



wwPDB EM Map/Model Validation Report ⓘ

May 5, 2016 – 10:46 PM EDT

PDB ID : 5FLZ
EMDB ID: : EMD-2799
Title : Cryo-EM structure of gamma-TuSC oligomers in a closed conformation
Authors : Greenberg, C.H.; Kollman, J.; Zelter, A.; Johnson, R.; MacCoss, M.J.; Davis, T.N.; Agard, D.A.; Sali, A.
Deposited on : 2015-10-29
Resolution : 6.90 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

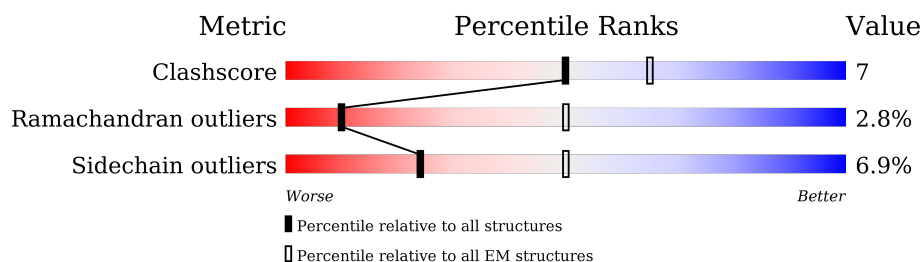
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




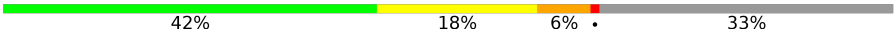
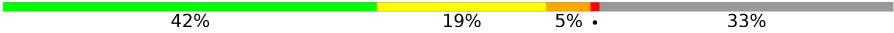
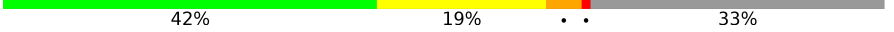
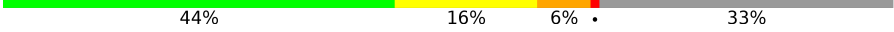
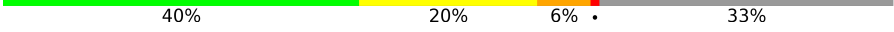
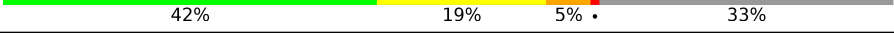
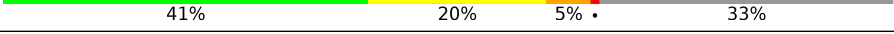
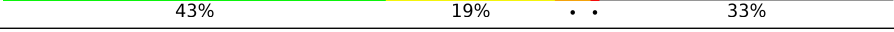
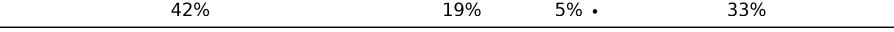
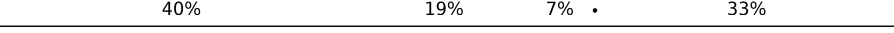
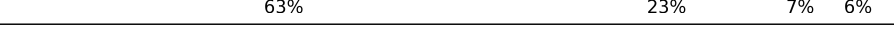
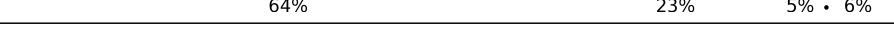


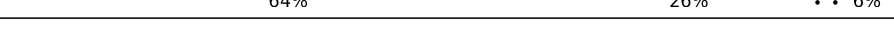









Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	1-A	823	46% 18% 5% • 30%
1	10-A	823	44% 20% 5% • 30%
1	2-A	823	45% 18% 5% • 30%
1	3-A	823	44% 20% 5% • 30%
1	4-A	823	44% 20% 5% • 30%
1	5-A	823	43% 20% 5% • 30%
1	6-A	823	44% 20% 5% • 30%
1	7-A	823	45% 17% 6% • 30%
1	8-A	823	43% 22% 5% • 30%








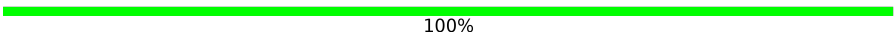
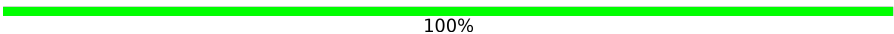
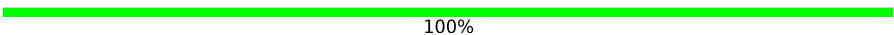
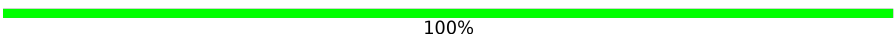




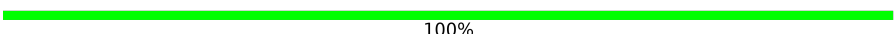
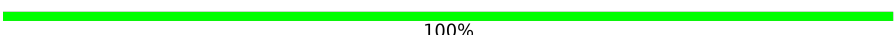
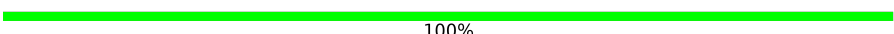
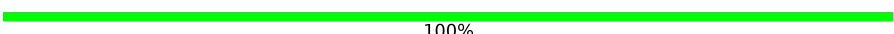
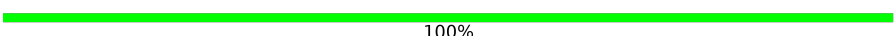
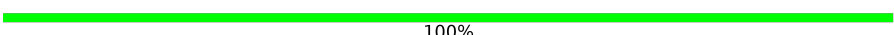
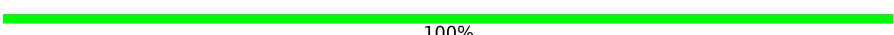
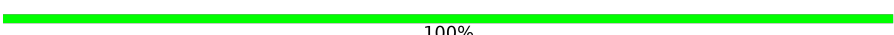
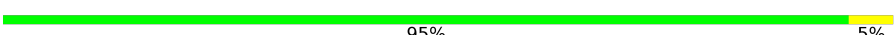
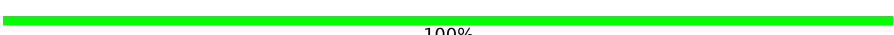
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Mol	Chain	Length	Quality of chain
1	9-A	823	
2	1-B	846	
2	10-B	846	
2	2-B	846	
2	3-B	846	
2	4-B	846	
2	5-B	846	
2	6-B	846	
2	7-B	846	
2	8-B	846	
2	9-B	846	
3	1-C	473	
3	1-D	473	
3	10-C	473	
3	10-D	473	
3	2-C	473	
3	2-D	473	
3	3-C	473	
3	3-D	473	
3	4-C	473	
3	4-D	473	
3	5-C	473	
3	5-D	473	
3	6-C	473	
3	6-D	473	


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Mol	Chain	Length	Quality of chain
3	7-C	473	 60%29%5%6%
3	7-D	473	 63%25%5%6%
3	8-C	473	 65%23%5%6%
3	8-D	473	 65%25%5%6%
3	9-C	473	 68%21%5%6%
3	9-D	473	 64%25%5%6%
4	1-E	44	 100%
4	1-F	44	 100%
4	10-E	44	 100%
4	10-F	44	 100%
4	2-E	44	 100%
4	2-F	44	 100%
4	3-E	44	 100%
4	3-F	44	 100%
4	4-E	44	 100%
4	4-F	44	 100%
4	5-E	44	 100%
4	5-F	44	 100%
4	6-E	44	 100%
4	6-F	44	 100%
4	7-E	44	 100%
4	7-F	44	 100%
4	8-E	44	 100%
4	8-F	44	 95%5%
4	9-E	44	 100%

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Mol	Chain	Length	Quality of chain
4	9-F	44	 100%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 169420 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called SPINDLE POLE BODY COMPONENT SPC97.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	2-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	3-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	4-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	5-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	6-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	7-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	8-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	9-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		
1	10-A	575	Total	C	N	O	S	0	0
			4831	3110	806	889	26		

- Molecule 2 is a protein called SPINDLE POLE BODY COMPONENT SPC98.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	2-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	3-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	4-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	5-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	6-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	7-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	8-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	9-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		
2	10-B	565	Total	C	N	O	S	0	0
			4701	3058	775	853	15		

- Molecule 3 is a protein called TUBULIN GAMMA CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	2-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	3-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	4-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	5-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	6-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	7-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	8-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	9-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	10-C	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	1-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	2-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	3-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	4-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	5-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	6-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	7-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	8-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	9-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		
3	10-D	445	Total	C	N	O	S	0	0
			3485	2180	591	695	19		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	58	CYS	SER	ENGINEERED MUTATION	UNP P53378
C	288	CYS	GLY	ENGINEERED MUTATION	UNP P53378
D	58	CYS	SER	ENGINEERED MUTATION	UNP P53378
D	288	CYS	GLY	ENGINEERED MUTATION	UNP P53378

- Molecule 4 is a protein called SPINDLE POLE BODY COMPONENT 110.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	1-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	2-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	3-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	4-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	5-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	6-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	7-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	8-E	44	Total	C	N	O	0	0
			220	132	44	44		
4	9-E	44	Total	C	N	O	0	0
			220	132	44	44		

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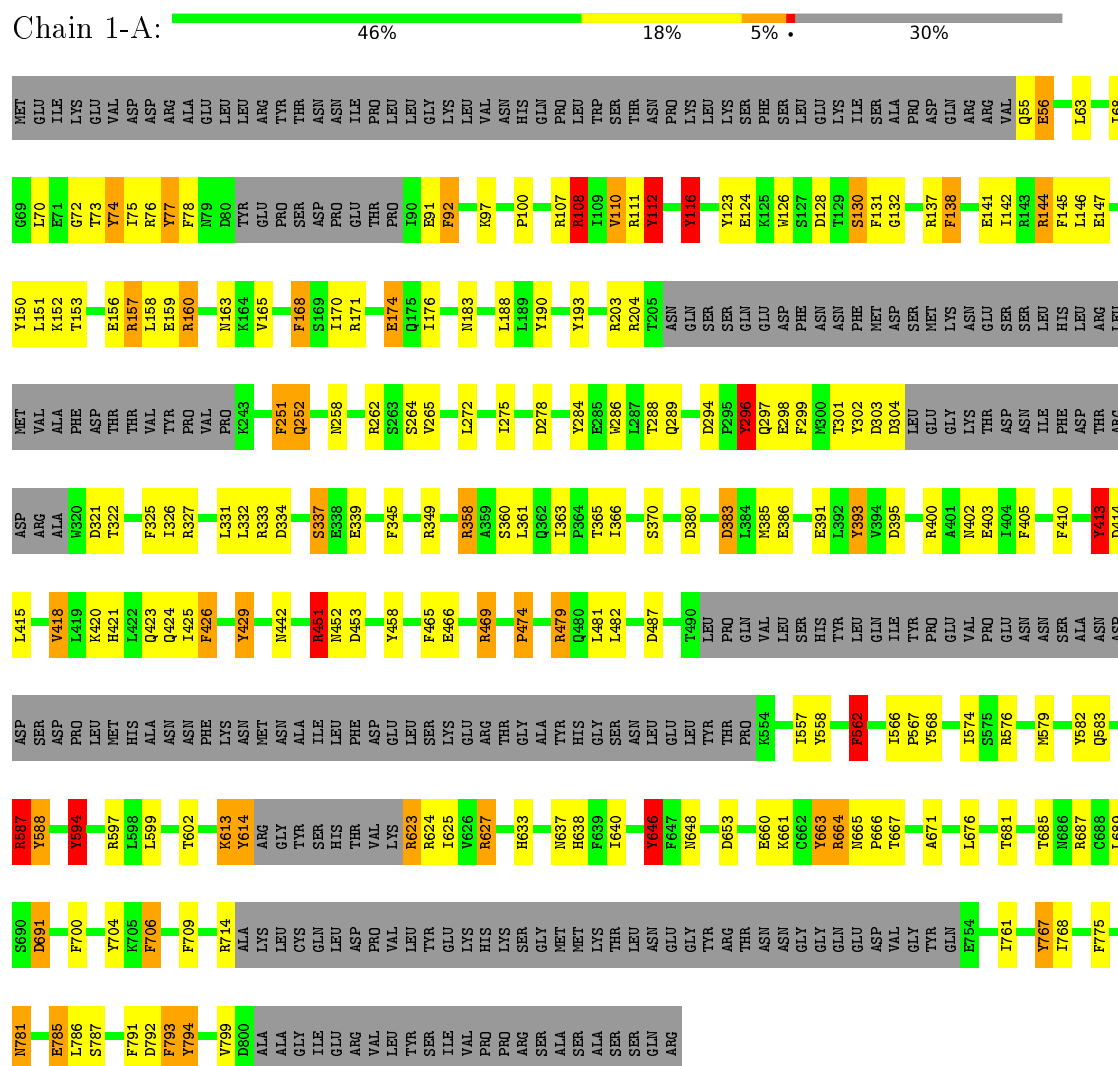
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Mol	Chain	Residues	Atoms				AltConf	Trace
4	10-E	44	Total 220	C 132	N 44	O 44	0	0
4	1-F	44	Total 220	C 132	N 44	O 44	0	0
4	2-F	44	Total 220	C 132	N 44	O 44	0	0
4	3-F	44	Total 220	C 132	N 44	O 44	0	0
4	4-F	44	Total 220	C 132	N 44	O 44	0	0
4	5-F	44	Total 220	C 132	N 44	O 44	0	0
4	6-F	44	Total 220	C 132	N 44	O 44	0	0
4	7-F	44	Total 220	C 132	N 44	O 44	0	0
4	8-F	44	Total 220	C 132	N 44	O 44	0	0
4	9-F	44	Total 220	C 132	N 44	O 44	0	0
4	10-F	44	Total 220	C 132	N 44	O 44	0	0

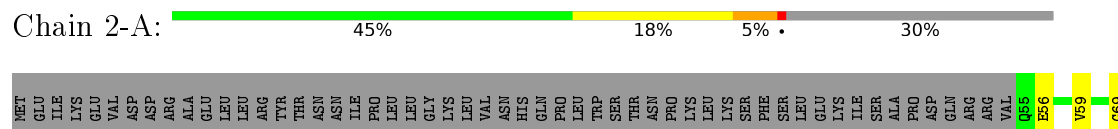
3 Residue-property plots

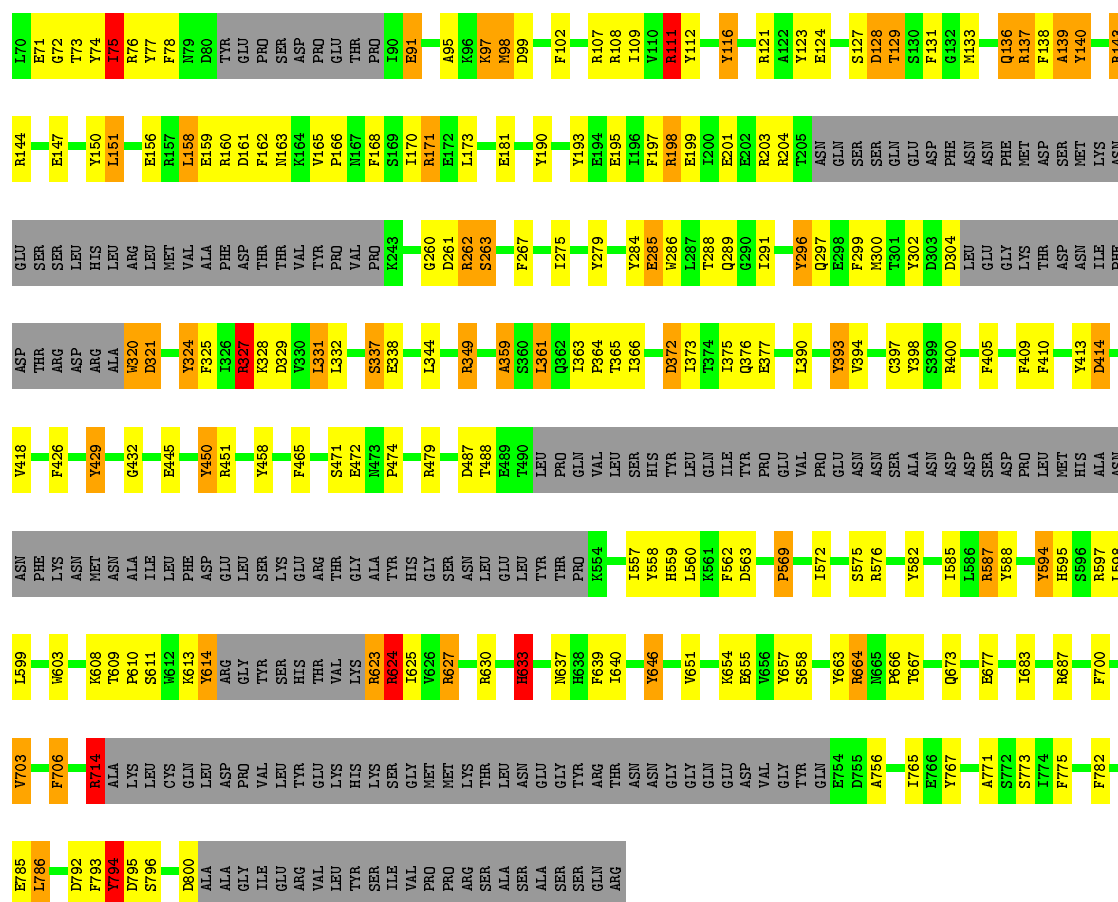
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97



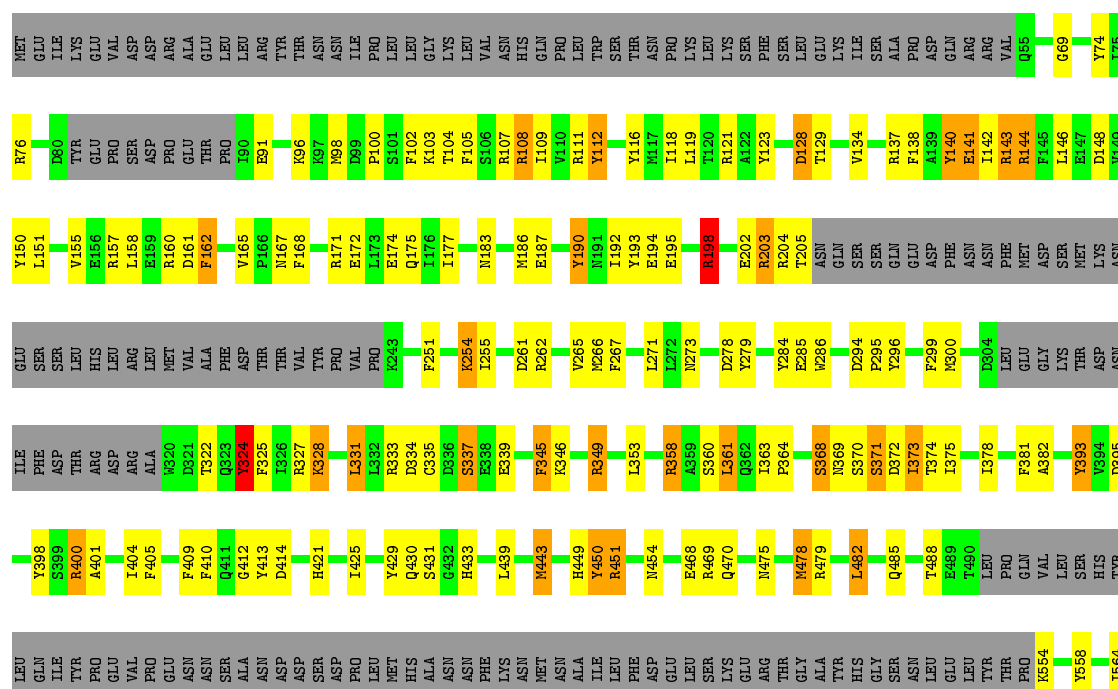
- Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

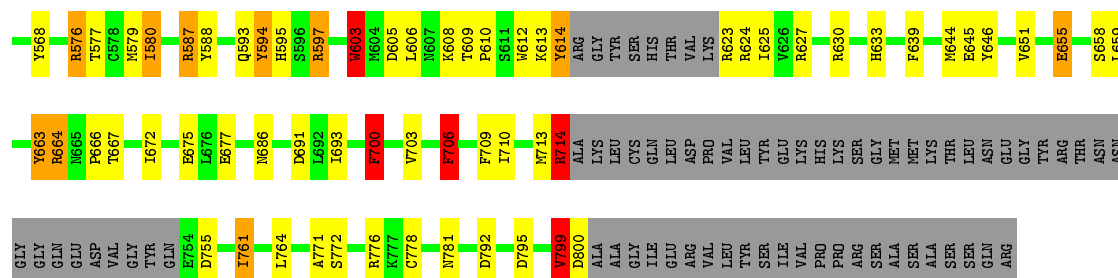




• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

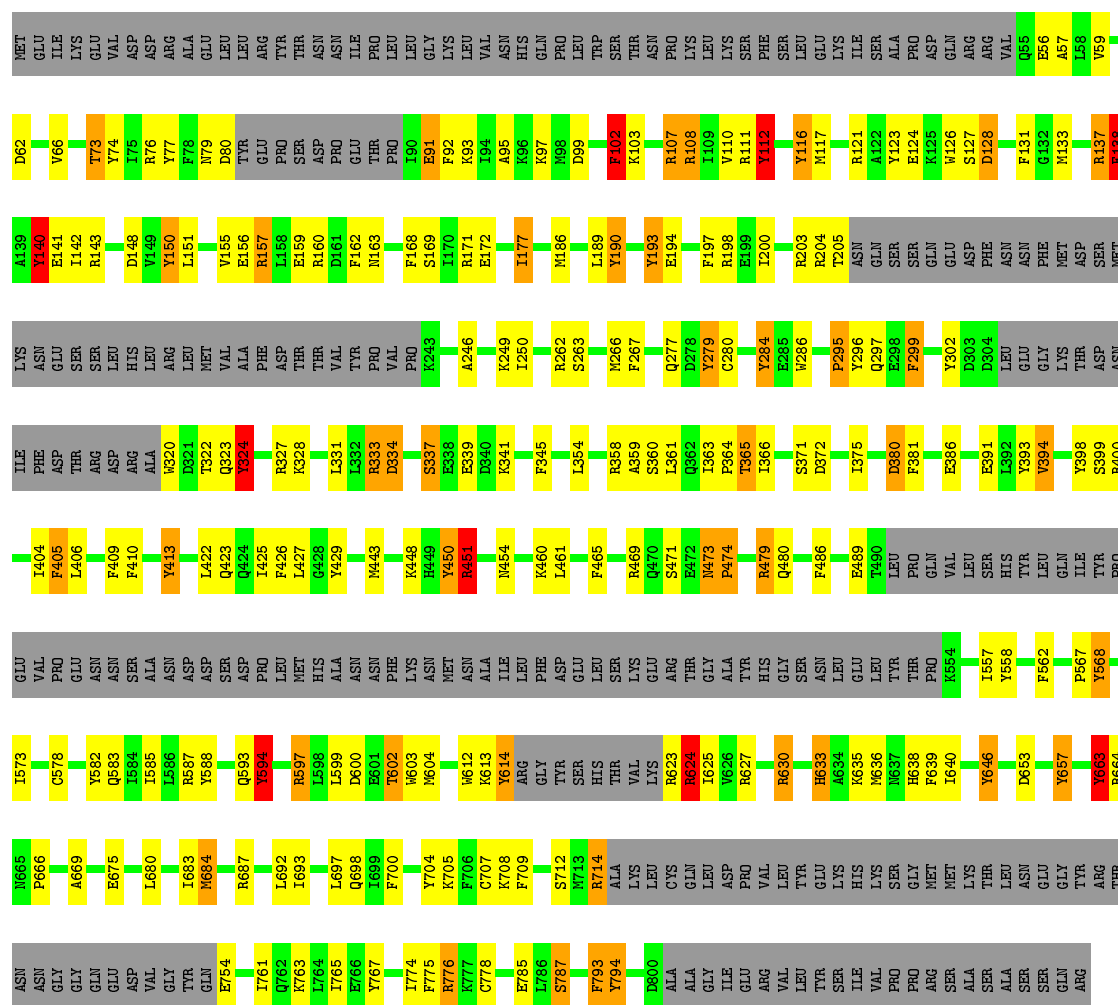
Chain 3-A: 44% 20% 5% 30%





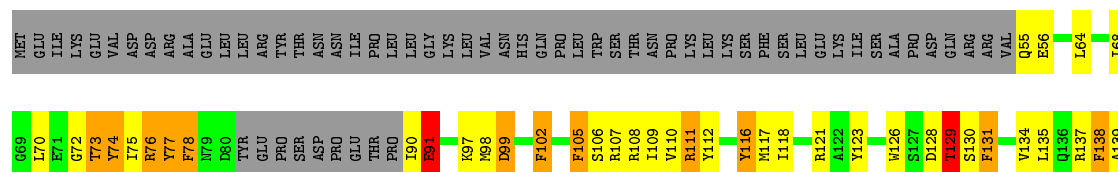
• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

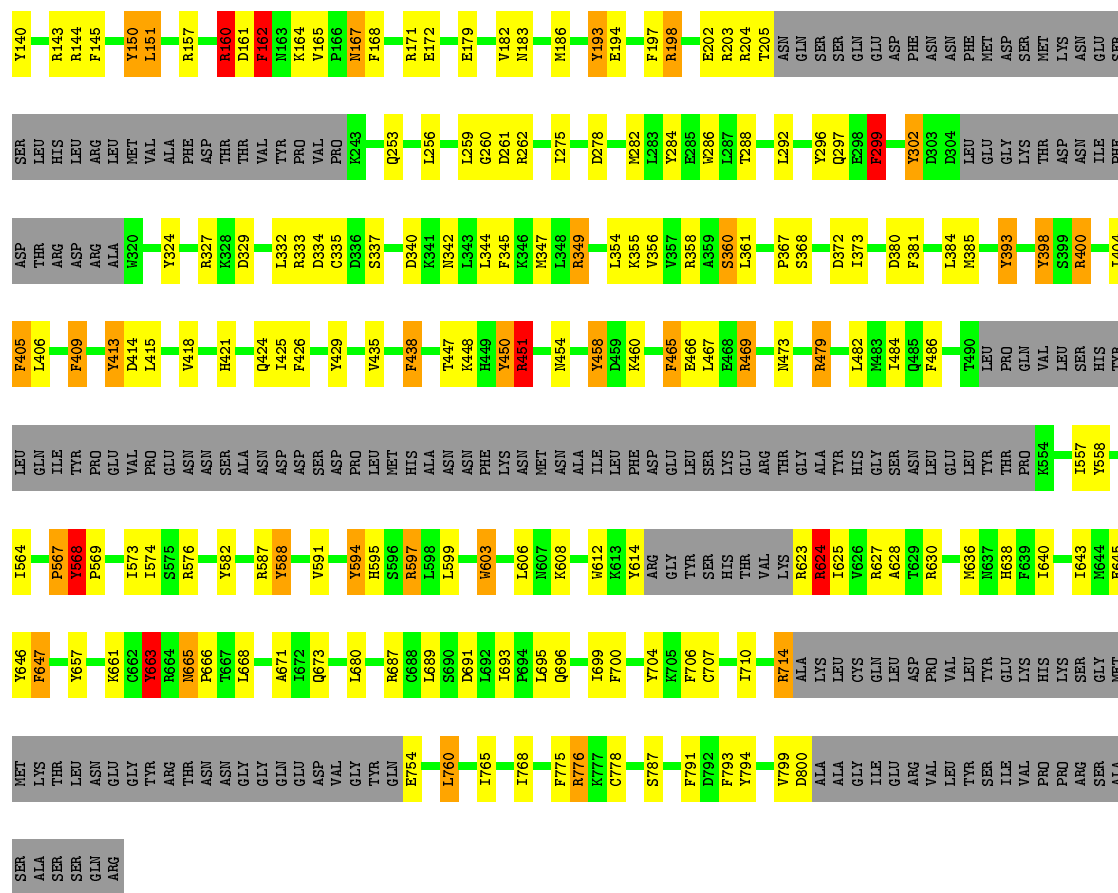
Chain 4-A: 44% 20% 5% 30%



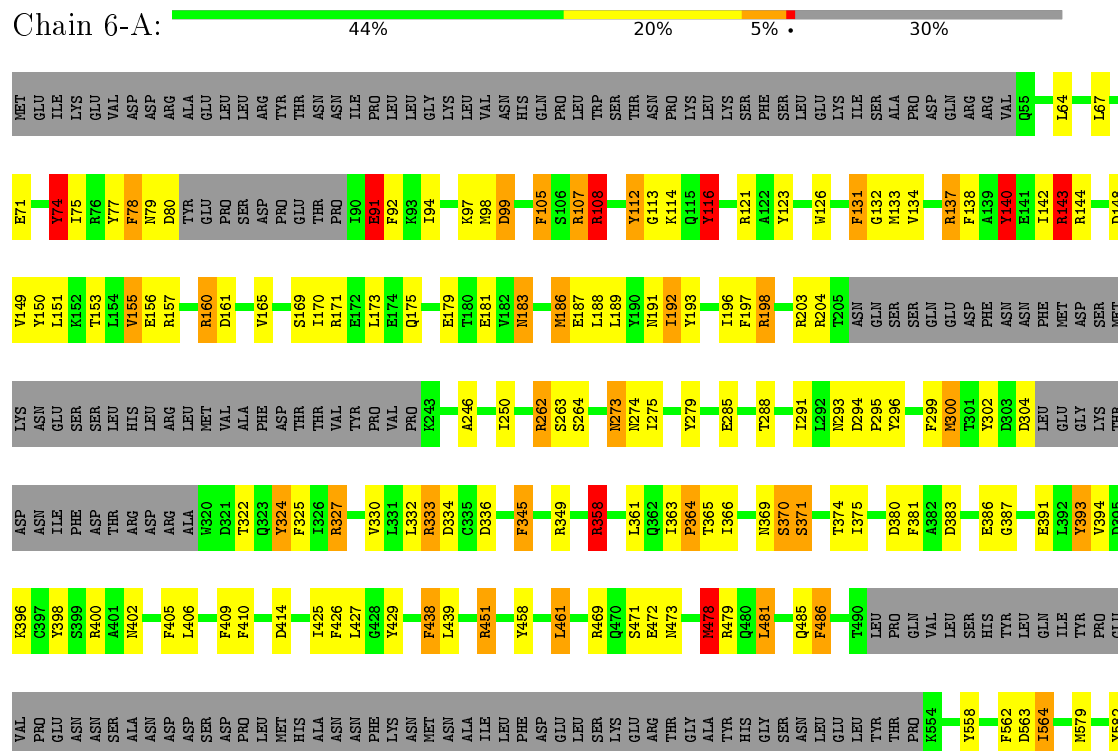
• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

