.743974 -16.171433 -4.449136
1ESR        A          VAL             60                   H -12.566389 11.665136 -16.161954 -4.383408
1ESR        A          ARG             61                   H -12.805598 11.527401 -16.179903 -4.219442
1ESR        A          ASP             62                   H -12.105983 10.880400 -16.579990 -5.045495
1ESR        A          SER             63                   H -12.168636 11.008333 -16.866447 -5.313933
1ESR        A          MET             64                   H -12.095935 11.151845 -17.075611 -5.420219
1ESR        A          LYS             65                   H -11.375683 10.354776 -19.374102 -7.491370
1ESR        A          HIS             66                   H -10.491763 10.152675 -18.901002 -7.964652
1ESR        A          LEU             67                   H -9.920431  9.462345 -18.282158 -7.779801
1ESR        A          ASP             68                   H -8.438296  6.026153 -16.397535 -6.841840
```

1ESR	A	GLN	69	H	-6.787676	5.309827	-13.330312	-5.895388
1ESR	A	ILE	70	H	-5.796464	4.802912	-11.312277	-4.963238
1ESR	A	PHE	71	H	-5.245710	4.162786	-10.777564	-4.586982
1ESR	A	GLN	72	H	-4.377589	3.593305	-8.801649	-3.774538
1ESR	A	ASN	73	H	-3.224551	2.390909	-6.260452	-2.633658
1ESR	A	LEU	74	C	-3.224551	2.390909	-6.260452	-2.633658
1ESR	A	LYS	75	C	-3.224551	2.390909	-6.260452	-2.633658
1ESR	A	PRO	76	C	-3.224551	2.390909	-6.260452	-2.633658
1FAO	A	PRO	162	C	-2.002069	2.045140	-6.032130	-3.208614
1FAO	A	SER	163	T	-2.002069	2.045140	-6.032130	-3.208614
1FAO	A	LEU	164	T	-2.002069	2.045140	-6.032130	-3.208614
1FAO	A	GLY	165	T	-2.002069	2.045140	-6.032130	-3.208614
1FAO	A	THR	166	T	-2.613995	3.305164	-6.141108	-3.666566
1FAO	A	LYS	167	E	-5.260508	6.655115	-10.231506	-5.330361
1FAO	A	GLU	168	E	-6.350434	8.926030	-12.085753	-6.595697
1FAO	A	GLY	169	E	-7.302837	9.404836	-13.931334	-7.460865
1FAO	A	TYR	170	E	-9.669404	14.216870	-14.006815	-6.518330
1FAO	A	LEU	171	E	-10.610287	15.307223	-13.233422	-5.612711
1FAO	A	THR	172	E	-10.932214	14.600859	-13.685887	-5.556609
1FAO	A	LYS	173	E	-9.842573	8.405557	-16.297618	-6.288402
1FAO	A	GLN	174	E	-6.360380	4.254184	-12.131157	-5.016149
1FAO	A	GLY	175	T	-2.233727	1.846932	-7.047398	-4.166161
1FAO	A	GLY	176	T	-1.754112	2.509401	-6.678667	-4.117669
1FAO	A	LEU	177	T	-1.753777	2.512625	-6.680528	-4.118081
1FAO	A	VAL	178	T	-1.753773	2.512677	-6.680571	-4.118088
1FAO	A	LYS	179	T	-1.754043	2.511822	-6.677791	-4.117500
1FAO	A	THR	180	C	-2.129803	2.959959	-6.060916	-3.886777
1FAO	A	TRP	181	E	-6.227585	8.029876	-9.409971	-4.468195
1FAO	A	LYS	182	E	-8.350453	10.259402	-12.795680	-5.412940
1FAO	A	THR	183	E	-8.800214	11.450879	-13.179569	-5.968593
1FAO	A	ARG	184	E	-10.237456	13.209487	-16.808754	-8.037085
1FAO	A	TRP	185	E	-13.699097	20.315010	-15.962763	-6.336251
1FAO	A	PHE	186	E	-11.900678	15.883103	-12.992419	-4.681502
1FAO	A	THR	187	E	-10.035251	11.017572	-13.163107	-4.763494
1FAO	A	LEU	188	E	-8.544702	10.622640	-11.424141	-4.722505
1FAO	A	HIS	189	E	-8.261784	10.821463	-11.337091	-4.695012
1FAO	A	ARG	190	T	-8.223538	10.956651	-11.371937	-4.704604
1FAO	A	ASN	191	T	-8.224562	10.949225	-11.369581	-4.705026
1FAO	A	GLU	192	E	-8.251889	10.956098	-11.284519	-4.702065
1FAO	A	LEU	193	E	-8.739325	11.426157	-11.301433	-4.680572
1FAO	A	LYS	194	E	-9.863442	13.014164	-11.906998	-4.853791
1FAO	A	TYR	195	E	-13.001645	19.537113	-15.181286	-6.287456
1FAO	A	PHE	196	E	-10.438750	14.129434	-16.410377	-7.839077
1FAO	A	LYS	197	T	-8.263146	6.831915	-13.252046	-4.927234
1FAO	A	ASP	198	T	-6.689262	5.222635	-11.344501	-4.325019
1FAO	A	GLN	199	T	-5.129523	4.676340	-9.261134	-4.045121
1FAO	A	MET	200	T	-4.531032	5.283765	-8.219806	-3.756209
1FAO	A	SER	201	T	-4.294797	6.329809	-7.652060	-3.719422
1FAO	A	PRO	202	T	-4.252024	6.539655	-7.593087	-3.705033
1FAO	A	GLU	203	T	-4.240827	6.718433	-7.506209	-3.696234
1FAO	A	PRO	204	T	-4.377631	7.272050	-7.087786	-3.609722
1FAO	A	ILE	205	T	-4.777362	8.852777	-6.572141	-3.627589
1FAO	A	ARG	206	E	-5.579921	9.976602	-6.816150	-3.587001
1FAO	A	ILE	207	E	-6.220311	11.384347	-6.682081	-3.711029
1FAO	A	LEU	208	E	-7.930923	14.681065	-8.274772	-4.054867
1FAO	A	ASP	209	E	-7.409209	12.489587	-9.278638	-4.755380
1FAO	A	LEU	210	G	-7.384903	12.358262	-9.399641	-4.766416
1FAO	A	THR	211	G	-7.210545	11.140741	-10.054930	-4.695723
1FAO	A	GLU	212	G	-7.235323	10.815919	-10.192576	-4.698128
1FAO	A	CYS	213	C	-7.247209	10.692816	-10.225402	-4.696880
1FAO	A	SER	214	C	-7.838020	8.474085	-11.890251	-4.503734
1FAO	A	ALA	215	E	-7.951516	7.807449	-12.042474	-4.456684
1FAO	A	VAL	216	E	-9.280287	9.413325	-12.666546	-4.178443
1FAO	A	GLN	217	E	-9.944792	8.826399	-13.805101	-4.243877
1FAO	A	PHE	218	E	-10.348368	9.645969	-15.057982	-4.942414
1FAO	A	ASP	219	E	-8.395596	6.580356	-13.506169	-4.924170
1FAO	A	TYR	220	T	-8.230234	6.941349	-13.572160	-4.966482
1FAO	A	SER	221	T	-7.909263	6.500419	-13.741959	-4.953722
1FAO	A	GLN	222	T	-7.868469	6.554368	-13.813579	-4.976732
1FAO	A	GLU	223	T	-7.554985	6.508177	-13.368315	-4.869540
1FAO	A	ARG	224	T	-7.713174	6.514709	-13.343885	-4.854285
1FAO	A	VAL	225	T	-7.776041	6.345932	-13.296756	-4.826833
1FAO	A	ASN	226	T	-8.017105	6.574328	-12.953756	-4.771968
1FAO	A	CYS	227	E	-8.071808	6.500645	-12.768777	-4.722221
1FAO	A	PHE	228	E	-11.529903	12.470972	-15.080688	-4.958984
1FAO	A	CYS	229	E	-11.188394	13.440859	-13.668184	-4.596580
1FAO	A	LEU	230	E	-11.037301	15.198146	-12.237856	-4.367913
1FAO	A	VAL	231	E	-10.980114	15.080987	-12.453812	-4.409049
1FAO	A	PHE	232	E	-10.052905	15.526043	-11.067012	-4.664704
1FAO	A	PRO	233	T	-10.027152	15.523751	-11.153363	-4.674049
1FAO	A	PHE	234	T	-10.074113	15.619979	-11.040336	-4.705161

1FAO	A	ARG	235	E	-10.140119	15.605552	-10.952195	-4.744655
1FAO	A	THR	236	E	-10.120540	15.794863	-10.960828	-4.790327
1FAO	A	PHE	237	E	-11.436690	17.062807	-12.923945	-5.265803
1FAO	A	TYR	238	E	-11.371643	16.281547	-13.212730	-5.249513
1FAO	A	LEU	239	E	-8.137175	9.911159	-10.497308	-4.284029
1FAO	A	CYS	240	E	-6.872272	6.030735	-11.553413	-4.523251
1FAO	A	ALA	241	C	-5.427956	4.453337	-10.023178	-4.086584
1FAO	A	LYS	242	C	-5.232322	4.418995	-10.226924	-4.154256
1FAO	A	THR	243	C	-5.224586	4.444199	-10.248338	-4.155682
1FAO	A	GLY	244	H	-5.228423	4.406229	-10.249916	-4.155145
1FAO	A	VAL	245	H	-5.261894	4.342211	-10.166170	-4.131848
1FAO	A	GLU	246	H	-5.955085	4.429521	-10.807628	-4.324582
1FAO	A	ALA	247	H	-7.756918	6.407869	-12.043205	-4.288689
1FAO	A	ASP	248	H	-9.346159	7.029428	-14.331625	-4.636985
1FAO	A	GLU	249	H	-10.572873	9.729587	-15.162226	-4.861569
1FAO	A	TRP	250	H	-11.055495	18.296717	-11.377688	-4.741640
1FAO	A	ILE	251	H	-10.830018	17.468867	-11.306564	-4.429632
1FAO	A	LYS	252	H	-10.756081	17.191143	-11.489242	-4.432968
1FAO	A	ILE	253	H	-10.848477	17.627506	-11.148107	-4.361828
1FAO	A	LEU	254	H	-10.947798	17.661053	-11.070782	-4.322758
1FAO	A	ARG	255	H	-10.949913	15.509306	-13.084708	-5.003183
1FAO	A	TRP	256	H	-9.142590	13.310005	-11.932232	-5.547612
1FAO	A	LYS	257	H	-7.849133	10.483035	-10.601949	-4.631120
1FAO	A	LEU	258	H	-5.203308	6.990747	-6.505527	-2.903375
1FAO	A	SER	259	H	-5.203308	6.990747	-6.505527	-2.903375
1FAO	A	GLN	260	H	-5.203308	6.990747	-6.505527	-2.903375
1FAO	A	ILE	261	C	-5.203308	6.990747	-6.505527	-2.903375
1FIL	A	ALA	1	C	-6.809249	7.210418	-8.649396	-2.967913
1FIL	A	GLY	2	C	-6.809249	7.210418	-8.649396	-2.967913
1FIL	A	TRP	3	H	-6.809249	7.210418	-8.649396	-2.967913
1FIL	A	ASN	4	H	-6.809249	7.210418	-8.649396	-2.967913
1FIL	A	ALA	5	H	-7.723575	8.317813	-10.568665	-4.049026
1FIL	A	TYR	6	H	-10.056845	12.167670	-12.280231	-4.276907
1FIL	A	ILE	7	H	-10.240995	12.069067	-11.729825	-3.829548
1FIL	A	ASP	8	H	-9.920812	10.886491	-12.053829	-3.735130
1FIL	A	ASN	9	H	-9.687407	10.510089	-12.192618	-3.776869
1FIL	A	LEU	10	H	-9.129268	8.645565	-12.126633	-3.809776
1FIL	A	MET	11	H	-7.194148	5.587163	-11.666354	-4.271530
1FIL	A	ALA	12	H	-6.348870	5.249838	-11.276036	-4.426493
1FIL	A	ASP	13	C	-6.348899	5.247155	-11.279104	-4.427919
1FIL	A	GLY	14	C	-6.349596	5.241716	-11.277701	-4.428545
1FIL	A	THR	15	C	-6.353633	5.221638	-11.273024	-4.432849
1FIL	A	CYS	16	E	-6.510695	5.146784	-11.159004	-4.476190
1FIL	A	GLN	17	E	-10.429215	7.082009	-15.769099	-5.062092
1FIL	A	ASP	18	E	-11.051400	13.938555	-10.407369	-2.941216
1FIL	A	ALA	19	E	-9.184519	12.693232	-7.859129	-2.487481
1FIL	A	ALA	20	E	-9.177690	12.740596	-7.880888	-2.495436
1FIL	A	ILE	21	E	-9.160713	12.846398	-7.965649	-2.542020
1FIL	A	VAL	22	E	-8.247930	12.342816	-9.049008	-3.752765
1FIL	A	GLY	23	E	-6.612082	8.837580	-7.912810	-3.443441
1FIL	A	TYR	24	T	-5.992864	9.563860	-6.643804	-3.130482
1FIL	A	LYS	25	T	-5.585686	7.737743	-6.894400	-2.785089
1FIL	A	ASP	26	T	-5.509080	7.775507	-6.990427	-2.778395
1FIL	A	SER	27	T	-5.513266	7.744225	-6.973885	-2.768336
1FIL	A	PRO	28	T	-5.607084	7.597878	-6.826000	-2.655753
1FIL	A	SER	29	E	-5.853089	6.375634	-7.270463	-2.500001
1FIL	A	VAL	30	E	-6.746405	8.163732	-7.703397	-2.729571
1FIL	A	TRP	31	E	-8.076516	12.945499	-7.992800	-3.245295
1FIL	A	ALA	32	E	-5.013162	8.113852	-5.881809	-3.078221
1FIL	A	ALA	33	E	-4.821736	7.662923	-6.174728	-3.036072
1FIL	A	VAL	34	T	-4.790719	7.589591	-6.313815	-3.054713
1FIL	A	PRO	35	T	-4.789044	7.596809	-6.323126	-3.057489
1FIL	A	GLY	36	T	-4.790869	7.580668	-6.318628	-3.056577
1FIL	A	LYS	37	T	-5.472630	6.483223	-7.283224	-3.010794
1FIL	A	THR	38	C	-6.514615	6.528466	-8.929361	-3.428212
1FIL	A	PHE	39	G	-8.097312	11.427705	-9.171658	-3.814466
1FIL	A	VAL	40	G	-7.874204	10.227631	-7.851258	-2.606340
1FIL	A	ASN	41	G	-7.065883	8.935019	-8.505715	-3.087321
1FIL	A	ILE	42	C	-7.056308	8.934562	-8.554329	-3.092505
1FIL	A	THR	43	C	-7.049773	8.876342	-8.594688	-3.084514
1FIL	A	PRO	44	H	-7.058214	8.751871	-8.632636	-3.084166
1FIL	A	ALA	45	H	-7.203597	8.506755	-8.898738	-3.248947
1FIL	A	GLU	46	H	-8.890179	8.544995	-11.457743	-3.114506
1FIL	A	VAL	47	H	-8.869115	9.772230	-10.657641	-3.017571
1FIL	A	GLY	48	H	-8.689327	9.773930	-10.406507	-3.107294
1FIL	A	VAL	49	H	-8.589150	9.774121	-10.269040	-3.034704
1FIL	A	LEU	50	H	-8.181570	8.973015	-10.274073	-3.205646
1FIL	A	VAL	51	H	-8.059713	8.332192	-10.937577	-3.396365
1FIL	A	GLY	52	T	-8.025308	7.214256	-11.674971	-3.514073
1FIL	A	LYS	53	T	-8.105454	6.666439	-12.103227	-3.592348
1FIL	A	ASP	54	T	-8.162753	6.386348	-12.296073	-3.677473

1FIL	A	ARG	55	T	-8.601429	4.515957	-14.311594	-4.027539
1FIL	A	SER	56	T	-8.976158	3.558374	-14.733986	-3.847044
1FIL	A	SER	57	T	-9.516434	6.324755	-13.461886	-3.454868
1FIL	A	PHE	58	T	-8.857688	10.131506	-10.445783	-3.592988
1FIL	A	TYR	59	T	-7.884616	8.790938	-9.739955	-3.414723
1FIL	A	VAL	60	T	-6.404750	8.678606	-7.919257	-3.569406
1FIL	A	ASN	61	T	-6.399210	8.721100	-7.944319	-3.580317
1FIL	A	GLY	62	T	-6.360869	9.004191	-7.992910	-3.637053
1FIL	A	LEU	63	E	-6.347358	9.076357	-8.006486	-3.648449
1FIL	A	THR	64	E	-6.376908	9.118645	-7.953838	-3.676547
1FIL	A	LEU	65	E	-7.589610	12.159487	-9.490683	-4.351432
1FIL	A	GLY	66	T	-7.589020	11.697362	-9.814857	-4.413682
1FIL	A	GLY	67	T	-8.012628	10.178915	-10.873762	-4.362905
1FIL	A	GLN	68	E	-8.532805	8.341288	-13.304012	-4.962649
1FIL	A	LYS	69	E	-8.891465	7.507658	-14.555972	-5.324862
1FIL	A	CYS	70	E	-9.032293	7.479893	-14.531712	-5.216919
1FIL	A	SER	71	E	-9.759391	10.980211	-11.926322	-3.728206
1FIL	A	VAL	72	E	-9.604891	11.192126	-11.833964	-3.761263
1FIL	A	ILE	73	E	-9.588615	11.200028	-11.871622	-3.762935
1FIL	A	ARG	74	E	-9.620630	11.158978	-11.816036	-3.743687
1FIL	A	ASP	75	E	-9.886145	11.226953	-12.585043	-4.096211
1FIL	A	SER	76	E	-9.227304	10.402522	-12.234095	-4.402991
1FIL	A	LEU	77	T	-7.406341	8.502186	-10.581594	-4.408969
1FIL	A	LEU	78	T	-6.480103	6.537902	-10.124705	-4.147449
1FIL	A	GLN	79	T	-6.460652	6.539608	-10.200152	-4.154471
1FIL	A	ASP	80	T	-6.457621	6.546651	-10.216053	-4.156624
1FIL	A	GLY	81	T	-6.462130	6.518790	-10.201606	-4.154322
1FIL	A	GLU	82	T	-6.590753	6.055202	-10.125596	-4.092913
1FIL	A	PHE	83	T	-8.403152	6.800587	-12.589817	-4.393778
1FIL	A	SER	84	E	-9.556411	8.054268	-13.361263	-4.568369
1FIL	A	MET	85	E	-12.772812	12.498037	-17.108725	-5.826592
1FIL	A	ASP	86	E	-15.345457	14.500649	-22.116365	-7.323288
1FIL	A	LEU	87	E	-12.377802	14.564606	-18.521326	-8.124744
1FIL	A	ARG	88	E	-9.424741	11.093593	-16.628699	-8.378121
1FIL	A	THR	89	E	-6.158740	6.552048	-9.592387	-4.401683
1FIL	A	LYS	90	C	-3.624025	3.415519	-7.503331	-4.035146
1FIL	A	SER	91	C	-1.084895	1.975686	-4.724373	-3.625466
1FIL	A	THR	92	T	-0.578833	2.694638	-5.167815	-4.129628
1FIL	A	GLY	93	T	-0.566669	2.765613	-5.236347	-4.164364
1FIL	A	GLY	94	T	-0.566752	2.764895	-5.235347	-4.164010
1FIL	A	ALA	95	T	-0.573180	2.741754	-5.179697	-4.140524
1FIL	A	PRO	96	C	-1.078052	2.661400	-4.063434	-3.362125
1FIL	A	THR	97	C	-3.254215	4.704464	-5.699981	-3.568899
1FIL	A	PHE	98	C	-7.684962	8.819760	-10.885419	-4.586539
1FIL	A	ASN	99	E	-11.301014	12.273269	-17.762107	-6.994248
1FIL	A	VAL	100	E	-11.497718	13.930072	-15.392855	-5.729021
1FIL	A	THR	101	E	-11.372559	14.485944	-13.603618	-4.776982
1FIL	A	VAL	102	E	-11.344750	14.325387	-13.676106	-4.744749
1FIL	A	THR	103	E	-11.319122	14.189215	-13.835529	-4.783359
1FIL	A	LYS	104	E	-11.374315	14.162726	-14.114743	-4.967962
1FIL	A	THR	105	T	-11.264864	13.884344	-14.196214	-5.060037
1FIL	A	ASP	106	T	-11.325721	13.839982	-14.085429	-4.885153
1FIL	A	LYS	107	T	-11.254416	14.659996	-13.513860	-4.776310
1FIL	A	THR	108	E	-11.218329	15.112797	-13.055722	-4.604353
1FIL	A	LEU	109	E	-11.231416	15.451232	-12.768111	-4.525315
1FIL	A	VAL	110	E	-11.252162	16.470564	-11.941613	-4.268914
1FIL	A	LEU	111	E	-11.387396	17.317795	-11.515501	-4.162099
1FIL	A	LEU	112	E	-10.716824	15.356739	-13.284778	-5.474893
1FIL	A	MET	113	E	-8.122960	9.891909	-10.792930	-4.636638
1FIL	A	GLY	114	E	-6.282444	6.886774	-8.535851	-3.527415
1FIL	A	LYS	115	T	-4.819809	6.256929	-6.576739	-3.141509
1FIL	A	GLU	116	T	-4.107262	5.587455	-7.173595	-3.632460
1FIL	A	GLY	117	T	-3.760255	4.826733	-7.628488	-3.762522
1FIL	A	VAL	118	T	-3.732615	4.854347	-7.639673	-3.739962
1FIL	A	HIS	119	C	-3.703645	4.966105	-7.584561	-3.720075
1FIL	A	GLY	120	H	-3.792504	4.764939	-7.774637	-3.817832
1FIL	A	GLY	121	H	-4.106873	4.387694	-8.008613	-3.796326
1FIL	A	LEU	122	H	-5.044278	6.415417	-7.312074	-3.317726
1FIL	A	ILE	123	H	-5.368262	7.100078	-6.893928	-3.350280
1FIL	A	ASN	124	H	-8.358604	8.665567	-11.737990	-4.360913
1FIL	A	LYS	125	H	-9.303687	9.844239	-13.377666	-5.126595
1FIL	A	LYS	126	H	-12.040070	12.259459	-18.098797	-6.576917
1FIL	A	CYS	127	H	-12.721903	11.635666	-17.480426	-5.223523
1FIL	A	TYR	128	H	-12.534628	11.606109	-16.547730	-4.747680
1FIL	A	GLU	129	H	-11.645712	10.361830	-14.995939	-4.238340
1FIL	A	MET	130	H	-11.542612	10.880195	-14.615666	-4.136360
1FIL	A	ALA	131	H	-11.536056	10.887463	-14.635323	-4.133612
1FIL	A	SER	132	H	-11.570623	10.776410	-14.498395	-4.061815
1FIL	A	HIS	133	H	-11.623254	10.697299	-14.418765	-4.056851
1FIL	A	LEU	134	H	-12.444049	12.770836	-13.978967	-3.939267
1FIL	A	ARG	135	H	-13.873163	11.660993	-17.385512	-4.303337

1FIL	A	ARG	136	H	-10.858544	7.818374	-13.865951	-3.324207
1FIL	A	SER	137	C	-10.858544	7.818374	-13.865951	-3.324207
1FIL	A	GLN	138	C	-10.858544	7.818374	-13.865951	-3.324207
1FIL	A	TYR	139	C	-10.858544	7.818374	-13.865951	-3.324207
1FL0	A	ILE	150	C	-8.321273	9.866298	-10.376860	-3.754495
1FL0	A	ASP	151	C	-8.321273	9.866298	-10.376860	-3.754495
1FL0	A	VAL	152	G	-8.321273	9.866298	-10.376860	-3.754495
1FL0	A	SER	153	G	-8.321273	9.866298	-10.376860	-3.754495
1FL0	A	ARG	154	G	-10.947352	12.591047	-13.695147	-4.716392
1FL0	A	LEU	155	C	-12.479796	17.552688	-14.197788	-5.566812
1FL0	A	ASP	156	C	-13.011384	15.289050	-15.945036	-5.308636
1FL0	A	LEU	157	E	-12.891083	15.027508	-16.155746	-5.283858
1FL0	A	ARG	158	E	-12.516777	14.121176	-16.195586	-5.169384
1FL0	A	ILE	159	E	-9.125877	12.503680	-10.609441	-4.247817
1FL0	A	GLY	160	E	-8.808338	11.064364	-11.511637	-4.281532
1FL0	A	CYS	161	E	-8.685367	10.916611	-11.671521	-4.261144
1FL0	A	ILE	162	E	-8.622827	10.924367	-11.677517	-4.198558
1FL0	A	ILE	163	E	-8.560827	10.861396	-11.760895	-4.184258
1FL0	A	THR	164	E	-8.843765	9.854968	-12.506505	-4.149590
1FL0	A	ALA	165	E	-8.954030	10.784114	-12.053790	-4.021473
1FL0	A	ARG	166	E	-8.257902	9.855589	-11.430511	-4.227822
1FL0	A	LYS	167	E	-7.578231	10.151926	-11.072712	-4.711773
1FL0	A	HIS	168	T	-6.793718	8.225641	-10.945268	-4.649381
1FL0	A	PRO	169	T	-6.448916	7.410890	-11.019787	-4.514419
1FL0	A	ASP	170	T	-6.431782	7.421054	-11.060600	-4.517381
1FL0	A	ALA	171	T	-6.453381	7.342729	-11.052191	-4.525368
1FL0	A	ASP	172	T	-6.518973	6.995698	-11.066873	-4.480906
1FL0	A	SER	173	T	-6.889352	6.517318	-11.202732	-4.357553
1FL0	A	LEU	174	T	-8.448938	8.285229	-12.335185	-4.539479
1FL0	A	TYR	175	E	-11.896765	13.412045	-14.623051	-4.761123
1FL0	A	VAL	176	E	-12.295459	13.967474	-15.344995	-5.018116
1FL0	A	GLU	177	E	-12.117538	13.933437	-15.445036	-5.104076
1FL0	A	GLU	178	E	-9.602738	12.739995	-11.559707	-4.566450
1FL0	A	VAL	179	E	-9.259952	11.925169	-12.176657	-4.658011
1FL0	A	ASP	180	E	-7.195473	6.462795	-11.613453	-4.406065
1FL0	A	VAL	181	T	-4.934561	4.868262	-9.055956	-4.060039
1FL0	A	GLY	182	T	-3.018528	3.460165	-7.119683	-3.840705
1FL0	A	GLU	183	T	-3.018285	3.461163	-7.121681	-3.840846
1FL0	A	ILE	184	T	-3.018142	3.462120	-7.122731	-3.840904
1FL0	A	ALA	185	T	-3.018646	3.459681	-7.118854	-3.840390
1FL0	A	PRO	186	T	-3.042215	3.402361	-7.039239	-3.829974
1FL0	A	ARG	187	E	-7.348040	6.641594	-11.734894	-4.121751
1FL0	A	THR	188	E	-7.786554	8.434097	-11.320654	-4.173901
1FL0	A	VAL	189	E	-8.327477	12.525380	-10.473758	-4.538788
1FL0	A	VAL	190	E	-8.032600	12.944103	-10.147795	-4.530732
1FL0	A	SER	191	E	-7.574336	11.802206	-10.454883	-4.700272
1FL0	A	GLY	192	C	-6.390994	11.835220	-8.600384	-4.798614
1FL0	A	LEU	193	T	-6.345164	11.948365	-8.572823	-4.767419
1FL0	A	VAL	194	T	-6.257606	11.556983	-8.722331	-4.666062
1FL0	A	ASN	195	T	-6.260216	11.489007	-8.747355	-4.662953
1FL0	A	HIS	196	T	-6.293847	11.524220	-8.639902	-4.650714
1FL0	A	VAL	197	T	-6.969324	10.125065	-9.930233	-4.205329
1FL0	A	PRO	198	C	-7.029068	9.220664	-10.547325	-4.271532
1FL0	A	LEU	199	G	-7.505318	8.884252	-11.652874	-4.528578
1FL0	A	GLU	200	G	-7.580463	8.758275	-11.700564	-4.574299
1FL0	A	GLN	201	G	-7.599783	8.721554	-11.663091	-4.579563
1FL0	A	MET	202	T	-7.991586	9.877154	-11.510643	-4.909465
1FL0	A	GLN	203	T	-9.894112	9.704302	-15.249816	-5.539097
1FL0	A	ASN	204	T	-10.438064	8.697262	-16.289309	-5.692136
1FL0	A	ARG	205	E	-12.342588	13.600794	-16.103033	-5.098867
1FL0	A	MET	206	E	-11.957004	16.769291	-13.493876	-4.730098
1FL0	A	VAL	207	E	-11.682441	17.266416	-12.832023	-4.584460
1FL0	A	ILE	208	E	-11.704393	17.565861	-12.596960	-4.556563
1FL0	A	LEU	209	E	-11.835518	18.521826	-11.968084	-4.462809
1FL0	A	LEU	210	E	-11.770440	17.829260	-12.553110	-4.618623
1FL0	A	CYS	211	T	-10.932646	12.281329	-14.766798	-5.264350
1FL0	A	ASN	212	T	-10.080547	10.770925	-13.927684	-4.817872
1FL0	A	LEU	213	T	-6.783139	11.098887	-8.219566	-4.158358
1FL0	A	LYS	214	C	-6.495977	10.756765	-8.685521	-4.276438
1FL0	A	PRO	215	C	-6.430028	10.753241	-8.796505	-4.270107
1FL0	A	ALA	216	E	-5.570516	8.476146	-8.945737	-4.424054
1FL0	A	LYS	217	E	-4.726526	9.069802	-7.567480	-4.444454
1FL0	A	MET	218	T	-4.707122	9.157618	-7.583133	-4.467579
1FL0	A	ARG	219	T	-4.714500	9.146282	-7.565938	-4.468828
1FL0	A	GLY	220	T	-4.717556	9.137860	-7.556578	-4.470613
1FL0	A	VAL	221	T	-4.836264	9.438202	-7.237362	-4.469937
1FL0	A	LEU	222	E	-6.289101	11.358852	-8.372033	-4.676830
1FL0	A	SER	223	E	-7.639733	10.497322	-10.582995	-4.687855
1FL0	A	GLN	224	C	-9.014673	10.458094	-12.580921	-4.935997
1FL0	A	ALA	225	C	-10.478532	13.886304	-13.223769	-4.897014
1FL0	A	MET	226	E	-10.313463	14.384748	-12.772026	-4.936099

1FL0	A	VAL	227	E	-10.231078	14.309229	-12.883170	-4.956624
1FL0	A	MET	228	C	-10.244643	14.317333	-12.852715	-4.960264
1FL0	A	CYS	229	E	-9.618600	10.317210	-13.880271	-4.815089
1FL0	A	ALA	230	E	-7.033979	5.849814	-11.588087	-4.352241
1FL0	A	SER	231	E	-5.580117	5.534123	-10.706320	-4.856104
1FL0	A	SER	232	E	-4.727286	6.820635	-8.985393	-4.692664
1FL0	A	PRO	233	T	-4.724706	6.827506	-9.001304	-4.695501
1FL0	A	GLU	234	T	-4.724794	6.827376	-9.000507	-4.695514
1FL0	A	LYS	235	E	-4.736816	6.848165	-8.947915	-4.702586
1FL0	A	ILE	236	E	-4.884289	7.226504	-8.473094	-4.645132
1FL0	A	GLU	237	E	-7.943276	8.428929	-12.655567	-5.343194
1FL0	A	ILE	238	E	-10.282182	14.519817	-11.847573	-4.316193
1FL0	A	LEU	239	C	-7.775694	11.342104	-8.686192	-3.598551
1FL0	A	ALA	240	B	-4.971215	6.975452	-7.514780	-3.720570
1FL0	A	PRO	241	C	-4.346379	8.254651	-6.962936	-4.057961
1FL0	A	PRO	242	T	-4.122746	7.778686	-7.328313	-4.123472
1FL0	A	ASN	243	T	-3.952093	7.451566	-7.571700	-4.180465
1FL0	A	GLY	244	T	-3.925136	7.426295	-7.658765	-4.197195
1FL0	A	SER	245	T	-4.033449	7.524516	-7.698900	-4.293318
1FL0	A	VAL	246	T	-4.320724	6.638214	-8.341078	-4.325174
1FL0	A	PRO	247	T	-4.663067	6.562688	-8.512162	-4.372733
1FL0	A	GLY	248	T	-5.711011	7.071111	-9.601672	-4.512935
1FL0	A	ASP	249	E	-7.323296	7.959619	-11.292085	-4.480559
1FL0	A	ARG	250	E	-8.615274	8.614125	-12.563484	-4.490907
1FL0	A	ILE	251	B	-6.918134	13.790320	-7.149688	-4.281236
1FL0	A	THR	252	C	-6.652048	14.591293	-7.018087	-4.392417
1FL0	A	PHE	253	T	-6.182004	14.232718	-6.553575	-4.174718
1FL0	A	ASP	254	T	-4.110393	8.864587	-6.075012	-4.172272
1FL0	A	ALA	255	T	-4.088918	8.891085	-6.163109	-4.185104
1FL0	A	PHE	256	T	-4.092580	8.852720	-6.164617	-4.185335
1FL0	A	PRO	257	T	-4.094509	8.813042	-6.172656	-4.184154
1FL0	A	GLY	258	C	-4.101185	8.708911	-6.206172	-4.190035
1FL0	A	GLU	259	C	-5.927131	8.929619	-9.346049	-4.568883
1FL0	A	PRO	260	C	-6.851613	6.433624	-12.403672	-4.735417
1FL0	A	ASP	261	T	-7.002348	5.272517	-13.042833	-4.769504
1FL0	A	LYS	262	T	-7.085292	5.670386	-12.878013	-4.807181
1FL0	A	GLU	263	T	-7.789133	9.035516	-12.716128	-4.986146
1FL0	A	LEU	264	T	-6.029319	8.477372	-8.998482	-4.350463
1FL0	A	ASN	265	T	-4.696558	6.719420	-8.492763	-4.471955
1FL0	A	PRO	266	T	-4.666282	6.825425	-8.535780	-4.473220
1FL0	A	LYS	267	T	-4.666956	6.822334	-8.532014	-4.472681
1FL0	A	LYS	268	T	-4.667371	6.822204	-8.528813	-4.472388
1FL0	A	LYS	269	T	-4.727755	6.651782	-8.490233	-4.487740
1FL0	A	ILE	270	H	-6.424406	8.971907	-9.429133	-4.515614
1FL0	A	TRP	271	H	-8.603698	14.039008	-11.105264	-5.126935
1FL0	A	GLU	272	H	-8.674677	13.582782	-11.393659	-5.107182
1FL0	A	GLN	273	H	-9.019181	12.502837	-12.503349	-5.078391
1FL0	A	ILE	274	H	-9.052370	12.112649	-12.547329	-4.973938
1FL0	A	GLN	275	G	-9.103532	11.215740	-12.759901	-4.846980
1FL0	A	PRO	276	G	-9.061271	11.245358	-12.797147	-4.827699
1FL0	A	ASP	277	G	-9.569485	11.804201	-13.017364	-4.767549
1FL0	A	LEU	278	E	-10.070128	12.712071	-13.048259	-4.673904
1FL0	A	HIS	279	E	-9.708618	8.604107	-15.177585	-5.165734
1FL0	A	THR	280	E	-8.549163	7.081362	-14.636080	-5.462635
1FL0	A	ASN	281	T	-6.852156	6.898968	-11.982727	-5.171589
1FL0	A	ASP	282	T	-6.719390	7.106021	-11.920563	-5.067464
1FL0	A	GLU	283	T	-6.716222	7.123764	-11.926955	-5.065677
1FL0	A	CYS	284	T	-6.718956	7.122691	-11.909468	-5.064338
1FL0	A	VAL	285	B	-6.742720	7.134250	-11.801228	-5.046196
1FL0	A	ALA	286	E	-7.647752	8.070906	-11.722705	-4.661276
1FL0	A	THR	287	E	-8.422891	13.909640	-10.444005	-5.096507
1FL0	A	TYR	288	E	-7.076746	14.036253	-8.010336	-4.727125
1FL0	A	LYS	289	T	-6.564964	14.190593	-7.459091	-4.581772
1FL0	A	GLY	290	T	-6.535134	14.191491	-7.525314	-4.570572
1FL0	A	VAL	291	E	-6.535926	14.193043	-7.518391	-4.569656
1FL0	A	PRO	292	E	-6.556855	14.191180	-7.429627	-4.549057
1FL0	A	PHE	293	C	-6.816448	14.237072	-7.339838	-4.478887
1FL0	A	GLU	294	E	-6.142172	7.742471	-9.860317	-4.607201
1FL0	A	VAL	295	E	-4.316242	6.449838	-8.231743	-4.639293
1FL0	A	LYS	296	T	-4.012977	6.483024	-8.299641	-4.640481
1FL0	A	GLY	297	T	-4.005137	6.504857	-8.328347	-4.643653
1FL0	A	LYS	298	T	-4.005302	6.503145	-8.327677	-4.643593
1FL0	A	GLY	299	E	-4.021016	6.475705	-8.285684	-4.644171
1FL0	A	VAL	300	E	-4.536291	6.576548	-8.457654	-4.643580
1FL0	A	CYS	301	C	-6.570150	8.144459	-10.477579	-4.869272
1FL0	A	ARG	302	B	-9.858934	10.323972	-13.755544	-4.429024
1FL0	A	ALA	303	T	-10.045748	9.492498	-14.837380	-4.730699
1FL0	A	GLN	304	T	-10.250570	7.783087	-17.478791	-5.773489
1FL0	A	THR	305	T	-9.343748	7.561062	-15.793731	-5.606528
1FL0	A	MET	306	T	-9.358369	7.536682	-15.768329	-5.620868
1FL0	A	SER	307	T	-9.365012	7.515067	-15.749354	-5.622089

1FL0	A	ASN	308	T	-9.411165	7.533688	-15.616563	-5.608052
1FL0	A	SER	309	E	-9.437055	7.969175	-15.277118	-5.553319
1FL0	A	GLY	310	E	-7.969287	11.784904	-9.628884	-4.340380
1FL0	A	ILE	311	E	-7.969287	11.784904	-9.628884	-4.340380
1FL0	A	LYS	312	E	-7.969287	11.784904	-9.628884	-4.340380
1FL0	A	LEU	313	C	-7.969287	11.784904	-9.628884	-4.340380
1FNA	A	GLY	6	C	-7.052953	9.158720	-9.320463	-3.675061
1FNA	A	SER	7	C	-7.052953	9.158720	-9.320463	-3.675061
1FNA	A	LEU	8	E	-7.052953	9.158720	-9.320463	-3.675061
1FNA	A	GLU	9	E	-7.052953	9.158720	-9.320463	-3.675061
1FNA	A	VAL	10	E	-5.899319	9.801555	-6.729343	-3.437474
1FNA	A	VAL	11	E	-5.852794	9.600739	-6.854260	-3.390058
1FNA	A	ALA	12	E	-5.855304	9.517919	-6.859121	-3.366076
1FNA	A	ALA	13	E	-5.834089	9.494386	-6.925183	-3.357533
1FNA	A	THR	14	E	-5.830597	9.503809	-6.939647	-3.357880
1FNA	A	PRO	15	T	-6.955193	8.488613	-8.726441	-3.083704
1FNA	A	THR	16	T	-7.540191	9.059096	-9.177641	-3.179918
1FNA	A	SER	17	E	-7.693812	9.439191	-8.963038	-3.263504
1FNA	A	LEU	18	E	-8.807222	11.546153	-9.665375	-3.593636
1FNA	A	LEU	19	E	-10.599676	14.435970	-11.560384	-3.956990
1FNA	A	ILE	20	E	-10.760761	15.325260	-11.474179	-4.106666
1FNA	A	SER	21	E	-10.280662	13.491893	-11.557892	-4.114337
1FNA	A	TRP	22	E	-7.745120	10.848966	-8.268825	-3.500517
1FNA	A	ASP	23	C	-4.896765	5.755769	-6.503983	-2.916466
1FNA	A	ALA	24	C	-4.296029	5.823516	-6.411310	-3.028934
1FNA	A	PRO	25	C	-4.149077	6.152768	-6.453402	-3.087151
1FNA	A	ALA	26	C	-4.117778	6.227693	-6.461473	-3.067013
1FNA	A	VAL	27	C	-4.118961	6.218756	-6.458042	-3.066087
1FNA	A	THR	28	C	-4.303190	6.399665	-6.443312	-3.120821
1FNA	A	VAL	29	C	-4.916697	7.374866	-6.597398	-3.171275
1FNA	A	ARG	30	C	-5.874522	7.615849	-6.608446	-2.692202
1FNA	A	TYR	31	E	-9.250224	12.310290	-8.919185	-3.121552
1FNA	A	TYR	32	E	-12.537130	16.297322	-11.657734	-3.524676
1FNA	A	ARG	33	E	-13.291269	19.383676	-15.264840	-6.320350
1FNA	A	ILE	34	E	-11.491639	18.650455	-14.033202	-6.923212
1FNA	A	THR	35	E	-10.350647	15.259858	-16.320324	-8.579491
1FNA	A	TYR	36	E	-7.718086	11.800066	-13.928639	-8.167088
1FNA	A	GLY	37	E	-4.276322	4.387441	-9.188357	-4.865228
1FNA	A	GLU	38	E	-3.119444	3.296257	-7.740410	-4.374601
1FNA	A	THR	39	T	-1.696907	2.532383	-5.631973	-3.834915
1FNA	A	GLY	40	T	-0.926630	1.662094	-5.852899	-3.996432
1FNA	A	GLY	41	T	-0.786753	1.970671	-5.987261	-4.063551
1FNA	A	ASN	42	C	-0.777632	2.001041	-6.007061	-4.062209
1FNA	A	SER	43	C	-0.792953	1.953000	-5.905338	-4.012896
1FNA	A	PRO	44	C	-0.987042	1.563921	-5.416719	-3.643980
1FNA	A	VAL	45	C	-1.885013	2.630504	-4.551651	-2.902737
1FNA	A	GLN	46	E	-3.359869	3.560772	-5.932662	-2.947762
1FNA	A	GLU	47	E	-5.232991	7.229392	-9.962971	-5.217084
1FNA	A	PHE	48	E	-6.027166	11.553381	-9.285831	-5.520610
1FNA	A	THR	49	E	-5.104707	8.726077	-6.801740	-3.642041
1FNA	A	VAL	50	E	-4.882413	7.495050	-6.898316	-3.272365
1FNA	A	PRO	51	E	-4.752436	7.114997	-7.134869	-3.267021
1FNA	A	GLY	52	T	-4.557238	7.053030	-7.113670	-3.337359
1FNA	A	SER	53	T	-4.563110	6.954500	-7.156327	-3.336998
1FNA	A	LYS	54	T	-4.750762	6.742246	-7.557808	-3.433091
1FNA	A	SER	55	C	-4.950659	7.228281	-7.392993	-3.476630
1FNA	A	THR	56	E	-5.098967	8.188181	-7.011824	-3.543235
1FNA	A	ALA	57	E	-5.070841	10.041717	-5.718343	-3.344307
1FNA	A	THR	58	E	-4.551098	10.893870	-4.754096	-3.442931
1FNA	A	ILE	59	E	-4.558246	10.916475	-4.729628	-3.444873
1FNA	A	SER	60	C	-4.522815	10.733820	-4.942290	-3.479747
1FNA	A	GLY	61	C	-4.404344	10.239530	-5.338394	-3.569469
1FNA	A	LEU	62	C	-4.556375	10.402845	-5.394380	-3.665359
1FNA	A	LYS	63	T	-5.073090	8.717260	-7.459008	-3.943920
1FNA	A	PRO	64	T	-5.126675	8.488524	-7.486555	-3.943384
1FNA	A	GLY	65	T	-5.255327	8.422240	-7.331080	-3.923359
1FNA	A	VAL	66	E	-6.410540	7.828526	-9.459450	-4.013260
1FNA	A	ASP	67	E	-6.702560	6.940870	-10.334083	-4.348615
1FNA	A	TYR	68	E	-9.250401	13.229006	-10.723715	-4.682425
1FNA	A	THR	69	E	-11.290315	14.238327	-13.632573	-4.774910
1FNA	A	ILE	70	E	-11.151013	17.585295	-11.106266	-4.377854
1FNA	A	THR	71	E	-10.930153	17.343799	-10.950093	-4.251587
1FNA	A	VAL	72	E	-10.652146	17.599867	-10.435164	-4.179939
1FNA	A	TYR	73	E	-10.001977	15.981820	-10.546918	-4.477901
1FNA	A	ALA	74	E	-8.632189	11.265733	-11.647770	-4.826097
1FNA	A	VAL	75	E	-6.774616	7.658013	-10.763142	-4.677290
1FNA	A	THR	76	T	-5.946787	6.037104	-10.317941	-4.434644
1FNA	A	GLY	77	T	-5.643712	5.297583	-10.279955	-4.221856
1FNA	A	ARG	78	T	-5.520956	4.795567	-10.370757	-4.059625
1FNA	A	GLY	79	T	-4.380718	2.123054	-9.006397	-3.449259
1FNA	A	ASP	80	T	-4.313847	2.226700	-9.063587	-3.454825

1FNA	A	SER	81	T	-4.342107	2.065003	-9.012306	-3.409638
1FNA	A	PRO	82	T	-4.368350	1.969671	-8.959412	-3.386635
1FNA	A	ALA	83	T	-4.384336	1.952230	-8.910202	-3.387406
1FNA	A	SER	84	T	-5.548814	3.666780	-9.739311	-3.641392
1FNA	A	SER	85	T	-7.705699	5.612403	-12.242895	-3.630759
1FNA	A	LYS	86	C	-7.864191	7.184369	-11.408940	-3.502818
1FNA	A	PRO	87	C	-7.822154	9.960769	-9.669102	-3.376857
1FNA	A	ILE	88	E	-7.863873	10.198457	-9.440896	-3.356193
1FNA	A	SER	89	E	-7.878989	10.227077	-9.343990	-3.338619
1FNA	A	ILE	90	E	-8.020403	10.611642	-8.821114	-3.218323
1FNA	A	ASN	91	E	-8.217971	10.813841	-8.594191	-3.292782
1FNA	A	TYR	92	E	-10.210531	13.301455	-10.752772	-3.662195
1FNA	A	ARG	93	E	-7.387733	8.570063	-7.720019	-2.516009
1FNA	A	THR	94	E	-7.387733	8.570063	-7.720019	-2.516009
1FNA	A	GLU	95	C	-7.387733	8.570063	-7.720019	-2.516009
1FNA	A	ILE	96	C	-7.387733	8.570063	-7.720019	-2.516009
1FNL	A	GLU	3	C	-3.469823	0.683156	-8.475379	-3.212219
1FNL	A	ASP	4	C	-3.469823	0.683156	-8.475379	-3.212219
1FNL	A	LEU	5	C	-3.469823	0.683156	-8.475379	-3.212219
1FNL	A	PRO	6	C	-3.469823	0.683156	-8.475379	-3.212219
1FNL	A	LYS	7	C	-4.943915	2.750699	-10.801686	-4.405702
1FNL	A	ALA	8	C	-6.455665	4.838862	-12.479461	-5.053605
1FNL	A	VAL	9	E	-7.975199	7.251399	-14.187283	-5.537627
1FNL	A	VAL	10	E	-8.807243	12.626558	-11.902690	-4.723282
1FNL	A	PHE	11	E	-8.932749	13.712267	-10.728038	-4.173854
1FNL	A	LEU	12	E	-8.961429	14.015015	-10.580710	-4.196735
1FNL	A	GLU	13	E	-9.189475	14.136657	-10.742396	-4.314602
1FNL	A	PRO	14	T	-9.751888	14.186334	-11.571972	-4.431857
1FNL	A	GLN	15	T	-10.144968	13.664777	-12.594888	-4.831682
1FNL	A	TRP	16	T	-10.669201	15.226646	-12.247348	-5.067536
1FNL	A	TYR	17	T	-14.262180	18.109430	-16.685754	-5.489673
1FNL	A	SER	18	E	-12.206573	16.280787	-14.019940	-5.282448
1FNL	A	VAL	19	E	-11.746086	15.652730	-14.177995	-5.240429
1FNL	A	LEU	20	E	-11.517163	15.072147	-14.566184	-5.303126
1FNL	A	GLU	21	T	-11.204179	14.041620	-14.780983	-5.236163
1FNL	A	LYS	22	T	-10.880608	13.567603	-14.594379	-5.150047
1FNL	A	ASP	23	b	-10.878104	13.338186	-14.624007	-5.079875
1FNL	A	SER	24	C	-10.583184	13.915784	-13.636557	-4.911167
1FNL	A	VAL	25	E	-10.383076	14.023549	-13.452207	-4.967820
1FNL	A	THR	26	E	-10.157552	13.314444	-13.830199	-5.203364
1FNL	A	LEU	27	E	-8.587650	10.636844	-12.833044	-5.552304
1FNL	A	LYS	28	E	-7.574948	7.678888	-13.208218	-5.519664
1FNL	A	CYS	29	E	-7.353082	8.373896	-12.930887	-5.548937
1FNL	A	GLN	30	E	-7.337173	8.416252	-12.953124	-5.546439
1FNL	A	GLY	31	C	-7.220043	8.409035	-12.869719	-5.439010
1FNL	A	ALA	32	C	-7.198037	8.119180	-12.870553	-5.323661
1FNL	A	TYR	33	C	-7.453979	8.706604	-12.744177	-5.174451
1FNL	A	SER	34	B	-6.039924	3.187350	-12.479188	-4.797849
1FNL	A	PRO	35	T	-5.924478	3.358755	-12.570405	-4.816240
1FNL	A	GLU	36	T	-5.935375	3.260808	-12.578750	-4.814846
1FNL	A	ASP	37	B	-5.944319	3.195253	-12.575362	-4.817795
1FNL	A	ASN	38	C	-5.950272	3.156680	-12.560124	-4.814529
1FNL	A	SER	39	C	-6.934274	4.275348	-13.039236	-4.916476
1FNL	A	THR	40	C	-9.539470	6.756544	-15.835225	-5.504632
1FNL	A	GLN	41	E	-12.477632	8.852918	-18.973482	-5.820733
1FNL	A	TRP	42	E	-13.994619	15.624033	-17.802174	-5.835312
1FNL	A	PHE	43	E	-10.298000	9.710450	-14.512018	-4.943727
1FNL	A	HIS	44	E	-7.998092	7.660777	-12.446052	-4.755727
1FNL	A	ASN	45	T	-7.107712	7.727027	-11.282043	-4.502924
1FNL	A	GLU	46	T	-7.049772	7.823891	-11.333004	-4.487005
1FNL	A	SER	47	E	-6.984174	7.944914	-11.327354	-4.448091
1FNL	A	LEU	48	E	-6.960531	8.016345	-11.349374	-4.451839
1FNL	A	ILE	49	E	-7.064431	8.099096	-11.164158	-4.391013
1FNL	A	SER	50	E	-7.819411	8.995168	-11.764061	-4.290227
1FNL	A	SER	51	C	-8.038202	8.962376	-11.909914	-4.286318
1FNL	A	GLN	52	C	-8.604412	8.951753	-12.977298	-4.571004
1FNL	A	ALA	53	C	-9.262955	7.417112	-14.832571	-4.579709
1FNL	A	SER	54	C	-9.588678	7.123756	-15.457768	-4.697711
1FNL	A	SER	55	E	-9.479465	9.410486	-14.356777	-4.853070
1FNL	A	TYR	56	E	-8.614847	13.635956	-10.428335	-4.812204
1FNL	A	PHE	57	E	-7.854240	11.878125	-10.003887	-4.372630
1FNL	A	ILE	58	E	-7.473884	10.421705	-10.266416	-4.152958
1FNL	A	ASP	59	T	-7.104853	8.895239	-10.579384	-4.023565
1FNL	A	ALA	60	T	-6.752628	7.610909	-10.730368	-3.903778
1FNL	A	ALA	61	b	-6.589147	7.157665	-10.914536	-3.946868
1FNL	A	THR	62	C	-6.575766	6.673411	-11.200739	-3.972839
1FNL	A	VAL	63	G	-6.620328	6.379056	-11.383932	-4.005603
1FNL	A	ASN	64	G	-6.756068	6.183206	-11.498479	-4.039450
1FNL	A	ASP	65	G	-7.114454	6.265110	-11.974600	-4.266907
1FNL	A	SER	66	C	-7.746959	5.649355	-13.175167	-4.475432
1FNL	A	GLY	67	E	-8.612115	5.161033	-14.476972	-4.732992

1FNL	A	GLU	68	E	-11.876786	6.923297	-18.842932	-5.571202
1FNL	A	TYR	69	E	-14.912473	14.362835	-20.315408	-6.079022
1FNL	A	ARG	70	E	-14.426725	12.238450	-20.876777	-6.325112
1FNL	A	CYS	71	E	-11.744924	9.702346	-17.700447	-5.943214
1FNL	A	GLN	72	E	-11.380746	10.223974	-17.452125	-5.917763
1FNL	A	THR	73	T	-10.097866	9.612803	-15.095068	-5.279450
1FNL	A	ASN	74	T	-9.880218	9.634057	-15.107470	-5.234778
1FNL	A	LEU	75	T	-9.831166	9.674881	-15.149232	-5.215143
1FNL	A	SER	76	T	-9.824756	9.631646	-15.152357	-5.193818
1FNL	A	THR	77	C	-9.305861	9.155315	-14.531584	-5.066635
1FNL	A	LEU	78	C	-9.263162	9.117796	-14.332962	-4.933007
1FNL	A	SER	79	C	-9.242716	9.023419	-14.359515	-4.917854
1FNL	A	ASP	80	C	-9.109648	9.614490	-13.934534	-4.850127
1FNL	A	PRO	81	C	-9.100924	9.720469	-13.878318	-4.837190
1FNL	A	VAL	82	E	-9.415460	10.416688	-13.675705	-4.720532
1FNL	A	GLN	83	E	-9.686313	11.079671	-13.477783	-4.736608
1FNL	A	LEU	84	E	-9.380867	13.275299	-11.750464	-4.647469
1FNL	A	GLU	85	E	-7.743563	10.059498	-10.878540	-4.724540
1FNL	A	VAL	86	E	-7.243454	11.441548	-9.786654	-4.606031
1FNL	A	HIS	87	E	-6.972906	12.320947	-9.346969	-4.666391
1FNL	A	ILE	88	C	-6.711428	13.598407	-8.518838	-4.653861
1FNL	A	GLY	89	C	-6.713570	13.607979	-8.507167	-4.655182
1FNL	A	TRP	90	C	-6.823003	14.362578	-8.029545	-4.640544
1FNL	A	LEU	91	E	-7.018442	15.096431	-7.660729	-4.688833
1FNL	A	LEU	92	E	-7.317344	15.920441	-7.050095	-4.635151
1FNL	A	LEU	93	E	-10.192050	18.417037	-10.073138	-5.130405
1FNL	A	GLN	94	E	-12.638886	16.729662	-15.065359	-5.072999
1FNL	A	ALA	95	T	-9.129716	14.021303	-9.332035	-3.856579
1FNL	A	PRO	96	T	-9.024365	14.209359	-9.491708	-3.902939
1FNL	A	ARG	97	T	-8.968212	14.207015	-9.683063	-3.950891
1FNL	A	TRP	98	T	-8.965854	14.215086	-9.699711	-3.957039
1FNL	A	VAL	99	E	-8.953686	14.198662	-9.792085	-3.985707
1FNL	A	PHE	100	E	-9.664935	14.445557	-11.581517	-4.514249
1FNL	A	LYS	101	E	-8.190244	7.874913	-12.749130	-4.800775
1FNL	A	GLU	102	T	-8.120768	8.065922	-12.777922	-4.812516
1FNL	A	GLU	103	T	-8.076254	8.300169	-12.758510	-4.808644
1FNL	A	ASP	104	b	-8.070080	8.366105	-12.737691	-4.801437
1FNL	A	PRO	105	C	-8.075504	8.327272	-12.723841	-4.795307
1FNL	A	ILE	106	E	-8.995872	11.000310	-12.629877	-4.784488
1FNL	A	HIS	107	E	-9.509182	11.893103	-12.421675	-4.722404
1FNL	A	LEU	108	E	-10.540277	14.339415	-11.908345	-4.508256
1FNL	A	ARG	109	E	-12.703032	16.244661	-14.185037	-4.786806
1FNL	A	CYS	110	E	-14.108940	14.477527	-19.007107	-5.819592
1FNL	A	HIS	111	E	-10.932786	11.904175	-15.387952	-5.887520
1FNL	A	SER	112	E	-7.557729	10.869622	-10.935071	-5.371240
1FNL	A	TRP	113	T	-6.083423	10.115352	-9.281231	-5.096188
1FNL	A	LYS	114	T	-5.339323	9.927604	-8.467716	-4.907666
1FNL	A	ASN	115	T	-5.310151	9.930159	-8.537869	-4.897622
1FNL	A	THR	116	T	-5.309919	9.931224	-8.539134	-4.897534
1FNL	A	ALA	117	C	-5.323256	9.910313	-8.485104	-4.886580
1FNL	A	LEU	118	E	-5.497025	9.863336	-8.264453	-4.823324
1FNL	A	HIS	119	E	-7.100551	10.018337	-9.959027	-4.697985
1FNL	A	LYS	120	E	-9.630384	12.876006	-12.311570	-4.740556
1FNL	A	VAL	121	E	-10.316380	13.647688	-12.239019	-4.464211
1FNL	A	THR	122	E	-11.405747	16.017813	-12.883450	-4.893436
1FNL	A	TYR	123	E	-12.479099	17.283010	-14.861357	-5.503580
1FNL	A	LEU	124	E	-8.175244	7.308148	-13.502509	-5.310937
1FNL	A	GLN	125	E	-6.000164	5.169983	-12.154160	-5.499005
1FNL	A	ASN	126	T	-5.880929	5.292029	-12.213462	-5.445595
1FNL	A	GLY	127	T	-5.820069	5.573835	-12.155198	-5.418861
1FNL	A	LYS	128	E	-5.818204	5.590241	-12.158065	-5.418618
1FNL	A	ASP	129	E	-5.829368	5.557964	-12.132545	-5.420676
1FNL	A	ARG	130	E	-6.606220	6.760560	-12.168641	-5.194689
1FNL	A	LYS	131	E	-7.174151	8.306119	-11.672489	-5.177596
1FNL	A	TYR	132	E	-9.068080	11.344798	-13.052869	-5.332380
1FNL	A	PHE	133	E	-9.820585	12.622655	-13.341422	-5.266480
1FNL	A	HIS	134	E	-9.311032	9.725630	-14.343267	-5.267418
1FNL	A	HIS	135	E	-9.311638	9.710146	-14.347952	-5.266905
1FNL	A	ASN	136	T	-9.541394	8.137766	-15.150487	-5.273398
1FNL	A	SER	137	C	-9.544654	8.150891	-15.119669	-5.262999
1FNL	A	ASP	138	E	-9.421272	9.433620	-14.338880	-5.161070
1FNL	A	PHE	139	E	-8.030167	13.127722	-9.349489	-4.534538
1FNL	A	HIS	140	E	-6.617103	10.299913	-8.433662	-3.973138
1FNL	A	ILE	141	E	-6.555599	10.157523	-8.635974	-3.961591
1FNL	A	PRO	142	T	-6.520434	10.039356	-8.795820	-3.962282
1FNL	A	LYS	143	T	-6.388923	9.365616	-9.265707	-3.985052
1FNL	A	ALA	144	b	-6.406464	9.022158	-9.394654	-3.961790
1FNL	A	THR	145	C	-6.987916	7.227218	-11.342191	-4.056362
1FNL	A	LEU	146	G	-7.117229	6.782561	-11.615198	-4.116181
1FNL	A	LYS	147	G	-7.218917	6.531030	-11.656071	-4.143010
1FNL	A	ASP	148	G	-8.216161	5.755762	-13.811539	-4.409316

```
1FNL           A          SER           149                    C -8.917791  5.057621 -15.205831 -4.633357
1FNL           A          GLY           150                    E -9.786913  4.483224 -16.667854 -4.918309
1FNL           A          SER           151                    E -11.834122  4.585693 -19.575014 -5.204114
1FNL           A          TYR           152                    E -14.315322 15.097674 -19.115531 -5.906520
1FNL           A          PHE           153                    E -13.113648 14.156482 -16.946145 -5.534442
1FNL           A          CYS           154                    E -11.621139 12.716582 -16.804012 -6.099743
1FNL           A          ARG           155                    E -9.722968 11.720707 -14.306634 -5.718196
1FNL           A          GLY           156                    E -7.548190  7.175978 -11.406811 -4.149620
1FNL           A          LEU           157                    E -6.241187  7.959224 -9.337928 -4.054684
1FNL           A          VAL           158                    E -3.873342  7.194925 -6.515841 -4.082142
1FNL           A          GLY           159                    T -3.823323  7.146579 -6.685396 -4.081669
1FNL           A          SER           160                    T -3.810158  7.172151 -6.727173 -4.079970
1FNL           A          LYS           161                    E -3.810794  7.174005 -6.722410 -4.080387
1FNL           A          ASN           162                    E -3.819230  7.160993 -6.690329 -4.081134
1FNL           A          VAL           163                    E -5.151555  7.018967 -8.666716 -4.068414
1FNL           A          SER           164                    E -5.989352  8.419518 -8.943152 -4.086215
1FNL           A          SER           165                    C -7.066852  8.979884 -11.542697 -4.698951
1FNL           A          GLU           166                    C -6.917693  9.489440 -10.882787 -4.575852
1FNL           A          THR           167                    C -6.556256 10.761846 -9.417236 -4.412219
1FNL           A          VAL           168                    E -6.669910 11.001406 -9.142820 -4.357185
1FNL           A          ASN           169                    E -6.678235 11.158444 -9.087608 -4.391326
1FNL           A          ILE           170                    E -6.648438 11.762735 -8.891394 -4.482303
1FNL           A          THR           171                    E -5.713665  9.417596 -8.516643 -4.450159
1FNL           A          ILE           172                    E -4.820640  7.932375 -7.324932 -3.808434
1FNL           A          THR           173                    E -4.820640  7.932375 -7.324932 -3.808434
1FNL           A          GLN           174                    C -4.820640  7.932375 -7.324932 -3.808434
1FNL           A          ALA           175                    C -4.820640  7.932375 -7.324932 -3.808434
1FP5           A          VAL           336                    I -9.523826  9.219287 -11.109340 -2.985913
1FP5           A          SER           337                    C -9.523826  9.219287 -11.109340 -2.985913
1FP5           A          ALA           338                    E -9.523826  9.219287 -11.109340 -2.985913
1FP5           A          TYR           339                    E -9.523826  9.219287 -11.109340 -2.985913
1FP5           A          LEU           340                    E -10.924458 13.204723 -12.452145 -4.122912
1FP5           A          SER           341                    E -12.061885 12.009157 -14.928881 -4.247085
1FP5           A          ARG           342                    E -12.081434 11.991723 -14.877489 -4.229922
1FP5           A          PRO           343                    C -11.760226 12.474875 -14.604090 -4.307429
1FP5           A          SER           344                    C -11.706635 12.728021 -14.598951 -4.344665
1FP5           A          PRO           345                    C -11.946445 13.437390 -14.578268 -4.431573
1FP5           A          PHE           346                    H -12.032526 14.423507 -14.300071 -4.611479
1FP5           A          ASP           347                    H -11.519934 15.551394 -13.252499 -4.736377
1FP5           A          LEU           348                    H -9.146037 14.671142 -9.204868 -4.225572
1FP5           A          PHE           349                    H -8.190826 11.966772 -9.354195 -3.962851
1FP5           A          ILE           350                    H -7.931153 10.690051 -9.734867 -3.717850
1FP5           A          ARG           351                    H -7.896339 10.564366 -9.893320 -3.721987
1FP5           A          LYS           352                    C -7.893291 10.557357 -9.910733 -3.721668
1FP5           A          SER           353                    C -7.956694 10.050934 -10.043786 -3.662403
1FP5           A          PRO           354                    C -8.360788  8.972677 -10.815500 -3.462599
1FP5           A          THR           355                    C -8.977852 11.159364 -11.767864 -4.131883
1FP5           A          ILE           356                    E -9.188274 12.688292 -11.401400 -4.313675
1FP5           A          THR           357                    E -9.186509 12.764559 -11.383025 -4.330435
1FP5           A          CYS           358                    E -9.284829 12.832834 -11.358972 -4.382081
1FP5           A          LEU           359                    E -9.601539 12.807922 -11.722572 -4.476936
1FP5           A          VAL           360                    E -10.022051 11.543877 -12.647581 -3.977556
1FP5           A          VAL           361                    E -8.951941  8.709413 -11.843960 -3.673562
1FP5           A          ASP           362                    E -8.402932  7.598849 -12.448562 -3.957969
1FP5           A          LEU           363                    E -5.475133  3.866402 -8.633823 -3.031497
1FP5           A          ALA           364                    T -3.415507  3.949625 -6.356614 -3.356848
1FP5           A          PRO           365                    T -2.903016  3.898232 -6.231233 -3.380661
1FP5           A          SER           366                    T -2.885852  3.942865 -6.288036 -3.391664
1FP5           A          LYS           367                    C -2.823318  3.996097 -6.412513 -3.418936
1FP5           A          GLY           368                    C -2.829747  4.000713 -6.388094 -3.423456
1FP5           A          THR           369                    C -3.098221  4.004490 -6.409610 -3.434996
1FP5           A          VAL           370                    C -4.056357  4.644683 -7.593998 -3.638282
1FP5           A          ASN           371                    C -4.191118  4.448038 -7.453283 -3.616893
1FP5           A          LEU           372                    E -7.125931  9.001323 -9.626233 -4.221916
1FP5           A          THR           373                    E -9.441082  9.789902 -12.469381 -4.363064
1FP5           A          TRP           374                    E -11.458957 14.239960 -14.559944 -5.304287
1FP5           A          SER           375                    E -9.358414  7.675506 -16.103396 -6.133565
1FP5           A          ARG           376                    E -7.317586  7.307900 -12.913476 -5.547779
1FP5           A          ALA           377                    E -4.635601  3.256435 -9.502173 -4.242748
1FP5           A          SER           378                    T -4.515887  3.445368 -9.571325 -4.229526
1FP5           A          GLY           379                    T -4.257856  3.931412 -9.279472 -4.215868
1FP5           A          LYS           380                    T -4.052500  4.191777 -8.908923 -4.066698
1FP5           A          PRO           381                    C -3.504533  4.999357 -7.391988 -3.794224
1FP5           A          VAL           382                    C -3.476238  5.618540 -6.963226 -3.725766
1FP5           A          ASN           383                    C -3.494904  5.662071 -6.870403 -3.711152
1FP5           A          HIS           384                    C -3.555627  5.750252 -6.667336 -3.657916
1FP5           A          SER           385                    C -3.635910  5.883167 -6.470948 -3.649693
1FP5           A          THR           386                    C -4.467129  6.958210 -6.695965 -3.756111
1FP5           A          ARG           387                    E -7.278437  6.624827 -12.438017 -4.531823
1FP5           A          LYS           388                    E -7.471672  6.887513 -13.301692 -4.972657
1FP5           A          GLU           389                    E -5.807584  6.552246 -10.186597 -4.750496
```

```
1FP5        A          GLU            390                     E -4.150542  3.836110 -8.092596 -3.844323
1FP5        A          LYS            391                     E -2.916544  2.877104 -7.443102 -3.997527
1FP5        A          GLN            392                     E -2.347910  3.056446 -6.660212 -3.775086
1FP5        A          ARG            393                     E -2.345651  3.073528 -6.664757 -3.774883
1FP5        A          ASN            394                     T -2.347104  3.067054 -6.656861 -3.773345
1FP5        A          GLY            395                     T -2.375238  3.033306 -6.582336 -3.766389
1FP5        A          THR            396                     T -2.638473  3.159885 -6.081700 -3.582346
1FP5        A          LEU            397                     E -5.590946  7.924502 -8.217294 -4.027767
1FP5        A          THR            398                     E -6.887481 11.812240 -12.423661 -7.349100
1FP5        A          VAL            399                     E -8.241652 13.564812 -13.064548 -7.387510
1FP5        A          THR            400                     E -9.674332 14.169037 -11.665059 -4.701548
1FP5        A          SER            401                     E -10.318814 13.723857 -13.115431 -4.813771
1FP5        A          THR            402                     E -9.417192 13.016354 -11.713359 -4.678849
1FP5        A          LEU            403                     E -8.903011 12.206100 -10.734878 -4.113449
1FP5        A          PRO            404                     E -8.866037 11.949641 -10.915397 -4.100758
1FP5        A          VAL            405                     E -8.778446 11.346766 -11.342894 -4.157239
1FP5        A          GLY            406                     C -8.783233 11.318787 -11.338668 -4.156739
1FP5        A          THR            407                     C -8.983861 10.677542 -11.316489 -3.960634
1FP5        A          ARG            408                     H -9.648572  8.614960 -13.922225 -4.435668
1FP5        A          ASP            409                     H -8.351700 11.623539 -10.531585 -4.690863
1FP5        A          TRP            410                     H -8.062219 12.135065 -10.378243 -4.832251
1FP5        A          ILE            411                     H -6.216580  8.828482 -9.649506 -4.955247
1FP5        A          GLU            412                     H -6.215628  8.835905 -9.654818 -4.956606
1FP5        A          GLY            413                     H -6.215758  8.835345 -9.653907 -4.956690
1FP5        A          GLU            414                     C -6.230706  8.757005 -9.639586 -4.963222
1FP5        A          THR            415                     C -6.242436  8.683287 -9.621706 -4.962403
1FP5        A          TYR            416                     E -10.015319 13.470019 -13.016045 -5.792678
1FP5        A          GLN            417                     E -12.804332 14.580263 -17.005119 -6.206086
1FP5        A          CYS            418                     E -13.260649 12.321527 -17.753629 -5.137770
1FP5        A          ARG            419                     E -12.163813 14.356429 -15.323219 -5.214992
1FP5        A          VAL            420                     E -9.027058 11.931743 -11.039502 -4.469259
1FP5        A          THR            421                     E -7.589174 11.029926 -9.568730 -4.312834
1FP5        A          HIS            422                     E -5.617082  8.979953 -7.159716 -3.732389
1FP5        A          PRO            423                     T -3.527934  6.939705 -4.547178 -3.030643
1FP5        A          HIS            424                     T -3.346846  6.855165 -4.819465 -3.070180
1FP5        A          LEU            425                     T -3.342670  6.863403 -4.836994 -3.069594
1FP5        A          PRO            426                     T -3.340516  6.865391 -4.850017 -3.070751
1FP5        A          ARG            427                     C -3.352960  6.821169 -4.802332 -3.056714
1FP5        A          ALA            428                     C -4.114978  6.643024 -5.652590 -3.166299
1FP5        A          LEU            429                     C -5.992844  8.005176 -7.807673 -3.189073
1FP5        A          MET            430                     E -6.554878  8.034185 -8.628134 -3.542568
1FP5        A          ARG            431                     E -8.754750 11.941640 -11.714859 -4.642433
1FP5        A          SER            432                     E -8.303297 11.653464 -11.679867 -5.185989
1FP5        A          THR            433                     E -7.989449 10.844080 -11.609570 -5.040490
1FP5        A          THR            434                     E -6.747043  7.876202 -10.654512 -4.751815
1FP5        A          LYS            435                     E -6.202212  6.343564 -10.758461 -4.548374
1FP5        A          THR            436                     C -5.642917  6.497298 -9.740267 -4.223889
1FP5        A          SER            437                     C -5.596508  6.398246 -9.800368 -4.175999
1FP5        A          GLY            438                     C -5.580469  6.387266 -9.815577 -4.156492
1FP5        A          PRO            439                     C -5.657140  6.241374 -9.717586 -4.077446
1FP5        A          ARG            440                     C -5.821365  6.510254 -9.361225 -3.968120
1FP5        A          ALA            441                     C -6.855724  6.107031 -10.635593 -3.731657
1FP5        A          ALA            442                     B -7.547707  7.048774 -10.663923 -3.740639
1FP5        A          PRO            443                     C -9.284833 10.567436 -11.102613 -3.401805
1FP5        A          GLU            444                     C -9.972530 11.577922 -12.029799 -3.807039
1FP5        A          VAL            445                     E -9.977435 11.735702 -11.946640 -3.813383
1FP5        A          TYR            446                     E -10.587884 14.206184 -13.116888 -4.815087
1FP5        A          ALA            447                     E -8.696132 12.051235 -11.978556 -5.321345
1FP5        A          PHE            448                     E -8.274320 11.554439 -12.232617 -5.404387
1FP5        A          ALA            449                     E -5.273896  6.895558 -7.935439 -3.918868
1FP5        A          THR            450                     E -3.894541  4.436057 -7.279972 -3.645224
1FP5        A          PRO            451                     E -1.991443  2.877876 -6.012580 -3.939223
1FP5        A          GLU            452                     C -1.819334  3.101003 -6.239933 -4.038944
1FP5        A          TRP            453                     C -1.731142  2.908716 -6.478031 -4.035703
1FP5        A          PRO            454                     C -1.730638  2.896242 -6.489143 -4.037235
1FP5        A          GLY            455                     C -1.745731  2.856321 -6.458708 -4.039604
1FP5        A          SER            456                     C -2.377241  2.770627 -6.964050 -3.951305
1FP5        A          ARG            457                     C -2.938406  1.479261 -7.518934 -3.685733
1FP5        A          ASP            458                     C -5.002279  2.840297 -10.988713 -4.590297
1FP5        A          LYS            459                     C -6.017298  4.636829 -13.322973 -6.071719
1FP5        A          ARG            460                     C -7.959951  8.047620 -16.756232 -8.314409
1FP5        A          THR            461                     E -10.184228 11.059845 -18.961168 -8.874870
1FP5        A          LEU            462                     E -10.944301 14.770627 -13.619052 -5.187221
1FP5        A          ALA            463                     E -10.811910 13.711770 -12.663336 -4.288936
1FP5        A          CYS            464                     E -10.529649 12.801142 -13.211697 -4.492698
1FP5        A          LEU            465                     E -10.503428 12.964616 -13.178640 -4.497280
1FP5        A          ILE            466                     E -10.524147 12.943197 -13.146278 -4.495021
1FP5        A          GLN            467                     E -10.700700 12.196340 -13.695940 -4.632464
1FP5        A          ASN            468                     E -11.001668 12.131587 -14.040337 -4.841207
1FP5        A          PHE            469                     E -12.099745 16.467654 -13.516888 -4.826798
1FP5        A          MET            470                     E -11.047667 14.185359 -12.708297 -4.759426
```

```
1FP5        A          PRO            471                   B -10.632714 13.556784 -13.053700 -4.833914
1FP5        A          GLU            472                   T -10.287428 13.571454 -12.894692 -4.858438
1FP5        A          ASP            473                   T -10.271009 13.565174 -12.955097 -4.868174
1FP5        A          ILE            474                   C -10.269950 13.578134 -12.955390 -4.870042
1FP5        A          SER            475                   C -10.445082 13.415135 -13.083565 -4.916170
1FP5        A          VAL            476                   E -10.723833 13.643666 -12.883640 -4.917864
1FP5        A          GLN            477                   E -12.284190 14.111608 -15.112324 -5.260343
1FP5        A          TRP            478                   E -12.504456 16.264451 -14.403115 -5.293237
1FP5        A          LEU            479                   E -7.398731  8.116076 -10.400688 -4.302363
1FP5        A          HIS            480                   E -6.421909  6.522236 -10.781191 -4.625626
1FP5        A          ASN            481                   E -6.401657  6.572310 -10.837935 -4.629375
1FP5        A          GLU            482                   T -5.963113  6.903861 -10.061354 -4.347068
1FP5        A          VAL            483                   T -5.938200  6.913948 -10.115284 -4.340871
1FP5        A          GLN            484                   E -5.920954  6.823259 -10.151022 -4.329644
1FP5        A          LEU            485                   E -6.152018  7.152253 -9.835212 -4.119506
1FP5        A          PRO            486                   C -6.149786  7.124670 -9.841161 -4.108544
1FP5        A          ASP            487                   C -6.896318  6.919258 -11.081005 -4.157088
1FP5        A          ALA            488                   G -7.033938  6.859428 -11.006489 -4.146882
1FP5        A          ARG            489                   G -7.805083  6.510644 -11.966418 -3.974882
1FP5        A          HIS            490                   G -8.154397  7.181992 -12.347428 -4.225924
1FP5        A          SER            491                   E -6.622143  8.280362 -8.953475 -3.808689
1FP5        A          THR            492                   E -5.626283  8.435430 -7.373353 -3.451939
1FP5        A          THR            493                   E -5.180016  8.241125 -7.131951 -3.367353
1FP5        A          GLN            494                   C -5.108265  8.317355 -7.171100 -3.362583
1FP5        A          PRO            495                   C -4.916071  8.295046 -7.053310 -3.326805
1FP5        A          ARG            496                   C -3.150585  4.478042 -6.367065 -3.666620
1FP5        A          LYS            497                   E -2.796471  3.585323 -6.948289 -3.788843
1FP5        A          THR            498                   E -2.539742  3.024392 -7.327946 -3.916102
1FP5        A          LYS            499                   T -2.540480  3.016390 -7.328730 -3.917099
1FP5        A          GLY            500                   T -2.543552  2.988907 -7.330710 -3.920132
1FP5        A          SER            501                   T -2.796684  2.278299 -7.788036 -4.008310
1FP5        A          GLY            502                   T -3.158481  2.039513 -7.891733 -4.070807
1FP5        A          PHE            503                   C -7.357619  7.243084 -11.732207 -4.788135
1FP5        A          PHE            504                   E -9.303199 15.081539 -14.289501 -7.829398
1FP5        A          VAL            505                   E -10.219892 15.523689 -15.107457 -8.018874
1FP5        A          PHE            506                   E -12.873705 19.575965 -15.103798 -6.191673
1FP5        A          SER            507                   E -12.859862 14.909008 -15.649954 -5.074688
1FP5        A          ARG            508                   E -11.443708 13.364430 -13.815969 -4.796525
1FP5        A          LEU            509                   E -11.367516 13.200366 -14.043431 -4.804328
1FP5        A          GLU            510                   E -10.313903  9.649665 -14.223294 -4.635695
1FP5        A          VAL            511                   E -9.724217  9.181963 -14.018770 -4.632851
1FP5        A          THR            512                   E -9.719496  9.190932 -14.042074 -4.640036
1FP5        A          ARG            513                   C -9.738139  9.014397 -14.108699 -4.646966
1FP5        A          ALA            514                   H -9.742536  8.990218 -14.099222 -4.646017
1FP5        A          GLU            515                   H -9.968576  9.014795 -14.024640 -4.666870
1FP5        A          TRP            516                   H -11.760719 11.107795 -16.610234 -5.405598
1FP5        A          GLU            517                   H -11.739146 10.270270 -17.272275 -5.601352
1FP5        A          GLN            518                   H -12.218365  9.707263 -18.380266 -5.929776
1FP5        A          LYS            519                   H -12.211644  9.979163 -18.192164 -5.884394
1FP5        A          ASP            520                   G -12.122134 10.396145 -17.893998 -5.738035
1FP5        A          GLU            521                   G -12.158417 10.268663 -17.825250 -5.705507
1FP5        A          PHE            522                   G -13.049627 13.845796 -16.312419 -5.015393
1FP5        A          ILE            523                   E -12.856001 13.653524 -16.005993 -4.786937
1FP5        A          CYS            524                   E -12.911071 13.242323 -16.140995 -4.741503
1FP5        A          ARG            525                   E -13.324430 13.614203 -16.220329 -4.605146
1FP5        A          ALA            526                   E -11.277904 12.988454 -13.217291 -4.390315
1FP5        A          VAL            527                   E -10.252501 13.021327 -11.953803 -4.277657
1FP5        A          HIS            528                   E -9.260292 10.856990 -11.620329 -4.125578
1FP5        A          GLU            529                   T -7.559758  6.644976 -10.579854 -3.529578
1FP5        A          ALA            530                   T -6.272862  5.417679 -8.931035 -2.949447
1FP5        A          ALA            531                   T -6.241470  5.415572 -9.086865 -2.987471
1FP5        A          SER            532                   T -6.180726  5.414666 -9.332416 -3.078227
1FP5        A          PRO            533                   T -6.179482  5.405746 -9.344062 -3.079395
1FP5        A          SER            534                   T -6.236489  5.306467 -9.225997 -3.037654
1FP5        A          GLN            535                   T -7.297896  5.539890 -11.760524 -3.851510
1FP5        A          THR            536                   T -7.516071  5.600446 -11.674422 -3.924136
1FP5        A          VAL            537                   E -9.141181  7.522726 -12.681527 -3.970319
1FP5        A          GLN            538                   E -10.068735 10.808069 -13.109310 -4.516998
1FP5        A          ARG            539                   E -8.167232  8.434353 -9.771782 -3.074355
1FP5        A          ALA            540                   E -5.185615  6.449631 -6.029729 -2.409459
1FP5        A          VAL            541                   E -5.185615  6.449631 -6.029729 -2.409459
1FP5        A          SER            542                   C -5.185615  6.449631 -6.029729 -2.409459
1FP5        A          VAL            543                   C -5.185615  6.449631 -6.029729 -2.409459
1FW1        A          LYS              5                   C -6.706242 11.984151 -6.521707 -3.313724
1FW1        A          PRO              6                   C -6.706242 11.984151 -6.521707 -3.313724
1FW1        A          ILE              7                   E -6.706242 11.984151 -6.521707 -3.313724
1FW1        A          LEU              8                   E -6.706242 11.984151 -6.521707 -3.313724
1FW1        A          TYR              9                   E -10.534189 18.145865 -9.950051 -4.659682
1FW1        A          SER             10                   E -13.446501 20.200910 -14.150254 -5.835069
1FW1        A          TYR             11                   T -15.552825 17.169766 -19.322604 -6.035586
1FW1        A          PHE             12                   T -14.727711 14.736652 -19.380727 -5.980992
```

1FW1	A	ARG	13	T	-13.959742	12.029405	-19.973707	-6.072926
1FW1	A	SER	14	T	-13.809501	12.414518	-19.856207	-6.075842
1FW1	A	SER	15	H	-13.812263	12.373669	-19.881195	-6.083750
1FW1	A	CYS	16	H	-13.813157	12.387329	-19.869855	-6.081753
1FW1	A	SER	17	H	-13.917287	12.079651	-19.961521	-6.103436
1FW1	A	TRP	18	H	-14.584950	14.318307	-19.470834	-6.094756
1FW1	A	ARG	19	H	-15.470729	16.875697	-19.446617	-5.954410
1FW1	A	VAL	20	H	-12.877738	17.072205	-13.460478	-4.606891
1FW1	A	ARG	21	H	-12.638637	16.763152	-13.775011	-4.607507
1FW1	A	ILE	22	H	-10.566449	17.384234	-9.143839	-3.629675
1FW1	A	ALA	23	H	-10.490670	17.397031	-9.444237	-3.734533
1FW1	A	LEU	24	H	-9.565117	15.326923	-10.527844	-4.573157
1FW1	A	ALA	25	H	-8.885520	14.125163	-10.519211	-4.657049
1FW1	A	LEU	26	H	-7.570048	12.092162	-9.903942	-4.892069
1FW1	A	LYS	27	H	-7.024944	12.794005	-9.635767	-5.281835
1FW1	A	GLY	28	C	-6.118590	12.439314	-8.328894	-5.098854
1FW1	A	ILE	29	C	-6.062750	12.761337	-8.282946	-5.109869
1FW1	A	ASP	30	C	-6.015647	12.892384	-8.270667	-5.096150
1FW1	A	TYR	31	C	-6.041286	13.014188	-8.173247	-5.097987
1FW1	A	LYS	32	E	-6.047229	13.019642	-7.980190	-4.951175
1FW1	A	THR	33	E	-6.746141	14.558840	-8.030906	-4.732516
1FW1	A	VAL	34	E	-6.949670	13.971426	-8.097985	-4.536991
1FW1	A	PRO	35	E	-7.247187	13.682844	-7.992081	-4.294634
1FW1	A	ILE	36	C	-7.321529	13.296531	-8.069181	-4.243068
1FW1	A	ASN	37	T	-6.308828	7.335830	-9.954696	-4.448245
1FW1	A	LEU	38	T	-4.814630	6.180212	-8.638770	-4.329512
1FW1	A	ILE	39	T	-2.810146	3.058364	-7.681197	-4.343565
1FW1	A	LYS	40	T	-2.801879	3.069250	-7.733051	-4.354518
1FW1	A	ASP	41	T	-2.801891	3.068991	-7.733053	-4.354527
1FW1	A	GLY	42	T	-2.803488	3.057578	-7.726753	-4.354085
1FW1	A	GLY	43	T	-2.822390	2.957933	-7.696677	-4.352829
1FW1	A	GLN	44	G	-5.346793	3.794986	-11.295912	-5.059888
1FW1	A	GLN	45	G	-9.313250	6.973189	-15.889362	-5.644541
1FW1	A	PHE	46	G	-8.828431	11.014276	-11.710158	-4.672329
1FW1	A	SER	47	C	-8.722454	10.685671	-12.007222	-4.644576
1FW1	A	LYS	48	H	-7.965174	9.336715	-11.641480	-4.505836
1FW1	A	ASP	49	H	-7.953709	9.395459	-11.667365	-4.513937
1FW1	A	PHE	50	H	-7.964289	9.428781	-11.593240	-4.502520
1FW1	A	GLN	51	H	-8.098962	8.919120	-11.709974	-4.474606
1FW1	A	ALA	52	H	-8.058149	8.797159	-11.849202	-4.494363
1FW1	A	LEU	53	H	-9.029895	9.211065	-13.788517	-4.889643
1FW1	A	ASN	54	T	-8.967205	8.677625	-14.285947	-5.071028
1FW1	A	PRO	55	T	-8.651874	9.152854	-13.812145	-5.102732
1FW1	A	MET	56	T	-8.635939	9.328848	-13.750315	-5.114983
1FW1	A	LYS	57	T	-8.858362	10.017192	-13.779284	-5.330700
1FW1	A	GLN	58	C	-8.947802	9.837027	-13.736336	-5.285210
1FW1	A	VAL	59	C	-9.060840	10.455726	-13.156017	-5.145881
1FW1	A	PRO	60	C	-10.048201	13.827944	-13.142262	-5.183137
1FW1	A	THR	61	E	-10.518714	17.069729	-12.853466	-5.471547
1FW1	A	LEU	62	E	-8.742988	11.626518	-11.701848	-5.031948
1FW1	A	LYS	63	E	-6.243606	7.955189	-9.825819	-4.668977
1FW1	A	ILE	64	E	-3.421238	8.247525	-5.878369	-4.520653
1FW1	A	ASP	65	T	-3.338206	8.114250	-6.094911	-4.495478
1FW1	A	GLY	66	T	-3.322854	8.149295	-6.134811	-4.492567
1FW1	A	ILE	67	E	-3.322845	8.149314	-6.134815	-4.492515
1FW1	A	THR	68	E	-3.327092	8.150826	-6.108226	-4.491068
1FW1	A	ILE	69	E	-4.438220	7.558343	-7.521833	-4.309443
1FW1	A	HIS	70	E	-5.495546	9.438612	-7.633968	-4.351623
1FW1	A	GLN	71	C	-8.491223	11.444014	-11.454722	-4.665628
1FW1	A	SER	72	H	-9.163657	12.462704	-12.387517	-4.999540
1FW1	A	LEU	73	H	-9.738254	12.588352	-12.724510	-4.691399
1FW1	A	ALA	74	H	-9.754876	12.578695	-12.663966	-4.676943
1FW1	A	ILE	75	H	-9.846381	12.935835	-12.277828	-4.608460
1FW1	A	ILE	76	H	-10.468751	14.778657	-11.631927	-4.506787
1FW1	A	GLU	77	H	-11.984584	14.974037	-14.235897	-4.911637
1FW1	A	TYR	78	H	-12.026035	14.600860	-15.271314	-5.503698
1FW1	A	LEU	79	H	-11.826833	13.854446	-15.640810	-5.544489
1FW1	A	GLU	80	H	-10.739283	8.670023	-16.116758	-5.070027
1FW1	A	GLU	81	H	-7.461643	6.893306	-11.293470	-4.192163
1FW1	A	THR	82	H	-7.329713	6.854734	-11.426959	-4.119459
1FW1	A	ARG	83	C	-7.328869	6.853019	-11.433402	-4.119126
1FW1	A	PRO	84	T	-7.318476	6.898354	-11.453399	-4.116846
1FW1	A	THR	85	T	-7.318886	6.909691	-11.443230	-4.115430
1FW1	A	PRO	86	T	-8.223289	6.997362	-12.052656	-3.851789
1FW1	A	ARG	87	T	-9.595609	9.770236	-12.894889	-4.077072
1FW1	A	LEU	88	C	-9.592650	10.535265	-12.648124	-4.195341
1FW1	A	LEU	89	C	-8.986572	11.596063	-12.327827	-5.178230
1FW1	A	PRO	90	C	-6.562496	6.059829	-10.727533	-4.282552
1FW1	A	GLN	91	C	-5.037610	4.272956	-9.694844	-4.157363
1FW1	A	ASP	92	C	-5.036048	4.277064	-9.703988	-4.157322
1FW1	A	PRO	93	H	-5.035574	4.277826	-9.707455	-4.157169

1FW1	A	LYS	94	H	-5.036209	4.269844	-9.705014	-4.155999
1FW1	A	LYS	95	H	-5.082313	4.132164	-9.624125	-4.146858
1FW1	A	ARG	96	H	-8.370880	5.892826	-13.426905	-4.135197
1FW1	A	ALA	97	H	-9.150399	6.054268	-14.152890	-4.121386
1FW1	A	SER	98	H	-10.347740	8.261164	-15.336061	-4.678837
1FW1	A	VAL	99	H	-11.706019	11.997868	-16.320132	-5.030025
1FW1	A	ARG	100	H	-11.933485	11.952707	-15.995383	-4.719042
1FW1	A	MET	101	H	-11.371607	12.773980	-14.705463	-4.720611
1FW1	A	ILE	102	H	-11.163252	13.966883	-13.722177	-4.656957
1FW1	A	SER	103	H	-11.087055	13.752836	-13.823052	-4.641137
1FW1	A	ASP	104	H	-9.357675	11.644421	-11.711566	-4.375499
1FW1	A	LEU	105	H	-7.846087	11.152800	-9.930362	-4.336278
1FW1	A	ILE	106	H	-7.013037	11.170077	-9.042067	-4.288831
1FW1	A	ALA	107	H	-6.997640	11.133567	-9.150610	-4.313625
1FW1	A	GLY	108	H	-6.992454	11.114503	-9.196376	-4.321094
1FW1	A	GLY	109	H	-7.001664	11.105625	-9.164793	-4.321506
1FW1	A	ILE	110	H	-7.150180	11.103983	-8.989449	-4.318215
1FW1	A	GLN	111	G	-8.949354	9.660728	-13.611763	-5.202167
1FW1	A	PRO	112	G	-9.666910	9.279885	-14.421825	-5.102898
1FW1	A	LEU	113	G	-10.651838	10.391689	-14.497755	-4.860294
1FW1	A	GLN	114	G	-12.969604	10.400517	-19.108457	-5.606008
1FW1	A	ASN	115	C	-11.066828	11.143478	-14.556032	-4.729401
1FW1	A	LEU	116	H	-10.832412	11.702971	-15.275669	-5.293760
1FW1	A	SER	117	H	-10.513006	11.172504	-15.211547	-5.111156
1FW1	A	VAL	118	H	-9.767085	11.723976	-13.450455	-4.807779
1FW1	A	LEU	119	H	-8.708646	10.783981	-12.177828	-4.766313
1FW1	A	LYS	120	H	-6.295597	6.751732	-10.326940	-4.512030
1FW1	A	GLN	121	H	-3.722756	4.960155	-7.412124	-4.103033
1FW1	A	VAL	122	H	-3.342171	5.212215	-7.362509	-4.151527
1FW1	A	GLY	123	C	-3.316910	5.208015	-7.473023	-4.174939
1FW1	A	GLU	124	H	-3.315107	5.216503	-7.481837	-4.176408
1FW1	A	GLU	125	H	-3.318801	5.207558	-7.464368	-4.174195
1FW1	A	MET	126	H	-3.730600	5.459767	-7.528078	-4.235613
1FW1	A	GLN	127	H	-5.156352	5.303872	-10.001053	-4.680133
1FW1	A	LEU	128	H	-6.687468	8.083204	-10.512659	-4.642737
1FW1	A	THR	129	H	-8.198341	8.591595	-12.259866	-4.778966
1FW1	A	TRP	130	H	-10.356670	12.620390	-17.392107	-7.508719
1FW1	A	ALA	131	H	-10.768358	13.146975	-16.712020	-6.837293
1FW1	A	GLN	132	H	-11.144229	11.517744	-15.660427	-4.877355
1FW1	A	ASN	133	H	-9.501771	9.676260	-12.661870	-4.221188
1FW1	A	ALA	134	H	-8.754441	9.796882	-11.878688	-4.152143
1FW1	A	ILE	135	H	-8.638823	10.501925	-11.713590	-4.225821
1FW1	A	THR	136	H	-8.540362	10.503104	-11.906660	-4.322112
1FW1	A	CYS	137	H	-8.397103	10.414969	-12.045769	-4.401623
1FW1	A	GLY	138	H	-8.482793	10.623181	-11.972967	-4.445929
1FW1	A	PHE	139	H	-8.842344	11.272298	-12.292804	-4.710795
1FW1	A	ASN	140	H	-8.995268	10.419512	-12.813894	-4.762660
1FW1	A	ALA	141	H	-9.206735	10.452598	-12.760875	-4.715399
1FW1	A	LEU	142	H	-10.278104	12.701918	-13.722858	-4.859777
1FW1	A	GLU	143	H	-10.482654	11.636637	-14.386974	-4.836171
1FW1	A	GLN	144	H	-9.869054	10.146971	-13.934013	-4.524871
1FW1	A	ILE	145	H	-9.353578	10.442759	-12.987967	-4.519653
1FW1	A	LEU	146	H	-8.840700	9.823281	-12.604345	-4.471022
1FW1	A	GLN	147	H	-7.775029	6.378931	-12.776880	-4.483512
1FW1	A	SER	148	H	-6.692597	6.794343	-10.705265	-4.158008
1FW1	A	THR	149	H	-6.688258	6.842737	-10.708802	-4.164971
1FW1	A	ALA	150	B	-6.689772	6.838631	-10.704519	-4.165361
1FW1	A	GLY	151	T	-6.698586	6.804123	-10.679911	-4.161817
1FW1	A	ILE	152	T	-6.782839	7.000776	-10.350714	-4.113332
1FW1	A	TYR	153	T	-8.971150	12.499400	-12.231017	-4.893359
1FW1	A	CYS	154	T	-8.623541	9.598696	-13.328172	-5.124199
1FW1	A	VAL	155	T	-7.649868	9.985086	-11.001051	-4.716577
1FW1	A	GLY	156	B	-7.535843	9.742766	-11.289148	-4.754572
1FW1	A	ASP	157	C	-7.541207	9.706359	-11.292366	-4.757350
1FW1	A	GLU	158	C	-7.545288	9.681831	-11.281989	-4.754844
1FW1	A	VAL	159	C	-7.617318	9.864213	-10.976207	-4.695232
1FW1	A	THR	160	C	-8.527841	8.920037	-12.703196	-4.951409
1FW1	A	MET	161	H	-10.478136	13.375353	-14.065880	-5.406068
1FW1	A	ALA	162	H	-11.119315	14.277687	-14.367003	-5.228986
1FW1	A	ASP	163	H	-11.240248	14.663077	-14.200259	-5.178626
1FW1	A	LEU	164	H	-11.213829	15.993790	-12.728972	-4.623808
1FW1	A	CYS	165	H	-11.266412	16.045398	-12.580219	-4.544759
1FW1	A	LEU	166	H	-11.223956	16.166832	-12.495756	-4.505983
1FW1	A	VAL	167	H	-11.079166	15.731495	-12.617261	-4.460533
1FW1	A	PRO	168	H	-11.123058	15.678481	-12.609159	-4.453070
1FW1	A	GLN	169	H	-11.595723	14.617023	-13.931480	-4.601803
1FW1	A	VAL	170	H	-10.959960	11.785733	-14.370920	-4.568962
1FW1	A	ALA	171	H	-10.991569	11.401089	-14.531942	-4.579033
1FW1	A	ASN	172	H	-11.134627	10.636492	-14.854624	-4.633826
1FW1	A	ALA	173	H	-11.104402	10.654891	-14.894491	-4.626900
1FW1	A	GLU	174	H	-11.032591	10.920640	-14.923227	-4.664808

1FW1	A	ARG	175	H	-11.761030	12.110378	-16.058081	-4.962972
1FW1	A	PHE	176	H	-10.087258	14.637063	-11.357735	-4.634423
1FW1	A	LYS	177	C	-6.171752	9.057914	-8.121022	-3.917023
1FW1	A	VAL	178	C	-5.346201	9.367624	-7.112584	-3.753325
1FW1	A	ASP	179	C	-5.338074	9.396799	-7.148053	-3.762159
1FW1	A	LEU	180	T	-5.337415	9.399808	-7.152545	-3.762839
1FW1	A	THR	181	T	-5.337014	9.399395	-7.156441	-3.763386
1FW1	A	PRO	182	T	-5.502797	9.511933	-6.846357	-3.713932
1FW1	A	TYR	183	T	-7.795592	11.509096	-9.999972	-4.412224
1FW1	A	PRO	184	H	-8.899018	11.460298	-11.938393	-4.499170
1FW1	A	THR	185	H	-9.243016	11.008182	-12.570577	-4.608203
1FW1	A	ILE	186	H	-9.997392	11.892638	-13.206811	-4.672995
1FW1	A	SER	187	H	-10.071557	11.389137	-13.403118	-4.671208
1FW1	A	SER	188	H	-10.067579	11.325037	-13.440229	-4.664573
1FW1	A	ILE	189	H	-11.073256	12.816532	-14.434087	-4.776941
1FW1	A	ASN	190	H	-11.407601	11.524631	-15.724667	-4.747065
1FW1	A	LYS	191	H	-9.970560	10.166401	-13.039535	-4.161012
1FW1	A	ARG	192	H	-9.906314	10.383919	-12.967471	-4.128548
1FW1	A	LEU	193	H	-9.393677	10.025139	-12.594943	-4.028007
1FW1	A	LEU	194	H	-8.627799	8.457113	-12.213520	-3.867415
1FW1	A	VAL	195	H	-8.573290	8.755218	-12.153075	-3.874085
1FW1	A	LEU	196	C	-8.626086	8.638830	-12.096548	-3.853014
1FW1	A	GLU	197	G	-8.633679	8.600729	-12.086699	-3.852096
1FW1	A	ALA	198	G	-8.738500	8.374872	-12.033017	-3.831014
1FW1	A	PHE	199	G	-9.972562	11.919556	-11.757915	-3.995369
1FW1	A	GLN	200	T	-11.815142	13.010035	-15.129824	-4.757215
1FW1	A	VAL	201	T	-8.784387	9.549742	-11.786483	-4.337661
1FW1	A	SER	202	T	-8.632214	9.656425	-11.970660	-4.370979
1FW1	A	HIS	203	T	-8.480877	10.265146	-12.301749	-4.709072
1FW1	A	PRO	204	T	-8.342901	10.866977	-12.689016	-5.149123
1FW1	A	CYS	205	T	-7.678932	11.113375	-13.016417	-6.395638
1FW1	A	ARG	206	T	-7.638154	11.303196	-13.245927	-6.668845
1FW1	A	GLN	207	T	-5.931254	9.041938	-10.005472	-5.463065
1FW1	A	PRO	208	T	-3.424714	6.791206	-5.647008	-3.768733
1FW1	A	ASP	209	T	-2.843482	5.838473	-5.424281	-3.382026
1FW1	A	THR	210	T	-2.843482	5.838473	-5.424281	-3.382026
1FW1	A	PRO	211	C	-2.843482	5.838473	-5.424281	-3.382026
1FW1	A	THR	212	C	-2.843482	5.838473	-5.424281	-3.382026
1G1T	A	TRP	1	C	-14.433225	16.310522	-17.155768	-5.213913
1G1T	A	SER	2	E	-14.433225	16.310522	-17.155768	-5.213913
1G1T	A	TYR	3	E	-14.433225	16.310522	-17.155768	-5.213913
1G1T	A	ASN	4	E	-14.433225	16.310522	-17.155768	-5.213913
1G1T	A	THR	5	E	-4.310727	9.093548	-6.690063	-4.614535
1G1T	A	SER	6	E	-4.286738	9.072572	-6.807695	-4.622185
1G1T	A	THR	7	E	-4.254257	9.087100	-6.930508	-4.637618
1G1T	A	GLU	8	E	-4.254256	9.087108	-6.930522	-4.637620
1G1T	A	ALA	9	E	-4.254255	9.087112	-6.930529	-4.637621
1G1T	A	MET	10	E	-5.675772	9.010208	-9.325940	-4.862104
1G1T	A	THR	11	C	-5.991519	9.332546	-9.101520	-4.904995
1G1T	A	TYR	12	H	-10.924983	12.394591	-15.544830	-5.630446
1G1T	A	ASP	13	H	-9.644812	7.113805	-15.113963	-4.773141
1G1T	A	GLU	14	H	-9.647427	7.073054	-15.112652	-4.765892
1G1T	A	ALA	15	H	-9.649746	7.049500	-15.103580	-4.758844
1G1T	A	SER	16	H	-9.699863	6.616153	-15.102078	-4.690788
1G1T	A	ALA	17	H	-9.702889	6.583173	-15.098946	-4.687499
1G1T	A	TYR	18	H	-11.995131	9.892065	-18.244252	-5.500416
1G1T	A	CYS	19	H	-11.227482	9.924425	-17.019982	-5.598322
1G1T	A	GLN	20	H	-10.057790	10.763397	-14.690741	-5.473659
1G1T	A	GLN	21	H	-10.023118	10.887071	-14.725067	-5.475911
1G1T	A	ARG	22	H	-10.022744	10.931217	-14.703810	-5.476135
1G1T	A	TYR	23	C	-10.026894	11.062701	-14.617367	-5.472792
1G1T	A	THR	24	C	-9.903469	12.643326	-13.447201	-5.218474
1G1T	A	HIS	25	E	-10.207896	17.027369	-10.854427	-4.583010
1G1T	A	LEU	26	E	-10.195283	17.328723	-10.611805	-4.513244
1G1T	A	VAL	27	C	-10.150917	17.147607	-10.829766	-4.558758
1G1T	A	ALA	28	C	-10.159581	17.119150	-10.803760	-4.549029
1G1T	A	ILE	29	C	-10.444488	17.106605	-11.120521	-4.601417
1G1T	A	GLN	30	C	-11.072896	14.950205	-13.784858	-5.071091
1G1T	A	ASN	31	C	-11.263162	12.714594	-15.755016	-5.483824
1G1T	A	LYS	32	H	-11.248632	9.738813	-17.467299	-5.618036
1G1T	A	GLU	33	H	-11.213122	9.965757	-17.401873	-5.625822
1G1T	A	GLU	34	H	-11.330254	10.003326	-17.309754	-5.578015
1G1T	A	ILE	35	H	-11.285971	10.688875	-16.912230	-5.523267
1G1T	A	GLU	36	H	-11.308707	11.470475	-16.343434	-5.387051
1G1T	A	TYR	37	H	-11.421478	13.672254	-14.877448	-4.966176
1G1T	A	LEU	38	H	-10.562257	12.899374	-13.201361	-4.535957
1G1T	A	ASN	39	H	-9.514121	8.970387	-13.302564	-4.154588
1G1T	A	SER	40	H	-8.868242	10.246174	-11.854311	-4.051214
1G1T	A	ILE	41	H	-8.738204	10.786825	-11.728227	-4.114716
1G1T	A	LEU	42	C	-8.574970	10.906192	-11.738078	-4.182985
1G1T	A	SER	43	C	-7.977339	9.547590	-11.501558	-4.209905

1G1T	A	TYR	44	C	-7.985010	9.798433	-11.423247	-4.257704
1G1T	A	SER	45	T	-8.081028	9.605203	-11.476190	-4.303120
1G1T	A	PRO	46	T	-8.121383	9.366023	-11.491144	-4.297557
1G1T	A	SER	47	T	-8.193027	9.116454	-11.449600	-4.284079
1G1T	A	TYR	48	T	-9.758223	12.866504	-12.248835	-5.004924
1G1T	A	TYR	49	E	-12.571524	18.461217	-13.854147	-5.335138
1G1T	A	TRP	50	E	-13.048601	22.073453	-12.331760	-5.214290
1G1T	A	ILE	51	E	-12.742674	19.959965	-13.505481	-5.323289
1G1T	A	GLY	52	T	-12.296579	16.094179	-15.132505	-5.325256
1G1T	A	ILE	53	E	-11.446632	12.926297	-15.227486	-5.178963
1G1T	A	ARG	54	E	-9.886005	8.002299	-15.638910	-5.362361
1G1T	A	LYS	55	E	-4.553205	5.374696	-8.897845	-4.564003
1G1T	A	VAL	56	E	-4.263478	7.231869	-8.027562	-4.541962
1G1T	A	ASN	57	T	-4.259979	7.258693	-8.032603	-4.541260
1G1T	A	ASN	58	T	-4.259980	7.258680	-8.032577	-4.541257
1G1T	A	VAL	59	E	-4.260022	7.258651	-8.032042	-4.541198
1G1T	A	TRP	60	E	-4.817839	10.195927	-6.673271	-4.501551
1G1T	A	VAL	61	E	-7.298682	11.801136	-8.890917	-4.418087
1G1T	A	TRP	62	E	-8.340459	13.097928	-10.128779	-4.782409
1G1T	A	VAL	63	T	-5.122890	8.101883	-8.073260	-4.455410
1G1T	A	GLY	64	T	-4.537864	7.174678	-8.158068	-4.345180
1G1T	A	THR	65	T	-4.503268	7.337150	-8.153970	-4.336134
1G1T	A	GLN	66	T	-4.500366	7.346374	-8.164323	-4.335179
1G1T	A	LYS	67	E	-4.499954	7.341106	-8.168967	-4.334799
1G1T	A	PRO	68	E	-4.740899	6.978265	-8.265937	-4.274228
1G1T	A	LEU	69	C	-6.009047	9.676134	-8.759118	-4.245531
1G1T	A	THR	70	T	-6.660809	8.594370	-10.744350	-4.460567
1G1T	A	GLU	71	T	-6.779120	8.445894	-10.887732	-4.545307
1G1T	A	GLU	72	T	-6.842234	8.413030	-10.807558	-4.554623
1G1T	A	ALA	73	T	-7.616551	8.014915	-12.170311	-4.745870
1G1T	A	LYS	74	T	-7.720459	7.861333	-12.137822	-4.780802
1G1T	A	ASN	75	C	-8.712231	11.503319	-12.476944	-5.243009
1G1T	A	TRP	76	B	-8.031859	11.898032	-10.935141	-4.984519
1G1T	A	ALA	77	T	-5.946617	7.656912	-9.277740	-4.313021
1G1T	A	PRO	78	T	-5.397573	6.498457	-9.881053	-4.512038
1G1T	A	GLY	79	T	-5.395653	6.499167	-9.897032	-4.515389
1G1T	A	GLU	80	T	-5.397169	6.485067	-9.892342	-4.513864
1G1T	A	PRO	81	T	-5.402387	6.436198	-9.887039	-4.510085
1G1T	A	ASN	82	T	-5.691591	5.741328	-10.315582	-4.648247
1G1T	A	ASN	83	C	-8.038263	4.750540	-15.285257	-5.199414
1G1T	A	ARG	84	C	-6.433840	4.515895	-12.202571	-4.771187
1G1T	A	GLN	85	T	-6.411632	4.554437	-12.297270	-4.794124
1G1T	A	LYS	86	T	-6.412099	4.554614	-12.294295	-4.794523
1G1T	A	ASP	87	T	-6.415745	4.561846	-12.264878	-4.791933
1G1T	A	GLU	88	T	-6.438967	4.589031	-12.148250	-4.782121
1G1T	A	ASP	89	C	-8.357993	5.589863	-14.834917	-5.403594
1G1T	A	CYS	90	E	-10.824226	7.151085	-18.059518	-5.977660
1G1T	A	VAL	91	E	-12.461866	13.910283	-17.078764	-5.630222
1G1T	A	GLU	92	E	-12.694952	15.995960	-15.973202	-5.457162
1G1T	A	ILE	93	E	-12.725174	16.341307	-15.699145	-5.415302
1G1T	A	TYR	94	E	-12.814714	17.966891	-15.091227	-5.490016
1G1T	A	ILE	95	T	-8.605892	10.721785	-11.713097	-4.880233
1G1T	A	LYS	96	T	-7.455984	8.462596	-11.939031	-5.043427
1G1T	A	ARG	97	T	-5.535898	7.275229	-9.227602	-4.510829
1G1T	A	GLU	98	T	-4.957299	6.523354	-9.490125	-4.658997
1G1T	A	LYS	99	T	-4.955411	6.526850	-9.501896	-4.660097
1G1T	A	ASP	100	T	-4.956651	6.518111	-9.497304	-4.659638
1G1T	A	VAL	101	T	-4.964172	6.498065	-9.465571	-4.654358
1G1T	A	GLY	102	T	-5.234349	6.076001	-9.665286	-4.749037
1G1T	A	MET	103	E	-8.358960	7.653757	-13.191661	-5.003833
1G1T	A	TRP	104	E	-11.414896	13.444893	-14.400396	-5.202873
1G1T	A	ASN	105	E	-13.597045	13.088033	-18.195889	-5.595707
1G1T	A	ASP	106	E	-13.688454	9.213388	-20.852811	-5.947468
1G1T	A	GLU	107	E	-11.122143	7.654987	-17.484168	-5.553608
1G1T	A	ARG	108	T	-9.581812	7.249762	-15.573408	-5.326334
1G1T	A	CYS	109	T	-9.482965	7.579027	-15.740534	-5.459858
1G1T	A	SER	110	T	-9.464325	7.720008	-15.750924	-5.474423
1G1T	A	LYS	111	T	-9.458193	7.782436	-15.748909	-5.476689
1G1T	A	LYS	112	C	-9.491221	7.838775	-15.635569	-5.471511
1G1T	A	LYS	113	E	-10.420782	10.305387	-16.458740	-6.094323
1G1T	A	LEU	114	E	-11.234803	13.039279	-15.856947	-5.790427
1G1T	A	ALA	115	E	-11.775473	14.534737	-15.509191	-5.542819
1G1T	A	LEU	116	E	-12.189687	15.764416	-15.182428	-5.338798
1G1T	A	CYS	117	E	-12.049127	13.708310	-15.758975	-5.167724
1G1T	A	TYR	118	E	-11.431670	13.001988	-15.190026	-5.214967
1G1T	A	THR	119	E	-8.325870	6.610911	-13.426562	-4.791233
1G1T	A	ALA	120	C	-5.927734	5.539763	-10.707415	-4.608449
1G1T	A	ALA	121	C	-4.733905	4.479301	-9.586649	-4.314546
1G1T	A	CYS	122	C	-4.342630	4.050551	-9.800505	-4.400606
1G1T	A	THR	123	T	-4.263824	4.043989	-9.924893	-4.416392
1G1T	A	ASN	124	T	-4.263889	4.042101	-9.925722	-4.416561

1G1T	A	THR	125	T	-4.299924	3.948786	-9.880763	-4.404601
1G1T	A	SER	126	T	-4.619486	3.684596	-10.209723	-4.499147
1G1T	A	CYS	127	G	-5.482815	4.037745	-10.883378	-4.541815
1G1T	A	SER	128	G	-7.301702	6.085879	-13.923804	-5.233099
1G1T	A	GLY	129	G	-6.792164	6.470005	-12.946665	-5.311042
1G1T	A	HIS	130	C	-6.756702	6.508985	-12.941154	-5.292222
1G1T	A	GLY	131	E	-6.736238	6.496425	-13.010264	-5.303331
1G1T	A	GLU	132	E	-6.820360	6.552560	-12.873480	-5.294404
1G1T	A	CYS	133	E	-6.940838	6.555501	-12.797512	-5.324223
1G1T	A	VAL	134	E	-7.965361	6.649136	-14.298714	-5.293249
1G1T	A	GLU	135	E	-8.440550	7.197097	-15.120758	-5.607275
1G1T	A	THR	136	E	-8.583047	10.315407	-13.477013	-5.372499
1G1T	A	ILE	137	T	-8.518338	10.561805	-13.325546	-5.359541
1G1T	A	ASN	138	T	-8.561629	10.602263	-13.285524	-5.367011
1G1T	A	ASN	139	E	-8.579025	10.530869	-13.311024	-5.367360
1G1T	A	TYR	140	E	-8.626061	10.575041	-13.299397	-5.363099
1G1T	A	THR	141	E	-8.405326	6.531855	-14.647650	-5.113994
1G1T	A	CYS	142	E	-6.791037	3.735204	-12.905300	-4.619779
1G1T	A	LYS	143	E	-5.137902	3.348965	-10.593865	-4.324433
1G1T	A	CYS	144	E	-5.075016	3.765725	-10.572511	-4.358981
1G1T	A	ASP	145	T	-5.071108	3.797041	-10.579046	-4.360128
1G1T	A	PRO	146	T	-5.070896	3.808021	-10.573983	-4.359690
1G1T	A	GLY	147	T	-5.102146	3.820871	-10.454438	-4.347194
1G1T	A	PHE	148	E	-6.376348	7.595488	-10.544189	-4.665917
1G1T	A	SER	149	E	-7.685191	8.030071	-12.712396	-4.785006
1G1T	A	GLY	150	T	-8.133502	7.379905	-14.342502	-5.259012
1G1T	A	LEU	151	T	-8.493155	5.962063	-16.557932	-5.929376
1G1T	A	LYS	152	T	-8.442788	6.076223	-16.585949	-6.029856
1G1T	A	CYS	153	T	-6.450825	6.122793	-11.390590	-4.794873
1G1T	A	GLU	154	C	-4.496528	5.247265	-7.715005	-3.556026
1G1T	A	GLN	155	E	-4.496528	5.247265	-7.715005	-3.556026
1G1T	A	ILE	156	E	-4.496528	5.247265	-7.715005	-3.556026
1G1T	A	VAL	157	C	-4.496528	5.247265	-7.715005	-3.556026
1G96	A	VAL	10	C	-0.245025	1.142165	-4.076298	-3.306670
1G96	A	GLY	11	C	-0.245025	1.142165	-4.076298	-3.306670
1G96	A	GLY	12	C	-0.245025	1.142165	-4.076298	-3.306670
1G96	A	PRO	13	C	-0.245025	1.142165	-4.076298	-3.306670
1G96	A	MET	14	E	-1.630798	1.933859	-5.565092	-3.465621
1G96	A	ASP	15	E	-2.402227	2.248347	-6.072927	-3.702350
1G96	A	ALA	16	C	-3.896910	4.318426	-7.858750	-4.473335
1G96	A	SER	17	T	-6.031296	5.370386	-11.621292	-5.152513
1G96	A	VAL	18	T	-6.508387	5.768661	-11.222334	-4.138228
1G96	A	GLU	19	T	-6.405327	5.732315	-11.131015	-4.147658
1G96	A	GLU	20	T	-6.528815	5.520090	-10.970715	-4.040696
1G96	A	GLU	21	H	-6.558277	5.487622	-10.971742	-4.057602
1G96	A	GLY	22	H	-6.625828	5.459234	-10.939543	-4.096018
1G96	A	VAL	23	H	-7.067189	6.245750	-11.600991	-4.586646
1G96	A	ARG	24	H	-8.477749	6.433016	-10.201240	-2.305066
1G96	A	ARG	25	H	-8.486219	6.434306	-10.122999	-2.268746
1G96	A	ALA	26	H	-9.550827	7.099531	-11.999206	-2.481878
1G96	A	LEU	27	H	-10.018163	7.764386	-13.197525	-2.911108
1G96	A	ASP	28	H	-9.538907	6.263288	-12.935960	-2.875429
1G96	A	PHE	29	H	-8.650223	6.031806	-13.040262	-3.832499
1G96	A	ALA	30	H	-8.366100	6.730619	-12.863817	-4.016579
1G96	A	VAL	31	H	-8.332429	6.868822	-13.239473	-4.308801
1G96	A	GLY	32	H	-8.082275	6.688425	-13.765917	-4.755024
1G96	A	GLU	33	H	-7.717383	6.748057	-13.542697	-4.968360
1G96	A	TYR	34	H	-7.467618	7.046560	-15.059572	-6.414512
1G96	A	ASN	35	H	-7.005589	5.239657	-13.982313	-5.403644
1G96	A	LYS	36	H	-5.726451	3.043553	-9.798242	-3.303735
1G96	A	ALA	37	H	-4.664812	2.853998	-7.673996	-2.770848
1G96	A	SER	38	C	-4.124539	3.128020	-7.075765	-2.785759
1G96	A	ASN	39	C	-2.720729	3.711597	-6.818329	-4.164254
1G96	A	ASP	40	C	-2.716962	3.718919	-6.829972	-4.159930
1G96	A	MET	41	C	-2.717978	3.740778	-6.824729	-4.167001
1G96	A	TYR	42	C	-2.736767	3.772832	-6.808958	-4.214623
1G96	A	HIS	43	C	-2.763404	3.823707	-6.802237	-4.268026
1G96	A	SER	44	C	-4.297535	5.961095	-7.657553	-3.587971
1G96	A	ARG	45	C	-3.673352	6.895771	-4.523278	-2.495379
1G96	A	ALA	46	T	-2.941647	5.374881	-3.516813	-2.033547
1G96	A	LEU	47	T	-2.368443	4.944898	-2.879161	-1.912721
1G96	A	GLN	48	T	-2.347806	5.026945	-2.885232	-1.915164
1G96	A	VAL	49	T	-2.346113	5.119970	-2.846245	-1.924083
1G96	A	VAL	50	C	-2.391982	4.936552	-2.825729	-1.919884
1G96	A	ARG	51	C	-2.593625	4.964158	-2.677482	-1.929001
1G96	A	ALA	52	C	-3.922888	7.989479	-4.864322	-3.082683
1G96	A	ARG	53	E	-4.429810	9.525347	-6.679333	-4.588464
1G96	A	LYS	54	E	-4.270865	4.010931	-9.767957	-5.094402
1G96	A	GLN	55	C	-2.160269	3.586039	-4.950468	-3.369759
1G96	A	ILE	56	C	-2.084547	3.540681	-4.886132	-3.192983
1G96	A	VAL	57	C	-2.083144	3.538606	-4.879947	-3.181643

1G96	A	ALA	58	C	-2.082957	3.540375	-4.879896	-3.181256
1G96	A	GLY	59	C	-2.097209	3.542937	-4.762696	-3.139310
1G96	A	VAL	60	E	-3.348442	3.168873	-4.262519	-1.769873
1G96	A	ASN	61	E	-5.298062	6.715201	-6.567271	-2.748635
1G96	A	TYR	62	E	-6.202352	9.729771	-7.622198	-3.577029
1G96	A	PHE	63	E	-6.490308	10.422623	-8.420110	-4.090184
1G96	A	LEU	64	E	-7.057375	10.051454	-8.513254	-3.322326
1G96	A	ASP	65	E	-6.495759	8.522943	-8.321817	-3.344498
1G96	A	VAL	66	E	-6.535626	8.273094	-8.338655	-3.315678
1G96	A	GLU	67	E	-6.554835	8.161378	-8.380328	-3.336765
1G96	A	LEU	68	E	-6.659655	7.957988	-8.533967	-3.429093
1G96	A	GLY	69	E	-6.690227	7.987229	-8.720186	-3.607786
1G96	A	ARG	70	E	-8.111369	9.574508	-15.834683	-7.413182
1G96	A	THR	71	B	-6.916201	6.783504	-13.282198	-5.955810
1G96	A	THR	72	C	-4.591520	3.232865	-8.820451	-3.874314
1G96	A	CYS	73	C	-3.916576	3.147086	-8.913416	-4.239601
1G96	A	THR	74	T	-3.076300	3.196013	-7.954367	-4.137044
1G96	A	LYS	75	T	-3.025095	3.183130	-7.959464	-4.072443
1G96	A	THR	76	T	-3.024520	3.183308	-7.961517	-4.071603
1G96	A	GLN	77	T	-3.054542	3.215356	-7.983266	-4.129761
1G96	A	PRO	78	C	-2.927111	3.012939	-7.511430	-3.809954
1G96	A	ASN	79	T	-3.231545	3.086993	-8.285649	-4.110502
1G96	A	LEU	80	T	-3.298896	3.097363	-8.357441	-4.213891
1G96	A	ASP	81	T	-3.297072	3.095951	-8.356414	-4.208046
1G96	A	ASN	82	T	-3.316960	3.043021	-8.239944	-4.146077
1G96	A	CYS	83	T	-3.888220	3.867073	-10.428272	-5.613045
1G96	A	PRO	84	C	-5.690617	3.771503	-10.898122	-4.113990
1G96	A	PHE	85	B	-6.169685	4.907422	-10.005699	-3.709906
1G96	A	HIS	86	C	-5.408097	6.070735	-7.308200	-3.214842
1G96	A	ASP	87	C	-4.193737	3.117639	-6.578375	-2.614424
1G96	A	GLN	88	T	-4.125821	3.229957	-6.646449	-2.609952
1G96	A	PRO	89	T	-4.117071	3.266658	-6.693416	-2.628111
1G96	A	HIS	90	T	-4.118786	3.247914	-6.687886	-2.625027
1G96	A	LEU	91	T	-4.186750	2.926605	-6.630315	-2.561667
1G96	A	LYS	92	T	-5.358715	4.422217	-7.573722	-2.753514
1G96	A	ARG	93	E	-6.560750	6.136928	-9.959001	-3.925295
1G96	A	LYS	94	E	-9.193904	8.187379	-12.180012	-3.825487
1G96	A	ALA	95	E	-10.896697	10.257315	-14.206204	-4.373501
1G96	A	PHE	96	E	-12.244144	12.538393	-16.092740	-5.294049
1G96	A	CYS	97	E	-13.407604	11.665540	-16.478686	-3.994482
1G96	A	SER	98	E	-13.906659	12.232711	-17.838236	-4.567864
1G96	A	PHE	99	E	-14.232236	13.644522	-16.973156	-4.310030
1G96	A	GLN	100	E	-13.340045	19.229627	-20.433959	-9.974217
1G96	A	ILE	101	E	-9.895878	15.311731	-15.873375	-8.882028
1G96	A	TYR	102	E	-8.437238	13.554588	-13.119602	-7.439748
1G96	A	ALA	103	E	-6.092421	11.567146	-8.516813	-5.655591
1G96	A	VAL	104	E	-3.954476	5.923484	-6.856433	-3.951992
1G96	A	PRO	105	G	-3.509790	5.291094	-6.351383	-3.488188
1G96	A	TRP	106	G	-3.284193	5.317592	-6.084099	-3.368804
1G96	A	GLN	107	G	-3.213277	5.375533	-6.067579	-3.342297
1G96	A	GLY	108	C	-3.083423	5.704723	-5.726313	-3.256303
1G96	A	THR	109	E	-3.221949	5.773439	-5.468246	-3.110107
1G96	A	MET	110	E	-3.433007	6.333223	-5.300756	-3.133042
1G96	A	THR	111	E	-3.734964	6.988771	-5.199474	-3.150685
1G96	A	LEU	112	E	-3.915881	7.405396	-4.970271	-3.157631
1G96	A	SER	113	E	-4.933342	8.603372	-7.529351	-4.053359
1G96	A	LYS	114	E	-5.219655	7.553436	-6.852546	-3.244975
1G96	A	SER	115	E	-6.007958	6.337662	-8.232313	-3.022383
1G96	A	THR	116	E	-6.230259	5.463989	-9.082662	-3.079175
1G96	A	CYS	117	E	-5.676760	4.555897	-7.733539	-2.492927
1G96	A	GLN	118	E	-5.676760	4.555897	-7.733539	-2.492927
1G96	A	ASP	119	E	-5.676760	4.555897	-7.733539	-2.492927
1G96	A	ALA	120	C	-5.676760	4.555897	-7.733539	-2.492927
1GEN	A	LEU	461	C	1.903951	0.075884	-2.207330	-3.177996
1GEN	A	GLY	462	C	1.903951	0.075884	-2.207330	-3.177996
1GEN	A	PRO	463	C	1.903951	0.075884	-2.207330	-3.177996
1GEN	A	VAL	464	C	1.903951	0.075884	-2.207330	-3.177996
1GEN	A	THR	465	C	0.454534	1.697981	0.025228	-1.186298
1GEN	A	PRO	466	C	-1.764794	4.112224	-1.236842	-1.168387
1GEN	A	GLU	467	T	-3.404062	5.448197	-4.156909	-2.368029
1GEN	A	ILE	468	T	-4.707159	9.180080	-4.874337	-3.250759
1GEN	A	CYS	469	T	-6.620303	10.936051	-9.840305	-5.283313
1GEN	A	LYS	470	T	-6.762994	10.933471	-10.128651	-5.485241
1GEN	A	GLN	471	T	-7.393657	11.373748	-11.539687	-6.099127
1GEN	A	ASP	472	C	-8.083527	11.627028	-12.705011	-6.273656
1GEN	A	ILE	473	C	-8.367868	11.133795	-12.418014	-5.725882
1GEN	A	VAL	474	C	-8.746441	8.029390	-11.988382	-4.039248
1GEN	A	PHE	475	C	-10.277470	14.687189	-11.819701	-5.126541
1GEN	A	ASP	476	C	-11.820217	16.437736	-11.866683	-3.883908
1GEN	A	GLY	477	E	-12.303165	16.385727	-12.372994	-3.561568
1GEN	A	ILE	478	E	-12.449539	16.646693	-12.741140	-3.948943

```
1GEN        A          ALA            479                     E -12.408830 16.202987 -12.855169 -3.831385
1GEN        A          GLN            480                     E -11.787188 12.031782 -15.047871 -4.616530
1GEN        A          ILE            481                     E -9.955417 13.437333 -12.107785 -5.226748
1GEN        A          ARG            482                     T -9.961029 13.399285 -12.113747 -5.241157
1GEN        A          GLY            483                     T -9.960979 13.400045 -12.113658 -5.240991
1GEN        A          GLU            484                     E -9.961772 13.402979 -12.111131 -5.245206
1GEN        A          ILE            485                     E -9.981002 13.509937 -11.980402 -5.254597
1GEN        A          PHE            486                     E -13.818625 17.294883 -14.533264 -4.449591
1GEN        A          PHE            487                     E -14.983896 21.191797 -12.971980 -3.531396
1GEN        A          PHE            488                     E -14.960580 21.456348 -13.429392 -3.917060
1GEN        A          LYS            489                     E -13.719193 18.158557 -10.891470 -2.310421
1GEN        A          ASP            490                     T -13.710040 18.176773 -10.884970 -2.288434
1GEN        A          ARG            491                     T -13.713303 18.133430 -10.862943 -2.264262
1GEN        A          PHE            492                     E -13.724940 18.041098 -10.792565 -2.216320
1GEN        A          ILE            493                     E -13.775548 17.821131 -10.613645 -2.106219
1GEN        A          TRP            494                     E -15.278310 17.881334 -13.713376 -2.525630
1GEN        A          ARG            495                     E -12.534369  9.952865 -15.600122 -3.947548
1GEN        A          THR            496                     E -9.674182  9.255453 -12.349581 -4.087248
1GEN        A          VAL            497                     T -9.239864  9.082860 -11.763133 -3.455609
1GEN        A          THR            498                     T -9.075608  8.993706 -11.202749 -2.954000
1GEN        A          PRO            499                     T -9.065116  9.033552 -11.171479 -2.919543
1GEN        A          ARG            500                     T -8.972275  8.860029 -11.452797 -3.024949
1GEN        A          ASP            501                     T -7.189704  8.890459 -10.383762 -4.808810
1GEN        A          LYS            502                     C -6.865404 10.546004 -9.272100 -4.523527
1GEN        A          PRO            503                     C -6.848014 10.562602 -9.212108 -4.444621
1GEN        A          MET            504                     E -6.821059 10.548178 -9.109533 -4.309486
1GEN        A          GLY            505                     E -6.763664 10.656169 -8.978693 -4.189995
1GEN        A          PRO            506                     E -7.124247 12.256418 -7.781262 -3.570035
1GEN        A          LEU            507                     E -7.733736 11.433893 -7.743861 -2.514102
1GEN        A          LEU            508                     E -7.823503 11.579239 -7.774707 -2.634801
1GEN        A          VAL            509                     G -7.988784 12.009854 -8.047681 -3.031299
1GEN        A          ALA            510                     G -8.809758 13.360303 -8.622499 -3.029501
1GEN        A          THR            511                     G -9.172980 13.132477 -8.460663 -2.550065
1GEN        A          PHE            512                     T -10.067855 12.830099 -8.820472 -1.975336
1GEN        A          TRP            513                     T -10.762834 13.382330 -11.420686 -3.645069
1GEN        A          PRO            514                     T -10.252496 12.226190 -9.822809 -2.337766
1GEN        A          GLU            515                     T -10.389442 11.603308 -9.946956 -2.134883
1GEN        A          LEU            516                     T -9.777976 13.368280 -10.543223 -3.812156
1GEN        A          PRO            517                     T -9.772693 13.369646 -10.574785 -3.814684
1GEN        A          GLU            518                     T -9.774152 13.356480 -10.580104 -3.820256
1GEN        A          LYS            519                     T -9.955285 14.017516 -11.270539 -4.692146
1GEN        A          ILE            520                     T -10.019376 14.350937 -10.975464 -4.734482
1GEN        A          ASP            521                     C -12.501152 13.602001 -14.080438 -3.912912
1GEN        A          ALA            522                     E -13.683518 14.606007 -13.830440 -2.580860
1GEN        A          VAL            523                     E -13.853347 16.041962 -13.319195 -2.616050
1GEN        A          TYR            524                     E -13.834568 16.785613 -13.356781 -2.980497
1GEN        A          GLU            525                     E -11.070804 10.170826 -14.583808 -4.702530
1GEN        A          ALA            526                     E -9.035333  9.808031 -13.084865 -5.463013
1GEN        A          PRO            527                     T -9.028765  9.832484 -13.108900 -5.460572
1GEN        A          GLN            528                     T -9.028638  9.832444 -13.109693 -5.460176
1GEN        A          GLU            529                     T -9.028647  9.832040 -13.109915 -5.460260
1GEN        A          GLU            530                     T -9.047618  9.823299 -13.061646 -5.484398
1GEN        A          LYS            531                     E -11.667255 12.162024 -15.251182 -5.159775
1GEN        A          ALA            532                     E -13.451000 14.921593 -14.778876 -3.645018
1GEN        A          VAL            533                     E -13.501104 18.702957 -12.079765 -3.015906
1GEN        A          PHE            534                     E -13.444292 19.375049 -11.377634 -2.818107
1GEN        A          PHE            535                     E -10.879019 12.378050 -12.622138 -4.263821
1GEN        A          ALA            536                     E -10.627694 12.645817 -13.146020 -4.701602
1GEN        A          GLY            537                     T -10.628174 12.636294 -13.149492 -4.703321
1GEN        A          ASN            538                     T -10.629931 12.615720 -13.160493 -4.712281
1GEN        A          GLU            539                     E -10.631322 12.605309 -13.164897 -4.718579
1GEN        A          TYR            540                     E -11.254163 13.192688 -14.135845 -5.528258
1GEN        A          TRP            541                     E -15.096987 18.791020 -16.350107 -5.026693
1GEN        A          ILE            542                     E -14.873218 16.033164 -16.640781 -4.348977
1GEN        A          TYR            543                     E -13.108462  9.507880 -14.027842 -1.924721
1GEN        A          SER            544                     E -10.550365  7.878650 -10.291593 -1.134647
1GEN        A          ALA            545                     T -10.349106  7.958231 -11.512593 -1.918774
1GEN        A          SER            546                     T -9.509544  8.908894 -12.503268 -3.847107
1GEN        A          THR            547                     E -8.513992  9.196333 -11.208707 -3.778255
1GEN        A          LEU            548                     E -8.492986  9.300604 -11.165415 -3.739898
1GEN        A          GLU            549                     T -8.472292  9.453065 -11.071298 -3.713460
1GEN        A          ARG            550                     T -7.967704  9.735614 -10.541696 -3.882003
1GEN        A          GLY            551                     T -7.903719 10.149513 -10.556989 -4.063944
1GEN        A          TYR            552                     T -8.107005 10.513338 -10.411681 -4.187360
1GEN        A          PRO            553                     T -8.116410 10.488870 -10.417944 -4.209224
1GEN        A          LYS            554                     E -8.133192 10.473954 -10.452974 -4.264049
1GEN        A          PRO            555                     E -8.890670 12.329648 -11.130208 -4.839508
1GEN        A          LEU            556                     G -8.808089 13.623343 -9.895726 -4.519051
1GEN        A          THR            557                     G -8.677995 14.108590 -9.679399 -4.399281
1GEN        A          SER            558                     G -8.665521 14.130026 -9.633281 -4.346439
1GEN        A          LEU            559                     G -8.647440 14.156520 -9.524722 -4.252601
```

```
1GEN        A          GLY           560                        C -6.697223  7.811441 -8.616573 -3.413858
1GEN        A          LEU           561                        C -6.271844  9.122432 -8.051393 -3.656942
1GEN        A          PRO           562                        T -6.215574  9.059754 -8.131676 -3.595279
1GEN        A          PRO           563                        T -6.213925  9.052633 -8.135941 -3.588438
1GEN        A          ASP           564                        T -6.214359  9.049163 -8.136716 -3.590113
1GEN        A          VAL           565                        T -6.545216 10.142466 -7.799436 -3.746005
1GEN        A          GLN           566                        C -7.597989  8.647843 -8.951750 -2.946996
1GEN        A          ARG           567                        C -9.601257  7.667060 -9.503374 -1.240677
1GEN        A          VAL           568                        C -11.884172 10.765111 -12.080086 -1.747498
1GEN        A          ASP           569                        C -12.568733 11.976701 -14.911132 -3.473293
1GEN        A          ALA           570                        E -12.732348 12.693731 -14.510094 -3.459056
1GEN        A          ALA           571                        E -13.091583 14.720756 -12.872285 -2.802327
1GEN        A          PHE           572                        E -14.346082 17.207365 -14.190293 -3.356881
1GEN        A          ASN           573                        E -14.492786 16.648998 -15.795246 -4.263136
1GEN        A          TRP           574                        E -13.034010 11.251786 -14.267143 -2.932988
1GEN        A          SER           575                        T -10.666643  6.941832 -16.294385 -5.099429
1GEN        A          LYS           576                        T -10.187881  8.724090 -16.021894 -5.766125
1GEN        A          ASN           577                        T -10.187746  8.725598 -16.022402 -5.766115
1GEN        A          LYS           578                        T -10.187779  8.725634 -16.022177 -5.766221
1GEN        A          LYS           579                        E -10.192254  8.710267 -16.036531 -5.788674
1GEN        A          THR           580                        E -10.536649 10.169668 -15.802118 -6.300076
1GEN        A          TYR           581                        E -13.143448 20.066102 -12.639935 -5.023780
1GEN        A          ILE           582                        E -12.186071 17.963068 -11.617163 -4.049839
1GEN        A          PHE           583                        E -11.563707 15.688035 -10.593851 -2.909721
1GEN        A          ALA           584                        E -11.319389 14.956212 -10.431105 -2.581308
1GEN        A          GLY           585                        T -11.317408 14.952301 -10.451746 -2.589047
1GEN        A          ASP           586                        T -11.342222 14.727768 -10.370691 -2.483228
1GEN        A          LYS           587                        E -11.470539 14.075029 -10.114909 -2.158499
1GEN        A          PHE           588                        E -11.951471 13.585406 -10.200966 -1.985198
1GEN        A          TRP           589                        E -14.339013 16.979295 -15.072391 -4.592030
1GEN        A          ARG           590                        E -16.761523 19.910197 -18.535576 -5.862511
1GEN        A          TYR           591                        E -13.956503 13.124462 -19.200656 -6.724682
1GEN        A          ASN           592                        E -11.892625  9.645571 -17.041236 -5.346464
1GEN        A          GLU           593                        T -11.752062  9.120152 -16.819121 -4.864866
1GEN        A          VAL           594                        T -10.855911  8.005262 -13.442066 -2.907368
1GEN        A          LYS           595                        T -10.827502  8.017402 -13.654831 -3.006749
1GEN        A          LYS           596                        T -10.786245  7.997038 -13.962837 -3.174134
1GEN        A          LYS           597                        E -10.579026  8.116206 -14.226491 -3.497215
1GEN        A          MET           598                        E -10.380519  8.981031 -13.376087 -3.276113
1GEN        A          ASP           599                        T -9.383061  9.560961 -9.391836 -2.019320
1GEN        A          PRO           600                        T -7.726025  9.356707 -9.496251 -3.659353
1GEN        A          GLY           601                        T -7.653236  9.798764 -9.603377 -3.812138
1GEN        A          PHE           602                        T -7.654900  9.802543 -9.586802 -3.810035
1GEN        A          PRO           603                        C -7.656606  9.799791 -9.581015 -3.812871
1GEN        A          LYS           604                        E -7.682440  9.810677 -9.622668 -3.900897
1GEN        A          LEU           605                        E -7.274292  7.877672 -8.879072 -3.027433
1GEN        A          ILE           606                        G -7.231977  8.386839 -8.729893 -3.080797
1GEN        A          ALA           607                        G -7.224058  8.431325 -8.713964 -3.058758
1GEN        A          ASP           608                        G -7.216516  8.480750 -8.703016 -3.042319
1GEN        A          ALA           609                        C -7.210099  8.567994 -8.657316 -3.022575
1GEN        A          TRP           610                        T -8.177046 14.239274 -8.009413 -3.601902
1GEN        A          ASN           611                        T -7.700081 12.632028 -8.440246 -4.038635
1GEN        A          ALA           612                        T -7.689968 12.701561 -8.513079 -4.090920
1GEN        A          ILE           613                        T -7.706045 12.716793 -8.532014 -4.155541
1GEN        A          PRO           614                        T -7.724244 12.636124 -8.629131 -4.247148
1GEN        A          ASP           615                        T -7.776407 12.401562 -8.703899 -4.322893
1GEN        A          ASN           616                        T -9.470536 13.661765 -9.546749 -3.498730
1GEN        A          LEU           617                        T -11.058137 14.741223 -10.884854 -3.238577
1GEN        A          ASP           618                        C -11.422117 13.960874 -12.760139 -4.263886
1GEN        A          ALA           619                        E -11.446106 14.030078 -12.765375 -4.335244
1GEN        A          VAL           620                        E -11.495804 14.266674 -12.555313 -4.356646
1GEN        A          VAL           621                        E -10.534359 10.027346 -14.716631 -5.370717
1GEN        A          ASP           622                        E -9.783086  9.070217 -14.362660 -4.932912
1GEN        A          LEU           623                        T -7.748443  5.563558 -10.194085 -2.739654
1GEN        A          GLN           624                        T -7.648469  5.302371 -10.450982 -2.715356
1GEN        A          GLY           625                        T -7.323193  4.709755 -11.837875 -3.575603
1GEN        A          GLY           626                        T -7.325345  4.691395 -11.828515 -3.569425
1GEN        A          GLY           627                        C -7.332111  4.645333 -11.801009 -3.555746
1GEN        A          HIS           628                        E -7.718734  3.907706 -13.407874 -4.374169
1GEN        A          SER           629                        E -7.832608  3.912830 -13.738344 -4.753761
1GEN        A          TYR           630                        E -11.575894 11.084576 -16.254083 -5.988503
1GEN        A          PHE           631                        E -12.456009 18.075020 -12.960581 -5.400551
1GEN        A          PHE           632                        E -12.060911 17.535799 -12.749986 -4.874552
1GEN        A          LYS           633                        E -12.034334 17.411137 -12.768127 -4.780991
1GEN        A          GLY           634                        T -12.030909 17.397732 -12.771271 -4.764658
1GEN        A          ALA           635                        T -12.030271 17.390979 -12.777065 -4.763530
1GEN        A          TYR           636                        E -12.423512 16.760816 -12.618650 -4.162579
1GEN        A          TYR           637                        E -13.775647 14.943007 -13.393474 -2.776487
1GEN        A          LEU           638                        E -14.792876 16.139827 -14.609455 -2.962013
1GEN        A          LYS           639                        E -14.649109 13.574704 -16.301578 -3.462407
1GEN        A          LEU           640                        E -11.936982  8.359267 -16.550949 -4.626886
```

1GEN	A	GLU	641	E	-10.798935	8.206899	-16.358925	-5.409527
1GEN	A	ASN	642	T	-10.304715	9.017362	-14.941724	-4.721067
1GEN	A	GLN	643	T	-9.489952	8.115163	-11.382644	-2.562843
1GEN	A	SER	644	T	-9.321334	8.721947	-10.730770	-2.296172
1GEN	A	LEU	645	T	-8.102577	8.971610	-10.004628	-3.364651
1GEN	A	LYS	646	T	-6.060206	8.801036	-8.341883	-4.339301
1GEN	A	SER	647	T	-6.043682	8.821332	-8.379016	-4.314535
1GEN	A	VAL	648	E	-6.019285	8.792441	-8.334581	-4.203749
1GEN	A	LYS	649	E	-6.018706	8.791343	-8.335356	-4.201032
1GEN	A	PHE	650	E	-6.034147	8.785632	-8.294704	-4.219032
1GEN	A	GLY	651	E	-7.582896	8.663761	-8.361868	-2.287395
1GEN	A	SER	652	E	-7.861577	8.137577	-7.525304	-1.589131
1GEN	A	ILE	653	H	-9.657813	9.081864	-9.548206	-1.743738
1GEN	A	LYS	654	H	-10.973294	9.030287	-14.505164	-4.125813
1GEN	A	SER	655	H	-12.356808	9.210358	-16.926545	-4.936140
1GEN	A	ASP	656	H	-12.772083	16.469145	-14.499913	-5.583752
1GEN	A	TRP	657	H	-10.713939	16.600340	-9.393849	-3.434340
1GEN	A	LEU	658	H	-10.713939	16.600340	-9.393849	-3.434340
1GEN	A	GLY	659	C	-10.713939	16.600340	-9.393849	-3.434340
1GEN	A	CYS	660	C	-10.713939	16.600340	-9.393849	-3.434340
1GGZ	A	LEU	4	C	-4.778484	5.253219	-8.577129	-3.778734
1GGZ	A	THR	5	C	-4.778484	5.253219	-8.577129	-3.778734
1GGZ	A	GLU	6	H	-4.778484	5.253219	-8.577129	-3.778734
1GGZ	A	GLU	7	H	-4.778484	5.253219	-8.577129	-3.778734
1GGZ	A	GLN	8	H	-6.004975	7.287825	-11.061928	-5.058359
1GGZ	A	VAL	9	H	-6.670197	8.661992	-12.080034	-5.778154
1GGZ	A	THR	10	H	-7.077409	9.254675	-12.514487	-6.221811
1GGZ	A	GLU	11	H	-8.338340	10.313931	-14.583039	-6.906634
1GGZ	A	PHE	12	H	-9.526021	11.930606	-14.045314	-5.520471
1GGZ	A	LYS	13	H	-9.567519	11.590050	-13.716733	-5.151436
1GGZ	A	GLU	14	H	-9.581319	11.183823	-13.653570	-4.976557
1GGZ	A	ALA	15	H	-10.131396	11.671331	-13.770411	-4.735484
1GGZ	A	PHE	16	H	-10.712908	11.229044	-14.134393	-4.281260
1GGZ	A	SER	17	H	-10.589144	11.323224	-14.251709	-4.382941
1GGZ	A	LEU	18	H	-10.688510	11.201281	-14.523066	-4.469067
1GGZ	A	PHE	19	H	-9.925729	11.084156	-14.384031	-5.486033
1GGZ	A	ASP	20	T	-7.958801	4.750190	-14.935692	-5.527234
1GGZ	A	LYS	21	T	-5.614245	3.161786	-12.573849	-5.424212
1GGZ	A	ASP	22	T	-4.839051	2.478843	-12.076685	-5.231917
1GGZ	A	GLY	23	T	-4.803799	2.690792	-12.041548	-5.216475
1GGZ	A	ASP	24	C	-4.802124	2.705116	-12.043805	-5.215909
1GGZ	A	GLY	25	C	-4.804391	2.703559	-12.030502	-5.214403
1GGZ	A	CYS	26	E	-4.974444	2.567271	-11.863072	-5.143797
1GGZ	A	ILE	27	E	-6.446661	6.357107	-11.558765	-4.963021
1GGZ	A	THR	28	C	-7.960947	8.951638	-12.754176	-4.977536
1GGZ	A	THR	29	H	-8.503966	10.609476	-12.567181	-4.878674
1GGZ	A	ARG	30	H	-8.829831	10.461156	-12.710206	-4.648020
1GGZ	A	GLU	31	H	-9.298163	10.683895	-13.521755	-4.824138
1GGZ	A	LEU	32	H	-9.410454	11.843654	-13.462576	-5.052826
1GGZ	A	GLY	33	H	-9.315547	11.999199	-14.944991	-6.342396
1GGZ	A	THR	34	H	-9.240071	12.245145	-15.601496	-6.999909
1GGZ	A	VAL	35	H	-9.260899	12.372347	-15.728368	-7.131974
1GGZ	A	MET	36	H	-9.014752	10.429829	-15.650724	-6.448286
1GGZ	A	ARG	37	H	-7.322700	4.606368	-12.952202	-4.475165
1GGZ	A	SER	38	H	-4.103140	4.006179	-8.776012	-4.372827
1GGZ	A	LEU	39	H	-3.600021	5.760619	-7.790950	-4.423309
1GGZ	A	GLY	40	C	-3.543720	5.862127	-7.883079	-4.449690
1GGZ	A	GLN	41	C	-3.525133	5.945662	-7.908885	-4.457727
1GGZ	A	ASN	42	C	-3.411256	6.094440	-7.845494	-4.419679
1GGZ	A	PRO	43	C	-3.626087	7.025223	-7.444435	-4.430479
1GGZ	A	THR	44	C	-4.157389	6.960901	-8.059531	-4.386858
1GGZ	A	GLU	45	H	-4.331404	6.994393	-7.813277	-4.280077
1GGZ	A	ALA	46	H	-4.407188	6.783019	-7.693185	-4.223774
1GGZ	A	GLU	47	H	-6.086645	7.339225	-10.068455	-4.310916
1GGZ	A	LEU	48	H	-6.677954	7.816115	-10.270119	-4.440241
1GGZ	A	ARG	49	H	-9.663081	9.789515	-15.540511	-5.664606
1GGZ	A	ASP	50	H	-10.236101	9.739638	-16.458160	-5.912328
1GGZ	A	MET	51	H	-10.983734	11.722548	-17.847828	-6.913580
1GGZ	A	MET	52	H	-11.271720	10.429125	-16.754867	-5.338970
1GGZ	A	SER	53	H	-10.850196	9.703942	-16.670619	-5.277675
1GGZ	A	GLU	54	H	-10.540323	9.237252	-16.521203	-5.194617
1GGZ	A	ILE	55	C	-9.378697	7.689401	-14.779282	-4.944317
1GGZ	A	ASP	56	T	-8.143467	3.383860	-15.445170	-5.017566
1GGZ	A	ARG	57	T	-5.946781	1.581179	-13.324611	-5.013883
1GGZ	A	ASP	58	T	-4.338290	2.676354	-11.051943	-5.230398
1GGZ	A	GLY	59	T	-4.284912	2.961174	-11.015268	-5.209243
1GGZ	A	ASN	60	C	-4.283325	2.973688	-11.018931	-5.209017
1GGZ	A	GLY	61	C	-4.284078	2.974272	-11.013068	-5.209240
1GGZ	A	THR	62	C	-4.320080	3.064995	-10.870540	-5.221005
1GGZ	A	VAL	63	E	-5.718056	6.042529	-10.674576	-4.981634
1GGZ	A	ASP	64	E	-7.732186	7.883708	-12.475586	-5.087564

1GGZ	A	PHE	65	H	-9.562026	13.317113	-12.149996	-4.711255
1GGZ	A	PRO	66	H	-9.699514	13.199011	-12.059910	-4.595278
1GGZ	A	GLU	67	H	-10.348094	13.107783	-12.887227	-4.669953
1GGZ	A	PHE	68	H	-11.169559	15.883573	-13.511269	-5.152251
1GGZ	A	LEU	69	H	-10.767199	14.255840	-13.808167	-5.210655
1GGZ	A	GLY	70	H	-10.728352	13.802816	-14.102022	-5.221468
1GGZ	A	MET	71	H	-10.842588	13.281561	-14.458002	-5.254938
1GGZ	A	MET	72	H	-10.839996	13.232743	-14.488823	-5.250892
1GGZ	A	ALA	73	H	-10.918126	12.516646	-14.734859	-5.212043
1GGZ	A	ARG	74	H	-11.758945	10.015452	-17.261320	-5.128521
1GGZ	A	LYS	75	H	-11.057846	6.331354	-17.699961	-4.982192
1GGZ	A	MET	76	H	-10.368785	5.409236	-17.318645	-4.942570
1GGZ	A	LYS	77	H	-9.235049	4.648119	-16.037582	-4.857017
1GGZ	A	ASP	78	H	-8.664418	4.961412	-15.441104	-4.886965
1GGZ	A	THR	79	H	-8.648679	4.974570	-15.502697	-4.897564
1GGZ	A	ASP	80	H	-8.653524	4.971550	-15.492297	-4.901053
1GGZ	A	ASN	81	H	-8.674889	4.975252	-15.434824	-4.901754
1GGZ	A	GLU	82	H	-8.913232	5.202340	-15.246059	-4.931259
1GGZ	A	GLU	83	H	-10.588360	5.985237	-18.001074	-5.343836
1GGZ	A	GLU	84	H	-11.277552	7.267787	-18.427949	-5.451142
1GGZ	A	ILE	85	H	-11.730701	8.581355	-17.785152	-5.238990
1GGZ	A	ARG	86	H	-12.756023	10.074503	-18.630713	-5.063538
1GGZ	A	GLU	87	H	-11.708883	10.819793	-15.477867	-4.449169
1GGZ	A	ALA	88	H	-11.716983	11.163513	-15.206794	-4.390976
1GGZ	A	PHE	89	H	-11.749220	11.244890	-15.029667	-4.355498
1GGZ	A	ARG	90	H	-11.608124	11.468927	-15.161817	-4.432875
1GGZ	A	VAL	91	H	-11.146413	11.647599	-14.970027	-4.673162
1GGZ	A	PHE	92	H	-10.109449	10.526802	-14.536272	-5.270415
1GGZ	A	ASP	93	T	-7.582198	3.590261	-14.722829	-5.311885
1GGZ	A	LYS	94	T	-5.027275	2.496306	-11.878058	-5.204461
1GGZ	A	ASP	95	T	-4.952228	2.722754	-11.944974	-5.214758
1GGZ	A	GLY	96	T	-4.943970	2.788821	-11.945674	-5.210983
1GGZ	A	ASN	97	C	-4.944027	2.788030	-11.945484	-5.210959
1GGZ	A	GLY	98	C	-4.950867	2.779924	-11.913148	-5.209744
1GGZ	A	PHE	99	C	-6.147254	4.729579	-12.390858	-5.251658
1GGZ	A	VAL	100	B	-7.471809	7.518836	-12.030385	-4.934400
1GGZ	A	SER	101	C	-9.845995	9.275040	-14.710506	-4.573538
1GGZ	A	ALA	102	H	-9.963957	9.341653	-14.509764	-4.462314
1GGZ	A	ALA	103	H	-9.991092	9.296979	-14.487011	-4.463253
1GGZ	A	GLU	104	H	-10.071177	9.152032	-14.499084	-4.495303
1GGZ	A	LEU	105	H	-10.511698	10.603314	-14.528626	-4.852944
1GGZ	A	ARG	106	H	-9.867939	14.829230	-15.465387	-8.094773
1GGZ	A	HIS	107	H	-8.006729	14.346179	-13.058520	-7.690723
1GGZ	A	VAL	108	H	-7.808667	13.650605	-12.345709	-6.761294
1GGZ	A	MET	109	H	-6.467432	9.698405	-9.751215	-4.835645
1GGZ	A	THR	110	H	-4.561165	7.019244	-7.850997	-4.343553
1GGZ	A	ARG	111	H	-3.431817	6.340574	-6.656803	-4.103788
1GGZ	A	LEU	112	H	-3.252061	6.633460	-6.759521	-4.206833
1GGZ	A	GLY	113	C	-3.246178	6.632583	-6.794978	-4.212454
1GGZ	A	GLU	114	C	-3.248224	6.622476	-6.787050	-4.211098
1GGZ	A	LYS	115	C	-3.313938	6.583042	-6.668464	-4.194582
1GGZ	A	LEU	116	C	-4.024657	7.395940	-7.158586	-4.487872
1GGZ	A	SER	117	C	-5.914392	6.597343	-10.551316	-4.748790
1GGZ	A	ASP	118	H	-7.245889	6.937713	-12.825010	-4.862325
1GGZ	A	GLU	119	H	-7.556197	6.625542	-13.123392	-4.828028
1GGZ	A	GLU	120	H	-8.212821	7.295099	-13.674497	-4.920448
1GGZ	A	VAL	121	H	-8.273064	7.302342	-13.435004	-4.852566
1GGZ	A	ASP	122	H	-9.340149	7.856991	-15.147612	-5.271741
1GGZ	A	GLU	123	H	-9.970487	8.807787	-15.021393	-4.654360
1GGZ	A	MET	124	H	-9.998346	9.870088	-13.719898	-4.057283
1GGZ	A	ILE	125	H	-9.818283	9.774714	-13.403432	-3.874774
1GGZ	A	ARG	126	H	-9.583179	9.013470	-13.761718	-3.969940
1GGZ	A	ALA	127	H	-9.497897	8.715401	-14.048615	-4.068127
1GGZ	A	ALA	128	H	-8.908053	6.816288	-14.728647	-4.763316
1GGZ	A	ASP	129	T	-8.212655	4.575087	-15.524977	-5.246670
1GGZ	A	THR	130	T	-6.266407	2.889136	-13.549624	-5.373262
1GGZ	A	ASP	131	T	-6.006050	3.355034	-13.516382	-5.452351
1GGZ	A	GLY	132	T	-5.926667	3.859695	-13.308062	-5.410662
1GGZ	A	ASP	133	C	-5.929263	3.850746	-13.301018	-5.412385
1GGZ	A	GLY	134	C	-5.938231	3.852318	-13.262885	-5.412301
1GGZ	A	GLN	135	C	-6.416161	5.121382	-13.002242	-5.456047
1GGZ	A	VAL	136	B	-7.153871	7.383254	-11.875108	-5.119131
1GGZ	A	ASN	137	C	-10.787398	9.505295	-16.208602	-5.563979
1GGZ	A	TYR	138	H	-12.418220	13.661679	-16.802779	-5.744901
1GGZ	A	GLU	139	H	-12.761530	14.405300	-18.526746	-6.740996
1GGZ	A	GLU	140	H	-11.793834	14.712009	-16.199049	-6.476674
1GGZ	A	PHE	141	H	-8.758445	12.451562	-11.043509	-4.926019
1GGZ	A	VAL	142	H	-6.447660	6.851581	-9.801069	-3.948712
1GGZ	A	ARG	143	H	-5.715375	5.728211	-9.301395	-3.518144
1GGZ	A	VAL	144	H	-3.340948	4.241947	-5.215206	-2.415148
1GGZ	A	LEU	145	H	-3.340948	4.241947	-5.215206	-2.415148

1GGZ	A	VAL	146	C	-3.340948	4.241947	-5.215206	-2.415148
1GGZ	A	SER	147	C	-3.340948	4.241947	-5.215206	-2.415148
1GH2	A	VAL	2	C	-3.760248	4.507322	-8.028623	-3.826098
1GH2	A	GLY	3	C	-3.760248	4.507322	-8.028623	-3.826098
1GH2	A	VAL	4	C	-3.760248	4.507322	-8.028623	-3.826098
1GH2	A	LYS	5	E	-3.760248	4.507322	-8.028623	-3.826098
1GH2	A	PRO	6	E	-4.199674	4.760981	-8.480793	-4.167599
1GH2	A	VAL	7	E	-5.826911	7.748333	-10.849615	-5.339299
1GH2	A	GLY	8	C	-6.029202	6.886016	-11.707162	-5.510540
1GH2	A	SER	9	C	-6.806501	4.160368	-12.472297	-4.475825
1GH2	A	ASP	10	G	-6.817247	4.075865	-12.407626	-4.429306
1GH2	A	PRO	11	G	-6.813852	4.114587	-12.405028	-4.429006
1GH2	A	ASP	12	G	-6.820864	4.088107	-12.380841	-4.429085
1GH2	A	PHE	13	H	-9.476699	10.271836	-13.370979	-4.585396
1GH2	A	GLN	14	H	-9.524594	10.290516	-13.287156	-4.583665
1GH2	A	PRO	15	H	-9.382941	10.157292	-13.302212	-4.596887
1GH2	A	GLU	16	H	-9.741981	10.670005	-13.879031	-4.834628
1GH2	A	LEU	17	H	-8.851087	8.180045	-13.537693	-4.601070
1GH2	A	SER	18	H	-7.878622	4.566688	-13.866789	-4.394419
1GH2	A	GLY	19	H	-7.756581	4.574702	-13.894260	-4.328067
1GH2	A	ALA	20	T	-7.763793	4.498300	-13.898085	-4.315834
1GH2	A	GLY	21	T	-7.769022	4.438060	-13.899040	-4.309100
1GH2	A	SER	22	T	-7.848981	3.995566	-13.961907	-4.274654
1GH2	A	ARG	23	T	-8.712721	4.959540	-14.012922	-4.041312
1GH2	A	LEU	24	E	-10.332006	10.405384	-13.725690	-4.058865
1GH2	A	ALA	25	E	-11.081652	13.650309	-13.303722	-4.063260
1GH2	A	VAL	26	E	-11.395262	17.309098	-12.010867	-4.169329
1GH2	A	VAL	27	E	-11.553611	18.740197	-11.831884	-4.499969
1GH2	A	LYS	28	E	-11.558160	18.762457	-12.114530	-4.727142
1GH2	A	PHE	29	E	-8.617391	11.854771	-11.280983	-4.980037
1GH2	A	THR	30	E	-6.597759	5.692272	-11.961099	-4.934990
1GH2	A	MET	31	T	-4.880600	3.638102	-10.683101	-4.773384
1GH2	A	ARG	32	T	-4.574732	3.676762	-10.439672	-4.558386
1GH2	A	GLY	33	T	-4.571495	3.682771	-10.458594	-4.561275
1GH2	A	CYS	34	T	-4.571222	3.676505	-10.463041	-4.560842
1GH2	A	GLY	35	H	-4.585752	3.632732	-10.421717	-4.542767
1GH2	A	PRO	36	H	-5.092054	3.787547	-10.165335	-4.241877
1GH2	A	CYS	37	H	-7.062631	5.432529	-12.669163	-4.343783
1GH2	A	LEU	38	H	-7.205764	6.306579	-11.632631	-3.779956
1GH2	A	ARG	39	H	-7.225365	6.819489	-11.162529	-3.626808
1GH2	A	ILE	40	H	-7.834639	9.229493	-10.433262	-3.346203
1GH2	A	ALA	41	H	-7.847076	9.219574	-10.393877	-3.338591
1GH2	A	PRO	42	H	-7.909489	9.186414	-10.220737	-3.275007
1GH2	A	ALA	43	H	-8.493831	10.487416	-10.180354	-3.410123
1GH2	A	PHE	44	H	-9.694361	13.538077	-10.956883	-3.925249
1GH2	A	SER	45	H	-10.448464	11.541270	-13.040530	-3.958685
1GH2	A	SER	46	H	-10.874386	10.060382	-15.551124	-4.698780
1GH2	A	MET	47	H	-11.148462	9.310052	-16.762568	-5.244537
1GH2	A	SER	48	H	-10.828180	9.096805	-16.716514	-5.251362
1GH2	A	ASN	49	H	-10.565700	8.714495	-16.754051	-5.225907
1GH2	A	LYS	50	H	-9.901762	10.253300	-14.489738	-4.979033
1GH2	A	TYR	51	T	-9.790834	11.047055	-13.848053	-4.832931
1GH2	A	PRO	52	T	-9.608131	11.800827	-13.220737	-4.671150
1GH2	A	GLN	53	T	-9.636823	12.009677	-13.021379	-4.637460
1GH2	A	ALA	54	T	-9.676079	12.400967	-12.707486	-4.594186
1GH2	A	VAL	55	E	-10.053022	13.805829	-11.963727	-4.352658
1GH2	A	PHE	56	E	-10.339949	14.259495	-11.596011	-4.269731
1GH2	A	LEU	57	E	-11.670959	18.121512	-12.664780	-4.736076
1GH2	A	GLU	58	E	-10.952145	14.281415	-13.657205	-5.027669
1GH2	A	VAL	59	E	-10.105656	11.343613	-13.660021	-4.768879
1GH2	A	ASP	60	E	-9.639117	9.997408	-14.215388	-4.929836
1GH2	A	VAL	61	T	-9.254006	8.959718	-14.338755	-4.842103
1GH2	A	HIS	62	T	-8.839252	7.252630	-14.963230	-4.994339
1GH2	A	GLN	63	T	-8.838597	7.131821	-15.040005	-5.003183
1GH2	A	CYS	64	T	-8.836203	6.841851	-15.235651	-5.031424
1GH2	A	GLN	65	H	-8.191087	6.493626	-13.719578	-4.575022
1GH2	A	GLY	66	H	-6.965058	5.723106	-11.710604	-4.206604
1GH2	A	THR	67	H	-6.964832	5.760216	-11.673749	-4.192375
1GH2	A	ALA	68	H	-6.871854	5.573435	-11.940429	-4.212604
1GH2	A	ALA	69	H	-6.725921	5.653551	-12.031017	-4.262491
1GH2	A	THR	70	H	-6.705454	5.648031	-12.071230	-4.282685
1GH2	A	ASN	71	C	-7.125818	5.759609	-12.963248	-4.480328
1GH2	A	ASN	72	C	-5.667725	7.420176	-9.231085	-4.304551
1GH2	A	ILE	73	C	-5.655825	7.597158	-9.157342	-4.294338
1GH2	A	SER	74	C	-5.675877	7.668501	-9.044479	-4.289528
1GH2	A	ALA	75	T	-5.685502	7.694313	-8.977680	-4.285044
1GH2	A	THR	76	T	-5.692121	7.708508	-8.927113	-4.280122
1GH2	A	PRO	77	T	-7.537802	10.595550	-9.601274	-4.097243
1GH2	A	THR	78	E	-9.079302	10.819379	-11.990941	-4.609023
1GH2	A	PHE	79	E	-11.479781	15.944615	-12.648097	-4.819040
1GH2	A	GLN	80	E	-13.979136	17.798809	-16.304087	-5.704702

1GH2	A	PHE	81	E	-14.395482	19.122365	-16.190043	-5.601570
1GH2	A	PHE	82	E	-11.118197	12.299087	-14.361735	-5.051513
1GH2	A	ARG	83	E	-9.973892	9.628841	-14.637391	-5.087507
1GH2	A	ASN	84	T	-8.160667	8.721844	-12.153089	-4.725517
1GH2	A	LYS	85	T	-8.131261	8.743422	-12.251101	-4.730987
1GH2	A	VAL	86	E	-8.123188	8.733173	-12.300934	-4.734243
1GH2	A	ARG	87	E	-8.126943	8.710680	-12.288032	-4.732267
1GH2	A	ILE	88	E	-8.149403	8.695669	-12.196865	-4.718975
1GH2	A	ASP	89	E	-9.766270	8.973972	-14.620468	-4.890882
1GH2	A	GLN	90	E	-10.512426	8.954037	-16.039692	-5.167385
1GH2	A	TYR	91	E	-10.240236	10.724809	-14.859863	-5.363564
1GH2	A	GLN	92	E	-8.302021	7.922639	-12.791502	-4.763113
1GH2	A	GLY	93	C	-6.338710	5.883530	-10.334067	-4.002645
1GH2	A	ALA	94	C	-5.456141	5.794208	-9.613646	-4.047719
1GH2	A	ASP	95	C	-5.440396	5.853395	-9.651986	-4.054514
1GH2	A	ALA	96	H	-5.439903	5.856902	-9.654618	-4.055180
1GH2	A	VAL	97	H	-5.444106	5.843625	-9.634085	-4.050605
1GH2	A	GLY	98	H	-5.585967	5.853375	-9.469399	-4.071166
1GH2	A	LEU	99	H	-7.559758	8.156058	-11.244643	-4.353601
1GH2	A	GLU	100	H	-9.216412	9.714082	-13.782881	-5.059478
1GH2	A	GLU	101	H	-9.819083	8.907956	-14.745783	-5.240042
1GH2	A	LYS	102	H	-12.531899	13.167691	-18.252709	-6.465621
1GH2	A	ILE	103	H	-11.395919	14.732663	-15.488923	-6.531799
1GH2	A	LYS	104	H	-9.993558	10.905767	-14.826582	-5.790393
1GH2	A	GLN	105	H	-8.286758	9.169501	-11.896812	-4.569484
1GH2	A	HIS	106	H	-8.286758	9.169501	-11.896812	-4.569484
1GH2	A	LEU	107	H	-8.286758	9.169501	-11.896812	-4.569484
1GH2	A	GLU	108	C	-8.286758	9.169501	-11.896812	-4.569484
1GLO	A	LEU	1	C	-5.091884	3.896805	-8.249970	-2.796585
1GLO	A	PRO	2	T	-5.091884	3.896805	-8.249970	-2.796585
1GLO	A	ASP	3	T	-5.091884	3.896805	-8.249970	-2.796585
1GLO	A	SER	4	T	-5.091884	3.896805	-8.249970	-2.796585
1GLO	A	VAL	5	E	-6.825076	5.767985	-10.132358	-3.364018
1GLO	A	ASP	6	E	-9.175948	7.907524	-13.974204	-4.701211
1GLO	A	TRP	7	G	-10.120575	11.146474	-14.456117	-5.135848
1GLO	A	ARG	8	G	-8.412997	7.816353	-13.779832	-5.332658
1GLO	A	GLU	9	G	-7.559546	8.668997	-12.064883	-5.005115
1GLO	A	LYS	10	G	-7.532042	8.766111	-12.109829	-5.016885
1GLO	A	GLY	11	C	-7.179578	8.866459	-11.842259	-5.006964
1GLO	A	CYS	12	C	-6.823868	9.873064	-10.736919	-4.808751
1GLO	A	VAL	13	C	-6.817380	10.138568	-10.576863	-4.790465
1GLO	A	THR	14	C	-6.915851	10.575649	-10.383564	-4.788826
1GLO	A	GLU	15	C	-6.924951	10.572732	-10.343708	-4.781836
1GLO	A	VAL	16	C	-7.130575	11.224259	-9.853762	-4.693614
1GLO	A	LYS	17	C	-7.975828	11.629497	-11.265451	-5.086278
1GLO	A	TYR	18	B	-8.155427	10.131896	-12.358320	-5.151807
1GLO	A	GLN	19	T	-7.919259	5.107062	-14.700337	-5.226230
1GLO	A	GLY	20	T	-6.868928	4.541827	-12.763397	-4.580066
1GLO	A	SER	21	T	-6.860640	4.558417	-12.792279	-4.579622
1GLO	A	CYS	22	T	-6.861011	4.555593	-12.789809	-4.579023
1GLO	A	GLY	23	T	-6.885476	4.444156	-12.735296	-4.555254
1GLO	A	ALA	24	H	-6.968179	4.462376	-12.412882	-4.451192
1GLO	A	SER	25	H	-9.372975	5.975823	-14.862484	-4.571434
1GLO	A	TRP	26	H	-11.810729	12.722701	-14.902640	-4.673540
1GLO	A	ALA	27	H	-11.578434	14.085831	-13.968113	-4.534385
1GLO	A	PHE	28	H	-11.287688	15.476882	-12.956167	-4.715124
1GLO	A	SER	29	H	-10.910333	13.473387	-13.497111	-4.502449
1GLO	A	ALA	30	H	-10.249630	13.706393	-11.957055	-4.086435
1GLO	A	VAL	31	H	-10.240168	13.708294	-12.003286	-4.095591
1GLO	A	GLY	32	H	-10.245176	13.582733	-12.071989	-4.104485
1GLO	A	ALA	33	H	-10.327063	13.358638	-11.935216	-3.998826
1GLO	A	LEU	34	H	-10.444553	13.790001	-11.461437	-3.937997
1GLO	A	GLU	35	H	-12.057168	13.340362	-15.072724	-4.706562
1GLO	A	ALA	36	H	-12.308007	12.947228	-15.301980	-4.770041
1GLO	A	GLN	37	H	-13.586506	15.882208	-19.030291	-6.875061
1GLO	A	LEU	38	H	-10.121213	11.764071	-13.436901	-5.045807
1GLO	A	LYS	39	H	-6.742880	8.024954	-11.056714	-5.126263
1GLO	A	LEU	40	H	-5.313950	6.963259	-9.408181	-4.673977
1GLO	A	LYS	41	H	-4.794811	7.683423	-8.698066	-4.638807
1GLO	A	THR	42	H	-4.315817	8.022741	-7.885207	-4.478682
1GLO	A	GLY	43	C	-4.272133	8.100477	-7.944405	-4.492394
1GLO	A	LYS	44	C	-4.280324	8.110507	-7.897901	-4.482469
1GLO	A	LEU	45	C	-4.383044	8.346214	-7.641197	-4.453657
1GLO	A	VAL	46	C	-4.587180	8.405322	-7.413247	-4.386740
1GLO	A	SER	47	C	-5.824468	9.208762	-8.725821	-4.663001
1GLO	A	LEU	48	B	-8.027644	13.286174	-9.334945	-4.552703
1GLO	A	SER	49	C	-9.874354	14.210019	-11.744315	-4.840209
1GLO	A	ALA	50	H	-11.196527	13.693856	-13.498619	-4.692384
1GLO	A	GLN	51	H	-12.844812	13.622485	-17.476461	-5.474914
1GLO	A	ASN	52	H	-12.975081	13.396921	-17.876687	-5.528357
1GLO	A	LEU	53	H	-12.594406	13.294861	-16.974086	-5.335957

1GLO	A	VAL	54	H	-11.915713	10.440130	-17.061506	-5.124889
1GLO	A	ASP	55	H	-10.226063	6.946847	-16.431496	-5.234302
1GLO	A	CYS	56	H	-6.912666	6.309304	-11.854215	-4.871882
1GLO	A	SER	57	C	-6.868643	6.466886	-11.911912	-4.873079
1GLO	A	THR	58	C	-5.581713	7.325978	-9.740528	-4.757134
1GLO	A	GLU	59	G	-5.562721	7.349352	-9.828238	-4.778272
1GLO	A	LYS	60	G	-5.562267	7.351271	-9.831282	-4.778816
1GLO	A	TYR	61	G	-5.625896	7.470259	-9.604527	-4.768524
1GLO	A	GLY	62	C	-5.627428	7.448054	-9.612381	-4.771182
1GLO	A	ASN	63	C	-7.410020	7.353125	-13.277215	-5.394361
1GLO	A	LYS	64	C	-6.371440	3.669521	-12.691939	-4.852550
1GLO	A	GLY	65	G	-5.469587	4.080438	-11.800354	-5.037183
1GLO	A	CYS	66	G	-5.366214	4.300777	-11.809011	-5.031558
1GLO	A	ASN	67	G	-5.342601	4.473148	-11.789800	-5.041706
1GLO	A	GLY	68	C	-5.336378	4.545967	-11.779686	-5.046832
1GLO	A	GLY	69	C	-5.440337	4.772702	-11.626999	-5.091323
1GLO	A	PHE	70	C	-6.249521	6.447611	-11.837929	-5.097505
1GLO	A	MET	71	H	-6.985557	8.886740	-11.795065	-5.333427
1GLO	A	THR	72	H	-7.673244	9.929397	-12.086683	-5.413422
1GLO	A	THR	73	H	-8.480899	10.681965	-12.271668	-5.310076
1GLO	A	ALA	74	H	-10.330984	12.626701	-13.570657	-5.055615
1GLO	A	PHE	75	H	-11.382752	16.156038	-13.395369	-5.288773
1GLO	A	GLN	76	H	-12.168453	15.246362	-14.767273	-5.217959
1GLO	A	TYR	77	H	-13.167093	15.755791	-16.265069	-5.302486
1GLO	A	ILE	78	H	-9.979239	8.948875	-14.271547	-4.747556
1GLO	A	ILE	79	H	-8.873241	6.722008	-14.654121	-5.009762
1GLO	A	ASP	80	H	-8.513185	7.277305	-14.344912	-5.065973
1GLO	A	ASN	81	H	-8.505937	7.303098	-14.366476	-5.068990
1GLO	A	LYS	82	C	-8.499509	7.325444	-14.383323	-5.068740
1GLO	A	GLY	83	C	-8.548078	7.195143	-14.401936	-5.098550
1GLO	A	ILE	84	E	-8.941331	8.046197	-14.109458	-5.135992
1GLO	A	ASP	85	E	-10.406597	9.230303	-16.295687	-5.163212
1GLO	A	SER	86	B	-10.346807	10.083147	-15.759098	-5.177653
1GLO	A	ASP	87	G	-9.487444	10.071943	-14.123557	-5.213707
1GLO	A	ALA	88	G	-9.489562	10.111195	-14.095779	-5.213550
1GLO	A	SER	89	G	-9.494070	10.159922	-14.066686	-5.223352
1GLO	A	TYR	90	C	-9.512590	10.415521	-13.906057	-5.232855
1GLO	A	PRO	91	C	-8.548996	11.153733	-11.728858	-4.827502
1GLO	A	TYR	92	C	-8.540380	11.333012	-11.646768	-4.835218
1GLO	A	LYS	93	C	-7.531120	8.716140	-11.690836	-4.783162
1GLO	A	ALA	94	C	-7.183042	7.803243	-11.877698	-4.648687
1GLO	A	MET	95	C	-6.294908	6.186688	-11.363738	-4.626340
1GLO	A	ASP	96	C	-5.898979	5.937863	-11.149903	-4.589656
1GLO	A	LEU	97	C	-5.897103	5.946307	-11.155307	-4.590520
1GLO	A	LYS	98	C	-5.927781	5.829998	-11.131209	-4.581588
1GLO	A	CYS	99	C	-5.960235	5.783221	-11.076519	-4.587356
1GLO	A	GLN	100	C	-6.304417	5.836369	-10.972326	-4.562653
1GLO	A	TYR	101	C	-8.583265	9.490896	-13.625398	-5.160109
1GLO	A	ASP	102	C	-7.752308	8.701304	-12.104615	-4.912337
1GLO	A	SER	103	G	-7.604020	8.962813	-11.937512	-4.840136
1GLO	A	LYS	104	G	-7.558058	9.142796	-11.912024	-4.825624
1GLO	A	TYR	105	G	-7.561655	9.175695	-11.874359	-4.818798
1GLO	A	ARG	106	E	-7.581577	9.177261	-11.796981	-4.787454
1GLO	A	ALA	107	E	-7.901512	10.397547	-11.455921	-4.559723
1GLO	A	ALA	108	E	-7.838529	10.342508	-11.389407	-4.573350
1GLO	A	THR	109	C	-7.876931	10.394607	-11.396039	-4.610476
1GLO	A	CYS	110	C	-7.852824	10.420529	-11.467931	-4.644259
1GLO	A	SER	111	C	-7.300725	10.993817	-10.807636	-4.969794
1GLO	A	LYS	112	E	-7.102185	12.688849	-9.900241	-5.117099
1GLO	A	TYR	113	E	-7.077409	13.479183	-9.492169	-5.128881
1GLO	A	THR	114	E	-6.998109	13.459282	-9.451444	-5.059352
1GLO	A	GLU	115	E	-6.795306	13.225032	-9.320209	-4.963493
1GLO	A	LEU	116	C	-6.967020	13.859806	-8.962258	-4.879102
1GLO	A	PRO	117	T	-7.187336	13.243551	-9.163107	-4.735663
1GLO	A	TYR	118	T	-7.323158	12.766768	-9.275021	-4.708504
1GLO	A	GLY	119	T	-7.476292	12.500440	-9.313802	-4.726413
1GLO	A	ARG	120	T	-9.154081	10.521168	-12.601148	-4.414183
1GLO	A	GLU	121	H	-9.730370	7.943834	-14.947572	-4.755706
1GLO	A	ASP	122	H	-9.741542	7.915519	-14.947399	-4.760758
1GLO	A	VAL	123	H	-9.729321	8.143577	-14.822779	-4.738533
1GLO	A	LEU	124	H	-10.707781	11.959204	-14.508101	-4.679134
1GLO	A	LYS	125	H	-10.988858	12.548799	-14.626056	-4.740896
1GLO	A	GLU	126	H	-8.845148	10.143161	-11.224872	-3.943124
1GLO	A	ALA	127	H	-8.701230	10.259213	-11.397361	-3.994464
1GLO	A	VAL	128	H	-8.195534	10.121026	-11.521602	-4.355036
1GLO	A	ALA	129	H	-7.918406	10.449671	-11.373647	-4.469514
1GLO	A	ASN	130	H	-7.813887	10.711281	-11.309554	-4.488752
1GLO	A	LYS	131	H	-7.912721	10.890515	-11.362977	-4.607146
1GLO	A	GLY	132	C	-7.918388	11.019683	-11.277671	-4.597348
1GLO	A	PRO	133	C	-8.169239	11.629039	-11.080439	-4.565804
1GLO	A	VAL	134	E	-8.598002	12.483528	-11.014863	-4.375816

