disorder				disorder				phi				psi			
Resi MCC	Struct MCC	p-val	n	Resi FPR	Struct FPR	p-val	n	Resi MAE	Struct MAE	p-val	n	Resi MAE	Struct MAE	p-val	n
0.660	0.518		21	0.015	0.015	0.5322	21	20.256	20.255	0.3548	21	31.832	31.170	0.7975	21
0.604	0.502	0.6304	21	0.011	0.013		21	20.013	19.991		21	31.157	30.971		21
0.597	0.476	0.4121	21	0.026	0.041	0.0181	21	21.607	21.855	0.0012	21	33.223	33.384	0.0054	21
0.621	0.514	0.9059	21	0.045	0.068	0.0006	21								

disorder				disorder				phi				psi			
Resi MCC	Struct MCC	p-val	n	Resi FPR	Struct FPR	p-val	n	Resi MAE	Struct MAE	p-val	n	Resi MAE	Struct MAE	p-val	n
0.656	0.533	0.8115	115	0.006	0.007		115	17.228	16.934		115	25.754	25.289		115
0.663	0.529		115	0.008	0.010	0.0282	115	17.465	17.084	0.2340	115	26.545	25.881	0.1129	115
0.604	0.505	0.3207	115	0.027	0.044	0.0000	115	17.998	17.607	0.0000	115	27.035	26.646	0.0012	115
0.567	0.500	0.1800	115	0.044	0.062	0.0000	115								

disorder				disorder				phi				psi			
Resi MCC	Struct MCC	p-val	n	Resi FPR	Struct FPR	p-val	n	Resi MAE	Struct MAE	p-val	n	Resi MAE	Struct MAE	p-val	n
								20.070	20.218	0.3941	513	27.981	28.240	0.4796	513
								20.231	20.325	0.7879	513	28.635	28.798	0.1268	513
								20.061	20.299		513	27.883	28.410		513

Resi [] = Per-residue performance

Struct [] = Mean of per-structure performance

CASP12	rsa				asa				q3				q8			
	Resi PCC	Struct PCC	p-val	n	Resi PCC	Struct PCC	p-val	n	Resi ACC	Struct ACC	p-val	n	Resi ACC	Struct ACC	p-val	n
mmseqs	0.726	0.712		21	0.735	0.735	0.5292	21	0.819	0.818	0.5181	21	0.703	0.716	0.7597	21
hhblits	0.725	0.712	0.9156	21	0.737	0.738		21	0.824	0.825		21	0.711	0.718		21
nsp1	0.617	0.613	0.0000	21	0.641	0.653	0.0000	21	0.709	0.682	0.0001	21				
spider					0.687	0.688	0.0029	21	0.791	0.774	0.0004	21				
raptorx									0.786	0.772	0.0017	21	0.661	0.657	0.0022	21
jpred4									0.760	0.746	0.0000	21				
TS115	**rsa**				**asa**				**q3**				**q8**			
	Resi PCC	**Struct PCC**	**p-val**	**n**	**Resi PCC**	**Struct PCC**	**p-val**	**n**	**Resi ACC**	**Struct ACC**	**p-val**	**n**	**Resi ACC**	**Struct ACC**	**p-val**	**n**
mmseqs	0.778	0.751		115	0.797	0.785		115	0.857	0.862		115	0.750	0.763		115
hhblits	0.775	0.750	0.7936	115	0.795	0.785	0.9783	115	0.853	0.859	0.3780	115	0.744	0.756	0.0401	115
nsp1	0.661	0.640	0.0000	115	0.691	0.679	0.0000	115	0.326	0.317	0.0000	115				
spider					0.771	0.755	0.0000	115	0.838	0.843	0.0000	115				
raptorx									0.822	0.829	0.0000	115	0.716	0.731	0.0000	115
jpred4									0.751	0.784	0.0000	108				
CB513	**rsa**				**asa**				**q3**				**q8**			
	Resi PCC	**Struct PCC**	**p-val**	**n**	**Resi PCC**	**Struct PCC**	**p-val**	**n**	**Resi ACC**	**Struct ACC**	**p-val**	**n**	**Resi ACC**	**Struct ACC**	**p-val**	**n**
mmseqs	0.794	0.778		513	0.807	0.799		513	0.853	0.851		513	0.723	0.722		513
hhblits	0.788	0.774	0.1115	513	0.804	0.796	0.1614	513	0.853	0.849	0.3244	513	0.720	0.719	0.2298	513
nsp1	0.701	0.693	0.0000	513	0.723	0.721	0.0000	513	0.787	0.783	0.0000	513				
spider					0.797	0.790	0.0000	513	0.848	0.844	0.0025	513				
raptorx									0.827	0.827	0.0000	508	0.703	0.704	0.0000	508
jpred4									0.683	0.775	0.0000	416				