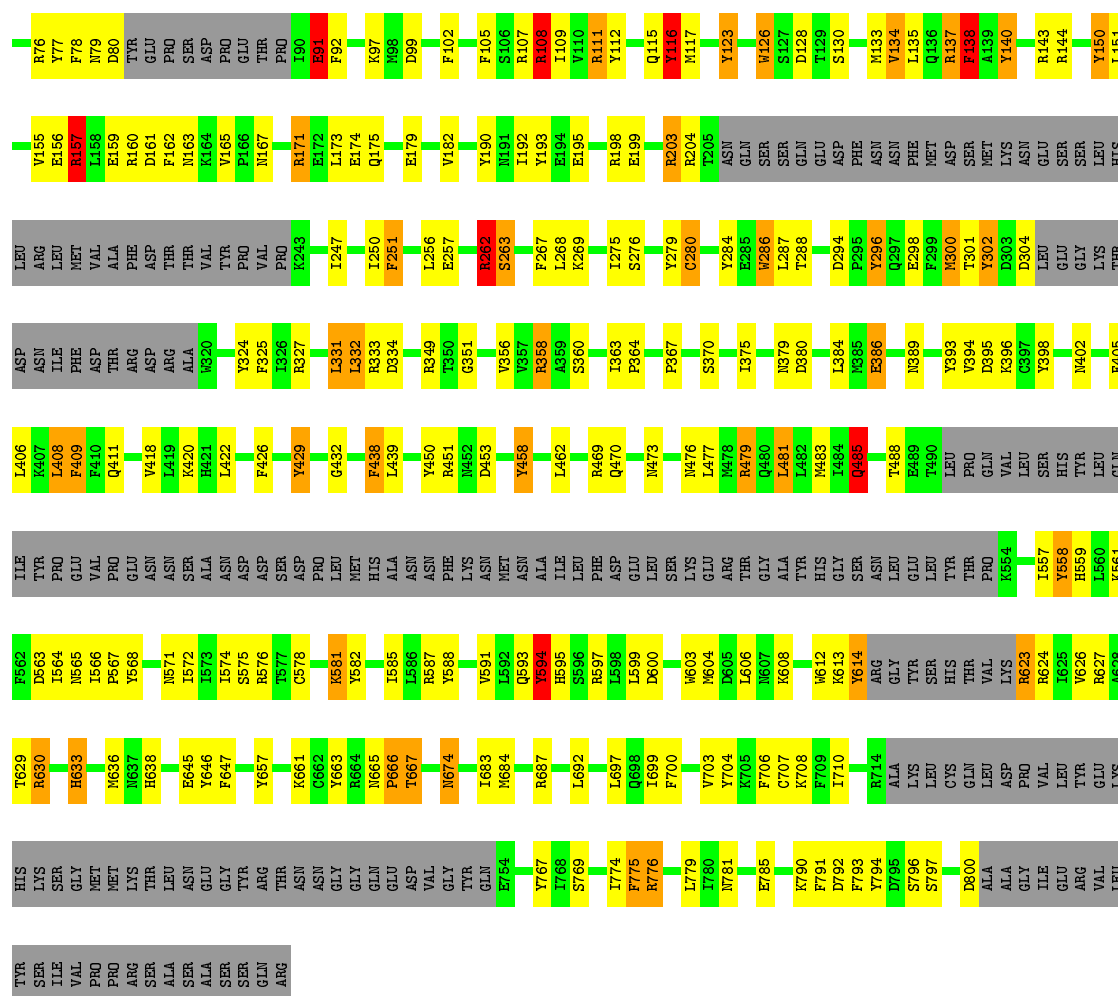
Chain 5-A: 43% 20% 5% 30%



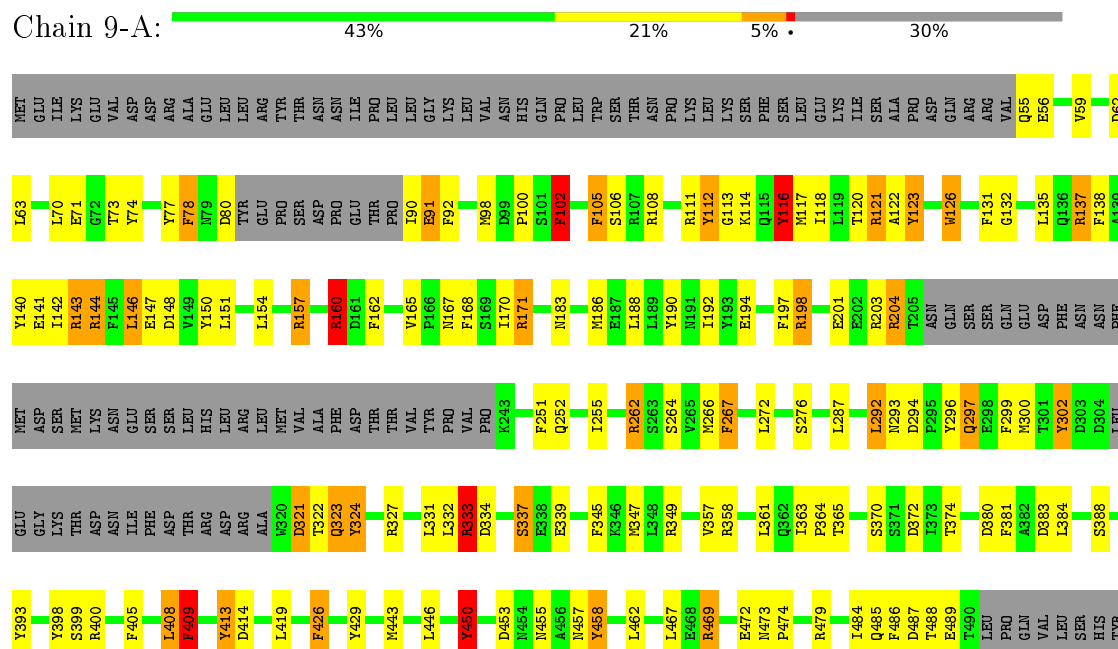


• Molecule 1: SPINDLE POLE BODY COMPONENT SPC97



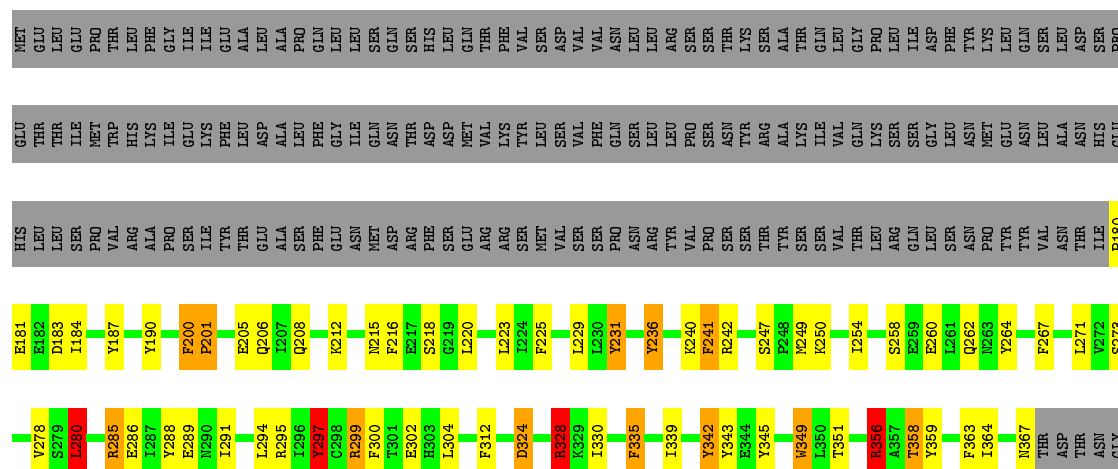


Molecule 1: SPINDLE POLE BODY COMPONENT SPC97

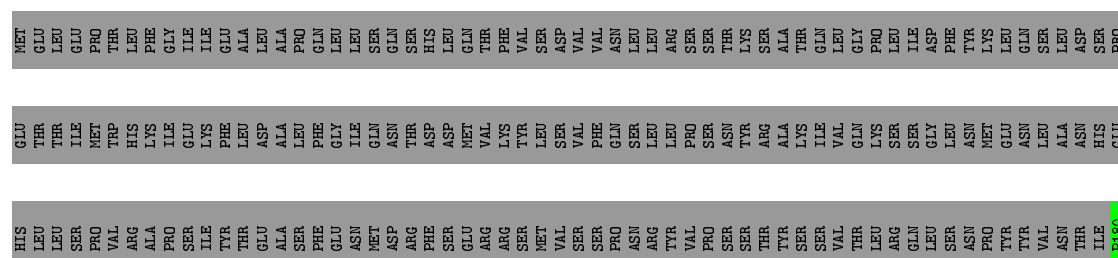


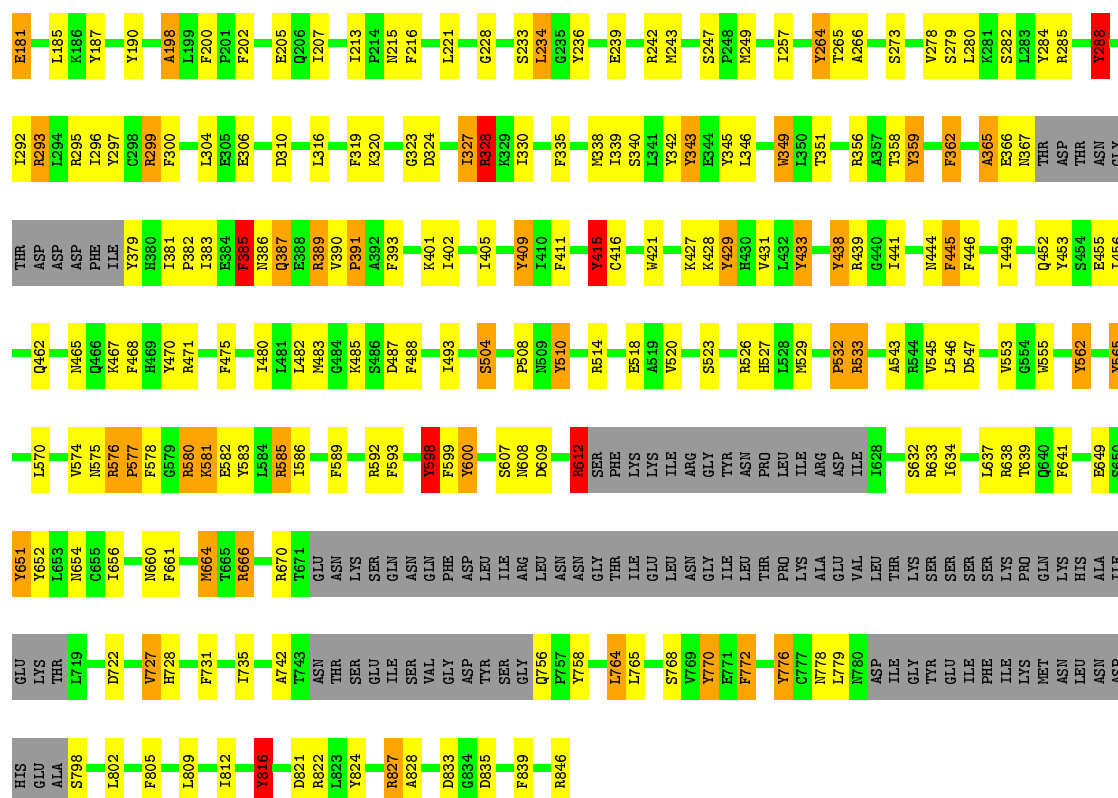


Chain 2-B:



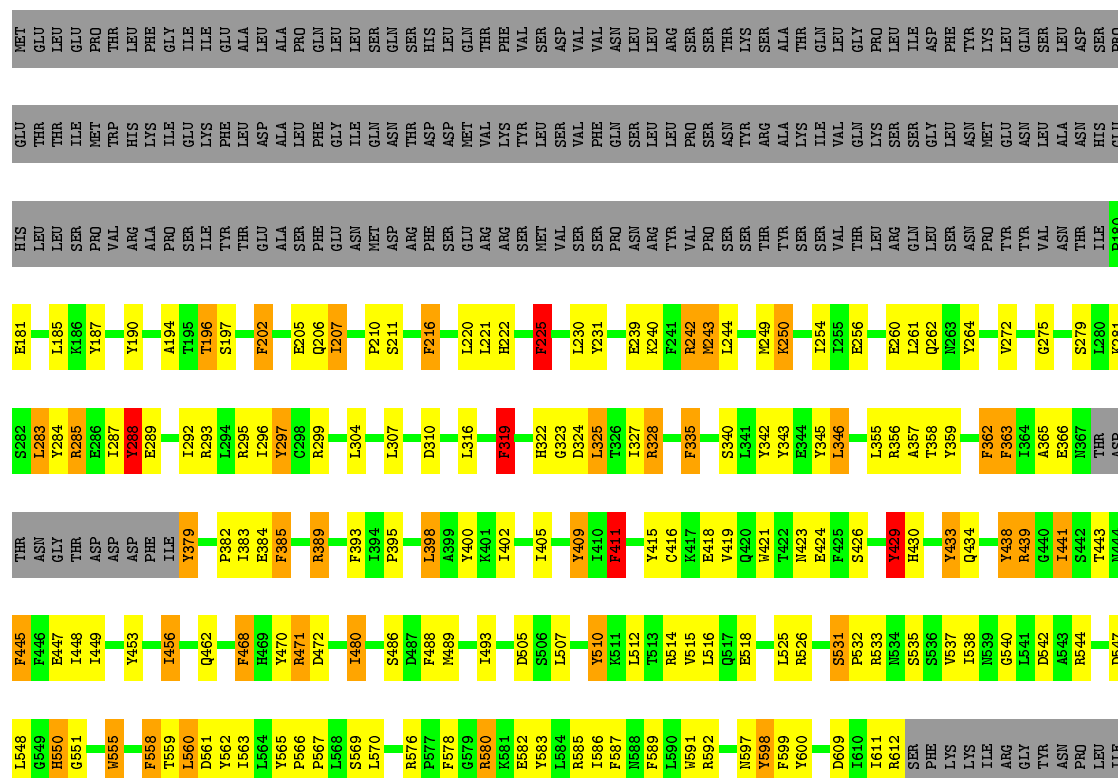






• Molecule 2: SPINDLE POLE BODY COMPONENT SPC98

Chain 6-B: 41% 20% 5% 33%

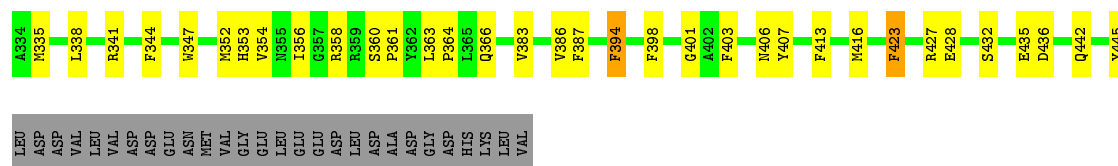




[illegible]

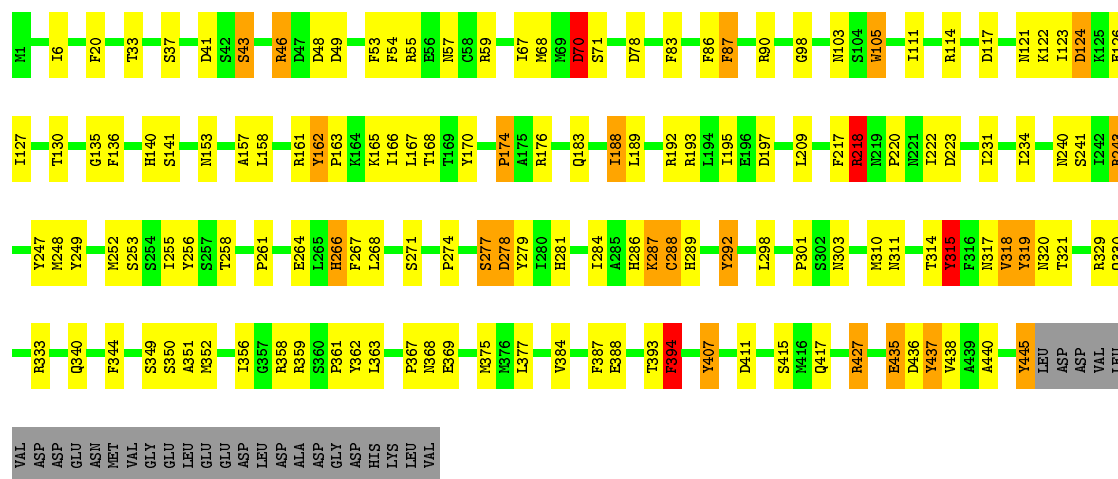
Chain 1-D:

Chain 2-C:



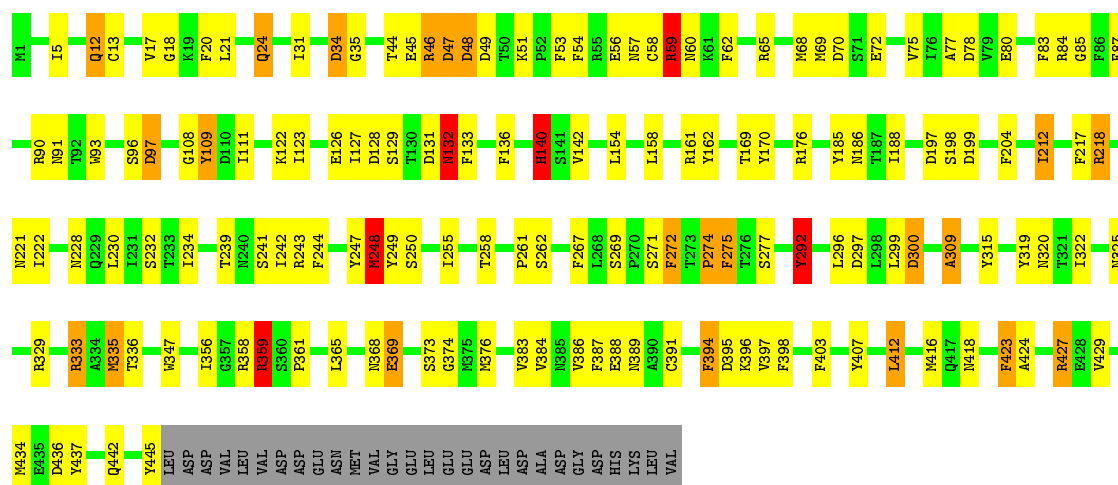
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 2-D: 64% 25% 5% • 6%



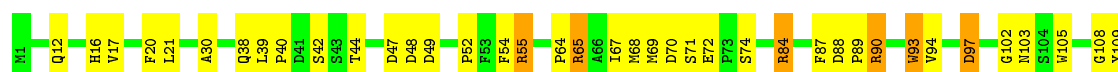
• Molecule 3: TUBULIN GAMMA CHAIN

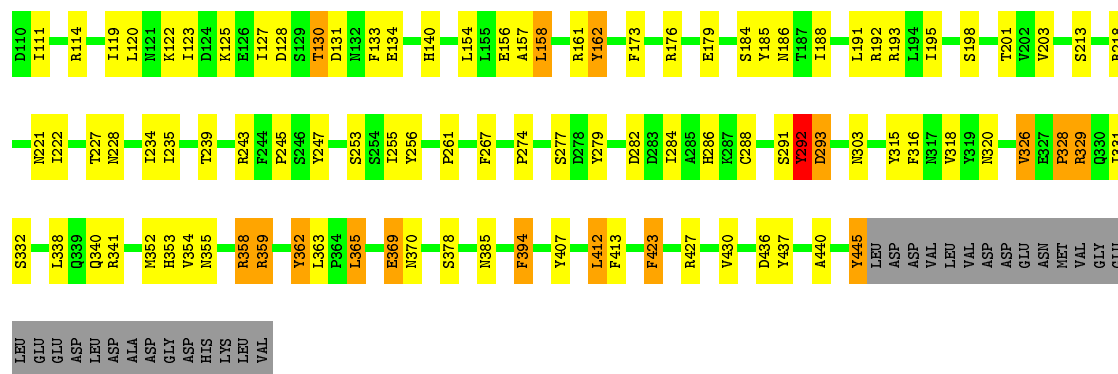
Chain 3-C: 62% 27% 5% • 6%



• Molecule 3: TUBULIN GAMMA CHAIN

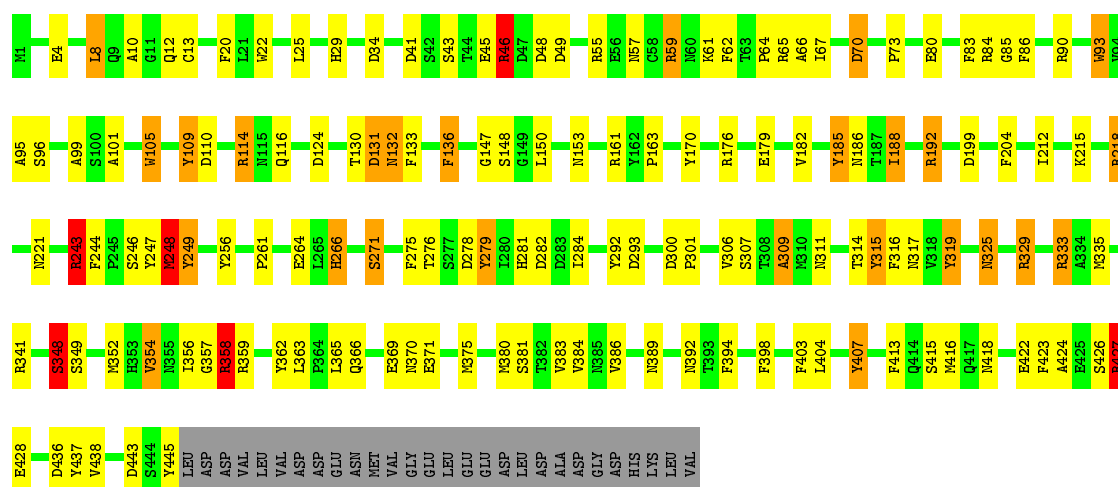
Chain 3-D: 65% 24% 5% • 6%





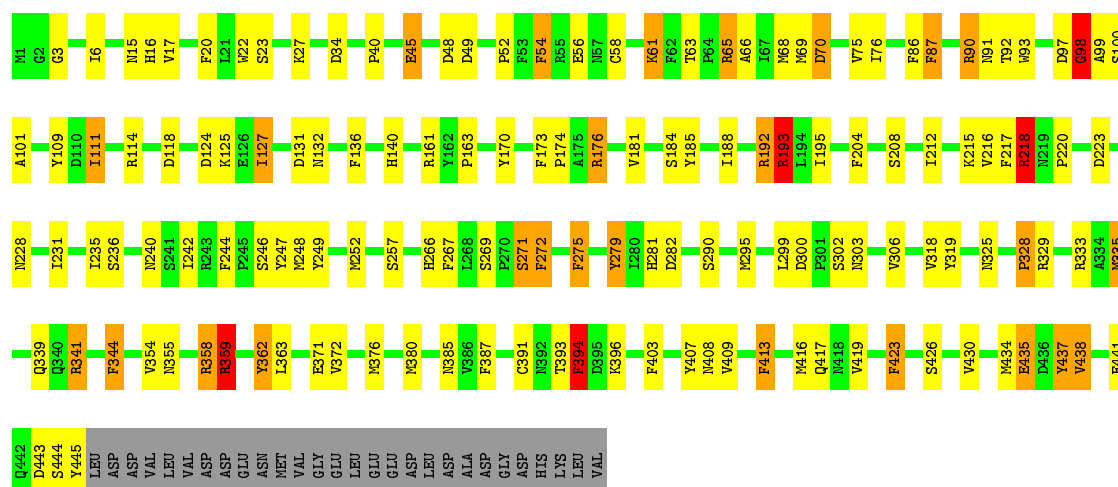
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 4-C: 63% 25% 5% • 6%



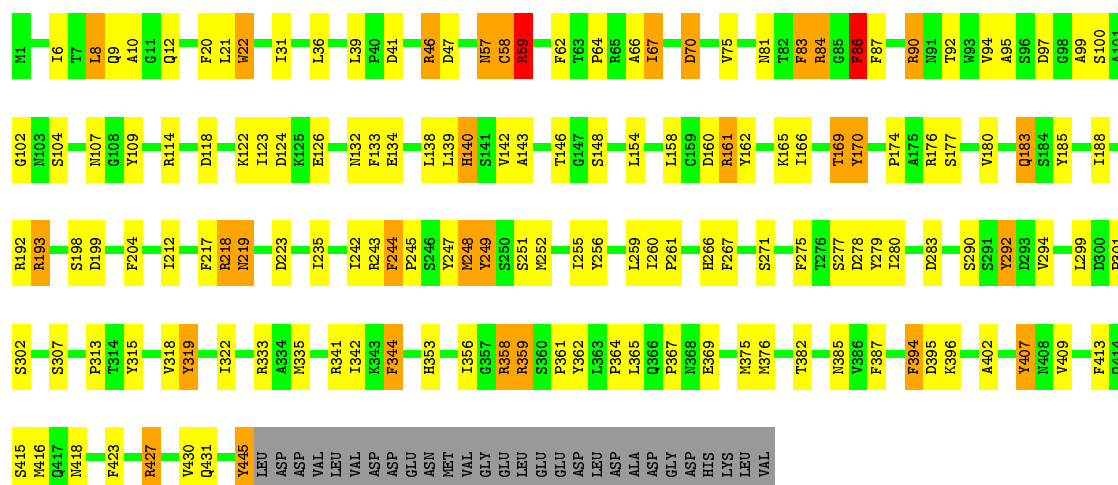
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 4-D: 63% 24% 5% • 6%



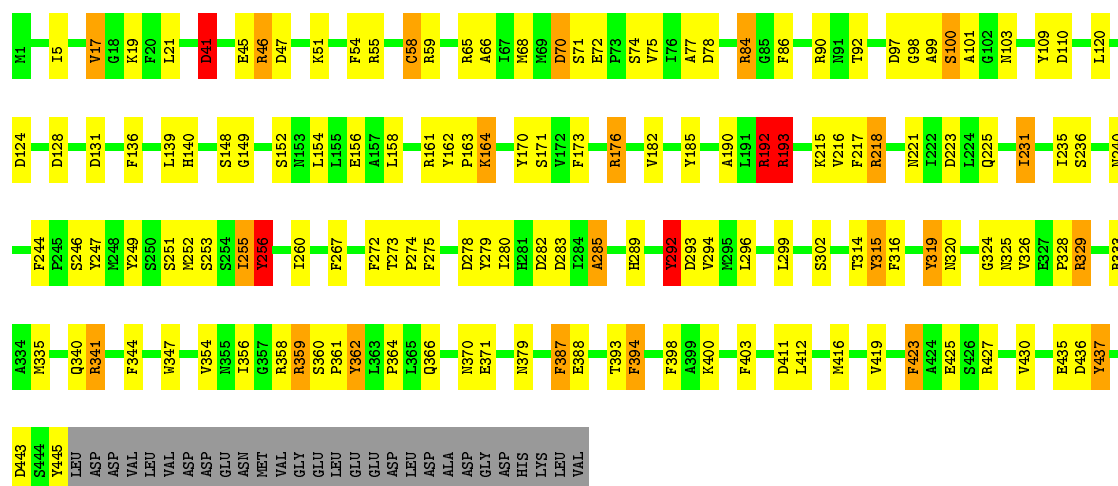
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 5-C: 



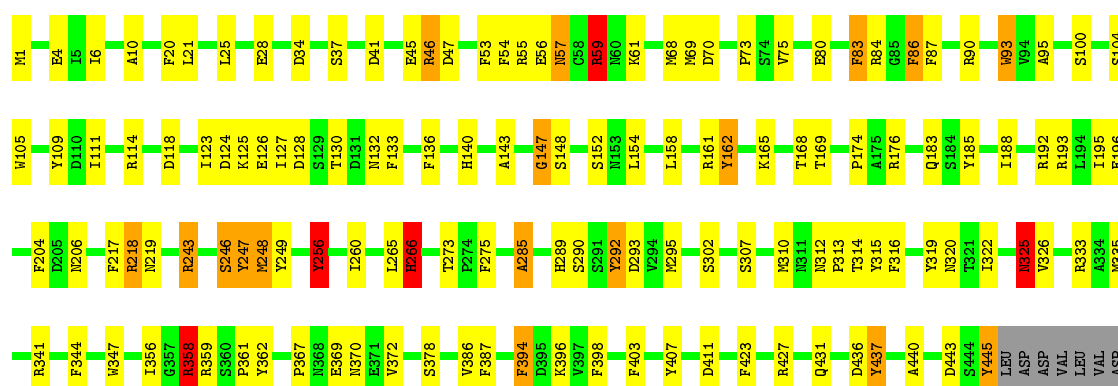
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 5-D: 



• Molecule 3: TUBULIN GAMMA CHAIN

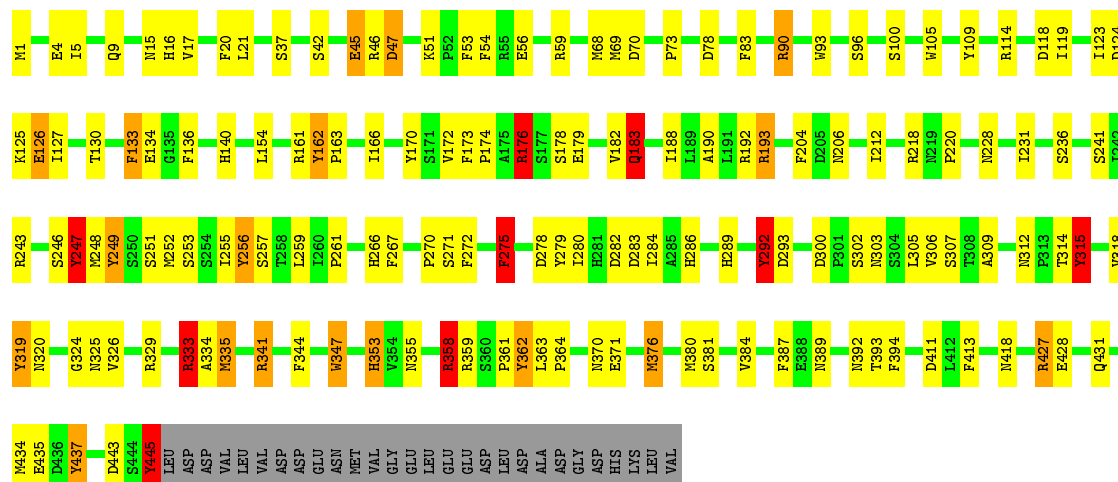
Chain 6-C: 



ASP
GLU
ASN
MET
VAL
GLY
GLU
LEU
GLU
ASP
LEU
ASP
ALA
ASP
GLY
ASP
HIS
LYS
LEU
VAL

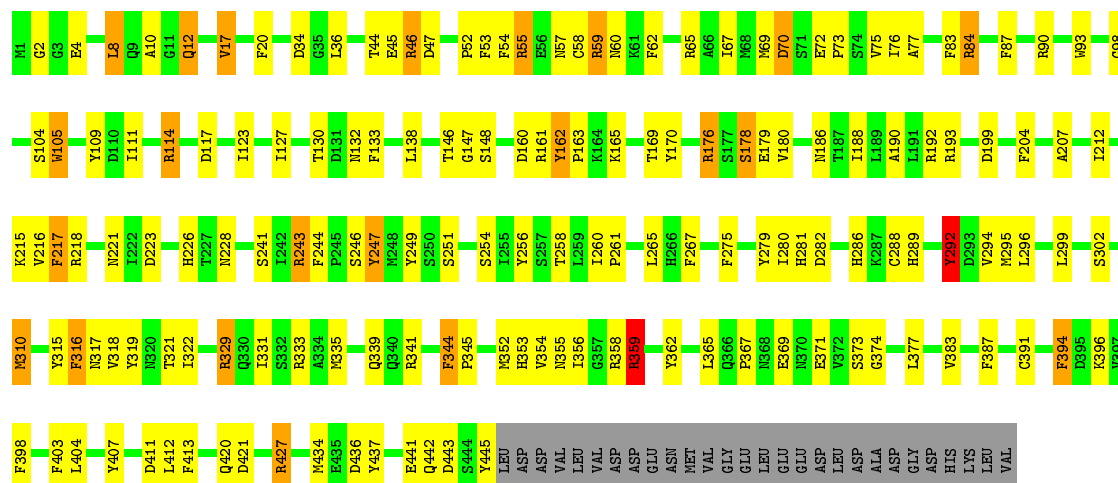
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 6-D: 62% 27% 6%