```
1GLO        A         SER            135                   E -9.136944 13.072333 -11.155964 -4.059907
1GLO        A         VAL            136                   E -9.196292 12.967674 -11.088625 -3.953809
1GLO        A         GLY            137                   E -9.360991 12.089265 -11.951662 -4.056357
1GLO        A         VAL            138                   E -9.372365 11.618583 -12.348688 -4.164207
1GLO        A         ASP            139                   C -9.090159  9.012687 -13.405120 -4.378358
1GLO        A         ALA            140                   C -8.432450  8.368694 -12.649212 -4.266890
1GLO        A         ARG            141                   C -8.438995  8.330242 -12.657128 -4.272650
1GLO        A         HIS            142                   C -8.469143  8.250173 -12.621527 -4.271866
1GLO        A         PRO            143                   H -8.445247  8.433118 -12.544601 -4.261138
1GLO        A         SER            144                   H -8.590961  8.546274 -12.295645 -4.226193
1GLO        A         PHE            145                   H -9.885019 12.147565 -12.214287 -4.303172
1GLO        A         PHE            146                   H -9.864101 11.945172 -12.238592 -4.225671
1GLO        A         LEU            147                   H -9.608736 10.820583 -12.786891 -4.208635
1GLO        A         TYR            148                   C -9.850542  9.935012 -13.632022 -4.229515
1GLO        A         ARG            149                   C -9.753104 10.158353 -13.649045 -4.270848
1GLO        A         SER            150                   C -8.812638 14.151945 -10.733609 -4.872772
1GLO        A         GLY            151                   C -8.779574 14.465478 -10.757410 -4.978681
1GLO        A         VAL            152                   C -8.737305 15.122021 -10.606851 -5.122108
1GLO        A         TYR            153                   B -8.705149 15.088105 -10.736554 -5.189107
1GLO        A         TYR            154                   C -6.643356  9.296359 -10.370530 -5.130116
1GLO        A         GLU            155                   T -6.557556  8.718937 -10.784367 -5.111956
1GLO        A         PRO            156                   T -6.555652  8.685698 -10.808260 -5.108833
1GLO        A         SER            157                   T -6.556172  8.646876 -10.823801 -5.107198
1GLO        A         CYS            158                   T -6.545070  8.609388 -10.879138 -5.101286
1GLO        A         THR            159                   C -7.545406  6.330727 -13.320911 -4.985888
1GLO        A         GLN            160                   C -8.505394  7.002844 -14.541215 -4.952988
1GLO        A         ASN            161                   C -8.288298  8.105054 -13.972137 -5.160035
1GLO        A         VAL            162                   C -8.293212  8.472262 -13.786384 -5.169738
1GLO        A         ASN            163                   C -8.596494  9.220786 -13.835635 -5.373918
1GLO        A         HIS            164                   E -8.719991  9.772524 -13.519768 -5.405482
1GLO        A         GLY            165                   E -8.573165 11.029793 -12.310213 -4.957603
1GLO        A         VAL            166                   E -8.883061 14.530441 -9.611970 -3.855087
1GLO        A         LEU            167                   E -8.959429 14.943563 -9.060747 -3.656045
1GLO        A         VAL            168                   E -8.897073 14.925018 -9.233684 -3.726516
1GLO        A         VAL            169                   E -8.886532 14.818368 -9.358259 -3.768865
1GLO        A         GLY            170                   E -9.193353 14.726143 -9.835228 -3.907058
1GLO        A         TYR            171                   E -8.938473 11.286111 -12.643868 -5.073164
1GLO        A         GLY            172                   E -4.020458  4.393729 -8.963276 -4.745210
1GLO        A         ASP            173                   E -3.419541  5.004555 -8.360963 -4.733720
1GLO        A         LEU            174                   E -3.407835  5.019830 -8.410560 -4.740457
1GLO        A         ASN            175                   T -3.407640  5.021278 -8.411992 -4.740748
1GLO        A         GLY            176                   T -3.407681  5.020886 -8.411686 -4.740716
1GLO        A         LYS            177                   E -3.669199  5.357676 -8.087803 -4.727557
1GLO        A         GLU            178                   E -5.732307  5.817005 -10.876350 -5.057772
1GLO        A         TYR            179                   E -8.159359  9.420359 -12.737366 -5.592898
1GLO        A         TRP            180                   E -12.390895 15.704051 -15.675837 -6.014978
1GLO        A         LEU            181                   E -13.693851 18.501469 -16.930877 -6.092197
1GLO        A         VAL            182                   E -13.674783 17.631590 -16.839383 -5.743278
1GLO        A         LYS            183                   E -13.443804 15.640889 -17.865844 -6.033548
1GLO        A         ASN            184                   C -12.336616 12.463228 -17.093246 -5.700073
1GLO        A         SER            185                   C -9.513699 10.332055 -13.454886 -5.141776
1GLO        A         TRP            186                   B -8.744118 12.208990 -11.674747 -4.973609
1GLO        A         GLY            187                   T -7.548126  8.934839 -11.523718 -4.788972
1GLO        A         HIS            188                   T -7.545992  8.935919 -11.539245 -4.790537
1GLO        A         ASN            189                   T -7.544952  8.935082 -11.548222 -4.791545
1GLO        A         PHE            190                   T -7.563463  8.887102 -11.499156 -4.780974
1GLO        A         GLY            191                   T -7.622093  8.449638 -11.576937 -4.770891
1GLO        A         GLU            192                   B -9.887915 10.078185 -15.476002 -5.331850
1GLO        A         GLU            193                   T -10.005618 10.323679 -15.382142 -5.355073
1GLO        A         GLY            194                   T -10.086907 10.532065 -15.189818 -5.348510
1GLO        A         TYR            195                   E -10.354916 11.124486 -15.036799 -5.425640
1GLO        A         ILE            196                   E -10.825120 13.110251 -13.977084 -5.291095
1GLO        A         ARG            197                   E -12.715044 16.041094 -14.956090 -5.358306
1GLO        A         MET            198                   E -14.180304 15.817008 -18.944180 -6.352144
1GLO        A         ALA            199                   E -11.171316  9.321346 -17.591777 -6.234295
1GLO        A         ARG            200                   T -11.130484  9.249928 -17.813063 -6.279387
1GLO        A         ASN            201                   T -10.912482  8.593240 -18.318818 -6.323452
1GLO        A         LYS            202                   T -10.774455  8.442791 -18.457674 -6.311118
1GLO        A         GLY            203                   T -10.523274  7.811293 -18.486279 -6.192597
1GLO        A         ASN            204                   T -10.703377  7.440813 -18.752584 -6.117117
1GLO        A         HIS            205                   G -10.397816  9.298988 -16.721111 -5.573492
1GLO        A         CYS            206                   G -9.937748  9.990948 -14.863758 -5.028278
1GLO        A         GLY            207                   G -9.800975 10.718924 -14.207096 -4.854502
1GLO        A         ILE            208                   T -9.801883 11.537456 -13.522510 -4.657895
1GLO        A         ALA            209                   T -9.778292 11.600154 -13.470329 -4.621682
1GLO        A         SER            210                   T -9.873509 11.551213 -13.370731 -4.579025
1GLO        A         PHE            211                   T -10.330819 13.079924 -12.762027 -4.382239
1GLO        A         PRO            212                   E -10.876812 13.815114 -12.599473 -4.168786
1GLO        A         SER            213                   E -11.387901 13.112165 -13.863875 -4.550304
1GLO        A         TYR            214                   E -9.779522 17.248812 -9.841490 -4.906971
1GLO        A         PRO            215                   E -9.779522 17.248812 -9.841490 -4.906971
```

1GLO	A	GLU	216	E	-9.779522	17.248812	-9.841490	-4.906971
1GLO	A	ILE	217	C	-9.779522	17.248812	-9.841490	-4.906971
1GNU	A	MET	1	C	-9.245012	10.999576	-11.646575	-4.299133
1GNU	A	LYS	2	C	-9.245012	10.999576	-11.646575	-4.299133
1GNU	A	PHE	3	C	-9.245012	10.999576	-11.646575	-4.299133
1GNU	A	VAL	4	H	-9.245012	10.999576	-11.646575	-4.299133
1GNU	A	TYR	5	H	-10.079799	13.726929	-13.845110	-6.277129
1GNU	A	LYS	6	H	-7.343931	8.739601	-11.874248	-5.422097
1GNU	A	GLU	7	H	-7.087092	9.291718	-11.582045	-5.305589
1GNU	A	GLU	8	H	-7.038366	9.297012	-11.674562	-5.296601
1GNU	A	HIS	9	C	-6.988948	9.185798	-11.794848	-5.271427
1GNU	A	PRO	10	C	-6.988744	9.164094	-11.800383	-5.266226
1GNU	A	PHE	11	H	-7.453500	9.729180	-11.736370	-5.090663
1GNU	A	GLU	12	H	-8.080227	8.638692	-13.040789	-5.090311
1GNU	A	LYS	13	H	-8.443305	8.029877	-13.283584	-5.004590
1GNU	A	ARG	14	H	-10.033203	9.702746	-14.729385	-5.313017
1GNU	A	ARG	15	H	-11.827585	9.801433	-17.618566	-5.295801
1GNU	A	SER	16	H	-10.083859	7.535664	-16.082421	-5.376862
1GNU	A	GLU	17	H	-9.498047	9.296977	-14.800784	-5.378091
1GNU	A	GLY	18	H	-9.486639	9.367075	-14.836806	-5.392853
1GNU	A	GLU	19	H	-9.472646	9.416608	-14.868723	-5.393961
1GNU	A	LYS	20	H	-9.447217	9.515609	-14.844505	-5.375367
1GNU	A	ILE	21	H	-9.656390	10.652622	-14.284084	-5.370548
1GNU	A	ARG	22	H	-10.150905	10.954521	-14.981532	-5.221241
1GNU	A	LYS	23	H	-7.197402	7.563461	-11.685248	-4.945992
1GNU	A	LYS	24	H	-7.076825	7.978686	-11.639309	-4.923950
1GNU	A	TYR	25	T	-7.068316	8.039089	-11.635877	-4.916653
1GNU	A	PRO	26	T	-7.058078	8.113977	-11.615012	-4.897265
1GNU	A	ASP	27	T	-7.058089	8.129259	-11.601303	-4.892923
1GNU	A	ARG	28	E	-7.966252	10.323063	-11.357126	-4.696846
1GNU	A	VAL	29	E	-8.873788	13.746433	-10.219864	-3.892881
1GNU	A	PRO	30	E	-9.094187	14.532472	-9.582687	-3.636653
1GNU	A	VAL	31	E	-9.560777	17.067453	-8.460988	-3.413662
1GNU	A	ILE	32	E	-9.690683	17.625303	-8.045981	-3.360325
1GNU	A	VAL	33	E	-9.688556	17.095217	-8.590521	-3.550020
1GNU	A	GLU	34	E	-9.467087	9.874442	-14.159781	-5.143539
1GNU	A	LYS	35	E	-6.915207	7.651206	-10.404315	-4.238344
1GNU	A	ALA	36	T	-5.504041	5.395397	-8.796492	-3.350268
1GNU	A	PRO	37	T	-5.034898	6.643388	-7.899177	-3.328298
1GNU	A	LYS	38	T	-4.645125	7.193542	-7.578821	-3.520784
1GNU	A	ALA	39	T	-4.607991	7.299536	-7.653578	-3.564542
1GNU	A	ARG	40	C	-4.581214	7.497737	-7.625883	-3.600125
1GNU	A	ILE	41	C	-4.696124	8.090484	-7.434680	-3.703344
1GNU	A	GLY	42	C	-4.910265	8.268343	-7.600669	-3.890045
1GNU	A	ASP	43	C	-5.739345	9.753555	-8.743079	-4.393611
1GNU	A	LEU	44	T	-6.052889	10.326554	-8.690437	-4.500451
1GNU	A	ASP	45	T	-6.897267	9.716721	-10.773883	-5.057122
1GNU	A	LYS	46	T	-7.714159	7.795713	-13.004043	-5.358943
1GNU	A	LYS	47	T	-9.111107	9.915445	-14.277513	-5.701632
1GNU	A	LYS	48	E	-10.127606	12.020922	-14.886737	-5.812395
1GNU	A	TYR	49	E	-10.831300	15.493100	-13.937432	-5.445811
1GNU	A	LEU	50	E	-9.153587	11.553379	-11.414563	-4.269578
1GNU	A	VAL	51	E	-8.230525	10.888060	-10.630943	-4.155947
1GNU	A	PRO	52	E	-7.957698	10.660199	-10.965765	-4.331714
1GNU	A	SER	53	T	-7.934287	10.695164	-11.019431	-4.341776
1GNU	A	ASP	54	T	-7.821976	10.752534	-11.129406	-4.406824
1GNU	A	LEU	55	T	-7.838642	10.666003	-11.198184	-4.425876
1GNU	A	THR	56	B	-8.131504	10.727534	-11.724679	-4.630483
1GNU	A	VAL	57	H	-8.538104	11.155625	-11.902093	-4.625166
1GNU	A	GLY	58	H	-8.607981	11.086896	-11.846309	-4.629047
1GNU	A	GLN	59	H	-9.235965	11.156572	-12.197771	-4.461464
1GNU	A	PHE	60	H	-10.134534	14.163980	-11.939208	-4.751154
1GNU	A	TYR	61	H	-11.778661	17.791932	-13.697094	-5.379885
1GNU	A	PHE	62	H	-11.126008	13.329738	-14.068719	-4.711114
1GNU	A	LEU	63	H	-11.207360	12.738234	-14.108452	-4.540806
1GNU	A	ILE	64	H	-11.224943	12.582358	-14.122638	-4.518578
1GNU	A	ARG	65	H	-11.054949	11.788521	-14.733806	-4.643317
1GNU	A	LYS	66	H	-8.188293	11.844260	-9.934462	-4.333767
1GNU	A	ARG	67	H	-8.094228	11.812356	-10.083033	-4.300030
1GNU	A	ILE	68	H	-7.074953	9.660786	-9.393877	-3.847211
1GNU	A	HIS	69	C	-5.977743	6.660476	-9.638324	-3.924193
1GNU	A	LEU	70	C	-5.645302	6.398158	-9.845463	-4.039754
1GNU	A	ARG	71	T	-4.704142	5.178919	-8.931276	-3.946074
1GNU	A	ALA	72	T	-4.694896	5.246122	-8.951710	-3.958892
1GNU	A	GLU	73	T	-4.703491	5.189941	-8.948353	-3.962473
1GNU	A	ASP	74	T	-4.764728	5.090333	-8.867668	-3.964811
1GNU	A	ALA	75	C	-4.825312	4.986749	-8.732254	-3.939992
1GNU	A	LEU	76	C	-7.131959	9.664242	-10.305155	-4.760073
1GNU	A	PHE	77	E	-9.338945	13.085122	-11.776074	-5.127418
1GNU	A	PHE	78	E	-12.206443	19.433879	-12.484474	-5.138838
1GNU	A	PHE	79	E	-10.337633	11.832156	-13.001152	-4.519571

1GNU	A	VAL	80	B	-7.339308	9.193091	-9.979749	-4.150670
1GNU	A	ASN	81	T	-7.203118	9.316877	-10.095396	-4.131041
1GNU	A	ASN	82	T	-6.925508	9.407878	-9.730286	-3.889208
1GNU	A	VAL	83	B	-5.942268	9.892478	-7.175465	-3.279542
1GNU	A	ILE	84	C	-5.619111	10.037704	-6.906895	-3.219656
1GNU	A	PRO	85	C	-5.438071	9.884793	-6.838320	-3.181180
1GNU	A	PRO	86	T	-5.329628	9.489200	-7.191240	-3.278224
1GNU	A	THR	87	T	-5.343876	9.489851	-7.148595	-3.274915
1GNU	A	SER	88	T	-5.550679	9.273511	-7.391281	-3.333464
1GNU	A	ALA	89	T	-5.828734	8.694647	-7.903847	-3.451232
1GNU	A	THR	90	B	-6.351708	7.670726	-9.070540	-3.786996
1GNU	A	MET	91	H	-8.943923	10.851913	-12.578372	-4.706064
1GNU	A	GLY	92	H	-9.625771	10.374210	-14.238271	-5.006003
1GNU	A	GLN	93	H	-9.991909	10.858248	-14.504998	-5.136949
1GNU	A	LEU	94	H	-10.430277	12.940803	-14.034000	-5.315950
1GNU	A	TYR	95	H	-10.973534	13.556011	-15.076742	-5.520692
1GNU	A	GLN	96	H	-10.665014	11.841663	-15.733854	-5.560480
1GNU	A	GLU	97	H	-10.135238	10.375858	-15.519943	-5.523551
1GNU	A	HIS	98	H	-10.161830	10.169411	-15.580014	-5.527774
1GNU	A	HIS	99	C	-10.125790	10.109010	-15.669760	-5.539636
1GNU	A	GLU	100	T	-10.194435	9.778555	-15.751992	-5.542034
1GNU	A	GLU	101	T	-10.313956	9.894411	-15.532903	-5.523303
1GNU	A	ASP	102	T	-11.507841	11.464966	-16.472867	-5.660007
1GNU	A	PHE	103	T	-11.556250	11.553325	-16.279774	-5.642512
1GNU	A	PHE	104	C	-13.067640	19.485551	-14.537311	-5.490008
1GNU	A	LEU	105	E	-13.333752	21.625406	-13.217438	-5.152704
1GNU	A	TYR	106	E	-13.762984	23.678186	-12.275434	-4.874538
1GNU	A	ILE	107	E	-13.560141	21.937143	-13.180692	-4.910399
1GNU	A	ALA	108	E	-12.466332	15.963361	-14.769854	-5.172876
1GNU	A	TYR	109	E	-11.808352	15.646762	-14.713021	-5.494647
1GNU	A	SER	110	E	-9.615898	15.727669	-13.655526	-7.343045
1GNU	A	ASP	111	C	-7.466888	13.278772	-11.127182	-6.531472
1GNU	A	GLU	112	C	-5.610431	11.024941	-8.456852	-5.361950
1GNU	A	SER	113	C	-4.836847	10.263930	-7.316012	-4.671159
1GNU	A	VAL	114	C	-3.967637	8.571632	-6.061574	-3.839916
1GNU	A	TYR	115	C	-3.967637	8.571632	-6.061574	-3.839916
1GNU	A	GLY	116	C	-3.967637	8.571632	-6.061574	-3.839916
1GNU	A	LEU	117	C	-3.967637	8.571632	-6.061574	-3.839916
1GP0	A	ASP	1515	C	-8.232721	6.764177	-13.008861	-4.349732
1GP0	A	CYS	1516	C	-8.232721	6.764177	-13.008861	-4.349732
1GP0	A	GLN	1517	E	-8.232721	6.764177	-13.008861	-4.349732
1GP0	A	VAL	1518	E	-8.232721	6.764177	-13.008861	-4.349732
1GP0	A	THR	1519	E	-5.958181	5.737613	-10.053874	-4.265383
1GP0	A	ASN	1520	T	-4.675063	3.488235	-10.051409	-4.439953
1GP0	A	PRO	1521	T	-4.576875	3.583430	-10.140548	-4.422807
1GP0	A	SER	1522	T	-4.544319	3.747620	-10.166351	-4.440079
1GP0	A	THR	1523	T	-4.543792	3.754605	-10.167571	-4.440628
1GP0	A	GLY	1524	T	-4.600463	3.557907	-10.180785	-4.458432
1GP0	A	HIS	1525	C	-5.501172	4.830822	-10.630127	-4.440599
1GP0	A	LEU	1526	E	-6.268828	6.745492	-10.635292	-4.748324
1GP0	A	PHE	1527	E	-8.623989	11.684459	-11.737859	-5.079384
1GP0	A	ASP	1528	E	-9.356211	11.862386	-12.529919	-4.799894
1GP0	A	LEU	1529	C	-9.422884	11.936997	-12.037052	-4.403022
1GP0	A	SER	1530	G	-8.902857	9.133318	-12.895126	-4.348919
1GP0	A	SER	1531	G	-8.886369	9.083850	-12.966563	-4.348010
1GP0	A	LEU	1532	G	-8.868893	9.049356	-13.035418	-4.350817
1GP0	A	SER	1533	B	-8.096888	5.598341	-13.798783	-4.576151
1GP0	A	GLY	1534	T	-8.065510	5.553589	-13.883856	-4.591541
1GP0	A	ARG	1535	T	-8.144319	5.391946	-13.941261	-4.638232
1GP0	A	ALA	1536	T	-8.057401	6.120402	-13.632371	-4.609497
1GP0	A	GLY	1537	T	-8.044145	6.264980	-13.594067	-4.608562
1GP0	A	PHE	1538	E	-8.810198	9.899222	-12.747138	-4.527276
1GP0	A	THR	1539	E	-8.808250	12.021186	-12.577674	-5.141487
1GP0	A	ALA	1540	E	-7.662083	9.789833	-10.416857	-4.182242
1GP0	A	ALA	1541	E	-4.968619	6.655455	-7.787752	-3.849014
1GP0	A	TYR	1542	E	-3.611570	5.888580	-7.096209	-4.170717
1GP0	A	SER	1543	T	-3.042893	4.873840	-7.084929	-4.032485
1GP0	A	GLU	1544	T	-3.015728	4.974250	-7.098586	-4.023912
1GP0	A	LYS	1545	T	-3.015885	4.973273	-7.097781	-4.023928
1GP0	A	GLY	1546	E	-3.038290	4.907392	-7.068942	-4.028960
1GP0	A	LEU	1547	E	-3.288121	4.421586	-7.068520	-3.920560
1GP0	A	VAL	1548	E	-4.861211	7.069602	-7.314387	-3.796204
1GP0	A	TYR	1549	E	-8.623164	12.282064	-10.269391	-4.419535
1GP0	A	MET	1550	E	-10.940733	12.134866	-15.053160	-5.478022
1GP0	A	SER	1551	T	-10.238639	10.217185	-15.229756	-5.475195
1GP0	A	ILE	1552	B	-9.952811	10.120216	-15.482335	-5.662170
1GP0	A	CYS	1553	T	-9.876305	9.844213	-15.828521	-5.752785
1GP0	A	GLY	1554	T	-9.866779	9.790570	-15.902451	-5.764989
1GP0	A	GLU	1555	C	-9.948596	9.523495	-16.070187	-5.819390
1GP0	A	ASN	1556	T	-10.226473	9.226744	-16.866564	-6.065593
1GP0	A	GLU	1557	T	-8.933186	6.896430	-14.370495	-4.970085

1GP0	A	ASN	1558	T	-8.110077	5.818395	-13.963833	-4.824792
1GP0	A	CYS	1559	T	-5.708848	5.920551	-9.454719	-4.090346
1GP0	A	PRO	1560	T	-4.787319	6.364769	-8.167283	-3.934016
1GP0	A	PRO	1561	T	-4.743402	6.466586	-8.226251	-3.934578
1GP0	A	GLY	1562	T	-4.742583	6.470069	-8.230405	-3.935262
1GP0	A	VAL	1563	E	-4.744105	6.472691	-8.215894	-3.933056
1GP0	A	GLY	1564	E	-4.871017	6.604330	-7.938577	-3.898217
1GP0	A	ALA	1565	E	-6.286698	7.814457	-9.104117	-3.963059
1GP0	A	CYS	1566	E	-7.744098	9.444291	-11.729075	-4.788317
1GP0	A	PHE	1567	E	-7.749154	10.240031	-11.288675	-4.763650
1GP0	A	GLY	1568	T	-5.926674	5.736279	-9.947315	-4.062481
1GP0	A	GLN	1569	T	-5.914299	5.763895	-9.987424	-4.063699
1GP0	A	THR	1570	T	-5.913767	5.765365	-9.989187	-4.062972
1GP0	A	ARG	1571	T	-5.930124	5.647285	-9.953103	-4.039556
1GP0	A	ILE	1572	C	-5.937329	5.587480	-9.943538	-4.033103
1GP0	A	SER	1573	E	-8.018539	7.992396	-12.023226	-4.186939
1GP0	A	VAL	1574	E	-8.828804	10.104058	-12.429849	-4.300232
1GP0	A	GLY	1575	E	-8.962836	9.965861	-12.794522	-4.453052
1GP0	A	LYS	1576	E	-8.973402	9.892052	-12.828555	-4.464497
1GP0	A	ALA	1577	C	-9.515969	9.177811	-14.299086	-4.594680
1GP0	A	ASN	1578	C	-9.852670	8.108299	-15.596059	-4.872645
1GP0	A	LYS	1579	T	-10.024204	7.917785	-15.787466	-4.941464
1GP0	A	ARG	1580	T	-10.551919	9.211520	-15.617983	-4.847631
1GP0	A	LEU	1581	T	-10.117364	12.137230	-12.935134	-4.488965
1GP0	A	ARG	1582	E	-8.807408	9.209978	-12.116787	-4.254529
1GP0	A	TYR	1583	E	-5.703834	9.086530	-7.740413	-4.064932
1GP0	A	VAL	1584	E	-5.435910	8.964267	-7.764323	-3.931950
1GP0	A	ASP	1585	T	-5.435566	8.965725	-7.766901	-3.932238
1GP0	A	GLN	1586	T	-5.435708	8.964714	-7.765928	-3.932148
1GP0	A	VAL	1587	E	-5.437556	8.964974	-7.752341	-3.931158
1GP0	A	LEU	1588	E	-6.034152	8.753802	-7.812350	-3.700025
1GP0	A	GLN	1589	E	-9.839299	11.545511	-12.238816	-4.428454
1GP0	A	LEU	1590	E	-12.103104	15.210498	-14.620376	-4.848134
1GP0	A	VAL	1591	E	-9.947464	12.154726	-13.448474	-5.483943
1GP0	A	TYR	1592	E	-9.616534	12.277852	-13.606734	-5.615729
1GP0	A	LYS	1593	E	-6.162546	6.541326	-10.897063	-5.022687
1GP0	A	ASP	1594	E	-5.996518	6.548268	-11.128190	-5.051826
1GP0	A	GLY	1595	E	-5.835884	6.149457	-11.222250	-4.882314
1GP0	A	SER	1596	E	-5.799681	6.122064	-11.285539	-4.860201
1GP0	A	PRO	1597	E	-5.779647	6.135137	-11.334474	-4.861108
1GP0	A	CYS	1598	T	-6.171911	5.725183	-11.889525	-4.684518
1GP0	A	PRO	1599	T	-5.215623	4.842251	-10.152979	-4.422470
1GP0	A	SER	1600	T	-5.166861	4.937056	-10.170902	-4.449190
1GP0	A	LYS	1601	T	-5.005076	5.158666	-10.068772	-4.422514
1GP0	A	SER	1602	T	-4.998696	5.259252	-10.026674	-4.416312
1GP0	A	GLY	1603	T	-5.004493	5.256724	-9.999301	-4.414094
1GP0	A	LEU	1604	T	-5.557399	6.006680	-10.179119	-4.409412
1GP0	A	SER	1605	E	-5.769685	6.240583	-9.849830	-4.347947
1GP0	A	TYR	1606	E	-7.307853	10.989377	-9.240963	-4.350473
1GP0	A	LYS	1607	E	-9.485667	13.837630	-11.544790	-5.171630
1GP0	A	SER	1608	E	-12.421806	16.133036	-14.855414	-5.039429
1GP0	A	VAL	1609	E	-12.168429	16.938535	-13.704829	-4.705386
1GP0	A	ILE	1610	E	-11.421490	16.213016	-12.585923	-4.543313
1GP0	A	SER	1611	E	-11.352337	16.052537	-12.839003	-4.593902
1GP0	A	PHE	1612	E	-9.562220	15.533375	-13.063339	-6.519454
1GP0	A	VAL	1613	E	-6.571245	8.190630	-11.309163	-5.242402
1GP0	A	CYS	1614	E	-5.634960	7.108578	-9.378118	-4.194540
1GP0	A	ARG	1615	T	-4.496812	6.752926	-7.491111	-3.857252
1GP0	A	PRO	1616	T	-3.222876	4.894147	-6.703084	-3.813547
1GP0	A	GLU	1617	T	-2.554316	5.361509	-6.191083	-4.036749
1GP0	A	ALA	1618	T	-2.326354	5.386156	-6.357785	-4.156327
1GP0	A	GLY	1619	T	-2.319791	5.390433	-6.386687	-4.162211
1GP0	A	PRO	1620	T	-2.333002	5.357726	-6.364661	-4.166993
1GP0	A	THR	1621	T	-2.467211	5.496982	-6.258395	-4.226423
1GP0	A	ASN	1622	T	-2.990306	5.335022	-6.662125	-4.312339
1GP0	A	ARG	1623	C	-4.848299	5.966905	-8.800542	-4.396952
1GP0	A	PRO	1624	C	-6.812812	9.689431	-9.742725	-4.313327
1GP0	A	MET	1625	E	-7.132918	11.381486	-9.260014	-4.270297
1GP0	A	LEU	1626	E	-7.079962	11.543648	-8.820698	-4.036535
1GP0	A	ILE	1627	E	-6.585951	10.031138	-9.409462	-4.253286
1GP0	A	SER	1628	E	-6.574886	9.958735	-9.497477	-4.269600
1GP0	A	LEU	1629	E	-6.522049	9.652841	-9.841055	-4.399667
1GP0	A	ASP	1630	E	-6.686826	8.968745	-10.446122	-4.560982
1GP0	A	LYS	1631	T	-6.743497	8.627655	-10.591749	-4.599667
1GP0	A	GLN	1632	T	-7.535721	7.942885	-12.647602	-5.101054
1GP0	A	THR	1633	T	-7.613837	7.942806	-12.555775	-5.124591
1GP0	A	CYS	1634	T	-8.695510	7.570977	-14.874124	-5.571721
1GP0	A	THR	1635	E	-9.490723	10.059196	-14.704178	-5.690286
1GP0	A	LEU	1636	E	-10.404929	13.160700	-13.815617	-5.308938
1GP0	A	PHE	1637	E	-10.900031	14.862687	-12.879984	-5.145894
1GP0	A	PHE	1638	E	-12.886669	19.381680	-13.633278	-5.393115

```
1GP0        A          SER          1639                   E -13.075591 17.529586 -14.784750 -5.230327
1GP0        A          TRP          1640                   E -13.134937 17.277156 -14.787123 -5.222454
1GP0        A          HIS          1641                   E -12.088920 16.819090 -15.626749 -6.668113
1GP0        A          THR          1642                   E -10.096380 13.420443 -13.359094 -5.716065
1GP0        A          PRO          1643                   G -8.726631 10.769453 -11.931877 -4.789719
1GP0        A          LEU          1644                   G -8.027353  9.358844 -11.387657 -4.293066
1GP0        A          ALA          1645                   G -8.027353  9.358844 -11.387657 -4.293066
1GP0        A          CYS          1646                   C -8.027353  9.358844 -11.387657 -4.293066
1GP0        A          GLU          1647                   C -8.027353  9.358844 -11.387657 -4.293066
1GQV        A          MET             0                   C -7.627094  7.939531 -11.120989 -4.092088
1GQV        A          LYS             1                   C -7.627094  7.939531 -11.120989 -4.092088
1GQV        A          PRO             2                   T -7.627094  7.939531 -11.120989 -4.092088
1GQV        A          PRO             3                   T -7.627094  7.939531 -11.120989 -4.092088
1GQV        A          GLN             4                   T -9.169941  9.259297 -13.768118 -5.176534
1GQV        A          PHE             5                   T -10.964551 14.328657 -15.100362 -6.255950
1GQV        A          THR             6                   C -11.910438 16.105866 -15.004208 -5.831143
1GQV        A          TRP             7                   H -11.980609 16.127794 -14.572499 -5.602934
1GQV        A          ALA             8                   H -11.985578 16.112709 -14.520784 -5.575889
1GQV        A          GLN             9                   H -13.155545 16.504773 -16.195610 -5.680090
1GQV        A          TRP            10                   H -13.545407 17.482498 -16.075767 -5.810681
1GQV        A          PHE            11                   H -14.835418 20.061818 -17.459846 -6.109351
1GQV        A          GLU            12                   H -14.864860 19.653918 -17.738359 -6.158463
1GQV        A          THR            13                   H -14.355030 16.238623 -18.481307 -6.006666
1GQV        A          GLN            14                   H -14.069983 15.495964 -18.644480 -6.058893
1GQV        A          HIS            15                   H -10.664984 13.663293 -13.428904 -5.335565
1GQV        A          ILE            16                   H -8.542105 11.856872 -11.305345 -5.009784
1GQV        A          ASN            17                   T -7.539314  9.412340 -11.648245 -5.058048
1GQV        A          MET            18                   T -7.474417  9.341630 -11.857210 -5.089377
1GQV        A          THR            19                   T -7.445763  9.183520 -12.036058 -5.101377
1GQV        A          SER            20                   T -7.448054  9.162706 -12.033630 -5.100676
1GQV        A          GLN            21                   T -7.543787  8.674689 -12.205348 -5.123567
1GQV        A          GLN            22                   C -8.565200  7.815489 -14.435037 -5.377916
1GQV        A          CYS            23                   H -9.191339  6.109935 -15.903127 -5.415190
1GQV        A          THR            24                   H -10.529373  7.272880 -18.179678 -6.048315
1GQV        A          ASN            25                   H -10.535291  7.681479 -17.951922 -6.042251
1GQV        A          ALA            26                   H -11.331751 10.996257 -17.480014 -5.833906
1GQV        A          MET            27                   H -11.501600 12.162507 -16.915607 -5.752199
1GQV        A          GLN            28                   H -11.619188 12.230259 -16.764928 -5.628316
1GQV        A          VAL            29                   H -11.589070 12.632129 -16.426744 -5.553479
1GQV        A          ILE            30                   H -11.976986 13.539854 -16.290384 -5.495400
1GQV        A          ASN            31                   H -12.166022 12.990701 -16.987084 -5.699155
1GQV        A          ASN            32                   H -11.538851 13.016446 -15.802614 -5.572048
1GQV        A          TYR            33                   H -11.279063 13.373224 -15.526182 -5.602667
1GQV        A          GLN            34                   H -11.329705 13.198874 -15.628248 -5.624436
1GQV        A          ARG            35                   C -10.928382 10.959759 -16.355060 -5.548545
1GQV        A          ARG            36                   C -10.002261  9.131112 -16.159596 -5.835935
1GQV        A          CYS            37                   C -9.994172  8.822110 -16.411404 -5.896439
1GQV        A          LYS            38                   C -9.956901  8.653289 -16.613057 -5.953586
1GQV        A          ASN            39                   C -9.958630  8.656056 -16.604691 -5.954245
1GQV        A          GLN            40                   E -10.018197  8.658017 -16.551705 -6.005479
1GQV        A          ASN            41                   E -11.014863  8.683265 -18.458236 -6.410101
1GQV        A          THR            42                   E -11.149885 11.398448 -16.707998 -6.096820
1GQV        A          PHE            43                   E -10.921094 17.045703 -11.777935 -4.890581
1GQV        A          LEU            44                   E -10.417582 17.691254 -11.008663 -4.852405
1GQV        A          LEU            45                   C -9.707249 15.124433 -11.227355 -4.676440
1GQV        A          THR            46                   C -9.021563 12.748769 -11.631432 -4.691457
1GQV        A          THR            47                   C -8.890028 12.556890 -11.693729 -4.615741
1GQV        A          PHE            48                   H -8.903597 12.447222 -11.706412 -4.608853
1GQV        A          ALA            49                   H -8.718296 10.829618 -12.212120 -4.420892
1GQV        A          ASN            50                   H -8.746738 10.236906 -12.443979 -4.356133
1GQV        A          VAL            51                   H -9.050013  9.192762 -12.962858 -4.086778
1GQV        A          VAL            52                   H -8.380269  7.120770 -13.055686 -4.233366
1GQV        A          ASN            53                   H -7.848314  6.335610 -13.418756 -4.586039
1GQV        A          VAL            54                   H -7.684783  5.808858 -13.622736 -4.585824
1GQV        A          CYS            55                   H -6.902819  4.511975 -13.560931 -4.959291
1GQV        A          GLY            56                   H -6.749562  4.578917 -13.595533 -4.969516
1GQV        A          ASN            57                   C -6.736184  4.674006 -13.600678 -5.004200
1GQV        A          PRO            58                   C -6.627600  5.458160 -13.174440 -5.044371
1GQV        A          ASN            59                   E -6.629409  5.715952 -13.087364 -5.083122
1GQV        A          MET            60                   E -6.970787  7.247638 -12.725600 -5.087272
1GQV        A          THR            61                   C -7.138712  8.366792 -12.388777 -5.146523
1GQV        A          CYS            62                   T -6.741796  7.705473 -12.233413 -5.236683
1GQV        A          PRO            63                   T -4.656884  6.417781 -8.783533 -4.717920
1GQV        A          SER            64                   T -4.523251  6.073227 -9.147777 -4.713587
1GQV        A          ASN            65                   T -4.375719  5.963052 -9.309385 -4.707394
1GQV        A          LYS            66                   T -4.375383  5.961252 -9.312273 -4.707346
1GQV        A          THR            67                   T -4.381504  5.949666 -9.282138 -4.701229
1GQV        A          ARG            68                   T -4.947681  5.232983 -10.195677 -4.690570
1GQV        A          LYS            69                   C -5.266188  5.580693 -9.911824 -4.685314
1GQV        A          ASN            70                   C -8.163991  6.000894 -13.939706 -5.049558
1GQV        A          CYS            71                   E -10.478674  6.262663 -17.434299 -5.459153
```

1GQV	A	HIS	72	E	-10.905936	8.294594	-16.678059	-5.183528
1GQV	A	HIS	73	E	-8.434303	8.367825	-12.992052	-5.022682
1GQV	A	SER	74	T	-7.479082	8.348309	-11.668491	-4.688833
1GQV	A	GLY	75	T	-7.226462	8.087723	-11.600832	-4.505955
1GQV	A	SER	76	T	-7.225064	8.096998	-11.602767	-4.504632
1GQV	A	GLN	77	C	-7.225668	8.101579	-11.595277	-4.503561
1GQV	A	VAL	78	E	-7.306827	8.062474	-11.398724	-4.427698
1GQV	A	PRO	79	E	-7.847549	7.644192	-11.488761	-4.162409
1GQV	A	LEU	80	E	-10.588402	12.384943	-13.064925	-4.214257
1GQV	A	ILE	81	E	-11.437877	14.691220	-13.257539	-4.521740
1GQV	A	HIS	82	E	-11.587341	10.909395	-16.862432	-5.555875
1GQV	A	CYS	83	E	-9.671248	9.877360	-14.218647	-5.296045
1GQV	A	ASN	84	E	-7.230940	8.510229	-10.837938	-4.614105
1GQV	A	LEU	85	E	-6.243787	8.733545	-9.527273	-4.428824
1GQV	A	THR	86	E	-5.788807	7.798193	-9.618782	-4.320761
1GQV	A	THR	87	E	-5.484485	6.825963	-9.811150	-4.197858
1GQV	A	PRO	88	T	-5.158098	5.627567	-10.154659	-4.206321
1GQV	A	SER	89	T	-5.150360	5.537815	-10.206555	-4.202705
1GQV	A	PRO	90	T	-5.226635	5.065945	-10.372642	-4.177058
1GQV	A	GLN	91	T	-5.361634	4.568421	-10.567686	-4.167800
1GQV	A	ASN	92	T	-5.594601	4.181430	-10.804978	-4.244548
1GQV	A	ILE	93	G	-6.878434	5.579609	-12.212136	-4.450288
1GQV	A	SER	94	G	-7.781511	5.899349	-13.643310	-4.647651
1GQV	A	ASN	95	G	-8.357968	6.179484	-14.773850	-5.150121
1GQV	A	CYS	96	C	-9.188961	7.135017	-15.711112	-5.573418
1GQV	A	ARG	97	E	-10.447010	9.918364	-16.284515	-5.677486
1GQV	A	TYR	98	E	-9.691147	11.408449	-13.083080	-4.973279
1GQV	A	ALA	99	E	-7.621445	6.443096	-11.906429	-4.175277
1GQV	A	GLN	100	E	-6.928679	6.763879	-11.586298	-4.441360
1GQV	A	THR	101	E	-6.584957	7.133579	-11.119340	-4.340374
1GQV	A	PRO	102	E	-6.578531	7.180336	-11.126622	-4.343353
1GQV	A	ALA	103	E	-6.581459	7.159892	-11.117847	-4.340433
1GQV	A	ASN	104	E	-6.690200	7.335196	-10.965894	-4.378572
1GQV	A	MET	105	E	-7.056445	7.699329	-10.557565	-4.222068
1GQV	A	PHE	106	C	-9.254541	11.509293	-11.836810	-4.626740
1GQV	A	TYR	107	E	-12.384356	17.477859	-14.529934	-5.353600
1GQV	A	ILE	108	E	-11.785998	12.770091	-14.818513	-4.576081
1GQV	A	VAL	109	E	-10.181151	9.053883	-14.311894	-4.473928
1GQV	A	ALA	110	E	-10.160713	9.035332	-14.431616	-4.498745
1GQV	A	CYS	111	E	-10.142437	8.965186	-14.582497	-4.535416
1GQV	A	ASP	112	E	-10.033566	8.505652	-15.105765	-4.658289
1GQV	A	ASN	113	E	-8.202318	5.917260	-13.363633	-4.466472
1GQV	A	ARG	114	C	-8.211381	5.815256	-13.387644	-4.465812
1GQV	A	ASP	115	T	-8.196312	5.808104	-13.468184	-4.476262
1GQV	A	GLN	116	T	-8.186521	5.796862	-13.516405	-4.474454
1GQV	A	ARG	117	T	-8.134573	5.743266	-13.599524	-4.429812
1GQV	A	ARG	118	T	-9.137427	5.603525	-15.501921	-4.377253
1GQV	A	ASP	119	T	-7.396148	9.231306	-10.750904	-4.578783
1GQV	A	PRO	120	T	-5.650492	8.424113	-8.108208	-3.963169
1GQV	A	PRO	121	T	-5.408615	8.693696	-8.094777	-3.970694
1GQV	A	GLN	122	T	-5.395891	8.770193	-8.100386	-3.970143
1GQV	A	TYR	123	T	-5.395800	8.774304	-8.098401	-3.969759
1GQV	A	PRO	124	T	-5.414286	8.761748	-8.018263	-3.947357
1GQV	A	VAL	125	E	-6.012568	9.437578	-8.112978	-3.977389
1GQV	A	VAL	126	E	-7.573143	12.283932	-8.668114	-3.869526
1GQV	A	PRO	127	E	-8.796041	14.179582	-9.033705	-3.330175
1GQV	A	VAL	128	E	-8.899490	14.010038	-8.914130	-3.240374
1GQV	A	HIS	129	E	-9.534623	14.898434	-9.659181	-3.559585
1GQV	A	LEU	130	E	-9.728931	15.760676	-10.289855	-4.184438
1GQV	A	ASP	131	E	-8.365172	11.211061	-10.025271	-3.884611
1GQV	A	ARG	132	E	-8.365172	11.211061	-10.025271	-3.884611
1GQV	A	ILE	133	E	-8.365172	11.211061	-10.025271	-3.884611
1GQV	A	ILE	134	C	-8.365172	11.211061	-10.025271	-3.884611
1GSM	A	VAL	1	C	-5.739952	6.235785	-5.167111	-1.381939
1GSM	A	LYS	2	T	-5.739952	6.235785	-5.167111	-1.381939
1GSM	A	PRO	3	T	-5.739952	6.235785	-5.167111	-1.381939
1GSM	A	LEU	4	E	-5.739952	6.235785	-5.167111	-1.381939
1GSM	A	GLN	5	E	-6.859402	6.824061	-7.291328	-2.205021
1GSM	A	VAL	6	E	-8.019292	9.259200	-8.493183	-2.627740
1GSM	A	GLU	7	E	-8.253649	7.392608	-9.166647	-2.152602
1GSM	A	PRO	8	T	-7.264755	7.999449	-8.960446	-2.951137
1GSM	A	PRO	9	T	-6.990734	7.862831	-8.106264	-2.410503
1GSM	A	GLU	10	T	-6.953300	7.978081	-8.019709	-2.356148
1GSM	A	PRO	11	T	-6.966513	8.152120	-7.891358	-2.330519
1GSM	A	VAL	12	E	-6.981393	8.339531	-7.773080	-2.332904
1GSM	A	VAL	13	E	-7.385120	8.667269	-6.627773	-1.540563
1GSM	A	ALA	14	E	-7.882666	11.270033	-6.550701	-1.755979
1GSM	A	VAL	15	E	-7.660376	9.978467	-6.800444	-1.767349
1GSM	A	ALA	16	E	-7.207495	7.783568	-7.450434	-1.939293
1GSM	A	LEU	17	T	-7.216536	7.667753	-7.494986	-1.948884
1GSM	A	GLY	18	T	-7.220206	7.555762	-7.544527	-1.953100

```
1GSM        A          ALA            19                  b -7.292626  7.089571 -7.677430 -1.957812
1GSM        A          SER            20                  C -7.488115  6.666453 -7.885062 -2.060122
1GSM        A          ARG            21                  E -9.612685  9.204115 -12.527509 -3.763431
1GSM        A          GLN            22                  E -9.844524  9.196272 -13.491906 -4.415070
1GSM        A          LEU            23                  E -11.563427 12.670562 -12.014356 -3.008334
1GSM        A          THR            24                  E -11.839109 12.863008 -12.714421 -3.326194
1GSM        A          CYS            25                  E -11.423699  9.471125 -13.547303 -3.237338
1GSM        A          ARG            26                  E -9.196913  7.619069 -10.256986 -2.593100
1GSM        A          LEU            27                  E -6.955496  5.927226 -8.129206 -2.448907
1GSM        A          ALA            28                  C -4.615768  3.007973 -8.553302 -3.416115
1GSM        A          CYS            29                  C -3.239978  1.475945 -5.586971 -2.243137
1GSM        A          ALA            30                  C -3.091577  1.671955 -5.461825 -2.123253
1GSM        A          ASP            31                  T -3.091027  1.674271 -5.465198 -2.123480
1GSM        A          ARG            32                  T -3.091856  1.668414 -5.461532 -2.122980
1GSM        A          GLY            33                  T -3.138468  1.562203 -5.203560 -2.013944
1GSM        A          ALA            34                  T -3.986748  2.357692 -4.994071 -1.686228
1GSM        A          SER            35                  E -7.181614  4.423107 -9.102884 -2.341883
1GSM        A          VAL            36                  E -8.922309  7.196236 -9.531155 -2.138222
1GSM        A          GLN            37                  E -12.804098 10.911635 -17.413766 -5.257579
1GSM        A          TRP            38                  E -12.087696 14.169529 -15.817060 -6.377699
1GSM        A          ARG            39                  E -9.066378  7.444790 -12.533786 -4.085996
1GSM        A          GLY            40                  T -6.917665  5.395121 -9.363917 -3.064340
1GSM        A          LEU            41                  T -6.193970  4.200771 -8.125791 -2.182875
1GSM        A          ASP            42                  T -4.295864  1.837992 -6.419037 -2.060077
1GSM        A          THR            43                  T -3.159190  3.963882 -6.140591 -3.216690
1GSM        A          SER            44                  T -3.118913  3.874101 -6.123729 -3.113838
1GSM        A          LEU            45                  T -3.108135  3.879111 -6.137923 -3.103539
1GSM        A          GLY            46                  T -3.110076  3.879769 -6.134508 -3.108308
1GSM        A          ALA            47                  C -3.192690  4.197227 -6.097373 -3.262308
1GSM        A          VAL            48                  E -4.570268  2.974458 -6.182374 -1.859434
1GSM        A          GLN            49                  E -5.395085  4.237376 -7.318365 -2.598208
1GSM        A          SER            50                  E -6.835461  4.598132 -10.521436 -3.100008
1GSM        A          ASP            51                  E -7.037499  4.974969 -10.706632 -3.228732
1GSM        A          THR            52                  C -7.350982  5.207153 -11.241754 -3.321588
1GSM        A          GLY            53                  C -7.415509  5.304292 -10.886102 -3.174999
1GSM        A          ARG            54                  E -7.695122  6.097189 -10.461401 -2.989872
1GSM        A          SER            55                  E -8.030743  7.058498 -10.391412 -3.069364
1GSM        A          VAL            56                  E -7.527875  9.670332 -7.303270 -2.430152
1GSM        A          LEU            57                  E -7.303466  9.735339 -6.916811 -2.320118
1GSM        A          THR            58                  E -6.538605  9.162360 -8.010732 -3.312568
1GSM        A          VAL            59                  E -6.530976  9.139293 -8.017396 -3.291417
1GSM        A          ARG            60                  T -6.525225  9.130062 -8.021927 -3.277774
1GSM        A          ASN            61                  T -6.608376  8.914005 -8.303688 -3.438973
1GSM        A          ALA            62                  b -6.702220  8.919868 -8.461866 -3.619629
1GSM        A          SER            63                  C -8.400035  8.385923 -9.586279 -2.347464
1GSM        A          LEU            64                  G -8.293401  7.716390 -9.803467 -2.405616
1GSM        A          SER            65                  G -8.347977  7.054995 -10.315284 -2.482479
1GSM        A          ALA            66                  G -8.367970  7.044616 -10.303330 -2.502006
1GSM        A          ALA            67                  C -8.387706  7.006485 -10.300632 -2.524698
1GSM        A          GLY            68                  E -8.564438  6.434752 -9.973098 -2.233979
1GSM        A          THR            69                  E -9.383154  5.640555 -11.165431 -2.328887
1GSM        A          ARG            70                  E -11.433944 10.460830 -13.421797 -3.310368
1GSM        A          VAL            71                  E -11.198862  8.577023 -13.949629 -3.330897
1GSM        A          CYS            72                  E -10.687079  7.833446 -14.558000 -3.859300
1GSM        A          VAL            73                  E -9.361535  7.371934 -14.527434 -4.853184
1GSM        A          GLY            74                  E -7.320548  3.707645 -12.219558 -4.123122
1GSM        A          SER            75                  E -5.990250  2.986128 -9.051511 -2.847184
1GSM        A          CYS            76                  E -3.711042  3.610657 -5.301341 -2.623728
1GSM        A          GLY            77                  T -3.669134  3.777354 -5.338427 -2.613422
1GSM        A          GLY            78                  T -3.667445  3.789660 -5.350457 -2.617187
1GSM        A          ARG            79                  E -3.668656  3.790048 -5.336522 -2.614134
1GSM        A          THR            80                  E -3.679297  3.806275 -5.275620 -2.612476
1GSM        A          PHE            81                  E -5.236471  6.125063 -5.983132 -2.524074
1GSM        A          GLN            82                  E -7.122035  8.132970 -9.638467 -3.935426
1GSM        A          HIS            83                  E -9.641847 12.471341 -9.000742 -3.098212
1GSM        A          THR            84                  E -9.651008 12.520747 -8.935646 -3.100360
1GSM        A          VAL            85                  E -11.388532 13.505354 -11.257369 -2.900437
1GSM        A          GLN            86                  E -11.905629 13.491324 -11.945691 -2.817594
1GSM        A          LEU            87                  E -12.002685 16.086785 -10.425756 -2.592700
1GSM        A          LEU            88                  E -11.927426 17.286191 -9.911991 -2.676738
1GSM        A          VAL            89                  E -11.708439 19.045498 -8.340681 -2.496616
1GSM        A          TYR            90                  E -11.757555 19.508191 -8.377546 -2.667597
1GSM        A          ALA            91                  B -10.515118 12.827430 -9.828144 -2.844917
1GSM        A          PHE            92                  C -10.381025 12.963806 -10.015285 -2.964049
1GSM        A          PRO            93                  C -10.089245 12.200572 -11.611424 -3.773705
1GSM        A          ASN            94                  C -9.997166 11.593710 -11.884458 -3.761438
1GSM        A          GLN            95                  E -9.924828 11.363197 -11.834581 -3.627951
1GSM        A          LEU            96                  E -9.948512 10.881937 -11.857682 -3.409639
1GSM        A          THR            97                  E -8.261436  6.947806 -8.480543 -1.729228
1GSM        A          VAL            98                  E -6.363536  9.123679 -7.355894 -3.118095
1GSM        A          SER            99                  E -6.345446  9.118235 -7.341567 -3.066308
```

1GSM	A	PRO	100	T	-6.343070	9.124476	-7.343163	-3.060393
1GSM	A	ALA	101	T	-6.340807	9.140821	-7.343420	-3.057561
1GSM	A	ALA	102	T	-6.317855	9.463246	-7.361092	-3.162900
1GSM	A	LEU	103	B	-6.105955	11.175345	-7.601359	-4.217452
1GSM	A	VAL	104	T	-5.476948	7.825614	-6.294716	-2.709751
1GSM	A	PRO	105	T	-5.464760	7.803154	-6.347863	-2.712623
1GSM	A	GLY	106	T	-5.463397	7.797976	-6.358552	-2.713771
1GSM	A	ASP	107	T	-5.473796	7.717114	-6.328837	-2.694515
1GSM	A	PRO	108	C	-5.699942	6.119387	-5.743194	-1.940476
1GSM	A	GLU	109	E	-7.655771	7.039718	-9.037684	-2.817655
1GSM	A	VAL	110	E	-8.794569	8.019817	-10.136797	-2.926290
1GSM	A	ALA	111	E	-10.234357	10.186950	-11.662295	-2.983110
1GSM	A	CYS	112	E	-10.258213	10.183336	-11.664337	-3.010416
1GSM	A	THR	113	E	-10.343947	10.398901	-11.211364	-2.816538
1GSM	A	ALA	114	E	-10.407938	10.570929	-11.001371	-2.754595
1GSM	A	HIS	115	E	-11.122118	12.275191	-12.908705	-3.676472
1GSM	A	LYS	116	E	-10.009940	13.536306	-8.210224	-2.381291
1GSM	A	VAL	117	E	-8.490437	12.455224	-6.242419	-2.007843
1GSM	A	THR	118	B	-7.662021	10.803964	-8.006326	-3.002047
1GSM	A	PRO	119	T	-6.273314	6.938789	-5.984364	-1.736913
1GSM	A	VAL	120	T	-5.768012	6.223019	-5.884697	-1.650892
1GSM	A	ASP	121	T	-5.742201	6.286854	-5.941328	-1.665512
1GSM	A	PRO	122	T	-5.745986	6.238031	-5.948632	-1.663945
1GSM	A	ASN	123	T	-5.763794	6.115494	-5.868324	-1.613190
1GSM	A	ALA	124	T	-6.049522	5.859121	-5.929014	-1.619627
1GSM	A	LEU	125	E	-7.567165	7.864159	-7.343773	-2.009798
1GSM	A	SER	126	E	-9.254248	8.750650	-9.371884	-2.219378
1GSM	A	PHE	127	E	-11.224278	14.374129	-12.026989	-4.112297
1GSM	A	SER	128	E	-11.017495	14.996435	-13.417348	-5.533483
1GSM	A	LEU	129	E	-8.152685	11.645584	-8.605392	-3.733393
1GSM	A	LEU	130	E	-5.475685	5.717926	-6.310540	-2.532333
1GSM	A	VAL	131	E	-4.272495	4.134249	-5.971570	-2.618832
1GSM	A	GLY	132	T	-4.261574	4.172493	-6.014507	-2.626550
1GSM	A	GLY	133	T	-4.192137	4.538895	-6.288042	-2.815722
1GSM	A	GLN	134	E	-4.178116	4.572675	-6.311659	-2.810173
1GSM	A	GLU	135	E	-4.066912	5.392601	-5.726590	-2.727228
1GSM	A	LEU	136	T	-4.573843	7.810393	-5.431963	-2.838270
1GSM	A	GLU	137	T	-4.439945	7.359529	-5.487063	-2.725420
1GSM	A	GLY	138	T	-4.415748	7.444947	-5.468903	-2.744334
1GSM	A	ALA	139	T	-4.371221	7.417729	-5.458706	-2.722605
1GSM	A	GLN	140	E	-4.575208	6.847222	-6.339272	-2.852596
1GSM	A	ALA	141	E	-4.625908	6.709746	-6.434323	-2.889477
1GSM	A	LEU	142	C	-4.816548	7.216727	-6.641919	-3.099275
1GSM	A	GLY	143	C	-5.112583	6.780415	-5.912083	-2.445657
1GSM	A	PRO	144	C	-5.385386	6.771102	-5.891361	-2.413138
1GSM	A	GLU	145	E	-6.397482	7.499814	-7.351551	-2.640371
1GSM	A	VAL	146	E	-6.558119	7.731278	-7.108424	-2.637405
1GSM	A	GLN	147	E	-8.005225	7.140365	-11.825447	-3.964212
1GSM	A	GLU	148	E	-7.618875	6.890430	-14.478584	-6.676734
1GSM	A	GLU	149	T	-7.605139	6.445758	-15.864119	-7.526140
1GSM	A	GLU	150	T	-6.430418	4.419879	-12.888459	-5.564425
1GSM	A	GLU	151	T	-3.750460	1.688864	-6.234571	-2.456658
1GSM	A	GLU	152	T	-2.708764	1.530675	-5.102004	-2.340636
1GSM	A	PRO	153	C	-0.335607	1.273714	-4.245804	-3.649985
1GSM	A	GLN	154	C	-0.317551	1.307815	-4.375695	-3.702238
1GSM	A	GLY	155	C	-0.315537	1.318359	-4.392347	-3.708303
1GSM	A	ASP	156	C	-0.319832	1.311007	-4.357251	-3.698990
1GSM	A	GLU	157	C	-0.341467	1.269840	-4.224492	-3.651948
1GSM	A	ASP	158	C	-2.859749	1.748591	-5.584545	-2.767785
1GSM	A	VAL	159	C	-4.167419	3.892174	-6.494814	-3.090564
1GSM	A	LEU	160	C	-5.651060	8.727384	-10.030680	-6.290153
1GSM	A	PHE	161	E	-8.446288	13.035813	-11.728911	-6.731313
1GSM	A	ARG	162	E	-12.282612	16.200131	-15.192385	-6.322945
1GSM	A	VAL	163	E	-13.045454	16.522166	-12.469704	-3.471747
1GSM	A	THR	164	E	-13.805631	16.983979	-14.662056	-4.287524
1GSM	A	GLU	165	E	-14.011603	17.127936	-15.303663	-4.702747
1GSM	A	ARG	166	E	-14.146549	17.547621	-15.485712	-4.973887
1GSM	A	TRP	167	E	-12.327683	18.135680	-10.891882	-3.747468
1GSM	A	ARG	168	E	-9.085693	16.982990	-8.745543	-4.804147
1GSM	A	LEU	169	C	-5.651647	13.292705	-4.029641	-3.339176
1GSM	A	PRO	170	C	-3.891564	8.733861	-2.005764	-1.788556
1GSM	A	PRO	171	C	-2.901648	5.937563	-1.991476	-1.543302
1GSM	A	LEU	172	C	-2.626750	6.667256	-1.715128	-1.594693
1GSM	A	GLY	173	T	-1.986403	6.432669	-2.620457	-2.463048
1GSM	A	THR	174	T	-1.930072	6.360711	-2.547873	-2.330864
1GSM	A	PRO	175	T	-1.948962	6.286982	-2.574044	-2.350127
1GSM	A	VAL	176	T	-2.060834	6.422681	-2.664754	-2.500342
1GSM	A	PRO	177	C	-2.155888	6.125556	-2.890771	-2.623325
1GSM	A	PRO	178	C	-3.341908	5.689895	-1.824755	-0.994182
1GSM	A	ALA	179	E	-4.990703	10.335829	-3.779568	-2.512602
1GSM	A	LEU	180	E	-6.805315	15.559128	-5.081014	-4.115754

1GSM	A	TYR	181	E	-10.368209	17.099660	-9.520242	-3.949607
1GSM	A	CYS	182	E	-11.153455	14.724849	-12.569477	-4.631939
1GSM	A	GLN	183	E	-13.673090	12.892558	-16.792033	-4.569550
1GSM	A	ALA	184	E	-13.211403	14.479743	-15.302635	-4.464083
1GSM	A	THR	185	E	-12.654881	15.469217	-14.652567	-4.881263
1GSM	A	MET	186	E	-10.464602	10.780062	-10.644395	-2.915217
1GSM	A	ARG	187	E	-7.683492	9.234535	-7.205985	-2.390702
1GSM	A	LEU	188	E	-4.874224	10.636438	-5.759042	-4.132314
1GSM	A	PRO	189	T	-4.810651	10.326658	-5.780794	-3.952042
1GSM	A	GLY	190	T	-4.771157	10.114209	-5.860632	-3.875966
1GSM	A	LEU	191	E	-4.771158	10.114180	-5.860650	-3.875977
1GSM	A	GLU	192	E	-4.775077	10.121819	-5.853061	-3.886501
1GSM	A	LEU	193	E	-5.855713	7.380098	-6.404813	-2.528332
1GSM	A	SER	194	E	-6.387703	7.084047	-7.046900	-2.776970
1GSM	A	HIS	195	E	-8.888112	11.449707	-9.340111	-3.240856
1GSM	A	ARG	196	E	-8.865572	11.548011	-9.199431	-3.161872
1GSM	A	GLN	197	E	-9.507398	11.127362	-9.908682	-2.756817
1GSM	A	ALA	198	E	-8.502161	14.246826	-9.276573	-4.380413
1GSM	A	ILE	199	E	-7.732979	13.734800	-7.000813	-3.465867
1GSM	A	PRO	200	E	-5.825793	8.879658	-4.763445	-2.217273
1GSM	A	VAL	201	B	-4.003876	7.251334	-2.683187	-1.735411
1GSM	A	LEU	202	T	-2.561860	4.410927	-1.837693	-1.242096
1GSM	A	ILE	203	T	-1.075917	3.446271	-2.421829	-2.224559
1GSM	A	GLU	204	T	-1.075917	3.446271	-2.421829	-2.224559
1GSM	A	GLY	205	T	-1.075917	3.446271	-2.421829	-2.224559
1GSM	A	ARG	206	C	-1.075917	3.446271	-2.421829	-2.224559
1H6H	A	ALA	2	H	-3.590481	1.175666	-7.419517	-2.619603
1H6H	A	VAL	3	H	-3.590481	1.175666	-7.419517	-2.619603
1H6H	A	ALA	4	H	-3.590481	1.175666	-7.419517	-2.619603
1H6H	A	GLN	5	H	-3.590481	1.175666	-7.419517	-2.619603
1H6H	A	GLN	6	H	-4.826309	2.139190	-10.337613	-3.810091
1H6H	A	LEU	7	H	-5.457767	2.089841	-11.365937	-4.236269
1H6H	A	ARG	8	H	-7.095047	2.877884	-14.513517	-5.048517
1H6H	A	ALA	9	H	-7.785750	3.352870	-16.188073	-5.746836
1H6H	A	GLU	10	H	-8.176413	3.832524	-16.707805	-6.080351
1H6H	A	SER	11	H	-9.222986	5.219461	-18.286037	-6.337657
1H6H	A	ASP	12	H	-9.435105	7.294049	-16.503961	-5.603629
1H6H	A	PHE	13	H	-9.503756	9.164363	-14.530431	-4.892449
1H6H	A	GLU	14	H	-8.797261	8.465574	-12.858771	-4.326901
1H6H	A	GLN	15	H	-8.727184	8.570377	-12.853200	-4.321402
1H6H	A	LEU	16	C	-8.699073	8.918612	-12.630407	-4.285397
1H6H	A	PRO	17	T	-8.307420	10.016442	-11.431847	-4.208735
1H6H	A	ASP	18	T	-7.501365	11.231689	-9.371840	-4.080554
1H6H	A	ASP	19	T	-7.525522	11.472280	-9.198738	-4.066439
1H6H	A	VAL	20	T	-7.497311	11.520016	-9.155478	-4.014676
1H6H	A	ALA	21	E	-7.408253	11.259708	-9.274659	-3.951139
1H6H	A	ILE	22	E	-7.397144	11.252650	-9.247027	-3.927163
1H6H	A	SER	23	E	-7.852522	10.391290	-10.364103	-3.786606
1H6H	A	ALA	24	E	-7.212383	9.580840	-9.663112	-3.850976
1H6H	A	ASN	25	E	-6.602476	10.355708	-8.438656	-3.898940
1H6H	A	ILE	26	E	-6.464079	10.643751	-8.325582	-3.924372
1H6H	A	ALA	27	E	-6.330687	10.959884	-8.640101	-4.248380
1H6H	A	ASP	28	E	-6.327098	11.011121	-8.667706	-4.280680
1H6H	A	ILE	29	E	-6.256536	11.248791	-8.546975	-4.345862
1H6H	A	GLU	30	E	-5.383303	8.238863	-8.532994	-4.537176
1H6H	A	GLU	31	E	-4.015746	6.650563	-7.241205	-4.372357
1H6H	A	LYS	32	E	-2.992779	5.397288	-6.427540	-4.073641
1H6H	A	ARG	33	T	-2.771150	4.943804	-6.678127	-4.021145
1H6H	A	GLY	34	T	-2.771243	4.940178	-6.680013	-4.021539
1H6H	A	PHE	35	T	-2.777553	4.909854	-6.659704	-4.015347
1H6H	A	THR	36	T	-2.849058	4.696826	-6.589382	-3.963995
1H6H	A	SER	37	T	-3.467533	3.880943	-7.159019	-3.856121
1H6H	A	HIS	38	E	-7.226094	6.202836	-12.593892	-5.168594
1H6H	A	PHE	39	E	-10.196904	15.621722	-16.022401	-8.185731
1H6H	A	VAL	40	E	-10.627257	17.078203	-15.919560	-8.713137
1H6H	A	PHE	41	E	-11.916405	20.373811	-10.569812	-4.247964
1H6H	A	VAL	42	E	-10.573813	16.628438	-10.822988	-4.553110
1H6H	A	ILE	43	E	-10.318038	16.325010	-11.275200	-4.745189
1H6H	A	GLU	44	E	-10.312138	16.282490	-11.353477	-4.769964
1H6H	A	VAL	45	E	-10.240683	15.797194	-11.752610	-4.853943
1H6H	A	LYS	46	E	-8.615013	9.986583	-13.012161	-5.645966
1H6H	A	THR	47	E	-7.026792	8.245643	-11.351350	-5.183317
1H6H	A	LYS	48	T	-6.066045	7.655864	-10.821397	-5.325856
1H6H	A	GLY	49	T	-5.839159	7.808514	-10.636875	-5.234367
1H6H	A	GLY	50	T	-5.837914	7.817356	-10.639146	-5.233689
1H6H	A	SER	51	C	-5.843013	7.802354	-10.617856	-5.229620
1H6H	A	LYS	52	E	-5.923231	7.753782	-10.529222	-5.241397
1H6H	A	TYR	53	E	-6.513536	8.164126	-10.251895	-5.037141
1H6H	A	LEU	54	E	-9.449407	12.223218	-11.818567	-4.924860
1H6H	A	ILE	55	E	-11.464081	16.804150	-12.102554	-4.911011
1H6H	A	TYR	56	E	-13.169756	21.526064	-12.788316	-5.722297

1H6H	A	ARG	57	E	-14.817150	14.618333	-18.273961	-5.427478
1H6H	A	ARG	58	E	-13.323551	18.140744	-14.264981	-5.178655
1H6H	A	TYR	59	H	-13.197879	18.284676	-14.431830	-5.257499
1H6H	A	ARG	60	H	-11.524135	14.664410	-13.280922	-4.913788
1H6H	A	GLN	61	H	-11.491178	14.816788	-13.331810	-4.929804
1H6H	A	PHE	62	H	-11.492811	14.820974	-13.318091	-4.928867
1H6H	A	HIS	63	H	-11.505403	14.598915	-13.391692	-4.923309
1H6H	A	ALA	64	H	-11.508119	14.525777	-13.409871	-4.916715
1H6H	A	LEU	65	H	-12.969248	15.491893	-15.619850	-5.184657
1H6H	A	GLN	66	H	-13.486618	11.785866	-18.393518	-5.186919
1H6H	A	SER	67	H	-10.847229	10.757271	-14.469411	-4.912235
1H6H	A	LYS	68	H	-10.744225	10.939204	-14.565769	-4.928267
1H6H	A	LEU	69	H	-10.742564	10.961487	-14.569937	-4.932365
1H6H	A	GLU	70	H	-10.714461	11.017511	-14.653767	-4.951113
1H6H	A	GLU	71	H	-10.489642	10.773921	-14.610179	-4.818517
1H6H	A	ARG	72	H	-9.619507	9.524585	-13.362602	-4.568270
1H6H	A	PHE	73	H	-7.180255	8.676688	-10.070666	-4.311145
1H6H	A	GLY	74	T	-3.466249	1.535810	-7.956621	-3.602323
1H6H	A	PRO	75	T	-3.449921	1.558597	-8.013528	-3.598414
1H6H	A	ASP	76	T	-3.448784	1.561033	-8.021079	-3.598214
1H6H	A	SER	77	T	-3.447519	1.564046	-8.029188	-3.597975
1H6H	A	LYS	78	T	-3.434689	1.592889	-8.055305	-3.585012
1H6H	A	SER	79	T	-5.077760	3.101702	-9.919112	-3.360329
1H6H	A	SER	80	G	-5.396552	3.657551	-9.874701	-3.305179
1H6H	A	ALA	81	G	-5.392821	3.807435	-9.794871	-3.301810
1H6H	A	LEU	82	G	-5.412424	4.006990	-9.661626	-3.302833
1H6H	A	ALA	83	C	-5.827301	6.626962	-9.594446	-3.703697
1H6H	A	CYS	84	C	-4.756039	8.927723	-5.844901	-3.491272
1H6H	A	THR	85	C	-4.264136	10.761355	-4.533744	-3.447336
1H6H	A	LEU	86	C	-4.264000	10.842455	-4.495210	-3.449741
1H6H	A	PRO	87	C	-4.231348	10.934240	-4.603667	-3.495556
1H6H	A	THR	88	C	-4.125678	11.241612	-5.022125	-3.846843
1H6H	A	LEU	89	C	-4.348596	12.310889	-4.774829	-4.020144
1H6H	A	PRO	90	C	-4.878543	12.069920	-7.123101	-4.934482
1H6H	A	ALA	91	C	-3.266455	6.050570	-5.616851	-3.626533
1H6H	A	LYS	92	C	-1.788572	5.886471	-4.355835	-3.981452
1H6H	A	VAL	93	C	-1.401819	5.721813	-4.520043	-4.016320
1H6H	A	TYR	94	C	-1.387008	5.745493	-4.593841	-4.036809
1H6H	A	VAL	95	C	-1.386952	5.744385	-4.595479	-4.037296
1H6H	A	GLY	96	C	-1.415166	5.703118	-4.515180	-4.029180
1H6H	A	VAL	97	C	-1.861043	5.068070	-4.440083	-3.718403
1H6H	A	LYS	98	H	-3.663892	5.768685	-6.860496	-4.185201
1H6H	A	GLN	99	H	-5.642156	7.301013	-10.248314	-4.948079
1H6H	A	GLU	100	H	-6.244410	8.782621	-11.530029	-5.848994
1H6H	A	ILE	101	H	-6.981312	12.488161	-12.864434	-7.606608
1H6H	A	ALA	102	H	-7.742058	12.961623	-12.875960	-6.988177
1H6H	A	GLU	103	H	-8.162646	12.089813	-11.960229	-5.568804
1H6H	A	MET	104	H	-8.593733	10.609458	-11.314211	-4.373713
1H6H	A	ARG	105	H	-9.925546	11.499712	-12.995049	-4.252731
1H6H	A	ILE	106	H	-9.610064	10.775051	-12.247319	-3.769647
1H6H	A	PRO	107	H	-9.181193	9.403985	-12.294060	-3.697706
1H6H	A	ALA	108	H	-9.217571	9.309594	-12.197796	-3.646181
1H6H	A	LEU	109	H	-9.318070	9.158480	-12.174555	-3.642156
1H6H	A	ASN	110	H	-9.336663	9.003771	-12.190987	-3.639607
1H6H	A	ALA	111	H	-9.536271	8.477891	-12.425816	-3.709805
1H6H	A	TYR	112	H	-12.212424	12.968613	-15.002523	-4.477725
1H6H	A	MET	113	H	-11.594125	14.635596	-13.187897	-4.397139
1H6H	A	LYS	114	H	-10.066719	12.088454	-11.027351	-3.520056
1H6H	A	SER	115	H	-9.920803	12.733671	-10.839511	-3.521854
1H6H	A	LEU	116	H	-9.847885	13.093231	-10.702617	-3.499382
1H6H	A	LEU	117	H	-8.721435	12.349763	-9.296906	-3.396063
1H6H	A	SER	118	C	-8.396815	11.608541	-9.657145	-3.445835
1H6H	A	LEU	119	C	-8.333686	11.802500	-9.553171	-3.435967
1H6H	A	PRO	120	C	-8.280709	12.009569	-9.468246	-3.424202
1H6H	A	VAL	121	H	-8.280257	12.020455	-9.470182	-3.429124
1H6H	A	TRP	122	H	-8.586827	11.885917	-9.755057	-3.463859
1H6H	A	VAL	123	H	-9.083709	13.633603	-9.328513	-3.433373
1H6H	A	LEU	124	H	-9.529269	14.342010	-9.373117	-3.514228
1H6H	A	MET	125	H	-10.306933	13.049638	-12.871359	-4.529282
1H6H	A	ASP	126	C	-10.515981	11.602715	-14.018718	-4.788469
1H6H	A	GLU	127	H	-10.369394	10.941963	-14.254993	-4.652727
1H6H	A	ASP	128	H	-10.638145	9.790746	-15.009399	-4.699829
1H6H	A	VAL	129	H	-10.686992	9.648297	-14.928286	-4.655175
1H6H	A	ARG	130	H	-11.238972	8.751776	-15.193906	-4.199588
1H6H	A	ILE	131	H	-11.258131	8.732183	-15.101587	-4.179302
1H6H	A	PHE	132	H	-14.189043	15.930064	-16.258569	-4.693822
1H6H	A	PHE	133	H	-13.998698	15.801346	-16.813576	-5.338070
1H6H	A	TYR	134	C	-11.491936	10.235223	-16.090898	-5.339389
1H6H	A	GLN	135	C	-9.586255	10.139765	-17.045135	-7.680980
1H6H	A	SER	136	C	-8.421469	9.049445	-15.664311	-7.313511
1H6H	A	PRO	137	H	-7.454641	9.238412	-13.951140	-6.973941

```
1H6H        A          TYR            138               H -7.302726  9.168658 -13.883406 -6.810398
1H6H        A          ASP            139               H -7.005463  8.150426 -13.344729 -6.151112
1H6H        A          SER            140               H -4.685036  5.030433 -8.069501 -3.859981
1H6H        A          GLU            141               H -3.289121  4.059633 -5.820842 -2.957688
1H6H        A          GLN            142               C -3.289121  4.059633 -5.820842 -2.957688
1H6H        A          VAL            143               C -3.289121  4.059633 -5.820842 -2.957688
1H6H        A          PRO            144               C -3.289121  4.059633 -5.820842 -2.957688
1HDO        A          MET              1               C -2.856840  4.705653 -4.949980 -2.925842
1HDO        A          ALA              2               C -2.856840  4.705653 -4.949980 -2.925842
1HDO        A          VAL              3               C -2.856840  4.705653 -4.949980 -2.925842
1HDO        A          LYS              4               C -2.856840  4.705653 -4.949980 -2.925842
1HDO        A          LYS              5               E -6.535638  6.917654 -10.479220 -4.377157
1HDO        A          ILE              6               E -8.465577 10.802531 -11.962399 -5.128290
1HDO        A          ALA              7               E -9.908345 15.247481 -11.658021 -4.736777
1HDO        A          ILE              8               E -9.512246 16.871061 -9.673579 -4.413563
1HDO        A          PHE              9               E -8.721971 14.817567 -10.155672 -4.795058
1HDO        A          GLY             10               T -8.433494 12.848757 -11.380085 -5.008721
1HDO        A          ALA             11               T -8.363214 12.651546 -11.631872 -5.095904
1HDO        A          THR             12               T -7.813051 11.123165 -12.256378 -5.615974
1HDO        A          GLY             13               T -7.766511 10.697390 -12.501631 -5.612522
1HDO        A          GLN             14               H -7.848201 10.139797 -12.895167 -5.720900
1HDO        A          THR             15               H -7.921944 10.260469 -12.828953 -5.760173
1HDO        A          GLY             16               H -7.955239 10.164632 -12.815451 -5.765610
1HDO        A          LEU             17               H -8.841256 10.054159 -13.477156 -5.176777
1HDO        A          THR             18               H -9.512372 11.960227 -13.315034 -5.028335
1HDO        A          THR             19               H -9.762848 12.264662 -13.046627 -4.871509
1HDO        A          LEU             20               H -10.424109 13.082840 -13.048196 -4.569527
1HDO        A          ALA             21               H -10.824433 12.905489 -13.260600 -4.374254
1HDO        A          GLN             22               H -10.522323  9.580100 -14.224441 -4.193635
1HDO        A          ALA             23               H -6.767801  6.486339 -9.890824 -3.601063
1HDO        A          VAL             24               H -6.673536  6.961372 -9.958048 -3.696307
1HDO        A          GLN             25               H -6.669500  6.984375 -9.987789 -3.708884
1HDO        A          ALA             26               H -6.667483  7.002184 -9.996816 -3.712891
1HDO        A          GLY             27               C -6.668141  7.000672 -9.992432 -3.712677
1HDO        A          TYR             28               C -7.767768  9.806459 -10.581320 -4.320568
1HDO        A          GLU             29               E -9.360277 11.100256 -13.798809 -5.309286
1HDO        A          VAL             30               E -9.876723 12.885749 -12.550330 -4.737771
1HDO        A          THR             31               E -10.369674 15.017463 -11.454709 -3.998227
1HDO        A          VAL             32               E -9.835668 13.726294 -11.046739 -3.805757
1HDO        A          LEU             33               E -9.292598 12.713288 -11.093813 -3.937232
1HDO        A          VAL             34               E -7.631399  8.635326 -10.294067 -3.765717
1HDO        A          ARG             35               T -6.955536  7.768056 -10.477409 -3.922395
1HDO        A          ASP             36               T -6.641726  8.521037 -10.131979 -4.057469
1HDO        A          SER             37               G -6.621679  8.601815 -10.156637 -4.065717
1HDO        A          SER             38               G -6.618817  8.606167 -10.173245 -4.070532
1HDO        A          ARG             39               G -6.673357  8.764272 -10.196151 -4.135243
1HDO        A          LEU             40               C -4.804633  7.120157 -7.568281 -3.922789
1HDO        A          PRO             41               C -3.955465  5.881092 -7.224343 -3.766362
1HDO        A          SER             42               C -3.806495  5.875032 -7.250372 -3.692469
1HDO        A          GLU             43               C -3.791736  5.949853 -7.258075 -3.689573
1HDO        A          GLY             44               C -3.789777  5.964245 -7.259349 -3.688416
1HDO        A          PRO             45               C -3.904715  5.728222 -7.202037 -3.637873
1HDO        A          ARG             46               C -4.621091  6.255570 -7.379205 -3.445637
1HDO        A          PRO             47               T -5.829017  9.325316 -7.784946 -3.591640
1HDO        A          ALA             48               T -6.357076 10.105282 -8.572015 -3.684307
1HDO        A          HIS             49               E -6.347984  9.615959 -9.035403 -3.858530
1HDO        A          VAL             50               E -6.046827  9.559130 -9.000535 -4.024064
1HDO        A          VAL             51               E -6.068044  9.475678 -8.990514 -4.016429
1HDO        A          VAL             52               E -6.080009  9.402905 -9.104779 -4.077242
1HDO        A          GLY             53               C -6.205221  9.500080 -9.385290 -4.257414
1HDO        A          ASP             54               T -6.341675  9.795202 -9.365054 -4.325903
1HDO        A          VAL             55               T -6.845300 10.180820 -10.105949 -4.300588
1HDO        A          LEU             56               T -6.754815  9.511601 -10.368660 -4.297437
1HDO        A          GLN             57               T -6.883046  9.089027 -10.667558 -4.272758
1HDO        A          ALA             58               H -7.096494  8.637442 -10.842675 -4.119038
1HDO        A          ALA             59               H -7.214267  8.301449 -10.942838 -4.094431
1HDO        A          ASP             60               H -7.494650  7.633923 -11.527565 -4.256199
1HDO        A          VAL             61               H -8.405575  8.362984 -12.142230 -4.124807
1HDO        A          ASP             62               H -9.229334  9.771844 -13.298477 -4.340865
1HDO        A          LYS             63               H -7.633797  9.547588 -10.583126 -4.396644
1HDO        A          THR             64               H -7.571961  9.647614 -10.734898 -4.459992
1HDO        A          VAL             65               H -7.544047  9.634836 -10.858652 -4.483027
1HDO        A          ALA             66               T -7.520663  9.559104 -10.993205 -4.507904
1HDO        A          GLY             67               T -7.527888  9.549010 -10.981708 -4.512987
1HDO        A          GLN             68               T -8.477178  9.755533 -13.023650 -4.971840
1HDO        A          ASP             69               C -8.855355  9.439925 -13.556940 -4.892512
1HDO        A          ALA             70               E -9.157476  9.842092 -13.434968 -4.782324
1HDO        A          VAL             71               E -9.859741 13.635433 -11.841966 -4.218716
1HDO        A          ILE             72               E -9.077876 16.526588 -8.804136 -4.220977
1HDO        A          VAL             73               E -8.839444 16.055916 -9.271133 -4.380436
1HDO        A          LEU             74               C -8.769456 15.622951 -9.751860 -4.549267
```

1HDO	A	LEU	75	C	-7.582342	10.092422	-11.073303	-4.846452
1HDO	A	GLY	76	C	-5.466865	5.056265	-10.857154	-4.986401
1HDO	A	THR	77	T	-5.435537	5.150595	-10.895021	-4.974178
1HDO	A	ARG	78	T	-5.429693	5.147906	-10.917197	-4.967477
1HDO	A	ASN	79	T	-4.803702	5.195331	-9.394677	-4.201287
1HDO	A	ASP	80	T	-4.802063	5.189863	-9.395554	-4.194903
1HDO	A	LEU	81	C	-5.013966	5.402968	-8.753612	-3.837702
1HDO	A	SER	82	C	-4.934406	5.753259	-8.710003	-3.865015
1HDO	A	PRO	83	C	-4.926854	5.853349	-8.707392	-3.881750
1HDO	A	THR	84	C	-5.889839	8.428795	-9.216402	-4.245457
1HDO	A	THR	85	H	-5.930950	8.481590	-9.098525	-4.255120
1HDO	A	VAL	86	H	-5.997834	8.414199	-8.966688	-4.243456
1HDO	A	MET	87	H	-7.325591	11.567437	-9.712723	-4.959825
1HDO	A	SER	88	H	-10.008251	11.500492	-14.740624	-5.362891
1HDO	A	GLU	89	H	-10.078340	10.318166	-15.128391	-5.091094
1HDO	A	GLY	90	H	-10.088359	10.344015	-14.762841	-4.808962
1HDO	A	ALA	91	H	-10.115574	10.408918	-14.578182	-4.705002
1HDO	A	ARG	92	H	-10.081396	10.512491	-14.405519	-4.605681
1HDO	A	ASN	93	H	-9.958405	11.484808	-13.208425	-4.253819
1HDO	A	ILE	94	H	-9.775628	12.939558	-11.862586	-4.031160
1HDO	A	VAL	95	H	-9.764391	12.885171	-11.874043	-4.018465
1HDO	A	ALA	96	H	-9.252206	10.751216	-12.380717	-4.109366
1HDO	A	ALA	97	H	-9.216107	10.767538	-12.455249	-4.147020
1HDO	A	MET	98	H	-8.283193	8.989051	-12.531496	-4.779533
1HDO	A	LYS	99	H	-7.222371	7.759410	-11.065386	-4.280089
1HDO	A	ALA	100	H	-6.826389	7.453145	-11.039865	-4.263168
1HDO	A	HIS	101	H	-6.828834	7.450016	-11.041171	-4.270016
1HDO	A	GLY	102	C	-6.827043	7.462453	-11.047269	-4.272841
1HDO	A	VAL	103	C	-6.870138	7.373840	-10.935166	-4.224622
1HDO	A	ASP	104	C	-7.238474	7.215091	-11.076078	-4.264504
1HDO	A	LYS	105	E	-9.533379	10.755739	-13.819739	-5.167328
1HDO	A	VAL	106	E	-9.753088	12.354210	-12.714845	-4.741814
1HDO	A	VAL	107	E	-10.167312	13.532246	-12.235329	-4.416938
1HDO	A	ALA	108	E	-10.062327	13.105710	-12.578428	-4.470948
1HDO	A	CYS	109	E	-10.070270	13.103877	-12.561305	-4.473175
1HDO	A	THR	110	C	-10.039659	13.353056	-12.530949	-4.505030
1HDO	A	SER	111	C	-10.462192	13.298312	-13.576727	-4.793565
1HDO	A	ALA	112	G	-10.729542	14.222837	-13.567854	-4.915138
1HDO	A	PHE	113	G	-11.170057	18.328209	-12.761500	-5.332772
1HDO	A	LEU	114	G	-10.628799	17.327480	-12.890584	-5.593307
1HDO	A	LEU	115	C	-9.014921	12.181890	-11.796005	-4.855483
1HDO	A	TRP	116	C	-6.863573	7.878553	-10.300788	-4.312660
1HDO	A	ASP	117	T	-3.902904	5.628248	-6.789199	-3.688146
1HDO	A	PRO	118	T	-3.840616	5.904265	-6.787825	-3.671437
1HDO	A	THR	119	T	-3.752125	6.171748	-6.777100	-3.651492
1HDO	A	LYS	120	T	-3.714457	6.327111	-6.759217	-3.626172
1HDO	A	VAL	121	T	-3.700345	6.427696	-6.722188	-3.606456
1HDO	A	PRO	122	C	-4.424048	8.367672	-6.617846	-3.413637
1HDO	A	PRO	123	G	-4.607459	8.361859	-6.568172	-3.377640
1HDO	A	ARG	124	G	-5.130148	9.132551	-6.392582	-3.179374
1HDO	A	LEU	125	G	-5.788620	10.055977	-6.226811	-3.074155
1HDO	A	GLN	126	H	-7.618759	8.935854	-10.808967	-4.041230
1HDO	A	ALA	127	H	-9.030479	9.777949	-11.734596	-3.892141
1HDO	A	VAL	128	H	-11.119006	12.583069	-14.992621	-4.729067
1HDO	A	THR	129	H	-11.369683	12.043528	-16.109233	-5.133328
1HDO	A	ASP	130	H	-11.523073	11.457616	-16.639543	-5.265128
1HDO	A	ASP	131	H	-11.847959	11.509404	-17.119318	-5.479642
1HDO	A	HIS	132	H	-11.999141	11.562315	-17.188301	-5.601862
1HDO	A	ILE	133	H	-12.369416	10.945246	-17.571525	-5.568610
1HDO	A	ARG	134	H	-13.696893	10.968518	-19.648391	-5.690623
1HDO	A	MET	135	H	-13.838564	16.128347	-17.362553	-5.807089
1HDO	A	HIS	136	H	-12.852146	15.034087	-15.707729	-5.174130
1HDO	A	LYS	137	H	-10.301548	12.017355	-12.859706	-4.592712
1HDO	A	VAL	138	H	-10.276100	12.092844	-12.938337	-4.609589
1HDO	A	LEU	139	H	-9.608241	10.821550	-13.714684	-5.091105
1HDO	A	ARG	140	H	-8.861490	9.615753	-13.815084	-5.353443
1HDO	A	GLU	141	H	-8.761187	9.430863	-14.102017	-5.423677
1HDO	A	SER	142	C	-8.804726	9.240362	-14.208300	-5.490519
1HDO	A	GLY	143	C	-8.804676	9.243505	-14.207683	-5.491140
1HDO	A	LEU	144	C	-8.918029	9.039529	-14.233242	-5.526803
1HDO	A	LYS	145	E	-9.838023	8.665154	-15.640810	-5.785321
1HDO	A	TYR	146	E	-11.797328	14.123739	-15.241185	-5.373753
1HDO	A	VAL	147	E	-11.334978	14.767852	-12.734601	-4.251748
1HDO	A	ALA	148	E	-10.780643	14.977833	-11.366084	-3.838759
1HDO	A	VAL	149	E	-10.284917	14.555416	-11.199100	-3.844239
1HDO	A	MET	150	C	-9.073555	13.908571	-9.970715	-4.079433
1HDO	A	PRO	151	C	-7.238780	10.662091	-8.623612	-3.739126
1HDO	A	PRO	152	C	-6.812860	9.560078	-9.362202	-3.939608
1HDO	A	HIS	153	E	-6.709554	9.319864	-9.819359	-4.115600
1HDO	A	ILE	154	E	-6.581905	8.974480	-10.251920	-4.278160
1HDO	A	GLY	155	E	-5.729409	7.906912	-10.050993	-4.829104

1HDO	A	ASP	156	C	-5.370214	8.153637	-9.646823	-4.888944
1HDO	A	GLN	157	C	-5.284121	8.251232	-9.669048	-4.934274
1HDO	A	PRO	158	C	-3.973384	7.330742	-7.064718	-4.279220
1HDO	A	LEU	159	C	-3.970447	7.365861	-7.065370	-4.282611
1HDO	A	THR	160	C	-3.992587	7.367217	-6.953569	-4.255062
1HDO	A	GLY	161	C	-4.020091	7.320082	-6.849072	-4.224953
1HDO	A	ALA	162	C	-4.032315	7.290053	-6.785951	-4.208886
1HDO	A	TYR	163	C	-6.526817	12.135528	-9.045787	-4.862131
1HDO	A	THR	164	E	-6.954023	11.912155	-9.524845	-4.723995
1HDO	A	VAL	165	E	-6.964994	10.987378	-9.798362	-4.545580
1HDO	A	THR	166	E	-6.803990	7.682142	-10.852298	-4.239263
1HDO	A	LEU	167	T	-5.253000	5.998017	-9.184722	-4.186303
1HDO	A	ASP	168	T	-4.896771	5.799940	-9.247196	-4.188462
1HDO	A	GLY	169	T	-4.880726	5.793657	-9.313635	-4.198619
1HDO	A	ARG	170	C	-4.883523	5.762140	-9.314759	-4.194226
1HDO	A	GLY	171	C	-4.892013	5.771434	-9.293650	-4.200493
1HDO	A	PRO	172	C	-5.308722	5.661137	-9.534912	-4.217806
1HDO	A	SER	173	C	-6.708427	6.617544	-11.590370	-4.484084
1HDO	A	ARG	174	C	-7.292760	7.920039	-11.403091	-4.376280
1HDO	A	VAL	175	E	-7.634410	8.584267	-11.151736	-4.480489
1HDO	A	ILE	176	E	-9.708798	12.118315	-12.532303	-4.358024
1HDO	A	SER	177	E	-10.205154	12.539081	-13.473170	-4.785278
1HDO	A	LYS	178	H	-10.248062	13.130120	-13.629177	-5.120322
1HDO	A	HIS	179	H	-10.733584	13.006839	-15.041358	-5.573745
1HDO	A	ASP	180	H	-10.945574	12.873705	-15.455573	-5.732807
1HDO	A	LEU	181	H	-10.884835	13.408372	-15.138635	-5.691106
1HDO	A	GLY	182	H	-10.890673	13.542612	-15.039952	-5.674397
1HDO	A	HIS	183	H	-11.448681	14.507228	-14.962494	-5.387636
1HDO	A	PHE	184	H	-11.714508	16.179688	-14.235300	-5.385044
1HDO	A	MET	185	H	-11.851122	16.554016	-14.046369	-5.419145
1HDO	A	LEU	186	H	-11.813516	14.172338	-14.756141	-5.049778
1HDO	A	ARG	187	H	-10.801385	11.304452	-14.728623	-5.031497
1HDO	A	CYS	188	H	-9.510433	9.634168	-14.010012	-5.111571
1HDO	A	LEU	189	T	-8.683968	9.498213	-13.204710	-5.109392
1HDO	A	THR	190	T	-8.286249	10.066619	-12.997400	-5.341486
1HDO	A	THR	191	T	-8.205955	10.214558	-13.074338	-5.401355
1HDO	A	ASP	192	T	-8.063884	10.258010	-13.152386	-5.498642
1HDO	A	GLU	193	T	-8.084169	10.344986	-13.142615	-5.533257
1HDO	A	TYR	194	T	-8.259734	10.707533	-13.242471	-5.687992
1HDO	A	ASP	195	T	-8.242358	9.512967	-13.592197	-5.501445
1HDO	A	GLY	196	T	-8.320722	9.282073	-13.595813	-5.450961
1HDO	A	HIS	197	T	-8.568358	8.684992	-13.651659	-5.255485
1HDO	A	SER	198	E	-8.632094	8.455508	-13.578696	-5.216482
1HDO	A	THR	199	E	-8.657857	8.302903	-13.548621	-5.205002
1HDO	A	TYR	200	E	-10.817597	12.480220	-14.134268	-5.241429
1HDO	A	PRO	201	E	-10.672240	15.927535	-12.092157	-5.221023
1HDO	A	SER	202	E	-8.719575	12.032763	-10.972927	-4.670265
1HDO	A	HIS	203	C	-8.719575	12.032763	-10.972927	-4.670265
1HDO	A	GLN	204	C	-8.719575	12.032763	-10.972927	-4.670265
1HDO	A	TYR	205	C	-8.719575	12.032763	-10.972927	-4.670265
1HDR	A	GLU	8	C	-7.811675	7.790085	-10.055458	-3.156377
1HDR	A	ALA	9	C	-7.811675	7.790085	-10.055458	-3.156377
1HDR	A	ARG	10	C	-7.811675	7.790085	-10.055458	-3.156377
1HDR	A	ARG	11	E	-7.811675	7.790085	-10.055458	-3.156377
1HDR	A	VAL	12	E	-10.102200	11.242583	-11.948307	-3.757600
1HDR	A	LEU	13	E	-11.560552	16.958715	-12.423178	-4.705818
1HDR	A	VAL	14	E	-11.352197	16.342629	-12.892308	-4.847943
1HDR	A	TYR	15	E	-10.861858	13.723067	-14.354601	-5.289434
1HDR	A	GLY	16	T	-7.688131	6.939015	-12.650455	-4.978412
1HDR	A	GLY	17	T	-7.540503	7.628831	-12.451760	-4.948011
1HDR	A	ARG	18	T	-7.285820	8.553316	-11.894380	-4.885163
1HDR	A	GLY	19	T	-7.266177	8.570209	-11.934719	-4.878578
1HDR	A	ALA	20	H	-7.266935	8.566227	-11.930210	-4.877603
1HDR	A	LEU	21	H	-7.664583	10.153413	-11.249047	-4.782573
1HDR	A	GLY	22	H	-7.852733	10.183908	-11.062006	-4.761006
1HDR	A	SER	23	H	-9.287454	9.137536	-13.146265	-4.688317
1HDR	A	ARG	24	H	-12.999955	12.011863	-17.999379	-5.193291
1HDR	A	CYS	25	H	-13.123920	12.386686	-18.003139	-5.211487
1HDR	A	VAL	26	H	-13.193408	12.418790	-17.856141	-5.167552
1HDR	A	GLN	27	H	-13.176876	12.632526	-17.722484	-5.148576
1HDR	A	ALA	28	H	-12.979498	12.862324	-17.213023	-4.914779
1HDR	A	PHE	29	H	-11.835944	12.127081	-14.974875	-4.559195
1HDR	A	ARG	30	H	-10.863210	11.435882	-14.306650	-4.630551
1HDR	A	ALA	31	H	-10.814330	11.738107	-14.330891	-4.683492
1HDR	A	ARG	32	H	-10.813490	11.758913	-14.326351	-4.685071
1HDR	A	ASN	33	C	-10.815452	11.775959	-14.314898	-4.689646
1HDR	A	TRP	34	C	-10.920542	11.744077	-14.221104	-4.720160
1HDR	A	TRP	35	E	-12.124227	15.829225	-14.525263	-5.162334
1HDR	A	VAL	36	E	-12.060780	13.798297	-14.256853	-4.218433
1HDR	A	ALA	37	E	-11.302977	11.799427	-14.131763	-4.075016
1HDR	A	SER	38	E	-9.432609	9.899273	-12.408693	-4.166111

1HDR	A	VAL	39	E	-7.815359	10.498314	-10.468506	-4.493469
1HDR	A	ASP	40	E	-7.759731	10.411338	-10.791124	-4.597767
1HDR	A	VAL	41	T	-7.223404	9.050371	-11.733047	-5.092238
1HDR	A	VAL	42	T	-7.041031	8.744255	-12.220065	-5.327529
1HDR	A	GLU	43	T	-6.739588	8.650747	-12.246001	-5.533011
1HDR	A	ASN	44	T	-6.817484	8.302589	-12.649059	-5.713849
1HDR	A	GLU	45	T	-6.781689	8.243294	-12.635319	-5.648010
1HDR	A	GLU	46	T	-6.967871	8.315486	-12.750506	-5.723222
1HDR	A	ALA	47	T	-7.113469	8.507434	-12.480620	-5.618742
1HDR	A	SER	48	T	-7.935473	8.580684	-13.039193	-4.960835
1HDR	A	ALA	49	E	-8.041522	8.993791	-12.523521	-4.701601
1HDR	A	SER	50	E	-8.616220	11.189515	-12.070908	-4.485759
1HDR	A	ILE	51	E	-8.580728	12.116692	-11.282795	-4.300805
1HDR	A	ILE	52	E	-7.607847	10.647459	-10.532671	-4.611484
1HDR	A	VAL	53	C	-6.729908	9.353810	-10.538088	-4.949210
1HDR	A	LYS	54	C	-6.547847	8.642740	-11.125848	-5.066419
1HDR	A	MET	55	C	-6.520272	8.712836	-11.156978	-5.066815
1HDR	A	THR	56	C	-6.481583	8.756945	-11.177237	-5.058466
1HDR	A	ASP	57	C	-6.533623	8.525244	-11.340292	-5.102565
1HDR	A	SER	58	C	-7.021969	7.922083	-12.346650	-5.183694
1HDR	A	PHE	59	H	-7.564416	9.637987	-11.795803	-4.917553
1HDR	A	THR	60	H	-7.743560	9.381860	-11.842502	-4.868034
1HDR	A	GLU	61	H	-8.304627	8.626515	-12.562782	-4.870445
1HDR	A	GLN	62	H	-10.081312	9.105902	-15.660574	-5.373669
1HDR	A	ALA	63	H	-10.154802	8.763165	-15.695425	-5.348853
1HDR	A	ASP	64	H	-10.231167	8.209700	-15.814241	-5.311115
1HDR	A	GLN	65	H	-11.994265	9.835686	-17.730439	-5.080764
1HDR	A	VAL	66	H	-10.858249	12.103835	-13.782608	-4.462628
1HDR	A	THR	67	H	-10.248152	10.611527	-14.309851	-4.703053
1HDR	A	ALA	68	H	-7.983404	6.762601	-11.997951	-4.052643
1HDR	A	GLU	69	H	-7.543251	8.177509	-11.269346	-4.138824
1HDR	A	VAL	70	H	-7.287245	9.250074	-10.580821	-4.067059
1HDR	A	GLY	71	H	-6.465152	7.852788	-10.191511	-4.189269
1HDR	A	LYS	72	H	-6.268973	7.710303	-10.281309	-4.189961
1HDR	A	LEU	73	H	-6.244714	7.853639	-10.291457	-4.247005
1HDR	A	LEU	74	H	-6.215956	7.732780	-10.467827	-4.327866
1HDR	A	GLY	75	T	-6.207608	7.508001	-10.666312	-4.386306
1HDR	A	GLU	76	T	-6.601923	7.619000	-11.237282	-4.534271
1HDR	A	GLU	77	T	-7.007623	7.879842	-11.941550	-4.869437
1HDR	A	LYS	78	C	-7.248281	7.477905	-12.247160	-4.942535
1HDR	A	VAL	79	E	-7.775412	7.374996	-12.353531	-4.839210
1HDR	A	ASP	80	E	-11.234887	11.633281	-15.542171	-5.051608
1HDR	A	ALA	81	E	-11.140098	15.987669	-12.011938	-4.250594
1HDR	A	ILE	82	E	-10.878628	16.091910	-11.783894	-4.216773
1HDR	A	LEU	83	E	-9.305734	12.579434	-11.186078	-4.374178
1HDR	A	CYS	84	E	-7.137969	8.386907	-10.769752	-4.617201
1HDR	A	VAL	85	C	-6.391724	9.371192	-9.552268	-4.509817
1HDR	A	ALA	86	C	-6.306427	9.213059	-9.793174	-4.535225
1HDR	A	GLY	87	C	-5.091010	7.240078	-9.485912	-4.969487
1HDR	A	GLY	88	C	-5.005733	7.215141	-9.636586	-4.970949
1HDR	A	TRP	89	C	-5.016497	7.195064	-9.631175	-4.982986
1HDR	A	ALA	90	C	-5.058190	7.002339	-9.683044	-5.021788
1HDR	A	GLY	91	C	-5.051483	6.924313	-9.750158	-5.025979
1HDR	A	GLY	92	B	-6.012941	6.700780	-11.254663	-4.977163
1HDR	A	ASN	93	T	-6.321024	4.735871	-12.431515	-4.586890
1HDR	A	ALA	94	T	-6.264059	4.323610	-12.489973	-4.471665
1HDR	A	LYS	95	T	-6.272411	4.269133	-12.481717	-4.461271
1HDR	A	SER	96	T	-6.410984	4.128787	-12.323293	-4.318863
1HDR	A	LYS	97	C	-6.451849	4.142905	-12.208735	-4.256380
1HDR	A	SER	98	H	-7.147090	4.487998	-12.869529	-4.221956
1HDR	A	LEU	99	H	-7.899696	6.529266	-13.061827	-4.333900
1HDR	A	PHE	100	H	-7.945571	6.574140	-12.971200	-4.334651
1HDR	A	LYS	101	H	-8.012745	6.552683	-12.857794	-4.330636
1HDR	A	ASN	102	H	-9.226627	8.216152	-14.561791	-4.789487
1HDR	A	CYS	103	H	-9.681320	8.790675	-14.857163	-4.970808
1HDR	A	ASP	104	H	-10.309420	8.195650	-16.112528	-5.248916
1HDR	A	LEU	105	H	-11.193405	8.373150	-16.873396	-5.322378
1HDR	A	MET	106	H	-14.111868	11.949262	-20.150102	-5.856553
1HDR	A	TRP	107	H	-14.536072	12.398048	-20.049143	-5.745810
1HDR	A	LYS	108	H	-15.406366	13.440559	-21.047207	-5.906857
1HDR	A	GLN	109	H	-15.234865	15.590245	-19.387131	-5.767062
1HDR	A	SER	110	H	-14.075281	15.631794	-17.298457	-5.502319
1HDR	A	ILE	111	H	-12.098698	15.579603	-14.044722	-5.103401
1HDR	A	TRP	112	H	-12.034656	15.751067	-14.141600	-5.128972
1HDR	A	THR	113	H	-11.850249	14.960469	-14.693941	-5.154653
1HDR	A	SER	114	H	-11.802486	14.769183	-14.874797	-5.152734
1HDR	A	THR	115	H	-11.168370	12.491455	-15.014059	-5.034158
1HDR	A	ILE	116	H	-11.224468	11.986906	-15.281722	-5.028562
1HDR	A	SER	117	H	-11.165056	11.965867	-15.332853	-5.019899
1HDR	A	SER	118	H	-11.069082	12.175223	-15.089036	-4.941931
1HDR	A	HIS	119	H	-10.348720	12.584267	-13.594552	-4.837104

1HDR	A	LEU	120	H	-10.421162	12.959971	-13.344869	-4.824473
1HDR	A	ALA	121	H	-10.418670	13.014999	-13.324132	-4.826649
1HDR	A	THR	122	H	-10.437812	13.025722	-13.251092	-4.821821
1HDR	A	LYS	123	H	-10.461674	13.113276	-13.217642	-4.861679
1HDR	A	HIS	124	H	-10.794663	13.643593	-14.095295	-5.265611
1HDR	A	LEU	125	E	-8.280713	9.433674	-12.194795	-5.019997
1HDR	A	LYS	126	E	-7.886110	9.407046	-12.260724	-5.069956
1HDR	A	GLU	127	E	-7.700885	10.069757	-11.867298	-4.995558
1HDR	A	GLY	128	E	-7.694132	10.100780	-11.877252	-4.994550
1HDR	A	GLY	129	E	-7.695334	10.102136	-11.869106	-4.993167
1HDR	A	LEU	130	E	-7.966574	10.523579	-11.694457	-4.979441
1HDR	A	LEU	131	E	-8.442059	11.993434	-10.910603	-4.797509
1HDR	A	THR	132	E	-9.944756	13.641438	-12.689520	-4.794354
1HDR	A	LEU	133	E	-10.337485	14.384213	-12.687755	-4.657807
1HDR	A	ALA	134	E	-9.979488	11.906100	-13.396874	-4.612990
1HDR	A	GLY	135	C	-8.771334	11.226649	-12.220832	-4.856886
1HDR	A	ALA	136	C	-8.452670	12.296290	-12.975340	-5.876317
1HDR	A	LYS	137	G	-7.521401	10.913742	-10.903079	-4.890019
1HDR	A	ALA	138	G	-5.142817	8.011849	-7.654733	-4.051333
1HDR	A	ALA	139	G	-4.859223	8.340685	-7.704992	-4.139206
1HDR	A	LEU	140	G	-4.243104	7.177670	-7.718343	-4.174272
1HDR	A	ASP	141	C	-3.332771	4.929332	-7.840951	-4.369282
1HDR	A	GLY	142	C	-3.279298	5.088603	-7.896499	-4.394018
1HDR	A	THR	143	T	-3.304338	4.964559	-7.910125	-4.408395
1HDR	A	PRO	144	T	-3.320824	4.852910	-7.913416	-4.411140
1HDR	A	GLY	145	T	-3.408254	4.580015	-7.935513	-4.441572
1HDR	A	MET	146	B	-4.720468	6.803304	-8.477855	-4.619777
1HDR	A	ILE	147	H	-7.121791	8.864292	-10.495391	-4.346340
1HDR	A	GLY	148	H	-8.047332	7.953115	-11.988894	-4.479592
1HDR	A	TYR	149	H	-10.572069	12.377230	-14.689038	-5.186211
1HDR	A	GLY	150	H	-10.436146	11.368305	-15.129726	-5.198876
1HDR	A	MET	151	H	-10.362996	10.878602	-15.246933	-5.130637
1HDR	A	ALA	152	H	-10.525415	10.466700	-15.627439	-5.099944
1HDR	A	LYS	153	H	-10.678758	10.034229	-15.930646	-5.109176
1HDR	A	GLY	154	H	-10.639527	10.079358	-15.935841	-5.086532
1HDR	A	ALA	155	H	-10.900083	10.917068	-15.596844	-4.955681
1HDR	A	VAL	156	H	-11.289551	11.896470	-15.433417	-4.892195
1HDR	A	HIS	157	H	-11.789714	12.104980	-16.037979	-4.951337
1HDR	A	GLN	158	H	-11.890964	11.667626	-16.254947	-4.916336
1HDR	A	LEU	159	H	-12.308412	12.438170	-16.752133	-5.137197
1HDR	A	CYS	160	H	-12.419442	11.383142	-20.091119	-6.910694
1HDR	A	GLN	161	H	-10.750358	10.026291	-16.740387	-5.968960
1HDR	A	SER	162	H	-8.962504	8.100729	-13.941121	-4.992034
1HDR	A	LEU	163	H	-5.589526	6.392936	-9.529795	-4.446763
1HDR	A	ALA	164	H	-4.691107	3.851395	-9.983965	-4.352816
1HDR	A	GLY	165	T	-3.310467	2.213429	-9.405030	-4.697318
1HDR	A	LYS	166	T	-3.271532	2.494986	-9.408645	-4.726464
1HDR	A	ASN	167	T	-3.271075	2.500922	-9.409639	-4.726771
1HDR	A	SER	168	T	-3.282761	2.425112	-9.406714	-4.731749
1HDR	A	GLY	169	C	-3.316493	2.475005	-9.338530	-4.757478
1HDR	A	MET	170	C	-4.737487	7.066941	-9.307940	-4.972376
1HDR	A	PRO	171	T	-5.450954	8.372849	-8.988938	-4.377335
1HDR	A	PRO	172	T	-5.450845	8.314969	-8.968150	-4.337719
1HDR	A	GLY	173	T	-5.460725	8.293213	-8.937682	-4.330111
1HDR	A	ALA	174	T	-6.156010	8.738512	-9.072889	-3.864674
1HDR	A	ALA	175	E	-6.394856	8.357674	-8.964927	-3.674611
1HDR	A	ALA	176	E	-7.387974	8.678207	-10.243846	-3.892167
1HDR	A	ILE	177	E	-8.577711	11.708527	-10.336423	-4.001537
1HDR	A	ALA	178	E	-9.689111	14.594050	-10.392213	-3.487826
1HDR	A	VAL	179	E	-8.321631	14.326696	-8.135471	-3.683149
1HDR	A	LEU	180	E	-7.297200	14.513620	-7.271509	-4.004012
1HDR	A	PRO	181	T	-7.262105	14.359876	-7.476945	-4.028255
1HDR	A	VAL	182	T	-7.253268	14.335872	-7.546699	-4.046388
1HDR	A	THR	183	T	-7.255843	14.332896	-7.542022	-4.051773
1HDR	A	LEU	184	B	-7.350881	14.322913	-7.502236	-4.119587
1HDR	A	ASP	185	C	-8.581238	11.216092	-12.110430	-4.742774
1HDR	A	THR	186	C	-8.916310	10.225660	-13.990054	-5.284832
1HDR	A	PRO	187	H	-8.893296	8.502429	-14.997454	-5.331015
1HDR	A	MET	188	H	-8.881655	8.390273	-15.072415	-5.327716
1HDR	A	ASN	189	H	-8.916965	8.217899	-15.184161	-5.357715
1HDR	A	ARG	190	H	-9.002935	8.440664	-14.877563	-5.083039
1HDR	A	LYS	191	T	-6.839833	5.653528	-11.317277	-4.210180
1HDR	A	SER	192	T	-5.116561	6.262700	-8.384357	-3.862537
1HDR	A	MET	193	T	-4.718121	6.293202	-8.528089	-4.037911
1HDR	A	PRO	194	T	-4.697394	6.367156	-8.569216	-4.048541
1HDR	A	GLU	195	T	-4.696923	6.369018	-8.572247	-4.049026
1HDR	A	ALA	196	T	-4.712738	6.389548	-8.499801	-4.044957
1HDR	A	ASP	197	C	-5.098657	6.471063	-8.754771	-4.228832
1HDR	A	PHE	198	G	-6.676963	8.446680	-9.809442	-4.352582
1HDR	A	SER	199	G	-8.776351	8.648104	-12.740194	-4.613904
1HDR	A	SER	200	G	-11.102302	9.336620	-15.380526	-4.551014

1HDR	A	TRP	201	C	-12.672660	15.151620	-15.967946	-5.277372
1HDR	A	THR	202	B	-12.033264	14.845095	-14.650688	-5.093408
1HDR	A	PRO	203	C	-11.555440	15.957944	-13.576267	-4.987415
1HDR	A	LEU	204	H	-11.546836	16.016838	-13.575044	-4.987429
1HDR	A	GLU	205	H	-11.386530	15.641526	-13.747384	-4.965403
1HDR	A	PHE	206	H	-11.092302	16.044644	-13.039745	-4.831231
1HDR	A	LEU	207	H	-11.153083	16.563437	-12.723731	-4.786604
1HDR	A	VAL	208	H	-11.345382	16.454307	-12.743193	-4.743368
1HDR	A	GLU	209	H	-11.333252	16.385916	-12.845684	-4.772628
1HDR	A	THR	210	H	-11.484735	16.927258	-12.406971	-4.736619
1HDR	A	PHE	211	H	-12.478715	18.009809	-13.571009	-5.041077
1HDR	A	HIS	212	H	-13.225798	15.844536	-16.501525	-5.692737
1HDR	A	ASP	213	H	-13.105034	15.623752	-16.608811	-5.709324
1HDR	A	TRP	214	H	-11.494369	14.362218	-14.095901	-5.286463
1HDR	A	ILE	215	H	-7.548454	7.148477	-11.984462	-4.696059
1HDR	A	THR	216	H	-7.470549	7.006995	-12.292961	-4.735804
1HDR	A	GLY	217	T	-7.403677	7.032525	-12.408990	-4.727379
1HDR	A	LYS	218	T	-7.399340	7.036529	-12.427651	-4.725393
1HDR	A	ASN	219	T	-7.397631	7.036717	-12.435555	-4.724178
1HDR	A	ARG	220	T	-8.277004	6.695742	-13.999514	-4.822008
1HDR	A	PRO	221	C	-8.493838	7.483735	-13.477695	-4.543178
1HDR	A	SER	222	T	-9.080439	8.080726	-13.766771	-4.337051
1HDR	A	SER	223	T	-9.152293	8.201813	-13.607200	-4.325079
1HDR	A	GLY	224	T	-9.197360	8.151397	-13.508813	-4.308664
1HDR	A	SER	225	T	-9.209042	8.131274	-13.463354	-4.304176
1HDR	A	LEU	226	E	-10.291900	9.283224	-14.475488	-4.566619
1HDR	A	ILE	227	E	-11.573308	13.368487	-14.748979	-4.860429
1HDR	A	GLN	228	E	-11.048895	12.929373	-14.360527	-5.115657
1HDR	A	VAL	229	E	-7.607342	10.706418	-9.957851	-4.507911
1HDR	A	VAL	230	E	-6.518761	7.911754	-10.832114	-4.863210
1HDR	A	THR	231	E	-6.037716	6.711218	-10.996117	-4.735874
1HDR	A	THR	232	E	-4.417792	6.858363	-8.404020	-4.769615
1HDR	A	GLU	233	T	-4.407595	6.854899	-8.459071	-4.772993
1HDR	A	GLY	234	T	-4.407993	6.847100	-8.462389	-4.774013
1HDR	A	ARG	235	E	-4.421670	6.838345	-8.404321	-4.770620
1HDR	A	THR	236	E	-4.443621	6.879283	-8.301269	-4.775627
1HDR	A	GLU	237	E	-6.666805	7.385297	-11.564703	-4.946788
1HDR	A	LEU	238	E	-6.428739	14.004201	-7.803859	-5.072258
1HDR	A	THR	239	E	-5.856553	12.405547	-7.348022	-4.540987
1HDR	A	PRO	240	E	-4.365078	10.703976	-4.619789	-3.427468
1HDR	A	ALA	241	E	-4.365078	10.703976	-4.619789	-3.427468
1HDR	A	TYR	242	C	-4.365078	10.703976	-4.619789	-3.427468
1HDR	A	PHE	243	C	-4.365078	10.703976	-4.619789	-3.427468
1HMT	A	VAL	1	C	-7.810381	11.702841	-8.876253	-3.638721
1HMT	A	ASP	2	G	-7.810381	11.702841	-8.876253	-3.638721
1HMT	A	ALA	3	G	-7.810381	11.702841	-8.876253	-3.638721
1HMT	A	PHE	4	G	-7.810381	11.702841	-8.876253	-3.638721
1HMT	A	LEU	5	C	-8.909588	13.902863	-10.424736	-4.640323
1HMT	A	GLY	6	E	-10.287301	14.051318	-13.169206	-5.461479
1HMT	A	THR	7	E	-11.331822	16.302858	-14.561673	-6.108708
1HMT	A	TRP	8	E	-11.902229	15.967909	-14.742319	-5.429115
1HMT	A	LYS	9	E	-10.400776	9.966288	-14.960638	-5.156119
1HMT	A	LEU	10	E	-8.406570	8.350787	-12.461832	-4.677655
1HMT	A	VAL	11	E	-7.978271	7.038715	-13.175710	-4.746162
1HMT	A	ASP	12	E	-7.976397	7.039203	-13.189029	-4.748322
1HMT	A	SER	13	E	-7.975716	7.040837	-13.194610	-4.749466
1HMT	A	LYS	14	E	-7.980661	7.020348	-13.188749	-4.749909
1HMT	A	ASN	15	T	-8.357013	5.895442	-13.914925	-4.830248
1HMT	A	PHE	16	H	-10.572262	9.382226	-16.588906	-5.602356
1HMT	A	ASP	17	H	-10.770540	9.778541	-16.480072	-5.690087
1HMT	A	ASP	18	H	-10.849824	10.002514	-16.251364	-5.689193
1HMT	A	TYR	19	H	-12.186448	15.549882	-16.182557	-6.061183
1HMT	A	MET	20	H	-9.502013	11.370520	-13.193588	-5.452188
1HMT	A	LYS	21	H	-8.006283	10.133547	-11.528773	-4.979501
1HMT	A	SER	22	H	-6.884000	8.980148	-10.590250	-4.823785
1HMT	A	LEU	23	H	-6.646076	8.962481	-10.672290	-4.825361
1HMT	A	GLY	24	C	-5.875892	6.274663	-10.660431	-4.552896
1HMT	A	VAL	25	C	-5.757810	6.538314	-10.554166	-4.513159
1HMT	A	GLY	26	C	-5.761332	6.495856	-10.562595	-4.509119
1HMT	A	PHE	27	H	-5.840963	6.170136	-10.587984	-4.467483
1HMT	A	ALA	28	H	-5.893307	5.916480	-10.566298	-4.434155
1HMT	A	THR	29	H	-6.712479	7.856038	-10.300563	-4.385316
1HMT	A	ARG	30	H	-8.166147	8.786276	-12.416552	-4.830005
1HMT	A	GLN	31	H	-8.559870	7.274973	-12.880213	-4.023747
1HMT	A	VAL	32	H	-7.698997	7.083355	-11.372644	-3.801102
1HMT	A	ALA	33	H	-6.834373	7.070617	-10.643555	-4.007644
1HMT	A	SER	34	H	-6.677145	7.283297	-10.687352	-4.058976
1HMT	A	MET	35	H	-6.633299	7.468060	-10.731962	-4.105741
1HMT	A	THR	36	C	-6.648433	7.521819	-10.679720	-4.119914
1HMT	A	LYS	37	C	-6.736212	7.582294	-10.624389	-4.173730
1HMT	A	PRO	38	C	-7.362091	8.529015	-10.982607	-4.363201

1HMT	A	THR	39	E	-8.162994	10.078135	-11.397786	-4.741485
1HMT	A	THR	40	E	-9.850633	13.520920	-12.816123	-5.191169
1HMT	A	ILE	41	E	-9.947911	12.894575	-13.258347	-5.072863
1HMT	A	ILE	42	E	-7.209464	8.933116	-10.860109	-4.942776
1HMT	A	GLU	43	E	-6.020086	5.142110	-11.847603	-5.113807
1HMT	A	LYS	44	E	-3.651203	5.308977	-7.939758	-4.714281
1HMT	A	ASN	45	E	-3.607623	5.487923	-7.960626	-4.697443
1HMT	A	GLY	46	T	-3.607307	5.490322	-7.962403	-4.697546
1HMT	A	ASP	47	T	-3.608660	5.482464	-7.955744	-4.696940
1HMT	A	ILE	48	E	-3.617524	5.496092	-7.894246	-4.689944
1HMT	A	LEU	49	E	-5.173401	7.827333	-8.224774	-4.460284
1HMT	A	THR	50	E	-8.057623	10.055376	-11.332908	-4.879227
1HMT	A	LEU	51	E	-11.083189	15.351328	-13.677706	-5.339941
1HMT	A	LYS	52	E	-10.750911	11.072224	-16.000517	-5.847075
1HMT	A	THR	53	E	-9.528519	12.445967	-13.008709	-5.413723
1HMT	A	HIS	54	E	-8.627517	12.002349	-11.964767	-5.272092
1HMT	A	SER	55	T	-6.349845	10.790984	-9.050548	-5.110141
1HMT	A	THR	56	T	-6.309546	10.797659	-9.180518	-5.112749
1HMT	A	PHE	57	T	-6.301822	10.827200	-9.211808	-5.119815
1HMT	A	LYS	58	T	-6.292531	10.829290	-9.252986	-5.123383
1HMT	A	ASN	59	E	-6.149663	10.737598	-9.336726	-5.075149
1HMT	A	THR	60	E	-6.851935	10.734962	-10.144043	-5.000185
1HMT	A	GLU	61	E	-6.951557	10.776556	-9.969093	-4.972357
1HMT	A	ILE	62	E	-6.975577	10.688270	-9.894561	-4.943156
1HMT	A	SER	63	E	-7.002885	10.736709	-9.759936	-4.915007
1HMT	A	PHE	64	E	-7.874515	14.372304	-8.996626	-4.581934
1HMT	A	LYS	65	E	-4.690063	10.121521	-6.430056	-4.502692
1HMT	A	LEU	66	T	-4.681155	10.161805	-6.458739	-4.504789
1HMT	A	GLY	67	T	-4.659322	10.153828	-6.565244	-4.516640
1HMT	A	VAL	68	T	-4.659367	10.152422	-6.565737	-4.516762
1HMT	A	GLU	69	C	-4.660811	10.141887	-6.563430	-4.517951
1HMT	A	PHE	70	E	-6.408374	10.834188	-9.181861	-4.797944
1HMT	A	ASP	71	E	-6.574344	9.999264	-9.651429	-4.880589
1HMT	A	GLU	72	E	-8.025307	10.671326	-12.491967	-5.450419
1HMT	A	THR	73	E	-7.167412	8.415214	-12.024235	-5.247161
1HMT	A	THR	74	T	-7.211540	8.065469	-12.080062	-5.223298
1HMT	A	ALA	75	T	-7.216423	8.030404	-12.069078	-5.220539
1HMT	A	ASP	76	T	-7.304473	7.843023	-11.951369	-5.195793
1HMT	A	ASP	77	T	-7.309777	7.821945	-11.926307	-5.192029
1HMT	A	ARG	78	C	-10.367292	9.334924	-15.884369	-5.616665
1HMT	A	LYS	79	E	-11.479538	9.352263	-17.403178	-5.204424
1HMT	A	VAL	80	E	-11.272088	11.597472	-15.036761	-4.576126
1HMT	A	LYS	81	E	-11.076537	12.055206	-14.515949	-4.493662
1HMT	A	SER	82	E	-10.273571	12.840190	-12.281444	-4.072359
1HMT	A	ILE	83	E	-8.901544	13.153187	-10.371417	-4.166097
1HMT	A	VAL	84	E	-6.511942	9.503977	-8.534069	-4.027692
1HMT	A	THR	85	E	-3.956493	5.907148	-7.524254	-4.347360
1HMT	A	LEU	86	E	-2.478186	6.388839	-5.956040	-4.637656
1HMT	A	ASP	87	E	-2.462239	6.480806	-5.989673	-4.647894
1HMT	A	GLY	88	T	-2.462088	6.482087	-5.990586	-4.647957
1HMT	A	GLY	89	T	-2.462734	6.478650	-5.987649	-4.648481
1HMT	A	LYS	90	E	-2.513157	6.517345	-5.837666	-4.663096
1HMT	A	LEU	91	E	-4.623944	9.678367	-7.068248	-4.882041
1HMT	A	VAL	92	E	-7.344882	11.463061	-9.460241	-4.719052
1HMT	A	HIS	93	E	-11.198906	18.631199	-14.616875	-7.324485
1HMT	A	LEU	94	E	-12.844289	20.163695	-16.812053	-7.913287
1HMT	A	GLN	95	E	-11.008587	10.746008	-16.557729	-6.298856
1HMT	A	LYS	96	E	-7.310432	8.373778	-12.165981	-5.607104
1HMT	A	TRP	97	E	-6.106893	8.038663	-10.916158	-5.513919
1HMT	A	ASP	98	T	-5.871015	7.353852	-11.316615	-5.473108
1HMT	A	GLY	99	T	-5.867245	7.359388	-11.333344	-5.472747
1HMT	A	GLN	100	E	-5.867339	7.358873	-11.332522	-5.472607
1HMT	A	GLU	101	E	-5.921475	7.262408	-11.253647	-5.459777
1HMT	A	THR	102	E	-6.519243	5.997638	-12.170041	-5.389714
1HMT	A	THR	103	E	-8.859192	8.274561	-13.965021	-5.411461
1HMT	A	LEU	104	E	-11.529773	12.954055	-14.984603	-5.028824
1HMT	A	VAL	105	E	-11.205367	14.482319	-13.794451	-4.959058
1HMT	A	ARG	106	E	-9.347012	13.538753	-11.586286	-5.147811
1HMT	A	GLU	107	E	-4.450486	7.769013	-7.191628	-4.403611
1HMT	A	LEU	108	E	-2.707404	7.264629	-5.384345	-4.386881
1HMT	A	ILE	109	E	-2.690905	7.320242	-5.437147	-4.394701
1HMT	A	ASP	110	T	-2.690796	7.320978	-5.438064	-4.394811
1HMT	A	GLY	111	T	-2.690804	7.320899	-5.437987	-4.394801
1HMT	A	LYS	112	E	-2.722650	7.288186	-5.335318	-4.389476
1HMT	A	LEU	113	E	-4.829087	9.154441	-7.217590	-4.583799
1HMT	A	ILE	114	E	-7.799583	11.236805	-10.373927	-4.911944
1HMT	A	LEU	115	E	-10.804900	15.894200	-13.260360	-5.246548
1HMT	A	THR	116	E	-10.401249	12.732450	-14.153637	-5.255933
1HMT	A	LEU	117	E	-8.078157	8.929615	-11.780429	-4.748003
1HMT	A	THR	118	E	-6.018458	6.532280	-10.215066	-4.566947
1HMT	A	HIS	119	E	-5.100728	6.166232	-9.296056	-4.397986

1HMT	A	GLY	120	T	-4.497145	5.438428	-8.878541	-4.202100
1HMT	A	THR	121	T	-4.483423	5.497223	-8.898372	-4.201506
1HMT	A	ALA	122	E	-4.484773	5.489531	-8.891883	-4.200266
1HMT	A	VAL	123	E	-4.529603	5.413167	-8.791160	-4.171589
1HMT	A	CYS	124	E	-4.741381	5.130693	-8.678564	-4.092874
1HMT	A	THR	125	E	-6.720784	8.007131	-9.743934	-4.173758
1HMT	A	ARG	126	E	-11.767835	12.976795	-15.625093	-5.434518
1HMT	A	THR	127	E	-11.381122	15.215318	-14.431509	-5.725766
1HMT	A	TYR	128	E	-9.776021	13.871359	-11.889635	-5.009088
1HMT	A	GLU	129	E	-9.776021	13.871359	-11.889635	-5.009088
1HMT	A	LYS	130	E	-9.776021	13.871359	-11.889635	-5.009088
1HMT	A	GLU	131	C	-9.776021	13.871359	-11.889635	-5.009088
1HNA	A	PRO	1	C	-9.816064	12.588382	-12.238731	-4.552501
1HNA	A	MET	2	E	-9.816064	12.588382	-12.238731	-4.552501
1HNA	A	THR	3	E	-9.816064	12.588382	-12.238731	-4.552501
1HNA	A	LEU	4	E	-9.816064	12.588382	-12.238731	-4.552501
1HNA	A	GLY	5	E	-10.784322	13.379247	-13.836936	-5.362686
1HNA	A	TYR	6	E	-12.884104	18.753492	-14.586086	-6.055055
1HNA	A	TRP	7	E	-12.863008	18.681863	-14.708820	-6.074447
1HNA	A	ASN	8	C	-12.721475	17.834584	-15.390602	-6.120217
1HNA	A	ILE	9	C	-12.290238	16.162058	-15.454064	-5.719543
1HNA	A	ARG	10	T	-12.487663	14.658193	-16.183121	-5.573632
1HNA	A	GLY	11	T	-11.675094	13.936916	-15.520691	-5.622077
1HNA	A	LEU	12	T	-11.410974	15.091388	-14.717799	-5.529342
1HNA	A	ALA	13	H	-11.424450	15.101940	-14.644848	-5.511359
1HNA	A	HIS	14	H	-11.499971	15.171468	-14.527666	-5.534107
1HNA	A	SER	15	H	-11.511787	15.192513	-14.460347	-5.526933
1HNA	A	ILE	16	H	-12.000510	17.188719	-13.384501	-5.379131
1HNA	A	ARG	17	H	-14.473863	19.696527	-15.872140	-5.363569
1HNA	A	LEU	18	H	-13.405643	21.878658	-13.111676	-5.436275
1HNA	A	LEU	19	H	-12.449146	20.436320	-13.024115	-5.683173
1HNA	A	LEU	20	H	-11.520652	17.000270	-13.927821	-5.877340
1HNA	A	GLU	21	H	-11.173810	15.577010	-14.657958	-5.980120
1HNA	A	TYR	22	H	-10.004031	11.948271	-13.983857	-5.428133
1HNA	A	THR	23	H	-9.842968	11.806582	-14.173097	-5.436893
1HNA	A	ASP	24	C	-9.813478	11.639101	-14.305914	-5.428555
1HNA	A	SER	25	C	-9.817403	11.449386	-14.382831	-5.415099
1HNA	A	SER	26	C	-9.839836	11.347802	-14.350806	-5.386732
1HNA	A	TYR	27	E	-10.462636	11.332243	-15.267185	-5.483445
1HNA	A	GLU	28	E	-11.139478	11.100798	-16.384627	-5.532294
1HNA	A	GLU	29	E	-11.601824	12.111216	-16.525676	-5.760821
1HNA	A	LYS	30	E	-12.479616	12.878966	-17.753779	-6.098962
1HNA	A	LYS	31	E	-13.161838	13.679160	-19.094750	-6.653309
1HNA	A	TYR	32	E	-11.316844	13.626923	-15.504994	-6.197803
1HNA	A	THR	33	C	-7.865180	9.027174	-12.265812	-5.344129
1HNA	A	MET	34	C	-6.284372	8.221599	-10.232475	-4.884715
1HNA	A	GLY	35	C	-3.826335	3.279071	-8.479683	-4.054586
1HNA	A	ASP	36	C	-3.766955	3.624033	-8.482941	-4.075223
1HNA	A	ALA	37	T	-3.758552	3.672755	-8.504662	-4.079720
1HNA	A	PRO	38	T	-3.759025	3.668699	-8.501626	-4.078596
1HNA	A	ASP	39	T	-3.766871	3.608648	-8.480195	-4.068120
1HNA	A	TYR	40	T	-5.077473	6.916315	-8.690300	-4.275265
1HNA	A	ASP	41	C	-6.278501	7.112890	-10.025162	-4.385709
1HNA	A	ARG	42	H	-8.863542	10.253797	-12.211560	-4.765810
1HNA	A	SER	43	H	-11.405978	12.160212	-15.913488	-5.462666
1HNA	A	GLN	44	H	-12.520193	13.086616	-17.618094	-5.827460
1HNA	A	TRP	45	H	-11.644043	15.080970	-15.192021	-5.908716
1HNA	A	LEU	46	H	-9.835462	12.169427	-13.839732	-5.671097
1HNA	A	ASN	47	H	-8.246607	9.684051	-12.524488	-5.269042
1HNA	A	GLU	48	T	-8.115464	10.018880	-12.532812	-5.260744
1HNA	A	LYS	49	T	-6.634377	9.953123	-9.854472	-4.877125
1HNA	A	PHE	50	T	-5.966313	11.146646	-8.512462	-4.759451
1HNA	A	LYS	51	T	-5.486181	10.670742	-8.277990	-4.710644
1HNA	A	LEU	52	T	-5.269353	10.492556	-8.286704	-4.699802
1HNA	A	GLY	53	T	-4.295328	9.307937	-6.906635	-4.446881
1HNA	A	LEU	54	T	-4.297475	9.310533	-6.891654	-4.441567
1HNA	A	ASP	55	T	-4.317579	9.219422	-6.869436	-4.430824
1HNA	A	PHE	56	T	-4.365032	9.130937	-6.767248	-4.410037
1HNA	A	PRO	57	T	-4.406757	9.061254	-6.648607	-4.389566
1HNA	A	ASN	58	T	-6.566208	10.501930	-9.336614	-4.541432
1HNA	A	LEU	59	T	-7.190385	10.883572	-9.490711	-4.486510
1HNA	A	PRO	60	T	-8.857605	13.898433	-9.671602	-4.299041
1HNA	A	TYR	61	E	-11.370277	17.718307	-12.483345	-4.973798
1HNA	A	LEU	62	E	-7.082014	9.677767	-9.986077	-4.639316
1HNA	A	ILE	63	E	-4.749649	6.443065	-8.612369	-4.528034
1HNA	A	ASP	64	E	-4.469155	6.415730	-8.911380	-4.657013
1HNA	A	GLY	65	T	-4.317842	6.692731	-8.773879	-4.592453
1HNA	A	THR	66	T	-4.313557	6.726181	-8.776883	-4.592041
1HNA	A	HIS	67	E	-4.319102	6.698492	-8.765559	-4.591561
1HNA	A	LYS	68	E	-4.700185	6.982984	-8.923009	-4.647972
1HNA	A	ILE	69	E	-5.182273	7.754795	-8.321286	-4.371060

1HNA	A	THR	70	E	-7.226512	11.338570	-9.263340	-4.544360
1HNA	A	GLN	71	C	-9.562009	12.010161	-14.048324	-5.389919
1HNA	A	SER	72	H	-9.720087	12.089448	-14.243303	-5.474230
1HNA	A	ASN	73	H	-9.830935	11.702601	-14.392172	-5.487102
1HNA	A	ALA	74	H	-9.896557	11.507047	-14.377000	-5.475423
1HNA	A	ILE	75	H	-10.567074	13.276666	-13.866235	-5.237867
1HNA	A	LEU	76	H	-11.149984	15.460891	-12.943432	-5.203604
1HNA	A	ARG	77	H	-13.955015	15.995896	-17.133078	-5.333077
1HNA	A	TYR	78	H	-12.634821	14.151057	-15.287546	-4.909743
1HNA	A	ILE	79	H	-10.295776	11.888169	-13.146357	-4.724102
1HNA	A	ALA	80	H	-8.678049	7.727796	-13.297391	-4.665331
1HNA	A	ARG	81	H	-8.336151	8.345957	-13.059639	-4.736919
1HNA	A	LYS	82	H	-8.234167	8.578081	-13.127291	-4.805377
1HNA	A	HIS	83	C	-7.910915	9.060377	-12.800365	-4.951804
1HNA	A	ASN	84	C	-7.677173	8.824781	-12.826007	-5.023409
1HNA	A	LEU	85	C	-7.726052	9.087400	-12.824730	-5.106358
1HNA	A	CYS	86	C	-7.064054	6.522489	-13.088140	-5.233693
1HNA	A	GLY	87	C	-5.387383	5.217288	-10.749347	-4.945691
1HNA	A	GLU	88	C	-5.248702	5.355213	-10.811695	-4.931306
1HNA	A	SER	89	C	-5.249413	5.343868	-10.812445	-4.929819
1HNA	A	GLU	90	H	-5.246568	5.349382	-10.823383	-4.929439
1HNA	A	LYS	91	H	-5.266878	5.342407	-10.741004	-4.917781
1HNA	A	GLU	92	H	-6.134807	6.008673	-11.186312	-4.883106
1HNA	A	GLN	93	H	-7.933322	6.933072	-13.400356	-4.909023
1HNA	A	ILE	94	H	-8.245078	7.070783	-13.246909	-4.929157
1HNA	A	ARG	95	H	-12.423710	10.196600	-19.577506	-6.380301
1HNA	A	GLU	96	H	-13.699517	11.400409	-21.500209	-6.815805
1HNA	A	ASP	97	H	-11.724271	10.033555	-16.507984	-5.125081
1HNA	A	ILE	98	H	-11.163412	10.607917	-15.930916	-5.129722
1HNA	A	LEU	99	H	-11.163013	10.649125	-15.914958	-5.132925
1HNA	A	GLU	100	H	-11.163578	10.647122	-15.911862	-5.132748
1HNA	A	ASN	101	H	-11.129828	10.734029	-15.992481	-5.164041
1HNA	A	GLN	102	H	-11.391644	11.133051	-15.760760	-5.190326
1HNA	A	PHE	103	H	-12.761637	12.611130	-17.455316	-5.708226
1HNA	A	MET	104	H	-12.805686	12.233100	-17.581965	-5.717862
1HNA	A	ASP	105	H	-12.800729	12.197227	-17.623078	-5.718731
1HNA	A	SER	106	H	-14.511798	11.738635	-21.103154	-6.017137
1HNA	A	ARG	107	H	-14.570012	11.592126	-21.137850	-5.956897
1HNA	A	MET	108	H	-11.899749	12.546402	-15.299147	-5.074797
1HNA	A	GLN	109	H	-11.701622	13.343494	-15.000514	-5.039371
1HNA	A	LEU	110	H	-10.802919	14.165584	-13.112086	-4.785530
1HNA	A	ALA	111	H	-10.530830	14.453204	-12.967929	-4.818829
1HNA	A	LYS	112	H	-10.448590	14.524748	-13.076095	-4.866453
1HNA	A	LEU	113	H	-10.395439	14.541481	-13.020167	-4.841557
1HNA	A	CYS	114	T	-9.146402	10.010718	-13.200698	-4.894852
1HNA	A	TYR	115	T	-9.020230	10.780941	-12.947679	-4.938973
1HNA	A	ASP	116	T	-6.814192	9.781538	-9.457482	-4.451932
1HNA	A	PRO	117	T	-5.428286	8.986870	-7.926334	-4.217979
1HNA	A	ASP	118	T	-5.358620	9.154854	-8.026811	-4.249525
1HNA	A	PHE	119	H	-5.317446	9.492696	-7.979100	-4.275470
1HNA	A	GLU	120	H	-5.055153	9.560457	-7.909847	-4.301724
1HNA	A	LYS	121	H	-5.077187	9.554262	-7.872393	-4.299788
1HNA	A	LEU	122	H	-5.487488	10.203788	-7.980273	-4.405667
1HNA	A	LYS	123	H	-5.575410	10.156156	-7.843917	-4.390222
1HNA	A	PRO	124	H	-5.641695	9.690365	-7.892683	-4.360543
1HNA	A	GLU	125	H	-7.597235	9.876320	-10.660923	-4.678939
1HNA	A	TYR	126	H	-11.132986	13.428947	-15.004266	-5.115752
1HNA	A	LEU	127	H	-10.435792	11.328203	-13.923053	-4.507331
1HNA	A	GLN	128	H	-9.038568	9.253790	-12.565974	-4.295531
1HNA	A	ALA	129	H	-8.984865	9.485882	-12.593045	-4.329890
1HNA	A	LEU	130	H	-8.971891	9.637746	-12.572168	-4.343121
1HNA	A	PRO	131	H	-8.891333	10.148254	-12.498538	-4.402726
1HNA	A	GLU	132	H	-8.810549	10.400394	-12.524072	-4.514706
1HNA	A	MET	133	H	-9.382769	12.575328	-12.668766	-4.900688
1HNA	A	LEU	134	H	-9.507538	12.721207	-12.572552	-4.945946
1HNA	A	LYS	135	H	-9.545057	12.503291	-12.602298	-4.942708
1HNA	A	LEU	136	H	-9.832760	11.779347	-12.975226	-5.023619
1HNA	A	TYR	137	H	-12.412790	12.969219	-16.520955	-5.203944
1HNA	A	SER	138	H	-12.168747	11.778353	-17.046234	-5.266437
1HNA	A	GLN	139	H	-10.297459	8.876985	-15.076406	-4.936653
1HNA	A	PHE	140	H	-10.034991	9.088061	-15.204185	-5.069525
1HNA	A	LEU	141	H	-8.423039	6.898376	-13.395673	-4.638962
1HNA	A	GLY	142	T	-8.384981	7.077248	-13.453544	-4.667696
1HNA	A	LYS	143	T	-8.385140	7.078936	-13.451035	-4.667398
1HNA	A	GLN	144	T	-8.408188	7.011251	-13.389938	-4.657243
1HNA	A	PRO	145	T	-8.421531	6.971516	-13.336384	-4.642684
1HNA	A	TRP	146	B	-9.838696	12.511791	-13.270051	-5.191367
1HNA	A	PHE	147	T	-9.489989	15.730743	-11.332915	-5.470853
1HNA	A	LEU	148	T	-7.685489	12.265567	-10.224940	-5.151070
1HNA	A	GLY	149	B	-7.315228	11.072642	-10.779405	-5.115362
1HNA	A	ASP	150	T	-7.314639	11.076147	-10.781910	-5.115501

1HNA	A	LYS	151	T	-7.316751	11.045531	-10.783566	-5.114347
1HNA	A	ILE	152	C	-7.329474	10.960776	-10.768551	-5.106242
1HNA	A	THR	153	C	-7.767158	9.723409	-11.422887	-5.074669
1HNA	A	PHE	154	H	-11.100334	16.692971	-12.767117	-5.202762
1HNA	A	VAL	155	H	-11.816242	18.936748	-12.289222	-4.931160
1HNA	A	ASP	156	H	-11.860721	18.957096	-12.158555	-4.911776
1HNA	A	PHE	157	H	-12.760744	19.562266	-13.025716	-4.788312
1HNA	A	ILE	158	H	-12.953121	18.408535	-13.464806	-4.607896
1HNA	A	ALA	159	H	-12.946713	17.865924	-13.781098	-4.629221
1HNA	A	TYR	160	H	-13.835402	17.469521	-16.091889	-5.217707
1HNA	A	ASP	161	H	-13.861063	17.287664	-16.127807	-5.219648
1HNA	A	VAL	162	H	-13.877927	17.175793	-16.141201	-5.217485
1HNA	A	LEU	163	H	-14.140719	17.593004	-15.856608	-5.241039
1HNA	A	GLU	164	H	-15.682509	15.406509	-21.154297	-6.269366
1HNA	A	ARG	165	H	-15.637560	15.617277	-21.066174	-6.338877
1HNA	A	ASN	166	H	-12.795583	16.133075	-15.705913	-5.975648
1HNA	A	GLN	167	H	-10.739034	13.725294	-13.276820	-5.110810
1HNA	A	VAL	168	H	-9.557096	12.004956	-11.902243	-4.358173
1HNA	A	PHE	169	H	-9.436039	12.006796	-12.109949	-4.403394
1HNA	A	GLU	170	C	-9.288610	11.685189	-12.365727	-4.410890
1HNA	A	PRO	171	H	-9.201896	11.407570	-12.589921	-4.423525
1HNA	A	SER	172	H	-9.066182	10.750409	-12.813884	-4.415019
1HNA	A	CYS	173	H	-9.288551	10.529126	-13.421561	-4.562019
1HNA	A	LEU	174	H	-9.199933	10.789367	-13.127391	-4.521055
1HNA	A	ASP	175	H	-9.274420	10.641567	-13.299055	-4.559839
1HNA	A	ALA	176	H	-9.295084	10.983665	-13.141505	-4.567674
1HNA	A	PHE	177	C	-9.583623	11.984556	-12.870515	-4.588177
1HNA	A	PRO	178	H	-9.629413	11.403671	-13.153133	-4.566766
1HNA	A	ASN	179	H	-10.092959	10.436729	-14.386470	-4.735005
1HNA	A	LEU	180	H	-10.313542	11.539908	-13.802034	-4.723299
1HNA	A	LYS	181	H	-11.023084	10.017269	-15.737605	-5.059822
1HNA	A	ASP	182	H	-11.020173	10.027144	-15.732354	-5.050650
1HNA	A	PHE	183	H	-12.385582	15.411632	-15.121805	-5.039563
1HNA	A	ILE	184	H	-12.384782	15.443117	-15.081755	-5.020152
1HNA	A	SER	185	H	-12.330914	12.632872	-16.480506	-5.038109
1HNA	A	ARG	186	H	-12.043271	13.489115	-15.897262	-5.245587
1HNA	A	PHE	187	H	-9.498757	12.008507	-12.696809	-5.235870
1HNA	A	GLU	188	H	-8.411279	8.012307	-13.666140	-5.217565
1HNA	A	GLY	189	H	-7.490033	9.020073	-11.424151	-4.718622
1HNA	A	LEU	190	C	-7.487976	9.025266	-11.433244	-4.717821
1HNA	A	GLU	191	H	-7.477174	9.015151	-11.477867	-4.713072
1HNA	A	LYS	192	H	-7.496779	8.915118	-11.438272	-4.695514
1HNA	A	ILE	193	H	-7.614010	9.278924	-10.910637	-4.582052
1HNA	A	SER	194	H	-9.725341	8.951353	-14.019283	-4.495299
1HNA	A	ALA	195	H	-9.782101	8.909050	-14.064714	-4.551306
1HNA	A	TYR	196	H	-11.078402	12.063463	-15.405904	-5.293990
1HNA	A	MET	197	H	-8.259411	5.471722	-13.342931	-4.316171
1HNA	A	LYS	198	H	-8.200389	5.710194	-13.365069	-4.307479
1HNA	A	SER	199	T	-8.066746	6.395220	-13.050269	-4.227929
1HNA	A	SER	200	T	-7.727714	8.703490	-11.497189	-4.108181
1HNA	A	ARG	201	T	-7.727778	8.703403	-11.496392	-4.107941
1HNA	A	PHE	202	T	-8.034299	10.935311	-10.258041	-3.972695
1HNA	A	LEU	203	T	-8.076335	11.164159	-10.015489	-3.954187
1HNA	A	PRO	204	T	-8.213601	11.697426	-9.540300	-3.962301
1HNA	A	ARG	205	T	-11.307021	12.111499	-14.287194	-4.354275
1HNA	A	PRO	206	T	-11.321738	12.122339	-14.255450	-4.356405
1HNA	A	VAL	207	C	-11.394978	11.997433	-14.158133	-4.333920
1HNA	A	PHE	208	T	-12.911897	17.104928	-15.923329	-5.644309
1HNA	A	THR	209	T	-11.702243	12.855001	-15.739138	-5.470827
1HNA	A	LYS	210	T	-11.718906	12.726246	-15.742889	-5.472060
1HNA	A	MET	211	T	-11.700617	12.861853	-15.808762	-5.557941
1HNA	A	ALA	212	T	-10.859090	13.191782	-14.339839	-5.294800
1HNA	A	VAL	213	T	-9.038396	11.990664	-11.406622	-4.603217
1HNA	A	PHE	214	T	-8.167962	10.650284	-10.676162	-4.148730
1HNA	A	GLY	215	T	-8.167962	10.650284	-10.676162	-4.148730
1HNA	A	ASN	216	T	-8.167962	10.650284	-10.676162	-4.148730
1HNA	A	LYS	217	C	-8.167962	10.650284	-10.676162	-4.148730
1HUP	A	ALA	88	C	-4.167585	2.305957	-8.441890	-3.125890
1HUP	A	ALA	89	C	-4.167585	2.305957	-8.441890	-3.125890
1HUP	A	SER	90	H	-4.167585	2.305957	-8.441890	-3.125890
1HUP	A	GLU	91	H	-4.167585	2.305957	-8.441890	-3.125890
1HUP	A	ARG	92	H	-5.617505	3.464737	-11.205754	-4.000684
1HUP	A	LYS	93	H	-6.468432	4.239031	-13.983953	-5.170869
1HUP	A	ALA	94	H	-6.783379	4.617891	-14.814440	-5.625595
1HUP	A	LEU	95	H	-7.076964	4.891199	-15.391480	-5.878108
1HUP	A	GLN	96	H	-7.311681	5.194959	-15.489646	-5.877520
1HUP	A	THR	97	H	-7.518811	5.544452	-15.255768	-5.776755
1HUP	A	GLU	98	H	-8.244598	7.574615	-14.705599	-5.192724
1HUP	A	MET	99	H	-8.372175	8.215465	-13.871861	-4.807230
1HUP	A	ALA	100	H	-8.390211	8.509002	-13.345535	-4.557717
1HUP	A	ARG	101	H	-8.350309	8.701481	-12.996040	-4.404251