Supplementary table S1: Results of the method's validation on independent test datasets. The performance of NetSurfP-2.0 using HH-suite and MMSeqs2 profiles, NetSurfP-1.0, Spider3, SPOT-disorder, RaptorX, and JPred4, is displayed for the CASP12, TS115, and CB513 datasets. SPOT-disorder and Spider3 predictions are reported as a single row. The following performance metrics are

used: Pearson Correlation Coefficient (PCC), Q3 and Q8 accuracy, Matthew's Correlation Coefficient (MCC), False Positive Rate (FPR), and mean absolute error (MAE) in degrees. The different predicted features are reported in the column header, together with the corresponding performance metric. All metrics are calculated both *per residue,* i.e. as an average over all residues in all structures, and *per structure,* i.e. as the average of the metric per structure, which is in turn calculated as the average of all its residues. For each feature and each dataset, a p-value is calculated by performing a 2-tailed paired Student's t-test on the corresponding performances per structure.

CASP12	pcc	pcc		Q8	Q3		MCC		MAE	MAE
	RSA	**ASA**		**Q8**	**Q3**		**Disorder**		**Phi**	**Psi**
Fold 1	0.7282	0.7365		0.7000	0.8189		0.6237		20.3031	31.6195
Fold 2	0.7284	0.7373		0.7041	0.8218		0.6448		20.1904	31.6913
Fold 3	0.7294	0.7383		0.6917	0.8069		0.5708		20.2208	31.6077
Fold 4	0.7291	0.7404		0.7062	0.8184		0.6597		20.3522	31.8715
TS115										
	RSA	**ASA**		**Q8**	**Q3**		**Disorder**		**Phi**	**Psi**
Fold 1	0.7833	0.8025		0.7482	0.8577		0.6650		17.1660	25.4516
Fold 2	0.7826	0.8016		0.7506	0.8590		0.6618		17.2033	25.4277
Fold 3	0.7830	0.8020		0.7464	0.8561		0.6548		17.2587	25.5880
Fold 4	0.7806	0.7998		0.7482	0.8565		0.6601		17.2485	25.7665
CB513										
	RSA	**ASA**		**Q8**	**Q3**		**Disorder**		**Phi**	**Psi**
Fold 1	0.8002	0.8132		0.7211	0.8519		0.1045		20.1689	27.9715
Fold 2	0.7991	0.8123		0.7221	0.8533		0.1283		20.1562	28.0746
Fold 3	0.7990	0.8123		0.7212	0.8526		0.0815		20.1293	27.9960
Fold 4	0.7985	0.8116		0.7194	0.8508		0.1244		20.2399	28.1678

Supplementary table S2: Results of the method's validation using a 4-fold validation approach. The metric used for teach column is reported in the first row.