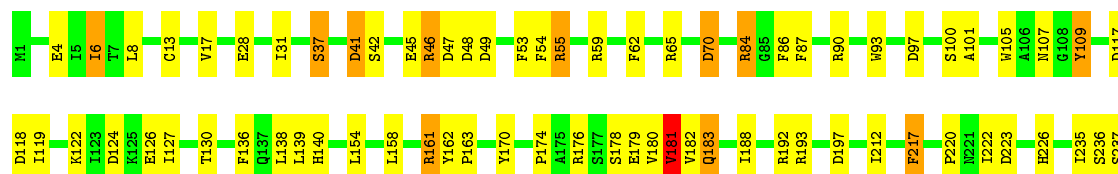
• Molecule 3: TUBULIN GAMMA CHAIN

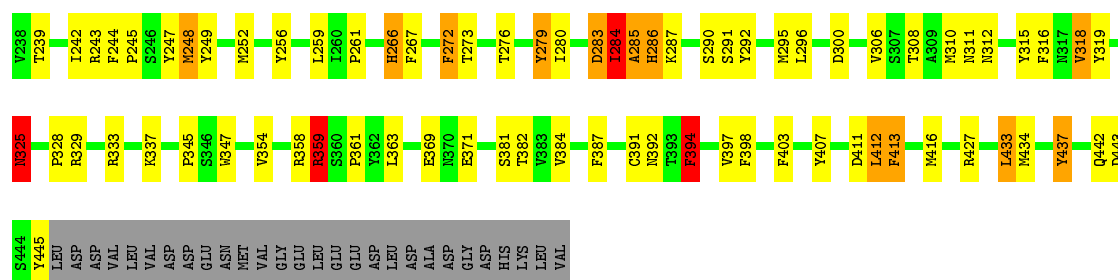
Chain 7-C: 60% 29% 5% 6%



• Molecule 3: TUBULIN GAMMA CHAIN

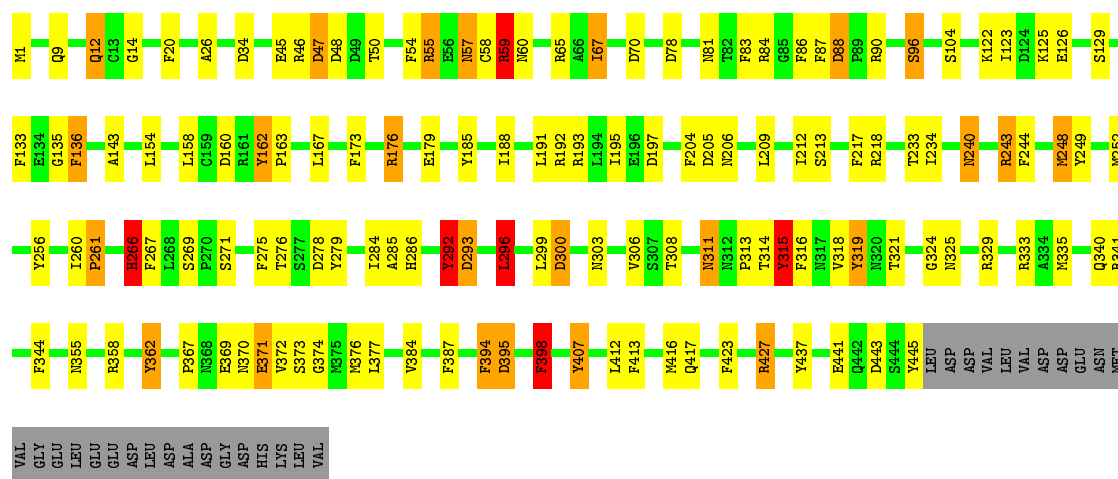
Chain 7-D: 63% 25% 5% 6%





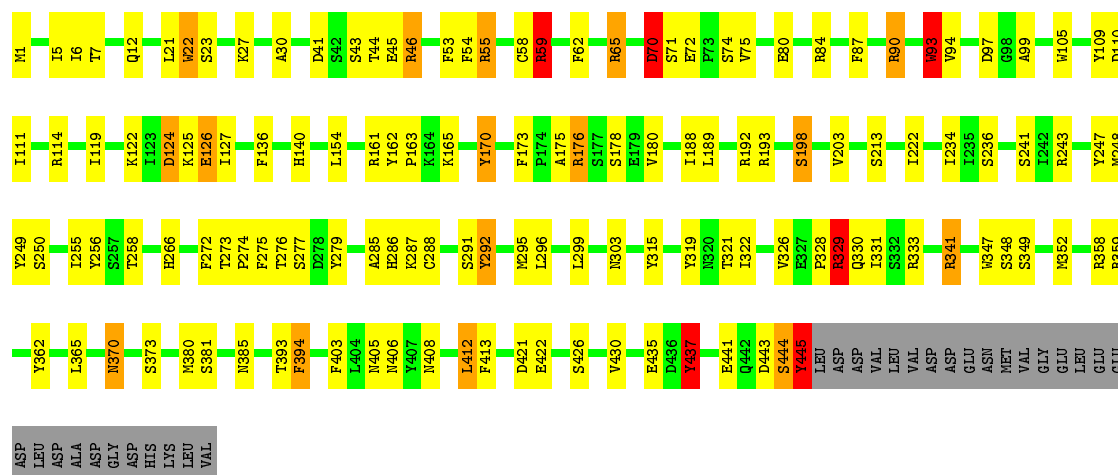
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 8-C: 65% 23% 5% • 6%



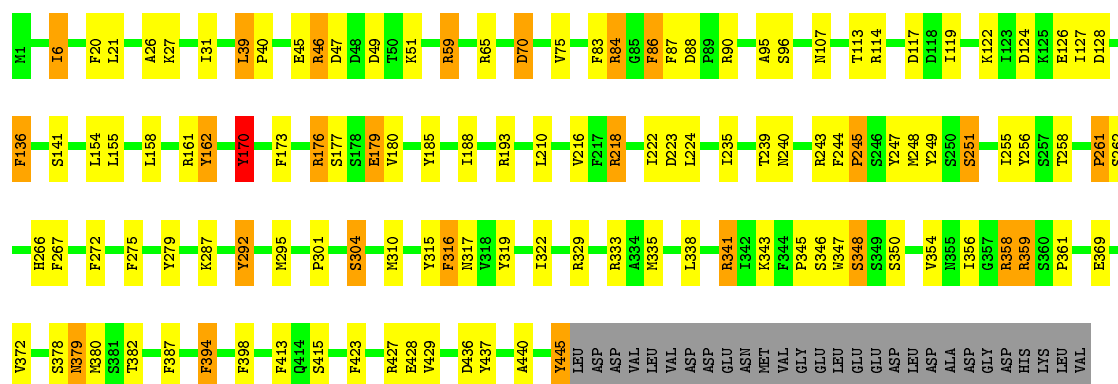
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 8-D: 65% 25% • 6%



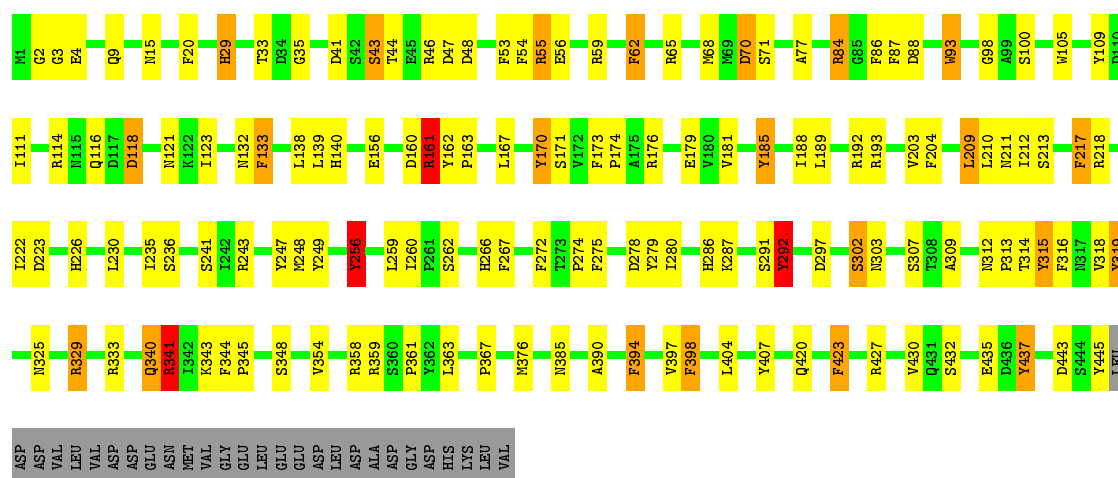
- Molecule 3: TUBULIN GAMMA CHAIN

Chain 9-C: 68% 21% 5% 6%



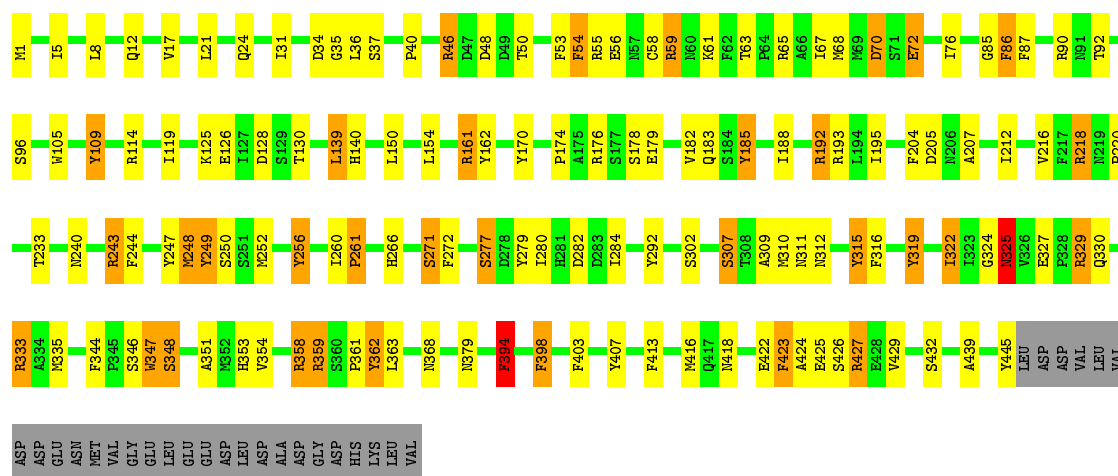
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 9-D: 64% 25% 5% • 6%



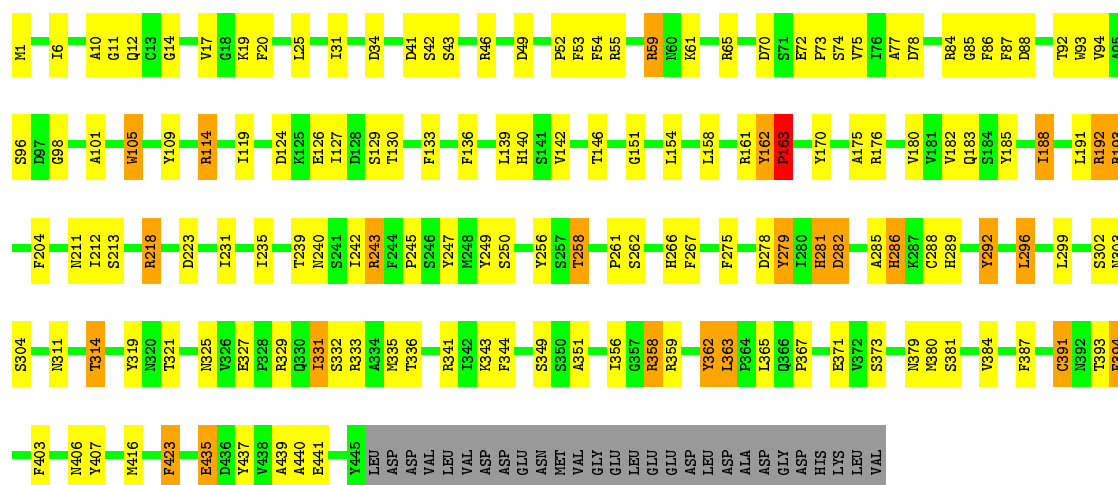
• Molecule 3: TUBULIN GAMMA CHAIN

Chain 10-C: 65% 22% 7% 6%



• Molecule 3: TUBULIN GAMMA CHAIN

Chain 10-D:  61% 27% 5% 6%



- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 1-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 1-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 2-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 2-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 3-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 3-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 4-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 4-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 5-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 5-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 6-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 6-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 7-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 7-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 8-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 8-F:  95% 5%



- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 9-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 9-F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 10-E:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: SPINDLE POLE BODY COMPONENT 110

Chain 10-F:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	HELICAL	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	EACH MICROGRAPH	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	Depositor
Image detector	TVIPS TEMCAM-F816 (8K X 8K)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	1-A	1.76	45/4917 (0.9%)	1.98	139/6616 (2.1%)
1	10-A	1.72	38/4917 (0.8%)	1.96	138/6616 (2.1%)
1	2-A	1.75	66/4917 (1.3%)	2.00	129/6616 (1.9%)
1	3-A	1.75	49/4917 (1.0%)	1.98	139/6616 (2.1%)
1	4-A	1.75	48/4917 (1.0%)	2.07	156/6616 (2.4%)
1	5-A	1.74	50/4917 (1.0%)	2.01	144/6616 (2.2%)
1	6-A	1.76	54/4917 (1.1%)	2.01	146/6616 (2.2%)
1	7-A	1.72	40/4917 (0.8%)	2.06	154/6616 (2.3%)
1	8-A	1.77	58/4917 (1.2%)	2.06	158/6616 (2.4%)
1	9-A	1.75	53/4917 (1.1%)	2.00	140/6616 (2.1%)
2	1-B	1.73	52/4803 (1.1%)	1.99	135/6481 (2.1%)
2	10-B	1.76	49/4803 (1.0%)	2.06	143/6481 (2.2%)
2	2-B	1.76	54/4803 (1.1%)	1.99	144/6481 (2.2%)
2	3-B	1.73	42/4803 (0.9%)	2.01	136/6481 (2.1%)
2	4-B	1.74	48/4803 (1.0%)	2.07	147/6481 (2.3%)
2	5-B	1.75	58/4803 (1.2%)	2.07	162/6481 (2.5%)
2	6-B	1.71	51/4803 (1.1%)	2.03	147/6481 (2.3%)
2	7-B	1.75	49/4803 (1.0%)	2.02	144/6481 (2.2%)
2	8-B	1.73	40/4803 (0.8%)	2.00	141/6481 (2.2%)
2	9-B	1.75	45/4803 (0.9%)	2.09	151/6481 (2.3%)
3	1-C	1.73	27/3560 (0.8%)	1.95	92/4834 (1.9%)
3	1-D	1.72	29/3560 (0.8%)	1.93	92/4834 (1.9%)
3	10-C	1.68	27/3560 (0.8%)	1.99	99/4834 (2.0%)
3	10-D	1.75	35/3560 (1.0%)	1.94	86/4834 (1.8%)
3	2-C	1.76	43/3560 (1.2%)	1.98	93/4834 (1.9%)
3	2-D	1.70	28/3560 (0.8%)	1.94	86/4834 (1.8%)
3	3-C	1.73	40/3560 (1.1%)	1.93	89/4834 (1.8%)
3	3-D	1.74	29/3560 (0.8%)	1.95	83/4834 (1.7%)
3	4-C	1.73	29/3560 (0.8%)	1.92	95/4834 (2.0%)
3	4-D	1.72	31/3560 (0.9%)	1.94	85/4834 (1.8%)
3	5-C	1.71	29/3560 (0.8%)	1.99	99/4834 (2.0%)
3	5-D	1.77	48/3560 (1.3%)	1.93	86/4834 (1.8%)
3	6-C	1.74	32/3560 (0.9%)	2.01	102/4834 (2.1%)
3	6-D	1.69	22/3560 (0.6%)	1.98	89/4834 (1.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
3	7-C	1.75	39/3560 (1.1%)	1.97	102/4834 (2.1%)
3	7-D	1.72	16/3560 (0.4%)	1.98	102/4834 (2.1%)
3	8-C	1.71	22/3560 (0.6%)	1.97	88/4834 (1.8%)
3	8-D	1.73	35/3560 (1.0%)	1.92	81/4834 (1.7%)
3	9-C	1.71	32/3560 (0.9%)	1.93	77/4834 (1.6%)
3	9-D	1.70	29/3560 (0.8%)	1.98	95/4834 (2.0%)
All	All	1.74	1611/168400 (1.0%)	1.99	4714/227650 (2.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1-A	0	25
1	10-A	0	19
1	2-A	0	20
1	3-A	0	22
1	4-A	0	25
1	5-A	0	27
1	6-A	0	18
1	7-A	0	26
1	8-A	0	19
1	9-A	0	29
2	1-B	0	27
2	10-B	0	25
2	2-B	0	21
2	3-B	0	28
2	4-B	0	23
2	5-B	0	22
2	6-B	0	23
2	7-B	0	20
2	8-B	0	19
2	9-B	0	28
3	1-C	0	16
3	1-D	0	13
3	10-C	0	13
3	10-D	0	10
3	2-C	0	11
3	2-D	0	12
3	3-C	0	9
3	3-D	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	4-C	0	15
3	4-D	0	14
3	5-C	0	14
3	5-D	0	17
3	6-C	0	16
3	6-D	0	12
3	7-C	0	13
3	7-D	0	13
3	8-C	0	12
3	8-D	0	13
3	9-C	0	6
3	9-D	0	15
All	All	0	717