```
1HUP          A          ILE            102                    H -8.221937  9.088358 -12.761877 -4.500710
1HUP          A          LYS            103                    H -8.339505  9.599168 -12.906105 -4.681020
1HUP          A          LYS            104                    H -8.133642  9.472489 -12.676475 -4.647329
1HUP          A          TRP            105                    H -8.063542  9.357633 -12.629396 -4.594934
1HUP          A          LEU            106                    H -7.810580  8.866453 -12.140142 -4.328886
1HUP          A          THR            107                    H -6.133193  7.258338 -9.737604 -4.257089
1HUP          A          PHE            108                    H -5.852104  7.471895 -9.708554 -4.276091
1HUP          A          SER            109                    H -5.850280  7.493366 -9.711116 -4.281571
1HUP          A          LEU            110                    H -5.851720  7.496419 -9.703405 -4.282828
1HUP          A          GLY            111                    C -5.821517  7.589308 -9.790118 -4.345189
1HUP          A          LYS            112                    E -6.168306  8.254437 -10.251062 -4.615852
1HUP          A          GLN            113                    E -6.485627  8.870771 -11.451761 -5.343481
1HUP          A          VAL            114                    E -6.497381  8.846431 -11.451530 -5.354573
1HUP          A          GLY            115                    T -6.500010  8.828774 -11.448696 -5.356316
1HUP          A          ASN            116                    T -6.632847  8.765264 -11.444771 -5.401274
1HUP          A          LYS            117                    E -7.013278  8.751274 -11.695011 -5.586361
1HUP          A          PHE            118                    E -9.199387 12.229373 -12.379141 -5.396450
1HUP          A          PHE            119                    E -8.714428 14.582964 -10.325571 -5.266189
1HUP          A          LEU            120                    E -6.099493  8.860803 -9.699005 -5.029756
1HUP          A          THR            121                    E -4.496979  7.750474 -8.362387 -5.032301
1HUP          A          ASN            122                    E -4.435129  7.789296 -8.514732 -5.050757
1HUP          A          GLY            123                    E -4.423457  7.811440 -8.558786 -5.054893
1HUP          A          GLU            124                    E -4.423873  7.806693 -8.557594 -5.054745
1HUP          A          ILE            125                    E -4.459565  7.745113 -8.486655 -5.056143
1HUP          A          MET            126                    E -5.696616  8.266771 -10.038078 -5.220887
1HUP          A          THR            127                    C -6.754556  8.933433 -10.773119 -5.256998
1HUP          A          PHE            128                    H -10.037039 13.739593 -13.449805 -5.209602
1HUP          A          GLU            129                    H -9.385260 10.668499 -13.250519 -4.745180
1HUP          A          LYS            130                    H -9.360629 10.644318 -13.250582 -4.709257
1HUP          A          VAL            131                    H -9.386359 10.553633 -13.196518 -4.668741
1HUP          A          LYS            132                    H -9.454820  9.907364 -13.440984 -4.625553
1HUP          A          ALA            133                    H -9.180501  8.151917 -13.979416 -4.410624
1HUP          A          LEU            134                    H -9.247580  6.747064 -14.701316 -4.307761
1HUP          A          CYS            135                    H -8.362427  5.595806 -13.789396 -4.227510
1HUP          A          VAL            136                    H -6.312294  6.491983 -9.599707 -3.715862
1HUP          A          LYS            137                    H -6.305301  6.507125 -9.634961 -3.720445
1HUP          A          PHE            138                    H -6.306436  6.515126 -9.622545 -3.719742
1HUP          A          GLN            139                    C -6.307062  6.522408 -9.612157 -3.717625
1HUP          A          ALA            140                    C -6.320908  6.560252 -9.516976 -3.705823
1HUP          A          SER            141                    E -8.709856  8.954303 -12.508360 -4.077105
1HUP          A          VAL            142                    E -9.411776 11.593942 -12.122859 -3.978244
1HUP          A          ALA            143                    C -9.552493 11.695519 -11.987019 -3.942176
1HUP          A          THR            144                    C -9.958326 12.926584 -11.934598 -4.152662
1HUP          A          PRO            145                    C -10.188406 11.002054 -13.614665 -4.351718
1HUP          A          ARG            146                    C -10.228630  8.629559 -15.380862 -4.715143
1HUP          A          ASN            147                    C -10.062064  8.386907 -15.667739 -4.829149
1HUP          A          ALA            148                    H -9.900412  7.919070 -16.020661 -4.940804
1HUP          A          ALA            149                    H -9.889682  7.891879 -16.067092 -4.953523
1HUP          A          GLU            150                    H -10.113467  7.588887 -16.732967 -5.199890
1HUP          A          ASN            151                    H -10.294945  7.504780 -16.920236 -5.242920
1HUP          A          GLY            152                    H -9.327349  9.524963 -13.572947 -4.841538
1HUP          A          ALA            153                    H -9.336869 10.186280 -13.163334 -4.803516
1HUP          A          ILE            154                    H -9.123521 11.991824 -12.297422 -4.825218
1HUP          A          GLN            155                    H -8.732638 11.906872 -12.079316 -4.860812
1HUP          A          ASN            156                    H -6.912568 12.056204 -8.905526 -4.801643
1HUP          A          LEU            157                    H -6.899250 12.120894 -8.926754 -4.812547
1HUP          A          ILE            158                    C -6.888664 12.102517 -8.981815 -4.811710
1HUP          A          LYS            159                    C -6.892788 12.075627 -8.971847 -4.811224
1HUP          A          GLU            160                    C -6.905819 12.081535 -8.907341 -4.809211
1HUP          A          GLU            161                    C -8.601970 12.388911 -11.474975 -4.981109
1HUP          A          ALA            162                    E -9.205970 11.624291 -12.043681 -4.762301
1HUP          A          PHE            163                    E -10.664553 18.327430 -10.922550 -4.621970
1HUP          A          LEU            164                    E -10.442145 17.143580 -11.329588 -4.665038
1HUP          A          GLY            165                    E -10.394527 16.698838 -11.728464 -4.733539
1HUP          A          ILE            166                    E -9.841322 12.882666 -13.113027 -4.934568
1HUP          A          THR            167                    E -8.029021  7.421147 -13.204669 -5.141760
1HUP          A          ASP            168                    T -7.951020  7.151332 -13.547950 -5.180689
1HUP          A          GLU            169                    T -6.236504  4.369555 -12.634607 -5.232358
1HUP          A          LYS            170                    T -5.123798  4.726104 -10.925365 -5.027030
1HUP          A          THR            171                    T -5.121218  4.753589 -10.929715 -5.029372
1HUP          A          GLU            172                    T -5.125270  4.738286 -10.914146 -5.028655
1HUP          A          GLY            173                    T -5.125885  4.737711 -10.909042 -5.028289
1HUP          A          GLN            174                    T -5.218717  4.827016 -10.624906 -4.992952
1HUP          A          PHE            175                    C -8.263295 11.347473 -12.179484 -5.623664
1HUP          A          VAL            176                    B -8.188436  8.258918 -12.886118 -4.993411
1HUP          A          ASP            177                    T -5.589776  5.800095 -10.547783 -4.941184
1HUP          A          LEU            178                    T -3.831133  7.331841 -7.035042 -4.517779
1HUP          A          THR            179                    T -3.734054  7.538034 -7.088327 -4.506219
1HUP          A          GLY            180                    T -3.581109  7.632793 -7.079411 -4.451240
1HUP          A          ASN            181                    C -3.580867  7.636262 -7.079104 -4.451100
1HUP          A          ARG            182                    B -3.584595  7.853807 -6.928425 -4.428806
```

1HUP	A	LEU	183	T	-4.164305	8.595538	-7.062766	-4.310295
1HUP	A	THR	184	T	-4.385399	8.559540	-6.923175	-4.255431
1HUP	A	TYR	185	T	-5.647279	13.232453	-6.173227	-4.304219
1HUP	A	THR	186	T	-5.662486	13.264222	-6.090020	-4.300682
1HUP	A	ASN	187	C	-7.071117	12.810367	-8.869054	-4.870021
1HUP	A	TRP	188	B	-8.511019	13.686402	-11.636796	-5.477269
1HUP	A	ASN	189	T	-6.881465	6.689224	-12.324496	-5.349718
1HUP	A	GLU	190	T	-6.363288	6.065216	-12.240880	-5.195427
1HUP	A	GLY	191	T	-6.351008	6.079320	-12.282669	-5.199434
1HUP	A	GLU	192	T	-6.351345	6.076129	-12.280812	-5.198432
1HUP	A	PRO	193	T	-6.283527	6.008179	-12.353414	-5.158866
1HUP	A	ASN	194	T	-6.325903	4.915667	-12.746172	-4.976925
1HUP	A	ASN	195	C	-6.013868	3.569134	-12.391374	-4.610666
1HUP	A	ALA	196	G	-5.738726	3.899801	-12.048761	-4.561791
1HUP	A	GLY	197	G	-5.737008	3.904593	-12.057774	-4.563136
1HUP	A	SER	198	G	-5.764698	3.817109	-12.011640	-4.547023
1HUP	A	ASP	199	C	-5.839788	3.906165	-11.806385	-4.515086
1HUP	A	GLU	200	C	-6.307913	4.527945	-11.557655	-4.503171
1HUP	A	ASP	201	C	-9.145251	5.802774	-15.258324	-5.035894
1HUP	A	CYS	202	E	-11.438909	12.949755	-15.110441	-4.834167
1HUP	A	VAL	203	E	-11.547230	14.854616	-13.937004	-4.674713
1HUP	A	LEU	204	E	-11.453455	14.786209	-14.083179	-4.767080
1HUP	A	LEU	205	E	-10.628483	11.184786	-15.317989	-5.345691
1HUP	A	LEU	206	T	-10.451459	9.733511	-16.308982	-5.587224
1HUP	A	LYS	207	T	-10.488596	9.292593	-16.583035	-5.671440
1HUP	A	ASN	208	T	-10.494106	9.218198	-16.619363	-5.686358
1HUP	A	GLY	209	T	-10.516464	9.062879	-16.649504	-5.701293
1HUP	A	GLN	210	C	-11.100013	7.464466	-18.176467	-5.979972
1HUP	A	TRP	211	E	-12.925071	12.724218	-18.424875	-5.967960
1HUP	A	ASN	212	E	-12.489812	11.574850	-17.412457	-5.352502
1HUP	A	ASP	213	E	-11.635385	9.528826	-16.522760	-4.729090
1HUP	A	VAL	214	E	-9.083574	7.725681	-12.979078	-4.120909
1HUP	A	PRO	215	T	-8.277075	7.538185	-12.703724	-4.332773
1HUP	A	CYS	216	T	-8.009893	7.956893	-12.696719	-4.505297
1HUP	A	SER	217	T	-7.974233	8.172554	-12.658726	-4.504672
1HUP	A	THR	218	T	-7.971969	8.197452	-12.655464	-4.504375
1HUP	A	SER	219	C	-8.067590	8.302872	-12.605849	-4.573278
1HUP	A	HIS	220	E	-8.504859	9.211611	-12.603755	-4.756148
1HUP	A	LEU	221	E	-9.580020	11.875512	-12.186104	-4.488813
1HUP	A	ALA	222	E	-10.855313	13.649722	-12.986317	-4.408143
1HUP	A	VAL	223	E	-11.570097	15.251715	-12.640713	-4.276566
1HUP	A	CYS	224	E	-11.588318	14.732099	-14.024281	-5.114638
1HUP	A	GLU	225	E	-8.946525	13.286025	-9.807641	-4.080077
1HUP	A	PHE	226	E	-8.946525	13.286025	-9.807641	-4.080077
1HUP	A	PRO	227	E	-8.946525	13.286025	-9.807641	-4.080077
1HUP	A	ILE	228	C	-8.946525	13.286025	-9.807641	-4.080077
1HZI	A	HIS	1	T	-5.483398	4.762984	-11.489501	-4.712137
1HZI	A	LYS	2	T	-5.483398	4.762984	-11.489501	-4.712137
1HZI	A	CYS	3	T	-5.483398	4.762984	-11.489501	-4.712137
1HZI	A	ASP	4	T	-5.483398	4.762984	-11.489501	-4.712137
1HZI	A	ILE	5	H	-5.734462	5.258967	-11.705642	-5.053760
1HZI	A	THR	6	H	-6.164260	6.569059	-11.746298	-5.561444
1HZI	A	LEU	7	H	-8.298843	10.336334	-13.807557	-6.355655
1HZI	A	GLN	8	H	-9.334431	11.196188	-13.467708	-5.027059
1HZI	A	ALA	9	H	-9.105604	11.728443	-12.520552	-4.693058
1HZI	A	ILE	10	H	-9.251070	13.255770	-11.907426	-4.720252
1HZI	A	ILE	11	H	-9.243540	13.157150	-11.969633	-4.723893
1HZI	A	LYS	12	H	-9.207855	12.991634	-12.155651	-4.762419
1HZI	A	THR	13	H	-9.327193	13.383591	-11.967872	-4.811918
1HZI	A	LEU	14	H	-9.822116	14.322370	-12.251347	-5.014057
1HZI	A	ASN	15	H	-10.214288	11.243466	-15.074458	-5.375465
1HZI	A	SER	16	H	-10.299836	11.079761	-15.250999	-5.426754
1HZI	A	LEU	17	H	-10.549460	10.966329	-15.733504	-5.554476
1HZI	A	THR	18	H	-10.119793	9.808366	-16.306646	-5.906440
1HZI	A	GLU	19	C	-9.950026	9.545556	-16.408428	-5.894886
1HZI	A	GLN	20	C	-10.096285	9.218631	-16.816727	-6.041564
1HZI	A	LYS	21	C	-9.118786	10.067857	-14.092049	-5.554113
1HZI	A	THR	22	T	-8.993961	10.355494	-14.087840	-5.601129
1HZI	A	LEU	23	T	-8.967735	10.639994	-13.890698	-5.556609
1HZI	A	CYS	24	T	-8.520365	11.147513	-13.178216	-5.630781
1HZI	A	THR	25	T	-8.363992	11.600104	-12.782926	-5.499713
1HZI	A	GLU	26	T	-8.257622	12.171797	-12.101902	-5.324450
1HZI	A	LEU	27	T	-8.282166	12.227184	-11.997658	-5.291408
1HZI	A	THR	28	E	-8.259591	12.386941	-11.883229	-5.254092
1HZI	A	VAL	29	E	-8.517981	12.905194	-11.425360	-5.006502
1HZI	A	THR	30	E	-8.695949	13.033949	-11.397876	-4.997839
1HZI	A	ASP	31	T	-9.229323	14.846638	-11.567573	-5.049189
1HZI	A	ILE	32	T	-8.293919	13.623422	-9.741181	-4.430312
1HZI	A	PHE	33	T	-6.872399	10.752663	-8.900629	-4.245936
1HZI	A	ALA	34	T	-6.132762	6.907370	-10.256794	-4.248551
1HZI	A	ALA	35	T	-5.801090	5.907496	-10.793415	-4.360737

1HZI	A	SER	36	T	-5.327878	5.531126	-10.702158	-4.553053
1HZI	A	LYS	37	T	-5.325375	5.510652	-10.739159	-4.566561
1HZI	A	ASN	38	T	-5.366257	5.153211	-10.879506	-4.591499
1HZI	A	THR	39	C	-5.494473	5.107643	-10.902512	-4.675755
1HZI	A	THR	40	C	-5.669355	5.287982	-10.695031	-4.732529
1HZI	A	GLU	41	H	-7.978398	7.986342	-13.988304	-5.811382
1HZI	A	LYS	42	H	-9.092781	9.172187	-15.104022	-5.840981
1HZI	A	GLU	43	H	-9.370806	9.495010	-14.821699	-5.777352
1HZI	A	THR	44	H	-10.582563	11.456562	-15.477397	-6.043808
1HZI	A	PHE	45	H	-13.161247	16.562771	-17.616383	-6.605266
1HZI	A	CYS	46	H	-13.309187	13.544051	-18.045061	-5.631302
1HZI	A	ARG	47	H	-13.112863	12.378400	-17.328566	-4.866812
1HZI	A	ALA	48	H	-10.971454	13.681261	-12.055076	-3.898713
1HZI	A	ALA	49	H	-10.674991	13.580129	-12.206965	-3.910540
1HZI	A	THR	50	H	-10.597128	13.496617	-12.453820	-3.981710
1HZI	A	VAL	51	H	-10.598042	13.526351	-12.429996	-3.978542
1HZI	A	LEU	52	H	-10.602937	13.533659	-12.396760	-3.973576
1HZI	A	ARG	53	H	-11.039630	13.340596	-12.937137	-4.087179
1HZI	A	GLN	54	H	-11.784409	13.260467	-14.344311	-4.558923
1HZI	A	PHE	55	H	-12.984215	16.983463	-15.668333	-5.369170
1HZI	A	TYR	56	H	-12.648617	14.882412	-16.701936	-5.730333
1HZI	A	SER	57	H	-10.593476	8.670721	-15.969208	-5.248951
1HZI	A	HIS	58	H	-10.453916	8.562726	-16.332520	-5.345556
1HZI	A	HIS	59	H	-10.304625	8.537761	-16.477580	-5.379762
1HZI	A	GLU	60	H	-9.059277	6.560678	-14.855430	-4.867252
1HZI	A	LYS	61	C	-8.638479	6.277256	-14.785027	-4.851735
1HZI	A	ASP	62	T	-8.602301	6.295417	-14.784094	-4.829580
1HZI	A	THR	63	T	-8.029853	7.419134	-13.312915	-4.724621
1HZI	A	ARG	64	T	-7.969039	7.497399	-13.351554	-4.729045
1HZI	A	CYS	65	T	-6.686128	6.890992	-11.487804	-4.805533
1HZI	A	LEU	66	T	-4.884586	5.650697	-8.831396	-4.163435
1HZI	A	GLY	67	C	-4.448578	4.738479	-9.476773	-4.379513
1HZI	A	ALA	68	C	-4.426897	4.769466	-9.540910	-4.392239
1HZI	A	THR	69	C	-4.426888	4.769709	-9.541007	-4.392355
1HZI	A	ALA	70	H	-4.438805	4.728318	-9.504973	-4.383678
1HZI	A	GLN	71	H	-4.792365	4.024143	-10.154142	-4.587028
1HZI	A	GLN	72	H	-6.370679	5.716860	-11.318032	-4.730607
1HZI	A	PHE	73	H	-9.263751	9.025669	-14.112403	-5.268060
1HZI	A	HIS	74	H	-11.193791	11.521206	-18.078773	-6.987012
1HZI	A	ARG	75	H	-11.941847	13.869025	-19.957689	-8.988886
1HZI	A	HIS	76	H	-13.708314	14.666888	-19.130900	-6.354860
1HZI	A	LYS	77	H	-13.129080	15.189403	-16.981684	-5.671750
1HZI	A	GLN	78	H	-13.152008	15.664650	-16.664924	-5.654570
1HZI	A	LEU	79	H	-13.152122	16.125862	-16.384555	-5.626208
1HZI	A	ILE	80	H	-13.127877	16.269498	-16.381727	-5.633195
1HZI	A	ARG	81	H	-13.211791	16.262463	-16.335234	-5.605075
1HZI	A	PHE	82	H	-14.015366	19.002082	-16.781969	-5.868142
1HZI	A	LEU	83	H	-14.115681	19.019020	-16.841133	-5.825447
1HZI	A	LYS	84	H	-13.991260	16.067973	-17.996146	-5.683666
1HZI	A	ARG	85	H	-13.468548	13.057224	-18.160977	-5.348148
1HZI	A	LEU	86	H	-13.358914	13.140157	-17.933158	-5.245836
1HZI	A	ASP	87	H	-13.370812	12.937281	-17.977346	-5.220258
1HZI	A	ARG	88	H	-13.158023	12.797481	-17.890658	-5.198514
1HZI	A	ASN	89	H	-13.156638	13.150833	-17.758807	-5.234421
1HZI	A	LEU	90	H	-12.950207	14.744781	-16.293518	-5.017345
1HZI	A	TRP	91	H	-11.046970	11.201227	-14.776667	-4.886191
1HZI	A	GLY	92	H	-8.514194	8.721772	-12.238937	-4.504504
1HZI	A	LEU	93	H	-7.775077	9.468872	-11.293627	-4.495463
1HZI	A	ALA	94	H	-5.509455	5.329652	-9.571952	-4.034884
1HZI	A	GLY	95	C	-5.171995	5.064326	-10.119205	-4.312684
1HZI	A	LEU	96	C	-5.145958	5.074972	-10.199491	-4.319519
1HZI	A	ASN	97	C	-4.831457	6.031364	-9.549831	-4.344534
1HZI	A	SER	98	C	-4.740647	6.090702	-9.551785	-4.330579
1HZI	A	CYS	99	C	-4.914697	6.431268	-9.592819	-4.452122
1HZI	A	PRO	100	C	-5.043199	7.093622	-9.222744	-4.370231
1HZI	A	VAL	101	C	-5.045499	7.184208	-9.189141	-4.384147
1HZI	A	LYS	102	C	-5.574956	6.862743	-10.028865	-4.397913
1HZI	A	GLU	103	C	-6.114422	7.338512	-10.675405	-4.616902
1HZI	A	ALA	104	C	-6.195828	7.214529	-10.540310	-4.552118
1HZI	A	ASN	105	C	-7.017439	7.770075	-11.614737	-4.964400
1HZI	A	GLN	106	E	-8.408221	6.577934	-14.760336	-5.460274
1HZI	A	SER	107	E	-9.623786	6.795857	-16.454689	-5.476260
1HZI	A	THR	108	E	-9.873015	6.890199	-16.238521	-5.413260
1HZI	A	LEU	109	H	-11.545321	13.422581	-15.868782	-5.549740
1HZI	A	GLU	110	H	-11.591934	13.789241	-15.654751	-5.555546
1HZI	A	ASN	111	H	-11.441643	14.416145	-15.318739	-5.536509
1HZI	A	PHE	112	H	-11.777476	17.073580	-14.372281	-5.584275
1HZI	A	LEU	113	H	-11.920669	17.244617	-14.292516	-5.558900
1HZI	A	GLU	114	H	-11.559521	14.862653	-14.925719	-5.569220
1HZI	A	ARG	115	H	-11.060708	14.974915	-13.984310	-5.328981
1HZI	A	LEU	116	H	-11.042606	15.050663	-14.051855	-5.412147

1HZI	A	LYS	117	H	-11.019925	14.948925	-14.181646	-5.433300
1HZI	A	THR	118	H	-10.718760	13.869112	-14.548699	-5.463530
1HZI	A	ILE	119	H	-10.797530	13.894424	-14.526454	-5.465742
1HZI	A	MET	120	H	-11.074184	13.198262	-15.235910	-5.649384
1HZI	A	ARG	121	H	-11.151400	12.562759	-15.537493	-5.661704
1HZI	A	GLU	122	H	-10.810909	11.839699	-16.919137	-6.608576
1HZI	A	LYS	123	H	-10.695364	10.928400	-17.963354	-7.192318
1HZI	A	TYR	124	H	-7.962637	6.711090	-13.448500	-5.189166
1HZI	A	SER	125	H	-6.615038	3.952601	-12.142422	-4.229824
1HZI	A	LYS	126	H	-5.419452	2.902302	-10.254025	-3.469956
1HZI	A	CYS	127	H	-5.419452	2.902302	-10.254025	-3.469956
1HZI	A	SER	128	C	-5.419452	2.902302	-10.254025	-3.469956
1HZI	A	SER	129	C	-5.419452	2.902302	-10.254025	-3.469956
1I1N	A	TRP	2	C	-6.485750	5.164649	-11.564837	-4.361494
1I1N	A	LYS	3	C	-6.485750	5.164649	-11.564837	-4.361494
1I1N	A	SER	4	C	-6.485750	5.164649	-11.564837	-4.361494
1I1N	A	GLY	5	C	-6.485750	5.164649	-11.564837	-4.361494
1I1N	A	GLY	6	T	-7.269798	6.073611	-13.252300	-5.207637
1I1N	A	ALA	7	T	-8.031371	6.636889	-14.303212	-5.472702
1I1N	A	SER	8	T	-8.720705	7.022972	-13.640468	-4.570116
1I1N	A	HIS	9	H	-8.764780	6.965781	-13.290166	-4.376825
1I1N	A	SER	10	H	-8.763590	6.976898	-13.292125	-4.376424
1I1N	A	GLU	11	H	-10.145630	7.673491	-14.851526	-4.527251
1I1N	A	LEU	12	H	-11.839299	12.736585	-15.781194	-4.889547
1I1N	A	ILE	13	H	-11.943364	13.115063	-15.621202	-4.913681
1I1N	A	HIS	14	H	-11.701384	11.886798	-16.051087	-5.002437
1I1N	A	ASN	15	H	-11.776915	11.540098	-16.568609	-5.177397
1I1N	A	LEU	16	H	-9.841019	9.642231	-13.910278	-4.950738
1I1N	A	ARG	17	H	-9.198176	8.978472	-13.702714	-4.861645
1I1N	A	LYS	18	H	-8.127577	10.117543	-11.477633	-4.744132
1I1N	A	ASN	19	H	-7.633333	10.436601	-11.201971	-4.867074
1I1N	A	GLY	20	T	-6.743888	10.055605	-9.510223	-4.464190
1I1N	A	ILE	21	T	-6.660433	10.148944	-9.527329	-4.440492
1I1N	A	ILE	22	T	-6.604329	10.086937	-9.667485	-4.472171
1I1N	A	LYS	23	T	-6.601843	9.987608	-9.716664	-4.468445
1I1N	A	THR	24	C	-6.663425	9.913838	-9.578116	-4.414573
1I1N	A	ASP	25	H	-7.335072	9.848981	-10.747425	-4.553882
1I1N	A	LYS	26	H	-7.662146	9.203015	-11.461942	-4.736885
1I1N	A	VAL	27	H	-8.187382	8.937431	-11.706960	-4.656516
1I1N	A	PHE	28	H	-10.659425	14.220153	-13.457149	-5.035373
1I1N	A	GLU	29	H	-10.231684	12.306781	-13.168698	-4.649102
1I1N	A	VAL	30	H	-10.088491	12.475087	-12.996457	-4.664827
1I1N	A	MET	31	H	-10.028146	12.409823	-13.181927	-4.727999
1I1N	A	LEU	32	H	-10.036551	12.314457	-13.216348	-4.733455
1I1N	A	ALA	33	H	-10.048378	12.232301	-13.216524	-4.731307
1I1N	A	THR	34	C	-10.551299	12.869629	-13.430355	-4.910098
1I1N	A	ASP	35	C	-11.323659	12.054332	-15.067354	-5.287734
1I1N	A	ARG	36	G	-12.851200	12.336991	-17.344602	-5.468972
1I1N	A	SER	37	G	-11.574616	12.015663	-14.592513	-4.764272
1I1N	A	HIS	38	G	-9.225113	11.254526	-11.636283	-4.509499
1I1N	A	TYR	39	C	-6.430551	9.956541	-8.950525	-4.588222
1I1N	A	ALA	40	C	-4.567169	6.760762	-7.050715	-3.726972
1I1N	A	LYS	41	T	-4.553443	6.824513	-7.095390	-3.739338
1I1N	A	CYS	42	T	-4.553311	6.825333	-7.096625	-3.739571
1I1N	A	ASN	43	T	-4.553528	6.823719	-7.094994	-3.739293
1I1N	A	PRO	44	T	-4.578792	6.687497	-7.014949	-3.702138
1I1N	A	TYR	45	T	-6.785461	9.549067	-9.033244	-4.268994
1I1N	A	MET	46	T	-9.484811	10.533165	-12.827288	-4.798834
1I1N	A	ASP	47	C	-11.058264	10.106415	-16.416439	-5.192787
1I1N	A	SER	48	C	-10.805990	9.549819	-15.761174	-4.767108
1I1N	A	PRO	49	C	-8.875524	9.102801	-12.818096	-4.707815
1I1N	A	GLN	50	E	-8.848417	9.227309	-12.847043	-4.715491
1I1N	A	SER	51	E	-8.619475	10.043706	-12.292901	-4.608654
1I1N	A	ILE	52	C	-8.560142	10.346249	-12.212698	-4.609086
1I1N	A	GLY	53	T	-8.336872	11.153972	-11.712423	-4.645231
1I1N	A	PHE	54	T	-8.590601	12.680821	-11.068573	-4.614902
1I1N	A	GLN	55	T	-8.340217	12.411652	-10.831396	-4.490635
1I1N	A	ALA	56	T	-8.163567	12.832093	-10.040939	-4.259865
1I1N	A	THR	57	E	-8.046888	13.002240	-9.765306	-4.157830
1I1N	A	ILE	58	E	-8.168440	13.039992	-9.567766	-4.022256
1I1N	A	SER	59	C	-8.182953	12.947047	-9.552455	-4.003776
1I1N	A	ALA	60	C	-8.374302	13.364407	-9.181683	-3.898521
1I1N	A	PRO	61	H	-8.889643	13.638396	-9.397021	-3.914712
1I1N	A	HIS	62	H	-10.349408	13.680220	-12.550671	-4.422936
1I1N	A	MET	63	H	-10.832461	14.581582	-13.193191	-4.806520
1I1N	A	HIS	64	H	-11.203420	16.129997	-12.847619	-4.984590
1I1N	A	ALA	65	H	-11.687428	16.599504	-12.998346	-4.986649
1I1N	A	TYR	66	H	-12.734647	18.106764	-14.522655	-5.273011
1I1N	A	ALA	67	H	-12.920282	18.021789	-14.526293	-4.980426
1I1N	A	LEU	68	H	-12.931466	18.046557	-14.492421	-4.962255
1I1N	A	GLU	69	H	-12.379313	14.910274	-15.560258	-5.371128

1I1N	A	LEU	70	H	-12.218371	14.660485	-15.641364	-5.374825
1I1N	A	LEU	71	H	-11.828125	15.019656	-14.869596	-5.289486
1I1N	A	PHE	72	G	-11.600471	14.168391	-15.092729	-5.257664
1I1N	A	ASP	73	G	-11.295426	12.248830	-15.691453	-5.185289
1I1N	A	GLN	74	G	-11.331422	11.842704	-15.873516	-5.164672
1I1N	A	LEU	75	C	-9.339769	8.559878	-12.944906	-4.259731
1I1N	A	HIS	76	T	-9.161203	8.129913	-13.483432	-4.388258
1I1N	A	GLU	77	T	-9.009061	8.229953	-13.565507	-4.432152
1I1N	A	GLY	78	T	-8.892717	8.775355	-13.287899	-4.404824
1I1N	A	ALA	79	T	-8.892943	8.777054	-13.284265	-4.403815
1I1N	A	LYS	80	E	-9.251505	9.056815	-13.651835	-4.549085
1I1N	A	ALA	81	E	-9.457396	10.007415	-13.052812	-4.442745
1I1N	A	LEU	82	E	-9.854229	11.329149	-12.279556	-4.299206
1I1N	A	ASP	83	E	-10.943294	10.387931	-15.000289	-4.513489
1I1N	A	VAL	84	E	-10.457640	9.899271	-15.203681	-4.841338
1I1N	A	GLY	85	T	-9.116702	7.588146	-14.740012	-5.330698
1I1N	A	SER	86	T	-8.940065	8.222697	-14.494949	-5.331900
1I1N	A	GLY	87	T	-8.827077	8.963303	-14.117092	-5.273450
1I1N	A	SER	88	T	-8.793646	9.312279	-13.963902	-5.264764
1I1N	A	GLY	89	T	-8.620901	10.638042	-13.016450	-5.116190
1I1N	A	ILE	90	H	-8.889101	12.825192	-11.950973	-4.933807
1I1N	A	LEU	91	H	-9.053848	13.706435	-11.364933	-4.818570
1I1N	A	THR	92	H	-9.222963	14.141042	-11.045185	-4.754678
1I1N	A	ALA	93	H	-9.317154	14.197422	-10.822013	-4.707285
1I1N	A	CYS	94	H	-10.694424	15.132915	-12.013742	-4.631244
1I1N	A	PHE	95	H	-11.696258	16.016877	-12.721738	-4.489972
1I1N	A	ALA	96	H	-11.835276	15.161414	-13.076167	-4.434362
1I1N	A	ARG	97	H	-11.872587	11.738141	-15.640339	-4.976018
1I1N	A	MET	98	H	-8.386266	8.294817	-11.955775	-4.430194
1I1N	A	VAL	99	H	-6.076635	5.632890	-10.517744	-4.363718
1I1N	A	GLY	100	T	-5.349708	5.222250	-10.323140	-4.551373
1I1N	A	CYS	101	T	-5.246361	5.595477	-10.130227	-4.464130
1I1N	A	THR	102	T	-5.244141	5.613564	-10.131610	-4.462526
1I1N	A	GLY	103	T	-5.245736	5.610742	-10.125242	-4.462213
1I1N	A	LYS	104	E	-5.408810	5.625907	-10.009767	-4.493495
1I1N	A	VAL	105	E	-6.308157	7.674579	-9.182807	-4.010131
1I1N	A	ILE	106	E	-8.222286	10.637073	-10.821437	-4.129449
1I1N	A	GLY	107	E	-8.723031	10.917707	-11.242547	-4.253928
1I1N	A	ILE	108	E	-9.695295	13.874150	-11.008444	-4.259775
1I1N	A	ASP	109	E	-10.773779	13.204835	-12.665930	-4.218747
1I1N	A	HIS	110	C	-11.665324	13.467915	-14.998577	-4.801989
1I1N	A	ILE	111	C	-10.911438	13.529936	-12.892484	-4.334730
1I1N	A	LYS	112	H	-10.604139	12.359800	-13.167612	-4.281313
1I1N	A	GLU	113	H	-10.602889	12.325037	-13.191233	-4.282389
1I1N	A	LEU	114	H	-10.610682	12.325906	-13.140263	-4.266533
1I1N	A	VAL	115	H	-10.625558	12.248762	-13.114802	-4.248319
1I1N	A	ASP	116	H	-11.003449	10.959609	-13.996752	-4.316041
1I1N	A	ASP	117	H	-12.447801	8.884694	-18.637451	-4.910586
1I1N	A	SER	118	H	-12.564305	8.291425	-19.186061	-4.977644
1I1N	A	VAL	119	H	-12.155086	9.148474	-17.413605	-4.508766
1I1N	A	ASN	120	H	-12.057370	8.888624	-17.472496	-4.489150
1I1N	A	ASN	121	H	-12.122320	9.131244	-17.189619	-4.419165
1I1N	A	VAL	122	H	-12.190449	9.464651	-16.846062	-4.292210
1I1N	A	ARG	123	H	-12.031112	8.474651	-17.392557	-4.379572
1I1N	A	LYS	124	H	-10.451579	5.842340	-16.974484	-5.027360
1I1N	A	ASP	125	H	-9.831592	7.251258	-15.410355	-4.807997
1I1N	A	ASP	126	C	-9.569016	8.553295	-14.427523	-4.618104
1I1N	A	PRO	127	H	-9.006534	9.874523	-12.356253	-4.132005
1I1N	A	THR	128	H	-8.849396	9.921083	-12.327790	-4.120046
1I1N	A	LEU	129	H	-8.554909	10.014960	-11.986308	-4.199453
1I1N	A	LEU	130	H	-8.596004	10.162865	-11.812519	-4.164240
1I1N	A	SER	131	H	-8.634872	10.100460	-11.774753	-4.157579
1I1N	A	SER	132	H	-8.869816	9.804543	-12.128300	-4.319461
1I1N	A	GLY	133	T	-9.034259	9.726524	-12.082920	-4.394966
1I1N	A	ARG	134	T	-11.063169	8.640842	-16.002144	-4.592367
1I1N	A	VAL	135	E	-9.569180	14.626152	-9.613195	-3.954337
1I1N	A	GLN	136	E	-8.690338	12.407895	-10.254314	-4.200422
1I1N	A	LEU	137	E	-7.471237	11.410487	-9.168900	-4.215670
1I1N	A	VAL	138	E	-6.627918	8.893758	-9.689147	-4.298170
1I1N	A	VAL	139	E	-6.614815	8.892969	-9.760303	-4.309526
1I1N	A	GLY	140	C	-6.610603	8.826049	-9.818392	-4.315335
1I1N	A	ASP	141	C	-6.603023	8.717288	-9.902062	-4.322855
1I1N	A	GLY	142	G	-6.736305	8.074775	-10.127352	-4.349348
1I1N	A	ARG	143	G	-8.172675	7.866924	-12.940128	-4.606936
1I1N	A	MET	144	G	-8.026361	8.181867	-12.641841	-4.637927
1I1N	A	GLY	145	C	-8.055960	8.499063	-12.568352	-4.709676
1I1N	A	TYR	146	C	-8.206004	9.310611	-12.529967	-4.865102
1I1N	A	ALA	147	G	-6.701344	7.646208	-10.310832	-4.382322
1I1N	A	GLU	148	G	-6.700923	7.649887	-10.313245	-4.382840
1I1N	A	GLU	149	G	-6.730466	7.577219	-10.212428	-4.362328
1I1N	A	ALA	150	C	-6.736897	7.561787	-10.173493	-4.352854

1I1N	A	PRO	151	C	-6.749191	7.512241	-10.125427	-4.341670
1I1N	A	TYR	152	E	-10.651200	13.571432	-13.317254	-4.827311
1I1N	A	ASP	153	E	-11.094256	14.672195	-12.736968	-4.427902
1I1N	A	ALA	154	E	-10.566654	14.460907	-11.820227	-4.112459
1I1N	A	ILE	155	E	-10.273735	14.513686	-11.146895	-3.942394
1I1N	A	HIS	156	E	-9.989198	13.746508	-11.254158	-3.865858
1I1N	A	VAL	157	E	-9.388684	12.785033	-10.479034	-3.508514
1I1N	A	GLY	158	C	-9.084335	11.726113	-10.719067	-3.407908
1I1N	A	ALA	159	C	-7.818023	8.140499	-9.896834	-2.939740
1I1N	A	ALA	160	B	-6.669275	8.240905	-7.807565	-2.631441
1I1N	A	ALA	161	B	-5.863734	8.701951	-6.577249	-2.559103
1I1N	A	PRO	162	T	-5.704937	8.590892	-6.851948	-2.662172
1I1N	A	VAL	163	T	-5.694096	8.596985	-6.899767	-2.673069
1I1N	A	VAL	164	T	-5.708686	8.620930	-6.828083	-2.668121
1I1N	A	PRO	165	C	-5.818671	8.693325	-6.699037	-2.685792
1I1N	A	GLN	166	H	-6.506782	8.335905	-7.929185	-3.027680
1I1N	A	ALA	167	H	-7.965331	9.258831	-9.778313	-3.337893
1I1N	A	LEU	168	H	-9.322354	11.482889	-11.401335	-4.010915
1I1N	A	ILE	169	H	-9.411725	11.221191	-11.383971	-4.034340
1I1N	A	ASP	170	H	-9.424800	11.148930	-11.398262	-4.052133
1I1N	A	GLN	171	H	-11.325627	13.459121	-14.955636	-5.058876
1I1N	A	LEU	172	E	-7.869151	9.872920	-10.796158	-4.700017
1I1N	A	LYS	173	E	-7.805417	9.688323	-11.115918	-4.742897
1I1N	A	PRO	174	E	-7.780101	9.716224	-11.207389	-4.751190
1I1N	A	GLY	175	E	-7.777814	9.727493	-11.215500	-4.751599
1I1N	A	GLY	176	E	-7.777803	9.731229	-11.212979	-4.751112
1I1N	A	ARG	177	E	-8.921587	8.964311	-13.724948	-5.056747
1I1N	A	LEU	178	E	-9.531382	11.429415	-12.890123	-4.791597
1I1N	A	ILE	179	E	-9.681179	15.813611	-10.101125	-4.110098
1I1N	A	LEU	180	E	-9.481891	14.860924	-10.054192	-3.794839
1I1N	A	PRO	181	E	-7.635607	9.699477	-8.640794	-3.049907
1I1N	A	VAL	182	E	-5.772314	6.370975	-8.460510	-3.451829
1I1N	A	GLY	183	C	-3.290013	3.196781	-7.420583	-3.886534
1I1N	A	PRO	184	T	-1.539529	2.857157	-5.713654	-3.950415
1I1N	A	ALA	185	T	-1.537506	2.864465	-5.729726	-3.954308
1I1N	A	GLY	186	T	-1.537505	2.864311	-5.729909	-3.954382
1I1N	A	GLY	187	T	-1.538020	2.861047	-5.726851	-3.954327
1I1N	A	ASN	188	C	-1.573820	2.820076	-5.576625	-3.925945
1I1N	A	GLN	189	E	-4.981996	4.615087	-9.679037	-4.550057
1I1N	A	MET	190	E	-7.642335	5.327382	-13.277223	-4.960432
1I1N	A	LEU	191	E	-10.506353	11.200151	-15.647912	-5.918595
1I1N	A	GLU	192	E	-13.303348	12.923345	-16.964340	-5.262055
1I1N	A	GLN	193	E	-15.874141	18.387082	-20.937873	-7.052122
1I1N	A	TYR	194	E	-13.360188	15.952938	-19.723160	-8.223291
1I1N	A	ASP	195	E	-10.770944	9.821383	-17.598830	-6.635493
1I1N	A	LYS	196	E	-7.348291	7.185029	-11.620899	-4.762466
1I1N	A	LEU	197	T	-5.423235	4.475338	-9.945476	-4.187844
1I1N	A	GLN	198	T	-4.708670	5.477982	-8.781479	-4.112967
1I1N	A	ASP	199	T	-4.679145	5.560566	-8.863664	-4.137498
1I1N	A	GLY	200	T	-4.674291	5.582985	-8.880876	-4.140974
1I1N	A	SER	201	C	-4.678786	5.579560	-8.857481	-4.135390
1I1N	A	ILE	202	E	-4.750507	6.791721	-8.267693	-4.148953
1I1N	A	LYS	203	E	-5.443785	9.622019	-8.254051	-4.373504
1I1N	A	MET	204	E	-5.461262	10.263616	-7.933140	-4.384827
1I1N	A	LYS	205	E	-5.119918	10.018313	-7.755306	-4.421877
1I1N	A	PRO	206	E	-4.849870	10.309028	-7.197637	-4.276179
1I1N	A	LEU	207	E	-4.336330	9.564826	-6.183958	-3.938338
1I1N	A	MET	208	E	-4.352008	9.550803	-6.128816	-3.923974
1I1N	A	GLY	209	E	-4.363478	9.521212	-6.080264	-3.905277
1I1N	A	VAL	210	E	-4.443646	9.502715	-5.851877	-3.821859
1I1N	A	ILE	211	C	-4.566108	9.204140	-5.751436	-3.773677
1I1N	A	TYR	212	C	-7.093695	10.754483	-9.417129	-4.174406
1I1N	A	VAL	213	C	-7.509171	10.517620	-9.623753	-4.032585
1I1N	A	PRO	214	B	-8.714308	12.110367	-9.593074	-3.541119
1I1N	A	LEU	215	C	-9.934647	13.625140	-11.046954	-3.888685
1I1N	A	THR	216	C	-9.601552	7.737401	-15.347061	-5.301750
1I1N	A	ASP	217	C	-9.604999	7.569801	-15.479313	-5.340811
1I1N	A	LYS	218	H	-9.667484	7.025180	-15.915658	-5.535334
1I1N	A	GLU	219	H	-9.502916	7.976441	-16.105907	-5.941059
1I1N	A	LYS	220	H	-9.365835	8.396215	-15.939925	-5.936953
1I1N	A	GLN	221	H	-8.550436	8.743037	-12.864326	-4.908762
1I1N	A	TRP	222	C	-4.012511	6.465125	-5.415091	-2.997071
1I1N	A	SER	223	C	-4.012511	6.465125	-5.415091	-2.997071
1I1N	A	ARG	224	C	-4.012511	6.465125	-5.415091	-2.997071
1I1N	A	TRP	225	C	-4.012511	6.465125	-5.415091	-2.997071
1I27	A	GLY	445	C	-2.324716	-0.648962	-8.787863	-3.702097
1I27	A	PRO	446	G	-2.324716	-0.648962	-8.787863	-3.702097
1I27	A	LEU	447	G	-2.324716	-0.648962	-8.787863	-3.702097
1I27	A	GLY	448	G	-2.324716	-0.648962	-8.787863	-3.702097
1I27	A	SER	449	C	-2.774373	-0.267728	-9.651908	-4.274094
1I27	A	GLY	450	C	-3.177841	-0.040300	-10.326881	-4.852227

1I27	A	ASP	451	C	-5.951385	3.720361	-14.079509	-5.817290
1I27	A	VAL	452	C	-6.327038	7.116232	-12.624922	-5.494460
1I27	A	GLN	453	C	-6.382064	8.644770	-11.374906	-5.087883
1I27	A	VAL	454	C	-6.476810	9.696603	-10.157053	-4.581630
1I27	A	THR	455	C	-6.788936	10.149013	-10.141105	-4.519796
1I27	A	GLU	456	H	-6.986360	10.348215	-10.079665	-4.565608
1I27	A	ASP	457	H	-7.306033	10.236628	-10.468950	-4.719726
1I27	A	ALA	458	H	-8.059600	10.745473	-11.092590	-4.741945
1I27	A	VAL	459	H	-9.016371	10.548347	-12.241012	-4.721074
1I27	A	ARG	460	H	-10.344903	10.865256	-13.594361	-4.543685
1I27	A	ARG	461	H	-11.764458	9.381080	-15.286429	-3.981771
1I27	A	TYR	462	H	-12.127071	14.092203	-14.581367	-4.956351
1I27	A	LEU	463	H	-9.228368	12.201152	-10.859849	-4.333309
1I27	A	THR	464	H	-8.750611	11.971061	-11.231116	-4.593181
1I27	A	ARG	465	H	-8.684101	12.123872	-11.334729	-4.646329
1I27	A	LYS	466	C	-8.487509	12.844958	-11.265325	-4.859784
1I27	A	PRO	467	C	-7.870232	13.905507	-9.892414	-4.972078
1I27	A	MET	468	B	-7.455740	12.507832	-10.215407	-5.101841
1I27	A	THR	469	C	-6.442834	12.301721	-8.269581	-4.784701
1I27	A	THR	470	H	-6.425968	12.312421	-8.306229	-4.773933
1I27	A	LYS	471	H	-6.411313	12.244115	-8.365554	-4.758567
1I27	A	ASP	472	H	-6.444097	12.116965	-8.325214	-4.743148
1I27	A	LEU	473	H	-6.506509	12.218830	-8.076869	-4.698055
1I27	A	LEU	474	H	-8.030638	11.889716	-10.387524	-4.490127
1I27	A	LYS	475	H	-8.384090	11.213811	-10.929887	-4.529483
1I27	A	LYS	476	H	-9.800426	15.257564	-12.307847	-5.246308
1I27	A	PHE	477	C	-9.817469	14.448068	-12.630405	-5.147326
1I27	A	GLN	478	C	-8.844714	9.915701	-12.813585	-4.890006
1I27	A	THR	479	H	-6.220364	7.888400	-10.636787	-5.170933
1I27	A	LYS	480	H	-6.068517	8.223692	-10.665291	-5.184225
1I27	A	LYS	481	H	-6.067007	8.227232	-10.674514	-5.185191
1I27	A	THR	482	H	-6.062734	8.211396	-10.695820	-5.179621
1I27	A	GLY	483	C	-6.062369	8.179381	-10.709510	-5.176145
1I27	A	LEU	484	C	-6.898021	9.129193	-11.037457	-5.176075
1I27	A	SER	485	C	-8.330436	6.423503	-14.112189	-4.569813
1I27	A	SER	486	H	-8.383065	6.006028	-14.132104	-4.442157
1I27	A	GLU	487	H	-8.585684	5.902243	-14.504214	-4.487145
1I27	A	GLN	488	H	-9.023244	7.327060	-14.682219	-4.575786
1I27	A	THR	489	H	-9.115597	7.977332	-14.467224	-4.645525
1I27	A	VAL	490	H	-9.013352	8.712860	-13.471438	-4.317287
1I27	A	ASN	491	H	-9.078833	8.820461	-13.307980	-4.259603
1I27	A	VAL	492	H	-9.320906	9.508558	-12.695562	-3.974938
1I27	A	LEU	493	H	-9.432825	9.595028	-12.352520	-3.821425
1I27	A	ALA	494	H	-9.372309	9.546776	-12.429035	-3.842285
1I27	A	GLN	495	H	-9.442035	10.605868	-12.259153	-4.037942
1I27	A	ILE	496	H	-9.422387	10.978486	-12.088470	-4.040112
1I27	A	LEU	497	H	-9.009258	11.078204	-11.906079	-4.257044
1I27	A	LYS	498	H	-8.433646	10.074950	-11.596650	-4.218915
1I27	A	ARG	499	H	-8.449923	10.073519	-11.568446	-4.227135
1I27	A	LEU	500	H	-8.193071	10.613409	-11.079636	-4.269347
1I27	A	ASN	501	C	-8.114659	10.539463	-11.386395	-4.397133
1I27	A	PRO	502	C	-8.164515	10.517890	-11.455665	-4.446470
1I27	A	GLU	503	E	-8.175292	11.820397	-13.054357	-6.131286
1I27	A	ARG	504	E	-7.171773	9.913096	-10.792461	-4.907291
1I27	A	LYS	505	E	-4.649835	7.039542	-7.883627	-4.453279
1I27	A	MET	506	E	-1.989857	5.884952	-4.839947	-4.203264
1I27	A	ILE	507	E	-1.925616	6.123905	-4.972987	-4.267656
1I27	A	ASN	508	T	-1.923411	6.136199	-4.987149	-4.271892
1I27	A	ASP	509	T	-1.923481	6.135790	-4.986497	-4.271829
1I27	A	LYS	510	E	-1.929844	6.121522	-4.951669	-4.266527
1I27	A	MET	511	E	-3.293131	7.856766	-5.902190	-4.566978
1I27	A	HIS	512	E	-5.280694	8.998616	-8.442895	-5.103042
1I27	A	PHE	513	E	-8.975190	15.311114	-13.015866	-7.049010
1I27	A	SER	514	E	-7.265403	8.072922	-10.047590	-3.963299
1I27	A	LEU	515	C	-7.265403	8.072922	-10.047590	-3.963299
1I27	A	LYS	516	C	-7.265403	8.072922	-10.047590	-3.963299
1I27	A	GLU	517	C	-7.265403	8.072922	-10.047590	-3.963299
1I2T	A	HIS	1009	H	-8.350529	5.413890	-12.787005	-3.509264
1I2T	A	ARG	1010	H	-8.350529	5.413890	-12.787005	-3.509264
1I2T	A	GLN	1011	H	-8.350529	5.413890	-12.787005	-3.509264
1I2T	A	ALA	1012	H	-8.350529	5.413890	-12.787005	-3.509264
1I2T	A	LEU	1013	H	-8.652050	11.811175	-11.066279	-4.309686
1I2T	A	GLY	1014	H	-8.649135	13.190199	-10.499896	-4.435713
1I2T	A	GLU	1015	H	-8.630688	13.443988	-10.298639	-4.374224
1I2T	A	ARG	1016	H	-8.661060	13.644647	-10.003039	-4.289880
1I2T	A	LEU	1017	H	-8.680510	13.738104	-9.811915	-4.227723
1I2T	A	TYR	1018	H	-9.317342	13.715414	-10.779518	-4.463407
1I2T	A	PRO	1019	H	-10.031572	13.195375	-11.247099	-4.191926
1I2T	A	ARG	1020	H	-12.342088	10.993899	-16.232290	-4.278958
1I2T	A	VAL	1021	H	-11.259813	12.090843	-14.864152	-5.008837
1I2T	A	GLN	1022	H	-10.008763	8.940186	-14.564725	-4.883349

1I2T	A	ALA	1023	H	-8.268872	7.628134	-12.156147	-4.340624
1I2T	A	MET	1024	H	-8.219298	7.885031	-12.208716	-4.382058
1I2T	A	GLN	1025	T	-8.019546	8.458824	-11.941856	-4.326407
1I2T	A	PRO	1026	T	-7.551248	8.920956	-10.712737	-3.874322
1I2T	A	ALA	1027	T	-7.508786	8.981753	-10.705820	-3.859357
1I2T	A	PHE	1028	T	-7.680735	9.540343	-10.250910	-3.703245
1I2T	A	ALA	1029	H	-7.675331	9.604345	-10.192541	-3.678126
1I2T	A	SER	1030	H	-7.586230	9.509564	-10.304606	-3.786023
1I2T	A	LYS	1031	H	-8.026677	10.034072	-11.250887	-4.281328
1I2T	A	ILE	1032	H	-8.134374	10.296072	-11.259627	-4.402085
1I2T	A	THR	1033	H	-8.139877	10.273512	-11.287398	-4.423429
1I2T	A	GLY	1034	H	-8.029283	10.238960	-11.345784	-4.483228
1I2T	A	MET	1035	H	-8.493443	11.569411	-11.632896	-4.697622
1I2T	A	LEU	1036	H	-8.592778	11.590322	-11.492601	-4.558950
1I2T	A	LEU	1037	H	-8.454612	10.352185	-11.851637	-4.400828
1I2T	A	GLU	1038	H	-7.386549	5.819146	-11.717053	-3.908220
1I2T	A	LEU	1039	C	-7.413882	5.386109	-11.844025	-3.863612
1I2T	A	SER	1040	C	-7.408815	5.353059	-11.877861	-3.863789
1I2T	A	PRO	1041	H	-7.416225	5.250289	-11.892692	-3.857232
1I2T	A	ALA	1042	H	-7.444270	5.135631	-11.851215	-3.849389
1I2T	A	GLN	1043	H	-8.996627	7.078248	-13.832739	-4.246359
1I2T	A	LEU	1044	H	-9.497607	9.159956	-13.321650	-4.367679
1I2T	A	LEU	1045	H	-9.578616	11.522231	-12.076677	-4.252096
1I2T	A	LEU	1046	H	-9.530016	11.616054	-12.042225	-4.268138
1I2T	A	LEU	1047	H	-9.515729	11.590206	-12.109224	-4.289059
1I2T	A	LEU	1048	H	-9.306735	10.072521	-13.139225	-4.477476
1I2T	A	ALA	1049	H	-8.951297	7.786886	-14.184930	-4.631609
1I2T	A	SER	1050	C	-9.107318	6.413144	-15.226162	-4.827037
1I2T	A	GLU	1051	H	-9.159474	5.951032	-15.492537	-4.875387
1I2T	A	ASP	1052	H	-9.090575	6.194971	-15.306004	-4.799714
1I2T	A	SER	1053	H	-9.227923	6.112822	-15.236929	-4.767506
1I2T	A	LEU	1054	H	-9.989503	8.841066	-14.703110	-4.638938
1I2T	A	ARG	1055	H	-10.123900	8.875144	-14.396663	-4.503246
1I2T	A	ALA	1056	H	-10.220036	8.693388	-14.241342	-4.357860
1I2T	A	ARG	1057	H	-11.413024	9.908919	-16.248068	-4.826890
1I2T	A	VAL	1058	H	-10.346186	14.038336	-17.078734	-8.292047
1I2T	A	ASP	1059	H	-8.942648	12.342021	-16.418293	-8.710640
1I2T	A	GLU	1060	H	-7.638333	11.855171	-13.871019	-7.874538
1I2T	A	ALA	1061	H	-6.738400	11.168388	-12.080646	-7.019477
1I2T	A	MET	1062	H	-5.402955	8.650787	-10.362435	-6.138235
1I2T	A	GLU	1063	H	-3.636001	6.445150	-7.572138	-4.937796
1I2T	A	LEU	1064	H	-2.830600	5.987809	-6.308076	-4.312609
1I2T	A	ILE	1065	H	-2.264122	5.128462	-5.603365	-3.772203
1I2T	A	ILE	1066	H	-1.459832	2.623027	-5.087124	-3.065595
1I2T	A	ALA	1067	H	-1.459832	2.623027	-5.087124	-3.065595
1I2T	A	HIS	1068	H	-1.459832	2.623027	-5.087124	-3.065595
1I2T	A	GLY	1069	C	-1.459832	2.623027	-5.087124	-3.065595
1I4M	A	GLY	119	C	-3.389287	5.061983	-9.107608	-4.912687
1I4M	A	ALA	120	C	-3.389287	5.061983	-9.107608	-4.912687
1I4M	A	VAL	121	C	-3.389287	5.061983	-9.107608	-4.912687
1I4M	A	VAL	122	T	-3.389287	5.061983	-9.107608	-4.912687
1I4M	A	GLY	123	T	-2.743306	4.914773	-8.078189	-4.963221
1I4M	A	GLY	124	T	-2.788552	4.975899	-8.067973	-5.044029
1I4M	A	LEU	125	T	-2.896896	5.063235	-7.869352	-5.044625
1I4M	A	GLY	126	T	-2.910260	5.007420	-7.814540	-5.024340
1I4M	A	GLY	127	T	-2.931701	4.928541	-7.680576	-4.953872
1I4M	A	TYR	128	T	-5.685947	10.758652	-9.088791	-5.544429
1I4M	A	MET	129	E	-6.510276	9.212576	-10.067969	-4.609452
1I4M	A	LEU	130	E	-6.315083	8.073985	-10.175963	-4.334858
1I4M	A	GLY	131	C	-6.020121	6.130235	-10.437044	-3.971986
1I4M	A	SER	132	C	-6.024193	6.050078	-10.440991	-3.952699
1I4M	A	ALA	133	C	-6.021269	6.034198	-10.454366	-3.948068
1I4M	A	MET	134	C	-6.207355	5.211935	-10.787905	-3.783435
1I4M	A	SER	135	C	-6.374265	4.835208	-10.849840	-3.658744
1I4M	A	ARG	136	C	-6.996949	8.064668	-10.540149	-3.766040
1I4M	A	PRO	137	C	-5.609856	8.589283	-7.528119	-3.534140
1I4M	A	ILE	138	C	-4.268118	7.984733	-6.581326	-3.898780
1I4M	A	ILE	139	C	-4.255719	7.979259	-6.648544	-3.912052
1I4M	A	HIS	140	C	-4.223518	7.936832	-6.821470	-3.959057
1I4M	A	PHE	141	T	-4.198662	7.949884	-6.934423	-3.999997
1I4M	A	GLY	142	T	-4.009190	7.026130	-7.631927	-4.231677
1I4M	A	SER	143	T	-4.520708	5.813258	-9.235295	-4.638099
1I4M	A	ASP	144	H	-4.543062	5.739634	-9.209274	-4.645702
1I4M	A	TYR	145	H	-4.601285	5.588425	-9.134322	-4.633781
1I4M	A	GLU	146	H	-4.656179	5.330614	-9.087649	-4.612445
1I4M	A	ASP	147	H	-7.899425	11.216578	-14.900665	-7.999922
1I4M	A	ARG	148	H	-10.193897	9.364668	-16.712648	-6.298934
1I4M	A	TYR	149	H	-13.623987	12.531088	-22.036105	-8.215516
1I4M	A	TYR	150	H	-15.559146	15.073526	-22.207305	-7.084088
1I4M	A	ARG	151	H	-13.261935	10.121822	-19.524256	-6.018704
1I4M	A	GLU	152	H	-13.257253	10.109126	-19.538623	-6.010819

1I4M	A	ASN	153	H	-13.231679	10.265330	-19.568945	-6.026293
1I4M	A	MET	154	G	-13.204194	10.459783	-19.540979	-6.012583
1I4M	A	HIS	155	G	-13.203344	10.444552	-19.547609	-6.009009
1I4M	A	ARG	156	G	-14.408703	13.810793	-20.198303	-6.096701
1I4M	A	TYR	157	C	-11.160660	13.925839	-14.141025	-5.546172
1I4M	A	PRO	158	C	-10.800596	15.105583	-13.721794	-5.648332
1I4M	A	ASN	159	C	-10.799445	15.118047	-13.725994	-5.650810
1I4M	A	GLN	160	C	-10.799555	15.118889	-13.724492	-5.650785
1I4M	A	VAL	161	C	-10.799693	15.119733	-13.722656	-5.650655
1I4M	A	TYR	162	E	-11.260968	16.535703	-13.259555	-5.775983
1I4M	A	TYR	163	E	-11.412046	12.914029	-14.625924	-5.136366
1I4M	A	ARG	164	C	-7.843972	7.323479	-12.042912	-4.533955
1I4M	A	PRO	165	C	-7.071070	7.933489	-11.352975	-4.675424
1I4M	A	MET	166	G	-6.834088	7.817177	-11.398550	-4.646652
1I4M	A	ASP	167	G	-6.821990	7.806939	-11.461940	-4.657654
1I4M	A	GLU	168	G	-6.817116	7.807361	-11.489764	-4.662319
1I4M	A	TYR	169	C	-6.839844	7.876648	-11.505283	-4.697625
1I4M	A	SER	170	C	-4.858241	4.051848	-9.791200	-4.391258
1I4M	A	ASN	171	C	-4.863862	4.020946	-9.777606	-4.390298
1I4M	A	GLN	172	H	-4.861764	4.040950	-9.781690	-4.391118
1I4M	A	ASN	173	H	-4.861844	4.040709	-9.780862	-4.390959
1I4M	A	ASN	174	H	-4.864880	4.022138	-9.767952	-4.389144
1I4M	A	PHE	175	H	-7.820409	9.111229	-11.995159	-4.819381
1I4M	A	VAL	176	H	-8.062720	9.263499	-11.706898	-4.726857
1I4M	A	HIS	177	H	-9.741079	8.804540	-14.849379	-4.864194
1I4M	A	ASP	178	H	-10.408808	6.767037	-16.637848	-4.651029
1I4M	A	CYS	179	H	-10.333774	7.204080	-16.377251	-4.636061
1I4M	A	VAL	180	H	-9.495194	8.546442	-13.771410	-4.247843
1I4M	A	ASN	181	H	-9.198652	9.295320	-13.163116	-4.289656
1I4M	A	ILE	182	H	-9.227156	9.461740	-12.975245	-4.267753
1I4M	A	THR	183	H	-9.230187	9.462073	-12.956613	-4.265365
1I4M	A	ILE	184	H	-9.232699	9.418742	-12.974140	-4.264317
1I4M	A	LYS	185	H	-9.621956	9.839261	-13.065580	-4.418794
1I4M	A	GLN	186	H	-10.273594	8.493853	-15.435354	-4.742321
1I4M	A	HIS	187	H	-7.573823	6.983825	-11.280689	-3.937757
1I4M	A	THR	188	H	-6.524569	6.279580	-10.930691	-4.131184
1I4M	A	VAL	189	H	-6.450060	6.225125	-11.130389	-4.154954
1I4M	A	THR	190	C	-5.756656	4.943586	-10.972592	-4.238015
1I4M	A	THR	191	C	-4.906689	4.429488	-10.086806	-4.321329
1I4M	A	THR	192	C	-4.404096	4.023149	-9.866860	-4.365488
1I4M	A	THR	193	C	-4.389037	3.979459	-9.958406	-4.399663
1I4M	A	LYS	194	G	-4.389143	3.985328	-9.959906	-4.403990
1I4M	A	GLY	195	G	-4.431269	3.957120	-9.890060	-4.413286
1I4M	A	GLU	196	G	-4.678834	3.795878	-9.930705	-4.447403
1I4M	A	ASN	197	G	-6.147988	4.374754	-12.346330	-5.046982
1I4M	A	PHE	198	C	-7.663346	8.028275	-13.559557	-5.794511
1I4M	A	THR	199	C	-7.207784	8.098013	-11.643024	-5.015068
1I4M	A	GLU	200	H	-7.147960	8.030417	-11.805570	-5.012213
1I4M	A	THR	201	H	-7.150621	7.980576	-11.722039	-4.934742
1I4M	A	ASP	202	H	-7.148042	7.986228	-11.712292	-4.920756
1I4M	A	VAL	203	H	-7.126218	8.005923	-11.719994	-4.899458
1I4M	A	LYS	204	H	-8.090415	8.492675	-13.370022	-5.018413
1I4M	A	MET	205	H	-8.411238	9.467012	-13.305391	-4.937161
1I4M	A	MET	206	H	-8.392854	9.535871	-13.331194	-4.946683
1I4M	A	GLU	207	H	-8.155539	8.557121	-13.569975	-4.887051
1I4M	A	ARG	208	H	-8.138984	7.437886	-13.824336	-4.651894
1I4M	A	VAL	209	H	-7.524911	6.178792	-12.802954	-4.317514
1I4M	A	VAL	210	H	-7.195878	6.149022	-12.449384	-4.281530
1I4M	A	GLU	211	H	-6.938078	6.000285	-12.248500	-4.230863
1I4M	A	GLN	212	H	-6.853051	6.138488	-12.167928	-4.240204
1I4M	A	MET	213	H	-6.866694	6.156343	-12.175835	-4.265340
1I4M	A	CYS	214	H	-7.009495	6.322644	-12.200801	-4.328048
1I4M	A	ILE	215	H	-7.230911	6.410594	-12.361003	-4.411374
1I4M	A	THR	216	H	-7.750659	7.369034	-13.135031	-4.898568
1I4M	A	GLN	217	H	-8.605179	8.827802	-16.986602	-6.995707
1I4M	A	TYR	218	H	-8.565313	9.663047	-17.702490	-7.964235
1I4M	A	GLU	219	H	-8.062863	9.267730	-16.106664	-7.447988
1I4M	A	ARG	220	H	-7.224780	7.981871	-13.779480	-6.282503
1I4M	A	GLU	221	H	-6.013554	6.462497	-11.371455	-5.223597
1I4M	A	SER	222	H	-5.069028	5.817291	-9.330820	-4.251871
1I4M	A	GLN	223	H	-3.420389	4.730209	-6.196543	-3.185948
1I4M	A	ALA	224	H	-3.420389	4.730209	-6.196543	-3.185948
1I4M	A	TYR	225	C	-3.420389	4.730209	-6.196543	-3.185948
1I4M	A	TYR	226	C	-3.420389	4.730209	-6.196543	-3.185948
1I71	A	ASP	0	C	-9.603302	10.629815	-15.703979	-6.526285
1I71	A	CYS	1	E	-9.603302	10.629815	-15.703979	-6.526285
1I71	A	TYR	2	E	-9.603302	10.629815	-15.703979	-6.526285
1I71	A	HIS	3	T	-9.603302	10.629815	-15.703979	-6.526285
1I71	A	GLY	4	T	-9.547593	7.093802	-17.282867	-6.407223
1I71	A	ASP	5	T	-9.776317	4.555739	-17.284803	-5.430467
1I71	A	GLY	6	T	-9.843583	3.854307	-16.947791	-4.991824

1I71	A	GLN	7	T	-9.848444	3.792897	-16.902240	-4.952144
1I71	A	SER	8	T	-9.848060	3.795882	-16.902852	-4.951035
1I71	A	TYR	9	T	-13.392041	9.279560	-18.044893	-3.656376
1I71	A	ARG	10	C	-13.163340	9.558410	-17.015717	-3.342208
1I71	A	GLY	11	C	-10.272617	10.013715	-11.199027	-2.770500
1I71	A	SER	12	C	-10.104467	10.495776	-11.243025	-2.833010
1I71	A	PHE	13	C	-10.060428	10.650523	-11.416034	-2.926376
1I71	A	SER	14	C	-8.894946	9.727700	-12.360116	-4.524641
1I71	A	THR	15	B	-7.577439	7.646407	-9.362012	-2.891542
1I71	A	THR	16	B	-7.519743	7.673823	-9.482345	-2.908921
1I71	A	VAL	17	T	-7.197336	7.468349	-9.519588	-2.902600
1I71	A	THR	18	T	-7.137331	7.438315	-9.861249	-3.056792
1I71	A	GLY	19	T	-7.163843	7.340319	-9.742670	-2.978438
1I71	A	ARG	20	C	-7.511332	7.297494	-10.336234	-3.205800
1I71	A	THR	21	B	-7.574337	7.203507	-10.294786	-3.223312
1I71	A	CYS	22	B	-8.517403	7.197977	-13.095130	-4.510015
1I71	A	GLN	23	C	-11.611705	9.433858	-17.672020	-6.087053
1I71	A	SER	24	T	-12.726850	10.926566	-16.729852	-4.801516
1I71	A	TRP	25	T	-11.463612	10.438482	-13.000266	-2.982150
1I71	A	SER	26	T	-8.073746	7.113234	-9.030505	-2.114827
1I71	A	SER	27	T	-8.055292	7.167424	-9.107887	-2.132813
1I71	A	MET	28	T	-8.033695	7.248113	-9.252760	-2.199506
1I71	A	THR	29	T	-8.027715	7.283177	-9.305271	-2.228718
1I71	A	PRO	30	T	-8.029164	7.275896	-9.297899	-2.227607
1I71	A	HIS	31	T	-9.559712	9.400890	-12.730977	-3.643034
1I71	A	TRP	32	T	-9.849842	9.737821	-13.483328	-4.240602
1I71	A	HIS	33	C	-10.695402	10.852703	-14.603519	-5.038148
1I71	A	GLN	34	C	-9.439875	11.315694	-12.655182	-5.078505
1I71	A	ARG	35	C	-9.232013	11.064547	-12.012547	-4.408005
1I71	A	THR	36	T	-8.959315	11.581578	-11.164995	-3.969380
1I71	A	THR	37	T	-8.803421	11.230649	-11.028258	-3.704085
1I71	A	GLU	38	T	-8.622699	10.587196	-11.464566	-3.775780
1I71	A	TYR	39	T	-8.477051	10.169481	-11.704729	-4.005846
1I71	A	TYR	40	T	-8.158735	8.572400	-11.240024	-3.453878
1I71	A	PRO	41	T	-6.565752	6.884556	-7.976913	-2.539107
1I71	A	ASN	42	T	-6.462136	7.100829	-8.131923	-2.622402
1I71	A	GLY	43	T	-6.421213	7.279452	-8.252428	-2.702219
1I71	A	GLY	44	T	-6.379708	7.488352	-8.398460	-2.843027
1I71	A	LEU	45	T	-6.393284	7.508009	-8.347922	-2.846681
1I71	A	THR	46	T	-7.109366	9.169849	-9.748301	-3.713969
1I71	A	ARG	47	T	-7.510203	10.028472	-10.484385	-4.354238
1I71	A	ASN	48	T	-7.874987	10.315526	-10.743654	-4.798264
1I71	A	TYR	49	T	-10.870542	12.875026	-11.293627	-3.171793
1I71	A	CYS	50	C	-11.784319	10.148814	-13.956792	-3.476961
1I71	A	ARG	51	B	-14.950440	10.344496	-18.199398	-3.493509
1I71	A	ASN	52	T	-11.473258	9.117409	-14.012737	-3.341391
1I71	A	PRO	53	T	-9.396047	8.537017	-12.516930	-3.677359
1I71	A	ASP	54	T	-9.340488	8.530107	-12.794463	-3.791303
1I71	A	ALA	55	T	-9.300321	8.724913	-12.644384	-3.691692
1I71	A	GLU	56	C	-9.300292	8.725816	-12.644098	-3.691622
1I71	A	ILE	57	C	-9.315497	8.716631	-12.608813	-3.700689
1I71	A	ARG	58	C	-10.426541	9.807818	-13.371907	-3.772117
1I71	A	PRO	59	C	-10.908873	11.567324	-10.545532	-2.295459
1I71	A	TRP	60	E	-13.627654	18.025805	-14.581401	-4.645748
1I71	A	CYS	61	E	-13.539680	16.709977	-15.307045	-4.736881
1I71	A	TYR	62	E	-12.760495	13.654752	-14.484262	-3.866135
1I71	A	THR	63	B	-9.033980	7.683312	-12.442725	-3.695895
1I71	A	MET	64	C	-6.978309	6.344952	-10.804046	-4.053270
1I71	A	ASP	65	T	-6.975373	6.345472	-10.809058	-4.043215
1I71	A	PRO	66	T	-6.965416	6.414421	-10.775461	-4.009261
1I71	A	SER	67	T	-6.965126	6.416796	-10.776104	-4.008726
1I71	A	VAL	68	T	-6.983390	6.377763	-10.724128	-4.018565
1I71	A	ARG	69	T	-9.223503	9.631658	-9.560259	-2.040620
1I71	A	TRP	70	E	-9.369670	10.534847	-8.931386	-2.049434
1I71	A	GLU	71	E	-11.339615	11.964141	-12.649706	-3.228361
1I71	A	TYR	72	E	-11.875722	14.228270	-14.122479	-4.322264
1I71	A	CYS	73	B	-9.039596	10.214222	-13.607227	-5.687467
1I71	A	ASN	74	T	-7.074107	9.138124	-10.839153	-5.265949
1I71	A	LEU	75	T	-6.133091	7.685573	-9.553834	-4.423759
1I71	A	THR	76	E	-3.855190	3.198573	-7.199504	-3.297540
1I71	A	GLN	77	E	-3.032348	2.597842	-6.142434	-2.757112
1I71	A	CYS	78	C	-1.601837	0.704693	-3.786721	-1.598437
1I71	A	PRO	79	C	1.346211	0.172233	-1.413033	-2.350798
1I71	A	VAL	80	C	1.346211	0.172233	-1.413033	-2.350798
1I71	A	MET	81	C	1.346211	0.172233	-1.413033	-2.350798
1I71	A	GLU	82	C	1.346211	0.172233	-1.413033	-2.350798
1I76	A	MET	80	C	-6.296794	9.185948	-10.523908	-5.157845
1I76	A	LEU	81	B	-6.296794	9.185948	-10.523908	-5.157845
1I76	A	THR	82	T	-6.296794	9.185948	-10.523908	-5.157845
1I76	A	PRO	83	T	-6.296794	9.185948	-10.523908	-5.157845
1I76	A	GLY	84	T	-6.322553	9.208620	-10.536387	-5.233415

1I76	A	ASN	85	T	-6.436901	9.271661	-10.527107	-5.382802
1I76	A	PRO	86	C	-8.037550	10.636396	-12.747670	-6.016534
1I76	A	LYS	87	C	-9.476165	13.133960	-13.886638	-5.941347
1I76	A	TRP	88	T	-9.538303	12.801387	-13.108619	-5.129710
1I76	A	GLU	89	T	-8.565665	10.444321	-11.951843	-4.729920
1I76	A	ARG	90	T	-8.553279	10.456747	-11.974510	-4.726589
1I76	A	THR	91	T	-8.550392	10.495049	-11.974971	-4.730879
1I76	A	ASN	92	E	-8.568471	10.414280	-11.935475	-4.721893
1I76	A	LEU	93	E	-8.603693	10.312878	-11.848887	-4.701790
1I76	A	THR	94	E	-10.395210	12.954217	-13.186360	-4.908832
1I76	A	TYR	95	E	-11.541752	17.309953	-12.719777	-5.417098
1I76	A	ARG	96	E	-14.474439	16.021535	-18.270982	-5.759978
1I76	A	ILE	97	E	-11.685495	16.097805	-13.932166	-5.690114
1I76	A	ARG	98	C	-10.533255	12.685372	-14.196016	-5.435978
1I76	A	ASN	99	C	-10.179293	11.562177	-14.634666	-5.378562
1I76	A	TYR	100	C	-9.504864	12.892147	-12.780477	-5.158590
1I76	A	THR	101	T	-8.909999	10.122737	-13.121796	-4.842066
1I76	A	PRO	102	T	-8.660905	9.233684	-13.397627	-4.779449
1I76	A	GLN	103	T	-8.668120	9.103191	-13.429099	-4.759556
1I76	A	LEU	104	T	-8.407883	8.644333	-13.335893	-4.686582
1I76	A	SER	105	T	-7.958327	8.298917	-12.563604	-4.518023
1I76	A	GLU	106	H	-8.016781	8.336558	-12.516520	-4.523351
1I76	A	ALA	107	H	-8.090302	8.425957	-12.333858	-4.503394
1I76	A	GLU	108	H	-8.095661	8.428575	-12.301304	-4.499896
1I76	A	VAL	109	H	-8.244089	8.577226	-12.020576	-4.470993
1I76	A	GLU	110	H	-9.925342	10.355316	-14.247045	-5.155163
1I76	A	ARG	111	H	-9.870422	10.631044	-12.595536	-4.058049
1I76	A	ALA	112	H	-9.669381	11.054754	-12.549518	-4.140156
1I76	A	ILE	113	H	-9.651459	11.219935	-12.539803	-4.159138
1I76	A	LYS	114	H	-9.635470	11.210914	-12.620902	-4.195474
1I76	A	ASP	115	H	-9.636666	11.239027	-12.603206	-4.196733
1I76	A	ALA	116	H	-10.215032	12.478693	-12.946488	-4.500420
1I76	A	PHE	117	H	-11.074909	14.115269	-13.818328	-4.892120
1I76	A	GLU	118	H	-11.197807	13.073673	-14.450266	-4.874494
1I76	A	LEU	119	H	-11.702711	14.335083	-14.256591	-4.599228
1I76	A	TRP	120	H	-11.102849	13.241787	-14.006978	-4.730480
1I76	A	SER	121	H	-9.764026	8.116866	-14.014188	-4.204121
1I76	A	VAL	122	H	-8.783830	10.802559	-11.325646	-4.102162
1I76	A	ALA	123	C	-8.699790	10.854177	-11.403415	-4.089427
1I76	A	SER	124	C	-8.628954	11.413712	-11.263902	-4.134973
1I76	A	PRO	125	C	-8.510229	12.165827	-10.936216	-4.168516
1I76	A	LEU	126	C	-8.571516	12.766315	-10.582377	-4.180491
1I76	A	ILE	127	E	-9.048210	14.486204	-10.508922	-4.322124
1I76	A	PHE	128	E	-9.152231	15.430534	-10.238450	-4.457135
1I76	A	THR	129	E	-8.777464	10.658226	-12.260589	-4.552738
1I76	A	ARG	130	E	-8.215220	6.831591	-13.711745	-4.815691
1I76	A	ILE	131	C	-7.889137	5.719630	-14.313740	-4.940563
1I76	A	SER	132	C	-7.649329	5.192592	-14.510662	-4.958566
1I76	A	GLN	133	C	-7.620135	5.111381	-14.622393	-4.977769
1I76	A	GLY	134	C	-7.639108	5.058672	-14.684506	-5.008164
1I76	A	GLU	135	C	-7.829665	4.642033	-15.007136	-5.057058
1I76	A	ALA	136	T	-8.118482	4.857608	-14.941729	-5.023915
1I76	A	ASP	137	T	-8.917641	6.694716	-15.092753	-5.115946
1I76	A	ILE	138	E	-9.323672	8.384340	-14.005710	-4.951324
1I76	A	ASN	139	E	-11.947219	11.439728	-16.635334	-5.261706
1I76	A	ILE	140	E	-12.690418	16.549654	-15.235678	-5.165576
1I76	A	ALA	141	E	-12.906265	17.756688	-14.747604	-5.179451
1I76	A	PHE	142	E	-12.812844	18.478086	-14.378292	-5.294466
1I76	A	TYR	143	E	-11.112604	13.312753	-15.346929	-5.874396
1I76	A	GLN	144	T	-7.317484	8.653635	-11.446344	-5.103382
1I76	A	ARG	145	T	-7.261837	8.569194	-11.657396	-5.110138
1I76	A	ASP	146	T	-4.648684	5.455782	-9.721203	-5.103240
1I76	A	HIS	147	T	-4.388962	5.928505	-9.568519	-5.064453
1I76	A	GLY	148	C	-3.632448	5.157544	-8.419697	-4.553642
1I76	A	ASP	149	C	-3.632754	5.158862	-8.415605	-4.552414
1I76	A	ASN	150	C	-3.632515	5.161169	-8.416010	-4.552210
1I76	A	SER	151	C	-3.748912	5.101809	-8.131715	-4.429189
1I76	A	PRO	152	C	-3.825110	4.869343	-7.970529	-4.350307
1I76	A	PHE	153	C	-7.255980	10.500726	-10.232312	-4.472162
1I76	A	ASP	154	C	-6.668199	4.304197	-12.888037	-4.840907
1I76	A	GLY	155	C	-5.554014	3.626285	-11.205715	-4.396637
1I76	A	PRO	156	C	-5.463549	4.004785	-11.096848	-4.353196
1I76	A	ASN	157	T	-5.367957	4.623340	-10.839063	-4.323542
1I76	A	GLY	158	T	-5.336298	4.914958	-10.755494	-4.322407
1I76	A	ILE	159	T	-5.392503	5.076064	-10.512491	-4.263565
1I76	A	LEU	160	T	-6.026360	7.871251	-9.766496	-4.158462
1I76	A	ALA	161	E	-6.297998	8.773483	-9.369310	-4.196032
1I76	A	HIS	162	E	-7.058095	10.321587	-9.313656	-4.297443
1I76	A	ALA	163	E	-8.840000	12.965006	-10.392839	-4.131152
1I76	A	PHE	164	E	-9.293043	12.956785	-11.719981	-4.510401
1I76	A	GLN	165	C	-6.811790	6.786372	-10.937482	-4.418013

1I76	A	PRO	166	C	-5.113462	6.001771	-8.633327	-3.926643
1I76	A	GLY	167	C	-3.908514	3.614623	-8.932783	-4.267980
1I76	A	GLN	168	T	-3.773648	3.795164	-9.000353	-4.277526
1I76	A	GLY	169	T	-3.773252	3.796567	-9.003353	-4.277955
1I76	A	ILE	170	T	-3.776639	3.780214	-8.992414	-4.277080
1I76	A	GLY	171	T	-3.838456	3.539923	-9.044188	-4.317434
1I76	A	GLY	172	T	-4.715664	4.503032	-9.257854	-4.305411
1I76	A	ASP	173	E	-7.947214	6.740292	-13.231137	-4.798825
1I76	A	ALA	174	E	-8.950852	8.860885	-12.684292	-4.452413
1I76	A	HIS	175	E	-11.078435	9.247837	-16.117022	-5.021934
1I76	A	PHE	176	E	-12.595845	14.674496	-15.858390	-5.115280
1I76	A	ASP	177	E	-11.801121	10.546036	-17.174680	-5.618949
1I76	A	ALA	178	T	-11.745960	10.912393	-17.136236	-5.646807
1I76	A	GLU	179	T	-11.757829	10.796843	-17.228619	-5.693463
1I76	A	GLU	180	T	-11.759399	10.760175	-17.255818	-5.703348
1I76	A	THR	181	C	-11.130594	11.839817	-15.748655	-5.468442
1I76	A	TRP	182	E	-10.836807	12.784590	-14.623102	-5.276078
1I76	A	THR	183	E	-7.881819	6.402933	-12.570692	-4.477669
1I76	A	ASN	184	C	-6.531920	6.054621	-11.394713	-4.607752
1I76	A	THR	185	C	-6.522198	6.119249	-11.410119	-4.609812
1I76	A	SER	186	C	-6.522223	6.118692	-11.410156	-4.609783
1I76	A	ALA	187	T	-6.522448	6.116112	-11.409107	-4.609566
1I76	A	ASN	188	T	-6.584974	6.088926	-11.281290	-4.624820
1I76	A	TYR	189	E	-8.953100	10.045660	-12.393778	-4.743766
1I76	A	ASN	190	E	-11.389579	12.116603	-15.502301	-5.324980
1I76	A	LEU	191	H	-11.690719	19.857342	-10.790244	-4.414775
1I76	A	PHE	192	H	-11.157285	18.763178	-10.404469	-4.111183
1I76	A	LEU	193	H	-10.860299	16.924734	-11.168311	-4.047963
1I76	A	VAL	194	H	-10.757404	16.284372	-11.616903	-4.089646
1I76	A	ALA	195	H	-10.772263	16.162598	-11.620354	-4.068334
1I76	A	ALA	196	H	-10.870835	15.333369	-12.009367	-4.056460
1I76	A	HIS	197	H	-11.157254	13.777857	-12.989627	-4.106227
1I76	A	GLU	198	H	-11.779009	13.172362	-14.211094	-4.398647
1I76	A	PHE	199	H	-12.965267	15.531019	-16.108995	-5.157529
1I76	A	GLY	200	H	-12.432085	12.589526	-16.765934	-5.196073
1I76	A	HIS	201	H	-12.504157	12.287076	-16.906672	-5.186212
1I76	A	SER	202	H	-12.225481	12.754330	-16.276251	-4.979264
1I76	A	LEU	203	H	-11.284863	13.928769	-13.666449	-4.604386
1I76	A	GLY	204	C	-11.083135	13.233865	-14.106373	-4.654987
1I76	A	LEU	205	B	-10.595223	12.055543	-13.715035	-4.381557
1I76	A	ALA	206	C	-8.970176	9.253317	-12.461961	-4.322301
1I76	A	HIS	207	C	-8.318388	8.301581	-12.380859	-4.265632
1I76	A	SER	208	C	-6.762348	5.324485	-11.718396	-4.338370
1I76	A	SER	209	C	-5.206452	5.909806	-8.932817	-3.994985
1I76	A	ASP	210	T	-5.182958	6.027423	-8.972488	-4.006730
1I76	A	PRO	211	T	-5.183517	6.025965	-8.969248	-4.006652
1I76	A	GLY	212	T	-5.185506	6.019985	-8.957912	-4.005883
1I76	A	ALA	213	T	-5.225224	6.083959	-8.769888	-3.982352
1I76	A	LEU	214	T	-7.095495	8.986662	-10.000127	-4.302964
1I76	A	MET	215	T	-9.426646	12.094203	-12.393789	-4.745634
1I76	A	TYR	216	T	-7.988220	12.887036	-9.413775	-4.543119
1I76	A	PRO	217	C	-7.640252	13.689349	-9.227575	-4.683473
1I76	A	ASN	218	C	-7.611171	13.714899	-9.300779	-4.687502
1I76	A	TYR	219	C	-7.604573	13.719828	-9.321387	-4.687169
1I76	A	ALA	220	C	-7.467893	13.415144	-9.471756	-4.641023
1I76	A	PHE	221	C	-7.657488	13.351592	-9.799987	-4.666708
1I76	A	ARG	222	C	-6.469874	7.368042	-10.076903	-4.175255
1I76	A	GLU	223	C	-5.912909	8.792646	-9.378890	-4.508912
1I76	A	THR	224	T	-5.806181	8.958999	-9.375775	-4.496551
1I76	A	SER	225	T	-5.790364	9.031610	-9.360032	-4.489316
1I76	A	ASN	226	T	-5.793477	9.024967	-9.350844	-4.489182
1I76	A	TYR	227	T	-6.001208	9.883665	-9.059402	-4.631795
1I76	A	SER	228	C	-6.734557	10.270948	-9.361129	-4.407902
1I76	A	LEU	229	C	-7.668458	11.999419	-9.333492	-4.304754
1I76	A	PRO	230	C	-9.156650	13.063270	-11.042311	-4.336985
1I76	A	GLN	231	H	-9.869753	10.749959	-13.846696	-4.501481
1I76	A	ASP	232	H	-10.026124	9.407443	-14.711642	-4.584954
1I76	A	ASP	233	H	-10.105740	9.784718	-15.011359	-4.873201
1I76	A	ILE	234	H	-9.904067	9.964500	-14.725658	-4.799322
1I76	A	ASP	235	H	-9.946462	10.056719	-14.654060	-4.831488
1I76	A	GLY	236	H	-10.179489	11.199325	-14.163993	-4.840572
1I76	A	ILE	237	H	-10.164530	11.737157	-13.963160	-4.891933
1I76	A	GLN	238	H	-10.190633	12.636963	-13.596238	-4.945149
1I76	A	ALA	239	H	-9.247345	12.917652	-10.718106	-4.135448
1I76	A	ILE	240	H	-9.247345	12.917652	-10.718106	-4.135448
1I76	A	TYR	241	H	-9.247345	12.917652	-10.718106	-4.135448
1I76	A	GLY	242	C	-9.247345	12.917652	-10.718106	-4.135448
1IAM	A	GLN	1	C	-7.933662	9.068920	-10.935529	-4.187845
1IAM	A	THR	2	E	-7.933662	9.068920	-10.935529	-4.187845
1IAM	A	SER	3	E	-7.933662	9.068920	-10.935529	-4.187845
1IAM	A	VAL	4	E	-7.933662	9.068920	-10.935529	-4.187845

```
1IAM        A          SER              5                  E -9.295493  8.980712 -12.879655 -3.977689
1IAM        A          PRO              6                  T -8.235209 11.615900 -9.759047 -3.882061
1IAM        A          SER              7                  T -8.093709 12.261284 -9.613127 -3.920391
1IAM        A          LYS              8                  E -7.803721 13.376358 -8.984584 -3.966401
1IAM        A          VAL              9                  E -7.797256 13.406346 -8.999004 -3.968290
1IAM        A          ILE             10                  E -7.805740 13.717409 -8.885690 -4.014806
1IAM        A          LEU             11                  E -8.073956 14.427459 -8.973370 -4.147649
1IAM        A          PRO             12                  E -7.878834 11.544061 -10.696605 -4.498195
1IAM        A          ARG             13                  T -8.157650  8.828858 -12.889845 -4.871239
1IAM        A          GLY             14                  T -6.597216  8.694349 -9.760204 -4.353241
1IAM        A          GLY             15                  E -6.504460  9.073868 -9.621283 -4.288264
1IAM        A          SER             16                  E -6.491119  9.211258 -9.577709 -4.279111
1IAM        A          VAL             17                  E -6.512705  9.294698 -9.436599 -4.250485
1IAM        A          LEU             18                  E -6.516045  9.294241 -9.413358 -4.246111
1IAM        A          VAL             19                  E -7.500533 11.858664 -8.972264 -3.963169
1IAM        A          THR             20                  E -8.449244 13.635663 -9.540173 -4.141721
1IAM        A          CYS             21                  E -9.365155 12.438353 -12.029384 -4.480178
1IAM        A          SER             22                  E -9.125779  7.149362 -15.206795 -5.165240
1IAM        A          THR             23                  E -7.133044  5.063190 -12.846538 -4.822561
1IAM        A          SER             24                  C -6.283633  5.475597 -11.313121 -4.380858
1IAM        A          CYS             25                  T -5.837462  5.618629 -10.950957 -4.389639
1IAM        A          ASP             26                  T -5.554938  6.112528 -10.382301 -4.261143
1IAM        A          GLN             27                  T -5.544691  6.207572 -10.360456 -4.258532
1IAM        A          PRO             28                  T -5.565996  6.446601 -10.172979 -4.226359
1IAM        A          LYS             29                  T -5.715480  6.723430 -9.982602 -4.224020
1IAM        A          LEU             30                  E -6.048901  7.466947 -9.494178 -4.093086
1IAM        A          LEU             31                  E -7.257190 11.313651 -9.820914 -4.408754
1IAM        A          GLY             32                  E -6.601120  9.730295 -9.988904 -4.763124
1IAM        A          ILE             33                  E -6.008043 11.748995 -8.179241 -4.758883
1IAM        A          GLU             34                  E -5.470440 10.176335 -8.270511 -4.572167
1IAM        A          THR             35                  C -5.160645  9.998950 -8.153413 -4.543011
1IAM        A          PRO             36                  C -5.159914  9.991505 -8.160961 -4.542580
1IAM        A          LEU             37                  C -5.202021 10.045297 -8.024559 -4.521168
1IAM        A          PRO             38                  C -5.319123  9.453729 -8.169525 -4.476482
1IAM        A          LYS             39                  E -5.681456  9.719715 -8.074391 -4.508212
1IAM        A          LYS             40                  E -7.025536  8.885309 -10.768604 -4.601592
1IAM        A          GLU             41                  E -5.522592  9.362571 -7.804056 -4.196289
1IAM        A          LEU             42                  E -4.884481  7.953756 -7.839279 -4.024812
1IAM        A          LEU             43                  E -4.076815  6.301582 -7.722755 -4.054064
1IAM        A          LEU             44                  T -4.070267  6.301040 -7.759738 -4.059898
1IAM        A          PRO             45                  T -4.065136  6.300494 -7.788389 -4.067344
1IAM        A          GLY             46                  T -4.113965  6.033507 -7.806069 -4.058533
1IAM        A          ASN             47                  T -4.231467  5.770187 -7.792208 -4.084072
1IAM        A          ASN             48                  T -6.229989  6.902159 -10.963023 -4.696210
1IAM        A          ARG             49                  E -6.587610  7.297072 -10.788449 -4.768501
1IAM        A          LYS             50                  E -10.152559 11.913760 -16.499346 -6.954363
1IAM        A          VAL             51                  E -11.538071 14.042762 -17.525412 -7.386249
1IAM        A          TYR             52                  E -14.061529 18.044053 -18.545281 -6.727705
1IAM        A          GLU             53                  E -12.154123 13.741800 -15.374255 -5.312566
1IAM        A          LEU             54                  E -11.449452 13.082498 -14.851454 -5.036793
1IAM        A          SER             55                  E -9.477720  9.164982 -13.689548 -4.795837
1IAM        A          ASN             56                  E -8.299191  8.942597 -12.551848 -4.861598
1IAM        A          VAL             57                  E -8.239896  8.952042 -12.680904 -4.862698
1IAM        A          GLN             58                  C -8.157509  8.867846 -12.945625 -4.944614
1IAM        A          GLU             59                  C -7.734062  9.126982 -12.292154 -4.858079
1IAM        A          ASP             60                  C -7.763141  9.142899 -12.228364 -4.864152
1IAM        A          SER             61                  B -8.016429  9.276592 -12.159402 -4.861927
1IAM        A          GLN             62                  C -8.056361  9.293947 -12.037893 -4.861310
1IAM        A          PRO             63                  C -8.125665  9.411227 -11.704534 -4.783067
1IAM        A          MET             64                  E -10.950772 12.580420 -15.326727 -5.665954
1IAM        A          CYS             65                  E -11.595648 12.838443 -15.914987 -5.808660
1IAM        A          TYR             66                  E -12.737533 14.797594 -19.057158 -7.240076
1IAM        A          SER             67                  E -10.125234  7.737739 -16.708203 -5.898724
1IAM        A          ASN             68                  E -6.574369  5.783691 -12.496490 -5.488252
1IAM        A          CYS             69                  E -4.339745  4.834857 -9.684456 -5.096752
1IAM        A          PRO             70                  T -4.278121  4.836205 -9.819384 -5.078861
1IAM        A          ASP             71                  T -4.246053  4.894572 -9.903179 -5.090660
1IAM        A          GLY             72                  E -4.244288  4.899796 -9.911532 -5.090240
1IAM        A          GLN             73                  E -4.254853  4.891986 -9.863645 -5.082598
1IAM        A          SER             74                  E -5.364746  5.339442 -11.209938 -5.050343
1IAM        A          THR             75                  E -5.928432  6.204732 -11.484181 -5.277703
1IAM        A          ALA             76                  E -7.290962  8.635826 -12.281638 -5.117507
1IAM        A          LYS             77                  E -7.716141 10.788257 -11.772608 -5.289927
1IAM        A          THR             78                  C -8.358164 12.399981 -11.694480 -5.266071
1IAM        A          PHE             79                  E -8.626242 12.966139 -11.320930 -5.247578
1IAM        A          LEU             80                  E -10.084103 15.725755 -12.147412 -5.158034
1IAM        A          THR             81                  E -10.358335 16.235701 -12.041229 -5.248043
1IAM        A          VAL             82                  E -11.139095 17.065934 -11.844646 -4.787453
1IAM        A          TYR             83                  E -12.109911 19.533834 -12.871341 -5.178174
1IAM        A          TRP             84                  B -12.223981 17.932795 -14.094798 -5.369182
1IAM        A          THR             85                  C -9.907455 12.072821 -12.708036 -4.834326
```

1IAM	A	PRO	86	T	-9.871474	11.942371	-12.893175	-4.836165
1IAM	A	GLU	87	T	-9.865472	11.913803	-12.943553	-4.842113
1IAM	A	ARG	88	E	-9.867600	11.857725	-12.956100	-4.836139
1IAM	A	VAL	89	E	-9.134630	12.191547	-11.816140	-4.618147
1IAM	A	GLU	90	E	-8.100015	11.606590	-10.307078	-4.419658
1IAM	A	LEU	91	E	-6.625183	10.826305	-7.865360	-3.732457
1IAM	A	ALA	92	C	-6.465847	10.213422	-8.312505	-3.709069
1IAM	A	PRO	93	C	-6.371805	9.836853	-8.614275	-3.704315
1IAM	A	LEU	94	C	-6.375178	9.820920	-8.600932	-3.699556
1IAM	A	PRO	95	C	-6.401063	9.730005	-8.548731	-3.667660
1IAM	A	SER	96	C	-6.984578	8.007062	-10.090021	-3.666286
1IAM	A	TRP	97	E	-7.199422	8.300021	-10.699371	-4.029333
1IAM	A	GLN	98	E	-6.763888	7.319912	-10.832572	-4.317092
1IAM	A	PRO	99	T	-4.945348	6.077125	-8.572527	-4.075978
1IAM	A	VAL	100	T	-4.903031	6.276733	-8.621642	-4.099634
1IAM	A	GLY	101	T	-4.858627	6.516369	-8.678810	-4.152608
1IAM	A	LYS	102	E	-4.862302	6.504172	-8.663584	-4.150275
1IAM	A	GLN	103	E	-4.881830	6.493383	-8.593655	-4.146550
1IAM	A	LEU	104	E	-6.032893	9.340958	-9.373479	-4.637201
1IAM	A	THR	105	E	-6.405183	9.668178	-9.433636	-4.830035
1IAM	A	LEU	106	E	-8.841136	14.148151	-10.466465	-4.810506
1IAM	A	ARG	107	E	-10.097284	16.235948	-11.642650	-5.163576
1IAM	A	CYS	108	E	-10.769838	15.726854	-12.268322	-5.084579
1IAM	A	GLN	109	E	-11.404052	9.784872	-17.185094	-5.700645
1IAM	A	VAL	110	E	-9.001373	9.355762	-12.911334	-4.804963
1IAM	A	GLU	111	E	-8.805351	9.398025	-13.102364	-4.829773
1IAM	A	GLY	112	C	-8.792354	9.399584	-13.144134	-4.822421
1IAM	A	GLY	113	T	-8.722871	9.245672	-13.236639	-4.745497
1IAM	A	ALA	114	B	-8.726285	9.238800	-13.213317	-4.734842
1IAM	A	PRO	115	T	-9.286489	9.095529	-13.839197	-4.644933
1IAM	A	ARG	116	G	-9.880134	8.395505	-14.285895	-4.217539
1IAM	A	ALA	117	G	-9.688156	10.012777	-13.393273	-4.277362
1IAM	A	GLN	118	G	-10.180864	12.650521	-12.599140	-4.463908
1IAM	A	LEU	119	E	-10.182623	13.072707	-12.358011	-4.452670
1IAM	A	THR	120	E	-10.206970	13.352744	-12.145355	-4.436198
1IAM	A	VAL	121	E	-10.208528	13.399489	-12.109080	-4.432375
1IAM	A	VAL	122	E	-11.525494	17.082539	-12.461345	-4.369094
1IAM	A	LEU	123	E	-11.003545	14.318400	-13.750988	-4.869909
1IAM	A	LEU	124	E	-8.367522	8.288745	-12.764699	-4.901481
1IAM	A	ARG	125	E	-5.865467	6.530273	-10.544794	-4.956723
1IAM	A	GLY	126	T	-5.625539	6.524612	-10.742780	-4.986267
1IAM	A	GLU	127	T	-5.622837	6.533220	-10.756923	-4.988112
1IAM	A	LYS	128	E	-5.622825	6.533110	-10.757156	-4.988152
1IAM	A	GLU	129	E	-5.627674	6.523256	-10.741350	-4.989359
1IAM	A	LEU	130	E	-6.264856	6.569004	-11.190406	-5.050359
1IAM	A	LYS	131	E	-8.536412	9.295149	-13.697291	-5.272197
1IAM	A	ARG	132	E	-8.023783	8.133318	-11.971080	-4.244989
1IAM	A	GLU	133	E	-6.084316	4.733588	-10.625431	-4.001308
1IAM	A	PRO	134	E	-5.006793	4.485840	-9.543001	-3.965924
1IAM	A	ALA	135	C	-4.819356	4.704924	-9.586935	-4.007505
1IAM	A	VAL	136	C	-4.771651	4.714284	-9.682411	-4.014667
1IAM	A	GLY	137	T	-4.772861	4.706453	-9.681708	-4.015658
1IAM	A	GLU	138	T	-4.838706	4.719064	-9.576509	-4.018213
1IAM	A	PRO	139	T	-5.429393	5.197469	-9.988109	-4.117368
1IAM	A	ALA	140	E	-6.273620	4.891613	-10.887176	-4.114780
1IAM	A	GLU	141	E	-8.070514	10.088398	-12.394230	-5.066574
1IAM	A	VAL	142	E	-7.326740	13.281303	-8.853205	-4.646895
1IAM	A	THR	143	E	-6.579799	12.204108	-8.696291	-4.728415
1IAM	A	THR	144	E	-6.545619	12.234280	-8.737276	-4.711746
1IAM	A	THR	145	E	-6.542524	12.231048	-8.748141	-4.707018
1IAM	A	VAL	146	E	-6.563515	12.215918	-8.660137	-4.675840
1IAM	A	LEU	147	E	-6.610195	11.288549	-8.914160	-4.485831
1IAM	A	VAL	148	E	-7.071772	9.847905	-9.466832	-3.641872
1IAM	A	ARG	149	T	-6.588107	8.517991	-9.427689	-3.646025
1IAM	A	ARG	150	T	-6.352882	7.991569	-10.010060	-3.947587
1IAM	A	ASP	151	T	-6.333138	7.946459	-10.126911	-3.984794
1IAM	A	HIS	152	T	-6.390045	7.904821	-10.214697	-4.075104
1IAM	A	HIS	153	T	-6.480089	7.589730	-10.412781	-4.154940
1IAM	A	GLY	154	T	-6.914667	7.135950	-11.484944	-4.613448
1IAM	A	ALA	155	T	-8.070299	8.080071	-13.166233	-4.944445
1IAM	A	GLN	156	E	-8.729746	10.238125	-12.815488	-4.978268
1IAM	A	PHE	157	E	-9.296087	11.916966	-12.021708	-4.835555
1IAM	A	SER	158	E	-11.364458	14.075702	-14.002887	-5.200943
1IAM	A	CYS	159	E	-13.491808	14.664455	-17.677070	-5.601139
1IAM	A	ARG	160	E	-13.855056	14.483653	-18.838844	-5.954696
1IAM	A	THR	161	E	-12.671818	15.722840	-15.759590	-5.675599
1IAM	A	GLU	162	E	-12.258128	15.797597	-15.159605	-5.412112
1IAM	A	LEU	163	E	-10.248536	13.174883	-12.185317	-4.444221
1IAM	A	ASP	164	E	-9.837899	12.124357	-13.078818	-4.770269
1IAM	A	LEU	165	E	-8.341880	9.569228	-12.275538	-4.904832
1IAM	A	ARG	166	G	-7.007793	7.958708	-11.341151	-4.842105

1IAM	A	PRO	167	G	-6.168283	8.118117	-10.568745	-4.986667
1IAM	A	GLN	168	G	-6.089342	8.462722	-10.590581	-5.050713
1IAM	A	GLY	169	C	-5.894402	9.564869	-9.931755	-4.990108
1IAM	A	LEU	170	C	-5.897135	9.615672	-9.902088	-4.993682
1IAM	A	GLU	171	E	-5.981736	9.920969	-9.704322	-5.021962
1IAM	A	LEU	172	E	-6.455119	12.098831	-8.962670	-5.014377
1IAM	A	PHE	173	E	-6.611518	12.464345	-8.426720	-4.870773
1IAM	A	GLU	174	E	-8.250624	13.249864	-11.634989	-5.490536
1IAM	A	ASN	175	E	-8.108413	9.261040	-13.180270	-5.289681
1IAM	A	THR	176	E	-8.205044	8.692622	-13.328596	-5.207374
1IAM	A	SER	177	C	-8.273495	8.022935	-13.441668	-5.102055
1IAM	A	ALA	178	C	-8.284630	7.933917	-13.412184	-5.080918
1IAM	A	PRO	179	C	-8.342639	7.849698	-13.216268	-5.008266
1IAM	A	TYR	180	E	-10.132190	11.421615	-13.947534	-5.070502
1IAM	A	GLN	181	E	-9.517823	12.685353	-12.512922	-5.238801
1IAM	A	LEU	182	C	-7.588916	10.937269	-9.388059	-4.091919
1IAM	A	GLN	183	E	-7.588916	10.937269	-9.388059	-4.091919
1IAM	A	THR	184	E	-7.588916	10.937269	-9.388059	-4.091919
1IAM	A	PHE	185	C	-7.588916	10.937269	-9.388059	-4.091919
1IAP	A	SER	44	T	-10.677568	11.159277	-14.436055	-5.081034
1IAP	A	GLN	45	T	-10.677568	11.159277	-14.436055	-5.081034
1IAP	A	PHE	46	T	-10.677568	11.159277	-14.436055	-5.081034
1IAP	A	GLN	47	T	-10.677568	11.159277	-14.436055	-5.081034
1IAP	A	SER	48	C	-11.378921	10.881479	-15.675404	-5.189377
1IAP	A	LEU	49	H	-11.364564	10.936827	-15.719469	-5.213235
1IAP	A	GLU	50	H	-11.341308	10.904539	-15.844064	-5.228491
1IAP	A	GLN	51	H	-11.341155	10.904959	-15.845582	-5.228667
1IAP	A	VAL	52	H	-11.339253	10.915308	-15.853386	-5.228717
1IAP	A	LYS	53	H	-12.788925	11.617919	-18.623184	-5.875379
1IAP	A	ARG	54	C	-13.115820	11.042471	-18.798061	-5.540037
1IAP	A	ARG	55	C	-13.904350	14.602660	-18.016914	-5.262789
1IAP	A	PRO	56	H	-12.498935	17.875736	-13.396353	-4.971960
1IAP	A	ALA	57	H	-12.165893	17.637033	-13.445352	-4.981731
1IAP	A	HIS	58	H	-12.090543	17.881555	-13.426569	-5.002831
1IAP	A	LEU	59	H	-11.651673	19.095693	-12.058571	-4.837694
1IAP	A	MET	60	H	-11.649823	19.103184	-12.064533	-4.839538
1IAP	A	ALA	61	H	-11.791512	19.352115	-11.843240	-4.812987
1IAP	A	LEU	62	H	-11.945827	20.004975	-11.320744	-4.759633
1IAP	A	LEU	63	H	-12.000095	20.044229	-11.134465	-4.720232
1IAP	A	GLN	64	H	-13.736507	17.802080	-16.240735	-5.220038
1IAP	A	HIS	65	H	-12.093242	13.060987	-14.800153	-4.589995
1IAP	A	VAL	66	H	-11.097072	13.405987	-13.487739	-4.559628
1IAP	A	ALA	67	H	-10.205608	12.363000	-13.366683	-4.856232
1IAP	A	LEU	68	H	-9.657773	12.702787	-12.718429	-4.874101
1IAP	A	GLN	69	H	-8.889081	12.779335	-11.787492	-5.003057
1IAP	A	PHE	70	C	-8.603951	13.030521	-11.269707	-4.792449
1IAP	A	GLU	71	C	-8.431805	13.398624	-10.840485	-4.645486
1IAP	A	PRO	72	H	-8.404548	13.807630	-10.558292	-4.583044
1IAP	A	GLY	73	H	-8.443658	13.896815	-10.436200	-4.559605
1IAP	A	PRO	74	H	-8.691504	14.467657	-9.918567	-4.303771
1IAP	A	LEU	75	H	-9.038923	15.309780	-9.495893	-4.187504
1IAP	A	LEU	76	H	-9.806672	17.591291	-8.997938	-4.103444
1IAP	A	CYS	77	H	-11.018787	16.265925	-12.390866	-4.717183
1IAP	A	CYS	78	H	-11.713971	16.709840	-13.979626	-5.078140
1IAP	A	LEU	79	H	-11.824873	16.672619	-14.179896	-5.166419
1IAP	A	HIS	80	H	-12.090969	15.952770	-15.111256	-5.269628
1IAP	A	ALA	81	H	-10.759444	12.861396	-13.884960	-5.064892
1IAP	A	ASP	82	H	-10.541451	12.280246	-14.370266	-5.159431
1IAP	A	MET	83	H	-9.075451	11.768058	-12.015190	-4.863540
1IAP	A	LEU	84	H	-7.629033	9.357143	-11.060069	-4.603263
1IAP	A	GLY	85	H	-6.894430	6.770543	-11.686500	-4.543783
1IAP	A	SER	86	C	-6.721549	6.901750	-11.691289	-4.547753
1IAP	A	LEU	87	C	-5.639332	7.392636	-9.582459	-4.468762
1IAP	A	GLY	88	C	-5.452309	7.355910	-9.669592	-4.468574
1IAP	A	PRO	89	H	-5.466118	7.314165	-9.639488	-4.466012
1IAP	A	LYS	90	H	-5.505063	7.423035	-9.483630	-4.462390
1IAP	A	GLU	91	H	-5.524699	7.426830	-9.408501	-4.459036
1IAP	A	ALA	92	H	-6.221539	7.291007	-9.923482	-4.470694
1IAP	A	LYS	93	H	-10.225530	9.011466	-15.480983	-4.935702
1IAP	A	LYS	94	H	-10.185844	11.050596	-14.158927	-4.792545
1IAP	A	ALA	95	H	-10.570924	13.726122	-12.717950	-4.676645
1IAP	A	PHE	96	H	-10.607132	13.945513	-12.438920	-4.646100
1IAP	A	LEU	97	H	-10.603463	13.956362	-12.455328	-4.647383
1IAP	A	ASP	98	H	-10.612103	13.940069	-12.420235	-4.641233
1IAP	A	PHE	99	H	-12.671760	17.376777	-14.348086	-4.913272
1IAP	A	TYR	100	H	-13.086403	16.069778	-15.727081	-5.093083
1IAP	A	HIS	101	H	-12.595168	16.217459	-14.949921	-5.011560
1IAP	A	SER	102	H	-11.827072	15.486612	-13.949716	-4.937636
1IAP	A	PHE	103	H	-8.949771	13.280713	-10.494170	-4.612558
1IAP	A	LEU	104	H	-6.264334	9.345328	-8.612599	-4.220977
1IAP	A	GLU	105	T	-5.246179	6.964033	-8.617970	-4.015994

1IAP	A	LYS	106	T	-4.829347	8.113864	-7.541291	-3.801761
1IAP	A	THR	107	T	-4.828804	8.117798	-7.543439	-3.801764
1IAP	A	ALA	108	T	-4.829329	8.113307	-7.540853	-3.800983
1IAP	A	VAL	109	T	-4.883751	7.998814	-7.439545	-3.760751
1IAP	A	LEU	110	T	-5.232747	9.246153	-6.492429	-3.591178
1IAP	A	ARG	111	T	-8.541415	12.559231	-9.891731	-3.623421
1IAP	A	VAL	112	C	-7.005221	9.950338	-8.022953	-3.186678
1IAP	A	PRO	113	C	-5.715779	8.394924	-7.507396	-3.337162
1IAP	A	VAL	114	C	-5.499407	9.035458	-7.284078	-3.345899
1IAP	A	PRO	115	C	-5.472754	9.026190	-7.366159	-3.349126
1IAP	A	PRO	116	H	-5.468744	9.019629	-7.393749	-3.354765
1IAP	A	ASN	117	H	-5.512614	8.957017	-7.353951	-3.369286
1IAP	A	VAL	118	H	-6.100735	10.245716	-7.203328	-3.390754
1IAP	A	ALA	119	H	-7.203555	8.921665	-9.511136	-3.529420
1IAP	A	PHE	120	H	-8.205773	9.260020	-11.239747	-4.062188
1IAP	A	GLU	121	H	-9.033749	11.974458	-12.508527	-4.888669
1IAP	A	LEU	122	H	-8.760359	11.929963	-11.842385	-4.651981
1IAP	A	ASP	123	H	-8.328677	10.300552	-11.904242	-4.398989
1IAP	A	ARG	124	C	-7.432803	9.272693	-10.662731	-4.177346
1IAP	A	THR	125	C	-5.409918	6.144487	-8.765507	-3.816303
1IAP	A	ARG	126	C	-4.749847	7.478584	-7.581179	-3.799038
1IAP	A	ALA	127	G	-4.739213	7.509463	-7.622817	-3.810343
1IAP	A	ASP	128	G	-4.730115	7.560755	-7.653274	-3.826679
1IAP	A	LEU	129	G	-4.733383	7.557088	-7.641258	-3.827153
1IAP	A	ILE	130	C	-4.951393	8.237549	-7.173292	-3.838301
1IAP	A	SER	131	C	-6.662717	10.024772	-10.057022	-4.648940
1IAP	A	GLU	132	H	-7.039849	10.685942	-10.149175	-4.845396
1IAP	A	ASP	133	H	-8.021425	10.536941	-11.706211	-4.918959
1IAP	A	VAL	134	H	-8.710483	10.454663	-12.486529	-4.964272
1IAP	A	GLN	135	H	-10.129571	10.073238	-15.381438	-5.366588
1IAP	A	ARG	136	H	-10.672771	10.403646	-15.457642	-5.150581
1IAP	A	ARG	137	H	-11.238812	9.893787	-15.573063	-4.646239
1IAP	A	PHE	138	H	-12.085757	15.837523	-13.683608	-4.435465
1IAP	A	VAL	139	H	-10.924287	11.905158	-13.596723	-4.196930
1IAP	A	GLN	140	H	-10.612049	10.972412	-14.214300	-4.334979
1IAP	A	GLU	141	H	-10.564697	10.882236	-14.364046	-4.363017
1IAP	A	VAL	142	H	-10.567333	10.792643	-14.414895	-4.370910
1IAP	A	VAL	143	H	-10.592584	10.482637	-14.522254	-4.369543
1IAP	A	GLN	144	H	-10.946187	9.439443	-15.745463	-4.625041
1IAP	A	SER	145	H	-11.653483	8.824468	-17.586576	-4.895900
1IAP	A	GLN	146	H	-11.909310	7.883004	-18.940721	-5.189872
1IAP	A	GLN	147	H	-9.410122	7.702383	-13.946522	-4.526678
1IAP	A	VAL	148	H	-8.068217	6.751252	-11.803781	-3.666196
1IAP	A	ALA	149	H	-8.067305	6.759083	-11.806652	-3.666790
1IAP	A	VAL	150	H	-8.067315	6.759896	-11.805937	-3.666643
1IAP	A	GLY	151	H	-8.067513	6.759048	-11.803979	-3.666142
1IAP	A	ARG	152	H	-8.131519	6.651352	-11.567098	-3.569008
1IAP	A	GLN	153	H	-11.634116	10.422688	-15.562285	-4.443235
1IAP	A	LEU	154	H	-12.883349	11.885295	-17.297678	-4.852325
1IAP	A	GLU	155	H	-13.132278	11.827566	-18.191555	-5.221143
1IAP	A	ASP	156	H	-13.513923	13.669745	-18.054320	-5.455837
1IAP	A	PHE	157	H	-13.598546	13.876312	-17.895762	-5.491177
1IAP	A	ARG	158	H	-13.542345	13.506453	-18.214645	-5.522056
1IAP	A	SER	159	H	-11.910893	9.024341	-17.630922	-5.311555
1IAP	A	LYS	160	H	-9.990479	8.425350	-15.818301	-5.645245
1IAP	A	ARG	161	H	-7.476661	6.836844	-12.555792	-5.032353
1IAP	A	LEU	162	H	-4.436319	6.839287	-8.274662	-4.772679
1IAP	A	MET	163	H	-4.377042	7.018305	-8.353459	-4.781935
1IAP	A	GLY	164	C	-4.376674	7.021915	-8.355373	-4.782315
1IAP	A	MET	165	C	-4.376714	7.021858	-8.354865	-4.782256
1IAP	A	THR	166	T	-4.379843	7.022947	-8.332831	-4.780951
1IAP	A	PRO	167	T	-5.767112	8.739224	-9.109105	-4.868067
1IAP	A	TRP	168	T	-8.738657	12.819870	-11.511754	-5.392261
1IAP	A	GLU	169	H	-11.119239	13.933622	-14.905759	-5.685470
1IAP	A	GLN	170	H	-11.399169	12.479614	-15.847082	-5.549786
1IAP	A	GLU	171	H	-12.039521	10.367831	-17.239457	-5.261810
1IAP	A	LEU	172	H	-11.783978	11.254468	-17.057162	-5.401983
1IAP	A	ALA	173	H	-10.153688	9.172876	-14.862954	-4.820458
1IAP	A	GLN	174	H	-9.868785	9.458984	-14.767363	-4.878521
1IAP	A	LEU	175	H	-9.572080	9.584576	-14.295815	-4.719574
1IAP	A	GLU	176	H	-6.954195	5.991475	-11.684967	-4.531160
1IAP	A	ALA	177	H	-4.755498	4.292664	-8.501641	-3.540790
1IAP	A	TRP	178	C	-4.559439	4.459870	-8.767007	-3.678808
1IAP	A	VAL	179	C	-4.381002	4.274499	-8.963544	-3.698563
1IAP	A	GLY	180	C	-4.325125	4.169209	-9.122021	-3.712027
1IAP	A	ARG	181	C	-4.330886	4.148197	-9.099498	-3.702212
1IAP	A	ASP	182	C	-4.714650	4.052844	-9.710918	-3.869509
1IAP	A	ARG	183	H	-4.984764	3.571597	-9.865220	-3.776670
1IAP	A	ALA	184	H	-5.738974	3.127684	-10.760994	-3.839902
1IAP	A	SER	185	H	-8.001144	4.195529	-12.794057	-3.654972
1IAP	A	TYR	186	H	-13.466606	10.065987	-20.819102	-6.069132

1IAP	A	GLU	187	H	-14.297271	11.014688	-22.629219	-6.756052
1IAP	A	ALA	188	H	-13.883534	10.790466	-20.494908	-5.683716
1IAP	A	ARG	189	H	-13.714306	11.814607	-18.765598	-5.060301
1IAP	A	GLU	190	H	-13.078351	12.150753	-17.279176	-4.763950
1IAP	A	ARG	191	H	-12.382239	11.107922	-16.599068	-4.522937
1IAP	A	HIS	192	H	-10.303330	9.444559	-13.684524	-4.096753
1IAP	A	VAL	193	H	-10.276032	9.627840	-13.700321	-4.110410
1IAP	A	ALA	194	H	-10.274818	9.642828	-13.701075	-4.111386
1IAP	A	GLU	195	H	-10.269354	9.678814	-13.717282	-4.120011
1IAP	A	ARG	196	H	-10.251575	9.869396	-13.687757	-4.139866
1IAP	A	LEU	197	H	-11.465998	14.215001	-14.312500	-4.660556
1IAP	A	LEU	198	H	-11.171813	14.981612	-13.817459	-5.023543
1IAP	A	MET	199	H	-9.688966	12.340707	-12.924219	-5.184090
1IAP	A	HIS	200	H	-9.508810	12.411430	-13.082951	-5.243732
1IAP	A	LEU	201	H	-9.502374	12.424022	-13.123808	-5.266517
1IAP	A	GLU	202	H	-9.234812	11.264520	-13.791478	-5.384432
1IAP	A	GLU	203	H	-8.663950	8.927011	-14.062096	-5.277447
1IAP	A	MET	204	H	-8.606706	8.884749	-13.977866	-5.221258
1IAP	A	GLN	205	G	-8.615373	8.744007	-14.036092	-5.216448
1IAP	A	HIS	206	G	-7.189642	8.375477	-10.866098	-4.447397
1IAP	A	THR	207	G	-7.071545	8.475185	-10.996788	-4.492227
1IAP	A	ILE	208	C	-6.619932	7.603456	-11.070303	-4.526764
1IAP	A	SER	209	T	-5.395452	4.956178	-10.641119	-4.612447
1IAP	A	THR	210	T	-5.361092	5.047540	-10.729515	-4.640997
1IAP	A	ASP	211	T	-5.386044	4.905675	-10.738921	-4.652981
1IAP	A	GLU	212	H	-5.392616	4.860581	-10.727721	-4.652022
1IAP	A	GLU	213	H	-5.435434	4.710111	-10.688808	-4.657320
1IAP	A	LYS	214	H	-7.059384	6.600533	-12.242939	-5.122267
1IAP	A	SER	215	H	-9.962757	8.431667	-15.968649	-5.489669
1IAP	A	ALA	216	H	-9.109714	9.951690	-11.246173	-3.572175
1IAP	A	ALA	217	H	-8.612531	10.620318	-10.576857	-3.514391
1IAP	A	VAL	218	H	-8.538295	10.985096	-10.514688	-3.531968
1IAP	A	VAL	219	H	-8.318050	11.051778	-10.666192	-3.717712
1IAP	A	ASN	220	H	-8.240615	10.946189	-10.882960	-3.805334
1IAP	A	ALA	221	H	-8.388364	11.235002	-10.837529	-3.887406
1IAP	A	ILE	222	H	-8.685184	11.327076	-11.277067	-4.141939
1IAP	A	GLY	223	H	-8.783622	10.903626	-11.480631	-4.224157
1IAP	A	LEU	224	H	-9.462988	10.264574	-12.487273	-4.422659
1IAP	A	TYR	225	H	-12.835793	14.993265	-15.694617	-5.081238
1IAP	A	MET	226	H	-12.834314	16.238785	-17.580346	-7.056465
1IAP	A	ARG	227	H	-10.940432	13.016456	-15.330627	-6.199978
1IAP	A	HIS	228	H	-9.221741	11.926819	-12.963601	-5.600623
1IAP	A	LEU	229	H	-7.327659	10.269422	-9.837142	-4.414856
1IAP	A	GLY	230	C	-4.143272	6.661688	-6.201484	-3.386700
1IAP	A	VAL	231	C	-4.143272	6.661688	-6.201484	-3.386700
1IAP	A	ARG	232	C	-4.143272	6.661688	-6.201484	-3.386700
1IAP	A	THR	233	C	-4.143272	6.661688	-6.201484	-3.386700
1IFR	A	GLY	432	C	-8.925111	5.169385	-15.179315	-4.569605
1IFR	A	SER	433	E	-8.925111	5.169385	-15.179315	-4.569605
1IFR	A	HIS	434	E	-8.925111	5.169385	-15.179315	-4.569605
1IFR	A	ARG	435	E	-8.925111	5.169385	-15.179315	-4.569605
1IFR	A	THR	436	E	-7.844378	9.171444	-11.884888	-5.018424
1IFR	A	SER	437	C	-7.842959	9.350181	-11.756591	-4.989842
1IFR	A	GLY	438	C	-7.827695	9.434575	-11.755834	-4.975599
1IFR	A	ARG	439	C	-7.828414	9.438735	-11.745045	-4.973206
1IFR	A	VAL	440	E	-7.827943	9.441319	-11.747762	-4.973222
1IFR	A	ALA	441	E	-9.225909	10.321155	-12.893139	-4.639914
1IFR	A	VAL	442	E	-9.940910	12.510657	-12.207435	-4.521233
1IFR	A	GLU	443	E	-11.230951	12.340893	-15.886378	-5.441008
1IFR	A	GLU	444	E	-8.851778	10.451034	-12.664713	-5.254401
1IFR	A	VAL	445	E	-7.631023	9.191633	-11.816362	-5.129485
1IFR	A	ASP	446	T	-6.726881	7.597908	-11.821954	-5.206510
1IFR	A	GLU	447	T	-6.707799	7.730563	-11.827999	-5.213662
1IFR	A	GLU	448	T	-6.705952	7.749822	-11.828410	-5.213146
1IFR	A	GLY	449	T	-6.721721	7.677885	-11.807414	-5.212128
1IFR	A	LYS	450	C	-6.845242	7.369049	-11.833466	-5.235504
1IFR	A	PHE	451	E	-8.693627	11.973658	-12.035823	-5.400272
1IFR	A	VAL	452	E	-10.088984	13.786397	-12.243265	-5.096273
1IFR	A	ARG	453	E	-13.305393	16.235330	-16.091623	-5.380450
1IFR	A	LEU	454	E	-13.055488	12.846131	-17.221312	-5.263797
1IFR	A	ARG	455	E	-10.745604	8.356790	-16.378898	-5.382310
1IFR	A	ASN	456	E	-8.709858	7.116606	-14.960083	-5.766559
1IFR	A	LYS	457	C	-7.057467	7.036673	-12.663411	-5.557056
1IFR	A	SER	458	C	-7.052725	7.042369	-12.693488	-5.561169
1IFR	A	ASN	459	C	-7.041273	7.047374	-12.747443	-5.564120
1IFR	A	GLU	460	C	-7.042290	7.045671	-12.741517	-5.564562
1IFR	A	ASP	461	C	-7.076857	7.048924	-12.612533	-5.551711
1IFR	A	GLN	462	E	-9.141415	7.648479	-15.817403	-5.819517
1IFR	A	SER	463	E	-9.303590	7.874800	-15.528629	-5.719987
1IFR	A	MET	464	T	-10.519857	11.794492	-15.633881	-5.766899
1IFR	A	GLY	465	T	-10.546035	11.968997	-15.483379	-5.748460

1IFR	A	ASN	466	T	-10.946897	13.244747	-15.020895	-5.680155
1IFR	A	TRP	467	E	-11.138408	14.249734	-14.321877	-5.650949
1IFR	A	GLN	468	E	-12.582120	16.555631	-16.028640	-6.257625
1IFR	A	ILE	469	E	-12.836074	16.646389	-15.608276	-6.071296
1IFR	A	LYS	470	E	-14.971087	18.056850	-17.865236	-6.221456
1IFR	A	ARG	471	E	-14.090736	7.782382	-22.628943	-6.513075
1IFR	A	GLN	472	E	-8.296122	4.895634	-15.158332	-5.518131
1IFR	A	ASN	473	E	-6.086795	2.945823	-12.590516	-4.885553
1IFR	A	GLY	474	T	-4.615825	3.042672	-10.273260	-4.492365
1IFR	A	ASP	475	T	-4.569049	3.211283	-10.283249	-4.469203
1IFR	A	ASP	476	T	-4.566824	3.227798	-10.289737	-4.469690
1IFR	A	PRO	477	C	-4.567906	3.224949	-10.280769	-4.467751
1IFR	A	LEU	478	C	-4.614244	3.251465	-10.097338	-4.434731
1IFR	A	LEU	479	E	-6.068151	5.376136	-10.473423	-4.203278
1IFR	A	THR	480	E	-7.868329	7.732418	-12.004854	-4.597890
1IFR	A	TYR	481	E	-10.011327	15.890073	-11.289149	-4.536163
1IFR	A	ARG	482	E	-7.280504	10.527060	-8.412253	-3.572747
1IFR	A	PHE	483	E	-7.239926	10.739084	-8.451985	-3.592069
1IFR	A	PRO	484	T	-5.891646	10.817529	-6.732866	-3.609162
1IFR	A	PRO	485	T	-5.843227	10.981897	-6.806858	-3.636299
1IFR	A	LYS	486	T	-5.812476	11.109304	-6.877562	-3.673649
1IFR	A	PHE	487	T	-5.862130	11.178373	-6.749457	-3.686049
1IFR	A	THR	488	E	-5.831771	11.094907	-6.933960	-3.735725
1IFR	A	LEU	489	E	-6.786626	12.012009	-8.855105	-4.286609
1IFR	A	LYS	490	T	-6.439228	8.287974	-10.334236	-4.442220
1IFR	A	ALA	491	T	-6.471214	7.518533	-10.710463	-4.424972
1IFR	A	GLY	492	T	-6.454255	7.550953	-10.746362	-4.434029
1IFR	A	GLN	493	T	-6.554149	7.129682	-10.831936	-4.403435
1IFR	A	VAL	494	E	-6.575706	7.104880	-10.763794	-4.396938
1IFR	A	VAL	495	E	-7.623249	9.287325	-10.989010	-4.309306
1IFR	A	THR	496	E	-8.325888	10.635120	-11.363437	-4.645871
1IFR	A	ILE	497	E	-9.369379	14.046681	-10.824173	-4.388107
1IFR	A	TRP	498	E	-9.644616	14.192354	-12.110771	-4.847761
1IFR	A	ALA	499	T	-5.209369	6.768861	-8.267537	-4.006979
1IFR	A	ALA	500	T	-3.830604	6.380813	-6.945549	-4.019059
1IFR	A	GLY	501	T	-2.806231	5.850681	-6.106998	-4.043322
1IFR	A	ALA	502	T	-2.610256	6.412105	-5.859049	-3.999789
1IFR	A	GLY	503	C	-2.541335	6.452100	-5.915692	-3.982366
1IFR	A	ALA	504	C	-2.537961	6.476769	-5.898418	-3.971856
1IFR	A	THR	505	C	-2.582126	6.476345	-5.816574	-3.935597
1IFR	A	HIS	506	C	-3.073771	7.362413	-5.650993	-3.748968
1IFR	A	SER	507	B	-3.623966	6.728146	-6.457290	-3.619609
1IFR	A	PRO	508	T	-4.275795	6.923082	-6.888233	-3.359714
1IFR	A	PRO	509	T	-4.496365	6.410152	-7.101256	-3.365543
1IFR	A	THR	510	T	-5.681571	6.691441	-9.224826	-3.768254
1IFR	A	ASP	511	E	-6.529717	6.776957	-10.208236	-3.972188
1IFR	A	LEU	512	E	-8.629506	12.218132	-11.835203	-4.848224
1IFR	A	VAL	513	E	-8.142881	12.935947	-9.637499	-4.352544
1IFR	A	TRP	514	T	-7.101056	11.529792	-9.182500	-4.491446
1IFR	A	LYS	515	T	-5.224701	7.712443	-8.373386	-4.323253
1IFR	A	ALA	516	T	-5.224173	7.717308	-8.376097	-4.323753
1IFR	A	GLN	517	T	-5.224425	7.713382	-8.376455	-4.324076
1IFR	A	ASN	518	T	-5.226437	7.692641	-8.378979	-4.326056
1IFR	A	THR	519	T	-5.244777	7.576101	-8.367912	-4.321619
1IFR	A	TRP	520	T	-6.537808	9.222234	-10.268113	-5.045906
1IFR	A	GLY	521	C	-4.225308	4.522727	-9.025739	-4.609029
1IFR	A	CYS	522	C	-4.212060	4.576698	-9.052523	-4.603896
1IFR	A	GLY	523	T	-4.212320	4.573797	-9.051560	-4.603782
1IFR	A	ASN	524	T	-4.212832	4.568701	-9.049294	-4.603434
1IFR	A	SER	525	T	-4.223708	4.485281	-9.028694	-4.594947
1IFR	A	LEU	526	E	-6.467701	6.983663	-10.240635	-4.373652
1IFR	A	ARG	527	E	-9.814670	10.394994	-13.551464	-4.917939
1IFR	A	THR	528	E	-11.639681	15.597264	-14.207693	-5.018809
1IFR	A	ALA	529	E	-11.526633	15.616630	-14.192048	-5.056753
1IFR	A	LEU	530	E	-9.103896	13.138767	-10.779171	-4.620691
1IFR	A	ILE	531	E	-5.823563	8.649321	-9.081683	-4.788264
1IFR	A	ASN	532	T	-3.875120	5.908649	-8.024245	-4.724726
1IFR	A	SER	533	T	-3.781267	5.927887	-8.280711	-4.792548
1IFR	A	THR	534	T	-3.776664	5.935846	-8.305540	-4.795365
1IFR	A	GLY	535	T	-3.776632	5.935353	-8.306193	-4.795439
1IFR	A	GLU	536	C	-3.795640	5.846825	-8.280242	-4.795137
1IFR	A	GLU	537	E	-4.889571	6.071697	-9.842893	-5.172392
1IFR	A	VAL	538	E	-6.645656	6.963617	-11.511459	-5.139272
1IFR	A	ALA	539	E	-8.896780	8.120750	-13.676088	-5.083611
1IFR	A	MET	540	E	-12.101840	13.801428	-16.310083	-5.771079
1IFR	A	ARG	541	E	-8.907751	11.571457	-10.847704	-4.259160
1IFR	A	LYS	542	E	-8.907751	11.571457	-10.847704	-4.259160
1IFR	A	LEU	543	E	-8.907751	11.571457	-10.847704	-4.259160
1IFR	A	VAL	544	C	-8.907751	11.571457	-10.847704	-4.259160
1IHK	A	THR	52	H	-2.608878	2.984961	-6.161421	-3.204193
1IHK	A	ASP	53	H	-2.608878	2.984961	-6.161421	-3.204193

1IHK	A	LEU	54	H	-2.608878	2.984961	-6.161421	-3.204193
1IHK	A	ASP	55	H	-2.608878	2.984961	-6.161421	-3.204193
1IHK	A	HIS	56	H	-3.663736	4.302558	-8.168197	-4.130717
1IHK	A	LEU	57	H	-4.350625	5.211223	-9.318765	-4.785062
1IHK	A	LYS	58	H	-5.240361	6.163337	-11.370336	-5.814108
1IHK	A	GLY	59	H	-6.067227	6.803006	-13.241844	-6.776103
1IHK	A	ILE	60	H	-7.136889	8.921688	-14.768000	-7.600571
1IHK	A	LEU	61	H	-7.485786	8.587020	-15.264960	-7.793661
1IHK	A	ARG	62	C	-9.153862	10.116628	-16.911420	-8.007990
1IHK	A	ARG	63	E	-12.585007	13.787088	-20.868764	-8.874677
1IHK	A	ARG	64	E	-14.019529	15.364134	-19.159176	-6.868330
1IHK	A	GLN	65	E	-15.891377	17.410793	-19.072072	-5.946681
1IHK	A	LEU	66	E	-13.148254	16.921273	-14.627555	-5.261997
1IHK	A	TYR	67	E	-10.747445	12.055065	-14.241515	-5.384711
1IHK	A	CYS	68	E	-10.297577	12.755355	-13.776549	-5.377386
1IHK	A	ARG	69	T	-10.284491	12.801508	-13.813163	-5.383405
1IHK	A	THR	70	T	-10.283435	12.808557	-13.817003	-5.383511
1IHK	A	GLY	71	T	-10.287889	12.777849	-13.812184	-5.384672
1IHK	A	PHE	72	E	-10.644625	13.446916	-13.463483	-5.382850
1IHK	A	HIS	73	E	-12.487085	15.107461	-15.535589	-5.639376
1IHK	A	LEU	74	E	-12.587381	19.060730	-13.026563	-5.135697
1IHK	A	GLU	75	E	-10.811046	15.292564	-12.896559	-5.386564
1IHK	A	ILE	76	E	-7.834943	12.521576	-9.293657	-4.645841
1IHK	A	PHE	77	T	-6.502953	9.107626	-9.283090	-4.423270
1IHK	A	PRO	78	T	-4.936211	7.731582	-7.345572	-3.960259
1IHK	A	ASN	79	T	-4.922389	7.740679	-7.419208	-3.972236
1IHK	A	GLY	80	T	-4.918545	7.748280	-7.444066	-3.976530
1IHK	A	THR	81	C	-4.921792	7.719059	-7.437972	-3.973197
1IHK	A	ILE	82	E	-4.959625	7.654556	-7.316741	-3.945169
1IHK	A	GLN	83	E	-6.943122	8.438381	-10.844678	-4.532578
1IHK	A	GLY	84	E	-6.992343	7.399878	-11.637261	-4.647518
1IHK	A	THR	85	E	-7.119445	6.998768	-11.800212	-4.658925
1IHK	A	ARG	86	C	-7.163068	6.702327	-11.833645	-4.646610
1IHK	A	LYS	87	T	-7.167276	6.657332	-11.837826	-4.647962
1IHK	A	ASP	88	T	-7.206389	6.584346	-11.767081	-4.654438
1IHK	A	HIS	89	T	-9.179023	7.869755	-14.250021	-4.995794
1IHK	A	SER	90	T	-10.340899	9.331540	-15.556018	-5.005258
1IHK	A	ARG	91	T	-10.600784	11.399686	-14.619168	-4.938516
1IHK	A	PHE	92	T	-10.917660	14.203898	-13.070304	-4.736799
1IHK	A	GLY	93	T	-10.919499	14.323255	-12.989891	-4.727281
1IHK	A	ILE	94	E	-10.930294	14.578837	-12.802028	-4.701905
1IHK	A	LEU	95	E	-11.376143	17.553898	-12.494685	-4.928776
1IHK	A	GLU	96	E	-9.699976	16.057117	-10.065322	-4.707360
1IHK	A	PHE	97	E	-8.549792	13.921942	-8.975079	-4.039689
1IHK	A	ILE	98	E	-5.091065	6.981393	-6.722254	-3.167925
1IHK	A	SER	99	E	-3.671309	5.102774	-6.481602	-3.403862
1IHK	A	ILE	100	E	-3.343203	5.467226	-6.384007	-3.468025
1IHK	A	ALA	101	E	-3.334905	5.481663	-6.414329	-3.469689
1IHK	A	VAL	102	T	-3.334874	5.481172	-6.414908	-3.469726
1IHK	A	GLY	103	T	-3.366391	5.398338	-6.396121	-3.485068
1IHK	A	LEU	104	E	-3.832652	5.958236	-6.302258	-3.542217
1IHK	A	VAL	105	E	-5.863422	6.509255	-8.557772	-3.570797
1IHK	A	SER	106	E	-8.429555	8.658377	-11.309723	-4.021488
1IHK	A	ILE	107	E	-10.736710	14.993451	-13.629201	-5.303208
1IHK	A	ARG	108	E	-11.034474	11.629672	-14.974221	-4.763617
1IHK	A	GLY	109	E	-7.955549	6.616414	-13.139241	-5.059075
1IHK	A	VAL	110	T	-7.912490	6.776409	-13.170114	-5.044514
1IHK	A	ASP	111	T	-7.912812	6.772114	-13.170573	-5.045056
1IHK	A	SER	112	T	-7.913441	6.765992	-13.169361	-5.045537
1IHK	A	GLY	113	T	-7.914753	6.761082	-13.163294	-5.045822
1IHK	A	LEU	114	C	-9.476390	8.991126	-13.606671	-4.853404
1IHK	A	TYR	115	E	-12.174972	14.101211	-15.823390	-5.339484
1IHK	A	LEU	116	E	-10.885529	13.703056	-13.942188	-5.543857
1IHK	A	GLY	117	E	-8.521276	9.360308	-12.954055	-5.505485
1IHK	A	MET	118	E	-8.012711	9.632309	-12.704053	-5.560974
1IHK	A	ASN	119	E	-5.914574	6.637175	-10.592823	-5.067934
1IHK	A	GLU	120	T	-5.824993	7.101860	-10.496793	-5.044562
1IHK	A	LYS	121	T	-5.824800	7.103251	-10.497610	-5.044532
1IHK	A	GLY	122	T	-5.830505	7.084339	-10.474150	-5.039853
1IHK	A	GLU	123	E	-5.839145	7.043975	-10.444129	-5.031588
1IHK	A	LEU	124	E	-6.981841	9.974052	-9.945050	-4.903929
1IHK	A	TYR	125	E	-8.305718	8.645495	-12.568195	-4.853245
1IHK	A	GLY	126	E	-4.821475	8.433832	-7.428888	-4.553866
1IHK	A	SER	127	E	-4.667874	8.129870	-7.740528	-4.516159
1IHK	A	GLU	128	T	-4.040110	7.324816	-7.322727	-4.333294
1IHK	A	LYS	129	T	-4.039116	7.325675	-7.330339	-4.333976
1IHK	A	LEU	130	T	-4.039454	7.325265	-7.327503	-4.333720
1IHK	A	THR	131	C	-4.223350	6.917898	-7.291729	-4.251424
1IHK	A	GLN	132	G	-4.291056	6.894627	-7.108962	-4.234338
1IHK	A	GLU	133	G	-7.777152	7.969713	-12.008373	-4.754894
1IHK	A	CYS	134	G	-9.326724	9.298696	-13.878339	-5.033857

```
1IHK         A          VAL            135                    E -10.116273  9.168471 -14.420758 -4.950596
1IHK         A          PHE            136                    E -13.656980 14.409132 -16.560566 -5.133743
1IHK         A          ARG            137                    E -14.684313 13.285299 -20.375021 -6.393468
1IHK         A          GLU            138                    E -11.500797 10.755154 -16.626947 -5.981054
1IHK         A          GLN            139                    E -9.395498  8.801021 -14.636842 -5.622821
1IHK         A          PHE            140                    E -6.023784  7.952060 -9.583582 -4.784459
1IHK         A          GLU            141                    E -5.981125  8.288604 -9.582469 -4.818121
1IHK         A          GLU            142                    E -5.973961  8.333668 -9.600580 -4.821969
1IHK         A          ASN            143                    T -5.973897  8.334579 -9.600759 -4.822000
1IHK         A          TRP            144                    T -5.975687  8.333342 -9.585702 -4.819609
1IHK         A          TYR            145                    E -7.464194 12.686249 -9.803068 -5.249788
1IHK         A          ASN            146                    E -8.583909 12.069915 -11.130373 -5.143745
1IHK         A          THR            147                    E -11.027011 14.036355 -13.655594 -5.500803
1IHK         A          TYR            148                    E -14.265479 16.210954 -18.342402 -6.048255
1IHK         A          SER            149                    E -13.182470 13.178729 -18.042797 -6.047857
1IHK         A          SER            150                    E -11.687077 13.105460 -16.010343 -6.021189
1IHK         A          ASN            151                    E -11.536387 13.371671 -16.180980 -6.120571
1IHK         A          LEU            152                    E -11.006097 13.308168 -14.895617 -5.566240
1IHK         A          TYR            153                    E -9.831240 11.669396 -13.285888 -5.129797
1IHK         A          LYS            154                    E -5.456636  6.703183 -9.202282 -4.558622
1IHK         A          HIS            155                    T -3.703637  4.576359 -8.040101 -4.418460
1IHK         A          VAL            156                    T -3.610041  4.563459 -8.212434 -4.415348
1IHK         A          ASP            157                    T -3.610031  4.563494 -8.212569 -4.415371
1IHK         A          THR            158                    T -3.610045  4.563331 -8.212454 -4.415356
1IHK         A          GLY            159                    T -3.636995  4.462998 -8.164872 -4.407821
1IHK         A          ARG            160                    C -4.751754  4.470866 -9.189378 -4.380328
1IHK         A          ARG            161                    E -10.062937  7.470008 -16.179278 -5.744358
1IHK         A          TYR            162                    E -13.718374 16.553662 -16.896355 -5.957474
1IHK         A          TYR            163                    E -13.712765 19.408459 -14.315779 -5.141152
1IHK         A          VAL            164                    C -10.581479 12.788913 -12.368557 -4.361631
1IHK         A          ALA            165                    C -8.978814  9.392400 -12.679888 -4.688260
1IHK         A          LEU            166                    B -8.024792  8.245793 -12.533426 -4.913024
1IHK         A          ASN            167                    T -5.641645  4.792154 -10.523673 -4.628716
1IHK         A          LYS            168                    T -4.882391  5.826508 -8.805463 -4.168073
1IHK         A          ASP            169                    T -4.882387  5.826223 -8.805699 -4.168107
1IHK         A          GLY            170                    T -4.882935  5.823146 -8.802111 -4.167604
1IHK         A          THR            171                    C -4.885295  5.814613 -8.787384 -4.164398
1IHK         A          PRO            172                    B -5.075088  6.223614 -8.144502 -3.990470
1IHK         A          ARG            173                    C -10.216110  8.442466 -15.675375 -4.916464
1IHK         A          GLU            174                    T -9.085934  8.437530 -13.979375 -5.177537
1IHK         A          GLY            175                    T -8.924368  8.664820 -14.160821 -5.290516
1IHK         A          THR            176                    T -8.929020  8.664767 -14.138048 -5.291221
1IHK         A          ARG            177                    T -8.931502  8.655511 -14.128043 -5.290991
1IHK         A          THR            178                    T -8.947737  8.663472 -14.089185 -5.303399
1IHK         A          LYS            179                    T -9.744705  9.372193 -14.908736 -5.658539
1IHK         A          ARG            180                    T -11.689376  9.472472 -18.515951 -6.063456
1IHK         A          HIS            181                    T -10.104249 12.398480 -13.954132 -5.777849
1IHK         A          GLN            182                    T -10.080897 12.485170 -14.005135 -5.789696
1IHK         A          LYS            183                    G -10.094768 12.570175 -13.898727 -5.783604
1IHK         A          PHE            184                    G -10.113642 12.702803 -13.740238 -5.774331
1IHK         A          THR            185                    G -10.114167 12.763590 -13.693745 -5.764975
1IHK         A          HIS            186                    E -11.856698 15.564039 -14.953259 -5.896236
1IHK         A          PHE            187                    E -11.990760 16.257169 -13.124307 -4.553797
1IHK         A          LEU            188                    E -9.318893 11.854861 -10.537576 -3.862073
1IHK         A          PRO            189                    E -8.689584 11.538427 -10.898378 -4.215039
1IHK         A          ARG            190                    E -8.222362 10.200429 -11.220799 -4.194905
1IHK         A          PRO            191                    C -4.677991  6.906068 -6.902659 -3.663360
1IHK         A          VAL            192                    C -4.219399  7.274059 -6.796645 -3.802300
1IHK         A          ASP            193                    T -4.158497  7.357415 -6.885801 -3.818593
1IHK         A          PRO            194                    T -4.122574  7.349964 -6.963926 -3.810109
1IHK         A          ASP            195                    T -4.120628  7.349051 -6.977866 -3.812309
1IHK         A          LYS            196                    T -4.413220  7.632404 -7.028794 -3.905766
1IHK         A          VAL            197                    T -5.226929  7.775949 -7.997314 -3.868396
1IHK         A          PRO            198                    T -5.755383  7.304468 -8.463002 -3.751258
1IHK         A          GLU            199                    T -7.305941  8.274246 -11.780825 -4.871093
1IHK         A          LEU            200                    G -8.207258 12.468819 -14.374354 -6.948609
1IHK         A          TYR            201                    G -7.368721  9.434016 -13.383916 -6.476006
1IHK         A          LYS            202                    G -6.440718  7.201929 -12.091188 -5.668538
1IHK         A          ASP            203                    G -4.680235  5.635330 -8.569832 -4.330945
1IHK         A          ILE            204                    C -2.205671  4.104258 -4.516451 -3.066593
1IHK         A          LEU            205                    C -1.797637  3.348726 -4.698855 -2.855739
1IHK         A          SER            206                    C -1.797637  3.348726 -4.698855 -2.855739
1IHK         A          GLN            207                    C -1.797637  3.348726 -4.698855 -2.855739
1IHK         A          SER            208                    C -1.797637  3.348726 -4.698855 -2.855739
1IJR         A          ALA              1                    C -3.429037  3.263078 -6.459753 -2.929943
1IJR         A          PRO              2                    C -3.429037  3.263078 -6.459753 -2.929943
1IJR         A          GLU              3                    T -3.429037  3.263078 -6.459753 -2.929943
1IJR         A          PRO              4                    T -3.429037  3.263078 -6.459753 -2.929943
1IJR         A          TRP              5                    T -6.273440 10.185641 -8.168146 -4.099246
1IJR         A          PHE              6                    B -7.558480 14.201319 -9.001130 -4.959062
1IJR         A          PHE              7                    T -8.283282 12.607313 -10.628634 -4.712457
```