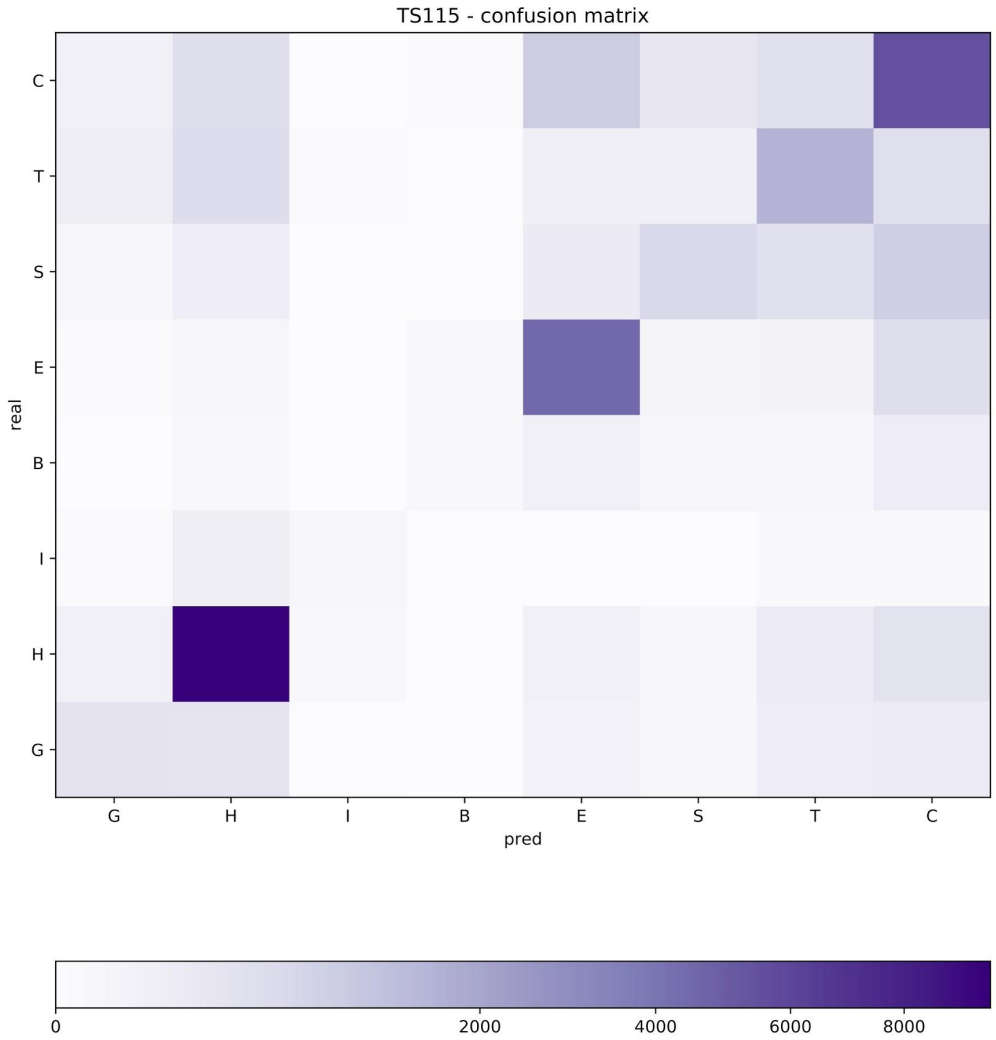
			CASP12			TS115			CB513		
output	metric	dist	SEQ	ATOM	Diff	SEQ	ATOM	Diff	SEQ	ATOM	Diff
q3	acc	1	0.761	0.702	0.060	0.764	0.633	0.131	0.750	0.687	0.062
	acc	2	0.682	0.712	-0.030	0.686	0.668	0.019	0.747	0.714	0.034
	acc	3	0.712	0.712	0.000	0.725	0.725	0.000	0.773	0.768	0.005
	acc	4	0.773	0.758	0.015	0.797	0.819	-0.022	0.785	0.799	-0.014
	acc	5	0.862	0.785	0.077	0.798	0.811	-0.013	0.855	0.869	-0.014
q8	acc	1	0.627	0.508	0.119	0.648	0.481	0.167	0.643	0.532	0.111
	acc	2	0.530	0.561	-0.030	0.594	0.548	0.046	0.647	0.588	0.059
	acc	3	0.591	0.621	-0.030	0.603	0.613	-0.009	0.608	0.601	0.007
	acc	4	0.621	0.652	-0.030	0.676	0.698	-0.022	0.663	0.680	-0.017
	acc	5	0.739	0.723	0.015	0.689	0.699	-0.010	0.732	0.742	-0.010
rsa	pcc	1	0.260	0.194	0.066	0.343	0.336	0.007	0.485	0.460	0.025
	pcc	2	0.452	0.455	-0.003	0.465	0.486	-0.021	0.603	0.616	-0.013
	pcc	3	0.631	0.610	0.021	0.674	0.660	0.013	0.630	0.641	-0.012
	pcc	4	0.587	0.560	0.027	0.664	0.667	-0.002	0.716	0.722	-0.006
	pcc	5	0.533	0.537	-0.004	0.739	0.753	-0.014	0.762	0.772	-0.010
asa	pcc	1	0.452	0.344	0.109	0.510	0.492	0.018	0.552	0.535	0.017
	pcc	2	0.548	0.531	0.017	0.553	0.567	-0.014	0.630	0.645	-0.014
	pcc	3	0.634	0.587	0.047	0.694	0.686	0.009	0.676	0.676	0.001
	pcc	4	0.605	0.577	0.028	0.689	0.689	0.000	0.731	0.744	-0.013
	pcc	5	0.555	0.537	0.018	0.763	0.772	-0.009	0.776	0.784	-0.008

Supplementary table S3: Accuracy of the method in the residues preceding and following disordered regions. The distance of the residue to the disordered region is reported in the dist column. The "SEQ" and "ATOM" columns contain the results obtained with the version of NetSurfP-2.0 trained without and with disordered residues, respectively. The "Diff" column shows the difference between the two methods, and it is colored in dark green, green, whilte, and orange, for results where the "ATOM" version has a difference of more than 10%, more than 3%, between 3% and -3%, and below -3%. No difference below -10% was present.