All (1611) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	7-B	592	ARG	CZ-NH2	9.95	1.46	1.33
1	3-A	141	GLU	CD-OE2	9.33	1.35	1.25
1	7-A	160	ARG	CD-NE	9.23	1.62	1.46
2	1-B	585	ARG	CZ-NH1	9.02	1.44	1.33
3	10-D	192	ARG	CD-NE	8.88	1.61	1.46
3	5-D	152	SER	CA-CB	8.86	1.66	1.52
3	4-C	333	ARG	CD-NE	8.83	1.61	1.46
3	9-C	279	TYR	CG-CD2	8.65	1.50	1.39
3	4-D	90	ARG	NE-CZ	8.58	1.44	1.33
2	3-B	827	ARG	CZ-NH2	8.57	1.44	1.33
1	7-A	568	TYR	CE2-CZ	8.54	1.49	1.38
2	8-B	651	TYR	CG-CD2	8.53	1.50	1.39
1	7-A	279	TYR	CB-CG	8.46	1.64	1.51
3	10-D	74	SER	CA-CB	8.30	1.65	1.52
3	5-C	90	ARG	CZ-NH2	8.24	1.43	1.33
3	6-C	218	ARG	CZ-NH2	8.20	1.43	1.33
2	10-B	273	SER	CA-CB	8.13	1.65	1.52
1	9-A	388	SER	CA-CB	8.13	1.65	1.52
3	6-C	192	ARG	NE-CZ	8.12	1.43	1.33
1	1-A	284	TYR	CE2-CZ	8.08	1.49	1.38
1	1-A	451	ARG	NE-CZ	8.07	1.43	1.33
1	6-A	108	ARG	CD-NE	8.07	1.60	1.46
3	3-C	65	ARG	CD-NE	8.06	1.60	1.46
1	8-A	111	ARG	CD-NE	8.05	1.60	1.46
2	3-B	409	TYR	CB-CG	-8.04	1.39	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5-B	632	SER	CA-CB	8.00	1.65	1.52
1	1-A	174	GLU	CD-OE1	8.00	1.34	1.25
2	6-B	535	SER	CA-CB	7.95	1.64	1.52
1	5-A	714	ARG	CZ-NH2	7.94	1.43	1.33
2	5-B	827	ARG	NE-CZ	7.94	1.43	1.33
1	2-A	127	SER	CA-CB	7.93	1.64	1.52
3	1-D	114	ARG	CZ-NH2	7.88	1.43	1.33
1	2-A	190	TYR	CB-CG	7.87	1.63	1.51
1	4-A	663	TYR	CB-CG	-7.84	1.39	1.51
2	3-B	471	ARG	NE-CZ	7.81	1.43	1.33
1	8-A	144	ARG	NE-CZ	7.80	1.43	1.33
1	9-A	664	ARG	CZ-NH2	7.78	1.43	1.33
3	2-D	445	TYR	CG-CD1	7.77	1.49	1.39
1	2-A	588	TYR	CG-CD1	7.76	1.49	1.39
1	2-A	793	PHE	CG-CD1	7.76	1.50	1.38
3	7-C	52	PRO	N-CD	-7.75	1.36	1.47
1	8-A	76	ARG	NE-CZ	7.75	1.43	1.33
3	5-D	427	ARG	CZ-NH2	7.71	1.43	1.33
3	10-C	204	PHE	CG-CD1	7.70	1.50	1.38
2	2-B	592	ARG	CZ-NH1	7.69	1.43	1.33
1	8-A	398	TYR	CE1-CZ	7.68	1.48	1.38
3	2-D	362	TYR	CG-CD1	7.67	1.49	1.39
3	5-D	84	ARG	NE-CZ	7.65	1.43	1.33
3	7-C	373	SER	CA-CB	7.64	1.64	1.52
1	8-A	111	ARG	NE-CZ	7.63	1.43	1.33
3	5-D	46	ARG	CZ-NH2	7.59	1.43	1.33
1	9-A	576	ARG	NE-CZ	7.58	1.43	1.33
3	9-D	176	ARG	CZ-NH1	7.58	1.42	1.33
3	3-D	329	ARG	NE-CZ	7.57	1.42	1.33
3	3-C	437	TYR	CB-CG	7.56	1.62	1.51
3	6-D	96	SER	CA-CB	7.56	1.64	1.52
2	8-B	670	ARG	CD-NE	7.55	1.59	1.46
1	2-A	144	ARG	CD-NE	7.54	1.59	1.46
3	8-D	109	TYR	CE2-CZ	-7.54	1.28	1.38
1	8-A	623	ARG	CZ-NH2	7.53	1.42	1.33
1	6-A	137	ARG	CZ-NH2	7.53	1.42	1.33
2	1-B	335	PHE	CE2-CZ	7.50	1.51	1.37
2	10-B	421	TRP	CD2-CE3	-7.50	1.29	1.40
2	6-B	409	TYR	CG-CD2	7.48	1.48	1.39
1	2-A	159	GLU	CD-OE1	7.48	1.33	1.25
1	3-A	371	SER	CA-CB	7.48	1.64	1.52
2	8-B	592	ARG	NE-CZ	7.46	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2-A	796	SER	CA-CB	7.44	1.64	1.52
2	10-B	670	ARG	CD-NE	7.44	1.59	1.46
3	4-C	13	CYS	CB-SG	7.43	1.94	1.82
2	1-B	453	TYR	CE1-CZ	7.43	1.48	1.38
3	9-C	358	ARG	CZ-NH1	7.43	1.42	1.33
3	1-D	381	SER	CB-OG	7.42	1.51	1.42
1	9-A	405	PHE	CG-CD1	7.42	1.49	1.38
1	8-A	204	ARG	CD-NE	7.42	1.59	1.46
2	4-B	288	TYR	CE2-CZ	7.41	1.48	1.38
3	2-D	349	SER	CA-CB	7.40	1.64	1.52
1	5-A	111	ARG	CD-NE	7.39	1.59	1.46
1	4-A	624	ARG	CD-NE	7.38	1.59	1.46
2	5-B	187	TYR	CG-CD2	7.38	1.48	1.39
2	2-B	576	ARG	NE-CZ	7.37	1.42	1.33
3	1-C	185	TYR	CE1-CZ	7.37	1.48	1.38
1	8-A	327	ARG	NE-CZ	7.37	1.42	1.33
1	3-A	451	ARG	NE-CZ	7.37	1.42	1.33
3	3-C	96	SER	CA-CB	7.36	1.64	1.52
1	5-A	393	TYR	CE1-CZ	7.35	1.48	1.38
1	4-A	284	TYR	CB-CG	-7.34	1.40	1.51
1	3-A	194	GLU	CD-OE1	7.34	1.33	1.25
1	3-A	663	TYR	CE2-CZ	7.31	1.48	1.38
3	1-C	87	PHE	CG-CD1	7.31	1.49	1.38
3	9-C	141	SER	CA-CB	7.31	1.64	1.52
2	7-B	758	TYR	CG-CD2	7.30	1.48	1.39
3	3-D	90	ARG	CZ-NH2	7.30	1.42	1.33
1	9-A	131	PHE	CG-CD2	7.28	1.49	1.38
3	8-C	90	ARG	CZ-NH2	7.28	1.42	1.33
3	3-C	373	SER	CA-CB	7.26	1.63	1.52
1	8-A	349	ARG	CZ-NH2	7.25	1.42	1.33
1	6-A	327	ARG	CD-NE	7.25	1.58	1.46
2	2-B	328	ARG	CZ-NH2	7.21	1.42	1.33
2	7-B	190	TYR	CZ-OH	7.21	1.50	1.37
2	1-B	633	ARG	CZ-NH2	7.21	1.42	1.33
3	5-D	247	TYR	CE2-CZ	7.21	1.48	1.38
3	7-C	109	TYR	CG-CD2	7.21	1.48	1.39
1	8-A	645	GLU	CD-OE1	7.20	1.33	1.25
3	3-C	13	CYS	CB-SG	7.20	1.94	1.82
1	1-A	150	TYR	CE1-CZ	7.18	1.47	1.38
1	4-A	712	SER	CA-CB	7.18	1.63	1.52
1	5-A	123	TYR	CZ-OH	7.17	1.50	1.37
1	4-A	77	TYR	CE2-CZ	7.17	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	5-C	204	PHE	CG-CD1	7.17	1.49	1.38
1	1-A	112	TYR	CE2-CZ	7.15	1.47	1.38
3	2-D	170	TYR	CD1-CE1	7.15	1.50	1.39
3	2-C	445	TYR	CZ-OH	7.14	1.50	1.37
1	3-A	172	GLU	CB-CG	7.13	1.65	1.52
2	4-B	600	TYR	CB-CG	7.13	1.62	1.51
3	3-D	279	TYR	CG-CD1	7.12	1.48	1.39
3	1-D	161	ARG	NE-CZ	7.12	1.42	1.33
1	9-A	337	SER	CA-CB	7.12	1.63	1.52
3	10-D	55	ARG	CZ-NH2	7.10	1.42	1.33
3	8-C	427	ARG	NE-CZ	7.09	1.42	1.33
3	10-C	59	ARG	CZ-NH2	7.09	1.42	1.33
2	3-B	201	PRO	N-CD	-7.08	1.38	1.47
3	1-D	291	SER	CA-CB	7.08	1.63	1.52
1	5-A	645	GLU	CD-OE1	7.07	1.33	1.25
3	7-C	247	TYR	CD2-CE2	7.07	1.50	1.39
2	7-B	328	ARG	CD-NE	7.06	1.58	1.46
2	7-B	388	GLU	CB-CG	7.05	1.65	1.52
1	5-A	614	TYR	CG-CD1	7.04	1.48	1.39
3	1-D	319	TYR	CE2-CZ	7.04	1.47	1.38
1	5-A	624	ARG	CZ-NH1	7.03	1.42	1.33
1	2-A	198	ARG	NE-CZ	7.03	1.42	1.33
2	9-B	846	ARG	CZ-NH2	7.03	1.42	1.33
3	6-C	378	SER	CB-OG	7.03	1.51	1.42
3	8-D	84	ARG	NE-CZ	7.03	1.42	1.33
2	10-B	389	ARG	CD-NE	7.02	1.58	1.46
1	3-A	284	TYR	CG-CD2	7.01	1.48	1.39
1	1-A	111	ARG	CD-NE	7.01	1.58	1.46
3	10-D	114	ARG	CZ-NH2	6.99	1.42	1.33
2	9-B	666	ARG	CZ-NH1	6.99	1.42	1.33
3	7-C	407	TYR	CE2-CZ	6.99	1.47	1.38
3	2-C	65	ARG	CZ-NH2	6.97	1.42	1.33
2	7-B	388	GLU	CD-OE2	-6.97	1.18	1.25
1	9-A	333	ARG	NE-CZ	6.97	1.42	1.33
2	9-B	578	PHE	CG-CD1	6.96	1.49	1.38
1	5-A	687	ARG	NE-CZ	6.95	1.42	1.33
2	3-B	514	ARG	NE-CZ	6.94	1.42	1.33
2	10-B	359	TYR	CG-CD1	6.94	1.48	1.39
2	8-B	666	ARG	CZ-NH1	6.93	1.42	1.33
2	3-B	345	TYR	CG-CD1	6.93	1.48	1.39
3	10-D	59	ARG	CZ-NH1	6.92	1.42	1.33
2	9-B	379	TYR	CG-CD1	6.92	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	3-B	758	TYR	CZ-OH	6.91	1.49	1.37
2	6-B	433	TYR	CE2-CZ	6.91	1.47	1.38
2	9-B	343	TYR	CG-CD2	6.90	1.48	1.39
2	3-B	445	PHE	CG-CD2	6.90	1.49	1.38
3	5-C	46	ARG	CZ-NH1	6.89	1.42	1.33
3	8-D	333	ARG	CZ-NH1	6.89	1.42	1.33
1	2-A	429	TYR	CE1-CZ	6.88	1.47	1.38
3	7-D	347	TRP	CB-CG	6.88	1.62	1.50
3	5-D	362	TYR	CG-CD1	6.88	1.48	1.39
3	10-D	213	SER	CA-CB	6.87	1.63	1.52
1	3-A	368	SER	CA-CB	6.87	1.63	1.52
2	3-B	190	TYR	CG-CD1	6.87	1.48	1.39
2	4-B	772	PHE	CA-CB	6.86	1.69	1.53
3	5-D	302	SER	CA-CB	6.86	1.63	1.52
3	7-C	59	ARG	CZ-NH1	6.86	1.42	1.33
2	8-B	526	ARG	CZ-NH2	6.84	1.42	1.33
3	2-C	319	TYR	CB-CG	6.84	1.61	1.51
3	9-C	90	ARG	CD-NE	6.84	1.58	1.46
2	10-B	670	ARG	NE-CZ	6.83	1.42	1.33
3	4-C	369	GLU	CD-OE1	6.82	1.33	1.25
3	2-C	243	ARG	CZ-NH1	6.82	1.42	1.33
3	3-D	243	ARG	NE-CZ	6.82	1.42	1.33
2	9-B	344	GLU	CG-CD	6.80	1.62	1.51
3	1-C	256	TYR	CG-CD1	6.80	1.48	1.39
2	4-B	409	TYR	CE2-CZ	6.79	1.47	1.38
3	8-C	218	ARG	CZ-NH1	6.78	1.41	1.33
1	1-A	76	ARG	CD-NE	6.78	1.57	1.46
3	2-D	427	ARG	CZ-NH2	6.77	1.41	1.33
3	10-D	193	ARG	NE-CZ	6.77	1.41	1.33
2	4-B	453	TYR	CG-CD1	6.76	1.48	1.39
3	2-C	358	ARG	CZ-NH1	6.76	1.41	1.33
3	9-D	100	SER	CA-CB	6.76	1.63	1.52
2	8-B	593	PHE	CG-CD1	6.75	1.48	1.38
1	8-A	203	ARG	CD-NE	6.75	1.57	1.46
1	3-A	772	SER	CA-CB	6.74	1.63	1.52
2	6-B	325	LEU	N-CA	-6.74	1.32	1.46
1	7-A	286	TRP	CZ2-CH2	6.73	1.50	1.37
3	1-C	359	ARG	CD-NE	6.73	1.57	1.46
1	3-A	413	TYR	CG-CD1	6.72	1.47	1.39
3	10-D	373	SER	CA-CB	6.71	1.63	1.52
3	10-C	427	ARG	CZ-NH1	6.71	1.41	1.33
3	3-C	80	GLU	CD-OE2	6.70	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1-B	411	PHE	CG-CD1	6.70	1.48	1.38
3	2-C	161	ARG	CZ-NH2	6.70	1.41	1.33
1	10-A	458	TYR	CG-CD1	6.70	1.47	1.39
3	1-C	332	SER	CA-CB	6.69	1.62	1.52
1	4-A	143	ARG	CZ-NH2	6.68	1.41	1.33
3	10-C	445	TYR	CE2-CZ	6.67	1.47	1.38
2	7-B	439	ARG	NE-CZ	6.67	1.41	1.33
3	9-C	136	PHE	CG-CD1	6.67	1.48	1.38
2	10-B	288	TYR	CG-CD1	6.66	1.47	1.39
3	2-C	109	TYR	CG-CD2	6.66	1.47	1.39
3	4-D	244	PHE	CG-CD1	6.66	1.48	1.38
2	6-B	356	ARG	NE-CZ	6.66	1.41	1.33
1	4-A	198	ARG	NE-CZ	6.65	1.41	1.33
3	10-C	250	SER	CA-CB	6.64	1.62	1.52
1	8-A	358	ARG	CD-NE	6.64	1.57	1.46
2	1-B	612	ARG	CZ-NH2	6.64	1.41	1.33
2	2-B	506	SER	CA-CB	6.64	1.62	1.52
3	5-C	170	TYR	CZ-OH	6.62	1.49	1.37
2	7-B	259	GLU	CG-CD	6.62	1.61	1.51
2	2-B	302	GLU	CD-OE2	6.61	1.32	1.25
2	5-B	651	TYR	CE1-CZ	6.61	1.47	1.38
3	5-D	17	VAL	C-N	6.60	1.45	1.33
3	7-D	315	TYR	CZ-OH	6.60	1.49	1.37
3	3-C	277	SER	CB-OG	6.60	1.50	1.42
2	8-B	356	ARG	CZ-NH2	6.60	1.41	1.33
1	1-A	203	ARG	CZ-NH2	6.59	1.41	1.33
1	2-A	111	ARG	CD-NE	6.58	1.57	1.46
3	8-D	176	ARG	CZ-NH1	6.58	1.41	1.33
2	6-B	297	TYR	CG-CD2	6.58	1.47	1.39
2	3-B	666	ARG	NE-CZ	6.58	1.41	1.33
1	8-A	687	ARG	CD-NE	6.58	1.57	1.46
2	1-B	286	GLU	CD-OE2	6.58	1.32	1.25
1	4-A	371	SER	CA-CB	6.57	1.62	1.52
2	1-B	293	ARG	CZ-NH1	6.57	1.41	1.33
2	2-B	425	PHE	CG-CD1	6.57	1.48	1.38
1	4-A	597	ARG	CZ-NH2	6.57	1.41	1.33
1	6-A	451	ARG	NE-CZ	6.57	1.41	1.33
2	7-B	225	PHE	CG-CD2	6.57	1.48	1.38
2	2-B	526	ARG	CD-NE	6.56	1.57	1.46
3	5-C	160	ASP	CA-CB	6.56	1.68	1.53
1	10-A	123	TYR	CD1-CE1	6.56	1.49	1.39
3	7-D	291	SER	CA-CB	6.56	1.62	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-D	56	GLU	CD-OE1	6.56	1.32	1.25
3	1-D	192	ARG	CD-NE	6.56	1.57	1.46
3	10-C	114	ARG	CD-NE	6.56	1.57	1.46
3	1-C	161	ARG	NE-CZ	6.55	1.41	1.33
1	1-A	627	ARG	CZ-NH2	6.55	1.41	1.33
1	10-A	675	GLU	CD-OE1	6.54	1.32	1.25
3	9-C	427	ARG	CZ-NH1	6.54	1.41	1.33
3	4-C	136	PHE	CG-CD1	6.54	1.48	1.38
1	4-A	204	ARG	NE-CZ	6.54	1.41	1.33
3	8-D	170	TYR	CG-CD1	6.54	1.47	1.39
2	5-B	228	GLY	CA-C	-6.53	1.41	1.51
2	6-B	635	SER	CA-CB	6.53	1.62	1.52
3	9-C	346	SER	CA-CB	6.52	1.62	1.52
3	7-C	427	ARG	CZ-NH1	6.52	1.41	1.33
3	2-D	162	TYR	CE2-CZ	6.52	1.47	1.38
2	9-B	839	PHE	CG-CD2	6.52	1.48	1.38
2	3-B	846	ARG	NE-CZ	6.51	1.41	1.33
2	7-B	776	TYR	CG-CD1	6.50	1.47	1.39
3	7-C	249	TYR	CG-CD1	6.50	1.47	1.39
3	10-C	277	SER	CA-CB	6.50	1.62	1.52
1	8-A	302	TYR	CG-CD1	6.49	1.47	1.39
2	4-B	299	ARG	CZ-NH1	6.49	1.41	1.33
2	9-B	288	TYR	CE2-CZ	6.49	1.47	1.38
1	1-A	111	ARG	CZ-NH2	6.49	1.41	1.33
2	8-B	822	ARG	CD-NE	6.49	1.57	1.46
2	2-B	600	TYR	CG-CD1	6.48	1.47	1.39
1	4-A	623	ARG	CZ-NH2	6.47	1.41	1.33
3	6-C	256	TYR	CG-CD2	6.47	1.47	1.39
3	2-D	55	ARG	CD-NE	6.46	1.57	1.46
3	6-D	218	ARG	NE-CZ	6.46	1.41	1.33
1	7-A	111	ARG	CZ-NH2	6.45	1.41	1.33
1	7-A	714	ARG	CD-NE	6.45	1.57	1.46
2	1-B	438	TYR	CG-CD2	6.45	1.47	1.39
2	3-B	306	GLU	CG-CD	6.45	1.61	1.51
1	2-A	262	ARG	CZ-NH2	6.44	1.41	1.33
3	3-D	291	SER	CA-CB	6.44	1.62	1.52
3	4-D	86	PHE	CG-CD1	6.44	1.48	1.38
3	6-D	275	PHE	CG-CD1	6.43	1.48	1.38
1	5-A	582	TYR	CZ-OH	6.42	1.48	1.37
2	6-B	598	TYR	CG-CD1	6.42	1.47	1.39
2	10-B	827	ARG	CD-NE	6.42	1.57	1.46
2	9-B	577	PRO	N-CD	-6.42	1.38	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	8-A	663	TYR	CZ-OH	6.41	1.48	1.37
3	9-D	292	TYR	CZ-OH	6.41	1.48	1.37
3	7-C	333	ARG	NE-CZ	6.41	1.41	1.33
2	10-B	578	PHE	CG-CD1	6.41	1.48	1.38
1	9-A	203	ARG	CZ-NH2	6.40	1.41	1.33
2	10-B	510	TYR	CZ-OH	6.40	1.48	1.37
3	6-C	341	ARG	CD-NE	6.40	1.57	1.46
3	1-C	394	PHE	CG-CD2	6.39	1.48	1.38
2	4-B	470	TYR	CE2-CZ	6.39	1.46	1.38
2	4-B	225	PHE	CG-CD2	6.38	1.48	1.38
3	1-D	43	SER	CA-CB	6.38	1.62	1.52
2	5-B	216	PHE	CB-CG	-6.38	1.40	1.51
3	7-D	358	ARG	NE-CZ	6.37	1.41	1.33
1	5-A	324	TYR	CD2-CE2	6.37	1.48	1.39
1	6-A	123	TYR	CE2-CZ	6.37	1.46	1.38
2	4-B	592	ARG	CZ-NH2	6.36	1.41	1.33
1	8-A	137	ARG	NE-CZ	6.36	1.41	1.33
3	9-C	59	ARG	CZ-NH2	6.36	1.41	1.33
1	6-A	193	TYR	CZ-OH	6.36	1.48	1.37
1	6-A	264	SER	CA-CB	-6.35	1.43	1.52
1	8-A	393	TYR	CE2-CZ	6.35	1.46	1.38
3	2-C	302	SER	CA-CB	6.34	1.62	1.52
2	5-B	508	PRO	N-CA	-6.34	1.36	1.47
3	9-D	59	ARG	NE-CZ	6.34	1.41	1.33
3	9-D	407	TYR	CB-CG	6.34	1.61	1.51
1	8-A	393	TYR	CZ-OH	6.33	1.48	1.37
1	8-A	597	ARG	CZ-NH1	6.33	1.41	1.33
3	8-C	46	ARG	NE-CZ	6.33	1.41	1.33
2	7-B	289	GLU	CB-CG	6.33	1.64	1.52
3	6-D	161	ARG	CD-NE	6.33	1.57	1.46
3	4-C	415	SER	CA-CB	6.33	1.62	1.52
1	8-A	190	TYR	CE1-CZ	6.33	1.46	1.38
3	1-D	173	PHE	CG-CD2	6.32	1.48	1.38
2	4-B	181	GLU	CG-CD	6.32	1.61	1.51
1	5-A	479	ARG	NE-CZ	6.32	1.41	1.33
1	3-A	160	ARG	CD-NE	6.32	1.57	1.46
3	2-C	244	PHE	CG-CD2	6.32	1.48	1.38
3	5-D	445	TYR	CD1-CE1	6.31	1.48	1.39
1	9-A	794	TYR	CE2-CZ	6.31	1.46	1.38
2	2-B	236	TYR	CE2-CZ	6.31	1.46	1.38
3	7-C	217	PHE	CG-CD2	6.31	1.48	1.38
1	2-A	139	ALA	N-CA	-6.30	1.33	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	6-B	651	TYR	CE2-CZ	6.29	1.46	1.38
3	3-D	179	GLU	CD-OE2	6.29	1.32	1.25
3	4-C	45	GLU	CD-OE1	6.29	1.32	1.25
3	10-D	344	PHE	CG-CD2	6.29	1.48	1.38
3	9-D	156	GLU	CG-CD	6.28	1.61	1.51
3	4-D	66	ALA	CA-C	-6.28	1.36	1.52
1	7-A	77	TYR	CE2-CZ	6.28	1.46	1.38
3	8-D	358	ARG	CZ-NH1	6.28	1.41	1.33
2	9-B	361	GLU	CD-OE2	6.28	1.32	1.25
2	6-B	844	SER	CA-CB	6.27	1.62	1.52
1	5-A	398	TYR	CE1-CZ	6.27	1.46	1.38
2	7-B	824	TYR	CE1-CZ	6.26	1.46	1.38
3	7-C	339	GLN	CG-CD	6.26	1.65	1.51
2	4-B	670	ARG	CZ-NH2	6.26	1.41	1.33
1	7-A	262	ARG	CZ-NH2	6.26	1.41	1.33
2	7-B	328	ARG	NE-CZ	6.26	1.41	1.33
3	7-C	178	SER	CA-CB	6.26	1.62	1.52
3	7-D	93	TRP	CD1-NE1	6.26	1.48	1.38
2	8-B	811	GLU	C-N	6.26	1.48	1.34
3	2-C	170	TYR	CG-CD2	6.25	1.47	1.39
3	3-D	203	VAL	CA-CB	-6.25	1.41	1.54
1	5-A	587	ARG	NE-CZ	6.25	1.41	1.33
1	9-A	74	TYR	CG-CD1	6.25	1.47	1.39
2	9-B	433	TYR	CG-CD1	6.25	1.47	1.39
3	3-C	398	PHE	CB-CG	6.24	1.61	1.51
2	10-B	585	ARG	CD-NE	6.24	1.57	1.46
1	6-A	387	GLY	CA-C	-6.24	1.41	1.51
3	9-C	162	TYR	CG-CD2	6.24	1.47	1.39
3	3-C	383	VAL	CB-CG1	6.23	1.66	1.52
3	3-D	64	PRO	N-CD	-6.23	1.39	1.47
3	7-D	90	ARG	NE-CZ	6.23	1.41	1.33
3	3-D	362	TYR	CE1-CZ	6.23	1.46	1.38
2	5-B	598	TYR	CE1-CZ	6.23	1.46	1.38
1	8-A	623	ARG	NE-CZ	6.22	1.41	1.33
3	2-D	375	MET	CA-C	-6.22	1.36	1.52
3	10-D	105	TRP	NE1-CE2	6.22	1.45	1.37
1	7-A	345	PHE	CB-CG	6.22	1.61	1.51
2	5-B	768	SER	CA-CB	6.22	1.62	1.52
3	4-C	218	ARG	NE-CZ	6.21	1.41	1.33
3	5-D	173	PHE	CG-CD1	6.21	1.48	1.38
1	4-A	489	GLU	CD-OE1	6.21	1.32	1.25
2	1-B	228	GLY	CA-C	-6.21	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	5-D	90	ARG	CZ-NH1	6.20	1.41	1.33
1	4-A	386	GLU	CD-OE1	6.20	1.32	1.25
3	6-C	218	ARG	CA-CB	6.19	1.67	1.53
2	3-B	504	SER	CA-CB	6.19	1.62	1.52
2	1-B	641	PHE	CB-CG	-6.19	1.40	1.51
1	9-A	597	ARG	NE-CZ	6.19	1.41	1.33
1	4-A	687	ARG	NE-CZ	6.19	1.41	1.33
1	3-A	285	GLU	CD-OE1	6.18	1.32	1.25
2	5-B	598	TYR	CG-CD1	6.18	1.47	1.39
3	8-D	359	ARG	NE-CZ	6.18	1.41	1.33
1	5-A	450	TYR	CG-CD1	6.18	1.47	1.39
3	10-D	11	GLY	N-CA	-6.18	1.36	1.46
2	2-B	644	PHE	CG-CD2	6.18	1.48	1.38
3	4-D	185	TYR	CZ-OH	6.18	1.48	1.37
3	9-C	359	ARG	CZ-NH2	6.18	1.41	1.33
3	3-D	161	ARG	CZ-NH2	6.18	1.41	1.33
2	9-B	824	TYR	CG-CD2	6.18	1.47	1.39
3	2-C	232	SER	CA-CB	6.17	1.62	1.52
3	7-D	427	ARG	CZ-NH2	6.17	1.41	1.33
1	8-A	157	ARG	NE-CZ	6.17	1.41	1.33
1	9-A	105	PHE	N-CA	-6.17	1.34	1.46
3	5-D	192	ARG	CZ-NH2	6.17	1.41	1.33
3	5-D	236	SER	CA-CB	6.17	1.62	1.52
3	7-D	62	PHE	CE1-CZ	6.17	1.49	1.37
3	2-D	135	GLY	N-CA	-6.17	1.36	1.46
1	7-A	594	TYR	CG-CD1	6.16	1.47	1.39
1	10-A	400	ARG	CZ-NH1	6.16	1.41	1.33
1	7-A	107	ARG	NE-CZ	6.16	1.41	1.33
1	7-A	469	ARG	NE-CZ	6.16	1.41	1.33
3	1-C	161	ARG	CZ-NH1	6.16	1.41	1.33
2	6-B	670	ARG	NE-CZ	6.15	1.41	1.33
3	3-D	55	ARG	NE-CZ	6.15	1.41	1.33
3	3-D	47	ASP	CB-CG	6.15	1.64	1.51
1	4-A	156	GLU	CG-CD	6.15	1.61	1.51
3	5-C	183	GLN	CA-CB	6.15	1.67	1.53
2	9-B	231	TYR	CG-CD1	6.15	1.47	1.39
2	10-B	666	ARG	CZ-NH2	6.15	1.41	1.33
3	10-D	292	TYR	CE1-CZ	6.14	1.46	1.38
2	8-B	297	TYR	CZ-OH	6.14	1.48	1.37
1	2-A	558	TYR	CZ-OH	6.13	1.48	1.37
1	3-A	143	ARG	CZ-NH2	6.13	1.41	1.33