```
1IJR         A          LYS              8                    T -8.167177 11.815876 -11.106028 -4.717149
1IJR         A          ASN              9                    T -8.163756 11.777238 -11.141150 -4.717398
1IJR         A          LEU             10                    T -8.166466 11.737100 -11.136262 -4.709559
1IJR         A          SER             11                    C -8.629490  9.953160 -12.636517 -4.811206
1IJR         A          ARG             12                    H -9.082735  9.167962 -13.400340 -4.904296
1IJR         A          LYS             13                    H -10.109224  8.608027 -15.743553 -4.965347
1IJR         A          ASP             14                    H -10.250742  8.445343 -15.631086 -4.848738
1IJR         A          ALA             15                    H -10.272425  8.413093 -15.555320 -4.826730
1IJR         A          GLU             16                    H -10.368779  8.311524 -15.392213 -4.758685
1IJR         A          ARG             17                    H -10.384830  8.447015 -15.183564 -4.667190
1IJR         A          GLN             18                    H -10.624531 10.082306 -14.553885 -4.527667
1IJR         A          LEU             19                    H -6.777457  6.824124 -10.336065 -4.046076
1IJR         A          LEU             20                    H -6.291305  5.437318 -11.325465 -4.343107
1IJR         A          ALA             21                    T -6.146705  4.885037 -11.821717 -4.431145
1IJR         A          PRO             22                    T -6.113974  4.865608 -11.959669 -4.474128
1IJR         A          GLY             23                    T -6.110237  4.867431 -11.986846 -4.482665
1IJR         A          ASN             24                    T -6.341760  3.934302 -12.782598 -4.692554
1IJR         A          THR             25                    T -6.898194  3.302090 -13.843367 -4.873945
1IJR         A          HIS             26                    T -7.768415  4.693748 -14.601989 -5.290371
1IJR         A          GLY             27                    T -9.012965  5.903057 -16.128621 -5.722334
1IJR         A          SER             28                    E -10.373015 10.030469 -15.814921 -5.490968
1IJR         A          PHE             29                    E -10.751203 12.598298 -14.199899 -5.211955
1IJR         A          LEU             30                    E -12.052566 16.652953 -13.702166 -5.036620
1IJR         A          ILE             31                    E -12.349278 17.282641 -13.110978 -4.883927
1IJR         A          ARG             32                    E -13.286105 10.388910 -19.812510 -6.149142
1IJR         A          GLU             33                    E -8.263534  7.271876 -13.765329 -5.446152
1IJR         A          SER             34                    T -5.409613  5.613201 -10.425604 -4.967597
1IJR         A          GLU             35                    T -4.415674  4.517153 -9.912625 -4.869843
1IJR         A          SER             36                    T -4.312555  4.499749 -10.004271 -4.825239
1IJR         A          THR             37                    T -4.309771  4.519491 -10.009913 -4.825224
1IJR         A          ALA             38                    T -4.310491  4.516295 -10.005370 -4.824457
1IJR         A          GLY             39                    T -4.410523  4.316116 -9.930962 -4.797819
1IJR         A          SER             40                    T -5.382574  4.528063 -10.496810 -4.591850
1IJR         A          PHE             41                    E -7.481503  8.724103 -11.231220 -4.821628
1IJR         A          CYS             42                    E -10.156163 10.391438 -14.527708 -5.367037
1IJR         A          LEU             43                    E -12.913185 15.473096 -16.357658 -5.718620
1IJR         A          SER             44                    E -13.886420 17.470785 -15.749924 -5.230294
1IJR         A          VAL             45                    E -13.941693 17.465729 -15.588863 -5.181633
1IJR         A          ARG             46                    E -14.238055 10.634585 -23.223662 -7.562535
1IJR         A          ASP             47                    E -8.783877  6.013664 -14.905360 -5.231866
1IJR         A          PHE             48                    E -6.175513  4.978157 -11.337348 -4.673236
1IJR         A          ASP             49                    T -4.387510  3.566733 -10.022315 -4.751230
1IJR         A          GLN             50                    T -4.357749  3.575443 -10.137554 -4.764647
1IJR         A          ASN             51                    T -4.354192  3.585062 -10.155440 -4.765865
1IJR         A          GLN             52                    T -4.354164  3.586627 -10.154542 -4.765640
1IJR         A          GLY             53                    T -4.381835  3.521023 -10.099779 -4.770165
1IJR         A          GLU             54                    E -6.069075  3.959824 -12.454880 -5.011567
1IJR         A          VAL             55                    E -7.320322  5.558731 -13.126612 -4.955159
1IJR         A          VAL             56                    E -8.642262  8.725822 -13.237227 -4.897581
1IJR         A          LYS             57                    E -9.777556 10.770193 -14.184850 -5.299680
1IJR         A          HIS             58                    E -10.938196 13.191474 -14.929628 -5.629876
1IJR         A          TYR             59                    E -11.830522 15.396099 -15.149966 -5.620559
1IJR         A          LYS             60                    E -11.608737 13.601887 -15.621355 -5.514338
1IJR         A          ILE             61                    E -10.104220 11.643824 -13.530322 -4.999319
1IJR         A          ARG             62                    E -8.135719  7.280901 -13.069314 -4.940340
1IJR         A          ASN             63                    E -4.986196  3.802066 -10.581981 -4.817050
1IJR         A          LEU             64                    T -2.687113  3.654289 -7.538826 -4.614957
1IJR         A          ASP             65                    T -2.685934  3.661284 -7.545273 -4.615527
1IJR         A          ASN             66                    T -2.685935  3.661270 -7.545260 -4.615526
1IJR         A          GLY             67                    T -2.685994  3.660918 -7.544695 -4.615484
1IJR         A          GLY             68                    C -2.698530  3.656639 -7.476682 -4.609135
1IJR         A          PHE             69                    E -6.384048  7.102780 -10.626161 -4.804069
1IJR         A          TYR             70                    E -9.260219 12.489594 -11.280513 -4.444086
1IJR         A          ILE             71                    T -7.457888  9.359060 -9.510405 -3.695965
1IJR         A          SER             72                    T -5.605607  7.907998 -7.905196 -3.707408
1IJR         A          PRO             73                    T -5.590909  8.014199 -7.928113 -3.717808
1IJR         A          ARG             74                    T -5.587807  8.036023 -7.940201 -3.720406
1IJR         A          ILE             75                    T -5.567468  8.189884 -7.959853 -3.741652
1IJR         A          THR             76                    E -5.526202  8.866512 -7.758998 -3.815905
1IJR         A          PHE             77                    E -6.578597 14.080479 -7.458959 -4.368386
1IJR         A          PRO             78                    C -6.476241 13.045460 -8.034300 -4.445797
1IJR         A          GLY             79                    C -6.486640 13.066228 -8.004440 -4.454761
1IJR         A          LEU             80                    H -6.595182 13.164395 -7.875981 -4.476019
1IJR         A          HIS             81                    H -7.186697  9.914751 -10.151327 -4.557209
1IJR         A          GLU             82                    H -7.242855  9.553679 -10.208407 -4.570714
1IJR         A          LEU             83                    H -9.471466 13.234425 -11.835958 -4.990926
1IJR         A          VAL             84                    H -11.190536 14.909382 -13.121600 -4.610340
1IJR         A          ARG             85                    H -11.856040 12.582261 -14.727305 -4.359393
1IJR         A          HIS             86                    H -11.762006 12.513317 -15.423907 -5.003712
1IJR         A          TYR             87                    H -11.479946 12.032755 -15.449828 -5.045881
1IJR         A          THR             88                    H -9.420181  6.571919 -14.790622 -4.704570
```

1IJR	A	ASN	89	H	-6.801465	5.103823	-12.242992	-4.766169
1IJR	A	ALA	90	C	-6.619636	5.940953	-11.925880	-4.718444
1IJR	A	SER	91	T	-6.551904	6.197911	-11.962714	-4.760889
1IJR	A	ASP	92	T	-6.507888	6.437324	-11.999671	-4.819328
1IJR	A	GLY	93	T	-6.491532	6.591806	-11.982335	-4.839856
1IJR	A	LEU	94	T	-7.012984	8.723848	-11.658737	-4.943026
1IJR	A	CYS	95	T	-7.439131	9.204104	-12.310176	-5.319828
1IJR	A	THR	96	T	-7.830424	10.028466	-12.348093	-5.514905
1IJR	A	ARG	97	T	-8.484442	11.001815	-12.075785	-5.391989
1IJR	A	LEU	98	C	-11.026977	14.497893	-13.831397	-5.188294
1IJR	A	SER	99	C	-10.851683	10.925250	-15.887836	-5.555956
1IJR	A	ARG	100	C	-9.571221	8.580193	-14.298299	-4.889126
1IJR	A	PRO	101	B	-6.030417	8.140729	-8.358735	-3.829200
1IJR	A	CYS	102	C	-6.030417	8.140729	-8.358735	-3.829200
1IJR	A	GLN	103	C	-6.030417	8.140729	-8.358735	-3.829200
1IJR	A	THR	104	C	-6.030417	8.140729	-8.358735	-3.829200
1IJT	A	GLY	79	C	-3.161135	3.835615	-7.423715	-3.822438
1IJT	A	ILE	80	C	-3.161135	3.835615	-7.423715	-3.822438
1IJT	A	LYS	81	C	-3.161135	3.835615	-7.423715	-3.822438
1IJT	A	ARG	82	E	-3.161135	3.835615	-7.423715	-3.822438
1IJT	A	LEU	83	E	-3.745668	5.543098	-7.435015	-4.334211
1IJT	A	ARG	84	E	-6.868635	8.786773	-10.727499	-5.094101
1IJT	A	ARG	85	E	-11.376365	12.591413	-16.349936	-6.467313
1IJT	A	LEU	86	E	-12.138265	15.614954	-13.969810	-5.018850
1IJT	A	TYR	87	E	-9.375621	11.350600	-12.528375	-5.029495
1IJT	A	CYS	88	E	-6.401528	7.829738	-9.756487	-4.409257
1IJT	A	ASN	89	T	-4.339960	7.196891	-7.435483	-4.353178
1IJT	A	VAL	90	T	-4.334467	7.232293	-7.447414	-4.351944
1IJT	A	GLY	91	T	-4.334349	7.233190	-7.448358	-4.352056
1IJT	A	ILE	92	T	-4.334466	7.232381	-7.447347	-4.351920
1IJT	A	GLY	93	T	-4.352742	7.214110	-7.375291	-4.350077
1IJT	A	PHE	94	E	-7.098423	11.039584	-8.792971	-4.228687
1IJT	A	HIS	95	E	-9.373871	11.770900	-12.182313	-4.909904
1IJT	A	LEU	96	E	-12.120023	16.088488	-14.045390	-4.899716
1IJT	A	GLN	97	E	-10.340972	10.727267	-14.282916	-5.026942
1IJT	A	ALA	98	E	-7.478950	8.613708	-10.848316	-4.494424
1IJT	A	LEU	99	T	-6.122802	6.733614	-9.616578	-3.958589
1IJT	A	PRO	100	T	-5.427922	8.150795	-8.128778	-3.840367
1IJT	A	ASP	101	T	-5.356880	8.150110	-8.309987	-3.890349
1IJT	A	GLY	102	T	-5.345232	8.161666	-8.360092	-3.901195
1IJT	A	ARG	103	C	-5.359798	8.154632	-8.300862	-3.885812
1IJT	A	ILE	104	E	-5.527891	8.695211	-7.918091	-3.882473
1IJT	A	GLY	105	E	-6.490764	8.181048	-10.140352	-4.317382
1IJT	A	GLY	106	E	-6.895316	7.659099	-11.467892	-4.512282
1IJT	A	ALA	107	E	-6.911051	7.028019	-11.838648	-4.529901
1IJT	A	HIS	108	C	-6.359235	6.415726	-11.022185	-4.256567
1IJT	A	ALA	109	C	-6.320332	6.400142	-11.092180	-4.253105
1IJT	A	ASP	110	C	-6.349655	6.388622	-11.033493	-4.246408
1IJT	A	THR	111	C	-6.491112	6.201066	-10.922259	-4.156181
1IJT	A	ARG	112	G	-6.568718	6.180590	-10.723284	-4.105638
1IJT	A	ASP	113	G	-7.850199	6.684889	-12.309097	-4.280619
1IJT	A	SER	114	G	-9.232737	8.484928	-13.827721	-4.731491
1IJT	A	LEU	115	C	-10.295637	10.418710	-13.698947	-4.517031
1IJT	A	LEU	116	E	-11.752256	14.299174	-14.185132	-4.665365
1IJT	A	GLU	117	E	-9.504475	13.041466	-11.594800	-4.833131
1IJT	A	LEU	118	E	-8.702247	11.799835	-11.550677	-4.715541
1IJT	A	SER	119	E	-5.417991	6.718879	-8.052256	-3.622739
1IJT	A	PRO	120	E	-3.031195	5.223703	-5.531060	-3.394964
1IJT	A	VAL	121	E	-2.604318	5.884812	-5.206431	-3.433975
1IJT	A	GLU	122	E	-2.597238	5.912511	-5.227158	-3.434984
1IJT	A	ARG	123	T	-2.597112	5.913240	-5.228035	-3.435033
1IJT	A	GLY	124	T	-2.602308	5.905073	-5.202171	-3.432684
1IJT	A	VAL	125	E	-2.992342	6.489004	-4.881728	-3.431459
1IJT	A	VAL	126	E	-5.225864	8.105188	-6.881214	-3.441940
1IJT	A	SER	127	E	-7.545818	9.504787	-9.509503	-3.720658
1IJT	A	ILE	128	E	-9.554582	14.723515	-11.421341	-4.719849
1IJT	A	PHE	129	E	-9.608224	13.579365	-11.399726	-4.335918
1IJT	A	GLY	130	E	-7.139306	8.055555	-9.919744	-3.849900
1IJT	A	VAL	131	T	-7.132637	8.107742	-9.926970	-3.848555
1IJT	A	ALA	132	T	-7.132897	8.104973	-9.925610	-3.848179
1IJT	A	SER	133	T	-7.138767	8.043440	-9.920009	-3.844937
1IJT	A	ARG	134	T	-7.141478	8.027210	-9.905550	-3.841361
1IJT	A	PHE	135	E	-9.772173	12.851695	-10.646485	-3.758078
1IJT	A	PHE	136	E	-12.401489	16.642289	-13.269718	-4.257383
1IJT	A	VAL	137	E	-11.784406	14.213846	-13.887553	-4.630882
1IJT	A	ALA	138	E	-9.949903	9.942211	-13.731728	-4.715495
1IJT	A	MET	139	E	-9.006705	8.630994	-13.898551	-5.049231
1IJT	A	SER	140	T	-8.190596	6.798353	-13.807941	-4.943805
1IJT	A	SER	141	T	-7.933973	7.679454	-13.425629	-5.024549
1IJT	A	LYS	142	T	-7.930742	7.695613	-13.437240	-5.029054
1IJT	A	GLY	143	T	-7.922876	7.822686	-13.422033	-5.060396

1IJT	A	LYS	144	C	-8.001832	7.771493	-13.351088	-5.051236
1IJT	A	LEU	145	E	-8.460901	9.711096	-12.846928	-5.218215
1IJT	A	TYR	146	E	-9.190225	11.350506	-13.178416	-5.089460
1IJT	A	GLY	147	E	-6.942852	11.931839	-8.621018	-4.626310
1IJT	A	SER	148	E	-6.728875	11.463328	-8.973711	-4.594999
1IJT	A	PRO	149	T	-6.498305	10.725641	-9.420689	-4.625367
1IJT	A	PHE	150	T	-6.498145	10.724015	-9.423464	-4.625957
1IJT	A	PHE	151	T	-6.501044	10.724545	-9.408723	-4.626165
1IJT	A	THR	152	T	-6.870404	9.666767	-10.180290	-4.635063
1IJT	A	ASP	153	T	-7.165622	9.182248	-10.392584	-4.695164
1IJT	A	GLU	154	T	-10.319147	10.033766	-16.247946	-5.787876
1IJT	A	CYS	155	T	-10.616147	10.085230	-16.412750	-5.844970
1IJT	A	THR	156	E	-11.020043	9.928955	-16.573219	-5.770292
1IJT	A	PHE	157	E	-11.404740	15.385746	-13.333391	-4.942003
1IJT	A	LYS	158	E	-9.060119	12.382614	-11.076216	-4.596893
1IJT	A	GLU	159	E	-7.656462	9.442676	-10.206379	-3.996828
1IJT	A	ILE	160	E	-5.461481	7.385708	-7.764024	-3.562619
1IJT	A	LEU	161	E	-4.419228	6.407856	-7.618656	-3.877269
1IJT	A	LEU	162	T	-4.405109	6.513873	-7.640887	-3.893070
1IJT	A	PRO	163	T	-4.403627	6.523538	-7.649269	-3.896203
1IJT	A	ASN	164	T	-4.405839	6.513809	-7.640083	-3.896070
1IJT	A	ASN	165	T	-4.512228	6.351293	-7.626355	-3.963049
1IJT	A	TYR	166	T	-6.557799	10.876062	-8.825083	-4.601881
1IJT	A	ASN	167	E	-7.866934	10.651185	-11.014437	-5.072140
1IJT	A	ALA	168	E	-10.817773	13.236310	-13.933986	-5.360402
1IJT	A	TYR	169	E	-14.722862	19.259506	-18.516451	-6.692305
1IJT	A	GLU	170	E	-14.454289	17.200523	-18.565863	-6.541843
1IJT	A	SER	171	E	-11.847144	14.245340	-15.505646	-5.936643
1IJT	A	TYR	172	T	-10.582780	12.528264	-14.816320	-5.875776
1IJT	A	LYS	173	T	-10.087211	11.320924	-15.058042	-5.787306
1IJT	A	TYR	174	T	-10.068160	11.441194	-15.043114	-5.776761
1IJT	A	PRO	175	T	-9.953887	12.086801	-14.542884	-5.591491
1IJT	A	GLY	176	T	-9.948500	12.248182	-14.392798	-5.539604
1IJT	A	MET	177	T	-10.157275	12.295591	-14.227771	-5.391726
1IJT	A	PHE	178	B	-10.446851	17.245498	-11.203719	-4.643465
1IJT	A	ILE	179	C	-8.679529	14.080399	-9.108963	-4.062119
1IJT	A	ALA	180	C	-7.288506	10.228496	-9.685273	-4.269977
1IJT	A	LEU	181	B	-5.961032	8.416165	-9.337403	-4.555122
1IJT	A	GLY	182	T	-5.175407	5.936875	-10.184985	-4.820878
1IJT	A	LYS	183	T	-5.047585	6.163459	-10.239384	-4.868937
1IJT	A	ASN	184	T	-5.044376	6.170214	-10.257628	-4.875073
1IJT	A	GLY	185	T	-5.056596	6.094016	-10.268785	-4.887395
1IJT	A	LYS	186	C	-5.184316	5.588003	-10.504115	-4.959409
1IJT	A	THR	187	B	-5.994756	7.197139	-10.544720	-5.084607
1IJT	A	LYS	188	C	-7.718832	9.558736	-12.451740	-5.418733
1IJT	A	LYS	189	T	-7.299718	9.413407	-11.030479	-4.852422
1IJT	A	GLY	190	T	-7.055700	8.953682	-11.158411	-4.744390
1IJT	A	ASN	191	T	-7.024788	8.980806	-11.141949	-4.698414
1IJT	A	ARG	192	T	-6.666826	8.861769	-10.174300	-4.161773
1IJT	A	VAL	193	T	-6.498669	8.727265	-9.927598	-3.998748
1IJT	A	SER	194	T	-6.525242	8.395730	-9.989289	-3.889806
1IJT	A	PRO	195	T	-6.463872	8.574667	-9.870516	-3.913480
1IJT	A	THR	196	T	-6.458590	8.568632	-9.910912	-3.936194
1IJT	A	MET	197	T	-6.687311	8.492401	-10.326478	-4.129204
1IJT	A	LYS	198	G	-6.975908	8.473039	-10.819082	-4.398674
1IJT	A	VAL	199	G	-7.268560	9.057469	-10.537090	-4.425004
1IJT	A	THR	200	G	-8.483699	9.309051	-12.286062	-4.828892
1IJT	A	HIS	201	E	-10.643570	11.964110	-14.112594	-5.125434
1IJT	A	PHE	202	E	-11.618258	17.444805	-11.973897	-4.633781
1IJT	A	LEU	203	E	-8.022586	10.736687	-9.004255	-3.408397
1IJT	A	PRO	204	E	-8.022586	10.736687	-9.004255	-3.408397
1IJT	A	ARG	205	E	-8.022586	10.736687	-9.004255	-3.408397
1IJT	A	LEU	206	C	-8.022586	10.736687	-9.004255	-3.408397
1IKT	A	LEU	6	C	-9.565040	9.460720	-13.223585	-4.436737
1IKT	A	GLN	7	H	-9.565040	9.460720	-13.223585	-4.436737
1IKT	A	SER	8	H	-9.565040	9.460720	-13.223585	-4.436737
1IKT	A	THR	9	H	-9.565040	9.460720	-13.223585	-4.436737
1IKT	A	PHE	10	H	-10.816398	10.632029	-14.908006	-4.951823
1IKT	A	VAL	11	H	-11.587917	13.773661	-14.646349	-5.071445
1IKT	A	PHE	12	H	-11.832020	14.971210	-14.278761	-4.943211
1IKT	A	GLU	13	H	-10.450486	9.779214	-13.788184	-4.342788
1IKT	A	GLU	14	H	-10.276035	9.469216	-13.862235	-4.166062
1IKT	A	ILE	15	H	-10.275285	9.460519	-13.847509	-4.148851
1IKT	A	GLY	16	H	-10.260975	9.233419	-13.969593	-4.128909
1IKT	A	ARG	17	H	-10.210377	9.069842	-14.031226	-4.068571
1IKT	A	ARG	18	H	-9.983076	9.220021	-12.786742	-3.532121
1IKT	A	LEU	19	H	-8.347965	9.931487	-10.134809	-3.764935
1IKT	A	LYS	20	H	-6.869256	7.567070	-9.930807	-3.957986
1IKT	A	ASP	21	H	-6.546496	7.646368	-9.982154	-4.020958
1IKT	A	ILE	22	H	-6.496698	7.861229	-9.898716	-3.981355
1IKT	A	GLY	23	H	-6.494250	7.867421	-9.901457	-3.978120

1IKT	A	PRO	24	H	-6.505333	7.792469	-9.903819	-3.962491
1IKT	A	GLU	25	H	-6.907355	8.230163	-9.916218	-3.949645
1IKT	A	VAL	26	H	-7.598232	10.169795	-9.367706	-3.419820
1IKT	A	VAL	27	H	-7.880669	9.579975	-10.141840	-3.378496
1IKT	A	LYS	28	H	-7.859772	9.493029	-10.253414	-3.429181
1IKT	A	LYS	29	H	-8.011795	9.808421	-10.288576	-3.573721
1IKT	A	VAL	30	H	-8.041062	9.850613	-10.166081	-3.555527
1IKT	A	ASN	31	C	-8.540508	8.246133	-11.508228	-3.708837
1IKT	A	ALA	32	E	-9.223333	8.658422	-11.961479	-3.846214
1IKT	A	VAL	33	E	-11.146353	11.628946	-13.303666	-3.936547
1IKT	A	PHE	34	E	-12.172688	14.809069	-12.985185	-4.011553
1IKT	A	GLU	35	E	-13.554942	17.828715	-15.822916	-5.470091
1IKT	A	TRP	36	E	-10.568496	19.065648	-14.893374	-9.065408
1IKT	A	HIS	37	E	-7.639157	14.012698	-12.438275	-7.768232
1IKT	A	ILE	38	E	-4.594182	7.915130	-7.185066	-4.413851
1IKT	A	THR	39	E	-2.770088	3.768724	-6.707022	-4.188934
1IKT	A	LYS	40	T	-1.415446	4.690002	-4.998262	-4.352778
1IKT	A	GLY	41	T	-0.985397	4.638407	-5.579588	-4.740370
1IKT	A	GLY	42	T	-0.983956	4.643602	-5.588917	-4.741504
1IKT	A	ASN	43	T	-0.985550	4.632329	-5.580870	-4.739032
1IKT	A	ILE	44	E	-1.025419	4.609400	-5.390277	-4.679341
1IKT	A	GLY	45	E	-1.482401	3.755985	-5.227708	-4.309511
1IKT	A	ALA	46	E	-4.643646	6.274468	-7.921587	-4.065020
1IKT	A	LYS	47	E	-5.705062	10.821425	-9.143119	-5.751784
1IKT	A	TRP	48	E	-8.792354	15.255655	-12.055730	-6.513212
1IKT	A	THR	49	E	-9.960804	15.818200	-12.683247	-6.262216
1IKT	A	ILE	50	E	-11.349495	13.964859	-12.996264	-4.210987
1IKT	A	ASP	51	E	-9.158440	8.891532	-12.334680	-4.176263
1IKT	A	LEU	52	E	-8.820198	8.384258	-12.328381	-3.994503
1IKT	A	LYS	53	C	-7.095228	5.157902	-11.259599	-3.955889
1IKT	A	SER	54	T	-6.726493	5.299446	-11.210894	-3.988804
1IKT	A	GLY	55	T	-6.621705	5.844788	-11.151206	-4.064765
1IKT	A	SER	56	T	-6.629649	5.805852	-11.135817	-4.063364
1IKT	A	GLY	57	T	-6.634401	5.801783	-11.126604	-4.068282
1IKT	A	LYS	58	E	-6.966224	6.488618	-11.080992	-4.160602
1IKT	A	VAL	59	E	-7.486979	9.580163	-10.545507	-4.393092
1IKT	A	TYR	60	E	-7.960179	11.346681	-10.284422	-4.354696
1IKT	A	GLN	61	E	-6.705416	7.027576	-10.457354	-4.197488
1IKT	A	GLY	62	C	-5.549624	4.561742	-9.628446	-3.835230
1IKT	A	PRO	63	C	-4.814499	4.072796	-8.579106	-3.421460
1IKT	A	ALA	64	T	-4.301945	4.372890	-7.889425	-3.361424
1IKT	A	LYS	65	T	-4.216999	4.472056	-8.062729	-3.448899
1IKT	A	GLY	66	T	-4.207308	4.515338	-8.073654	-3.457339
1IKT	A	ALA	67	T	-4.259493	4.577219	-7.938844	-3.428018
1IKT	A	ALA	68	T	-4.453112	4.848466	-7.853563	-3.494405
1IKT	A	ASP	69	T	-5.271140	5.573415	-9.234460	-4.017655
1IKT	A	THR	70	E	-6.206604	7.269699	-9.424347	-4.030683
1IKT	A	THR	71	E	-7.338898	9.848517	-8.957719	-3.872567
1IKT	A	ILE	72	E	-9.289651	13.999290	-10.108465	-4.199646
1IKT	A	ILE	73	E	-10.289490	16.663783	-10.997509	-4.591270
1IKT	A	LEU	74	E	-10.515539	17.226914	-10.801101	-4.616015
1IKT	A	SER	75	E	-11.187169	15.790724	-12.248890	-4.536867
1IKT	A	ASP	76	H	-12.090178	13.143840	-14.985894	-4.506777
1IKT	A	GLU	77	H	-12.451877	11.646334	-16.788660	-4.935003
1IKT	A	ASP	78	H	-12.943087	11.649248	-18.444422	-5.587297
1IKT	A	PHE	79	H	-12.326294	16.297735	-16.038964	-6.325472
1IKT	A	MET	80	H	-10.243150	10.866089	-13.389215	-4.602909
1IKT	A	GLU	81	H	-7.064220	7.732609	-10.036933	-4.063501
1IKT	A	VAL	82	H	-3.544330	5.568192	-4.958864	-2.921809
1IKT	A	VAL	83	H	-3.467610	5.723917	-5.126217	-2.972810
1IKT	A	LEU	84	H	-3.434558	5.822862	-5.254720	-3.031030
1IKT	A	GLY	85	T	-3.431534	5.844888	-5.271857	-3.038302
1IKT	A	LYS	86	T	-3.432822	5.840752	-5.261466	-3.036041
1IKT	A	LEU	87	T	-4.472740	7.136697	-6.740149	-3.579211
1IKT	A	ASP	88	T	-5.110737	7.740288	-7.565506	-4.064696
1IKT	A	PRO	89	H	-6.559873	10.114232	-8.619489	-4.441544
1IKT	A	GLN	90	H	-9.772817	9.937969	-13.558532	-4.489686
1IKT	A	LYS	91	H	-8.928248	10.562834	-11.292695	-4.005740
1IKT	A	ALA	92	H	-8.342735	9.516229	-10.860555	-3.794415
1IKT	A	PHE	93	H	-8.352188	9.474973	-10.838910	-3.773552
1IKT	A	PHE	94	H	-8.302223	9.427707	-10.976058	-3.784058
1IKT	A	SER	95	H	-8.265278	9.338337	-11.132117	-3.804367
1IKT	A	GLY	96	T	-8.375481	9.008836	-11.352637	-3.813785
1IKT	A	ARG	97	T	-9.042912	9.223691	-12.763895	-4.072663
1IKT	A	LEU	98	T	-7.041180	10.189300	-7.582975	-3.265148
1IKT	A	LYS	99	E	-6.144392	7.808957	-8.283624	-3.484653
1IKT	A	ALA	100	E	-5.428688	7.717442	-7.871767	-3.615630
1IKT	A	ARG	101	E	-5.232169	7.075218	-8.339444	-3.679189
1IKT	A	GLY	102	E	-5.141645	6.969202	-8.472321	-3.701403
1IKT	A	ASN	103	T	-5.164314	6.838744	-8.520794	-3.720482
1IKT	A	ILE	104	H	-5.260291	6.785253	-8.525725	-3.750756

1IKT	A	MET	105	H	-5.705290	5.784953	-9.448559	-3.838846
1IKT	A	LEU	106	H	-6.291924	6.349252	-9.306785	-3.835178
1IKT	A	SER	107	H	-8.875726	8.176773	-11.751265	-3.860430
1IKT	A	GLN	108	H	-10.990888	9.548496	-14.829538	-4.476963
1IKT	A	LYS	109	H	-12.250746	10.309312	-17.403371	-5.384143
1IKT	A	LEU	110	H	-13.068499	13.359749	-16.553008	-4.922305
1IKT	A	GLN	111	H	-12.436061	11.022098	-16.789086	-4.803798
1IKT	A	MET	112	H	-10.852207	10.199195	-14.311996	-4.423465
1IKT	A	ILE	113	H	-10.676923	11.454458	-14.445586	-4.971822
1IKT	A	LEU	114	H	-10.203984	11.889904	-14.334954	-5.447816
1IKT	A	LYS	115	H	-9.164223	9.652121	-13.867905	-5.380682
1IKT	A	ASP	116	H	-7.413375	8.791302	-10.437704	-4.337841
1IKT	A	TYR	117	H	-6.284273	8.102050	-7.782701	-3.127430
1IKT	A	ALA	118	C	-6.284273	8.102050	-7.782701	-3.127430
1IKT	A	LYS	119	C	-6.284273	8.102050	-7.782701	-3.127430
1IKT	A	LEU	120	C	-6.284273	8.102050	-7.782701	-3.127430
1IMJ	A	ALA	2	C	-4.787656	4.517475	-8.055057	-3.182661
1IMJ	A	ALA	3	C	-4.787656	4.517475	-8.055057	-3.182661
1IMJ	A	SER	4	C	-4.787656	4.517475	-8.055057	-3.182661
1IMJ	A	VAL	5	E	-4.787656	4.517475	-8.055057	-3.182661
1IMJ	A	GLU	6	E	-6.413323	6.145965	-10.605063	-4.314947
1IMJ	A	GLN	7	E	-8.623901	7.653103	-14.583138	-5.359916
1IMJ	A	ARG	8	C	-7.896530	9.234068	-12.033724	-4.826652
1IMJ	A	GLU	9	C	-6.882122	9.182881	-10.285156	-4.539232
1IMJ	A	GLY	10	C	-6.774667	9.421394	-10.162424	-4.442169
1IMJ	A	THR	11	C	-6.776093	9.451879	-10.127218	-4.431749
1IMJ	A	ILE	12	E	-6.738563	9.610416	-10.071020	-4.420606
1IMJ	A	GLN	13	E	-6.766345	9.485004	-10.129087	-4.427678
1IMJ	A	VAL	14	E	-7.318759	9.894402	-10.907500	-4.419796
1IMJ	A	GLN	15	T	-7.633144	9.382665	-11.896206	-4.753928
1IMJ	A	GLY	16	T	-7.647531	9.319497	-11.899395	-4.766700
1IMJ	A	GLN	17	E	-7.970794	8.365056	-12.719764	-4.912551
1IMJ	A	ALA	18	E	-8.347660	8.778316	-12.449802	-4.874828
1IMJ	A	LEU	19	E	-10.598207	10.184387	-15.237194	-5.290961
1IMJ	A	PHE	20	E	-12.826996	13.611492	-16.227082	-5.312987
1IMJ	A	PHE	21	E	-16.076420	20.050260	-17.971738	-5.576061
1IMJ	A	ARG	22	E	-16.063621	17.437326	-19.853631	-5.890519
1IMJ	A	GLU	23	E	-11.457093	13.316142	-13.702908	-4.652329
1IMJ	A	ALA	24	E	-9.676443	11.404463	-11.581017	-3.898612
1IMJ	A	LEU	25	E	-6.487864	8.186227	-9.344300	-4.135958
1IMJ	A	PRO	26	T	-4.298233	4.978478	-8.089175	-3.971437
1IMJ	A	GLY	27	T	-3.089757	4.872835	-6.997780	-4.110647
1IMJ	A	SER	28	T	-3.089147	4.873631	-7.002500	-4.110666
1IMJ	A	GLY	29	T	-3.089138	4.873677	-7.002593	-4.110681
1IMJ	A	GLN	30	C	-3.091065	4.862770	-6.994759	-4.110451
1IMJ	A	ALA	31	C	-3.172433	4.851082	-6.828937	-4.125835
1IMJ	A	ARG	32	C	-7.154258	5.715209	-11.539407	-4.096753
1IMJ	A	PHE	33	E	-9.287396	9.864960	-12.646061	-4.498207
1IMJ	A	SER	34	E	-11.221183	13.254472	-14.111362	-4.586066
1IMJ	A	VAL	35	E	-11.665162	16.015716	-12.989639	-4.416663
1IMJ	A	LEU	36	E	-11.622209	18.233809	-12.125355	-4.735512
1IMJ	A	LEU	37	E	-10.513960	17.146256	-11.076153	-4.784252
1IMJ	A	LEU	38	C	-9.110220	14.717934	-10.012345	-4.497816
1IMJ	A	HIS	39	C	-8.156365	13.303155	-9.683160	-4.502026
1IMJ	A	GLY	40	T	-7.316214	11.637855	-9.541141	-4.479793
1IMJ	A	ILE	41	T	-7.304975	11.650686	-9.582196	-4.481738
1IMJ	A	ARG	42	T	-7.307108	11.630742	-9.578448	-4.480722
1IMJ	A	PHE	43	T	-7.333219	11.502695	-9.564649	-4.481452
1IMJ	A	SER	44	C	-7.465043	11.141314	-9.555910	-4.476245
1IMJ	A	SER	45	H	-9.633852	12.467806	-11.828824	-4.611737
1IMJ	A	GLU	46	H	-11.417942	12.966996	-16.307140	-5.927536
1IMJ	A	THR	47	H	-11.414328	13.542749	-16.096941	-6.001142
1IMJ	A	TRP	48	H	-11.022072	13.585709	-15.467435	-5.939772
1IMJ	A	GLN	49	H	-8.680744	9.502254	-13.574897	-5.717476
1IMJ	A	ASN	50	H	-8.502436	10.212857	-13.164944	-5.545757
1IMJ	A	LEU	51	H	-8.487396	10.302302	-13.147148	-5.530971
1IMJ	A	GLY	52	C	-8.487245	10.299383	-13.149314	-5.530730
1IMJ	A	THR	53	H	-8.491651	10.275505	-13.135282	-5.528094
1IMJ	A	LEU	54	H	-9.232031	12.388080	-12.127640	-5.066918
1IMJ	A	HIS	55	H	-10.539002	13.618498	-13.201331	-5.148468
1IMJ	A	ARG	56	H	-11.956051	13.217325	-16.010219	-5.265760
1IMJ	A	LEU	57	H	-8.677380	11.163520	-11.062073	-4.486277
1IMJ	A	ALA	58	H	-8.591646	11.283096	-11.250966	-4.537015
1IMJ	A	GLN	59	H	-8.591516	11.283243	-11.252477	-4.537277
1IMJ	A	ALA	60	H	-8.591525	11.283170	-11.252388	-4.537243
1IMJ	A	GLY	61	C	-8.592171	11.281026	-11.248119	-4.537097
1IMJ	A	TYR	62	E	-9.776366	12.062340	-12.486338	-4.865283
1IMJ	A	ARG	63	E	-12.788262	14.146571	-16.165808	-4.839979
1IMJ	A	ALA	64	E	-11.503088	14.311942	-12.783076	-4.104997
1IMJ	A	VAL	65	E	-11.338878	14.828625	-12.669497	-4.156029
1IMJ	A	ALA	66	E	-11.075686	15.467563	-12.382425	-4.236145

```
1IMJ        A          ILE              67                      E -10.542336 15.115574 -12.200887 -4.467335
1IMJ        A          ASP              68                      E -10.062596 14.377812 -12.174632 -4.602573
1IMJ        A          LEU              69                      T -7.576061 12.649681 -8.833711 -4.439767
1IMJ        A          PRO              70                      T -7.057442 10.884134 -9.594601 -4.455881
1IMJ        A          GLY              71                      T -7.017454 10.696228 -9.854533 -4.503687
1IMJ        A          LEU              72                      T -6.974609 10.503696 -10.068481 -4.524345
1IMJ        A          GLY              73                      G -6.125293  6.421515 -11.063401 -4.645593
1IMJ        A          HIS              74                      G -6.134998  5.898875 -11.321696 -4.639681
1IMJ        A          SER              75                      G -6.186917  5.378055 -11.545014 -4.641948
1IMJ        A          LYS              76                      T -5.908389  5.359615 -11.030146 -4.279996
1IMJ        A          GLU              77                      T -5.739319  5.858778 -10.536405 -4.092186
1IMJ        A          ALA              78                      T -5.851471  7.168448 -9.402012 -3.596184
1IMJ        A          ALA              79                      C -5.451539  7.617347 -8.305777 -3.375812
1IMJ        A          ALA              80                      T -4.771122  9.238361 -6.121959 -3.192806
1IMJ        A          PRO              81                      T -4.338917  9.174997 -5.888196 -3.379132
1IMJ        A          ALA              82                      T -3.857406  7.317751 -6.624401 -3.639759
1IMJ        A          PRO              83                      T -3.483609  7.773034 -6.292774 -3.855449
1IMJ        A          ILE              84                      T -3.481867  7.822681 -6.294690 -3.874347
1IMJ        A          GLY              85                      T -3.529014  7.643553 -6.395322 -3.938273
1IMJ        A          GLU              86                      T -3.617097  7.437106 -6.475524 -3.997299
1IMJ        A          LEU              87                      C -3.898444  8.388902 -6.002093 -4.087125
1IMJ        A          ALA              88                      C -5.670097 10.393319 -7.599234 -4.177069
1IMJ        A          PRO              89                      C -6.828438 11.043592 -9.363950 -4.262747
1IMJ        A          GLY              90                      H -7.260770 11.423059 -9.279488 -4.119313
1IMJ        A          SER              91                      H -8.009046 10.820939 -9.803297 -3.755880
1IMJ        A          PHE              92                      H -9.309297 13.651979 -10.801705 -3.998454
1IMJ        A          LEU              93                      H -9.358719 14.948320 -9.861063 -3.725742
1IMJ        A          ALA              94                      H -8.053951 10.374454 -9.386983 -3.313714
1IMJ        A          ALA              95                      H -7.761249 10.308207 -9.440073 -3.317448
1IMJ        A          VAL              96                      H -7.706686 10.535824 -9.463681 -3.353143
1IMJ        A          VAL              97                      H -7.010118  9.377958 -9.513401 -3.677354
1IMJ        A          ASP              98                      H -6.868830  9.615613 -9.612639 -3.825756
1IMJ        A          ALA              99                      H -6.876446  9.728217 -9.745209 -3.973640
1IMJ        A          LEU             100                      H -6.731386  9.888971 -9.759966 -4.139068
1IMJ        A          GLU             101                      C -5.609247 10.046690 -7.480022 -3.981343
1IMJ        A          LEU             102                      T -5.592967 10.379308 -7.294708 -3.958025
1IMJ        A          GLY             103                      T -5.596891 10.410781 -7.235906 -3.933723
1IMJ        A          PRO             104                      T -5.604234 10.407807 -7.192667 -3.924921
1IMJ        A          PRO             105                      T -5.629923 10.409372 -7.079127 -3.903735
1IMJ        A          VAL             106                      E -6.895447 12.868215 -7.050987 -3.537266
1IMJ        A          VAL             107                      E -7.892145 12.720050 -7.862699 -3.213749
1IMJ        A          ILE             108                      E -9.347139 16.383711 -8.671057 -3.392105
1IMJ        A          SER             109                      E -9.711720 15.831988 -9.749477 -3.758977
1IMJ        A          PRO             110                      E -9.900349 15.221195 -10.503932 -3.973283
1IMJ        A          SER             111                      G -10.606621 13.745798 -13.134799 -4.603014
1IMJ        A          LEU             112                      G -10.909118 13.337491 -13.733230 -4.813641
1IMJ        A          SER             113                      G -11.001866 12.926289 -13.856418 -4.851222
1IMJ        A          GLY             114                      G -11.020556 12.920109 -13.796277 -4.852439
1IMJ        A          MET             115                      G -12.747844 15.226389 -16.553721 -5.708487
1IMJ        A          TYR             116                      H -13.279660 17.627324 -16.054732 -5.763121
1IMJ        A          SER             117                      H -13.288901 19.821719 -14.563180 -5.403105
1IMJ        A          LEU             118                      H -12.499887 21.555340 -11.283514 -4.685442
1IMJ        A          PRO             119                      H -11.526238 20.880938 -11.400671 -5.282371
1IMJ        A          PHE             120                      H -10.290410 16.402266 -10.919876 -4.595462
1IMJ        A          LEU             121                      H -5.767853  9.495305 -7.797915 -4.199217
1IMJ        A          THR             122                      H -4.805650  6.282625 -8.709510 -4.250822
1IMJ        A          ALA             123                      T -4.277281  4.813498 -8.883153 -4.091432
1IMJ        A          PRO             124                      T -4.120636  5.503457 -8.617812 -4.125715
1IMJ        A          GLY             125                      T -4.114651  5.549830 -8.621370 -4.127492
1IMJ        A          SER             126                      T -4.151876  5.295071 -8.675505 -4.122508
1IMJ        A          GLN             127                      C -4.335550  5.222371 -8.578044 -4.069530
1IMJ        A          LEU             128                      C -4.959135  7.889700 -7.787155 -4.236281
1IMJ        A          PRO             129                      C -6.796682 10.328264 -9.042053 -4.301248
1IMJ        A          GLY             130                      E -8.357638 13.147584 -10.115777 -4.367358
1IMJ        A          PHE             131                      E -9.183923 17.180750 -9.117644 -4.191723
1IMJ        A          VAL             132                      E -9.386705 16.626977 -9.013745 -3.600564
1IMJ        A          PRO             133                      E -9.481667 16.233655 -9.088379 -3.489357
1IMJ        A          VAL             134                      E -9.536844 15.350840 -9.782809 -3.594994
1IMJ        A          ALA             135                      T -9.129823 14.528919 -10.275453 -4.166356
1IMJ        A          PRO             136                      T -8.448372 12.993956 -10.686532 -4.637503
1IMJ        A          ILE             137                      T -7.512898 10.782595 -10.936149 -5.016192
1IMJ        A          CYS             138                      T -6.561422 11.698657 -9.566382 -5.229101
1IMJ        A          THR             139                      T -6.486422 11.522999 -9.752877 -5.221365
1IMJ        A          ASP             140                      T -6.454743 11.320357 -9.892328 -5.201139
1IMJ        A          LYS             141                      T -6.451390 11.208425 -9.945460 -5.191662
1IMJ        A          ILE             142                      T -6.428494 10.681777 -10.092039 -5.098490
1IMJ        A          ASN             143                      C -7.025518  8.491269 -11.652405 -4.777943
1IMJ        A          ALA             144                      H -7.236423  7.723721 -11.880650 -4.620315
1IMJ        A          ALA             145                      H -7.381881  7.555654 -11.785425 -4.567975
1IMJ        A          ASN             146                      H -7.471785  7.430875 -11.671164 -4.564518
1IMJ        A          TYR             147                      H -9.623459 10.228281 -13.932033 -5.097748
```

```
1IMJ        A          ALA           148                  H -9.665341  8.478011 -13.732065 -4.169237
1IMJ        A          SER           149                  H -9.496307  8.611842 -13.577041 -4.101319
1IMJ        A          VAL           150                  C -9.435856  8.869328 -13.436304 -4.062531
1IMJ        A          LYS           151                  C -9.428335  8.938697 -13.417824 -4.061134
1IMJ        A          THR           152                  C -9.397573  9.354928 -13.257928 -4.056272
1IMJ        A          PRO           153                  C -9.720948 12.247107 -12.119308 -3.917156
1IMJ        A          ALA           154                  E -10.057146 14.525224 -11.092204 -3.801641
1IMJ        A          LEU           155                  E -10.324441 16.639988 -10.025352 -3.721234
1IMJ        A          ILE           156                  E -10.366997 16.954871 -9.798367 -3.704949
1IMJ        A          VAL           157                  E -10.457416 16.425187 -10.275809 -3.838892
1IMJ        A          TYR           158                  E -11.287663 14.362450 -14.333692 -5.096176
1IMJ        A          GLY           159                  E -8.588197  6.358244 -13.874592 -4.779907
1IMJ        A          ASP           160                  T -8.505653  6.483638 -14.021497 -4.806869
1IMJ        A          GLN           161                  T -8.125678  6.900180 -13.758919 -4.868903
1IMJ        A          ASP           162                  T -8.119091  6.878917 -13.796461 -4.870022
1IMJ        A          PRO           163                  H -7.912358  6.655548 -13.777259 -4.779575
1IMJ        A          MET           164                  H -8.125650  6.847239 -13.778880 -4.787208
1IMJ        A          GLY           165                  H -8.167063  6.811930 -13.693920 -4.773132
1IMJ        A          GLN           166                  H -8.586771  6.233274 -13.934953 -4.603986
1IMJ        A          THR           167                  H -8.604379  6.225212 -13.855648 -4.592495
1IMJ        A          SER           168                  H -10.355260  8.035224 -16.077712 -5.115408
1IMJ        A          PHE           169                  H -11.249711 12.288751 -15.883382 -5.314591
1IMJ        A          GLU           170                  H -11.042590 13.124179 -15.253835 -5.450107
1IMJ        A          HIS           171                  H -11.077167 13.897163 -14.898866 -5.489773
1IMJ        A          LEU           172                  H -11.063177 14.453280 -14.544229 -5.443025
1IMJ        A          LYS           173                  H -10.991704 14.171123 -14.687057 -5.405873
1IMJ        A          GLN           174                  C -10.915810 13.512746 -14.735883 -5.263068
1IMJ        A          LEU           175                  T -10.810631 12.681157 -14.270091 -4.721770
1IMJ        A          PRO           176                  T -8.717796 10.152106 -11.310322 -4.153614
1IMJ        A          ASN           177                  T -8.704382 10.189521 -11.353114 -4.158507
1IMJ        A          HIS           178                  E -8.506177 11.104925 -10.965567 -4.125896
1IMJ        A          ARG           179                  E -8.480649 11.260803 -10.957245 -4.134680
1IMJ        A          VAL           180                  E -8.147315 12.035821 -10.464123 -4.245034
1IMJ        A          LEU           181                  E -8.038560 12.229798 -10.636858 -4.597464
1IMJ        A          ILE           182                  E -7.013384 10.287324 -10.387330 -4.890971
1IMJ        A          MET           183                  E -6.796454  9.580239 -10.971972 -5.067273
1IMJ        A          LYS           184                  T -6.679003  9.354993 -11.212606 -5.117249
1IMJ        A          GLY           185                  T -6.645497  9.266756 -11.301818 -5.135626
1IMJ        A          ALA           186                  T -6.671241  9.178934 -11.309258 -5.145732
1IMJ        A          GLY           187                  T -7.039148  8.582107 -12.145164 -5.311388
1IMJ        A          HIS           188                  T -7.433284  8.896873 -12.110476 -5.231519
1IMJ        A          PRO           189                  T -8.053375  9.838560 -11.767477 -5.041269
1IMJ        A          CYS           190                  H -10.011809 11.117545 -13.884250 -5.026939
1IMJ        A          TYR           191                  H -10.937628 16.061246 -12.891288 -5.018648
1IMJ        A          LEU           192                  H -9.689347  9.608068 -13.877716 -4.770417
1IMJ        A          ASP           193                  H -9.618681  9.362984 -14.193912 -4.814104
1IMJ        A          LYS           194                  C -9.656291  8.925915 -14.321173 -4.810751
1IMJ        A          PRO           195                  H -9.659029  8.888008 -14.320892 -4.807159
1IMJ        A          GLU           196                  H -9.677472  8.652042 -14.367551 -4.801222
1IMJ        A          GLU           197                  H -10.885402  7.812220 -16.676160 -5.183436
1IMJ        A          TRP           198                  H -12.563890 15.562274 -16.095023 -5.586469
1IMJ        A          HIS           199                  H -11.512937 13.613310 -14.591763 -5.064648
1IMJ        A          THR           200                  H -10.592730 11.406896 -14.269003 -4.817660
1IMJ        A          GLY           201                  H -10.589492 11.439485 -14.272583 -4.820171
1IMJ        A          LEU           202                  H -10.596282 11.405255 -14.244557 -4.809029
1IMJ        A          LEU           203                  H -10.596374 11.423517 -14.266833 -4.834010
1IMJ        A          ASP           204                  H -10.263698 12.883706 -13.906892 -5.386556
1IMJ        A          PHE           205                  H -8.884438 14.024377 -10.400958 -4.837050
1IMJ        A          LEU           206                  H -6.289184  8.751437 -8.335568 -3.753053
1IMJ        A          GLN           207                  H -6.289184  8.751437 -8.335568 -3.753053
1IMJ        A          GLY           208                  H -6.289184  8.751437 -8.335568 -3.753053
1IMJ        A          LEU           209                  C -6.289184  8.751437 -8.335568 -3.753053
1J74        A          VAL             7                  C -1.859415  1.836614 -4.873755 -2.685760
1J74        A          LYS             8                  C -1.859415  1.836614 -4.873755 -2.685760
1J74        A          VAL             9                  H -1.859415  1.836614 -4.873755 -2.685760
1J74        A          PRO            10                  H -1.859415  1.836614 -4.873755 -2.685760
1J74        A          ARG            11                  H -6.979982  4.258148 -12.057136 -3.991229
1J74        A          ASN            12                  H -8.249016  5.119688 -14.401112 -4.922683
1J74        A          PHE            13                  H -9.517547  6.805865 -15.957338 -5.669655
1J74        A          ARG            14                  H -11.489309 11.688057 -14.930406 -4.664359
1J74        A          LEU            15                  H -11.449169 12.214964 -14.601222 -4.594749
1J74        A          LEU            16                  H -11.304458 12.017747 -15.196522 -4.861117
1J74        A          GLU            17                  H -11.283839 12.010743 -15.353100 -4.937012
1J74        A          GLU            18                  H -11.751466 12.458838 -17.614900 -6.132222
1J74        A          LEU            19                  H -10.039057 10.042218 -16.860686 -6.735890
1J74        A          GLU            20                  H -8.092300  6.811874 -14.864850 -5.952786
1J74        A          GLU            21                  H -7.249429  6.463603 -13.662119 -5.544887
1J74        A          GLY            22                  H -6.120889  5.295623 -11.697757 -4.835920
1J74        A          GLN            23                  H -5.044600  4.846878 -10.260232 -4.684652
1J74        A          LYS            24                  H -4.652267  4.316171 -10.370645 -4.694724
1J74        A          GLY            25                  C -3.913922  3.268860 -9.914167 -4.707121
```

1J74	A	VAL	26	T	-3.796711	3.526527	-9.925871	-4.740280
1J74	A	GLY	27	T	-3.687966	3.991635	-9.719004	-4.757495
1J74	A	ASP	28	T	-3.738149	3.933807	-9.696691	-4.764785
1J74	A	GLY	29	T	-3.803105	3.953611	-9.601687	-4.770031
1J74	A	THR	30	C	-4.334102	5.547628	-9.400717	-4.847888
1J74	A	VAL	31	E	-4.687504	6.222315	-8.911667	-4.814086
1J74	A	SER	32	E	-6.972920	7.423292	-10.900495	-4.599367
1J74	A	TRP	33	E	-10.620690	15.136757	-14.574515	-5.932137
1J74	A	GLY	34	E	-8.451425	8.764512	-13.290364	-5.493813
1J74	A	LEU	35	E	-7.238148	7.863634	-12.072833	-5.226339
1J74	A	GLU	36	T	-6.955290	6.950941	-12.864436	-5.408780
1J74	A	ASP	37	T	-5.656705	3.485809	-11.689075	-4.680458
1J74	A	ASP	38	T	-5.291402	3.257201	-11.469909	-4.499472
1J74	A	GLU	39	T	-5.265413	3.368335	-11.456739	-4.488499
1J74	A	ASP	40	T	-5.281538	3.248301	-11.447395	-4.466356
1J74	A	MET	41	T	-5.295036	3.197158	-11.384975	-4.437769
1J74	A	THR	42	T	-5.685336	3.333963	-11.238013	-4.296427
1J74	A	LEU	43	T	-7.018760	6.264668	-11.463978	-4.379783
1J74	A	THR	44	C	-8.480686	7.869017	-12.557615	-4.571525
1J74	A	ARG	45	E	-11.724627	10.340492	-17.658773	-5.906057
1J74	A	TRP	46	E	-11.808223	16.632842	-13.201770	-5.220850
1J74	A	THR	47	E	-9.397331	12.041928	-11.492562	-4.499605
1J74	A	GLY	48	E	-8.421749	11.138367	-11.162254	-4.606860
1J74	A	MET	49	E	-8.207301	11.720285	-10.809361	-4.514019
1J74	A	ILE	50	E	-7.722055	11.670321	-9.951066	-4.224977
1J74	A	ILE	51	E	-6.772750	9.119032	-9.211576	-3.707779
1J74	A	GLY	52	C	-6.252354	8.972052	-8.841475	-3.792768
1J74	A	PRO	53	T	-6.236622	8.950212	-8.879418	-3.791738
1J74	A	PRO	54	T	-6.242977	8.905617	-8.868380	-3.786367
1J74	A	ARG	55	T	-6.270859	8.774403	-8.849368	-3.776337
1J74	A	THR	56	T	-6.518994	8.929986	-8.759736	-3.880433
1J74	A	ASN	57	T	-8.048680	9.382714	-10.687364	-4.150525
1J74	A	TYR	58	T	-10.552143	12.235577	-14.958310	-5.347243
1J74	A	GLU	59	T	-10.658432	12.628436	-15.200704	-5.568959
1J74	A	ASN	60	T	-10.740054	12.600586	-15.257896	-5.600637
1J74	A	ARG	61	T	-11.087956	13.052859	-14.868774	-5.330093
1J74	A	ILE	62	E	-11.073052	13.207894	-14.803829	-5.316439
1J74	A	TYR	63	E	-11.404756	13.314461	-14.831129	-5.288008
1J74	A	SER	64	E	-12.348447	14.882505	-15.445996	-5.224442
1J74	A	LEU	65	E	-12.600239	16.477635	-15.138333	-5.294728
1J74	A	LYS	66	E	-11.109477	12.837616	-15.279416	-5.807567
1J74	A	VAL	67	E	-9.182378	9.901531	-13.047008	-5.001200
1J74	A	GLU	68	E	-6.308161	6.093973	-11.246959	-4.999173
1J74	A	CYS	69	C	-6.274136	6.279347	-11.260265	-4.993298
1J74	A	GLY	70	T	-6.246538	6.506885	-11.207145	-4.969930
1J74	A	PRO	71	T	-6.234866	6.620325	-11.192127	-4.961847
1J74	A	LYS	72	T	-6.228464	6.693282	-11.163536	-4.950819
1J74	A	TYR	73	T	-7.419256	10.841429	-10.713228	-4.631866
1J74	A	PRO	74	T	-7.270760	12.280235	-8.768791	-3.936888
1J74	A	GLU	75	T	-7.278536	11.959170	-8.668704	-3.721300
1J74	A	ALA	76	T	-7.238087	11.989356	-8.418521	-3.552879
1J74	A	PRO	77	T	-7.294170	11.995853	-8.241900	-3.472171
1J74	A	PRO	78	C	-7.298898	11.976999	-8.219987	-3.465107
1J74	A	SER	79	E	-7.768205	11.008776	-9.174302	-3.482838
1J74	A	VAL	80	E	-8.259282	12.410598	-8.420668	-3.287199
1J74	A	ARG	81	E	-10.371487	14.185711	-10.574410	-3.658532
1J74	A	PHE	82	E	-11.504905	19.625445	-11.554255	-5.181923
1J74	A	VAL	83	T	-10.630219	16.223822	-12.351634	-5.323619
1J74	A	THR	84	B	-10.420687	16.049749	-12.668375	-5.486867
1J74	A	LYS	85	T	-10.270787	15.602918	-13.065462	-5.591911
1J74	A	ILE	86	C	-8.804818	11.693962	-12.733095	-5.644061
1J74	A	ASN	87	C	-8.317961	11.367857	-12.381695	-5.515103
1J74	A	MET	88	B	-7.944053	10.815251	-12.368934	-5.518089
1J74	A	ASN	89	T	-7.189272	8.160361	-12.245586	-5.231595
1J74	A	GLY	90	T	-6.633473	7.144521	-11.570275	-4.776877
1J74	A	ILE	91	B	-6.546152	7.001787	-11.631076	-4.720938
1J74	A	ASN	92	T	-6.348939	6.150247	-11.941548	-4.705515
1J74	A	ASN	93	T	-6.244154	5.758194	-12.070774	-4.670238
1J74	A	SER	94	T	-6.324112	5.559797	-12.058252	-4.583452
1J74	A	SER	95	T	-6.588172	5.034434	-12.585718	-4.638851
1J74	A	GLY	96	T	-6.677748	4.766193	-12.701998	-4.656709
1J74	A	MET	97	B	-7.007575	5.456374	-12.452229	-4.431500
1J74	A	VAL	98	B	-7.105857	7.627508	-10.463780	-3.620111
1J74	A	ASP	99	C	-6.832785	8.413690	-9.706799	-3.565362
1J74	A	ALA	100	G	-6.802710	8.524365	-9.692715	-3.555390
1J74	A	ARG	101	G	-6.810984	8.673314	-9.550945	-3.516862
1J74	A	SER	102	G	-6.888298	8.933533	-9.309905	-3.492056
1J74	A	ILE	103	C	-7.218955	9.827312	-9.085907	-3.559571
1J74	A	PRO	104	H	-7.791186	11.558990	-9.181728	-3.447977
1J74	A	VAL	105	H	-7.965066	12.223539	-8.903080	-3.458744
1J74	A	LEU	106	H	-8.077895	12.338595	-8.721074	-3.433359

1J74	A	ALA	107	H	-8.046923	12.076391	-9.024550	-3.531538
1J74	A	LYS	108	H	-8.063499	11.796889	-9.192407	-3.570360
1J74	A	TRP	109	C	-9.030317	12.736304	-11.512210	-4.456980
1J74	A	GLN	110	T	-9.147357	11.290058	-12.607595	-4.678674
1J74	A	ASN	111	T	-9.231832	10.660275	-12.918157	-4.731420
1J74	A	SER	112	T	-9.892921	10.380041	-14.056126	-4.881538
1J74	A	TYR	113	T	-10.590524	10.634637	-15.146753	-5.158802
1J74	A	SER	114	C	-10.345835	12.248173	-13.894201	-4.979067
1J74	A	ILE	115	H	-10.653464	15.274403	-12.415135	-4.783910
1J74	A	LYS	116	H	-10.709415	15.572533	-12.117102	-4.724835
1J74	A	VAL	117	H	-10.686901	15.534038	-12.188050	-4.719180
1J74	A	VAL	118	H	-10.690079	15.542249	-12.164206	-4.711336
1J74	A	LEU	119	H	-11.455021	16.944283	-12.537697	-4.731515
1J74	A	GLN	120	H	-12.113935	15.329527	-14.419727	-4.816551
1J74	A	GLU	121	H	-12.386635	15.260053	-14.409936	-4.784077
1J74	A	LEU	122	H	-13.222194	17.049037	-14.678207	-5.049521
1J74	A	ARG	123	H	-14.501633	15.548968	-18.648787	-5.585077
1J74	A	ARG	124	H	-12.870465	12.082959	-16.965875	-5.171480
1J74	A	LEU	125	H	-11.254473	11.696444	-15.247203	-5.320180
1J74	A	MET	126	H	-10.020121	9.482834	-15.198304	-5.436498
1J74	A	MET	127	H	-9.378474	7.842200	-15.376953	-5.383636
1J74	A	SER	128	T	-9.310440	7.708691	-15.538235	-5.372641
1J74	A	LYS	129	T	-9.286788	7.630623	-15.635993	-5.372669
1J74	A	GLU	130	T	-9.306286	7.490863	-15.659376	-5.374450
1J74	A	ASN	131	T	-9.482876	6.894646	-15.844458	-5.344159
1J74	A	MET	132	T	-10.340993	6.675419	-17.248578	-5.287223
1J74	A	LYS	133	T	-10.647237	7.345289	-17.305861	-5.165154
1J74	A	LEU	134	T	-10.194396	8.260653	-15.378651	-4.729144
1J74	A	PRO	135	C	-9.366961	7.971064	-14.747745	-4.999155
1J74	A	GLN	136	C	-8.449697	7.743303	-14.411963	-5.534862
1J74	A	PRO	137	C	-5.705014	6.523045	-10.063113	-4.841085
1J74	A	PRO	138	T	-5.694527	6.622378	-10.132395	-4.894730
1J74	A	GLU	139	T	-5.690086	6.664281	-10.160759	-4.913836
1J74	A	GLY	140	T	-5.670533	6.791206	-10.223298	-4.956385
1J74	A	GLN	141	T	-5.664072	6.849104	-10.219838	-4.956574
1J74	A	THR	142	B	-4.798612	7.807607	-6.832728	-3.740288
1J74	A	TYR	143	C	-4.798612	7.807607	-6.832728	-3.740288
1J74	A	ASN	144	C	-4.798612	7.807607	-6.832728	-3.740288
1J74	A	ASN	145	C	-4.798612	7.807607	-6.832728	-3.740288
1JHJ	A	ALA	2	C	-1.758074	2.966954	-4.965381	-3.133377
1JHJ	A	THR	3	T	-1.758074	2.966954	-4.965381	-3.133377
1JHJ	A	PRO	4	T	-1.758074	2.966954	-4.965381	-3.133377
1JHJ	A	ASN	5	T	-1.758074	2.966954	-4.965381	-3.133377
1JHJ	A	LYS	6	T	-2.677563	4.485025	-5.266872	-3.471519
1JHJ	A	THR	7	C	-4.405189	6.652628	-8.636633	-4.633694
1JHJ	A	PRO	8	C	-4.473647	6.332691	-8.808421	-4.591838
1JHJ	A	PRO	9	C	-4.898655	6.089589	-9.736557	-4.602832
1JHJ	A	GLY	10	C	-5.126496	5.569695	-9.868302	-4.284666
1JHJ	A	ALA	11	C	-5.421979	4.615174	-8.804486	-3.164837
1JHJ	A	ASP	12	C	-5.792822	4.433458	-8.561378	-2.983485
1JHJ	A	PRO	13	H	-7.169223	7.389759	-9.190356	-3.205276
1JHJ	A	LYS	14	H	-8.235938	8.132156	-11.372019	-3.919900
1JHJ	A	GLN	15	H	-8.974015	8.970792	-13.125910	-4.307406
1JHJ	A	LEU	16	H	-7.923037	7.317754	-12.054477	-4.313518
1JHJ	A	GLU	17	H	-6.182166	3.974240	-10.073873	-3.493573
1JHJ	A	ARG	18	H	-5.496030	4.973921	-8.043629	-2.874168
1JHJ	A	THR	19	H	-5.349045	5.271349	-7.869380	-2.799907
1JHJ	A	GLY	20	C	-5.346367	5.286989	-7.878420	-2.802871
1JHJ	A	THR	21	C	-5.352745	5.272014	-7.833481	-2.786256
1JHJ	A	VAL	22	E	-5.509872	5.730633	-7.184806	-2.585208
1JHJ	A	ARG	23	E	-6.226859	6.435263	-7.356888	-2.573198
1JHJ	A	GLU	24	E	-8.251288	9.560610	-10.438175	-3.658534
1JHJ	A	ILE	25	C	-8.129934	8.479880	-10.731465	-3.648604
1JHJ	A	GLY	26	G	-7.915296	6.812827	-11.814061	-3.806792
1JHJ	A	SER	27	G	-7.968582	6.303052	-11.984916	-3.788875
1JHJ	A	GLN	28	G	-7.981189	6.266944	-11.963104	-3.790516
1JHJ	A	ALA	29	E	-7.980529	6.312592	-11.924864	-3.777740
1JHJ	A	VAL	30	E	-8.483485	4.887612	-13.692555	-4.165090
1JHJ	A	TRP	31	E	-10.229203	11.137619	-11.892653	-3.468194
1JHJ	A	SER	32	E	-10.059698	9.506286	-12.569550	-3.534696
1JHJ	A	LEU	33	E	-9.432204	9.916657	-11.863263	-3.811117
1JHJ	A	SER	34	T	-8.434464	6.431592	-11.924510	-3.676884
1JHJ	A	SER	35	T	-6.483428	4.666460	-9.991140	-3.620035
1JHJ	A	CYS	36	T	-4.690402	6.902394	-8.083544	-4.460744
1JHJ	A	LYS	37	B	-4.556127	6.690107	-8.228257	-4.385518
1JHJ	A	PRO	38	T	-4.548228	6.707408	-8.231802	-4.371905
1JHJ	A	GLY	39	T	-4.547221	6.713891	-8.232422	-4.371090
1JHJ	A	PHE	40	B	-4.569321	6.794609	-8.168318	-4.399608
1JHJ	A	GLY	41	T	-5.448963	6.071490	-8.813456	-4.044279
1JHJ	A	VAL	42	G	-6.907852	8.435169	-9.035578	-3.591218
1JHJ	A	ASP	43	G	-7.660342	9.503304	-10.337121	-4.179943

1JHJ	A	GLN	44	G	-8.134069	10.633570	-10.812758	-4.666212
1JHJ	A	LEU	45	G	-8.157548	10.634802	-10.770076	-4.692154
1JHJ	A	ARG	46	C	-11.776363	9.822321	-16.903627	-5.050575
1JHJ	A	ASP	47	C	-8.669468	5.849054	-13.637098	-4.663575
1JHJ	A	ASP	48	C	-7.645834	5.955524	-11.828218	-4.222735
1JHJ	A	ASN	49	T	-7.572086	6.500384	-11.684808	-4.230971
1JHJ	A	LEU	50	T	-7.572009	6.502044	-11.684729	-4.231017
1JHJ	A	GLU	51	T	-7.572249	6.501435	-11.681899	-4.230391
1JHJ	A	THR	52	T	-7.673055	6.623860	-11.322094	-4.150601
1JHJ	A	TYR	53	C	-8.842177	10.620286	-10.606986	-4.293783
1JHJ	A	TRP	54	E	-12.544617	15.643647	-13.966681	-4.837212
1JHJ	A	GLN	55	E	-11.287891	6.403043	-16.900410	-4.906524
1JHJ	A	SER	56	C	-9.983913	6.188716	-16.640506	-5.447103
1JHJ	A	ASP	57	C	-8.096725	5.255636	-12.761859	-4.210143
1JHJ	A	GLY	58	C	-8.057895	5.305134	-12.811752	-4.187875
1JHJ	A	SER	59	T	-8.054271	5.328871	-12.815405	-4.184954
1JHJ	A	GLN	60	T	-8.056666	5.326000	-12.798704	-4.181989
1JHJ	A	PRO	61	T	-8.077227	5.298483	-12.663875	-4.134751
1JHJ	A	HIS	62	E	-9.631878	6.377668	-13.554054	-3.853633
1JHJ	A	LEU	63	E	-11.010037	9.671586	-13.613740	-3.806273
1JHJ	A	VAL	64	E	-12.410333	14.092256	-14.990272	-4.526626
1JHJ	A	ASN	65	E	-12.351080	14.621275	-14.475738	-4.413653
1JHJ	A	ILE	66	E	-11.880301	15.040815	-13.008230	-4.088893
1JHJ	A	GLN	67	E	-11.738671	14.351650	-13.288385	-4.076958
1JHJ	A	PHE	68	E	-10.700434	11.676479	-11.864492	-3.444966
1JHJ	A	ARG	69	E	-8.595302	8.840353	-10.231026	-3.437704
1JHJ	A	ARG	70	E	-8.580276	8.915526	-10.279802	-3.454803
1JHJ	A	LYS	71	E	-8.572352	8.987576	-10.325105	-3.486497
1JHJ	A	THR	72	E	-8.427495	10.109451	-10.142169	-3.646959
1JHJ	A	THR	73	E	-8.382963	10.600516	-9.946483	-3.647926
1JHJ	A	VAL	74	C	-8.954418	14.455745	-9.422638	-4.007654
1JHJ	A	LYS	75	C	-8.934943	14.627272	-9.311550	-3.984642
1JHJ	A	THR	76	E	-8.951389	14.643587	-9.189982	-3.939629
1JHJ	A	LEU	77	E	-9.393352	15.203313	-8.849126	-3.621296
1JHJ	A	CYS	78	E	-9.791154	14.616932	-9.467506	-3.646454
1JHJ	A	ILE	79	E	-10.406344	15.310962	-9.784958	-3.817680
1JHJ	A	TYR	80	E	-12.089244	18.230297	-12.217520	-4.483456
1JHJ	A	ALA	81	E	-11.110247	11.827223	-14.507035	-4.922710
1JHJ	A	ASP	82	E	-11.022071	11.029229	-15.072671	-5.013601
1JHJ	A	TYR	83	G	-10.671501	9.542407	-15.112071	-4.744958
1JHJ	A	LYS	84	G	-9.662213	6.378350	-14.106666	-4.038647
1JHJ	A	SER	85	G	-9.655164	6.401738	-14.127996	-4.039662
1JHJ	A	ASP	86	C	-9.669967	6.276571	-14.136785	-4.020353
1JHJ	A	GLU	87	G	-9.650777	6.551998	-14.005565	-3.994332
1JHJ	A	SER	88	G	-9.699097	6.455339	-13.907125	-3.956778
1JHJ	A	TYR	89	G	-10.892122	11.782266	-14.060070	-4.453884
1JHJ	A	THR	90	C	-10.759023	12.745931	-13.122663	-4.241581
1JHJ	A	PRO	91	E	-10.897589	13.727096	-12.286937	-3.926136
1JHJ	A	SER	92	E	-11.169011	14.247177	-12.302847	-3.938366
1JHJ	A	LYS	93	E	-11.185177	14.347788	-12.242042	-3.947986
1JHJ	A	ILE	94	E	-11.196278	14.392199	-12.173245	-3.922229
1JHJ	A	SER	95	E	-11.518704	13.689901	-13.567508	-4.183358
1JHJ	A	VAL	96	E	-10.678653	12.423431	-13.316419	-4.620363
1JHJ	A	ARG	97	E	-10.309362	11.047013	-13.783864	-4.648042
1JHJ	A	VAL	98	E	-9.381780	10.290381	-12.563163	-4.550515
1JHJ	A	GLY	99	E	-7.239346	6.329272	-10.578415	-4.035549
1JHJ	A	ASN	100	C	-6.367652	6.049879	-9.766067	-3.897421
1JHJ	A	ASN	101	T	-6.180972	6.848863	-9.909287	-4.170487
1JHJ	A	PHE	102	T	-6.134046	7.007168	-9.911566	-4.164812
1JHJ	A	HIS	103	T	-6.076046	7.059573	-9.933707	-4.162243
1JHJ	A	ASN	104	T	-6.155156	7.227357	-9.850232	-4.182981
1JHJ	A	LEU	105	E	-6.611271	8.705832	-10.233123	-4.562233
1JHJ	A	GLN	106	E	-7.042655	8.409868	-10.284959	-4.164049
1JHJ	A	GLU	107	E	-7.281514	8.219311	-10.468668	-4.186873
1JHJ	A	ILE	108	E	-8.048027	9.846109	-11.169933	-4.257890
1JHJ	A	ARG	109	E	-8.277169	9.863595	-11.452901	-4.344443
1JHJ	A	GLN	110	E	-8.150205	9.920923	-11.085055	-4.144367
1JHJ	A	LEU	111	E	-8.607633	10.916566	-10.504916	-3.748994
1JHJ	A	GLU	112	E	-8.816276	11.066160	-10.534755	-3.779152
1JHJ	A	LEU	113	T	-8.901359	11.163687	-10.494610	-3.851658
1JHJ	A	VAL	114	T	-8.870290	11.272951	-10.704783	-3.991583
1JHJ	A	GLU	115	T	-9.763584	14.106643	-13.770888	-5.975565
1JHJ	A	PRO	116	T	-10.156441	13.856141	-13.698930	-5.702688
1JHJ	A	SER	117	E	-10.418248	13.358144	-14.074447	-5.851847
1JHJ	A	GLY	118	E	-10.359299	13.732323	-13.435606	-5.530181
1JHJ	A	TRP	119	E	-11.073852	17.004197	-10.260505	-3.688332
1JHJ	A	ILE	120	E	-9.662801	15.339028	-7.969909	-3.113160
1JHJ	A	HIS	121	E	-9.279187	15.470258	-10.159811	-4.761939
1JHJ	A	VAL	122	E	-8.219319	14.999153	-10.964488	-6.535982
1JHJ	A	PRO	123	E	-7.818198	13.706978	-11.451838	-6.465268
1JHJ	A	LEU	124	C	-6.342341	9.539442	-8.184003	-4.119017

1JHJ	A	THR	125	B	-3.180646	4.046400	-5.616389	-3.367575
1JHJ	A	ASP	126	T	-0.795237	2.394558	-4.372645	-3.707827
1JHJ	A	ASN	127	T	-0.608596	3.195616	-4.514612	-3.906104
1JHJ	A	HIS	128	T	-0.608053	3.200276	-4.518229	-3.907045
1JHJ	A	LYS	129	T	-0.608068	3.200079	-4.518052	-3.906957
1JHJ	A	LYS	130	C	-0.622233	3.140623	-4.435792	-3.871275
1JHJ	A	PRO	131	B	-1.666079	4.272621	-2.983174	-2.803800
1JHJ	A	THR	132	C	-5.059444	6.858583	-6.257208	-2.954345
1JHJ	A	ARG	133	E	-6.521513	9.384630	-7.854319	-3.643042
1JHJ	A	THR	134	E	-8.103351	11.389884	-11.613568	-5.697263
1JHJ	A	PHE	135	E	-10.902768	15.098843	-14.595754	-6.606759
1JHJ	A	MET	136	E	-12.660624	16.249414	-14.517226	-4.897363
1JHJ	A	ILE	137	E	-12.341981	16.765678	-12.559110	-4.097190
1JHJ	A	GLN	138	E	-12.229402	16.443119	-12.472726	-3.979814
1JHJ	A	ILE	139	E	-10.125397	14.203642	-8.656204	-2.870677
1JHJ	A	ALA	140	E	-10.006786	13.635063	-9.317055	-3.003429
1JHJ	A	VAL	141	E	-9.997023	13.597383	-9.430223	-3.040784
1JHJ	A	LEU	142	E	-9.994459	13.502117	-9.524401	-3.067591
1JHJ	A	ALA	143	E	-9.720414	10.509792	-11.678244	-3.567762
1JHJ	A	ASN	144	E	-8.333862	5.371448	-13.369683	-4.669002
1JHJ	A	HIS	145	T	-8.286841	5.293005	-13.485206	-4.641026
1JHJ	A	GLN	146	T	-8.189080	5.215258	-13.833186	-4.706325
1JHJ	A	ASN	147	T	-8.162239	5.246385	-13.881104	-4.693101
1JHJ	A	GLY	148	T	-8.178431	5.238513	-13.841651	-4.700928
1JHJ	A	ARG	149	C	-8.957478	5.108053	-15.313700	-4.731785
1JHJ	A	ASP	150	C	-9.141926	5.103629	-15.579644	-4.918133
1JHJ	A	THR	151	C	-9.998135	5.996352	-14.949768	-4.420736
1JHJ	A	HIS	152	E	-14.151464	9.392616	-18.697025	-4.564754
1JHJ	A	MET	153	E	-15.582230	13.925773	-18.741594	-4.925621
1JHJ	A	ARG	154	C	-16.695221	16.802293	-20.334873	-5.702444
1JHJ	A	GLN	155	E	-17.149127	17.996473	-20.675086	-5.916835
1JHJ	A	ILE	156	E	-15.210616	25.097430	-15.500549	-7.153514
1JHJ	A	LYS	157	E	-13.173218	21.160887	-12.887342	-5.736198
1JHJ	A	ILE	158	E	-9.233319	16.418223	-6.851300	-3.356219
1JHJ	A	TYR	159	E	-7.160463	12.148940	-5.552271	-2.590496
1JHJ	A	THR	160	E	-7.160463	12.148940	-5.552271	-2.590496
1JHJ	A	PRO	161	E	-7.160463	12.148940	-5.552271	-2.590496
1JHJ	A	VAL	162	C	-7.160463	12.148940	-5.552271	-2.590496
1JK3	A	GLY	106	C	-4.989832	9.131896	-6.814544	-3.565233
1JK3	A	PRO	107	C	-4.989832	9.131896	-6.814544	-3.565233
1JK3	A	VAL	108	C	-4.989832	9.131896	-6.814544	-3.565233
1JK3	A	TRP	109	C	-4.989832	9.131896	-6.814544	-3.565233
1JK3	A	ARG	110	C	-4.875737	9.284946	-6.842323	-3.713272
1JK3	A	LYS	111	C	-5.405196	9.814288	-7.509005	-4.082228
1JK3	A	HIS	112	C	-5.479272	9.744838	-7.301709	-4.010833
1JK3	A	TYR	113	E	-5.499954	9.676051	-7.192384	-3.962467
1JK3	A	ILE	114	E	-5.510742	9.603107	-7.120261	-3.918501
1JK3	A	THR	115	E	-8.070708	11.187555	-10.715730	-4.768828
1JK3	A	TYR	116	E	-10.457646	15.863701	-11.649597	-5.008756
1JK3	A	ARG	117	E	-12.196968	16.167735	-15.211327	-5.446171
1JK3	A	ILE	118	E	-10.348005	14.653226	-13.037505	-5.661805
1JK3	A	ASN	119	C	-9.672784	12.565977	-13.452216	-5.524361
1JK3	A	ASN	120	C	-9.638845	12.478802	-13.580222	-5.523374
1JK3	A	TYR	121	C	-9.489353	12.894360	-13.463155	-5.548616
1JK3	A	THR	122	T	-8.213679	9.734761	-12.564894	-5.252035
1JK3	A	PRO	123	T	-8.045279	9.569466	-12.547088	-5.120088
1JK3	A	ASP	124	T	-7.932487	9.476967	-12.578634	-5.092008
1JK3	A	MET	125	T	-6.766225	9.289523	-10.572129	-4.937256
1JK3	A	ASN	126	C	-6.254675	9.652738	-9.546001	-4.590175
1JK3	A	ARG	127	H	-6.272329	9.668649	-9.458387	-4.569495
1JK3	A	GLU	128	H	-6.278574	9.677348	-9.427766	-4.568691
1JK3	A	ASP	129	H	-6.286032	9.681166	-9.384255	-4.562694
1JK3	A	VAL	130	H	-6.571561	9.945406	-8.849393	-4.345899
1JK3	A	ASP	131	H	-9.226135	11.801370	-12.840250	-4.944860
1JK3	A	TYR	132	H	-9.554192	12.335813	-13.136854	-5.165271
1JK3	A	ALA	133	H	-10.298251	14.065771	-13.059504	-4.722654
1JK3	A	ILE	134	H	-10.497192	14.489184	-12.746300	-4.551199
1JK3	A	ARG	135	H	-10.748811	13.527678	-13.572533	-4.539144
1JK3	A	LYS	136	H	-10.835577	13.585731	-13.535894	-4.540427
1JK3	A	ALA	137	H	-11.302291	14.475724	-13.704721	-4.610508
1JK3	A	PHE	138	H	-11.727693	14.915779	-14.184785	-4.882423
1JK3	A	GLN	139	H	-11.789356	14.269841	-14.532578	-4.917324
1JK3	A	VAL	140	H	-11.502854	14.206011	-13.660170	-4.613795
1JK3	A	TRP	141	H	-10.404876	14.267646	-12.597823	-4.981565
1JK3	A	SER	142	H	-8.726692	9.831670	-11.957640	-4.452709
1JK3	A	ASN	143	H	-7.936930	11.604144	-10.225638	-4.385758
1JK3	A	VAL	144	C	-7.893505	11.720643	-10.274716	-4.391152
1JK3	A	THR	145	C	-7.849475	12.101605	-10.215365	-4.429610
1JK3	A	PRO	146	C	-7.847264	12.129093	-10.201047	-4.424579
1JK3	A	LEU	147	C	-7.987776	12.838298	-9.744735	-4.428942
1JK3	A	LYS	148	E	-8.903440	15.269327	-10.520903	-4.781661

1JK3	A	PHE	149	E	-8.762108	15.240065	-10.649585	-5.069965
1JK3	A	SER	150	E	-6.473997	7.856559	-10.183050	-4.619555
1JK3	A	LYS	151	E	-4.636156	6.379599	-9.090087	-4.942658
1JK3	A	ILE	152	C	-4.328112	5.291522	-9.530315	-4.790409
1JK3	A	ASN	153	C	-4.016804	4.939948	-9.469347	-4.694748
1JK3	A	THR	154	C	-4.008132	4.938457	-9.502197	-4.693636
1JK3	A	GLY	155	C	-4.016597	4.898071	-9.494524	-4.694716
1JK3	A	MET	156	C	-4.259296	4.180294	-9.718327	-4.558065
1JK3	A	ALA	157	T	-4.524671	4.454453	-9.458729	-4.552682
1JK3	A	ASP	158	T	-6.460404	5.201403	-11.724966	-4.616941
1JK3	A	ILE	159	E	-7.958022	8.308360	-12.005488	-4.652220
1JK3	A	LEU	160	E	-9.718096	11.567047	-12.506962	-4.476001
1JK3	A	VAL	161	E	-11.064905	15.451072	-12.717814	-4.316871
1JK3	A	VAL	162	E	-11.246503	15.159117	-13.178451	-4.276327
1JK3	A	PHE	163	E	-10.131654	12.182916	-12.675327	-4.377046
1JK3	A	ALA	164	E	-8.688616	8.046525	-13.227645	-4.555719
1JK3	A	ARG	165	T	-6.107616	5.793504	-10.684374	-4.531699
1JK3	A	GLY	166	T	-5.406133	5.351098	-10.676824	-4.713459
1JK3	A	ALA	167	T	-4.371712	5.135588	-9.308266	-4.636677
1JK3	A	HIS	168	T	-4.236462	5.370398	-9.383099	-4.693759
1JK3	A	GLY	169	C	-3.860967	5.418016	-8.908378	-4.577631
1JK3	A	ASP	170	T	-3.873201	5.422301	-8.869164	-4.578476
1JK3	A	PHE	171	T	-3.904742	5.439408	-8.769293	-4.565965
1JK3	A	HIS	172	T	-4.183986	5.645561	-8.611957	-4.529145
1JK3	A	ALA	173	T	-4.306458	5.498487	-8.368215	-4.440122
1JK3	A	PHE	174	C	-7.353260	11.419742	-10.230289	-4.661071
1JK3	A	ASP	175	C	-5.518971	1.585217	-12.624634	-4.899624
1JK3	A	GLY	176	C	-5.284293	1.931135	-12.421220	-4.777070
1JK3	A	LYS	177	C	-5.203748	2.401237	-12.235460	-4.732964
1JK3	A	GLY	178	T	-4.941208	4.418791	-10.873104	-4.579138
1JK3	A	GLY	179	T	-4.935750	4.484408	-10.856318	-4.576749
1JK3	A	ILE	180	T	-5.207214	6.259644	-9.816899	-4.386086
1JK3	A	LEU	181	T	-5.411676	7.691159	-8.924251	-4.328072
1JK3	A	ALA	182	E	-5.529515	8.148309	-8.474814	-4.305367
1JK3	A	HIS	183	E	-7.547450	11.379437	-9.766162	-4.398548
1JK3	A	ALA	184	E	-7.770482	11.898226	-9.747938	-4.238897
1JK3	A	PHE	185	E	-7.693348	11.351030	-10.013837	-4.216403
1JK3	A	GLY	186	C	-5.102984	5.492548	-8.894781	-4.021305
1JK3	A	PRO	187	C	-4.719092	5.438204	-8.677408	-3.828947
1JK3	A	GLY	188	C	-3.890912	3.879893	-8.750849	-4.066052
1JK3	A	SER	189	T	-3.809134	3.955398	-8.830437	-4.072123
1JK3	A	GLY	190	T	-3.806967	3.958874	-8.843418	-4.074317
1JK3	A	ILE	191	T	-3.876637	3.775938	-8.836427	-4.079851
1JK3	A	GLY	192	T	-3.949285	3.565102	-8.885479	-4.138820
1JK3	A	GLY	193	T	-5.001286	4.537665	-9.436728	-4.118288
1JK3	A	ASP	194	E	-7.061114	5.415829	-12.289681	-4.605915
1JK3	A	ALA	195	E	-8.937578	7.974620	-13.148680	-4.404999
1JK3	A	HIS	196	E	-11.268812	10.053459	-15.847266	-4.985061
1JK3	A	PHE	197	E	-12.963733	15.269612	-15.195882	-4.983273
1JK3	A	ASP	198	E	-14.954961	16.073158	-18.565299	-5.436903
1JK3	A	GLU	199	T	-15.548063	15.597775	-20.457342	-6.012499
1JK3	A	ASP	200	T	-15.554170	15.139983	-21.293436	-6.439204
1JK3	A	GLU	201	T	-14.470623	16.511703	-18.409125	-6.189390
1JK3	A	PHE	202	C	-12.052530	14.440877	-14.729126	-5.241431
1JK3	A	TRP	203	E	-10.994688	13.605093	-13.912823	-5.107455
1JK3	A	THR	204	E	-6.574519	7.051679	-10.797355	-4.712019
1JK3	A	THR	205	C	-4.837064	5.913637	-9.444104	-4.813960
1JK3	A	HIS	206	C	-4.726293	6.039284	-9.582905	-4.833604
1JK3	A	SER	207	C	-4.723002	6.048463	-9.601016	-4.836442
1JK3	A	GLY	208	C	-4.722903	6.049170	-9.601766	-4.836557
1JK3	A	GLY	209	C	-4.749521	6.003113	-9.546629	-4.842145
1JK3	A	THR	210	E	-5.754962	6.684724	-10.338896	-4.940188
1JK3	A	ASN	211	E	-7.781401	7.797917	-12.887240	-5.346909
1JK3	A	LEU	212	H	-9.792369	10.841638	-14.032259	-5.465794
1JK3	A	PHE	213	H	-11.469511	18.327943	-11.941890	-4.626478
1JK3	A	LEU	214	H	-11.146265	16.426813	-12.103205	-4.326240
1JK3	A	THR	215	H	-10.433987	13.839498	-12.095803	-4.090287
1JK3	A	ALA	216	H	-10.321544	13.956029	-12.007496	-4.022858
1JK3	A	VAL	217	H	-10.218087	13.761683	-12.129592	-4.036373
1JK3	A	HIS	218	H	-10.236315	13.419568	-12.306967	-4.044472
1JK3	A	ALA	219	H	-10.276658	13.291861	-12.371271	-4.053822
1JK3	A	ILE	220	H	-10.684253	13.936894	-12.829048	-4.184188
1JK3	A	GLY	221	H	-10.773141	12.978765	-13.932195	-4.549825
1JK3	A	HIS	222	H	-11.120678	12.457803	-15.123440	-4.881266
1JK3	A	SER	223	H	-9.564909	11.848468	-12.578249	-4.888464
1JK3	A	LEU	224	H	-7.606686	12.180616	-9.617269	-4.767148
1JK3	A	GLY	225	C	-7.092426	10.419513	-10.554125	-4.942996
1JK3	A	LEU	226	C	-7.011029	10.261351	-10.690631	-4.896878
1JK3	A	GLY	227	C	-6.564167	8.740372	-10.945386	-4.833647
1JK3	A	HIS	228	C	-6.458532	8.738653	-10.902842	-4.768044
1JK3	A	SER	229	C	-6.388446	7.842436	-11.156686	-4.650828

1JK3	A	SER	230	C	-5.596828	7.961577	-8.915808	-4.144313
1JK3	A	ASP	231	T	-5.571794	8.027266	-8.929832	-4.140260
1JK3	A	PRO	232	T	-5.633278	8.099867	-8.685610	-4.070409
1JK3	A	LYS	233	T	-5.658569	8.068433	-8.596190	-4.054045
1JK3	A	ALA	234	T	-5.700628	8.166359	-8.400839	-4.038415
1JK3	A	VAL	235	T	-7.306879	9.505887	-9.806455	-4.168095
1JK3	A	MET	236	T	-9.781568	12.085710	-12.680554	-4.619923
1JK3	A	PHE	237	T	-9.366260	13.208991	-11.093633	-4.420455
1JK3	A	PRO	238	C	-8.863939	14.477389	-10.699883	-4.808085
1JK3	A	THR	239	C	-8.726581	14.554946	-10.748650	-4.830773
1JK3	A	TYR	240	C	-8.725220	14.609640	-10.771875	-4.863224
1JK3	A	LYS	241	C	-8.296017	14.218032	-10.818935	-5.042535
1JK3	A	TYR	242	C	-6.214583	11.444187	-8.081501	-4.671207
1JK3	A	VAL	243	C	-4.611279	6.980032	-7.580672	-3.997250
1JK3	A	ASP	244	T	-4.538224	7.439804	-7.541717	-4.033729
1JK3	A	ILE	245	T	-4.429387	8.049653	-7.275080	-3.974920
1JK3	A	ASN	246	T	-4.346791	8.819752	-6.956076	-3.969901
1JK3	A	THR	247	T	-4.371547	8.713436	-6.911315	-3.939933
1JK3	A	PHE	248	T	-4.948618	12.099138	-5.864189	-3.922178
1JK3	A	ARG	249	C	-5.104512	12.443999	-5.453736	-3.805380
1JK3	A	LEU	250	C	-5.544422	13.957162	-4.910545	-3.943076
1JK3	A	SER	251	C	-8.079655	13.868276	-9.518872	-4.282573
1JK3	A	ALA	252	H	-8.404615	13.095428	-10.175795	-4.339890
1JK3	A	ASP	253	H	-9.124947	9.289218	-12.907290	-4.464622
1JK3	A	ASP	254	H	-10.531389	8.332354	-16.304347	-4.718828
1JK3	A	ILE	255	H	-10.426930	8.634306	-15.817765	-4.537186
1JK3	A	ARG	256	H	-10.499719	8.669729	-15.654246	-4.469552
1JK3	A	GLY	257	H	-10.677078	11.227530	-15.205689	-4.963687
1JK3	A	ILE	258	H	-10.566620	14.452863	-13.747846	-5.293856
1JK3	A	GLN	259	H	-9.895025	13.603996	-12.677932	-4.979926
1JK3	A	SER	260	H	-8.255999	11.666255	-9.477877	-3.744505
1JK3	A	LEU	261	H	-8.255999	11.666255	-9.477877	-3.744505
1JK3	A	TYR	262	C	-8.255999	11.666255	-9.477877	-3.744505
1JK3	A	GLY	263	C	-8.255999	11.666255	-9.477877	-3.744505
1JSF	A	LYS	1	C	-8.805779	8.918315	-11.890694	-4.074837
1JSF	A	VAL	2	B	-8.805779	8.918315	-11.890694	-4.074837
1JSF	A	PHE	3	C	-8.805779	8.918315	-11.890694	-4.074837
1JSF	A	GLU	4	C	-8.805779	8.918315	-11.890694	-4.074837
1JSF	A	ARG	5	H	-12.222708	11.182183	-16.799053	-5.201198
1JSF	A	CYS	6	H	-12.613424	11.356600	-17.208129	-5.055362
1JSF	A	GLU	7	H	-11.922792	12.911073	-15.433625	-4.907682
1JSF	A	LEU	8	H	-11.646726	13.938922	-14.601421	-4.736082
1JSF	A	ALA	9	H	-11.578516	14.052814	-14.627822	-4.739517
1JSF	A	ARG	10	H	-10.247536	12.466608	-12.408917	-4.211478
1JSF	A	THR	11	H	-8.711605	13.090424	-9.850705	-4.128067
1JSF	A	LEU	12	H	-8.075957	11.706857	-10.280898	-4.233595
1JSF	A	LYS	13	H	-7.769938	11.078618	-10.711680	-4.411633
1JSF	A	ARG	14	H	-7.582281	10.866221	-10.872520	-4.476195
1JSF	A	LEU	15	H	-7.522900	10.757498	-11.082521	-4.566039
1JSF	A	GLY	16	C	-7.584857	10.437288	-11.367981	-4.664103
1JSF	A	MET	17	T	-7.785365	10.215831	-11.717410	-4.816268
1JSF	A	ASP	18	T	-7.526151	9.390853	-12.178391	-5.206531
1JSF	A	GLY	19	T	-6.983584	9.497809	-11.071552	-5.050356
1JSF	A	TYR	20	G	-7.005783	9.485508	-11.000933	-5.037953
1JSF	A	ARG	21	G	-7.005915	9.482983	-10.982201	-5.022765
1JSF	A	GLY	22	G	-6.992201	9.513829	-10.992012	-5.001340
1JSF	A	ILE	23	C	-7.164522	9.734378	-10.550686	-4.872265
1JSF	A	SER	24	C	-8.917934	10.873113	-12.017104	-4.289317
1JSF	A	LEU	25	H	-9.005075	10.879789	-11.779807	-4.201761
1JSF	A	ALA	26	H	-9.218095	10.883516	-11.483937	-4.106316
1JSF	A	ASN	27	H	-11.892842	13.561875	-14.175133	-4.418420
1JSF	A	TRP	28	H	-13.075095	17.775502	-14.955036	-5.196209
1JSF	A	MET	29	H	-12.429008	16.170841	-14.883322	-5.454981
1JSF	A	CYS	30	H	-11.931073	15.321175	-14.902812	-5.423054
1JSF	A	LEU	31	H	-11.719275	15.764770	-14.652923	-5.427819
1JSF	A	ALA	32	H	-11.612899	15.511346	-14.924421	-5.490341
1JSF	A	LYS	33	H	-10.256057	12.452090	-14.838223	-6.098195
1JSF	A	TRP	34	H	-10.267220	12.388472	-14.850114	-6.114963
1JSF	A	GLU	35	H	-10.273876	12.335004	-14.896358	-6.143349
1JSF	A	SER	36	H	-10.265906	12.245464	-14.975057	-6.151552
1JSF	A	GLY	37	T	-10.257914	12.211011	-14.983373	-6.124940
1JSF	A	TYR	38	T	-11.511303	13.130378	-16.166252	-5.553743
1JSF	A	ASN	39	B	-8.018320	9.770417	-10.706239	-4.291749
1JSF	A	THR	40	T	-7.777038	9.224184	-11.208542	-4.327636
1JSF	A	ARG	41	T	-7.423359	9.350164	-11.081385	-4.400182
1JSF	A	ALA	42	T	-7.416613	9.343545	-11.127052	-4.410352
1JSF	A	THR	43	E	-7.307427	9.057544	-11.501531	-4.534239
1JSF	A	ASN	44	E	-7.122229	6.921858	-12.773305	-4.904241
1JSF	A	TYR	45	E	-7.046672	6.238815	-13.271638	-5.046804
1JSF	A	ASN	46	E	-6.815244	4.315588	-13.831021	-4.986387
1JSF	A	ALA	47	T	-6.614314	4.526464	-13.558863	-4.917866

1JSF	A	GLY	48	T	-6.642143	4.373155	-13.583364	-4.908559
1JSF	A	ASP	49	T	-6.787173	4.199275	-13.539402	-4.832864
1JSF	A	ARG	50	T	-6.876712	4.178317	-13.331385	-4.751076
1JSF	A	SER	51	E	-7.333561	5.133379	-12.964711	-4.767587
1JSF	A	THR	52	E	-9.603598	7.211366	-15.548683	-5.397899
1JSF	A	ASP	53	E	-12.723043	13.470340	-18.186209	-5.988736
1JSF	A	TYR	54	E	-12.808418	14.896840	-17.270994	-5.881373
1JSF	A	GLY	55	T	-12.560840	16.372604	-15.976021	-5.701034
1JSF	A	ILE	56	T	-12.703114	17.666887	-15.148880	-5.571263
1JSF	A	PHE	57	T	-12.916982	19.009316	-14.370201	-5.507766
1JSF	A	GLN	58	T	-13.052977	18.941344	-14.234066	-5.481688
1JSF	A	ILE	59	E	-13.101454	18.543266	-14.274864	-5.421982
1JSF	A	ASN	60	E	-14.699491	15.769313	-19.063314	-5.860184
1JSF	A	SER	61	T	-14.929106	13.425352	-20.646658	-5.896434
1JSF	A	ARG	62	T	-14.885552	13.391890	-20.660570	-5.885154
1JSF	A	TYR	63	T	-14.386884	14.167470	-19.918783	-6.127651
1JSF	A	TRP	64	T	-11.722063	11.034158	-17.154115	-6.078002
1JSF	A	CYS	65	C	-8.849816	5.090034	-16.205538	-5.770329
1JSF	A	ASN	66	B	-6.802894	6.417911	-12.741880	-5.642151
1JSF	A	ASP	67	T	-6.616633	6.436941	-12.792380	-5.548900
1JSF	A	GLY	68	T	-5.940634	5.687425	-11.997657	-5.211723
1JSF	A	LYS	69	T	-5.771571	6.014775	-11.717508	-5.090276
1JSF	A	THR	70	T	-5.201719	6.180720	-10.042215	-4.479921
1JSF	A	PRO	71	T	-5.220526	6.159170	-9.920009	-4.393852
1JSF	A	GLY	72	T	-5.223217	6.158997	-9.880621	-4.367907
1JSF	A	ALA	73	T	-5.356968	6.369479	-9.440568	-4.193652
1JSF	A	VAL	74	C	-5.425192	6.269681	-9.297368	-4.123726
1JSF	A	ASN	75	T	-6.791202	6.244782	-11.871473	-4.294223
1JSF	A	ALA	76	T	-7.137974	6.451720	-12.294598	-4.365499
1JSF	A	CYS	77	T	-7.518392	6.310379	-13.138395	-4.535728
1JSF	A	HIS	78	T	-7.531267	6.255752	-13.135374	-4.531347
1JSF	A	LEU	79	C	-8.010764	7.075097	-13.619475	-4.692908
1JSF	A	SER	80	B	-8.186297	6.860024	-13.738727	-4.650245
1JSF	A	CYS	81	G	-8.599821	6.737998	-14.387499	-4.758961
1JSF	A	SER	82	G	-9.342305	8.454269	-14.186719	-4.300878
1JSF	A	ALA	83	G	-9.518062	9.290667	-13.845104	-4.320575
1JSF	A	LEU	84	G	-9.657970	10.458971	-13.750163	-4.528749
1JSF	A	LEU	85	C	-8.374580	9.782786	-11.998698	-4.750223
1JSF	A	GLN	86	T	-7.889886	9.024768	-11.981815	-4.655376
1JSF	A	ASP	87	T	-7.140125	9.442667	-10.778758	-4.613601
1JSF	A	ASN	88	T	-6.997193	9.684938	-10.614155	-4.526556
1JSF	A	ILE	89	H	-6.987713	9.757521	-10.587147	-4.513215
1JSF	A	ALA	90	H	-7.031945	9.765130	-10.487867	-4.476368
1JSF	A	ASP	91	H	-7.113518	9.963486	-10.273295	-4.459686
1JSF	A	ALA	92	H	-7.789070	10.731029	-10.245909	-4.153911
1JSF	A	VAL	93	H	-8.778737	11.395229	-11.355377	-3.930642
1JSF	A	ALA	94	H	-9.086188	9.993645	-12.332921	-3.947239
1JSF	A	CYS	95	H	-9.609726	10.193946	-13.133061	-4.186674
1JSF	A	ALA	96	H	-9.946197	10.175666	-13.092757	-4.076974
1JSF	A	LYS	97	H	-10.920354	10.169345	-14.703410	-4.598651
1JSF	A	ARG	98	H	-12.714346	13.049437	-16.346473	-4.659931
1JSF	A	VAL	99	H	-10.740322	10.339343	-14.046802	-4.309322
1JSF	A	VAL	100	H	-10.436142	9.193673	-15.022967	-4.546777
1JSF	A	ARG	101	H	-9.589153	6.087368	-16.243623	-5.094036
1JSF	A	ASP	102	T	-8.300087	7.433188	-13.338297	-4.837073
1JSF	A	PRO	103	T	-8.090206	8.100962	-12.970559	-4.756179
1JSF	A	GLN	104	T	-8.065397	8.219809	-12.960419	-4.758482
1JSF	A	GLY	105	G	-8.069089	8.233937	-12.934880	-4.757523
1JSF	A	ILE	106	G	-8.104264	8.433761	-12.706344	-4.725838
1JSF	A	ARG	107	G	-8.703519	9.891558	-12.256265	-4.588506
1JSF	A	ALA	108	G	-9.788214	11.060736	-13.043503	-4.709049
1JSF	A	TRP	109	C	-11.508540	14.835038	-14.099466	-4.740256
1JSF	A	VAL	110	H	-11.155347	12.003057	-15.106687	-4.903126
1JSF	A	ALA	111	H	-11.254247	11.436862	-15.395728	-4.962406
1JSF	A	TRP	112	H	-11.343792	11.285984	-15.390374	-5.014957
1JSF	A	ARG	113	H	-11.367795	10.910945	-15.606654	-5.065981
1JSF	A	ASN	114	H	-9.969346	8.261187	-16.120166	-5.730613
1JSF	A	ARG	115	H	-9.293154	8.058659	-14.994720	-5.291071
1JSF	A	CYS	116	H	-8.187420	5.346572	-14.900443	-5.269591
1JSF	A	GLN	117	T	-8.006520	5.482173	-14.779735	-5.148697
1JSF	A	ASN	118	T	-7.273117	5.766398	-12.496471	-4.278583
1JSF	A	ARG	119	T	-7.212522	5.900997	-12.438950	-4.229208
1JSF	A	ASP	120	C	-7.215720	5.935468	-12.399951	-4.219105
1JSF	A	VAL	121	C	-7.321674	6.150369	-11.913434	-4.013986
1JSF	A	ARG	122	G	-7.372582	6.179628	-11.687342	-3.942802
1JSF	A	GLN	123	G	-8.456144	7.753765	-12.349180	-4.056606
1JSF	A	TYR	124	G	-9.512335	11.706244	-13.501201	-5.342740
1JSF	A	VAL	125	G	-5.764929	7.898945	-10.884202	-5.927986
1JSF	A	GLN	126	T	-5.014922	6.542350	-10.503438	-5.476490
1JSF	A	GLY	127	T	-3.193766	4.971188	-7.060281	-4.191962
1JSF	A	CYS	128	T	-3.193766	4.971188	-7.060281	-4.191962

1JSF	A	GLY	129	C	-3.193766	4.971188	-7.060281	-4.191962
1JSF	A	VAL	130	C	-3.193766	4.971188	-7.060281	-4.191962
1JSG	A	CYS	4	C	-1.595062	0.255659	-5.743578	-2.957329
1JSG	A	PRO	5	C	-1.595062	0.255659	-5.743578	-2.957329
1JSG	A	THR	6	C	-1.595062	0.255659	-5.743578	-2.957329
1JSG	A	LEU	7	C	-1.595062	0.255659	-5.743578	-2.957329
1JSG	A	GLY	8	E	-1.702885	0.522831	-5.682716	-3.136396
1JSG	A	GLU	9	E	-3.050500	2.570676	-8.735756	-4.482838
1JSG	A	ALA	10	E	-3.236271	3.516360	-8.508575	-4.572651
1JSG	A	VAL	11	C	-3.937233	5.035874	-7.881931	-3.785244
1JSG	A	THR	12	C	-3.990097	5.072985	-7.603041	-3.627103
1JSG	A	ASP	13	C	-4.281009	5.334828	-7.568445	-3.635514
1JSG	A	HIS	14	C	-4.611331	5.931562	-7.016752	-3.498736
1JSG	A	PRO	15	C	-6.247843	8.481654	-8.128819	-3.657107
1JSG	A	ASP	16	C	-7.487565	7.538972	-10.035369	-3.838207
1JSG	A	ARG	17	E	-11.011567	11.563842	-13.967014	-4.504940
1JSG	A	LEU	18	E	-11.828448	15.375940	-13.516088	-4.498733
1JSG	A	TRP	19	E	-12.023234	16.234484	-13.578073	-4.696326
1JSG	A	ALA	20	E	-11.527846	21.219854	-17.136541	-10.037930
1JSG	A	TRP	21	E	-10.569274	20.334414	-13.221291	-7.772050
1JSG	A	GLU	22	E	-10.510228	20.029459	-13.084699	-7.484268
1JSG	A	LYS	23	T	-10.510375	20.025068	-13.077745	-7.479667
1JSG	A	PHE	24	T	-10.512879	20.025420	-13.059798	-7.477771
1JSG	A	VAL	25	E	-10.596283	19.597527	-12.255702	-6.801053
1JSG	A	TYR	26	E	-11.808330	17.395959	-11.916566	-4.707145
1JSG	A	LEU	27	E	-10.514533	9.427967	-14.182260	-4.775172
1JSG	A	ASP	28	E	-8.661968	6.693047	-13.124141	-4.725793
1JSG	A	GLU	29	T	-8.214706	6.840933	-12.854830	-4.616704
1JSG	A	LYS	30	T	-8.210257	6.878687	-12.858056	-4.616295
1JSG	A	GLN	31	T	-8.209027	6.897191	-12.856899	-4.616074
1JSG	A	HIS	32	E	-8.220949	6.850165	-12.828895	-4.612478
1JSG	A	ALA	33	E	-8.578481	7.104672	-12.618733	-4.517617
1JSG	A	TRP	34	E	-10.331576	15.317804	-10.691886	-4.079109
1JSG	A	LEU	35	E	-6.917974	13.843595	-5.230118	-3.230489
1JSG	A	PRO	36	E	-6.268231	13.038479	-5.872894	-3.595158
1JSG	A	LEU	37	E	-5.545337	11.460733	-5.663375	-3.496358
1JSG	A	THR	38	E	-5.515934	11.381381	-5.796558	-3.509771
1JSG	A	ILE	39	E	-5.304536	10.817612	-6.292610	-3.694190
1JSG	A	GLU	40	E	-4.736157	7.814663	-6.902894	-3.660158
1JSG	A	ILE	41	E	-3.729062	6.462933	-5.701026	-3.361252
1JSG	A	LYS	42	E	-3.738136	6.308923	-5.766505	-3.366976
1JSG	A	ASP	43	T	-3.739219	6.302499	-5.762388	-3.366280
1JSG	A	ARG	44	T	-3.752067	6.231866	-5.724986	-3.349430
1JSG	A	LEU	45	T	-3.829353	6.225883	-5.517095	-3.309999
1JSG	A	GLN	46	E	-6.099409	6.121103	-9.131323	-3.863491
1JSG	A	LEU	47	E	-8.140292	9.931222	-9.726584	-3.908393
1JSG	A	ARG	48	E	-11.282971	17.359848	-15.216255	-7.867961
1JSG	A	VAL	49	E	-13.229062	18.476979	-17.062438	-7.822391
1JSG	A	LEU	50	E	-14.925956	20.299195	-16.715488	-5.955169
1JSG	A	LEU	51	E	-11.760928	16.525486	-15.086151	-7.000268
1JSG	A	ARG	52	E	-9.527638	12.445777	-13.586205	-6.304362
1JSG	A	ARG	53	E	-5.744915	5.889750	-8.351325	-3.673103
1JSG	A	GLU	54	C	-3.743131	5.568462	-5.866840	-3.452465
1JSG	A	ASP	55	C	-1.749672	3.825538	-3.732134	-3.121662
1JSG	A	VAL	56	C	-0.985485	5.011450	-2.450124	-2.901484
1JSG	A	VAL	57	C	-0.770957	5.285214	-2.624204	-3.004305
1JSG	A	LEU	58	C	-0.769894	5.292763	-2.630169	-3.006188
1JSG	A	GLY	59	C	-0.774379	5.275148	-2.602536	-2.994418
1JSG	A	ARG	60	C	-0.959259	5.183591	-1.972904	-2.622433
1JSG	A	PRO	61	C	-1.677342	4.280486	-2.293379	-2.296760
1JSG	A	MET	62	C	-3.987593	7.163597	-7.406068	-4.085456
1JSG	A	THR	63	C	-4.156970	7.288455	-8.174883	-4.505880
1JSG	A	PRO	64	H	-4.387258	8.670607	-8.785733	-5.140843
1JSG	A	THR	65	H	-4.369825	8.351818	-8.805308	-5.065618
1JSG	A	GLN	66	H	-4.422084	8.237117	-8.826603	-5.060201
1JSG	A	ILE	67	H	-4.537368	8.540612	-8.685734	-4.991636
1JSG	A	GLY	68	C	-4.418299	8.450307	-8.110453	-4.707538
1JSG	A	PRO	69	C	-4.621741	8.344858	-7.950378	-4.512929
1JSG	A	SER	70	C	-4.899316	8.182299	-6.750988	-3.623000
1JSG	A	LEU	71	C	-4.921228	8.093315	-6.547174	-3.503650
1JSG	A	LEU	72	C	-5.092202	8.248774	-6.143466	-3.417728
1JSG	A	PRO	73	T	-6.653407	10.954497	-6.756652	-3.281918
1JSG	A	ILE	74	T	-7.863964	13.522323	-7.054289	-3.477871
1JSG	A	MET	75	E	-9.778562	16.159624	-9.067772	-4.195051
1JSG	A	TRP	76	E	-11.824214	17.414137	-12.217233	-4.700506
1JSG	A	GLN	77	E	-9.619016	9.033819	-12.791024	-4.413257
1JSG	A	LEU	78	E	-6.369868	6.718439	-8.927482	-3.866340
1JSG	A	TYR	79	T	-6.251507	6.808758	-9.189308	-3.928921
1JSG	A	PRO	80	T	-6.250887	6.811721	-9.193448	-3.929317
1JSG	A	ASP	81	T	-6.250923	6.811122	-9.193261	-3.929268
1JSG	A	GLY	82	T	-6.252900	6.804215	-9.181213	-3.927672

1JSG	A	ARG	83	C	-7.260547	7.231045	-10.389016	-4.212333
1JSG	A	TYR	84	E	-10.316211	9.649454	-13.149840	-4.308256
1JSG	A	ARG	85	E	-11.599157	5.876854	-16.707512	-4.229694
1JSG	A	SER	86	E	-9.903113	5.085395	-15.518657	-4.467720
1JSG	A	SER	87	T	-9.881026	5.207578	-15.537733	-4.469924
1JSG	A	ASP	88	T	-9.880827	5.210651	-15.538095	-4.470005
1JSG	A	SER	89	T	-9.880903	5.209813	-15.537617	-4.469934
1JSG	A	SER	90	C	-9.914305	5.172518	-15.470313	-4.484048
1JSG	A	PHE	91	E	-11.834484	8.498566	-16.043764	-4.530009
1JSG	A	TRP	92	E	-13.880902	17.717877	-14.353609	-4.528930
1JSG	A	ARG	93	E	-12.290182	15.227007	-12.714822	-4.250077
1JSG	A	LEU	94	E	-10.569473	15.662096	-10.213901	-4.105064
1JSG	A	VAL	95	E	-10.463110	15.614959	-10.548499	-4.188857
1JSG	A	TYR	96	E	-10.445946	15.617826	-10.650729	-4.212105
1JSG	A	HIS	97	E	-10.251999	14.420039	-12.540322	-5.054807
1JSG	A	ILE	98	E	-7.211554	7.324011	-11.491894	-4.793102
1JSG	A	LYS	99	E	-5.178738	5.266789	-11.045185	-5.619189
1JSG	A	ILE	100	E	-5.038347	5.626223	-10.665003	-5.372006
1JSG	A	ASP	101	T	-5.037817	5.627068	-10.668500	-5.371812
1JSG	A	GLY	102	T	-5.037831	5.626918	-10.668312	-5.371733
1JSG	A	VAL	103	E	-5.053057	5.583746	-10.646922	-5.386783
1JSG	A	GLU	104	E	-5.957841	6.968272	-9.263034	-4.448841
1JSG	A	ASP	105	E	-9.182567	6.685001	-14.597017	-5.156069
1JSG	A	MET	106	E	-11.449034	10.435043	-15.603297	-5.326530
1JSG	A	LEU	107	E	-13.787004	15.617789	-16.876764	-5.338302
1JSG	A	LEU	108	E	-13.537243	15.038359	-17.243801	-5.865276
1JSG	A	GLU	109	E	-11.337883	9.076889	-16.398355	-5.509246
1JSG	A	LEU	110	E	-7.390514	6.938068	-10.115853	-3.766565
1JSG	A	LEU	111	E	-4.854360	4.566958	-7.289219	-3.000683
1JSG	A	PRO	112	C	-4.854360	4.566958	-7.289219	-3.000683
1JSG	A	ASP	113	C	-4.854360	4.566958	-7.289219	-3.000683
1JSG	A	ASP	114	C	-4.854360	4.566958	-7.289219	-3.000683
1JWF	A	PRO	7	C	-7.013708	5.888834	-11.285083	-3.977380
1JWF	A	GLU	8	C	-7.013708	5.888834	-11.285083	-3.977380
1JWF	A	THR	9	C	-7.013708	5.888834	-11.285083	-3.977380
1JWF	A	LEU	10	H	-7.013708	5.888834	-11.285083	-3.977380
1JWF	A	GLU	11	H	-8.503370	7.637285	-13.688654	-5.044675
1JWF	A	ALA	12	H	-9.821657	8.186962	-15.758301	-5.718881
1JWF	A	ARG	13	H	-12.412833	11.277874	-18.887709	-6.323952
1JWF	A	ILE	14	H	-12.165439	11.959524	-16.722205	-5.266327
1JWF	A	ASN	15	H	-11.734137	10.358047	-17.264564	-5.313103
1JWF	A	ARG	16	H	-11.543243	10.533113	-16.967084	-5.246934
1JWF	A	ALA	17	H	-8.510661	8.892122	-12.036628	-4.448894
1JWF	A	THR	18	H	-7.944395	7.770549	-12.800112	-4.768719
1JWF	A	ASN	19	T	-5.484843	4.024182	-10.524083	-4.281021
1JWF	A	PRO	20	T	-4.695991	3.987915	-9.800331	-4.190971
1JWF	A	LEU	21	T	-4.368057	4.575252	-9.435152	-4.221874
1JWF	A	ASN	22	T	-4.361496	4.591849	-9.461614	-4.228416
1JWF	A	LYS	23	T	-4.308332	4.950533	-9.395748	-4.262058
1JWF	A	GLU	24	T	-4.389520	5.134830	-9.235955	-4.263433
1JWF	A	LEU	25	T	-4.731399	6.042870	-8.997774	-4.344361
1JWF	A	ASP	26	C	-5.639970	8.500071	-9.227523	-4.646712
1JWF	A	TRP	27	H	-5.704049	8.755180	-8.929964	-4.631233
1JWF	A	ALA	28	H	-7.177472	8.943540	-10.963930	-4.760727
1JWF	A	SER	29	H	-8.638046	10.134447	-13.241529	-5.119252
1JWF	A	ILE	30	H	-9.227690	10.777794	-13.901770	-5.207916
1JWF	A	ASN	31	H	-9.438793	10.480760	-14.375083	-5.345110
1JWF	A	GLY	32	H	-9.644104	10.114203	-14.718039	-5.477250
1JWF	A	PHE	33	H	-10.835333	11.364237	-15.998283	-5.687129
1JWF	A	CYS	34	H	-10.870821	11.044401	-16.104293	-5.692315
1JWF	A	GLU	35	H	-10.844161	9.901350	-16.641242	-5.650429
1JWF	A	GLN	36	H	-11.469521	9.311800	-17.725520	-5.592465
1JWF	A	LEU	37	H	-10.023806	7.914495	-15.550128	-5.104387
1JWF	A	ASN	38	H	-7.251736	4.240006	-13.456440	-4.902099
1JWF	A	GLU	39	H	-4.777517	4.790370	-9.664827	-4.642100
1JWF	A	ASP	40	C	-4.755616	4.907851	-9.684951	-4.636904
1JWF	A	PHE	41	C	-4.743055	4.979136	-9.694710	-4.628698
1JWF	A	GLU	42	H	-4.740096	5.005113	-9.697519	-4.627177
1JWF	A	GLY	43	H	-4.748392	5.019446	-9.643738	-4.622961
1JWF	A	PRO	44	H	-6.390151	8.322256	-10.210701	-4.394834
1JWF	A	PRO	45	H	-6.886612	8.741045	-10.218030	-4.250860
1JWF	A	LEU	46	H	-7.781323	10.323544	-10.496658	-4.276217
1JWF	A	ALA	47	H	-8.957945	11.595142	-11.278190	-3.881058
1JWF	A	THR	48	H	-9.342823	11.210671	-11.545425	-3.696442
1JWF	A	ARG	49	H	-9.339836	11.142665	-11.547064	-3.671638
1JWF	A	LEU	50	H	-10.104966	13.053627	-12.225005	-4.001753
1JWF	A	LEU	51	H	-10.434981	13.790656	-12.388646	-4.134161
1JWF	A	ALA	52	H	-10.547488	13.469756	-12.548931	-4.169336
1JWF	A	HIS	53	H	-10.583233	13.335896	-12.561227	-4.181655
1JWF	A	LYS	54	H	-11.481837	14.311627	-14.446188	-4.974925
1JWF	A	ILE	55	H	-11.789723	13.815397	-15.068717	-5.006535

1JWF	A	GLN	56	H	-12.176063	10.732330	-18.504750	-5.804607
1JWF	A	SER	57	T	-10.878586	10.497971	-16.036149	-5.645904
1JWF	A	PRO	58	T	-10.810866	10.629836	-16.147404	-5.696168
1JWF	A	GLN	59	T	-10.809431	10.637136	-16.153498	-5.697120
1JWF	A	GLU	60	H	-10.819510	10.650278	-16.115913	-5.701138
1JWF	A	TRP	61	H	-10.845577	10.723243	-15.962399	-5.679145
1JWF	A	GLU	62	H	-12.005784	12.065207	-17.237236	-6.037148
1JWF	A	ALA	63	H	-12.433156	15.227336	-15.014171	-4.989582
1JWF	A	ILE	64	H	-11.890831	15.667023	-14.366371	-5.139376
1JWF	A	GLN	65	H	-11.820316	15.709813	-14.379877	-5.131063
1JWF	A	ALA	66	H	-11.083530	17.125852	-11.919156	-4.638542
1JWF	A	LEU	67	H	-11.073773	17.178150	-11.929021	-4.646912
1JWF	A	THR	68	H	-11.037604	17.026570	-12.139354	-4.738975
1JWF	A	VAL	69	H	-11.060435	16.778223	-12.281152	-4.747995
1JWF	A	LEU	70	H	-11.077205	16.782744	-12.240144	-4.747849
1JWF	A	GLU	71	H	-11.418319	11.929014	-16.726631	-5.709708
1JWF	A	THR	72	H	-10.742855	9.275905	-16.975988	-5.668754
1JWF	A	CYS	73	H	-10.542327	8.467245	-17.332256	-5.714452
1JWF	A	MET	74	H	-9.760599	7.116516	-16.712039	-5.643364
1JWF	A	LYS	75	H	-8.647666	4.283203	-16.014980	-5.214377
1JWF	A	SER	76	H	-8.645346	4.267848	-16.028480	-5.210424
1JWF	A	CYS	77	H	-8.655467	4.204395	-16.010834	-5.201245
1JWF	A	GLY	78	H	-8.663732	4.154033	-15.987815	-5.193099
1JWF	A	LYS	79	H	-8.737476	3.811806	-15.922886	-5.137053
1JWF	A	ARG	80	H	-11.268379	6.460442	-18.262658	-5.124422
1JWF	A	PHE	81	H	-11.972314	9.988965	-17.010078	-5.102417
1JWF	A	HIS	82	H	-12.995612	11.968941	-17.853365	-5.324017
1JWF	A	ASP	83	H	-10.839457	9.266373	-15.822933	-5.205286
1JWF	A	GLU	84	H	-10.357260	11.380217	-14.669779	-5.268789
1JWF	A	VAL	85	H	-8.488593	10.441094	-11.140557	-4.312268
1JWF	A	GLY	86	H	-8.313000	11.199077	-11.044776	-4.417555
1JWF	A	LYS	87	C	-8.305046	11.270418	-11.043711	-4.418059
1JWF	A	PHE	88	H	-8.285838	11.543180	-10.931682	-4.409239
1JWF	A	ARG	89	H	-8.295639	11.519887	-10.884675	-4.393920
1JWF	A	PHE	90	H	-8.991874	14.028775	-10.664257	-4.672198
1JWF	A	LEU	91	H	-9.961502	16.671650	-10.262551	-4.466947
1JWF	A	ASN	92	H	-10.093873	16.697334	-10.162733	-4.497589
1JWF	A	GLU	93	H	-11.918115	16.568443	-14.520666	-5.465137
1JWF	A	LEU	94	H	-11.552756	18.105242	-12.688931	-5.106870
1JWF	A	ILE	95	H	-11.301518	17.843758	-12.779146	-5.122096
1JWF	A	LYS	96	H	-11.030212	16.765908	-13.207521	-5.178847
1JWF	A	VAL	97	H	-7.828393	11.519646	-9.183752	-3.995987
1JWF	A	VAL	98	H	-5.780484	11.035836	-7.357599	-4.367999
1JWF	A	SER	99	T	-5.398497	10.516322	-7.818887	-4.524223
1JWF	A	PRO	100	T	-4.936447	10.004472	-7.844657	-4.633135
1JWF	A	LYS	101	T	-4.904284	9.935523	-7.957997	-4.635072
1JWF	A	TYR	102	T	-4.908478	9.924267	-7.949909	-4.639724
1JWF	A	LEU	103	T	-5.056162	9.606319	-8.145488	-4.712820
1JWF	A	GLY	104	G	-5.238853	9.478280	-8.089783	-4.718543
1JWF	A	SER	105	G	-6.612968	8.635020	-10.177586	-4.664940
1JWF	A	ARG	106	G	-8.325065	7.588656	-13.461659	-4.622822
1JWF	A	THR	107	C	-8.283520	7.683803	-13.519079	-4.680378
1JWF	A	SER	108	C	-8.702257	7.403715	-14.463342	-4.955769
1JWF	A	GLU	109	H	-9.044718	9.213041	-14.535881	-5.248829
1JWF	A	LYS	110	H	-9.188694	9.900193	-14.219353	-5.329294
1JWF	A	VAL	111	H	-9.203202	9.962793	-14.131760	-5.323653
1JWF	A	LYS	112	H	-9.585201	10.420509	-14.048647	-5.368257
1JWF	A	ASN	113	H	-9.632411	10.418742	-13.925104	-5.344193
1JWF	A	LYS	114	H	-11.463829	14.250219	-14.816468	-5.227545
1JWF	A	ILE	115	H	-11.279807	15.744988	-13.702639	-5.046230
1JWF	A	LEU	116	H	-11.309313	15.815804	-13.582814	-5.014041
1JWF	A	GLU	117	H	-11.139034	15.703182	-13.506155	-4.940051
1JWF	A	LEU	118	H	-11.360248	17.072621	-12.808819	-4.829674
1JWF	A	LEU	119	H	-11.511289	17.382367	-12.565423	-4.765418
1JWF	A	TYR	120	H	-11.209351	14.946133	-13.146648	-4.616992
1JWF	A	SER	121	H	-9.096661	12.253472	-11.288033	-4.591324
1JWF	A	TRP	122	H	-8.674979	13.574210	-10.674279	-4.726712
1JWF	A	THR	123	H	-7.027687	8.197839	-10.281477	-4.148334
1JWF	A	VAL	124	H	-5.993040	6.360588	-9.851310	-3.958202
1JWF	A	GLY	125	H	-5.979549	6.384916	-9.914049	-3.973703
1JWF	A	LEU	126	T	-5.974708	6.374379	-9.940490	-3.974852
1JWF	A	PRO	127	T	-5.974429	6.338502	-9.960535	-3.974752
1JWF	A	GLU	128	T	-6.076608	6.056015	-9.905687	-3.949394
1JWF	A	GLU	129	T	-7.858271	7.672216	-12.707667	-4.554472
1JWF	A	VAL	130	H	-8.184547	8.289777	-12.652885	-4.414416
1JWF	A	LYS	131	H	-8.630320	9.053158	-12.912062	-4.555922
1JWF	A	ILE	132	H	-9.061916	10.145764	-12.260150	-4.328464
1JWF	A	ALA	133	H	-9.077820	10.105985	-12.193923	-4.309283
1JWF	A	GLU	134	H	-9.083342	10.092804	-12.167185	-4.305821
1JWF	A	ALA	135	H	-10.482337	13.598499	-12.959811	-4.893427
1JWF	A	TYR	136	H	-10.468633	20.495824	-14.970473	-9.231779

1JWF	A	GLN	137	H	-7.954258	14.886464	-12.293598	-7.282435
1JWF	A	MET	138	H	-7.157278	15.318353	-11.189567	-7.355065
1JWF	A	LEU	139	H	-6.556133	14.158043	-10.445873	-6.798814
1JWF	A	LYS	140	H	-5.600662	10.774637	-9.586207	-5.847061
1JWF	A	LYS	141	H	-4.881483	9.258372	-8.347101	-4.908578
1JWF	A	GLN	142	H	-4.545103	8.774210	-7.781354	-4.414330
1JWF	A	GLY	143	C	-4.545103	8.774210	-7.781354	-4.414330
1JWF	A	ILE	144	C	-4.545103	8.774210	-7.781354	-4.414330
1JWF	A	VAL	145	C	-4.545103	8.774210	-7.781354	-4.414330
1JWO	A	LEU	117	T	-5.960272	6.460114	-8.548067	-3.117896
1JWO	A	SER	118	T	-5.960272	6.460114	-8.548067	-3.117896
1JWO	A	LEU	119	T	-5.960272	6.460114	-8.548067	-3.117896
1JWO	A	MET	120	T	-5.960272	6.460114	-8.548067	-3.117896
1JWO	A	PRO	121	T	-7.257339	7.442176	-10.185225	-3.676901
1JWO	A	TRP	122	T	-10.183134	14.311469	-12.224556	-4.884986
1JWO	A	PHE	123	B	-9.189122	13.474053	-11.395595	-5.099887
1JWO	A	HIS	124	T	-8.165723	10.028605	-12.224439	-5.152580
1JWO	A	GLY	125	T	-7.142607	7.631168	-12.212688	-5.129793
1JWO	A	LYS	126	T	-7.091208	7.577484	-12.340777	-5.117061
1JWO	A	ILE	127	T	-6.950607	7.405570	-12.454629	-5.072751
1JWO	A	SER	128	C	-6.825226	7.190694	-12.513149	-5.033779
1JWO	A	GLY	129	H	-6.812747	7.078968	-12.548657	-5.015875
1JWO	A	GLN	130	H	-7.140813	7.118593	-12.860483	-4.898430
1JWO	A	GLU	131	H	-7.186598	7.168928	-12.788716	-4.890522
1JWO	A	ALA	132	H	-7.408249	7.370434	-12.749236	-4.881733
1JWO	A	VAL	133	H	-7.888948	7.998540	-12.896490	-4.874715
1JWO	A	GLN	134	H	-8.472504	8.420812	-13.178392	-4.712341
1JWO	A	GLN	135	H	-9.139812	10.067466	-13.696909	-4.809598
1JWO	A	LEU	136	H	-9.199172	9.622786	-13.832675	-4.650689
1JWO	A	GLN	137	T	-8.591420	6.721019	-14.284855	-4.635251
1JWO	A	PRO	138	T	-7.166031	6.042653	-12.234795	-4.580579
1JWO	A	PRO	139	T	-7.160079	6.072421	-12.251601	-4.586869
1JWO	A	GLU	140	T	-7.165146	6.037107	-12.242359	-4.586508
1JWO	A	ASP	141	T	-7.172958	6.012467	-12.217490	-4.587523
1JWO	A	GLY	142	T	-7.210238	6.055104	-12.069413	-4.584804
1JWO	A	LEU	143	E	-9.601677	9.838537	-13.920372	-5.084803
1JWO	A	PHE	144	E	-11.361041	16.119078	-13.349863	-4.958753
1JWO	A	LEU	145	E	-11.680489	17.886299	-12.179369	-4.670815
1JWO	A	VAL	146	E	-11.951300	17.966189	-12.048686	-4.551459
1JWO	A	ARG	147	E	-10.554205	10.376534	-14.111693	-4.622546
1JWO	A	GLU	148	E	-6.822620	7.179410	-10.829320	-4.522316
1JWO	A	SER	149	T	-5.198457	4.114255	-9.616785	-3.817893
1JWO	A	ALA	150	T	-3.706314	2.192185	-8.598774	-3.690705
1JWO	A	ARG	151	T	-3.695092	2.212318	-8.654164	-3.701108
1JWO	A	HIS	152	T	-3.695068	2.212576	-8.654396	-3.701179
1JWO	A	PRO	153	T	-3.698092	2.187229	-8.643175	-3.696912
1JWO	A	GLY	154	T	-3.744037	2.048307	-8.568944	-3.690010
1JWO	A	ASP	155	T	-6.050852	3.280127	-11.527265	-4.234483
1JWO	A	TYR	156	E	-9.382394	9.724503	-14.111373	-5.193348
1JWO	A	VAL	157	E	-10.132944	11.548520	-13.359092	-4.898666
1JWO	A	LEU	158	E	-12.456305	17.085279	-14.640272	-5.117724
1JWO	A	CYS	159	E	-11.814602	12.665160	-15.843577	-5.217219
1JWO	A	VAL	160	E	-10.415583	11.204338	-13.566897	-4.476425
1JWO	A	SER	161	E	-7.674962	7.737690	-11.652299	-4.510961
1JWO	A	PHE	162	E	-5.386563	8.945221	-7.569437	-4.098155
1JWO	A	GLY	163	T	-4.689772	8.213280	-6.979879	-3.712696
1JWO	A	ARG	164	T	-4.683617	8.238316	-6.996004	-3.711483
1JWO	A	ASP	165	E	-4.683618	8.238414	-6.995948	-3.711488
1JWO	A	VAL	166	E	-4.687396	8.241822	-6.966258	-3.706356
1JWO	A	ILE	167	E	-4.899528	7.926099	-6.742850	-3.540722
1JWO	A	HIS	168	E	-7.389318	10.644298	-8.561539	-3.598782
1JWO	A	TYR	169	E	-10.452475	13.133065	-12.607233	-4.542889
1JWO	A	ARG	170	E	-12.051122	16.093169	-13.817104	-4.949644
1JWO	A	VAL	171	E	-10.143201	9.189019	-13.708843	-4.234515
1JWO	A	LEU	172	E	-7.041306	6.389426	-11.461757	-4.460703
1JWO	A	HIS	173	E	-6.717413	6.588673	-11.555547	-4.543237
1JWO	A	ARG	174	T	-6.697645	6.707646	-11.564870	-4.546915
1JWO	A	ASP	175	T	-6.694997	6.730672	-11.571274	-4.549112
1JWO	A	GLY	176	T	-6.696646	6.724826	-11.565402	-4.550108
1JWO	A	HIS	177	E	-7.177031	7.171275	-11.711510	-4.660793
1JWO	A	LEU	178	E	-7.724840	11.654133	-10.130229	-4.539445
1JWO	A	THR	179	T	-5.372263	9.698913	-7.388896	-4.291800
1JWO	A	ILE	180	T	-4.890359	8.388677	-7.580732	-4.003739
1JWO	A	ASP	181	T	-4.665766	8.681768	-7.490756	-4.044584
1JWO	A	GLU	182	T	-4.661953	8.710125	-7.495786	-4.045226
1JWO	A	ALA	183	T	-4.657839	8.753970	-7.484975	-4.043598
1JWO	A	VAL	184	T	-4.863205	8.389471	-7.543833	-3.942679
1JWO	A	PHE	185	C	-5.312243	9.583532	-7.328257	-4.134518
1JWO	A	PHE	186	B	-6.951934	13.771138	-7.958299	-4.210002
1JWO	A	CYS	187	T	-6.243413	10.855707	-8.851694	-4.685288
1JWO	A	ASN	188	T	-6.349619	10.270099	-9.147974	-4.806490

1JWO	A	LEU	189	H	-6.371437	10.113900	-9.145064	-4.808716
1JWO	A	MET	190	H	-6.375670	10.061527	-9.144331	-4.807032
1JWO	A	ASP	191	H	-6.382146	10.008704	-9.131915	-4.804639
1JWO	A	MET	192	H	-10.349174	14.600645	-13.452346	-5.653955
1JWO	A	VAL	193	H	-11.303011	14.483717	-14.858393	-5.532765
1JWO	A	GLU	194	H	-11.448284	13.456033	-15.511276	-5.578896
1JWO	A	HIS	195	H	-11.932414	13.543054	-16.061962	-5.473723
1JWO	A	TYR	196	H	-12.316299	13.011062	-16.933488	-5.440726
1JWO	A	SER	197	H	-8.323090	6.393950	-13.901069	-5.083270
1JWO	A	LYS	198	H	-6.039650	6.639135	-10.433110	-4.723773
1JWO	A	ASP	199	C	-5.764735	7.804430	-9.850219	-4.654267
1JWO	A	LYS	200	T	-5.718453	7.918903	-9.893759	-4.654817
1JWO	A	GLY	201	T	-5.696763	8.024724	-9.917288	-4.666291
1JWO	A	ALA	202	T	-5.698881	8.088927	-9.873446	-4.663896
1JWO	A	ILE	203	T	-6.171873	9.869415	-9.282143	-4.600658
1JWO	A	CYS	204	T	-6.952152	10.178584	-10.487892	-4.782895
1JWO	A	THR	205	C	-7.497701	11.472551	-10.585674	-4.967253
1JWO	A	LYS	206	C	-8.321808	13.316409	-10.701183	-4.948672
1JWO	A	LEU	207	C	-9.025445	13.153637	-11.543061	-4.894162
1JWO	A	VAL	208	C	-8.913480	11.334454	-12.320691	-4.820169
1JWO	A	ARG	209	C	-8.907984	9.047094	-13.029077	-4.444377
1JWO	A	PRO	210	B	-6.155903	7.051124	-8.674185	-3.429954
1JWO	A	LYS	211	C	-6.155903	7.051124	-8.674185	-3.429954
1JWO	A	ARG	212	C	-6.155903	7.051124	-8.674185	-3.429954
1JWO	A	LYS	213	C	-6.155903	7.051124	-8.674185	-3.429954
1K04	A	GLU	908	C	1.117405	-0.008610	-2.909204	-2.818333
1K04	A	ILE	909	C	1.117405	-0.008610	-2.909204	-2.818333
1K04	A	SER	910	C	1.117405	-0.008610	-2.909204	-2.818333
1K04	A	PRO	911	C	1.117405	-0.008610	-2.909204	-2.818333
1K04	A	PRO	912	C	0.573721	0.105139	-2.173436	-2.121579
1K04	A	PRO	913	C	-0.591441	1.191831	-3.875668	-2.606932
1K04	A	THR	914	T	-0.969333	1.513570	-4.980521	-3.438146
1K04	A	ALA	915	T	-1.080410	1.470455	-5.111070	-3.620384
1K04	A	ASN	916	T	-1.149094	1.427104	-4.989065	-3.636105
1K04	A	LEU	917	T	-1.966321	1.696530	-6.339480	-4.135584
1K04	A	ASP	918	C	-2.805413	2.115001	-8.162918	-4.961472
1K04	A	ARG	919	T	-4.041100	3.890373	-11.344607	-6.498651
1K04	A	SER	920	T	-4.342362	4.010143	-12.324173	-7.118340
1K04	A	ASN	921	T	-4.506204	4.042478	-12.411658	-7.296253
1K04	A	ASP	922	T	-5.217343	4.579715	-13.845929	-8.082589
1K04	A	LYS	923	H	-6.434261	5.162908	-16.675924	-9.034397
1K04	A	VAL	924	H	-6.995163	5.180784	-17.403273	-9.129799
1K04	A	TYR	925	H	-8.138681	6.612353	-18.747563	-9.172065
1K04	A	GLU	926	H	-8.572587	7.019012	-16.397059	-6.542661
1K04	A	ASN	927	H	-7.942301	5.745927	-13.699802	-4.639764
1K04	A	VAL	928	H	-6.718128	5.085850	-10.105873	-3.450148
1K04	A	THR	929	H	-6.560846	5.101384	-10.022946	-3.286798
1K04	A	GLY	930	H	-6.515408	5.072526	-9.845897	-3.089297
1K04	A	LEU	931	H	-6.458664	5.075554	-9.686021	-2.920203
1K04	A	VAL	932	H	-6.313118	4.968544	-9.716765	-2.908592
1K04	A	LYS	933	H	-6.559252	4.992690	-10.090278	-2.817906
1K04	A	ALA	934	H	-6.686380	4.989154	-10.286058	-2.874711
1K04	A	VAL	935	H	-6.741222	5.004537	-10.503096	-3.037139
1K04	A	ILE	936	H	-6.834591	4.997095	-10.937026	-3.364228
1K04	A	GLU	937	H	-7.389141	5.580615	-12.263805	-4.029659
1K04	A	MET	938	H	-7.557109	4.677352	-12.497427	-3.670159
1K04	A	SER	939	H	-7.388897	4.473726	-11.725182	-3.271862
1K04	A	SER	940	H	-6.784532	3.906291	-9.514550	-2.190914
1K04	A	LYS	941	H	-5.951236	4.962415	-7.228460	-1.823419
1K04	A	ILE	942	H	-5.523929	5.098054	-7.675875	-2.370517
1K04	A	GLN	943	C	-5.516656	5.166707	-7.652986	-2.372300
1K04	A	PRO	944	C	-5.489631	5.275717	-7.620903	-2.364498
1K04	A	ALA	945	C	-5.523921	5.450638	-7.551124	-2.407398
1K04	A	PRO	946	C	-5.795893	5.536642	-8.154673	-2.810571
1K04	A	PRO	947	G	-6.800528	6.901884	-8.269854	-2.425263
1K04	A	GLU	948	G	-6.980856	7.070557	-7.844901	-2.211783
1K04	A	GLU	949	G	-7.839062	7.917566	-7.466787	-1.753201
1K04	A	TYR	950	H	-9.769258	12.499733	-10.192453	-3.234684
1K04	A	VAL	951	H	-9.398655	9.982855	-9.543929	-2.282217
1K04	A	PRO	952	H	-8.828977	9.574385	-10.239986	-2.968679
1K04	A	MET	953	H	-8.584679	9.377577	-10.269698	-3.090012
1K04	A	VAL	954	H	-8.441456	9.285685	-10.281495	-3.053350
1K04	A	LYS	955	H	-8.400518	9.119325	-10.342140	-2.993998
1K04	A	GLU	956	H	-8.429659	8.771050	-10.671896	-3.091652
1K04	A	VAL	957	H	-8.620538	8.562908	-10.760515	-2.988346
1K04	A	GLY	958	H	-8.866524	7.994272	-11.070634	-2.727019
1K04	A	LEU	959	H	-9.175131	7.196695	-11.654255	-2.531277
1K04	A	ALA	960	H	-9.322166	7.434700	-11.750121	-2.613745
1K04	A	LEU	961	H	-9.686213	8.874562	-12.061624	-3.108197
1K04	A	ARG	962	H	-9.912857	8.394236	-12.015807	-2.810393
1K04	A	THR	963	H	-9.783807	9.021507	-11.778698	-3.044699