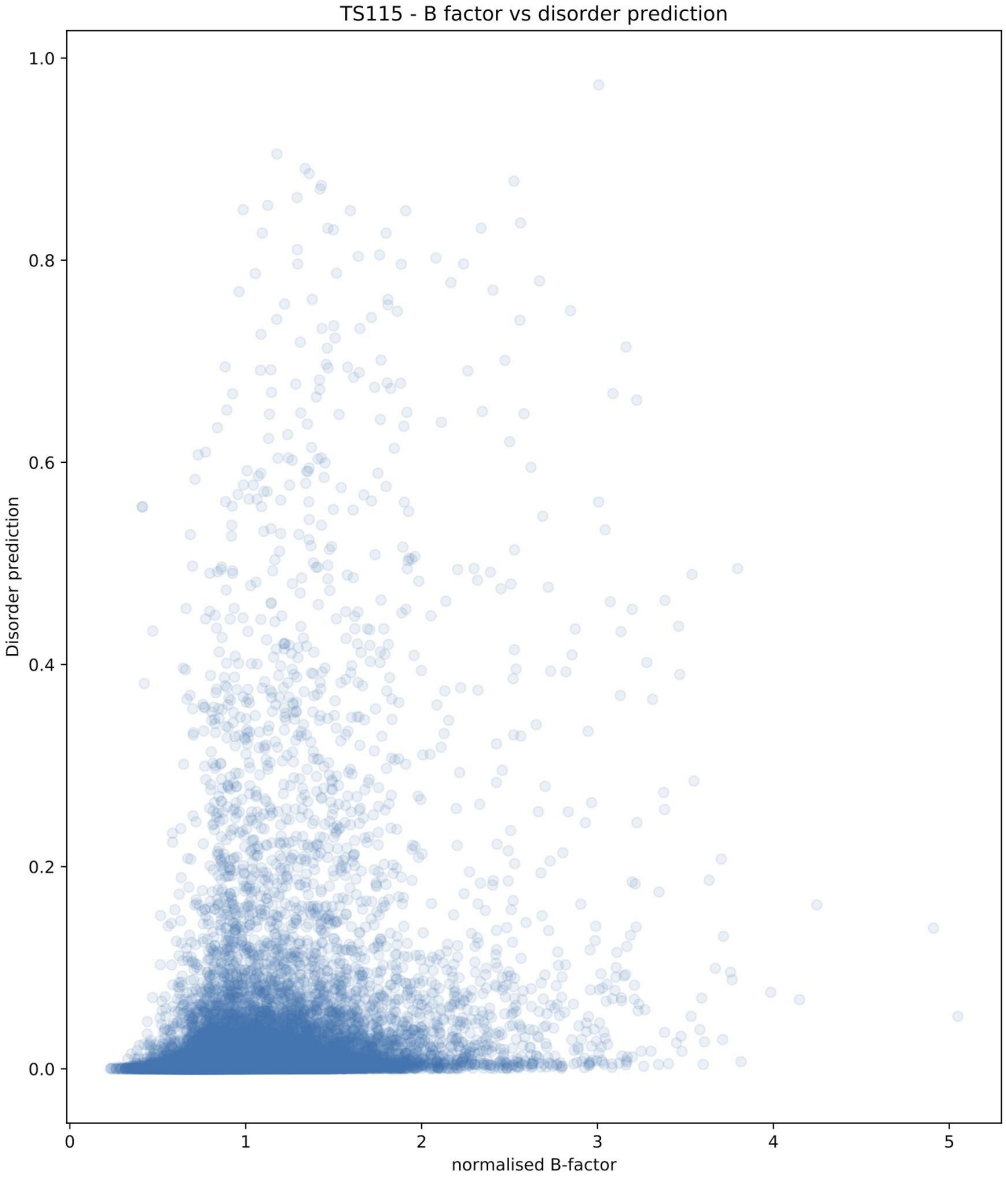
CASP12							
	RSA	**ASA**	**Q8**	**Q3**	**Disorder**	**Phi**	**Psi**
Current	0.7322	0.7414	0.7029	0.8177	0.6608	20.1658	31.5859
PDBSEQ PRO	0.7237	0.7315	0.6706	0.7962		19.9052	31.1891
PDBSEQ	0.7245	0.7329	0.6739	0.7982		19.7819	30.7876
1 output	0.7138	0.7242	0.6963	0.8225	0.7016		