2	5-B	518	GLU	CA-C	-6.13	1.37	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	10-D	20	PHE	CG-CD1	6.13	1.48	1.38
1	2-A	111	ARG	NE-CZ	6.13	1.41	1.33
3	2-D	193	ARG	CZ-NH2	6.13	1.41	1.33
2	3-B	827	ARG	CZ-NH1	6.13	1.41	1.33
2	1-B	239	GLU	CA-CB	6.12	1.67	1.53
3	4-D	114	ARG	NE-CZ	6.12	1.41	1.33
2	8-B	288	TYR	CD1-CE1	6.12	1.48	1.39
2	8-B	638	ARG	NE-CZ	6.12	1.41	1.33
3	5-D	274	PRO	N-CD	-6.11	1.39	1.47
1	8-A	458	TYR	CG-CD1	6.11	1.47	1.39
3	9-C	372	VAL	CB-CG1	6.11	1.65	1.52
1	6-A	630	ARG	CD-NE	6.11	1.56	1.46
2	3-B	562	TYR	CD2-CE2	-6.11	1.30	1.39
1	1-A	156	GLU	CB-CG	6.11	1.63	1.52
1	6-A	171	ARG	CZ-NH1	6.11	1.41	1.33
1	10-A	614	TYR	CB-CG	-6.11	1.42	1.51
2	1-B	557	VAL	N-CA	-6.11	1.34	1.46
3	3-C	267	PHE	CG-CD1	6.11	1.48	1.38
1	2-A	359	ALA	CA-CB	6.10	1.65	1.52
3	4-D	358	ARG	CZ-NH2	6.09	1.41	1.33
3	5-C	427	ARG	CZ-NH2	6.09	1.41	1.33
2	7-B	260	GLU	CD-OE1	6.09	1.32	1.25
1	9-A	262	ARG	NE-CZ	6.09	1.41	1.33
1	6-A	137	ARG	NE-CZ	6.09	1.41	1.33
1	3-A	108	ARG	CZ-NH1	-6.09	1.25	1.33
3	1-D	319	TYR	CD1-CE1	6.08	1.48	1.39
1	10-A	168	PHE	CG-CD2	6.08	1.47	1.38
1	5-A	171	ARG	CZ-NH1	6.07	1.41	1.33
3	7-C	218	ARG	CD-NE	6.07	1.56	1.46
1	7-A	251	PHE	CG-CD1	6.07	1.47	1.38
1	5-A	138	PHE	CE2-CZ	6.07	1.48	1.37
2	10-B	526	ARG	CZ-NH1	6.07	1.41	1.33
3	3-D	445	TYR	CE2-CZ	6.07	1.46	1.38
1	2-A	400	ARG	NE-CZ	6.07	1.41	1.33
3	6-C	84	ARG	NE-CZ	6.07	1.41	1.33
1	1-A	767	TYR	CG-CD1	6.06	1.47	1.39
3	2-D	264	GLU	CD-OE1	6.06	1.32	1.25
3	7-C	329	ARG	NE-CZ	6.06	1.41	1.33
2	2-B	435	SER	CA-CB	6.06	1.62	1.52
1	6-A	759	GLU	CB-CG	6.06	1.63	1.52
3	8-C	129	SER	CA-CB	6.06	1.62	1.52
3	1-C	249	TYR	CG-CD2	6.05	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	10-D	281	HIS	CB-CG	6.05	1.60	1.50
3	1-C	253	SER	CA-CB	6.05	1.62	1.52
1	2-A	190	TYR	CE1-CZ	6.05	1.46	1.38
3	5-D	192	ARG	NE-CZ	6.05	1.41	1.33
1	9-A	126	TRP	CB-CG	6.05	1.61	1.50
3	10-C	325	ASN	N-CA	-6.05	1.34	1.46
1	2-A	203	ARG	CZ-NH2	6.05	1.41	1.33
1	1-A	400	ARG	NE-CZ	6.04	1.41	1.33
3	3-C	359	ARG	CZ-NH1	6.04	1.41	1.33
3	5-D	171	SER	CA-CB	6.04	1.62	1.52
2	3-B	587	PHE	CG-CD2	6.04	1.47	1.38
1	5-A	663	TYR	CE1-CZ	6.04	1.46	1.38
3	2-D	315	TYR	CG-CD1	6.04	1.47	1.39
1	7-A	400	ARG	NE-CZ	6.04	1.41	1.33
1	6-A	596	SER	CA-CB	6.04	1.62	1.52
3	3-C	90	ARG	CZ-NH1	6.04	1.40	1.33
3	6-C	69	MET	N-CA	-6.04	1.34	1.46
1	1-A	138	PHE	CG-CD2	6.03	1.47	1.38
3	1-D	84	ARG	CZ-NH1	6.03	1.40	1.33
1	6-A	664	ARG	CD-NE	6.03	1.56	1.46
2	9-B	670	ARG	NE-CZ	6.03	1.40	1.33
2	6-B	582	GLU	CG-CD	6.03	1.60	1.51
2	1-B	592	ARG	CZ-NH1	6.03	1.40	1.33
2	10-B	836	GLU	CG-CD	6.03	1.60	1.51
2	1-B	337	SER	CA-CB	6.03	1.61	1.52
3	4-D	65	ARG	CZ-NH2	6.03	1.40	1.33
1	10-A	627	ARG	NE-CZ	6.03	1.40	1.33
3	10-C	193	ARG	CD-NE	6.02	1.56	1.46
1	3-A	381	PHE	CG-CD1	6.02	1.47	1.38
1	9-A	798	SER	CA-CB	6.02	1.61	1.52
3	1-D	90	ARG	CZ-NH2	6.02	1.40	1.33
3	1-D	161	ARG	CZ-NH1	6.02	1.40	1.33
2	1-B	576	ARG	NE-CZ	6.02	1.40	1.33
1	9-A	469	ARG	CD-NE	6.01	1.56	1.46
2	9-B	585	ARG	NE-CZ	6.01	1.40	1.33
2	3-B	187	TYR	CG-CD1	6.01	1.47	1.39
3	7-C	55	ARG	NE-CZ	6.01	1.40	1.33
3	3-C	369	GLU	CB-CG	6.00	1.63	1.52
3	5-C	100	SER	CA-CB	6.00	1.61	1.52
2	6-B	514	ARG	CD-NE	6.00	1.56	1.46
2	6-B	805	PHE	CB-CG	6.00	1.61	1.51
2	2-B	600	TYR	CZ-OH	6.00	1.48	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4-C	148	SER	C-N	6.00	1.43	1.33
1	2-A	429	TYR	CG-CD1	6.00	1.47	1.39
2	9-B	356	ARG	NE-CZ	6.00	1.40	1.33
3	9-D	274	PRO	CA-C	6.00	1.64	1.52
3	4-D	87	PHE	CG-CD1	6.00	1.47	1.38
1	5-A	78	PHE	CG-CD2	6.00	1.47	1.38
3	8-D	236	SER	CA-CB	5.99	1.61	1.52
1	2-A	714	ARG	CZ-NH1	5.99	1.40	1.33
1	7-A	413	TYR	CG-CD2	5.99	1.47	1.39
3	7-C	445	TYR	CE2-CZ	5.99	1.46	1.38
3	9-C	315	TYR	CE1-CZ	5.99	1.46	1.38
3	3-C	161	ARG	CZ-NH1	5.99	1.40	1.33
3	9-C	170	TYR	CG-CD1	5.98	1.47	1.39
1	6-A	626	VAL	CB-CG2	5.98	1.65	1.52
1	9-A	262	ARG	CA-C	-5.98	1.37	1.52
2	10-B	628	ILE	N-CA	5.98	1.58	1.46
2	9-B	576	ARG	CD-NE	5.98	1.56	1.46
3	4-C	317	ASN	CB-CG	5.98	1.64	1.51
3	3-D	315	TYR	CE2-CZ	5.97	1.46	1.38
2	5-B	340	SER	CA-CB	5.97	1.61	1.52
1	1-A	627	ARG	CZ-NH1	5.97	1.40	1.33
1	5-A	137	ARG	NE-CZ	5.97	1.40	1.33
3	8-C	173	PHE	CG-CD2	5.97	1.47	1.38
3	3-C	185	TYR	CE1-CZ	5.97	1.46	1.38
1	9-A	62	ASP	CB-CG	5.97	1.64	1.51
2	5-B	345	TYR	CE1-CZ	5.97	1.46	1.38
2	1-B	670	ARG	NE-CZ	5.97	1.40	1.33
1	2-A	324	TYR	CE2-CZ	5.97	1.46	1.38
2	5-B	328	ARG	CZ-NH2	5.97	1.40	1.33
3	1-D	35	GLY	CA-C	-5.96	1.42	1.51
2	5-B	297	TYR	CG-CD1	5.96	1.47	1.39
3	7-C	65	ARG	CZ-NH1	5.96	1.40	1.33
3	8-D	109	TYR	CE1-CZ	5.96	1.46	1.38
1	7-A	624	ARG	NE-CZ	5.96	1.40	1.33
3	6-C	344	PHE	CG-CD2	5.96	1.47	1.38
3	2-C	193	ARG	CZ-NH1	5.95	1.40	1.33
3	6-D	83	PHE	CE1-CZ	5.95	1.48	1.37
1	5-A	286	TRP	CD1-NE1	5.95	1.48	1.38
1	9-A	664	ARG	CD-NE	5.95	1.56	1.46
1	9-A	658	SER	CA-CB	5.95	1.61	1.52
3	3-D	341	ARG	NE-CZ	5.94	1.40	1.33
3	5-D	161	ARG	CZ-NH2	5.94	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	8-A	451	ARG	CZ-NH1	5.94	1.40	1.33
1	2-A	646	TYR	CG-CD1	5.94	1.46	1.39
1	1-A	646	TYR	CD2-CE2	5.94	1.48	1.39
3	3-C	437	TYR	CE1-CZ	5.94	1.46	1.38
3	4-C	407	TYR	CG-CD1	5.94	1.46	1.39
1	5-A	450	TYR	CG-CD2	5.94	1.46	1.39
2	5-B	504	SER	CA-CB	5.94	1.61	1.52
2	10-B	533	ARG	CZ-NH1	5.94	1.40	1.33
1	1-A	333	ARG	NE-CZ	5.94	1.40	1.33
1	2-A	161	ASP	CA-CB	5.94	1.67	1.53
3	4-D	371	GLU	CG-CD	5.93	1.60	1.51
2	6-B	526	ARG	CZ-NH1	5.93	1.40	1.33
2	9-B	628	ILE	N-CA	5.93	1.58	1.46
1	6-A	349	ARG	CD-NE	5.93	1.56	1.46
3	1-D	256	TYR	CB-CG	-5.93	1.42	1.51
2	4-B	439	ARG	CZ-NH2	5.93	1.40	1.33
3	1-D	3	GLY	CA-C	5.92	1.61	1.51
1	1-A	144	ARG	NE-CZ	5.92	1.40	1.33
2	8-B	741	PHE	CG-CD1	5.92	1.47	1.38
3	10-D	367	PRO	CA-C	-5.92	1.41	1.52
3	4-C	161	ARG	CZ-NH2	5.92	1.40	1.33
3	5-D	84	ARG	CZ-NH2	5.91	1.40	1.33
2	10-B	424	GLU	CD-OE2	5.91	1.32	1.25
1	2-A	664	ARG	NE-CZ	5.91	1.40	1.33
2	2-B	533	ARG	CZ-NH2	5.91	1.40	1.33
1	6-A	325	PHE	CG-CD1	5.91	1.47	1.38
1	7-A	124	GLU	CD-OE1	5.90	1.32	1.25
1	2-A	262	ARG	CZ-NH1	5.90	1.40	1.33
2	3-B	719	LEU	N-CA	5.90	1.58	1.46
2	6-B	319	PHE	CB-CG	5.90	1.61	1.51
1	2-A	143	ARG	CD-NE	5.90	1.56	1.46
2	3-B	822	ARG	CZ-NH1	5.90	1.40	1.33
3	1-C	262	SER	CA-CB	5.89	1.61	1.52
3	5-C	292	TYR	CZ-OH	5.89	1.47	1.37
2	1-B	447	GLU	CD-OE1	5.89	1.32	1.25
3	4-D	184	SER	CA-CB	5.88	1.61	1.52
1	5-A	76	ARG	CZ-NH2	5.88	1.40	1.33
2	2-B	592	ARG	CZ-NH2	5.88	1.40	1.33
3	10-C	358	ARG	CZ-NH2	5.88	1.40	1.33
2	7-B	343	TYR	CB-CG	5.87	1.60	1.51
3	5-C	148	SER	C-N	5.87	1.43	1.33
3	8-C	329	ARG	NE-CZ	5.87	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	9-A	409	PHE	CG-CD1	5.87	1.47	1.38
2	9-B	264	TYR	CG-CD1	5.87	1.46	1.39
3	10-C	161	ARG	NE-CZ	5.87	1.40	1.33
1	4-A	443	MET	C-N	5.86	1.43	1.33
2	8-B	264	TYR	CE2-CZ	5.86	1.46	1.38
1	10-A	201	GLU	CD-OE1	5.86	1.32	1.25
2	6-B	638	ARG	CD-NE	5.86	1.56	1.46
1	2-A	97	LYS	CA-CB	5.86	1.66	1.53
1	9-A	171	ARG	CD-NE	5.86	1.56	1.46
3	9-D	272	PHE	CG-CD1	5.86	1.47	1.38
2	3-B	285	ARG	CZ-NH1	5.86	1.40	1.33
3	5-D	359	ARG	CZ-NH1	5.86	1.40	1.33
1	5-A	161	ASP	N-CA	-5.86	1.34	1.46
3	5-C	409	VAL	CA-CB	5.86	1.67	1.54
2	9-B	583	TYR	CG-CD2	5.86	1.46	1.39
3	1-D	59	ARG	CZ-NH2	5.85	1.40	1.33
2	4-B	544	ARG	CZ-NH2	5.85	1.40	1.33
3	4-D	161	ARG	NE-CZ	5.85	1.40	1.33
3	4-C	359	ARG	NE-CZ	5.85	1.40	1.33
3	8-D	441	GLU	CD-OE2	5.85	1.32	1.25
2	9-B	471	ARG	NE-CZ	5.85	1.40	1.33
2	4-B	200	PHE	CB-CG	5.85	1.61	1.51
1	6-A	471	SER	CA-CB	5.85	1.61	1.52
3	2-C	360	SER	CB-OG	5.84	1.49	1.42
2	3-B	582	GLU	CG-CD	5.84	1.60	1.51
2	7-B	827	ARG	CD-NE	5.84	1.56	1.46
2	5-B	585	ARG	NE-CZ	5.84	1.40	1.33
3	5-D	176	ARG	CZ-NH1	5.84	1.40	1.33
3	10-C	327	GLU	CB-CG	5.84	1.63	1.52
3	10-D	358	ARG	NE-CZ	5.83	1.40	1.33
1	1-A	74	TYR	CG-CD2	-5.83	1.31	1.39
1	4-A	582	TYR	CG-CD2	5.83	1.46	1.39
1	8-A	333	ARG	CZ-NH2	5.83	1.40	1.33
1	9-A	624	ARG	CZ-NH1	5.83	1.40	1.33
3	2-D	329	ARG	NE-CZ	5.83	1.40	1.33
1	5-A	150	TYR	CG-CD2	5.83	1.46	1.39
2	5-B	565	TYR	CG-CD2	5.83	1.46	1.39
2	8-B	670	ARG	NE-CZ	5.82	1.40	1.33
1	6-A	71	GLU	N-CA	-5.82	1.34	1.46
3	7-C	176	ARG	CZ-NH2	5.82	1.40	1.33
1	3-A	273	ASN	CB-CG	5.82	1.64	1.51
2	4-B	415	TYR	CZ-OH	5.82	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	6-B	565	TYR	CE2-CZ	5.82	1.46	1.38
3	9-D	266	HIS	CB-CG	-5.82	1.39	1.50
1	9-A	558	TYR	CD1-CE1	5.81	1.48	1.39
1	10-A	144	ARG	CZ-NH2	5.81	1.40	1.33
2	6-B	424	GLU	CG-CD	5.81	1.60	1.51
2	2-B	725	GLU	CG-CD	5.81	1.60	1.51
2	3-B	592	ARG	CD-NE	5.81	1.56	1.46
1	2-A	587	ARG	CZ-NH1	5.81	1.40	1.33
3	2-D	368	ASN	N-CA	-5.81	1.34	1.46
2	10-B	453	TYR	CB-CG	5.81	1.60	1.51
1	2-A	655	GLU	CD-OE1	5.81	1.32	1.25
3	3-C	136	PHE	CB-CG	-5.81	1.41	1.51
1	4-A	111	ARG	CZ-NH1	5.81	1.40	1.33
3	4-C	403	PHE	CG-CD2	5.81	1.47	1.38
1	7-A	204	ARG	CZ-NH2	5.81	1.40	1.33
2	10-B	413	GLU	CB-CG	5.80	1.63	1.52
2	10-B	343	TYR	CE1-CZ	5.80	1.46	1.38
3	6-C	185	TYR	CG-CD2	5.80	1.46	1.39
3	1-C	196	GLU	CD-OE2	5.80	1.32	1.25
3	10-D	43	SER	CB-OG	5.80	1.49	1.42
2	2-B	839	PHE	CG-CD1	5.80	1.47	1.38
3	7-D	107	ASN	C-N	5.80	1.43	1.33
2	2-B	258	SER	CA-CB	5.80	1.61	1.52
2	10-B	418	GLU	CG-CD	5.80	1.60	1.51
3	6-C	1	MET	C-N	5.79	1.43	1.33
2	7-B	360	GLY	N-CA	-5.79	1.37	1.46
1	10-A	162	PHE	CG-CD2	5.79	1.47	1.38
1	10-A	393	TYR	CD1-CE1	5.79	1.48	1.39
3	4-C	275	PHE	CB-CG	-5.79	1.41	1.51
1	2-A	687	ARG	CZ-NH2	5.79	1.40	1.33
1	10-A	358	ARG	NE-CZ	5.79	1.40	1.33
2	2-B	486	SER	CA-CB	5.79	1.61	1.52
1	5-A	400	ARG	CD-NE	5.78	1.56	1.46
2	5-B	356	ARG	CZ-NH1	5.78	1.40	1.33
2	6-B	260	GLU	CB-CG	5.78	1.63	1.52
2	6-B	293	ARG	CD-NE	5.78	1.56	1.46
3	9-D	71	SER	CB-OG	5.78	1.49	1.42
1	1-A	131	PHE	CG-CD1	5.78	1.47	1.38
1	3-A	587	ARG	CZ-NH1	5.78	1.40	1.33
3	4-D	204	PHE	CE2-CZ	5.78	1.48	1.37
3	10-D	304	SER	N-CA	-5.78	1.34	1.46
3	2-C	184	SER	CA-CB	5.78	1.61	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	6-A	794	TYR	CG-CD2	5.78	1.46	1.39
2	6-B	328	ARG	CD-NE	5.78	1.56	1.46
2	8-B	425	PHE	CG-CD2	5.78	1.47	1.38
3	2-C	333	ARG	CD-NE	5.77	1.56	1.46
3	4-D	136	PHE	CG-CD1	5.77	1.47	1.38
3	10-D	362	TYR	CZ-OH	5.77	1.47	1.37
2	3-B	562	TYR	CG-CD2	5.77	1.46	1.39
2	4-B	578	PHE	CG-CD1	5.77	1.47	1.38
1	2-A	588	TYR	CB-CG	-5.76	1.43	1.51
1	3-A	337	SER	CA-CB	5.76	1.61	1.52
3	10-D	34	ASP	CB-CG	5.76	1.63	1.51
2	5-B	306	GLU	CG-CD	5.76	1.60	1.51
2	2-B	411	PHE	CB-CG	5.76	1.61	1.51
2	8-B	231	TYR	CZ-OH	5.76	1.47	1.37
3	1-C	437	TYR	CG-CD1	5.76	1.46	1.39
2	7-B	328	ARG	CZ-NH2	5.75	1.40	1.33
3	7-C	353	HIS	CB-CG	-5.75	1.39	1.50
1	3-A	143	ARG	NE-CZ	5.75	1.40	1.33
2	9-B	802	LEU	C-N	5.75	1.43	1.33
2	10-B	242	ARG	CZ-NH1	5.75	1.40	1.33
1	4-A	320	TRP	CZ2-CH2	5.75	1.48	1.37
1	7-A	627	ARG	CZ-NH2	5.75	1.40	1.33
3	6-D	45	GLU	CB-CG	5.75	1.63	1.52
3	5-C	59	ARG	CZ-NH2	5.75	1.40	1.33
1	9-A	400	ARG	CZ-NH1	5.75	1.40	1.33
2	5-B	562	TYR	CZ-OH	5.75	1.47	1.37
3	5-C	415	SER	CA-CB	-5.75	1.44	1.52
2	6-B	345	TYR	CZ-OH	5.74	1.47	1.37
2	8-B	503	PRO	N-CD	-5.74	1.39	1.47
3	2-C	161	ARG	CD-NE	5.74	1.56	1.46
3	8-C	261	PRO	CA-C	-5.74	1.41	1.52
3	9-D	109	TYR	CG-CD2	5.74	1.46	1.39
1	6-A	333	ARG	CZ-NH1	5.74	1.40	1.33
2	1-B	216	PHE	CG-CD1	5.73	1.47	1.38
3	8-D	193	ARG	CZ-NH1	5.73	1.40	1.33
3	3-C	84	ARG	NE-CZ	5.73	1.40	1.33
2	3-B	589	PHE	C-N	5.73	1.47	1.34
2	4-B	453	TYR	CE1-CZ	5.73	1.46	1.38
1	1-A	429	TYR	CG-CD2	5.72	1.46	1.39
1	2-A	771	ALA	CA-CB	5.72	1.64	1.52
1	8-A	776	ARG	CD-NE	5.72	1.56	1.46
1	4-A	337	SER	CA-CB	-5.72	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	7-A	658	SER	CA-C	-5.72	1.38	1.52
2	8-B	837	GLU	CG-CD	5.72	1.60	1.51
1	2-A	775	PHE	CA-CB	5.71	1.66	1.53
3	5-D	329	ARG	NE-CZ	5.71	1.40	1.33
2	6-B	661	PHE	CG-CD2	5.71	1.47	1.38
1	8-A	262	ARG	CZ-NH2	5.71	1.40	1.33
2	2-B	299	ARG	CZ-NH1	5.71	1.40	1.33
3	4-C	176	ARG	CZ-NH2	5.71	1.40	1.33
1	1-A	474	PRO	N-CA	-5.71	1.37	1.47
1	2-A	664	ARG	CZ-NH1	5.71	1.40	1.33
1	5-A	794	TYR	CG-CD1	5.71	1.46	1.39
3	7-C	192	ARG	CD-NE	5.71	1.56	1.46
1	5-A	138	PHE	CG-CD2	5.70	1.47	1.38
1	6-A	193	TYR	CE1-CZ	5.70	1.46	1.38
2	10-B	510	TYR	CG-CD2	5.70	1.46	1.39
2	7-B	438	TYR	CG-CD2	5.70	1.46	1.39
3	9-D	292	TYR	CE2-CZ	5.70	1.46	1.38
2	3-B	293	ARG	NE-CZ	5.70	1.40	1.33
3	5-D	354	VAL	CB-CG2	5.70	1.64	1.52
3	6-D	333	ARG	CZ-NH2	5.70	1.40	1.33
2	7-B	197	SER	CA-CB	5.70	1.61	1.52
1	8-A	558	TYR	CZ-OH	5.70	1.47	1.37
2	7-B	295	ARG	CZ-NH2	5.70	1.40	1.33
1	3-A	568	TYR	CG-CD1	5.69	1.46	1.39
2	9-B	758	TYR	CZ-OH	5.69	1.47	1.37
2	4-B	265	THR	C-N	5.69	1.47	1.34
1	6-A	479	ARG	CD-NE	5.69	1.56	1.46
1	8-A	107	ARG	CZ-NH2	5.69	1.40	1.33
1	2-A	267	PHE	CG-CD1	5.69	1.47	1.38
3	2-D	333	ARG	NE-CZ	5.69	1.40	1.33
3	3-C	247	TYR	CZ-OH	5.69	1.47	1.37
3	8-C	12	GLN	CG-CD	5.69	1.64	1.51
2	3-B	379	TYR	CB-CG	5.68	1.60	1.51
1	9-A	704	TYR	CG-CD1	5.68	1.46	1.39
2	10-B	814	SER	CA-CB	5.68	1.61	1.52
1	2-A	624	ARG	CZ-NH1	5.68	1.40	1.33
3	7-C	403	PHE	CG-CD2	5.68	1.47	1.38
3	10-D	151	GLY	CA-C	-5.68	1.42	1.51
3	2-C	46	ARG	CD-NE	5.68	1.56	1.46
3	4-C	215	LYS	N-CA	-5.68	1.34	1.46
3	8-C	329	ARG	CZ-NH1	5.68	1.40	1.33
1	3-A	587	ARG	CZ-NH2	5.67	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	9-A	302	TYR	CE1-CZ	5.67	1.46	1.38
1	10-A	121	ARG	CD-NE	5.67	1.56	1.46
3	2-D	350	SER	CA-CB	5.67	1.61	1.52
3	6-D	126	GLU	CD-OE1	5.67	1.31	1.25
3	3-C	249	TYR	CG-CD1	5.67	1.46	1.39
3	3-D	427	ARG	CA-CB	5.67	1.66	1.53
1	10-A	157	ARG	CZ-NH2	5.67	1.40	1.33
3	5-D	170	TYR	CB-CG	5.67	1.60	1.51
1	1-A	410	PHE	CA-CB	5.67	1.66	1.53
2	8-B	533	ARG	NE-CZ	5.66	1.40	1.33
3	8-C	315	TYR	CG-CD2	5.66	1.46	1.39
1	8-A	665	ASN	CB-CG	5.66	1.64	1.51
1	9-A	143	ARG	CD-NE	5.66	1.56	1.46
2	1-B	565	TYR	CG-CD1	5.66	1.46	1.39
1	3-A	612	TRP	CG-CD1	5.66	1.44	1.36
3	3-C	24	GLN	CG-CD	5.66	1.64	1.51
2	6-B	598	TYR	CB-CG	5.66	1.60	1.51
3	7-C	445	TYR	CZ-OH	5.66	1.47	1.37
1	8-A	451	ARG	NE-CZ	5.66	1.40	1.33
3	8-D	277	SER	CA-CB	5.66	1.61	1.52
3	9-C	20	PHE	CG-CD1	5.66	1.47	1.38
1	10-A	296	TYR	CG-CD2	5.66	1.46	1.39
1	2-A	124	GLU	CB-CG	5.66	1.62	1.52
1	4-A	594	TYR	CE2-CZ	5.65	1.46	1.38
2	5-B	288	TYR	CG-CD2	5.65	1.46	1.39
3	3-D	173	PHE	CG-CD1	5.65	1.47	1.38
1	7-A	687	ARG	NE-CZ	5.65	1.40	1.33
2	8-B	288	TYR	CE2-CZ	5.65	1.45	1.38
1	2-A	320	TRP	CB-CG	5.65	1.60	1.50
3	2-D	271	SER	CA-CB	5.65	1.61	1.52
2	1-B	666	ARG	NE-CZ	5.65	1.40	1.33
2	2-B	652	TYR	CE1-CZ	5.64	1.45	1.38
1	4-A	121	ARG	NE-CZ	5.64	1.40	1.33
1	2-A	398	TYR	CG-CD2	5.64	1.46	1.39
1	1-A	458	TYR	CB-CG	5.64	1.60	1.51
1	4-A	66	VAL	CB-CG1	5.64	1.64	1.52
2	1-B	421	TRP	CE3-CZ3	5.64	1.48	1.38
2	6-B	322	HIS	CB-CG	-5.64	1.40	1.50
2	1-B	302	GLU	CD-OE2	5.63	1.31	1.25
1	3-A	468	GLU	CD-OE1	5.63	1.31	1.25
1	5-A	74	TYR	CG-CD2	5.63	1.46	1.39
1	7-A	348	LEU	CA-C	-5.63	1.38	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	10-D	292	TYR	CG-CD2	5.63	1.46	1.39
1	2-A	327	ARG	CZ-NH2	5.63	1.40	1.33
2	5-B	520	VAL	CA-CB	-5.63	1.43	1.54
2	9-B	514	ARG	NE-CZ	5.63	1.40	1.33
2	2-B	533	ARG	CZ-NH1	5.63	1.40	1.33
1	3-A	157	ARG	NE-CZ	5.63	1.40	1.33
1	8-A	276	SER	CB-OG	5.63	1.49	1.42
3	9-D	218	ARG	CZ-NH1	5.63	1.40	1.33
2	10-B	663	GLU	CD-OE2	5.63	1.31	1.25
2	6-B	433	TYR	CZ-OH	5.62	1.47	1.37
3	9-C	155	LEU	N-CA	-5.62	1.35	1.46
1	7-A	794	TYR	CZ-OH	5.62	1.47	1.37
3	9-C	161	ARG	CZ-NH1	5.62	1.40	1.33
1	10-A	714	ARG	NE-CZ	5.62	1.40	1.33
3	10-C	329	ARG	CZ-NH1	5.62	1.40	1.33
1	5-A	203	ARG	CZ-NH1	5.62	1.40	1.33
1	6-A	179	GLU	CG-CD	5.62	1.60	1.51
2	10-B	270	ASN	CA-C	-5.62	1.38	1.52
3	2-C	407	TYR	CE2-CZ	5.61	1.45	1.38
3	6-C	218	ARG	CD-NE	5.61	1.55	1.46
3	6-C	4	GLU	CD-OE1	5.61	1.31	1.25
3	9-D	313	PRO	N-CD	-5.61	1.40	1.47
3	10-D	435	GLU	CB-CG	5.61	1.62	1.52