```
1K04        A          LEU            964                  H -9.891729  9.332766 -11.772270 -3.200392
1K04        A          LEU            965                  H -9.931652  9.228654 -11.946175 -3.334098
1K04        A          ALA            966                  H -9.142554  7.408570 -10.586923 -2.299001
1K04        A          THR            967                  H -8.425432  8.739186 -10.776504 -3.485938
1K04        A          VAL            968                  H -8.340985  9.328058 -10.537078 -3.566573
1K04        A          ASP            969                  H -8.258937  9.334245 -10.577761 -3.542621
1K04        A          GLU            970                  H -7.977647  9.324227 -9.563732 -2.976366
1K04        A          THR            971                  H -8.002817  9.760589 -9.410958 -3.032548
1K04        A          ILE            972                  G -8.230016 10.114678 -8.699951 -2.564187
1K04        A          PRO            973                  G -8.001963  9.630234 -8.855489 -2.694937
1K04        A          LEU            974                  G -8.027298  9.637956 -8.776625 -2.650119
1K04        A          LEU            975                  C -8.063406 10.291280 -8.594457 -2.751809
1K04        A          PRO            976                  C -7.972367  9.996974 -8.665283 -2.705958
1K04        A          ALA            977                  G -7.914504  9.714647 -8.991616 -2.800622
1K04        A          SER            978                  G -8.137078  9.830974 -9.029145 -2.678441
1K04        A          THR            979                  G -8.152452  9.957601 -8.935811 -2.677331
1K04        A          HIS            980                  H -8.481183  9.214403 -10.206188 -3.022380
1K04        A          ARG            981                  H -8.685323  9.517846 -10.717420 -3.243200
1K04        A          GLU            982                  H -8.932578 10.790767 -10.111824 -3.088205
1K04        A          ILE            983                  H -9.147959 11.465867 -9.362565 -2.702516
1K04        A          GLU            984                  H -9.248756 11.106152 -9.329553 -2.595722
1K04        A          MET            985                  H -9.274385 10.943060 -9.401936 -2.613186
1K04        A          ALA            986                  H -10.024997 11.855984 -11.682675 -3.962983
1K04        A          GLN            987                  H -11.117721  9.146174 -13.847111 -3.231950
1K04        A          LYS            988                  H -9.793262  8.420234 -11.978659 -3.398340
1K04        A          LEU            989                  H -9.800567  8.432670 -11.924432 -3.384530
1K04        A          LEU            990                  H -9.835425  8.456841 -11.866226 -3.433812
1K04        A          ASN            991                  H -9.812227  8.491997 -11.896638 -3.412609
1K04        A          SER            992                  H -9.788993  8.550115 -12.000407 -3.454014
1K04        A          ASP            993                  H -11.038996 10.491233 -13.860318 -3.784733
1K04        A          LEU            994                  H -10.641466 11.761237 -12.412483 -3.615238
1K04        A          GLY            995                  H -9.295425 10.469741 -9.373704 -2.685092
1K04        A          GLU            996                  H -9.283847 10.605513 -9.348265 -2.695475
1K04        A          LEU            997                  H -9.295363 10.624890 -9.238864 -2.660550
1K04        A          ILE            998                  H -9.290826 10.617304 -9.291354 -2.683209
1K04        A          ASN            999                  H -9.322569 10.490963 -9.198493 -2.644889
1K04        A          LYS           1000                  H -10.986089 13.089325 -11.870297 -3.684173
1K04        A          MET           1001                  H -11.666285 11.957900 -15.091559 -5.074665
1K04        A          LYS           1002                  H -11.602345 11.467153 -14.905745 -4.754397
1K04        A          LEU           1003                  H -12.096854 12.419916 -14.524854 -4.159852
1K04        A          ALA           1004                  H -12.043263 12.804241 -14.159491 -4.050216
1K04        A          GLN           1005                  H -10.826658 11.283701 -11.738988 -3.268326
1K04        A          GLN           1006                  H -8.576557  9.198034 -8.689524 -2.474744
1K04        A          TYR           1007                  H -7.854098  8.814825 -9.692509 -3.338403
1K04        A          VAL           1008                  T -4.834523  6.312271 -6.107830 -3.091146
1K04        A          MET           1009                  T -4.831272  6.321920 -6.125010 -3.091129
1K04        A          THR           1010                  T -4.831225  6.321976 -6.125415 -3.091073
1K04        A          SER           1011                  C -4.832263  6.317004 -6.121071 -3.092188
1K04        A          LEU           1012                  H -4.834816  6.306895 -6.103817 -3.089555
1K04        A          GLN           1013                  H -7.904015  8.078783 -9.293463 -3.077360
1K04        A          GLN           1014                  H -10.157587  8.396166 -11.523473 -2.703948
1K04        A          GLU           1015                  H -11.639678 10.013110 -14.406177 -3.697018
1K04        A          TYR           1016                  H -12.351707 13.138964 -15.364614 -4.966441
1K04        A          LYS           1017                  H -12.314771 12.537650 -15.685696 -4.979298
1K04        A          LYS           1018                  H -10.659587  9.349709 -14.330124 -4.750434
1K04        A          GLN           1019                  H -10.636597  9.293211 -14.307009 -4.671918
1K04        A          MET           1020                  H -10.410089  9.663496 -13.031328 -3.787018
1K04        A          LEU           1021                  H -8.942177  7.818175 -8.785365 -1.476100
1K04        A          THR           1022                  H -8.493521  7.799725 -9.686030 -2.189800
1K04        A          ALA           1023                  H -8.489202  7.862394 -9.613400 -2.152627
1K04        A          ALA           1024                  H -8.456317  7.961579 -9.646741 -2.162768
1K04        A          HIS           1025                  H -8.404111  7.941858 -9.605203 -2.092846
1K04        A          ALA           1026                  H -8.674933  8.123878 -10.318595 -2.576064
1K04        A          LEU           1027                  H -9.397525  9.106462 -9.941571 -1.964365
1K04        A          ALA           1028                  H -8.735844  7.356804 -10.931667 -2.883368
1K04        A          VAL           1029                  H -8.721934  7.190549 -11.116497 -2.950369
1K04        A          ASP           1030                  H -8.823449  7.053572 -11.471223 -3.246512
1K04        A          ALA           1031                  H -8.811707  7.108773 -11.449842 -3.221032
1K04        A          LYS           1032                  H -8.758721  7.247721 -11.581047 -3.296548
1K04        A          ASN           1033                  H -9.499275  8.857494 -12.153146 -3.307044
1K04        A          LEU           1034                  H -9.799522  9.736069 -12.136890 -3.443481
1K04        A          LEU           1035                  H -9.808493  9.687125 -12.170767 -3.461033
1K04        A          ASP           1036                  H -9.884968  9.646708 -12.412763 -3.674642
1K04        A          VAL           1037                  H -10.536630 11.109113 -12.192352 -3.522106
1K04        A          ILE           1038                  H -10.679240 13.215237 -15.261615 -6.298681
1K04        A          ASP           1039                  H -10.143434 11.719761 -16.295289 -7.095201
1K04        A          GLN           1040                  H -9.470671 10.872859 -14.586090 -6.288277
1K04        A          ALA           1041                  H -8.748314 10.181161 -12.580257 -5.412218
1K04        A          ARG           1042                  H -6.814104  7.676566 -12.443562 -6.253724
1K04        A          LEU           1043                  H -4.660039  4.634150 -9.709854 -5.317848
1K04        A          LYS           1044                  H -4.127065  4.485732 -8.639565 -4.549623
```

1K04	A	MET	1045	H	-3.551675	3.361609	-6.416827	-2.911870
1K04	A	LEU	1046	H	-2.314446	1.597213	-2.845603	-1.018007
1K04	A	GLY	1047	T	-2.314446	1.597213	-2.845603	-1.018007
1K04	A	GLN	1048	T	-2.314446	1.597213	-2.845603	-1.018007
1K04	A	THR	1049	C	-2.314446	1.597213	-2.845603	-1.018007
1K1B	A	GLU	125	T	-1.353229	1.354325	-6.859083	-4.046474
1K1B	A	ASP	126	T	-1.353229	1.354325	-6.859083	-4.046474
1K1B	A	GLY	127	T	-1.353229	1.354325	-6.859083	-4.046474
1K1B	A	ASP	128	T	-1.353229	1.354325	-6.859083	-4.046474
1K1B	A	THR	129	T	-1.920899	3.162466	-6.793917	-4.520546
1K1B	A	PRO	130	C	-3.013409	4.205220	-7.878463	-4.942405
1K1B	A	LEU	131	H	-4.902167	8.945468	-8.724039	-5.744824
1K1B	A	HIS	132	H	-7.450678	12.055584	-12.322758	-6.847787
1K1B	A	ILE	133	H	-7.817530	10.551371	-11.181968	-4.786549
1K1B	A	ALA	134	H	-7.200708	9.585366	-9.231713	-3.684954
1K1B	A	VAL	135	H	-6.343026	8.699132	-8.986665	-3.965475
1K1B	A	VAL	136	H	-5.750777	8.955373	-8.392708	-4.094147
1K1B	A	GLN	137	H	-5.355936	8.165904	-8.449526	-4.090883
1K1B	A	GLY	138	H	-5.254688	8.056912	-8.505098	-4.063297
1K1B	A	ASN	139	C	-5.264302	8.032206	-8.501558	-4.066537
1K1B	A	LEU	140	C	-5.341731	7.976807	-8.442980	-4.064348
1K1B	A	PRO	141	H	-5.565039	7.460139	-8.632874	-4.011497
1K1B	A	ALA	142	H	-6.263061	7.751282	-8.911287	-3.840565
1K1B	A	VAL	143	H	-7.624866	9.884796	-9.624118	-3.546485
1K1B	A	HIS	144	H	-8.373297	10.000815	-10.372205	-3.295178
1K1B	A	ARG	145	H	-8.614807	9.690574	-10.580828	-3.191322
1K1B	A	LEU	146	H	-9.375990	11.203009	-11.626793	-3.565874
1K1B	A	VAL	147	H	-9.543482	10.810483	-12.056359	-3.699451
1K1B	A	ASN	148	H	-9.613136	10.354192	-12.313636	-3.764313
1K1B	A	LEU	149	H	-9.903845	9.893072	-13.040129	-3.920350
1K1B	A	PHE	150	H	-9.069305	6.905812	-14.387791	-4.914906
1K1B	A	GLN	151	H	-7.314634	3.401153	-13.041869	-4.279447
1K1B	A	GLN	152	H	-6.114632	3.229150	-11.373637	-4.045432
1K1B	A	GLY	153	H	-5.970871	4.371105	-10.929500	-4.058367
1K1B	A	GLY	154	H	-5.966667	4.418813	-10.931984	-4.062217
1K1B	A	ARG	155	C	-5.968389	4.424692	-10.914798	-4.058067
1K1B	A	GLU	156	C	-6.027073	4.592632	-10.690015	-4.039792
1K1B	A	LEU	157	T	-6.845661	8.734558	-9.406985	-4.128624
1K1B	A	ASP	158	T	-8.515771	12.083224	-11.117412	-4.549361
1K1B	A	ILE	159	T	-8.272056	10.450417	-12.384123	-5.122287
1K1B	A	TYR	160	T	-8.129529	9.913828	-12.935675	-5.352449
1K1B	A	ASN	161	C	-7.741406	8.841495	-12.847934	-5.317396
1K1B	A	ASN	162	B	-7.678971	9.023475	-12.782916	-5.291208
1K1B	A	LEU	163	T	-7.685015	9.006860	-12.770761	-5.291005
1K1B	A	ARG	164	T	-7.861265	8.945339	-12.659754	-5.251492
1K1B	A	GLN	165	T	-7.983561	8.884448	-12.390613	-5.164034
1K1B	A	THR	166	B	-9.016634	10.906343	-12.188072	-5.033898
1K1B	A	PRO	167	C	-10.845531	16.399410	-11.820753	-4.479673
1K1B	A	LEU	168	H	-11.012174	17.571309	-11.177040	-4.357068
1K1B	A	HIS	169	H	-10.962006	17.263266	-11.220674	-4.265368
1K1B	A	LEU	170	H	-10.213217	14.882986	-10.669546	-3.854116
1K1B	A	ALA	171	H	-8.551509	11.874100	-9.419651	-3.702946
1K1B	A	VAL	172	H	-8.071421	12.079155	-9.090580	-3.706589
1K1B	A	ILE	173	H	-7.888500	11.531912	-9.413992	-3.704718
1K1B	A	THR	174	H	-7.497329	10.320133	-9.766673	-3.740045
1K1B	A	THR	175	H	-7.345525	10.508432	-9.551737	-3.670355
1K1B	A	LEU	176	C	-7.382645	10.514820	-9.487180	-3.616625
1K1B	A	PRO	177	C	-7.492066	10.168428	-9.629124	-3.593733
1K1B	A	SER	178	H	-7.578152	10.195410	-9.523811	-3.576800
1K1B	A	VAL	179	H	-8.056810	11.648175	-8.751009	-3.326606
1K1B	A	VAL	180	H	-8.928693	13.060811	-8.385345	-2.946621
1K1B	A	ARG	181	H	-10.359967	13.531792	-10.511483	-3.166203
1K1B	A	LEU	182	H	-9.892392	13.902411	-9.679723	-3.328782
1K1B	A	LEU	183	H	-7.853663	10.237379	-8.987855	-3.494689
1K1B	A	VAL	184	H	-6.586033	8.027114	-8.914682	-3.544877
1K1B	A	THR	185	H	-6.485029	7.773125	-9.253396	-3.585427
1K1B	A	ALA	186	H	-6.480888	7.782824	-9.269437	-3.585116
1K1B	A	GLY	187	H	-6.481780	7.768786	-9.273740	-3.586426
1K1B	A	ALA	188	C	-6.540977	7.522561	-9.307889	-3.595601
1K1B	A	SER	189	C	-7.547522	6.597158	-11.120910	-3.793775
1K1B	A	PRO	190	T	-9.231857	9.686564	-11.864203	-3.638731
1K1B	A	MET	191	T	-10.005433	10.950640	-12.700561	-3.903543
1K1B	A	ALA	192	T	-10.304162	11.460760	-12.877088	-3.903396
1K1B	A	LEU	193	T	-9.195796	9.508499	-12.441902	-4.387115
1K1B	A	ASP	194	C	-9.130952	9.373081	-12.819726	-4.559506
1K1B	A	ARG	195	T	-9.086026	9.474250	-12.958301	-4.623045
1K1B	A	HIS	196	T	-9.083022	9.481550	-12.975676	-4.627892
1K1B	A	GLY	197	T	-9.091563	9.499849	-12.963202	-4.644029
1K1B	A	GLN	198	T	-9.944011	9.994572	-14.977263	-5.375232
1K1B	A	THR	199	C	-10.444313	11.301307	-14.720119	-5.278498
1K1B	A	ALA	200	C	-11.145059	13.014566	-14.412153	-4.766502

1K1B	A	ALA	201	H	-11.257427	13.556908	-13.933652	-4.595519
1K1B	A	HIS	202	H	-11.610600	14.861181	-13.357727	-4.348794
1K1B	A	LEU	203	H	-11.187742	13.367226	-13.814551	-4.513625
1K1B	A	ALA	204	H	-10.767593	11.158448	-14.543059	-4.689698
1K1B	A	CYS	205	H	-10.606563	10.645756	-15.003029	-4.899338
1K1B	A	GLU	206	H	-10.439022	10.591180	-14.923466	-4.854373
1K1B	A	HIS	207	H	-9.922730	10.336621	-13.832504	-4.541014
1K1B	A	ARG	208	H	-9.621773	9.989083	-13.492069	-4.418418
1K1B	A	SER	209	C	-9.403462	10.927095	-12.831252	-4.443661
1K1B	A	PRO	210	C	-9.354782	11.188183	-12.653028	-4.399101
1K1B	A	THR	211	H	-9.352452	11.269737	-12.585497	-4.378450
1K1B	A	CYS	212	H	-9.500153	11.598463	-12.452261	-4.395050
1K1B	A	LEU	213	H	-9.753937	12.698729	-12.099139	-4.459026
1K1B	A	ARG	214	H	-10.408345	12.992784	-12.453724	-4.278038
1K1B	A	ALA	215	H	-10.973789	13.307397	-13.359771	-4.442034
1K1B	A	LEU	216	H	-10.661090	14.559937	-13.519233	-5.346378
1K1B	A	LEU	217	H	-9.807522	11.674843	-13.548412	-5.102680
1K1B	A	ASP	218	H	-8.289167	6.426232	-12.512017	-4.106763
1K1B	A	SER	219	H	-5.369427	5.165882	-9.063443	-3.889914
1K1B	A	ALA	220	H	-3.379274	3.665272	-6.599780	-3.320331
1K1B	A	ALA	221	C	-2.758649	5.711774	-5.205878	-3.391281
1K1B	A	PRO	222	T	-2.730767	5.810848	-5.265056	-3.414718
1K1B	A	GLY	223	T	-2.730648	5.812652	-5.265395	-3.414910
1K1B	A	THR	224	T	-2.737668	5.819126	-5.219219	-3.408476
1K1B	A	LEU	225	T	-2.975896	6.868043	-4.551370	-3.440371
1K1B	A	ASP	226	C	-4.562884	7.788201	-6.409657	-3.839958
1K1B	A	LEU	227	T	-7.564979	12.265361	-8.565052	-4.242483
1K1B	A	GLU	228	T	-9.452159	13.015771	-11.656502	-4.654878
1K1B	A	ALA	229	T	-9.505046	12.959071	-11.516627	-4.629350
1K1B	A	ARG	230	T	-10.708925	10.921032	-14.543411	-4.814890
1K1B	A	ASN	231	B	-9.340807	10.252963	-13.092063	-5.176327
1K1B	A	TYR	232	T	-8.998441	11.018717	-12.691720	-5.160737
1K1B	A	ASP	233	T	-8.829366	11.148440	-12.545742	-5.053753
1K1B	A	GLY	234	T	-8.782937	11.409245	-12.451917	-5.018471
1K1B	A	LEU	235	T	-8.787996	11.442519	-12.409092	-5.013855
1K1B	A	THR	236	C	-9.067286	12.204031	-12.048440	-4.909724
1K1B	A	ALA	237	B	-9.464689	12.434510	-11.920956	-4.678240
1K1B	A	LEU	238	H	-10.208551	14.853356	-11.439228	-4.512978
1K1B	A	HIS	239	H	-11.243370	15.949980	-12.262926	-4.147202
1K1B	A	VAL	240	H	-10.944770	13.503345	-13.114025	-4.163700
1K1B	A	ALA	241	H	-11.044771	12.381694	-13.842771	-4.215871
1K1B	A	VAL	242	H	-11.088953	11.694886	-14.346696	-4.329186
1K1B	A	ASN	243	H	-11.154449	10.605457	-15.219633	-4.557378
1K1B	A	THR	244	H	-10.352424	9.141063	-16.223629	-5.678866
1K1B	A	GLU	245	H	-9.759429	9.601428	-15.446701	-5.891100
1K1B	A	CYS	246	C	-9.175795	10.941846	-13.319239	-5.300582
1K1B	A	GLN	247	C	-9.107027	11.046812	-13.303508	-5.267238
1K1B	A	GLU	248	H	-9.093966	11.114259	-13.287177	-5.253181
1K1B	A	THR	249	H	-9.147440	11.379348	-12.962353	-5.173659
1K1B	A	VAL	250	H	-9.315687	11.851871	-12.318511	-4.949420
1K1B	A	GLN	251	H	-10.236025	12.503149	-13.245650	-4.944336
1K1B	A	LEU	252	H	-11.051150	14.518278	-13.177492	-4.761666
1K1B	A	LEU	253	H	-10.878043	13.369868	-13.423107	-4.758951
1K1B	A	LEU	254	H	-9.837461	11.013621	-13.235495	-4.784404
1K1B	A	GLU	255	H	-9.546330	9.806322	-13.935062	-4.862257
1K1B	A	ARG	256	H	-9.288657	9.882462	-13.499674	-4.681023
1K1B	A	GLY	257	H	-8.074152	8.907563	-11.210781	-4.203539
1K1B	A	ALA	258	C	-7.935199	9.226579	-11.043236	-4.123765
1K1B	A	ASP	259	C	-7.738008	9.317176	-10.926590	-4.084685
1K1B	A	ILE	260	T	-7.746701	9.347337	-10.862062	-4.068846
1K1B	A	ASP	261	T	-7.759065	9.307657	-10.839166	-4.060617
1K1B	A	ALA	262	T	-8.168710	9.780557	-10.898510	-3.976625
1K1B	A	VAL	263	T	-8.337470	9.104367	-11.396309	-4.034885
1K1B	A	ASP	264	C	-8.933469	5.791929	-14.631994	-4.310154
1K1B	A	ILE	265	T	-8.755344	6.156483	-14.483460	-4.396986
1K1B	A	LYS	266	T	-8.769795	6.178868	-14.471652	-4.418517
1K1B	A	SER	267	T	-8.811822	6.199194	-14.471455	-4.476009
1K1B	A	GLY	268	T	-8.947985	6.349547	-14.495979	-4.599337
1K1B	A	ARG	269	T	-9.479154	7.610527	-14.133236	-4.642684
1K1B	A	SER	270	C	-11.181933	12.230472	-14.998039	-5.000022
1K1B	A	PRO	271	C	-11.569278	15.937895	-13.159996	-4.523227
1K1B	A	LEU	272	H	-11.534354	17.310289	-12.152757	-4.343395
1K1B	A	ILE	273	H	-11.568466	17.438105	-12.120604	-4.362013
1K1B	A	HIS	274	H	-11.556417	17.083092	-12.390948	-4.417551
1K1B	A	ALA	275	H	-11.394580	13.468354	-14.495285	-4.807363
1K1B	A	VAL	276	H	-11.413878	12.142606	-15.506408	-5.041552
1K1B	A	GLU	277	H	-11.495933	10.361931	-16.926422	-5.368985
1K1B	A	ASN	278	H	-10.812296	9.141821	-16.131427	-5.159945
1K1B	A	ASN	279	H	-10.438216	10.270051	-15.425684	-5.262644
1K1B	A	SER	280	C	-10.400331	10.817108	-15.047059	-5.194667
1K1B	A	LEU	281	C	-10.271237	11.367540	-14.588083	-5.082687

1K1B	A	SER	282	H	-10.265816	11.470974	-14.528578	-5.070635
1K1B	A	MET	283	H	-10.447977	12.649354	-14.024797	-5.069612
1K1B	A	VAL	284	H	-10.797233	13.988494	-13.323423	-4.766283
1K1B	A	GLN	285	H	-10.666221	14.353345	-12.916025	-4.747934
1K1B	A	LEU	286	H	-10.075890	15.626168	-10.912998	-4.588736
1K1B	A	LEU	287	H	-8.207330	12.577536	-9.608282	-4.538794
1K1B	A	LEU	288	H	-6.481043	10.503165	-8.278890	-4.378281
1K1B	A	GLN	289	H	-6.439385	10.357100	-8.532507	-4.410165
1K1B	A	HIS	290	H	-6.426595	10.362779	-8.586437	-4.410803
1K1B	A	GLY	291	H	-6.416996	10.328375	-8.643245	-4.409487
1K1B	A	ALA	292	C	-6.442917	10.226127	-8.612339	-4.402320
1K1B	A	ASN	293	C	-7.703537	9.054988	-11.851977	-4.663484
1K1B	A	VAL	294	T	-8.208451	9.995015	-11.636781	-4.416358
1K1B	A	ASN	295	T	-8.550955	9.453240	-12.073330	-4.394294
1K1B	A	ALA	296	T	-9.170742	10.446415	-12.280174	-4.480262
1K1B	A	GLN	297	T	-9.457458	10.331431	-12.611865	-4.708616
1K1B	A	MET	298	B	-10.823316	8.909088	-16.484188	-5.311866
1K1B	A	TYR	299	T	-10.745578	8.836357	-16.581133	-5.326750
1K1B	A	SER	300	T	-10.680282	8.883057	-16.600479	-5.305264
1K1B	A	GLY	301	T	-10.527523	9.803576	-15.922970	-5.190028
1K1B	A	SER	302	T	-10.649176	10.066648	-15.729523	-5.139847
1K1B	A	SER	303	C	-10.957664	11.588919	-15.200829	-5.032429
1K1B	A	ALA	304	B	-11.060398	12.502275	-14.538271	-4.859324
1K1B	A	LEU	305	H	-11.168919	13.350241	-13.987068	-4.782537
1K1B	A	HIS	306	H	-11.515103	12.596514	-15.150756	-4.800408
1K1B	A	SER	307	H	-11.225521	11.206157	-15.345268	-4.672291
1K1B	A	ALA	308	H	-9.819697	9.048925	-13.670172	-4.528654
1K1B	A	SER	309	H	-9.641970	9.026970	-13.969770	-4.639966
1K1B	A	GLY	310	H	-8.908608	10.385804	-12.432608	-4.684094
1K1B	A	ARG	311	H	-8.804458	10.562348	-12.334746	-4.620704
1K1B	A	GLY	312	H	-8.592145	11.380239	-11.633899	-4.496747
1K1B	A	LEU	313	T	-8.650756	11.807940	-11.358509	-4.477478
1K1B	A	LEU	314	T	-8.634407	12.198885	-11.052309	-4.388956
1K1B	A	PRO	315	H	-8.917956	13.421010	-10.392394	-4.107024
1K1B	A	LEU	316	H	-9.043953	13.965508	-10.008687	-4.056673
1K1B	A	VAL	317	H	-9.654149	15.405951	-9.890706	-3.757674
1K1B	A	ARG	318	H	-9.141185	12.964804	-9.802222	-3.392548
1K1B	A	THR	319	H	-8.260100	11.155051	-9.428547	-3.419064
1K1B	A	LEU	320	H	-6.702073	8.628442	-8.295294	-3.264645
1K1B	A	VAL	321	H	-5.520114	6.898913	-7.452050	-3.042403
1K1B	A	ARG	322	H	-5.511242	6.889151	-7.511090	-3.052016
1K1B	A	SER	323	H	-5.511522	6.883390	-7.513564	-3.053029
1K1B	A	GLY	324	H	-5.511517	6.852527	-7.537464	-3.058943
1K1B	A	ALA	325	C	-5.589027	6.631277	-7.452021	-3.033623
1K1B	A	ASP	326	C	-7.647388	6.866215	-11.898825	-3.931685
1K1B	A	SER	327	T	-8.116646	7.601637	-12.484224	-4.227862
1K1B	A	SER	328	T	-8.158045	7.594984	-12.417360	-4.222519
1K1B	A	LEU	329	T	-8.818008	8.936102	-12.725505	-4.342539
1K1B	A	LYS	330	T	-7.491229	4.473097	-13.589641	-4.929237
1K1B	A	ASN	331	C	-6.418517	4.437702	-12.279785	-4.878732
1K1B	A	CYS	332	T	-6.201932	4.927824	-12.040466	-4.841380
1K1B	A	HIS	333	T	-6.197299	4.958652	-12.042769	-4.838631
1K1B	A	ASN	334	T	-6.197330	4.961019	-12.040852	-4.838346
1K1B	A	ASP	335	T	-6.260671	5.085251	-11.851617	-4.822735
1K1B	A	THR	336	C	-6.775355	7.052983	-11.077545	-4.596366
1K1B	A	PRO	337	C	-7.381642	11.452744	-8.808507	-3.759835
1K1B	A	LEU	338	G	-7.150388	11.058232	-8.663841	-3.629102
1K1B	A	MET	339	G	-7.084343	10.788735	-8.887987	-3.629043
1K1B	A	VAL	340	G	-7.090204	10.732258	-8.876987	-3.606515
1K1B	A	ALA	341	G	-7.171778	10.031679	-9.154696	-3.469312
1K1B	A	ARG	342	C	-7.351397	9.290636	-9.667537	-3.414394
1K1B	A	SER	343	C	-7.686871	8.857799	-10.554616	-3.420744
1K1B	A	ARG	344	C	-7.677435	10.678643	-10.540815	-4.055684
1K1B	A	ARG	345	H	-7.690809	10.923353	-10.506893	-4.138894
1K1B	A	VAL	346	H	-7.705148	13.335856	-10.270407	-4.917196
1K1B	A	ILE	347	H	-6.724763	11.442157	-8.793120	-4.622790
1K1B	A	ASP	348	H	-5.973254	9.824546	-8.120060	-4.165346
1K1B	A	ILE	349	H	-4.859741	9.072775	-5.974915	-3.327295
1K1B	A	LEU	350	H	-4.859741	9.072775	-5.974915	-3.327295
1K1B	A	ARG	351	H	-4.859741	9.072775	-5.974915	-3.327295
1K1B	A	GLY	352	H	-4.859741	9.072775	-5.974915	-3.327295
1K59	A	ASP	2	C	-5.274884	3.757898	-9.074314	-3.316776
1K59	A	ASN	3	C	-5.274884	3.757898	-9.074314	-3.316776
1K59	A	SER	4	H	-5.274884	3.757898	-9.074314	-3.316776
1K59	A	ARG	5	H	-5.274884	3.757898	-9.074314	-3.316776
1K59	A	TYR	6	H	-9.002668	10.046781	-13.479526	-5.045394
1K59	A	THR	7	H	-9.393992	10.962079	-13.795913	-5.378837
1K59	A	HIS	8	H	-10.211394	12.743393	-14.284095	-5.630280
1K59	A	PHE	9	H	-10.683311	14.451572	-12.562210	-4.838595
1K59	A	LEU	10	H	-10.686914	14.432038	-12.530025	-4.822818
1K59	A	THR	11	H	-10.691946	14.397519	-12.508812	-4.816580

1K59	A	GLN	12	H	-12.535222	15.533302	-14.871704	-5.347031
1K59	A	HIS	13	H	-13.325215	12.275686	-17.579133	-5.246568
1K59	A	TYR	14	B	-10.592448	10.738862	-13.933246	-4.606353
1K59	A	ASP	15	T	-7.053009	6.918369	-10.565081	-3.987915
1K59	A	ALA	16	T	-4.111184	5.531442	-7.232269	-3.762792
1K59	A	LYS	17	T	-4.094878	5.579260	-7.301796	-3.779205
1K59	A	PRO	18	T	-4.093045	5.585048	-7.315787	-3.782148
1K59	A	GLN	19	T	-4.092871	5.585119	-7.317991	-3.782547
1K59	A	GLY	20	T	-4.096861	5.576090	-7.296250	-3.781160
1K59	A	ARG	21	T	-6.161792	7.285411	-10.045735	-4.405374
1K59	A	ASP	22	C	-7.452145	7.313348	-12.142421	-4.760432
1K59	A	ASP	23	H	-8.782518	6.234014	-14.907656	-5.068315
1K59	A	ARG	24	H	-9.891187	7.034975	-15.589858	-4.846983
1K59	A	TYR	25	H	-11.034947	9.121865	-15.957801	-5.011782
1K59	A	CYS	26	H	-11.035050	9.123153	-15.960503	-5.017147
1K59	A	GLU	27	H	-12.989147	11.503363	-18.817826	-5.554818
1K59	A	SER	28	H	-12.741891	11.021247	-18.096623	-5.108783
1K59	A	ILE	29	H	-12.770331	11.059628	-18.005432	-5.090258
1K59	A	MET	30	H	-12.646126	10.705164	-18.297963	-5.153569
1K59	A	ARG	31	H	-12.289342	9.454186	-18.138121	-5.001877
1K59	A	ARG	32	H	-11.673980	9.914707	-17.325092	-5.304714
1K59	A	ARG	33	H	-10.221251	10.762920	-14.458464	-5.233260
1K59	A	GLY	34	C	-6.623501	9.758747	-9.119464	-4.461463
1K59	A	LEU	35	T	-6.612740	9.789948	-9.166229	-4.467157
1K59	A	THR	36	T	-6.605317	9.785808	-9.218167	-4.473899
1K59	A	SER	37	T	-6.600587	9.765587	-9.260311	-4.476781
1K59	A	PRO	38	T	-6.599712	9.763887	-9.267702	-4.477732
1K59	A	CYS	39	T	-8.479381	9.933372	-13.003293	-4.902715
1K59	A	LYS	40	T	-8.792360	8.851221	-13.969732	-5.010719
1K59	A	ASP	41	T	-9.203454	8.251119	-14.590060	-5.013440
1K59	A	ILE	42	E	-9.831055	10.076144	-14.654637	-5.329796
1K59	A	ASN	43	E	-10.851701	10.868804	-16.583721	-6.021294
1K59	A	THR	44	E	-11.172905	11.868455	-16.053295	-6.001388
1K59	A	PHE	45	E	-12.512497	15.270722	-16.142573	-5.529927
1K59	A	ILE	46	E	-10.824130	11.594131	-15.118133	-5.531773
1K59	A	HIS	47	C	-10.496206	10.161784	-15.918520	-5.566785
1K59	A	GLY	48	C	-9.137210	6.766592	-15.110879	-5.145453
1K59	A	ASN	49	C	-9.022256	7.593579	-14.764505	-5.097767
1K59	A	LYS	50	H	-9.019163	7.619683	-14.764682	-5.096786
1K59	A	ARG	51	H	-9.043439	7.463441	-14.752781	-5.073405
1K59	A	SER	52	H	-9.063234	7.465391	-14.663825	-5.052046
1K59	A	ILE	53	H	-9.939006	12.015377	-13.255293	-4.902154
1K59	A	LYS	54	H	-10.800851	13.765604	-14.392134	-5.174747
1K59	A	ALA	55	G	-10.196310	10.127721	-15.152585	-5.138226
1K59	A	ILE	56	G	-8.336132	6.559861	-13.934249	-5.060632
1K59	A	CYS	57	G	-7.921293	5.336330	-14.851229	-5.341902
1K59	A	GLU	58	T	-7.543784	4.755885	-14.989167	-5.409629
1K59	A	ASN	59	T	-7.265070	5.259529	-14.705956	-5.529077
1K59	A	LYS	60	T	-7.017631	5.535052	-14.301437	-5.470391
1K59	A	ASN	61	T	-7.073875	5.476607	-14.363457	-5.521380
1K59	A	GLY	62	E	-6.770208	6.635030	-12.834316	-5.159903
1K59	A	ASN	63	E	-5.725468	7.007924	-10.017448	-4.600801
1K59	A	PRO	64	E	-4.474215	5.820468	-8.361847	-4.174752
1K59	A	HIS	65	E	-4.012710	6.832864	-7.603846	-4.190494
1K59	A	ARG	66	T	-4.012586	6.833170	-7.604740	-4.190469
1K59	A	GLU	67	T	-4.015265	6.829090	-7.587731	-4.187792
1K59	A	ASN	68	T	-4.044121	6.819372	-7.487415	-4.171220
1K59	A	LEU	69	E	-4.374513	7.679375	-6.981722	-4.204276
1K59	A	ARG	70	E	-8.830703	8.355453	-12.869340	-4.550766
1K59	A	ILE	71	E	-10.568944	9.770169	-15.843774	-5.328804
1K59	A	SER	72	E	-10.588375	9.801718	-15.595062	-5.219936
1K59	A	LYS	73	C	-10.544722	9.970790	-15.616950	-5.234549
1K59	A	SER	74	C	-10.529442	10.083705	-15.604057	-5.227711
1K59	A	SER	75	C	-10.513769	10.255426	-15.572316	-5.231136
1K59	A	PHE	76	E	-11.203887	12.645650	-15.570955	-5.408905
1K59	A	GLN	77	E	-11.632081	13.502230	-15.878843	-5.437476
1K59	A	VAL	78	E	-11.547782	13.149269	-15.832499	-5.396346
1K59	A	THR	79	E	-11.608258	12.890399	-16.065190	-5.480044
1K59	A	THR	80	E	-11.690021	12.114675	-16.507514	-5.521648
1K59	A	CYS	81	E	-11.350349	10.584337	-17.237732	-5.670215
1K59	A	LYS	82	E	-8.055137	7.000488	-13.815640	-5.529014
1K59	A	LEU	83	E	-6.049551	5.860794	-11.154068	-4.943046
1K59	A	HIS	84	E	-4.369354	3.846460	-9.677324	-4.599642
1K59	A	GLY	85	C	-3.718954	4.636776	-8.391204	-4.285167
1K59	A	GLY	86	C	-3.663231	4.812079	-8.353259	-4.241053
1K59	A	SER	87	C	-3.658709	4.822712	-8.359112	-4.233463
1K59	A	PRO	88	C	-3.665682	4.817412	-8.322691	-4.220967
1K59	A	TRP	89	T	-3.865482	5.260285	-7.814247	-4.074586
1K59	A	PRO	90	T	-4.999747	6.592616	-8.253620	-3.791697
1K59	A	PRO	91	T	-6.137500	6.708114	-10.092975	-3.872063
1K59	A	CYS	92	T	-6.592401	7.237938	-10.854564	-4.424423

1K59	A	GLN	93	E	-7.457128	7.874227	-12.586554	-5.255010
1K59	A	TYR	94	E	-9.463879	11.276521	-12.934727	-5.158027
1K59	A	ARG	95	E	-9.099629	6.754255	-14.005608	-4.537772
1K59	A	ALA	96	E	-6.379154	8.471653	-9.843743	-4.714947
1K59	A	THR	97	E	-6.374396	8.477080	-9.873434	-4.717644
1K59	A	ALA	98	E	-6.370261	8.483158	-9.900547	-4.721194
1K59	A	GLY	99	E	-6.369603	8.486608	-9.904976	-4.721745
1K59	A	PHE	100	E	-6.375340	8.506302	-9.864725	-4.723666
1K59	A	ARG	101	E	-8.806185	9.540043	-13.654734	-5.132745
1K59	A	ASN	102	C	-9.184881	10.013095	-13.713930	-5.181571
1K59	A	VAL	103	C	-9.715091	13.721561	-11.795016	-4.402865
1K59	A	VAL	104	E	-9.710912	13.987092	-11.309940	-4.127972
1K59	A	VAL	105	E	-7.471401	9.176765	-10.610484	-4.457950
1K59	A	ALA	106	E	-4.740558	5.865788	-9.287848	-4.855142
1K59	A	CYS	107	E	-3.740607	6.778045	-8.059626	-5.018096
1K59	A	GLU	108	E	-3.652395	7.163616	-7.925487	-4.960757
1K59	A	ASN	109	T	-3.647787	7.202319	-7.923884	-4.956787
1K59	A	GLY	110	T	-3.648643	7.200052	-7.919919	-4.957457
1K59	A	LEU	111	E	-3.750060	7.450550	-7.661950	-4.972511
1K59	A	PRO	112	E	-4.793394	9.683895	-7.097766	-4.576891
1K59	A	VAL	113	E	-6.506833	12.157676	-7.804437	-4.435234
1K59	A	HIS	114	E	-8.268062	11.989915	-11.277041	-4.676057
1K59	A	LEU	115	E	-8.329890	11.284670	-11.851073	-4.797386
1K59	A	ASP	116	C	-8.279427	11.459194	-12.066028	-5.013454
1K59	A	GLY	117	C	-8.074338	11.937403	-12.026967	-5.278938
1K59	A	SER	118	G	-8.063061	12.191062	-11.876320	-5.280991
1K59	A	ILE	119	G	-7.476409	12.679524	-9.452357	-4.491058
1K59	A	PHE	120	G	-5.805397	10.692014	-6.255814	-3.286408
1K59	A	ARG	121	C	-5.805397	10.692014	-6.255814	-3.286408
1K59	A	ARG	122	C	-5.805397	10.692014	-6.255814	-3.286408
1K59	A	PRO	123	C	-5.805397	10.692014	-6.255814	-3.286408
1KAO	A	MET	1	C	-8.180909	10.604419	-10.480058	-4.255988
1KAO	A	ARG	2	C	-8.180909	10.604419	-10.480058	-4.255988
1KAO	A	GLU	3	E	-8.180909	10.604419	-10.480058	-4.255988
1KAO	A	TYR	4	E	-8.180909	10.604419	-10.480058	-4.255988
1KAO	A	LYS	5	E	-10.856847	13.054275	-14.501351	-5.589624
1KAO	A	VAL	6	E	-10.250055	16.049177	-10.054139	-4.053338
1KAO	A	VAL	7	E	-10.153998	15.782889	-10.446953	-4.117487
1KAO	A	VAL	8	E	-9.193270	12.862219	-11.662521	-4.769297
1KAO	A	LEU	9	E	-8.569188	10.245545	-12.971771	-5.185667
1KAO	A	GLY	10	C	-7.327972	7.293708	-12.665698	-5.203689
1KAO	A	SER	11	T	-6.826187	7.504523	-12.275517	-5.258096
1KAO	A	GLY	12	T	-6.757250	7.631968	-12.356100	-5.295112
1KAO	A	GLY	13	T	-6.764691	7.573494	-12.363876	-5.300116
1KAO	A	VAL	14	T	-6.783050	7.534835	-12.323230	-5.296485
1KAO	A	GLY	15	C	-7.037649	7.889016	-12.163196	-5.344900
1KAO	A	LYS	16	H	-8.055517	8.723732	-13.038329	-5.585764
1KAO	A	SER	17	H	-10.520812	12.014698	-14.850412	-5.103519
1KAO	A	ALA	18	H	-10.802001	13.277684	-14.077063	-4.854551
1KAO	A	LEU	19	H	-11.128224	14.494112	-13.515573	-4.771999
1KAO	A	THR	20	H	-11.499144	15.579879	-12.714040	-4.495349
1KAO	A	VAL	21	H	-11.520104	15.554848	-12.663649	-4.475545
1KAO	A	GLN	22	H	-11.213597	13.851690	-14.608797	-5.659260
1KAO	A	PHE	23	H	-7.486730	11.001105	-9.825298	-4.633507
1KAO	A	VAL	24	H	-6.869800	10.420629	-9.923011	-4.704255
1KAO	A	THR	25	H	-6.450299	10.929734	-9.350649	-4.669432
1KAO	A	GLY	26	C	-5.911940	10.179624	-9.028489	-4.614563
1KAO	A	THR	27	C	-5.738323	10.022377	-9.008388	-4.536381
1KAO	A	PHE	28	C	-5.748746	10.069166	-8.980874	-4.541480
1KAO	A	ILE	29	C	-5.733255	10.060209	-8.993356	-4.549241
1KAO	A	GLU	30	C	-5.758959	9.672435	-9.227081	-4.563347
1KAO	A	LYS	31	C	-6.021182	9.545319	-9.717320	-4.560722
1KAO	A	TYR	32	C	-6.280948	9.472279	-10.319456	-4.711622
1KAO	A	ASP	33	T	-5.980404	8.833792	-9.911069	-4.486723
1KAO	A	PRO	34	T	-6.098522	8.570871	-9.932042	-4.425571
1KAO	A	THR	35	T	-6.221954	8.611820	-9.752246	-4.339804
1KAO	A	ILE	36	T	-6.373748	8.531807	-9.558370	-4.260766
1KAO	A	GLU	37	C	-6.435437	8.502747	-9.391439	-4.241146
1KAO	A	ASP	38	E	-8.518143	10.516125	-12.041693	-4.772308
1KAO	A	PHE	39	E	-8.639734	10.712296	-11.729845	-4.772474
1KAO	A	TYR	40	E	-11.004927	15.823294	-13.710201	-5.280868
1KAO	A	ARG	41	E	-7.983184	12.828119	-9.679021	-4.754954
1KAO	A	LYS	42	E	-7.858121	12.892068	-9.860719	-4.764993
1KAO	A	GLU	43	E	-7.626817	12.229413	-10.323009	-4.805297
1KAO	A	ILE	44	E	-7.028449	10.187194	-10.175299	-4.438724
1KAO	A	GLU	45	E	-5.947126	7.231542	-9.639860	-4.135645
1KAO	A	VAL	46	E	-5.798215	6.948620	-9.763023	-4.078326
1KAO	A	ASP	47	T	-5.792534	6.902449	-9.806278	-4.078028
1KAO	A	SER	48	T	-5.800096	6.849327	-9.789771	-4.066095
1KAO	A	SER	49	E	-5.849407	6.661389	-9.763908	-4.051884
1KAO	A	PRO	50	E	-6.585432	6.655845	-10.322574	-3.988885

1KAO	A	SER	51	E	-8.188054	6.759763	-12.877738	-4.314835
1KAO	A	VAL	52	E	-9.434580	9.933346	-12.645461	-4.150075
1KAO	A	LEU	53	E	-10.838150	13.513253	-13.043540	-4.385779
1KAO	A	GLU	54	E	-11.787673	16.899539	-13.530971	-5.096525
1KAO	A	ILE	55	E	-12.070015	17.344027	-13.634635	-4.928472
1KAO	A	LEU	56	E	-11.465950	14.002866	-14.661816	-5.109555
1KAO	A	ASP	57	E	-10.667598	11.279686	-15.155730	-5.304761
1KAO	A	THR	58	C	-7.134348	8.382397	-10.882069	-4.729910
1KAO	A	ALA	59	C	-6.842514	7.813350	-11.431436	-4.824561
1KAO	A	GLY	60	T	-6.610237	7.716083	-11.693100	-4.977343
1KAO	A	THR	61	T	-6.566501	7.697764	-11.792084	-4.985098
1KAO	A	GLU	62	T	-6.562205	7.688417	-11.815526	-4.985309
1KAO	A	GLN	63	T	-6.843536	7.266930	-12.403558	-5.141704
1KAO	A	PHE	64	C	-7.133493	7.492487	-12.483822	-5.246796
1KAO	A	ALA	65	H	-8.042297	7.413055	-13.381188	-5.069498
1KAO	A	SER	66	H	-9.209902	7.063608	-15.201180	-4.964331
1KAO	A	MET	67	H	-9.915254	7.654394	-15.538510	-4.777442
1KAO	A	ARG	68	H	-10.327734	8.416001	-15.155036	-4.705154
1KAO	A	ASP	69	H	-11.835148	9.985470	-17.268332	-5.031663
1KAO	A	LEU	70	H	-10.702771	12.265731	-13.816081	-4.858305
1KAO	A	TYR	71	H	-9.918487	13.219555	-12.980649	-5.208572
1KAO	A	ILE	72	H	-8.304373	9.616812	-12.534365	-5.193341
1KAO	A	LYS	73	H	-7.113969	7.173127	-12.575945	-5.327868
1KAO	A	ASN	74	H	-7.110367	7.198957	-12.584877	-5.328809
1KAO	A	GLY	75	C	-7.109715	7.211841	-12.582327	-5.329195
1KAO	A	GLN	76	C	-7.113407	7.173974	-12.581040	-5.329073
1KAO	A	GLY	77	E	-7.191396	6.886436	-12.585231	-5.346201
1KAO	A	PHE	78	E	-9.754184	13.745317	-12.797625	-5.159493
1KAO	A	ILE	79	E	-10.197920	16.360928	-11.368216	-4.797062
1KAO	A	LEU	80	E	-10.735395	19.064682	-9.752441	-4.308511
1KAO	A	VAL	81	E	-10.812289	19.137174	-9.463558	-4.215310
1KAO	A	TYR	82	E	-12.055238	17.482932	-13.714839	-5.069704
1KAO	A	SER	83	E	-10.613619	12.287498	-14.256828	-5.257400
1KAO	A	LEU	84	T	-10.387662	11.780221	-14.612123	-5.280731
1KAO	A	VAL	85	T	-9.915876	9.861198	-15.340363	-5.401096
1KAO	A	ASN	86	T	-9.911986	9.857232	-15.366596	-5.407895
1KAO	A	GLN	87	H	-9.921255	9.756605	-15.387754	-5.409742
1KAO	A	GLN	88	H	-10.119100	8.933623	-15.825229	-5.464777
1KAO	A	SER	89	H	-10.257428	8.391832	-15.972186	-5.506545
1KAO	A	PHE	90	H	-12.279163	13.403510	-17.067852	-5.839194
1KAO	A	GLN	91	H	-11.001113	10.592591	-15.559686	-5.258471
1KAO	A	ASP	92	H	-10.842857	10.946861	-15.567090	-5.294048
1KAO	A	ILE	93	H	-10.831563	11.052949	-15.553384	-5.295675
1KAO	A	LYS	94	H	-10.795813	11.133880	-15.621653	-5.315770
1KAO	A	PRO	95	H	-10.812694	10.991967	-15.634005	-5.305178
1KAO	A	MET	96	H	-11.498812	12.423690	-15.932036	-5.475577
1KAO	A	ARG	97	H	-12.160646	13.091197	-16.756113	-5.561528
1KAO	A	ASP	98	H	-11.770861	10.792056	-16.672764	-5.005079
1KAO	A	GLN	99	H	-11.158490	11.522826	-14.588890	-4.461468
1KAO	A	ILE	100	H	-9.838957	16.675127	-13.084429	-6.629710
1KAO	A	ILE	101	H	-9.258559	13.723680	-12.766968	-5.480322
1KAO	A	ARG	102	H	-8.334622	10.483342	-11.624333	-4.449212
1KAO	A	VAL	103	H	-7.268150	9.277059	-10.782312	-4.545070
1KAO	A	LYS	104	H	-6.374236	7.399563	-10.577394	-4.474695
1KAO	A	ARG	105	T	-4.511714	8.045967	-6.707062	-3.863599
1KAO	A	TYR	106	T	-4.480779	8.164136	-6.765877	-3.876039
1KAO	A	GLU	107	T	-4.443839	8.381167	-6.746373	-3.868614
1KAO	A	LYS	108	C	-4.442565	8.440259	-6.709705	-3.860223
1KAO	A	VAL	109	C	-4.460438	8.490755	-6.592039	-3.841732
1KAO	A	PRO	110	C	-5.705415	11.459265	-7.010254	-3.877591
1KAO	A	VAL	111	E	-6.010286	12.202130	-6.430573	-3.722987
1KAO	A	ILE	112	E	-7.196541	15.367661	-5.832523	-3.506216
1KAO	A	LEU	113	E	-9.163400	17.800404	-8.072863	-3.844706
1KAO	A	VAL	114	E	-9.705532	16.097668	-9.881337	-4.079637
1KAO	A	GLY	115	E	-9.771327	15.491250	-10.363612	-4.247845
1KAO	A	ASN	116	E	-10.652591	11.551481	-15.706616	-5.399869
1KAO	A	LYS	117	T	-9.679145	9.946421	-14.798820	-5.504050
1KAO	A	VAL	118	T	-7.713522	7.062044	-12.570055	-4.829748
1KAO	A	ASP	119	T	-7.115072	6.002289	-12.763001	-4.825055
1KAO	A	LEU	120	T	-7.066084	6.088862	-12.800802	-4.809976
1KAO	A	GLU	121	G	-7.061816	6.093155	-12.821270	-4.812120
1KAO	A	SER	122	G	-7.067525	6.057636	-12.805601	-4.805265
1KAO	A	GLU	123	G	-7.299509	5.627543	-12.958409	-4.805637
1KAO	A	ARG	124	C	-8.502690	7.126532	-13.507941	-4.693462
1KAO	A	GLU	125	C	-9.880450	7.215880	-15.794682	-5.153522
1KAO	A	VAL	126	C	-11.000744	8.644239	-16.532908	-4.812687
1KAO	A	SER	127	C	-10.268527	6.829134	-16.297790	-4.865912
1KAO	A	SER	128	H	-10.058450	7.082946	-16.157252	-4.809910
1KAO	A	SER	129	H	-9.441689	6.741838	-15.247925	-4.568111
1KAO	A	GLU	130	H	-9.361727	7.223858	-15.090591	-4.579391
1KAO	A	GLY	131	H	-9.094312	8.404046	-14.122210	-4.463437

1KAO	A	ARG	132	H	-8.858597	8.727384	-13.246017	-4.162461
1KAO	A	ALA	133	H	-7.539328	7.360379	-11.172102	-3.868830
1KAO	A	LEU	134	H	-7.548028	7.444468	-11.094571	-3.865234
1KAO	A	ALA	135	H	-7.301577	8.118206	-11.258595	-4.230248
1KAO	A	GLU	136	H	-6.572581	8.482723	-11.028212	-4.964869
1KAO	A	GLU	137	H	-6.553641	8.572170	-11.051176	-4.982954
1KAO	A	TRP	138	H	-6.662660	8.868689	-11.074304	-5.217624
1KAO	A	GLY	139	C	-6.657473	8.895384	-11.082409	-5.217004
1KAO	A	CYS	140	C	-6.730441	8.825693	-11.014446	-5.254140
1KAO	A	PRO	141	C	-8.308321	11.304489	-11.945287	-5.171579
1KAO	A	PHE	142	E	-9.172233	12.946047	-12.167220	-5.153596
1KAO	A	MET	143	E	-9.262739	12.407638	-12.257554	-5.116794
1KAO	A	GLU	144	E	-10.581417	15.223655	-13.808142	-5.614213
1KAO	A	THR	145	C	-10.283604	13.248318	-14.223738	-5.470772
1KAO	A	SER	146	T	-10.460103	11.857953	-15.031994	-5.464489
1KAO	A	ALA	147	T	-9.811748	9.901866	-14.861163	-5.232551
1KAO	A	LYS	148	T	-9.426960	9.030833	-15.099145	-5.315867
1KAO	A	SER	149	T	-9.376755	8.841753	-15.139020	-5.248101
1KAO	A	LYS	150	H	-9.381801	8.593222	-15.227011	-5.214907
1KAO	A	THR	151	H	-9.165306	8.388773	-14.991941	-5.045452
1KAO	A	MET	152	H	-9.315272	8.220979	-15.054621	-5.019519
1KAO	A	VAL	153	H	-9.616602	8.304413	-14.837150	-4.757270
1KAO	A	ASP	154	H	-9.725677	8.244870	-14.723851	-4.737942
1KAO	A	GLU	155	H	-9.840338	8.138420	-14.529803	-4.686711
1KAO	A	LEU	156	H	-12.029045	14.992845	-14.991650	-4.936945
1KAO	A	PHE	157	H	-12.109634	17.499977	-13.737063	-4.867030
1KAO	A	ALA	158	H	-12.268971	17.492734	-13.870456	-4.887023
1KAO	A	GLU	159	H	-12.448237	18.226803	-13.543496	-4.892887
1KAO	A	ILE	160	H	-12.515498	18.354682	-13.327412	-4.845601
1KAO	A	VAL	161	H	-12.550884	17.869676	-13.844528	-5.057544
1KAO	A	ARG	162	H	-12.474289	13.287867	-18.033730	-6.548518
1KAO	A	GLN	163	H	-8.338146	11.217603	-11.768955	-5.382652
1KAO	A	MET	164	H	-5.765551	8.264495	-8.350298	-4.057496
1KAO	A	ASN	165	H	-5.765551	8.264495	-8.350298	-4.057496
1KAO	A	TYR	166	H	-5.765551	8.264495	-8.350298	-4.057496
1KAO	A	ALA	167	C	-5.765551	8.264495	-8.350298	-4.057496
1KCQ	A	VAL	158	C	-8.351816	8.719827	-11.030197	-3.745668
1KCQ	A	VAL	159	C	-8.351816	8.719827	-11.030197	-3.745668
1KCQ	A	GLN	160	E	-8.351816	8.719827	-11.030197	-3.745668
1KCQ	A	ARG	161	E	-8.351816	8.719827	-11.030197	-3.745668
1KCQ	A	LEU	162	E	-11.069250	13.061978	-13.298235	-4.595169
1KCQ	A	PHE	163	E	-13.830133	16.807482	-16.943812	-5.784906
1KCQ	A	GLN	164	E	-13.732785	14.821288	-17.905822	-5.772662
1KCQ	A	VAL	165	E	-13.385162	13.398801	-18.637248	-5.812885
1KCQ	A	LYS	166	T	-12.447962	9.640662	-20.554727	-6.681293
1KCQ	A	GLY	167	T	-9.541509	9.218747	-13.833525	-4.862012
1KCQ	A	ARG	168	T	-9.357521	9.157354	-13.700729	-4.607126
1KCQ	A	ARG	169	T	-8.373505	9.203079	-11.250561	-3.764787
1KCQ	A	VAL	170	T	-6.498227	9.636875	-7.681819	-3.295111
1KCQ	A	VAL	171	E	-6.349975	10.213880	-7.740922	-3.436774
1KCQ	A	ARG	172	E	-6.283259	10.283514	-7.876578	-3.489781
1KCQ	A	ALA	173	E	-5.958284	9.985161	-8.302183	-3.860262
1KCQ	A	THR	174	E	-5.606871	9.691570	-8.404999	-4.110332
1KCQ	A	GLU	175	E	-5.691012	9.709551	-8.756001	-4.357754
1KCQ	A	VAL	176	C	-5.735160	9.516337	-8.821293	-4.391164
1KCQ	A	PRO	177	C	-5.756161	9.494278	-8.812653	-4.411323
1KCQ	A	VAL	178	C	-5.967409	9.465469	-8.780851	-4.431115
1KCQ	A	SER	179	G	-7.038361	10.181995	-9.872243	-4.566415
1KCQ	A	TRP	180	G	-8.405200	13.705402	-9.948101	-4.546325
1KCQ	A	GLU	181	G	-8.466073	13.579788	-9.863184	-4.536023
1KCQ	A	SER	182	C	-9.859795	14.962814	-11.503447	-4.941383
1KCQ	A	PHE	183	T	-11.120493	17.879604	-12.298366	-5.435166
1KCQ	A	ASN	184	T	-12.243556	16.899635	-15.440918	-6.059365
1KCQ	A	ASN	185	T	-12.813346	13.162436	-18.335055	-6.155771
1KCQ	A	GLY	186	T	-12.937985	13.150018	-18.377961	-5.983074
1KCQ	A	ASP	187	E	-12.919892	13.577642	-18.045760	-5.902170
1KCQ	A	CYS	188	E	-12.826470	14.447320	-17.405295	-5.774420
1KCQ	A	PHE	189	E	-12.928288	16.674400	-15.953480	-5.498301
1KCQ	A	ILE	190	E	-12.267185	16.350793	-14.557686	-5.143455
1KCQ	A	LEU	191	E	-11.384790	13.420633	-14.777018	-5.218589
1KCQ	A	ASP	192	E	-9.480075	9.551371	-14.343648	-5.450375
1KCQ	A	LEU	193	T	-7.985225	11.065122	-11.143163	-5.029125
1KCQ	A	GLY	194	T	-7.975875	11.082406	-11.188956	-5.036146
1KCQ	A	ASN	195	E	-7.976131	11.080159	-11.187956	-5.036230
1KCQ	A	ASN	196	E	-7.977660	11.076027	-11.178313	-5.035654
1KCQ	A	ILE	197	E	-8.024520	11.214579	-10.919249	-5.000724
1KCQ	A	HIS	198	E	-10.435508	12.193847	-14.081825	-5.479360
1KCQ	A	GLN	199	E	-13.692814	14.792030	-17.891326	-6.136019
1KCQ	A	TRP	200	E	-11.933989	11.487875	-16.917336	-5.888516
1KCQ	A	CYS	201	T	-10.041615	7.231355	-16.698707	-5.775503
1KCQ	A	GLY	202	T	-10.040181	7.238951	-16.717863	-5.784516

1KCQ	A	SER	203	T	-9.925217	7.231742	-16.805080	-5.710563
1KCQ	A	ASN	204	T	-9.880175	7.447334	-16.796725	-5.709905
1KCQ	A	SER	205	C	-9.897113	7.329398	-16.799563	-5.704835
1KCQ	A	ASN	206	H	-10.721032	8.180819	-17.136971	-5.506065
1KCQ	A	ARG	207	H	-10.708876	8.237234	-17.084742	-5.462096
1KCQ	A	TYR	208	H	-11.346878	10.298934	-16.849049	-5.653673
1KCQ	A	GLU	209	H	-12.501666	11.252790	-17.925990	-5.340182
1KCQ	A	ARG	210	H	-11.727673	11.696807	-15.988687	-5.080047
1KCQ	A	LEU	211	H	-8.989005	10.557268	-12.073092	-4.663994
1KCQ	A	LYS	212	H	-8.989460	10.563140	-12.070170	-4.666419
1KCQ	A	ALA	213	H	-8.936486	10.660420	-12.182832	-4.678226
1KCQ	A	THR	214	H	-8.892244	10.676813	-12.333806	-4.709302
1KCQ	A	GLN	215	H	-8.854543	10.673854	-12.479714	-4.755551
1KCQ	A	VAL	216	H	-9.688236	11.407807	-14.132062	-5.147660
1KCQ	A	SER	217	H	-9.688743	11.393104	-14.126405	-5.140217
1KCQ	A	LYS	218	H	-9.872703	11.285626	-14.514114	-5.293549
1KCQ	A	GLY	219	H	-9.713066	10.577238	-14.551064	-5.254139
1KCQ	A	ILE	220	H	-9.791463	10.525072	-14.599120	-5.218012
1KCQ	A	ARG	221	H	-9.892945	10.032865	-14.745241	-5.195480
1KCQ	A	ASP	222	H	-9.433007	8.591752	-15.226061	-5.284906
1KCQ	A	ASN	223	H	-8.402223	7.656760	-14.092328	-5.312618
1KCQ	A	GLU	224	H	-8.432238	7.511503	-14.102837	-5.320434
1KCQ	A	ARG	225	T	-8.432865	7.421972	-14.123882	-5.301773
1KCQ	A	SER	226	T	-8.430042	7.404656	-14.140877	-5.295451
1KCQ	A	GLY	227	T	-8.492147	7.407944	-13.975406	-5.288173
1KCQ	A	ARG	228	C	-10.470759	5.438466	-17.103855	-4.447195
1KCQ	A	ALA	229	E	-10.003299	8.606649	-14.767702	-4.499315
1KCQ	A	ARG	230	E	-10.132250	9.566150	-14.360918	-4.590834
1KCQ	A	VAL	231	E	-9.114583	11.077330	-12.913889	-5.151187
1KCQ	A	HIS	232	E	-9.105204	11.065215	-12.977499	-5.161901
1KCQ	A	VAL	233	E	-8.703786	9.523710	-13.947946	-5.442802
1KCQ	A	SER	234	E	-8.340938	8.138953	-14.462184	-5.580870
1KCQ	A	GLU	235	T	-7.387901	7.767604	-13.635236	-5.958546
1KCQ	A	GLU	236	T	-7.332604	7.783323	-13.714930	-5.989227
1KCQ	A	GLY	237	T	-6.171083	8.446566	-10.778004	-5.349736
1KCQ	A	THR	238	T	-6.079839	8.758214	-10.658470	-5.292254
1KCQ	A	GLU	239	C	-6.085557	8.786998	-10.613557	-5.288561
1KCQ	A	PRO	240	H	-6.136040	8.931632	-10.343354	-5.211730
1KCQ	A	GLU	241	H	-6.137632	8.973339	-10.291308	-5.192305
1KCQ	A	ALA	242	H	-7.125258	10.798271	-10.274957	-4.965093
1KCQ	A	MET	243	H	-8.308811	12.709801	-11.170672	-4.885695
1KCQ	A	LEU	244	H	-7.561123	12.786121	-9.521653	-4.567132
1KCQ	A	GLN	245	H	-6.667923	10.478278	-9.037849	-4.268785
1KCQ	A	VAL	246	H	-6.634324	10.615774	-9.064818	-4.307733
1KCQ	A	LEU	247	C	-6.577438	10.721489	-9.183080	-4.359644
1KCQ	A	GLY	248	C	-5.330140	7.785468	-8.924385	-4.505071
1KCQ	A	PRO	249	C	-5.016799	9.123151	-8.115637	-4.481128
1KCQ	A	LYS	250	C	-5.017823	9.163687	-8.114620	-4.496922
1KCQ	A	PRO	251	C	-4.935466	9.046948	-8.154442	-4.404815
1KCQ	A	ALA	252	C	-4.641297	8.694286	-7.997622	-4.296625
1KCQ	A	LEU	253	C	-4.826714	9.204286	-7.706245	-4.233755
1KCQ	A	PRO	254	C	-4.815892	7.893935	-9.088479	-4.781689
1KCQ	A	ALA	255	C	-4.139247	6.425955	-9.510890	-5.320861
1KCQ	A	GLY	256	C	-3.564225	5.756652	-8.848849	-5.094801
1KCQ	A	THR	257	C	-3.564225	5.756652	-8.848849	-5.094801
1KCQ	A	GLU	258	C	-3.564225	5.756652	-8.848849	-5.094801
1KCQ	A	ASP	259	C	-3.564225	5.756652	-8.848849	-5.094801
1KEX	A	PHE	1	T	-4.537036	1.895251	-8.466935	-3.072229
1KEX	A	LYS	2	T	-4.537036	1.895251	-8.466935	-3.072229
1KEX	A	CYS	3	T	-4.537036	1.895251	-8.466935	-3.072229
1KEX	A	MET	4	T	-4.537036	1.895251	-8.466935	-3.072229
1KEX	A	GLU	5	E	-6.966413	4.298760	-13.354154	-4.869526
1KEX	A	ALA	6	E	-7.698319	6.330438	-13.793981	-5.384341
1KEX	A	LEU	7	C	-8.755523	10.663661	-13.145517	-5.244055
1KEX	A	GLY	8	T	-8.007237	7.193484	-13.220957	-5.007973
1KEX	A	MET	9	T	-7.776753	6.845894	-13.225438	-4.931273
1KEX	A	GLU	10	T	-7.502241	6.389849	-12.797105	-4.644321
1KEX	A	SER	11	T	-7.193934	6.188083	-12.518379	-4.522334
1KEX	A	GLY	12	T	-7.189590	6.165049	-12.543792	-4.522175
1KEX	A	GLU	13	T	-7.309561	6.201964	-12.375479	-4.415053
1KEX	A	ILE	14	T	-7.407011	6.187069	-12.198699	-4.330857
1KEX	A	HIS	15	T	-7.649711	6.203057	-12.336255	-4.392697
1KEX	A	SER	16	G	-9.041211	7.131586	-14.478175	-4.603389
1KEX	A	ASP	17	G	-9.218341	7.541204	-14.191498	-4.469113
1KEX	A	GLN	18	G	-9.378417	8.091070	-13.905045	-4.500613
1KEX	A	ILE	19	E	-9.335976	8.284756	-13.681682	-4.394191
1KEX	A	THR	20	E	-9.760278	8.495008	-14.221477	-4.213742
1KEX	A	ALA	21	E	-9.681961	8.787682	-14.115944	-4.293889
1KEX	A	SER	22	C	-9.786251	8.509776	-14.245569	-4.292380
1KEX	A	SER	23	C	-9.311350	7.480141	-14.030748	-4.209539
1KEX	A	GLN	24	C	-7.766370	7.061803	-11.946604	-4.538651

1KEX	A	TYR	25	C	-7.738143	7.202842	-11.961969	-4.550710
1KEX	A	SER	26	T	-7.741755	7.186701	-11.951622	-4.550516
1KEX	A	THR	27	T	-7.742188	7.187005	-11.947790	-4.550328
1KEX	A	ASN	28	T	-7.765853	7.208631	-11.869842	-4.567001
1KEX	A	TRP	29	T	-9.387046	9.539271	-12.942471	-4.732539
1KEX	A	SER	30	T	-11.109883	9.712643	-16.281943	-5.387665
1KEX	A	ALA	31	G	-12.311051	11.092158	-17.247992	-5.411779
1KEX	A	GLU	32	G	-13.293962	11.795490	-18.117291	-5.413679
1KEX	A	ARG	33	G	-13.801767	10.727999	-18.608990	-5.130755
1KEX	A	SER	34	C	-13.849119	10.442871	-18.634268	-5.115355
1KEX	A	ARG	35	B	-14.613837	12.671938	-18.838561	-5.264861
1KEX	A	LEU	36	T	-10.341303	11.752207	-13.928467	-5.439422
1KEX	A	ASN	37	T	-10.179484	11.087818	-14.654303	-5.563693
1KEX	A	TYR	38	T	-9.412812	9.843236	-14.079733	-5.377603
1KEX	A	PRO	39	C	-9.396368	9.896898	-14.101742	-5.372105
1KEX	A	GLU	40	C	-9.392458	9.919490	-14.111199	-5.373095
1KEX	A	ASN	41	C	-9.522867	9.480754	-14.162644	-5.354785
1KEX	A	GLY	42	C	-9.413216	10.266265	-13.553445	-5.150005
1KEX	A	TRP	43	B	-9.731675	12.027710	-12.320262	-4.444541
1KEX	A	THR	44	C	-7.089393	7.360722	-10.132159	-4.067266
1KEX	A	PRO	45	T	-6.877636	7.166754	-10.471769	-4.112854
1KEX	A	GLY	46	T	-6.875066	7.171215	-10.491506	-4.117249
1KEX	A	GLU	47	T	-6.874109	7.156538	-10.502951	-4.116185
1KEX	A	ASP	48	T	-6.875570	7.142326	-10.503104	-4.116548
1KEX	A	SER	49	T	-7.568029	6.775899	-11.378705	-4.234634
1KEX	A	TYR	50	T	-9.531674	8.405780	-14.455163	-4.648596
1KEX	A	ARG	51	T	-9.822294	8.494177	-14.091008	-4.346143
1KEX	A	GLU	52	T	-10.539147	10.087283	-14.089334	-4.565514
1KEX	A	TRP	53	C	-11.793764	13.957080	-14.614975	-5.103121
1KEX	A	ILE	54	E	-12.254368	15.443857	-14.319718	-5.177127
1KEX	A	GLN	55	E	-12.497947	12.638038	-16.050649	-5.024114
1KEX	A	VAL	56	E	-10.278048	10.871770	-13.521288	-4.764793
1KEX	A	ASP	57	E	-8.764884	10.608638	-12.305956	-5.108400
1KEX	A	LEU	58	E	-7.816970	11.199154	-9.956942	-4.442880
1KEX	A	GLY	59	E	-7.806499	11.224541	-9.988842	-4.442916
1KEX	A	LEU	60	E	-7.806374	11.226376	-9.988349	-4.442510
1KEX	A	LEU	61	E	-7.815350	11.232723	-9.935268	-4.437651
1KEX	A	ARG	62	E	-7.937043	11.380344	-9.418153	-4.278077
1KEX	A	PHE	63	E	-10.142230	12.978558	-11.732638	-4.363246
1KEX	A	VAL	64	E	-9.382334	12.578811	-9.341096	-3.250143
1KEX	A	THR	65	E	-9.188907	12.316489	-9.827308	-3.399689
1KEX	A	ALA	66	E	-9.185249	12.307410	-9.863488	-3.408155
1KEX	A	VAL	67	E	-9.176031	12.269226	-9.961873	-3.435630
1KEX	A	GLY	68	E	-9.169845	12.132330	-10.097249	-3.470763
1KEX	A	THR	69	E	-9.826479	11.350338	-11.932660	-3.984768
1KEX	A	GLN	70	E	-10.793505	9.598819	-16.008617	-4.923578
1KEX	A	GLY	71	C	-10.346649	9.199450	-15.455213	-4.853025
1KEX	A	ALA	72	E	-10.367082	9.178538	-15.498951	-4.865392
1KEX	A	ILE	73	E	-9.937705	8.576799	-15.134044	-4.945847
1KEX	A	SER	74	T	-8.720846	5.581885	-14.445951	-4.800271
1KEX	A	LYS	75	T	-7.577683	4.846548	-13.280951	-4.747103
1KEX	A	GLU	76	T	-6.461744	6.617904	-11.377494	-4.974238
1KEX	A	THR	77	T	-6.396882	7.116588	-11.271373	-4.989772
1KEX	A	LYS	78	T	-6.397725	7.116040	-11.265882	-4.989766
1KEX	A	LYS	79	C	-6.408094	7.150793	-11.211337	-4.993491
1KEX	A	LYS	80	E	-6.483032	7.477868	-10.958642	-5.027905
1KEX	A	TYR	81	E	-7.738317	11.432574	-10.363347	-5.124227
1KEX	A	TYR	82	E	-11.691635	17.056723	-12.833177	-5.156131
1KEX	A	VAL	83	E	-12.487636	18.940959	-12.536767	-4.977488
1KEX	A	LYS	84	E	-13.350379	19.359311	-14.328795	-5.283139
1KEX	A	THR	85	E	-13.447558	18.560094	-15.057215	-5.387485
1KEX	A	TYR	86	E	-13.079202	19.260885	-14.184166	-5.307483
1KEX	A	LYS	87	E	-12.138304	16.887447	-14.136528	-5.410275
1KEX	A	ILE	88	E	-11.920182	15.539578	-14.296013	-5.052266
1KEX	A	ASP	89	E	-11.713115	13.707933	-15.350819	-5.164330
1KEX	A	VAL	90	E	-9.794614	8.552950	-14.021660	-4.656590
1KEX	A	SER	91	E	-8.053619	5.738905	-13.578019	-4.871355
1KEX	A	SER	92	T	-5.388466	4.315437	-10.615370	-4.728312
1KEX	A	ASN	93	T	-5.133296	5.287140	-10.314562	-4.834708
1KEX	A	GLY	94	T	-5.095870	5.363765	-10.322078	-4.804731
1KEX	A	GLU	95	T	-5.090724	5.399765	-10.322563	-4.801614
1KEX	A	ASP	96	T	-5.094400	5.400583	-10.302465	-4.801471
1KEX	A	TRP	97	E	-5.633976	7.165665	-9.874813	-4.922824
1KEX	A	ILE	98	E	-5.876256	12.247405	-9.428413	-6.195355
1KEX	A	THR	99	E	-5.653533	14.458580	-8.894634	-6.735061
1KEX	A	ILE	100	C	-4.367629	9.027380	-6.255619	-4.211441
1KEX	A	LYS	101	E	-1.538404	5.005931	-4.346291	-4.036516
1KEX	A	GLU	102	E	-1.032807	5.441344	-4.577333	-4.334716
1KEX	A	GLY	103	T	-1.025440	5.462722	-4.610213	-4.338330
1KEX	A	ASN	104	T	-1.025056	5.465397	-4.612303	-4.338456
1KEX	A	LYS	105	E	-1.027643	5.445750	-4.600519	-4.334745

1KEX	A	PRO	106	E	-1.436790	5.047536	-4.151163	-3.947915
1KEX	A	VAL	107	C	-3.764894	6.030776	-6.023123	-3.470003
1KEX	A	LEU	108	C	-5.360127	10.057588	-7.113325	-4.253938
1KEX	A	PHE	109	E	-8.091467	15.443567	-10.436716	-5.641212
1KEX	A	GLN	110	E	-8.532634	14.109074	-11.440162	-5.530948
1KEX	A	GLY	111	C	-8.662737	11.558253	-12.224900	-5.058713
1KEX	A	ASN	112	C	-9.027683	7.946674	-14.003636	-4.668048
1KEX	A	THR	113	C	-6.863193	6.320698	-10.091289	-3.782171
1KEX	A	ASN	114	T	-6.737633	6.582145	-10.143043	-3.785077
1KEX	A	PRO	115	T	-6.732488	6.600374	-10.148939	-3.779458
1KEX	A	THR	116	T	-6.618258	6.742257	-10.144838	-3.736961
1KEX	A	ASP	117	T	-6.613328	6.748391	-10.147870	-3.726981
1KEX	A	VAL	118	C	-6.614418	7.863515	-8.389019	-2.816175
1KEX	A	VAL	119	E	-6.706824	7.953351	-8.030639	-2.636231
1KEX	A	VAL	120	E	-6.703939	8.050358	-7.981863	-2.630228
1KEX	A	ALA	121	E	-6.811813	8.559239	-7.454321	-2.484000
1KEX	A	VAL	122	E	-5.790560	12.016514	-6.244386	-3.707542
1KEX	A	PHE	123	E	-5.870070	12.783382	-6.088338	-3.937848
1KEX	A	PRO	124	E	-5.227130	11.155155	-5.290134	-3.231711
1KEX	A	LYS	125	E	-5.068875	10.978460	-5.447676	-3.244578
1KEX	A	PRO	126	E	-5.070186	10.971461	-5.439273	-3.241578
1KEX	A	LEU	127	E	-5.236384	10.395516	-5.255741	-3.005266
1KEX	A	ILE	128	E	-5.244193	10.359604	-5.234373	-3.002764
1KEX	A	THR	129	E	-5.924059	10.428626	-5.978370	-3.286048
1KEX	A	ARG	130	E	-9.287537	14.472646	-9.259084	-3.956766
1KEX	A	PHE	131	E	-12.189967	17.735193	-12.012330	-4.125575
1KEX	A	VAL	132	E	-12.385543	18.236975	-11.849535	-4.074834
1KEX	A	ARG	133	E	-12.373679	17.610092	-12.622977	-4.436302
1KEX	A	ILE	134	E	-10.454022	14.700442	-10.599349	-3.991576
1KEX	A	LYS	135	E	-10.151143	14.926473	-10.693516	-4.106590
1KEX	A	PRO	136	E	-9.820401	14.549093	-10.916857	-4.188515
1KEX	A	ALA	137	E	-8.093554	12.200839	-9.924573	-4.594950
1KEX	A	THR	138	E	-7.538957	11.052175	-10.054986	-4.580544
1KEX	A	TRP	139	E	-7.328521	11.635179	-9.638595	-4.517582
1KEX	A	GLU	140	E	-7.156500	11.303905	-9.749100	-4.493520
1KEX	A	THR	141	T	-7.148559	11.341805	-9.766897	-4.504414
1KEX	A	GLY	142	T	-7.274832	11.169410	-9.742861	-4.477371
1KEX	A	ILE	143	C	-7.567042	11.715246	-9.489731	-4.417561
1KEX	A	SER	144	C	-7.926103	10.621650	-10.154238	-4.462596
1KEX	A	MET	145	B	-9.527682	14.125180	-11.123329	-5.047160
1KEX	A	ARG	146	E	-14.104608	14.741609	-17.395377	-5.452395
1KEX	A	PHE	147	E	-13.644212	19.203332	-13.784268	-4.992653
1KEX	A	GLU	148	E	-13.625713	19.198607	-13.963073	-5.088615
1KEX	A	VAL	149	E	-12.147056	16.466131	-14.309672	-5.823988
1KEX	A	TYR	150	E	-10.027856	12.730724	-12.766274	-5.322848
1KEX	A	GLY	151	E	-5.725016	7.231385	-9.095637	-4.453236
1KEX	A	CYS	152	E	-4.675078	6.535806	-7.444556	-3.657358
1KEX	A	LYS	153	C	-4.675078	6.535806	-7.444556	-3.657358
1KEX	A	ILE	154	C	-4.675078	6.535806	-7.444556	-3.657358
1KEX	A	THR	155	C	-4.675078	6.535806	-7.444556	-3.657358
1KPF	A	ASP	16	C	-8.758497	9.502619	-10.460143	-3.145907
1KPF	A	THR	17	C	-8.758497	9.502619	-10.460143	-3.145907
1KPF	A	ILE	18	H	-8.758497	9.502619	-10.460143	-3.145907
1KPF	A	PHE	19	H	-8.758497	9.502619	-10.460143	-3.145907
1KPF	A	GLY	20	H	-9.102177	11.930791	-13.186227	-5.619116
1KPF	A	LYS	21	H	-8.680229	11.598539	-12.796748	-5.841885
1KPF	A	ILE	22	H	-6.571280	10.157569	-8.247633	-3.874576
1KPF	A	ILE	23	H	-5.645723	9.922769	-7.889331	-4.188771
1KPF	A	ARG	24	H	-4.913960	5.220061	-6.981855	-2.592628
1KPF	A	LYS	25	T	-3.532773	4.527865	-4.199015	-1.920577
1KPF	A	GLU	26	T	-2.919618	4.593208	-3.608368	-1.856458
1KPF	A	ILE	27	T	-2.515769	5.444697	-3.090235	-1.891809
1KPF	A	PRO	28	T	-2.324558	6.278883	-3.182872	-2.242026
1KPF	A	ALA	29	C	-2.329775	6.306541	-3.150937	-2.243945
1KPF	A	LYS	30	C	-2.407069	6.536104	-3.033809	-2.288809
1KPF	A	ILE	31	E	-2.599107	7.206846	-2.918952	-2.448426
1KPF	A	ILE	32	E	-3.096321	8.336165	-3.395648	-3.118344
1KPF	A	PHE	33	E	-6.544413	9.654289	-6.248418	-2.311737
1KPF	A	GLU	34	E	-7.176762	10.242188	-7.610316	-3.087961
1KPF	A	ASP	35	E	-8.944262	8.062152	-13.244367	-4.096789
1KPF	A	ASP	36	T	-9.069595	7.521712	-13.704301	-4.204952
1KPF	A	ARG	37	T	-9.323619	6.812403	-13.893093	-4.102781
1KPF	A	CYS	38	E	-9.493845	6.036908	-13.507160	-3.673640
1KPF	A	LEU	39	E	-10.508774	9.226646	-12.743828	-3.256823
1KPF	A	ALA	40	E	-9.898457	10.016234	-10.226485	-2.415138
1KPF	A	PHE	41	E	-8.874502	8.576301	-9.632204	-2.380638
1KPF	A	HIS	42	E	-6.094236	3.759138	-8.751738	-2.504918
1KPF	A	ASP	43	T	-5.475497	3.345863	-9.655526	-3.217508
1KPF	A	ILE	44	T	-5.396712	3.140894	-9.550729	-3.001768
1KPF	A	SER	45	T	-5.385939	3.151107	-9.550092	-2.979820
1KPF	A	PRO	46	T	-5.376581	3.191501	-9.538929	-2.967349

1KPF	A	GLN	47	T	-5.583493	2.975510	-9.872769	-3.160553
1KPF	A	ALA	48	T	-6.473416	2.483122	-8.919584	-1.612365
1KPF	A	PRO	49	T	-7.334467	5.054520	-9.272237	-2.032542
1KPF	A	THR	50	E	-7.737877	6.234758	-9.029902	-2.265302
1KPF	A	HIS	51	E	-9.779761	11.428327	-11.971031	-3.924151
1KPF	A	PHE	52	E	-10.356491	15.349838	-10.746604	-4.324266
1KPF	A	LEU	53	E	-11.635034	17.478203	-10.826297	-3.632872
1KPF	A	VAL	54	E	-11.644562	17.131098	-10.983965	-3.605385
1KPF	A	ILE	55	E	-10.958583	13.629723	-11.301682	-3.341145
1KPF	A	PRO	56	E	-10.485460	12.247006	-11.355437	-3.222921
1KPF	A	LYS	57	C	-10.141222	11.134474	-12.184468	-3.558659
1KPF	A	LYS	58	C	-10.066392	10.985354	-12.598043	-3.793314
1KPF	A	HIS	59	C	-10.038338	11.041374	-12.552810	-3.763223
1KPF	A	ILE	60	C	-10.120896	10.888403	-12.752347	-3.844227
1KPF	A	SER	61	C	-9.843766	8.493319	-12.858350	-3.390864
1KPF	A	GLN	62	C	-8.286262	8.180813	-10.392029	-3.292893
1KPF	A	ILE	63	G	-6.276058	7.853561	-8.817411	-3.872820
1KPF	A	SER	64	G	-6.107016	6.655106	-9.034140	-3.509289
1KPF	A	VAL	65	G	-5.338433	3.429921	-8.391829	-2.623221
1KPF	A	ALA	66	C	-5.293566	3.394274	-8.516992	-2.633941
1KPF	A	GLU	67	C	-5.216761	3.246447	-8.839985	-2.740909
1KPF	A	ASP	68	G	-5.302184	2.417582	-8.977561	-2.578585
1KPF	A	ASP	69	G	-5.341238	2.376148	-8.929104	-2.590197
1KPF	A	ASP	70	G	-6.117329	2.807527	-11.036362	-3.402596
1KPF	A	GLU	71	H	-6.323123	2.750669	-11.420469	-3.665559
1KPF	A	SER	72	H	-7.342429	4.222608	-12.738740	-4.406241
1KPF	A	LEU	73	H	-10.325935	9.305396	-13.302892	-3.455306
1KPF	A	LEU	74	H	-10.438531	10.372728	-12.789860	-3.451233
1KPF	A	GLY	75	H	-10.104414	9.431534	-12.291126	-3.071653
1KPF	A	HIS	76	H	-10.353051	9.772653	-12.210697	-3.064226
1KPF	A	LEU	77	H	-10.000330	10.415411	-11.625686	-3.031277
1KPF	A	MET	78	H	-9.134190	9.511831	-12.164489	-3.998845
1KPF	A	ILE	79	H	-8.242033	6.577234	-10.362219	-2.588449
1KPF	A	VAL	80	H	-8.200854	6.688170	-10.407377	-2.619449
1KPF	A	GLY	81	H	-8.171564	6.722573	-10.488779	-2.640062
1KPF	A	LYS	82	H	-8.157267	6.684909	-10.607356	-2.681900
1KPF	A	LYS	83	H	-7.747046	7.416641	-11.568672	-3.845686
1KPF	A	CYS	84	H	-7.545205	8.205613	-12.382692	-4.973657
1KPF	A	ALA	85	H	-6.668929	5.282401	-9.491437	-2.837448
1KPF	A	ALA	86	H	-6.570490	5.340520	-9.432437	-2.757300
1KPF	A	ASP	87	H	-6.264503	5.593052	-9.379080	-2.927452
1KPF	A	LEU	88	H	-5.306192	6.589371	-8.559428	-3.834183
1KPF	A	GLY	89	C	-3.423594	2.013035	-5.895493	-2.437284
1KPF	A	LEU	90	T	-3.404444	2.196055	-5.881839	-2.446544
1KPF	A	ASN	91	T	-3.404688	2.195323	-5.880827	-2.446962
1KPF	A	LYS	92	T	-3.406548	2.184329	-5.870292	-2.445024
1KPF	A	GLY	93	T	-3.426454	2.024482	-5.782561	-2.389075
1KPF	A	TYR	94	E	-5.386586	7.482291	-5.792809	-2.690218
1KPF	A	ARG	95	E	-7.928358	9.400213	-10.839130	-4.280416
1KPF	A	MET	96	E	-8.592673	12.900522	-12.311108	-6.108508
1KPF	A	VAL	97	E	-9.263812	10.160820	-13.002877	-4.523751
1KPF	A	VAL	98	C	-9.227369	9.027501	-13.982107	-4.737420
1KPF	A	ASN	99	C	-8.895596	6.504982	-13.996262	-4.138775
1KPF	A	GLU	100	C	-5.929333	0.654063	-10.165547	-2.782348
1KPF	A	GLY	101	C	-3.806223	-1.881684	-8.319935	-2.370874
1KPF	A	SER	102	G	-3.804031	-1.869616	-8.335970	-2.375451
1KPF	A	ASP	103	G	-3.802464	-1.854865	-8.349603	-2.382053
1KPF	A	GLY	104	G	-3.802421	-1.854273	-8.349774	-2.382091
1KPF	A	GLY	105	C	-3.818933	-1.923728	-8.298508	-2.370841
1KPF	A	GLN	106	C	-6.780982	2.511756	-12.989115	-4.114512
1KPF	A	SER	107	C	-7.277176	3.866337	-13.438122	-4.776055
1KPF	A	VAL	108	C	-8.923386	5.187283	-12.490084	-3.180332
1KPF	A	TYR	109	C	-10.134076	7.547255	-12.987942	-3.473301
1KPF	A	HIS	110	C	-12.599579	12.714227	-14.966762	-3.986739
1KPF	A	VAL	111	C	-12.765131	13.792500	-13.560030	-3.348803
1KPF	A	HIS	112	C	-13.551479	15.886470	-13.663019	-3.293117
1KPF	A	LEU	113	E	-12.120896	15.238896	-13.221246	-4.382803
1KPF	A	HIS	114	E	-11.041397	10.715527	-12.455155	-3.197376
1KPF	A	VAL	115	E	-10.391782	10.524608	-12.724179	-3.669082
1KPF	A	LEU	116	E	-9.403747	10.102521	-15.055225	-6.275887
1KPF	A	GLY	117	E	-7.709896	7.246870	-14.592969	-6.780943
1KPF	A	GLY	118	C	-6.764987	6.620556	-13.048856	-6.169754
1KPF	A	ARG	119	C	-6.503632	6.298865	-12.730203	-5.839450
1KPF	A	GLN	120	C	-5.690231	4.984400	-11.015641	-4.971601
1KPF	A	MET	121	C	-5.086711	4.644833	-9.676496	-4.316553
1KPF	A	HIS	122	T	-1.537086	1.502379	-3.557790	-2.270251
1KPF	A	TRP	123	T	0.245483	3.380779	-1.777011	-2.942946
1KPF	A	PRO	124	T	0.245483	3.380779	-1.777011	-2.942946
1KPF	A	PRO	125	T	0.245483	3.380779	-1.777011	-2.942946
1KPF	A	GLY	126	C	0.245483	3.380779	-1.777011	-2.942946
1KTH	A	GLU	1	C	-6.742044	5.215069	-11.601104	-4.129149

1KTH	A	THR	2	C	-6.742044	5.215069	-11.601104	-4.129149
1KTH	A	ASP	3	G	-6.742044	5.215069	-11.601104	-4.129149
1KTH	A	ILE	4	G	-6.742044	5.215069	-11.601104	-4.129149
1KTH	A	CYS	5	G	-7.885814	7.246231	-14.085623	-5.353893
1KTH	A	LYS	6	G	-8.298148	8.748730	-14.321357	-5.650805
1KTH	A	LEU	7	C	-8.435573	9.291224	-13.896020	-5.358994
1KTH	A	PRO	8	C	-6.885429	7.192845	-11.569077	-4.889184
1KTH	A	LYS	9	C	-6.666955	7.238432	-11.673320	-4.900278
1KTH	A	ASP	10	C	-6.611899	7.034398	-11.859881	-4.911922
1KTH	A	GLU	11	C	-5.223597	6.242003	-10.150579	-4.816017
1KTH	A	GLY	12	C	-3.723136	3.992796	-8.021642	-3.968253
1KTH	A	THR	13	B	-3.619211	4.401894	-7.909300	-3.932238
1KTH	A	CYS	14	C	-3.529073	4.726081	-7.781776	-3.877067
1KTH	A	ARG	15	C	-3.518169	4.825639	-7.762612	-3.871644
1KTH	A	ASP	16	C	-3.548529	4.762290	-7.643180	-3.821299
1KTH	A	PHE	17	C	-4.235804	6.852273	-7.197408	-3.650106
1KTH	A	ILE	18	E	-4.606292	7.124263	-7.025623	-3.555449
1KTH	A	LEU	19	E	-5.839287	10.184777	-7.026481	-3.666270
1KTH	A	LYS	20	E	-7.523591	12.775145	-8.918726	-4.627546
1KTH	A	TRP	21	E	-10.802483	18.676066	-11.060566	-5.346792
1KTH	A	TYR	22	E	-11.834558	14.749254	-14.556475	-5.347221
1KTH	A	TYR	23	E	-9.087160	9.674163	-12.911950	-4.899808
1KTH	A	ASP	24	E	-4.911592	6.374253	-8.569350	-4.378535
1KTH	A	PRO	25	T	-4.708671	6.300556	-8.719923	-4.301697
1KTH	A	ASN	26	T	-4.696354	6.277107	-8.795271	-4.311082
1KTH	A	THR	27	T	-4.695704	6.276711	-8.800832	-4.311290
1KTH	A	LYS	28	T	-4.695980	6.275158	-8.799016	-4.310976
1KTH	A	SER	29	E	-5.398529	6.053665	-9.325221	-4.156369
1KTH	A	CYS	30	E	-6.960750	5.268516	-12.454342	-4.741614
1KTH	A	ALA	31	E	-8.621609	7.021875	-13.672896	-4.538001
1KTH	A	ARG	32	E	-9.661490	12.355661	-12.689268	-4.717820
1KTH	A	PHE	33	E	-10.147951	16.080042	-11.517935	-4.929891
1KTH	A	TRP	34	E	-9.680364	13.932526	-13.122457	-5.537280
1KTH	A	TYR	35	E	-8.176389	7.541590	-13.646945	-5.368130
1KTH	A	GLY	36	C	-4.277391	3.372707	-10.411815	-5.155543
1KTH	A	GLY	37	C	-4.262772	3.389111	-10.495794	-5.171647
1KTH	A	CYS	38	B	-4.257180	3.400185	-10.526190	-5.174875
1KTH	A	GLY	39	C	-4.256703	3.402559	-10.529670	-5.175430
1KTH	A	GLY	40	C	-4.257093	3.401500	-10.527762	-5.175767
1KTH	A	ASN	41	T	-6.243831	4.349947	-13.832050	-5.733963
1KTH	A	GLU	42	T	-6.935823	5.041404	-13.810195	-5.568344
1KTH	A	ASN	43	T	-8.111331	8.026998	-14.405867	-5.950313
1KTH	A	LYS	44	T	-8.603787	9.901114	-13.857103	-6.063201
1KTH	A	PHE	45	B	-9.269848	11.999467	-13.139648	-5.498318
1KTH	A	GLY	46	C	-6.810706	7.982320	-11.397526	-5.283350
1KTH	A	SER	47	C	-6.778175	7.996527	-11.509921	-5.289814
1KTH	A	GLN	48	H	-6.776502	8.006364	-11.527139	-5.296931
1KTH	A	LYS	49	H	-6.739726	8.029587	-11.721547	-5.354558
1KTH	A	GLU	50	H	-6.730387	8.025007	-11.781103	-5.368322
1KTH	A	CYS	51	H	-7.761690	9.324339	-14.302640	-6.185185
1KTH	A	GLU	52	H	-6.761397	10.904299	-11.199989	-6.074320
1KTH	A	LYS	53	H	-4.972720	9.585028	-7.695776	-4.827300
1KTH	A	VAL	54	H	-4.423134	8.744791	-6.983002	-4.163436
1KTH	A	CYS	55	H	-2.957147	6.166838	-4.743464	-3.053221
1KTH	A	ALA	56	C	-2.957147	6.166838	-4.743464	-3.053221
1KTH	A	PRO	57	C	-2.957147	6.166838	-4.743464	-3.053221
1KTH	A	VAL	58	C	-2.957147	6.166838	-4.743464	-3.053221
1L8J	A	LEU	8	C	-9.911735	11.631997	-10.696206	-3.462242
1L8J	A	GLN	9	E	-9.911735	11.631997	-10.696206	-3.462242
1L8J	A	ARG	10	E	-9.911735	11.631997	-10.696206	-3.462242
1L8J	A	LEU	11	E	-9.911735	11.631997	-10.696206	-3.462242
1L8J	A	HIS	12	E	-12.751162	14.127378	-14.982775	-4.787319
1L8J	A	MET	13	E	-14.786349	15.752295	-18.801941	-5.842102
1L8J	A	LEU	14	E	-15.029569	14.476541	-19.128574	-5.513724
1L8J	A	GLN	15	E	-14.980075	14.758610	-19.050254	-5.502974
1L8J	A	ILE	16	E	-14.178254	16.881191	-15.784521	-4.798685
1L8J	A	SER	17	E	-13.859432	16.698406	-15.472171	-4.689884
1L8J	A	TYR	18	E	-13.215877	17.607006	-13.562194	-4.317098
1L8J	A	PHE	19	E	-11.407419	16.940082	-11.941618	-4.756328
1L8J	A	ARG	20	E	-8.121323	10.218624	-9.620902	-3.853526
1L8J	A	ASP	21	E	-8.066810	10.339262	-9.751617	-3.883181
1L8J	A	PRO	22	T	-8.062983	10.362796	-9.764220	-3.884730
1L8J	A	TYR	23	T	-8.062984	10.362645	-9.764403	-3.884809
1L8J	A	HIS	24	E	-8.064976	10.340598	-9.757408	-3.881807
1L8J	A	VAL	25	E	-9.462383	11.773065	-11.166437	-4.188561
1L8J	A	TRP	26	E	-11.008499	14.061143	-11.933640	-4.164463
1L8J	A	TYR	27	E	-12.324059	14.095201	-15.098623	-4.723730
1L8J	A	GLN	28	E	-10.751823	8.722838	-14.772188	-4.426161
1L8J	A	GLY	29	E	-10.435609	9.725359	-14.637470	-4.608295
1L8J	A	ASN	30	E	-10.273712	10.049902	-14.371069	-4.546876
1L8J	A	ALA	31	E	-9.070073	9.720610	-11.989997	-4.214811

1L8J	A	SER	32	E	-6.083509	7.418263	-8.770934	-4.082894
1L8J	A	LEU	33	E	-4.702099	7.832064	-7.193092	-4.213630
1L8J	A	GLY	34	T	-4.552921	7.466449	-7.824687	-4.380602
1L8J	A	GLY	35	T	-4.551973	7.468025	-7.831000	-4.380959
1L8J	A	HIS	36	E	-4.552216	7.467139	-7.829468	-4.381047
1L8J	A	LEU	37	E	-4.598408	7.471852	-7.754316	-4.404989
1L8J	A	THR	38	E	-5.439109	6.201513	-10.038899	-4.958068
1L8J	A	HIS	39	E	-8.347800	8.561986	-11.823814	-4.594918
1L8J	A	VAL	40	E	-10.062846	11.888893	-13.597724	-4.753741
1L8J	A	LEU	41	E	-9.850934	13.816273	-14.035756	-6.065550
1L8J	A	GLU	42	E	-8.349946	6.731796	-12.684343	-4.280292
1L8J	A	GLY	43	E	-5.089498	3.806534	-8.885168	-3.664231
1L8J	A	PRO	44	E	-3.834552	6.387179	-6.971991	-4.087552
1L8J	A	ASP	45	T	-3.680478	6.453852	-6.987493	-4.061960
1L8J	A	THR	46	T	-3.562126	7.040329	-6.691987	-4.026077
1L8J	A	ASN	47	T	-3.557563	7.068273	-6.693833	-4.023776
1L8J	A	THR	48	T	-3.603943	7.333040	-6.514375	-4.051836
1L8J	A	THR	49	E	-4.142303	8.191833	-6.212373	-3.904671
1L8J	A	ILE	50	E	-4.550843	9.705069	-5.407235	-3.843043
1L8J	A	ILE	51	E	-6.408321	10.521826	-7.206264	-3.739114
1L8J	A	GLN	52	E	-8.397270	11.251102	-11.237618	-4.378640
1L8J	A	LEU	53	T	-8.615835	10.342053	-11.810981	-4.340115
1L8J	A	GLN	54	T	-8.736752	9.608212	-12.065573	-4.302885
1L8J	A	PRO	55	T	-8.678638	9.315906	-12.314554	-4.349490
1L8J	A	LEU	56	T	-9.029389	9.296346	-12.850387	-4.546823
1L8J	A	GLN	57	T	-9.647774	8.396827	-14.791727	-4.909844
1L8J	A	GLU	58	T	-9.660803	8.228662	-14.841631	-4.885166
1L8J	A	PRO	59	H	-9.704923	8.118437	-14.709765	-4.783677
1L8J	A	GLU	60	H	-10.414840	7.367830	-16.481596	-4.849197
1L8J	A	SER	61	H	-10.528633	7.302576	-16.448602	-4.798848
1L8J	A	TRP	62	H	-10.878890	9.414132	-15.768335	-4.845380
1L8J	A	ALA	63	H	-11.208786	8.806522	-16.515359	-4.693467
1L8J	A	ARG	64	H	-11.289550	6.809240	-17.426063	-4.479605
1L8J	A	THR	65	H	-10.965912	7.109599	-16.789371	-4.551102
1L8J	A	GLN	66	H	-10.834857	7.385252	-16.663963	-4.594402
1L8J	A	SER	67	H	-9.867720	7.248133	-14.320694	-4.109843
1L8J	A	GLY	68	H	-9.876304	7.335400	-14.267453	-4.122940
1L8J	A	LEU	69	H	-9.900023	7.402951	-14.101259	-4.091421
1L8J	A	GLN	70	H	-9.951802	7.365517	-13.934194	-4.044321
1L8J	A	SER	71	H	-9.981901	7.296691	-13.816717	-4.007940
1L8J	A	TYR	72	H	-12.277946	10.606124	-16.308447	-4.659175
1L8J	A	LEU	73	H	-13.293942	11.659480	-17.199242	-4.541461
1L8J	A	LEU	74	H	-13.190491	10.647654	-17.989357	-4.765592
1L8J	A	GLN	75	H	-13.572595	10.551075	-19.260467	-5.237473
1L8J	A	PHE	76	H	-12.703881	14.155443	-14.916584	-4.621709
1L8J	A	HIS	77	H	-11.417623	12.849657	-12.983803	-4.011393
1L8J	A	GLY	78	H	-10.345603	12.390815	-11.789724	-3.889697
1L8J	A	LEU	79	H	-10.270605	12.796409	-11.764608	-3.910289
1L8J	A	VAL	80	H	-10.263280	12.828592	-11.774718	-3.906675
1L8J	A	ARG	81	H	-10.166114	12.689247	-11.915242	-3.909206
1L8J	A	LEU	82	H	-9.821000	11.777904	-12.032716	-3.986347
1L8J	A	VAL	83	H	-9.796504	11.597491	-12.243032	-4.095849
1L8J	A	HIS	84	H	-7.798854	9.294245	-11.049532	-4.573233
1L8J	A	GLN	85	H	-7.619823	9.821622	-10.651837	-4.411736
1L8J	A	GLU	86	H	-7.358566	10.167979	-10.009320	-4.145023
1L8J	A	ARG	87	H	-7.263091	10.911914	-9.519854	-4.047019
1L8J	A	THR	88	C	-6.290983	12.376512	-6.044434	-3.324502
1L8J	A	LEU	89	C	-6.275612	12.808032	-5.766415	-3.269704
1L8J	A	ALA	90	C	-6.284025	12.858156	-5.696300	-3.253307
1L8J	A	PHE	91	C	-6.319432	12.987533	-5.501219	-3.227896
1L8J	A	PRO	92	C	-6.338414	12.922629	-5.454223	-3.218669
1L8J	A	LEU	93	E	-7.567557	14.282359	-7.105545	-3.682883
1L8J	A	THR	94	E	-8.830329	13.648926	-8.341733	-3.454931
1L8J	A	ILE	95	E	-10.753170	16.789605	-9.998137	-3.629658
1L8J	A	ARG	96	E	-11.336410	15.393469	-12.339288	-4.006468
1L8J	A	CYS	97	E	-11.388380	14.202513	-13.751882	-4.576398
1L8J	A	PHE	98	E	-11.485407	13.794666	-14.286414	-4.778673
1L8J	A	LEU	99	E	-11.275552	13.914330	-15.357784	-5.761538
1L8J	A	GLY	100	E	-10.929329	12.671590	-15.746150	-5.777755
1L8J	A	CYS	101	E	-9.925263	10.757727	-14.228509	-5.169670
1L8J	A	GLU	102	E	-6.940945	8.433552	-9.053069	-3.778590
1L8J	A	LEU	103	E	-2.908070	6.027234	-4.226455	-3.155279
1L8J	A	PRO	104	T	-0.957097	2.867366	-3.843346	-3.177385
1L8J	A	PRO	105	T	-0.946202	2.865328	-3.922237	-3.191651
1L8J	A	GLU	106	T	-0.944568	2.871667	-3.935218	-3.194293
1L8J	A	GLY	107	T	-0.944559	2.871554	-3.935357	-3.194283
1L8J	A	SER	108	C	-0.976025	2.652280	-3.851433	-3.140670
1L8J	A	ARG	109	C	-3.448234	2.138551	-6.965734	-2.930922
1L8J	A	ALA	110	C	-4.636272	4.279209	-7.396385	-3.092150
1L8J	A	HIS	111	E	-6.677660	6.632829	-9.897335	-3.595332
1L8J	A	VAL	112	E	-7.596939	10.481789	-10.483579	-4.646963

1L8J	A	PHE	113	E	-9.228511	13.999915	-12.622636	-6.419344
1L8J	A	PHE	114	E	-10.871017	18.213832	-10.646649	-4.274988
1L8J	A	GLU	115	E	-9.874373	12.205757	-11.152250	-3.784365
1L8J	A	VAL	116	E	-7.628260	9.012258	-9.368526	-3.597121
1L8J	A	ALA	117	E	-6.097131	6.103883	-8.791885	-3.408722
1L8J	A	VAL	118	E	-4.761099	5.738853	-7.394785	-3.429834
1L8J	A	ASN	119	T	-4.756649	5.770594	-7.415109	-3.436858
1L8J	A	GLY	120	T	-4.755534	5.783103	-7.416567	-3.436890
1L8J	A	SER	121	E	-4.760099	5.758578	-7.401752	-3.435661
1L8J	A	SER	122	E	-4.820458	5.746632	-7.257263	-3.439985
1L8J	A	PHE	123	E	-7.513853	10.491485	-9.747056	-4.174987
1L8J	A	VAL	124	E	-8.426592	12.344640	-8.425989	-3.473296
1L8J	A	SER	125	E	-11.991331	14.746744	-13.705562	-4.215370
1L8J	A	PHE	126	E	-10.905229	13.206492	-11.822690	-3.837345
1L8J	A	ARG	127	E	-9.514579	10.463281	-11.191537	-3.601071
1L8J	A	PRO	128	G	-9.390336	10.375747	-11.455846	-3.639540
1L8J	A	GLU	129	G	-9.380253	10.420858	-11.505247	-3.662632
1L8J	A	ARG	130	G	-9.380306	10.420407	-11.505306	-3.662750
1L8J	A	ALA	131	C	-9.422381	10.230621	-11.504480	-3.656573
1L8J	A	LEU	132	E	-10.297609	10.434142	-12.855076	-3.953725
1L8J	A	TRP	133	E	-11.334901	13.407321	-15.417251	-5.470530
1L8J	A	GLN	134	E	-8.166119	7.656423	-13.181246	-5.243249
1L8J	A	ALA	135	E	-4.261785	5.309741	-6.937073	-3.631721
1L8J	A	ASP	136	C	-2.929696	4.690146	-5.919544	-3.717917
1L8J	A	THR	137	C	-2.691585	4.356173	-5.977019	-3.544492
1L8J	A	GLN	138	C	-2.540615	3.851038	-6.318802	-3.535464
1L8J	A	VAL	139	C	-2.535683	3.858860	-6.345522	-3.539478
1L8J	A	THR	140	C	-2.569264	3.770304	-6.303578	-3.529054
1L8J	A	SER	141	C	-2.971001	2.920648	-6.718187	-3.299291
1L8J	A	GLY	142	H	-3.413490	2.136212	-7.453806	-3.451077
1L8J	A	VAL	143	H	-5.337426	5.016860	-9.464669	-3.961541
1L8J	A	VAL	144	H	-6.842051	8.511626	-10.144568	-4.258425
1L8J	A	THR	145	H	-7.694901	10.258727	-11.904937	-5.497317
1L8J	A	PHE	146	H	-8.985932	15.174889	-12.983621	-7.204593
1L8J	A	THR	147	H	-10.449612	17.430787	-13.926896	-7.246244
1L8J	A	LEU	148	H	-11.610548	15.718402	-14.000635	-5.122435
1L8J	A	GLN	149	H	-11.695583	13.624521	-15.033084	-5.089621
1L8J	A	GLN	150	H	-11.625229	12.076378	-15.671090	-5.092227
1L8J	A	LEU	151	H	-9.918468	9.291562	-13.476733	-4.514906
1L8J	A	ASN	152	H	-9.720187	8.533533	-13.972919	-4.497280
1L8J	A	ALA	153	C	-8.741805	7.584411	-12.717476	-4.175927
1L8J	A	TYR	154	C	-8.742441	7.577657	-12.714024	-4.173765
1L8J	A	ASN	155	H	-8.744866	7.562935	-12.703807	-4.171062
1L8J	A	ARG	156	H	-8.827641	7.326846	-12.607260	-4.124487
1L8J	A	THR	157	H	-8.866764	7.366925	-12.429491	-4.101653
1L8J	A	ARG	158	H	-12.604167	10.904140	-17.383602	-5.067439
1L8J	A	TYR	159	H	-12.571896	12.839986	-16.284645	-5.050966
1L8J	A	GLU	160	H	-12.387803	13.502462	-15.585869	-4.907243
1L8J	A	LEU	161	H	-12.364201	13.771814	-15.438679	-4.877259
1L8J	A	ARG	162	H	-12.373692	13.774754	-15.408451	-4.878628
1L8J	A	GLU	163	H	-12.314616	13.772593	-15.487993	-4.891848
1L8J	A	PHE	164	H	-12.569947	14.478164	-15.350206	-4.817240
1L8J	A	LEU	165	H	-12.098185	11.542744	-16.057725	-4.925217
1L8J	A	GLU	166	H	-11.402777	9.153698	-16.278298	-4.817941
1L8J	A	ASP	167	H	-10.186478	7.397838	-14.622670	-4.245952
1L8J	A	THR	168	H	-10.180159	7.440488	-14.636479	-4.251277
1L8J	A	CYS	169	H	-10.181252	7.433682	-14.636286	-4.252190
1L8J	A	VAL	170	H	-10.175092	7.831512	-14.548756	-4.336432
1L8J	A	GLN	171	H	-10.121032	9.448771	-14.098262	-4.624330
1L8J	A	TYR	172	H	-9.564561	16.821906	-10.188648	-5.360257
1L8J	A	VAL	173	H	-5.714757	11.376698	-6.006028	-3.904479
1L8J	A	GLN	174	H	-4.184308	8.838156	-5.625230	-3.745993
1L8J	A	LYS	175	H	-4.184308	8.838156	-5.625230	-3.745993
1L8J	A	HIS	176	H	-4.184308	8.838156	-5.625230	-3.745993
1L8J	A	ILE	177	C	-4.184308	8.838156	-5.625230	-3.745993
1L9L	A	GLY	1	H	-10.986313	9.744895	-16.488861	-5.268003
1L9L	A	ARG	2	H	-10.986313	9.744895	-16.488861	-5.268003
1L9L	A	ASP	3	H	-10.986313	9.744895	-16.488861	-5.268003
1L9L	A	TYR	4	H	-10.986313	9.744895	-16.488861	-5.268003
1L9L	A	ARG	5	H	-10.406142	10.908195	-14.533248	-5.046874
1L9L	A	THR	6	H	-9.506934	13.049515	-12.184866	-4.973282
1L9L	A	CYS	7	H	-9.026075	12.907639	-11.508955	-4.652366
1L9L	A	LEU	8	H	-9.000044	12.917992	-11.571133	-4.649484
1L9L	A	THR	9	H	-8.976929	12.912977	-11.652177	-4.660855
1L9L	A	ILE	10	H	-9.023368	13.081678	-11.450979	-4.636599
1L9L	A	VAL	11	H	-9.281586	12.833222	-11.345434	-4.462860
1L9L	A	GLN	12	H	-10.319820	12.654308	-13.961699	-4.953705
1L9L	A	LYS	13	H	-10.383063	12.527463	-14.751810	-5.390563
1L9L	A	LEU	14	H	-10.119950	12.339587	-14.008970	-5.145548
1L9L	A	LYS	15	H	-8.545035	8.704193	-12.930181	-4.859271
1L9L	A	LYS	16	H	-6.352657	7.926702	-9.983294	-4.565930

1L9L	A	MET	17	H	-5.698887	8.682864	-8.775350	-4.264793
1L9L	A	VAL	18	T	-4.734470	7.281796	-7.627028	-3.792252
1L9L	A	ASP	19	T	-4.653738	7.154382	-7.870347	-3.830975
1L9L	A	LYS	20	T	-4.648649	7.149343	-7.893417	-3.829693
1L9L	A	PRO	21	T	-4.682041	7.105035	-7.777080	-3.787175
1L9L	A	THR	22	C	-4.757699	6.838214	-7.723787	-3.742145
1L9L	A	GLN	23	H	-5.827971	6.324727	-9.643932	-4.075117
1L9L	A	ARG	24	H	-7.354299	6.878291	-11.000337	-3.846093
1L9L	A	SER	25	H	-9.090432	8.163524	-13.466263	-4.121244
1L9L	A	VAL	26	H	-9.311487	8.709597	-13.318764	-4.142706
1L9L	A	SER	27	H	-9.367199	7.466970	-14.320321	-4.331293
1L9L	A	ASN	28	H	-8.904572	7.409548	-13.771620	-4.217510
1L9L	A	ALA	29	H	-8.883560	7.621329	-13.649028	-4.195526
1L9L	A	ALA	30	H	-8.872356	7.646295	-13.676029	-4.201247
1L9L	A	THR	31	H	-8.852178	7.516263	-13.759027	-4.197755
1L9L	A	ARG	32	H	-9.013767	7.807076	-13.664742	-4.138953
1L9L	A	VAL	33	H	-8.245690	7.241342	-12.859696	-4.441694
1L9L	A	CYS	34	T	-6.271326	4.469731	-10.886975	-3.912792
1L9L	A	ARG	35	T	-5.794851	4.119876	-10.610213	-3.677831
1L9L	A	THR	36	T	-5.622044	3.983252	-10.681817	-3.630106
1L9L	A	GLY	37	C	-5.616521	4.011657	-10.694300	-3.632891
1L9L	A	ARG	38	C	-5.622745	3.979694	-10.673075	-3.623801
1L9L	A	SER	39	H	-5.853894	3.791858	-10.604335	-3.495024
1L9L	A	ARG	40	H	-6.412679	3.719932	-10.944906	-3.506438
1L9L	A	TRP	41	H	-8.348285	7.139878	-12.157223	-3.930616
1L9L	A	ARG	42	H	-10.442765	9.360714	-13.337772	-3.649179
1L9L	A	ASP	43	H	-10.464443	6.335279	-16.700357	-5.001984
1L9L	A	VAL	44	H	-10.466688	6.329802	-16.689434	-5.002080
1L9L	A	CYS	45	H	-10.468344	6.318125	-16.679020	-4.999171
1L9L	A	ARG	46	H	-10.465066	6.355169	-16.672533	-4.996068
1L9L	A	ASN	47	H	-9.989716	10.124506	-14.330252	-4.846360
1L9L	A	PHE	48	H	-10.295703	13.334285	-12.561902	-4.740019
1L9L	A	MET	49	H	-10.021766	13.017782	-12.767724	-4.725076
1L9L	A	ARG	50	H	-9.574854	11.503916	-12.679902	-4.334697
1L9L	A	ARG	51	H	-9.575731	11.501828	-12.673755	-4.333494
1L9L	A	TYR	52	H	-9.767196	10.874212	-12.749955	-4.183697
1L9L	A	GLN	53	H	-9.781271	10.736457	-12.746457	-4.167160
1L9L	A	SER	54	H	-9.950056	10.162081	-12.616211	-3.989964
1L9L	A	ARG	55	H	-13.219641	10.889313	-18.449422	-4.737280
1L9L	A	VAL	56	H	-11.187670	13.666165	-13.339473	-4.652488
1L9L	A	ILE	57	H	-10.623669	12.535262	-13.561817	-4.597884
1L9L	A	GLN	58	H	-8.781572	9.540078	-12.070813	-4.360453
1L9L	A	GLY	59	H	-6.807820	8.293096	-9.844152	-4.125675
1L9L	A	LEU	60	H	-6.729891	8.362355	-10.032197	-4.169089
1L9L	A	VAL	61	H	-6.585694	7.745611	-10.630171	-4.284492
1L9L	A	ALA	62	H	-6.502760	7.581789	-10.917043	-4.367567
1L9L	A	GLY	63	C	-6.509935	7.542924	-10.928257	-4.375464
1L9L	A	GLU	64	C	-7.022051	6.573647	-12.585463	-4.741154
1L9L	A	THR	65	C	-7.119053	6.285558	-12.822858	-4.803650
1L9L	A	ALA	66	H	-7.568284	7.162069	-12.853659	-4.919154
1L9L	A	GLN	67	H	-8.499504	9.637030	-12.948094	-4.922959
1L9L	A	GLN	68	H	-8.657069	10.400187	-12.372098	-4.844908
1L9L	A	ILE	69	H	-8.475631	11.462020	-12.048717	-5.107073
1L9L	A	CYS	70	H	-6.922375	8.803953	-10.426968	-4.689928
1L9L	A	GLU	71	G	-5.179519	7.702843	-7.307648	-3.517674
1L9L	A	ASP	72	G	-5.179519	7.702843	-7.307648	-3.517674
1L9L	A	LEU	73	G	-5.179519	7.702843	-7.307648	-3.517674
1L9L	A	ARG	74	C	-5.179519	7.702843	-7.307648	-3.517674
1LCL	A	SER	2	C	-6.104190	6.415938	-9.310967	-3.265954
1LCL	A	LEU	3	C	-6.104190	6.415938	-9.310967	-3.265954
1LCL	A	LEU	4	B	-6.104190	6.415938	-9.310967	-3.265954
1LCL	A	PRO	5	T	-6.104190	6.415938	-9.310967	-3.265954
1LCL	A	VAL	6	T	-6.830250	8.885040	-9.662088	-3.871428
1LCL	A	PRO	7	T	-7.255284	9.595478	-9.841979	-4.198582
1LCL	A	TYR	8	E	-9.116672	12.990395	-12.072334	-4.838867
1LCL	A	THR	9	E	-8.999224	12.046960	-12.331158	-4.691974
1LCL	A	GLU	10	E	-8.995299	11.933822	-12.321263	-4.633046
1LCL	A	ALA	11	E	-9.069510	11.561851	-12.480747	-4.617079
1LCL	A	ALA	12	C	-9.443527	10.553140	-13.289069	-4.451036
1LCL	A	SER	13	C	-9.397901	9.998296	-13.570941	-4.497402
1LCL	A	LEU	14	C	-9.619231	11.000867	-13.698307	-4.753827
1LCL	A	SER	15	T	-9.323586	10.329990	-14.224317	-5.178042
1LCL	A	THR	16	T	-9.187970	10.590560	-14.108308	-5.251252
1LCL	A	GLY	17	T	-9.054382	10.641307	-14.059083	-5.295408
1LCL	A	SER	18	E	-9.189737	10.679970	-14.205426	-5.406144
1LCL	A	THR	19	E	-9.241048	10.637467	-14.206461	-5.429249
1LCL	A	VAL	20	E	-9.482470	11.585617	-13.746116	-5.295486
1LCL	A	THR	21	E	-9.785937	11.672741	-13.795058	-5.296678
1LCL	A	ILE	22	E	-10.731699	14.450570	-13.726772	-5.203134
1LCL	A	LYS	23	E	-10.717783	13.996054	-13.959358	-5.200109
1LCL	A	GLY	24	E	-9.161186	9.989629	-11.963405	-4.043174

1LCL	A	ARG	25	E	-8.786596	9.645500	-11.895019	-3.949091
1LCL	A	PRO	26	E	-8.546579	10.891313	-11.256538	-3.974673
1LCL	A	LEU	27	C	-8.253916	10.629561	-11.250439	-4.023141
1LCL	A	VAL	28	C	-7.371931	8.992099	-10.708479	-4.121945
1LCL	A	CYS	29	C	-6.922155	9.233784	-10.683073	-4.558121
1LCL	A	PHE	30	G	-6.911745	9.318709	-10.692122	-4.584097
1LCL	A	LEU	31	G	-6.877577	9.316536	-10.802897	-4.635704
1LCL	A	ASN	32	G	-6.899952	9.288202	-10.787568	-4.657870
1LCL	A	GLU	33	C	-7.154592	9.702319	-10.912950	-4.929844
1LCL	A	PRO	34	C	-8.167952	10.810514	-11.850021	-5.045956
1LCL	A	TYR	35	E	-8.395194	10.440459	-11.977270	-5.121334
1LCL	A	LEU	36	E	-10.856013	15.634920	-12.733663	-5.369811
1LCL	A	GLN	37	E	-13.396763	17.671213	-15.899627	-5.671332
1LCL	A	VAL	38	E	-13.711407	17.966553	-15.600021	-5.231320
1LCL	A	ASP	39	E	-13.987492	16.400186	-17.401113	-5.607210
1LCL	A	PHE	40	E	-12.938443	16.209600	-16.224290	-5.934157
1LCL	A	HIS	41	E	-10.146006	11.309358	-15.087885	-6.155783
1LCL	A	THR	42	C	-8.303565	9.513032	-13.597617	-6.030842
1LCL	A	GLU	43	C	-6.996058	7.162720	-12.897711	-5.726001
1LCL	A	MET	44	C	-6.770460	6.935271	-13.015555	-5.648944
1LCL	A	LYS	45	T	-6.763142	6.922111	-13.054535	-5.648373
1LCL	A	GLU	46	T	-6.764697	6.909024	-13.050465	-5.646690
1LCL	A	GLU	47	T	-6.808389	6.716307	-13.014105	-5.617678
1LCL	A	SER	48	T	-7.427592	6.429089	-13.388146	-5.487406
1LCL	A	ASP	49	C	-9.334712	6.064143	-16.231042	-5.603161
1LCL	A	ILE	50	E	-11.038678	9.159479	-16.899994	-5.600976
1LCL	A	VAL	51	E	-12.413480	12.951266	-16.370615	-5.238135
1LCL	A	PHE	52	E	-13.535229	19.550074	-14.682639	-5.080311
1LCL	A	HIS	53	E	-13.687179	20.547211	-14.492871	-5.195340
1LCL	A	PHE	54	E	-13.891132	21.312455	-14.374469	-5.282196
1LCL	A	GLN	55	E	-12.388868	14.784048	-15.599386	-5.653824
1LCL	A	VAL	56	E	-11.482870	13.759115	-14.626332	-5.166313
1LCL	A	CYS	57	E	-11.429877	13.782029	-14.794759	-5.217692
1LCL	A	PHE	58	T	-11.420198	13.820570	-14.811280	-5.220040
1LCL	A	GLY	59	T	-11.363405	13.629447	-15.012007	-5.222854
1LCL	A	ARG	60	T	-11.474567	13.420271	-14.900767	-5.134222
1LCL	A	ARG	61	E	-12.348551	13.214458	-16.768400	-5.484261
1LCL	A	VAL	62	E	-12.569313	12.820927	-16.955094	-5.323908
1LCL	A	VAL	63	E	-12.656028	12.263863	-17.098389	-5.307526
1LCL	A	MET	64	E	-13.666599	14.278109	-17.545682	-5.551276
1LCL	A	ASN	65	E	-13.599909	13.991123	-17.968549	-5.659233
1LCL	A	SER	66	E	-11.645895	9.381309	-17.781639	-5.891774
1LCL	A	ARG	67	E	-9.259250	7.598003	-14.925228	-5.379818
1LCL	A	GLU	68	E	-6.232775	8.925503	-10.478748	-5.527909
1LCL	A	TYR	69	T	-5.884457	8.505086	-10.565987	-5.374696
1LCL	A	GLY	70	T	-5.851763	8.423728	-10.691640	-5.370180
1LCL	A	ALA	71	E	-5.850870	8.424631	-10.697783	-5.370446
1LCL	A	TRP	72	E	-5.852085	8.428624	-10.689294	-5.370749
1LCL	A	LYS	73	C	-6.279041	7.879616	-11.007570	-5.204537
1LCL	A	GLN	74	C	-7.432530	7.286599	-13.215982	-5.344248
1LCL	A	GLN	75	C	-8.239505	8.357764	-14.316586	-5.516162
1LCL	A	VAL	76	E	-8.166446	8.171784	-14.322606	-5.472261
1LCL	A	GLU	77	E	-8.141797	8.210010	-14.326712	-5.485604
1LCL	A	SER	78	E	-8.471555	8.306368	-14.588372	-5.407076
1LCL	A	LYS	79	C	-8.694092	8.456154	-14.651504	-5.425090
1LCL	A	ASN	80	C	-8.854216	8.461260	-14.643870	-5.424815
1LCL	A	MET	81	C	-9.310575	10.741041	-14.245845	-5.533005
1LCL	A	PRO	82	C	-9.423105	13.303461	-12.576387	-5.103734
1LCL	A	PHE	83	C	-9.169671	12.467075	-12.781070	-5.149523
1LCL	A	GLN	84	T	-8.100819	7.623167	-14.058714	-5.558445
1LCL	A	ASP	85	T	-8.089962	7.695973	-14.070137	-5.567909
1LCL	A	GLY	86	T	-8.103129	7.522080	-14.122794	-5.578053
1LCL	A	GLN	87	T	-8.141989	7.131491	-14.262971	-5.613407
1LCL	A	GLU	88	C	-8.188711	6.848932	-14.316354	-5.645543
1LCL	A	PHE	89	E	-10.310149	12.289797	-14.521670	-5.909352
1LCL	A	GLU	90	E	-12.272842	14.992444	-16.392516	-5.879160
1LCL	A	LEU	91	E	-12.324847	16.454852	-14.515057	-4.946481
1LCL	A	SER	92	E	-11.806275	15.409659	-13.854131	-4.618157
1LCL	A	ILE	93	E	-10.409018	13.706111	-11.817082	-4.131892
1LCL	A	SER	94	E	-9.116405	9.839513	-12.456499	-4.340746
1LCL	A	VAL	95	E	-7.339995	10.433314	-10.077114	-4.619459
1LCL	A	LEU	96	T	-7.324225	10.504896	-10.128921	-4.636450
1LCL	A	PRO	97	T	-7.323621	10.508992	-10.133714	-4.638320
1LCL	A	ASP	98	T	-7.326562	10.493970	-10.126425	-4.641103
1LCL	A	LYS	99	E	-7.352765	10.545720	-10.017372	-4.653477
1LCL	A	TYR	100	E	-9.448656	13.242125	-12.177398	-5.299190
1LCL	A	GLN	101	E	-11.223948	14.606871	-14.609963	-5.984347
1LCL	A	VAL	102	E	-10.647153	10.408192	-14.569923	-4.870760
1LCL	A	MET	103	E	-9.339249	8.027771	-14.724696	-5.164094
1LCL	A	VAL	104	E	-7.991670	7.261666	-13.164609	-4.977697
1LCL	A	ASN	105	T	-7.913792	7.043856	-13.508922	-5.039491

1LCL	A	GLY	106	T	-7.911657	7.054265	-13.519585	-5.041716
1LCL	A	GLN	107	E	-7.916286	7.031864	-13.514108	-5.044601
1LCL	A	SER	108	E	-7.966055	6.970718	-13.406362	-5.030966
1LCL	A	SER	109	E	-9.119456	5.877260	-15.943289	-5.490717
1LCL	A	TYR	110	E	-10.775112	12.551214	-15.548594	-5.682701
1LCL	A	THR	111	E	-10.921532	14.890971	-14.578799	-5.688899
1LCL	A	PHE	112	E	-11.035129	16.109795	-14.036782	-5.660148
1LCL	A	ASP	113	E	-8.919078	12.092242	-11.773037	-5.067277
1LCL	A	HIS	114	T	-8.847525	12.199081	-11.792640	-5.017090
1LCL	A	ARG	115	T	-8.784442	12.191382	-11.875098	-4.981105
1LCL	A	ILE	116	T	-7.141047	10.015701	-9.237831	-3.961677
1LCL	A	LYS	117	T	-6.761982	10.341587	-8.902795	-3.881954
1LCL	A	PRO	118	G	-6.773525	10.307174	-8.849067	-3.853919
1LCL	A	GLU	119	G	-6.775518	10.296576	-8.839267	-3.851149
1LCL	A	ALA	120	G	-6.777549	10.289917	-8.826357	-3.848275
1LCL	A	VAL	121	C	-7.197699	10.719298	-8.579851	-3.800239
1LCL	A	LYS	122	C	-9.737436	11.638054	-12.132603	-4.294213
1LCL	A	MET	123	E	-11.431181	11.785885	-15.213214	-4.951694
1LCL	A	VAL	124	E	-12.621795	13.586313	-14.892085	-4.393379
1LCL	A	GLN	125	E	-14.504321	15.242986	-18.965602	-5.570094
1LCL	A	VAL	126	E	-12.767834	17.334816	-13.889144	-4.960347
1LCL	A	TRP	127	E	-12.673264	17.158018	-14.213493	-5.036831
1LCL	A	ARG	128	E	-12.391259	16.972789	-14.292104	-5.047602
1LCL	A	ASP	129	T	-11.749793	15.808772	-14.013596	-5.014576
1LCL	A	ILE	130	E	-11.587148	15.768973	-14.168002	-5.100184
1LCL	A	SER	131	E	-11.637180	15.652576	-14.304229	-5.164094
1LCL	A	LEU	132	E	-11.330027	15.806066	-14.190223	-5.369563
1LCL	A	THR	133	E	-10.545075	15.405404	-13.083318	-5.406989
1LCL	A	LYS	134	E	-10.539763	15.369863	-13.124167	-5.420648
1LCL	A	PHE	135	E	-10.562380	15.363186	-13.079558	-5.431177
1LCL	A	ASN	136	E	-10.361793	13.810665	-14.259165	-5.701770
1LCL	A	VAL	137	E	-9.488425	10.006699	-14.343069	-5.320786
1LCL	A	SER	138	E	-8.043431	6.739735	-12.964889	-4.598901
1LCL	A	TYR	139	C	-6.366084	5.677430	-10.146383	-3.688000
1LCL	A	LEU	140	C	-6.366084	5.677430	-10.146383	-3.688000
1LCL	A	LYS	141	C	-6.366084	5.677430	-10.146383	-3.688000
1LCL	A	ARG	142	C	-6.366084	5.677430	-10.146383	-3.688000
1LDS	A	MET	0	C	-5.031051	5.933665	-7.499339	-3.165858
1LDS	A	ILE	1	C	-5.031051	5.933665	-7.499339	-3.165858
1LDS	A	GLN	2	C	-5.031051	5.933665	-7.499339	-3.165858
1LDS	A	ARG	3	B	-5.031051	5.933665	-7.499339	-3.165858
1LDS	A	THR	4	C	-6.338502	7.462728	-9.666114	-4.129636
1LDS	A	PRO	5	C	-7.708690	11.511634	-10.212937	-4.430182
1LDS	A	LYS	6	E	-8.089568	12.328237	-9.988721	-4.319774
1LDS	A	ILE	7	E	-8.109760	12.353093	-9.853856	-4.270759
1LDS	A	GLN	8	E	-8.115576	12.316420	-9.817053	-4.247528
1LDS	A	VAL	9	E	-8.612179	13.597018	-9.372654	-4.213097
1LDS	A	TYR	10	E	-9.764677	11.335268	-16.365535	-7.206236
1LDS	A	SER	11	E	-6.844158	7.874660	-14.013952	-7.226070
1LDS	A	ARG	12	E	-5.557948	5.935583	-9.166553	-3.875836
1LDS	A	HIS	13	C	-3.721008	4.813383	-6.982613	-3.776440
1LDS	A	PRO	14	T	-2.125969	3.408762	-5.912852	-3.870808
1LDS	A	ALA	15	T	-1.393613	1.806329	-6.532263	-4.036854
1LDS	A	GLU	16	T	-1.365840	1.857626	-6.640861	-4.067983
1LDS	A	ASN	17	T	-1.366290	1.854396	-6.639234	-4.068236
1LDS	A	GLY	18	T	-1.379231	1.783281	-6.608069	-4.058888
1LDS	A	LYS	19	T	-1.591396	1.072956	-6.581405	-3.921782
1LDS	A	SER	20	T	-3.297229	2.634380	-7.799344	-4.026878
1LDS	A	ASN	21	C	-6.663824	5.543674	-13.591427	-5.896494
1LDS	A	PHE	22	E	-8.291960	10.555246	-15.527846	-8.227974
1LDS	A	LEU	23	E	-11.680428	15.000311	-17.429854	-7.861402
1LDS	A	ASN	24	E	-13.520351	14.991865	-17.164113	-5.412651
1LDS	A	CYS	25	E	-11.775186	11.312123	-15.852237	-5.118992
1LDS	A	TYR	26	E	-11.712348	11.788243	-15.675519	-5.082024
1LDS	A	VAL	27	E	-11.480119	12.911942	-14.883131	-4.929093
1LDS	A	SER	28	E	-11.297283	13.119948	-14.608847	-4.845506
1LDS	A	GLY	29	E	-11.070792	13.521580	-14.154459	-4.753569
1LDS	A	PHE	30	E	-10.455137	13.562039	-12.512200	-4.417515
1LDS	A	HIS	31	B	-7.360932	11.410101	-8.149469	-3.822971
1LDS	A	PRO	32	T	-6.763528	10.403193	-8.443393	-3.878648
1LDS	A	SER	33	T	-6.340232	10.590854	-8.074171	-3.886623
1LDS	A	ASP	34	C	-6.333825	10.583773	-8.115347	-3.893056
1LDS	A	ILE	35	C	-6.333453	10.586876	-8.117101	-3.893811
1LDS	A	GLU	36	E	-6.447840	10.414082	-8.115349	-3.909583
1LDS	A	VAL	37	E	-6.724286	10.763972	-7.819518	-3.908883
1LDS	A	ASP	38	E	-8.941501	10.478175	-11.887904	-4.510791
1LDS	A	LEU	39	E	-10.068938	14.019545	-12.183604	-4.831625
1LDS	A	LEU	40	E	-7.633524	8.090802	-12.013598	-5.088440
1LDS	A	LYS	41	E	-7.527733	7.802874	-12.366430	-5.106249
1LDS	A	ASN	42	T	-7.522411	7.795214	-12.394608	-5.103607
1LDS	A	GLY	43	T	-7.368043	7.466062	-12.390689	-4.896659

1LDS	A	GLU	44	E	-7.310295	7.316056	-12.469676	-4.830999
1LDS	A	ARG	45	E	-7.416017	7.361643	-12.028298	-4.348989
1LDS	A	ILE	46	T	-6.707946	7.828272	-10.445634	-4.305740
1LDS	A	GLU	47	T	-6.511631	7.462460	-10.662678	-4.325282
1LDS	A	LYS	48	T	-6.445420	7.685075	-10.516755	-4.302843
1LDS	A	VAL	49	T	-6.425595	7.778187	-10.500461	-4.307860
1LDS	A	GLU	50	C	-6.417192	7.809205	-10.544529	-4.353796
1LDS	A	HIS	51	E	-6.759825	7.715908	-11.015597	-4.358079
1LDS	A	SER	52	E	-7.025143	8.656672	-10.814051	-4.282163
1LDS	A	ASP	53	E	-7.310207	8.691872	-11.247168	-4.355243
1LDS	A	LEU	54	E	-7.163449	8.698100	-10.773614	-4.165299
1LDS	A	SER	55	E	-6.812392	7.266454	-10.711180	-4.027917
1LDS	A	PHE	56	E	-5.427019	7.632604	-8.391815	-4.181216
1LDS	A	SER	57	T	-5.353636	7.519273	-8.582110	-4.188777
1LDS	A	LYS	58	T	-5.351573	7.540793	-8.585376	-4.191863
1LDS	A	ASP	59	T	-5.363039	7.517544	-8.555605	-4.197713
1LDS	A	TRP	60	T	-5.397542	7.578834	-8.418478	-4.202833
1LDS	A	SER	61	T	-6.570810	6.988941	-10.065337	-4.239033
1LDS	A	PHE	62	E	-8.474734	11.883363	-10.380748	-4.672411
1LDS	A	TYR	63	E	-12.653448	17.481420	-15.052678	-6.037851
1LDS	A	LEU	64	E	-14.840899	20.374189	-16.696184	-6.027493
1LDS	A	LEU	65	E	-14.939767	19.133947	-16.854531	-5.672713
1LDS	A	TYR	66	E	-14.743359	20.182176	-16.395869	-5.817195
1LDS	A	TYR	67	E	-10.065944	16.663391	-10.326468	-4.976650
1LDS	A	THR	68	E	-7.564089	13.825001	-7.821433	-4.343533
1LDS	A	GLU	69	E	-6.979477	12.659880	-8.185131	-4.333566
1LDS	A	PHE	70	C	-6.028674	10.866526	-7.782910	-4.200208
1LDS	A	THR	71	C	-3.420243	4.930515	-6.041793	-3.457357
1LDS	A	PRO	72	C	-3.282199	5.115349	-6.291586	-3.571420
1LDS	A	THR	73	T	-3.270249	5.103971	-6.372323	-3.591686
1LDS	A	GLU	74	T	-3.270948	5.095785	-6.370009	-3.590817
1LDS	A	LYS	75	T	-3.275508	5.054386	-6.359494	-3.586151
1LDS	A	ASP	76	T	-4.159284	5.702226	-7.484026	-4.037692
1LDS	A	GLU	77	C	-5.572236	4.831459	-10.205050	-4.552214
1LDS	A	TYR	78	E	-9.464195	10.923210	-13.515011	-5.519635
1LDS	A	ALA	79	E	-11.567585	14.751570	-16.061090	-6.400775
1LDS	A	CYS	80	E	-12.623369	15.623172	-18.067793	-7.277351
1LDS	A	ARG	81	E	-12.672004	13.097145	-15.836541	-4.653608
1LDS	A	VAL	82	E	-9.672063	11.738168	-11.842674	-4.508774
1LDS	A	ASN	83	E	-8.981423	11.616523	-11.757768	-4.722437
1LDS	A	HIS	84	E	-7.246267	10.334653	-9.354690	-4.269378
1LDS	A	VAL	85	T	-5.937908	8.330849	-8.609608	-4.044007
1LDS	A	THR	86	T	-5.736375	8.230226	-8.670782	-3.988910
1LDS	A	LEU	87	E	-5.724503	8.204812	-8.715766	-3.982467
1LDS	A	SER	88	E	-5.461031	8.129653	-8.426425	-3.842352
1LDS	A	GLN	89	E	-5.489136	8.027155	-8.388652	-3.823273
1LDS	A	PRO	90	E	-5.805779	8.031791	-8.307717	-3.696989
1LDS	A	LYS	91	E	-6.017646	8.248008	-8.093422	-3.662381
1LDS	A	ILE	92	E	-5.359499	10.428681	-6.326791	-3.642544
1LDS	A	VAL	93	E	-5.139897	10.270325	-5.759903	-3.324356
1LDS	A	LYS	94	E	-5.139897	10.270325	-5.759903	-3.324356
1LDS	A	TRP	95	C	-5.139897	10.270325	-5.759903	-3.324356
1LDS	A	ASP	96	C	-5.139897	10.270325	-5.759903	-3.324356
1LN1	A	PHE	8	C	-10.805145	8.202169	-15.167843	-4.408019
1LN1	A	SER	9	C	-10.805145	8.202169	-15.167843	-4.408019
1LN1	A	GLU	10	H	-10.805145	8.202169	-15.167843	-4.408019
1LN1	A	GLU	11	H	-10.805145	8.202169	-15.167843	-4.408019
1LN1	A	GLN	12	H	-12.520591	9.613851	-17.959652	-5.421201
1LN1	A	PHE	13	H	-13.369338	15.318422	-15.850583	-5.029199
1LN1	A	TRP	14	H	-10.968442	10.004899	-14.441925	-4.500860
1LN1	A	GLU	15	H	-10.580672	9.132708	-15.033040	-4.593053
1LN1	A	ALA	16	H	-10.514261	9.478086	-15.011329	-4.615927
1LN1	A	CYS	17	H	-10.297110	9.792684	-14.957133	-4.739571
1LN1	A	ALA	18	H	-9.770876	9.846007	-14.215489	-4.733013
1LN1	A	GLU	19	H	-9.364494	10.425550	-13.231062	-4.674159
1LN1	A	LEU	20	H	-7.982882	8.450946	-11.103534	-4.019143
1LN1	A	GLN	21	H	-7.500287	8.145127	-11.226811	-4.118988
1LN1	A	GLN	22	C	-6.609609	7.245541	-9.515818	-3.483115
1LN1	A	PRO	23	C	-4.815537	5.940065	-7.330557	-3.401426
1LN1	A	ALA	24	C	-4.078298	5.563123	-6.881852	-3.370975
1LN1	A	LEU	25	T	-3.478678	5.722661	-6.533241	-3.603176
1LN1	A	ALA	26	T	-3.452059	5.890255	-6.578686	-3.645580
1LN1	A	GLY	27	T	-3.452578	5.898144	-6.576905	-3.649340
1LN1	A	ALA	28	T	-3.512182	5.899008	-6.505674	-3.674211
1LN1	A	ASP	29	C	-3.702448	6.076951	-6.424249	-3.788999
1LN1	A	TRP	30	C	-5.258366	9.541567	-7.690340	-4.541658
1LN1	A	GLN	31	E	-6.760629	10.692974	-9.227897	-4.517576
1LN1	A	LEU	32	E	-7.097046	13.224556	-8.238880	-4.282734
1LN1	A	LEU	33	E	-7.124068	13.113299	-8.191425	-4.236003
1LN1	A	VAL	34	E	-6.289607	9.128813	-8.870005	-4.102027
1LN1	A	GLU	35	E	-5.136716	9.182259	-7.325063	-4.203793

1LN1	A	THR	36	E	-5.139203	9.152003	-7.327735	-4.202218
1LN1	A	SER	37	T	-5.152293	9.056506	-7.325779	-4.205149
1LN1	A	GLY	38	T	-5.153144	9.052195	-7.321657	-4.205232
1LN1	A	ILE	39	E	-5.223393	9.197192	-7.098021	-4.222679
1LN1	A	SER	40	E	-8.099182	9.914040	-10.987521	-4.479993
1LN1	A	ILE	41	E	-10.204205	13.763558	-11.431490	-4.107918
1LN1	A	TYR	42	E	-10.782916	17.743242	-11.200544	-4.999163
1LN1	A	ARG	43	E	-9.325824	13.500829	-13.163967	-6.186829
1LN1	A	LEU	44	E	-4.996167	6.927866	-7.173230	-3.615290
1LN1	A	LEU	45	E	-2.826152	4.082718	-5.865925	-3.522741
1LN1	A	ASP	46	E	-1.430443	2.739987	-5.856241	-4.090133
1LN1	A	LYS	47	T	-1.372591	3.000633	-5.929210	-4.127428
1LN1	A	LYS	48	T	-1.372406	3.003047	-5.930240	-4.127766
1LN1	A	THR	49	T	-1.373978	2.991301	-5.924187	-4.127214
1LN1	A	GLY	50	T	-1.436115	2.827807	-5.828954	-4.119748
1LN1	A	LEU	51	E	-2.879487	5.105240	-5.680787	-3.816989
1LN1	A	TYR	52	E	-6.240214	10.357802	-8.324507	-4.587977
1LN1	A	GLU	53	E	-8.261474	15.695271	-12.742885	-8.007674
1LN1	A	TYR	54	E	-11.078307	18.307898	-15.891942	-8.787144
1LN1	A	LYS	55	E	-11.973455	15.487857	-13.353660	-4.750535
1LN1	A	VAL	56	E	-11.685452	15.678563	-13.144033	-4.601546
1LN1	A	PHE	57	E	-10.623680	14.788349	-12.023418	-4.610762
1LN1	A	GLY	58	E	-8.175889	10.122316	-10.817927	-4.539168
1LN1	A	VAL	59	E	-8.007095	10.159305	-11.075293	-4.589673
1LN1	A	LEU	60	E	-7.911118	10.292568	-11.224055	-4.657989
1LN1	A	GLU	61	T	-7.688331	10.202930	-11.443062	-4.783127
1LN1	A	ASP	62	T	-7.665502	10.083744	-11.529471	-4.768860
1LN1	A	CYS	63	T	-7.890218	9.912259	-12.040314	-4.809691
1LN1	A	SER	64	C	-7.991601	9.951762	-12.020708	-4.778675
1LN1	A	PRO	65	H	-8.088293	9.835451	-11.975687	-4.707860
1LN1	A	THR	66	H	-8.637645	9.635722	-12.099168	-4.169764
1LN1	A	LEU	67	H	-8.787468	10.103549	-11.703082	-4.094233
1LN1	A	LEU	68	H	-9.435716	12.782051	-11.143819	-4.104046
1LN1	A	ALA	69	H	-10.022670	13.734074	-11.597159	-4.361605
1LN1	A	ASP	70	H	-10.685895	12.539994	-13.412009	-4.861784
1LN1	A	ILE	71	H	-12.858846	15.356635	-14.306952	-4.583479
1LN1	A	TYR	72	H	-14.533664	16.793285	-17.372742	-5.423103
1LN1	A	MET	73	H	-14.611736	12.231240	-20.738248	-6.037898
1LN1	A	ASP	74	C	-14.630184	11.763235	-21.034744	-6.074885
1LN1	A	SER	75	H	-14.667153	11.544276	-21.108680	-6.068923
1LN1	A	ASP	76	H	-14.076712	12.307388	-19.748396	-5.851447
1LN1	A	TYR	77	H	-14.093113	12.381157	-19.643002	-5.828490
1LN1	A	ARG	78	H	-14.148322	13.403400	-19.009119	-5.724024
1LN1	A	LYS	79	H	-12.751040	12.332255	-17.005068	-5.494245
1LN1	A	GLN	80	H	-12.537127	13.114945	-16.682176	-5.476444
1LN1	A	TRP	81	H	-12.313475	14.512079	-15.873927	-5.458620
1LN1	A	ASP	82	T	-11.686580	13.664653	-15.313769	-5.374645
1LN1	A	GLN	83	T	-11.295902	13.768755	-14.850930	-5.358278
1LN1	A	TYR	84	T	-10.949791	15.816415	-13.381955	-5.404542
1LN1	A	VAL	85	E	-10.437563	15.664306	-12.678165	-5.334975
1LN1	A	LYS	86	E	-10.193950	15.379324	-13.128728	-5.646088
1LN1	A	GLU	87	E	-10.222148	15.488738	-13.050201	-5.665342
1LN1	A	LEU	88	E	-10.264199	15.586664	-12.992354	-5.696766
1LN1	A	TYR	89	E	-10.348718	15.086602	-13.334260	-5.780588
1LN1	A	GLU	90	E	-9.606964	7.211395	-16.074699	-5.703287
1LN1	A	GLN	91	E	-7.127695	3.482095	-14.237785	-5.386060
1LN1	A	GLU	92	E	-4.853997	2.862634	-10.745637	-4.801600
1LN1	A	CYS	93	E	-4.686111	3.134397	-10.814970	-4.825337
1LN1	A	ASN	94	T	-4.682952	3.153681	-10.822500	-4.824651
1LN1	A	GLY	95	T	-4.682993	3.154042	-10.821682	-4.824453
1LN1	A	GLU	96	E	-4.692514	3.149257	-10.766682	-4.815350
1LN1	A	THR	97	E	-5.502504	4.025143	-11.047563	-4.890722
1LN1	A	VAL	98	E	-7.770248	6.841945	-12.252794	-4.690990
1LN1	A	VAL	99	E	-9.932350	9.924507	-13.273874	-4.591815
1LN1	A	TYR	100	E	-14.576708	16.899326	-17.284420	-5.480137
1LN1	A	TRP	101	E	-15.512040	19.542117	-18.006826	-5.860764
1LN1	A	GLU	102	E	-12.947523	15.427286	-15.129154	-5.270185
1LN1	A	VAL	103	E	-9.535539	14.006047	-10.104646	-4.258609
1LN1	A	LYS	104	C	-7.831162	11.963457	-8.935262	-4.093923
1LN1	A	TYR	105	C	-7.410367	12.127200	-8.792066	-4.103919
1LN1	A	PRO	106	T	-6.583723	9.576765	-9.066870	-4.031362
1LN1	A	PHE	107	T	-6.576068	9.549438	-9.122471	-4.037437
1LN1	A	PRO	108	T	-6.580076	9.519198	-9.115968	-4.035964
1LN1	A	MET	109	T	-6.651943	9.219673	-9.148242	-4.029743
1LN1	A	SER	110	T	-6.742244	8.714896	-9.229644	-4.015927
1LN1	A	ASN	111	C	-9.155234	7.463729	-13.402995	-4.506126
1LN1	A	ARG	112	E	-13.534646	11.963800	-17.565357	-5.188527
1LN1	A	ASP	113	E	-16.255732	13.770188	-21.378768	-5.742666
1LN1	A	TYR	114	E	-17.120336	19.575434	-19.202209	-5.492957
1LN1	A	VAL	115	E	-17.140973	19.910006	-18.968758	-5.475277
1LN1	A	TYR	116	E	-17.219502	20.437578	-18.440078	-5.402354

1LN1	A	LEU	117	E	-17.254195	20.413217	-18.347301	-5.391028
1LN1	A	ARG	118	E	-17.817041	14.959606	-23.367805	-6.306186
1LN1	A	GLN	119	E	-15.321511	12.296191	-20.054637	-5.449866
1LN1	A	ARG	120	E	-13.294502	10.708128	-17.954672	-5.126856
1LN1	A	ARG	121	E	-11.989846	11.379961	-16.846203	-5.547465
1LN1	A	ASP	122	E	-9.403810	9.282007	-13.666204	-5.158836
1LN1	A	LEU	123	E	-7.535541	7.958039	-11.750048	-4.967548
1LN1	A	ASP	124	T	-6.760402	6.723712	-11.919982	-5.095714
1LN1	A	MET	125	T	-6.611101	6.595310	-12.074479	-5.074232
1LN1	A	GLU	126	T	-6.578837	6.590436	-12.147816	-5.063625
1LN1	A	GLY	127	T	-6.583747	6.568310	-12.135951	-5.062871
1LN1	A	ARG	128	T	-6.710083	6.252053	-12.247959	-5.087529
1LN1	A	LYS	129	C	-7.366467	6.236823	-12.784375	-4.972438
1LN1	A	ILE	130	E	-8.310707	6.603834	-13.452293	-4.866336
1LN1	A	HIS	131	E	-10.789667	14.325847	-12.403710	-4.169110
1LN1	A	VAL	132	E	-10.831851	15.365529	-11.540393	-3.937354
1LN1	A	ILE	133	E	-10.829474	15.368651	-11.530563	-3.927074
1LN1	A	LEU	134	E	-11.298460	16.371058	-11.978977	-4.039947
1LN1	A	ALA	135	E	-10.660866	11.653897	-13.089113	-3.930139
1LN1	A	ARG	136	E	-10.573760	10.899500	-13.743738	-4.141535
1LN1	A	SER	137	E	-8.454135	8.407643	-11.858850	-4.311727
1LN1	A	THR	138	C	-6.711414	6.378170	-10.479416	-4.135921
1LN1	A	SER	139	C	-6.614608	6.413772	-10.627808	-4.129351
1LN1	A	MET	140	B	-6.450401	6.324580	-10.936492	-4.249122
1LN1	A	PRO	141	T	-6.108121	6.092065	-11.239387	-4.525868
1LN1	A	GLN	142	T	-6.119107	6.049541	-11.229865	-4.529980
1LN1	A	LEU	143	B	-6.370161	5.939511	-11.683373	-4.744358
1LN1	A	GLY	144	T	-5.648972	4.120491	-11.256917	-4.534085
1LN1	A	GLU	145	C	-5.444692	4.656812	-10.720319	-4.388085
1LN1	A	ARG	146	T	-5.520236	4.530602	-10.586741	-4.296543
1LN1	A	SER	147	T	-5.519717	4.534463	-10.588691	-4.296545
1LN1	A	GLY	148	T	-5.520389	4.531699	-10.584893	-4.296418
1LN1	A	VAL	149	T	-6.049250	6.037672	-9.851889	-4.101643
1LN1	A	ILE	150	E	-7.643927	6.945015	-11.324415	-3.975825
1LN1	A	ARG	151	E	-9.621825	8.901672	-13.217588	-4.379476
1LN1	A	VAL	152	E	-11.414378	12.352483	-15.248270	-4.942623
1LN1	A	LYS	153	T	-11.794491	13.165509	-15.733237	-5.309972
1LN1	A	GLN	154	E	-11.962108	13.407842	-15.615414	-5.411172
1LN1	A	TYR	155	E	-12.110724	14.203437	-15.153627	-5.509301
1LN1	A	LYS	156	E	-12.112577	14.179945	-15.134633	-5.490141
1LN1	A	GLN	157	E	-13.572247	14.376872	-17.478127	-5.362009
1LN1	A	SER	158	E	-12.761051	15.421763	-14.343026	-4.561827
1LN1	A	LEU	159	E	-11.904175	15.069170	-13.269104	-4.344863
1LN1	A	ALA	160	E	-11.600949	13.972663	-13.953496	-4.482051
1LN1	A	ILE	161	E	-9.958372	10.100809	-14.368314	-5.223866
1LN1	A	GLU	162	E	-7.880451	6.733645	-12.920429	-5.021931
1LN1	A	SER	163	E	-5.380628	4.439218	-9.921286	-4.325231
1LN1	A	ASP	164	T	-3.902289	4.022815	-8.870952	-4.683042
1LN1	A	GLY	165	T	-3.869366	4.052307	-8.963661	-4.682373
1LN1	A	LYS	166	T	-3.869212	4.053151	-8.964810	-4.682431
1LN1	A	LYS	167	T	-3.869870	4.050297	-8.960444	-4.682042
1LN1	A	GLY	168	C	-3.917439	4.019747	-8.881872	-4.711684
1LN1	A	SER	169	E	-5.596485	4.574419	-10.577921	-4.659227
1LN1	A	LYS	170	E	-8.678829	7.631593	-13.487653	-4.925420
1LN1	A	VAL	171	E	-10.922245	10.254935	-14.219253	-4.394595
1LN1	A	PHE	172	E	-12.818826	14.875182	-14.484939	-4.614285
1LN1	A	MET	173	E	-14.652866	17.694943	-15.931191	-4.973187
1LN1	A	TYR	174	E	-16.010145	20.137502	-17.051168	-5.396075
1LN1	A	TYR	175	E	-15.264979	17.596521	-17.305104	-5.429978
1LN1	A	PHE	176	E	-11.589780	13.819510	-14.472764	-5.359824
1LN1	A	ASP	177	E	-8.391184	8.567727	-12.621306	-5.026653
1LN1	A	ASN	178	E	-6.450275	6.365548	-10.584350	-4.505207
1LN1	A	PRO	179	C	-5.024347	6.581396	-8.056677	-3.959915
1LN1	A	GLY	180	C	-4.118508	6.146990	-7.170706	-3.811703
1LN1	A	GLY	181	C	-4.078362	6.189289	-7.240442	-3.794438
1LN1	A	GLN	182	C	-4.073987	6.219523	-7.238560	-3.788911
1LN1	A	ILE	183	C	-4.082981	6.235702	-7.179335	-3.775320
1LN1	A	PRO	184	C	-4.204902	6.150196	-7.033683	-3.744068
1LN1	A	SER	185	H	-5.604607	7.362855	-8.100155	-3.499836
1LN1	A	TRP	186	H	-6.767544	10.923604	-7.356496	-3.248157
1LN1	A	LEU	187	H	-7.602473	13.362939	-7.083506	-3.386237
1LN1	A	ILE	188	H	-9.134575	13.463095	-10.710807	-4.148558
1LN1	A	ASN	189	H	-9.234272	12.596472	-11.516213	-4.312966
1LN1	A	TRP	190	H	-9.788213	11.107604	-12.259734	-3.845727
1LN1	A	ALA	191	H	-8.978518	8.057253	-13.038754	-4.090703
1LN1	A	ALA	192	H	-8.134029	7.692057	-11.775892	-3.925166
1LN1	A	LYS	193	H	-8.062905	7.657349	-11.896137	-3.928684
1LN1	A	ASN	194	H	-7.970951	7.694839	-11.954444	-3.972666
1LN1	A	GLY	195	H	-7.971900	7.695508	-11.951252	-3.973940
1LN1	A	VAL	196	H	-8.059990	7.781951	-11.735550	-3.939307
1LN1	A	PRO	197	H	-8.728300	8.096280	-12.478439	-4.074100

1LN1	A	ASN	198	H	-8.990562	8.405332	-12.286957	-4.141572
1LN1	A	PHE	199	H	-11.309120	12.928345	-14.202187	-4.522488
1LN1	A	LEU	200	H	-11.185729	13.182258	-14.066994	-4.727378
1LN1	A	LYS	201	H	-11.058219	12.096810	-14.651628	-4.730711
1LN1	A	ASP	202	H	-11.096619	11.889900	-14.732091	-4.742623
1LN1	A	MET	203	H	-11.153890	11.816691	-14.659355	-4.728707
1LN1	A	ALA	204	H	-11.138834	11.610775	-14.881995	-4.801380
1LN1	A	ARG	205	H	-11.220633	9.753264	-16.595201	-5.249628
1LN1	A	ALA	206	H	-10.799384	9.646976	-16.328935	-5.464910
1LN1	A	CYS	207	H	-8.518279	6.891068	-12.941666	-4.482365
1LN1	A	GLN	208	H	-8.518279	6.891068	-12.941666	-4.482365
1LN1	A	ASN	209	H	-8.518279	6.891068	-12.941666	-4.482365
1LN1	A	TYR	210	C	-8.518279	6.891068	-12.941666	-4.482365
1LPJ	A	PRO	1	C	-7.642003	8.442192	-10.062738	-3.515044
1LPJ	A	ALA	2	C	-7.642003	8.442192	-10.062738	-3.515044
1LPJ	A	ASP	3	C	-7.642003	8.442192	-10.062738	-3.515044
1LPJ	A	LEU	4	C	-7.642003	8.442192	-10.062738	-3.515044
1LPJ	A	SER	5	C	-9.593828	10.035530	-13.302614	-4.545091
1LPJ	A	GLY	6	E	-10.555895	11.991684	-15.055982	-5.473594
1LPJ	A	THR	7	E	-10.895726	15.772027	-13.640331	-5.452453
1LPJ	A	TRP	8	E	-10.899924	15.940048	-13.442084	-5.369955
1LPJ	A	THR	9	E	-10.076338	11.655616	-14.031516	-5.078175
1LPJ	A	LEU	10	E	-9.734824	10.148576	-14.479104	-5.008051
1LPJ	A	LEU	11	E	-9.571420	8.512294	-15.255290	-5.011221
1LPJ	A	SER	12	E	-9.582021	8.167098	-15.413060	-5.006545
1LPJ	A	SER	13	T	-9.552541	8.207791	-15.495481	-5.047508
1LPJ	A	ASP	14	T	-9.577302	8.047599	-15.955464	-5.311816
1LPJ	A	ASN	15	T	-9.831069	7.873301	-16.421613	-5.512263
1LPJ	A	PHE	16	H	-10.182374	9.892282	-15.987002	-5.867164
1LPJ	A	GLU	17	H	-10.211370	10.017932	-15.886942	-5.896204
1LPJ	A	GLY	18	H	-10.313676	10.136366	-15.692469	-5.917749
1LPJ	A	TYR	19	H	-12.425971	16.155610	-16.387576	-6.073767
1LPJ	A	MET	20	H	-10.596914	12.911441	-13.807903	-5.265857
1LPJ	A	LEU	21	H	-9.595005	12.014099	-12.517710	-4.732734
1LPJ	A	ALA	22	H	-9.132621	11.459707	-12.549805	-4.753842
1LPJ	A	LEU	23	H	-8.704708	11.222637	-12.533854	-4.941745
1LPJ	A	GLY	24	C	-6.869480	7.128206	-11.411474	-4.763232
1LPJ	A	ILE	25	C	-6.753878	7.450682	-11.396835	-4.752093
1LPJ	A	ASP	26	C	-6.751807	7.448490	-11.413599	-4.757549
1LPJ	A	PHE	27	H	-6.756206	7.420557	-11.409742	-4.758525
1LPJ	A	ALA	28	H	-6.766783	7.356423	-11.392264	-4.751826
1LPJ	A	THR	29	H	-7.728225	9.081780	-11.534875	-4.741266
1LPJ	A	ARG	30	H	-9.249845	10.444712	-13.860128	-5.187531
1LPJ	A	LYS	31	H	-7.451347	9.043062	-10.001857	-3.953529
1LPJ	A	ILE	32	H	-6.974578	9.904517	-9.496330	-4.026552
1LPJ	A	ALA	33	H	-6.948848	9.928272	-9.583854	-4.048675
1LPJ	A	LYS	34	H	-6.890810	9.968815	-9.738439	-4.107608
1LPJ	A	LEU	35	C	-6.885285	9.977023	-9.766887	-4.114495
1LPJ	A	LEU	36	C	-7.167473	10.566956	-9.665072	-4.223988
1LPJ	A	LYS	37	C	-8.038849	10.456065	-11.487691	-4.664058
1LPJ	A	PRO	38	C	-8.233948	10.439441	-11.413686	-4.701583
1LPJ	A	GLN	39	E	-9.617532	11.027772	-12.916140	-4.863216
1LPJ	A	LYS	40	E	-12.096126	14.507378	-16.334471	-5.690628
1LPJ	A	VAL	41	E	-10.667804	11.535503	-14.826340	-5.410412
1LPJ	A	ILE	42	E	-8.072526	9.557634	-12.694768	-5.648746
1LPJ	A	GLU	43	E	-7.292623	7.367426	-13.493571	-5.838646
1LPJ	A	GLN	44	E	-6.766209	6.333343	-13.312579	-5.609409
1LPJ	A	ASN	45	E	-6.710497	6.629513	-13.195545	-5.565478
1LPJ	A	GLY	46	T	-6.710080	6.633965	-13.195372	-5.565359
1LPJ	A	ASP	47	T	-6.771862	6.315632	-13.253328	-5.555828
1LPJ	A	SER	48	E	-6.986502	6.206579	-13.020578	-5.401959
1LPJ	A	PHE	49	E	-8.125912	9.688008	-12.053428	-5.125770
1LPJ	A	THR	50	E	-10.394424	12.179425	-14.109928	-5.395247
1LPJ	A	ILE	51	E	-12.188977	16.392689	-14.999339	-5.337445
1LPJ	A	HIS	52	E	-11.957688	12.406964	-16.684469	-5.392690
1LPJ	A	THR	53	E	-10.540854	11.419791	-14.753690	-5.352774
1LPJ	A	ASN	54	E	-9.940186	10.679344	-14.351955	-5.111226
1LPJ	A	SER	55	E	-7.186756	9.560057	-10.172015	-4.581318
1LPJ	A	SER	56	T	-7.182831	9.568458	-10.193754	-4.582313
1LPJ	A	LEU	57	T	-7.182508	9.571383	-10.195318	-4.582582
1LPJ	A	ARG	58	E	-7.184254	9.566469	-10.182572	-4.580228
1LPJ	A	ASN	59	E	-7.165294	9.689828	-10.204272	-4.594890
1LPJ	A	TYR	60	E	-8.985160	12.857420	-11.726591	-4.989383
1LPJ	A	PHE	61	E	-8.853767	13.923689	-11.097057	-4.969019
1LPJ	A	VAL	62	E	-8.752939	14.338529	-10.852725	-4.891799
1LPJ	A	LYS	63	E	-7.960867	13.981076	-9.819013	-4.871760
1LPJ	A	PHE	64	E	-7.733247	13.380864	-9.809455	-4.771169
1LPJ	A	LYS	65	E	-6.394035	9.733156	-9.846783	-4.971868
1LPJ	A	VAL	66	T	-6.369798	9.795233	-9.887553	-4.972671
1LPJ	A	GLY	67	T	-6.314752	9.830619	-10.041022	-5.021035
1LPJ	A	GLU	68	B	-6.342436	9.637745	-10.070456	-5.028758

1LPJ	A	GLU	69	C	-6.366156	9.528172	-10.070037	-5.044337
1LPJ	A	PHE	70	E	-7.509529	10.799921	-11.360645	-5.334434
1LPJ	A	ASP	71	E	-7.709085	10.324457	-11.718673	-5.496117
1LPJ	A	GLU	72	E	-9.209959	7.671991	-15.883151	-5.627847
1LPJ	A	ASP	73	E	-8.337805	8.066757	-13.826314	-5.252529
1LPJ	A	ASN	74	E	-8.345005	8.014819	-13.811581	-5.240246
1LPJ	A	ARG	75	T	-7.767061	8.342965	-12.880487	-5.098416
1LPJ	A	GLY	76	T	-7.785533	8.351416	-12.797736	-5.083207
1LPJ	A	LEU	77	T	-7.813407	8.447366	-12.639721	-5.061064
1LPJ	A	ASP	78	T	-8.042148	8.556768	-12.362157	-5.020939
1LPJ	A	ASN	79	T	-8.043915	8.554953	-12.347838	-5.019040
1LPJ	A	ARG	80	E	-11.287097	10.713569	-17.597162	-6.087732
1LPJ	A	LYS	81	E	-11.507410	10.846006	-17.648408	-6.076640
1LPJ	A	CYS	82	E	-12.065623	9.768289	-19.125793	-6.129746
1LPJ	A	LYS	83	E	-11.711722	12.695345	-15.349744	-4.954330
1LPJ	A	SER	84	E	-11.590061	13.708858	-14.620594	-4.778489
1LPJ	A	LEU	85	E	-10.994276	15.082452	-12.754242	-4.468351
1LPJ	A	VAL	86	E	-8.879585	13.303715	-10.119955	-4.326473
1LPJ	A	ILE	87	E	-8.399199	12.198062	-10.802625	-4.528401
1LPJ	A	TRP	88	E	-7.537233	11.385142	-10.224007	-4.631852
1LPJ	A	ASP	89	E	-6.672260	9.950304	-9.628309	-4.451339
1LPJ	A	ASN	90	T	-6.665186	9.971340	-9.652053	-4.453331
1LPJ	A	ASP	91	T	-6.678799	9.895105	-9.644574	-4.456653
1LPJ	A	ARG	92	E	-6.695749	9.858709	-9.597096	-4.449837
1LPJ	A	LEU	93	E	-6.817236	9.567279	-9.493745	-4.401241
1LPJ	A	THR	94	E	-9.154379	12.129748	-11.800297	-4.631621
1LPJ	A	CYS	95	E	-10.164718	13.266558	-12.677635	-4.759754
1LPJ	A	ILE	96	E	-10.157934	12.354824	-13.404293	-4.950587
1LPJ	A	GLN	97	E	-10.940611	8.666729	-18.466262	-6.396417
1LPJ	A	LYS	98	E	-9.149356	7.496468	-16.161140	-6.324057
1LPJ	A	GLY	99	E	-6.675601	5.693233	-13.061443	-5.741506
1LPJ	A	GLU	100	T	-6.675596	5.693273	-13.061514	-5.741531
1LPJ	A	LYS	101	T	-6.675875	5.692198	-13.059213	-5.741374
1LPJ	A	LYS	102	T	-6.675985	5.691438	-13.058052	-5.741070
1LPJ	A	ASN	103	T	-6.684728	5.665414	-13.013653	-5.732467
1LPJ	A	ARG	104	E	-12.252567	9.449764	-19.890586	-6.415056
1LPJ	A	GLY	105	E	-12.689531	11.667698	-19.224875	-6.260769
1LPJ	A	TRP	106	E	-13.010198	14.431120	-18.008049	-6.209904
1LPJ	A	THR	107	E	-12.367517	16.197005	-15.342618	-5.803255
1LPJ	A	HIS	108	E	-9.864031	13.794193	-12.688067	-5.578418
1LPJ	A	TRP	109	E	-7.775730	11.189293	-11.232806	-5.438540
1LPJ	A	ILE	110	E	-5.254128	7.592539	-9.199734	-4.945619
1LPJ	A	GLU	111	E	-5.220980	7.668415	-9.295889	-4.961649
1LPJ	A	GLY	112	T	-5.219921	7.675096	-9.301722	-4.962537
1LPJ	A	ASP	113	T	-5.220147	7.672798	-9.300462	-4.962302
1LPJ	A	LYS	114	E	-5.227897	7.627521	-9.275572	-4.956069
1LPJ	A	LEU	115	E	-6.926615	9.064477	-11.016333	-5.245927
1LPJ	A	HIS	116	E	-8.963122	11.464443	-12.584226	-5.459309
1LPJ	A	LEU	117	E	-11.670004	16.688875	-14.548243	-5.633463
1LPJ	A	GLU	118	E	-11.977983	17.444920	-14.853512	-5.799813
1LPJ	A	MET	119	E	-11.055203	13.863986	-14.930676	-5.802252
1LPJ	A	PHE	120	E	-9.887914	11.312424	-14.409319	-5.652617
1LPJ	A	CYS	121	E	-7.316459	7.817973	-12.209895	-5.313375
1LPJ	A	GLU	122	T	-7.144548	7.683390	-12.483681	-5.320099
1LPJ	A	GLY	123	T	-7.106446	7.711347	-12.566585	-5.318825
1LPJ	A	GLN	124	E	-7.107058	7.705731	-12.564213	-5.318333
1LPJ	A	VAL	125	E	-7.111732	7.679957	-12.550600	-5.315899
1LPJ	A	CYS	126	E	-7.822378	7.466136	-13.407485	-5.332056
1LPJ	A	LYS	127	E	-8.749818	8.142371	-13.823977	-5.301306
1LPJ	A	GLN	128	E	-12.473412	11.539182	-18.209898	-6.044597
1LPJ	A	THR	129	E	-11.382385	15.194197	-13.978429	-5.455613
1LPJ	A	PHE	130	E	-8.861342	13.394320	-9.796733	-4.176118
1LPJ	A	GLN	131	E	-8.861342	13.394320	-9.796733	-4.176118
1LPJ	A	ARG	132	E	-8.861342	13.394320	-9.796733	-4.176118
1LPJ	A	ALA	133	C	-8.861342	13.394320	-9.796733	-4.176118
1LSL	A	GLN	416	C	-6.334041	4.948789	-12.949140	-5.432377
1LSL	A	ASP	417	C	-6.334041	4.948789	-12.949140	-5.432377
1LSL	A	GLY	418	C	-6.334041	4.948789	-12.949140	-5.432377
1LSL	A	GLY	419	B	-6.334041	4.948789	-12.949140	-5.432377
1LSL	A	TRP	420	C	-10.414007	10.239581	-16.310776	-6.161536
1LSL	A	SER	421	C	-9.085805	7.688643	-14.048557	-5.006092
1LSL	A	HIS	422	C	-8.462637	10.392809	-12.521084	-5.194379
1LSL	A	TRP	423	C	-8.457812	10.406770	-12.540642	-5.195621
1LSL	A	SER	424	C	-8.229839	9.376697	-12.700786	-4.881403
1LSL	A	PRO	425	C	-7.437340	7.925413	-11.868692	-4.575345
1LSL	A	TRP	426	C	-7.461821	7.951797	-11.779774	-4.551442
1LSL	A	SER	427	C	-7.448883	6.966818	-12.094783	-4.386125
1LSL	A	SER	428	C	-5.811679	4.457110	-10.299612	-3.919507
1LSL	A	CYS	429	T	-5.330052	4.764835	-10.334859	-4.237131
1LSL	A	SER	430	T	-5.214030	4.581363	-10.491358	-4.240534
1LSL	A	VAL	431	T	-5.007838	4.610784	-10.571692	-4.339566

1LSL	A	THR	432	T	-4.509353	5.440734	-10.658399	-5.128253
1LSL	A	CYS	433	T	-4.561998	5.572345	-10.749220	-5.267950
1LSL	A	GLY	434	E	-4.628108	5.738093	-10.798931	-5.367724
1LSL	A	ASP	435	E	-4.664911	5.905069	-10.766001	-5.445061
1LSL	A	GLY	436	E	-4.771722	6.145808	-10.764939	-5.615994
1LSL	A	VAL	437	E	-6.063334	6.782352	-11.071446	-4.787853
1LSL	A	ILE	438	E	-6.243966	7.243437	-10.583625	-4.683060
1LSL	A	THR	439	E	-7.225743	8.596402	-10.969922	-4.844365
1LSL	A	ARG	440	E	-10.234301	12.020458	-13.934237	-5.076975
1LSL	A	ILE	441	E	-9.535946	9.828187	-14.164323	-5.290361
1LSL	A	ARG	442	C	-9.437261	9.327424	-14.510159	-5.341000
1LSL	A	LEU	443	C	-8.048032	6.519722	-13.106805	-4.644499
1LSL	A	CYS	444	T	-7.652358	6.562889	-12.933133	-4.588505
1LSL	A	ASN	445	T	-7.387399	7.029963	-12.322179	-4.371479
1LSL	A	SER	446	T	-7.391365	7.002866	-12.318610	-4.358832
1LSL	A	PRO	447	B	-7.156751	6.995558	-11.897800	-4.140788
1LSL	A	SER	448	T	-4.925330	4.701936	-8.672905	-3.743785
1LSL	A	PRO	449	C	-3.155104	3.995029	-7.234430	-4.027231
1LSL	A	GLN	450	T	-2.946939	3.722050	-7.673004	-4.127200
1LSL	A	MET	451	T	-2.584817	3.141415	-7.632195	-3.997972
1LSL	A	ASN	452	T	-2.578067	3.154254	-7.663092	-4.004190
1LSL	A	GLY	453	T	-2.588275	3.125537	-7.649243	-4.008403
1LSL	A	LYS	454	C	-2.839318	2.638856	-7.960991	-3.974585
1LSL	A	PRO	455	C	-2.973542	2.535302	-7.852236	-3.886854
1LSL	A	CYS	456	C	-4.141598	3.431366	-10.391038	-4.547383
1LSL	A	GLU	457	C	-4.035822	3.815394	-9.888923	-4.415998
1LSL	A	GLY	458	C	-4.032165	3.900552	-9.849842	-4.416855
1LSL	A	GLU	459	T	-4.211269	4.303587	-9.676955	-4.392811
1LSL	A	ALA	460	T	-4.562170	5.309136	-9.216958	-4.249717
1LSL	A	ARG	461	E	-4.594331	6.019348	-8.650771	-4.141000
1LSL	A	GLU	462	E	-5.390986	8.854184	-8.980913	-4.455522
1LSL	A	THR	463	E	-4.935905	8.367599	-8.454263	-4.539656
1LSL	A	LYS	464	E	-4.960521	8.218801	-8.583435	-4.590818
1LSL	A	ALA	465	E	-4.858011	7.754495	-8.899505	-4.607496
1LSL	A	CYS	466	E	-4.810856	7.109050	-9.260612	-4.641475
1LSL	A	LYS	467	E	-4.417534	7.569067	-9.303648	-5.069888
1LSL	A	LYS	468	E	-4.554409	7.525693	-9.615690	-5.178783
1LSL	A	ASP	469	B	-4.538896	7.522309	-9.533581	-5.105320
1LSL	A	ALA	470	C	-4.593368	7.741281	-9.425093	-5.135804
1LSL	A	CYS	471	C	-4.651739	7.937755	-9.350276	-5.155810
1LSL	A	PRO	472	C	-5.130358	7.467960	-9.099123	-4.208547
1LSL	A	ILE	473	B	-5.297116	7.393870	-9.094588	-4.161388
1LSL	A	ASN	474	C	-5.431192	7.434166	-9.176457	-4.277886
1LSL	A	GLY	475	C	-5.444109	7.340603	-9.273334	-4.329143
1LSL	A	GLY	476	E	-5.604532	7.359270	-9.142372	-4.348277
1LSL	A	TRP	477	E	-7.078849	8.155842	-12.084283	-5.191860
1LSL	A	GLY	478	E	-6.811350	7.394702	-12.018565	-4.965671
1LSL	A	PRO	479	C	-6.885166	7.162155	-11.944109	-4.869178
1LSL	A	TRP	480	C	-7.306192	6.878144	-12.028021	-4.692414
1LSL	A	SER	481	C	-7.072402	6.349533	-12.137393	-4.557403
1LSL	A	PRO	482	C	-6.291529	6.306252	-11.258434	-4.645470
1LSL	A	TRP	483	C	-6.386594	6.299729	-11.174501	-4.657132
1LSL	A	ASP	484	C	-6.288203	5.791452	-11.481995	-4.577308
1LSL	A	ILE	485	C	-5.525488	3.941468	-10.702344	-3.962130
1LSL	A	CYS	486	C	-5.525275	3.895542	-10.726223	-3.961457
1LSL	A	SER	487	C	-5.631383	3.317068	-10.779512	-3.805305
1LSL	A	VAL	488	T	-4.996170	3.816025	-10.677977	-4.377852
1LSL	A	THR	489	T	-4.227052	4.967899	-10.421845	-5.268728
1LSL	A	CYS	490	T	-4.225270	5.131866	-10.520272	-5.395232
1LSL	A	GLY	491	T	-4.224822	5.138928	-10.523185	-5.398805
1LSL	A	GLY	492	C	-4.227173	5.144454	-10.513381	-5.403270
1LSL	A	GLY	493	E	-4.344973	5.376359	-10.484275	-5.561659
1LSL	A	VAL	494	E	-5.667912	5.300336	-11.670396	-5.303608
1LSL	A	GLN	495	E	-7.505799	6.246525	-13.589454	-5.541688
1LSL	A	LYS	496	E	-9.279401	7.169018	-15.433335	-5.701738
1LSL	A	ARG	497	E	-12.657719	9.993615	-19.231504	-5.933012
1LSL	A	SER	498	E	-10.979740	8.359308	-16.300036	-5.115808
1LSL	A	ARG	499	C	-9.526790	8.998121	-14.353980	-5.160887
1LSL	A	LEU	500	E	-7.233744	6.098838	-11.661688	-4.312437
1LSL	A	CYS	501	E	-6.163187	7.218274	-10.174781	-4.467116
1LSL	A	ASN	502	E	-5.749290	7.987330	-9.256068	-4.223201
1LSL	A	ASN	503	E	-5.708301	8.079346	-9.270054	-4.204858
1LSL	A	PRO	504	B	-5.704624	8.103806	-9.269069	-4.201351
1LSL	A	THR	505	T	-5.602147	8.466673	-9.058139	-4.209783
1LSL	A	PRO	506	C	-5.141786	8.924267	-8.169382	-4.365439
1LSL	A	GLN	507	B	-5.049699	8.525399	-8.531976	-4.525727
1LSL	A	PHE	508	T	-4.584998	7.463751	-8.587859	-4.554889
1LSL	A	GLY	509	T	-4.008057	5.094034	-9.307182	-4.703727
1LSL	A	GLY	510	T	-3.892955	4.530227	-9.544835	-4.639007
1LSL	A	LYS	511	C	-3.571354	3.096309	-9.708151	-4.517434
1LSL	A	ASP	512	C	-3.566106	2.953915	-9.791734	-4.518431

1LSL	A	CYS	513	C	-3.622808	2.546557	-9.938231	-4.510295
1LSL	A	VAL	514	C	-3.616330	2.692224	-9.668557	-4.367102
1LSL	A	GLY	515	C	-3.683862	2.779141	-9.567908	-4.378498
1LSL	A	ASP	516	T	-4.175870	3.904440	-9.376000	-4.402685
1LSL	A	VAL	517	T	-4.233586	4.094190	-9.102992	-4.373874
1LSL	A	THR	518	E	-4.248224	4.142537	-9.016130	-4.373767
1LSL	A	GLU	519	E	-6.230083	6.507319	-11.304900	-5.018790
1LSL	A	ASN	520	E	-7.563833	7.844371	-13.183330	-5.361395
1LSL	A	GLN	521	E	-8.111143	8.601872	-13.545859	-5.523119
1LSL	A	ILE	522	E	-7.688183	7.189860	-14.597597	-6.084511
1LSL	A	CYS	523	E	-6.928194	6.291610	-17.062408	-8.368504
1LSL	A	ASN	524	T	-5.062869	6.879792	-12.834808	-7.261720
1LSL	A	LYS	525	T	-3.670461	4.118790	-7.906869	-3.970376
1LSL	A	GLN	526	C	-3.670461	4.118790	-7.906869	-3.970376
1LSL	A	ASP	527	C	-3.670461	4.118790	-7.906869	-3.970376
1LSL	A	CYS	528	C	-3.670461	4.118790	-7.906869	-3.970376
1M7B	A	VAL	22	C	-9.761125	7.582881	-14.479724	-4.615596
1M7B	A	LYS	23	E	-9.761125	7.582881	-14.479724	-4.615596
1M7B	A	CYS	24	E	-9.761125	7.582881	-14.479724	-4.615596
1M7B	A	LYS	25	E	-9.761125	7.582881	-14.479724	-4.615596
1M7B	A	ILE	26	E	-8.902016	15.546866	-7.965830	-3.719384
1M7B	A	VAL	27	E	-8.864894	15.386330	-8.211618	-3.754387
1M7B	A	VAL	28	E	-8.856903	15.326233	-8.300017	-3.766564
1M7B	A	VAL	29	E	-8.847673	15.229251	-8.427163	-3.789684
1M7B	A	GLY	30	E	-8.843496	15.168358	-8.507192	-3.806316
1M7B	A	ASP	31	T	-10.138980	10.938929	-14.430541	-4.842567
1M7B	A	SER	32	T	-10.548540	8.613930	-17.239385	-5.498121
1M7B	A	GLN	33	T	-10.600424	8.203181	-17.920803	-5.806844
1M7B	A	CYS	34	T	-10.531245	8.437584	-17.648113	-5.802606
1M7B	A	GLY	35	C	-10.503287	9.231088	-17.008424	-5.659646
1M7B	A	LYS	36	H	-10.671428	9.969383	-16.532855	-5.555541
1M7B	A	THR	37	H	-10.738637	10.244622	-16.240080	-5.479626
1M7B	A	ALA	38	H	-10.864868	10.514261	-15.822048	-5.297118
1M7B	A	LEU	39	H	-11.499544	12.650642	-15.069949	-5.075317
1M7B	A	LEU	40	H	-12.322696	18.007936	-13.064386	-4.464469
1M7B	A	HIS	41	H	-11.164206	16.146703	-12.119308	-4.550457
1M7B	A	VAL	42	H	-8.949305	14.044115	-9.738771	-4.370828
1M7B	A	PHE	43	H	-8.207063	11.705115	-10.534021	-4.478156
1M7B	A	ALA	44	H	-7.721925	10.873234	-10.808051	-4.563545
1M7B	A	LYS	45	H	-7.575508	11.357102	-11.347344	-5.063824
1M7B	A	ASP	46	C	-6.880107	10.582768	-10.352439	-4.781958
1M7B	A	CYS	47	C	-5.037159	9.446895	-6.839984	-4.071902
1M7B	A	PHE	48	C	-4.895081	10.013550	-6.787405	-4.138651
1M7B	A	PRO	49	C	-3.593527	8.029389	-5.705262	-3.955530
1M7B	A	GLU	50	C	-2.419455	5.368285	-5.699678	-3.940686
1M7B	A	ASN	51	C	-2.396252	5.431025	-5.771534	-3.959366
1M7B	A	TYR	52	C	-2.401589	5.392996	-5.765745	-3.958055
1M7B	A	VAL	53	C	-2.403006	5.376652	-5.763699	-3.956442
1M7B	A	PRO	54	C	-2.480583	5.020542	-5.767187	-3.943681
1M7B	A	THR	55	C	-4.289586	7.137809	-7.466712	-4.300091
1M7B	A	VAL	56	C	-5.757222	10.193090	-8.120193	-4.296815
1M7B	A	PHE	57	C	-6.481245	12.539449	-7.604874	-4.321091
1M7B	A	GLU	58	E	-7.725478	14.876978	-10.599870	-5.941912
1M7B	A	ASN	59	E	-8.675309	15.239087	-12.903313	-6.757230
1M7B	A	TYR	60	E	-9.350064	13.103186	-12.751532	-5.227203
1M7B	A	THR	61	E	-7.710125	11.740796	-9.977011	-4.702426
1M7B	A	ALA	62	E	-7.673237	11.898442	-10.065628	-4.750566
1M7B	A	SER	63	E	-7.248007	11.872163	-9.849505	-4.778662
1M7B	A	PHE	64	E	-4.706005	9.760113	-6.194932	-4.135511
1M7B	A	GLU	65	E	-2.618604	6.315967	-5.461950	-4.143131
1M7B	A	ILE	66	T	-2.578874	6.358942	-5.569972	-4.147697
1M7B	A	ASP	67	T	-2.577825	6.359660	-5.577866	-4.147892
1M7B	A	THR	68	T	-2.577937	6.358569	-5.577116	-4.147754
1M7B	A	GLN	69	T	-2.594677	6.257482	-5.556904	-4.145417
1M7B	A	ARG	70	E	-4.196115	6.837036	-7.083943	-4.118037
1M7B	A	ILE	71	E	-6.338169	6.693334	-9.934537	-4.172471
1M7B	A	GLU	72	E	-9.222845	9.832794	-13.800229	-5.303463
1M7B	A	LEU	73	E	-12.138006	15.910198	-16.621631	-6.584502
1M7B	A	SER	74	E	-12.740655	13.290262	-16.599834	-5.152569
1M7B	A	LEU	75	E	-13.593009	15.838396	-17.058707	-5.406200
1M7B	A	TRP	76	E	-12.674103	14.266903	-16.983314	-6.113161
1M7B	A	ASP	77	E	-12.081531	11.808354	-17.596654	-6.006187
1M7B	A	THR	78	C	-10.449042	8.631952	-15.982602	-5.412948
1M7B	A	SER	79	C	-8.921749	6.339851	-14.588879	-4.914523
1M7B	A	GLY	80	C	-7.825623	8.085334	-12.488292	-4.920784
1M7B	A	SER	81	C	-7.789090	8.068877	-12.588232	-4.915525
1M7B	A	PRO	82	G	-6.892688	8.303423	-11.094167	-4.799501
1M7B	A	TYR	83	G	-6.652183	8.635115	-10.819719	-4.729903
1M7B	A	TYR	84	G	-6.663821	8.688194	-10.747049	-4.727219
1M7B	A	ASP	85	T	-6.738142	8.726968	-10.568714	-4.701021
1M7B	A	ASN	86	T	-6.731917	8.767689	-10.548040	-4.686341

1M7B	A	VAL	87	T	-7.266519	9.352010	-10.366124	-4.568183
1M7B	A	ARG	88	G	-8.988627	10.366154	-11.558795	-4.114515
1M7B	A	PRO	89	G	-9.001813	10.314236	-11.500118	-4.082932
1M7B	A	LEU	90	G	-8.964050	10.157326	-11.698655	-4.115910
1M7B	A	SER	91	G	-10.187172	9.386855	-14.786002	-4.692392
1M7B	A	TYR	92	T	-9.844959	9.290730	-14.848100	-4.936499
1M7B	A	PRO	93	T	-8.206169	6.227356	-13.133114	-4.456275
1M7B	A	ASP	94	T	-8.169498	6.389439	-13.162534	-4.463425
1M7B	A	SER	95	T	-8.184443	6.329793	-13.124192	-4.458443
1M7B	A	ASP	96	C	-8.185823	6.329340	-13.111533	-4.454630
1M7B	A	ALA	97	E	-8.200387	6.281360	-13.052348	-4.431152
1M7B	A	VAL	98	E	-9.757569	9.655238	-13.490580	-4.522380
1M7B	A	LEU	99	E	-11.169835	15.863064	-11.945180	-4.119878
1M7B	A	ILE	100	E	-11.194277	16.040864	-11.785901	-4.106469
1M7B	A	CYS	101	E	-11.385683	16.213460	-11.580561	-4.099068
1M7B	A	PHE	102	E	-12.818411	18.333395	-13.886871	-4.790877
1M7B	A	ASP	103	E	-13.082430	15.937629	-16.088215	-5.158550
1M7B	A	ILE	104	T	-12.482259	12.969570	-16.194194	-4.913945
1M7B	A	SER	105	T	-11.746978	10.889892	-16.440117	-5.089940
1M7B	A	ARG	106	T	-11.514232	11.336173	-16.045124	-4.997944
1M7B	A	PRO	107	H	-9.591344	11.857378	-12.410959	-4.866503
1M7B	A	GLU	108	H	-9.484482	11.795561	-12.705837	-4.934316
1M7B	A	THR	109	H	-9.469543	11.853193	-12.721407	-4.932068
1M7B	A	LEU	110	H	-9.476348	11.886831	-12.672441	-4.928613
1M7B	A	ASP	111	H	-9.304313	11.211443	-12.942838	-4.818265
1M7B	A	SER	112	H	-9.801357	10.246541	-14.017838	-4.762162
1M7B	A	VAL	113	H	-9.991722	9.815841	-13.954212	-4.566949
1M7B	A	LEU	114	H	-10.031894	9.542512	-13.984651	-4.554013
1M7B	A	LYS	115	H	-10.030663	9.544707	-14.013367	-4.573534
1M7B	A	LYS	116	H	-11.312348	11.444442	-15.753394	-5.148071
1M7B	A	TRP	117	H	-12.056581	14.395441	-16.350153	-5.878305
1M7B	A	LYS	118	H	-11.354550	12.040545	-16.296211	-5.855082
1M7B	A	GLY	119	H	-10.172316	10.193598	-15.074460	-5.478077
1M7B	A	GLU	120	H	-10.082333	10.667010	-14.890192	-5.441482
1M7B	A	ILE	121	H	-9.665864	11.987168	-13.569055	-5.210712
1M7B	A	GLN	122	H	-8.750779	9.864830	-12.783587	-4.858817
1M7B	A	GLU	123	H	-6.999648	7.951190	-10.559425	-4.407888
1M7B	A	PHE	124	H	-6.724091	8.476917	-10.454418	-4.483845
1M7B	A	CYS	125	H	-6.648896	8.290383	-10.726446	-4.526276
1M7B	A	PRO	126	T	-6.634894	8.308435	-10.766737	-4.533661
1M7B	A	ASN	127	T	-6.647737	8.289867	-10.727900	-4.528940
1M7B	A	THR	128	T	-7.087167	8.775511	-11.043916	-4.688372
1M7B	A	LYS	129	E	-7.783325	7.448189	-12.689086	-4.846614
1M7B	A	MET	130	E	-8.767711	9.717501	-12.456035	-4.865885
1M7B	A	LEU	131	E	-10.491522	14.430935	-12.856850	-4.847960
1M7B	A	LEU	132	E	-10.782153	14.850176	-12.593093	-4.578943
1M7B	A	VAL	133	E	-10.724425	14.342729	-13.013080	-4.637235
1M7B	A	GLY	134	E	-10.719887	14.284796	-13.078616	-4.650546
1M7B	A	CYS	135	E	-10.879945	13.342877	-13.591066	-4.682974
1M7B	A	LYS	136	T	-11.605922	10.876979	-16.627473	-5.193713
1M7B	A	SER	137	G	-11.553047	10.278264	-17.049854	-5.340629
1M7B	A	ASP	138	G	-11.449556	10.177468	-17.013992	-5.382379
1M7B	A	LEU	139	G	-10.314732	8.659797	-15.020963	-4.646773
1M7B	A	ARG	140	T	-8.691352	5.897568	-13.474809	-4.043093
1M7B	A	THR	141	T	-5.652375	5.804028	-9.068846	-3.830842
1M7B	A	ASP	142	T	-5.633485	5.863508	-9.120206	-3.832242
1M7B	A	VAL	143	H	-5.617644	5.886883	-9.171087	-3.827781
1M7B	A	SER	144	H	-5.617220	5.888684	-9.174058	-3.828113
1M7B	A	THR	145	H	-5.620214	5.890640	-9.153202	-3.827543
1M7B	A	LEU	146	H	-7.287403	7.373704	-11.069844	-3.882190
1M7B	A	VAL	147	H	-7.668327	7.218063	-11.669854	-4.016745
1M7B	A	GLU	148	H	-8.133885	7.698232	-13.511146	-4.833600
1M7B	A	LEU	149	H	-7.172390	5.937399	-11.388279	-3.782622
1M7B	A	SER	150	H	-5.837251	3.945716	-10.620331	-3.806922
1M7B	A	ASN	151	H	-5.261934	3.949842	-10.046882	-3.736308
1M7B	A	HIS	152	C	-5.121594	4.682916	-9.625502	-3.654468
1M7B	A	ARG	153	C	-5.109044	4.819457	-9.570395	-3.641156
1M7B	A	GLN	154	C	-5.123995	4.801887	-9.536173	-3.643889
1M7B	A	THR	155	C	-5.309317	5.201798	-9.169964	-3.582501
1M7B	A	PRO	156	C	-5.972849	7.768828	-8.065822	-3.344780
1M7B	A	VAL	157	C	-7.281802	10.490365	-8.033594	-3.248514
1M7B	A	SER	158	C	-8.650685	8.762126	-13.323429	-4.833630
1M7B	A	TYR	159	H	-8.355303	8.551295	-13.352757	-4.963105
1M7B	A	ASP	160	H	-7.470132	6.651950	-13.052577	-4.974308
1M7B	A	GLN	161	H	-7.468465	6.630595	-13.080222	-4.982165
1M7B	A	GLY	162	H	-7.465896	6.652810	-13.085233	-4.986228
1M7B	A	ALA	163	H	-7.494288	6.605650	-13.044475	-4.950913
1M7B	A	ASN	164	H	-7.486722	6.547735	-13.005428	-4.891686
1M7B	A	MET	165	H	-8.375393	8.608398	-13.060119	-4.561947
1M7B	A	ALA	166	H	-6.993371	8.178367	-10.455589	-4.312163
1M7B	A	LYS	167	H	-6.204856	8.648524	-9.426261	-4.346557

1M7B	A	GLN	168	H	-6.131602	8.858048	-9.426890	-4.353237
1M7B	A	ILE	169	H	-5.918341	9.368820	-8.988395	-4.259025
1M7B	A	GLY	170	C	-5.904971	9.437715	-8.998153	-4.262975
1M7B	A	ALA	171	C	-5.996514	9.667203	-8.795645	-4.257708
1M7B	A	ALA	172	C	-6.429341	10.587749	-8.503354	-4.147608
1M7B	A	THR	173	E	-6.562718	10.649369	-8.226790	-4.084036
1M7B	A	TYR	174	E	-8.064922	12.639796	-9.656047	-4.430145
1M7B	A	ILE	175	E	-9.554463	15.208511	-10.168709	-4.242033
1M7B	A	GLU	176	E	-10.275471	15.404316	-11.825497	-4.943875
1M7B	A	CYS	177	C	-9.852686	10.086607	-13.918311	-4.963406
1M7B	A	SER	178	B	-8.454084	9.249630	-12.036098	-4.573880
1M7B	A	ALA	179	T	-8.104494	9.632474	-11.909930	-4.658938
1M7B	A	LEU	180	T	-7.823350	8.890231	-12.556040	-4.914817
1M7B	A	GLN	181	T	-7.792020	8.788429	-12.701583	-4.938272
1M7B	A	SER	182	B	-7.806911	8.757214	-12.682493	-4.938856
1M7B	A	GLU	183	H	-8.015588	8.588501	-13.064397	-5.111007
1M7B	A	ASN	184	H	-8.294836	7.659452	-13.895236	-5.317290
1M7B	A	SER	185	H	-9.374115	7.590821	-15.302909	-5.214381
1M7B	A	VAL	186	H	-10.212272	9.506872	-14.979272	-4.705530
1M7B	A	ARG	187	H	-10.354892	9.781235	-14.714009	-4.646112
1M7B	A	ASP	188	H	-10.500674	12.833562	-13.123566	-4.484977
1M7B	A	ILE	189	H	-10.775585	17.211029	-10.920765	-4.304447
1M7B	A	PHE	190	H	-10.630559	17.350158	-10.938907	-4.365200
1M7B	A	HIS	191	H	-10.052413	14.071159	-11.661023	-4.214699
1M7B	A	VAL	192	H	-9.816287	13.386771	-11.844353	-4.147071
1M7B	A	ALA	193	H	-9.892455	12.826099	-12.130062	-4.169246
1M7B	A	THR	194	H	-9.816083	12.355053	-12.921284	-4.590198
1M7B	A	LEU	195	H	-9.164429	10.159454	-14.055665	-5.332244
1M7B	A	ALA	196	H	-8.444270	7.943093	-13.570729	-4.966813
1M7B	A	CYS	197	H	-6.400721	5.424396	-10.511801	-3.983363
1M7B	A	VAL	198	H	-6.400721	5.424396	-10.511801	-3.983363
1M7B	A	ASN	199	C	-6.400721	5.424396	-10.511801	-3.983363
1M7B	A	LYS	200	C	-6.400721	5.424396	-10.511801	-3.983363
1M9Z	A	ALA	26	C	-11.406451	9.212287	-15.779298	-4.611586
1M9Z	A	LEU	27	E	-11.406451	9.212287	-15.779298	-4.611586
1M9Z	A	CYS	28	E	-11.406451	9.212287	-15.779298	-4.611586
1M9Z	A	LYS	29	E	-11.406451	9.212287	-15.779298	-4.611586
1M9Z	A	PHE	30	C	-10.046627	9.662688	-13.981834	-4.773691
1M9Z	A	CYS	31	T	-8.348267	8.047191	-12.653336	-4.653449
1M9Z	A	ASP	32	E	-8.297835	8.169055	-12.739812	-4.662964
1M9Z	A	VAL	33	E	-7.758120	8.378629	-12.076973	-4.534619
1M9Z	A	ARG	34	E	-7.665687	8.232521	-12.305529	-4.575335
1M9Z	A	PHE	35	E	-7.590960	8.127859	-12.528293	-4.675641
1M9Z	A	SER	36	C	-7.390321	6.812160	-13.286290	-4.989748
1M9Z	A	THR	37	C	-6.912129	5.283810	-13.692174	-5.175954
1M9Z	A	CYS	38	T	-6.988903	4.739903	-14.099638	-5.304842
1M9Z	A	ASP	39	T	-6.735272	5.041768	-13.712473	-5.271413
1M9Z	A	ASN	40	T	-6.707716	5.002303	-13.740782	-5.257964
1M9Z	A	GLN	41	T	-6.802729	4.957209	-13.675571	-5.246092
1M9Z	A	LYS	42	T	-7.173363	5.692731	-13.389025	-5.184438
1M9Z	A	SER	43	E	-7.167036	5.777148	-13.351440	-5.179700
1M9Z	A	CYS	44	E	-7.938141	5.878078	-14.702896	-5.275314
1M9Z	A	MET	45	E	-7.735994	5.876898	-14.307852	-5.280932
1M9Z	A	SER	46	C	-7.574870	5.543652	-14.426559	-5.214476
1M9Z	A	ASN	47	C	-7.188989	5.315990	-14.020934	-5.122649
1M9Z	A	CYS	48	C	-7.196648	5.270794	-14.005562	-5.099551
1M9Z	A	SER	49	C	-6.384028	5.671854	-11.127040	-4.107342
1M9Z	A	ILE	50	C	-6.392930	5.720354	-11.007198	-4.042197
1M9Z	A	THR	51	E	-6.200162	5.886289	-11.147564	-4.240953
1M9Z	A	SER	52	E	-6.022275	5.719665	-11.242747	-4.346474
1M9Z	A	ILE	53	E	-5.037828	3.882756	-10.614240	-4.383279
1M9Z	A	CYS	54	T	-5.061468	3.717374	-10.758475	-4.455109
1M9Z	A	GLU	55	T	-4.985742	3.941387	-10.837220	-4.523675
1M9Z	A	LYS	56	T	-5.007415	3.866637	-10.804363	-4.514826
1M9Z	A	PRO	57	T	-5.043139	3.784745	-10.734253	-4.501813
1M9Z	A	GLN	58	T	-6.053646	5.270088	-11.917127	-4.994852
1M9Z	A	GLU	59	T	-6.199728	5.714542	-11.496753	-4.996884
1M9Z	A	VAL	60	E	-8.328330	9.176888	-12.738819	-4.981659
1M9Z	A	CYS	61	E	-9.395901	10.259121	-13.596771	-4.861976
1M9Z	A	VAL	62	E	-10.105972	12.332485	-12.348568	-4.089969
1M9Z	A	ALA	63	E	-10.124062	12.317588	-12.209743	-4.033951
1M9Z	A	VAL	64	E	-10.252940	12.274481	-11.847652	-3.880551
1M9Z	A	TRP	65	E	-12.163908	15.732235	-13.272559	-4.515404
1M9Z	A	ARG	66	E	-9.947271	7.344643	-16.233698	-5.659023
1M9Z	A	LYS	67	E	-5.166138	4.806228	-10.919833	-5.281990
1M9Z	A	ASN	68	E	-4.144463	5.820917	-9.003552	-4.957083
1M9Z	A	ASP	69	T	-4.125558	5.886460	-9.038044	-4.955493
1M9Z	A	GLU	70	T	-4.125531	5.886776	-9.038217	-4.955505
1M9Z	A	ASN	71	E	-4.125563	5.886698	-9.037827	-4.955466
1M9Z	A	ILE	72	E	-4.238034	6.110733	-8.641929	-4.885636
1M9Z	A	THR	73	E	-6.176254	7.904554	-10.089396	-4.897832

1M9Z	A	LEU	74	E	-10.049689	12.915761	-12.892814	-5.215181
1M9Z	A	GLU	75	E	-12.555354	15.378036	-16.385840	-5.546644
1M9Z	A	THR	76	E	-11.482235	13.421330	-15.252834	-5.497490
1M9Z	A	VAL	77	E	-11.311876	13.391197	-15.100751	-5.338012
1M9Z	A	CYS	78	E	-9.490924	11.393385	-12.842818	-5.018010
1M9Z	A	HIS	79	E	-7.591931	9.871770	-10.323611	-4.368898
1M9Z	A	ASP	80	T	-5.818026	8.590711	-8.096825	-3.873704
1M9Z	A	PRO	81	T	-5.815682	8.605355	-8.105421	-3.874100
1M9Z	A	LYS	82	T	-5.814963	8.608963	-8.110678	-3.875060
1M9Z	A	LEU	83	T	-5.815705	8.605501	-8.105394	-3.873579
1M9Z	A	PRO	84	T	-5.844224	8.549869	-8.003324	-3.851421
1M9Z	A	TYR	85	B	-8.766753	12.290754	-11.352123	-4.395042
1M9Z	A	HIS	86	T	-9.255000	12.375071	-12.784080	-4.961294
1M9Z	A	ASP	87	T	-7.917615	11.877927	-9.985841	-4.518262
1M9Z	A	PHE	88	B	-7.915787	11.886998	-9.981794	-4.514464
1M9Z	A	ILE	89	C	-7.679574	10.830111	-10.435422	-4.406257
1M9Z	A	LEU	90	T	-7.597772	10.470642	-10.749435	-4.420551
1M9Z	A	GLU	91	T	-7.466001	9.362151	-11.375040	-4.421399
1M9Z	A	ASP	92	T	-7.764735	7.295176	-12.764019	-4.371611
1M9Z	A	ALA	93	T	-6.844911	6.079041	-11.466672	-4.102694
1M9Z	A	ALA	94	T	-6.516878	5.635197	-11.698777	-4.312402
1M9Z	A	SER	95	T	-6.501138	5.683703	-11.712545	-4.320780
1M9Z	A	PRO	96	C	-6.518568	5.761711	-11.640125	-4.326762
1M9Z	A	THR	97	C	-6.523101	5.771200	-11.616086	-4.328247
1M9Z	A	CYS	98	E	-6.885919	5.787796	-12.041573	-4.584025
1M9Z	A	ILE	99	E	-8.132717	8.670142	-12.738105	-4.809627
1M9Z	A	MET	100	C	-8.214077	11.215084	-12.456170	-5.496029
1M9Z	A	LYS	101	E	-7.511321	11.241557	-11.469942	-5.582997
1M9Z	A	GLU	102	E	-5.984603	9.179233	-9.738132	-5.146659
1M9Z	A	LYS	103	E	-4.936788	7.454175	-9.396952	-5.113523
1M9Z	A	LYS	104	C	-4.326661	5.873708	-9.596334	-5.043155
1M9Z	A	LYS	105	T	-4.276555	5.967858	-9.675037	-5.068950
1M9Z	A	PRO	106	T	-4.275021	5.982734	-9.673665	-5.068790
1M9Z	A	GLY	107	T	-4.306446	5.817553	-9.677154	-5.066148
1M9Z	A	GLU	108	T	-4.506501	5.300491	-9.813891	-5.047966
1M9Z	A	THR	109	E	-5.718583	7.362717	-10.551863	-5.354957
1M9Z	A	PHE	110	E	-7.326557	11.441124	-10.287986	-5.334362
1M9Z	A	PHE	111	E	-10.705282	17.567191	-13.925705	-6.875504
1M9Z	A	MET	112	E	-12.659582	16.156897	-16.624467	-6.024257
1M9Z	A	CYS	113	E	-12.426083	12.109895	-18.088193	-5.745006
1M9Z	A	SER	114	E	-10.740354	6.719260	-17.147520	-5.203810
1M9Z	A	CYS	115	E	-9.117968	6.643958	-15.079277	-5.171907
1M9Z	A	SER	116	C	-8.775392	6.463975	-15.109290	-5.125355
1M9Z	A	SER	117	T	-8.763503	6.461604	-15.170141	-5.136117
1M9Z	A	ASP	118	T	-8.727493	6.555967	-15.288383	-5.203399
1M9Z	A	GLU	119	T	-8.741486	6.572923	-15.262972	-5.217285
1M9Z	A	CYS	120	G	-9.141586	6.538371	-15.605701	-5.272436
1M9Z	A	ASN	121	G	-10.124292	7.998600	-17.587416	-6.170532
1M9Z	A	ASP	122	G	-10.252079	8.466093	-17.417912	-6.290182
1M9Z	A	ASN	123	E	-11.122598	10.566329	-18.077111	-6.495509
1M9Z	A	ILE	124	E	-10.380982	17.953410	-13.437427	-7.063716
1M9Z	A	ILE	125	E	-8.149768	14.779961	-10.839627	-6.259759
1M9Z	A	PHE	126	C	-6.161683	12.460102	-8.537705	-5.488032
1M9Z	A	SER	127	C	-3.592370	7.140632	-6.575245	-4.397589
1M9Z	A	GLU	128	C	-3.592370	7.140632	-6.575245	-4.397589
1M9Z	A	GLU	129	C	-3.592370	7.140632	-6.575245	-4.397589
1M9Z	A	TYR	130	C	-3.592370	7.140632	-6.575245	-4.397589
1MFM	A	ALA	1	C	-6.154258	7.934343	-8.233098	-3.435340
1MFM	A	THR	2	E	-6.154258	7.934343	-8.233098	-3.435340
1MFM	A	LYS	3	E	-6.154258	7.934343	-8.233098	-3.435340
1MFM	A	ALA	4	E	-6.154258	7.934343	-8.233098	-3.435340
1MFM	A	VAL	5	E	-8.584911	11.207886	-10.576028	-3.861414
1MFM	A	ALA	6	E	-8.338225	11.060192	-10.178345	-3.813066
1MFM	A	VAL	7	E	-6.452906	8.737936	-8.918123	-4.009620
1MFM	A	LEU	8	E	-4.805905	7.610844	-7.820695	-4.352688
1MFM	A	LYS	9	B	-3.142344	3.581937	-7.478092	-4.095029
1MFM	A	GLY	10	C	-2.436287	4.225334	-6.414345	-3.915617
1MFM	A	ASP	11	C	-2.422961	4.285058	-6.440229	-3.918582
1MFM	A	GLY	12	C	-2.423294	4.282098	-6.439456	-3.918584
1MFM	A	PRO	13	C	-2.433656	4.222373	-6.412833	-3.908291
1MFM	A	VAL	14	C	-2.637082	4.549679	-5.931142	-3.803534
1MFM	A	GLN	15	E	-4.679875	6.819151	-7.455151	-3.931982
1MFM	A	GLY	16	E	-6.819521	8.201446	-10.305636	-4.269729
1MFM	A	ILE	17	E	-8.044649	10.740238	-11.204871	-4.331877
1MFM	A	ILE	18	E	-8.399331	11.168615	-11.215922	-4.402527
1MFM	A	ASN	19	E	-8.791142	10.485688	-11.725280	-4.528442
1MFM	A	PHE	20	E	-10.522201	14.617896	-11.381276	-4.265502
1MFM	A	GLU	21	E	-10.587383	9.366863	-16.162619	-5.687650
1MFM	A	GLN	22	E	-8.699785	6.022301	-14.873159	-5.316076
1MFM	A	LYS	23	T	-4.681421	4.645916	-9.524998	-4.733316
1MFM	A	GLU	24	T	-4.330548	4.874759	-9.381435	-4.653886

1MFM	A	SER	25	T	-4.298313	5.043498	-9.363374	-4.636751
1MFM	A	ASN	26	T	-4.277581	5.167219	-9.353006	-4.629143
1MFM	A	GLY	27	T	-4.277404	5.172550	-9.350276	-4.628268
1MFM	A	PRO	28	C	-4.694534	5.708747	-9.171223	-4.518214
1MFM	A	VAL	29	E	-5.728421	8.331651	-9.047494	-4.355310
1MFM	A	LYS	30	E	-6.257081	8.735628	-9.081672	-4.400374
1MFM	A	VAL	31	E	-8.296920	12.189576	-10.079307	-4.094826
1MFM	A	TRP	32	E	-8.878779	12.598610	-11.468954	-4.388474
1MFM	A	GLY	33	E	-7.723878	9.231205	-10.991133	-4.368421
1MFM	A	SER	34	E	-7.703400	9.353246	-10.955899	-4.359730
1MFM	A	ILE	35	E	-7.329220	10.577466	-10.192725	-4.365498
1MFM	A	LYS	36	E	-6.290525	10.046487	-9.053667	-4.536072
1MFM	A	GLY	37	C	-5.373850	8.214278	-8.727590	-4.480659
1MFM	A	LEU	38	C	-5.240658	8.253055	-8.733420	-4.447326
1MFM	A	THR	39	C	-5.226865	8.225585	-8.795928	-4.449267
1MFM	A	GLU	40	C	-5.230826	8.171102	-8.815431	-4.453983
1MFM	A	GLY	41	E	-5.319272	7.885096	-8.814438	-4.435074
1MFM	A	LEU	42	E	-6.070759	8.297906	-9.251775	-4.356268
1MFM	A	HIS	43	E	-7.281433	7.436727	-11.704937	-4.619966
1MFM	A	GLY	44	E	-8.150720	7.891264	-12.697484	-4.964697
1MFM	A	PHE	45	E	-10.981226	12.686525	-13.758392	-4.885010
1MFM	A	HIS	46	E	-12.887360	16.561617	-15.134490	-5.050882
1MFM	A	VAL	47	E	-12.813421	15.639426	-17.167299	-6.203312
1MFM	A	HIS	48	E	-11.888487	10.436697	-18.591877	-6.392951
1MFM	A	GLU	49	C	-7.335784	5.864870	-13.299812	-5.452717
1MFM	A	GLU	50	C	-5.819796	4.709971	-11.943688	-5.252416
1MFM	A	GLU	51	C	-3.820635	3.047481	-9.162897	-4.565505
1MFM	A	ASP	52	C	-2.973408	2.452339	-8.613002	-4.472425
1MFM	A	ASN	53	C	-2.907087	2.534476	-8.735312	-4.500787
1MFM	A	THR	54	C	-2.896327	2.546535	-8.775662	-4.504079
1MFM	A	ALA	55	T	-2.899274	2.534025	-8.761825	-4.499341
1MFM	A	GLY	56	T	-3.036100	2.409281	-8.658286	-4.475297
1MFM	A	CYS	57	T	-4.138344	3.214123	-9.905493	-4.682682
1MFM	A	THR	58	T	-5.202885	3.320417	-11.172898	-4.680543
1MFM	A	SER	59	T	-6.549164	3.958745	-13.351488	-5.006462
1MFM	A	ALA	60	T	-7.606080	6.377983	-15.226060	-5.971084
1MFM	A	GLY	61	C	-7.905958	6.405776	-14.388225	-5.307639
1MFM	A	PRO	62	C	-8.126311	6.318379	-13.203075	-4.524676
1MFM	A	HIS	63	B	-9.610523	9.898610	-13.972527	-4.883462
1MFM	A	PHE	64	C	-8.608630	12.506089	-10.148729	-4.348601
1MFM	A	ASN	65	T	-7.823461	9.650932	-10.655523	-4.117482
1MFM	A	PRO	66	T	-7.465581	9.290506	-10.480002	-3.969932
1MFM	A	LEU	67	T	-7.456707	9.281219	-10.526403	-3.975747
1MFM	A	SER	68	T	-7.453721	9.275435	-10.548077	-3.978838
1MFM	A	ARG	69	C	-7.536024	8.784988	-10.663579	-3.934059
1MFM	A	LYS	70	C	-7.772247	9.140773	-10.770951	-4.019086
1MFM	A	HIS	71	C	-8.506292	9.658302	-12.623899	-4.717999
1MFM	A	GLY	72	C	-8.095698	7.468540	-13.237718	-4.706383
1MFM	A	GLY	73	T	-7.919900	6.704117	-13.620234	-4.724987
1MFM	A	PRO	74	T	-7.907637	6.622102	-13.699936	-4.734966
1MFM	A	LYS	75	T	-8.071367	5.469563	-14.259557	-4.723440
1MFM	A	ASP	76	T	-8.125063	5.230153	-14.296801	-4.731633
1MFM	A	GLU	77	T	-8.629279	4.762574	-14.921396	-4.816019
1MFM	A	GLU	78	T	-9.940549	5.326216	-16.517471	-5.167070
1MFM	A	ARG	79	T	-14.039419	8.954787	-21.691771	-5.870893
1MFM	A	HIS	80	T	-12.955987	14.392577	-15.822270	-5.086618
1MFM	A	VAL	81	T	-10.669632	12.852752	-12.883264	-4.647143
1MFM	A	GLY	82	T	-10.364711	12.213856	-13.699522	-4.946474
1MFM	A	ASP	83	E	-10.290392	12.307486	-13.753802	-4.939841
1MFM	A	LEU	84	E	-9.110208	13.013820	-10.981161	-4.531816
1MFM	A	GLY	85	E	-8.422437	11.059774	-11.056432	-4.294914
1MFM	A	ASN	86	E	-8.398907	10.933915	-11.140124	-4.277441
1MFM	A	VAL	87	E	-8.370913	10.808392	-11.222356	-4.249936
1MFM	A	THR	88	E	-7.974665	8.398042	-12.139946	-4.277037
1MFM	A	ALA	89	E	-7.468790	5.646603	-12.991394	-4.436150
1MFM	A	ASP	90	T	-6.416890	4.348270	-12.206006	-4.598377
1MFM	A	LYS	91	T	-6.388474	4.421947	-12.232973	-4.587771
1MFM	A	ASP	92	T	-6.369506	4.457233	-12.257739	-4.575901
1MFM	A	GLY	93	T	-6.378782	4.479338	-12.218743	-4.572045
1MFM	A	VAL	94	C	-6.404199	4.756542	-11.959945	-4.503945
1MFM	A	ALA	95	E	-7.309289	7.853942	-11.160456	-3.755288
1MFM	A	ASP	96	E	-7.032706	9.177689	-9.849247	-3.695339
1MFM	A	VAL	97	E	-7.091250	9.582826	-9.508917	-3.641766
1MFM	A	SER	98	E	-7.111569	9.632551	-9.456246	-3.643377
1MFM	A	ILE	99	E	-7.230012	9.796489	-9.416389	-3.718665
1MFM	A	GLU	100	E	-7.305710	10.036572	-9.538612	-3.925939
1MFM	A	ASP	101	E	-8.248325	10.543858	-11.688015	-4.431704
1MFM	A	SER	102	T	-8.070688	11.398624	-10.927193	-4.322133
1MFM	A	VAL	103	T	-8.148764	11.760867	-10.706740	-4.342210
1MFM	A	ILE	104	T	-8.187212	11.987773	-10.599861	-4.368016
1MFM	A	SER	105	C	-7.679999	9.506337	-11.724364	-4.955412

1MFM	A	LEU	106	C	-5.629055	9.123739	-8.897118	-5.043234
1MFM	A	SER	107	C	-5.321932	7.814972	-9.542402	-4.958161
1MFM	A	GLY	108	T	-5.057131	8.070037	-9.105474	-4.762366
1MFM	A	ASP	109	T	-5.054906	8.087086	-9.105771	-4.760146
1MFM	A	HIS	110	T	-5.060224	8.083776	-9.077945	-4.756065
1MFM	A	SER	111	T	-5.335298	7.475247	-9.235146	-4.584743
1MFM	A	ILE	112	T	-5.654704	8.571019	-8.343500	-4.411749
1MFM	A	ILE	113	T	-8.271294	12.677540	-9.630039	-4.254557
1MFM	A	GLY	114	T	-9.654711	13.512710	-11.936247	-4.620209
1MFM	A	ARG	115	E	-10.295309	13.627021	-12.803818	-4.746554
1MFM	A	THR	116	E	-10.816990	15.136646	-12.812797	-4.831230
1MFM	A	LEU	117	E	-11.311979	15.475342	-13.351938	-4.654600
1MFM	A	VAL	118	E	-11.558934	15.517714	-13.489251	-4.526305
1MFM	A	VAL	119	E	-11.392742	13.874365	-14.190005	-4.581903
1MFM	A	HIS	120	E	-11.376002	13.316948	-14.591059	-4.658791
1MFM	A	GLU	121	C	-11.364881	11.107792	-16.043243	-4.892682
1MFM	A	LYS	122	C	-11.497948	9.378421	-17.256062	-5.039915
1MFM	A	ALA	123	C	-10.909838	8.043631	-16.881619	-4.964339
1MFM	A	ASP	124	C	-10.708672	6.946568	-17.364393	-5.058336
1MFM	A	ASP	125	T	-8.117519	4.854803	-14.481077	-5.123891
1MFM	A	LEU	126	T	-5.393337	3.991809	-11.021733	-4.886199
1MFM	A	GLY	127	T	-4.384377	2.050441	-11.604400	-5.289165
1MFM	A	LYS	128	T	-4.121043	2.236315	-11.570761	-5.320746
1MFM	A	GLY	129	C	-4.065365	2.345555	-11.652111	-5.355433
1MFM	A	GLY	130	C	-4.065318	2.345986	-11.653281	-5.356289
1MFM	A	ASN	131	C	-4.131315	2.152682	-11.729390	-5.410794
1MFM	A	GLU	132	C	-4.583277	2.765995	-11.716653	-5.443209
1MFM	A	GLN	133	H	-5.486037	3.481723	-12.498464	-5.699587
1MFM	A	SER	134	H	-7.951315	5.580894	-15.268236	-5.850875
1MFM	A	THR	135	H	-8.890354	7.823548	-15.331983	-5.702066
1MFM	A	LYS	136	H	-8.872292	7.850501	-15.257798	-5.650675
1MFM	A	THR	137	H	-8.398539	6.312187	-14.354372	-5.123225
1MFM	A	GLY	138	T	-8.166721	5.906356	-14.479311	-5.038603
1MFM	A	ASN	139	T	-8.179717	5.843852	-14.427077	-5.006261
1MFM	A	ALA	140	T	-8.170767	5.918146	-14.389041	-4.986703
1MFM	A	GLY	141	C	-8.167855	5.998549	-14.318145	-4.960155
1MFM	A	SER	142	C	-8.708393	5.883608	-14.702197	-4.838978
1MFM	A	ARG	143	E	-9.709478	9.495823	-14.279178	-4.627182
1MFM	A	LEU	144	E	-9.070646	9.138046	-12.971346	-4.265988
1MFM	A	ALA	145	E	-8.420914	8.705358	-11.927786	-4.012934
1MFM	A	CYS	146	E	-8.329903	9.116679	-12.213664	-4.385332
1MFM	A	GLY	147	E	-7.115823	9.996104	-10.405312	-4.853412
1MFM	A	VAL	148	E	-5.915948	9.684107	-7.933950	-4.056299
1MFM	A	ILE	149	E	-4.582314	8.685056	-5.995336	-3.511617
1MFM	A	GLY	150	E	-2.640628	4.891899	-4.498028	-2.809235
1MFM	A	ILE	151	E	-2.640628	4.891899	-4.498028	-2.809235
1MFM	A	ALA	152	C	-2.640628	4.891899	-4.498028	-2.809235
1MFM	A	GLN	153	C	-2.640628	4.891899	-4.498028	-2.809235
1MH1	A	PRO	1	C	-7.036179	6.391454	-7.145792	-1.505740
1MH1	A	GLN	2	E	-7.036179	6.391454	-7.145792	-1.505740
1MH1	A	ALA	3	E	-7.036179	6.391454	-7.145792	-1.505740
1MH1	A	ILE	4	E	-7.036179	6.391454	-7.145792	-1.505740
1MH1	A	LYS	5	E	-10.435401	9.260042	-12.475151	-3.158090
1MH1	A	CYS	6	E	-9.764152	10.990182	-9.740785	-2.612288
1MH1	A	VAL	7	E	-9.704147	11.027864	-9.887878	-2.625248
1MH1	A	VAL	8	E	-8.994974	10.561353	-11.477710	-3.964773
1MH1	A	VAL	9	E	-8.592748	8.512096	-11.498382	-3.473307
1MH1	A	GLY	10	E	-8.014886	6.388083	-11.539582	-3.292574
1MH1	A	ASP	11	T	-7.686428	6.119406	-11.441127	-3.374811
1MH1	A	GLY	12	T	-7.626327	6.318023	-11.484919	-3.428007
1MH1	A	ALA	13	T	-7.665550	6.044918	-11.453453	-3.356301
1MH1	A	VAL	14	T	-7.727671	6.023587	-11.451487	-3.403048
1MH1	A	GLY	15	C	-8.012474	6.614418	-11.386077	-3.542277
1MH1	A	LYS	16	H	-8.933165	8.565060	-12.077773	-3.968578
1MH1	A	THR	17	H	-10.275094	11.566176	-13.666850	-4.569793
1MH1	A	CYS	18	H	-10.602284	12.255010	-12.674775	-3.918086
1MH1	A	LEU	19	H	-11.011387	13.416272	-12.456627	-3.901203
1MH1	A	LEU	20	H	-11.567321	15.573970	-11.809065	-3.672421
1MH1	A	ILE	21	H	-11.458568	15.077569	-11.987321	-3.617806
1MH1	A	SER	22	H	-10.666574	11.635104	-12.812969	-4.022542
1MH1	A	TYR	23	H	-8.215661	9.902523	-11.495350	-4.782398
1MH1	A	THR	24	H	-7.700522	9.158176	-10.523173	-3.988296
1MH1	A	THR	25	H	-7.566922	9.342387	-10.718780	-4.101238
1MH1	A	ASN	26	C	-7.272514	8.545971	-10.390474	-3.742273
1MH1	A	ALA	27	C	-6.544631	7.657306	-9.087681	-3.277805
1MH1	A	PHE	28	C	-6.033315	8.971301	-8.949508	-4.118911
1MH1	A	PRO	29	C	-4.440938	6.467162	-5.421639	-2.638729
1MH1	A	GLY	30	C	-3.867679	5.125926	-5.630747	-2.549791
1MH1	A	GLU	31	C	-3.855814	5.150010	-5.664616	-2.551429
1MH1	A	TYR	32	C	-3.850830	5.185771	-5.661852	-2.549667
1MH1	A	ILE	33	C	-3.830204	5.431640	-5.632437	-2.583261

1MH1	A	PRO	34	C	-4.070328	5.002357	-5.858240	-2.606234
1MH1	A	THR	35	C	-5.289569	9.797102	-6.553035	-3.372044
1MH1	A	VAL	36	C	-5.449042	10.852234	-6.269427	-3.592636
1MH1	A	PHE	37	C	-5.608085	11.605319	-6.090653	-3.870407
1MH1	A	ASP	38	C	-7.913418	10.514836	-8.718316	-3.052548
1MH1	A	ASN	39	E	-8.698776	10.778774	-10.216532	-3.613892
1MH1	A	TYR	40	E	-10.061422	12.012192	-12.335328	-4.042472
1MH1	A	SER	41	E	-9.083269	7.500580	-10.945806	-2.615552
1MH1	A	ALA	42	E	-8.819404	7.786419	-10.779658	-2.542676
1MH1	A	ASN	43	E	-8.552166	8.116064	-11.706452	-3.382838
1MH1	A	VAL	44	E	-7.973238	7.181494	-10.739244	-3.001317
1MH1	A	MET	45	E	-7.323633	7.193520	-10.137105	-3.234496
1MH1	A	VAL	46	E	-7.053064	7.831407	-10.139046	-3.562245
1MH1	A	ASP	47	T	-6.996877	7.951835	-10.321173	-3.695400
1MH1	A	GLY	48	T	-6.943964	8.110286	-10.401845	-3.818905
1MH1	A	LYS	49	E	-7.013123	8.293567	-10.430867	-3.948318
1MH1	A	PRO	50	E	-7.309236	9.008987	-10.819516	-4.334306
1MH1	A	VAL	51	E	-7.865193	9.347607	-11.822240	-4.849636
1MH1	A	ASN	52	E	-8.235090	9.618712	-11.758288	-5.042870
1MH1	A	LEU	53	E	-10.709312	11.929074	-11.374927	-2.896492
1MH1	A	GLY	54	E	-10.720134	11.920756	-11.340394	-2.897441
1MH1	A	LEU	55	E	-11.177010	12.921364	-11.153990	-3.057654
1MH1	A	TRP	56	E	-12.850826	12.959553	-15.776584	-4.267169
1MH1	A	ASP	57	C	-11.666068	10.696184	-14.546982	-4.041392
1MH1	A	THR	58	C	-8.570689	9.107336	-12.649951	-5.022614
1MH1	A	ALA	59	C	-6.997308	5.970271	-9.635694	-3.166957
1MH1	A	GLY	60	C	-6.640427	7.049786	-9.180520	-3.266454
1MH1	A	GLN	61	C	-6.634084	7.063817	-9.208029	-3.270274
1MH1	A	GLU	62	G	-6.516897	7.057835	-9.221129	-3.190069
1MH1	A	ASP	63	G	-6.459124	7.273548	-9.227399	-3.234355
1MH1	A	TYR	64	G	-6.737465	8.197157	-9.119066	-3.358815
1MH1	A	ASP	65	T	-7.188425	8.016086	-9.678655	-3.326633
1MH1	A	ARG	66	T	-7.201336	8.009287	-9.626873	-3.310652
1MH1	A	LEU	67	T	-7.701529	9.304537	-10.080912	-3.955778
1MH1	A	ARG	68	G	-10.220211	8.638709	-10.954977	-2.042769
1MH1	A	PRO	69	G	-10.218009	8.646525	-10.964092	-2.044705
1MH1	A	LEU	70	G	-10.237556	8.636183	-10.894356	-2.031239
1MH1	A	SER	71	G	-11.984939	11.165274	-14.448382	-3.349200
1MH1	A	TYR	72	T	-10.901706	10.762392	-13.182214	-3.723616
1MH1	A	PRO	73	T	-8.431269	9.005094	-11.595349	-4.274414
1MH1	A	GLN	74	T	-8.424194	9.019122	-11.605820	-4.262829
1MH1	A	THR	75	T	-8.424191	9.021653	-11.604744	-4.263007
1MH1	A	ASP	76	C	-8.424348	9.022830	-11.602597	-4.262691
1MH1	A	VAL	77	E	-8.432095	9.001910	-11.584136	-4.268828
1MH1	A	SER	78	E	-10.955295	10.746048	-12.547428	-3.278385
1MH1	A	LEU	79	E	-12.167957	14.492895	-12.744421	-3.228568
1MH1	A	ILE	80	E	-12.412509	15.259727	-12.539656	-3.184709
1MH1	A	CYS	81	E	-12.745325	15.925689	-13.029168	-3.455103
1MH1	A	PHE	82	E	-12.554682	16.393100	-12.548774	-3.591360
1MH1	A	SER	83	E	-10.962963	13.716298	-12.557529	-4.311158
1MH1	A	LEU	84	T	-10.198985	12.033064	-10.677758	-2.948337
1MH1	A	VAL	85	T	-9.665637	10.330011	-10.782586	-2.748954
1MH1	A	SER	86	T	-9.646273	10.366429	-10.830828	-2.756462
1MH1	A	PRO	87	H	-9.643229	10.352491	-10.856004	-2.761233
1MH1	A	ALA	88	H	-9.701481	10.001365	-10.718325	-2.604738
1MH1	A	SER	89	H	-9.923084	9.369436	-11.068501	-2.685993
1MH1	A	PHE	90	H	-11.395481	11.595054	-13.433718	-3.494733
1MH1	A	GLU	91	H	-11.239347	9.454929	-14.184467	-3.459912
1MH1	A	ASN	92	H	-11.327149	9.042735	-14.278776	-3.444634
1MH1	A	VAL	93	H	-11.403662	8.803887	-13.847131	-3.157680
1MH1	A	ARG	94	H	-11.418763	8.682263	-13.823110	-3.139981
1MH1	A	ALA	95	H	-11.423064	8.646458	-13.811758	-3.136272
1MH1	A	LYS	96	H	-13.526582	11.852780	-16.706547	-4.156994
1MH1	A	TRP	97	H	-14.360875	15.700486	-17.058799	-5.238460
1MH1	A	TYR	98	H	-13.837449	14.734310	-16.645711	-4.946179
1MH1	A	PRO	99	H	-12.259908	10.375393	-14.240393	-3.125540
1MH1	A	GLU	100	H	-11.844024	10.743291	-13.852240	-3.126148
1MH1	A	VAL	101	H	-10.889195	10.473040	-12.438435	-2.995481
1MH1	A	ARG	102	H	-10.269864	8.378282	-12.962725	-2.992256
1MH1	A	HIS	103	H	-6.536411	5.906104	-10.894315	-4.398335
1MH1	A	HIS	104	H	-6.381667	6.095045	-10.502361	-4.088930
1MH1	A	CYS	105	H	-6.192282	5.931399	-10.006646	-3.637781
1MH1	A	PRO	106	T	-6.053269	6.549128	-9.250169	-3.299530
1MH1	A	ASN	107	T	-6.044935	6.635719	-9.218726	-3.287544
1MH1	A	THR	108	T	-6.383491	7.205425	-7.929568	-2.429090
1MH1	A	PRO	109	C	-6.538796	7.348646	-7.551821	-2.242319
1MH1	A	ILE	110	E	-6.938606	9.139280	-6.454191	-2.051843
1MH1	A	ILE	111	E	-8.534912	12.665071	-7.298461	-2.480141
1MH1	A	LEU	112	E	-10.562385	16.070354	-9.773864	-3.094815
1MH1	A	VAL	113	E	-10.791067	15.038949	-10.339032	-2.967325
1MH1	A	GLY	114	E	-10.808810	14.863104	-10.494783	-3.037787

1MH1	A	THR	115	E	-11.136391	13.957594	-12.134211	-3.640046
1MH1	A	LYS	116	C	-11.654925	13.694646	-14.554859	-4.784642
1MH1	A	LEU	117	H	-11.723331	13.594666	-14.907631	-4.988054
1MH1	A	ASP	118	H	-11.644954	10.656056	-16.557266	-5.178882
1MH1	A	LEU	119	H	-11.620319	10.333622	-16.625473	-5.095948
1MH1	A	ARG	120	H	-10.494315	6.467261	-15.157708	-3.993637
1MH1	A	ASP	121	H	-7.694228	5.469370	-11.203810	-3.601466
1MH1	A	ASP	122	C	-7.515395	5.960859	-11.090870	-3.531747
1MH1	A	LYS	123	H	-7.483361	6.036279	-11.254158	-3.604990
1MH1	A	ASP	124	H	-7.480849	6.040005	-11.265562	-3.604202
1MH1	A	THR	125	H	-7.483755	6.042453	-11.247350	-3.603000
1MH1	A	ILE	126	H	-8.186881	7.367202	-11.427147	-3.614421
1MH1	A	GLU	127	H	-9.169039	7.407246	-14.214859	-4.805066
1MH1	A	LYS	128	H	-10.593896	7.210313	-14.416258	-3.567974
1MH1	A	LEU	129	H	-11.368727	7.355126	-16.469703	-3.997839
1MH1	A	LYS	130	H	-9.930978	4.058921	-14.880512	-3.513213
1MH1	A	GLU	131	H	-9.237910	4.807441	-13.638343	-3.294044
1MH1	A	LYS	132	C	-8.313800	7.535629	-10.790756	-3.053707
1MH1	A	LYS	133	C	-7.802681	10.138468	-9.909098	-3.637729
1MH1	A	LEU	134	C	-7.701374	10.391807	-9.545881	-3.434208
1MH1	A	THR	135	C	-7.706475	10.570909	-9.430743	-3.425555
1MH1	A	PRO	136	C	-7.731471	10.879513	-9.241000	-3.430426
1MH1	A	ILE	137	C	-7.910002	11.892889	-8.997873	-3.590866
1MH1	A	THR	138	C	-7.513690	9.312571	-10.709885	-4.394309
1MH1	A	TYR	139	H	-7.575199	9.008923	-11.116199	-4.635363
1MH1	A	PRO	140	H	-7.538962	8.847120	-11.137005	-4.535598
1MH1	A	GLN	141	H	-7.542961	8.825317	-11.148028	-4.549174
1MH1	A	GLY	142	H	-7.551578	8.809210	-11.162559	-4.573038
1MH1	A	LEU	143	H	-8.504723	8.914806	-11.512254	-3.625106
1MH1	A	ALA	144	H	-8.523722	8.827417	-11.567892	-3.633177
1MH1	A	MET	145	H	-8.784268	9.754918	-11.800581	-4.024858
1MH1	A	ALA	146	H	-8.296236	8.559251	-10.977716	-3.408008
1MH1	A	LYS	147	H	-7.582812	8.697842	-9.649795	-3.236890
1MH1	A	GLU	148	H	-7.174932	9.111915	-9.766658	-3.744641
1MH1	A	ILE	149	H	-6.578016	9.631736	-7.549391	-2.965648
1MH1	A	GLY	150	C	-6.553773	9.731338	-7.559472	-2.966646
1MH1	A	ALA	151	C	-6.569536	9.816406	-7.474804	-2.967656
1MH1	A	VAL	152	C	-6.650896	9.972141	-7.232690	-2.938775
1MH1	A	LYS	153	E	-6.803494	10.095748	-6.402529	-2.552913
1MH1	A	TYR	154	E	-8.396509	12.434227	-7.875615	-3.003356
1MH1	A	LEU	155	E	-9.803014	15.550132	-8.253908	-3.097160
1MH1	A	GLU	156	E	-11.027198	16.469340	-10.749253	-4.045511
1MH1	A	CYS	157	C	-10.287828	9.754813	-12.441065	-3.527515
1MH1	A	SER	158	T	-9.812943	9.522382	-13.577241	-4.353292
1MH1	A	ALA	159	T	-9.433681	9.085864	-12.622512	-3.727758
1MH1	A	LEU	160	T	-8.486160	6.883479	-11.634944	-3.318984
1MH1	A	THR	161	T	-8.459070	6.951302	-11.682380	-3.323337
1MH1	A	GLN	162	T	-8.484641	6.832476	-11.659357	-3.316873
1MH1	A	ARG	163	T	-7.952849	8.384403	-11.297272	-3.929833
1MH1	A	GLY	164	T	-7.735553	9.059764	-10.318406	-3.579298
1MH1	A	LEU	165	H	-7.885002	9.867526	-10.007370	-3.682713
1MH1	A	LYS	166	H	-7.893911	9.900433	-9.962472	-3.685572
1MH1	A	THR	167	H	-7.894332	9.901858	-9.958404	-3.685634
1MH1	A	VAL	168	H	-8.378988	10.471351	-8.406692	-2.808441
1MH1	A	PHE	169	H	-11.063940	14.808121	-10.220313	-2.884493
1MH1	A	ASP	170	H	-11.499219	13.446339	-11.105471	-2.941988
1MH1	A	GLU	171	H	-12.976827	16.432121	-14.475378	-4.593283
1MH1	A	ALA	172	H	-12.235236	16.405645	-13.784030	-4.959416
1MH1	A	ILE	173	H	-10.508097	14.347770	-11.819422	-4.767580
1MH1	A	ARG	174	H	-8.915437	10.017910	-11.158819	-4.101811
1MH1	A	ALA	175	H	-4.864859	8.419987	-5.017470	-2.879671
1MH1	A	VAL	176	H	-3.438069	6.380483	-3.761953	-2.325635
1MH1	A	LEU	177	C	-2.183626	4.187774	-2.656435	-1.710821
1MH1	A	CYS	178	C	0.549918	1.253470	-1.611827	-2.240885
1MH1	A	PRO	179	C	0.549918	1.253470	-1.611827	-2.240885
1MH1	A	PRO	180	C	0.549918	1.253470	-1.611827	-2.240885
1MH1	A	PRO	181	C	0.549918	1.253470	-1.611827	-2.240885
1MH9	A	ARG	34	C	-8.260062	8.905619	-9.910529	-3.073578
1MH9	A	ALA	35	C	-8.260062	8.905619	-9.910529	-3.073578
1MH9	A	LEU	36	E	-8.260062	8.905619	-9.910529	-3.073578
1MH9	A	ARG	37	E	-8.260062	8.905619	-9.910529	-3.073578
1MH9	A	VAL	38	E	-10.651107	12.222751	-12.205771	-3.771685
1MH9	A	LEU	39	E	-12.485083	16.550789	-14.292822	-4.835650
1MH9	A	VAL	40	E	-12.250659	14.416143	-15.561560	-5.197319
1MH9	A	ASP	41	C	-11.904190	13.051583	-16.158288	-5.315870
1MH9	A	MET	42	T	-11.748059	13.521668	-15.857233	-5.279498
1MH9	A	ASP	43	T	-11.388718	13.450147	-14.692636	-4.832672
1MH9	A	GLY	44	T	-10.879615	13.833619	-13.272104	-4.454207
1MH9	A	VAL	45	T	-10.898078	14.010772	-13.075864	-4.397733
1MH9	A	LEU	46	T	-10.946707	14.256248	-12.743579	-4.305454
1MH9	A	ALA	47	B	-10.928765	14.220391	-12.826743	-4.340896

1MH9	A	ASP	48	T	-10.344034	12.995397	-13.789242	-5.291529
1MH9	A	PHE	49	H	-10.491863	12.722164	-14.269217	-5.633580
1MH9	A	GLU	50	H	-10.480309	12.713596	-14.324608	-5.643233
1MH9	A	GLY	51	H	-10.334640	12.769008	-14.186817	-5.455194
1MH9	A	GLY	52	H	-10.349269	12.731248	-14.169545	-5.458245
1MH9	A	PHE	53	H	-11.118246	13.392150	-14.002447	-4.908762
1MH9	A	LEU	54	H	-11.156482	13.188059	-13.939549	-4.856504
1MH9	A	ARG	55	H	-11.190034	13.096606	-13.830291	-4.780891
1MH9	A	LYS	56	H	-12.402280	14.975645	-15.126382	-4.853073
1MH9	A	PHE	57	H	-11.365505	17.271451	-11.915503	-4.697339
1MH9	A	ARG	58	H	-9.092571	11.389901	-11.045892	-4.121465
1MH9	A	ALA	59	H	-7.921216	8.777314	-11.318335	-4.264665
1MH9	A	ARG	60	H	-7.837418	8.987333	-11.503649	-4.382213
1MH9	A	PHE	61	T	-7.520975	9.732758	-11.211899	-4.565782
1MH9	A	PRO	62	T	-7.341544	9.978538	-11.147973	-4.626882
1MH9	A	ASP	63	T	-7.358721	10.010548	-11.161759	-4.667296
1MH9	A	GLN	64	T	-7.593212	10.885021	-11.065625	-4.859238
1MH9	A	PRO	65	C	-7.621226	11.149732	-10.837777	-4.809325
1MH9	A	PHE	66	C	-7.761436	12.346950	-10.313401	-4.720313
1MH9	A	ILE	67	C	-6.520372	9.570291	-9.126548	-4.367099
1MH9	A	ALA	68	C	-6.522169	9.542370	-9.128018	-4.364495
1MH9	A	LEU	69	G	-6.523110	9.532463	-9.124339	-4.363373
1MH9	A	GLU	70	G	-6.527104	9.488713	-9.123635	-4.363650
1MH9	A	ASP	71	G	-6.553822	9.285223	-9.115948	-4.353344
1MH9	A	ARG	72	C	-10.039981	8.960500	-14.930757	-5.185517
1MH9	A	ARG	73	C	-11.743012	9.629383	-17.603715	-5.379303
1MH9	A	GLY	74	C	-10.159339	12.599744	-13.474844	-5.342494
1MH9	A	PHE	75	C	-9.915938	13.115354	-13.197253	-5.306608
1MH9	A	TRP	76	C	-9.901822	13.079011	-13.281039	-5.316066
1MH9	A	VAL	77	H	-9.901672	13.080160	-13.281943	-5.316236
1MH9	A	SER	78	H	-9.915556	13.116069	-13.214616	-5.317868
1MH9	A	GLU	79	H	-10.473860	13.564938	-13.342221	-5.283334
1MH9	A	GLN	80	H	-11.805336	11.852979	-16.854539	-5.564748
1MH9	A	TYR	81	H	-11.339605	13.651652	-13.927109	-4.730413
1MH9	A	GLY	82	H	-7.104507	6.829321	-10.382244	-3.788447
1MH9	A	ARG	83	H	-6.787844	6.732448	-10.553412	-3.800536
1MH9	A	LEU	84	H	-6.703515	7.075903	-10.546373	-3.843390
1MH9	A	ARG	85	T	-6.686250	7.113178	-10.600874	-3.858529
1MH9	A	PRO	86	T	-6.485240	7.294152	-10.660361	-4.015332
1MH9	A	GLY	87	T	-6.680082	7.783656	-10.885196	-4.225417
1MH9	A	LEU	88	H	-6.928911	8.423872	-10.938405	-4.441346
1MH9	A	SER	89	H	-7.051880	8.226671	-11.060177	-4.518590
1MH9	A	GLU	90	H	-7.083202	8.221833	-10.988932	-4.527338
1MH9	A	LYS	91	H	-8.006101	10.016964	-11.670142	-4.992102
1MH9	A	ALA	92	H	-9.538205	11.235713	-13.181776	-4.673972
1MH9	A	ILE	93	H	-9.715745	10.888089	-13.363027	-4.664687
1MH9	A	SER	94	H	-10.513039	11.945995	-14.213867	-4.819525
1MH9	A	ILE	95	H	-11.029586	15.015715	-13.612603	-4.955312
1MH9	A	TRP	96	H	-11.225192	15.856854	-13.846981	-5.249036
1MH9	A	GLU	97	H	-11.370817	15.572319	-14.540879	-5.542202
1MH9	A	SER	98	T	-11.680882	15.234485	-15.325211	-5.764582
1MH9	A	LYS	99	T	-11.684777	15.321579	-15.286292	-5.775070
1MH9	A	ASN	100	T	-11.854239	14.588688	-15.737614	-5.848222
1MH9	A	PHE	101	T	-12.410550	14.434972	-16.341095	-5.815193
1MH9	A	PHE	102	T	-12.995839	17.839527	-15.416962	-5.606031
1MH9	A	PHE	103	T	-11.148914	14.107523	-13.107666	-4.742806
1MH9	A	GLU	104	T	-10.529480	13.960777	-12.466322	-4.504840
1MH9	A	LEU	105	T	-9.105718	11.947588	-10.292105	-3.622926
1MH9	A	GLU	106	C	-6.193980	8.790123	-8.172198	-3.785215
1MH9	A	PRO	107	B	-5.842294	9.209727	-7.894712	-3.687600
1MH9	A	LEU	108	T	-5.800677	9.290383	-7.949117	-3.686565
1MH9	A	PRO	109	T	-5.700744	9.051887	-8.177382	-3.695353
1MH9	A	GLY	110	T	-5.669994	9.039004	-8.252940	-3.703955
1MH9	A	ALA	111	H	-5.981071	9.234935	-8.324575	-3.646104
1MH9	A	VAL	112	H	-6.473580	8.602936	-9.337307	-3.749350
1MH9	A	GLU	113	H	-6.613499	8.123080	-9.513835	-3.770780
1MH9	A	ALA	114	H	-7.378459	9.083277	-9.758186	-3.843238
1MH9	A	VAL	115	H	-9.184292	11.872063	-11.177093	-3.769152
1MH9	A	LYS	116	H	-9.637101	11.470069	-12.486279	-4.163135
1MH9	A	GLU	117	H	-10.126415	10.873959	-14.292717	-4.716066
1MH9	A	MET	118	H	-9.904358	10.454419	-14.002057	-4.697496
1MH9	A	ALA	119	H	-8.326769	6.721775	-13.035019	-4.419923
1MH9	A	SER	120	H	-8.242854	6.801711	-13.226149	-4.488896
1MH9	A	LEU	121	T	-8.204964	6.926867	-13.304122	-4.536674
1MH9	A	GLN	122	T	-8.145593	7.192637	-13.302210	-4.571985
1MH9	A	ASN	123	T	-8.165816	7.106783	-13.292950	-4.573028
1MH9	A	THR	124	E	-8.896827	8.751543	-14.082287	-4.994363
1MH9	A	ASP	125	E	-9.206462	9.641768	-13.815517	-5.029824
1MH9	A	VAL	126	E	-9.475237	10.093846	-13.376566	-4.911842
1MH9	A	PHE	127	E	-11.144167	15.588786	-13.521975	-5.008236
1MH9	A	ILE	128	E	-10.922617	14.773249	-13.343795	-4.872162

1MH9	A	CYS	129	E	-10.674690	13.102080	-13.972745	-4.958269
1MH9	A	THR	130	E	-9.709130	10.776115	-13.302475	-4.701672
1MH9	A	SER	131	C	-9.201164	10.732164	-12.923209	-4.729490
1MH9	A	PRO	132	C	-7.786276	10.067169	-10.594618	-4.369591
1MH9	A	ILE	133	T	-6.143310	8.761355	-9.107728	-4.408242
1MH9	A	LYS	134	T	-6.085408	8.822295	-9.258088	-4.440164
1MH9	A	MET	135	T	-6.081133	8.844410	-9.273807	-4.445515
1MH9	A	PHE	136	T	-6.078378	8.860935	-9.279937	-4.446949
1MH9	A	LYS	137	C	-6.107727	8.813386	-9.227847	-4.454368
1MH9	A	TYR	138	H	-7.378852	9.859598	-10.877838	-4.782767
1MH9	A	CYS	139	H	-8.421866	11.969932	-11.588686	-4.934035
1MH9	A	PRO	140	H	-8.793634	12.315626	-11.420741	-4.809808
1MH9	A	TYR	141	H	-9.602406	13.951444	-11.490484	-4.975801
1MH9	A	GLU	142	H	-11.672684	15.659595	-14.061989	-5.477860
1MH9	A	LYS	143	H	-13.167699	14.637325	-17.160994	-5.668458
1MH9	A	TYR	144	H	-13.077285	18.364354	-14.089411	-4.958029
1MH9	A	ALA	145	H	-11.232369	17.946023	-11.163939	-4.736721
1MH9	A	TRP	146	H	-11.164557	18.097471	-11.266370	-4.765662
1MH9	A	VAL	147	H	-10.991793	18.686547	-11.171581	-4.834009
1MH9	A	GLU	148	H	-10.094662	18.112602	-10.722374	-5.253589
1MH9	A	LYS	149	H	-9.732720	17.317348	-10.776884	-5.135228
1MH9	A	TYR	150	H	-9.467121	16.372590	-10.914828	-5.058017
1MH9	A	PHE	151	H	-7.740875	14.786179	-8.258229	-4.622345
1MH9	A	GLY	152	C	-7.122571	12.807983	-8.730241	-4.505441
1MH9	A	PRO	153	G	-6.755204	12.138435	-8.740619	-4.416051
1MH9	A	ASP	154	G	-6.750883	12.122065	-8.767650	-4.417472
1MH9	A	PHE	155	G	-6.752752	12.113803	-8.760374	-4.415725
1MH9	A	LEU	156	G	-6.863140	11.560010	-8.927421	-4.375711
1MH9	A	GLU	157	G	-7.170740	11.481779	-8.923944	-4.331130
1MH9	A	GLN	158	G	-8.773888	12.834528	-11.347615	-4.528502
1MH9	A	ILE	159	E	-8.576526	13.457604	-10.346663	-4.286744
1MH9	A	VAL	160	E	-8.448874	12.843039	-10.678502	-4.309427
1MH9	A	LEU	161	E	-8.542534	12.938850	-10.577611	-4.310646
1MH9	A	THR	162	T	-8.694552	12.732328	-10.560502	-4.265068
1MH9	A	ARG	163	T	-8.726336	12.632407	-10.511609	-4.249041
1MH9	A	ASP	164	T	-9.335003	10.843983	-12.215332	-4.485759
1MH9	A	LYS	165	T	-10.517929	11.698669	-15.011322	-5.295340
1MH9	A	THR	166	T	-8.317314	10.207276	-10.749501	-4.185769
1MH9	A	VAL	167	T	-7.933687	9.739283	-10.965876	-4.167136
1MH9	A	VAL	168	T	-7.930647	9.754220	-10.975045	-4.167968
1MH9	A	SER	169	C	-7.930778	9.759729	-10.968692	-4.166027
1MH9	A	ALA	170	C	-7.932644	9.780563	-10.940806	-4.159119
1MH9	A	ASP	171	C	-8.355194	9.384152	-11.241440	-4.158103
1MH9	A	LEU	172	E	-10.463362	14.771965	-12.369408	-4.500425
1MH9	A	LEU	173	E	-10.782981	16.431480	-11.714106	-4.514111
1MH9	A	ILE	174	E	-11.006974	17.474512	-11.016301	-4.433096
1MH9	A	ASP	175	E	-11.838296	15.927820	-13.872058	-4.991955
1MH9	A	ASP	176	C	-10.127484	13.371264	-12.352245	-4.865759
1MH9	A	ARG	177	T	-6.323266	11.379503	-7.953208	-4.410075
1MH9	A	PRO	178	T	-4.050338	9.299391	-6.124242	-4.458752
1MH9	A	ASP	179	T	-3.221657	7.501595	-6.188846	-4.336053
1MH9	A	ILE	180	T	-3.168147	7.660515	-6.243592	-4.352728
1MH9	A	THR	181	C	-3.022711	7.072539	-6.573142	-4.309141
1MH9	A	GLY	182	C	-2.520686	5.273698	-6.611553	-4.082793
1MH9	A	ALA	183	C	-2.438332	5.122433	-6.490212	-3.937195
1MH9	A	GLU	184	T	-2.561681	4.658800	-6.562128	-3.822859
1MH9	A	PRO	185	T	-2.580433	4.507105	-6.551213	-3.798153
1MH9	A	THR	186	T	-2.645873	4.450942	-6.400222	-3.751624
1MH9	A	PRO	187	T	-3.367491	5.762160	-5.912852	-3.432347
1MH9	A	SER	188	C	-4.836014	5.757445	-8.192940	-3.794956
1MH9	A	TRP	189	C	-7.210329	10.419352	-9.397025	-4.233509
1MH9	A	GLU	190	E	-10.987025	11.094912	-15.570512	-5.356078
1MH9	A	HIS	191	E	-13.032653	13.549409	-16.723107	-5.176019
1MH9	A	VAL	192	E	-12.701088	16.845506	-13.605141	-4.544197
1MH9	A	LEU	193	E	-11.954408	15.505129	-13.982581	-4.900885
1MH9	A	PHE	194	E	-11.922177	15.461945	-14.126955	-4.934769
1MH9	A	THR	195	C	-11.826691	14.724083	-14.783947	-5.068630
1MH9	A	ALA	196	T	-11.760484	14.293514	-15.218929	-5.181575
1MH9	A	CYS	197	T	-11.815905	13.378674	-16.076304	-5.452883
1MH9	A	HIS	198	T	-11.774905	10.476258	-18.247834	-5.979120
1MH9	A	ASN	199	T	-9.245297	7.340557	-15.042256	-5.438103
1MH9	A	GLN	200	T	-6.980823	9.462439	-10.351118	-4.932511
1MH9	A	HIS	201	T	-5.580612	9.527690	-8.334116	-4.662715
1MH9	A	LEU	202	T	-4.841718	8.680208	-7.526289	-4.191543
1MH9	A	GLN	203	C	-3.800759	6.903654	-6.643759	-3.885222
1MH9	A	LEU	204	C	-3.797032	6.902191	-6.665216	-3.884838
1MH9	A	GLN	205	T	-3.799711	6.890121	-6.649082	-3.880061
1MH9	A	PRO	206	T	-3.826979	6.764587	-6.578625	-3.843957
1MH9	A	PRO	207	T	-3.908728	6.529321	-6.484190	-3.819209
1MH9	A	ARG	208	T	-6.790922	6.652376	-10.153111	-3.839931
1MH9	A	ARG	209	E	-9.805386	5.726852	-15.124184	-4.341475

1MH9	A	ARG	210	E	-14.152366	10.802428	-20.652451	-5.734860
1MH9	A	LEU	211	E	-10.744680	14.614804	-11.974703	-4.590696
1MH9	A	HIS	212	C	-9.016713	10.987129	-11.798490	-4.555927
1MH9	A	SER	213	T	-8.614887	10.565193	-11.918540	-4.531514
1MH9	A	TRP	214	T	-8.602108	10.674567	-11.929584	-4.546831
1MH9	A	ALA	215	T	-8.489213	10.701761	-12.131632	-4.649543
1MH9	A	ASP	216	T	-8.474894	10.640754	-12.212254	-4.670595
1MH9	A	ASP	217	T	-8.707859	10.779095	-12.459157	-4.751559
1MH9	A	TRP	218	H	-9.212512	11.696550	-13.026187	-5.084255
1MH9	A	LYS	219	H	-9.211544	11.472987	-13.112263	-5.058653
1MH9	A	ALA	220	H	-9.735008	12.388876	-13.145391	-4.947896
1MH9	A	ILE	221	H	-10.015202	13.121639	-12.767393	-4.881452
1MH9	A	LEU	222	H	-10.244886	11.433825	-14.981035	-5.591699
1MH9	A	ASP	223	H	-8.295799	6.319196	-14.039813	-5.129667
1MH9	A	SER	224	H	-7.799924	5.936803	-13.358946	-4.620231
1MH9	A	LYS	225	C	-7.799924	5.936803	-13.358946	-4.620231
1MH9	A	ARG	226	C	-7.799924	5.936803	-13.358946	-4.620231
1MH9	A	PRO	227	C	-7.799924	5.936803	-13.358946	-4.620231
1MJ4	A	SER	3	C	-3.085671	6.684085	-4.599089	-3.187909
1MJ4	A	THR	4	C	-3.085671	6.684085	-4.599089	-3.187909
1MJ4	A	HIS	5	C	-3.085671	6.684085	-4.599089	-3.187909
1MJ4	A	ILE	6	C	-3.085671	6.684085	-4.599089	-3.187909
1MJ4	A	TYR	7	C	-6.124584	11.347568	-8.781435	-4.781382
1MJ4	A	THR	8	T	-6.173456	9.794451	-9.997816	-5.010809
1MJ4	A	LYS	9	T	-6.190789	9.743724	-9.964643	-4.999206
1MJ4	A	GLU	10	T	-6.210458	9.677875	-9.893452	-4.966197
1MJ4	A	GLU	11	T	-6.215815	9.659647	-9.854414	-4.949375
1MJ4	A	VAL	12	T	-6.367580	8.953000	-9.505573	-4.627288
1MJ4	A	SER	13	T	-9.151466	10.428392	-12.916188	-4.896292
1MJ4	A	SER	14	T	-10.749395	11.418065	-15.910338	-5.317559
1MJ4	A	HIS	15	E	-8.223833	9.886967	-11.634824	-4.837910
1MJ4	A	THR	16	E	-5.657835	8.397902	-8.775666	-4.567123
1MJ4	A	SER	17	G	-4.712064	7.835251	-8.690037	-4.856257
1MJ4	A	PRO	18	G	-4.661863	8.074100	-8.692356	-4.871154
1MJ4	A	GLU	19	G	-4.661842	8.074447	-8.692455	-4.871190
1MJ4	A	THR	20	E	-4.663284	8.070049	-8.685354	-4.871271
1MJ4	A	GLY	21	E	-4.783973	7.999339	-8.672334	-4.940108
1MJ4	A	ILE	22	E	-6.149236	10.773018	-8.715123	-5.036620
1MJ4	A	TRP	23	E	-10.561385	16.367366	-12.406295	-5.653707
1MJ4	A	VAL	24	E	-10.359568	13.748943	-12.186949	-4.653028
1MJ4	A	THR	25	E	-8.492740	12.078596	-11.494403	-5.283484
1MJ4	A	LEU	26	T	-8.260524	12.373093	-11.363823	-5.195843
1MJ4	A	GLY	27	T	-8.250559	12.420865	-11.383039	-5.195365
1MJ4	A	SER	28	E	-8.250544	12.420804	-11.383178	-5.195341
1MJ4	A	GLU	29	E	-8.267143	12.388238	-11.361347	-5.211223
1MJ4	A	VAL	30	E	-8.896277	13.113172	-11.167278	-5.020849
1MJ4	A	PHE	31	E	-10.474977	15.814882	-12.379865	-5.113939
1MJ4	A	ASP	32	T	-10.814448	17.374471	-12.047591	-5.075665
1MJ4	A	VAL	33	T	-10.202336	18.189580	-10.733976	-4.932829
1MJ4	A	THR	34	T	-9.649420	17.509887	-11.534524	-5.619310
1MJ4	A	GLU	35	T	-9.206501	16.188362	-11.619784	-5.474832
1MJ4	A	PHE	36	G	-9.209819	16.165024	-11.665238	-5.494718
1MJ4	A	VAL	37	G	-8.880946	14.073641	-11.843332	-5.058717
1MJ4	A	ASP	38	G	-6.639454	7.899471	-10.289109	-4.513382
1MJ4	A	LEU	39	T	-5.403065	7.545776	-9.217383	-4.627539
1MJ4	A	HIS	40	T	-5.342651	7.546352	-9.342125	-4.620878
1MJ4	A	PRO	41	T	-5.280534	7.322343	-9.515751	-4.573191
1MJ4	A	GLY	42	T	-5.259854	7.329154	-9.588342	-4.581404
1MJ4	A	GLY	43	H	-5.319175	7.282794	-9.518687	-4.589799
1MJ4	A	PRO	44	H	-6.166408	6.589859	-10.953086	-4.415569
1MJ4	A	SER	45	H	-6.461385	5.933824	-11.238892	-4.319775
1MJ4	A	LYS	46	H	-7.237932	7.660083	-11.655895	-4.803696
1MJ4	A	LEU	47	H	-10.128399	13.444918	-13.489723	-4.889759
1MJ4	A	MET	48	H	-9.631716	13.273302	-11.987777	-4.607139
1MJ4	A	LEU	49	T	-8.795082	11.992001	-11.276182	-4.450425
1MJ4	A	ALA	50	T	-8.061771	10.695042	-10.909534	-4.337992
1MJ4	A	ALA	51	T	-8.008042	10.845673	-10.949045	-4.353126
1MJ4	A	GLY	52	T	-8.003672	10.828146	-10.983382	-4.360756
1MJ4	A	GLY	53	B	-8.024304	10.735140	-10.980714	-4.351114
1MJ4	A	PRO	54	H	-8.160223	10.525023	-10.961244	-4.337465
1MJ4	A	LEU	55	H	-9.262608	12.374074	-11.925293	-4.560407
1MJ4	A	GLU	56	H	-10.035089	12.137130	-13.357227	-4.675492
1MJ4	A	PRO	57	H	-10.124594	13.536026	-12.408160	-4.431382
1MJ4	A	PHE	58	H	-10.569768	16.189347	-11.617412	-4.477902
1MJ4	A	TRP	59	H	-10.496558	15.532985	-12.046115	-4.594331
1MJ4	A	ALA	60	T	-8.429489	7.487959	-12.355988	-4.145013
1MJ4	A	LEU	61	T	-8.410133	7.543493	-12.425339	-4.161248
1MJ4	A	TYR	62	G	-8.408280	7.435880	-12.515014	-4.181570
1MJ4	A	ALA	63	G	-8.388873	7.455316	-12.622535	-4.217498
1MJ4	A	VAL	64	G	-8.392896	7.404018	-12.626351	-4.215030
1MJ4	A	HIS	65	C	-9.822607	9.129319	-15.346549	-5.086708

1MJ4	A	ASN	66	C	-9.279068	8.169173	-14.619535	-4.941215
1MJ4	A	GLN	67	H	-9.327974	8.018586	-14.540462	-4.892985
1MJ4	A	SER	68	H	-9.420717	7.979232	-14.337991	-4.810825
1MJ4	A	HIS	69	H	-9.425976	7.979444	-14.304362	-4.804528
1MJ4	A	VAL	70	H	-9.429501	7.973442	-14.280251	-4.799733
1MJ4	A	ARG	71	H	-11.272891	10.221931	-15.917938	-4.625532
1MJ4	A	GLU	72	H	-10.756146	12.288868	-14.140969	-4.738587
1MJ4	A	LEU	73	H	-10.899376	12.996712	-13.730957	-4.791870
1MJ4	A	LEU	74	H	-10.920287	13.032675	-13.633064	-4.791732
1MJ4	A	ALA	75	H	-10.923578	13.018606	-13.620800	-4.792188
1MJ4	A	GLN	76	C	-10.930252	13.003409	-13.593588	-4.792276
1MJ4	A	TYR	77	E	-13.087697	17.799775	-16.478393	-6.309747
1MJ4	A	LYS	78	E	-13.087697	17.799775	-16.478393	-6.309747
1MJ4	A	ILE	79	E	-13.087697	17.799775	-16.478393	-6.309747
1MJ4	A	GLY	80	E	-13.087697	17.799775	-16.478393	-6.309747
1MWP	A	LEU	28	C	-4.553637	2.263172	-5.525961	-1.096883
1MWP	A	LEU	29	C	-4.553637	2.263172	-5.525961	-1.096883
1MWP	A	ALA	30	C	-4.553637	2.263172	-5.525961	-1.096883
1MWP	A	GLU	31	C	-4.553637	2.263172	-5.525961	-1.096883
1MWP	A	PRO	32	C	-5.969081	4.900828	-6.728509	-1.773698
1MWP	A	GLN	33	E	-8.089765	9.314977	-11.169821	-4.551315
1MWP	A	ILE	34	E	-9.830070	13.590617	-12.207271	-4.981888
1MWP	A	ALA	35	E	-8.953868	11.015604	-11.848797	-4.770549
1MWP	A	MET	36	E	-8.939088	10.959426	-11.893812	-4.748081
1MWP	A	PHE	37	E	-8.933838	10.930535	-11.914786	-4.736969
1MWP	A	CYS	38	T	-8.933448	10.926532	-11.918909	-4.736378
1MWP	A	GLY	39	T	-8.990076	10.578712	-12.048705	-4.805819
1MWP	A	ARG	40	E	-10.857979	9.056900	-13.819837	-3.768024
1MWP	A	LEU	41	E	-11.557786	8.777662	-14.048505	-3.397435
1MWP	A	ASN	42	E	-13.108223	7.275764	-17.261889	-3.780718
1MWP	A	MET	43	E	-14.678462	12.037908	-18.042047	-4.233662
1MWP	A	HIS	44	E	-12.816815	10.820043	-16.160168	-4.322778
1MWP	A	MET	45	E	-10.803682	7.613989	-15.898658	-4.785332
1MWP	A	ASN	46	E	-8.021470	3.727018	-11.390776	-2.943272
1MWP	A	VAL	47	T	-7.367703	3.260462	-11.044925	-2.739445
1MWP	A	GLN	48	T	-7.328296	3.513211	-11.062855	-2.780869
1MWP	A	ASN	49	T	-7.322001	3.572355	-11.093982	-2.802933
1MWP	A	GLY	50	T	-7.323267	3.565746	-11.084005	-2.799080
1MWP	A	LYS	51	E	-7.538795	3.510710	-10.967625	-2.743261
1MWP	A	TRP	52	E	-8.857422	7.490487	-11.747441	-3.610483
1MWP	A	ASP	53	E	-9.980067	9.192659	-14.156316	-4.895075
1MWP	A	SER	54	C	-10.471815	7.025615	-15.614804	-4.545395
1MWP	A	ASP	55	T	-8.594077	6.622032	-13.374062	-4.624927
1MWP	A	PRO	56	T	-8.135962	5.536635	-12.346579	-3.704064
1MWP	A	SER	57	T	-8.072664	5.378793	-12.435801	-3.641891
1MWP	A	GLY	58	T	-7.976360	5.226778	-12.545740	-3.623032
1MWP	A	THR	59	C	-7.954732	5.315281	-12.588646	-3.657881
1MWP	A	LYS	60	C	-7.897734	5.243104	-12.708548	-3.773227
1MWP	A	THR	61	B	-6.641025	3.191378	-9.560211	-2.488829
1MWP	A	CYS	62	C	-6.432360	3.318087	-9.636846	-2.532351
1MWP	A	ILE	63	C	-6.012664	3.219519	-9.136521	-2.374552
1MWP	A	ASP	64	C	-5.383435	2.942259	-9.963560	-3.338378
1MWP	A	THR	65	C	-5.377562	2.990416	-9.969756	-3.346221
1MWP	A	LYS	66	H	-5.446100	2.991569	-10.059608	-3.469394
1MWP	A	GLU	67	H	-5.480539	2.956699	-10.071021	-3.518608
1MWP	A	GLY	68	H	-5.619440	2.909008	-10.433168	-3.857552
1MWP	A	ILE	69	H	-7.811136	7.207972	-11.597738	-4.224166
1MWP	A	LEU	70	H	-9.435757	7.098629	-11.399680	-2.594024
1MWP	A	GLN	71	H	-9.581699	6.835327	-11.285225	-2.557161
1MWP	A	TYR	72	H	-12.653345	12.354362	-14.135446	-3.457663
1MWP	A	CYS	73	H	-13.590510	13.068362	-16.946213	-4.390239
1MWP	A	GLN	74	H	-12.222477	13.636466	-15.651078	-5.390543
1MWP	A	GLU	75	H	-9.303532	10.434428	-11.539776	-4.116579
1MWP	A	VAL	76	H	-8.188854	9.556982	-7.771307	-2.066475
1MWP	A	TYR	77	T	-8.062688	9.273195	-8.081653	-2.082970
1MWP	A	PRO	78	T	-6.258021	8.817322	-6.540554	-2.646855
1MWP	A	GLU	79	T	-5.148711	10.848166	-7.362242	-5.284230
1MWP	A	LEU	80	T	-5.145738	10.854789	-7.378365	-5.286852
1MWP	A	GLN	81	C	-5.148443	10.862332	-7.380551	-5.303702
1MWP	A	ILE	82	E	-5.148329	10.866325	-7.378787	-5.303381
1MWP	A	THR	83	E	-5.236984	11.211270	-7.543741	-5.731028
1MWP	A	ASN	84	E	-7.565996	10.899429	-9.430322	-3.937299
1MWP	A	VAL	85	E	-6.427371	9.990824	-7.984742	-3.857030
1MWP	A	VAL	86	E	-5.721641	7.022208	-7.123439	-2.762439
1MWP	A	GLU	87	E	-4.911146	6.636416	-5.643391	-2.340198
1MWP	A	ALA	88	C	-4.798423	6.313685	-5.724489	-2.200918
1MWP	A	ASN	89	C	-4.256210	6.869895	-5.549176	-2.609122
1MWP	A	GLN	90	C	-4.253252	6.906342	-5.517132	-2.593623
1MWP	A	PRO	91	C	-4.287906	6.984636	-5.441981	-2.611239
1MWP	A	VAL	92	E	-4.466181	7.152717	-5.550043	-2.756335
1MWP	A	THR	93	E	-4.529426	7.406808	-5.480399	-2.889570

1MWP	A	ILE	94	E	-6.313926	10.629307	-6.421338	-3.053664
1MWP	A	GLN	95	E	-7.729791	9.913642	-7.175913	-2.086760
1MWP	A	ASN	96	C	-8.302413	9.404088	-8.179742	-2.410826
1MWP	A	TRP	97	C	-10.347806	13.714409	-10.444212	-3.470755
1MWP	A	CYS	98	B	-10.111383	7.256673	-13.341281	-3.437159
1MWP	A	LYS	99	B	-8.977302	7.298326	-13.128223	-4.234416
1MWP	A	ARG	100	G	-8.218419	6.887972	-13.025307	-4.531017
1MWP	A	GLY	101	G	-7.979674	6.067050	-12.846759	-4.189154
1MWP	A	ARG	102	G	-7.978747	6.050952	-12.857928	-4.188269
1MWP	A	LYS	103	B	-7.940617	5.815674	-12.948656	-4.146402
1MWP	A	GLN	104	T	-7.725051	5.153670	-13.114885	-4.177444
1MWP	A	CYS	105	T	-6.539900	5.376932	-10.863280	-4.099830
1MWP	A	LYS	106	C	-6.438105	5.392140	-10.486496	-3.798490
1MWP	A	THR	107	C	-6.183294	6.250983	-9.129732	-3.224638
1MWP	A	HIS	108	C	-6.180097	6.288540	-9.102008	-3.210293
1MWP	A	PRO	109	E	-6.194322	6.380373	-8.968994	-3.176278
1MWP	A	HIS	110	E	-6.607923	7.354556	-7.283926	-2.222718
1MWP	A	PHE	111	E	-6.771627	8.017582	-6.728809	-2.175391
1MWP	A	VAL	112	E	-8.479369	10.889196	-8.737125	-2.477786
1MWP	A	ILE	113	C	-8.853942	12.711704	-8.993700	-3.037766
1MWP	A	PRO	114	C	-9.376746	13.300153	-8.947753	-2.993559
1MWP	A	TYR	115	E	-10.401375	14.324494	-7.592104	-1.867489
1MWP	A	ARG	116	E	-9.207103	9.239972	-12.821716	-5.133317
1MWP	A	CYS	117	E	-5.124390	6.275884	-7.651199	-4.002550
1MWP	A	LEU	118	E	-3.425957	5.174888	-4.815371	-2.914220
1MWP	A	VAL	119	E	-0.873425	3.243195	-1.969575	-2.339848
1MWP	A	GLY	120	C	0.229191	4.018354	-2.723485	-3.614369
1MWP	A	GLU	121	C	0.229191	4.018354	-2.723485	-3.614369
1MWP	A	PHE	122	C	0.229191	4.018354	-2.723485	-3.614369
1MWP	A	VAL	123	C	0.229191	4.018354	-2.723485	-3.614369
1N6H	A	GLY	15	C	-2.223615	2.194701	-6.696795	-3.551751
1N6H	A	ASN	16	C	-2.223615	2.194701	-6.696795	-3.551751
1N6H	A	LYS	17	E	-2.223615	2.194701	-6.696795	-3.551751
1N6H	A	ILE	18	E	-2.223615	2.194701	-6.696795	-3.551751
1N6H	A	CYS	19	E	-3.157012	3.069282	-7.965825	-4.240946
1N6H	A	GLN	20	E	-5.077050	5.242431	-10.889282	-5.575806
1N6H	A	PHE	21	E	-8.214653	10.710379	-13.408907	-6.643428
1N6H	A	LYS	22	E	-12.005996	14.368252	-18.357256	-7.838543
1N6H	A	LEU	23	E	-10.154320	17.474422	-9.316527	-4.270627
1N6H	A	VAL	24	E	-10.135098	17.404615	-9.455244	-4.290860
1N6H	A	LEU	25	E	-10.126628	17.367523	-9.538134	-4.307073
1N6H	A	LEU	26	E	-10.005892	15.985508	-10.643337	-4.466476
1N6H	A	GLY	27	C	-9.350601	10.191960	-13.409817	-4.796547
1N6H	A	GLU	28	T	-8.723783	7.674603	-14.076054	-5.017999
1N6H	A	SER	29	T	-8.638729	7.834654	-14.125743	-5.028480
1N6H	A	ALA	30	T	-8.633227	7.843013	-14.147237	-5.030363
1N6H	A	VAL	31	T	-8.642873	7.812267	-14.127408	-5.028769
1N6H	A	GLY	32	C	-8.776480	7.939407	-13.965460	-5.047175
1N6H	A	LYS	33	H	-9.762353	9.095752	-14.618826	-5.115574
1N6H	A	SER	34	H	-11.151334	10.320795	-16.337079	-5.295875
1N6H	A	SER	35	H	-11.925899	12.740020	-16.376328	-5.403869
1N6H	A	LEU	36	H	-12.377383	14.422244	-15.783145	-5.279977
1N6H	A	VAL	37	H	-12.759117	15.810925	-14.754394	-4.828461
1N6H	A	LEU	38	H	-12.734040	15.992404	-14.694945	-4.840705
1N6H	A	ARG	39	H	-10.158873	14.414445	-12.478229	-5.429556
1N6H	A	PHE	40	H	-8.931705	12.360825	-11.961367	-5.237820
1N6H	A	VAL	41	H	-7.905931	12.394944	-10.787318	-5.277158
1N6H	A	LYS	42	H	-7.575977	12.210782	-11.027315	-5.452472
1N6H	A	GLY	43	C	-7.499791	12.196553	-11.196560	-5.507708
1N6H	A	GLN	44	C	-7.366497	12.045847	-11.302026	-5.524482
1N6H	A	PHE	45	C	-7.000645	11.819801	-10.952062	-5.586498
1N6H	A	HIS	46	T	-5.712242	7.570789	-10.356867	-5.252566
1N6H	A	GLU	47	T	-5.656131	7.348439	-10.565466	-5.249435
1N6H	A	PHE	48	T	-5.642549	7.327511	-10.625074	-5.253015
1N6H	A	GLN	49	T	-5.621229	7.208493	-10.722360	-5.238856
1N6H	A	GLU	50	C	-5.538162	6.644367	-10.869101	-5.093511
1N6H	A	SER	51	C	-6.158374	5.757028	-12.031533	-4.810411
1N6H	A	THR	52	T	-6.156039	6.093191	-11.390594	-4.453316
1N6H	A	ILE	53	T	-5.894125	7.940684	-9.760766	-4.184942
1N6H	A	GLY	54	T	-5.924928	8.230751	-9.493177	-4.120792
1N6H	A	ALA	55	E	-6.064491	10.518384	-8.225376	-3.956225
1N6H	A	ALA	56	E	-6.103924	10.721091	-8.006417	-3.928306
1N6H	A	PHE	57	E	-6.247152	11.781471	-7.463849	-3.968969
1N6H	A	LEU	58	E	-6.992732	14.222175	-7.481108	-4.188644
1N6H	A	THR	59	E	-6.335062	11.513060	-8.462490	-4.541752
1N6H	A	GLN	60	E	-6.464700	10.673605	-9.047233	-4.687238
1N6H	A	THR	61	E	-6.134749	10.327379	-8.970950	-4.549957
1N6H	A	VAL	62	E	-6.088175	10.015751	-9.143164	-4.513396
1N6H	A	CYS	63	E	-5.603580	8.910589	-9.190545	-4.557846
1N6H	A	LEU	64	E	-5.674755	8.532670	-9.798399	-4.845232
1N6H	A	ASP	65	T	-5.660331	8.467222	-10.028978	-4.973472

1N6H	A	ASP	66	T	-5.786036	8.138224	-10.314100	-5.123894
1N6H	A	THR	67	E	-5.819701	8.150250	-10.282967	-5.175572
1N6H	A	THR	68	E	-6.801352	8.473587	-14.740037	-7.643481
1N6H	A	VAL	69	E	-7.564151	8.141107	-15.920417	-8.051381
1N6H	A	LYS	70	E	-9.668916	12.934998	-18.015195	-9.397993
1N6H	A	PHE	71	E	-11.499062	18.274010	-12.858130	-5.374153
1N6H	A	GLU	72	E	-11.672776	18.716730	-12.621651	-5.410696
1N6H	A	ILE	73	E	-12.125535	19.024297	-12.849061	-5.176891
1N6H	A	TRP	74	E	-11.780396	15.711981	-14.143784	-5.302991
1N6H	A	ASP	75	E	-11.662340	14.836011	-14.884659	-5.444738
1N6H	A	THR	76	E	-11.030129	11.383962	-16.291532	-5.765023
1N6H	A	ALA	77	C	-10.406615	9.188698	-16.314861	-5.511061
1N6H	A	GLY	78	C	-10.392276	9.053336	-16.435189	-5.526871
1N6H	A	GLN	79	C	-10.436018	8.549237	-16.636381	-5.540758
1N6H	A	GLU	80	G	-10.433329	8.492933	-16.631637	-5.509176
1N6H	A	ARG	81	G	-10.579913	8.202104	-16.516203	-5.354885
1N6H	A	TYR	82	G	-11.518543	10.462408	-16.667572	-4.929756
1N6H	A	HIS	83	G	-10.230662	9.247034	-13.539614	-3.908754
1N6H	A	SER	84	G	-9.377094	8.710688	-12.818221	-3.798119
1N6H	A	LEU	85	G	-9.342405	8.965762	-12.805388	-3.829928
1N6H	A	ALA	86	H	-9.344156	8.964542	-12.792875	-3.827815
1N6H	A	PRO	87	H	-9.349262	8.941028	-12.775002	-3.822182
1N6H	A	MET	88	H	-9.485486	8.914310	-12.642038	-3.820010
1N6H	A	TYR	89	H	-10.934123	13.262202	-13.100396	-4.457725
1N6H	A	TYR	90	H	-10.911783	12.781817	-13.956640	-4.955434
1N6H	A	ARG	91	H	-9.114269	8.752222	-12.704538	-4.275913
1N6H	A	GLY	92	C	-8.470563	9.404059	-11.834168	-4.218196
1N6H	A	ALA	93	T	-8.445962	9.561922	-11.804246	-4.201497
1N6H	A	GLN	94	T	-8.425618	9.713285	-11.766660	-4.184432
1N6H	A	ALA	95	E	-8.346568	10.390055	-11.296088	-4.045409
1N6H	A	ALA	96	E	-8.523252	11.065869	-10.819994	-3.975649
1N6H	A	ILE	97	E	-9.285820	14.564983	-9.322210	-3.417142
1N6H	A	VAL	98	E	-9.395065	14.825516	-8.957832	-3.336470
1N6H	A	VAL	99	E	-9.508331	14.986915	-8.590274	-3.259112
1N6H	A	TYR	100	E	-11.520024	17.810814	-11.944373	-4.374699
1N6H	A	ASP	101	E	-9.744814	11.265271	-13.406310	-5.267806
1N6H	A	ILE	102	T	-9.259336	10.376878	-13.538762	-5.138081
1N6H	A	THR	103	T	-9.135243	9.870861	-13.984161	-5.197910
1N6H	A	ASN	104	T	-9.132750	9.864513	-14.002330	-5.200568
1N6H	A	GLU	105	H	-9.122164	9.870647	-14.028695	-5.197557
1N6H	A	GLU	106	H	-9.370365	9.207455	-14.361151	-5.159529
1N6H	A	SER	107	H	-10.039977	8.156601	-15.874403	-5.422667
1N6H	A	PHE	108	H	-11.263067	11.046209	-15.808251	-5.229564
1N6H	A	ALA	109	H	-11.363135	10.893579	-15.687352	-5.119079
1N6H	A	ARG	110	H	-12.753854	10.761285	-17.629912	-5.071757
1N6H	A	ALA	111	H	-12.601831	12.178605	-17.000416	-5.084743
1N6H	A	LYS	112	H	-12.515225	12.618464	-16.952641	-5.174578
1N6H	A	ASN	113	H	-12.546184	12.504253	-16.983125	-5.190678
1N6H	A	TRP	114	H	-13.104055	16.236243	-15.943457	-5.412418
1N6H	A	VAL	115	H	-13.069446	15.993795	-16.133306	-5.428633
1N6H	A	LYS	116	H	-12.295553	11.161530	-17.212240	-5.377390
1N6H	A	GLU	117	H	-11.757931	10.592196	-16.973025	-5.363297
1N6H	A	LEU	118	H	-9.578080	11.272676	-12.475380	-4.702389
1N6H	A	GLN	119	H	-9.363523	10.425713	-13.132188	-4.724475
1N6H	A	ARG	120	H	-7.811054	7.082552	-11.620350	-3.979687
1N6H	A	GLN	121	H	-5.872891	5.399522	-9.761530	-3.886458
1N6H	A	ALA	122	C	-5.198359	6.397545	-8.356340	-3.577436
1N6H	A	SER	123	T	-5.062523	6.752514	-8.251625	-3.559394
1N6H	A	PRO	124	T	-4.928812	7.668452	-7.846862	-3.570855
1N6H	A	ASN	125	T	-4.928782	7.716839	-7.819081	-3.569004
1N6H	A	ILE	126	T	-5.057628	8.297202	-7.364066	-3.492390
1N6H	A	VAL	127	E	-5.512603	9.947437	-6.982422	-3.562074
1N6H	A	ILE	128	E	-5.854710	11.365063	-6.302853	-3.617645
1N6H	A	ALA	129	E	-7.831380	13.636584	-7.697254	-3.672042
1N6H	A	LEU	130	E	-9.836245	16.345844	-9.908891	-3.969504
1N6H	A	SER	131	E	-10.272412	14.542728	-12.002580	-4.484263
1N6H	A	GLY	132	E	-10.320994	13.770247	-12.643949	-4.671072
1N6H	A	ASN	133	E	-10.900191	10.874682	-16.365466	-5.471799
1N6H	A	LYS	134	T	-9.212342	10.931374	-12.987699	-5.239562
1N6H	A	ALA	135	G	-6.955189	8.638392	-10.659268	-4.846277
1N6H	A	ASP	136	G	-5.935780	7.035694	-10.420305	-4.814114
1N6H	A	LEU	137	G	-5.861732	7.117830	-10.478941	-4.787574
1N6H	A	ALA	138	G	-5.772674	7.012185	-10.544183	-4.710264
1N6H	A	ASN	139	G	-5.772398	7.008349	-10.543969	-4.707491
1N6H	A	LYS	140	G	-5.856548	6.768243	-10.535838	-4.687472
1N6H	A	ARG	141	C	-6.607021	6.977740	-10.963217	-4.382306
1N6H	A	ALA	142	C	-6.918890	6.473100	-11.007658	-4.240424
1N6H	A	VAL	143	C	-8.345549	9.664694	-12.372553	-4.687621
1N6H	A	ASP	144	C	-7.869949	9.256285	-12.060170	-4.831092
1N6H	A	PHE	145	H	-7.878656	9.241367	-12.036214	-4.834891
1N6H	A	GLN	146	H	-7.879668	9.236317	-12.033007	-4.835424

1N6H	A	GLU	147	H	-7.901422	9.186741	-11.993527	-4.840145
1N6H	A	ALA	148	H	-8.108572	8.983493	-11.925011	-4.839917
1N6H	A	GLN	149	H	-12.022436	9.492880	-17.540002	-5.068038
1N6H	A	SER	150	H	-11.292622	9.005596	-16.235353	-4.818790
1N6H	A	TYR	151	H	-10.876400	9.281741	-16.090885	-5.057251
1N6H	A	ALA	152	H	-8.681586	5.043917	-14.302498	-4.482002
1N6H	A	ASP	153	H	-8.214495	6.098680	-13.759435	-4.591293
1N6H	A	ASP	154	H	-8.185708	6.294866	-13.738808	-4.589881
1N6H	A	ASN	155	H	-8.187711	6.294895	-13.727393	-4.589052
1N6H	A	SER	156	C	-8.190484	6.290462	-13.710777	-4.584897
1N6H	A	LEU	157	C	-8.519028	7.297348	-13.305371	-4.672138
1N6H	A	LEU	158	E	-9.955926	10.638258	-13.295173	-4.571200
1N6H	A	PHE	159	E	-11.625460	17.084621	-12.872853	-4.749382
1N6H	A	MET	160	E	-11.924854	17.276312	-13.096125	-4.819599
1N6H	A	GLU	161	E	-12.259825	14.976477	-16.225208	-5.751268
1N6H	A	THR	162	C	-10.234124	10.661493	-14.509887	-5.373015
1N6H	A	SER	163	T	-9.807021	10.063551	-14.559054	-5.240572
1N6H	A	ALA	164	T	-8.654648	10.133999	-12.847718	-5.188194
1N6H	A	LYS	165	T	-8.279253	9.571649	-13.223404	-5.373375
1N6H	A	THR	166	T	-7.980656	9.801262	-12.720994	-5.218543
1N6H	A	SER	167	T	-7.953367	9.786987	-12.740827	-5.205144
1N6H	A	MET	168	T	-7.873372	9.743030	-12.738795	-5.177083
1N6H	A	ASN	169	T	-7.848245	10.030662	-12.477909	-5.117964
1N6H	A	VAL	170	H	-7.982461	10.531356	-12.079804	-4.972797
1N6H	A	ASN	171	H	-8.279585	10.805442	-12.163204	-4.966722
1N6H	A	GLU	172	H	-8.350288	10.942221	-11.984210	-4.954843
1N6H	A	ILE	173	H	-8.583089	11.688606	-11.500185	-4.932209
1N6H	A	PHE	174	H	-9.940173	16.785395	-10.643387	-4.831445
1N6H	A	MET	175	H	-8.712510	18.502504	-8.910849	-5.751105
1N6H	A	ALA	176	H	-6.408880	15.735758	-5.896307	-4.620448
1N6H	A	ILE	177	H	-5.463146	14.062770	-5.151803	-4.054114
1N6H	A	ALA	178	H	-4.011839	9.725950	-4.419374	-3.268322
1N6H	A	LYS	179	H	-4.011839	9.725950	-4.419374	-3.268322
1N6H	A	LYS	180	H	-4.011839	9.725950	-4.419374	-3.268322
1N6H	A	LEU	181	C	-4.011839	9.725950	-4.419374	-3.268322
1NKR	A	ARG	6	C	-8.604228	8.769063	-10.765084	-3.359139
1NKR	A	LYS	7	C	-8.604228	8.769063	-10.765084	-3.359139
1NKR	A	PRO	8	C	-8.604228	8.769063	-10.765084	-3.359139
1NKR	A	SER	9	E	-8.604228	8.769063	-10.765084	-3.359139
1NKR	A	LEU	10	E	-8.413086	11.321604	-9.698751	-3.788747
1NKR	A	LEU	11	E	-6.090303	7.257425	-8.654106	-3.702395
1NKR	A	ALA	12	E	-5.669259	7.424733	-8.368878	-3.587919
1NKR	A	HIS	13	E	-5.592823	7.652354	-8.401498	-3.612866
1NKR	A	PRO	14	T	-5.495295	8.032592	-8.263392	-3.586068
1NKR	A	GLY	15	T	-5.492751	8.063161	-8.261074	-3.590557
1NKR	A	PRO	16	C	-5.753890	8.567793	-8.055161	-3.529914
1NKR	A	LEU	17	E	-6.271332	9.997010	-8.025685	-3.616212
1NKR	A	VAL	18	E	-6.433562	10.162326	-8.185138	-3.703065
1NKR	A	LYS	19	E	-6.508867	8.664870	-10.326348	-4.641913
1NKR	A	SER	20	T	-6.505371	8.465147	-10.457102	-4.658865
1NKR	A	GLU	21	T	-6.500588	8.441585	-10.485190	-4.658963
1NKR	A	GLU	22	b	-6.504625	8.403749	-10.482664	-4.651393
1NKR	A	THR	23	C	-6.643287	8.242307	-10.468383	-4.674347
1NKR	A	VAL	24	E	-7.916483	9.862174	-11.005618	-4.345971
1NKR	A	ILE	25	E	-8.713010	10.991647	-11.184973	-4.212550
1NKR	A	LEU	26	E	-9.316589	12.981215	-10.066631	-3.898961
1NKR	A	GLN	27	E	-11.636782	14.139823	-13.717288	-4.652030
1NKR	A	CYS	28	E	-11.468163	10.089276	-16.323599	-5.241899
1NKR	A	TRP	29	E	-10.182912	10.608504	-14.406259	-5.203910
1NKR	A	SER	30	E	-9.820025	11.377910	-13.909447	-5.178785
1NKR	A	ASP	31	T	-9.732888	11.468969	-13.950290	-5.182752
1NKR	A	VAL	32	T	-9.726342	11.508819	-13.957891	-5.185691
1NKR	A	MET	33	T	-9.755802	11.597590	-13.840800	-5.183601
1NKR	A	PHE	34	T	-10.092719	12.287772	-13.586604	-5.172277
1NKR	A	GLU	35	T	-10.860398	12.283655	-14.279133	-5.232258
1NKR	A	HIS	36	E	-12.339716	14.961975	-15.033479	-5.498808
1NKR	A	PHE	37	E	-14.387122	19.606803	-16.250050	-5.634956
1NKR	A	LEU	38	E	-14.479637	19.413561	-16.351301	-5.625695
1NKR	A	LEU	39	E	-14.314174	17.001236	-17.698410	-5.777033
1NKR	A	HIS	40	E	-14.154067	12.483366	-20.331098	-6.164741
1NKR	A	ARG	41	E	-12.869390	10.666816	-18.657211	-5.856081
1NKR	A	GLU	42	E	-7.324979	7.058825	-12.218668	-5.207894
1NKR	A	GLY	43	E	-7.093981	6.856625	-12.490994	-5.183923
1NKR	A	MET	44	T	-7.055878	6.970245	-12.536028	-5.184105
1NKR	A	PHE	45	T	-7.045417	7.005587	-12.551786	-5.177191
1NKR	A	ASN	46	T	-6.894752	7.543566	-12.136461	-5.033484
1NKR	A	ASP	47	E	-7.268069	8.116520	-12.030464	-4.852611
1NKR	A	THR	48	E	-7.471423	10.018933	-10.805452	-4.478018
1NKR	A	LEU	49	E	-7.495352	10.335038	-10.451104	-4.336972
1NKR	A	ARG	50	E	-7.412776	10.261646	-10.484581	-4.301045
1NKR	A	LEU	51	E	-7.484348	9.887322	-10.539905	-4.067482

1NKR	A	ILE	52	E	-6.457979	6.827850	-10.570312	-4.286023
1NKR	A	GLY	53	C	-5.023794	5.228930	-9.758818	-4.618464
1NKR	A	GLU	54	E	-4.306232	4.968630	-9.419775	-4.712713
1NKR	A	HIS	55	E	-3.613560	5.993932	-7.887963	-4.575544
1NKR	A	HIS	56	E	-3.599510	5.995877	-7.938168	-4.577758
1NKR	A	ASP	57	T	-3.603056	5.996207	-7.923328	-4.579784
1NKR	A	GLY	58	T	-3.654684	6.075707	-7.760803	-4.571879
1NKR	A	VAL	59	E	-3.813070	6.442033	-7.290418	-4.512785
1NKR	A	SER	60	E	-5.790700	6.199238	-10.091914	-4.654374
1NKR	A	LYS	61	E	-7.852875	8.872248	-12.371493	-5.290356
1NKR	A	ALA	62	E	-9.537063	13.000157	-13.749949	-5.612790
1NKR	A	ASN	63	E	-9.162623	13.463067	-11.217992	-4.565570
1NKR	A	PHE	64	E	-9.137078	13.552469	-10.889160	-4.365265
1NKR	A	SER	65	E	-9.094146	13.449757	-11.013759	-4.360861
1NKR	A	ILE	66	E	-9.114845	13.344747	-10.973632	-4.302684
1NKR	A	SER	67	T	-9.216333	13.106489	-11.042853	-4.300881
1NKR	A	ARG	68	T	-9.957368	12.709675	-12.491408	-4.308258
1NKR	A	MET	69	b	-10.314825	12.062694	-13.518092	-4.537463
1NKR	A	THR	70	C	-10.070235	11.504200	-13.882664	-4.991168
1NKR	A	GLN	71	G	-9.927889	11.347526	-14.012906	-5.122905
1NKR	A	ASP	72	G	-9.826634	11.335398	-13.966964	-5.079755
1NKR	A	LEU	73	G	-9.839598	11.341577	-13.912478	-5.068214
1NKR	A	ALA	74	C	-9.851658	11.317134	-13.864730	-5.054806
1NKR	A	GLY	75	E	-10.253360	11.297858	-14.097022	-5.038677
1NKR	A	THR	76	E	-10.785642	11.245630	-14.160970	-4.885361
1NKR	A	TYR	77	E	-12.940275	15.397605	-15.976683	-5.395495
1NKR	A	ARG	78	E	-13.449419	14.525813	-17.788920	-5.654005
1NKR	A	CYS	79	E	-12.147760	12.985859	-15.701422	-5.194087
1NKR	A	TYR	80	E	-11.047358	13.307936	-14.012555	-5.041036
1NKR	A	GLY	81	E	-8.059646	7.865021	-13.166189	-5.216364
1NKR	A	SER	82	E	-7.571333	7.719144	-12.359625	-4.767388
1NKR	A	VAL	83	B	-5.591269	6.865016	-8.715585	-3.986930
1NKR	A	THR	84	T	-4.907975	6.595458	-8.585333	-4.137678
1NKR	A	HIS	85	T	-4.823658	6.416788	-8.758291	-4.109484
1NKR	A	SER	86	B	-4.706094	6.379756	-8.768863	-4.066374
1NKR	A	PRO	87	T	-4.625709	6.490119	-8.767534	-4.077450
1NKR	A	TYR	88	T	-4.738703	6.447500	-8.841304	-4.112754
1NKR	A	GLN	89	T	-5.157162	6.461956	-9.203673	-4.020685
1NKR	A	VAL	90	C	-5.310160	6.850237	-9.008476	-4.051199
1NKR	A	SER	91	C	-5.730412	7.482862	-9.128162	-4.214372
1NKR	A	ALA	92	C	-6.796660	8.696989	-10.736409	-4.505350
1NKR	A	PRO	93	C	-7.345936	9.088833	-11.122031	-4.461743
1NKR	A	SER	94	C	-7.954520	9.316466	-11.329866	-4.294772
1NKR	A	ASP	95	C	-8.488256	8.729356	-12.089327	-4.390209
1NKR	A	PRO	96	C	-8.515753	8.758798	-11.963190	-4.368353
1NKR	A	LEU	97	E	-10.225323	12.179048	-13.011153	-4.479286
1NKR	A	ASP	98	E	-10.935695	15.225092	-12.446394	-4.217976
1NKR	A	ILE	99	E	-8.543885	16.468504	-7.454293	-3.995873
1NKR	A	VAL	100	E	-7.856967	15.702001	-7.522915	-4.130794
1NKR	A	ILE	101	E	-7.765975	15.730004	-7.718894	-4.210965
1NKR	A	ILE	102	E	-7.520797	14.965351	-8.339264	-4.454849
1NKR	A	GLY	103	C	-7.416330	14.428576	-8.871042	-4.612967
1NKR	A	LEU	104	C	-7.495556	14.070934	-9.187890	-4.727666
1NKR	A	TYR	105	C	-7.770231	13.302950	-10.172142	-5.045831
1NKR	A	GLU	106	C	-7.801456	12.721752	-10.503346	-5.064478
1NKR	A	LYS	107	C	-8.253616	11.801425	-11.672743	-5.205042
1NKR	A	PRO	108	C	-8.647141	11.805332	-11.368914	-4.400980
1NKR	A	SER	109	E	-8.638319	11.071425	-11.530186	-4.227625
1NKR	A	LEU	110	E	-8.365438	10.757994	-11.190352	-4.017592
1NKR	A	SER	111	E	-7.066941	6.764250	-10.316097	-3.641126
1NKR	A	ALA	112	E	-5.968926	6.733886	-8.814609	-3.498841
1NKR	A	GLN	113	E	-5.482739	6.980515	-8.600573	-3.663286
1NKR	A	PRO	114	T	-4.964710	7.807211	-7.575517	-3.593509
1NKR	A	GLY	115	T	-4.950301	7.803249	-7.625308	-3.595934
1NKR	A	PRO	116	T	-4.962313	7.845653	-7.568843	-3.593730
1NKR	A	THR	117	E	-5.030544	8.012132	-7.502947	-3.624182
1NKR	A	VAL	118	E	-5.197068	8.275305	-7.246744	-3.568427
1NKR	A	LEU	119	T	-5.904109	6.523388	-10.114923	-3.996517
1NKR	A	ALA	120	T	-5.933067	6.522549	-10.177095	-4.045011
1NKR	A	GLY	121	T	-5.911962	6.686501	-10.168201	-4.087820
1NKR	A	GLU	122	E	-6.063118	6.508521	-10.343860	-4.177086
1NKR	A	ASN	123	E	-6.122670	6.458144	-10.317746	-4.222269
1NKR	A	VAL	124	E	-7.057244	9.285311	-10.058926	-4.237144
1NKR	A	THR	125	E	-7.528763	10.232820	-9.894814	-4.407416
1NKR	A	LEU	126	E	-9.783228	13.824086	-11.223778	-4.370476
1NKR	A	SER	127	E	-10.763615	13.056329	-13.106234	-4.552340
1NKR	A	CYS	128	E	-11.388385	9.675453	-16.641480	-4.985626
1NKR	A	SER	129	E	-10.438357	8.975533	-15.516903	-4.941072
1NKR	A	SER	130	E	-10.429341	9.112521	-15.498920	-4.956440
1NKR	A	ARG	131	C	-10.378740	9.442312	-15.378865	-4.931401
1NKR	A	SER	132	T	-10.373328	9.518005	-15.367364	-4.937473

1NKR	A	SER	133	T	-10.441733	9.721401	-15.158113	-4.939766
1NKR	A	TYR	134	T	-11.547726	13.536290	-14.816124	-5.021725
1NKR	A	ASP	135	C	-11.762064	13.416521	-14.357077	-4.787671
1NKR	A	MET	136	E	-12.997093	15.880302	-15.467749	-5.534175
1NKR	A	TYR	137	E	-14.875541	19.195240	-17.290541	-5.880439
1NKR	A	HIS	138	E	-15.125929	17.494211	-18.830437	-5.993462
1NKR	A	LEU	139	E	-11.619803	11.140698	-16.172756	-5.551899
1NKR	A	SER	140	E	-8.957072	6.532284	-14.864681	-5.314004
1NKR	A	ARG	141	E	-7.385369	5.545619	-12.932344	-4.926310
1NKR	A	GLU	142	T	-6.465257	4.786055	-12.330160	-4.886248
1NKR	A	GLY	143	T	-6.191649	5.567224	-12.022127	-4.962387
1NKR	A	GLU	144	T	-6.191562	5.567343	-12.022756	-4.962341
1NKR	A	ALA	145	C	-6.197082	5.558869	-11.996332	-4.959064
1NKR	A	HIS	146	C	-6.276266	5.571424	-11.883355	-4.967914
1NKR	A	GLU	147	C	-6.780548	6.899247	-11.500440	-5.091870
1NKR	A	ARG	148	E	-10.985824	8.821775	-16.205683	-4.895932
1NKR	A	ARG	149	E	-8.990159	9.867322	-12.520479	-4.599882
1NKR	A	LEU	150	E	-6.724842	7.498030	-11.281412	-4.805946
1NKR	A	PRO	151	E	-5.116789	6.233541	-7.951704	-3.562414
1NKR	A	ALA	152	C	-4.461486	5.455660	-7.815854	-3.548732
1NKR	A	GLY	153	E	-2.697090	3.119174	-6.601340	-3.687925
1NKR	A	PRO	154	E	-1.880588	3.461347	-6.024651	-3.884238
1NKR	A	LYS	155	E	-1.746869	3.794835	-6.196920	-4.036557
1NKR	A	VAL	156	E	-1.748608	3.788444	-6.191803	-4.037912
1NKR	A	ASN	157	T	-1.753118	3.775925	-6.175394	-4.038746
1NKR	A	GLY	158	T	-1.891982	3.902068	-5.956969	-4.045391
1NKR	A	THR	159	E	-2.740803	4.846450	-6.404989	-4.326126
1NKR	A	PHE	160	E	-6.214048	9.072808	-9.911365	-5.123970
1NKR	A	GLN	161	E	-8.277956	12.262808	-15.706136	-8.655921
1NKR	A	ALA	162	E	-9.414950	12.914109	-16.593467	-8.492118
1NKR	A	ASP	163	E	-9.444379	12.603149	-12.355924	-5.044440
1NKR	A	PHE	164	E	-9.152972	11.868410	-11.968826	-4.573078
1NKR	A	PRO	165	E	-7.489127	7.540560	-10.439260	-3.642304
1NKR	A	LEU	166	E	-6.203878	8.137186	-8.416887	-3.584306
1NKR	A	GLY	167	E	-5.037633	5.746776	-8.018617	-3.426838
1NKR	A	PRO	168	E	-4.361513	6.313156	-7.182625	-3.476135
1NKR	A	ALA	169	E	-4.254865	6.189417	-7.511238	-3.587546
1NKR	A	THR	170	C	-4.153177	6.274662	-7.746715	-3.758707
1NKR	A	HIS	171	C	-4.169805	6.219836	-7.735474	-3.764055
1NKR	A	GLY	172	C	-4.301366	6.431798	-7.678583	-3.852960
1NKR	A	GLY	173	E	-4.867026	6.192776	-9.093628	-4.416052
1NKR	A	THR	174	E	-5.235153	6.738068	-9.025343	-4.645676
1NKR	A	TYR	175	E	-9.237255	11.985915	-12.535852	-5.502787
1NKR	A	ARG	176	E	-11.749040	14.061247	-15.314788	-5.765222
1NKR	A	CYS	177	E	-12.880881	14.511384	-17.277656	-5.886891
1NKR	A	PHE	178	E	-12.632158	15.645130	-15.808373	-5.580594
1NKR	A	GLY	179	E	-9.408392	9.549021	-13.605206	-5.118904
1NKR	A	SER	180	E	-8.929556	9.835632	-13.231938	-5.053365
1NKR	A	PHE	181	E	-7.632418	9.203557	-11.043189	-4.606927
1NKR	A	HIS	182	T	-7.589338	9.200741	-11.157189	-4.605134
1NKR	A	ASP	183	T	-7.587456	9.206412	-11.168500	-4.606877
1NKR	A	SER	184	E	-7.615395	9.191165	-11.051309	-4.582251
1NKR	A	PRO	185	E	-7.652263	9.134949	-10.930546	-4.555379
1NKR	A	TYR	186	E	-9.136236	9.257580	-12.763204	-4.608139
1NKR	A	GLU	187	E	-10.969748	11.223919	-14.745004	-5.171050
1NKR	A	TRP	188	E	-13.441524	15.193993	-17.180000	-5.714138
1NKR	A	SER	189	C	-11.397789	9.231632	-16.819852	-5.422426
1NKR	A	LYS	190	C	-8.785417	8.101549	-13.265056	-4.908647
1NKR	A	SER	191	C	-8.674953	8.250862	-13.313308	-4.860955
1NKR	A	SER	192	C	-8.405624	8.199510	-13.078219	-4.660349
1NKR	A	ASP	193	C	-8.405579	8.200483	-13.078204	-4.660436
1NKR	A	PRO	194	C	-8.407930	8.214869	-13.054350	-4.656073
1NKR	A	LEU	195	E	-8.838574	8.430722	-12.863658	-4.382653
1NKR	A	LEU	196	E	-8.579984	9.783277	-11.097362	-3.719103
1NKR	A	VAL	197	E	-7.167519	10.249378	-6.954914	-2.446504
1NKR	A	SER	198	E	-7.167519	10.249378	-6.954914	-2.446504
1NKR	A	VAL	199	E	-7.167519	10.249378	-6.954914	-2.446504
1NKR	A	THR	200	C	-7.167519	10.249378	-6.954914	-2.446504
1PBK	A	PRO	109	C	-7.962991	11.095665	-10.101097	-4.235216
1PBK	A	LYS	110	C	-7.962991	11.095665	-10.101097	-4.235216
1PBK	A	TYR	111	E	-7.962991	11.095665	-10.101097	-4.235216
1PBK	A	THR	112	E	-7.962991	11.095665	-10.101097	-4.235216
1PBK	A	LYS	113	E	-7.902081	10.593165	-11.434029	-5.137779
1PBK	A	SER	114	E	-7.694756	9.752369	-11.775579	-5.048849
1PBK	A	VAL	115	E	-6.328860	9.164982	-10.235479	-5.154991
1PBK	A	LEU	116	E	-6.323336	9.155468	-10.276143	-5.159618
1PBK	A	LYS	117	E	-6.300823	9.029140	-10.436885	-5.170808
1PBK	A	LYS	118	T	-5.708668	6.786238	-11.001444	-5.173848
1PBK	A	GLY	119	C	-4.288315	5.836630	-9.430210	-5.227373
1PBK	A	ASP	120	T	-4.217749	6.102488	-9.394858	-5.233716
1PBK	A	LYS	121	T	-4.213290	6.140395	-9.392738	-5.229269