TS115								
	RSA	ASA	Q8	Q3	Disorder	Phi	Psi
Current	0.7845	0.8033	0.7489	0.8566	0.6664	17.2269	25.6000
PDBSEQ PRO	0.7860	0.8043	0.7349	0.8461		16.8226	24.9746
PDBSEQ	0.7851	0.8039	0.7381	0.8477		16.7593	24.8865
1 output	0.7716	0.7924	0.7495	0.8600	0.6374		
CB513							
	RSA	ASA	Q8	Q3	Disorder	Phi	Psi
Current	0.7992	0.8126	0.7208	0.8515		20.1228	28.2267
PDBSEQ PRO	0.8067	0.8193	0.7325	0.8582		19.7445	27.2077
PDBSEQ	0.8070	0.8196	0.7334	0.8585		19.7169	27.1891
1 output	0.7879	0.8022	0.7211	0.8534			

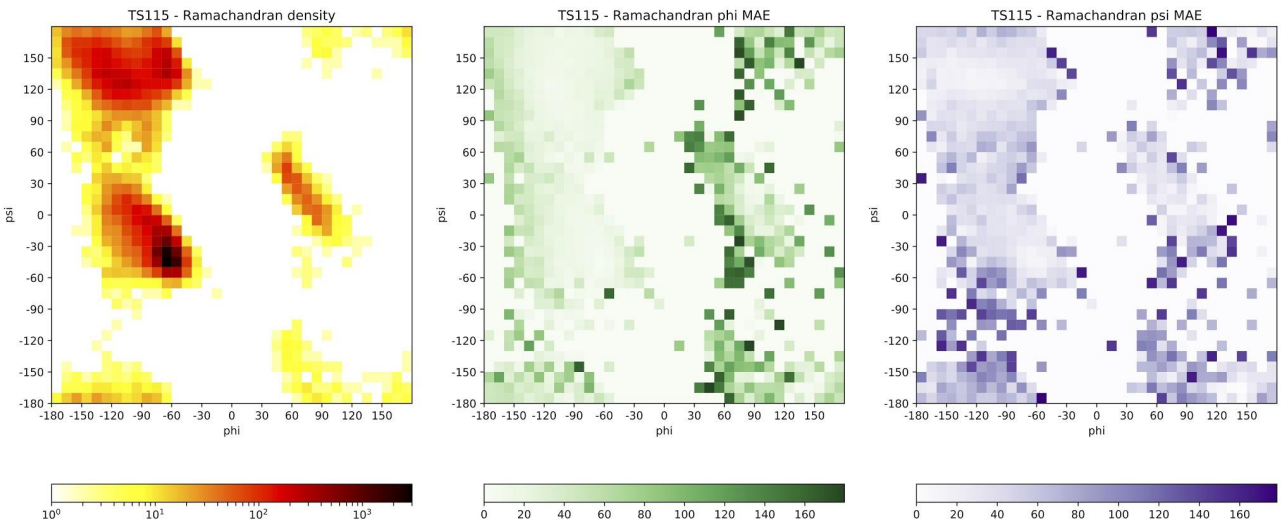
Supplementary table S4: A comparison of the results of NetSurfP-2.0 (Current) with respect of those obtained by training only on non-disordered region, using profiles obtained with the whole sequence (PDBSEQ PRO) or with the sequence of only non-disordered residue (PDBSEQ), and with models trained only on a single output variable (1 output).



Supplementary figure S1: Graphical representation of the 8-class secondary structure prediction confusion matrix. A non-linear scale was used for the coloring, as displayed in the bottom bar.



Supplementary figure S2: scatterplot of residue normalised B-factors plotted against their disorder prediction.



Supplementary figure S3: Ramachandran plot of all residues in the TS115 dataset (left panel), together with the average error in the prediction of their phi (central panel, shades of green) and psi (right panel, shades of blue).