3	2-C	307	SER	CA-CB	5.61	1.61	1.52
1	5-A	381	PHE	CG-CD1	5.61	1.47	1.38
1	10-A	597	ARG	CZ-NH2	5.61	1.40	1.33
2	7-B	666	ARG	CD-NE	5.61	1.55	1.46
3	4-D	114	ARG	CZ-NH2	5.60	1.40	1.33
1	7-A	576	ARG	CZ-NH1	5.60	1.40	1.33
2	10-B	571	VAL	N-CA	-5.60	1.35	1.46
1	2-A	107	ARG	NE-CZ	5.60	1.40	1.33
1	10-A	284	TYR	CZ-OH	5.60	1.47	1.37
1	5-A	794	TYR	CE2-CZ	5.60	1.45	1.38
2	6-B	363	PHE	CB-CG	5.59	1.60	1.51
2	2-B	260	GLU	CD-OE1	5.59	1.31	1.25
1	5-A	700	PHE	CG-CD1	5.59	1.47	1.38
1	6-A	143	ARG	NE-CZ	5.59	1.40	1.33
3	6-C	147	GLY	CA-C	-5.59	1.43	1.51
3	6-D	134	GLU	CG-CD	5.59	1.60	1.51
1	8-A	262	ARG	NE-CZ	5.59	1.40	1.33
3	5-D	216	VAL	CA-C	-5.59	1.38	1.52
3	6-C	162	TYR	CE2-CZ	5.59	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	7-A	624	ARG	CZ-NH1	5.59	1.40	1.33
3	8-C	14	GLY	N-CA	5.59	1.54	1.46
3	10-D	204	PHE	CG-CD2	5.58	1.47	1.38
3	3-D	114	ARG	NE-CZ	5.58	1.40	1.33
1	6-A	197	PHE	CG-CD1	5.58	1.47	1.38
1	4-A	603	TRP	CB-CG	5.58	1.60	1.50
2	5-B	633	ARG	NE-CZ	5.58	1.40	1.33
3	3-C	403	PHE	CG-CD1	5.58	1.47	1.38
3	7-C	53	PHE	CG-CD1	5.58	1.47	1.38
3	8-D	45	GLU	CB-CG	5.58	1.62	1.52
2	9-B	284	TYR	CG-CD1	5.58	1.46	1.39
3	2-C	214	GLY	CA-C	-5.58	1.43	1.51
1	6-A	78	PHE	CG-CD2	5.58	1.47	1.38
2	1-B	658	GLU	CD-OE1	5.57	1.31	1.25
2	6-B	288	TYR	CG-CD2	5.57	1.46	1.39
2	7-B	236	TYR	CE1-CZ	5.57	1.45	1.38
3	8-D	445	TYR	CG-CD2	5.57	1.46	1.39
3	1-D	329	ARG	CZ-NH2	5.57	1.40	1.33
1	7-A	759	GLU	CD-OE2	5.57	1.31	1.25
2	3-B	359	TYR	CG-CD2	5.57	1.46	1.39
3	4-C	264	GLU	CG-CD	5.57	1.60	1.51
2	8-B	231	TYR	CB-CG	-5.57	1.43	1.51
1	1-A	358	ARG	CD-NE	5.57	1.55	1.46
3	9-C	65	ARG	NE-CZ	5.57	1.40	1.33
2	9-B	247	SER	CA-CB	5.56	1.61	1.52
3	3-C	45	GLU	N-CA	-5.56	1.35	1.46
3	4-C	341	ARG	CZ-NH2	5.56	1.40	1.33
1	5-A	262	ARG	CZ-NH2	5.56	1.40	1.33
3	5-D	251	SER	CA-CB	5.56	1.61	1.52
1	6-A	74	TYR	CD1-CE1	5.56	1.47	1.39
1	9-A	398	TYR	CE2-CZ	5.56	1.45	1.38
3	6-C	90	ARG	CD-NE	5.56	1.55	1.46
2	8-B	417	LYS	N-CA	-5.56	1.35	1.46
2	2-B	824	TYR	CE1-CZ	5.56	1.45	1.38
3	2-D	279	TYR	CG-CD2	5.56	1.46	1.39
3	8-D	65	ARG	CD-NE	5.56	1.55	1.46
1	9-A	776	ARG	CZ-NH2	5.56	1.40	1.33
3	9-D	316	PHE	CG-CD2	5.56	1.47	1.38
3	6-D	353	HIS	CA-CB	5.56	1.66	1.53
3	8-D	46	ARG	NE-CZ	5.55	1.40	1.33
3	1-C	425	GLU	CG-CD	5.55	1.60	1.51
3	4-D	23	SER	CA-CB	5.55	1.61	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	5-D	59	ARG	CD-NE	5.55	1.55	1.46
1	3-A	171	ARG	CZ-NH2	5.55	1.40	1.33
2	10-B	389	ARG	NE-CZ	5.55	1.40	1.33
3	3-D	358	ARG	NE-CZ	5.55	1.40	1.33
1	6-A	144	ARG	CZ-NH2	5.55	1.40	1.33
2	7-B	633	ARG	CZ-NH1	5.55	1.40	1.33
1	3-A	108	ARG	CZ-NH2	5.54	1.40	1.33
1	3-A	691	ASP	CA-CB	5.54	1.66	1.53
3	3-D	316	PHE	CG-CD1	5.54	1.47	1.38
1	8-A	630	ARG	CD-NE	5.54	1.55	1.46
2	2-B	379	TYR	CE1-CZ	5.54	1.45	1.38
2	4-B	602	LYS	CA-C	-5.54	1.38	1.52
1	6-A	105	PHE	CG-CD1	5.54	1.47	1.38
2	6-B	299	ARG	CZ-NH1	5.54	1.40	1.33
3	2-C	256	TYR	CD1-CE1	5.54	1.47	1.39
3	3-D	114	ARG	CZ-NH2	5.54	1.40	1.33
3	1-D	105	TRP	CG-CD1	5.54	1.44	1.36
1	6-A	582	TYR	CD2-CE2	5.54	1.47	1.39
1	7-A	400	ARG	CD-NE	5.54	1.55	1.46
3	2-C	87	PHE	CA-CB	5.54	1.66	1.53
3	7-C	316	PHE	CG-CD1	5.54	1.47	1.38
1	1-A	265	VAL	CA-CB	-5.53	1.43	1.54
1	6-A	132	GLY	N-CA	-5.53	1.37	1.46
1	3-A	781	ASN	CA-CB	5.53	1.67	1.53
1	6-A	77	TYR	CG-CD2	5.53	1.46	1.39
3	5-D	253	SER	CB-OG	5.53	1.49	1.42
2	2-B	418	GLU	CG-CD	5.53	1.60	1.51
2	2-B	490	ASP	CA-CB	5.53	1.66	1.53
2	7-B	844	SER	CA-CB	5.53	1.61	1.52
1	2-A	794	TYR	CE1-CZ	5.52	1.45	1.38
2	1-B	440	GLY	CA-C	-5.52	1.43	1.51
3	1-D	22	TRP	CD2-CE3	5.52	1.48	1.40
3	2-C	59	ARG	NE-CZ	5.52	1.40	1.33
3	2-C	84	ARG	CZ-NH1	5.52	1.40	1.33
1	6-A	203	ARG	NE-CZ	5.52	1.40	1.33
1	8-A	614	TYR	CE2-CZ	5.52	1.45	1.38
2	8-B	582	GLU	CD-OE2	5.52	1.31	1.25
1	7-A	794	TYR	CD1-CE1	5.52	1.47	1.39
2	2-B	393	PHE	CB-CG	5.52	1.60	1.51
1	10-A	140	TYR	CB-CG	-5.52	1.43	1.51
2	7-B	598	TYR	CG-CD1	5.52	1.46	1.39
3	1-D	204	PHE	CG-CD1	5.52	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2-A	663	TYR	CE2-CZ	5.51	1.45	1.38
2	2-B	285	ARG	NE-CZ	5.51	1.40	1.33
1	3-A	286	TRP	CZ2-CH2	5.51	1.47	1.37
1	8-A	286	TRP	CB-CG	5.51	1.60	1.50
2	8-B	719	LEU	N-CA	5.51	1.57	1.46
1	3-A	203	ARG	NE-CZ	5.51	1.40	1.33
3	6-C	341	ARG	CZ-NH1	5.51	1.40	1.33
3	7-C	413	PHE	CE1-CZ	5.51	1.47	1.37
3	1-D	277	SER	CB-OG	5.51	1.49	1.42
2	5-B	592	ARG	CZ-NH2	5.51	1.40	1.33
3	5-D	445	TYR	CE2-CZ	5.51	1.45	1.38
3	6-C	302	SER	CA-CB	5.51	1.61	1.52
1	8-A	575	SER	CA-CB	5.51	1.61	1.52
3	9-D	65	ARG	CD-NE	5.51	1.55	1.46
2	5-B	446	PHE	CG-CD2	5.51	1.47	1.38
3	2-C	46	ARG	CZ-NH2	5.50	1.40	1.33
1	3-A	190	TYR	CE2-CZ	5.50	1.45	1.38
2	3-B	243	MET	CA-CB	5.50	1.66	1.53
3	5-D	65	ARG	NE-CZ	5.50	1.40	1.33
3	10-D	193	ARG	CZ-NH2	5.50	1.40	1.33
3	10-C	162	TYR	CE1-CZ	5.50	1.45	1.38
1	2-A	160	ARG	CD-NE	5.50	1.55	1.46
2	6-B	284	TYR	CE1-CZ	5.50	1.45	1.38
1	8-A	587	ARG	CZ-NH1	5.50	1.40	1.33
3	6-C	290	SER	CA-CB	5.49	1.61	1.52
3	6-C	427	ARG	CD-NE	5.49	1.55	1.46
1	9-A	276	SER	CA-CB	5.49	1.61	1.52
2	9-B	565	TYR	CG-CD2	5.49	1.46	1.39
3	10-C	324	GLY	CA-C	-5.49	1.43	1.51
3	10-D	329	ARG	NE-CZ	5.49	1.40	1.33
2	7-B	438	TYR	CZ-OH	5.49	1.47	1.37
1	4-A	263	SER	CA-CB	5.49	1.61	1.52
2	4-B	308	SER	CB-OG	-5.49	1.35	1.42
1	8-A	77	TYR	CG-CD1	5.49	1.46	1.39
3	9-D	3	GLY	CA-C	-5.49	1.43	1.51
3	9-D	236	SER	CA-CB	5.49	1.61	1.52
1	4-A	74	TYR	CG-CD1	5.49	1.46	1.39
1	4-A	107	ARG	CZ-NH2	5.49	1.40	1.33
1	7-A	444	GLY	N-CA	5.49	1.54	1.46
1	2-A	349	ARG	CD-NE	5.49	1.55	1.46
3	1-D	185	TYR	CE1-CZ	5.49	1.45	1.38
2	4-B	446	PHE	CG-CD1	5.48	1.47	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2-A	377	GLU	CD-OE2	5.48	1.31	1.25
3	8-D	178	SER	CA-CB	5.48	1.61	1.52
3	9-D	87	PHE	CG-CD1	5.48	1.47	1.38
3	10-C	65	ARG	CD-NE	5.48	1.55	1.46
1	4-A	203	ARG	CZ-NH2	5.48	1.40	1.33
3	3-C	56	GLU	CD-OE2	-5.47	1.19	1.25
3	4-C	319	TYR	CB-CG	-5.47	1.43	1.51
1	5-A	137	ARG	CZ-NH1	5.47	1.40	1.33
1	10-A	559	HIS	CB-CG	5.47	1.59	1.50
1	10-A	582	TYR	CZ-OH	5.47	1.47	1.37
3	1-D	171	SER	CA-CB	5.47	1.61	1.52
1	1-A	171	ARG	CZ-NH1	5.47	1.40	1.33
1	5-A	162	PHE	CG-CD2	5.47	1.47	1.38
2	3-B	612	ARG	CD-NE	5.47	1.55	1.46
3	3-C	108	GLY	CA-C	-5.47	1.43	1.51
3	5-C	427	ARG	CZ-NH1	5.47	1.40	1.33
1	7-A	76	ARG	CD-NE	5.47	1.55	1.46
2	5-B	523	SER	CB-OG	-5.47	1.35	1.42
2	6-B	471	ARG	NE-CZ	5.47	1.40	1.33
1	4-A	324	TYR	CZ-OH	5.46	1.47	1.37
2	7-B	768	SER	CA-CB	5.46	1.61	1.52
1	8-A	143	ARG	CZ-NH1	5.46	1.40	1.33
1	10-A	465	PHE	CG-CD1	5.46	1.47	1.38
2	10-B	397	GLU	CG-CD	5.46	1.60	1.51
2	5-B	532	PRO	N-CD	-5.46	1.40	1.47
3	7-C	162	TYR	CG-CD2	5.46	1.46	1.39
1	4-A	754	GLU	N-CA	5.46	1.57	1.46
2	6-B	827	ARG	CZ-NH2	5.46	1.40	1.33
1	2-A	588	TYR	CE1-CZ	5.45	1.45	1.38
3	4-D	208	SER	CA-CB	5.45	1.61	1.52
3	10-D	146	THR	C-N	5.45	1.42	1.33
1	2-A	639	PHE	CG-CD1	5.45	1.47	1.38
1	2-A	198	ARG	CZ-NH2	5.45	1.40	1.33
2	8-B	554	GLY	CA-C	-5.45	1.43	1.51
3	8-C	324	GLY	CA-C	-5.45	1.43	1.51
2	8-B	580	ARG	CZ-NH2	5.45	1.40	1.33
1	4-A	657	TYR	CG-CD2	5.45	1.46	1.39
1	4-A	776	ARG	CZ-NH2	5.44	1.40	1.33
3	6-D	364	PRO	CA-CB	-5.44	1.42	1.53
2	10-B	644	PHE	CG-CD1	5.44	1.47	1.38
2	4-B	531	SER	CA-CB	5.44	1.61	1.52
3	5-D	218	ARG	CZ-NH1	5.44	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	6-A	438	PHE	CG-CD2	5.44	1.47	1.38
3	9-D	302	SER	CA-CB	5.44	1.61	1.52
2	1-B	776	TYR	CE1-CZ	5.44	1.45	1.38
3	3-C	140	HIS	CB-CG	5.44	1.59	1.50
1	8-A	286	TRP	CG-CD1	5.44	1.44	1.36
1	1-A	410	PHE	CE2-CZ	5.44	1.47	1.37
2	2-B	514	ARG	CZ-NH1	5.43	1.40	1.33
1	3-A	645	GLU	CD-OE1	5.43	1.31	1.25
2	4-B	180	PRO	CA-C	-5.43	1.42	1.52
1	5-A	405	PHE	CG-CD1	5.43	1.47	1.38
2	5-B	778	ASN	CB-CG	5.43	1.63	1.51
2	7-B	816	TYR	CE1-CZ	5.43	1.45	1.38
3	10-C	398	PHE	CG-CD1	5.43	1.47	1.38
1	5-A	123	TYR	CB-CG	-5.43	1.43	1.51
3	5-C	413	PHE	CG-CD1	5.43	1.46	1.38
3	6-D	20	PHE	CG-CD2	5.43	1.46	1.38
2	9-B	359	TYR	C-N	5.43	1.42	1.33
3	1-D	361	PRO	N-CA	-5.43	1.38	1.47
1	3-A	413	TYR	CG-CD2	5.43	1.46	1.39
3	6-C	192	ARG	CZ-NH1	5.43	1.40	1.33
1	5-A	614	TYR	CE1-CZ	5.43	1.45	1.38
2	7-B	761	SER	CA-CB	5.42	1.61	1.52
2	8-B	323	GLY	CA-C	-5.42	1.43	1.51
2	9-B	297	TYR	CG-CD1	5.42	1.46	1.39
3	10-D	262	SER	CA-CB	5.42	1.61	1.52
1	2-A	782	PHE	CG-CD1	5.42	1.46	1.38
3	9-C	341	ARG	NE-CZ	5.42	1.40	1.33
2	2-B	510	TYR	CA-CB	5.42	1.65	1.53
3	8-C	59	ARG	CD-NE	5.42	1.55	1.46
1	2-A	201	GLU	CA-CB	5.42	1.65	1.53
2	4-B	651	TYR	CB-CG	-5.42	1.43	1.51
2	8-B	585	ARG	CD-NE	5.42	1.55	1.46
3	2-C	99	ALA	N-CA	-5.41	1.35	1.46
3	4-D	45	GLU	CD-OE1	5.41	1.31	1.25
1	6-A	714	ARG	CZ-NH2	5.41	1.40	1.33
2	2-B	816	TYR	CG-CD1	5.41	1.46	1.39
2	4-B	366	GLU	CB-CG	5.41	1.62	1.52
2	10-B	544	ARG	CD-NE	5.41	1.55	1.46
3	10-D	261	PRO	N-CD	-5.41	1.40	1.47
2	1-B	253	LEU	CA-CB	5.41	1.66	1.53
1	4-A	190	TYR	CZ-OH	5.41	1.47	1.37
1	10-A	568	TYR	CD2-CE2	5.41	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1-A	558	TYR	CG-CD1	5.41	1.46	1.39
3	5-C	275	PHE	CE1-CZ	5.41	1.47	1.37
2	7-B	592	ARG	CZ-NH1	5.41	1.40	1.33
3	9-C	359	ARG	NE-CZ	5.41	1.40	1.33
2	3-B	824	TYR	CG-CD1	5.40	1.46	1.39
2	5-B	190	TYR	CE1-CZ	5.40	1.45	1.38
1	7-A	712	SER	CA-CB	5.40	1.61	1.52
3	9-C	378	SER	CA-CB	5.40	1.61	1.52
1	3-A	658	SER	CA-CB	5.40	1.61	1.52
3	5-D	136	PHE	CG-CD1	5.40	1.46	1.38
1	8-A	794	TYR	CE2-CZ	5.40	1.45	1.38
2	8-B	293	ARG	CZ-NH2	5.40	1.40	1.33
3	9-D	4	GLU	CD-OE1	-5.40	1.19	1.25
3	3-D	326	VAL	N-CA	-5.40	1.35	1.46
3	5-C	22	TRP	CZ3-CH2	5.40	1.48	1.40
3	6-D	428	GLU	CB-CG	5.40	1.62	1.52
3	8-D	55	ARG	NE-CZ	5.40	1.40	1.33
2	2-B	776	TYR	CD1-CE1	5.40	1.47	1.39
3	6-C	358	ARG	CD-NE	5.40	1.55	1.46
2	7-B	638	ARG	NE-CZ	5.40	1.40	1.33
3	8-C	279	TYR	CG-CD1	5.40	1.46	1.39
3	8-D	80	GLU	CB-CG	5.40	1.62	1.52
2	4-B	425	PHE	CB-CG	5.39	1.60	1.51
1	5-A	140	TYR	CG-CD1	5.39	1.46	1.39
2	1-B	823	LEU	CB-CG	5.39	1.68	1.52
1	9-A	144	ARG	CZ-NH1	5.39	1.40	1.33
1	10-A	458	TYR	CZ-OH	5.39	1.47	1.37
3	1-C	247	TYR	CE2-CZ	5.39	1.45	1.38
2	2-B	216	PHE	CB-CG	5.39	1.60	1.51
2	2-B	356	ARG	NE-CZ	5.39	1.40	1.33
3	10-D	59	ARG	CZ-NH2	5.39	1.40	1.33
1	1-A	714	ARG	CD-NE	5.39	1.55	1.46
2	1-B	557	VAL	CB-CG1	5.39	1.64	1.52
3	7-C	148	SER	C-N	5.38	1.42	1.33
2	1-B	297	TYR	CE2-CZ	5.38	1.45	1.38
2	5-B	770	TYR	CG-CD2	5.38	1.46	1.39
1	7-A	687	ARG	CD-NE	5.38	1.55	1.46
3	3-C	18	GLY	CA-C	-5.38	1.43	1.51
3	6-C	80	GLU	CB-CG	5.38	1.62	1.52
2	10-B	342	TYR	CE1-CZ	5.38	1.45	1.38
2	10-B	415	TYR	CD1-CE1	5.38	1.47	1.39
1	5-A	687	ARG	CZ-NH1	5.38	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5-B	389	ARG	CZ-NH2	5.38	1.40	1.33
3	2-C	192	ARG	NE-CZ	5.38	1.40	1.33
3	10-C	348	SER	N-CA	-5.38	1.35	1.46
3	2-D	90	ARG	NE-CZ	5.37	1.40	1.33
1	4-A	295	PRO	CA-C	-5.37	1.42	1.52
3	7-C	216	VAL	CB-CG1	5.37	1.64	1.52
3	3-D	108	GLY	CA-C	-5.37	1.43	1.51
2	4-B	424	GLU	CD-OE1	5.37	1.31	1.25
1	1-A	262	ARG	CD-NE	5.36	1.55	1.46
3	5-C	177	SER	CA-CB	5.36	1.60	1.52
1	7-A	181	GLU	CB-CG	5.36	1.62	1.52
2	7-B	651	TYR	CZ-OH	5.36	1.47	1.37
2	9-B	526	ARG	CD-NE	5.36	1.55	1.46
1	10-A	345	PHE	CG-CD1	5.36	1.46	1.38
2	1-B	569	SER	CA-CB	5.36	1.60	1.52
3	4-C	407	TYR	CZ-OH	5.36	1.47	1.37
1	6-A	116	TYR	CZ-OH	5.36	1.47	1.37
3	6-C	37	SER	CA-CB	5.36	1.60	1.52
3	4-D	185	TYR	CE1-CZ	5.36	1.45	1.38
3	5-D	86	PHE	CE1-CZ	5.36	1.47	1.37
2	6-B	580	ARG	CD-NE	5.36	1.55	1.46
2	10-B	379	TYR	CD1-CE1	5.36	1.47	1.39
1	5-A	121	ARG	CZ-NH1	5.36	1.40	1.33
1	8-A	451	ARG	CD-NE	5.36	1.55	1.46
3	8-D	59	ARG	NE-CZ	5.36	1.40	1.33
1	10-A	646	TYR	CG-CD1	5.36	1.46	1.39
2	3-B	509	ASN	N-CA	-5.36	1.35	1.46
2	4-B	446	PHE	CB-CG	5.35	1.60	1.51
2	2-B	633	ARG	CD-NE	5.35	1.55	1.46
3	3-C	333	ARG	CZ-NH2	5.35	1.40	1.33
3	6-D	83	PHE	CG-CD1	5.35	1.46	1.38
3	7-C	105	TRP	NE1-CE2	5.35	1.44	1.37
3	3-D	162	TYR	CG-CD2	5.35	1.46	1.39
2	9-B	180	PRO	N-CD	5.35	1.55	1.47
3	9-D	35	GLY	CA-C	-5.35	1.43	1.51
1	2-A	630	ARG	CZ-NH2	5.34	1.40	1.33
2	2-B	737	SER	CA-CB	5.34	1.60	1.52
2	4-B	550	HIS	C-N	5.34	1.42	1.33
1	9-A	787	SER	CA-CB	5.34	1.60	1.52
1	9-A	327	ARG	CA-C	-5.34	1.39	1.52
2	9-B	433	TYR	CB-CG	-5.34	1.43	1.51
1	1-A	74	TYR	CZ-OH	5.34	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1-A	157	ARG	CD-NE	5.34	1.55	1.46
2	1-B	217	GLU	CD-OE2	5.34	1.31	1.25
3	6-C	46	ARG	CD-NE	5.34	1.55	1.46
3	10-C	432	SER	CA-CB	5.34	1.60	1.52
2	4-B	488	PHE	CB-CG	-5.34	1.42	1.51
2	5-B	809	LEU	C-N	5.34	1.46	1.34
3	9-C	347	TRP	CB-CG	5.34	1.59	1.50
1	4-A	588	TYR	CZ-OH	5.34	1.47	1.37
3	9-D	236	SER	CB-OG	5.34	1.49	1.42
3	10-D	362	TYR	CE2-CZ	5.34	1.45	1.38
2	6-B	737	SER	CA-CB	5.33	1.60	1.52
3	8-C	135	GLY	N-CA	-5.33	1.38	1.46
1	9-A	111	ARG	NE-CZ	5.33	1.40	1.33
2	1-B	600	TYR	CG-CD1	5.33	1.46	1.39
3	8-D	247	TYR	CE1-CZ	5.33	1.45	1.38
1	9-A	769	SER	CA-CB	-5.33	1.45	1.52
2	7-B	598	TYR	CZ-OH	5.33	1.47	1.37
3	5-C	217	PHE	CG-CD2	5.33	1.46	1.38
2	7-B	846	ARG	CZ-NH1	5.33	1.40	1.33
3	8-D	62	PHE	CB-CG	5.33	1.60	1.51
1	9-A	687	ARG	CD-NE	5.33	1.55	1.46
2	7-B	670	ARG	CZ-NH2	5.33	1.40	1.33
2	2-B	822	ARG	CD-NE	5.33	1.55	1.46
1	3-A	102	PHE	CD1-CE1	5.33	1.50	1.39
3	3-C	91	ASN	CB-CG	5.33	1.63	1.51
3	7-D	243	ARG	CZ-NH2	5.33	1.40	1.33
3	1-C	315	TYR	CG-CD1	5.32	1.46	1.39
1	8-A	776	ARG	NE-CZ	5.32	1.40	1.33
2	9-B	312	PHE	CG-CD1	5.32	1.46	1.38
3	1-C	65	ARG	NE-CZ	5.32	1.40	1.33
3	4-C	163	PRO	CA-C	-5.32	1.42	1.52
1	9-A	479	ARG	CZ-NH2	5.32	1.40	1.33
2	9-B	822	ARG	NE-CZ	5.32	1.40	1.33
3	10-C	359	ARG	CZ-NH2	5.32	1.40	1.33
2	1-B	379	TYR	CZ-OH	5.32	1.46	1.37
3	3-C	445	TYR	CE1-CZ	5.32	1.45	1.38
3	7-C	146	THR	C-N	5.32	1.42	1.33
3	3-D	84	ARG	CZ-NH2	5.32	1.40	1.33
1	5-A	333	ARG	CZ-NH2	5.32	1.40	1.33
2	2-B	585	ARG	CZ-NH1	5.31	1.40	1.33
2	3-B	641	PHE	CG-CD2	5.31	1.46	1.38
2	5-B	470	TYR	CE2-CZ	5.31	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	5-D	341	ARG	NE-CZ	5.31	1.40	1.33
2	9-B	770	TYR	CG-CD1	5.31	1.46	1.39
1	10-A	594	TYR	CB-CG	5.31	1.59	1.51
1	4-A	194	GLU	CB-CG	5.31	1.62	1.52
2	8-B	635	SER	CA-CB	5.31	1.60	1.52
3	2-C	109	TYR	CE2-CZ	5.31	1.45	1.38
3	2-C	176	ARG	CZ-NH2	5.31	1.40	1.33
2	4-B	603	GLU	CD-OE2	5.31	1.31	1.25
3	3-C	388	GLU	CA-CB	5.31	1.65	1.53
2	9-B	236	TYR	CZ-OH	5.31	1.46	1.37
3	9-C	319	TYR	CG-CD2	5.31	1.46	1.39
3	6-D	358	ARG	NE-CZ	5.31	1.40	1.33
2	10-B	569	SER	CA-CB	5.31	1.60	1.52
2	2-B	437	SER	CA-CB	5.30	1.60	1.52
2	3-B	408	SER	CA-CB	5.30	1.60	1.52
2	4-B	741	PHE	CE2-CZ	5.30	1.47	1.37
3	1-C	328	PRO	CA-C	-5.30	1.42	1.52
1	3-A	144	ARG	NE-CZ	5.30	1.40	1.33
3	5-C	369	GLU	CD-OE1	5.30	1.31	1.25
3	9-C	256	TYR	CG-CD1	5.30	1.46	1.39
1	10-A	587	ARG	CD-NE	5.30	1.55	1.46
2	4-B	221	LEU	N-CA	-5.30	1.35	1.46
3	4-C	426	SER	CB-OG	5.30	1.49	1.42
3	4-D	426	SER	CA-CB	5.30	1.60	1.52
1	4-A	262	ARG	CD-NE	5.29	1.55	1.46
1	6-A	630	ARG	CZ-NH2	5.29	1.40	1.33
2	1-B	285	ARG	CZ-NH1	5.29	1.40	1.33
2	4-B	384	GLU	CD-OE1	5.29	1.31	1.25
2	10-B	426	SER	CA-CB	5.29	1.60	1.52
2	6-B	411	PHE	CG-CD1	5.29	1.46	1.38
1	7-A	612	TRP	CE3-CZ3	5.29	1.47	1.38
1	9-A	112	TYR	CZ-OH	5.29	1.46	1.37
1	9-A	327	ARG	NE-CZ	5.29	1.40	1.33
2	2-B	273	SER	CB-OG	5.29	1.49	1.42
3	4-D	56	GLU	CB-CG	5.29	1.62	1.52
2	8-B	299	ARG	NE-CZ	5.29	1.40	1.33
3	9-C	350	SER	CA-CB	5.29	1.60	1.52
1	1-A	646	TYR	CB-CG	5.29	1.59	1.51
1	2-A	687	ARG	CD-NE	5.29	1.55	1.46
2	3-B	725	GLU	CG-CD	5.29	1.59	1.51
3	1-C	359	ARG	CZ-NH2	5.28	1.40	1.33
2	2-B	422	THR	N-CA	-5.28	1.35	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	7-D	161	ARG	CZ-NH2	5.28	1.40	1.33
3	8-D	381	SER	CA-CB	5.28	1.60	1.52
2	10-B	236	TYR	CG-CD2	5.28	1.46	1.39
3	5-D	326	VAL	CB-CG2	5.28	1.64	1.52
3	5-D	149	GLY	CA-C	-5.28	1.43	1.51
1	6-A	324	TYR	CB-CG	-5.28	1.43	1.51