```
1PBK          A           THR            122                       T -4.212730  6.147773 -9.389277 -5.226897
1PBK          A           ASN            123                       T -4.244640  6.175382 -9.281099 -5.229420
1PBK          A           PHE            124                       C -5.349708  8.525819 -9.306959 -5.207102
1PBK          A           PRO            125                       C -6.775344  9.791371 -10.136831 -4.488976
1PBK          A           LYS            126                       T -7.198619  7.685037 -11.661907 -4.279515
1PBK          A           LYS            127                       T -7.418396  6.839315 -12.219610 -4.321380
1PBK          A           GLY            128                       T -7.423842  6.800643 -12.213396 -4.320598
1PBK          A           ASP            129                       T -7.483766  6.541118 -12.248822 -4.334996
1PBK          A           VAL            130                       E -8.288704  5.955057 -13.508321 -4.520364
1PBK          A           VAL            131                       E -10.258499  8.524534 -14.715203 -4.516627
1PBK          A           HIS            132                       E -12.113930  9.682862 -17.080273 -4.971842
1PBK          A           CYS            133                       E -13.331350 15.764472 -16.747980 -5.544189
1PBK          A           TRP            134                       E -12.784178 18.933529 -14.435080 -5.767678
1PBK          A           TYR            135                       E -12.051500 16.932098 -15.230027 -6.053112
1PBK          A           THR            136                       E -9.914496 11.384255 -13.727561 -5.191533
1PBK          A           GLY            137                       E -8.181762  8.444426 -12.546964 -4.873814
1PBK          A           THR            138                       E -6.619295  7.110445 -11.154116 -4.807970
1PBK          A           LEU            139                       T -4.439648  5.353701 -8.753984 -4.497495
1PBK          A           GLN            140                       T -3.486000  4.753451 -8.151536 -4.495075
1PBK          A           ASP            141                       T -3.477962  4.814720 -8.160163 -4.496655
1PBK          A           GLY            142                       T -3.477981  4.814961 -8.159848 -4.496629
1PBK          A           THR            143                       C -3.480284  4.809763 -8.147528 -4.495212
1PBK          A           VAL            144                       E -3.607992  4.684991 -8.008079 -4.491759
1PBK          A           PHE            145                       E -5.985655  9.398917 -8.886565 -4.596601
1PBK          A           ASP            146                       E -7.505692 10.860521 -10.587771 -4.707890
1PBK          A           THR            147                       E -6.968539  8.526595 -11.074500 -4.729958
1PBK          A           ASN            148                       C -6.556514  6.504272 -11.372766 -4.542854
1PBK          A           ILE            149                       C -4.957463  5.638818 -8.568208 -3.843146
1PBK          A           GLN            150                       T -4.909257  5.659169 -8.740831 -3.881334
1PBK          A           THR            151                       T -4.833649  5.609564 -8.986834 -3.939461
1PBK          A           SER            152                       T -4.822219  5.538370 -9.043959 -3.934202
1PBK          A           ALA            153                       T -4.836714  5.530582 -8.999451 -3.924693
1PBK          A           LYS            154                       T -5.202358  6.220643 -10.364812 -4.663126
1PBK          A           LYS            155                       T -5.273548  6.281250 -10.357072 -4.723653
1PBK          A           LYS            156                       T -5.419851  6.648361 -10.353798 -4.886393
1PBK          A           LYS            157                       T -5.475521  6.912930 -10.222101 -4.961087
1PBK          A           ASN            158                       T -5.491979  6.938346 -10.160395 -4.967789
1PBK          A           ALA            159                       T -6.847095  7.660523 -12.953384 -5.322660
1PBK          A           LYS            160                       T -7.001648  7.923246 -12.771062 -5.280882
1PBK          A           PRO            161                       C -7.562749  9.284110 -11.417825 -4.387218
1PBK          A           LEU            162                       E -8.020727 10.221137 -10.772935 -4.033585
1PBK          A           SER            163                       E -8.159536 10.505209 -10.511882 -4.022601
1PBK          A           PHE            164                       E -9.266100 13.838356 -11.110841 -4.364985
1PBK          A           LYS            165                       E -6.954754  8.672804 -10.239049 -4.523562
1PBK          A           VAL            166                       T -4.821642  8.509546 -7.474522 -4.417919
1PBK          A           GLY            167                       T -3.546666  7.226418 -6.689506 -4.403563
1PBK          A           VAL            168                       T -3.320065  8.014714 -6.215072 -4.279231
1PBK          A           GLY            169                       T -3.308506  8.068630 -6.230557 -4.277989
1PBK          A           LYS            170                       T -3.309261  8.070833 -6.224057 -4.277357
1PBK          A           VAL            171                       T -3.356270  8.030421 -6.123727 -4.263568
1PBK          A           ILE            172                       T -3.965009  9.741070 -5.278357 -4.002626
1PBK          A           ARG            173                       H -5.625320 10.807761 -7.043794 -4.184262
1PBK          A           GLY            174                       H -7.499053 12.159443 -8.653725 -4.196666
1PBK          A           TRP            175                       H -10.701659 16.216071 -11.158287 -4.482165
1PBK          A           ASP            176                       H -12.534940 16.253489 -16.387711 -5.838338
1PBK          A           GLU            177                       H -11.514397 12.653763 -14.568407 -4.650345
1PBK          A           ALA            178                       H -10.985636 13.601141 -13.483424 -4.592745
1PBK          A           LEU            179                       H -10.962721 13.625640 -13.539599 -4.609693
1PBK          A           LEU            180                       H -10.951735 13.604610 -13.615313 -4.629126
1PBK          A           THR            181                       C -10.934890 13.481348 -13.785180 -4.685025
1PBK          A           MET            182                       C -11.162271 14.049798 -13.589441 -4.766715
1PBK          A           SER            183                       T -12.125593 12.533960 -17.411412 -5.705000
1PBK          A           LYS            184                       T -12.126411 11.367698 -18.457549 -6.035304
1PBK          A           GLY            185                       T -12.178526 11.199093 -18.640557 -6.103974
1PBK          A           GLU            186                       E -12.428293 11.602653 -18.716844 -6.191412
1PBK          A           LYS            187                       E -12.334269 12.585062 -18.051109 -6.100485
1PBK          A           ALA            188                       E -12.035203 14.880793 -15.599673 -5.489913
1PBK          A           ARG            189                       E -12.180726 16.594979 -14.547714 -5.293676
1PBK          A           LEU            190                       E -12.111046 16.877439 -14.341156 -5.246509
1PBK          A           GLU            191                       E -11.755021 15.634981 -14.916279 -5.472571
1PBK          A           ILE            192                       E -11.717349 15.718773 -14.847225 -5.456879
1PBK          A           GLU            193                       C -11.371671 15.152641 -14.649550 -5.577688
1PBK          A           PRO            194                       G -11.347153 15.340754 -14.575060 -5.574341
1PBK          A           GLU            195                       G -11.183141 15.750321 -14.411593 -5.679885
1PBK          A           TRP            196                       G -11.154813 15.924567 -14.189268 -5.598334
1PBK          A           ALA            197                       T -9.810380 10.343117 -13.892057 -4.941742
1PBK          A           TYR            198                       T -8.648752  8.594742 -13.563115 -5.149060
1PBK          A           GLY            199                       T -8.462556  7.911678 -14.035700 -5.142054
1PBK          A           LYS            200                       T -8.335450  7.590034 -14.243532 -5.090326
1PBK          A           LYS            201                       T -7.327062  5.737961 -12.980549 -4.650119
1PBK          A           GLY            202                       T -6.325093  5.416348 -11.608618 -4.564942
```

1PBK	A	GLN	203	B	-5.999457	5.097271	-11.456862	-4.419978
1PBK	A	PRO	204	G	-5.481388	6.659772	-9.569876	-4.057230
1PBK	A	ASP	205	G	-5.436743	6.850935	-9.519288	-4.036800
1PBK	A	ALA	206	G	-5.421597	7.083649	-9.340216	-3.980418
1PBK	A	LYS	207	C	-5.532167	7.480696	-8.926955	-3.856574
1PBK	A	ILE	208	B	-5.632705	8.250896	-8.362335	-3.750488
1PBK	A	PRO	209	T	-6.455435	9.725397	-8.792511	-3.608988
1PBK	A	PRO	210	T	-6.770339	10.074730	-8.657687	-3.478763
1PBK	A	ASN	211	T	-7.263913	10.175893	-9.214412	-3.638438
1PBK	A	ALA	212	T	-7.378634	10.233351	-8.982615	-3.614309
1PBK	A	LYS	213	C	-8.845233	10.067398	-12.120091	-4.535881
1PBK	A	LEU	214	E	-10.522751	12.649016	-13.589805	-4.957402
1PBK	A	THR	215	E	-11.781813	14.216405	-14.927529	-5.529827
1PBK	A	PHE	216	E	-13.601620	18.736141	-15.891613	-5.546836
1PBK	A	GLU	217	E	-13.729679	18.730447	-15.886053	-5.559732
1PBK	A	VAL	218	E	-13.649578	18.714105	-16.064094	-5.694096
1PBK	A	GLU	219	E	-12.523619	15.984533	-15.540599	-5.848063
1PBK	A	LEU	220	E	-9.667557	12.799943	-11.509686	-4.497211
1PBK	A	VAL	221	E	-7.100507	9.154092	-9.020719	-3.636177
1PBK	A	ASP	222	E	-7.100507	9.154092	-9.020719	-3.636177
1PBK	A	ILE	223	E	-7.100507	9.154092	-9.020719	-3.636177
1PBK	A	ASP	224	C	-7.100507	9.154092	-9.020719	-3.636177
1PBV	A	ALA	52	C	-1.992957	1.501318	-7.257937	-3.866818
1PBV	A	ASN	53	C	-1.992957	1.501318	-7.257937	-3.866818
1PBV	A	GLU	54	H	-1.992957	1.501318	-7.257937	-3.866818
1PBV	A	GLY	55	H	-1.992957	1.501318	-7.257937	-3.866818
1PBV	A	SER	56	H	-2.953770	2.488015	-9.598150	-4.872462
1PBV	A	LYS	57	H	-3.261833	2.823131	-10.229333	-5.377491
1PBV	A	THR	58	H	-3.723345	3.339236	-11.034563	-5.931378
1PBV	A	LEU	59	H	-4.425856	3.640046	-12.274075	-6.501134
1PBV	A	GLN	60	H	-5.600760	5.084002	-14.335057	-7.599607
1PBV	A	ARG	61	H	-7.349187	7.243267	-17.614648	-8.733087
1PBV	A	ASN	62	H	-7.626931	7.545667	-17.940686	-9.047322
1PBV	A	ARG	63	H	-8.310520	8.456541	-18.284928	-9.241747
1PBV	A	LYS	64	H	-9.926735	10.141650	-20.351621	-9.795534
1PBV	A	MET	65	H	-11.143613	10.970997	-16.566596	-5.512359
1PBV	A	ALA	66	H	-10.317817	9.521247	-15.369468	-5.101425
1PBV	A	MET	67	H	-10.161582	9.963050	-15.250583	-5.203466
1PBV	A	GLY	68	H	-10.208410	9.931925	-15.219127	-5.215416
1PBV	A	ARG	69	H	-10.230033	9.854411	-15.162704	-5.188370
1PBV	A	LYS	70	H	-9.660112	11.350270	-13.455561	-5.029932
1PBV	A	LYS	71	H	-9.642230	12.386229	-12.998963	-5.108285
1PBV	A	PHE	72	H	-9.628200	12.521679	-12.796472	-5.004661
1PBV	A	ASN	73	H	-9.519689	11.859385	-13.222628	-5.012291
1PBV	A	MET	74	H	-8.604284	8.962306	-12.872194	-4.756406
1PBV	A	ASP	75	C	-8.422497	8.550069	-13.047437	-4.796463
1PBV	A	PRO	76	H	-8.434114	8.455972	-13.048723	-4.780890
1PBV	A	LYS	77	H	-8.425899	8.434712	-13.105725	-4.800807
1PBV	A	LYS	78	H	-8.439649	8.444720	-13.051722	-4.795585
1PBV	A	GLY	79	H	-8.975898	8.845130	-13.457816	-4.955767
1PBV	A	ILE	80	H	-10.188994	11.133951	-14.556174	-5.233265
1PBV	A	GLN	81	H	-10.394506	10.406997	-15.010416	-5.334523
1PBV	A	PHE	82	H	-11.335520	13.384391	-14.907481	-5.211184
1PBV	A	LEU	83	H	-9.565266	9.385797	-13.504165	-4.839068
1PBV	A	VAL	84	H	-9.097365	9.466719	-13.515828	-4.992781
1PBV	A	GLU	85	H	-9.048145	9.635316	-13.562882	-5.018709
1PBV	A	ASN	86	H	-9.006274	9.815593	-13.596571	-5.050796
1PBV	A	GLU	87	T	-8.415636	11.892243	-11.747568	-5.063112
1PBV	A	LEU	88	T	-7.587707	13.876721	-9.132839	-4.927699
1PBV	A	LEU	89	T	-7.008450	12.447194	-8.734714	-4.527493
1PBV	A	GLN	90	T	-6.721916	10.976107	-9.411092	-4.543875
1PBV	A	ASN	91	C	-6.539468	10.565931	-9.777302	-4.669210
1PBV	A	THR	92	C	-6.534979	10.535876	-9.785243	-4.658030
1PBV	A	PRO	93	H	-6.618413	9.965839	-9.985732	-4.623490
1PBV	A	GLU	94	H	-6.853033	9.211155	-10.667199	-4.777971
1PBV	A	GLU	95	H	-7.240896	9.755422	-10.809533	-4.967237
1PBV	A	ILE	96	H	-8.446798	11.857944	-10.833191	-4.625568
1PBV	A	ALA	97	H	-9.602119	13.030673	-11.554475	-4.458900
1PBV	A	ARG	98	H	-9.838027	12.718674	-11.543793	-4.438912
1PBV	A	PHE	99	H	-10.874339	17.678008	-11.368480	-5.167528
1PBV	A	LEU	100	H	-8.876603	12.265386	-11.405917	-5.074570
1PBV	A	TYR	101	H	-6.703145	7.730054	-11.438870	-5.360241
1PBV	A	LYS	102	H	-5.420538	7.804162	-9.619001	-5.122952
1PBV	A	GLY	103	T	-5.328121	7.788043	-9.801604	-5.145838
1PBV	A	GLU	104	T	-5.327298	7.790868	-9.806741	-5.146434
1PBV	A	GLY	105	T	-5.326743	7.788491	-9.811086	-5.146610
1PBV	A	LEU	106	T	-5.385299	7.813485	-9.641864	-5.122604
1PBV	A	ASN	107	C	-6.447295	7.826795	-10.947445	-5.272205
1PBV	A	LYS	108	H	-8.239724	10.809544	-12.297256	-5.054704
1PBV	A	THR	109	H	-7.753527	10.162101	-10.786306	-4.321495
1PBV	A	ALA	110	H	-7.886234	10.164616	-10.417708	-4.114419

1PBV	A	ILE	111	H	-7.951257	9.948951	-10.285488	-4.038721
1PBV	A	GLY	112	H	-7.981633	9.867371	-10.192240	-4.013889
1PBV	A	ASP	113	H	-8.008729	9.751878	-10.123941	-3.994217
1PBV	A	TYR	114	H	-11.400014	15.330568	-13.845678	-5.018227
1PBV	A	LEU	115	H	-10.612695	11.360529	-14.463065	-5.055224
1PBV	A	GLY	116	H	-8.450071	6.444227	-13.818312	-4.929935
1PBV	A	GLU	117	C	-8.046023	7.012413	-13.206158	-4.729823
1PBV	A	ARG	118	C	-7.299779	7.137036	-11.680449	-4.352110
1PBV	A	GLU	119	C	-7.292995	7.154097	-11.708231	-4.356403
1PBV	A	GLU	120	H	-7.288796	7.164125	-11.715873	-4.353188
1PBV	A	LEU	121	H	-7.376211	7.298737	-11.384663	-4.261885
1PBV	A	ASN	122	H	-7.479503	7.239379	-11.156241	-4.211232
1PBV	A	LEU	123	H	-9.486848	9.314717	-13.516356	-4.375116
1PBV	A	ALA	124	H	-9.639712	10.697975	-12.328260	-3.851381
1PBV	A	VAL	125	H	-10.084510	12.510360	-11.220587	-3.418436
1PBV	A	LEU	126	H	-10.083626	12.608097	-11.169138	-3.416583
1PBV	A	HIS	127	H	-10.012910	12.736448	-11.307589	-3.510608
1PBV	A	ALA	128	H	-10.189342	13.028301	-11.206791	-3.559497
1PBV	A	PHE	129	H	-11.054288	14.695520	-12.548488	-4.260294
1PBV	A	VAL	130	H	-11.009590	14.220375	-12.996956	-4.399218
1PBV	A	ASP	131	H	-11.055594	13.895794	-13.175548	-4.454823
1PBV	A	LEU	132	H	-11.515840	14.286586	-14.745857	-5.142563
1PBV	A	HIS	133	C	-10.310312	10.807831	-14.344772	-5.154229
1PBV	A	GLU	134	C	-8.586558	9.940399	-11.864508	-4.720926
1PBV	A	PHE	135	T	-8.526375	10.062995	-11.985838	-4.756405
1PBV	A	THR	136	T	-8.395057	10.035212	-12.212837	-4.803657
1PBV	A	ASP	137	T	-8.389183	10.063425	-12.222117	-4.803515
1PBV	A	LEU	138	T	-8.408680	10.056184	-12.154770	-4.791116
1PBV	A	ASN	139	C	-9.058670	10.789953	-13.026133	-4.969859
1PBV	A	LEU	140	H	-9.197634	10.865869	-12.904673	-4.903174
1PBV	A	VAL	141	H	-10.070738	14.029276	-12.144054	-4.594664
1PBV	A	GLN	142	H	-10.205263	14.263604	-11.813108	-4.519890
1PBV	A	ALA	143	H	-10.242065	14.336717	-11.659337	-4.508809
1PBV	A	LEU	144	H	-11.080386	15.841300	-11.216374	-4.255062
1PBV	A	ARG	145	H	-14.144509	14.228995	-17.211879	-4.909066
1PBV	A	GLN	146	H	-15.410050	14.569959	-19.677197	-5.449000
1PBV	A	PHE	147	H	-15.225469	22.175416	-15.307529	-5.439208
1PBV	A	LEU	148	H	-15.202023	22.307479	-15.260082	-5.432686
1PBV	A	TRP	149	H	-14.090539	19.977018	-14.494509	-5.177090
1PBV	A	SER	150	H	-12.095275	18.522873	-11.469201	-4.454895
1PBV	A	PHE	151	C	-9.212983	16.292642	-8.846483	-4.383811
1PBV	A	ARG	152	C	-6.849344	11.898511	-8.336863	-4.538176
1PBV	A	LEU	153	C	-5.792517	10.140529	-7.981602	-4.426350
1PBV	A	PRO	154	C	-5.266152	7.746922	-8.839111	-4.411618
1PBV	A	GLY	155	C	-5.234836	7.620259	-9.021187	-4.439270
1PBV	A	GLU	156	C	-5.235330	7.609952	-9.023479	-4.439448
1PBV	A	ALA	157	H	-5.274750	7.320351	-9.071528	-4.432393
1PBV	A	GLN	158	H	-5.527492	6.008407	-9.688729	-4.447249
1PBV	A	LYS	159	H	-6.987813	5.308395	-12.391753	-4.946016
1PBV	A	ILE	160	H	-9.857539	8.025819	-14.742798	-4.770189
1PBV	A	ASP	161	H	-11.263760	8.662098	-16.439340	-5.047856
1PBV	A	ARG	162	H	-13.607768	13.737527	-19.524658	-6.507848
1PBV	A	MET	163	H	-14.029239	17.390430	-17.666213	-6.100346
1PBV	A	MET	164	H	-12.637354	16.723201	-14.012583	-5.034171
1PBV	A	GLU	165	H	-12.174816	14.645188	-14.536866	-4.778891
1PBV	A	ALA	166	H	-12.174352	14.647219	-14.536242	-4.777171
1PBV	A	PHE	167	H	-12.178731	14.635760	-14.507563	-4.768567
1PBV	A	ALA	168	H	-12.192385	14.547371	-14.476755	-4.749804
1PBV	A	GLN	169	H	-12.529037	12.932342	-15.035769	-4.577579
1PBV	A	ARG	170	H	-15.159513	13.196844	-19.978137	-5.258426
1PBV	A	TYR	171	H	-14.539303	11.224406	-20.221273	-5.453557
1PBV	A	CYS	172	H	-11.441821	4.543964	-18.342729	-4.735758
1PBV	A	LEU	173	H	-9.779007	3.695199	-16.564809	-4.612915
1PBV	A	CYS	174	H	-9.381787	4.281761	-16.184463	-4.616509
1PBV	A	ASN	175	T	-8.983312	6.930624	-14.460409	-4.588798
1PBV	A	PRO	176	T	-7.595752	9.826042	-10.549344	-4.460886
1PBV	A	GLY	177	T	-7.575309	9.885805	-10.616071	-4.482091
1PBV	A	VAL	178	T	-7.588728	10.032941	-10.481874	-4.479554
1PBV	A	PHE	179	T	-7.601849	10.161593	-10.361500	-4.477939
1PBV	A	GLN	180	T	-7.598657	10.122372	-10.437408	-4.515461
1PBV	A	SER	181	T	-8.759879	9.780774	-13.592900	-5.227665
1PBV	A	THR	182	H	-8.934971	9.271999	-13.901371	-5.286058
1PBV	A	ASP	183	H	-8.931133	9.278884	-13.910201	-5.283882
1PBV	A	THR	184	H	-8.940880	9.231062	-13.893339	-5.280479
1PBV	A	CYS	185	H	-9.359889	9.479760	-13.919684	-5.297107
1PBV	A	TYR	186	H	-11.270229	12.566384	-15.339108	-5.306019
1PBV	A	VAL	187	H	-11.381156	13.127005	-14.666800	-4.928633
1PBV	A	LEU	188	H	-11.851320	16.213806	-13.475695	-4.608279
1PBV	A	SER	189	H	-11.684770	16.238638	-13.068146	-4.454278
1PBV	A	PHE	190	H	-10.424326	14.764734	-10.794335	-3.875570
1PBV	A	ALA	191	H	-10.106685	14.975442	-10.624232	-3.843113

1PBV	A	VAL	192	H	-10.079254	15.003145	-10.676638	-3.865197
1PBV	A	ILE	193	H	-9.720732	14.053207	-11.220368	-4.157021
1PBV	A	MET	194	H	-9.619611	13.742822	-11.526957	-4.249437
1PBV	A	LEU	195	H	-9.762129	13.530947	-11.860622	-4.391798
1PBV	A	ASN	196	H	-9.896424	13.013549	-12.457198	-4.630136
1PBV	A	THR	197	H	-9.463756	12.817625	-14.139322	-6.090806
1PBV	A	SER	198	H	-8.884419	12.309104	-15.014399	-7.282119
1PBV	A	LEU	199	H	-6.668072	9.116760	-9.839065	-4.720516
1PBV	A	HIS	200	H	-5.714420	6.978545	-10.076821	-4.643452
1PBV	A	ASN	201	T	-3.597167	3.774691	-7.069956	-3.433848
1PBV	A	PRO	202	T	-2.228039	3.013929	-5.433942	-3.112886
1PBV	A	ASN	203	T	-2.201647	3.065714	-5.529846	-3.134886
1PBV	A	VAL	204	T	-2.200177	3.073683	-5.535786	-3.135374
1PBV	A	ARG	205	T	-2.192744	3.106698	-5.564419	-3.145308
1PBV	A	ASP	206	T	-2.251640	3.035090	-5.393269	-3.105669
1PBV	A	LYS	207	T	-3.878200	4.626210	-7.586612	-3.597544
1PBV	A	PRO	208	C	-4.601127	5.963312	-8.049728	-3.879083
1PBV	A	GLY	209	C	-4.708426	5.825257	-8.052054	-3.964167
1PBV	A	LEU	210	H	-6.921528	10.687358	-12.023373	-6.199058
1PBV	A	GLU	211	H	-7.966360	9.916280	-11.299071	-4.514125
1PBV	A	ARG	212	H	-8.076644	9.652692	-10.670603	-4.094611
1PBV	A	PHE	213	H	-9.699706	13.611777	-11.254070	-4.388387
1PBV	A	VAL	214	H	-10.599929	12.978412	-12.955199	-4.182983
1PBV	A	ALA	215	H	-10.392873	10.760675	-14.231068	-4.445236
1PBV	A	MET	216	H	-10.300303	10.447562	-14.611734	-4.597524
1PBV	A	ASN	217	T	-10.524748	9.140791	-16.337007	-5.193354
1PBV	A	ARG	218	T	-9.811629	11.079834	-16.492170	-6.808518
1PBV	A	GLY	219	T	-6.428047	7.093890	-10.960735	-5.105264
1PBV	A	ILE	220	T	-5.805141	7.219328	-10.498368	-5.069823
1PBV	A	ASN	221	B	-5.407107	6.011627	-11.184747	-5.252542
1PBV	A	GLU	222	T	-5.314593	6.325142	-11.101362	-5.248331
1PBV	A	GLY	223	T	-5.261311	6.381826	-11.049168	-5.180212
1PBV	A	GLY	224	B	-5.336007	6.329795	-11.068504	-5.183238
1PBV	A	ASP	225	C	-5.534644	5.974017	-11.407601	-5.229258
1PBV	A	LEU	226	C	-6.075076	7.941211	-10.635597	-4.888503
1PBV	A	PRO	227	C	-6.493000	7.819056	-10.647229	-4.516044
1PBV	A	GLU	228	H	-7.184352	9.660767	-10.943248	-4.624865
1PBV	A	GLU	229	H	-7.629303	10.575471	-10.689340	-4.454546
1PBV	A	LEU	230	H	-8.014343	11.906142	-10.153247	-4.333598
1PBV	A	LEU	231	H	-8.490845	12.182006	-10.143541	-4.276459
1PBV	A	ARG	232	H	-10.012557	14.020063	-11.499537	-4.312743
1PBV	A	ASN	233	H	-10.480045	13.719751	-11.914254	-4.353630
1PBV	A	LEU	234	H	-12.060561	16.957225	-13.153280	-4.733425
1PBV	A	TYR	235	H	-12.785996	15.405907	-15.555149	-5.150688
1PBV	A	ASP	236	H	-10.314165	8.998187	-14.453654	-4.626908
1PBV	A	SER	237	H	-9.516514	9.396609	-13.655834	-4.687338
1PBV	A	ILE	238	H	-7.950491	9.241490	-10.801110	-4.195565
1PBV	A	ARG	239	H	-7.949035	9.264471	-10.808948	-4.202819
1PBV	A	ASN	240	H	-7.933645	9.454761	-10.849724	-4.262279
1PBV	A	GLU	241	C	-7.877167	10.181061	-10.736719	-4.391373
1PBV	A	PRO	242	C	-7.015586	14.174982	-7.459638	-4.311436
1PBV	A	PHE	243	C	-6.108614	13.837540	-5.436170	-3.630109
1PBV	A	LYS	244	C	-6.108614	13.837540	-5.436170	-3.630109
1PBV	A	ILE	245	C	-6.108614	13.837540	-5.436170	-3.630109
1PBV	A	PRO	246	C	-6.108614	13.837540	-5.436170	-3.630109
1PHT	A	ALA	3	C	-8.921571	10.746672	-12.718808	-5.593618
1PHT	A	GLU	4	E	-8.921571	10.746672	-12.718808	-5.593618
1PHT	A	GLY	5	E	-8.921571	10.746672	-12.718808	-5.593618
1PHT	A	TYR	6	E	-8.921571	10.746672	-12.718808	-5.593618
1PHT	A	GLN	7	E	-13.541649	13.174687	-18.691033	-6.473544
1PHT	A	TYR	8	E	-14.315378	16.194862	-14.814972	-4.012725
1PHT	A	ARG	9	E	-11.592190	11.306378	-12.913809	-3.529016
1PHT	A	ALA	10	E	-11.527950	11.510106	-12.992652	-3.542820
1PHT	A	LEU	11	C	-10.488347	11.734954	-12.307219	-3.910086
1PHT	A	TYR	12	C	-10.431478	11.847846	-12.583038	-4.041633
1PHT	A	ASP	13	C	-9.529234	9.357568	-12.546940	-4.092219
1PHT	A	TYR	14	B	-8.656654	8.103348	-11.331720	-3.557680
1PHT	A	LYS	15	C	-5.307446	3.636844	-8.267962	-3.082927
1PHT	A	LYS	16	T	-5.042291	3.571346	-8.710054	-3.222914
1PHT	A	GLU	17	T	-4.658266	3.970507	-9.072241	-3.669669
1PHT	A	ARG	18	T	-4.656441	3.979052	-9.075091	-3.667905
1PHT	A	GLU	19	T	-4.656898	3.976238	-9.073900	-3.668217
1PHT	A	GLU	20	T	-4.896420	4.152142	-9.478414	-3.959651
1PHT	A	ASP	21	B	-5.092829	4.425014	-9.471794	-4.151413
1PHT	A	ILE	22	C	-8.017052	6.969922	-10.295412	-3.209191
1PHT	A	ASP	23	C	-9.437062	8.583744	-12.895829	-4.004218
1PHT	A	LEU	24	B	-9.230384	8.927182	-12.149763	-3.850389
1PHT	A	HIS	25	T	-8.621486	7.866016	-11.986028	-3.846461
1PHT	A	LEU	26	T	-8.519612	8.122359	-11.996370	-3.865893
1PHT	A	GLY	27	T	-8.514896	8.151809	-12.020769	-3.884145
1PHT	A	ASP	28	E	-8.579077	8.164461	-11.957971	-3.901389

1PHT	A	ILE	29	E	-8.709437	7.952551	-12.013354	-3.915976
1PHT	A	LEU	30	E	-9.526079	9.888760	-12.298903	-4.086814
1PHT	A	THR	31	E	-10.249841	10.489734	-14.135490	-4.664653
1PHT	A	VAL	32	E	-9.951262	8.829393	-14.718958	-4.700338
1PHT	A	ASN	33	E	-9.771633	8.871142	-14.514529	-4.621501
1PHT	A	LYS	34	H	-9.594692	8.407765	-14.285871	-4.393356
1PHT	A	GLY	35	H	-8.598509	6.380841	-11.987902	-3.318877
1PHT	A	SER	36	H	-8.532728	6.508823	-11.895578	-3.239155
1PHT	A	LEU	37	H	-6.644975	7.509666	-9.293953	-3.642906
1PHT	A	VAL	38	H	-6.370710	7.146712	-9.041385	-3.374294
1PHT	A	ALA	39	H	-6.352027	7.116459	-9.093440	-3.363988
1PHT	A	LEU	40	C	-6.346180	7.110568	-9.122005	-3.375006
1PHT	A	GLY	41	T	-6.261719	6.899386	-9.478446	-3.505951
1PHT	A	PHE	42	T	-6.671646	6.250572	-9.802736	-3.361385
1PHT	A	SER	43	T	-7.235251	5.784134	-11.736701	-4.075816
1PHT	A	ASP	44	T	-7.323002	5.715038	-11.911830	-4.247646
1PHT	A	GLY	45	T	-7.416169	5.644635	-11.956963	-4.363439
1PHT	A	GLN	46	G	-9.226659	7.119916	-15.028250	-5.018290
1PHT	A	GLU	47	G	-9.728567	5.718302	-15.481563	-4.668938
1PHT	A	ALA	48	G	-9.600990	7.649302	-12.995507	-3.702996
1PHT	A	ARG	49	C	-9.712250	8.653938	-11.909857	-3.255915
1PHT	A	PRO	50	H	-8.332948	10.365920	-9.611019	-3.649108
1PHT	A	GLU	51	H	-7.785780	11.185816	-9.587964	-4.147087
1PHT	A	GLU	52	H	-7.694280	11.662346	-9.620840	-4.244178
1PHT	A	ILE	53	H	-7.704023	11.776613	-9.570792	-4.267942
1PHT	A	GLY	54	C	-7.693416	11.744722	-9.616773	-4.269513
1PHT	A	TRP	55	E	-7.910625	12.275087	-9.726149	-4.525076
1PHT	A	LEU	56	E	-8.718577	13.873573	-10.172932	-4.670536
1PHT	A	ASN	57	E	-9.696908	11.201896	-11.610617	-4.021001
1PHT	A	GLY	58	E	-9.923130	10.275183	-12.108943	-4.133527
1PHT	A	TYR	59	E	-11.579990	9.476924	-16.090372	-4.812344
1PHT	A	ASN	60	E	-8.371311	6.246277	-12.996280	-4.739224
1PHT	A	GLU	61	T	-6.361933	6.275878	-10.661960	-4.728062
1PHT	A	THR	62	T	-6.132238	6.624658	-10.771514	-4.767599
1PHT	A	THR	63	T	-6.034288	6.477654	-10.759789	-4.647458
1PHT	A	GLY	64	T	-6.033381	6.476293	-10.765264	-4.646709
1PHT	A	GLU	65	E	-6.044895	6.481074	-10.721756	-4.644891
1PHT	A	ARG	66	E	-6.539321	6.747114	-10.905344	-4.536772
1PHT	A	GLY	67	E	-7.137629	5.722866	-10.743767	-3.986988
1PHT	A	ASP	68	E	-9.391749	9.557592	-12.898443	-4.267498
1PHT	A	PHE	69	E	-9.135356	14.321910	-9.131989	-3.702194
1PHT	A	PRO	70	E	-7.105845	12.404853	-5.922218	-2.959309
1PHT	A	GLY	71	T	-7.078970	12.406488	-6.083210	-3.001837
1PHT	A	THR	72	T	-7.081900	12.418602	-6.049556	-2.994158
1PHT	A	TYR	73	T	-7.083287	12.420760	-6.038321	-2.993268
1PHT	A	VAL	74	E	-7.080662	12.350726	-6.097613	-3.004118
1PHT	A	GLU	75	E	-8.457257	12.019308	-10.056475	-3.965089
1PHT	A	TYR	76	E	-8.658813	11.883061	-11.205101	-4.543156
1PHT	A	ILE	77	E	-7.268044	8.654736	-12.339578	-5.874206
1PHT	A	GLY	78	E	-6.787322	7.170602	-12.416336	-5.673302
1PHT	A	ARG	79	E	-5.744412	6.033822	-10.084884	-4.694641
1PHT	A	LYS	80	E	-3.834319	3.968334	-6.956353	-3.580098
1PHT	A	LYS	81	E	-1.708697	2.874129	-3.365705	-2.404647
1PHT	A	ILE	82	C	-0.083679	2.915359	-1.938591	-2.396322
1PHT	A	SER	83	C	-0.083679	2.915359	-1.938591	-2.396322
1PHT	A	PRO	84	C	-0.083679	2.915359	-1.938591	-2.396322
1PHT	A	PRO	85	C	-0.083679	2.915359	-1.938591	-2.396322
1POD	A	ASN	1	C	-10.844491	7.191097	-15.655771	-4.347284
1POD	A	LEU	2	H	-10.844491	7.191097	-15.655771	-4.347284
1POD	A	VAL	3	H	-10.844491	7.191097	-15.655771	-4.347284
1POD	A	ASN	4	H	-10.844491	7.191097	-15.655771	-4.347284
1POD	A	PHE	5	H	-13.305492	17.548359	-14.765196	-5.019837
1POD	A	HIS	6	H	-13.080461	16.609168	-14.947628	-4.893718
1POD	A	ARG	7	H	-12.727427	14.997128	-15.307155	-4.745258
1POD	A	MET	8	H	-12.506636	14.924742	-15.420569	-4.876529
1POD	A	ILE	9	H	-11.924401	14.084119	-15.049105	-4.933290
1POD	A	LYS	10	H	-9.888704	9.649713	-14.379394	-5.238677
1POD	A	LEU	11	H	-9.594011	10.493212	-14.403734	-5.513711
1POD	A	THR	12	H	-8.900591	9.884804	-14.397080	-5.933921
1POD	A	THR	13	H	-8.182315	9.083210	-13.690242	-5.776569
1POD	A	GLY	14	C	-7.948583	8.498096	-13.736254	-5.597492
1POD	A	LYS	15	C	-7.928156	8.430916	-13.731365	-5.551483
1POD	A	GLU	16	C	-7.841624	8.189918	-13.613514	-5.339203
1POD	A	ALA	17	H	-7.914184	8.005488	-13.511903	-5.236748
1POD	A	ALA	18	H	-8.264184	7.414111	-13.612224	-4.854712
1POD	A	LEU	19	H	-8.745889	7.555023	-13.335204	-4.388065
1POD	A	SER	20	H	-8.936994	7.365065	-13.089068	-4.248347
1POD	A	TYR	21	H	-11.843914	12.319254	-15.643597	-4.913057
1POD	A	GLY	22	H	-11.508855	11.729460	-15.859134	-5.213446
1POD	A	PHE	23	C	-11.770116	11.721720	-15.994755	-5.345937
1POD	A	TYR	24	C	-11.776866	11.696928	-16.024834	-5.372966