1	8-A	646	TYR	CB-CG	5.28	1.59	1.51
2	6-B	544	ARG	NE-CZ	5.28	1.40	1.33
3	8-D	74	SER	CA-CB	5.28	1.60	1.52
2	9-B	761	SER	CA-CB	5.28	1.60	1.52
1	4-A	687	ARG	CZ-NH2	5.27	1.40	1.33
3	7-C	59	ARG	CD-NE	5.27	1.55	1.46
2	1-B	345	TYR	CB-CG	-5.27	1.43	1.51
3	5-C	290	SER	CA-CB	5.27	1.60	1.52
3	9-C	86	PHE	CG-CD1	-5.27	1.30	1.38
3	2-D	358	ARG	CZ-NH2	5.27	1.40	1.33
2	1-B	488	PHE	CE2-CZ	5.27	1.47	1.37
3	1-C	423	PHE	CG-CD2	5.27	1.46	1.38
1	9-A	186	MET	CG-SD	5.27	1.94	1.81
1	9-A	472	GLU	CB-CG	5.27	1.62	1.52
2	2-B	297	TYR	CE2-CZ	5.27	1.45	1.38
3	2-C	401	GLY	N-CA	-5.27	1.38	1.46
2	5-B	387	GLN	N-CA	-5.27	1.35	1.46
3	6-C	285	ALA	CA-CB	5.27	1.63	1.52
3	8-D	126	GLU	CA-CB	5.27	1.65	1.53
2	4-B	227	ALA	C-N	5.26	1.42	1.33
3	5-C	356	ILE	C-N	5.26	1.42	1.33
1	1-A	576	ARG	NE-CZ	5.26	1.39	1.33
1	3-A	69	GLY	N-CA	-5.26	1.38	1.46
3	7-C	249	TYR	CZ-OH	5.26	1.46	1.37
2	10-B	544	ARG	CZ-NH2	5.26	1.39	1.33
3	2-D	437	TYR	CE2-CZ	5.26	1.45	1.38
3	3-D	218	ARG	NE-CZ	5.26	1.39	1.33
3	8-D	43	SER	N-CA	-5.26	1.35	1.46
2	2-B	231	TYR	CZ-OH	5.26	1.46	1.37
1	3-A	624	ARG	CD-NE	5.26	1.55	1.46
2	3-B	218	SER	CA-CB	5.26	1.60	1.52
1	5-A	661	LYS	CA-CB	5.26	1.65	1.53
3	6-D	218	ARG	CD-NE	5.26	1.55	1.46
2	9-B	638	ARG	NE-CZ	5.26	1.39	1.33
3	9-D	223	ASP	N-CA	-5.26	1.35	1.46
3	10-D	54	PHE	CE2-CZ	5.26	1.47	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3-D	94	VAL	CB-CG2	5.25	1.63	1.52
3	7-D	361	PRO	N-CD	-5.25	1.40	1.47
3	4-D	98	GLY	N-CA	-5.25	1.38	1.46
3	7-C	8	LEU	CA-C	-5.25	1.39	1.52
1	7-A	776	ARG	NE-CZ	5.25	1.39	1.33
2	3-B	457	VAL	CB-CG2	5.25	1.63	1.52
1	5-A	787	SER	CB-OG	5.25	1.49	1.42
3	6-C	359	ARG	CZ-NH2	5.25	1.39	1.33
1	3-A	400	ARG	CZ-NH1	5.25	1.39	1.33
3	7-D	437	TYR	CZ-OH	5.25	1.46	1.37
1	8-A	171	ARG	CZ-NH2	5.25	1.39	1.33
2	10-B	826	PHE	CE1-CZ	5.25	1.47	1.37
2	4-B	599	PHE	CE2-CZ	5.25	1.47	1.37
3	7-C	358	ARG	CZ-NH2	5.25	1.39	1.33
2	1-B	525	LEU	N-CA	-5.24	1.35	1.46
1	4-A	479	ARG	CZ-NH2	5.24	1.39	1.33
1	8-A	624	ARG	NE-CZ	5.24	1.39	1.33
2	10-B	598	TYR	CG-CD1	5.24	1.46	1.39
1	6-A	116	TYR	CG-CD1	5.24	1.46	1.39
3	6-D	361	PRO	CA-C	-5.24	1.42	1.52
3	1-C	173	PHE	CB-CG	-5.23	1.42	1.51
3	6-C	218	ARG	NE-CZ	5.23	1.39	1.33
3	8-C	192	ARG	NE-CZ	5.23	1.39	1.33
1	2-A	445	GLU	CG-CD	5.23	1.59	1.51
1	6-A	131	PHE	CA-CB	5.23	1.65	1.53
2	10-B	587	PHE	CA-CB	5.23	1.65	1.53
2	4-B	612	ARG	NE-CZ	5.23	1.39	1.33
3	8-D	180	VAL	CB-CG2	5.23	1.63	1.52
2	4-B	770	TYR	CE2-CZ	5.23	1.45	1.38
1	7-A	614	TYR	CG-CD2	5.23	1.46	1.39
2	7-B	846	ARG	NE-CZ	5.23	1.39	1.33
3	2-C	181	VAL	CB-CG1	5.22	1.63	1.52
1	10-A	56	GLU	CD-OE1	5.22	1.31	1.25
1	4-A	137	ARG	CZ-NH1	5.22	1.39	1.33
2	5-B	284	TYR	CG-CD1	5.22	1.46	1.39
2	5-B	323	GLY	CA-C	-5.22	1.43	1.51
2	7-B	544	ARG	CZ-NH1	5.22	1.39	1.33
1	8-A	159	GLU	CG-CD	-5.22	1.44	1.51
1	4-A	141	GLU	CD-OE2	5.22	1.31	1.25
2	8-B	389	ARG	CZ-NH1	5.22	1.39	1.33
2	2-B	663	GLU	CD-OE1	5.22	1.31	1.25
1	6-A	600	ASP	CA-CB	5.22	1.65	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1-B	638	ARG	CD-NE	5.22	1.55	1.46
3	4-C	84	ARG	CD-NE	5.22	1.55	1.46
2	6-B	343	TYR	CG-CD1	5.21	1.46	1.39
3	7-D	290	SER	CB-OG	5.21	1.49	1.42
1	6-A	74	TYR	CZ-OH	5.21	1.46	1.37
1	6-A	663	TYR	CZ-OH	5.21	1.46	1.37
3	2-C	177	SER	CA-CB	5.21	1.60	1.52
3	9-C	162	TYR	CB-CG	5.21	1.59	1.51
2	2-B	583	TYR	CG-CD1	5.21	1.46	1.39
2	6-B	264	TYR	CG-CD2	5.21	1.46	1.39
1	7-A	597	ARG	CZ-NH1	5.21	1.39	1.33
2	2-B	780	ASN	CA-CB	5.21	1.66	1.53
2	5-B	514	ARG	CD-NE	5.21	1.55	1.46
1	10-A	185	GLN	N-CA	-5.21	1.35	1.46
2	2-B	638	ARG	NE-CZ	5.21	1.39	1.33
2	2-B	544	ARG	CZ-NH1	5.20	1.39	1.33
3	1-D	90	ARG	NE-CZ	5.20	1.39	1.33
2	1-B	409	TYR	CE2-CZ	5.20	1.45	1.38
1	5-A	754	GLU	CB-CG	5.20	1.62	1.52
2	6-B	826	PHE	CE2-CZ	5.20	1.47	1.37
3	6-C	196	GLU	CD-OE2	5.20	1.31	1.25
1	8-A	776	ARG	CZ-NH2	5.20	1.39	1.33
3	3-C	319	TYR	CZ-OH	5.20	1.46	1.37
1	5-A	75	ILE	N-CA	-5.20	1.35	1.46
1	9-A	160	ARG	CZ-NH1	5.20	1.39	1.33
3	5-D	65	ARG	CZ-NH2	5.20	1.39	1.33
1	7-A	123	TYR	CG-CD2	5.20	1.46	1.39
3	2-C	96	SER	CA-CB	5.19	1.60	1.52
3	5-D	425	GLU	CD-OE2	5.19	1.31	1.25
3	2-D	277	SER	CA-CB	5.19	1.60	1.52
3	3-D	378	SER	CA-C	-5.19	1.39	1.52
3	6-D	257	SER	CA-CB	5.19	1.60	1.52
3	8-C	34	ASP	C-N	5.19	1.42	1.33
1	2-A	78	PHE	N-CA	5.19	1.56	1.46
2	6-B	379	TYR	CG-CD1	-5.19	1.32	1.39
3	8-D	90	ARG	CZ-NH1	5.19	1.39	1.33
2	4-B	342	TYR	CE2-CZ	5.19	1.45	1.38
2	7-B	293	ARG	CZ-NH1	5.19	1.39	1.33
2	8-B	225	PHE	CG-CD2	5.19	1.46	1.38
1	9-A	591	VAL	CB-CG2	5.19	1.63	1.52
3	10-D	46	ARG	CZ-NH2	5.19	1.39	1.33
2	1-B	562	TYR	CG-CD1	5.19	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2-A	69	GLY	CA-C	-5.19	1.43	1.51
3	2-D	264	GLU	C-N	5.18	1.46	1.34
2	3-B	598	TYR	CE2-CZ	5.18	1.45	1.38
2	5-B	666	ARG	CZ-NH2	5.18	1.39	1.33
2	1-B	531	SER	C-N	5.18	1.44	1.34
2	9-B	335	PHE	CE1-CZ	5.18	1.47	1.37
2	1-B	394	ILE	N-CA	-5.18	1.35	1.46
3	4-D	161	ARG	CZ-NH2	5.18	1.39	1.33
3	7-D	37	SER	CB-OG	5.18	1.49	1.42
3	7-C	302	SER	CA-CB	5.18	1.60	1.52
3	1-C	176	ARG	CZ-NH2	5.18	1.39	1.33
3	2-C	262	SER	CA-CB	5.18	1.60	1.52
2	6-B	486	SER	CA-CB	5.18	1.60	1.52
1	9-A	106	SER	CA-CB	5.17	1.60	1.52
3	10-C	59	ARG	NE-CZ	5.17	1.39	1.33
1	1-A	284	TYR	N-CA	-5.17	1.36	1.46
3	2-C	185	TYR	CG-CD2	5.17	1.45	1.39
3	4-D	359	ARG	CZ-NH1	5.17	1.39	1.33
3	8-D	22	TRP	CZ2-CH2	5.17	1.47	1.37
2	10-B	415	TYR	CG-CD2	5.17	1.45	1.39
2	5-B	764	LEU	CA-CB	5.17	1.65	1.53
1	3-A	204	ARG	CZ-NH2	5.17	1.39	1.33
3	9-D	398	PHE	CE2-CZ	5.17	1.47	1.37
2	1-B	308	SER	CA-CB	5.17	1.60	1.52
3	5-D	100	SER	N-CA	-5.17	1.36	1.46
3	2-C	403	PHE	CE2-CZ	5.16	1.47	1.37
3	4-C	59	ARG	CD-NE	5.16	1.55	1.46
3	6-D	105	TRP	NE1-CE2	-5.16	1.30	1.37
3	1-C	388	GLU	CD-OE1	5.16	1.31	1.25
1	3-A	123	TYR	CB-CG	5.16	1.59	1.51
2	4-B	576	ARG	NE-CZ	5.16	1.39	1.33
1	2-A	198	ARG	CZ-NH1	5.16	1.39	1.33
3	2-C	445	TYR	CE2-CZ	5.16	1.45	1.38
2	6-B	225	PHE	CG-CD2	5.16	1.46	1.38
1	3-A	203	ARG	CD-NE	5.16	1.55	1.46
3	5-C	418	ASN	N-CA	-5.16	1.36	1.46
3	8-D	329	ARG	CZ-NH1	5.16	1.39	1.33
2	5-B	345	TYR	CZ-OH	5.15	1.46	1.37
1	10-A	588	TYR	CG-CD2	5.15	1.45	1.39
1	4-A	400	ARG	CZ-NH1	5.15	1.39	1.33
2	4-B	532	PRO	CA-CB	5.15	1.63	1.53
3	5-D	319	TYR	CZ-OH	5.15	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	8-A	284	TYR	CB-CG	5.15	1.59	1.51
1	1-A	150	TYR	CD1-CE1	-5.15	1.31	1.39
3	10-C	425	GLU	CG-CD	5.15	1.59	1.51
1	1-A	370	SER	CA-CB	5.15	1.60	1.52
2	1-B	518	GLU	CD-OE1	5.15	1.31	1.25
3	5-C	198	SER	CA-CB	5.15	1.60	1.52
2	1-B	824	TYR	CZ-OH	5.15	1.46	1.37
2	7-B	577	PRO	CA-C	-5.15	1.42	1.52
1	8-A	578	CYS	CA-CB	5.15	1.65	1.53
1	5-A	116	TYR	CE1-CZ	5.14	1.45	1.38
2	6-B	567	PRO	CA-CB	5.14	1.63	1.53
1	9-A	137	ARG	CD-NE	5.14	1.55	1.46
2	9-B	651	TYR	CZ-OH	5.14	1.46	1.37
3	5-D	329	ARG	CZ-NH2	5.14	1.39	1.33
2	6-B	379	TYR	CG-CD2	5.14	1.45	1.39
1	8-A	576	ARG	CZ-NH1	5.14	1.39	1.33
3	1-D	304	SER	CA-CB	5.14	1.60	1.52
3	9-C	310	MET	CA-CB	5.14	1.65	1.53
1	10-A	113	GLY	CA-C	-5.14	1.43	1.51
3	1-D	237	SER	CA-CB	5.14	1.60	1.52
2	3-B	523	SER	CA-CB	5.14	1.60	1.52
3	3-C	45	GLU	CD-OE2	5.14	1.31	1.25
1	4-A	107	ARG	CD-NE	5.14	1.55	1.46
2	8-B	340	SER	CA-CB	5.14	1.60	1.52
2	5-B	185	LEU	CA-C	-5.14	1.39	1.52
2	5-B	299	ARG	CD-NE	5.14	1.55	1.46
1	6-A	327	ARG	NE-CZ	5.14	1.39	1.33
1	2-A	614	TYR	CE1-CZ	5.13	1.45	1.38
2	1-B	822	ARG	CZ-NH2	5.13	1.39	1.33
2	10-B	638	ARG	CZ-NH1	5.13	1.39	1.33
3	5-C	359	ARG	CZ-NH1	5.13	1.39	1.33
3	5-D	51	LYS	CD-CE	5.13	1.64	1.51
1	2-A	197	PHE	CG-CD2	5.13	1.46	1.38
1	2-A	338	GLU	CD-OE1	-5.13	1.20	1.25
3	6-D	178	SER	CA-CB	5.13	1.60	1.52
1	3-A	279	TYR	N-CA	-5.13	1.36	1.46
3	9-C	245	PRO	N-CA	-5.13	1.38	1.47
2	10-B	343	TYR	CD1-CE1	5.13	1.47	1.39
2	4-B	464	LEU	N-CA	-5.12	1.36	1.46
3	9-D	170	TYR	CE2-CZ	-5.12	1.31	1.38
2	8-B	297	TYR	CE2-CZ	5.12	1.45	1.38
1	9-A	446	LEU	CA-CB	5.12	1.65	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	9-D	114	ARG	CD-NE	5.12	1.55	1.46
1	4-A	767	TYR	CE2-CZ	5.12	1.45	1.38
3	4-D	45	GLU	CB-CG	5.12	1.61	1.52
3	3-C	292	TYR	CG-CD2	5.12	1.45	1.39
2	6-B	555	TRP	CE3-CZ3	5.12	1.47	1.38
2	7-B	526	ARG	CZ-NH2	5.12	1.39	1.33
3	9-C	267	PHE	CG-CD2	5.12	1.46	1.38
1	1-A	410	PHE	N-CA	-5.12	1.36	1.46
1	3-A	116	TYR	CD2-CE2	5.12	1.47	1.39
1	8-A	704	TYR	CE1-CZ	-5.12	1.31	1.38
3	8-C	67	ILE	CA-CB	-5.12	1.43	1.54
3	8-D	22	TRP	CD2-CE3	-5.12	1.32	1.40
1	4-A	669	ALA	CA-CB	5.12	1.63	1.52
3	5-D	292	TYR	CG-CD2	5.12	1.45	1.39
1	5-A	594	TYR	CE1-CZ	5.12	1.45	1.38
3	4-C	43	SER	CA-CB	5.11	1.60	1.52
3	2-D	437	TYR	CZ-OH	5.11	1.46	1.37
1	1-A	265	VAL	N-CA	-5.11	1.36	1.46
1	6-A	658	SER	CA-CB	5.11	1.60	1.52
3	4-D	306	VAL	CB-CG1	5.11	1.63	1.52
3	5-D	193	ARG	CZ-NH1	5.11	1.39	1.33
1	4-A	333	ARG	CZ-NH1	5.10	1.39	1.33
3	8-C	373	SER	CA-CB	5.10	1.60	1.52
1	3-A	646	TYR	CE1-CZ	5.10	1.45	1.38
2	7-B	598	TYR	CE1-CZ	5.10	1.45	1.38
3	10-C	346	SER	CB-OG	-5.10	1.35	1.42
2	1-B	214	PRO	N-CD	-5.10	1.40	1.47
3	3-C	109	TYR	CE2-CZ	5.10	1.45	1.38
3	3-D	369	GLU	CB-CG	5.10	1.61	1.52
2	5-B	359	TYR	CB-CG	-5.10	1.44	1.51
1	8-A	462	LEU	N-CA	-5.10	1.36	1.46
2	7-B	644	PHE	CG-CD1	5.10	1.46	1.38
3	1-C	341	ARG	CZ-NH1	5.09	1.39	1.33
1	2-A	108	ARG	CZ-NH2	5.09	1.39	1.33
1	2-A	140	TYR	CE1-CZ	5.09	1.45	1.38
2	4-B	197	SER	CB-OG	5.09	1.48	1.42
3	2-D	130	THR	CA-C	-5.09	1.39	1.52
2	4-B	439	ARG	NE-CZ	5.09	1.39	1.33
1	2-A	794	TYR	CD2-CE2	5.09	1.47	1.39
3	8-C	176	ARG	CD-NE	5.09	1.55	1.46
3	2-C	243	ARG	CD-NE	5.09	1.55	1.46
2	7-B	433	TYR	CG-CD1	5.09	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	3-B	362	PHE	CG-CD2	5.09	1.46	1.38
3	7-D	316	PHE	CG-CD1	5.09	1.46	1.38
1	2-A	296	TYR	CG-CD1	5.08	1.45	1.39
1	1-A	137	ARG	CZ-NH2	5.08	1.39	1.33
2	2-B	731	PHE	CG-CD1	5.08	1.46	1.38
3	4-D	192	ARG	CZ-NH2	5.08	1.39	1.33
1	7-A	647	PHE	CE1-CZ	5.08	1.47	1.37
2	5-B	523	SER	CA-C	-5.08	1.39	1.52
3	6-C	28	GLU	CG-CD	5.08	1.59	1.51
3	3-C	218	ARG	CZ-NH2	5.08	1.39	1.33
1	6-A	204	ARG	NE-CZ	5.08	1.39	1.33
2	7-B	200	PHE	C-N	-5.08	1.24	1.34
1	9-A	399	SER	CA-CB	5.08	1.60	1.52
3	9-C	251	SER	CA-CB	-5.08	1.45	1.52
3	2-C	55	ARG	CZ-NH2	5.08	1.39	1.33
1	6-A	198	ARG	CD-NE	5.08	1.55	1.46
1	6-A	198	ARG	NE-CZ	5.08	1.39	1.33
3	1-C	407	TYR	CE1-CZ	5.08	1.45	1.38
1	6-A	636	MET	CG-SD	5.08	1.94	1.81
1	9-A	262	ARG	CD-NE	5.08	1.55	1.46
1	1-A	176	ILE	CA-CB	-5.08	1.43	1.54
3	5-D	215	LYS	CA-C	-5.08	1.39	1.52
3	7-C	420	GLN	CB-CG	5.08	1.66	1.52
2	5-B	593	PHE	CE2-CZ	5.07	1.47	1.37
3	6-D	170	TYR	CE1-CZ	5.07	1.45	1.38
1	1-A	168	PHE	N-CA	-5.07	1.36	1.46
3	2-C	319	TYR	CG-CD2	5.07	1.45	1.39
1	3-A	107	ARG	CZ-NH1	5.07	1.39	1.33
3	3-C	198	SER	CA-CB	5.07	1.60	1.52
3	5-D	358	ARG	NE-CZ	5.07	1.39	1.33
1	3-A	74	TYR	CB-CG	5.07	1.59	1.51
2	3-B	658	GLU	CA-CB	-5.07	1.42	1.53
2	6-B	597	ASN	CB-CG	5.07	1.62	1.51
2	8-B	846	ARG	NE-CZ	5.07	1.39	1.33
3	8-C	407	TYR	CD2-CE2	5.07	1.47	1.39
2	9-B	651	TYR	CG-CD2	5.07	1.45	1.39
3	4-C	80	GLU	CD-OE2	5.07	1.31	1.25
3	5-D	72	GLU	CB-CG	5.07	1.61	1.52
3	3-C	93	TRP	CZ2-CH2	5.07	1.47	1.37
3	5-C	134	GLU	CD-OE1	5.07	1.31	1.25
3	7-C	161	ARG	CZ-NH2	5.07	1.39	1.33
3	9-C	185	TYR	CZ-OH	5.07	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	10-A	450	TYR	CG-CD1	5.07	1.45	1.39
3	10-C	266	HIS	CA-CB	5.07	1.65	1.53
3	9-D	65	ARG	CZ-NH1	5.06	1.39	1.33
2	1-B	471	ARG	CZ-NH1	5.06	1.39	1.33
2	2-B	510	TYR	CZ-OH	5.06	1.46	1.37
3	2-C	279	TYR	CD1-CE1	5.06	1.47	1.39
3	3-C	358	ARG	CD-NE	5.06	1.55	1.46
1	10-A	451	ARG	N-CA	-5.06	1.36	1.46
3	1-C	243	ARG	CZ-NH2	5.06	1.39	1.33
3	4-D	441	GLU	CG-CD	5.06	1.59	1.51
2	9-B	297	TYR	CZ-OH	5.06	1.46	1.37
2	2-B	423	ASN	CB-CG	5.06	1.62	1.51
3	3-C	212	ILE	N-CA	-5.06	1.36	1.46
3	6-C	367	PRO	N-CD	-5.06	1.40	1.47
3	2-C	84	ARG	NE-CZ	5.06	1.39	1.33
1	3-A	398	TYR	CZ-OH	5.06	1.46	1.37
2	5-B	532	PRO	CA-CB	-5.06	1.43	1.53
2	5-B	670	ARG	CZ-NH1	5.06	1.39	1.33
1	6-A	588	TYR	CG-CD1	5.06	1.45	1.39
1	6-A	773	SER	CA-CB	5.06	1.60	1.52
1	6-A	143	ARG	CZ-NH2	5.06	1.39	1.33
1	9-A	349	ARG	NE-CZ	5.06	1.39	1.33
3	2-D	220	PRO	N-CD	-5.05	1.40	1.47
1	7-A	121	ARG	CD-NE	5.05	1.55	1.46
2	7-B	284	TYR	CG-CD2	5.05	1.45	1.39
3	4-D	48	ASP	CB-CG	5.05	1.62	1.51
2	5-B	465	ASN	N-CA	-5.05	1.36	1.46
3	5-D	244	PHE	CG-CD2	5.05	1.46	1.38
2	1-B	285	ARG	CD-NE	5.05	1.55	1.46
2	4-B	471	ARG	CZ-NH2	5.05	1.39	1.33
2	7-B	343	TYR	CZ-OH	5.05	1.46	1.37
1	1-A	124	GLU	CD-OE2	-5.05	1.20	1.25
2	6-B	771	GLU	CG-CD	5.05	1.59	1.51
1	10-A	145	PHE	CG-CD1	5.05	1.46	1.38
2	5-B	455	GLU	CD-OE1	5.05	1.31	1.25
3	9-C	341	ARG	CZ-NH1	5.05	1.39	1.33
1	10-A	450	TYR	CB-CG	5.05	1.59	1.51
3	4-D	91	ASN	CA-CB	5.04	1.66	1.53
2	8-B	816	TYR	N-CA	5.04	1.56	1.46
3	9-D	179	GLU	CG-CD	5.04	1.59	1.51
3	10-D	250	SER	CA-C	-5.04	1.39	1.52
2	1-B	758	TYR	CE2-CZ	5.04	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2-D	417	GLN	N-CA	-5.04	1.36	1.46
1	9-A	140	TYR	CG-CD2	5.04	1.45	1.39
1	2-A	260	GLY	N-CA	5.04	1.53	1.46
2	3-B	802	LEU	C-N	5.04	1.42	1.33
3	10-C	407	TYR	CG-CD2	5.04	1.45	1.39
2	5-B	555	TRP	CE3-CZ3	5.04	1.47	1.38
2	2-B	218	SER	C-N	5.04	1.42	1.33
1	4-A	479	ARG	NE-CZ	5.04	1.39	1.33
3	4-D	344	PHE	CG-CD2	5.04	1.46	1.38
3	5-D	316	PHE	CG-CD2	5.04	1.46	1.38
2	6-B	293	ARG	CZ-NH1	5.04	1.39	1.33
2	5-B	300	PHE	CG-CD2	5.03	1.46	1.38
2	5-B	565	TYR	CG-CD1	5.03	1.45	1.39
3	5-C	109	TYR	CG-CD1	5.03	1.45	1.39
2	8-B	471	ARG	NE-CZ	5.03	1.39	1.33
3	10-C	243	ARG	CZ-NH2	5.03	1.39	1.33
3	1-D	218	ARG	NE-CZ	5.03	1.39	1.33
3	6-C	243	ARG	CZ-NH2	5.03	1.39	1.33
1	8-A	603	TRP	CE3-CZ3	5.03	1.47	1.38
2	10-B	348	ASN	N-CA	-5.03	1.36	1.46
2	4-B	805	PHE	CG-CD1	5.03	1.46	1.38
2	6-B	510	TYR	CE2-CZ	5.03	1.45	1.38
2	9-B	558	PHE	CG-CD1	5.03	1.46	1.38
1	2-A	131	PHE	CB-CG	5.03	1.59	1.51
1	9-A	469	ARG	NE-CZ	5.03	1.39	1.33
2	10-B	514	ARG	CZ-NH2	5.03	1.39	1.33
1	1-A	791	PHE	CE1-CZ	5.03	1.46	1.37
2	2-B	471	ARG	NE-CZ	5.02	1.39	1.33
2	5-B	592	ARG	CZ-NH1	5.02	1.39	1.33
2	7-B	239	GLU	CG-CD	5.02	1.59	1.51
3	8-D	1	MET	C-N	5.02	1.42	1.33
1	10-A	657	TYR	CZ-OH	5.02	1.46	1.37
3	2-D	407	TYR	CE2-CZ	5.02	1.45	1.38
3	5-C	243	ARG	CD-NE	5.02	1.54	1.46
3	8-D	275	PHE	CG-CD1	5.02	1.46	1.38
2	10-B	397	GLU	CD-OE1	5.02	1.31	1.25
1	8-A	112	TYR	CE1-CZ	5.02	1.45	1.38
3	10-C	249	TYR	CB-CG	-5.02	1.44	1.51
1	6-A	121	ARG	CZ-NH1	5.02	1.39	1.33
3	7-C	59	ARG	NE-CZ	5.02	1.39	1.33
3	4-C	392	ASN	CB-CG	5.02	1.62	1.51
3	4-C	422	GLU	CB-CG	5.02	1.61	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	8-B	544	ARG	NE-CZ	5.02	1.39	1.33
3	8-D	373	SER	CA-CB	5.02	1.60	1.52
1	9-A	121	ARG	NE-CZ	5.02	1.39	1.33
2	9-B	267	PHE	CG-CD2	5.02	1.46	1.38
3	2-C	445	TYR	CG-CD2	5.01	1.45	1.39
2	7-B	666	ARG	NE-CZ	5.01	1.39	1.33
2	9-B	612	ARG	CZ-NH2	5.01	1.39	1.33
3	1-C	410	GLY	CA-C	-5.01	1.43	1.51
3	4-C	133	PHE	CE1-CZ	5.01	1.46	1.37
1	5-A	450	TYR	CE2-CZ	5.01	1.45	1.38
3	6-D	271	SER	N-CA	-5.01	1.36	1.46
1	8-A	479	ARG	NE-CZ	5.01	1.39	1.33
1	10-A	472	GLU	CD-OE2	5.01	1.31	1.25
2	10-B	846	ARG	CD-NE	5.01	1.54	1.46
2	4-B	827	ARG	NE-CZ	5.01	1.39	1.33
3	5-C	218	ARG	CZ-NH1	5.01	1.39	1.33
2	10-B	776	TYR	CB-CG	5.01	1.59	1.51
2	5-B	359	TYR	CE2-CZ	5.01	1.45	1.38
2	3-B	526	ARG	CZ-NH2	5.01	1.39	1.33
1	4-A	451	ARG	CZ-NH1	5.01	1.39	1.33
2	5-B	236	TYR	CA-C	-5.01	1.40	1.52
2	5-B	431	VAL	CA-CB	-5.01	1.44	1.54
2	5-B	600	TYR	CG-CD1	5.01	1.45	1.39
3	7-C	288	CYS	C-N	5.01	1.45	1.34
1	3-A	603	TRP	CB-CG	5.00	1.59	1.50
1	5-A	558	TYR	CG-CD2	5.00	1.45	1.39
2	6-B	589	PHE	CG-CD1	5.00	1.46	1.38
3	10-D	129	SER	CA-CB	5.00	1.60	1.52
2	1-B	359	TYR	CZ-OH	5.00	1.46	1.37
2	4-B	771	GLU	CB-CG	5.00	1.61	1.52
1	8-A	687	ARG	CZ-NH2	5.00	1.39	1.33
3	8-D	286	HIS	CB-CG	5.00	1.59	1.50