```
1POD        A          GLY             25                   T -10.729054  7.470860 -17.215096 -5.504875
1POD        A          CYS             26                   T -9.766316  6.821726 -16.148354 -5.274474
1POD        A          HIS             27                   T -6.914549  5.421901 -12.308356 -4.962491
1POD        A          CYS             28                   T -4.076874  2.731928 -9.835191 -4.776473
1POD        A          GLY             29                   C -4.050719  2.753755 -9.914943 -4.768140
1POD        A          VAL             30                   C -4.042412  2.782547 -9.942759 -4.767614
1POD        A          GLY             31                   C -4.042412  2.782491 -9.942775 -4.767603
1POD        A          GLY             32                   C -4.047022  2.762067 -9.924456 -4.765995
1POD        A          ARG             33                   C -5.744878  3.629071 -11.725951 -4.610319
1POD        A          GLY             34                   C -6.570420  4.840116 -11.924428 -4.721902
1POD        A          SER             35                   C -9.202012  7.954127 -14.901786 -4.869766
1POD        A          PRO             36                   C -9.139869 10.071401 -13.863990 -5.025834
1POD        A          LYS             37                   C -9.330814 10.705316 -13.882604 -5.244343
1POD        A          ASP             38                   C -9.334396 10.706380 -13.868240 -5.245357
1POD        A          ALA             39                   H -9.425488 10.932854 -13.577524 -5.210151
1POD        A          THR             40                   H -9.700303 11.786474 -13.275773 -5.384738
1POD        A          ASP             41                   H -11.775232  9.893440 -17.643777 -5.539432
1POD        A          ARG             42                   H -11.009902  7.783770 -15.884948 -4.416800
1POD        A          CYS             43                   H -10.808246  8.142398 -15.938895 -4.570529
1POD        A          CYS             44                   H -10.774138  8.164742 -15.999873 -4.583363
1POD        A          VAL             45                   H -10.733236  8.224146 -16.088668 -4.608383
1POD        A          THR             46                   H -10.720414  8.224615 -16.171360 -4.638797
1POD        A          HIS             47                   H -11.212251  8.972835 -16.826643 -4.996668
1POD        A          ASP             48                   H -11.795289  8.892797 -17.798791 -5.085720
1POD        A          CYS             49                   H -12.118615  8.935072 -18.135684 -5.233662
1POD        A          CYS             50                   H -12.873686  8.552514 -19.936871 -5.893274
1POD        A          TYR             51                   H -15.222807 13.197549 -23.147672 -7.108989
1POD        A          LYS             52                   H -12.140998  9.397377 -17.921156 -5.571539
1POD        A          ARG             53                   H -11.030994  8.244786 -16.177676 -4.724873
1POD        A          LEU             54                   H -8.649069  7.040284 -13.671752 -4.886148
1POD        A          GLU             55                   H -6.890008  4.164626 -13.090120 -4.963822
1POD        A          LYS             56                   H -6.415632  4.123822 -13.050881 -5.007078
1POD        A          ARG             57                   H -6.233415  4.497766 -12.878626 -5.006507
1POD        A          GLY             58                   C -6.121124  5.254109 -12.650378 -5.104093
1POD        A          CYS             59                   C -5.967281  6.206624 -12.147147 -5.159797
1POD        A          GLY             60                   T -5.594805  9.084950 -9.783134 -5.075155
1POD        A          THR             61                   T -5.672465  9.919486 -9.287925 -5.080095
1POD        A          LYS             62                   T -5.736600 10.421707 -8.932153 -5.088682
1POD        A          PHE             63                   T -5.792679 10.575015 -8.671192 -5.040818
1POD        A          LEU             64                   T -5.908983 10.848659 -8.254835 -4.978648
1POD        A          SER             65                   C -8.075673 11.993334 -10.610523 -5.070162
1POD        A          TYR             66                   C -10.711452 13.287790 -14.163653 -5.394259
1POD        A          LYS             67                   C -10.906478 10.959860 -15.614395 -5.266781
1POD        A          PHE             68                   E -8.886888  8.212972 -13.295097 -4.836984
1POD        A          SER             69                   E -8.446451  6.028562 -14.054317 -4.597811
1POD        A          ASN             70                   E -7.362409  4.546909 -12.934479 -4.321911
1POD        A          SER             71                   E -7.161552  5.237523 -12.631129 -4.289492
1POD        A          GLY             72                   T -7.142902  5.305179 -12.655556 -4.295385
1POD        A          SER             73                   T -7.172601  5.161037 -12.630931 -4.268127
1POD        A          ARG             74                   E -7.204522  5.258578 -12.514087 -4.265941
1POD        A          ILE             75                   E -7.798817  7.138764 -12.208600 -4.299552
1POD        A          THR             76                   E -8.799759  8.009180 -14.400607 -4.993530
1POD        A          CYS             77                   E -8.880189  7.856394 -15.738518 -5.834559
1POD        A          ALA             78                   T -8.539242  7.225158 -15.520252 -5.769032
1POD        A          LYS             79                   T -8.555820  7.092182 -15.711498 -5.869036
1POD        A          GLN             80                   T -8.605921  6.733025 -15.867424 -5.877277
1POD        A          ASP             81                   C -8.672514  6.655817 -15.765927 -5.837475
1POD        A          SER             82                   H -8.902180  6.491905 -15.594587 -5.672853
1POD        A          CYS             83                   H -10.038103  6.185092 -17.658211 -5.865192
1POD        A          ARG             84                   H -10.840956  6.265229 -18.027471 -5.389011
1POD        A          SER             85                   H -11.594893  7.916727 -18.127617 -5.248394
1POD        A          GLN             86                   H -11.708393 10.269309 -17.657170 -5.672606
1POD        A          LEU             87                   H -11.759929 10.409545 -17.653619 -5.723227
1POD        A          CYS             88                   H -11.766757 10.320317 -17.689480 -5.728995
1POD        A          GLU             89                   H -11.712952  9.830511 -17.961482 -5.700210
1POD        A          CYS             90                   H -11.734893  9.612760 -18.028320 -5.665514
1POD        A          ASP             91                   H -12.139386  8.313094 -18.813043 -5.118550
1POD        A          LYS             92                   H -11.035809  9.287878 -15.293733 -4.453139
1POD        A          ALA             93                   H -9.926209  8.211899 -14.129688 -4.230128
1POD        A          ALA             94                   H -9.925768  8.258140 -14.104862 -4.228110
1POD        A          ALA             95                   H -9.924154  8.296244 -14.094918 -4.229921
1POD        A          THR             96                   H -9.801290  8.898283 -13.997580 -4.297608
1POD        A          CYS             97                   H -9.856521  8.893301 -13.937812 -4.302798
1POD        A          PHE             98                   H -10.648830 11.658838 -14.056019 -4.665739
1POD        A          ALA             99                   H -8.085467  7.124597 -12.218157 -4.379132
1POD        A          ARG            100                   H -7.457496  6.308025 -12.340140 -4.419252
1POD        A          ASN            101                   H -7.451786  6.335068 -12.366618 -4.432255
1POD        A          LYS            102                   G -7.424798  6.445611 -12.430277 -4.466871
1POD        A          THR            103                   G -7.330468  6.571775 -12.523443 -4.515482
1POD        A          THR            104                   G -7.469594  6.563803 -12.713068 -4.611319
1POD        A          TYR            105                   C -8.037396  8.505953 -13.192518 -5.014607
```

1POD	A	ASN	106	T	-7.937943	8.730728	-13.139825	-5.068171
1POD	A	LYS	107	T	-7.997462	8.764806	-13.068474	-5.055316
1POD	A	LYS	108	T	-8.356380	9.975383	-13.070360	-5.270093
1POD	A	TYR	109	T	-8.636700	10.855279	-12.864915	-5.389913
1POD	A	GLN	110	T	-8.903894	10.078838	-13.192031	-5.374394
1POD	A	TYR	111	T	-10.572960	12.438067	-13.963580	-5.363686
1POD	A	TYR	112	T	-10.725821	6.722493	-16.728043	-4.992130
1POD	A	SER	113	C	-9.035490	4.243292	-15.861672	-4.981648
1POD	A	ASN	114	G	-8.962083	4.313359	-16.048459	-5.019183
1POD	A	LYS	115	G	-6.958542	3.759100	-13.326657	-4.884518
1POD	A	HIS	116	G	-6.906493	3.929045	-13.484347	-4.940097
1POD	A	CYS	117	C	-6.683932	5.058799	-13.417145	-5.321620
1POD	A	ARG	118	C	-5.279309	6.700717	-9.811773	-4.973044
1POD	A	GLY	119	C	-3.040606	6.076259	-6.174833	-4.282159
1POD	A	SER	120	C	-2.704199	6.002661	-5.686493	-3.821337
1POD	A	THR	121	C	-1.781986	5.957788	-3.539311	-2.998978
1POD	A	PRO	122	C	-1.781986	5.957788	-3.539311	-2.998978
1POD	A	ARG	123	C	-1.781986	5.957788	-3.539311	-2.998978
1POD	A	CYS	124	C	-1.781986	5.957788	-3.539311	-2.998978
1QB0	A	ASP	374	C	-7.289827	4.914261	-12.889871	-4.331319
1QB0	A	HIS	375	C	-7.289827	4.914261	-12.889871	-4.331319
1QB0	A	ARG	376	C	-7.289827	4.914261	-12.889871	-4.331319
1QB0	A	GLU	377	C	-7.289827	4.914261	-12.889871	-4.331319
1QB0	A	LEU	378	B	-7.980579	6.952972	-13.010240	-4.841910
1QB0	A	ILE	379	T	-9.804965	11.094591	-14.706973	-5.622079
1QB0	A	GLY	380	T	-10.162311	11.520434	-15.248457	-5.650780
1QB0	A	ASP	381	T	-9.960053	11.720773	-14.528416	-5.390620
1QB0	A	TYR	382	T	-9.953918	11.771333	-14.525945	-5.391057
1QB0	A	SER	383	C	-10.006080	11.791508	-14.605724	-5.470057
1QB0	A	LYS	384	C	-10.058021	11.801872	-14.566054	-5.499727
1QB0	A	ALA	385	B	-10.337895	12.948178	-13.953766	-5.368045
1QB0	A	PHE	386	C	-10.478309	17.779119	-11.849290	-5.496676
1QB0	A	LEU	387	C	-8.010525	13.496374	-9.528583	-4.857005
1QB0	A	LEU	388	C	-7.143217	10.331242	-10.408434	-4.836686
1QB0	A	GLN	389	C	-5.203092	6.577051	-9.619439	-4.850930
1QB0	A	THR	390	C	-5.022709	6.901216	-9.787180	-4.979485
1QB0	A	VAL	391	B	-5.015330	6.910205	-9.822470	-4.983868
1QB0	A	ASP	392	C	-5.004206	6.849413	-9.896984	-4.989835
1QB0	A	GLY	393	T	-5.014375	6.790054	-9.899729	-4.994972
1QB0	A	LYS	394	T	-5.726684	7.629178	-10.627702	-5.328251
1QB0	A	HIS	395	T	-6.894309	6.516226	-12.936422	-5.261453
1QB0	A	GLN	396	T	-7.102844	6.022870	-13.067638	-5.231450
1QB0	A	ASP	397	T	-8.247059	5.708007	-14.961604	-5.480529
1QB0	A	LEU	398	T	-9.628215	8.806334	-15.560395	-5.677536
1QB0	A	LYS	399	C	-10.470757	10.924653	-15.595506	-5.996739
1QB0	A	TYR	400	E	-12.230211	15.328933	-15.398575	-5.481616
1QB0	A	ILE	401	E	-8.948449	12.421666	-10.545010	-4.310967
1QB0	A	SER	402	C	-8.734198	12.645587	-10.861752	-4.502782
1QB0	A	PRO	403	H	-8.651317	12.836635	-10.961165	-4.559719
1QB0	A	GLU	404	H	-8.449544	12.778512	-11.148058	-4.675663
1QB0	A	THR	405	H	-8.447006	12.801032	-11.151003	-4.677359
1QB0	A	MET	406	H	-8.775543	13.117992	-11.608939	-4.951288
1QB0	A	VAL	407	H	-8.808711	14.179963	-10.848271	-4.736406
1QB0	A	ALA	408	H	-8.151816	14.272797	-9.545405	-4.594944
1QB0	A	LEU	409	H	-6.155474	13.332718	-6.943176	-4.605850
1QB0	A	LEU	410	H	-6.019391	13.239208	-7.205952	-4.623201
1QB0	A	THR	411	H	-5.897510	12.481455	-7.648910	-4.562475
1QB0	A	GLY	412	T	-5.600535	10.808179	-8.256100	-4.485640
1QB0	A	LYS	413	T	-5.569618	10.741768	-8.302306	-4.459498
1QB0	A	PHE	414	T	-5.816699	9.410515	-9.087801	-4.363867
1QB0	A	SER	415	T	-5.900859	8.833763	-9.267208	-4.309349
1QB0	A	ASN	416	T	-6.021667	8.763588	-9.204906	-4.314035
1QB0	A	ILE	417	T	-6.989980	10.829061	-9.277530	-4.097254
1QB0	A	VAL	418	E	-7.629718	11.980084	-9.521344	-4.168312
1QB0	A	ASP	419	E	-8.271655	10.027684	-11.562662	-4.464784
1QB0	A	LYS	420	E	-9.353036	11.469510	-12.786722	-4.853224
1QB0	A	PHE	421	E	-10.515171	16.766416	-11.937695	-4.696378
1QB0	A	VAL	422	E	-10.593494	16.958078	-11.789357	-4.642497
1QB0	A	ILE	423	E	-10.832101	17.781898	-11.424440	-4.592922
1QB0	A	VAL	424	E	-11.090512	18.288533	-10.939674	-4.379778
1QB0	A	ASP	425	E	-11.769323	17.319629	-12.287163	-4.442947
1QB0	A	CYS	426	C	-12.323575	15.370497	-13.699482	-4.563493
1QB0	A	ARG	427	C	-14.983986	15.889146	-18.389840	-5.656626
1QB0	A	TYR	428	C	-16.628453	18.709242	-21.009256	-6.520039
1QB0	A	PRO	429	H	-14.996542	16.883650	-18.282977	-5.968545
1QB0	A	TYR	430	H	-14.815959	16.820418	-18.621598	-6.111429
1QB0	A	GLU	431	H	-12.249371	11.924570	-17.379252	-6.072557
1QB0	A	TYR	432	H	-11.578505	11.719273	-16.615877	-5.728434
1QB0	A	GLU	433	H	-10.312248	11.698271	-14.212401	-5.249447
1QB0	A	GLY	434	H	-10.240658	11.758581	-14.323912	-5.252899
1QB0	A	GLY	435	C	-9.854811	11.769480	-13.947215	-5.148038

1QB0	A	HIS	436	E	-9.317615	12.488701	-12.544400	-4.894189
1QB0	A	ILE	437	E	-8.438698	12.711026	-10.342249	-4.344180
1QB0	A	LYS	438	T	-8.375115	12.476543	-10.534313	-4.356765
1QB0	A	THR	439	T	-8.195582	12.524566	-10.466411	-4.318384
1QB0	A	ALA	440	T	-8.207791	12.562121	-10.386506	-4.293781
1QB0	A	VAL	441	E	-8.259145	12.559107	-10.265489	-4.248727
1QB0	A	ASN	442	E	-8.763285	12.279102	-10.997476	-4.330643
1QB0	A	LEU	443	C	-8.941933	12.827116	-10.419684	-4.219825
1QB0	A	PRO	444	C	-10.421543	14.796304	-12.060694	-4.308112
1QB0	A	LEU	445	C	-10.577069	14.494684	-12.795260	-4.620112
1QB0	A	GLU	446	H	-11.013751	12.679538	-14.678798	-5.005762
1QB0	A	ARG	447	H	-11.009937	12.310179	-14.829549	-4.968388
1QB0	A	ASP	448	H	-10.947573	12.333648	-14.890484	-4.968052
1QB0	A	ALA	449	H	-11.275763	12.149977	-15.410999	-4.976726
1QB0	A	GLU	450	H	-11.743215	13.199637	-15.559785	-4.901831
1QB0	A	SER	451	H	-10.514591	14.866524	-11.691831	-4.326718
1QB0	A	PHE	452	H	-9.599232	15.245419	-10.194644	-4.198216
1QB0	A	LEU	453	H	-8.069990	13.271758	-8.552491	-3.821396
1QB0	A	LEU	454	H	-7.177476	12.073446	-8.085354	-3.685661
1QB0	A	LYS	455	H	-6.632669	10.100262	-8.509195	-3.555306
1QB0	A	SER	456	C	-6.589706	10.188846	-8.521723	-3.533965
1QB0	A	PRO	457	C	-6.425532	10.408247	-8.372072	-3.515978
1QB0	A	ILE	458	C	-6.430370	10.226871	-8.470047	-3.520488
1QB0	A	ALA	459	C	-5.520439	6.554147	-8.780779	-3.605372
1QB0	A	PRO	460	T	-4.191078	4.920648	-7.884540	-3.735655
1QB0	A	CYS	461	T	-3.932748	4.776555	-8.302365	-3.949434
1QB0	A	SER	462	T	-3.934903	4.753153	-8.303906	-3.951208
1QB0	A	LEU	463	T	-3.935338	4.749359	-8.302385	-3.951228
1QB0	A	ASP	464	T	-3.970401	4.678554	-8.269975	-3.970242
1QB0	A	LYS	465	T	-4.548620	4.520874	-9.053569	-4.331965
1QB0	A	ARG	466	E	-9.861852	8.992215	-15.071256	-5.240015
1QB0	A	VAL	467	E	-10.913717	12.194525	-14.618628	-5.265195
1QB0	A	ILE	468	E	-12.543144	20.369512	-12.551487	-4.770709
1QB0	A	LEU	469	E	-12.677358	21.629598	-11.476410	-4.469120
1QB0	A	ILE	470	E	-12.686115	21.627854	-11.417142	-4.447136
1QB0	A	PHE	471	E	-12.731601	21.695492	-11.298613	-4.440914
1QB0	A	HIS	472	E	-13.463142	20.259645	-14.188693	-5.197901
1QB0	A	CYS	473	T	-12.828925	11.941578	-18.383764	-6.016704
1QB0	A	GLU	474	T	-12.450039	10.834722	-18.744555	-6.039928
1QB0	A	PHE	475	T	-12.367822	10.765034	-18.875965	-6.043802
1QB0	A	SER	476	T	-12.025209	9.714600	-19.101717	-6.019537
1QB0	A	SER	477	C	-11.891607	9.784469	-18.914107	-5.908540
1QB0	A	GLU	478	H	-11.961546	9.496925	-19.012773	-5.839925
1QB0	A	ARG	479	H	-12.108373	9.280089	-19.062400	-5.789315
1QB0	A	GLY	480	H	-12.065455	9.629828	-18.740104	-5.685873
1QB0	A	PRO	481	H	-12.443691	10.705724	-18.165670	-5.410062
1QB0	A	ARG	482	H	-12.889978	11.292168	-18.089531	-5.307011
1QB0	A	MET	483	H	-13.156329	12.360275	-17.406656	-5.271906
1QB0	A	CYS	484	H	-13.174931	12.363362	-17.315668	-5.261727
1QB0	A	ARG	485	H	-15.313022	15.307766	-19.840447	-5.637496
1QB0	A	PHE	486	H	-15.010781	16.761148	-18.530500	-5.646119
1QB0	A	ILE	487	H	-14.723382	15.866459	-18.760322	-5.589711
1QB0	A	ARG	488	H	-14.766409	15.669622	-18.753314	-5.557814
1QB0	A	GLU	489	H	-14.190741	12.255920	-19.527674	-5.352951
1QB0	A	ARG	490	H	-13.280400	10.392312	-18.495648	-4.911559
1QB0	A	ASP	491	H	-12.524364	9.282100	-18.375354	-5.094407
1QB0	A	ARG	492	H	-10.300037	6.660573	-16.118438	-4.865314
1QB0	A	ALA	493	H	-7.544394	7.818910	-11.630092	-4.655180
1QB0	A	VAL	494	H	-7.283560	7.838837	-11.722516	-4.620756
1QB0	A	ASN	495	C	-6.927680	7.629354	-11.624660	-4.587874
1QB0	A	ASP	496	T	-6.568379	9.223437	-10.368790	-4.502881
1QB0	A	TYR	497	T	-6.569046	9.232554	-10.359514	-4.502385
1QB0	A	PRO	498	T	-6.694581	9.563571	-10.069832	-4.466780
1QB0	A	SER	499	T	-6.778310	9.819897	-9.793569	-4.452844
1QB0	A	LEU	500	T	-7.034400	11.141792	-8.867629	-4.401414
1QB0	A	TYR	501	T	-10.889241	15.804973	-11.838282	-4.723982
1QB0	A	TYR	502	T	-13.504128	19.596428	-14.053519	-5.012885
1QB0	A	PRO	503	T	-14.328735	19.651344	-15.374577	-5.197386
1QB0	A	GLU	504	T	-15.087369	20.417928	-16.816449	-5.758196
1QB0	A	MET	505	E	-15.424811	20.737732	-17.529268	-5.934013
1QB0	A	TYR	506	E	-12.693332	18.304004	-13.636353	-5.341316
1QB0	A	ILE	507	E	-9.204974	14.194670	-11.000932	-5.133259
1QB0	A	LEU	508	E	-9.193432	14.216052	-11.059855	-5.143122
1QB0	A	LYS	509	T	-9.191113	14.217322	-11.079614	-5.146404
1QB0	A	GLY	510	T	-9.170870	14.154166	-11.214215	-5.160801
1QB0	A	GLY	511	H	-9.171388	14.150617	-11.213375	-5.161217
1QB0	A	TYR	512	H	-10.860824	13.623033	-14.800647	-5.627047
1QB0	A	LYS	513	H	-10.980973	13.671734	-14.692192	-5.499003
1QB0	A	GLU	514	H	-10.806419	14.759045	-13.742098	-5.267790
1QB0	A	PHE	515	H	-10.852680	17.812520	-11.604403	-4.792276
1QB0	A	PHE	516	H	-9.714102	13.190914	-11.531801	-4.308264

1QB0	A	PRO	517	H	-8.670090	9.880527	-12.034328	-4.389618
1QB0	A	GLN	518	H	-8.645331	9.969522	-12.091615	-4.414389
1QB0	A	HIS	519	C	-8.639313	9.967644	-12.128891	-4.426634
1QB0	A	PRO	520	G	-8.632521	9.932265	-12.195734	-4.448191
1QB0	A	ASN	521	G	-8.714702	9.554312	-12.332782	-4.491051
1QB0	A	PHE	522	G	-9.963032	12.556160	-14.026861	-5.198067
1QB0	A	CYS	523	E	-9.312098	8.449353	-14.557248	-4.999758
1QB0	A	GLU	524	E	-9.281648	8.674187	-14.467148	-4.999518
1QB0	A	PRO	525	T	-9.322857	8.400696	-14.469779	-4.964304
1QB0	A	GLN	526	T	-9.335683	8.351992	-14.443870	-4.956535
1QB0	A	ASP	527	C	-9.360493	8.176919	-14.441172	-4.946445
1QB0	A	TYR	528	C	-10.564016	13.290905	-13.578712	-5.166205
1QB0	A	ARG	529	C	-10.532279	13.002208	-13.783687	-5.229475
1QB0	A	PRO	530	T	-7.691909	9.960296	-11.421921	-5.210446
1QB0	A	MET	531	T	-7.044396	9.561488	-11.274454	-5.229352
1QB0	A	ASN	532	T	-6.435147	10.360939	-10.083692	-5.105407
1QB0	A	HIS	533	T	-6.326467	10.220566	-10.155599	-5.033261
1QB0	A	GLU	534	T	-6.269519	10.090785	-10.272888	-5.013847
1QB0	A	ALA	535	T	-6.318828	10.100993	-10.193312	-4.995265
1QB0	A	PHE	536	T	-6.447539	10.280889	-9.949501	-4.936172
1QB0	A	LYS	537	H	-7.069980	9.283429	-11.014767	-4.756124
1QB0	A	ASP	538	H	-7.546247	8.958308	-11.834588	-4.866288
1QB0	A	GLU	539	H	-8.488431	9.458573	-13.335146	-5.031743
1QB0	A	LEU	540	H	-8.816771	9.325681	-13.513392	-5.002073
1QB0	A	LYS	541	H	-8.814435	9.347916	-13.496385	-4.992291
1QB0	A	THR	542	H	-9.009218	9.424616	-13.065688	-4.791265
1QB0	A	PHE	543	H	-10.633957	13.305705	-13.457562	-4.697668
1QB0	A	ARG	544	H	-10.470250	12.136169	-14.668039	-5.208348
1QB0	A	LEU	545	H	-8.729321	8.121034	-14.447736	-5.649096
1QB0	A	LYS	546	C	-8.124180	7.906552	-13.665918	-5.289119
1QB0	A	THR	547	C	-5.794978	5.991394	-9.368785	-3.869516
1QB0	A	ARG	548	C	-5.794978	5.991394	-9.368785	-3.869516
1QB0	A	SER	549	C	-5.794978	5.991394	-9.368785	-3.869516
1QB0	A	TRP	550	C	-5.794978	5.991394	-9.368785	-3.869516
1QDD	A	GLN	1	T	-0.735342	0.313963	-8.526265	-5.388250
1QDD	A	GLU	2	T	-0.735342	0.313963	-8.526265	-5.388250
1QDD	A	ALA	3	T	-0.735342	0.313963	-8.526265	-5.388250
1QDD	A	GLN	4	T	-0.735342	0.313963	-8.526265	-5.388250
1QDD	A	THR	5	C	-0.737140	0.354914	-8.507569	-5.395080
1QDD	A	GLU	6	C	-0.773436	0.396908	-8.407930	-5.412744
1QDD	A	LEU	7	C	-0.912128	0.621841	-8.050773	-5.370036
1QDD	A	PRO	8	C	-1.551375	0.722518	-7.815632	-5.083634
1QDD	A	GLN	9	G	-3.235939	1.945052	-7.979686	-3.737452
1QDD	A	ALA	10	G	-4.366937	1.598468	-10.969651	-4.987132
1QDD	A	ARG	11	G	-7.361375	3.425012	-17.992479	-7.474652
1QDD	A	ILE	12	C	-5.968996	5.149061	-8.335237	-2.943891
1QDD	A	SER	13	C	-5.033976	4.040391	-8.860841	-3.532491
1QDD	A	CYS	14	C	-2.947705	4.995618	-5.539049	-3.721874
1QDD	A	PRO	15	T	-2.727276	5.267321	-5.282151	-3.551231
1QDD	A	GLU	16	T	-2.699297	5.310010	-5.329235	-3.544735
1QDD	A	GLY	17	T	-2.701608	5.310133	-5.319150	-3.547848
1QDD	A	THR	18	T	-2.711097	5.333590	-5.257182	-3.544068
1QDD	A	ASN	19	E	-3.342229	5.845243	-4.852462	-3.154088
1QDD	A	ALA	20	E	-4.533364	6.092344	-6.202142	-3.340529
1QDD	A	TYR	21	E	-8.818441	11.766220	-10.769234	-3.902322
1QDD	A	ARG	22	T	-8.940237	11.753894	-10.536290	-3.757139
1QDD	A	SER	23	T	-9.054302	11.748509	-10.241122	-3.634705
1QDD	A	TYR	24	E	-9.379615	12.776173	-9.284665	-3.421231
1QDD	A	CYS	25	E	-10.751369	12.543205	-11.491016	-3.819638
1QDD	A	TYR	26	E	-13.237066	14.191246	-14.502563	-4.259131
1QDD	A	TYR	27	E	-13.170808	15.784209	-14.821280	-5.230072
1QDD	A	PHE	28	E	-11.095077	12.552884	-14.197906	-5.299544
1QDD	A	ASN	29	E	-10.594137	10.418771	-14.724452	-5.028352
1QDD	A	GLU	30	E	-10.207135	9.669018	-14.194067	-4.592092
1QDD	A	ASP	31	E	-10.206244	9.673087	-14.196993	-4.591542
1QDD	A	ARG	32	E	-10.208897	9.639837	-14.196371	-4.586336
1QDD	A	GLU	33	E	-10.163420	9.477979	-14.035107	-4.415277
1QDD	A	THR	34	C	-9.303372	11.395444	-10.808713	-3.828939
1QDD	A	TRP	35	H	-9.363983	11.691884	-10.506813	-3.795198
1QDD	A	VAL	36	H	-9.251746	10.954217	-10.893925	-3.695210
1QDD	A	ASP	37	H	-9.251609	10.954097	-10.895201	-3.695371
1QDD	A	ALA	38	H	-9.287557	10.944612	-10.727052	-3.645883
1QDD	A	ASP	39	H	-10.266366	7.608453	-12.814907	-3.246285
1QDD	A	LEU	40	H	-10.257077	7.536028	-12.903905	-3.267578
1QDD	A	TYR	41	H	-11.754569	9.076096	-15.650425	-4.129910
1QDD	A	CYS	42	H	-9.621957	6.651868	-13.798502	-4.227777
1QDD	A	GLN	43	H	-7.712100	6.052854	-11.783299	-4.133592
1QDD	A	ASN	44	H	-6.259109	5.990322	-9.523594	-3.800097
1QDD	A	MET	45	T	-6.251154	6.012976	-9.548692	-3.799741
1QDD	A	ASN	46	T	-6.244975	6.048332	-9.559542	-3.798764
1QDD	A	SER	47	T	-6.246410	6.050573	-9.547480	-3.797018

```
1QDD        A          GLY              48                    T -6.296291  6.053710 -9.358793 -3.767903
1QDD        A          ASN              49                    E -8.437027  8.577065 -11.100787 -3.741149
1QDD        A          LEU              50                    E -8.888533  9.635554 -10.729112 -3.701429
1QDD        A          VAL              51                    C -10.064429 12.003119 -11.562399 -3.612586
1QDD        A          SER              52                    C -10.389478 12.909263 -11.956620 -3.870982
1QDD        A          VAL              53                    C -9.382884 10.568291 -11.372482 -3.774843
1QDD        A          LEU              54                    C -9.284673 10.126760 -11.764049 -3.827175
1QDD        A          THR              55                    C -9.112576  9.174001 -12.090102 -3.735234
1QDD        A          GLN              56                    H -9.002514  8.416564 -12.362633 -3.690060
1QDD        A          ALA              57                    H -9.010935  8.379741 -12.353137 -3.686027
1QDD        A          GLU              58                    H -9.364024  6.975474 -13.196248 -3.602320
1QDD        A          GLY              59                    H -9.412615  7.355142 -12.812287 -3.460507
1QDD        A          ALA              60                    H -9.734917  7.980700 -12.657588 -3.437806
1QDD        A          PHE              61                    H -10.537332 12.355578 -11.406906 -3.319809
1QDD        A          VAL              62                    H -10.502143 12.742952 -11.232716 -3.298689
1QDD        A          ALA              63                    H -10.328938 13.059017 -11.553023 -3.619389
1QDD        A          SER              64                    H -9.411938 11.540354 -10.410200 -3.528212
1QDD        A          LEU              65                    H -8.839027 11.809909 -9.449601 -3.341262
1QDD        A          ILE              66                    H -6.567617  7.616121 -8.033258 -3.278667
1QDD        A          LYS              67                    H -5.488503  6.125037 -8.324781 -3.716491
1QDD        A          GLU              68                    H -5.139126  5.334998 -9.126344 -3.993776
1QDD        A          SER              69                    H -5.129884  5.323791 -9.178070 -4.001272
1QDD        A          GLY              70                    C -5.106435  5.272919 -9.261586 -4.003304
1QDD        A          THR              71                    C -5.157294  5.070572 -9.379005 -4.069295
1QDD        A          ASP              72                    C -5.543793  4.365191 -10.297354 -4.315652
1QDD        A          ASP              73                    C -6.809682  4.466808 -11.600073 -4.146407
1QDD        A          PHE              74                    C -6.999980  4.310725 -11.307063 -4.036709
1QDD        A          ASN              75                    E -9.200938  7.256235 -13.314982 -4.366332
1QDD        A          VAL              76                    E -10.212151  9.868120 -12.938260 -3.995237
1QDD        A          TRP              77                    E -11.153048 18.499736 -8.949669 -3.292753
1QDD        A          ILE              78                    E -11.029979 18.003652 -9.550434 -3.473514
1QDD        A          GLY              79                    E -10.628662 15.454340 -10.701282 -3.710891
1QDD        A          LEU              80                    E -10.072755 13.345535 -10.486331 -3.448376
1QDD        A          HIS              81                    E -7.352860  8.988267 -8.383125 -3.365242
1QDD        A          ASP              82                    T -5.506864  6.923122 -7.383996 -3.451774
1QDD        A          PRO              83                    T -5.435958  6.946676 -7.632375 -3.507430
1QDD        A          LYS              84                    T -5.429233  6.928729 -7.680413 -3.510378
1QDD        A          LYS              85                    T -5.429323  6.927854 -7.680176 -3.510460
1QDD        A          ASN              86                    C -5.452593  6.846783 -7.653045 -3.516318
1QDD        A          ARG              87                    C -6.670696  6.978335 -9.800935 -3.928253
1QDD        A          ALA              88                    C -8.074219  5.492097 -11.891567 -3.769642
1QDD        A          TRP              89                    C -10.647294 11.788766 -12.217599 -3.799889
1QDD        A          HIS              90                    E -10.955048 11.847110 -13.028671 -4.060660
1QDD        A          TRP              91                    E -10.408241 11.038464 -12.957328 -4.425594
1QDD        A          SER              92                    T -7.432826  4.614960 -11.568870 -3.910351
1QDD        A          SER              93                    T -5.643379  4.879481 -9.324129 -3.801177
1QDD        A          GLY              94                    T -5.287250  4.432144 -9.170271 -3.537145
1QDD        A          SER              95                    C -5.287098  4.433250 -9.170828 -3.536999
1QDD        A          LEU              96                    C -5.272163  4.556994 -9.132229 -3.520853
1QDD        A          VAL              97                    C -5.287277  4.561063 -9.068746 -3.510551
1QDD        A          SER              98                    C -5.724022  4.199517 -8.914997 -3.199562
1QDD        A          TYR              99                    C -7.430847  9.470832 -7.791393 -2.924247
1QDD        A          LYS             100                    C -6.683780  9.582995 -7.325679 -3.110014
1QDD        A          SER             101                    C -6.246156  8.454291 -7.781644 -3.419706
1QDD        A          TRP             102                    B -4.091836  8.058854 -4.545611 -3.116853
1QDD        A          GLY             103                    T -2.173943  4.372109 -4.078512 -2.991219
1QDD        A          ILE             104                    T -2.168417  4.382397 -4.112614 -2.994804
1QDD        A          GLY             105                    T -2.168572  4.380624 -4.111966 -2.994653
1QDD        A          ALA             106                    T -2.168938  4.378223 -4.109443 -2.994105
1QDD        A          PRO             107                    T -2.184144  4.221581 -4.125832 -2.978626
1QDD        A          SER             108                    T -3.905469  3.899665 -7.665921 -3.242209
1QDD        A          SER             109                    T -3.118802  3.437577 -6.175918 -3.020673
1QDD        A          VAL             110                    T -3.115434  3.462173 -6.183268 -3.023500
1QDD        A          ASN             111                    T -3.115637  3.461430 -6.182458 -3.023888
1QDD        A          PRO             112                    T -3.157896  3.398278 -6.153420 -3.059039
1QDD        A          GLY             113                    C -3.263416  3.410111 -5.744982 -2.953967
1QDD        A          TYR             114                    C -6.128574  7.656671 -7.580394 -3.420265
1QDD        A          CYS             115                    E -8.835007  9.529039 -10.867432 -3.952177
1QDD        A          VAL             116                    E -10.720536 12.439800 -11.796178 -3.809653
1QDD        A          SER             117                    E -11.813954 11.489289 -14.410113 -3.873092
1QDD        A          LEU             118                    E -9.671537  9.853475 -12.076459 -3.981024
1QDD        A          THR             119                    E -6.740272  6.222859 -10.025936 -3.971981
1QDD        A          SER             120                    G -6.719569  6.366553 -10.011758 -3.958413
1QDD        A          SER             121                    G -6.711079  6.438378 -10.010480 -3.954950
1QDD        A          THR             122                    G -6.709548  6.454391 -10.014068 -3.956041
1QDD        A          GLY             123                    T -6.713457  6.432275 -10.000743 -3.955851
1QDD        A          PHE             124                    T -8.476214 10.808910 -9.804780 -3.657102
1QDD        A          GLN             125                    T -9.126891 11.609205 -10.181245 -3.817912
1QDD        A          LYS             126                    E -10.208036 12.647093 -11.537614 -4.358056
1QDD        A          TRP             127                    E -12.288631 16.825713 -13.042295 -4.401209
1QDD        A          LYS             128                    E -10.728278  9.854346 -13.920687 -4.283619
```

1QDD	A	ASP	129	E	-9.413142	7.997448	-12.556748	-3.779812
1QDD	A	VAL	130	E	-7.224854	6.891454	-8.845746	-2.952312
1QDD	A	PRO	131	T	-5.825457	6.956085	-7.527433	-3.241144
1QDD	A	CYS	132	T	-5.816076	7.016740	-7.558334	-3.253379
1QDD	A	GLU	133	T	-5.812403	7.045293	-7.577574	-3.261898
1QDD	A	ASP	134	T	-5.813601	7.044043	-7.567823	-3.260993
1QDD	A	LYS	135	C	-5.869527	7.061966	-7.450627	-3.293613
1QDD	A	PHE	136	E	-8.071948	11.043464	-9.875854	-4.194328
1QDD	A	SER	137	E	-8.800792	11.586567	-10.796768	-4.617486
1QDD	A	PHE	138	E	-11.907184	17.170834	-11.767287	-4.344342
1QDD	A	VAL	139	E	-12.731179	18.921764	-10.609336	-3.719039
1QDD	A	CYS	140	E	-14.419243	16.793109	-15.128024	-4.346503
1QDD	A	LYS	141	E	-12.487104	13.829001	-13.356859	-4.057985
1QDD	A	PHE	142	E	-12.487104	13.829001	-13.356859	-4.057985
1QDD	A	LYS	143	E	-12.487104	13.829001	-13.356859	-4.057985
1QDD	A	ASN	144	C	-12.487104	13.829001	-13.356859	-4.057985
1QKT	A	ASN	304	C	-5.144151	3.984058	-6.982800	-2.143034
1QKT	A	SER	305	T	-5.144151	3.984058	-6.982800	-2.143034
1QKT	A	LEU	306	T	-5.144151	3.984058	-6.982800	-2.143034
1QKT	A	ALA	307	T	-5.144151	3.984058	-6.982800	-2.143034
1QKT	A	LEU	308	T	-7.003321	5.596312	-9.066677	-2.458588
1QKT	A	SER	309	T	-7.708395	6.747161	-11.143855	-3.683172
1QKT	A	LEU	310	T	-8.445737	8.672347	-12.506236	-4.628378
1QKT	A	THR	311	C	-9.124079	8.393311	-13.756191	-4.505546
1QKT	A	ALA	312	H	-9.377600	7.546817	-13.010484	-3.382557
1QKT	A	ASP	313	H	-9.522424	6.768119	-12.906294	-3.112595
1QKT	A	GLN	314	H	-9.609912	6.881006	-12.962606	-3.256613
1QKT	A	MET	315	H	-10.304024	8.126414	-13.878998	-3.970042
1QKT	A	VAL	316	H	-11.753424	11.393808	-14.921523	-4.378640
1QKT	A	SER	317	H	-11.224384	9.691694	-14.092712	-3.818273
1QKT	A	ALA	318	H	-11.092250	9.916963	-13.756597	-3.613946
1QKT	A	LEU	319	H	-10.973347	9.927364	-13.485359	-3.398487
1QKT	A	LEU	320	H	-10.261516	9.668703	-12.233784	-3.093230
1QKT	A	ASP	321	H	-9.705240	9.145080	-12.035122	-3.177779
1QKT	A	ALA	322	H	-7.548277	10.847868	-8.346322	-3.730449
1QKT	A	GLU	323	C	-7.036793	11.030081	-7.605836	-3.332192
1QKT	A	PRO	324	C	-6.805544	11.207897	-6.692399	-2.800801
1QKT	A	PRO	325	C	-6.798919	11.224989	-6.711856	-2.803585
1QKT	A	ILE	326	C	-6.801351	11.236656	-6.690873	-2.802274
1QKT	A	LEU	327	C	-6.993130	11.368581	-6.092176	-2.441684
1QKT	A	TYR	328	C	-7.449840	11.607741	-4.958407	-1.744767
1QKT	A	SER	329	C	-9.238711	11.658575	-9.569260	-3.100290
1QKT	A	GLU	330	C	-7.268875	7.521520	-9.314672	-3.426910
1QKT	A	TYR	331	C	-6.240664	7.103948	-8.172315	-3.059748
1QKT	A	ASP	332	T	-3.900172	4.790193	-6.309070	-3.334449
1QKT	A	PRO	333	T	-3.899080	4.796900	-6.312957	-3.333241
1QKT	A	THR	334	T	-3.898643	4.798020	-6.314196	-3.331808
1QKT	A	ARG	335	T	-3.898816	4.794591	-6.310429	-3.328260
1QKT	A	PRO	336	T	-3.902622	4.781430	-6.301489	-3.329016
1QKT	A	PHE	337	T	-6.237297	7.550715	-8.497566	-2.964971
1QKT	A	SER	338	T	-6.290036	7.474958	-8.532406	-2.999385
1QKT	A	GLU	339	T	-6.315894	7.525023	-8.552810	-3.069493
1QKT	A	ALA	340	T	-6.434248	7.718679	-8.598746	-3.243673
1QKT	A	SER	341	C	-7.111266	8.943765	-9.673537	-4.123071
1QKT	A	MET	342	H	-8.934732	8.943352	-10.943563	-3.333981
1QKT	A	MET	343	H	-10.368728	10.533340	-13.077937	-3.745999
1QKT	A	GLY	344	H	-10.363818	10.369660	-13.112818	-3.711862
1QKT	A	LEU	345	H	-10.693595	11.012353	-13.172609	-3.807461
1QKT	A	LEU	346	H	-10.812544	11.116450	-12.935773	-3.711486
1QKT	A	THR	347	H	-10.461525	9.821411	-13.708545	-4.023279
1QKT	A	ASN	348	H	-10.769879	8.639014	-14.475835	-4.139744
1QKT	A	LEU	349	H	-10.877122	8.714130	-14.703117	-4.442695
1QKT	A	ALA	350	H	-10.879282	8.700024	-14.703812	-4.447279
1QKT	A	ASP	351	H	-10.895299	8.642259	-14.698297	-4.473140
1QKT	A	ARG	352	H	-13.896448	11.304161	-17.660008	-3.988206
1QKT	A	GLU	353	H	-13.662180	13.100958	-16.540727	-4.144498
1QKT	A	LEU	354	H	-13.350817	13.688729	-14.777061	-3.448643
1QKT	A	VAL	355	H	-11.925733	11.494725	-13.193066	-3.278807
1QKT	A	HIS	356	H	-11.924544	11.589807	-13.151800	-3.281966
1QKT	A	MET	357	H	-11.816570	12.553818	-13.162559	-3.565074
1QKT	A	ILE	358	H	-11.734881	13.091755	-12.990605	-3.579230
1QKT	A	ASN	359	H	-11.744524	13.064078	-13.011753	-3.597841
1QKT	A	TRP	360	H	-12.382095	16.843434	-12.893054	-4.259964
1QKT	A	ALA	361	H	-11.546564	14.761231	-11.819505	-3.565921
1QKT	A	LYS	362	H	-10.895101	12.440809	-10.071571	-2.195962
1QKT	A	ARG	363	H	-10.825747	12.780397	-10.032916	-2.231200
1QKT	A	VAL	364	T	-10.632447	13.021458	-9.681058	-2.093938
1QKT	A	PRO	365	T	-10.507992	12.751890	-9.850188	-2.118199
1QKT	A	GLY	366	T	-9.712736	12.802540	-10.293891	-3.468781
1QKT	A	PHE	367	G	-9.711935	13.116539	-10.591680	-3.799205
1QKT	A	VAL	368	G	-9.616456	12.556709	-10.662011	-3.636325

1QKT	A	ASP	369	G	-9.624535	12.424663	-10.816400	-3.707104
1QKT	A	LEU	370	C	-9.625086	12.397380	-10.937879	-3.778111
1QKT	A	THR	371	C	-10.252149	11.374774	-11.968763	-3.528770
1QKT	A	LEU	372	H	-10.405847	10.312556	-11.861095	-3.051589
1QKT	A	HIS	373	H	-10.999873	10.756197	-13.400049	-3.637880
1QKT	A	ASP	374	H	-11.283961	10.905336	-14.112238	-4.067162
1QKT	A	GLN	375	H	-11.985551	10.689624	-15.565755	-4.474508
1QKT	A	VAL	376	H	-12.689523	13.409183	-15.234183	-4.603098
1QKT	A	HIS	377	H	-13.222639	15.072274	-14.760502	-4.127785
1QKT	A	LEU	378	H	-13.133777	14.901140	-14.152319	-3.713408
1QKT	A	LEU	379	H	-13.101924	14.985922	-14.081650	-3.675236
1QKT	A	GLU	380	H	-13.045317	15.045661	-14.112700	-3.696750
1QKT	A	SER	381	H	-13.246243	14.713992	-14.642395	-3.854710
1QKT	A	ALA	382	H	-13.247297	16.447852	-13.926838	-4.006677
1QKT	A	TRP	383	H	-13.417793	17.862459	-14.212066	-4.627539
1QKT	A	LEU	384	H	-13.320006	17.636381	-14.024665	-4.486834
1QKT	A	GLU	385	H	-13.252012	18.057930	-13.740333	-4.489539
1QKT	A	ILE	386	H	-11.624803	16.470334	-11.185862	-3.995407
1QKT	A	LEU	387	H	-11.273570	16.281964	-11.695906	-4.407053
1QKT	A	MET	388	H	-11.178434	16.011437	-11.512839	-4.125859
1QKT	A	ILE	389	H	-11.148630	16.035319	-11.418180	-4.033421
1QKT	A	GLY	390	H	-11.152696	16.018234	-11.407720	-4.032416
1QKT	A	LEU	391	H	-11.479445	15.767164	-11.681431	-4.082165
1QKT	A	VAL	392	H	-12.106800	15.051935	-10.379002	-2.490877
1QKT	A	TRP	393	H	-12.842767	16.389785	-10.236389	-2.440861
1QKT	A	ARG	394	H	-14.477130	12.396154	-17.465109	-4.035738
1QKT	A	SER	395	H	-10.407851	7.975550	-13.545613	-3.811323
1QKT	A	MET	396	T	-8.061490	6.400044	-9.792358	-2.835024
1QKT	A	GLU	397	T	-6.274601	6.104935	-7.341045	-2.551440
1QKT	A	HIS	398	T	-6.259893	6.250883	-7.384990	-2.584842
1QKT	A	PRO	399	T	-6.258809	6.262012	-7.387813	-2.585076
1QKT	A	GLY	400	T	-6.259338	6.260659	-7.382273	-2.583983
1QKT	A	LYS	401	E	-6.287764	6.255326	-7.267397	-2.572574
1QKT	A	LEU	402	E	-8.412164	12.106734	-9.121060	-3.831533
1QKT	A	LEU	403	E	-9.959797	12.765502	-8.987578	-2.793641
1QKT	A	PHE	404	E	-11.596738	19.665152	-9.927988	-3.977705
1QKT	A	ALA	405	E	-10.417228	14.402298	-9.695665	-3.174985
1QKT	A	PRO	406	T	-10.309655	14.415262	-9.942863	-3.251236
1QKT	A	ASN	407	T	-10.352661	13.930159	-10.014135	-3.179832
1QKT	A	LEU	408	E	-10.359720	13.892481	-9.992508	-3.174623
1QKT	A	LEU	409	E	-10.365738	13.832283	-10.012755	-3.182543
1QKT	A	LEU	410	E	-11.327092	14.324349	-11.531538	-3.671037
1QKT	A	ASP	411	E	-11.662002	6.926859	-16.935768	-4.384150
1QKT	A	ARG	412	G	-10.651162	7.930601	-15.934259	-5.082413
1QKT	A	ASN	413	G	-9.786457	6.518391	-14.990587	-4.491991
1QKT	A	GLN	414	G	-9.727865	6.559521	-14.840317	-4.339061
1QKT	A	GLY	415	G	-7.347543	4.925383	-10.217481	-2.982541
1QKT	A	LYS	416	T	-6.394279	4.553877	-10.023533	-3.321994
1QKT	A	SER	417	T	-6.341804	4.792051	-10.151879	-3.433505
1QKT	A	VAL	418	T	-6.340600	4.806949	-10.149249	-3.432714
1QKT	A	GLU	419	T	-6.338083	4.812645	-10.154484	-3.429396
1QKT	A	GLY	420	T	-6.452461	4.816000	-10.162640	-3.532058
1QKT	A	MET	421	H	-7.721412	7.483320	-11.565076	-4.471390
1QKT	A	VAL	422	H	-8.955508	8.299312	-11.568021	-3.276063
1QKT	A	GLU	423	H	-9.216581	7.951056	-11.354548	-3.032423
1QKT	A	ILE	424	H	-9.739295	10.419267	-11.115210	-3.553134
1QKT	A	PHE	425	H	-12.360086	15.137120	-13.821086	-4.491243
1QKT	A	ASP	426	H	-12.514883	14.444768	-14.421026	-4.670257
1QKT	A	MET	427	H	-12.415645	15.482635	-14.016759	-4.921508
1QKT	A	LEU	428	H	-12.049875	14.715611	-13.575129	-4.382931
1QKT	A	LEU	429	H	-11.989034	14.068710	-13.741452	-4.208996
1QKT	A	ALA	430	H	-11.969839	13.866699	-13.879801	-4.192408
1QKT	A	THR	431	H	-11.994957	13.947967	-13.784153	-4.202847
1QKT	A	SER	432	H	-12.319240	12.569581	-13.832327	-3.571605
1QKT	A	SER	433	H	-13.169212	8.348720	-15.972148	-2.906341
1QKT	A	ARG	434	H	-13.963819	8.264606	-18.065309	-3.717603
1QKT	A	PHE	435	H	-15.428936	13.008630	-18.860666	-4.222162
1QKT	A	ARG	436	H	-14.800297	10.536700	-19.508725	-4.544014
1QKT	A	MET	437	H	-12.127173	9.821178	-17.254111	-5.692311
1QKT	A	MET	438	H	-11.754650	10.286194	-16.628277	-5.335989
1QKT	A	ASN	439	C	-10.052233	9.089873	-11.675449	-3.271286
1QKT	A	LEU	440	C	-10.036202	9.146486	-11.758235	-3.299417
1QKT	A	GLN	441	C	-10.030385	9.182760	-11.792234	-3.313590
1QKT	A	GLY	442	H	-10.007343	9.604527	-11.727946	-3.389873
1QKT	A	GLU	443	H	-10.021472	9.580787	-11.625972	-3.352561
1QKT	A	GLU	444	H	-11.359260	14.422695	-13.748441	-5.107775
1QKT	A	PHE	445	H	-11.528034	15.495493	-13.406735	-5.365146
1QKT	A	VAL	446	H	-11.598737	15.878307	-13.159922	-5.438764
1QKT	A	CYS	447	H	-13.032824	16.811578	-14.778078	-5.077533
1QKT	A	LEU	448	H	-12.934466	17.477156	-14.126695	-4.894318
1QKT	A	LYS	449	H	-12.823814	17.392617	-13.666578	-4.570375

1QKT	A	SER	450	H	-12.354558	17.876248	-11.672658	-3.729937
1QKT	A	ILE	451	H	-12.171211	17.956953	-11.366438	-3.607708
1QKT	A	ILE	452	H	-12.012911	17.756059	-11.533938	-3.814966
1QKT	A	LEU	453	H	-11.890314	16.700953	-12.120298	-3.884357
1QKT	A	LEU	454	H	-11.771425	15.510965	-12.365519	-3.699888
1QKT	A	ASN	455	H	-11.122676	10.364701	-13.954419	-3.846495
1QKT	A	SER	456	H	-10.303794	8.604472	-13.697859	-3.804124
1QKT	A	GLY	457	T	-9.826833	11.347705	-12.566312	-4.411225
1QKT	A	VAL	458	T	-9.220302	11.889240	-10.776099	-3.797089
1QKT	A	TYR	459	T	-8.938737	10.587072	-10.536024	-3.322000
1QKT	A	THR	460	T	-8.538040	8.744994	-9.986744	-2.657673
1QKT	A	PHE	461	T	-8.124318	7.832417	-10.450091	-2.946501
1QKT	A	LEU	462	C	-6.019534	3.223476	-10.284119	-3.639887
1QKT	A	SER	463	C	-5.988279	3.297695	-10.325862	-3.619865
1QKT	A	SER	464	C	-5.961545	3.355729	-10.286803	-3.559353
1QKT	A	THR	465	C	-5.960214	3.349020	-10.307790	-3.566348
1QKT	A	LEU	466	H	-5.962666	3.319823	-10.318791	-3.570548
1QKT	A	LYS	467	H	-7.234351	5.009338	-10.618424	-2.887258
1QKT	A	SER	468	H	-7.581501	4.976861	-10.291151	-2.590004
1QKT	A	LEU	469	H	-8.330870	5.378611	-12.358914	-3.419351
1QKT	A	GLU	470	H	-8.713416	5.543386	-12.574532	-3.609671
1QKT	A	GLU	471	H	-11.029014	8.893027	-17.204084	-6.030196
1QKT	A	LYS	472	H	-13.111607	10.801508	-17.412375	-4.482605
1QKT	A	ASP	473	H	-11.631503	12.405885	-12.649752	-3.448513
1QKT	A	HIS	474	H	-11.631154	12.550804	-12.517227	-3.408252
1QKT	A	ILE	475	H	-11.594692	12.718341	-12.443359	-3.346746
1QKT	A	HIS	476	H	-11.367505	12.126542	-12.667722	-3.231858
1QKT	A	ARG	477	H	-11.330247	12.108927	-12.783303	-3.279244
1QKT	A	VAL	478	H	-11.761090	11.883188	-13.357528	-3.189411
1QKT	A	LEU	479	H	-11.684459	11.785725	-13.311379	-3.134387
1QKT	A	ASP	480	H	-10.816025	9.280788	-13.249257	-3.259935
1QKT	A	LYS	481	H	-10.674133	9.801102	-13.231120	-3.488827
1QKT	A	ILE	482	H	-10.060285	12.931801	-11.875582	-4.334875
1QKT	A	THR	483	H	-9.930304	12.848809	-11.811226	-4.190993
1QKT	A	ASP	484	H	-9.927136	12.847080	-11.809970	-4.183411
1QKT	A	THR	485	H	-10.037197	13.742287	-11.514685	-4.363597
1QKT	A	LEU	486	H	-10.101622	14.020523	-11.319827	-4.411672
1QKT	A	ILE	487	H	-10.800074	12.663274	-11.737687	-3.558856
1QKT	A	HIS	488	H	-11.539231	12.230335	-13.386096	-3.577899
1QKT	A	LEU	489	H	-10.344265	9.263579	-11.143008	-2.510778
1QKT	A	MET	490	H	-8.823024	6.138740	-11.825992	-3.155675
1QKT	A	ALA	491	H	-6.451246	4.274500	-9.559396	-3.031866
1QKT	A	LYS	492	H	-6.289884	4.038840	-9.484667	-2.816902
1QKT	A	ALA	493	H	-6.117000	4.030404	-9.739062	-2.914293
1QKT	A	GLY	494	C	-6.111780	4.024038	-9.759851	-2.912551
1QKT	A	LEU	495	C	-6.115393	4.011085	-9.751056	-2.911271
1QKT	A	THR	496	C	-6.596874	3.727078	-10.052205	-2.764692
1QKT	A	LEU	497	H	-6.899355	4.024146	-10.594969	-3.189914
1QKT	A	GLN	498	H	-8.650344	4.342304	-12.513705	-2.979043
1QKT	A	GLN	499	H	-9.340127	5.710888	-13.614585	-3.618432
1QKT	A	GLN	500	H	-10.289052	6.785617	-15.667072	-4.629934
1QKT	A	HIS	501	H	-11.098612	8.140084	-16.978908	-5.636470
1QKT	A	GLN	502	H	-12.637610	9.784629	-20.304111	-7.002763
1QKT	A	ARG	503	H	-14.530863	11.789634	-18.937889	-4.776348
1QKT	A	LEU	504	H	-12.783771	12.851093	-12.434604	-2.671119
1QKT	A	ALA	505	H	-11.961229	11.115624	-13.274079	-3.028060
1QKT	A	GLN	506	H	-11.792531	11.618157	-13.359304	-3.208548
1QKT	A	LEU	507	H	-10.696152	14.811865	-10.869729	-3.899635
1QKT	A	LEU	508	H	-10.165371	12.667660	-10.733681	-3.194895
1QKT	A	LEU	509	H	-10.118287	12.395947	-10.776603	-3.089440
1QKT	A	ILE	510	H	-10.121183	12.491014	-10.712970	-3.083653
1QKT	A	LEU	511	H	-10.130017	12.481946	-10.668643	-3.073393
1QKT	A	SER	512	H	-10.360740	11.078782	-10.810496	-2.620386
1QKT	A	HIS	513	H	-11.385940	10.570613	-11.608102	-2.211817
1QKT	A	ILE	514	H	-12.180506	13.393868	-12.224151	-3.079965
1QKT	A	ARG	515	H	-13.532342	11.058281	-17.826619	-4.639586
1QKT	A	HIS	516	H	-12.502145	10.278376	-17.051146	-4.976201
1QKT	A	MET	517	H	-11.309041	11.517124	-16.048711	-6.063553
1QKT	A	SER	518	H	-10.964823	10.640761	-15.743758	-5.472588
1QKT	A	ASN	519	H	-10.075021	7.756458	-13.433659	-3.734421
1QKT	A	LYS	520	H	-10.049916	7.837359	-13.504544	-3.756082
1QKT	A	GLY	521	H	-10.043663	7.856320	-13.512471	-3.754002
1QKT	A	MET	522	H	-10.081269	7.527456	-13.362741	-3.542346
1QKT	A	GLU	523	H	-10.092360	7.381310	-13.358417	-3.474754
1QKT	A	HIS	524	H	-10.450301	8.057953	-15.484336	-4.514502
1QKT	A	LEU	525	H	-8.395444	6.029327	-13.095620	-4.437596
1QKT	A	TYR	526	H	-7.810894	5.529293	-13.083269	-4.431160
1QKT	A	SER	527	H	-6.802709	5.396119	-11.379636	-4.211616
1QKT	A	MET	528	H	-5.524913	5.000281	-8.697430	-3.366945
1QKT	A	LYS	529	C	-4.320895	1.870575	-6.300767	-1.748093
1QKT	A	SER	530	T	-3.455583	1.998876	-5.761280	-1.965629

1QKT	A	LYS	531	T	-3.320632	2.148222	-5.988870	-2.084363
1QKT	A	ASN	532	T	-3.319409	2.153449	-5.981356	-2.077249
1QKT	A	VAL	533	T	-3.332302	2.091659	-5.928402	-2.050978
1QKT	A	VAL	534	C	-3.438975	2.225989	-5.919553	-2.156455
1QKT	A	PRO	535	C	-4.253262	2.773550	-6.856132	-2.519227
1QKT	A	LEU	536	H	-6.540926	5.054865	-6.909295	-1.549185
1QKT	A	TYR	537	H	-9.820967	9.652122	-11.183876	-2.705270
1QKT	A	ASP	538	H	-9.795120	10.946129	-11.000735	-3.053141
1QKT	A	LEU	539	H	-9.739357	16.309401	-10.718338	-5.142481
1QKT	A	LEU	540	H	-9.299623	17.759764	-10.511658	-6.101886
1QKT	A	LEU	541	H	-7.497760	13.862030	-9.271389	-5.956541
1QKT	A	GLU	542	H	-6.176370	11.113695	-8.176195	-5.238930
1QKT	A	MET	543	H	-5.569252	10.527535	-7.280589	-4.673171
1QKT	A	LEU	544	H	-3.821428	6.242132	-4.933124	-3.155667
1QKT	A	ASP	545	C	-1.945978	1.842274	-3.713663	-2.229670
1QKT	A	ALA	546	C	-1.201060	0.935525	-2.941052	-1.607262
1QKT	A	HIS	547	C	0.412747	0.669300	-1.176982	-1.694408
1QKT	A	ARG	548	C	1.010464	2.192467	-1.693306	-2.717993
1QKT	A	LEU	549	C	1.010464	2.192467	-1.693306	-2.717993
1QKT	A	HIS	550	C	1.010464	2.192467	-1.693306	-2.717993
1QKT	A	ALA	551	C	1.010464	2.192467	-1.693306	-2.717993
1QUU	A	GLY	1	C	-5.465931	2.874654	-10.871034	-3.990394
1QUU	A	SER	2	C	-5.465931	2.874654	-10.871034	-3.990394
1QUU	A	SER	3	C	-5.465931	2.874654	-10.871034	-3.990394
1QUU	A	ASN	4	H	-5.465931	2.874654	-10.871034	-3.990394
1QUU	A	GLU	5	H	-7.174833	3.529363	-15.052288	-5.397625
1QUU	A	ILE	6	H	-7.623163	3.779542	-15.580663	-5.699678
1QUU	A	ARG	7	H	-8.671454	4.637437	-17.048164	-6.162692
1QUU	A	ARG	8	H	-9.922880	6.281297	-19.471641	-7.084397
1QUU	A	LEU	9	H	-10.327936	6.671444	-20.145998	-7.499346
1QUU	A	GLU	10	H	-10.818485	7.259181	-20.578518	-7.841502
1QUU	A	ARG	11	H	-12.584261	10.248856	-19.764090	-5.979754
1QUU	A	LEU	12	H	-12.620765	11.728398	-17.616861	-4.935028
1QUU	A	GLU	13	H	-11.210017	9.718305	-15.972592	-4.942077
1QUU	A	HIS	14	H	-8.526925	10.365499	-11.607821	-4.689473
1QUU	A	LEU	15	H	-8.520921	10.430131	-11.612705	-4.693444
1QUU	A	ALA	16	H	-8.520678	10.431679	-11.614214	-4.693584
1QUU	A	GLU	17	H	-8.520345	10.432726	-11.617110	-4.694108
1QUU	A	LYS	18	H	-8.526121	10.442264	-11.575990	-4.691848
1QUU	A	PHE	19	H	-11.143019	16.153286	-12.832751	-5.112503
1QUU	A	ARG	20	H	-12.299979	12.994034	-16.769133	-5.314495
1QUU	A	GLN	21	H	-10.370062	8.355276	-15.357225	-4.889131
1QUU	A	LYS	22	H	-10.362457	8.384546	-15.376445	-4.896618
1QUU	A	ALA	23	H	-10.355756	8.389469	-15.405519	-4.896896
1QUU	A	SER	24	H	-10.169500	8.327433	-15.596256	-4.901521
1QUU	A	THR	25	H	-10.150361	8.463082	-15.605933	-4.918421
1QUU	A	HIS	26	H	-10.802550	8.989761	-16.227779	-5.017482
1QUU	A	GLU	27	H	-10.637142	9.535537	-15.869710	-4.988998
1QUU	A	THR	28	H	-8.928538	10.140024	-12.416683	-4.705592
1QUU	A	TRP	29	H	-8.928567	10.306714	-12.346974	-4.719716
1QUU	A	ALA	30	H	-8.919710	10.310293	-12.405201	-4.737659
1QUU	A	TYR	31	T	-8.900617	10.291126	-12.533345	-4.772959
1QUU	A	GLY	32	T	-8.876108	10.189063	-12.694687	-4.810498
1QUU	A	LYS	33	H	-10.060376	10.297068	-15.750519	-5.588415
1QUU	A	GLU	34	H	-10.130945	9.673330	-16.093396	-5.559252
1QUU	A	GLN	35	H	-9.556033	9.806165	-14.126485	-4.856308
1QUU	A	ILE	36	H	-9.102156	10.630859	-12.934994	-4.711877
1QUU	A	LEU	37	H	-8.892546	10.489278	-13.003205	-4.820865
1QUU	A	LEU	38	H	-8.871448	10.525357	-13.071945	-4.846050
1QUU	A	GLN	39	C	-8.865168	10.529714	-13.112133	-4.868669
1QUU	A	LYS	40	T	-8.994602	10.688468	-13.135474	-4.963747
1QUU	A	ASP	41	T	-9.377765	10.230336	-13.979656	-5.227400
1QUU	A	TYR	42	T	-10.327657	11.541610	-15.384153	-5.545289
1QUU	A	GLU	43	T	-10.190764	10.873075	-14.758549	-4.995225
1QUU	A	SER	44	T	-8.482253	8.799564	-11.510917	-3.929206
1QUU	A	ALA	45	T	-7.716360	8.376284	-11.196720	-4.027384
1QUU	A	SER	46	C	-7.168395	9.332767	-10.207021	-4.030419
1QUU	A	LEU	47	H	-7.163093	9.346334	-10.230603	-4.034727
1QUU	A	THR	48	H	-7.151232	9.321884	-10.286019	-4.038714
1QUU	A	GLU	49	H	-7.214114	9.392093	-10.165552	-4.055506
1QUU	A	VAL	50	H	-7.435378	9.920872	-9.746827	-4.049707
1QUU	A	ARG	51	H	-9.180901	9.156619	-13.122439	-4.347742
1QUU	A	ALA	52	H	-9.278735	8.694591	-13.222125	-4.232395
1QUU	A	LEU	53	H	-10.322174	10.175912	-13.594356	-4.039378
1QUU	A	LEU	54	H	-10.327780	10.051342	-13.697607	-4.073209
1QUU	A	ARG	55	H	-9.756987	8.309627	-14.482947	-4.371912
1QUU	A	LYS	56	H	-9.752355	8.339368	-14.501223	-4.382941
1QUU	A	HIS	57	H	-9.977855	7.642880	-15.054420	-4.591421
1QUU	A	GLU	58	H	-9.985687	7.565393	-15.067940	-4.593740
1QUU	A	ALA	59	H	-10.020799	7.391632	-15.037636	-4.577468
1QUU	A	PHE	60	H	-12.098155	11.431405	-17.296223	-5.292486

1QUU	A	GLU	61	H	-11.323365	8.631847	-16.366024	-4.603164
1QUU	A	SER	62	H	-9.995724	7.226909	-14.554686	-4.032206
1QUU	A	ASP	63	H	-9.776465	8.002442	-14.424024	-4.185729
1QUU	A	LEU	64	H	-9.765440	8.047837	-14.452063	-4.198108
1QUU	A	ALA	65	H	-9.683487	7.917824	-14.758030	-4.309312
1QUU	A	ALA	66	H	-9.713255	7.896095	-14.702511	-4.301804
1QUU	A	HIS	67	H	-10.192416	8.935416	-15.157652	-4.721882
1QUU	A	GLN	68	H	-10.753482	7.546543	-16.923811	-5.037412
1QUU	A	ASP	69	H	-10.637246	7.579487	-16.899213	-5.053780
1QUU	A	ARG	70	H	-11.235703	8.671301	-17.034668	-5.045950
1QUU	A	VAL	71	H	-11.231933	8.882673	-16.896561	-5.022576
1QUU	A	GLU	72	H	-10.895920	8.884767	-16.647137	-4.992908
1QUU	A	GLN	73	H	-10.763236	9.615963	-16.092625	-4.911117
1QUU	A	ILE	74	H	-10.587628	11.521143	-14.066174	-4.358160
1QUU	A	ALA	75	H	-10.110361	10.181771	-13.950980	-4.187290
1QUU	A	ALA	76	H	-9.987149	10.135886	-14.071745	-4.253518
1QUU	A	ILE	77	H	-10.035855	10.331913	-13.848026	-4.190470
1QUU	A	ALA	78	H	-10.079932	10.241057	-13.781525	-4.155436
1QUU	A	GLN	79	H	-10.123769	9.551451	-14.471870	-4.391620
1QUU	A	GLU	80	H	-10.567369	10.189626	-15.368746	-4.880787
1QUU	A	LEU	81	H	-9.612372	9.271779	-14.095198	-4.891287
1QUU	A	ASN	82	H	-9.505752	9.541228	-14.187039	-4.970002
1QUU	A	GLU	83	H	-9.091099	10.068947	-13.668821	-5.012508
1QUU	A	LEU	84	H	-8.952089	10.171391	-13.636818	-5.038530
1QUU	A	ASP	85	C	-8.711085	9.896768	-13.554045	-4.991406
1QUU	A	TYR	86	C	-8.615752	9.706337	-13.416396	-4.912379
1QUU	A	HIS	87	C	-6.175907	4.665342	-11.104014	-4.296244
1QUU	A	ASP	88	H	-6.045243	5.075619	-11.016986	-4.253258
1QUU	A	ALA	89	H	-6.041062	5.084291	-11.030720	-4.251734
1QUU	A	VAL	90	H	-5.984493	5.166320	-11.116700	-4.268283
1QUU	A	ASN	91	H	-5.986661	5.152661	-11.109002	-4.266861
1QUU	A	VAL	92	H	-6.730828	6.575487	-11.211441	-4.216774
1QUU	A	ASN	93	H	-7.334227	6.187737	-12.116204	-4.435599
1QUU	A	ASP	94	H	-7.381873	6.109688	-12.032787	-4.451117
1QUU	A	ARG	95	H	-11.363235	8.957019	-17.506887	-5.366385
1QUU	A	CYS	96	H	-11.265398	9.107709	-17.051779	-5.228692
1QUU	A	GLN	97	H	-10.579363	8.563224	-16.202999	-5.025925
1QUU	A	LYS	98	H	-10.586342	8.597646	-16.148571	-5.013716
1QUU	A	ILE	99	H	-10.604130	8.632443	-16.041658	-4.994519
1QUU	A	CYS	100	H	-10.605287	8.628439	-16.036171	-4.993677
1QUU	A	ASP	101	H	-10.779998	8.385197	-15.932016	-4.956329
1QUU	A	GLN	102	H	-13.100149	10.021257	-19.315785	-5.632861
1QUU	A	TRP	103	H	-12.915541	12.191771	-17.160793	-5.103859
1QUU	A	ASP	104	H	-9.521633	8.636608	-13.596080	-4.554264
1QUU	A	ARG	105	H	-9.337209	9.444713	-13.368616	-4.553150
1QUU	A	LEU	106	H	-9.103528	10.825769	-12.822479	-4.669348
1QUU	A	GLY	107	H	-8.905540	10.380025	-13.219333	-4.813463
1QUU	A	THR	108	H	-8.865903	10.366986	-13.312719	-4.832340
1QUU	A	LEU	109	H	-9.102776	11.223301	-13.179298	-4.969930
1QUU	A	THR	110	H	-9.220512	11.127996	-13.273298	-5.061998
1QUU	A	GLN	111	H	-9.520330	9.445868	-14.313499	-5.162289
1QUU	A	LYS	112	H	-10.479305	10.211084	-14.693173	-5.104078
1QUU	A	ARG	113	H	-15.212277	12.981560	-21.028488	-6.008234
1QUU	A	ARG	114	H	-14.143502	12.317478	-19.049568	-5.575466
1QUU	A	GLU	115	H	-11.202279	11.575582	-14.586449	-4.829027
1QUU	A	ALA	116	H	-11.047271	12.357320	-14.419372	-4.861858
1QUU	A	LEU	117	H	-11.025551	12.493708	-14.455140	-4.887714
1QUU	A	GLU	118	H	-10.603011	12.021268	-14.732261	-5.136185
1QUU	A	ARG	119	H	-10.503585	12.121219	-14.729445	-5.121122
1QUU	A	MET	120	H	-10.701914	12.437315	-14.825572	-5.253481
1QUU	A	GLU	121	H	-10.771041	12.067917	-15.014959	-5.296317
1QUU	A	LYS	122	H	-10.428798	12.018103	-14.519918	-5.094340
1QUU	A	LEU	123	H	-10.627123	12.581058	-14.167948	-4.904948
1QUU	A	LEU	124	H	-10.732347	12.593554	-14.091973	-4.881466
1QUU	A	GLU	125	H	-10.655617	12.210180	-14.384950	-4.909028
1QUU	A	THR	126	H	-10.481384	12.296673	-14.277029	-4.881581
1QUU	A	ILE	127	H	-10.879181	12.525914	-14.633182	-4.905557
1QUU	A	ASP	128	H	-11.006890	12.029410	-14.888957	-4.936071
1QUU	A	GLN	129	H	-10.839045	11.873441	-14.922158	-4.939636
1QUU	A	LEU	130	H	-10.970989	12.258765	-14.572783	-4.889064
1QUU	A	HIS	131	H	-11.525080	11.864181	-15.298764	-4.987304
1QUU	A	LEU	132	H	-10.557897	13.083838	-13.320001	-4.820771
1QUU	A	GLU	133	H	-10.550079	13.109755	-13.342557	-4.826484
1QUU	A	PHE	134	H	-10.662807	13.420790	-12.969691	-4.794072
1QUU	A	ALA	135	H	-10.273173	11.623703	-13.574545	-4.560247
1QUU	A	LYS	136	H	-9.874827	9.736638	-14.051595	-4.375364
1QUU	A	ARG	137	H	-10.041669	8.555263	-14.465519	-4.240957
1QUU	A	ALA	138	H	-10.022522	8.687297	-14.450937	-4.245214
1QUU	A	ALA	139	H	-9.818699	9.340947	-14.273693	-4.373829
1QUU	A	PRO	140	H	-9.949753	9.439743	-14.272987	-4.416529
1QUU	A	PHE	141	H	-10.428358	11.547641	-13.932612	-4.713254

1QUU	A	ASN	142	H	-10.441442	11.496777	-13.925769	-4.721517
1QUU	A	ASN	143	H	-10.063286	11.470156	-14.212146	-5.154431
1QUU	A	TRP	144	H	-10.196151	12.282811	-14.326027	-5.460500
1QUU	A	MET	145	H	-10.059683	11.914330	-14.558738	-5.489229
1QUU	A	GLU	146	H	-9.457517	9.668759	-14.703158	-5.288829
1QUU	A	GLY	147	H	-8.804116	8.258347	-14.205164	-5.019979
1QUU	A	ALA	148	H	-8.823730	8.164663	-14.178462	-4.982410
1QUU	A	MET	149	H	-8.789218	8.315691	-14.168198	-4.998427
1QUU	A	GLU	150	H	-8.344781	8.137715	-13.663171	-4.903451
1QUU	A	ASP	151	G	-8.070143	8.022738	-13.326539	-4.839170
1QUU	A	LEU	152	G	-8.047115	9.144210	-12.791272	-4.897236
1QUU	A	GLN	153	G	-6.271148	8.013010	-9.955914	-4.586611
1QUU	A	ASP	154	C	-5.213090	9.087160	-7.809351	-4.276851
1QUU	A	MET	155	C	-4.122635	9.061075	-6.155306	-4.057177
1QUU	A	PHE	156	C	-4.121638	9.064528	-6.160962	-4.057862
1QUU	A	ILE	157	C	-4.118482	9.050124	-6.185878	-4.057107
1QUU	A	VAL	158	C	-4.131954	9.073331	-6.107449	-4.044820
1QUU	A	HIS	159	C	-4.212104	8.999917	-5.966225	-4.022804
1QUU	A	SER	160	T	-6.475842	6.642339	-11.537852	-4.391890
1QUU	A	ILE	161	T	-6.516102	6.381960	-11.687988	-4.406717
1QUU	A	GLU	162	T	-6.725261	6.365814	-12.087984	-4.623322
1QUU	A	GLU	163	H	-6.870819	6.086605	-12.202229	-4.669523
1QUU	A	ILE	164	H	-7.841430	10.080546	-12.036854	-4.956396
1QUU	A	GLN	165	H	-7.966192	10.107203	-11.956812	-4.918502
1QUU	A	SER	166	H	-8.250820	9.311188	-12.164346	-4.350701
1QUU	A	LEU	167	H	-8.560400	8.963234	-11.906703	-3.895031
1QUU	A	ILE	168	H	-8.490270	8.946902	-12.099145	-3.970937
1QUU	A	THR	169	H	-8.383053	8.594575	-12.495076	-4.097783
1QUU	A	ALA	170	H	-8.473082	8.520171	-12.471098	-4.102808
1QUU	A	HIS	171	H	-9.074915	8.296129	-14.100586	-4.664377
1QUU	A	GLU	172	H	-8.822771	9.297361	-13.463632	-4.743673
1QUU	A	GLN	173	H	-8.400853	11.503554	-11.655382	-4.770684
1QUU	A	PHE	174	H	-8.411363	12.874721	-10.895755	-4.739487
1QUU	A	LYS	175	H	-7.647589	10.602798	-10.430403	-4.286007
1QUU	A	ALA	176	H	-6.739503	8.266588	-9.713510	-3.769526
1QUU	A	THR	177	H	-6.640758	8.455380	-9.680677	-3.752167
1QUU	A	LEU	178	H	-6.646762	8.341413	-9.694912	-3.726653
1QUU	A	PRO	179	H	-6.512371	7.756601	-10.216157	-3.860510
1QUU	A	GLU	180	H	-6.573699	7.514698	-10.256166	-3.843310
1QUU	A	ALA	181	H	-7.106038	7.354517	-11.331541	-4.157119
1QUU	A	ASP	182	H	-7.369146	6.096504	-12.257844	-4.396755
1QUU	A	GLY	183	H	-7.414099	5.815613	-12.308006	-4.423489
1QUU	A	GLU	184	H	-9.332174	7.086595	-15.059176	-5.240852
1QUU	A	ARG	185	H	-12.711551	8.847632	-20.296963	-5.951582
1QUU	A	GLN	186	H	-11.455460	9.568552	-16.529006	-5.042244
1QUU	A	SER	187	H	-11.187902	10.548466	-15.802538	-4.924978
1QUU	A	ILE	188	H	-11.187397	10.661380	-15.734105	-4.916995
1QUU	A	MET	189	H	-11.136003	10.559981	-15.950053	-4.965294
1QUU	A	ALA	190	H	-10.892073	9.901509	-16.282844	-5.032112
1QUU	A	ILE	191	H	-11.104306	10.129746	-16.421621	-5.093288
1QUU	A	GLN	192	H	-10.987968	9.577213	-16.894303	-5.380268
1QUU	A	ASN	193	H	-9.718610	8.867776	-14.758136	-5.082840
1QUU	A	GLU	194	H	-9.162304	10.377372	-13.300553	-4.913123
1QUU	A	VAL	195	H	-9.131380	10.595480	-13.214516	-4.895658
1QUU	A	GLU	196	H	-9.050318	10.681248	-13.250937	-4.891639
1QUU	A	LYS	197	H	-8.970050	10.575521	-13.207768	-4.787337
1QUU	A	VAL	198	H	-9.137939	11.185718	-12.793636	-4.702911
1QUU	A	ILE	199	H	-9.661103	10.972881	-13.371667	-4.556045
1QUU	A	GLN	200	H	-9.707565	10.327757	-13.741476	-4.576494
1QUU	A	SER	201	H	-8.437519	7.737498	-12.373805	-4.159621
1QUU	A	TYR	202	H	-7.417181	8.831150	-10.357151	-3.962196
1QUU	A	ASN	203	T	-5.886758	5.478411	-9.303653	-3.401036
1QUU	A	ILE	204	T	-5.831443	5.546168	-9.408978	-3.403652
1QUU	A	ARG	205	T	-5.819420	5.549298	-9.459215	-3.404986
1QUU	A	ILE	206	T	-5.825833	5.527004	-9.430097	-3.397134
1QUU	A	SER	207	C	-5.859245	5.315522	-9.408567	-3.367632
1QUU	A	SER	208	C	-7.125588	6.162080	-10.859661	-3.467572
1QUU	A	SER	209	C	-7.967958	6.409862	-12.370988	-3.783848
1QUU	A	ASN	210	T	-7.606857	9.404361	-11.317838	-4.713971
1QUU	A	PRO	211	T	-7.209899	9.704599	-10.614076	-4.446113
1QUU	A	TYR	212	T	-7.182214	9.815987	-10.604077	-4.449825
1QUU	A	SER	213	T	-7.128673	9.828313	-10.710215	-4.480007
1QUU	A	THR	214	T	-7.002927	9.636188	-10.852260	-4.535940
1QUU	A	VAL	215	T	-7.210625	9.677950	-10.881131	-4.473645
1QUU	A	THR	216	T	-7.557823	9.602166	-11.837248	-4.818900
1QUU	A	MET	217	H	-7.632738	9.489357	-11.872856	-4.863891
1QUU	A	ASP	218	H	-7.765177	9.395303	-11.877883	-4.882559
1QUU	A	GLU	219	H	-8.688363	11.099574	-12.807972	-5.249124
1QUU	A	LEU	220	H	-8.908635	11.887379	-12.377792	-5.305747
1QUU	A	ARG	221	H	-10.145684	11.367992	-14.302143	-5.274738
1QUU	A	THR	222	H	-10.212790	11.158458	-14.277358	-5.231808

1QUU	A	LYS	223	H	-11.768726	13.202708	-16.661730	-5.972387
1QUU	A	TRP	224	H	-10.573290	13.678579	-13.273595	-5.109458
1QUU	A	ASP	225	H	-8.830338	10.059289	-12.243435	-4.657886
1QUU	A	LYS	226	H	-8.670736	10.753428	-12.036133	-4.650464
1QUU	A	VAL	227	H	-8.627392	11.034672	-11.936592	-4.617889
1QUU	A	LYS	228	H	-8.449974	11.155125	-11.788569	-4.530224
1QUU	A	GLN	229	H	-8.283529	10.757986	-11.689549	-4.348391
1QUU	A	LEU	230	H	-8.562224	11.303889	-11.395937	-4.176998
1QUU	A	VAL	231	H	-8.691729	10.886974	-11.404970	-4.066259
1QUU	A	PRO	232	H	-8.741786	10.546815	-11.460716	-4.049481
1QUU	A	ILE	233	H	-9.068039	9.845785	-11.532124	-3.880798
1QUU	A	ARG	234	H	-11.914606	11.217787	-16.058290	-4.491215
1QUU	A	ASP	235	H	-12.051196	10.030220	-17.452582	-4.897527
1QUU	A	GLN	236	H	-10.492257	10.105087	-14.587525	-4.817494
1QUU	A	SER	237	H	-10.475353	10.235076	-14.600745	-4.845057
1QUU	A	LEU	238	H	-10.444927	10.395682	-14.686141	-4.895288
1QUU	A	GLN	239	H	-9.635002	9.024577	-14.669306	-5.030456
1QUU	A	GLU	240	H	-9.386005	9.310867	-14.969541	-5.276373
1QUU	A	GLU	241	H	-8.801131	10.486407	-14.933526	-6.518096
1QUU	A	LEU	242	H	-7.579978	8.407646	-13.339150	-5.919778
1QUU	A	ALA	243	H	-6.712161	7.119585	-12.232966	-5.310211
1QUU	A	ARG	244	H	-6.075678	6.653367	-11.150469	-4.798252
1QUU	A	GLN	245	H	-5.379146	6.325115	-9.868039	-4.348108
1QUU	A	HIS	246	H	-5.379146	6.325115	-9.868039	-4.348108
1QUU	A	ALA	247	C	-5.379146	6.325115	-9.868039	-4.348108
1QUU	A	ASN	248	C	-5.379146	6.325115	-9.868039	-4.348108
1RBP	A	GLU	1	C	-3.795231	2.529654	-8.549897	-3.792688
1RBP	A	ARG	2	C	-3.795231	2.529654	-8.549897	-3.792688
1RBP	A	ASP	3	C	-3.795231	2.529654	-8.549897	-3.792688
1RBP	A	CYS	4	C	-3.795231	2.529654	-8.549897	-3.792688
1RBP	A	ARG	5	C	-5.694797	4.903843	-10.952826	-4.766194
1RBP	A	VAL	6	G	-7.870646	8.238193	-13.024129	-5.508473
1RBP	A	SER	7	G	-9.803745	9.282788	-16.096928	-5.864030
1RBP	A	SER	8	G	-10.296714	9.798458	-16.077730	-5.650767
1RBP	A	PHE	9	C	-10.858680	11.340984	-13.956335	-4.098172
1RBP	A	ARG	10	C	-8.678799	8.828245	-12.268554	-4.392300
1RBP	A	VAL	11	C	-8.654539	9.051069	-12.281220	-4.428913
1RBP	A	LYS	12	T	-8.654813	9.067104	-12.309997	-4.458626
1RBP	A	GLU	13	T	-8.651263	9.086427	-12.332239	-4.467329
1RBP	A	ASN	14	T	-8.618800	9.310147	-12.366896	-4.508941
1RBP	A	PHE	15	T	-9.863784	13.349840	-13.443928	-5.308986
1RBP	A	ASP	16	T	-10.102741	12.953905	-13.812972	-5.362920
1RBP	A	LYS	17	T	-10.235604	13.199090	-13.456811	-5.282002
1RBP	A	ALA	18	T	-10.272453	13.233479	-13.284541	-5.210735
1RBP	A	ARG	19	T	-11.576094	12.852200	-15.355055	-5.034884
1RBP	A	PHE	20	T	-12.109354	12.603929	-15.949710	-4.949863
1RBP	A	SER	21	T	-12.247426	12.117718	-16.056544	-4.897697
1RBP	A	GLY	22	E	-12.172880	12.738531	-15.855930	-4.930618
1RBP	A	THR	23	E	-13.068687	16.344124	-15.880899	-5.319566
1RBP	A	TRP	24	E	-13.143297	17.103018	-15.424239	-5.307766
1RBP	A	TYR	25	E	-13.172215	17.188428	-15.307744	-5.277518
1RBP	A	ALA	26	E	-13.225399	17.250463	-15.182859	-5.254019
1RBP	A	MET	27	E	-14.149703	17.334477	-17.594271	-5.679795
1RBP	A	ALA	28	E	-13.023822	14.083280	-16.760949	-5.435020
1RBP	A	LYS	29	E	-12.553909	12.574518	-17.372109	-5.574139
1RBP	A	LYS	30	E	-9.244179	7.767155	-14.527883	-5.208524
1RBP	A	ASP	31	C	-7.885300	7.584731	-12.412076	-4.680983
1RBP	A	PRO	32	C	-7.636980	9.074360	-11.713377	-4.674668
1RBP	A	GLU	33	C	-7.439597	10.405457	-11.052725	-4.697185
1RBP	A	GLY	34	C	-7.438631	10.414013	-11.055748	-4.698239
1RBP	A	LEU	35	C	-7.467340	10.546347	-10.883895	-4.672973
1RBP	A	PHE	36	C	-7.815182	12.928223	-9.852897	-4.713852
1RBP	A	LEU	37	C	-8.183025	13.782349	-9.406763	-4.758003
1RBP	A	GLN	38	C	-11.202868	15.420881	-13.226881	-5.366990
1RBP	A	ASP	39	E	-13.154150	14.182546	-16.556205	-5.109244
1RBP	A	ASN	40	E	-12.549193	13.491062	-15.972877	-4.921492
1RBP	A	ILE	41	E	-12.338624	14.815274	-15.089017	-4.771608
1RBP	A	VAL	42	E	-12.261802	14.809358	-15.094304	-4.726744
1RBP	A	ALA	43	E	-12.158524	14.849032	-15.028633	-4.684154
1RBP	A	GLU	44	E	-12.095610	14.573348	-15.142792	-4.716346
1RBP	A	PHE	45	E	-10.038588	11.946569	-12.782006	-4.702688
1RBP	A	SER	46	E	-5.669763	5.291970	-9.865474	-4.176174
1RBP	A	VAL	47	E	-3.240189	3.617807	-7.783900	-4.243810
1RBP	A	ASP	48	T	-3.216196	3.576298	-7.926577	-4.263909
1RBP	A	GLU	49	T	-3.216086	3.576995	-7.927688	-4.264137
1RBP	A	THR	50	T	-3.216091	3.576923	-7.927656	-4.264135
1RBP	A	GLY	51	T	-3.225665	3.548555	-7.895012	-4.264976
1RBP	A	GLN	52	C	-5.130186	2.564018	-11.325730	-4.718139
1RBP	A	MET	53	E	-8.306061	7.336460	-13.890250	-5.459162
1RBP	A	SER	54	E	-10.843957	9.677986	-16.564818	-5.422762
1RBP	A	ALA	55	E	-10.666317	10.695708	-14.568254	-4.577874

1RBP	A	THR	56	E	-10.683187	10.647922	-14.412572	-4.492548
1RBP	A	ALA	57	E	-10.685714	10.639665	-14.391400	-4.484797
1RBP	A	LYS	58	E	-10.729650	10.482657	-14.344617	-4.475792
1RBP	A	GLY	59	E	-10.803487	10.405076	-14.215813	-4.479234
1RBP	A	ARG	60	E	-13.761520	12.642416	-19.334617	-5.643850
1RBP	A	VAL	61	E	-10.328967	10.770340	-13.327815	-4.407616
1RBP	A	ARG	62	E	-7.411925	7.619272	-11.350399	-4.491064
1RBP	A	LEU	63	E	-5.705067	7.350834	-9.375476	-4.473346
1RBP	A	LEU	64	T	-5.626514	7.195915	-9.699045	-4.533626
1RBP	A	ASN	65	T	-5.625290	7.198096	-9.708019	-4.534600
1RBP	A	ASN	66	T	-5.625423	7.197093	-9.707581	-4.534748
1RBP	A	TRP	67	E	-5.654896	7.177102	-9.624987	-4.536941
1RBP	A	ASP	68	E	-6.849678	6.156247	-12.027691	-4.958103
1RBP	A	VAL	69	E	-9.096377	8.777710	-14.162021	-4.939733
1RBP	A	CYS	70	E	-9.826974	10.259642	-14.463077	-4.768952
1RBP	A	ALA	71	E	-9.884278	10.619966	-14.139131	-4.666548
1RBP	A	ASP	72	E	-9.955254	10.916805	-14.073150	-4.713248
1RBP	A	MET	73	E	-10.426457	12.597355	-14.024962	-4.804215
1RBP	A	VAL	74	E	-10.175746	13.306307	-13.092661	-4.780775
1RBP	A	GLY	75	E	-9.484057	12.225537	-12.894713	-5.034185
1RBP	A	THR	76	E	-9.248592	12.146047	-12.864457	-5.062111
1RBP	A	PHE	77	E	-8.014813	10.499333	-11.419860	-4.857020
1RBP	A	THR	78	E	-6.494976	6.917085	-11.229393	-4.891377
1RBP	A	ASP	79	E	-6.381160	6.744627	-11.427452	-4.849885
1RBP	A	THR	80	T	-6.207881	6.963448	-11.151938	-4.677370
1RBP	A	GLU	81	T	-6.206395	6.966275	-11.155266	-4.675705
1RBP	A	ASP	82	T	-6.231526	6.822974	-11.152098	-4.669042
1RBP	A	PRO	83	T	-6.762369	7.118384	-11.062564	-4.342439
1RBP	A	ALA	84	T	-7.003682	7.693072	-10.409180	-4.185710
1RBP	A	LYS	85	E	-9.394674	9.900613	-12.672023	-4.501337
1RBP	A	PHE	86	E	-12.726749	15.891144	-14.700160	-4.933353
1RBP	A	LYS	87	E	-14.063150	17.530920	-16.786648	-5.649881
1RBP	A	MET	88	E	-13.681188	15.595027	-17.057020	-5.745163
1RBP	A	LYS	89	E	-11.310999	14.045443	-13.779621	-5.099448
1RBP	A	TYR	90	E	-10.017954	14.868278	-11.620162	-4.884282
1RBP	A	TRP	91	E	-6.873014	10.301262	-8.554633	-3.986920
1RBP	A	GLY	92	E	-5.483103	8.605516	-7.617581	-3.766017
1RBP	A	VAL	93	T	-5.371450	8.987243	-7.516538	-3.719114
1RBP	A	ALA	94	T	-5.371144	8.987989	-7.519004	-3.719340
1RBP	A	SER	95	T	-5.369708	8.993982	-7.526901	-3.720964
1RBP	A	PHE	96	T	-5.417912	8.885983	-7.443553	-3.699357
1RBP	A	LEU	97	T	-6.400499	10.843537	-7.143948	-3.519641
1RBP	A	GLN	98	C	-8.579235	11.416677	-11.861986	-4.629072
1RBP	A	LYS	99	C	-8.626717	11.303504	-12.060323	-4.751733
1RBP	A	GLY	100	E	-9.290997	10.055139	-14.581233	-5.384196
1RBP	A	ASN	101	E	-9.620469	8.640624	-15.944355	-5.675963
1RBP	A	ASP	102	E	-10.135260	7.326650	-17.277254	-5.891154
1RBP	A	ASP	103	E	-10.360954	7.483262	-17.073604	-5.927505
1RBP	A	HIS	104	E	-12.811356	9.911445	-19.688816	-6.398147
1RBP	A	TRP	105	E	-13.738177	19.533777	-15.083400	-5.511981
1RBP	A	ILE	106	E	-12.225949	14.246757	-15.112908	-5.173926
1RBP	A	VAL	107	E	-12.212448	14.257097	-15.184367	-5.188690
1RBP	A	ASP	108	E	-12.196872	14.136498	-15.347849	-5.227582
1RBP	A	THR	109	E	-10.877575	12.363997	-15.308855	-5.854612
1RBP	A	ASP	110	T	-10.832298	12.580516	-15.317401	-5.868052
1RBP	A	TYR	111	T	-10.884105	12.489146	-15.337189	-5.936103
1RBP	A	ASP	112	T	-10.791353	13.113375	-14.961491	-5.782141
1RBP	A	THR	113	T	-10.792972	13.118895	-14.945938	-5.779991
1RBP	A	TYR	114	E	-11.673484	16.420482	-13.719542	-5.265992
1RBP	A	ALA	115	E	-11.908952	16.810117	-12.921993	-4.911392
1RBP	A	VAL	116	E	-11.924721	16.774553	-12.845713	-4.890431
1RBP	A	GLN	117	E	-15.152706	18.210100	-17.777559	-5.570783
1RBP	A	TYR	118	E	-15.110058	15.254266	-19.781014	-5.976939
1RBP	A	SER	119	E	-11.987082	9.964438	-16.912424	-5.200221
1RBP	A	CYS	120	E	-11.483831	9.745376	-16.950617	-5.220874
1RBP	A	ARG	121	E	-10.187429	7.972351	-15.441795	-4.751636
1RBP	A	LEU	122	E	-6.667965	4.911296	-11.370394	-4.138294
1RBP	A	LEU	123	E	-5.291750	4.414182	-10.454996	-4.459484
1RBP	A	ASN	124	T	-4.502236	4.546618	-9.876970	-4.656484
1RBP	A	LEU	125	T	-4.442009	4.617210	-9.998981	-4.688434
1RBP	A	ASP	126	T	-4.440848	4.622362	-10.005436	-4.689517
1RBP	A	GLY	127	T	-4.454627	4.616676	-9.974994	-4.703260
1RBP	A	THR	128	C	-4.601627	4.688027	-9.865845	-4.761039
1RBP	A	CYS	129	E	-5.812840	5.323542	-11.193853	-4.993637
1RBP	A	ALA	130	E	-8.033021	7.432563	-13.850329	-5.458893
1RBP	A	ASP	131	E	-9.212928	8.538727	-17.091912	-6.959499
1RBP	A	SER	132	E	-10.536987	9.023813	-16.795236	-5.965500
1RBP	A	TYR	133	E	-12.944074	12.856266	-17.894555	-5.939375
1RBP	A	SER	134	E	-13.876941	16.041443	-17.389016	-5.717728
1RBP	A	PHE	135	E	-14.483576	19.993832	-15.182977	-5.229829
1RBP	A	VAL	136	E	-14.466228	19.865049	-15.266835	-5.205422

1RBP	A	PHE	137	E	-14.378355	18.996023	-15.785175	-5.193033
1RBP	A	SER	138	E	-10.895041	7.721747	-16.178977	-4.823012
1RBP	A	ARG	139	T	-7.548303	6.572603	-12.507356	-4.859878
1RBP	A	ASP	140	T	-5.192524	8.558905	-8.356253	-4.754659
1RBP	A	PRO	141	T	-5.007850	9.063788	-8.157310	-4.663280
1RBP	A	ASN	142	T	-4.980723	9.064760	-8.233338	-4.657751
1RBP	A	GLY	143	T	-4.952859	9.054441	-8.299230	-4.644419
1RBP	A	LEU	144	C	-4.945815	9.113962	-8.259819	-4.623842
1RBP	A	PRO	145	C	-5.550821	10.018402	-8.285283	-4.379373
1RBP	A	PRO	146	H	-6.159127	8.987123	-9.800903	-4.298303
1RBP	A	GLU	147	H	-6.389585	8.939502	-9.802367	-4.185231
1RBP	A	ALA	148	H	-6.822375	9.057925	-9.953801	-3.991416
1RBP	A	GLN	149	H	-7.326652	7.460849	-11.493335	-4.112300
1RBP	A	LYS	150	H	-7.636932	7.056680	-11.747406	-4.158739
1RBP	A	ILE	151	H	-9.240323	9.108935	-13.704794	-4.659206
1RBP	A	VAL	152	H	-10.346690	11.257866	-13.879886	-4.642094
1RBP	A	ARG	153	H	-11.804121	9.471209	-16.680660	-4.587609
1RBP	A	GLN	154	H	-11.993317	9.318945	-16.489182	-4.538731
1RBP	A	ARG	155	H	-14.425194	12.266862	-20.182369	-5.489321
1RBP	A	GLN	156	H	-14.628678	12.301443	-21.325023	-6.101091
1RBP	A	GLU	157	H	-13.077033	11.574142	-18.318770	-5.691485
1RBP	A	GLU	158	H	-12.592906	12.260112	-17.365543	-5.433742
1RBP	A	LEU	159	H	-12.102157	12.475142	-16.409018	-5.156998
1RBP	A	CYS	160	C	-10.562107	9.109358	-15.791010	-5.188640
1RBP	A	LEU	161	T	-10.484979	9.771100	-15.641732	-5.233224
1RBP	A	ALA	162	T	-10.299345	9.942096	-15.365641	-5.065728
1RBP	A	ARG	163	T	-9.850968	9.841055	-14.502146	-4.757710
1RBP	A	GLN	164	T	-9.477557	11.226989	-13.168110	-4.600529
1RBP	A	TYR	165	C	-7.463563	12.083140	-8.254408	-3.808214
1RBP	A	ARG	166	E	-6.597730	10.034190	-8.118846	-3.486728
1RBP	A	LEU	167	E	-6.596068	10.046360	-8.141976	-3.501680
1RBP	A	ILE	168	C	-6.594116	10.060017	-8.169542	-3.520885
1RBP	A	VAL	169	C	-6.569281	9.991184	-8.448978	-3.655274
1RBP	A	HIS	170	C	-6.533413	9.222773	-9.592776	-4.240049
1RBP	A	ASN	171	C	-5.712102	6.642314	-10.517545	-5.007181
1RBP	A	GLY	172	C	-5.712102	6.642314	-10.517545	-5.007181
1RBP	A	TYR	173	C	-5.712102	6.642314	-10.517545	-5.007181
1RBP	A	CYS	174	C	-5.712102	6.642314	-10.517545	-5.007181
1RLW	A	SER	16	C	-11.820510	10.489817	-15.267158	-4.328905
1RLW	A	SER	17	C	-11.820510	10.489817	-15.267158	-4.328905
1RLW	A	HIS	18	E	-11.820510	10.489817	-15.267158	-4.328905
1RLW	A	LYS	19	E	-11.820510	10.489817	-15.267158	-4.328905
1RLW	A	PHE	20	E	-11.104378	16.546145	-10.928907	-4.164686
1RLW	A	THR	21	E	-10.256642	14.482203	-11.258984	-4.106365
1RLW	A	VAL	22	E	-10.228868	14.513944	-11.315823	-4.096041
1RLW	A	VAL	23	E	-10.175636	14.490237	-11.419816	-4.081338
1RLW	A	VAL	24	E	-10.117894	14.435453	-11.552838	-4.088804
1RLW	A	LEU	25	E	-10.174186	13.739213	-11.984815	-4.127123
1RLW	A	ARG	26	E	-10.484859	13.073944	-13.202993	-4.277145
1RLW	A	ALA	27	E	-9.846762	12.934547	-12.449150	-4.521706
1RLW	A	THR	28	E	-9.783897	13.054113	-12.637835	-4.697321
1RLW	A	LYS	29	T	-8.899225	12.191666	-12.324448	-5.238719
1RLW	A	VAL	30	T	-8.187217	10.478474	-12.173763	-5.047697
1RLW	A	THR	31	C	-7.487354	9.036952	-12.172232	-5.154298
1RLW	A	LYS	32	C	-6.382164	6.478936	-11.886930	-5.183728
1RLW	A	GLY	33	C	-6.278653	6.254549	-12.063213	-5.120173
1RLW	A	ALA	34	H	-6.234061	6.166623	-12.100142	-5.059665
1RLW	A	PHE	35	H	-6.196202	6.015746	-12.146195	-5.003975
1RLW	A	GLY	36	H	-6.241914	5.811321	-12.161920	-4.988580
1RLW	A	ASP	37	H	-6.852500	5.506440	-12.878247	-4.615071
1RLW	A	MET	38	H	-7.084038	6.379575	-12.573130	-4.478937
1RLW	A	LEU	39	H	-7.326651	6.713313	-12.601099	-4.519577
1RLW	A	ASP	40	C	-7.842807	8.494381	-12.549281	-4.703724
1RLW	A	THR	41	C	-7.887051	8.693805	-12.287081	-4.662003
1RLW	A	PRO	42	C	-8.197458	9.728189	-11.362537	-4.438448
1RLW	A	ASP	43	C	-10.197480	10.341673	-13.814728	-4.690934
1RLW	A	PRO	44	E	-12.319018	13.830650	-15.346982	-4.660051
1RLW	A	TYR	45	E	-12.895742	17.910195	-14.385549	-4.968806
1RLW	A	VAL	46	E	-12.475226	18.229428	-13.710389	-5.091084
1RLW	A	GLU	47	E	-12.413929	17.987221	-13.987771	-5.179963
1RLW	A	LEU	48	E	-11.263734	15.429351	-13.340836	-5.051705
1RLW	A	PHE	49	E	-9.900872	13.647767	-12.624279	-5.282590
1RLW	A	ILE	50	E	-6.723314	9.421679	-9.463933	-4.481750
1RLW	A	SER	51	T	-4.976789	5.637257	-9.196009	-4.371866
1RLW	A	THR	52	T	-4.903856	5.623127	-9.412406	-4.408502
1RLW	A	THR	53	T	-4.884563	5.656860	-9.467202	-4.409835
1RLW	A	PRO	54	T	-4.873690	5.688755	-9.499731	-4.412902
1RLW	A	ASP	55	T	-4.900255	5.518440	-9.502090	-4.409846
1RLW	A	SER	56	T	-5.959859	5.968504	-11.096585	-4.627830
1RLW	A	ARG	57	C	-6.650181	6.973661	-11.176125	-4.498738
1RLW	A	LYS	58	E	-7.240412	7.481072	-11.274827	-4.585284

1RLW	A	ARG	59	E	-10.655952	11.380344	-14.797330	-5.119523
1RLW	A	THR	60	C	-10.145596	10.679237	-14.101780	-4.986348
1RLW	A	ARG	61	C	-9.064876	9.686483	-13.203203	-4.880605
1RLW	A	HIS	62	C	-8.980053	9.723567	-13.408937	-4.948063
1RLW	A	PHE	63	T	-8.919187	9.742797	-13.514429	-4.968336
1RLW	A	ASN	64	T	-8.275353	8.305972	-13.624744	-5.141892
1RLW	A	ASN	65	T	-8.127504	8.549791	-13.309570	-5.015273
1RLW	A	ASP	66	T	-7.875465	8.688978	-12.375155	-4.615263
1RLW	A	ILE	67	T	-7.877094	8.766738	-12.305770	-4.596094
1RLW	A	ASN	68	T	-7.825643	9.193896	-12.139532	-4.605853
1RLW	A	PRO	69	T	-8.023834	10.043513	-11.459165	-4.337695
1RLW	A	VAL	70	E	-7.711733	11.336650	-10.726319	-4.653172
1RLW	A	TRP	71	E	-7.951438	12.636611	-10.489096	-4.957466
1RLW	A	ASN	72	E	-7.895060	12.613349	-10.685464	-5.044861
1RLW	A	GLU	73	E	-7.960237	12.572793	-10.659177	-5.084361
1RLW	A	THR	74	E	-7.866581	13.325422	-10.392396	-5.136150
1RLW	A	PHE	75	E	-8.566325	15.548574	-10.582604	-5.458747
1RLW	A	GLU	76	E	-8.599603	15.461263	-10.569644	-5.460074
1RLW	A	PHE	77	E	-8.860632	16.976965	-9.553808	-5.340475
1RLW	A	ILE	78	E	-8.499732	13.055027	-10.964276	-4.911156
1RLW	A	LEU	79	E	-8.309444	8.996026	-12.514864	-4.684830
1RLW	A	ASP	80	T	-7.062603	6.140375	-12.334220	-4.776681
1RLW	A	PRO	81	T	-7.032095	6.206332	-12.424441	-4.802228
1RLW	A	ASN	82	T	-7.018816	6.232592	-12.480620	-4.815787
1RLW	A	GLN	83	T	-7.041924	6.133564	-12.477391	-4.830580
1RLW	A	GLU	84	C	-7.087855	5.905763	-12.483421	-4.834294
1RLW	A	ASN	85	C	-8.557936	7.665599	-14.395723	-5.324572
1RLW	A	VAL	86	E	-9.133332	8.758892	-14.488300	-5.297205
1RLW	A	LEU	87	E	-10.005904	14.134278	-12.616992	-4.874945
1RLW	A	GLU	88	E	-10.061836	14.763828	-12.225403	-4.834369
1RLW	A	ILE	89	E	-10.166705	15.414766	-11.739536	-4.762512
1RLW	A	THR	90	E	-10.171028	15.424030	-11.729063	-4.766931
1RLW	A	LEU	91	E	-10.987750	16.977893	-12.647513	-5.131143
1RLW	A	MET	92	E	-11.209839	14.491851	-15.492233	-5.912569
1RLW	A	ASP	93	E	-8.244083	4.794744	-14.009363	-4.581552
1RLW	A	ALA	94	C	-4.760718	2.839004	-9.728367	-3.968131
1RLW	A	ASN	95	T	-3.905569	2.452607	-9.585335	-4.234261
1RLW	A	TYR	96	T	-3.870842	2.539749	-9.657324	-4.249204
1RLW	A	VAL	97	T	-3.857040	2.590216	-9.695339	-4.258083
1RLW	A	MET	98	T	-3.857375	2.589155	-9.692917	-4.257920
1RLW	A	ASP	99	C	-4.002745	2.519691	-9.680268	-4.336214
1RLW	A	GLU	100	E	-5.355479	4.281917	-10.972320	-4.535714
1RLW	A	THR	101	E	-5.934582	5.956950	-10.941003	-4.625271
1RLW	A	LEU	102	E	-6.524397	10.291387	-9.576071	-4.557546
1RLW	A	GLY	103	E	-6.341597	10.763142	-9.318344	-4.550972
1RLW	A	THR	104	E	-6.066302	11.702329	-8.570085	-4.527441
1RLW	A	ALA	105	E	-6.087283	11.883752	-8.400742	-4.491341
1RLW	A	THR	106	E	-6.246265	12.490975	-8.103022	-4.480086
1RLW	A	PHE	107	E	-6.398455	12.974177	-7.809698	-4.495684
1RLW	A	THR	108	E	-6.589945	13.286266	-7.567090	-4.482644
1RLW	A	VAL	109	G	-7.913378	13.004834	-10.088012	-4.442328
1RLW	A	SER	110	G	-8.034893	10.921897	-11.545365	-4.563386
1RLW	A	SER	111	G	-7.562742	8.640558	-12.069827	-4.782131
1RLW	A	MET	112	C	-6.422012	7.851410	-10.672521	-4.776886
1RLW	A	LYS	113	T	-4.361096	6.783792	-8.187761	-4.686189
1RLW	A	VAL	114	T	-4.335692	6.858566	-8.271575	-4.709071
1RLW	A	GLY	115	T	-4.311009	6.920202	-8.382883	-4.753927
1RLW	A	GLU	116	E	-4.310138	6.934760	-8.383235	-4.756561
1RLW	A	LYS	117	E	-4.303154	7.042575	-8.343826	-4.756171
1RLW	A	LYS	118	E	-5.555852	9.163187	-10.035118	-5.281506
1RLW	A	GLU	119	E	-5.722928	9.974268	-9.587947	-5.152966
1RLW	A	VAL	120	E	-6.072562	11.282476	-8.440541	-4.637136
1RLW	A	PRO	121	E	-6.124552	11.301837	-8.225520	-4.565279
1RLW	A	PHE	122	E	-6.965025	14.062089	-6.915179	-3.947082
1RLW	A	ILE	123	E	-4.746148	9.602866	-6.339596	-4.043108
1RLW	A	PHE	124	E	-4.736383	9.564899	-6.421625	-4.068174
1RLW	A	ASN	125	T	-4.732264	9.555063	-6.459684	-4.074572
1RLW	A	GLN	126	T	-4.732220	9.554877	-6.460450	-4.074754
1RLW	A	VAL	127	T	-4.732986	9.549238	-6.456641	-4.074388
1RLW	A	THR	128	E	-6.576011	10.667167	-9.212170	-4.688117
1RLW	A	GLU	129	E	-7.649167	8.451501	-11.865155	-4.969320
1RLW	A	MET	130	E	-9.838122	12.198968	-13.227059	-5.289467
1RLW	A	VAL	131	E	-11.556363	15.478481	-14.642418	-5.375146
1RLW	A	LEU	132	E	-12.010267	16.992754	-14.676454	-5.497231
1RLW	A	GLU	133	E	-12.145265	16.889064	-14.970366	-5.589094
1RLW	A	MET	134	E	-12.193929	16.619590	-15.308961	-5.730612
1RLW	A	SER	135	E	-10.791627	11.293533	-15.777511	-5.936885
1RLW	A	LEU	136	E	-7.996550	9.796975	-11.385038	-4.844956
1RLW	A	GLU	137	E	-5.037520	5.473424	-8.686064	-3.947028
1RLW	A	VAL	138	C	-3.247664	3.462827	-6.135006	-2.822289
1RLW	A	ALA	139	C	-3.247664	3.462827	-6.135006	-2.822289

1RLW	A	SER	140	C	-3.247664	3.462827	-6.135006	-2.822289
1RLW	A	SER	141	C	-3.247664	3.462827	-6.135006	-2.822289
1SRA	A	PRO	136	C	-5.048911	2.699035	-9.675283	-3.480006
1SRA	A	PRO	137	C	-5.048911	2.699035	-9.675283	-3.480006
1SRA	A	CYS	138	C	-5.048911	2.699035	-9.675283	-3.480006
1SRA	A	LEU	139	C	-5.048911	2.699035	-9.675283	-3.480006
1SRA	A	ASP	140	H	-7.072139	2.803491	-13.970520	-4.642403
1SRA	A	SER	141	H	-8.276452	3.937671	-15.976595	-5.313512
1SRA	A	GLU	142	H	-9.159542	6.482107	-16.262735	-5.610929
1SRA	A	LEU	143	H	-9.508699	8.005239	-14.678689	-4.952209
1SRA	A	THR	144	H	-9.504717	8.084307	-14.639062	-4.939555
1SRA	A	GLU	145	H	-10.989014	11.608064	-15.264073	-5.137051
1SRA	A	PHE	146	H	-11.833906	15.750451	-13.900116	-4.876995
1SRA	A	PRO	147	H	-11.874184	15.733746	-13.731148	-4.815419
1SRA	A	LEU	148	H	-12.192481	15.526673	-13.667678	-4.758804
1SRA	A	ARG	149	H	-15.571860	18.972578	-17.360893	-5.226845
1SRA	A	MET	150	H	-16.285563	20.172305	-17.725346	-5.365879
1SRA	A	ARG	151	H	-17.294061	19.689721	-19.728895	-5.631384
1SRA	A	ASP	152	H	-17.185170	18.700193	-20.771883	-6.196382
1SRA	A	TRP	153	H	-15.801724	16.962943	-19.126273	-5.778458
1SRA	A	LEU	154	H	-15.145478	17.028646	-18.284566	-5.573723
1SRA	A	LYS	155	H	-14.354185	15.471688	-17.829861	-5.364715
1SRA	A	ASN	156	H	-11.490354	12.408329	-13.968787	-4.399807
1SRA	A	VAL	157	H	-10.736820	13.753386	-12.324311	-4.101519
1SRA	A	LEU	158	H	-10.732829	13.794252	-12.331843	-4.107010
1SRA	A	VAL	159	H	-10.635650	14.107871	-12.489855	-4.262096
1SRA	A	THR	160	H	-9.820523	14.223966	-11.756949	-4.650060
1SRA	A	LEU	161	H	-9.808132	14.421455	-11.765752	-4.724008
1SRA	A	TYR	162	H	-9.734197	13.817139	-12.454992	-5.028972
1SRA	A	GLU	163	H	-6.951377	6.058422	-12.051533	-4.852843
1SRA	A	ARG	164	H	-6.864900	6.083241	-12.268509	-4.883785
1SRA	A	ASP	165	T	-6.448275	4.792303	-12.983991	-5.059642
1SRA	A	GLU	166	T	-4.818798	5.182834	-9.955188	-4.858523
1SRA	A	ASP	167	T	-4.813610	5.219821	-9.967581	-4.860565
1SRA	A	ASN	168	T	-4.829417	5.201164	-9.911989	-4.860951
1SRA	A	ASN	169	T	-4.829888	5.210979	-9.903061	-4.860064
1SRA	A	LEU	170	T	-4.847613	5.284782	-9.780227	-4.847420
1SRA	A	LEU	171	T	-7.247474	9.559238	-11.636907	-5.006352
1SRA	A	THR	172	C	-7.695518	9.686759	-11.947651	-4.911810
1SRA	A	GLU	173	H	-7.737696	9.671220	-11.839926	-4.889564
1SRA	A	LYS	174	H	-8.132157	10.093172	-11.696427	-4.895712
1SRA	A	GLN	175	H	-9.859240	8.896120	-15.550115	-5.368199
1SRA	A	LYS	176	H	-10.533166	8.484766	-16.775320	-5.664046
1SRA	A	LEU	177	H	-11.175357	10.067151	-16.598586	-5.410830
1SRA	A	ARG	178	H	-11.497279	12.303515	-15.148712	-4.918386
1SRA	A	VAL	179	H	-11.214768	12.911290	-14.865971	-4.984972
1SRA	A	LYS	180	H	-10.834724	12.030778	-15.235718	-5.178738
1SRA	A	LYS	181	H	-10.526272	11.502640	-15.523816	-5.398484
1SRA	A	ILE	182	H	-9.571769	10.016520	-14.662920	-5.523488
1SRA	A	HIS	183	H	-7.729778	5.505302	-14.193791	-5.424594
1SRA	A	GLU	184	H	-7.694814	5.562839	-14.292638	-5.439649
1SRA	A	ASN	185	T	-7.691246	5.579900	-14.303390	-5.440843
1SRA	A	GLU	186	T	-7.691974	5.567384	-14.304593	-5.439732
1SRA	A	LYS	187	T	-7.712633	5.420295	-14.299938	-5.436364
1SRA	A	ARG	188	T	-9.235457	7.091380	-15.983291	-5.625302
1SRA	A	LEU	189	C	-7.253227	5.157164	-12.962026	-4.891300
1SRA	A	GLU	190	C	-5.289249	4.834593	-10.625606	-4.849999
1SRA	A	ALA	191	C	-4.631218	5.104833	-9.680079	-4.569331
1SRA	A	GLY	192	C	-4.596896	5.216503	-9.712890	-4.569309
1SRA	A	ASP	193	C	-4.594057	5.230878	-9.720219	-4.568296
1SRA	A	HIS	194	C	-4.600122	5.236338	-9.685735	-4.564343
1SRA	A	PRO	195	C	-4.809964	5.440915	-9.316646	-4.439300
1SRA	A	VAL	196	H	-6.212705	7.444146	-10.320370	-4.524489
1SRA	A	GLU	197	H	-7.376196	9.653651	-10.723311	-4.274306
1SRA	A	LEU	198	H	-7.818074	11.241744	-10.122890	-4.181288
1SRA	A	LEU	199	H	-7.970052	11.711932	-9.685403	-4.161197
1SRA	A	ALA	200	H	-9.487796	12.848589	-11.431604	-4.408291
1SRA	A	ARG	201	H	-10.970281	11.788926	-14.514816	-4.641689
1SRA	A	ASP	202	H	-11.749326	10.804812	-16.792754	-5.160514
1SRA	A	PHE	203	H	-11.782038	10.724859	-16.835348	-5.207661
1SRA	A	GLU	204	H	-11.240304	10.527341	-17.096490	-5.757287
1SRA	A	LYS	205	H	-11.225394	10.677027	-17.160031	-5.857211
1SRA	A	ASN	206	H	-11.429682	10.776853	-17.454545	-6.172606
1SRA	A	TYR	207	G	-11.457241	10.820520	-17.360146	-6.171530
1SRA	A	ASN	208	G	-11.410030	11.566688	-17.020381	-6.136575
1SRA	A	MET	209	G	-12.357043	16.240141	-16.009819	-6.183916
1SRA	A	TYR	210	H	-12.687822	20.331906	-13.483180	-5.611338
1SRA	A	ILE	211	H	-12.364107	20.289791	-12.649489	-5.089082
1SRA	A	PHE	212	H	-12.391349	20.388430	-12.478884	-5.048593
1SRA	A	PRO	213	H	-12.733356	20.732201	-11.695327	-4.481861
1SRA	A	VAL	214	H	-12.739745	20.706740	-11.661898	-4.470253

1SRA	A	HIS	215	H	-12.862857	20.209783	-11.658308	-4.413815
1SRA	A	TRP	216	H	-14.799216	19.544086	-17.280158	-6.078897
1SRA	A	GLN	217	H	-13.691650	16.664873	-16.838527	-5.892878
1SRA	A	PHE	218	H	-13.262267	15.895832	-16.814191	-5.751951
1SRA	A	GLY	219	H	-11.251111	10.300603	-16.703127	-5.714110
1SRA	A	GLN	220	H	-10.798544	10.422091	-16.190121	-5.516655
1SRA	A	LEU	221	H	-10.195959	9.509304	-15.275938	-4.979905
1SRA	A	ASP	222	T	-6.591724	4.004550	-11.634303	-4.075367
1SRA	A	GLN	223	T	-5.233649	3.436443	-10.290198	-3.973295
1SRA	A	HIS	224	T	-4.565463	3.516485	-9.773702	-4.030393
1SRA	A	PRO	225	T	-4.548112	3.605792	-9.790634	-4.032449
1SRA	A	ILE	226	T	-4.547214	3.616809	-9.792184	-4.033206
1SRA	A	ASP	227	C	-4.566276	3.604583	-9.731989	-4.031796
1SRA	A	GLY	228	C	-4.770545	3.699197	-9.562041	-4.059590
1SRA	A	TYR	229	E	-6.616957	6.833151	-10.387899	-4.122005
1SRA	A	LEU	230	E	-8.359340	10.863024	-11.026922	-4.547362
1SRA	A	SER	231	C	-10.218928	11.504119	-14.703777	-5.037711
1SRA	A	HIS	232	G	-10.278643	11.095334	-14.965247	-5.022185
1SRA	A	THR	233	G	-9.562865	10.090221	-13.724315	-4.639736
1SRA	A	GLU	234	G	-9.600588	9.922507	-13.736979	-4.624279
1SRA	A	LEU	235	G	-9.597738	10.169673	-13.580399	-4.598792
1SRA	A	ALA	236	G	-9.348360	10.774466	-12.839107	-4.427903
1SRA	A	PRO	237	G	-9.196966	11.120073	-12.552620	-4.369438
1SRA	A	LEU	238	G	-8.756348	10.159043	-12.042424	-4.235420
1SRA	A	ARG	239	C	-7.683483	8.596411	-10.943094	-3.989166
1SRA	A	ALA	240	T	-5.313095	7.827247	-6.961402	-3.238961
1SRA	A	PRO	241	T	-5.252693	8.120679	-7.061839	-3.315819
1SRA	A	LEU	242	T	-5.252521	8.122386	-7.062962	-3.316309
1SRA	A	ILE	243	T	-5.253638	8.120120	-7.053682	-3.314648
1SRA	A	PRO	244	T	-5.261885	8.117801	-7.002284	-3.305916
1SRA	A	MET	245	T	-6.628804	10.871870	-8.041504	-4.037324
1SRA	A	GLU	246	G	-9.528120	13.015785	-12.093766	-4.795695
1SRA	A	HIS	247	G	-10.598094	13.119553	-15.166104	-5.706436
1SRA	A	CYS	248	G	-10.744717	12.688315	-15.620965	-5.857123
1SRA	A	THR	249	H	-11.074353	12.646210	-16.029185	-5.982815
1SRA	A	THR	250	H	-11.338329	12.251533	-16.025421	-5.814296
1SRA	A	ARG	251	H	-12.546188	14.664527	-16.800533	-5.689873
1SRA	A	PHE	252	H	-12.330729	16.335776	-15.425546	-5.619127
1SRA	A	PHE	253	H	-11.641581	14.017938	-15.463451	-5.658843
1SRA	A	GLU	254	H	-9.023887	6.879246	-14.710440	-5.164934
1SRA	A	THR	255	H	-8.891438	6.729177	-14.994753	-5.170652
1SRA	A	CYS	256	H	-8.600153	5.762684	-15.429291	-5.138391
1SRA	A	ASP	257	T	-7.991947	4.392167	-15.145314	-4.968354
1SRA	A	LEU	258	T	-6.255796	2.365981	-12.704565	-4.427406
1SRA	A	ASP	259	T	-6.148616	2.852206	-12.708681	-4.514722
1SRA	A	ASN	260	T	-6.140743	2.942405	-12.697693	-4.517703
1SRA	A	ASP	261	C	-6.143973	2.940219	-12.677246	-4.514335
1SRA	A	LYS	262	C	-6.160998	2.920689	-12.609784	-4.503832
1SRA	A	TYR	263	C	-7.134478	5.716185	-12.786544	-4.949467
1SRA	A	ILE	264	E	-8.587280	9.444337	-12.470805	-4.794868
1SRA	A	ALA	265	E	-10.252081	12.788883	-13.299208	-4.746739
1SRA	A	LEU	266	H	-10.969896	16.020830	-12.765046	-4.809159
1SRA	A	ASP	267	H	-11.045441	15.924856	-12.936529	-4.894029
1SRA	A	GLU	268	H	-11.404550	14.707692	-13.924159	-4.933576
1SRA	A	TRP	269	H	-11.768374	16.253988	-14.241649	-5.237131
1SRA	A	ALA	270	H	-9.300972	11.315437	-12.511002	-4.989696
1SRA	A	GLY	271	H	-8.934147	12.369087	-12.055254	-5.046150
1SRA	A	CYS	272	H	-8.926712	12.415968	-12.066590	-5.051028
1SRA	A	PHE	273	H	-8.682326	13.257444	-11.544231	-5.017051
1SRA	A	GLY	274	C	-5.580243	7.955599	-8.792185	-4.482814
1SRA	A	ILE	275	C	-5.411062	8.189543	-8.882199	-4.495812
1SRA	A	LYS	276	C	-4.588878	7.806834	-8.061968	-4.449354
1SRA	A	GLN	277	G	-4.505993	7.828108	-8.195821	-4.469708
1SRA	A	LYS	278	G	-4.504681	7.830427	-8.203702	-4.470579
1SRA	A	ASP	279	G	-4.609429	7.810467	-8.091466	-4.468058
1SRA	A	ILE	280	C	-4.648848	7.735709	-8.017540	-4.463393
1SRA	A	ASP	281	C	-5.692307	8.033720	-9.169463	-4.614578
1SRA	A	LYS	282	G	-7.439667	9.922426	-11.326157	-4.698038
1SRA	A	ASP	283	G	-7.214542	9.369025	-10.127873	-3.851319
1SRA	A	LEU	284	G	-7.214542	9.369025	-10.127873	-3.851319
1SRA	A	VAL	285	C	-7.214542	9.369025	-10.127873	-3.851319
1SRA	A	ILE	286	C	-7.214542	9.369025	-10.127873	-3.851319
1TEN	A	ARG	802	C	-10.347944	10.461446	-13.665665	-4.388944
1TEN	A	LEU	803	C	-10.347944	10.461446	-13.665665	-4.388944
1TEN	A	ASP	804	C	-10.347944	10.461446	-13.665665	-4.388944
1TEN	A	ALA	805	C	-10.347944	10.461446	-13.665665	-4.388944
1TEN	A	PRO	806	E	-10.251182	13.551052	-12.143132	-4.584399
1TEN	A	SER	807	E	-10.282103	13.534061	-12.015130	-4.564699
1TEN	A	GLN	808	E	-9.957455	13.536422	-12.365557	-4.767898
1TEN	A	ILE	809	E	-9.574343	13.393534	-12.385199	-4.887913
1TEN	A	GLU	810	E	-8.384136	11.281674	-11.271521	-4.658072

1TEN	A	VAL	811	E	-8.160376	10.916483	-11.294634	-4.536260
1TEN	A	LYS	812	E	-7.901494	9.852034	-11.779488	-4.539902
1TEN	A	ASP	813	E	-7.475658	8.939201	-11.488535	-4.347449
1TEN	A	VAL	814	E	-6.965010	8.671589	-10.552272	-4.060487
1TEN	A	THR	815	T	-6.961117	8.498310	-10.582439	-4.009995
1TEN	A	ASP	816	T	-6.988359	8.409810	-10.545176	-3.996860
1TEN	A	THR	817	E	-7.034929	8.452169	-10.372107	-3.951876
1TEN	A	THR	818	E	-7.202708	8.555305	-10.090855	-3.878748
1TEN	A	ALA	819	E	-8.418116	8.771891	-11.432405	-3.990213
1TEN	A	LEU	820	E	-11.406977	13.854210	-14.594523	-4.819961
1TEN	A	ILE	821	E	-11.841110	14.479595	-13.941242	-4.486487
1TEN	A	THR	822	E	-12.664104	14.836062	-14.732249	-4.681933
1TEN	A	TRP	823	E	-12.947986	15.513865	-15.145446	-4.956885
1TEN	A	PHE	824	C	-9.955149	10.520177	-13.056476	-4.455440
1TEN	A	LYS	825	C	-9.124370	9.310780	-12.982227	-4.421382
1TEN	A	PRO	826	C	-8.432601	10.348542	-11.598259	-4.325982
1TEN	A	LEU	827	C	-8.294265	10.054631	-11.903824	-4.377149
1TEN	A	ALA	828	C	-8.258700	10.012866	-12.040182	-4.410639
1TEN	A	GLU	829	C	-8.274734	10.035165	-12.026132	-4.422787
1TEN	A	ILE	830	C	-8.390671	10.290330	-11.829023	-4.427851
1TEN	A	ASP	831	E	-8.997169	9.363508	-13.367688	-4.689809
1TEN	A	GLY	832	E	-9.667475	10.363118	-14.019057	-4.951943
1TEN	A	ILE	833	E	-10.259071	12.067423	-13.625388	-4.952510
1TEN	A	GLU	834	E	-11.493053	15.286447	-14.700936	-5.474490
1TEN	A	LEU	835	E	-11.730446	16.578203	-14.409835	-5.525854
1TEN	A	THR	836	E	-11.914954	17.257459	-14.251430	-5.609543
1TEN	A	TYR	837	E	-12.298251	17.758025	-15.014262	-5.823820
1TEN	A	GLY	838	E	-8.796190	8.481879	-13.348974	-4.999895
1TEN	A	ILE	839	T	-7.967138	7.513155	-12.783051	-4.672220
1TEN	A	LYS	840	T	-6.145957	5.151105	-11.466347	-4.732731
1TEN	A	ASP	841	T	-5.462452	4.596312	-10.952773	-4.507213
1TEN	A	VAL	842	T	-5.456571	4.608577	-10.974314	-4.506035
1TEN	A	PRO	843	T	-5.456830	4.603559	-10.974261	-4.504970
1TEN	A	GLY	844	T	-5.462975	4.577833	-10.958695	-4.504875
1TEN	A	ASP	845	C	-5.675320	4.379830	-10.766824	-4.405144
1TEN	A	ARG	846	E	-7.990681	6.463098	-13.353523	-4.528792
1TEN	A	THR	847	E	-8.004714	11.253924	-11.030925	-4.664482
1TEN	A	THR	848	E	-7.931482	12.294733	-10.397746	-4.644932
1TEN	A	ILE	849	E	-7.953687	12.402729	-10.222361	-4.612022
1TEN	A	ASP	850	E	-7.952582	12.397340	-10.233598	-4.613270
1TEN	A	LEU	851	E	-7.962880	12.409034	-10.171820	-4.601934
1TEN	A	THR	852	T	-8.586977	11.927811	-10.933771	-4.664766
1TEN	A	GLU	853	T	-10.559121	8.381753	-17.061117	-5.341485
1TEN	A	ASP	854	T	-10.559878	8.374495	-17.092227	-5.363460
1TEN	A	GLU	855	C	-10.646514	8.354449	-17.140605	-5.376442
1TEN	A	ASN	856	E	-10.589529	10.763088	-15.665209	-5.282568
1TEN	A	GLN	857	E	-9.574013	14.763514	-11.337266	-5.019597
1TEN	A	TYR	858	E	-7.253503	12.891463	-8.495746	-4.549996
1TEN	A	SER	859	E	-6.390592	12.182101	-7.812379	-4.315377
1TEN	A	ILE	860	C	-6.250485	12.334827	-7.941481	-4.383705
1TEN	A	GLY	861	C	-5.804124	11.325068	-8.153947	-4.475049
1TEN	A	ASN	862	C	-5.805044	11.319625	-8.149464	-4.474235
1TEN	A	LEU	863	T	-5.814044	11.215358	-8.192016	-4.468213
1TEN	A	LYS	864	T	-5.752483	10.478674	-8.784194	-4.687442
1TEN	A	PRO	865	T	-5.808545	10.239286	-8.822026	-4.692696
1TEN	A	ASP	866	T	-6.260073	10.023871	-9.368248	-4.848431
1TEN	A	THR	867	E	-6.260076	10.023828	-9.368195	-4.848411
1TEN	A	GLU	868	E	-6.356936	9.723315	-9.415435	-4.915508
1TEN	A	TYR	869	E	-10.137898	15.466531	-12.070724	-5.506289
1TEN	A	GLU	870	E	-13.409062	16.826119	-16.995635	-6.111032
1TEN	A	VAL	871	E	-12.775438	15.544542	-14.712524	-4.736666
1TEN	A	SER	872	E	-12.771997	15.528562	-14.733419	-4.735249
1TEN	A	LEU	873	E	-12.772363	15.526697	-14.730253	-4.734214
1TEN	A	ILE	874	E	-12.770475	15.512165	-14.755501	-4.738609
1TEN	A	SER	875	E	-12.781219	14.760950	-15.260322	-4.826360
1TEN	A	ARG	876	E	-10.997566	8.018313	-16.873334	-5.347870
1TEN	A	ARG	877	T	-8.930872	6.885980	-14.575544	-5.114925
1TEN	A	GLY	878	T	-8.207458	6.631607	-14.236616	-5.170181
1TEN	A	ASP	879	E	-7.470236	7.765802	-12.500846	-4.940303
1TEN	A	MET	880	E	-7.277284	8.413152	-12.119670	-4.881637
1TEN	A	SER	881	C	-7.067062	8.745134	-11.619017	-4.687096
1TEN	A	SER	882	C	-6.576030	9.405491	-10.409739	-4.625169
1TEN	A	ASN	883	C	-6.603253	9.541026	-10.236473	-4.598469
1TEN	A	PRO	884	E	-6.709929	9.800722	-9.928358	-4.549386
1TEN	A	ALA	885	E	-6.776763	9.765750	-9.784934	-4.527920
1TEN	A	LYS	886	E	-6.896848	9.824747	-9.631549	-4.594193
1TEN	A	GLU	887	E	-6.896848	9.824747	-9.631549	-4.594193
1TEN	A	THR	888	E	-6.896848	9.824747	-9.631549	-4.594193
1TEN	A	PHE	889	E	-6.896848	9.824747	-9.631549	-4.594193
1TN3	A	ALA	45	C	-4.051094	5.978783	-7.022049	-3.628983
1TN3	A	LEU	46	C	-4.051094	5.978783	-7.022049	-3.628983

```
1TN3        A         GLN              47                  C -4.051094  5.978783 -7.022049 -3.628983
1TN3        A         THR              48                  C -4.051094  5.978783 -7.022049 -3.628983
1TN3        A         VAL              49                  E -5.381667  8.013508 -8.967842 -4.479934
1TN3        A         CYS              50                  E -6.062141  8.681018 -10.435278 -5.222791
1TN3        A         LEU              51                  E -6.933055  8.143299 -11.934237 -4.987628
1TN3        A         LYS              52                  E -5.929999  6.180918 -11.027965 -4.814748
1TN3        A         GLY              53                  T -5.827822  6.195595 -11.184350 -4.842093
1TN3        A         THR              54                  T -5.829236  6.207985 -11.188065 -4.852996
1TN3        A         LYS              55                  T -5.882924  6.071830 -11.145952 -4.847993
1TN3        A         VAL              56                  T -5.899720  6.034159 -11.095861 -4.842258
1TN3        A         HIS              57                  T -6.825778  6.721597 -12.002624 -4.997240
1TN3        A         MET              58                  E -7.975504  9.267307 -11.861656 -5.016665
1TN3        A         LYS              59                  E -10.978393 12.255791 -15.502688 -5.785852
1TN3        A         CYS              60                  E -12.122217 13.207340 -16.375617 -5.759095
1TN3        A         PHE              61                  E -12.201469 19.430113 -12.115119 -4.901811
1TN3        A         LEU              62                  E -11.005230 13.828440 -13.317894 -4.761818
1TN3        A         ALA              63                  E -8.629999 12.918320 -10.631811 -4.858437
1TN3        A         PHE              64                  E -8.401485 13.121812 -10.943218 -5.062263
1TN3        A         THR              65                  E -7.710908 11.503409 -11.411010 -5.376129
1TN3        A         GLN              66                  E -7.711011 11.500429 -11.412356 -5.376581
1TN3        A         THR              67                  E -7.712625 11.497855 -11.407765 -5.379187
1TN3        A         LYS              68                  E -7.851103 11.128421 -11.627696 -5.516338
1TN3        A         THR              69                  C -7.924633 10.808885 -11.650613 -5.518334
1TN3        A         PHE              70                  H -10.487472 13.762480 -13.866182 -5.520638
1TN3        A         HIS              71                  H -9.631913 10.061805 -14.233140 -5.159018
1TN3        A         GLU              72                  H -9.614139  9.960648 -14.332266 -5.162404
1TN3        A         ALA              73                  H -9.607778  9.911861 -14.382809 -5.163148
1TN3        A         SER              74                  H -9.711806  8.965182 -14.737470 -5.111231
1TN3        A         GLU              75                  H -9.608870  8.251525 -15.137303 -5.038370
1TN3        A         ASP              76                  H -10.258678  6.091337 -17.279602 -4.865377
1TN3        A         CYS              77                  H -8.477742  4.334465 -14.277856 -4.265382
1TN3        A         ILE              78                  H -5.451815  4.426354 -9.986353 -4.098261
1TN3        A         SER              79                  H -5.427197  4.465936 -10.087085 -4.117826
1TN3        A         ARG              80                  H -5.420393  4.527118 -10.103265 -4.127208
1TN3        A         GLY              81                  C -5.416322  4.557817 -10.120383 -4.134225
1TN3        A         GLY              82                  C -5.419459  4.560664 -10.099045 -4.133857
1TN3        A         THR              83                  E -7.097517  6.701640 -12.315452 -4.718372
1TN3        A         LEU              84                  E -7.777038  9.504697 -11.999529 -5.018974
1TN3        A         SER              85                  C -8.340899  9.115389 -12.708127 -5.157532
1TN3        A         THR              86                  C -9.194793 11.573468 -13.257218 -5.500878
1TN3        A         PRO              87                  C -8.827718 10.746577 -13.024237 -5.205533
1TN3        A         GLN              88                  C -8.798467 10.557728 -13.215448 -5.229620
1TN3        A         THR              89                  C -8.792081 10.510967 -13.267243 -5.231515
1TN3        A         GLY              90                  H -8.796834 10.435679 -13.284952 -5.225592
1TN3        A         SER              91                  H -9.127888  9.720800 -13.477430 -5.016815
1TN3        A         GLU              92                  H -10.286139  7.865116 -16.927771 -5.565243
1TN3        A         ASN              93                  H -11.005430  7.192209 -18.071117 -5.420350
1TN3        A         ASP              94                  H -11.231910  8.850880 -17.354123 -5.278392
1TN3        A         ALA              95                  H -11.731244 12.603255 -15.554947 -5.053908
1TN3        A         LEU              96                  H -11.821882 13.417196 -14.969191 -5.045255
1TN3        A         TYR              97                  H -11.871984 13.514823 -14.739243 -5.015154
1TN3        A         GLU              98                  H -11.893232 13.495342 -14.652170 -5.006719
1TN3        A         TYR              99                  H -15.280470 17.752205 -18.641082 -5.712410
1TN3        A         LEU             100                  H -13.424495 13.868034 -16.710756 -5.156940
1TN3        A         ARG             101                  H -11.163673  9.972951 -15.975114 -5.273481
1TN3        A         GLN             102                  H -9.343817  8.543397 -14.457292 -5.278856
1TN3        A         SER             103                  H -8.110567  8.381988 -12.758605 -4.995831
1TN3        A         VAL             104                  H -6.717199  7.371119 -10.711033 -4.422647
1TN3        A         GLY             105                  T -6.699371  7.366486 -10.813023 -4.445008
1TN3        A         ASN             106                  T -6.697918  7.376373 -10.818461 -4.446062
1TN3        A         GLU             107                  T -6.704408  7.364865 -10.779127 -4.436861
1TN3        A         ALA             108                  T -6.754804  7.276698 -10.624868 -4.390808
1TN3        A         GLU             109                  E -8.725293  7.606410 -14.095283 -5.155378
1TN3        A         ILE             110                  E -10.097040 11.767693 -13.415674 -4.940058
1TN3        A         TRP             111                  E -11.574060 19.091498 -12.008215 -4.895850
1TN3        A         LEU             112                  E -11.581159 18.359441 -12.524181 -4.991725
1TN3        A         GLY             113                  E -11.479182 17.215477 -13.413744 -5.182510
1TN3        A         LEU             114                  E -10.863809 13.442096 -14.451815 -5.268640
1TN3        A         ASN             115                  E -9.165728  7.665691 -14.498398 -5.112167
1TN3        A         ASP             116                  E -8.437688  7.746383 -14.009059 -5.230141
1TN3        A         MET             117                  E -5.985458  6.415878 -10.891700 -5.058831
1TN3        A         ALA             118                  E -4.752075  5.329329 -9.519636 -4.599361
1TN3        A         ALA             119                  E -4.749458  5.357418 -9.525359 -4.602257
1TN3        A         GLU             120                  T -4.749586  5.359039 -9.523404 -4.602206
1TN3        A         GLY             121                  T -4.750408  5.355751 -9.517455 -4.601259
1TN3        A         THR             122                  E -4.827804  5.210386 -9.331971 -4.537430
1TN3        A         TRP             123                  E -7.915401 11.841112 -10.916560 -5.255179
1TN3        A         VAL             124                  E -8.232841  7.027752 -13.587236 -4.966115
1TN3        A         ASP             125                  T -6.723299  5.056173 -12.522095 -4.937596
1TN3        A         MET             126                  T -5.924239  5.402968 -11.048845 -4.507858
1TN3        A         THR             127                  T -5.569394  6.072287 -10.067692 -4.135698
```

1TN3	A	GLY	128	T	-5.091503	6.350985	-8.993478	-3.820651
1TN3	A	ALA	129	C	-5.092885	6.362014	-8.975040	-3.815856
1TN3	A	ARG	130	B	-5.124778	6.496422	-8.759330	-3.748803
1TN3	A	ILE	131	C	-5.249738	6.739826	-8.344867	-3.607443
1TN3	A	ALA	132	C	-5.430299	6.687117	-8.157307	-3.580906
1TN3	A	TYR	133	C	-7.765665	12.360139	-9.749670	-4.334436
1TN3	A	LYS	134	C	-7.886335	12.621931	-9.627530	-4.449594
1TN3	A	ASN	135	C	-8.791959	12.045923	-11.598280	-5.075589
1TN3	A	TRP	136	B	-7.127079	11.036161	-9.572335	-4.831824
1TN3	A	GLU	137	T	-4.636258	4.988316	-8.983358	-4.351271
1TN3	A	THR	138	T	-3.487627	3.372063	-8.078049	-3.920630
1TN3	A	GLU	139	T	-3.487145	3.373548	-8.082335	-3.921325
1TN3	A	ILE	140	T	-3.487088	3.373986	-8.082835	-3.921386
1TN3	A	THR	141	T	-3.488333	3.357635	-8.079884	-3.919429
1TN3	A	ALA	142	T	-3.579447	3.099501	-7.925350	-3.845919
1TN3	A	GLN	143	T	-7.556896	5.697026	-13.598806	-4.832290
1TN3	A	PRO	144	T	-6.481468	4.428595	-12.220149	-4.710567
1TN3	A	ASP	145	T	-5.109471	2.476679	-11.715119	-4.823836
1TN3	A	GLY	146	C	-4.655524	3.241684	-11.190547	-4.880610
1TN3	A	GLY	147	G	-4.649426	3.264215	-11.210233	-4.883434
1TN3	A	LYS	148	G	-4.648687	3.268404	-11.213521	-4.883796
1TN3	A	THR	149	G	-4.675184	3.220542	-11.171265	-4.892232
1TN3	A	GLU	150	C	-5.012330	3.946266	-10.791589	-4.934048
1TN3	A	ASN	151	C	-7.267050	5.642095	-13.344288	-5.191699
1TN3	A	CYS	152	E	-8.510592	6.609848	-14.332036	-5.270526
1TN3	A	ALA	153	E	-10.172792	13.079838	-12.594013	-4.450118
1TN3	A	VAL	154	E	-9.995101	13.036042	-12.461707	-4.388401
1TN3	A	LEU	155	E	-9.402392	11.439663	-12.496831	-4.394091
1TN3	A	SER	156	E	-6.574352	6.563695	-10.735575	-4.434304
1TN3	A	GLY	157	T	-4.617201	5.539519	-8.880224	-4.467633
1TN3	A	ALA	158	T	-4.594793	5.583317	-8.957103	-4.476856
1TN3	A	ALA	159	T	-4.594768	5.583588	-8.957314	-4.476913
1TN3	A	ASN	160	T	-4.594880	5.582655	-8.956631	-4.476928
1TN3	A	GLY	161	T	-4.616075	5.548224	-8.892096	-4.478331
1TN3	A	LYS	162	E	-6.544567	6.737688	-10.951121	-4.712813
1TN3	A	TRP	163	E	-10.194380	12.068236	-13.477410	-5.177386
1TN3	A	PHE	164	E	-12.688199	16.082462	-15.463604	-5.775130
1TN3	A	ASP	165	E	-11.842921	8.712775	-17.227059	-5.071037
1TN3	A	LYS	166	E	-9.196109	7.698724	-13.955447	-4.770033
1TN3	A	ARG	167	T	-8.053282	7.171275	-12.936642	-4.690887
1TN3	A	CYS	168	T	-7.941697	7.608816	-12.970576	-4.777494
1TN3	A	ARG	169	T	-7.896773	7.924055	-12.886687	-4.766541
1TN3	A	ASP	170	T	-7.897446	7.924216	-12.881539	-4.766240
1TN3	A	GLN	171	C	-7.966453	7.959866	-12.752506	-4.766249
1TN3	A	LEU	172	E	-8.760107	10.440399	-12.722165	-5.016560
1TN3	A	PRO	173	E	-9.441128	11.995020	-11.834008	-4.630986
1TN3	A	TYR	174	E	-12.154550	18.641535	-12.923878	-4.951686
1TN3	A	ILE	175	E	-12.129737	18.522631	-13.471912	-5.336383
1TN3	A	CYS	176	E	-10.791688	12.134416	-15.598335	-6.180619
1TN3	A	GLN	177	E	-8.308447	10.826460	-11.563517	-5.068649
1TN3	A	PHE	178	E	-4.856135	7.884664	-6.435610	-3.362931
1TN3	A	GLY	179	E	-4.856135	7.884664	-6.435610	-3.362931
1TN3	A	ILE	180	C	-4.856135	7.884664	-6.435610	-3.362931
1TN3	A	VAL	181	C	-4.856135	7.884664	-6.435610	-3.362931
1ZON	A	GLY	128	C	-9.078199	7.853929	-13.425768	-4.524791
1ZON	A	ASN	129	C	-9.078199	7.853929	-13.425768	-4.524791
1ZON	A	VAL	130	E	-9.078199	7.853929	-13.425768	-4.524791
1ZON	A	ASP	131	E	-9.078199	7.853929	-13.425768	-4.524791
1ZON	A	LEU	132	E	-11.873051	13.016864	-15.642655	-5.397903
1ZON	A	VAL	133	E	-13.301122	19.331732	-14.542312	-5.311147
1ZON	A	PHE	134	E	-13.210770	21.450043	-12.917098	-5.039747
1ZON	A	LEU	135	E	-12.480872	17.269928	-14.545195	-5.355382
1ZON	A	PHE	136	E	-11.988153	15.075086	-15.304216	-5.425624
1ZON	A	ASP	137	E	-11.131764	8.918200	-16.935248	-5.217549
1ZON	A	GLY	138	C	-9.830364	8.595506	-14.791078	-4.912434
1ZON	A	SER	139	B	-9.513741	9.008829	-14.561109	-4.927643
1ZON	A	MET	140	T	-8.575447	8.100708	-13.134318	-4.525108
1ZON	A	SER	141	T	-8.196060	7.552073	-13.237227	-4.547100
1ZON	A	LEU	142	T	-7.710950	8.083111	-12.513915	-4.637532
1ZON	A	GLN	143	C	-7.681291	8.280342	-12.457692	-4.648552
1ZON	A	PRO	144	H	-7.691831	8.258875	-12.427555	-4.643573
1ZON	A	ASP	145	H	-7.808721	8.342820	-12.353392	-4.691886
1ZON	A	GLU	146	H	-7.976354	8.797240	-12.025213	-4.730629
1ZON	A	PHE	147	H	-9.226095	10.976498	-12.450805	-4.874829
1ZON	A	GLN	148	H	-11.554973	12.112507	-15.845302	-5.361613
1ZON	A	LYS	149	H	-12.596462	13.937626	-16.733656	-5.637406
1ZON	A	ILE	150	H	-12.539331	15.432104	-15.753447	-5.505653
1ZON	A	LEU	151	H	-12.535251	15.463749	-15.758304	-5.509965
1ZON	A	ASP	152	H	-12.499960	15.564904	-15.847519	-5.589835
1ZON	A	PHE	153	H	-13.013969	19.186930	-14.876552	-5.700484
1ZON	A	MET	154	H	-12.887104	18.783203	-15.159378	-5.780371

1ZON	A	LYS	155	H	-12.677744	16.071350	-16.334569	-5.916254
1ZON	A	ASP	156	H	-10.578584	12.353221	-13.849930	-5.129070
1ZON	A	VAL	157	H	-10.302390	12.892098	-13.590981	-5.076817
1ZON	A	MET	158	H	-10.218818	12.774304	-13.800586	-5.106620
1ZON	A	LYS	159	H	-9.350897	9.489693	-14.054211	-4.981111
1ZON	A	LYS	160	H	-7.918917	7.827684	-12.340240	-4.643573
1ZON	A	LEU	161	H	-7.877992	7.827459	-12.443985	-4.652049
1ZON	A	SER	162	T	-7.870676	7.833029	-12.477864	-4.659748
1ZON	A	ASN	163	T	-7.871739	7.825587	-12.474397	-4.659195
1ZON	A	THR	164	T	-7.910532	7.779373	-12.362241	-4.639912
1ZON	A	SER	165	C	-9.264234	8.774896	-14.029417	-4.896948
1ZON	A	TYR	166	E	-10.212755	10.223746	-14.624723	-5.221543
1ZON	A	GLN	167	E	-11.914308	14.040450	-15.738563	-5.639302
1ZON	A	PHE	168	E	-12.356079	17.311271	-13.266871	-4.590927
1ZON	A	ALA	169	E	-12.244063	17.069842	-13.445874	-4.563330
1ZON	A	ALA	170	E	-12.218833	16.995041	-13.572788	-4.582812
1ZON	A	VAL	171	E	-12.209991	16.923896	-13.649578	-4.594826
1ZON	A	GLN	172	E	-12.632962	16.069611	-14.691606	-4.651799
1ZON	A	PHE	173	E	-12.579902	15.535643	-15.323034	-5.002221
1ZON	A	SER	174	T	-11.264993	11.866806	-15.409147	-5.360516
1ZON	A	THR	175	T	-10.533680	12.350372	-14.411305	-5.301615
1ZON	A	SER	176	T	-10.486119	12.456136	-14.488723	-5.326169
1ZON	A	TYR	177	E	-10.479451	12.523389	-14.489578	-5.332163
1ZON	A	LYS	178	E	-10.457558	12.569330	-14.535907	-5.354970
1ZON	A	THR	179	E	-10.617118	12.880190	-14.275089	-5.350698
1ZON	A	GLU	180	E	-11.629844	14.335934	-15.473313	-5.685856
1ZON	A	PHE	181	E	-12.076798	15.088044	-15.510322	-5.754763
1ZON	A	ASP	182	T	-12.190753	14.451078	-15.650269	-5.734395
1ZON	A	PHE	183	H	-13.908112	17.740016	-16.542762	-5.456773
1ZON	A	SER	184	H	-12.613789	11.465389	-17.181379	-5.202018
1ZON	A	ASP	185	H	-11.688134	11.427015	-15.836500	-4.930533
1ZON	A	TYR	186	H	-9.943525	10.081174	-13.516648	-4.533910
1ZON	A	VAL	187	H	-7.466089	6.842995	-11.575312	-4.269034
1ZON	A	LYS	188	H	-7.324590	7.268306	-11.561646	-4.277919
1ZON	A	ARG	189	T	-7.321479	7.283634	-11.576033	-4.281186
1ZON	A	LYS	190	T	-7.292521	7.378208	-11.652420	-4.313084
1ZON	A	ASP	191	T	-7.282132	7.458098	-11.652711	-4.322205
1ZON	A	PRO	192	H	-8.037716	9.215426	-11.933632	-4.472490
1ZON	A	ASP	193	H	-8.699908	10.361895	-12.917021	-4.859624
1ZON	A	ALA	194	H	-7.950391	11.397729	-10.584544	-4.420508
1ZON	A	LEU	195	H	-7.335887	12.934740	-8.771998	-4.307881
1ZON	A	LEU	196	H	-5.731321	9.323599	-7.979299	-4.109364
1ZON	A	LYS	197	T	-5.367730	8.813689	-8.298822	-4.180235
1ZON	A	HIS	198	T	-5.363502	8.828003	-8.320593	-4.186616
1ZON	A	VAL	199	T	-5.368698	8.801829	-8.309677	-4.186314
1ZON	A	LYS	200	C	-5.382972	8.682744	-8.320562	-4.184738
1ZON	A	HIS	201	C	-5.815967	8.271036	-8.749083	-4.282162
1ZON	A	MET	202	C	-8.035334	10.902619	-11.981542	-5.109916
1ZON	A	LEU	203	C	-8.706694	10.898302	-13.200679	-5.211261
1ZON	A	LEU	204	B	-8.807722	10.823146	-13.281403	-5.279852
1ZON	A	LEU	205	C	-9.180363	12.067449	-13.038373	-5.425495
1ZON	A	THR	206	T	-9.879291	12.605311	-13.776998	-5.661470
1ZON	A	ASN	207	T	-10.938610	12.954330	-15.493804	-5.620250
1ZON	A	THR	208	H	-10.287766	15.956038	-11.788106	-4.961704
1ZON	A	PHE	209	H	-10.311986	16.169193	-11.500002	-4.842338
1ZON	A	GLY	210	H	-10.279531	16.013701	-11.665768	-4.846389
1ZON	A	ALA	211	H	-10.282811	16.027962	-11.616505	-4.821554
1ZON	A	ILE	212	H	-10.322878	16.146747	-11.407566	-4.776987
1ZON	A	ASN	213	H	-11.364914	14.127553	-14.324146	-4.778197
1ZON	A	TYR	214	H	-10.598169	13.074555	-12.955077	-4.453596
1ZON	A	VAL	215	H	-9.231854	12.050491	-10.848335	-3.922430
1ZON	A	ALA	216	H	-9.133638	12.596306	-10.836840	-4.017510
1ZON	A	THR	217	H	-9.119843	12.681430	-10.868062	-4.036194
1ZON	A	GLU	218	H	-9.119078	12.696543	-10.866877	-4.038279
1ZON	A	VAL	219	H	-9.115497	12.858674	-10.809870	-4.057371
1ZON	A	PHE	220	T	-9.681986	14.661311	-11.718388	-4.658001
1ZON	A	ARG	221	T	-7.851333	7.558227	-12.395630	-4.770586
1ZON	A	GLU	222	G	-7.310281	8.218728	-11.860437	-4.826734
1ZON	A	GLU	223	G	-7.310317	8.217416	-11.860835	-4.826770
1ZON	A	LEU	224	G	-7.312225	8.193441	-11.863051	-4.827574
1ZON	A	GLY	225	C	-7.311379	8.146229	-11.892480	-4.828363
1ZON	A	ALA	226	C	-7.576352	8.589552	-11.682029	-4.849730
1ZON	A	ARG	227	T	-9.002482	7.400323	-14.513031	-4.687096
1ZON	A	PRO	228	T	-7.252396	8.638803	-10.843656	-4.546487
1ZON	A	ASP	229	T	-7.239499	8.697236	-10.871176	-4.547297
1ZON	A	ALA	230	T	-7.235224	8.810792	-10.823129	-4.542684
1ZON	A	THR	231	E	-7.249847	8.867503	-10.735515	-4.542583
1ZON	A	LYS	232	E	-7.259284	8.904974	-10.665918	-4.537598
1ZON	A	VAL	233	E	-9.120914	13.923913	-11.052301	-4.481911
1ZON	A	LEU	234	E	-9.527080	17.004596	-9.775216	-4.374260
1ZON	A	ILE	235	E	-10.162914	19.997568	-9.296294	-4.373389

1ZON	A	ILE	236	E	-10.168330	19.035967	-10.036420	-4.547755
1ZON	A	ILE	237	E	-10.204939	17.919969	-10.928225	-4.756249
1ZON	A	THR	238	E	-9.340320	11.794864	-13.374867	-5.495507
1ZON	A	ASP	239	C	-8.224985	9.321981	-12.939322	-5.343725
1ZON	A	GLY	240	C	-7.786308	8.953421	-12.867674	-5.316510
1ZON	A	GLU	241	C	-7.275357	8.611324	-11.979065	-4.918665
1ZON	A	ALA	242	C	-5.557969	6.930291	-9.281436	-4.320757
1ZON	A	THR	243	C	-5.306560	6.262643	-9.891522	-4.449781
1ZON	A	ASP	244	C	-5.291589	6.290272	-9.918373	-4.448811
1ZON	A	SER	245	C	-4.941896	6.577861	-9.526274	-4.455057
1ZON	A	GLY	246	C	-4.847370	6.650129	-9.580221	-4.495725
1ZON	A	ASN	247	C	-5.033780	6.633856	-9.768866	-4.574811
1ZON	A	ILE	248	C	-5.174221	7.111839	-9.423953	-4.540250
1ZON	A	ASP	249	G	-5.187493	7.095511	-9.388463	-4.539732
1ZON	A	ALA	250	G	-5.858775	7.429488	-10.081752	-4.688970
1ZON	A	ALA	251	G	-7.031444	9.293977	-10.803688	-4.479313
1ZON	A	LYS	252	T	-7.569947	9.173363	-11.738260	-4.607582
1ZON	A	ASP	253	T	-8.059937	8.611520	-12.772685	-4.740938
1ZON	A	ILE	254	T	-8.389524	10.066485	-12.122891	-4.736628
1ZON	A	ILE	255	E	-9.148958	10.651049	-12.369298	-4.762414
1ZON	A	ARG	256	E	-12.053917	11.823139	-16.238522	-5.337605
1ZON	A	TYR	257	E	-11.385555	19.568383	-10.411568	-4.682257
1ZON	A	ILE	258	E	-8.860687	14.766028	-9.289270	-4.345406
1ZON	A	ILE	259	E	-7.794203	11.594347	-9.893320	-4.355017
1ZON	A	GLY	260	E	-7.552359	10.397928	-10.726160	-4.467294
1ZON	A	ILE	261	E	-7.525800	10.509127	-10.757680	-4.481621
1ZON	A	GLY	262	T	-7.359236	10.165825	-11.074336	-4.584857
1ZON	A	LYS	263	T	-7.363883	9.731062	-11.354253	-4.625280
1ZON	A	HIS	264	T	-7.668760	8.897019	-12.272033	-4.808172
1ZON	A	PHE	265	T	-7.693470	8.850548	-12.400509	-4.858284
1ZON	A	GLN	266	T	-6.566547	4.173397	-12.632208	-4.621741
1ZON	A	THR	267	C	-6.591697	3.871821	-12.722370	-4.610038
1ZON	A	LYS	268	H	-6.599950	3.787320	-12.732827	-4.608673
1ZON	A	GLU	269	H	-6.600122	3.785442	-12.732141	-4.608557
1ZON	A	SER	270	H	-6.637066	3.526777	-12.732546	-4.595735
1ZON	A	GLN	271	H	-8.676266	5.876708	-14.920040	-5.001345
1ZON	A	GLU	272	H	-9.597831	7.650547	-15.583892	-5.341858
1ZON	A	THR	273	H	-10.750431	12.548616	-14.896796	-5.409993
1ZON	A	LEU	274	C	-10.814913	13.330744	-14.315491	-5.322954
1ZON	A	HIS	275	G	-10.815711	13.335074	-14.301908	-5.318490
1ZON	A	LYS	276	G	-10.846365	13.344966	-14.175991	-5.291573
1ZON	A	PHE	277	G	-11.422587	14.414441	-14.305004	-4.989647
1ZON	A	ALA	278	C	-9.099561	7.774430	-13.115780	-4.211557
1ZON	A	SER	279	T	-8.314521	6.512766	-12.955682	-4.052756
1ZON	A	LYS	280	T	-7.747937	6.598881	-12.629110	-4.223798
1ZON	A	PRO	281	T	-7.699212	6.931805	-12.576457	-4.246196
1ZON	A	ALA	282	H	-7.695393	6.978492	-12.571600	-4.248401
1ZON	A	SER	283	H	-7.752516	6.908086	-12.519225	-4.253375
1ZON	A	GLU	284	H	-7.950790	7.245651	-12.368958	-4.355943
1ZON	A	PHE	285	H	-9.143917	11.143678	-12.004487	-4.523828
1ZON	A	VAL	286	E	-10.234859	14.081532	-12.715902	-4.859228
1ZON	A	LYS	287	E	-10.277638	13.792060	-13.579831	-5.356436
1ZON	A	ILE	288	E	-9.524360	16.037660	-11.179708	-5.223102
1ZON	A	LEU	289	E	-9.138437	15.652835	-11.259122	-5.343817
1ZON	A	ASP	290	C	-8.378942	13.220812	-11.397819	-5.347630
1ZON	A	THR	291	C	-8.376575	13.276087	-11.384913	-5.355365
1ZON	A	PHE	292	G	-8.388591	13.277531	-11.334953	-5.351722
1ZON	A	GLU	293	G	-8.406283	12.629562	-11.691319	-5.373533
1ZON	A	LYS	294	G	-8.486830	12.222344	-11.775619	-5.354811
1ZON	A	LEU	295	T	-9.662284	11.915080	-13.853299	-5.377641
1ZON	A	LYS	296	T	-9.274730	11.329548	-13.129254	-4.989975
1ZON	A	ASP	297	T	-8.253315	11.616104	-11.136525	-4.767131
1ZON	A	LEU	298	T	-8.242553	12.037673	-10.895396	-4.741547
1ZON	A	PHE	299	H	-8.240145	12.061481	-10.894814	-4.743804
1ZON	A	THR	300	H	-8.107971	11.622658	-11.276831	-4.781210
1ZON	A	GLU	301	H	-8.157275	11.626023	-11.188381	-4.787694
1ZON	A	LEU	302	H	-8.841098	11.744180	-12.351794	-5.019616
1ZON	A	GLN	303	H	-8.358346	12.139118	-11.995837	-5.437055
1ZON	A	LYS	304	H	-6.153406	11.006155	-8.005441	-4.486019
1ZON	A	LYS	305	H	-5.752857	10.959188	-7.492728	-4.109366
1ZON	A	ILE	306	H	-5.752857	10.959188	-7.492728	-4.109366
1ZON	A	TYR	307	C	-5.752857	10.959188	-7.492728	-4.109366
1ZON	A	VAL	308	C	-5.752857	10.959188	-7.492728	-4.109366
1ZXQ	A	LYS	1	C	-5.283067	6.859254	-8.587223	-4.009659
1ZXQ	A	VAL	2	C	-5.283067	6.859254	-8.587223	-4.009659
1ZXQ	A	PHE	3	C	-5.283067	6.859254	-8.587223	-4.009659
1ZXQ	A	GLU	4	C	-5.283067	6.859254	-8.587223	-4.009659
1ZXQ	A	VAL	5	E	-6.687607	9.790749	-9.605922	-4.722124
1ZXQ	A	HIS	6	E	-8.911439	11.280688	-13.377434	-5.745577
1ZXQ	A	VAL	7	E	-8.833458	11.462581	-11.508976	-4.478986
1ZXQ	A	ARG	8	E	-8.820078	11.290023	-11.499489	-4.381965

1ZXQ	A	PRO	9	T	-8.532464	11.645482	-11.210935	-4.333320
1ZXQ	A	LYS	10	T	-8.474313	11.774744	-11.188049	-4.313378
1ZXQ	A	LYS	11	E	-8.482739	11.898564	-11.095441	-4.299647
1ZXQ	A	LEU	12	E	-8.547621	12.691365	-10.411281	-4.001632
1ZXQ	A	ALA	13	E	-7.069795	11.352008	-8.306971	-3.809714
1ZXQ	A	VAL	14	E	-6.189257	8.818442	-8.910294	-4.003520
1ZXQ	A	GLU	15	T	-5.527987	8.049684	-8.982320	-4.264252
1ZXQ	A	PRO	16	T	-5.425308	8.374501	-8.898304	-4.252999
1ZXQ	A	LYS	17	T	-5.401044	8.441722	-8.945276	-4.272985
1ZXQ	A	GLY	18	E	-5.430626	8.309545	-8.997883	-4.301984
1ZXQ	A	SER	19	E	-5.575398	8.365244	-8.969722	-4.368540
1ZXQ	A	LEU	20	E	-6.349252	10.209741	-8.837196	-4.308434
1ZXQ	A	GLU	21	E	-7.188801	10.568650	-10.029709	-4.670357
1ZXQ	A	VAL	22	E	-8.354898	12.862577	-10.015901	-4.501446
1ZXQ	A	ASN	23	E	-9.823261	12.681453	-13.401481	-5.041014
1ZXQ	A	CYS	24	E	-9.996103	9.850041	-15.730915	-5.410193
1ZXQ	A	SER	25	E	-9.615010	8.795781	-15.834152	-5.542852
1ZXQ	A	THR	26	E	-8.323718	7.496358	-14.184335	-5.482330
1ZXQ	A	THR	27	C	-7.979086	7.381410	-13.850146	-5.252839
1ZXQ	A	CYS	28	T	-7.889855	7.272672	-13.921079	-5.206209
1ZXQ	A	ASN	29	T	-7.455491	6.746448	-13.106162	-4.763123
1ZXQ	A	GLN	30	T	-6.038931	6.908020	-9.997314	-4.312611
1ZXQ	A	PRO	31	T	-5.827171	7.003594	-10.049959	-4.348699
1ZXQ	A	GLU	32	T	-5.806701	7.089504	-10.073556	-4.366962
1ZXQ	A	VAL	33	E	-5.808571	7.092942	-10.060012	-4.365366
1ZXQ	A	GLY	34	E	-5.827766	7.122154	-9.985193	-4.366311
1ZXQ	A	GLY	35	E	-6.427435	7.466821	-10.504525	-4.537458
1ZXQ	A	LEU	36	E	-7.591982	9.025471	-11.642850	-4.928479
1ZXQ	A	GLU	37	E	-8.120355	8.165475	-13.226146	-5.064786
1ZXQ	A	THR	38	C	-7.265561	9.219188	-11.418839	-4.988760
1ZXQ	A	SER	39	C	-7.200007	9.101249	-11.507535	-4.933595
1ZXQ	A	LEU	40	C	-7.097811	9.482092	-11.336335	-4.894804
1ZXQ	A	ASN	41	E	-6.417716	10.199920	-9.649142	-4.679587
1ZXQ	A	LYS	42	E	-6.051346	10.408295	-9.030025	-4.565636
1ZXQ	A	ILE	43	E	-5.238854	9.794907	-7.620144	-4.251468
1ZXQ	A	LEU	44	E	-5.162793	9.847604	-7.763108	-4.304927
1ZXQ	A	LEU	45	E	-5.133023	9.754478	-7.886343	-4.316627
1ZXQ	A	ASP	46	E	-5.180964	9.685407	-7.806747	-4.294523
1ZXQ	A	GLU	47	E	-5.250655	9.581697	-7.719536	-4.274087
1ZXQ	A	GLN	48	E	-6.167402	9.572272	-9.398832	-4.652531
1ZXQ	A	ALA	49	T	-6.835266	8.322530	-10.416991	-4.574940
1ZXQ	A	GLN	50	T	-8.931022	8.445042	-14.158491	-5.094612
1ZXQ	A	TRP	51	E	-9.343181	9.614592	-13.706354	-5.202059
1ZXQ	A	LYS	52	E	-12.072758	12.048775	-16.676242	-5.677534
1ZXQ	A	HIS	53	E	-14.040712	17.645430	-17.600902	-6.045435
1ZXQ	A	TYR	54	E	-12.727828	16.506035	-14.677570	-5.234120
1ZXQ	A	LEU	55	E	-10.492239	13.830146	-12.109559	-4.493576
1ZXQ	A	VAL	56	E	-9.810057	12.710296	-12.055595	-4.353184
1ZXQ	A	SER	57	E	-8.502910	9.878707	-11.568133	-4.278772
1ZXQ	A	ASN	58	E	-7.745939	8.832327	-11.392511	-4.295989
1ZXQ	A	ILE	59	E	-7.490884	8.682880	-11.399074	-4.261012
1ZXQ	A	SER	60	C	-7.079152	7.409471	-11.573368	-4.217575
1ZXQ	A	HIS	61	C	-7.046768	7.483693	-11.614765	-4.240355
1ZXQ	A	ASP	62	C	-7.093124	7.318615	-11.627600	-4.239076
1ZXQ	A	THR	63	E	-7.254508	6.975998	-11.728708	-4.220984
1ZXQ	A	VAL	64	E	-7.413019	6.537086	-11.826337	-4.228682
1ZXQ	A	LEU	65	E	-8.696337	9.240587	-12.425196	-4.634763
1ZXQ	A	GLN	66	E	-10.685589	11.198627	-15.453348	-5.407684
1ZXQ	A	CYS	67	E	-11.002405	11.625562	-15.413344	-5.470157
1ZXQ	A	HIS	68	E	-12.034750	14.032685	-16.272354	-5.602445
1ZXQ	A	PHE	69	E	-9.437933	11.135896	-12.960741	-5.151740
1ZXQ	A	THR	70	E	-7.257688	6.618969	-12.652026	-5.190019
1ZXQ	A	CYS	71	E	-6.795885	6.335165	-12.899865	-5.369523
1ZXQ	A	SER	72	T	-6.721799	6.357480	-12.995861	-5.365983
1ZXQ	A	GLY	73	T	-6.547721	6.821069	-12.833566	-5.421688
1ZXQ	A	LYS	74	E	-6.550736	6.797744	-12.837828	-5.424542
1ZXQ	A	GLN	75	E	-6.751649	6.963786	-12.933994	-5.528074
1ZXQ	A	GLU	76	E	-7.163488	7.849905	-12.764083	-5.535491
1ZXQ	A	SER	77	E	-7.328107	8.297385	-12.469160	-5.600332
1ZXQ	A	MET	78	E	-9.085197	10.603107	-14.597767	-5.876777
1ZXQ	A	ASN	79	E	-9.193611	10.629679	-14.561637	-5.898177
1ZXQ	A	SER	80	E	-9.889650	10.577327	-15.276432	-5.619112
1ZXQ	A	ASN	81	E	-10.084583	10.457530	-15.198405	-5.522685
1ZXQ	A	VAL	82	E	-10.835792	11.621305	-15.140590	-5.225422
1ZXQ	A	SER	83	E	-11.601031	11.457605	-16.031410	-5.152618
1ZXQ	A	VAL	84	E	-12.403202	14.549451	-15.416933	-4.874636
1ZXQ	A	TYR	85	C	-12.724275	17.436010	-14.658241	-5.046407
1ZXQ	A	GLN	86	B	-11.125429	12.432097	-14.114499	-4.793869
1ZXQ	A	PRO	87	C	-9.599543	13.395955	-10.852823	-4.146545
1ZXQ	A	PRO	88	C	-9.558789	13.337572	-11.016056	-4.156543
1ZXQ	A	ARG	89	C	-9.550966	13.319204	-11.069313	-4.163927

1ZXQ	A	GLN	90	C	-9.258267	13.379507	-11.305244	-4.402090
1ZXQ	A	VAL	91	C	-9.063673	14.448199	-10.849997	-4.554558
1ZXQ	A	ILE	92	E	-9.319275	15.014116	-11.106602	-4.848965
1ZXQ	A	LEU	93	E	-9.288377	14.993864	-11.187999	-4.884017
1ZXQ	A	THR	94	E	-8.400973	11.102071	-11.459830	-4.593858
1ZXQ	A	LEU	95	E	-7.171498	10.914652	-9.432968	-4.381456
1ZXQ	A	GLN	96	E	-6.788051	9.916302	-9.590176	-4.206717
1ZXQ	A	PRO	97	T	-6.510781	9.839403	-9.143186	-3.909061
1ZXQ	A	THR	98	T	-6.466842	9.972483	-9.102507	-3.876172
1ZXQ	A	LEU	99	E	-6.295521	9.998750	-8.917184	-3.829063
1ZXQ	A	VAL	100	E	-6.380959	9.668114	-8.997453	-3.713302
1ZXQ	A	ALA	101	T	-6.315840	8.981772	-9.362011	-3.792047
1ZXQ	A	VAL	102	T	-6.498539	8.728896	-9.728798	-3.935704
1ZXQ	A	GLY	103	T	-6.544854	8.485709	-9.824878	-3.975898
1ZXQ	A	LYS	104	E	-6.863921	7.355885	-10.682135	-4.133182
1ZXQ	A	SER	105	E	-6.979131	7.105048	-10.675485	-4.178368
1ZXQ	A	PHE	106	E	-9.500381	12.011867	-12.374558	-4.734903
1ZXQ	A	THR	107	E	-10.534089	12.099111	-14.095454	-5.216647
1ZXQ	A	ILE	108	E	-12.114038	14.897414	-15.557578	-5.237453
1ZXQ	A	GLU	109	E	-12.292686	13.792563	-16.489873	-5.301965
1ZXQ	A	CYS	110	E	-12.020557	11.643953	-16.799205	-4.979875
1ZXQ	A	ARG	111	E	-11.689768	11.174965	-16.040648	-4.545759
1ZXQ	A	VAL	112	E	-10.850980	12.266151	-13.935905	-4.516384
1ZXQ	A	PRO	113	C	-10.731863	12.244634	-13.988546	-4.525464
1ZXQ	A	THR	114	C	-10.678062	12.440851	-13.958013	-4.535681
1ZXQ	A	VAL	115	T	-10.466858	13.044092	-13.512218	-4.564010
1ZXQ	A	GLU	116	B	-10.478735	13.128906	-13.521816	-4.614179
1ZXQ	A	PRO	117	T	-10.703769	13.540479	-13.681811	-4.666075
1ZXQ	A	LEU	118	G	-10.750055	13.866429	-13.594924	-4.705863
1ZXQ	A	ASP	119	G	-10.770429	13.856272	-13.625457	-4.726467
1ZXQ	A	SER	120	G	-11.236732	13.797531	-14.501003	-4.844786
1ZXQ	A	LEU	121	E	-11.287406	14.518426	-14.048404	-4.784048
1ZXQ	A	THR	122	E	-11.561154	14.968593	-14.119100	-4.881074
1ZXQ	A	LEU	123	E	-12.031960	16.065822	-13.953194	-4.855128
1ZXQ	A	PHE	124	E	-12.687757	20.052354	-12.425742	-4.707284
1ZXQ	A	LEU	125	E	-12.543406	18.314820	-13.799363	-5.136492
1ZXQ	A	PHE	126	E	-10.242734	10.513548	-15.020066	-5.694411
1ZXQ	A	ARG	127	E	-6.296718	8.116206	-10.880331	-5.475303
1ZXQ	A	GLY	128	T	-4.747012	8.421264	-8.344335	-5.024203
1ZXQ	A	ASN	129	T	-4.739663	8.452234	-8.367401	-5.024714
1ZXQ	A	GLU	130	E	-4.738264	8.466178	-8.371283	-5.025441
1ZXQ	A	THR	131	E	-4.736735	8.483709	-8.373024	-5.025627
1ZXQ	A	LEU	132	E	-4.780493	8.516508	-8.180631	-4.990840
1ZXQ	A	HIS	133	E	-7.119430	12.156262	-10.055894	-5.114999
1ZXQ	A	TYR	134	E	-7.774974	14.842023	-9.802852	-5.242659
1ZXQ	A	GLU	135	E	-7.784071	13.663118	-10.389199	-5.133882
1ZXQ	A	THR	136	E	-6.414208	10.299169	-8.649031	-4.357519
1ZXQ	A	PHE	137	C	-5.525041	9.678658	-7.724933	-4.099821
1ZXQ	A	GLY	138	C	-3.806501	4.735507	-7.217043	-3.592068
1ZXQ	A	LYS	139	C	-3.727310	4.801279	-7.281236	-3.542186
1ZXQ	A	ALA	140	T	-3.647494	4.842890	-7.296306	-3.470573
1ZXQ	A	ALA	141	T	-3.651834	4.798851	-7.290969	-3.463540
1ZXQ	A	PRO	142	T	-3.671295	4.639276	-7.287434	-3.444345
1ZXQ	A	ALA	143	T	-4.498317	5.217890	-7.580261	-3.079628
1ZXQ	A	PRO	144	T	-4.861039	5.196150	-7.474765	-2.993581
1ZXQ	A	GLN	145	T	-7.081999	7.888989	-11.168598	-4.102004
1ZXQ	A	GLU	146	T	-7.480806	8.850404	-11.555258	-4.390390
1ZXQ	A	ALA	147	E	-7.896499	10.147590	-11.656266	-4.564245
1ZXQ	A	THR	148	E	-7.704415	12.469925	-10.458408	-4.943478
1ZXQ	A	ALA	149	E	-7.783960	12.803495	-10.289614	-4.978917
1ZXQ	A	THR	150	E	-7.661633	12.381221	-10.670556	-5.038135
1ZXQ	A	PHE	151	E	-7.711420	12.320438	-10.710205	-5.084114
1ZXQ	A	ASN	152	E	-7.725747	12.164458	-10.791157	-5.107113
1ZXQ	A	SER	153	E	-8.378427	10.391590	-12.754286	-5.114335
1ZXQ	A	THR	154	E	-7.932336	8.886278	-12.211329	-4.595372
1ZXQ	A	ALA	155	E	-8.126328	8.167321	-12.221481	-4.308097
1ZXQ	A	ASP	156	C	-8.077716	8.075543	-12.428252	-4.394221
1ZXQ	A	ARG	157	G	-6.570890	6.979789	-11.037724	-4.672294
1ZXQ	A	GLU	158	G	-6.559933	6.985475	-11.102560	-4.691753
1ZXQ	A	ASP	159	G	-6.595770	6.921186	-11.058725	-4.720104
1ZXQ	A	GLY	160	G	-6.596806	6.920944	-11.052162	-4.720627
1ZXQ	A	HIS	161	C	-6.602690	6.909373	-11.018172	-4.715734
1ZXQ	A	ARG	162	C	-8.779588	7.684793	-14.401800	-5.441376
1ZXQ	A	ASN	163	E	-10.763433	11.642051	-15.724508	-5.759332
1ZXQ	A	PHE	164	E	-11.111955	13.344036	-14.710818	-5.666525
1ZXQ	A	SER	165	E	-11.962723	12.856438	-15.006561	-4.622312
1ZXQ	A	CYS	166	E	-11.119769	13.791390	-13.026130	-4.277308
1ZXQ	A	LEU	167	E	-10.538653	14.234710	-12.104723	-4.161489
1ZXQ	A	ALA	168	E	-10.196091	14.491325	-11.794754	-4.196503
1ZXQ	A	VAL	169	E	-10.065900	14.385272	-11.961208	-4.263112
1ZXQ	A	LEU	170	E	-9.720241	13.275798	-12.282631	-4.415888

1ZXQ	A	ASP	171	E	-9.729686	13.065673	-12.467009	-4.473773
1ZXQ	A	LEU	172	E	-9.781354	12.595128	-12.885547	-4.591293
1ZXQ	A	MET	173	T	-9.158146	8.369755	-14.516477	-5.024628
1ZXQ	A	SER	174	T	-8.911110	7.640452	-14.830130	-5.073309
1ZXQ	A	ARG	175	T	-8.297352	8.636099	-13.525005	-5.216449
1ZXQ	A	GLY	176	T	-6.366418	9.001627	-9.572882	-4.643376
1ZXQ	A	GLY	177	C	-5.768593	9.984300	-8.520964	-4.511659
1ZXQ	A	ASN	178	E	-5.761545	10.016536	-8.530214	-4.509775
1ZXQ	A	ILE	179	E	-5.752948	10.073605	-8.530820	-4.507452
1ZXQ	A	PHE	180	E	-5.758257	10.081643	-8.492400	-4.500590
1ZXQ	A	HIS	181	E	-6.003068	10.626404	-8.048777	-4.439773
1ZXQ	A	LYS	182	E	-7.496614	10.704401	-10.876194	-4.524235
1ZXQ	A	HIS	183	E	-7.379281	9.214658	-11.511811	-4.553201
1ZXQ	A	SER	184	C	-7.508249	7.855048	-12.359000	-4.600464
1ZXQ	A	ALA	185	C	-7.513442	7.812563	-12.353910	-4.597556
1ZXQ	A	PRO	186	C	-7.588297	7.647257	-12.323446	-4.583656
1ZXQ	A	LYS	187	E	-7.847521	7.542651	-12.331381	-4.590228
1ZXQ	A	MET	188	E	-8.783690	10.729656	-12.027922	-4.536383
1ZXQ	A	LEU	189	C	-7.366625	13.958004	-6.608358	-3.381914
1ZXQ	A	GLU	190	E	-7.366625	13.958004	-6.608358	-3.381914
1ZXQ	A	ILE	191	E	-7.366625	13.958004	-6.608358	-3.381914
1ZXQ	A	TYR	192	C	-7.366625	13.958004	-6.608358	-3.381914
2ABL	A	MET	75	C	-3.133744	3.439392	-7.091312	-3.396118
2ABL	A	GLY	76	C	-3.133744	3.439392	-7.091312	-3.396118
2ABL	A	PRO	77	C	-3.133744	3.439392	-7.091312	-3.396118
2ABL	A	SER	78	C	-3.133744	3.439392	-7.091312	-3.396118
2ABL	A	GLU	79	T	-3.989330	3.860900	-9.017474	-4.294586
2ABL	A	ASN	80	T	-4.769551	4.172662	-10.503574	-5.064620
2ABL	A	ASP	81	T	-6.681123	5.763495	-13.851309	-6.286677
2ABL	A	PRO	82	T	-8.109667	7.496125	-15.620769	-6.722860
2ABL	A	ASN	83	T	-9.014842	7.463580	-16.003943	-5.991317
2ABL	A	LEU	84	T	-10.579830	10.992999	-16.588732	-6.264505
2ABL	A	PHE	85	E	-11.415359	16.004306	-12.617006	-4.290335
2ABL	A	VAL	86	E	-9.305502	12.450103	-10.941960	-4.280644
2ABL	A	ALA	87	E	-9.297037	12.487241	-10.970752	-4.287797
2ABL	A	LEU	88	E	-8.760407	12.772515	-10.800444	-4.468860
2ABL	A	TYR	89	T	-8.320433	12.693620	-10.667064	-4.542333
2ABL	A	ASP	90	T	-7.353923	10.019814	-10.149242	-4.271127
2ABL	A	PHE	91	T	-6.183991	7.636428	-9.582548	-4.176631
2ABL	A	VAL	92	B	-4.506900	2.593039	-9.754224	-4.052749
2ABL	A	ALA	93	C	-4.367294	2.493444	-10.029646	-4.090973
2ABL	A	SER	94	C	-3.688783	3.263774	-9.153106	-4.284648
2ABL	A	GLY	95	C	-3.685754	3.277273	-9.163502	-4.287219
2ABL	A	ASP	96	T	-3.693305	3.226119	-9.159223	-4.288697
2ABL	A	ASN	97	T	-3.855154	3.521403	-8.960870	-4.361329
2ABL	A	THR	98	T	-3.910207	3.655677	-8.754581	-4.372831
2ABL	A	LEU	99	B	-6.631291	6.854824	-10.934726	-4.642034
2ABL	A	SER	100	T	-8.488259	9.666098	-12.866492	-4.774914
2ABL	A	ILE	101	C	-8.507201	8.769529	-13.293086	-4.768752
2ABL	A	THR	102	B	-7.946749	7.604754	-13.117767	-4.827484
2ABL	A	LYS	103	T	-7.942065	7.562401	-13.160841	-4.837157
2ABL	A	GLY	104	T	-7.949850	7.503006	-13.168746	-4.844594
2ABL	A	GLU	105	T	-8.032138	7.384170	-13.188809	-4.906377
2ABL	A	LYS	106	E	-8.189478	7.256478	-13.165136	-4.975123
2ABL	A	LEU	107	E	-10.077427	10.400018	-14.401688	-5.147997
2ABL	A	ARG	108	E	-10.984655	14.106626	-13.718356	-4.896533
2ABL	A	VAL	109	E	-10.836229	14.100703	-13.827108	-5.017681
2ABL	A	LEU	110	E	-9.760662	11.768999	-13.747438	-5.421661
2ABL	A	GLY	111	E	-9.216170	10.399808	-14.167362	-5.570518
2ABL	A	TYR	112	E	-8.870881	10.325953	-14.074343	-5.681851
2ABL	A	ASN	113	E	-6.618605	5.109935	-12.871363	-5.454037
2ABL	A	HIS	114	T	-6.543595	5.514873	-12.847317	-5.464803
2ABL	A	ASN	115	T	-6.543942	5.505826	-12.851327	-5.465671
2ABL	A	GLY	116	T	-6.547113	5.487079	-12.843245	-5.464816
2ABL	A	GLU	117	T	-6.552297	5.445373	-12.833744	-5.461843
2ABL	A	TRP	118	T	-7.781378	8.591732	-12.761854	-5.552935
2ABL	A	CYS	119	E	-9.717419	10.338728	-15.063280	-5.776233
2ABL	A	GLU	120	E	-10.248403	11.686438	-15.001944	-5.698001
2ABL	A	ALA	121	E	-9.353916	7.671388	-14.748212	-5.114928
2ABL	A	GLN	122	E	-6.550622	5.170043	-12.642591	-5.424017
2ABL	A	THR	123	E	-5.647680	5.422892	-11.565294	-5.299705
2ABL	A	LYS	124	E	-5.309202	4.695655	-11.813945	-5.232136
2ABL	A	ASN	125	T	-5.308687	4.699478	-11.816238	-5.232482
2ABL	A	GLY	126	T	-5.309201	4.697750	-11.813646	-5.232603
2ABL	A	GLN	127	E	-5.386281	4.635006	-11.700654	-5.205445
2ABL	A	GLY	128	E	-5.800710	3.765971	-12.140711	-5.144593
2ABL	A	TRP	129	E	-9.308540	9.910017	-14.291451	-5.435496
2ABL	A	VAL	130	E	-9.026477	12.299227	-10.996934	-4.279660
2ABL	A	PRO	131	E	-8.012097	12.461340	-9.505752	-4.243563
2ABL	A	SER	132	E	-7.810446	12.652376	-9.622766	-4.350272
2ABL	A	ASN	133	G	-7.511353	13.496469	-8.983944	-4.323498

2ABL	A	TYR	134	G	-7.386270	13.954687	-8.707596	-4.271614
2ABL	A	ILE	135	G	-7.337322	13.868423	-8.745568	-4.271454
2ABL	A	THR	136	E	-7.481355	14.059814	-8.796784	-4.284311
2ABL	A	PRO	137	E	-7.585746	14.229215	-8.598177	-4.220150
2ABL	A	VAL	138	E	-7.937595	13.770884	-9.093558	-4.172458
2ABL	A	ASN	139	T	-8.327654	11.744913	-10.584736	-4.297006
2ABL	A	SER	140	T	-8.644515	10.168188	-12.380825	-4.618409
2ABL	A	LEU	141	T	-8.908136	10.529321	-12.775739	-4.859309
2ABL	A	GLU	142	G	-8.934530	10.490876	-12.773411	-4.883567
2ABL	A	LYS	143	G	-8.950155	10.443064	-12.738201	-4.881604
2ABL	A	HIS	144	G	-8.972854	10.438952	-12.641700	-4.866106
2ABL	A	SER	145	T	-9.947847	9.820763	-14.142556	-4.950752
2ABL	A	TRP	146	T	-11.458946	12.542363	-14.976595	-5.156778
2ABL	A	TYR	147	T	-10.393392	13.565098	-12.260757	-4.700963
2ABL	A	HIS	148	E	-9.318092	10.335676	-12.605976	-4.494350
2ABL	A	GLY	149	E	-9.187555	10.132049	-12.840425	-4.475076
2ABL	A	PRO	150	E	-8.621591	9.661664	-12.198234	-4.280633
2ABL	A	VAL	151	E	-8.111009	8.822985	-11.958046	-4.204811
2ABL	A	SER	152	C	-7.682984	8.481219	-11.553840	-4.133805
2ABL	A	ARG	153	C	-7.561353	8.514389	-11.548685	-4.174006
2ABL	A	ASN	154	H	-7.422226	8.429986	-11.700644	-4.270124
2ABL	A	ALA	155	H	-7.450151	8.388409	-11.724810	-4.281010
2ABL	A	ALA	156	H	-7.572042	8.447523	-11.717171	-4.312977
2ABL	A	GLU	157	H	-7.894384	8.639889	-12.147689	-4.493366
2ABL	A	TYR	158	H	-8.036030	8.633626	-12.228013	-4.418290
2ABL	A	LEU	159	H	-7.898271	8.712092	-11.668077	-4.225953
2ABL	A	LEU	160	H	-7.662477	7.784725	-11.949169	-4.205643
2ABL	A	SER	161	H	-7.123451	5.377050	-12.723797	-4.371453
2ABL	A	SER	162	T	-6.307919	4.323602	-12.293867	-4.586142
2ABL	A	GLY	163	T	-6.219996	4.473035	-12.382848	-4.651697
2ABL	A	ILE	164	T	-6.244566	4.307652	-12.420912	-4.667441
2ABL	A	ASN	165	T	-6.265548	4.233027	-12.416955	-4.684882
2ABL	A	GLY	166	T	-6.355286	4.311234	-12.280709	-4.717781
2ABL	A	SER	167	T	-7.344631	5.723577	-12.839903	-4.974416
2ABL	A	PHE	168	E	-10.477972	13.872198	-12.871063	-4.756962
2ABL	A	LEU	169	E	-10.965443	16.000516	-11.725207	-4.587205
2ABL	A	VAL	170	E	-11.016309	16.040891	-11.477174	-4.526804
2ABL	A	ARG	171	E	-14.635854	14.667079	-19.467090	-5.697914
2ABL	A	GLU	172	E	-12.354344	9.793417	-17.737928	-5.434828
2ABL	A	SER	173	E	-10.742860	9.445421	-15.243805	-4.871967
2ABL	A	GLU	174	T	-10.052808	9.021077	-15.091994	-4.976408
2ABL	A	SER	175	T	-9.972896	8.929022	-15.312509	-5.022926
2ABL	A	SER	176	T	-9.955661	8.967090	-15.370947	-5.042422
2ABL	A	PRO	177	T	-9.961386	8.964841	-15.356104	-5.043052
2ABL	A	GLY	178	T	-10.130712	8.818512	-15.458256	-5.114959
2ABL	A	GLN	179	T	-11.040467	8.781518	-17.043961	-5.447311
2ABL	A	ARG	180	T	-11.896461	10.393839	-17.703178	-5.778299
2ABL	A	SER	181	E	-12.745717	10.843802	-18.771207	-6.013064
2ABL	A	ILE	182	E	-13.807681	13.204447	-19.048365	-6.055592
2ABL	A	SER	183	E	-14.525548	16.368126	-18.225088	-5.603838
2ABL	A	LEU	184	E	-12.238094	13.748828	-15.753388	-5.567864
2ABL	A	ARG	185	E	-10.955674	10.599484	-15.388790	-5.181977
2ABL	A	TYR	186	E	-7.764435	10.268926	-10.708079	-4.810328
2ABL	A	GLU	187	E	-7.692763	10.136593	-10.922095	-4.785321
2ABL	A	GLY	188	T	-7.685330	10.153811	-10.953807	-4.787364
2ABL	A	ARG	189	T	-7.685566	10.152510	-10.951901	-4.787025
2ABL	A	VAL	190	E	-7.687673	10.152358	-10.936256	-4.785795
2ABL	A	TYR	191	E	-8.917157	9.350981	-12.675592	-4.626810
2ABL	A	HIS	192	E	-10.279497	11.543894	-13.482533	-4.951133
2ABL	A	TYR	193	E	-12.343489	14.794400	-15.183348	-5.178216
2ABL	A	ARG	194	E	-10.000809	11.574490	-12.818971	-4.655747
2ABL	A	ILE	195	E	-7.275259	9.680137	-9.555708	-4.146231
2ABL	A	ASN	196	E	-6.632176	7.263472	-10.681214	-4.320124
2ABL	A	THR	197	E	-4.371722	4.251794	-8.756289	-4.170216
2ABL	A	ALA	198	E	-4.239585	4.354756	-9.018525	-4.262929
2ABL	A	SER	199	T	-4.236825	4.367211	-9.031960	-4.265242
2ABL	A	ASP	200	T	-4.240311	4.335968	-9.029033	-4.265951
2ABL	A	GLY	201	T	-4.247288	4.315816	-9.002502	-4.264182
2ABL	A	LYS	202	T	-5.180298	4.815702	-10.100228	-4.631755
2ABL	A	LEU	203	C	-7.411442	7.096941	-11.912125	-4.754683
2ABL	A	TYR	204	E	-10.185871	11.449246	-14.077240	-5.098442
2ABL	A	VAL	205	E	-8.286658	7.587604	-12.439132	-4.465372
2ABL	A	SER	206	T	-8.086064	7.537657	-12.759163	-4.564617
2ABL	A	SER	207	T	-8.072819	7.603874	-12.789702	-4.574785
2ABL	A	GLU	208	T	-8.071299	7.613138	-12.798224	-4.577488
2ABL	A	SER	209	T	-8.084156	7.541774	-12.775841	-4.570791
2ABL	A	ARG	210	T	-8.771872	7.716156	-13.624409	-4.837215
2ABL	A	PHE	211	E	-9.264282	13.934458	-11.146179	-4.805170
2ABL	A	ASN	212	E	-6.666222	10.895170	-8.545373	-4.463311
2ABL	A	THR	213	C	-6.648571	10.998924	-8.563838	-4.460880
2ABL	A	LEU	214	C	-6.647668	11.008026	-8.566363	-4.460884

2ABL	A	ALA	215	H	-6.646768	11.011535	-8.571245	-4.460710
2ABL	A	GLU	216	H	-6.652452	10.976261	-8.554448	-4.458114
2ABL	A	LEU	217	H	-8.670980	14.481216	-9.436326	-4.398014
2ABL	A	VAL	218	H	-10.026917	15.159777	-11.265331	-4.467273
2ABL	A	HIS	219	H	-10.358392	13.506616	-12.326894	-4.494539
2ABL	A	HIS	220	H	-9.912262	9.723730	-13.752919	-4.636971
2ABL	A	HIS	221	H	-9.268534	9.610273	-12.992767	-4.421332
2ABL	A	SER	222	H	-7.978047	6.650662	-12.522120	-4.271900
2ABL	A	THR	223	H	-5.540154	5.246643	-9.854286	-4.269769
2ABL	A	VAL	224	H	-5.497150	5.510476	-9.877610	-4.289309
2ABL	A	ALA	225	C	-5.470872	5.742237	-9.859447	-4.301385
2ABL	A	ASP	226	T	-5.410672	6.400243	-9.716030	-4.364476
2ABL	A	GLY	227	T	-5.126802	9.391169	-8.098944	-4.419127
2ABL	A	LEU	228	T	-5.513693	13.479621	-6.450830	-4.558492
2ABL	A	ILE	229	T	-5.549950	13.877136	-6.190051	-4.568892
2ABL	A	THR	230	T	-5.568570	14.112020	-6.079894	-4.610720
2ABL	A	THR	231	T	-5.580484	14.373805	-6.031486	-4.685968
2ABL	A	LEU	232	T	-5.231038	12.573985	-6.600684	-4.872141
2ABL	A	HIS	233	C	-3.381438	8.027155	-5.208469	-3.897837
2ABL	A	TYR	234	C	-2.508035	6.474431	-4.393737	-3.222325
2ABL	A	PRO	235	C	-2.508035	6.474431	-4.393737	-3.222325
2ABL	A	ALA	236	C	-2.508035	6.474431	-4.393737	-3.222325
2ABL	A	PRO	237	C	-2.508035	6.474431	-4.393737	-3.222325
2CPL	A	VAL	2	C	-6.212240	6.110085	-9.738762	-3.783733
2CPL	A	ASN	3	C	-6.212240	6.110085	-9.738762	-3.783733
2CPL	A	PRO	4	C	-6.212240	6.110085	-9.738762	-3.783733
2CPL	A	THR	5	E	-6.212240	6.110085	-9.738762	-3.783733
2CPL	A	VAL	6	E	-8.150705	9.098332	-11.466335	-4.480886
2CPL	A	PHE	7	E	-11.964029	14.714740	-14.941688	-5.601824
2CPL	A	PHE	8	E	-13.129229	17.815725	-14.179018	-4.703111
2CPL	A	ASP	9	E	-10.538088	15.121888	-16.293354	-8.188452
2CPL	A	ILE	10	E	-8.775572	11.371112	-11.683972	-4.710645
2CPL	A	ALA	11	E	-5.530569	7.379070	-8.648771	-4.217545
2CPL	A	VAL	12	E	-3.194620	5.839578	-6.313440	-4.057240
2CPL	A	ASP	13	T	-3.061291	5.955907	-6.491473	-4.084906
2CPL	A	GLY	14	T	-2.905368	5.927213	-6.612581	-4.075263
2CPL	A	GLU	15	E	-2.904689	5.929750	-6.616196	-4.075262
2CPL	A	PRO	16	E	-2.911726	5.912450	-6.591039	-4.072808
2CPL	A	LEU	17	E	-3.472182	6.023145	-7.040242	-4.066930
2CPL	A	GLY	18	E	-3.775711	5.781957	-6.957850	-3.997057
2CPL	A	ARG	19	E	-6.805212	8.661316	-9.670404	-4.013121
2CPL	A	VAL	20	E	-7.926402	11.365318	-9.248976	-3.891286
2CPL	A	SER	21	E	-10.633708	12.926072	-13.110785	-4.675109
2CPL	A	PHE	22	E	-12.571858	15.670518	-14.646018	-4.828905
2CPL	A	GLU	23	E	-12.405309	16.200016	-14.715764	-5.347505
2CPL	A	LEU	24	E	-10.063691	14.948723	-11.304371	-4.793271
2CPL	A	PHE	25	T	-9.080885	13.690879	-10.795316	-4.635119
2CPL	A	ALA	26	T	-8.023535	9.414360	-11.096942	-4.155883
2CPL	A	ASP	27	T	-8.004048	9.449634	-11.186111	-4.184351
2CPL	A	LYS	28	T	-8.003342	9.453893	-11.190235	-4.185620
2CPL	A	VAL	29	T	-8.019186	9.298687	-11.198152	-4.168908
2CPL	A	PRO	30	H	-8.104407	8.662363	-11.285326	-4.103300
2CPL	A	LYS	31	H	-9.926408	10.949204	-13.923288	-5.014817
2CPL	A	THR	32	H	-10.974421	13.096226	-14.289843	-4.916514
2CPL	A	ALA	33	H	-11.150211	12.846080	-14.160576	-4.789821
2CPL	A	GLU	34	H	-12.083243	11.486545	-16.546396	-5.326485
2CPL	A	ASN	35	H	-13.705044	14.235861	-18.139369	-5.793968
2CPL	A	PHE	36	H	-13.895450	14.976029	-17.445977	-5.650498
2CPL	A	ARG	37	H	-15.026560	14.773375	-19.983715	-5.857376
2CPL	A	ALA	38	H	-10.511360	11.309981	-13.848928	-4.871796
2CPL	A	LEU	39	H	-10.022359	10.492745	-14.576116	-5.197026
2CPL	A	SER	40	H	-8.713666	8.225882	-14.381531	-5.599465
2CPL	A	THR	41	H	-5.175213	6.112479	-10.423014	-5.438174
2CPL	A	GLY	42	T	-5.040143	6.562647	-10.404684	-5.442523
2CPL	A	GLU	43	T	-4.991015	6.799732	-10.399602	-5.444675
2CPL	A	LYS	44	T	-4.990488	6.807265	-10.399778	-5.444801
2CPL	A	GLY	45	T	-4.991399	6.806295	-10.393508	-5.444471
2CPL	A	PHE	46	C	-5.770360	8.708935	-10.337794	-5.461038
2CPL	A	GLY	47	C	-6.479530	9.618088	-10.369092	-5.468619
2CPL	A	TYR	48	T	-8.862257	13.825070	-11.957202	-5.574788
2CPL	A	LYS	49	T	-9.545551	11.982363	-13.889882	-5.590385
2CPL	A	GLY	50	T	-9.735199	11.168958	-14.259088	-5.603226
2CPL	A	SER	51	E	-9.787969	10.839309	-14.273196	-5.590169
2CPL	A	CYS	52	E	-11.507187	12.065370	-16.475246	-5.724201
2CPL	A	PHE	53	E	-11.737441	12.411164	-16.125205	-5.640814
2CPL	A	HIS	54	E	-12.525409	15.621056	-14.914077	-4.920554
2CPL	A	ARG	55	E	-10.013253	12.847958	-11.496777	-4.168437
2CPL	A	ILE	56	E	-8.854293	13.430706	-10.097513	-4.262698
2CPL	A	ILE	57	E	-8.625979	13.283529	-10.548271	-4.484206
2CPL	A	PRO	58	T	-8.598828	13.235315	-10.696820	-4.522883
2CPL	A	GLY	59	T	-8.599114	13.233102	-10.696822	-4.523558

2CPL	A	PHE	60	T	-8.655603	13.275139	-10.619982	-4.559624
2CPL	A	MET	61	E	-9.214536	12.855705	-11.868505	-5.017209
2CPL	A	CYS	62	E	-10.368008	11.965620	-14.373497	-5.440201
2CPL	A	GLN	63	E	-11.616134	10.275343	-18.353189	-6.183357
2CPL	A	GLY	64	E	-10.234389	11.779861	-14.624566	-5.685078
2CPL	A	GLY	65	C	-9.786822	12.382744	-14.001572	-5.570560
2CPL	A	ASP	66	T	-9.563449	12.128672	-14.072093	-5.530504
2CPL	A	PHE	67	T	-8.042698	10.717081	-11.222703	-4.847644
2CPL	A	THR	68	T	-6.555234	6.682209	-11.329772	-4.814136
2CPL	A	ARG	69	T	-5.529532	5.020963	-10.644434	-4.508210
2CPL	A	HIS	70	T	-5.385234	4.803388	-11.065633	-4.650581
2CPL	A	ASN	71	C	-4.627826	3.850255	-11.157039	-5.136491
2CPL	A	GLY	72	C	-4.575264	4.019083	-11.215488	-5.179613
2CPL	A	THR	73	C	-4.592203	3.960748	-11.218850	-5.193948
2CPL	A	GLY	74	C	-4.701458	3.824383	-11.365442	-5.346464
2CPL	A	GLY	75	C	-4.743344	3.809891	-11.275024	-5.359408
2CPL	A	LYS	76	C	-5.972033	6.284627	-11.847338	-5.612819
2CPL	A	SER	77	B	-7.235234	10.355487	-11.841866	-5.468819
2CPL	A	ILE	78	T	-6.341544	10.703088	-9.600641	-5.198039
2CPL	A	TYR	79	T	-6.349190	10.710136	-9.564486	-5.195748
2CPL	A	GLY	80	B	-6.346455	10.703493	-9.585012	-5.196829
2CPL	A	GLU	81	C	-6.369102	10.596675	-9.544314	-5.185075
2CPL	A	LYS	82	C	-6.420819	10.559869	-9.407261	-5.179000
2CPL	A	PHE	83	B	-9.041647	11.340633	-13.382771	-5.583711
2CPL	A	GLU	84	C	-9.447396	10.063055	-13.921520	-5.465581
2CPL	A	ASP	85	C	-11.561995	11.938177	-16.402635	-5.539253
2CPL	A	GLU	86	C	-10.571283	13.378083	-13.447003	-5.135759
2CPL	A	ASN	87	C	-9.070982	13.033812	-11.132254	-4.741107
2CPL	A	PHE	88	C	-8.996120	13.327833	-11.166354	-4.768946
2CPL	A	ILE	89	C	-8.229686	12.346097	-10.736489	-4.730198
2CPL	A	LEU	90	C	-8.032753	12.302560	-10.931242	-4.843058
2CPL	A	LYS	91	C	-6.824106	10.393029	-9.924765	-4.854291
2CPL	A	HIS	92	C	-6.060430	9.348802	-9.690128	-4.894121
2CPL	A	THR	93	C	-4.865937	8.464245	-7.724580	-4.332297
2CPL	A	GLY	94	T	-4.863766	8.471358	-7.730206	-4.330918
2CPL	A	PRO	95	T	-4.864438	8.467146	-7.726046	-4.329836
2CPL	A	GLY	96	T	-4.883659	8.412708	-7.658187	-4.312399
2CPL	A	ILE	97	E	-4.946240	8.348717	-7.440223	-4.245867
2CPL	A	LEU	98	E	-7.861408	11.081081	-9.858400	-4.263762
2CPL	A	SER	99	E	-9.857231	12.283399	-11.845815	-4.352545
2CPL	A	MET	100	E	-10.103192	8.493140	-15.515366	-5.384870
2CPL	A	ALA	101	E	-6.635681	4.584729	-11.947121	-4.535321
2CPL	A	ASN	102	E	-6.025551	4.213730	-12.197896	-4.800651
2CPL	A	ALA	103	C	-4.449270	4.711568	-9.252162	-4.509654
2CPL	A	GLY	104	T	-4.448529	4.714184	-9.258279	-4.510744
2CPL	A	PRO	105	T	-4.448386	4.715034	-9.259438	-4.510946
2CPL	A	ASN	106	T	-4.463314	4.718529	-9.190891	-4.510268
2CPL	A	THR	107	T	-4.491261	4.752636	-9.038501	-4.488911
2CPL	A	ASN	108	E	-8.276402	7.102500	-14.197330	-5.374001
2CPL	A	GLY	109	E	-9.226049	8.297116	-14.425690	-5.360623
2CPL	A	SER	110	E	-11.851770	9.809048	-18.129781	-6.021575
2CPL	A	GLN	111	E	-13.186294	10.630454	-19.740344	-6.321490
2CPL	A	PHE	112	E	-13.414828	20.780287	-13.624400	-5.439553
2CPL	A	PHE	113	E	-12.171224	17.591076	-13.192424	-5.048910
2CPL	A	ILE	114	E	-10.409048	13.516971	-12.814489	-4.964485
2CPL	A	CYS	115	E	-9.842418	12.240650	-13.363803	-5.126267
2CPL	A	THR	116	C	-9.398826	11.781551	-13.281695	-5.140640
2CPL	A	ALA	117	C	-9.164432	11.017187	-13.523104	-5.075950
2CPL	A	LYS	118	C	-9.021888	11.157740	-13.461561	-5.102127
2CPL	A	THR	119	C	-9.014897	11.026100	-13.601978	-5.158816
2CPL	A	GLU	120	G	-8.819455	10.796694	-13.546937	-5.264778
2CPL	A	TRP	121	G	-8.529302	10.620309	-13.054388	-5.211764
2CPL	A	LEU	122	G	-8.541302	10.787710	-13.013808	-5.249106
2CPL	A	ASP	123	T	-8.594147	10.682495	-13.019934	-5.253884
2CPL	A	GLY	124	T	-8.614430	10.660417	-12.962941	-5.228273
2CPL	A	LYS	125	T	-8.805697	10.703887	-12.762162	-5.143621
2CPL	A	HIS	126	T	-9.768066	11.459966	-13.813140	-5.164197
2CPL	A	VAL	127	C	-10.444090	13.651677	-13.394713	-4.761993
2CPL	A	VAL	128	E	-10.274452	15.879061	-11.613037	-4.517497
2CPL	A	PHE	129	E	-9.670472	15.847079	-11.236794	-5.080869
2CPL	A	GLY	130	E	-8.352003	10.251661	-12.441063	-5.280722
2CPL	A	LYS	131	E	-7.583775	9.710726	-11.999567	-5.324073
2CPL	A	VAL	132	E	-7.442902	9.773902	-12.077592	-5.334222
2CPL	A	LYS	133	E	-7.345669	9.542686	-12.359183	-5.407221
2CPL	A	GLU	134	E	-7.192913	9.273557	-12.280008	-5.273664
2CPL	A	GLY	135	C	-7.207489	9.424595	-12.093827	-5.185925
2CPL	A	MET	136	H	-7.477483	9.419946	-12.254697	-5.071248
2CPL	A	ASN	137	H	-7.617956	9.263959	-12.233538	-4.973454
2CPL	A	ILE	138	H	-7.783893	9.536814	-11.706623	-4.709813
2CPL	A	VAL	139	H	-8.399890	11.088049	-11.212118	-4.469275
2CPL	A	GLU	140	H	-9.266501	11.105703	-12.505107	-4.486347

2CPL	A	ALA	141	H	-9.853461	11.100376	-13.081694	-4.476418
2CPL	A	MET	142	H	-10.754045	12.812375	-14.352987	-5.029357
2CPL	A	GLU	143	H	-10.804195	12.452992	-14.548907	-5.058866
2CPL	A	ARG	144	H	-10.170183	10.224386	-13.877232	-4.300449
2CPL	A	PHE	145	C	-9.008370	8.504579	-12.979584	-4.349834
2CPL	A	GLY	146	C	-5.434879	4.016836	-10.293402	-4.221618
2CPL	A	SER	147	T	-5.372857	3.947381	-10.480300	-4.208086
2CPL	A	ARG	148	T	-5.220790	4.251696	-10.591725	-4.298488
2CPL	A	ASN	149	T	-5.215362	4.258602	-10.624688	-4.306323
2CPL	A	GLY	150	T	-5.213934	4.261759	-10.634314	-4.309227
2CPL	A	LYS	151	C	-5.901425	4.827366	-11.401144	-4.502801
2CPL	A	THR	152	T	-6.059514	5.384131	-11.165847	-4.646319
2CPL	A	SER	153	T	-7.641018	6.763341	-13.847554	-5.191514
2CPL	A	LYS	154	T	-8.118949	8.904834	-13.413662	-5.259259
2CPL	A	LYS	155	T	-8.552243	11.420678	-12.817662	-5.445211
2CPL	A	ILE	156	E	-8.622340	12.063170	-12.403551	-5.419770
2CPL	A	THR	157	E	-9.535626	11.931384	-13.270533	-4.883705
2CPL	A	ILE	158	E	-9.990854	12.870266	-13.010617	-4.647967
2CPL	A	ALA	159	E	-10.073644	12.698158	-13.042496	-4.642231
2CPL	A	ASP	160	E	-10.085294	12.493674	-13.529224	-4.936640
2CPL	A	CYS	161	E	-9.187029	9.925490	-14.266827	-5.703929
2CPL	A	GLY	162	E	-6.589429	7.988443	-10.201631	-4.578789
2CPL	A	GLN	163	E	-6.589429	7.988443	-10.201631	-4.578789
2CPL	A	LEU	164	C	-6.589429	7.988443	-10.201631	-4.578789
2CPL	A	GLU	165	C	-6.589429	7.988443	-10.201631	-4.578789
2FCB	A	ALA	6	C	-3.872827	4.643147	-6.878085	-3.219337
2FCB	A	PRO	7	C	-3.872827	4.643147	-6.878085	-3.219337
2FCB	A	PRO	8	C	-3.872827	4.643147	-6.878085	-3.219337
2FCB	A	LYS	9	B	-3.872827	4.643147	-6.878085	-3.219337
2FCB	A	ALA	10	C	-5.336358	6.617996	-8.372736	-3.822373
2FCB	A	VAL	11	E	-7.225765	8.065197	-11.082969	-4.643002
2FCB	A	LEU	12	E	-9.245450	12.560956	-12.848535	-5.585987
2FCB	A	LYS	13	E	-10.208674	12.027267	-14.002494	-4.771331
2FCB	A	LEU	14	E	-9.524108	13.587628	-11.953503	-4.758028
2FCB	A	GLU	15	E	-9.533559	13.616165	-11.930712	-4.763995
2FCB	A	PRO	16	T	-9.580354	13.685348	-11.795477	-4.759041
2FCB	A	GLN	17	T	-9.619212	13.716042	-11.698754	-4.774012
2FCB	A	TRP	18	T	-9.707775	14.280340	-11.243452	-4.784603
2FCB	A	ILE	19	T	-11.462528	14.250353	-13.620369	-4.751667
2FCB	A	ASN	20	E	-12.887739	15.970561	-15.741219	-5.169050
2FCB	A	VAL	21	E	-13.073172	15.205955	-16.683768	-5.301595
2FCB	A	LEU	22	E	-12.954562	14.042918	-17.326809	-5.418983
2FCB	A	GLN	23	T	-12.619041	12.218000	-17.846937	-5.454756
2FCB	A	GLU	24	T	-11.453216	11.234661	-15.826088	-5.183857
2FCB	A	ASP	25	E	-11.325524	11.636927	-15.587284	-5.068634
2FCB	A	SER	26	E	-10.637153	13.258617	-13.271882	-4.633023
2FCB	A	VAL	27	E	-10.281557	13.669229	-12.868251	-4.678011
2FCB	A	THR	28	E	-10.247896	13.605216	-13.001792	-4.705539
2FCB	A	LEU	29	E	-9.735550	12.182741	-13.211054	-4.887495
2FCB	A	THR	30	E	-8.395960	8.823321	-13.199521	-5.155095
2FCB	A	CYS	31	E	-7.022104	7.759306	-11.752532	-5.080613
2FCB	A	ARG	32	E	-5.773983	7.310818	-9.631660	-4.501449
2FCB	A	GLY	33	C	-3.053557	6.234271	-6.141667	-4.267235
2FCB	A	THR	34	C	-2.904161	6.247373	-6.328829	-4.254718
2FCB	A	HIS	35	C	-2.887896	6.242401	-6.392658	-4.252851
2FCB	A	SER	36	C	-2.871678	6.216723	-6.462187	-4.251279
2FCB	A	PRO	37	C	-2.875015	6.208746	-6.447702	-4.249935
2FCB	A	GLU	38	T	-3.662118	6.101974	-7.319261	-4.162749
2FCB	A	SER	39	T	-4.593858	5.627889	-8.851218	-4.152207
2FCB	A	ASP	40	T	-4.977496	5.305815	-9.070134	-4.174161
2FCB	A	SER	41	T	-6.861717	6.121875	-11.783197	-4.537177
2FCB	A	ILE	42	C	-8.024405	8.574023	-13.122384	-5.317321
2FCB	A	GLN	43	E	-9.571587	9.419277	-13.917571	-5.070314
2FCB	A	TRP	44	E	-12.398075	15.862332	-16.368293	-6.262610
2FCB	A	PHE	45	E	-8.799391	8.365278	-13.591635	-5.161172
2FCB	A	HIS	46	E	-5.809048	6.739499	-10.023060	-4.752623
2FCB	A	ASN	47	T	-5.620158	7.120958	-9.927613	-4.685382
2FCB	A	GLY	48	T	-5.190976	7.192014	-9.146671	-4.308306
2FCB	A	ASN	49	E	-4.815893	7.032246	-8.511300	-3.993553
2FCB	A	LEU	50	E	-4.026524	8.324744	-6.285832	-3.761821
2FCB	A	ILE	51	T	-3.941063	8.368383	-6.242406	-3.728390
2FCB	A	PRO	52	T	-3.949625	8.369118	-6.196070	-3.716604
2FCB	A	THR	53	T	-3.988523	8.443191	-6.044917	-3.699973
2FCB	A	HIS	54	T	-4.061765	8.650550	-5.813791	-3.707377
2FCB	A	THR	55	C	-4.962866	8.160875	-6.972487	-3.809592
2FCB	A	GLN	56	T	-7.702553	6.830776	-11.866136	-4.318937
2FCB	A	PRO	57	T	-10.465377	9.190771	-14.751651	-4.507457
2FCB	A	SER	58	E	-11.647373	14.279894	-14.990294	-5.078449
2FCB	A	TYR	59	E	-11.682753	15.642382	-14.271829	-5.078986
2FCB	A	ARG	60	E	-11.147449	13.042001	-14.750713	-4.984437
2FCB	A	PHE	61	E	-11.165143	12.962049	-14.770015	-4.993147

```
2FCB         A          LYS             62                   E -10.139511  6.582083 -16.611803 -5.149632
2FCB         A          ALA             63                   E -9.273938  5.715234 -15.999313 -5.150278
2FCB         A          ASN             64                   C -9.181641  5.548782 -16.244053 -5.184703
2FCB         A          ASN             65                   G -9.173865  5.376038 -16.372141 -5.200720
2FCB         A          ASN             66                   G -9.170095  5.379649 -16.391271 -5.202598
2FCB         A          ASP             67                   G -9.275194  5.378590 -16.282202 -5.207563
2FCB         A          SER             68                   C -10.165885  4.755365 -17.984650 -5.404276
2FCB         A          GLY             69                   E -11.000049  5.349237 -18.999941 -5.517006
2FCB         A          GLU             70                   E -11.821779  9.143930 -18.255654 -5.614032
2FCB         A          TYR             71                   E -12.364805 13.505903 -16.596848 -5.805034
2FCB         A          THR             72                   E -11.401449 10.272927 -17.579299 -6.160167
2FCB         A          CYS             73                   E -10.993322  9.036220 -18.331900 -6.363401
2FCB         A          GLN             74                   E -9.415476  9.891699 -15.267312 -6.277172
2FCB         A          THR             75                   T -8.713291  9.273760 -14.523190 -5.896267
2FCB         A          GLY             76                   T -8.647394  9.186431 -14.633223 -5.861480
2FCB         A          GLN             77                   T -8.651612  9.184889 -14.610886 -5.858421
2FCB         A          THR             78                   T -8.642436  9.208257 -14.596512 -5.839655
2FCB         A          SER             79                   B -8.280612  8.856717 -13.322817 -5.168433
2FCB         A          LEU             80                   C -8.159053  9.526389 -12.194961 -4.693924
2FCB         A          SER             81                   C -7.907450  9.431004 -11.915681 -4.566887
2FCB         A          ASP             82                   C -7.777511  9.972723 -11.544173 -4.473138
2FCB         A          PRO             83                   C -7.625535 10.824866 -10.883264 -4.344279
2FCB         A          VAL             84                   E -7.745126 11.389451 -10.467887 -4.226923
2FCB         A          HIS             85                   E -7.891053 11.722705 -10.210081 -4.159357
2FCB         A          LEU             86                   E -8.151899 13.206858 -9.374423 -4.013345
2FCB         A          THR             87                   E -8.376524 13.604686 -9.317548 -4.047625
2FCB         A          VAL             88                   E -9.365655 13.409307 -11.917916 -4.603894
2FCB         A          LEU             89                   E -9.517521 12.953142 -12.547611 -4.837584
2FCB         A          SER             90                   C -9.597095 12.726226 -12.838255 -4.963708
2FCB         A          GLU             91                   C -9.706638 12.402237 -13.050317 -5.056512
2FCB         A          TRP             92                   C -10.554117 16.089063 -12.867589 -5.342094
2FCB         A          LEU             93                   E -10.767962 16.781199 -12.567406 -5.353262
2FCB         A          VAL             94                   E -11.085112 16.966521 -12.474148 -5.264101
2FCB         A          LEU             95                   E -11.928481 17.031949 -14.178881 -5.337083
2FCB         A          GLN             96                   E -11.429477 13.849563 -14.808835 -5.248506
2FCB         A          THR             97                   C -8.272059 12.512563 -10.063270 -4.696812
2FCB         A          PRO             98                   C -8.235550 12.573040 -10.157045 -4.697373
2FCB         A          HIS             99                   C -8.229607 12.580949 -10.191226 -4.702028
2FCB         A          LEU            100                   C -8.228688 12.591119 -10.200669 -4.707936
2FCB         A          GLU            101                   E -8.227292 12.595698 -10.211186 -4.712189
2FCB         A          PHE            102                   E -9.668103 13.515854 -12.498559 -4.974607
2FCB         A          GLN            103                   T -8.262841  9.806698 -12.310528 -5.232397
2FCB         A          GLU            104                   T -7.765568 11.016145 -11.360731 -5.165672
2FCB         A          GLY            105                   T -6.527581 11.529046 -8.791487 -4.771412
2FCB         A          GLU            106                   b -6.515648 11.604046 -8.796048 -4.766451
2FCB         A          THR            107                   C -6.515500 11.607354 -8.794789 -4.765992
2FCB         A          ILE            108                   E -6.546342 11.710079 -8.610305 -4.741524
2FCB         A          VAL            109                   E -6.591347 11.691267 -8.448337 -4.712015
2FCB         A          LEU            110                   E -8.800354 15.299528 -9.203284 -4.544740
2FCB         A          ARG            111                   E -10.666373 16.049501 -11.380291 -4.626011
2FCB         A          CYS            112                   E -12.174749 14.993520 -14.523426 -4.985804
2FCB         A          HIS            113                   E -12.327842 12.680397 -17.420857 -6.077414
2FCB         A          SER            114                   E -9.928905 12.695375 -13.717549 -5.908079
2FCB         A          TRP            115                   G -8.442339 10.470453 -12.648657 -5.513096
2FCB         A          LYS            116                   G -7.190228 10.136817 -10.924329 -5.249964
2FCB         A          ASP            117                   G -7.068296 10.069831 -10.971966 -5.142694
2FCB         A          LYS            118                   C -7.048940 10.110274 -10.997147 -5.128737
2FCB         A          PRO            119                   C -7.038351 10.135454 -10.968233 -5.091472
2FCB         A          LEU            120                   E -7.090366 10.131849 -10.820876 -5.053697
2FCB         A          VAL            121                   E -7.894414 10.255055 -11.207673 -4.591263
2FCB         A          LYS            122                   E -8.715697 11.692753 -11.288900 -4.345264
2FCB         A          VAL            123                   E -9.172519 12.112023 -10.724535 -3.917624
2FCB         A          THR            124                   E -10.698587 14.962867 -11.774483 -4.376796
2FCB         A          PHE            125                   E -12.028044 16.828395 -12.867117 -4.634346
2FCB         A          PHE            126                   E -10.323589  8.963082 -15.955773 -5.757572
2FCB         A          GLN            127                   E -7.637080  6.087506 -13.509770 -5.364805
2FCB         A          ASN            128                   T -5.415868  5.721958 -10.321130 -4.909141
2FCB         A          GLY            129                   T -5.400409  5.771180 -10.370593 -4.914234
2FCB         A          LYS            130                   E -5.397287  5.794702 -10.380043 -4.915533
2FCB         A          SER            131                   E -5.396320  5.804427 -10.382816 -4.916168
2FCB         A          LYS            132                   E -5.408354  5.809938 -10.316207 -4.905852
2FCB         A          LYS            133                   E -7.373127  8.416904 -12.266907 -5.100836
2FCB         A          PHE            134                   E -8.048910 10.140780 -12.413677 -4.970516
2FCB         A          SER            135                   E -8.288057  9.362674 -12.751164 -4.599958
2FCB         A          ARG            136                   T -7.953352  7.384090 -12.531311 -4.125380
2FCB         A          SER            137                   T -8.070763  6.732828 -12.590444 -3.959120
2FCB         A          ASP            138                   T -8.090757  6.691145 -12.560178 -3.958335
2FCB         A          PRO            139                   C -8.167937  6.566737 -12.494419 -3.941635
2FCB         A          ASN            140                   E -8.235645  6.965469 -12.315044 -4.022097
2FCB         A          PHE            141                   E -7.982782 13.212271 -8.952647 -4.278202
2FCB         A          SER            142                   E -6.782017 10.461998 -8.364857 -3.801487
```

2FCB	A	ILE	143	E	-6.727544	10.336937	-8.604809	-3.837171
2FCB	A	PRO	144	T	-6.713537	10.241971	-8.721451	-3.848415
2FCB	A	GLN	145	T	-6.713039	10.207547	-8.741303	-3.847940
2FCB	A	ALA	146	b	-6.781876	9.828746	-8.749219	-3.798894
2FCB	A	ASN	147	C	-7.981540	8.393920	-11.872733	-4.257581
2FCB	A	HIS	148	G	-8.766338	6.519973	-13.984088	-4.380313
2FCB	A	SER	149	G	-9.640157	6.356512	-15.480099	-4.547172
2FCB	A	HIS	150	G	-10.393918	6.680307	-16.397674	-4.705611
2FCB	A	SER	151	C	-11.266814	5.902953	-18.394266	-5.023452
2FCB	A	GLY	152	E	-11.921717	6.469439	-19.227119	-5.234343
2FCB	A	ASP	153	E	-12.768829	10.567754	-19.078139	-5.653892
2FCB	A	TYR	154	E	-12.469732	13.803646	-16.977768	-5.809220
2FCB	A	HIS	155	E	-11.733771	11.143081	-17.465031	-5.890977
2FCB	A	CYS	156	E	-10.798900	11.980477	-16.287437	-6.169713
2FCB	A	THR	157	E	-9.252149	10.855523	-13.479974	-5.434632
2FCB	A	GLY	158	E	-7.223540	7.682232	-11.628743	-4.888621
2FCB	A	ASN	159	E	-5.584588	8.298690	-9.000824	-4.702611
2FCB	A	ILE	160	E	-3.511682	7.974325	-5.795469	-4.197255
2FCB	A	GLY	161	T	-3.502658	7.981153	-5.843129	-4.200966
2FCB	A	TYR	162	T	-3.501984	7.983303	-5.847730	-4.201137
2FCB	A	THR	163	E	-3.503053	7.984018	-5.837386	-4.199889
2FCB	A	LEU	164	E	-3.519922	7.972539	-5.750261	-4.185099
2FCB	A	TYR	165	E	-5.943237	8.499506	-9.008575	-4.418995
2FCB	A	SER	166	E	-7.439860	9.861370	-10.262884	-4.397022
2FCB	A	SER	167	C	-8.193032	9.375821	-11.971806	-4.474330
2FCB	A	LYS	168	B	-7.923873	10.417447	-11.057368	-4.319483
2FCB	A	PRO	169	C	-7.226387	12.115119	-8.849921	-4.089211
2FCB	A	VAL	170	E	-7.197771	12.204981	-8.851857	-4.079178
2FCB	A	THR	171	E	-7.221720	12.352094	-8.701538	-4.069711
2FCB	A	ILE	172	E	-7.288878	12.891019	-8.358118	-4.068020
2FCB	A	THR	173	E	-6.851929	11.376373	-9.292170	-4.551436
2FCB	A	VAL	174	E	-5.707701	8.504341	-8.150432	-3.950321
2FCB	A	GLN	175	C	-3.860525	5.500162	-6.383959	-3.263390
2FCB	A	ALA	176	C	-3.860525	5.500162	-6.383959	-3.263390
2FCB	A	PRO	177	C	-3.860525	5.500162	-6.383959	-3.263390
2FCB	A	ALA	178	C	-3.860525	5.500162	-6.383959	-3.263390
2FHA	A	THR	5	C	-3.022834	2.631436	-6.691494	-3.268201
2FHA	A	SER	6	T	-3.022834	2.631436	-6.691494	-3.268201
2FHA	A	GLN	7	T	-3.022834	2.631436	-6.691494	-3.268201
2FHA	A	VAL	8	T	-3.022834	2.631436	-6.691494	-3.268201
2FHA	A	ARG	9	T	-6.061134	4.449968	-11.464380	-4.468615
2FHA	A	GLN	10	T	-7.218309	4.905005	-13.483199	-5.230234
2FHA	A	ASN	11	T	-9.233238	5.427303	-17.282607	-6.289863
2FHA	A	TYR	12	T	-10.830429	11.388604	-16.778803	-6.251861
2FHA	A	HIS	13	C	-10.610431	10.834352	-16.733881	-6.100819
2FHA	A	GLN	14	H	-10.491313	10.277191	-16.900654	-5.995177
2FHA	A	ASP	15	H	-10.591307	10.216302	-16.888152	-5.968692
2FHA	A	SER	16	H	-10.852374	9.452293	-17.281547	-5.816573
2FHA	A	GLU	17	H	-10.911354	9.057337	-17.358775	-5.782323
2FHA	A	ALA	18	H	-11.304400	8.461364	-17.538387	-5.323088
2FHA	A	ALA	19	H	-12.105599	10.081553	-16.912992	-4.591601
2FHA	A	ILE	20	H	-12.230556	10.223562	-16.477725	-4.392344
2FHA	A	ASN	21	H	-12.351011	9.792878	-16.314289	-4.221376
2FHA	A	ARG	22	H	-12.361331	9.824145	-16.245640	-4.204018
2FHA	A	GLN	23	H	-14.361548	13.284564	-19.306684	-5.475140
2FHA	A	ILE	24	H	-13.864132	15.336999	-17.481486	-5.478023
2FHA	A	ASN	25	H	-13.854905	15.420771	-17.473580	-5.492213
2FHA	A	LEU	26	H	-13.665952	16.090853	-17.028434	-5.431449
2FHA	A	GLU	27	H	-13.773996	16.842572	-16.650754	-5.448435
2FHA	A	LEU	28	H	-13.539218	17.688443	-15.853082	-5.301179
2FHA	A	TYR	29	H	-13.177631	17.744352	-14.605890	-4.886303
2FHA	A	ALA	30	H	-13.042606	18.064062	-14.501286	-4.916096
2FHA	A	SER	31	H	-13.024950	18.050111	-14.517414	-4.924166
2FHA	A	TYR	32	H	-12.905643	17.987244	-14.559700	-4.927801
2FHA	A	VAL	33	H	-12.857007	17.686799	-14.732669	-4.968873
2FHA	A	TYR	34	H	-13.126549	17.849822	-15.167534	-5.141818
2FHA	A	LEU	35	H	-12.716779	14.722410	-16.139283	-5.233453
2FHA	A	SER	36	H	-12.758206	14.500883	-16.187186	-5.235387
2FHA	A	MET	37	H	-12.848771	14.012222	-16.408572	-5.286845
2FHA	A	SER	38	H	-12.938557	13.626468	-16.567291	-5.304014
2FHA	A	TYR	39	H	-12.927452	13.794325	-16.570076	-5.336341
2FHA	A	TYR	40	H	-13.574254	18.194514	-17.002168	-6.193562
2FHA	A	PHE	41	H	-9.240899	10.350389	-12.150658	-4.480122
2FHA	A	ASP	42	H	-6.292327	5.963244	-10.194783	-4.092507
2FHA	A	ARG	43	T	-5.626927	5.392230	-9.877938	-3.902919
2FHA	A	ASP	44	T	-5.359288	6.084425	-9.515617	-3.924028
2FHA	A	ASP	45	T	-5.345991	6.126121	-9.539000	-3.923981
2FHA	A	VAL	46	T	-5.345394	6.129741	-9.540122	-3.923886
2FHA	A	ALA	47	T	-5.478249	6.179189	-9.378623	-3.882007
2FHA	A	LEU	48	C	-5.919314	7.352905	-8.995265	-3.959743
2FHA	A	LYS	49	H	-7.534176	8.212917	-10.686147	-3.955144

2FHA	A	ASN	50	H	-8.849574	10.273716	-11.663506	-4.235192
2FHA	A	PHE	51	H	-10.153781	11.821915	-12.825581	-4.469944
2FHA	A	ALA	52	H	-10.201057	11.631341	-12.760242	-4.448635
2FHA	A	LYS	53	H	-10.208528	11.580128	-12.741698	-4.443984
2FHA	A	TYR	54	H	-13.575078	17.196824	-16.334894	-5.393242
2FHA	A	PHE	55	H	-13.813491	17.282520	-16.890324	-5.543059
2FHA	A	LEU	56	H	-11.527703	9.284378	-16.747176	-5.269606
2FHA	A	HIS	57	H	-11.283908	8.964988	-17.181281	-5.368389
2FHA	A	GLN	58	H	-11.285317	8.933875	-17.192703	-5.370040
2FHA	A	SER	59	H	-11.284364	8.930868	-17.201359	-5.370860
2FHA	A	HIS	60	H	-11.241530	8.965159	-17.292691	-5.383946
2FHA	A	GLU	61	H	-11.779940	8.718552	-18.191547	-5.579840
2FHA	A	GLU	62	H	-12.678689	9.934745	-18.817051	-5.650803
2FHA	A	ARG	63	H	-11.958089	10.038619	-17.328043	-5.185601
2FHA	A	GLU	64	H	-11.911245	10.066855	-17.448344	-5.226216
2FHA	A	HIS	65	H	-12.051078	10.257069	-17.168561	-5.138358
2FHA	A	ALA	66	H	-11.689915	11.958123	-16.142259	-5.220973
2FHA	A	GLU	67	H	-11.142809	12.392473	-15.551711	-5.436479
2FHA	A	LYS	68	H	-11.120258	13.646939	-14.992675	-5.524022
2FHA	A	LEU	69	H	-11.101310	13.862964	-14.925086	-5.536364
2FHA	A	MET	70	H	-11.081034	13.825729	-15.011567	-5.550812
2FHA	A	LYS	71	H	-10.858891	12.150911	-15.652271	-5.597200
2FHA	A	LEU	72	H	-11.136069	11.835648	-15.943089	-5.608753
2FHA	A	GLN	73	H	-11.274634	10.550771	-16.555395	-5.646458
2FHA	A	ASN	74	H	-10.940850	9.421283	-17.218379	-5.814320
2FHA	A	GLN	75	H	-10.938378	9.314936	-17.276023	-5.811554
2FHA	A	ARG	76	H	-11.164005	9.290948	-17.681672	-5.907185
2FHA	A	GLY	77	C	-8.446165	8.180126	-13.053399	-5.043054
2FHA	A	GLY	78	C	-7.776784	8.754908	-11.993990	-4.765117
2FHA	A	ARG	79	C	-7.626957	8.832157	-12.018924	-4.741197
2FHA	A	ILE	80	C	-6.059797	8.483621	-9.678634	-4.788973
2FHA	A	PHE	81	C	-5.792271	8.249792	-9.785709	-4.725743
2FHA	A	LEU	82	C	-5.368160	7.620373	-9.577663	-4.593793
2FHA	A	GLN	83	C	-5.345843	7.554673	-9.665407	-4.600756
2FHA	A	ASP	84	C	-5.276085	7.660498	-9.599226	-4.542838
2FHA	A	ILE	85	C	-5.399146	7.484580	-9.632884	-4.434638
2FHA	A	GLN	86	C	-5.393940	7.226666	-9.677014	-4.366742
2FHA	A	LYS	87	C	-4.799424	5.676746	-9.007980	-4.172055
2FHA	A	PRO	88	C	-4.704619	5.614335	-9.201034	-4.228878
2FHA	A	ASP	89	C	-4.729166	5.488909	-9.214965	-4.238336
2FHA	A	CYS	90	T	-4.742887	5.417465	-9.208410	-4.242664
2FHA	A	ASP	91	T	-4.782552	5.342646	-9.140528	-4.241519
2FHA	A	ASP	92	T	-5.759775	5.460368	-10.530215	-4.593057
2FHA	A	TRP	93	T	-7.919536	8.338137	-13.126479	-5.341570
2FHA	A	GLU	94	T	-8.688987	9.556940	-13.841719	-5.546081
2FHA	A	SER	95	T	-9.519332	10.058978	-14.722450	-5.492340
2FHA	A	GLY	96	H	-9.548612	10.026612	-14.643163	-5.460537
2FHA	A	LEU	97	H	-9.723607	9.460238	-14.611024	-5.316393
2FHA	A	ASN	98	H	-9.731385	9.315255	-14.656619	-5.310858
2FHA	A	ALA	99	H	-11.200678	12.407004	-15.893519	-5.414472
2FHA	A	MET	100	H	-11.353079	12.974352	-15.840593	-5.492544
2FHA	A	GLU	101	H	-10.833983	11.054043	-15.195612	-4.997973
2FHA	A	CYS	102	H	-10.391096	12.094499	-13.815068	-4.680618
2FHA	A	ALA	103	H	-10.425501	12.109358	-13.652035	-4.614998
2FHA	A	LEU	104	H	-10.450518	12.063008	-13.594876	-4.585747
2FHA	A	HIS	105	H	-10.266774	11.706471	-13.962600	-4.734518
2FHA	A	LEU	106	H	-10.439499	12.263412	-13.669975	-4.722476
2FHA	A	GLU	107	H	-10.932667	11.242250	-15.177258	-5.171267
2FHA	A	LYS	108	H	-10.356537	10.554339	-15.125996	-5.236708
2FHA	A	ASN	109	H	-10.345509	10.496124	-15.192090	-5.244667
2FHA	A	VAL	110	H	-10.569761	10.316452	-15.295336	-5.287434
2FHA	A	ASN	111	H	-10.557570	10.278101	-15.332814	-5.280892
2FHA	A	GLN	112	H	-10.314519	10.186661	-15.130290	-5.081782
2FHA	A	SER	113	H	-10.767805	10.641484	-15.091231	-4.826469
2FHA	A	LEU	114	H	-10.800162	10.771218	-14.924148	-4.792371
2FHA	A	LEU	115	H	-10.772693	10.772000	-14.989717	-4.798001
2FHA	A	GLU	116	H	-10.794231	10.783813	-14.930601	-4.778023
2FHA	A	LEU	117	H	-11.639570	13.305685	-15.388993	-4.977213
2FHA	A	HIS	118	H	-11.807237	11.742650	-16.472025	-4.944722
2FHA	A	LYS	119	H	-9.482312	7.675241	-13.875347	-4.403590
2FHA	A	LEU	120	H	-9.366939	8.100363	-13.972682	-4.521203
2FHA	A	ALA	121	H	-8.407613	7.611104	-13.544143	-4.924050
2FHA	A	THR	122	H	-8.307469	7.509123	-13.846931	-5.016980
2FHA	A	ASP	123	H	-8.293048	7.483037	-13.922990	-5.027138
2FHA	A	LYS	124	H	-8.359646	7.463983	-14.009058	-5.130831
2FHA	A	ASN	125	C	-8.371183	7.390098	-14.018056	-5.130089
2FHA	A	ASP	126	C	-9.180941	7.177235	-15.780024	-5.439215
2FHA	A	PRO	127	H	-9.557975	8.176774	-15.551234	-5.045347
2FHA	A	HIS	128	H	-9.693628	8.647108	-15.167885	-4.948291
2FHA	A	LEU	129	H	-9.878421	9.139056	-14.694123	-4.787172
2FHA	A	CYS	130	H	-9.994449	9.284872	-14.463419	-4.759161

2FHA	A	ASP	131	H	-9.993292	9.981453	-14.099674	-4.761357
2FHA	A	PHE	132	H	-10.950226	14.637283	-13.440496	-5.039192
2FHA	A	ILE	133	H	-10.959239	14.710625	-13.388972	-5.041794
2FHA	A	GLU	134	H	-10.974260	14.614115	-13.414691	-5.049049
2FHA	A	THR	135	H	-10.970341	14.610656	-13.435396	-5.056178
2FHA	A	HIS	136	H	-11.859151	15.084437	-15.192090	-5.391775
2FHA	A	TYR	137	H	-12.324726	14.798484	-16.281393	-5.582370
2FHA	A	LEU	138	H	-11.935051	11.486484	-17.190779	-5.537449
2FHA	A	ASN	139	H	-10.693855	7.300134	-17.039223	-5.300144
2FHA	A	GLU	140	H	-10.599517	7.250862	-17.131645	-5.270441
2FHA	A	GLN	141	H	-10.562577	7.352098	-17.120859	-5.247507
2FHA	A	VAL	142	H	-9.894040	6.807964	-15.485754	-4.420208
2FHA	A	LYS	143	H	-9.833428	6.890036	-15.507518	-4.423814
2FHA	A	ALA	144	H	-9.957490	7.006221	-15.124311	-4.208336
2FHA	A	ILE	145	H	-9.970210	7.083974	-15.020857	-4.176172
2FHA	A	LYS	146	H	-9.882077	7.074933	-15.206762	-4.269943
2FHA	A	GLU	147	H	-10.520495	8.125363	-16.220940	-4.758777
2FHA	A	LEU	148	H	-10.783795	8.254295	-16.367160	-4.841826
2FHA	A	GLY	149	H	-10.172629	8.887376	-15.503413	-5.053278
2FHA	A	ASP	150	H	-9.925960	9.607891	-15.085200	-5.126302
2FHA	A	HIS	151	H	-9.949071	10.726529	-14.550094	-5.160523
2FHA	A	VAL	152	H	-9.843903	11.048025	-14.295458	-5.037521
2FHA	A	THR	153	H	-8.808505	9.909574	-12.362304	-4.434130
2FHA	A	ASN	154	H	-8.729974	10.334176	-12.176474	-4.439863
2FHA	A	LEU	155	H	-8.488184	10.556413	-11.976281	-4.486319
2FHA	A	ARG	156	H	-7.509305	9.153289	-11.106233	-4.478067
2FHA	A	LYS	157	H	-6.920013	9.351593	-10.516894	-4.528469
2FHA	A	MET	158	H	-6.542502	8.947338	-10.318063	-4.490274
2FHA	A	GLY	159	T	-5.769948	6.850613	-9.804011	-4.159193
2FHA	A	ALA	160	T	-5.451432	6.450008	-9.769952	-4.120579
2FHA	A	PRO	161	T	-4.672299	5.118743	-9.109635	-4.041660
2FHA	A	GLU	162	T	-4.635138	5.061208	-9.188282	-4.031508
2FHA	A	SER	163	T	-4.646322	4.994343	-9.172149	-4.023743
2FHA	A	GLY	164	H	-4.714848	4.862981	-9.118261	-4.022233
2FHA	A	LEU	165	H	-4.790993	4.718882	-9.033499	-4.015545
2FHA	A	ALA	166	H	-6.166731	5.189398	-10.402093	-4.007789
2FHA	A	GLU	167	H	-8.573605	8.906423	-12.981193	-4.721844
2FHA	A	TYR	168	H	-9.221731	11.322147	-12.894392	-5.151426
2FHA	A	LEU	169	H	-9.889019	17.570322	-13.465371	-7.239567
2FHA	A	PHE	170	H	-9.374279	17.413008	-12.923249	-7.385060
2FHA	A	ASP	171	H	-7.349586	11.634453	-11.169187	-6.041125
2FHA	A	LYS	172	H	-3.917807	9.619958	-5.989236	-4.710659
2FHA	A	HIS	173	H	-2.645972	8.018191	-4.270356	-3.757743
2FHA	A	THR	174	H	-2.645972	8.018191	-4.270356	-3.757743
2FHA	A	LEU	175	C	-2.645972	8.018191	-4.270356	-3.757743
2FHA	A	GLY	176	C	-2.645972	8.018191	-4.270356	-3.757743
2ILK	A	THR	6	T	-8.461245	4.892886	-14.443687	-4.826048
2ILK	A	GLN	7	T	-8.461245	4.892886	-14.443687	-4.826048
2ILK	A	SER	8	T	-8.461245	4.892886	-14.443687	-4.826048
2ILK	A	GLU	9	C	-8.461245	4.892886	-14.443687	-4.826048
2ILK	A	ASN	10	C	-4.846381	1.793391	-10.283435	-4.106619
2ILK	A	SER	11	C	-4.477987	4.335856	-8.940748	-4.061660
2ILK	A	CYS	12	T	-4.374332	4.912048	-8.760191	-4.060279
2ILK	A	THR	13	T	-3.697506	6.644382	-6.501174	-3.779325
2ILK	A	HIS	14	T	-3.689353	6.673025	-6.534380	-3.789744
2ILK	A	PHE	15	T	-3.779940	7.482061	-5.911492	-3.735767
2ILK	A	PRO	16	T	-3.868163	7.512293	-5.687190	-3.691154
2ILK	A	GLY	17	T	-3.910134	7.480754	-5.530764	-3.664198
2ILK	A	ASN	18	H	-6.067080	8.599614	-9.180674	-4.452943
2ILK	A	LEU	19	H	-6.895910	8.249754	-10.019366	-4.226781
2ILK	A	PRO	20	H	-6.973364	7.627297	-10.075494	-4.154003
2ILK	A	ASN	21	H	-9.851498	7.475407	-15.522740	-5.046247
2ILK	A	MET	22	H	-10.992200	9.573700	-16.051070	-4.859439
2ILK	A	LEU	23	H	-10.928306	9.034780	-15.568463	-4.349858
2ILK	A	ARG	24	H	-10.765186	8.361815	-15.435258	-4.107316
2ILK	A	ASP	25	H	-10.896302	8.312024	-15.453306	-3.955317
2ILK	A	LEU	26	H	-10.766893	9.498853	-14.473838	-3.807803
2ILK	A	ARG	27	H	-10.080185	9.465656	-13.415997	-3.814873
2ILK	A	ASP	28	H	-9.741824	9.535972	-13.059974	-3.868461
2ILK	A	ALA	29	H	-9.750556	9.790662	-12.917768	-3.869569
2ILK	A	PHE	30	H	-9.733215	9.862455	-12.906657	-3.873888
2ILK	A	SER	31	H	-9.691112	9.793961	-12.989622	-3.899729
2ILK	A	ARG	32	H	-9.924732	10.203678	-13.022575	-3.978102
2ILK	A	VAL	33	H	-10.170512	13.836809	-12.695692	-4.667685
2ILK	A	LYS	34	H	-9.935332	14.153745	-13.126193	-5.254505
2ILK	A	THR	35	H	-9.487707	13.352614	-13.061148	-5.374941
2ILK	A	PHE	36	H	-9.394646	13.349339	-13.689819	-5.843475
2ILK	A	PHE	37	H	-8.727632	9.958427	-14.119145	-5.609404
2ILK	A	GLN	38	H	-7.342367	4.782026	-13.943497	-5.215403
2ILK	A	MET	39	H	-6.152360	3.702156	-11.914349	-4.467958
2ILK	A	LYS	40	H	-5.560373	2.863075	-11.890419	-4.447586

2ILK	A	ASP	41	C	-4.063656	1.098091	-9.722501	-3.938817
2ILK	A	GLN	42	C	-3.854627	1.328990	-9.702084	-3.922348
2ILK	A	LEU	43	C	-3.729945	1.517201	-9.603150	-3.876397
2ILK	A	ASP	44	C	-3.597838	2.048974	-9.273175	-3.846028
2ILK	A	ASN	45	C	-3.579458	2.178026	-9.215028	-3.836248
2ILK	A	LEU	46	T	-3.872444	3.085020	-9.014526	-3.799689
2ILK	A	LEU	47	T	-4.088703	3.618716	-8.737976	-3.764378
2ILK	A	LEU	48	T	-4.344648	4.308502	-8.481844	-3.805189
2ILK	A	LYS	49	T	-5.150774	4.801165	-9.523999	-3.974680
2ILK	A	GLU	50	H	-5.964774	5.348247	-10.335496	-4.192280
2ILK	A	SER	51	H	-7.946966	7.015419	-14.553022	-5.469001
2ILK	A	LEU	52	H	-8.609137	8.885540	-14.448044	-5.342206
2ILK	A	LEU	53	H	-8.263185	9.480343	-12.377318	-4.603515
2ILK	A	GLU	54	H	-7.703859	9.701378	-11.110104	-4.512981
2ILK	A	ASP	55	H	-7.071313	10.138680	-9.862054	-4.453949
2ILK	A	PHE	56	H	-6.104201	9.102077	-8.776082	-4.282936
2ILK	A	LYS	57	H	-5.066536	5.246427	-9.413970	-4.259778
2ILK	A	GLY	58	C	-5.027246	5.157990	-9.556722	-4.265821
2ILK	A	TYR	59	C	-5.024518	5.134093	-9.579181	-4.266000
2ILK	A	LEU	60	H	-5.037082	5.021377	-9.586816	-4.262712
2ILK	A	GLY	61	H	-5.121678	4.433523	-9.750120	-4.265626
2ILK	A	CYS	62	H	-6.530110	4.392388	-11.722016	-4.369581
2ILK	A	GLN	63	H	-7.611813	6.070734	-12.288222	-4.482564
2ILK	A	ALA	64	H	-9.077003	7.846236	-13.831479	-4.668972
2ILK	A	LEU	65	H	-9.929692	10.067699	-13.963764	-4.781943
2ILK	A	SER	66	H	-10.901017	12.257253	-14.442367	-4.728654
2ILK	A	GLU	67	H	-10.883156	12.600284	-14.272528	-4.741997
2ILK	A	MET	68	H	-11.123973	13.771372	-13.958525	-4.826951
2ILK	A	ILE	69	H	-11.358603	14.216241	-13.960706	-4.934576
2ILK	A	GLN	70	H	-11.839381	14.345737	-14.912944	-5.138742
2ILK	A	PHE	71	H	-11.476405	15.105026	-13.691561	-4.994433
2ILK	A	TYR	72	H	-10.296069	13.657125	-12.153485	-4.709915
2ILK	A	LEU	73	H	-9.538397	13.423798	-11.348654	-4.628875
2ILK	A	GLU	74	H	-9.440349	12.976980	-11.658416	-4.595454
2ILK	A	GLU	75	H	-9.363018	12.536221	-11.899532	-4.534285
2ILK	A	VAL	76	H	-9.329281	12.291109	-11.990275	-4.473451
2ILK	A	MET	77	H	-9.443246	12.034037	-11.993760	-4.429124
2ILK	A	PRO	78	H	-9.883903	9.433810	-13.874772	-4.190764
2ILK	A	GLN	79	H	-9.982407	8.644837	-14.513095	-4.254853
2ILK	A	ALA	80	H	-10.076920	8.646521	-15.068852	-4.567834
2ILK	A	GLU	81	H	-8.880087	7.108890	-14.320806	-5.120912
2ILK	A	ASN	82	T	-5.647319	4.422637	-10.488543	-4.493376
2ILK	A	GLN	83	T	-5.398766	5.133340	-9.977926	-4.294474
2ILK	A	ASP	84	T	-5.346391	5.200118	-10.006265	-4.261578
2ILK	A	PRO	85	T	-5.319980	5.231140	-10.037932	-4.242133
2ILK	A	ASP	86	T	-5.319835	5.233362	-10.035445	-4.240517
2ILK	A	ILE	87	H	-5.823769	6.337752	-9.449474	-3.904453
2ILK	A	LYS	88	H	-6.541011	5.964672	-10.514538	-3.886067
2ILK	A	ALA	89	H	-7.137357	6.044770	-10.873497	-3.852811
2ILK	A	HIS	90	H	-8.785596	7.975630	-12.924077	-4.393206
2ILK	A	VAL	91	H	-9.880100	9.657397	-13.932809	-4.339532
2ILK	A	ASN	92	H	-10.109019	8.602103	-14.661525	-4.362084
2ILK	A	SER	93	H	-10.202908	8.868293	-14.528452	-4.325376
2ILK	A	LEU	94	H	-10.778758	10.931181	-14.997942	-4.738493
2ILK	A	GLY	95	H	-10.431817	10.818908	-14.877368	-4.964283
2ILK	A	GLU	96	H	-9.814173	11.027424	-13.630487	-4.969302
2ILK	A	ASN	97	H	-9.788045	11.418600	-13.471603	-4.982190
2ILK	A	LEU	98	H	-9.815979	11.550183	-13.369656	-4.992106
2ILK	A	LYS	99	H	-9.807845	11.562332	-13.377182	-4.990303
2ILK	A	THR	100	H	-9.913050	11.711330	-13.112121	-4.946902
2ILK	A	LEU	101	H	-10.997336	14.582396	-13.357413	-5.040385
2ILK	A	ARG	102	H	-11.568158	14.112182	-13.953019	-4.950665
2ILK	A	LEU	103	H	-11.776984	13.362368	-14.230955	-4.991644
2ILK	A	ARG	104	H	-14.607062	13.558443	-18.841449	-5.103522
2ILK	A	LEU	105	H	-12.752099	14.114576	-14.962139	-4.783413
2ILK	A	ARG	106	H	-12.689633	13.913795	-15.233096	-4.795494
2ILK	A	ARG	107	H	-11.820050	13.352949	-14.359895	-4.623386
2ILK	A	CYS	108	T	-11.306210	14.279469	-13.491268	-4.711441
2ILK	A	HIS	109	T	-11.069938	14.271827	-13.273989	-4.593560
2ILK	A	ARG	110	T	-10.888508	13.965678	-13.370616	-4.643357
2ILK	A	PHE	111	T	-10.657442	13.643549	-13.699784	-4.892772
2ILK	A	LEU	112	T	-10.477733	12.509566	-14.492479	-5.222800
2ILK	A	PRO	113	G	-10.128589	8.958605	-15.890459	-5.361125
2ILK	A	CYS	114	G	-10.134303	8.444395	-16.267981	-5.446280
2ILK	A	GLU	115	G	-10.184661	7.989504	-16.517139	-5.509273
2ILK	A	ASN	116	C	-10.059846	6.675068	-16.974543	-5.352771
2ILK	A	LYS	117	C	-7.810980	5.183187	-12.665790	-4.188258
2ILK	A	SER	118	C	-7.159583	5.375239	-11.995609	-4.154735
2ILK	A	LYS	119	H	-7.046978	5.264669	-12.191303	-4.183748
2ILK	A	ALA	120	H	-6.977151	5.195128	-12.329146	-4.192070
2ILK	A	VAL	121	H	-6.889523	5.099006	-12.420831	-4.178642

2ILK	A	GLU	122	H	-6.996382	5.087128	-12.518805 -4.223156
2ILK	A	GLN	123	H	-7.368152	4.762798	-13.538104 -4.380092
2ILK	A	VAL	124	H	-7.563662	4.859110	-13.714869 -4.405607
2ILK	A	LYS	125	H	-7.735984	5.191809	-13.804178 -4.475959
2ILK	A	ASN	126	H	-7.987572	6.487333	-14.060279 -4.721329
2ILK	A	ALA	127	H	-8.000893	7.459772	-13.254615 -4.521441
2ILK	A	PHE	128	H	-7.952193	8.317891	-12.352957 -4.300915
2ILK	A	ASN	129	H	-7.149096	6.584009	-11.711684 -4.333659
2ILK	A	LYS	130	H	-6.262266	5.914936	-10.439209 -4.072124
2ILK	A	LEU	131	H	-6.105979	6.021292	-10.498432 -4.126506
2ILK	A	GLN	132	H	-5.968583	6.076212	-10.488554 -4.116704
2ILK	A	GLU	133	H	-5.793113	6.328016	-10.228865 -4.090390
2ILK	A	LYS	134	H	-5.824625	6.408521	-10.150535 -4.078244
2ILK	A	GLY	135	H	-6.066777	6.908073	-10.215570 -4.132174
2ILK	A	ILE	136	H	-6.181565	7.116753	-10.072935 -4.067418
2ILK	A	TYR	137	H	-6.391761	7.448040	-9.915690 -4.061921
2ILK	A	LYS	138	H	-7.037183	7.956451	-11.094058 -4.140151
2ILK	A	ALA	139	H	-7.154788	7.846257	-11.102342 -4.075975
2ILK	A	MET	140	H	-7.406872	7.439166	-11.347405 -3.983237
2ILK	A	SER	141	H	-7.837680	6.904648	-12.276063 -4.145346
2ILK	A	GLU	142	H	-7.895870	7.215101	-12.560425 -4.500042
2ILK	A	PHE	143	H	-8.382022	11.986457	-15.847756 -7.997377
2ILK	A	ASP	144	H	-7.738928	12.659161	-15.656312 -8.995916
2ILK	A	ILE	145	H	-7.265625	13.422665	-15.280224 -9.457407
2ILK	A	PHE	146	H	-6.955992	13.554659	-15.090996 -9.581696
2ILK	A	ILE	147	H	-6.263073	12.835738	-14.159902 -9.555304
2ILK	A	ASN	148	H	-5.984003	12.555049	-13.956576 -9.444104
2ILK	A	TYR	149	H	-5.528238	12.063580	-12.787559 -8.862651
2ILK	A	ILE	150	H	-4.774747	9.853805	-11.310901 -7.787380
2ILK	A	GLU	151	H	-4.133510	8.315747	-10.529793 -7.183960
2ILK	A	ALA	152	H	-3.666427	7.474314	-9.667257 -6.535947
2ILK	A	TYR	153	H	-3.195835	6.973112	-8.605270 -5.923288
2ILK	A	MET	154	H	-2.507785	6.066955	-6.985193 -5.072464
2ILK	A	THR	155	H	-1.833879	5.333563	-5.635500 -4.349422
2ILK	A	MET	156	H	-1.532325	5.103421	-5.246780 -4.006343
2ILK	A	LYS	157	H	-1.235403	4.811047	-4.792534 -3.610922
2ILK	A	ILE	158	H	-1.235403	4.811047	-4.792534 -3.610922
2ILK	A	ARG	159	C	-1.235403	4.811047	-4.792534 -3.610922
2ILK	A	ASN	160	C	-1.235403	4.811047	-4.792534 -3.610922
2PSR	A	SER	1	C	-6.296357	3.270417	-13.721813 -4.778403
2PSR	A	ASN	2	C	-6.296357	3.270417	-13.721813 -4.778403
2PSR	A	THR	3	C	-6.296357	3.270417	-13.721813 -4.778403
2PSR	A	GLN	4	H	-6.296357	3.270417	-13.721813 -4.778403
2PSR	A	ALA	5	H	-6.585249	3.562458	-14.546093 -5.309681
2PSR	A	GLU	6	H	-6.847590	3.855939	-15.071268 -5.697979
2PSR	A	ARG	7	H	-7.345248	4.411140	-15.974336 -6.062481
2PSR	A	SER	8	H	-7.837649	5.022042	-17.247967 -6.554168
2PSR	A	ILE	9	H	-7.843609	5.502266	-16.281237 -5.992184
2PSR	A	ILE	10	H	-7.963559	5.859174	-15.770763 -5.654280
2PSR	A	GLY	11	H	-8.118970	6.250916	-15.092668 -5.206151
2PSR	A	MET	12	H	-8.345517	6.820313	-13.485122 -4.185866
2PSR	A	ILE	13	H	-8.459936	7.127528	-13.038613 -4.064041
2PSR	A	ASP	14	H	-9.123242	7.951009	-13.921185 -4.519527
2PSR	A	MET	15	H	-10.065622	10.504219	-14.548708 -5.102026
2PSR	A	PHE	16	H	-10.901025	14.458527	-14.058226 -5.302300
2PSR	A	HIS	17	H	-10.591264	13.280123	-14.426817 -5.292152
2PSR	A	LYS	18	H	-8.826229	9.813060	-11.955115 -4.353303
2PSR	A	TYR	19	C	-8.609955	9.704170	-12.171695 -4.384914
2PSR	A	THR	20	C	-6.555953	4.965454	-11.152268 -4.035388
2PSR	A	ARG	21	B	-6.350603	5.193494	-11.326919 -4.139459
2PSR	A	ARG	22	T	-6.309993	5.441247	-11.324415 -4.164291
2PSR	A	ASP	23	T	-6.318189	5.382064	-11.317388 -4.162294
2PSR	A	ASP	24	T	-6.322082	5.354487	-11.308229 -4.160183
2PSR	A	LYS	25	B	-6.948631	6.376105	-11.664569 -4.416462
2PSR	A	ILE	26	B	-7.903339	8.991693	-11.365003 -4.529182
2PSR	A	ASP	27	C	-9.862606	11.565732	-13.975174 -5.123847
2PSR	A	LYS	28	H	-9.708274	11.847863	-13.682807 -5.018894
2PSR	A	PRO	29	H	-9.029960	12.598142	-11.800442 -4.679664
2PSR	A	SER	30	H	-9.036662	12.608196	-11.756790 -4.667955
2PSR	A	LEU	31	H	-9.106981	12.858917	-11.478524 -4.633299
2PSR	A	LEU	32	H	-9.169814	13.054166	-11.224058 -4.580751
2PSR	A	THR	33	H	-9.171051	13.129409	-11.296389 -4.668669
2PSR	A	MET	34	H	-10.310165	14.232158	-13.869772 -5.663876
2PSR	A	MET	35	H	-10.276118	14.241102	-13.950227 -5.706724
2PSR	A	LYS	36	H	-9.584897	11.886011	-13.671244 -5.343875
2PSR	A	GLU	37	H	-9.173077	10.715101	-13.749674 -5.260214
2PSR	A	ASN	38	H	-9.223648	10.483998	-13.752899 -5.217323
2PSR	A	PHE	39	H	-9.226575	10.499849	-13.712016 -5.199792
2PSR	A	PRO	40	H	-9.225648	10.470213	-13.699125 -5.175572
2PSR	A	ASN	41	H	-9.505831	10.214086	-13.802223 -5.166806
2PSR	A	PHE	42	H	-11.024525	14.455695	-13.871377 -4.871314

2PSR	A	LEU	43	H	-11.199348	13.818536	-14.322239	-4.765394
2PSR	A	SER	44	H	-9.970284	6.515126	-15.627665	-4.577275
2PSR	A	ALA	45	H	-9.895550	6.244792	-15.959584	-4.675302
2PSR	A	CYS	46	H	-8.698015	4.643603	-15.956915	-5.313046
2PSR	A	ASP	47	H	-7.088168	4.841797	-13.431646	-5.154915
2PSR	A	LYS	48	H	-6.788458	5.123332	-13.378471	-5.194683
2PSR	A	LYS	49	H	-6.789506	5.131940	-13.373482	-5.198408
2PSR	A	GLY	50	C	-6.788463	5.150740	-13.370324	-5.198907
2PSR	A	THR	51	C	-6.808410	5.189728	-13.277588	-5.191185
2PSR	A	ASN	52	T	-7.324521	5.670649	-13.313879	-5.257325
2PSR	A	TYR	53	T	-9.674722	11.963260	-14.129756	-5.371824
2PSR	A	LEU	54	T	-9.893031	12.962430	-13.562058	-5.249851
2PSR	A	ALA	55	T	-10.276287	13.078433	-13.780472	-5.127164
2PSR	A	ASP	56	H	-10.203805	12.362646	-13.926767	-5.057271
2PSR	A	VAL	57	H	-10.386283	12.421057	-13.830380	-5.000679
2PSR	A	PHE	58	H	-10.413964	12.324098	-13.808906	-5.002670
2PSR	A	GLU	59	H	-10.241900	10.910035	-14.835485	-5.196650
2PSR	A	LYS	60	H	-10.077072	9.888217	-15.573060	-5.381542
2PSR	A	LYS	61	H	-9.252386	6.886526	-15.949006	-5.651227
2PSR	A	ASP	62	T	-7.609189	3.264546	-14.930858	-5.159810
2PSR	A	LYS	63	T	-5.223640	2.260603	-11.658762	-4.693650
2PSR	A	ASN	64	T	-5.217833	2.286545	-11.687740	-4.700798
2PSR	A	GLU	65	T	-5.215924	2.307692	-11.691709	-4.702083
2PSR	A	ASP	66	C	-5.216480	2.303600	-11.687940	-4.701207
2PSR	A	LYS	67	C	-5.226355	2.291475	-11.634513	-4.694024
2PSR	A	LYS	68	C	-7.784604	5.927373	-14.240860	-5.349023
2PSR	A	ILE	69	B	-8.596402	8.855875	-13.058903	-5.120080
2PSR	A	ASP	70	C	-11.291544	11.900574	-16.268724	-5.546172
2PSR	A	PHE	71	H	-11.770774	14.813960	-15.261169	-5.317085
2PSR	A	SER	72	H	-11.908805	14.435934	-15.429476	-5.201627
2PSR	A	GLU	73	H	-11.979062	14.350645	-15.382520	-5.156223
2PSR	A	PHE	74	H	-12.051896	16.431727	-13.998767	-4.813014
2PSR	A	LEU	75	H	-10.483305	11.985848	-13.178033	-4.463417
2PSR	A	SER	76	H	-10.446190	11.843790	-13.377752	-4.494431
2PSR	A	LEU	77	H	-10.363784	11.953162	-13.472594	-4.520038
2PSR	A	LEU	78	H	-9.763289	10.348112	-13.546896	-4.429976
2PSR	A	GLY	79	H	-8.397766	7.656042	-12.710878	-4.356823
2PSR	A	ASP	80	H	-8.407325	7.564745	-12.728128	-4.357452
2PSR	A	ILE	81	H	-8.407096	7.568203	-12.727103	-4.357003
2PSR	A	ALA	82	H	-8.407441	7.545747	-12.738893	-4.358189
2PSR	A	THR	83	H	-8.446275	7.416698	-12.688353	-4.358673
2PSR	A	ASP	84	H	-10.714262	9.505016	-15.852918	-4.799504
2PSR	A	TYR	85	H	-11.169898	9.517296	-16.950393	-5.090485
2PSR	A	HIS	86	H	-9.478641	5.886162	-15.487636	-4.810620
2PSR	A	LYS	87	H	-8.788354	5.797897	-15.245865	-5.029124
2PSR	A	GLN	88	H	-7.137033	4.894268	-12.727563	-4.581990
2PSR	A	SER	89	H	-7.135664	4.901232	-12.742276	-4.588345
2PSR	A	HIS	90	H	-7.122806	4.965519	-12.820830	-4.631060
2PSR	A	GLY	91	C	-7.097811	5.088691	-12.897255	-4.694177
2PSR	A	ALA	92	C	-7.095682	5.161927	-12.847289	-4.681744
2PSR	A	ALA	93	C	-7.738721	6.743655	-13.188492	-4.622711
2PSR	A	PRO	94	C	-7.738721	6.743655	-13.188492	-4.622711
2PSR	A	CYS	95	C	-7.738721	6.743655	-13.188492	-4.622711
2PSR	A	SER	96	C	-7.738721	6.743655	-13.188492	-4.622711
2TGI	A	ALA	1	C	-7.686040	5.715165	-9.739842	-2.422415
2TGI	A	LEU	2	C	-7.686040	5.715165	-9.739842	-2.422415
2TGI	A	ASP	3	B	-7.686040	5.715165	-9.739842	-2.422415
2TGI	A	ALA	4	H	-7.686040	5.715165	-9.739842	-2.422415
2TGI	A	ALA	5	H	-8.926428	6.064881	-12.146054	-3.258570
2TGI	A	TYR	6	H	-11.249572	8.891581	-16.441896	-4.842819
2TGI	A	CYS	7	H	-8.764400	5.663967	-13.621135	-4.185036
2TGI	A	PHE	8	T	-8.743813	5.629612	-13.675366	-4.159369
2TGI	A	ARG	9	T	-8.241503	2.830014	-14.150826	-3.745621
2TGI	A	ASN	10	T	-8.083749	2.753485	-14.400447	-3.889112
2TGI	A	VAL	11	C	-7.806868	3.080168	-14.345395	-4.117734
2TGI	A	GLN	12	C	-7.935194	2.459762	-14.543054	-4.107899
2TGI	A	ASP	13	C	-7.935083	2.480580	-14.543019	-4.116099
2TGI	A	ASN	14	B	-8.181998	3.384570	-14.561600	-4.467937
2TGI	A	CYS	15	C	-8.374213	3.714921	-14.310368	-4.511628
2TGI	A	CYS	16	E	-10.506712	6.818507	-16.330205	-4.869816
2TGI	A	LEU	17	E	-10.703853	7.116596	-15.257729	-4.362042
2TGI	A	ARG	18	E	-12.338271	11.185754	-15.391811	-3.739813
2TGI	A	PRO	19	C	-10.622761	11.027685	-11.850215	-3.359275
2TGI	A	LEU	20	C	-10.625274	11.074025	-11.813296	-3.357909
2TGI	A	TYR	21	E	-10.630956	11.128578	-11.774339	-3.367119
2TGI	A	ILE	22	E	-10.355552	13.170633	-12.854386	-4.704128
2TGI	A	ASP	23	E	-9.842122	11.491638	-12.577618	-4.265995
2TGI	A	PHE	24	H	-9.789072	12.119874	-12.636159	-4.525349
2TGI	A	LYS	25	H	-6.395369	5.099056	-9.359609	-3.387517
2TGI	A	ARG	26	H	-6.353841	5.233999	-9.443469	-3.396493
2TGI	A	ASP	27	H	-5.991350	6.867895	-9.576252	-4.029701

2TGI	A	LEU	28	H	-5.628356	7.894033	-8.337865	-3.747993
2TGI	A	GLY	29	C	-5.364141	9.115631	-7.353620	-3.639083
2TGI	A	TRP	30	T	-5.449142	10.133305	-6.895686	-3.682342
2TGI	A	LYS	31	T	-5.451644	10.210021	-6.858354	-3.689054
2TGI	A	TRP	32	T	-5.572079	10.527178	-6.209983	-3.442689
2TGI	A	ILE	33	E	-5.882786	11.488340	-5.790705	-3.452811
2TGI	A	HIS	34	E	-6.738356	9.744197	-8.173583	-3.340602
2TGI	A	GLU	35	E	-7.059981	7.127849	-9.602054	-3.249153
2TGI	A	PRO	36	T	-7.162334	5.990495	-9.804295	-3.090164
2TGI	A	LYS	37	T	-7.164531	5.957739	-9.798952	-3.085120
2TGI	A	GLY	38	E	-7.247189	5.650187	-9.827495	-3.124195
2TGI	A	TYR	39	E	-10.695373	10.864816	-13.667930	-4.003305
2TGI	A	ASN	40	E	-10.550685	10.558259	-13.691744	-4.109185
2TGI	A	ALA	41	C	-10.330617	10.017023	-13.650177	-4.036363
2TGI	A	ASN	42	C	-8.955493	9.094896	-13.659724	-5.226944
2TGI	A	PHE	43	E	-8.195178	6.488241	-12.330900	-3.980063
2TGI	A	CYS	44	E	-7.894501	5.503560	-12.552270	-3.850526
2TGI	A	ALA	45	E	-7.684087	5.009555	-12.447691	-3.637981
2TGI	A	GLY	46	C	-7.588709	5.470040	-12.289524	-3.669478
2TGI	A	ALA	47	B	-7.587758	5.586903	-12.152757	-3.610729
2TGI	A	CYS	48	C	-7.764971	5.626108	-12.269601	-3.649369
2TGI	A	PRO	49	T	-7.984549	6.457705	-11.976313	-3.649191
2TGI	A	TYR	50	T	-8.391631	9.054748	-11.742906	-4.156236
2TGI	A	LEU	51	T	-8.920771	10.384355	-12.189228	-4.598509
2TGI	A	TRP	52	T	-10.115256	11.450609	-12.527220	-4.055781
2TGI	A	SER	53	T	-10.077101	9.877705	-13.456995	-4.159402
2TGI	A	SER	54	T	-9.598043	5.232346	-15.251273	-4.389132
2TGI	A	ASP	55	C	-9.271104	4.316282	-15.314138	-4.271538
2TGI	A	THR	56	C	-9.217461	4.435887	-15.299396	-4.239597
2TGI	A	GLN	57	H	-9.146113	4.686539	-15.341891	-4.279807
2TGI	A	HIS	58	H	-9.173138	4.694649	-15.267969	-4.259344
2TGI	A	SER	59	H	-9.457401	4.891896	-15.263172	-4.202887
2TGI	A	ARG	60	H	-10.082575	6.463955	-15.525845	-4.317969
2TGI	A	VAL	61	H	-10.333598	7.070962	-15.590530	-4.471722
2TGI	A	LEU	62	H	-11.498671	9.281189	-14.749056	-3.562803
2TGI	A	SER	63	H	-11.480354	10.515340	-15.571142	-4.561127
2TGI	A	LEU	64	H	-8.987989	7.904994	-12.138659	-3.781629
2TGI	A	TYR	65	H	-8.468425	7.810130	-12.215970	-3.950740
2TGI	A	ASN	66	H	-7.758565	5.282936	-12.210873	-3.624871
2TGI	A	THR	67	H	-5.912453	3.559871	-10.650810	-3.762860
2TGI	A	ILE	68	H	-5.572857	3.336746	-9.917413	-3.249133
2TGI	A	ASN	69	C	-5.344081	2.925397	-9.736763	-3.024822
2TGI	A	PRO	70	G	-5.100802	2.843135	-9.206163	-2.731383
2TGI	A	GLU	71	G	-5.079391	2.870275	-9.225681	-2.728847
2TGI	A	ALA	72	G	-5.226217	2.793803	-8.830468	-2.432367
2TGI	A	SER	73	C	-5.385759	2.743036	-8.795456	-2.383524
2TGI	A	ALA	74	C	-5.635585	3.099871	-8.498969	-2.293982
2TGI	A	SER	75	C	-6.676594	5.092050	-10.155462	-2.953785
2TGI	A	PRO	76	C	-7.161788	7.330281	-10.250709	-3.228420
2TGI	A	CYS	77	C	-7.526954	6.293932	-10.901718	-3.043279
2TGI	A	CYS	78	E	-7.766049	6.388862	-11.470936	-3.377976
2TGI	A	VAL	79	E	-7.650218	6.732734	-11.478938	-3.608224
2TGI	A	SER	80	E	-7.747476	7.277937	-11.601487	-3.870194
2TGI	A	GLN	81	E	-7.953115	8.291558	-12.175496	-4.467513
2TGI	A	ASP	82	E	-7.917605	9.138264	-11.724134	-4.466367
2TGI	A	LEU	83	E	-7.513050	10.759924	-9.712785	-4.029492
2TGI	A	GLU	84	E	-7.540211	11.804374	-9.025384	-3.900536
2TGI	A	PRO	85	E	-7.514002	12.362639	-8.563678	-3.769493
2TGI	A	LEU	86	E	-7.594736	12.876829	-8.056135	-3.650599
2TGI	A	THR	87	E	-7.663806	12.953727	-7.673951	-3.497608
2TGI	A	ILE	88	E	-8.266283	14.225575	-7.625394	-3.418168
2TGI	A	LEU	89	E	-7.583729	14.457741	-10.148677	-6.305826
2TGI	A	TYR	90	E	-6.582888	11.632027	-9.110173	-5.084924
2TGI	A	TYR	91	E	-2.044118	5.821093	-2.703253	-2.814638
2TGI	A	ILE	92	E	-0.378975	5.231500	-2.521131	-3.553391
2TGI	A	GLY	93	T	-0.375166	5.248753	-2.554308	-3.565315
2TGI	A	LYS	94	T	-0.374346	5.255633	-2.560771	-3.567400
2TGI	A	THR	95	E	-0.374345	5.255590	-2.560794	-3.567391
2TGI	A	PRO	96	E	-0.456567	4.705451	-2.311424	-3.350450
2TGI	A	LYS	97	E	-3.747144	4.780085	-5.909469	-2.917671
2TGI	A	ILE	98	E	-4.740767	6.844627	-5.727729	-2.748919
2TGI	A	GLU	99	E	-6.302184	9.614490	-9.559737	-4.473986
2TGI	A	GLN	100	E	-6.380327	9.062069	-9.136357	-3.988033
2TGI	A	LEU	101	E	-6.483507	8.697686	-8.798316	-3.643585
2TGI	A	SER	102	E	-6.511500	8.606332	-8.615268	-3.519544
2TGI	A	ASN	103	E	-6.549215	8.656959	-8.504399	-3.522537
2TGI	A	MET	104	E	-6.773155	9.242372	-8.048048	-3.488772
2TGI	A	ILE	105	E	-8.240703	11.432016	-9.378865	-3.640722
2TGI	A	VAL	106	E	-9.098194	13.521124	-10.235867	-4.324117
2TGI	A	LYS	107	E	-10.682523	13.406515	-11.439975	-4.036427
2TGI	A	SER	108	E	-12.808230	13.554824	-14.123490	-4.097372

2TGI	A	CYS	109	E	-12.108696	7.758786	-16.060771	-3.960776
2TGI	A	LYS	110	E	-12.108696	7.758786	-16.060771	-3.960776
2TGI	A	CYS	111	E	-12.108696	7.758786	-16.060771	-3.960776
2TGI	A	SER	112	C	-12.108696	7.758786	-16.060771	-3.960776
3FIB	A	GLN	144	C	-3.438145	7.631913	-5.662079	-3.648907
3FIB	A	ILE	145	E	-3.438145	7.631913	-5.662079	-3.648907
3FIB	A	HIS	146	E	-3.438145	7.631913	-5.662079	-3.648907
3FIB	A	ASP	147	E	-3.438145	7.631913	-5.662079	-3.648907
3FIB	A	ILE	148	E	-4.208368	9.526206	-6.311706	-4.269806
3FIB	A	THR	149	E	-5.169616	10.610151	-7.889150	-5.107022
3FIB	A	GLY	150	E	-6.478604	11.329415	-10.160812	-6.049838
3FIB	A	LYS	151	T	-9.859623	13.715309	-15.124900	-7.370248
3FIB	A	ASP	152	T	-11.612703	9.146674	-17.946328	-5.604637
3FIB	A	CYS	153	H	-12.035655	8.441313	-18.964906	-5.864526
3FIB	A	GLN	154	H	-11.663153	10.673669	-16.570045	-5.400857
3FIB	A	ASP	155	H	-8.992604	10.196493	-12.319023	-4.722708
3FIB	A	ILE	156	H	-7.529004	8.593956	-11.440647	-4.712502
3FIB	A	ALA	157	H	-7.151984	7.751935	-11.819549	-4.712422
3FIB	A	ASN	158	H	-6.451504	6.097463	-11.836313	-4.726729
3FIB	A	LYS	159	H	-5.862852	5.822317	-11.031598	-4.518742
3FIB	A	GLY	160	C	-5.824239	5.770957	-11.102990	-4.499268
3FIB	A	ALA	161	C	-5.850388	5.628018	-11.110289	-4.485857
3FIB	A	LYS	162	C	-5.880992	5.569024	-11.052843	-4.473349
3FIB	A	GLN	163	C	-6.063194	5.642206	-10.767916	-4.379760
3FIB	A	SER	164	C	-7.335159	5.501978	-12.349981	-4.254069
3FIB	A	GLY	165	E	-8.536369	6.391956	-13.539073	-4.315799
3FIB	A	LEU	166	E	-9.529468	8.520453	-13.594521	-4.491974
3FIB	A	TYR	167	E	-12.226388	15.639598	-15.118705	-5.314559
3FIB	A	PHE	168	E	-12.005297	17.822785	-13.824586	-5.427113
3FIB	A	ILE	169	E	-8.645340	12.890519	-9.921449	-4.332027
3FIB	A	LYS	170	C	-6.849534	11.238600	-8.487563	-4.240961
3FIB	A	PRO	171	T	-5.441958	9.026030	-7.589299	-3.968457
3FIB	A	LEU	172	T	-4.956943	7.641216	-8.275597	-4.121382
3FIB	A	LYS	173	T	-4.874050	7.740669	-8.442268	-4.208862
3FIB	A	ALA	174	T	-4.873994	7.738508	-8.445301	-4.210096
3FIB	A	ASN	175	T	-4.893393	7.628402	-8.450156	-4.210608
3FIB	A	GLN	176	T	-5.157289	6.970644	-8.983521	-4.361447
3FIB	A	GLN	177	T	-6.064555	8.504952	-9.589740	-4.795873
3FIB	A	PHE	178	E	-8.212751	12.351313	-11.097508	-5.027759
3FIB	A	LEU	179	E	-8.631252	13.316696	-10.677218	-5.052690
3FIB	A	VAL	180	E	-10.925625	16.583854	-11.874019	-4.967880
3FIB	A	TYR	181	E	-13.019448	19.542203	-14.377400	-5.323781
3FIB	A	CYS	182	E	-10.117118	7.483143	-16.176642	-5.498330
3FIB	A	GLU	183	E	-8.634521	6.707317	-14.287253	-5.043567
3FIB	A	ILE	184	E	-5.540613	4.668533	-10.595122	-4.591790
3FIB	A	ASP	185	T	-5.393704	4.222503	-11.186027	-4.707903
3FIB	A	GLY	186	T	-5.310832	4.129549	-11.462910	-4.781046
3FIB	A	SER	187	T	-5.310999	4.128670	-11.461585	-4.780848
3FIB	A	GLY	188	T	-5.312993	4.120240	-11.452637	-4.780102
3FIB	A	ASN	189	C	-5.983271	2.991763	-13.292973	-5.179768
3FIB	A	GLY	190	E	-6.517233	3.511281	-13.305374	-5.267338
3FIB	A	TRP	191	E	-11.584074	13.049368	-16.539111	-5.975670
3FIB	A	THR	192	E	-12.119086	16.092516	-15.768021	-6.100451
3FIB	A	VAL	193	E	-12.606609	19.190539	-14.240383	-5.830777
3FIB	A	PHE	194	E	-12.926561	21.116779	-13.062385	-5.732641
3FIB	A	GLN	195	E	-14.635041	19.773133	-16.867508	-6.257533
3FIB	A	LYS	196	E	-12.772841	13.037152	-17.735760	-6.248377
3FIB	A	ARG	197	E	-10.591940	10.495201	-15.398094	-5.606373
3FIB	A	LEU	198	C	-7.171473	9.115637	-10.434276	-4.658453
3FIB	A	ASP	199	C	-6.406292	6.877273	-11.181192	-4.753775
3FIB	A	GLY	200	C	-6.401131	6.910400	-11.194186	-4.756135
3FIB	A	SER	201	C	-6.400906	6.912480	-11.195223	-4.756210
3FIB	A	VAL	202	C	-6.401102	6.913640	-11.192708	-4.755841
3FIB	A	ASP	203	C	-6.588750	6.095888	-11.482015	-4.793505
3FIB	A	PHE	204	C	-9.145492	11.055282	-12.797292	-5.062845
3FIB	A	LYS	205	C	-10.449423	13.990945	-13.807111	-5.377534
3FIB	A	LYS	206	C	-10.650657	14.714498	-13.909823	-5.630058
3FIB	A	ASN	207	C	-11.227006	14.162979	-15.555292	-6.052323
3FIB	A	TRP	208	H	-11.718923	13.812628	-16.130698	-5.985655
3FIB	A	ILE	209	H	-11.359244	13.296692	-16.042881	-5.880686
3FIB	A	GLN	210	H	-11.305510	13.354377	-16.073376	-5.922923
3FIB	A	TYR	211	H	-11.524333	13.705988	-16.050447	-5.916045
3FIB	A	LYS	212	H	-8.237308	12.446487	-11.317887	-5.644916
3FIB	A	GLU	213	H	-6.645533	10.318956	-9.728044	-4.992680
3FIB	A	GLY	214	C	-6.110646	11.737656	-8.462371	-4.815616
3FIB	A	PHE	215	E	-6.088476	11.836023	-8.489056	-4.821099
3FIB	A	GLY	216	E	-5.966533	11.639608	-8.573918	-4.742669
3FIB	A	HIS	217	C	-5.944797	11.542361	-8.589905	-4.693496
3FIB	A	LEU	218	C	-6.030899	11.811551	-8.385719	-4.573508
3FIB	A	SER	219	T	-5.208889	6.848611	-8.932595	-4.238303
3FIB	A	PRO	220	T	-4.536717	6.981814	-8.437682	-4.427164

3FIB	A	THR	221	T	-4.541552	6.923323	-8.464449	-4.436737
3FIB	A	GLY	222	T	-4.544711	6.905675	-8.457023	-4.437954
3FIB	A	THR	223	C	-4.553163	6.854350	-8.443979	-4.437273
3FIB	A	THR	224	C	-4.757052	7.078641	-8.258175	-4.529257
3FIB	A	GLU	225	C	-7.358754	7.611036	-12.546498	-5.488543
3FIB	A	PHE	226	E	-11.551588	13.075404	-15.543592	-5.814033
3FIB	A	TRP	227	E	-13.914325	17.835951	-16.843785	-5.927297
3FIB	A	LEU	228	C	-12.866560	14.101779	-17.043727	-5.839352
3FIB	A	GLY	229	C	-12.145606	13.590027	-16.501795	-5.789936
3FIB	A	ASN	230	H	-12.131207	13.621389	-16.535344	-5.793273
3FIB	A	GLU	231	H	-11.983479	14.008777	-16.255229	-5.690141
3FIB	A	LYS	232	H	-11.930730	14.419587	-15.974549	-5.614615
3FIB	A	ILE	233	H	-11.987574	14.867752	-15.618450	-5.508056
3FIB	A	HIS	234	H	-12.156935	16.073141	-14.855227	-5.148168
3FIB	A	LEU	235	H	-12.142990	16.086793	-14.872774	-5.155924
3FIB	A	ILE	236	H	-12.248822	15.978037	-15.090920	-5.182604
3FIB	A	SER	237	H	-10.974127	9.753464	-16.314274	-5.448368
3FIB	A	THR	238	H	-8.263192	9.368575	-12.043243	-4.894028
3FIB	A	GLN	239	G	-7.861625	8.808269	-12.018584	-4.659138
3FIB	A	SER	240	G	-7.745105	9.183613	-11.775369	-4.540107
3FIB	A	ALA	241	G	-7.736076	9.239749	-11.768698	-4.530337
3FIB	A	ILE	242	C	-7.738185	9.242396	-11.750997	-4.526622
3FIB	A	PRO	243	C	-8.048863	9.157374	-11.579908	-4.277303
3FIB	A	TYR	244	E	-8.715810	11.080060	-10.716201	-3.985989
3FIB	A	ALA	245	E	-10.199964	13.023807	-11.411171	-3.919766
3FIB	A	LEU	246	E	-12.252699	17.493836	-13.288963	-4.604232
3FIB	A	ARG	247	E	-12.695654	17.285131	-14.795289	-5.208917
3FIB	A	VAL	248	E	-12.585896	16.809377	-15.237210	-5.369584
3FIB	A	GLU	249	E	-12.597266	16.745879	-15.262801	-5.387982
3FIB	A	LEU	250	E	-12.942225	16.724109	-16.178661	-5.738719
3FIB	A	GLU	251	E	-11.422917	10.940650	-17.437031	-6.470280
3FIB	A	ASP	252	T	-9.836448	8.539463	-15.461913	-5.525440
3FIB	A	TRP	253	T	-7.295388	9.457521	-11.206761	-5.239659
3FIB	A	ASN	254	T	-6.716674	7.581947	-11.796041	-5.148310
3FIB	A	GLY	255	T	-6.690338	7.605295	-11.867113	-5.151477
3FIB	A	ARG	256	C	-6.689540	7.608194	-11.869505	-5.150402
3FIB	A	THR	257	E	-6.691973	7.606627	-11.855191	-5.149026
3FIB	A	SER	258	E	-6.952895	6.575315	-12.246549	-5.101024
3FIB	A	THR	259	E	-8.519077	8.224077	-13.483962	-5.204480
3FIB	A	ALA	260	E	-10.320528	10.318288	-14.545291	-4.873478
3FIB	A	ASP	261	E	-11.182949	11.567584	-15.096937	-5.220322
3FIB	A	TYR	262	E	-13.532474	16.759236	-15.950229	-5.008839
3FIB	A	ALA	263	E	-12.039493	16.560020	-12.963154	-4.628274
3FIB	A	MET	264	E	-11.134099	15.500033	-12.905396	-4.922155
3FIB	A	PHE	265	E	-10.379686	14.893727	-12.229168	-4.788445
3FIB	A	LYS	266	E	-9.993600	12.450023	-13.298756	-4.804774
3FIB	A	VAL	267	E	-7.805978	8.199068	-11.338540	-4.285790
3FIB	A	GLY	268	C	-7.160917	6.024137	-12.507824	-4.622164
3FIB	A	PRO	269	C	-7.137738	6.022750	-12.607272	-4.643843
3FIB	A	GLU	270	G	-7.139469	5.997086	-12.609818	-4.643718
3FIB	A	ALA	271	G	-7.141764	5.982386	-12.602659	-4.643031
3FIB	A	ASP	272	G	-7.368364	5.000208	-13.214861	-4.815620
3FIB	A	LYS	273	T	-9.053540	6.222417	-15.057278	-5.185317
3FIB	A	TYR	274	T	-12.484934	11.248112	-18.059066	-6.014597
3FIB	A	ARG	275	T	-14.013058	13.351732	-18.799391	-5.747717
3FIB	A	LEU	276	E	-13.192422	16.507418	-15.038234	-5.130918
3FIB	A	THR	277	E	-12.376921	17.452523	-13.901077	-5.208001
3FIB	A	TYR	278	E	-11.397123	17.876986	-11.915636	-4.818997
3FIB	A	ALA	279	E	-8.285877	11.762395	-9.949244	-4.248505
3FIB	A	TYR	280	E	-7.339583	11.218321	-9.708107	-4.504642
3FIB	A	PHE	281	E	-6.252242	8.494521	-9.873106	-4.599305
3FIB	A	ALA	282	E	-5.550932	6.876433	-9.832632	-4.456525
3FIB	A	GLY	283	E	-5.275770	6.054661	-10.337703	-4.563972
3FIB	A	GLY	284	T	-5.265949	6.044818	-10.385158	-4.575842
3FIB	A	ASP	285	T	-5.279901	5.923241	-10.405855	-4.576100
3FIB	A	ALA	286	T	-5.385210	5.523748	-10.503063	-4.567905
3FIB	A	GLY	287	T	-5.825569	4.821533	-11.262424	-4.760165
3FIB	A	ASP	288	C	-7.477579	7.390537	-12.372730	-5.000805
3FIB	A	ALA	289	G	-9.149447	11.298995	-12.975787	-4.950908
3FIB	A	PHE	290	G	-9.593638	14.321597	-12.410461	-5.274117
3FIB	A	ASP	291	G	-9.381277	14.377607	-12.425680	-5.414867
3FIB	A	GLY	292	C	-7.859051	12.427632	-10.741706	-5.393241
3FIB	A	PHE	293	C	-7.740892	12.097788	-11.040809	-5.409221
3FIB	A	ASP	294	C	-7.360295	10.757059	-11.626818	-5.471056
3FIB	A	PHE	295	C	-6.828537	8.623900	-11.814387	-5.243964
3FIB	A	GLY	296	T	-4.786516	3.070423	-10.417121	-4.473990
3FIB	A	ASP	297	T	-4.777113	3.066694	-10.453019	-4.470231
3FIB	A	ASP	298	T	-4.777242	3.060007	-10.453898	-4.468882
3FIB	A	PRO	299	T	-4.780292	3.025920	-10.445481	-4.462282
3FIB	A	SER	300	H	-4.791482	2.946892	-10.416812	-4.450292
3FIB	A	ASP	301	H	-7.012003	5.331891	-12.298459	-4.512408

3FIB	A	LYS	302	H	-8.422750	7.044402	-13.429816	-4.463488
3FIB	A	PHE	303	H	-8.904052	7.204485	-13.417510	-4.419226
3FIB	A	PHE	304	H	-11.507079	10.755319	-16.601971	-5.242246
3FIB	A	THR	305	H	-11.925320	11.308902	-17.618799	-5.651955
3FIB	A	SER	306	C	-12.074687	10.230994	-18.117113	-5.537663
3FIB	A	HIS	307	T	-12.190981	9.731818	-18.545834	-5.671932
3FIB	A	ASN	308	T	-12.183938	9.757808	-18.582414	-5.697519
3FIB	A	GLY	309	T	-12.183081	9.762201	-18.587936	-5.700358
3FIB	A	MET	310	B	-12.716928	9.493479	-19.468959	-5.894736
3FIB	A	GLN	311	C	-13.665495	11.858440	-20.450182	-6.534021
3FIB	A	PHE	312	C	-13.702163	14.633419	-18.388719	-6.018312
3FIB	A	SER	313	B	-11.969791	11.826611	-16.920115	-5.926879
3FIB	A	THR	314	B	-10.923930	10.275679	-16.669828	-5.952187
3FIB	A	TRP	315	T	-10.906931	10.214641	-16.784926	-5.965960
3FIB	A	ASP	316	T	-10.897570	10.148826	-16.874080	-5.975511
3FIB	A	ASN	317	B	-10.895195	10.083672	-16.927479	-5.982467
3FIB	A	ASP	318	T	-10.988699	9.776038	-16.985660	-5.998050
3FIB	A	ASN	319	C	-12.372453	7.724834	-21.313844	-6.442532
3FIB	A	ASP	320	C	-9.249305	6.646104	-15.689837	-5.652998
3FIB	A	LYS	321	C	-8.566197	6.965522	-15.259104	-5.775407
3FIB	A	PHE	322	T	-8.153536	6.648322	-15.190633	-5.782574
3FIB	A	GLU	323	T	-7.968539	6.415318	-15.142719	-5.648955
3FIB	A	GLY	324	T	-7.958896	6.425313	-15.164316	-5.643575
3FIB	A	ASN	325	T	-8.029072	6.401652	-15.103789	-5.642987
3FIB	A	CYS	326	H	-8.220757	6.130614	-15.119786	-5.570725
3FIB	A	ALA	327	H	-8.708610	5.880096	-15.120915	-5.290750
3FIB	A	GLU	328	H	-10.329555	7.338560	-16.695619	-5.383694
3FIB	A	GLN	329	H	-11.570797	9.679636	-18.298359	-5.897628
3FIB	A	ASP	330	H	-11.917004	10.327067	-18.579721	-5.948310
3FIB	A	GLY	331	C	-11.935250	10.715614	-18.355217	-5.940746
3FIB	A	SER	332	C	-12.361131	11.422019	-18.675539	-6.058531
3FIB	A	GLY	333	C	-12.473351	11.752825	-18.372807	-6.008049
3FIB	A	TRP	334	B	-12.857448	13.841226	-17.329283	-5.899221
3FIB	A	TRP	335	C	-13.668208	18.165088	-15.920128	-5.923559
3FIB	A	MET	336	T	-14.545494	16.602359	-19.709375	-6.967361
3FIB	A	ASN	337	T	-13.379706	12.622920	-19.062457	-6.354492
3FIB	A	LYS	338	T	-10.972961	11.681485	-15.527501	-5.817061
3FIB	A	CYS	339	T	-10.883563	11.562869	-15.715856	-5.772443
3FIB	A	HIS	340	T	-10.810072	11.861664	-15.610756	-5.707883
3FIB	A	ALA	341	T	-10.738392	11.912736	-15.622222	-5.656495
3FIB	A	GLY	342	E	-10.462098	11.588797	-15.688621	-5.712881
3FIB	A	HIS	343	E	-10.721233	11.519545	-15.919535	-5.627295
3FIB	A	LEU	344	T	-10.768219	11.685119	-15.815752	-5.638481
3FIB	A	ASN	345	T	-10.831592	11.410416	-15.951823	-5.691401
3FIB	A	GLY	346	T	-10.458834	12.283916	-14.722554	-5.438288
3FIB	A	VAL	347	C	-9.527652	13.131509	-12.294583	-5.142897
3FIB	A	TYR	348	C	-8.699122	13.735256	-11.436936	-5.425601
3FIB	A	TYR	349	T	-5.968102	9.689629	-8.923702	-4.907707
3FIB	A	GLN	350	T	-5.735051	9.653244	-9.084748	-4.888599
3FIB	A	GLY	351	T	-5.732781	9.650727	-9.100165	-4.888822
3FIB	A	GLY	352	T	-5.733267	9.646105	-9.099188	-4.888607
3FIB	A	THR	353	B	-5.735207	9.625788	-9.097646	-4.886389
3FIB	A	TYR	354	C	-6.383906	9.583043	-9.524165	-4.851653
3FIB	A	SER	355	T	-6.825992	7.152160	-10.770896	-4.292378
3FIB	A	LYS	356	T	-5.423364	4.956642	-10.028243	-4.217662
3FIB	A	ALA	357	T	-4.653336	4.930858	-9.500184	-4.360114
3FIB	A	SER	358	T	-4.298325	5.285650	-9.349309	-4.510322
3FIB	A	THR	359	T	-4.234013	5.528831	-9.354428	-4.546743
3FIB	A	PRO	360	T	-4.238027	5.527132	-9.351954	-4.554302
3FIB	A	ASN	361	T	-4.315829	5.636374	-9.264937	-4.601487
3FIB	A	GLY	362	T	-4.630249	6.133820	-9.234599	-4.730979
3FIB	A	TYR	363	C	-5.552329	7.692719	-9.508242	-4.880289
3FIB	A	ASP	364	C	-7.359725	8.595241	-11.829159	-5.337480
3FIB	A	ASN	365	C	-11.516178	11.262861	-17.870846	-6.443833
3FIB	A	GLY	366	C	-12.226467	13.537419	-17.085125	-5.853827
3FIB	A	ILE	367	C	-12.584977	16.832279	-14.578000	-4.855444
3FIB	A	ILE	368	E	-12.593184	17.264436	-14.244914	-4.778525
3FIB	A	TRP	369	E	-12.305253	19.006084	-13.332614	-5.121609
3FIB	A	ALA	370	T	-10.192665	14.798548	-12.232336	-5.284745
3FIB	A	THR	371	T	-10.194832	14.779063	-12.245228	-5.295042
3FIB	A	TRP	372	T	-10.196427	14.764716	-12.246943	-5.298640
3FIB	A	LYS	373	T	-10.196911	14.758701	-12.246268	-5.298901
3FIB	A	THR	374	T	-10.205197	14.686006	-12.234168	-5.294237
3FIB	A	ARG	375	T	-13.200900	15.795186	-16.816305	-6.031603
3FIB	A	TRP	376	T	-14.322592	17.340707	-17.661281	-6.141580
3FIB	A	TYR	377	B	-15.272339	16.557068	-19.557145	-6.078159
3FIB	A	SER	378	C	-13.537120	14.599294	-18.176096	-6.457581
3FIB	A	MET	379	C	-12.882621	15.417809	-17.406562	-6.568889
3FIB	A	LYS	380	C	-12.232789	15.628210	-16.686018	-6.625864
3FIB	A	LYS	381	E	-12.143858	15.743830	-16.802746	-6.684547
3FIB	A	THR	382	E	-12.021586	16.111293	-16.589893	-6.634630

3FIB	A	THR	383	E	-11.903896	16.875035	-15.908850	-6.486037
3FIB	A	MET	384	E	-11.615041	18.354615	-14.112414	-6.057260
3FIB	A	LYS	385	E	-11.773525	19.159422	-13.434396	-5.874319
3FIB	A	ILE	386	E	-11.789048	19.404873	-13.215607	-5.815767
3FIB	A	ILE	387	E	-11.412702	17.498779	-13.554678	-5.673804
3FIB	A	PRO	388	E	-10.026860	12.840146	-12.697210	-4.888658
3FIB	A	PHE	389	T	-9.021120	10.010826	-12.188276	-4.252436
3FIB	A	ASN	390	T	-9.021120	10.010826	-12.188276	-4.252436
3FIB	A	ARG	391	T	-9.021120	10.010826	-12.188276	-4.252436
3FIB	A	LEU	392	C	-9.021120	10.010826	-12.188276	-4.252436
3IL8	A	LEU	5	C	-5.948819	3.876701	-10.940440	-3.827766
3IL8	A	ARG	6	C	-5.948819	3.876701	-10.940440	-3.827766
3IL8	A	CYS	7	C	-5.948819	3.876701	-10.940440	-3.827766
3IL8	A	GLN	8	C	-5.948819	3.876701	-10.940440	-3.827766
3IL8	A	CYS	9	T	-6.682358	7.014782	-12.403192	-5.121309
3IL8	A	ILE	10	T	-6.284552	8.300688	-10.515295	-4.646197
3IL8	A	LYS	11	T	-6.148951	8.974707	-9.954024	-4.545439
3IL8	A	THR	12	T	-5.774369	9.732129	-8.917905	-4.369373
3IL8	A	TYR	13	C	-5.772303	9.804942	-8.840712	-4.334954
3IL8	A	SER	14	C	-5.725171	10.425947	-8.350133	-4.230944
3IL8	A	LYS	15	C	-5.828101	11.042234	-8.054723	-4.216799
3IL8	A	PRO	16	C	-5.866519	11.601710	-7.705281	-4.167557
3IL8	A	PHE	17	C	-6.325529	12.998939	-7.563460	-4.145652
3IL8	A	HIS	18	C	-6.277744	13.016400	-7.621828	-4.180487
3IL8	A	PRO	19	G	-6.675574	13.854082	-7.762067	-4.264957
3IL8	A	LYS	20	G	-6.887183	13.932677	-7.848627	-4.325755
3IL8	A	PHE	21	G	-7.393748	13.423901	-8.895285	-4.532886
3IL8	A	ILE	22	E	-7.519127	13.308862	-8.844708	-4.524681
3IL8	A	LYS	23	E	-7.714242	13.193136	-9.520237	-4.729721
3IL8	A	GLU	24	E	-7.651723	12.811542	-9.665916	-4.646537
3IL8	A	LEU	25	E	-7.178028	11.648813	-9.368706	-4.289003
3IL8	A	ARG	26	E	-7.068746	11.043730	-9.709896	-4.261291
3IL8	A	VAL	27	E	-5.743551	8.346008	-9.054394	-4.412764
3IL8	A	ILE	28	E	-5.455355	7.120986	-9.651659	-4.398562
3IL8	A	GLU	29	C	-4.978833	5.493411	-9.951576	-4.343742
3IL8	A	SER	30	C	-4.952961	5.357713	-10.088223	-4.361655
3IL8	A	GLY	31	B	-4.683309	4.665791	-10.290033	-4.387362
3IL8	A	PRO	32	T	-4.766749	4.094938	-10.565553	-4.387715
3IL8	A	HIS	33	T	-4.843785	3.911238	-10.597231	-4.404433
3IL8	A	CYS	34	B	-5.185622	3.705748	-10.929920	-4.493418
3IL8	A	ALA	35	T	-5.235806	3.664118	-10.816320	-4.485827
3IL8	A	ASN	36	C	-6.870303	5.997133	-13.398549	-5.343092
3IL8	A	THR	37	C	-7.635296	8.424972	-15.167938	-6.809613
3IL8	A	GLU	38	E	-8.145375	8.400942	-13.775724	-5.577970
3IL8	A	ILE	39	E	-9.014436	11.173405	-12.395914	-5.139431
3IL8	A	ILE	40	E	-11.644941	15.756008	-14.802861	-5.459842
3IL8	A	VAL	41	E	-11.721408	15.669461	-15.764728	-5.895452
3IL8	A	LYS	42	E	-10.100708	9.428834	-15.568024	-5.681309
3IL8	A	LEU	43	E	-7.106089	6.165962	-11.455433	-4.292708
3IL8	A	SER	44	T	-5.576405	5.335471	-10.445819	-4.554891
3IL8	A	ASP	45	T	-5.322090	6.317670	-10.047021	-4.576521
3IL8	A	GLY	46	T	-5.311693	6.369728	-10.067179	-4.580452
3IL8	A	ARG	47	C	-5.311747	6.370322	-10.066025	-4.580139
3IL8	A	GLU	48	E	-5.340449	6.389120	-9.997951	-4.595668
3IL8	A	LEU	49	E	-5.914877	8.224172	-9.399079	-4.626697
3IL8	A	CYS	50	E	-7.649770	9.713879	-11.262587	-4.820691
3IL8	A	LEU	51	E	-8.063759	11.812442	-10.756692	-4.707849
3IL8	A	ASP	52	T	-7.135473	7.951083	-11.695955	-4.829015
3IL8	A	PRO	53	T	-7.131125	7.897407	-11.730045	-4.823859
3IL8	A	LYS	54	T	-7.077677	8.164010	-11.692996	-4.817780
3IL8	A	GLU	55	T	-7.087772	8.105047	-11.685842	-4.818463
3IL8	A	ASN	56	H	-7.186176	7.505291	-11.903024	-4.850821
3IL8	A	TRP	57	H	-8.380286	11.006870	-11.628910	-4.795092
3IL8	A	VAL	58	H	-8.513604	11.029647	-11.374387	-4.750177
3IL8	A	GLN	59	H	-10.613858	11.525789	-14.323584	-4.421671
3IL8	A	ARG	60	H	-9.351914	11.565349	-11.066443	-3.766517
3IL8	A	VAL	61	H	-9.369754	11.607597	-10.965542	-3.749771
3IL8	A	VAL	62	H	-9.329204	11.802520	-11.053005	-3.802742
3IL8	A	GLU	63	H	-9.208302	11.843278	-11.444704	-3.992169
3IL8	A	LYS	64	H	-9.192870	11.896007	-11.661693	-4.159217
3IL8	A	PHE	65	H	-9.702494	12.035047	-14.509138	-5.618321
3IL8	A	LEU	66	H	-7.724970	6.415953	-13.993330	-5.650749
3IL8	A	LYS	67	H	-6.901009	5.244639	-13.247956	-5.178942
3IL8	A	ARG	68	H	-6.395810	4.552351	-12.466826	-4.601663
3IL8	A	ALA	69	H	-3.773882	3.352596	-7.484440	-3.363095
3IL8	A	GLU	70	H	-3.773882	3.352596	-7.484440	-3.363095
3IL8	A	ASN	71	H	-3.773882	3.352596	-7.484440	-3.363095
3IL8	A	SER	72	C	-3.773882	3.352596	-7.484440	-3.363095
5PNT	A	ALA	1	C	-2.985387	1.180323	-8.641622	-3.743932
5PNT	A	GLU	2	C	-2.985387	1.180323	-8.641622	-3.743932
5PNT	A	GLN	3	C	-2.985387	1.180323	-8.641622	-3.743932

5PNT	A	ALA	4	C	-2.985387	1.180323	-8.641622	-3.743932
5PNT	A	THR	5	C	-3.440657	1.776234	-9.030143	-4.186966
5PNT	A	LYS	6	E	-5.150200	3.896317	-11.304366	-5.224865
5PNT	A	SER	7	E	-8.065901	5.875201	-15.796158	-6.523774
5PNT	A	VAL	8	E	-9.972580	9.580852	-16.996311	-6.889655
5PNT	A	LEU	9	E	-11.289404	15.267347	-14.101649	-5.082298
5PNT	A	PHE	10	E	-11.212489	15.202922	-13.466663	-4.859389
5PNT	A	VAL	11	E	-10.652749	11.632719	-15.046620	-5.179368
5PNT	A	CYS	12	E	-10.461941	10.745584	-15.583923	-5.325794
5PNT	A	LEU	13	T	-10.209266	10.406177	-15.594745	-5.384041
5PNT	A	GLY	14	T	-10.210230	10.376808	-15.616855	-5.391769
5PNT	A	ASN	15	T	-10.282381	9.954394	-15.807840	-5.428989
5PNT	A	ILE	16	T	-10.517149	10.233138	-15.694842	-5.452152
5PNT	A	CYS	17	T	-10.770574	10.498959	-15.384737	-5.415190
5PNT	A	ARG	18	H	-12.925309	13.637506	-17.898576	-5.820526
5PNT	A	SER	19	H	-13.075912	13.866915	-17.417313	-5.288100
5PNT	A	PRO	20	H	-12.710423	13.754690	-16.271899	-4.796883
5PNT	A	ILE	21	H	-12.080859	13.852785	-14.835717	-4.550854
5PNT	A	ALA	22	H	-12.034019	14.084978	-14.752918	-4.542975
5PNT	A	GLU	23	H	-12.044741	14.105660	-14.695531	-4.526448
5PNT	A	ALA	24	H	-12.075117	14.249695	-14.537035	-4.490505
5PNT	A	VAL	25	H	-12.158228	14.603543	-14.402304	-4.549715
5PNT	A	PHE	26	H	-12.984911	17.242707	-15.106444	-4.933217
5PNT	A	ARG	27	H	-12.686382	15.262216	-16.124158	-5.284857
5PNT	A	LYS	28	H	-9.201476	12.039919	-11.833913	-4.840451
5PNT	A	LEU	29	H	-8.731188	11.964954	-11.875001	-4.909995
5PNT	A	VAL	30	H	-6.555796	8.379154	-10.230307	-4.748404
5PNT	A	THR	31	H	-5.571120	6.255216	-10.266969	-4.673796
5PNT	A	ASP	32	H	-5.562081	6.265474	-10.303475	-4.673656
5PNT	A	GLN	33	H	-5.461503	6.244993	-10.367449	-4.620190
5PNT	A	ASN	34	C	-5.388693	6.244853	-10.437720	-4.604617
5PNT	A	ILE	35	C	-5.471634	5.966288	-10.477576	-4.584850
5PNT	A	SER	36	G	-6.155950	6.421122	-10.916958	-4.429412
5PNT	A	GLU	37	G	-6.180807	6.400651	-10.841675	-4.419502
5PNT	A	ASN	38	G	-6.630322	6.627389	-10.974708	-4.513888
5PNT	A	TRP	39	E	-8.478367	12.929172	-10.676761	-4.974952
5PNT	A	ARG	40	E	-10.615215	13.761727	-14.378875	-5.418704
5PNT	A	VAL	41	E	-10.404148	12.330129	-13.942608	-4.860887
5PNT	A	ASP	42	E	-10.461401	11.473707	-14.184908	-4.709819
5PNT	A	SER	43	E	-10.351908	11.437443	-14.308588	-4.729873
5PNT	A	ALA	44	E	-9.383479	10.425669	-13.116850	-4.650742
5PNT	A	ALA	45	E	-7.934729	9.953166	-11.489854	-4.865369
5PNT	A	THR	46	C	-7.309650	10.019703	-11.468084	-5.259808
5PNT	A	SER	47	C	-6.346086	8.715948	-10.341627	-4.894806
5PNT	A	GLY	48	T	-4.660242	7.837508	-8.406801	-4.950005
5PNT	A	TYR	49	T	-4.587104	8.041168	-8.434098	-4.933096
5PNT	A	GLU	50	T	-4.568980	8.028181	-8.473381	-4.912411
5PNT	A	ILE	51	T	-4.551121	8.004329	-8.479777	-4.867837
5PNT	A	GLY	52	T	-4.574390	7.987720	-8.417404	-4.870034
5PNT	A	ASN	53	b	-5.573731	8.882687	-8.987273	-4.500677
5PNT	A	PRO	54	C	-6.138984	7.758470	-9.534163	-4.022098
5PNT	A	PRO	55	C	-6.515291	7.703594	-9.225409	-3.773079
5PNT	A	ASP	56	C	-9.136018	7.091341	-14.237636	-4.512544
5PNT	A	TYR	57	H	-10.174495	8.327763	-15.244400	-4.767448
5PNT	A	ARG	58	H	-11.499283	9.961559	-16.527871	-4.935436
5PNT	A	GLY	59	H	-11.838707	10.304621	-16.823906	-5.223481
5PNT	A	GLN	60	H	-13.093929	9.610687	-20.821949	-6.179947
5PNT	A	SER	61	H	-12.860736	9.121054	-20.285227	-5.885529
5PNT	A	CYS	62	H	-12.494773	9.271805	-19.523916	-5.781702
5PNT	A	MET	63	H	-10.323439	7.928592	-16.237869	-5.466977
5PNT	A	LYS	64	H	-8.253085	7.995242	-12.822900	-4.918643
5PNT	A	ARG	65	H	-7.934229	7.913278	-12.719855	-4.751790
5PNT	A	HIS	66	H	-7.538303	9.424688	-11.889819	-4.928213
5PNT	A	GLY	67	C	-6.393896	9.570448	-9.402157	-4.512132
5PNT	A	ILE	68	C	-6.388111	9.598306	-9.414582	-4.512174
5PNT	A	PRO	69	C	-6.362280	9.619045	-9.392179	-4.474043
5PNT	A	MET	70	C	-6.374721	9.682095	-9.317982	-4.471553
5PNT	A	SER	71	C	-6.416684	9.584247	-9.193349	-4.424378
5PNT	A	HIS	72	C	-7.717072	9.497400	-10.889897	-4.286761
5PNT	A	VAL	73	C	-7.781744	9.218910	-10.841594	-4.247705
5PNT	A	ALA	74	b	-9.181432	10.595093	-11.845288	-4.339486
5PNT	A	ARG	75	C	-11.668799	9.882539	-16.647883	-4.694100
5PNT	A	GLN	76	B	-7.807865	9.546356	-11.145853	-4.761703
5PNT	A	ILE	77	C	-7.232220	9.500210	-10.879236	-4.730470
5PNT	A	THR	78	C	-7.209121	9.597674	-10.915799	-4.741124
5PNT	A	LYS	79	H	-7.206570	9.612614	-10.924575	-4.742319
5PNT	A	GLU	80	H	-7.205219	9.619332	-10.930639	-4.743267
5PNT	A	ASP	81	H	-7.470718	9.661271	-10.812744	-4.732896
5PNT	A	PHE	82	H	-9.042484	12.158168	-12.077770	-5.016187
5PNT	A	ALA	83	H	-10.146657	12.754808	-13.370976	-5.058208
5PNT	A	THR	84	H	-10.721400	12.272214	-13.967408	-5.127483

5PNT	A	PHE	85	T	-13.578147	17.623117	-16.198787	-5.789629
5PNT	A	ASP	86	T	-14.352959	18.097453	-17.705484	-6.058936
5PNT	A	TYR	87	E	-14.553086	18.885629	-16.979887	-5.640856
5PNT	A	ILE	88	E	-13.558969	16.529457	-16.329204	-5.568583
5PNT	A	LEU	89	E	-13.169052	15.691294	-16.919305	-5.840187
5PNT	A	CYS	90	E	-12.808243	13.389896	-18.022406	-5.967175
5PNT	A	MET	91	C	-12.634939	12.661444	-18.464520	-6.060179
5PNT	A	ASP	92	C	-12.207818	10.817858	-18.612865	-5.898889
5PNT	A	GLU	93	H	-11.502526	8.736882	-17.423275	-5.087675
5PNT	A	SER	94	H	-11.470423	8.458873	-17.557844	-5.047210
5PNT	A	ASN	95	H	-11.492406	8.384801	-17.488205	-4.998645
5PNT	A	LEU	96	H	-11.409122	8.606152	-17.326949	-4.936365
5PNT	A	ARG	97	H	-11.435262	8.530405	-17.206398	-4.813624
5PNT	A	ASP	98	H	-11.967051	9.410198	-17.937701	-5.002918
5PNT	A	LEU	99	H	-12.059821	10.133726	-17.849014	-5.205503
5PNT	A	ASN	100	H	-11.679496	9.917172	-19.168783	-6.310012
5PNT	A	ARG	101	H	-11.399163	8.389740	-19.330363	-6.188596
5PNT	A	LYS	102	H	-10.448458	8.986614	-16.704369	-5.756240
5PNT	A	SER	103	H	-6.826600	5.604830	-11.607821	-4.497631
5PNT	A	ASN	104	H	-4.662872	5.084217	-8.593903	-4.047537
5PNT	A	GLN	105	C	-4.437291	5.521563	-8.565031	-4.077552
5PNT	A	VAL	106	T	-4.146735	5.765476	-8.293319	-4.019301
5PNT	A	LYS	107	T	-4.041515	5.801072	-8.322291	-4.004768
5PNT	A	THR	108	T	-4.046282	5.805643	-8.296074	-4.000898
5PNT	A	CYS	109	T	-4.295254	6.197140	-8.181585	-3.981621
5PNT	A	LYS	110	C	-4.465044	6.107546	-8.074710	-3.927988
5PNT	A	ALA	111	C	-5.108983	6.032729	-8.502658	-3.935892
5PNT	A	LYS	112	E	-7.570184	9.734425	-11.370562	-4.756623
5PNT	A	ILE	113	E	-7.884016	10.703773	-10.967615	-4.839571
5PNT	A	GLU	114	E	-9.473080	12.800220	-12.814060	-5.067718
5PNT	A	LEU	115	E	-9.724735	13.957407	-12.229385	-5.059710
5PNT	A	LEU	116	G	-10.648794	16.196726	-12.834665	-5.345858
5PNT	A	GLY	117	G	-10.974988	15.886832	-13.282356	-5.386426
5PNT	A	SER	118	G	-11.718171	13.749017	-15.700533	-5.386073
5PNT	A	TYR	119	G	-10.676240	10.466788	-15.324394	-5.308802
5PNT	A	ASP	120	T	-9.629691	5.985614	-16.483623	-5.343877
5PNT	A	PRO	121	T	-8.753737	6.714913	-14.553956	-4.926790
5PNT	A	GLN	122	T	-8.572389	7.195090	-14.388027	-4.941208
5PNT	A	LYS	123	T	-8.550763	7.334482	-14.362481	-4.932884
5PNT	A	GLN	124	C	-8.536249	7.479129	-14.293887	-4.922779
5PNT	A	LEU	125	C	-7.970455	10.359678	-11.477348	-4.631591
5PNT	A	ILE	126	C	-7.519123	11.669737	-9.901526	-4.446670
5PNT	A	ILE	127	C	-7.528511	11.871474	-9.766838	-4.438053
5PNT	A	GLU	128	C	-7.063732	11.038337	-10.011850	-4.626931
5PNT	A	ASP	129	C	-6.603997	10.282568	-10.118369	-4.797016
5PNT	A	PRO	130	T	-6.565997	10.037002	-10.300693	-4.831401
5PNT	A	TYR	131	T	-6.610955	9.577133	-10.655566	-4.929127
5PNT	A	TYR	132	T	-6.332049	7.686409	-11.361957	-4.859406
5PNT	A	GLY	133	T	-6.219169	6.207722	-11.987167	-4.842530
5PNT	A	ASN	134	C	-6.412646	4.883974	-12.685918	-4.803716
5PNT	A	ASP	135	H	-6.472426	4.449132	-12.796005	-4.789882
5PNT	A	SER	136	H	-6.499735	4.354999	-12.726542	-4.759573
5PNT	A	ASP	137	H	-6.914505	4.071031	-12.929314	-4.773540
5PNT	A	PHE	138	H	-9.435429	10.315465	-13.064498	-4.884979
5PNT	A	GLU	139	H	-11.718393	11.744798	-16.127434	-5.136352
5PNT	A	THR	140	H	-11.775341	11.857932	-15.919553	-5.112002
5PNT	A	VAL	141	H	-12.757618	14.037403	-16.125881	-5.269139
5PNT	A	TYR	142	H	-14.148977	13.593685	-18.711471	-5.545307
5PNT	A	GLN	143	H	-14.186695	13.228677	-18.800818	-5.538024
5PNT	A	GLN	144	H	-15.384287	14.020717	-21.242543	-6.181503
5PNT	A	CYS	145	H	-15.379002	12.045673	-22.246189	-6.160419
5PNT	A	VAL	146	H	-14.905657	11.008444	-21.447029	-5.646164
5PNT	A	ARG	147	H	-14.869857	10.761000	-21.396119	-5.518082
5PNT	A	CYS	148	H	-13.765194	14.805067	-17.197059	-5.262623
5PNT	A	CYS	149	H	-13.133017	17.935881	-15.906907	-5.798215
5PNT	A	ARG	150	H	-11.921399	19.319148	-13.979939	-6.528861
5PNT	A	ALA	151	H	-10.130313	17.459680	-11.501414	-5.828262
5PNT	A	PHE	152	H	-8.805157	15.853411	-9.963653	-5.228071
5PNT	A	LEU	153	H	-6.435418	9.744396	-8.494430	-4.118285
5PNT	A	GLU	154	H	-4.931846	6.240022	-7.467402	-3.280151
5PNT	A	LYS	155	H	-4.931846	6.240022	-7.467402	-3.280151
5PNT	A	ALA	156	C	-4.931846	6.240022	-7.467402	-3.280151
5PNT	A	HIS	157	C	-4.931846	6.240022	-7.467402	-3.280151

Table S2. Eigenvectors and eigenvalues of the 4-dimensional energetic space of the 120 human proteins, computed from the data in Table S1.

The first line in each group represents the energetic center of mass, in kcal/mol (ΔG, ΔH_{ap}, ΔH_{pol}, $T\Delta S_{conf}$). In the second through fifth lines, each row is an eigenvector, each column is a thermodynamic quantity. The final value in each row is the square root of the eigenvalue of each eigenvector. The sixth line indicates the type and number of data points, subsets of Table S1, used to generate the eigenvectors and eigenvalues.

```
   -8.129790643     9.522003469   -11.716524440    -4.559127696
    0.554794467    -0.651216265     0.509542073     0.092126818  |  4.90692
   -0.145321982    -0.688576434    -0.701700634    -0.111176597  |  2.65339
   -0.592453412    -0.223876674     0.225075352     0.740418311  |  0.92355
    0.565759290     0.227286395    -0.444211866     0.656454978  |  0.16035
  17484 residues in the complete data set

   -9.345680715    10.295732346   -12.994411528    -4.622164034
    0.532872325    -0.689922965     0.479523825     0.100549936  |  4.13730
   -0.172712967    -0.655069672    -0.726722065    -0.113705746  |  2.63011
   -0.598555278    -0.206511833     0.211927368     0.744426781  |  0.99660
    0.572668224     0.228567039    -0.443867923     0.650222640  |  0.16213
   5493 helical residues (H, G, I)

   -8.874033970    11.118841191   -11.963001314    -4.705481633
    0.542709216    -0.680819908     0.483591962     0.089943171  |  4.74944
   -0.156204686    -0.657224249    -0.724233954    -0.138353037  |  2.69673
   -0.597441354    -0.235539961     0.201309288     0.739634590  |  0.90969
    0.569324716     0.221498232    -0.448440146     0.652464050  |  0.16319
   5101 strand residues (E, B, b)

   -6.609432243     7.722937874   -10.515259953    -4.400519562
    0.562979534    -0.575243061     0.583378627     0.108714504  |  4.40595
   -0.084313580    -0.754142729    -0.643159127    -0.102500255  |  2.45716
   -0.606738788    -0.225308473     0.227789606     0.727472357  |  0.83466
    0.554809254     0.222711150    -0.440599150     0.669670683  |  0.14705
   6890 coil residues (C, T)

   -7.934693021     9.065689824   -11.231849089    -4.192453242
    0.548752323    -0.666348163     0.496491335     0.091363933  |  4.45409
   -0.155101038    -0.674385316    -0.713689739    -0.108605112  |  2.30474
    0.597450298     0.221705085    -0.227278004    -0.736372667  |  0.94803
   -0.563797568    -0.228103982     0.438734567    -0.661523133  |  0.15439
   1118 ALA residues

   -8.468699070     8.497661859   -13.027411725    -4.812680016
    0.562114080    -0.618928142     0.540644760     0.093053527  |  4.93440
   -0.119397632    -0.717069711    -0.677898581    -0.109584437  |  2.44059
   -0.597538614    -0.230802608     0.230998444     0.732336999  |  0.86306
    0.559213350     0.222416592    -0.441357538     0.665593579  |  0.16251
    440 CYS residues

   -7.791749638     8.169441779   -12.101158942    -4.634624398
    0.573164954    -0.586094762     0.566018611     0.087165347  |  4.55600
   -0.108517454    -0.747004234    -0.649062111    -0.094482868  |  2.42087
   -0.581074307    -0.221824165     0.244144230     0.744002879  |  0.87288
    0.567502024     0.221972171    -0.445796929     0.655694217  |  0.15418
```

```
 992 ASP residues

-8.095154291     9.111000743   -12.195991569    -4.782776739
 0.562680244    -0.607501701     0.552243077     0.096748180  |  4.75664
-0.127898949    -0.733646408    -0.662219524    -0.082886117  |  2.44699
-0.588356927    -0.203209078     0.245755394     0.743065598  |  0.89353
 0.566452935     0.226739283    -0.442828603     0.656980364  |  0.15850
1149 GLU residues

-9.626764534    12.880710689   -12.201727535    -4.806243724
 0.538724540    -0.713717145     0.440836334     0.077762676  |  4.34913
-0.210321042    -0.628331442    -0.740895186    -0.109722291  |  2.38872
 0.582963769     0.213108751    -0.235466006    -0.747859388  |  0.91832
-0.570696218    -0.224481838     0.448657341    -0.650092548  |  0.15469
 721 PHE residues

-6.396875829     7.428780140   -10.566543536    -4.523816990
 0.566833488    -0.623278495     0.532115088     0.084126384  |  4.27926
-0.124990462    -0.711413423    -0.682501301    -0.111625719  |  2.32219
-0.596254130    -0.239389396     0.239687993     0.727820991  |  0.82886
 0.554579295     0.219334396    -0.439994516     0.671371026  |  0.14498
1182 GLY residues

-8.669477153    10.006104639   -12.315058345    -4.684310698
 0.565231152    -0.601771563     0.555687572     0.097959449  |  4.86526
-0.124197648    -0.738117128    -0.656522076    -0.093470921  |  2.49141
-0.585876450    -0.208322072     0.238857036     0.745853884  |  0.92156
 0.567307213     0.222836275    -0.450707669     0.652203279  |  0.16494
 443 HIS residues

-8.248504716    11.049984607   -10.876807284    -4.405631025
 0.545573980    -0.693062085     0.463839333     0.082867676  |  4.87727
-0.169862618    -0.641985594    -0.737485090    -0.122950925  |  2.56139
-0.591361676    -0.232803376     0.215249892     0.741458994  |  0.95708
 0.569022927     0.230915637    -0.441176040     0.654411627  |  0.15852
 863 ILE residues

-7.732935352     8.858890240   -11.714808212    -4.693669408
 0.563486840    -0.594061163     0.564862633     0.102489623  |  4.40801
-0.108665405    -0.742025970    -0.654231983    -0.097825365  |  2.49491
-0.591672801    -0.214222919     0.230250253     0.742304963  |  0.93256
 0.566213483     0.224938515    -0.447096790     0.654911762  |  0.16177
1133 LYS residues

-8.595834214    10.987111084   -11.356325599    -4.437591222
 0.536151002    -0.696889563     0.468063144     0.088339870  |  4.66455
-0.197497883    -0.651590327    -0.726730468    -0.091035483  |  2.46311
-0.593655294    -0.197735860     0.245891560     0.740277828  |  0.90493
 0.566665758     0.225112221    -0.438539692     0.660225224  |  0.16410
1533 LEU residues

-8.733040500    10.117706459   -12.529929319    -4.822137577
 0.566195322    -0.622136486     0.532883833     0.091672630  |  5.22819
-0.158839073    -0.725033863    -0.667536162    -0.059089068  |  2.36256
-0.591652938    -0.189378481     0.281745833     0.731233121  |  0.83777
-0.551488719    -0.226733062     0.437092184    -0.673351865  |  0.17197
 392 MET residues
```

```
-7.704065480     8.118910322   -12.170634084    -4.734736130
 0.579773904    -0.539367462     0.603196710     0.095387053  |  4.51497
-0.061659235    -0.776414321    -0.619224403    -0.099699945  |  2.36495
-0.589543302    -0.237452766     0.238192344     0.734383609  |  0.87009
 0.559016148     0.223337696    -0.442695465     0.664561469  |  0.15386
 777 ASN residues

-6.416408312     8.374496239    -9.413883246    -4.014081557
 0.548333358    -0.657604253     0.507838563     0.094800680  |  4.52197
-0.135907294    -0.679608300    -0.710020514    -0.124629997  |  2.31166
-0.613127951    -0.238280699     0.218936157     0.720668706  |  0.82694
 0.552208160     0.221159474    -0.435933278     0.675364206  |  0.14418
 805 PRO residues

-8.596583714     8.975238527   -12.882609403    -4.775286924
 0.557418841    -0.579266549     0.583273306     0.116304561  |  4.96375
-0.087085414    -0.752976225    -0.644217569    -0.102111014  |  2.32687
-0.606165688    -0.216172029     0.218330348     0.733597077  |  0.88344
 0.560592120     0.225270337    -0.443968279     0.661726468  |  0.16106
 790 GLN residues

-9.350945555     9.669734199   -13.307446179    -4.641403512
 0.566903592    -0.505209738     0.639009017     0.122682170  |  4.97678
-0.021124726    -0.798483488    -0.592634842    -0.103739142  |  2.53704
-0.582787987    -0.226122547     0.193054291     0.756278254  |  1.00964
 0.581835223     0.236761133    -0.450756543     0.634216429  |  0.16573
 898 ARG residues

-8.112398204     8.335346089   -12.207684980    -4.470031530
 0.563706426    -0.600960801     0.557956651     0.098820831  |  4.43821
-0.110456127    -0.734633382    -0.661602756    -0.101956024  |  2.38776
-0.601179000    -0.224104808     0.236778034     0.729586875  |  0.85133
 0.555534265     0.221216963    -0.441477441     0.668986102  |  0.15613
1158 SER residues

-7.399774980     9.169390730   -10.970804126    -4.575507383
 0.546823845    -0.651058418     0.516607963     0.101108020  |  4.42783
-0.147924019    -0.693686463    -0.696935110    -0.105825462  |  2.34976
-0.601006348    -0.211146487     0.225811364     0.737033079  |  0.83105
 0.563820483     0.224363965    -0.443178173     0.659818445  |  0.15741
1050 THR residues

-8.133288207    10.263927187   -10.925712458    -4.252779356
 0.541443644    -0.692618689     0.468521241     0.087212260  |  4.74383
-0.164277021    -0.643077505    -0.735529565    -0.135869945  |  2.40616
-0.597934245    -0.236505152     0.203960146     0.738200657  |  0.89476
 0.567738037     0.225379650    -0.444841955     0.654975701  |  0.15970
1158 VAL residues

-9.921118993    12.942561764   -12.677726118    -4.938081239
 0.563564577    -0.628193991     0.528944557     0.089358458  |  4.99226
-0.109500041    -0.700416726    -0.693322997    -0.129342077  |  2.38645
-0.587912890    -0.248698885     0.205720027     0.741745622  |  0.95257
 0.569879937     0.230081691    -0.444072234     0.651996261  |  0.14545
 280 TRP residues
```

```
-9.950454616    12.523347314   -12.960132100    -4.941445736
 0.561044296    -0.619681045     0.540314590     0.096357902  |  4.96615
-0.105286148    -0.711048249    -0.685238986    -0.117357347  |  2.59556
-0.593224161    -0.237854511     0.211311316     0.739498380  |  1.03869
 0.567652377     0.232015133    -0.440289909     0.655808320  |  0.17142
 602 TYR residues
```