All (4714) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	10-B	433	TYR	CB-CG-CD2	-20.70	108.58	121.00
1	1-A	107	ARG	NE-CZ-NH1	20.67	130.63	120.30
3	9-D	256	TYR	CB-CG-CD2	20.54	133.32	121.00
3	9-D	256	TYR	CB-CG-CD1	-19.19	109.48	121.00
2	10-B	264	TYR	CB-CG-CD1	18.97	132.38	121.00
1	4-A	400	ARG	NE-CZ-NH1	18.54	129.57	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	7-D	90	ARG	NE-CZ-NH2	-18.13	111.24	120.30
3	6-D	333	ARG	NE-CZ-NH2	-18.04	111.28	120.30
3	7-D	55	ARG	NE-CZ-NH1	17.93	129.26	120.30
1	2-A	102	PHE	CB-CG-CD1	17.55	133.09	120.80
2	3-B	433	TYR	CB-CG-CD2	-17.20	110.68	121.00
2	3-B	285	ARG	NE-CZ-NH2	-17.16	111.72	120.30
1	7-A	558	TYR	CB-CG-CD1	17.14	131.29	121.00
2	3-B	438	TYR	CB-CG-CD2	-16.99	110.81	121.00
2	4-B	343	TYR	CB-CG-CD2	-16.80	110.92	121.00
1	5-A	657	TYR	CB-CG-CD1	16.75	131.05	121.00
2	3-B	585	ARG	NE-CZ-NH2	-16.59	112.01	120.30
2	8-B	633	ARG	NE-CZ-NH1	16.54	128.57	120.30
2	4-B	342	TYR	CB-CG-CD1	-16.53	111.08	121.00
3	2-C	176	ARG	NE-CZ-NH2	-16.50	112.05	120.30
3	10-C	333	ARG	NE-CZ-NH1	16.41	128.50	120.30
3	6-C	218	ARG	NE-CZ-NH2	-16.36	112.12	120.30
2	6-B	824	TYR	CB-CG-CD1	16.27	130.76	121.00
2	3-B	438	TYR	CB-CG-CD1	16.25	130.75	121.00
3	10-C	333	ARG	NE-CZ-NH2	-16.14	112.23	120.30
3	7-D	427	ARG	NE-CZ-NH2	-16.11	112.25	120.30
2	6-B	328	ARG	NE-CZ-NH2	-16.08	112.26	120.30
2	6-B	429	TYR	CB-CG-CD2	-15.97	111.42	121.00
2	9-B	345	TYR	CB-CG-CD2	-15.96	111.42	121.00
2	6-B	824	TYR	CB-CG-CD2	-15.91	111.45	121.00
2	5-B	429	TYR	CB-CG-CD2	-15.91	111.46	121.00
2	10-B	264	TYR	CB-CG-CD2	-15.91	111.46	121.00
3	10-D	176	ARG	NE-CZ-NH2	-15.85	112.37	120.30
1	7-A	558	TYR	CB-CG-CD2	-15.85	111.49	121.00
3	10-C	359	ARG	NE-CZ-NH2	-15.84	112.38	120.30
1	2-A	111	ARG	NE-CZ-NH1	15.81	128.20	120.30
1	3-A	140	TYR	CB-CG-CD1	-15.79	111.53	121.00
2	4-B	328	ARG	NE-CZ-NH1	15.78	128.19	120.30
2	6-B	343	TYR	CB-CG-CD1	15.75	130.45	121.00
3	9-C	437	TYR	CB-CG-CD2	15.72	130.43	121.00
3	9-C	329	ARG	NE-CZ-NH2	-15.72	112.44	120.30
1	2-A	627	ARG	NE-CZ-NH2	-15.68	112.46	120.30
3	3-D	161	ARG	NE-CZ-NH2	-15.59	112.51	120.30
1	9-A	157	ARG	NE-CZ-NH2	-15.50	112.55	120.30
3	7-D	359	ARG	NE-CZ-NH1	15.40	128.00	120.30
1	8-A	137	ARG	NE-CZ-NH2	-15.25	112.67	120.30
3	3-D	193	ARG	NE-CZ-NH2	-15.17	112.71	120.30
2	1-B	666	ARG	NE-CZ-NH1	15.16	127.88	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	9-B	345	TYR	CB-CG-CD1	15.15	130.09	121.00
1	6-A	479	ARG	NE-CZ-NH2	-15.09	112.75	120.30
1	7-A	400	ARG	NE-CZ-NH2	-15.07	112.77	120.30
1	4-A	123	TYR	CB-CG-CD1	-15.04	111.97	121.00
2	6-B	345	TYR	CB-CG-CD2	-15.01	111.99	121.00
1	6-A	791	PHE	CB-CG-CD2	-14.95	110.33	120.80
3	4-D	341	ARG	NE-CZ-NH2	-14.89	112.86	120.30
2	8-B	758	TYR	CB-CG-CD2	14.87	129.92	121.00
2	7-B	190	TYR	CB-CG-CD2	-14.87	112.08	121.00
1	8-A	198	ARG	NE-CZ-NH2	14.77	127.69	120.30
2	6-B	816	TYR	CB-CG-CD2	-14.77	112.14	121.00
2	6-B	345	TYR	CB-CG-CD1	14.71	129.82	121.00
2	9-B	470	TYR	CB-CG-CD1	-14.65	112.21	121.00
3	2-D	161	ARG	NE-CZ-NH2	-14.61	113.00	120.30
1	1-A	107	ARG	NE-CZ-NH2	-14.60	113.00	120.30
1	2-A	108	ARG	NE-CZ-NH1	14.58	127.59	120.30
1	6-A	157	ARG	NE-CZ-NH1	14.57	127.58	120.30
1	4-A	614	TYR	CB-CG-CD1	-14.55	112.27	121.00
2	5-B	411	PHE	CB-CG-CD2	-14.51	110.64	120.80
2	6-B	343	TYR	CB-CG-CD2	-14.50	112.30	121.00
3	5-C	341	ARG	NE-CZ-NH1	14.49	127.55	120.30
1	7-A	479	ARG	NE-CZ-NH1	-14.49	113.06	120.30
2	4-B	285	ARG	NE-CZ-NH1	14.46	127.53	120.30
2	9-B	641	PHE	CB-CG-CD2	-14.44	110.69	120.80
1	7-A	704	TYR	CB-CG-CD2	14.42	129.65	121.00
2	10-B	445	PHE	CB-CG-CD1	14.41	130.89	120.80
3	6-C	46	ARG	NE-CZ-NH2	-14.39	113.11	120.30
1	4-A	630	ARG	NE-CZ-NH2	-14.38	113.11	120.30
2	9-B	583	TYR	CB-CG-CD2	-14.36	112.38	121.00
3	10-D	87	PHE	CB-CG-CD1	14.31	130.82	120.80
2	6-B	533	ARG	NE-CZ-NH1	14.30	127.45	120.30
2	10-B	445	PHE	CB-CG-CD2	-14.29	110.80	120.80
2	7-B	297	TYR	CB-CG-CD2	-14.22	112.47	121.00
1	6-A	791	PHE	CB-CG-CD1	14.21	130.75	120.80
2	5-B	651	TYR	CB-CG-CD2	-14.14	112.52	121.00
2	10-B	666	ARG	NE-CZ-NH2	-14.13	113.24	120.30
2	7-B	585	ARG	NE-CZ-NH2	-14.10	113.25	120.30
1	7-A	429	TYR	CB-CG-CD1	14.02	129.41	121.00
3	2-C	55	ARG	NE-CZ-NH2	-14.00	113.30	120.30
1	7-A	429	TYR	CB-CG-CD2	-13.97	112.61	121.00
3	8-D	136	PHE	CB-CG-CD2	-13.97	111.02	120.80
3	5-C	267	PHE	CB-CG-CD1	13.95	130.56	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6-A	709	PHE	CB-CG-CD2	-13.92	111.05	120.80
1	7-A	687	ARG	NE-CZ-NH2	-13.91	113.34	120.30
2	2-B	264	TYR	CB-CG-CD2	-13.86	112.68	121.00
2	9-B	772	PHE	CB-CG-CD2	-13.84	111.11	120.80
2	3-B	600	TYR	CB-CG-CD1	13.83	129.30	121.00
3	6-C	292	TYR	CB-CG-CD2	-13.83	112.70	121.00
2	5-B	187	TYR	CB-CG-CD1	13.79	129.28	121.00
3	1-C	387	PHE	CB-CG-CD1	13.79	130.45	120.80
3	6-C	176	ARG	NE-CZ-NH1	13.77	127.19	120.30
2	4-B	583	TYR	CB-CG-CD2	-13.77	112.74	121.00
3	2-C	86	PHE	CB-CG-CD1	13.76	130.43	120.80
2	4-B	438	TYR	CB-CG-CD2	-13.71	112.77	121.00
2	5-B	415	TYR	CB-CG-CD2	-13.71	112.77	121.00
1	5-A	138	PHE	CB-CG-CD1	13.68	130.38	120.80
2	10-B	345	TYR	CB-CG-CD2	-13.65	112.81	121.00
1	10-A	700	PHE	CB-CG-CD1	13.63	130.34	120.80
3	9-D	358	ARG	NE-CZ-NH2	-13.62	113.49	120.30
1	8-A	429	TYR	CB-CG-CD2	-13.62	112.83	121.00
1	4-A	450	TYR	CB-CG-CD2	-13.61	112.83	121.00
3	4-D	192	ARG	NE-CZ-NH2	-13.53	113.53	120.30
2	7-B	297	TYR	CB-CG-CD1	13.51	129.11	121.00
2	2-B	299	ARG	NE-CZ-NH1	13.46	127.03	120.30
3	2-D	83	PHE	CB-CG-CD2	-13.45	111.39	120.80
2	5-B	342	TYR	CB-CG-CD1	-13.45	112.93	121.00
3	5-D	362	TYR	CB-CG-CD2	-13.43	112.94	121.00
2	9-B	599	PHE	CB-CG-CD2	-13.40	111.42	120.80
1	10-A	469	ARG	NE-CZ-NH2	13.39	127.00	120.30
3	10-C	247	TYR	CB-CG-CD1	-13.36	112.98	121.00
1	2-A	627	ARG	NE-CZ-NH1	13.36	126.98	120.30
1	8-A	251	PHE	CB-CG-CD1	13.32	130.13	120.80
2	10-B	510	TYR	CB-CG-CD2	-13.28	113.03	121.00
1	2-A	111	ARG	NE-CZ-NH2	-13.27	113.66	120.30
2	4-B	593	PHE	CB-CG-CD1	13.26	130.08	120.80
2	4-B	612	ARG	NE-CZ-NH2	-13.26	113.67	120.30
2	10-B	638	ARG	NE-CZ-NH1	13.25	126.93	120.30
3	5-C	407	TYR	CB-CG-CD1	-13.25	113.05	121.00
2	2-B	299	ARG	NE-CZ-NH2	-13.17	113.72	120.30
1	8-A	144	ARG	NE-CZ-NH2	-13.16	113.72	120.30
2	2-B	805	PHE	CB-CG-CD2	-13.15	111.59	120.80
1	4-A	76	ARG	NE-CZ-NH1	13.15	126.88	120.30
1	2-A	706	PHE	CB-CG-CD2	-13.14	111.60	120.80
3	3-D	161	ARG	NE-CZ-NH1	13.12	126.86	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5-B	284	TYR	CB-CG-CD2	-13.12	113.13	121.00
2	10-B	356	ARG	NE-CZ-NH1	13.07	126.83	120.30
2	4-B	328	ARG	NE-CZ-NH2	-13.06	113.77	120.30
2	8-B	758	TYR	CB-CG-CD1	-13.04	113.17	121.00
1	3-A	479	ARG	NE-CZ-NH2	-13.03	113.79	120.30
1	6-A	639	PHE	CB-CG-CD1	-13.00	111.70	120.80
1	8-A	438	PHE	CB-CG-CD1	12.96	129.88	120.80
1	4-A	413	TYR	CB-CG-CD2	12.94	128.76	121.00
2	3-B	433	TYR	CB-CG-CD1	12.94	128.76	121.00
3	8-C	437	TYR	CB-CG-CD1	12.93	128.76	121.00
1	8-A	429	TYR	CB-CG-CD1	12.92	128.75	121.00
2	8-B	599	PHE	CB-CG-CD2	-12.91	111.76	120.80
2	9-B	565	TYR	CB-CG-CD2	-12.90	113.26	121.00
3	8-C	427	ARG	NE-CZ-NH2	-12.88	113.86	120.30
3	2-C	86	PHE	CB-CG-CD2	-12.87	111.79	120.80
2	5-B	772	PHE	CB-CG-CD2	-12.87	111.79	120.80
1	7-A	138	PHE	CB-CG-CD1	-12.82	111.82	120.80
2	4-B	583	TYR	CB-CG-CD1	12.80	128.68	121.00
2	7-B	342	TYR	CB-CG-CD1	-12.80	113.32	121.00
3	5-C	243	ARG	NE-CZ-NH1	12.79	126.69	120.30
1	1-A	451	ARG	NE-CZ-NH1	-12.78	113.91	120.30
3	10-D	87	PHE	CB-CG-CD2	-12.78	111.85	120.80
1	2-A	597	ARG	NE-CZ-NH2	-12.72	113.94	120.30
3	7-D	358	ARG	NE-CZ-NH1	-12.71	113.94	120.30
2	8-B	328	ARG	NE-CZ-NH1	12.68	126.64	120.30
2	8-B	433	TYR	CB-CG-CD2	-12.68	113.39	121.00
2	3-B	576	ARG	NE-CZ-NH1	12.68	126.64	120.30
3	7-C	162	TYR	CB-CG-CD2	-12.68	113.39	121.00
3	3-D	362	TYR	CB-CG-CD2	-12.61	113.43	121.00
1	2-A	296	TYR	CB-CG-CD2	-12.59	113.45	121.00
2	9-B	231	TYR	CB-CG-CD1	12.57	128.54	121.00
3	10-C	358	ARG	NE-CZ-NH2	-12.55	114.03	120.30
3	6-D	249	TYR	CB-CG-CD2	12.52	128.51	121.00
2	9-B	379	TYR	CB-CG-CD2	12.50	128.50	121.00
2	9-B	446	PHE	CB-CG-CD2	-12.49	112.06	120.80
3	8-D	341	ARG	NE-CZ-NH1	12.46	126.53	120.30
2	9-B	470	TYR	CB-CG-CD2	12.44	128.47	121.00
3	6-C	218	ARG	NE-CZ-NH1	12.42	126.51	120.30
3	3-D	437	TYR	CB-CG-CD1	-12.41	113.56	121.00
3	9-D	55	ARG	NE-CZ-NH1	12.40	126.50	120.30
1	7-A	775	PHE	CB-CG-CD2	-12.39	112.12	120.80
2	5-B	359	TYR	CB-CG-CD1	12.39	128.43	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	7-A	144	ARG	NE-CZ-NH1	12.39	126.50	120.30
2	10-B	776	TYR	CB-CG-CD2	-12.37	113.58	121.00
3	2-C	65	ARG	NE-CZ-NH2	-12.36	114.12	120.30
1	5-A	450	TYR	CB-CG-CD1	12.35	128.41	121.00
2	10-B	510	TYR	CB-CG-CD1	12.32	128.40	121.00
3	6-D	193	ARG	NE-CZ-NH1	12.31	126.46	120.30
2	8-B	772	PHE	CB-CG-CD1	12.29	129.41	120.80
1	4-A	160	ARG	NE-CZ-NH2	-12.27	114.17	120.30
2	4-B	533	ARG	NE-CZ-NH2	-12.26	114.17	120.30
3	8-C	90	ARG	NE-CZ-NH2	-12.24	114.18	120.30
1	2-A	302	TYR	CB-CG-CD2	-12.24	113.66	121.00
3	3-C	217	PHE	CB-CG-CD2	12.21	129.35	120.80
1	4-A	193	TYR	CB-CG-CD2	-12.20	113.68	121.00
1	10-A	409	PHE	CB-CG-CD2	-12.19	112.27	120.80
1	4-A	262	ARG	NE-CZ-NH1	12.17	126.39	120.30
3	7-C	362	TYR	CB-CG-CD1	12.09	128.25	121.00
1	8-A	627	ARG	NE-CZ-NH2	12.08	126.34	120.30
2	2-B	409	TYR	CB-CG-CD2	-12.08	113.75	121.00
3	6-D	176	ARG	NE-CZ-NH1	12.07	126.34	120.30
3	9-C	272	PHE	CB-CG-CD1	-12.05	112.36	120.80
2	5-B	343	TYR	CB-CG-CD1	12.05	128.23	121.00
1	6-A	479	ARG	NE-CZ-NH1	12.05	126.32	120.30
2	4-B	343	TYR	CB-CG-CD1	12.02	128.21	121.00
1	8-A	469	ARG	NE-CZ-NH1	11.98	126.29	120.30
3	6-C	445	TYR	CB-CG-CD1	11.98	128.19	121.00
2	8-B	772	PHE	CB-CG-CD2	-11.97	112.42	120.80
2	3-B	776	TYR	CB-CG-CD2	-11.97	113.82	121.00
2	5-B	342	TYR	CB-CG-CD2	11.96	128.18	121.00
2	2-B	345	TYR	CB-CG-CD2	-11.96	113.83	121.00
1	4-A	204	ARG	NE-CZ-NH1	11.95	126.27	120.30
2	5-B	429	TYR	CB-CG-CD1	11.95	128.17	121.00
2	8-B	599	PHE	CB-CG-CD1	11.94	129.16	120.80
2	1-B	580	ARG	NE-CZ-NH2	11.92	126.26	120.30
2	3-B	819	PHE	CB-CG-CD2	-11.92	112.45	120.80
3	5-D	427	ARG	NE-CZ-NH1	11.92	126.26	120.30
2	9-B	439	ARG	NE-CZ-NH2	-11.91	114.34	120.30
3	4-D	387	PHE	CB-CG-CD2	-11.91	112.46	120.80
1	2-A	102	PHE	CB-CG-CD2	-11.91	112.47	120.80
2	8-B	411	PHE	CB-CG-CD1	-11.90	112.47	120.80
1	8-A	775	PHE	CB-CG-CD2	-11.90	112.47	120.80
2	1-B	731	PHE	CB-CG-CD2	-11.87	112.49	120.80
2	7-B	741	PHE	CB-CG-CD1	11.86	129.10	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	6-D	333	ARG	NE-CZ-NH1	11.85	126.22	120.30
2	9-B	446	PHE	CB-CG-CD1	11.85	129.09	120.80
2	9-B	284	TYR	CB-CG-CD2	11.82	128.09	121.00
2	9-B	633	ARG	NE-CZ-NH2	-11.82	114.39	120.30
1	4-A	597	ARG	NE-CZ-NH2	-11.79	114.40	120.30
1	7-A	714	ARG	NE-CZ-NH2	-11.78	114.41	120.30
1	5-A	398	TYR	CB-CG-CD1	-11.77	113.94	121.00
3	9-D	59	ARG	NE-CZ-NH2	-11.75	114.42	120.30
1	9-A	405	PHE	CB-CG-CD2	-11.75	112.57	120.80
2	2-B	241	PHE	CB-CG-CD2	-11.75	112.58	120.80
3	3-D	162	TYR	CB-CG-CD2	11.72	128.03	121.00
3	5-C	90	ARG	NE-CZ-NH2	11.72	126.16	120.30
3	6-D	170	TYR	CB-CG-CD2	-11.71	113.97	121.00
1	4-A	469	ARG	NE-CZ-NH2	-11.70	114.45	120.30
2	9-B	670	ARG	NE-CZ-NH2	-11.69	114.45	120.30
2	2-B	816	TYR	CB-CG-CD2	11.69	128.01	121.00
2	1-B	587	PHE	CB-CG-CD2	-11.68	112.62	120.80
2	9-B	231	TYR	CB-CG-CD2	-11.67	114.00	121.00
3	2-C	387	PHE	CB-CG-CD2	11.66	128.96	120.80
3	10-D	84	ARG	NE-CZ-NH2	-11.66	114.47	120.30
2	6-B	187	TYR	CB-CG-CD1	11.66	127.99	121.00
1	9-A	576	ARG	NE-CZ-NH2	-11.64	114.48	120.30
2	10-B	433	TYR	CB-CG-CD1	11.62	127.97	121.00
3	3-D	87	PHE	CB-CG-CD1	11.62	128.93	120.80
3	6-C	86	PHE	CB-CG-CD1	11.60	128.92	120.80
2	2-B	470	TYR	CB-CG-CD2	-11.60	114.04	121.00
3	2-C	170	TYR	CB-CG-CD1	11.57	127.94	121.00
2	5-B	470	TYR	CB-CG-CD2	-11.55	114.07	121.00
1	5-A	657	TYR	CB-CG-CD2	-11.53	114.08	121.00
3	9-C	359	ARG	NE-CZ-NH1	11.53	126.06	120.30
2	4-B	359	TYR	CB-CG-CD2	-11.52	114.09	121.00
2	4-B	514	ARG	NE-CZ-NH2	-11.52	114.54	120.30
2	8-B	475	PHE	CB-CG-CD1	11.52	128.87	120.80
1	4-A	193	TYR	CB-CG-CD1	11.51	127.91	121.00
1	1-A	204	ARG	NE-CZ-NH2	11.49	126.05	120.30
1	5-A	197	PHE	CB-CG-CD2	-11.48	112.77	120.80
3	5-C	86	PHE	CB-CG-CD2	-11.48	112.77	120.80
2	2-B	264	TYR	CB-CG-CD1	11.46	127.88	121.00
1	6-A	349	ARG	NE-CZ-NH1	11.45	126.03	120.30
3	2-C	46	ARG	NE-CZ-NH1	-11.45	114.58	120.30
3	2-D	161	ARG	NE-CZ-NH1	11.40	126.00	120.30
2	7-B	393	PHE	CB-CG-CD2	-11.39	112.83	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6-A	381	PHE	CB-CG-CD1	11.38	128.77	120.80
3	1-D	65	ARG	NE-CZ-NH1	11.36	125.98	120.30
3	9-C	315	TYR	CB-CG-CD2	-11.35	114.19	121.00
1	8-A	576	ARG	NE-CZ-NH2	-11.33	114.63	120.30
3	5-C	20	PHE	CB-CG-CD1	11.32	128.73	120.80
2	4-B	544	ARG	NE-CZ-NH1	11.32	125.96	120.30
3	1-C	161	ARG	NE-CZ-NH2	11.31	125.95	120.30
2	4-B	544	ARG	NE-CZ-NH2	-11.29	114.65	120.30
3	6-D	413	PHE	CB-CG-CD2	-11.27	112.91	120.80
3	8-C	341	ARG	NE-CZ-NH2	-11.25	114.67	120.30
1	7-A	150	TYR	CB-CG-CD1	11.24	127.75	121.00
1	4-A	597	ARG	NE-CZ-NH1	11.23	125.91	120.30
2	10-B	612	ARG	NE-CZ-NH1	11.22	125.91	120.30
3	6-C	445	TYR	CB-CG-CD2	-11.19	114.28	121.00
1	9-A	105	PHE	CB-CG-CD2	-11.19	112.97	120.80
3	1-D	176	ARG	NE-CZ-NH1	11.19	125.89	120.30
3	2-C	161	ARG	NE-CZ-NH1	11.18	125.89	120.30
1	9-A	171	ARG	NE-CZ-NH2	-11.17	114.71	120.30
2	2-B	328	ARG	NE-CZ-NH2	-11.16	114.72	120.30
1	7-A	349	ARG	NE-CZ-NH2	11.16	125.88	120.30
2	1-B	514	ARG	NE-CZ-NH1	11.14	125.87	120.30
2	9-B	284	TYR	CB-CG-CD1	-11.12	114.33	121.00
2	10-B	187	TYR	CB-CG-CD1	11.12	127.67	121.00
1	3-A	251	PHE	CB-CG-CD1	11.11	128.58	120.80
2	6-B	400	TYR	CB-CG-CD2	-11.11	114.33	121.00
2	1-B	670	ARG	NE-CZ-NH1	-11.10	114.75	120.30
2	4-B	345	TYR	CB-CG-CD2	-11.10	114.34	121.00
3	9-D	84	ARG	NE-CZ-NH1	11.09	125.85	120.30
3	1-C	387	PHE	CB-CG-CD2	-11.08	113.05	120.80
2	8-B	433	TYR	CB-CG-CD1	11.07	127.64	121.00
2	2-B	345	TYR	CB-CG-CD1	11.07	127.64	121.00
2	4-B	666	ARG	NE-CZ-NH1	11.06	125.83	120.30
2	7-B	599	PHE	CB-CG-CD2	-11.06	113.06	120.80
1	6-A	709	PHE	CB-CG-CD1	11.06	128.54	120.80
3	4-C	359	ARG	NE-CZ-NH2	-11.05	114.78	120.30
3	5-D	423	PHE	CB-CG-CD2	-11.04	113.07	120.80
3	9-D	55	ARG	NE-CZ-NH2	-11.04	114.78	120.30
1	8-A	582	TYR	CB-CG-CD1	-11.03	114.38	121.00
3	5-C	247	TYR	CB-CG-CD2	-11.03	114.38	121.00
2	6-B	429	TYR	CB-CG-CD1	11.03	127.62	121.00
2	8-B	641	PHE	CB-CG-CD1	11.02	128.51	120.80
2	7-B	741	PHE	CB-CG-CD2	-11.02	113.09	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-D	362	TYR	CB-CG-CD2	-11.01	114.40	121.00
1	5-A	102	PHE	CB-CG-CD2	-11.01	113.10	120.80
2	3-B	600	TYR	CB-CG-CD2	-11.00	114.40	121.00
1	4-A	400	ARG	NE-CZ-NH2	-10.97	114.81	120.30
2	2-B	411	PHE	CB-CG-CD2	-10.96	113.12	120.80
2	7-B	819	PHE	CB-CG-CD2	-10.96	113.13	120.80
2	9-B	776	TYR	CB-CG-CD2	-10.96	114.42	121.00
2	9-B	816	TYR	CB-CG-CD1	-10.96	114.43	121.00
1	7-A	385	MET	CG-SD-CE	-10.95	82.68	100.20
2	1-B	433	TYR	CB-CG-CD1	-10.95	114.43	121.00
2	10-B	758	TYR	CB-CG-CD2	-10.94	114.43	121.00
1	9-A	636	MET	CG-SD-CE	-10.93	82.72	100.20
3	5-C	84	ARG	NE-CZ-NH2	-10.92	114.84	120.30
1	5-A	77	TYR	CB-CG-CD2	-10.92	114.45	121.00
1	7-A	657	TYR	CB-CG-CD1	-10.91	114.45	121.00
3	10-D	362	TYR	CB-CG-CD2	-10.90	114.46	121.00
2	10-B	824	TYR	CB-CG-CD1	10.90	127.54	121.00
3	2-C	176	ARG	NE-CZ-NH1	10.89	125.75	120.30
2	1-B	429	TYR	CB-CG-CD2	-10.88	114.47	121.00
3	2-D	359	ARG	NE-CZ-NH1	10.88	125.74	120.30
1	7-A	108	ARG	NE-CZ-NH2	-10.88	114.86	120.30
3	3-D	427	ARG	NE-CZ-NH2	10.86	125.73	120.30
1	1-A	296	TYR	CB-CG-CD2	-10.86	114.48	121.00
2	1-B	599	PHE	CB-CG-CD2	-10.86	113.20	120.80
2	5-B	439	ARG	NE-CZ-NH2	-10.86	114.87	120.30
2	9-B	343	TYR	CB-CG-CD2	-10.86	114.49	121.00
2	10-B	299	ARG	NE-CZ-NH1	10.85	125.72	120.30
2	2-B	612	ARG	NE-CZ-NH1	10.83	125.72	120.30
2	6-B	846	ARG	NE-CZ-NH1	10.83	125.71	120.30
3	3-C	218	ARG	NE-CZ-NH2	-10.81	114.89	120.30
1	9-A	604	MET	CG-SD-CE	-10.81	82.91	100.20
2	2-B	216	PHE	CB-CG-CD2	-10.80	113.24	120.80
3	9-D	133	PHE	CB-CG-CD1	10.80	128.36	120.80
3	10-D	192	ARG	NE-CZ-NH2	-10.79	114.91	120.30
2	3-B	827	ARG	NE-CZ-NH1	10.78	125.69	120.30
3	1-D	170	TYR	CB-CG-CD2	10.78	127.47	121.00
3	6-D	114	ARG	NE-CZ-NH2	10.76	125.68	120.30
2	7-B	345	TYR	CB-CG-CD1	10.75	127.45	121.00
2	9-B	776	TYR	CB-CG-CD1	10.75	127.45	121.00
1	3-A	198	ARG	NE-CZ-NH1	10.73	125.66	120.30
3	8-C	133	PHE	CB-CG-CD2	-10.72	113.29	120.80
1	5-A	261	ASP	CB-CG-OD2	-10.72	108.65	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	9-D	176	ARG	NE-CZ-NH1	-10.71	114.95	120.30
1	6-A	597	ARG	NE-CZ-NH2	-10.69	114.95	120.30
1	8-A	251	PHE	CB-CG-CD2	-10.68	113.33	120.80
2	7-B	824	TYR	CB-CG-CD2	10.67	127.40	121.00
1	3-A	450	TYR	CB-CG-CD2	-10.66	114.60	121.00
3	9-D	319	TYR	CB-CG-CD2	-10.66	114.60	121.00
2	6-B	600	TYR	CB-CG-CD1	10.65	127.39	121.00
3	6-C	362	TYR	CB-CG-CD2	-10.65	114.61	121.00
1	1-A	262	ARG	NE-CZ-NH1	10.64	125.62	120.30
2	4-B	824	TYR	CB-CG-CD1	10.62	127.37	121.00
2	5-B	236	TYR	CB-CG-CD2	10.62	127.37	121.00
2	4-B	533	ARG	NE-CZ-NH1	10.61	125.61	120.30
2	7-B	612	ARG	NE-CZ-NH2	-10.60	115.00	120.30
2	6-B	599	PHE	CB-CG-CD2	-10.59	113.39	120.80
3	2-D	83	PHE	CB-CG-CD1	10.57	128.20	120.80
1	8-A	627	ARG	NE-CZ-NH1	-10.57	115.02	120.30
1	3-A	140	TYR	CB-CG-CD2	10.56	127.34	121.00
3	5-C	87	PHE	CB-CG-CD2	-10.56	113.41	120.80
3	8-C	279	TYR	CB-CG-CD2	-10.56	114.67	121.00
3	10-D	282	ASP	CB-CG-OD1	10.56	127.80	118.30
3	5-D	387	PHE	CB-CG-CD1	10.55	128.18	120.80
2	9-B	312	PHE	CB-CG-CD1	10.55	128.18	120.80
3	4-D	387	PHE	CB-CG-CD1	10.54	128.18	120.80
3	3-C	427	ARG	NE-CZ-NH2	-10.54	115.03	120.30
2	8-B	822	ARG	NE-CZ-NH1	10.53	125.56	120.30
1	7-A	775	PHE	CB-CG-CD1	10.53	128.17	120.80
2	7-B	488	PHE	CB-CG-CD2	-10.52	113.44	120.80
3	10-D	218	ARG	NE-CZ-NH1	10.50	125.55	120.30
1	5-A	479	ARG	NE-CZ-NH1	10.50	125.55	120.30
3	7-C	84	ARG	NE-CZ-NH1	10.50	125.55	120.30
1	8-A	171	ARG	NE-CZ-NH2	-10.50	115.05	120.30
3	1-D	55	ARG	NE-CZ-NH1	10.49	125.55	120.30
1	4-A	627	ARG	NE-CZ-NH2	-10.49	115.05	120.30
2	5-B	585	ARG	NE-CZ-NH2	-10.49	115.05	120.30
2	10-B	293	ARG	NE-CZ-NH2	-10.48	115.06	120.30
2	5-B	433	TYR	CB-CG-CD1	10.47	127.28	121.00
2	1-B	183	ASP	CB-CG-OD2	10.45	127.71	118.30
2	4-B	342	TYR	CB-CG-CD2	10.45	127.27	121.00
3	5-D	292	TYR	CB-CG-CD1	-10.44	114.73	121.00
1	9-A	704	TYR	CB-CG-CD1	10.43	127.25	121.00
1	4-A	204	ARG	NE-CZ-NH2	-10.42	115.09	120.30
2	6-B	190	TYR	CB-CG-CD2	-10.40	114.76	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	405	PHE	CB-CG-CD1	10.40	128.08	120.80
1	1-A	296	TYR	CB-CG-CD1	10.39	127.24	121.00
3	10-C	243	ARG	NE-CZ-NH1	10.39	125.49	120.30
3	8-C	193	ARG	NE-CZ-NH2	-10.39	115.11	120.30
2	5-B	411	PHE	CB-CG-CD1	10.38	128.06	120.80
1	1-A	624	ARG	NE-CZ-NH2	-10.38	115.11	120.30
1	1-A	453	ASP	CB-CG-OD2	-10.36	108.97	118.30
2	4-B	593	PHE	CB-CG-CD2	-10.35	113.56	120.80
1	8-A	171	ARG	NE-CZ-NH1	10.35	125.47	120.30
3	7-D	90	ARG	NE-CZ-NH1	10.34	125.47	120.30
1	8-A	78	PHE	CB-CG-CD2	-10.34	113.56	120.80
1	3-A	108	ARG	NE-CZ-NH2	-10.34	115.13	120.30
3	9-D	437	TYR	CB-CG-CD1	10.33	127.20	121.00
1	1-A	171	ARG	NE-CZ-NH1	-10.32	115.14	120.30
3	7-D	244	PHE	CB-CG-CD1	10.32	128.02	120.80
2	9-B	816	TYR	CB-CG-CD2	10.32	127.19	121.00
1	4-A	262	ARG	NE-CZ-NH2	-10.32	115.14	120.30
3	3-C	247	TYR	CB-CG-CD2	-10.31	114.81	121.00
1	1-A	145	PHE	CB-CG-CD1	10.30	128.01	120.80
3	9-D	427	ARG	NE-CZ-NH2	-10.30	115.15	120.30
3	9-C	341	ARG	NE-CZ-NH1	10.30	125.45	120.30
1	5-A	138	PHE	CB-CG-CD2	-10.29	113.59	120.80
3	5-C	423	PHE	CB-CG-CD1	10.29	128.01	120.80
2	1-B	776	TYR	CB-CG-CD1	10.29	127.17	121.00
1	8-A	767	TYR	CB-CG-CD2	10.29	127.17	121.00
1	3-A	76	ARG	NE-CZ-NH1	10.28	125.44	120.30
2	8-B	526	ARG	NE-CZ-NH1	10.28	125.44	120.30
2	4-B	389	ARG	NE-CZ-NH1	10.26	125.43	120.30
2	10-B	598	TYR	CB-CG-CD1	-10.26	114.85	121.00
3	7-C	176	ARG	NE-CZ-NH1	10.25	125.43	120.30
2	5-B	839	PHE	CB-CG-CD1	10.25	127.97	120.80
2	7-B	819	PHE	CB-CG-CD1	10.22	127.95	120.80
2	6-B	816	TYR	CB-CG-CD1	10.21	127.12	121.00
3	5-D	443	ASP	CB-CG-OD1	10.19	127.47	118.30
3	6-C	247	TYR	CB-CG-CD2	-10.20	114.88	121.00
2	9-B	299	ARG	NE-CZ-NH2	-10.19	115.20	120.30
1	5-A	630	ARG	NE-CZ-NH2	-10.18	115.21	120.30
1	9-A	776	ARG	NE-CZ-NH1	10.18	125.39	120.30
3	9-D	192	ARG	NE-CZ-NH1	10.17	125.38	120.30
3	10-C	249	TYR	CD1-CE1-CZ	10.15	128.94	119.80
2	5-B	652	TYR	CB-CG-CD2	-10.15	114.91	121.00
3	10-C	362	TYR	CB-CG-CD2	-10.15	114.91	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-A	116	TYR	CB-CG-CD1	10.14	127.09	121.00
3	6-C	341	ARG	NE-CZ-NH2	-10.14	115.23	120.30
2	9-B	583	TYR	CB-CG-CD1	10.14	127.08	121.00
1	3-A	349	ARG	NE-CZ-NH1	10.13	125.36	120.30
3	9-C	176	ARG	NE-CZ-NH2	-10.12	115.24	120.30
1	2-A	398	TYR	CB-CG-CD1	-10.11	114.94	121.00
3	1-C	160	ASP	CB-CG-OD1	10.10	127.39	118.30
1	4-A	594	TYR	CB-CG-CD2	-10.10	114.94	121.00
1	9-A	691	ASP	CB-CG-OD1	-10.09	109.22	118.30
1	1-A	74	TYR	CB-CG-CD1	10.09	127.05	121.00
3	4-D	54	PHE	CB-CG-CD2	-10.09	113.74	120.80
3	7-C	407	TYR	CB-CG-CD2	10.08	127.05	121.00
1	10-A	594	TYR	CB-CG-CD1	10.07	127.05	121.00
3	7-D	161	ARG	NE-CZ-NH1	10.07	125.33	120.30
2	5-B	758	TYR	CB-CG-CD1	-10.06	114.96	121.00
1	8-A	349	ARG	NE-CZ-NH1	10.06	125.33	120.30
1	3-A	251	PHE	CB-CG-CD2	-10.06	113.76	120.80
2	2-B	187	TYR	CB-CG-CD2	-10.05	114.97	121.00
2	2-B	638	ARG	NE-CZ-NH1	10.05	125.33	120.30
2	5-B	293	ARG	NE-CZ-NH2	-10.04	115.28	120.30
3	5-D	362	TYR	CB-CG-CD1	10.04	127.03	121.00
1	6-A	458	TYR	CB-CG-CD1	-10.03	114.98	121.00
2	9-B	187	TYR	CB-CG-CD2	-10.03	114.98	121.00
3	5-C	170	TYR	CB-CG-CD2	10.02	127.01	121.00
3	8-D	341	ARG	NE-CZ-NH2	-10.02	115.29	120.30
3	5-C	249	TYR	CB-CG-CD2	-10.02	114.99	121.00
3	1-C	223	ASP	CB-CG-OD2	-10.01	109.29	118.30
3	1-C	437	TYR	CB-CG-CD2	-10.01	115.00	121.00
2	1-B	741	PHE	CB-CG-CD2	-10.01	113.80	120.80
2	1-B	285	ARG	NE-CZ-NH2	10.00	125.30	120.30
2	3-B	312	PHE	CB-CG-CD1	-10.00	113.80	120.80
2	6-B	592	ARG	NE-CZ-NH1	10.00	125.30	120.30
2	6-B	846	ARG	NE-CZ-NH2	-9.99	115.31	120.30
2	2-B	356	ARG	NE-CZ-NH2	-9.97	115.31	120.30
2	5-B	514	ARG	NE-CZ-NH1	9.96	125.28	120.30
3	4-C	131	ASP	CB-CG-OD1	9.95	127.25	118.30
3	5-C	247	TYR	CB-CG-CD1	9.95	126.97	121.00
2	7-B	362	PHE	CB-CG-CD2	-9.94	113.84	120.80
1	1-A	327	ARG	NE-CZ-NH2	-9.93	115.34	120.30
3	1-C	398	PHE	CB-CG-CD1	9.93	127.75	120.80
3	8-D	87	PHE	CB-CG-CD1	-9.93	113.85	120.80
1	3-A	325	PHE	CB-CG-CD1	-9.92	113.86	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	664	ARG	NE-CZ-NH2	-9.92	115.34	120.30
2	2-B	819	PHE	CB-CG-CD1	9.92	127.74	120.80
3	6-C	316	PHE	CB-CG-CD1	9.91	127.74	120.80
2	2-B	328	ARG	NE-CZ-NH1	9.91	125.25	120.30
1	3-A	144	ARG	NE-CZ-NH2	-9.90	115.35	120.30
1	4-A	793	PHE	CB-CG-CD2	9.90	127.73	120.80
2	4-B	585	ARG	NE-CZ-NH1	-9.90	115.35	120.30
3	1-D	176	ARG	NE-CZ-NH2	-9.90	115.35	120.30
1	6-A	562	PHE	CB-CG-CD2	9.90	127.73	120.80
2	6-B	438	TYR	CB-CG-CD1	-9.87	115.08	121.00
3	4-D	295	MET	CG-SD-CE	-9.87	84.42	100.20
1	7-A	486	PHE	CB-CG-CD2	9.86	127.70	120.80
3	2-D	114	ARG	NE-CZ-NH2	9.86	125.23	120.30
1	4-A	279	TYR	CB-CG-CD1	-9.84	115.10	121.00
3	5-C	86	PHE	CB-CG-CD1	9.83	127.68	120.80
1	9-A	646	TYR	CB-CG-CD1	-9.83	115.10	121.00
3	1-D	161	ARG	NE-CZ-NH2	-9.82	115.39	120.30
1	4-A	410	PHE	CB-CG-CD2	-9.82	113.92	120.80
1	6-A	438	PHE	CB-CG-CD1	9.82	127.67	120.80
1	6-A	92	PHE	CB-CG-CD2	-9.81	113.93	120.80
1	6-A	478	MET	CG-SD-CE	-9.80	84.52	100.20
1	2-A	116	TYR	CB-CG-CD2	-9.80	115.12	121.00
3	8-D	272	PHE	CB-CG-CD2	-9.80	113.94	120.80
2	5-B	824	TYR	CB-CG-CD2	-9.79	115.12	121.00
2	8-B	409	TYR	CB-CG-CD1	-9.79	115.12	121.00
2	9-B	731	PHE	CB-CG-CD2	-9.79	113.94	120.80
2	1-B	612	ARG	NE-CZ-NH2	-9.77	115.41	120.30
1	4-A	137	ARG	NE-CZ-NH2	-9.77	115.41	120.30
2	4-B	652	TYR	CB-CG-CD1	-9.77	115.14	121.00
1	10-A	121	ARG	NE-CZ-NH1	-9.77	115.42	120.30
1	6-A	197	PHE	CB-CG-CD2	-9.76	113.97	120.80
2	2-B	468	PHE	CB-CG-CD1	-9.75	113.98	120.80
3	8-D	192	ARG	NE-CZ-NH2	9.74	125.17	120.30
3	1-C	55	ARG	NE-CZ-NH2	-9.73	115.43	120.30
2	9-B	359	TYR	CB-CG-CD1	9.72	126.83	121.00
2	2-B	475	PHE	CB-CG-CD2	-9.71	114.00	120.80
3	3-C	243	ARG	NE-CZ-NH1	9.67	125.14	120.30
1	3-A	102	PHE	CB-CG-CD2	-9.67	114.03	120.80
1	7-A	400	ARG	NE-CZ-NH1	9.67	125.13	120.30
2	5-B	300	PHE	CB-CG-CD1	9.67	127.57	120.80
1	8-A	791	PHE	CB-CG-CD1	-9.67	114.03	120.80
3	5-D	136	PHE	CB-CG-CD1	9.66	127.56	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-D	423	PHE	CB-CG-CD2	-9.65	114.05	120.80
1	7-A	138	PHE	CB-CG-CD2	9.64	127.55	120.80
1	9-A	171	ARG	NE-CZ-NH1	9.63	125.12	120.30
2	8-B	284	TYR	CB-CG-CD1	-9.62	115.23	121.00
3	1-C	329	ARG	NE-CZ-NH1	9.62	125.11	120.30
2	4-B	824	TYR	CB-CG-CD2	-9.61	115.23	121.00
2	4-B	187	TYR	CG-CD1-CE1	-9.60	113.62	121.30
2	2-B	312	PHE	CB-CG-CD1	9.58	127.51	120.80
1	5-A	458	TYR	CB-CG-CD1	9.58	126.75	121.00
1	10-A	633	HIS	CA-CB-CG	9.58	129.88	113.60
1	6-A	193	TYR	CB-CG-CD2	-9.57	115.25	121.00
1	8-A	393	TYR	CB-CG-CD1	-9.57	115.26	121.00
1	5-A	381	PHE	CB-CG-CD1	9.56	127.50	120.80
1	5-A	623	ARG	NE-CZ-NH2	-9.56	115.52	120.30
2	9-B	319	PHE	CB-CG-CD1	9.56	127.49	120.80
2	7-B	295	ARG	NE-CZ-NH2	-9.55	115.52	120.30
2	9-B	839	PHE	CB-CG-CD1	9.55	127.49	120.80
3	6-C	398	PHE	CB-CG-CD2	-9.55	114.12	120.80
3	7-D	272	PHE	CB-CG-CD2	-9.55	114.12	120.80
3	6-C	443	ASP	CB-CG-OD1	9.54	126.89	118.30
1	6-A	588	TYR	CB-CG-CD1	9.54	126.72	121.00
3	10-C	329	ARG	NE-CZ-NH1	9.54	125.07	120.30
2	5-B	772	PHE	CB-CG-CD1	9.54	127.47	120.80
2	8-B	319	PHE	CB-CG-CD2	-9.54	114.13	120.80
1	6-A	381	PHE	CB-CG-CD2	-9.53	114.13	120.80
3	2-D	267	PHE	CB-CG-CD2	-9.52	114.13	120.80
1	6-A	663	TYR	CB-CG-CD1	9.51	126.71	121.00
1	3-A	410	PHE	CB-CG-CD1	9.51	127.45	120.80
3	8-C	78	ASP	CB-CG-OD2	-9.51	109.75	118.30
3	5-D	267	PHE	CB-CG-CD1	9.50	127.45	120.80
1	10-A	795	ASP	CB-CG-OD1	9.50	126.85	118.30
3	5-D	267	PHE	CB-CG-CD2	-9.50	114.15	120.80
2	4-B	666	ARG	NE-CZ-NH2	-9.50	115.55	120.30
3	8-C	437	TYR	CB-CG-CD2	-9.50	115.30	121.00
3	1-D	315	TYR	CB-CG-CD2	-9.49	115.30	121.00
1	9-A	624	ARG	NE-CZ-NH1	9.49	125.05	120.30
2	8-B	295	ARG	NE-CZ-NH2	-9.49	115.56	120.30
2	7-B	295	ARG	NE-CZ-NH1	9.48	125.04	120.30
3	7-C	244	PHE	CB-CG-CD1	9.48	127.44	120.80
3	8-C	217	PHE	CB-CG-CD1	-9.48	114.16	120.80
3	3-C	34	ASP	CB-CG-OD1	9.48	126.83	118.30
1	6-A	107	ARG	NE-CZ-NH1	9.47	125.03	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	7-B	200	PHE	CB-CG-CD2	-9.47	114.17	120.80
2	7-B	599	PHE	CB-CG-CD1	9.46	127.42	120.80
3	7-C	319	TYR	CB-CG-CD2	9.45	126.67	121.00
3	1-D	387	PHE	CB-CG-CD2	-9.45	114.19	120.80
2	8-B	544	ARG	NE-CZ-NH2	-9.44	115.58	120.30
3	1-D	315	TYR	CB-CG-CD1	9.44	126.66	121.00
2	6-B	295	ARG	NE-CZ-NH1	9.44	125.02	120.30
3	1-C	279	TYR	CB-CG-CD2	-9.44	115.34	121.00
2	6-B	533	ARG	NE-CZ-NH2	-9.44	115.58	120.30
1	3-A	587	ARG	NE-CZ-NH1	9.43	125.02	120.30
3	1-D	333	ARG	NE-CZ-NH2	-9.43	115.59	120.30
2	5-B	652	TYR	CB-CG-CD1	9.43	126.66	121.00
1	7-A	627	ARG	NE-CZ-NH1	9.42	125.01	120.30
3	2-D	437	TYR	CB-CG-CD2	-9.41	115.35	121.00
1	10-A	349	ARG	NE-CZ-NH2	-9.40	115.60	120.30
2	3-B	776	TYR	CB-CG-CD1	9.40	126.64	121.00
3	9-C	279	TYR	CB-CG-CD1	9.40	126.64	121.00
3	2-D	59	ARG	NE-CZ-NH1	9.39	125.00	120.30
3	7-C	411	ASP	CB-CG-OD2	9.39	126.75	118.30
2	8-B	587	PHE	CB-CG-CD2	-9.38	114.23	120.80
2	9-B	651	TYR	CB-CG-CD2	9.38	126.63	121.00
1	3-A	262	ARG	NE-CZ-NH1	9.38	124.99	120.30
3	7-D	55	ARG	NE-CZ-NH2	-9.35	115.63	120.30
3	7-C	362	TYR	CB-CG-CD2	-9.34	115.39	121.00
3	7-C	407	TYR	CB-CG-CD1	-9.33	115.40	121.00
2	8-B	236	TYR	CB-CG-CD2	-9.33	115.40	121.00
3	2-D	445	TYR	CB-CG-CD2	-9.32	115.41	121.00
1	10-A	793	PHE	CB-CG-CD2	-9.32	114.28	120.80
1	10-A	116	TYR	N-CA-CB	9.30	127.34	110.60
2	10-B	520	VAL	CA-CB-CG2	9.29	124.84	110.90
2	9-B	612	ARG	NE-CZ-NH1	9.29	124.94	120.30
1	7-A	410	PHE	CB-CG-CD2	-9.28	114.30	120.80
2	9-B	288	TYR	CB-CG-CD2	-9.28	115.43	121.00
1	6-A	171	ARG	NE-CZ-NH2	9.28	124.94	120.30
2	9-B	242	ARG	NE-CZ-NH2	-9.27	115.67	120.30
1	3-A	160	ARG	NE-CZ-NH1	9.26	124.93	120.30
3	9-D	65	ARG	NE-CZ-NH1	-9.26	115.67	120.30
3	5-D	403	PHE	CB-CG-CD2	-9.25	114.33	120.80
2	8-B	633	ARG	NE-CZ-NH2	-9.24	115.68	120.30
3	9-C	341	ARG	NE-CZ-NH2	-9.24	115.68	120.30
1	1-A	145	PHE	CB-CG-CD2	-9.23	114.33	120.80
2	9-B	187	TYR	CB-CG-CD1	9.23	126.54	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3-D	162	TYR	CB-CG-CD1	-9.22	115.47	121.00
1	9-A	597	ARG	NE-CZ-NH1	-9.22	115.69	120.30
2	4-B	393	PHE	CB-CG-CD2	-9.22	114.34	120.80
1	10-A	251	PHE	CB-CG-CD1	9.22	127.25	120.80
3	10-C	162	TYR	CB-CG-CD2	-9.22	115.47	121.00
1	6-A	203	ARG	NE-CZ-NH1	9.22	124.91	120.30
2	10-B	345	TYR	CB-CG-CD1	9.21	126.53	121.00
3	7-C	170	TYR	CB-CG-CD2	-9.21	115.47	121.00
2	6-B	514	ARG	NE-CZ-NH2	-9.21	115.69	120.30
2	9-B	453	TYR	CB-CG-CD2	9.20	126.52	121.00
2	3-B	651	TYR	CB-CG-CD1	9.19	126.52	121.00
1	4-A	469	ARG	NE-CZ-NH1	9.19	124.89	120.30
1	8-A	568	TYR	CG-CD2-CE2	-9.18	113.95	121.30
1	3-A	171	ARG	NE-CZ-NH1	9.18	124.89	120.30
1	5-A	450	TYR	CB-CG-CD2	-9.18	115.49	121.00
2	2-B	409	TYR	CB-CG-CD1	9.18	126.51	121.00
3	3-D	430	VAL	CA-CB-CG1	-9.18	97.14	110.90
3	6-C	124	ASP	CB-CG-OD1	-9.18	110.04	118.30
1	4-A	639	PHE	CB-CG-CD2	-9.17	114.38	120.80
1	10-A	105	PHE	CB-CG-CD1	-9.17	114.38	120.80
3	8-D	53	PHE	CB-CG-CD2	-9.16	114.39	120.80
2	10-B	599	PHE	CB-CG-CD1	9.16	127.21	120.80
2	10-B	776	TYR	CB-CG-CD1	9.16	126.49	121.00
3	3-D	84	ARG	NE-CZ-NH2	9.14	124.87	120.30
2	1-B	514	ARG	NE-CZ-NH2	-9.14	115.73	120.30
3	7-D	407	TYR	CB-CG-CD1	-9.14	115.52	121.00
3	7-C	398	PHE	CB-CG-CD2	-9.13	114.41	120.80
3	9-C	445	TYR	CB-CG-CD1	-9.13	115.52	121.00
1	9-A	112	TYR	CB-CG-CD2	-9.12	115.53	121.00
3	3-D	193	ARG	NE-CZ-NH1	9.11	124.85	120.30
3	3-D	256	TYR	CB-CG-CD2	-9.11	115.53	121.00
2	10-B	342	TYR	CB-CG-CD1	9.11	126.47	121.00
3	6-C	55	ARG	NE-CZ-NH2	-9.11	115.75	120.30
3	8-C	445	TYR	CB-CG-CD2	-9.11	115.54	121.00
2	8-B	190	TYR	CB-CG-CD1	9.10	126.46	121.00
1	3-A	706	PHE	CB-CG-CD1	-9.10	114.43	120.80
3	6-C	249	TYR	CB-CG-CD2	-9.09	115.54	121.00
3	4-C	109	TYR	CB-CG-CD2	-9.09	115.55	121.00
2	6-B	827	ARG	NE-CZ-NH2	-9.09	115.75	120.30
1	10-A	594	TYR	CB-CG-CD2	-9.09	115.55	121.00
3	6-D	437	TYR	CB-CG-CD1	9.09	126.45	121.00
1	10-A	251	PHE	CB-CG-CD2	-9.09	114.44	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	10-C	403	PHE	CB-CG-CD1	-9.09	114.44	120.80
3	5-D	292	TYR	CB-CG-CD2	9.08	126.45	121.00
3	9-D	314	THR	CA-CB-CG2	-9.08	99.68	112.40
1	4-A	714	ARG	NE-CZ-NH1	-9.08	115.76	120.30
3	3-D	173	PHE	CB-CG-CD1	9.08	127.15	120.80
1	2-A	687	ARG	NE-CZ-NH1	9.07	124.84	120.30
3	7-C	161	ARG	NE-CZ-NH1	9.06	124.83	120.30
3	7-D	427	ARG	NE-CZ-NH1	9.05	124.83	120.30
1	5-A	793	PHE	CB-CG-CD1	9.05	127.14	120.80
1	3-A	102	PHE	CB-CG-CD1	9.05	127.13	120.80
3	6-D	329	ARG	NE-CZ-NH2	9.04	124.82	120.30
1	6-A	639	PHE	CB-CG-CD2	9.04	127.13	120.80
2	9-B	200	PHE	CB-CG-CD2	-9.04	114.47	120.80
1	5-A	74	TYR	CB-CG-CD1	-9.04	115.58	121.00
1	5-A	102	PHE	CB-CG-CD1	9.03	127.12	120.80
3	9-C	87	PHE	CB-CG-CD2	-9.03	114.48	120.80
3	5-D	247	TYR	CZ-CE2-CD2	-9.02	111.68	119.80
3	10-C	50	THR	CA-CB-CG2	-9.02	99.77	112.40
3	8-D	403	PHE	CB-CG-CD2	-9.01	114.49	120.80
2	10-B	242	ARG	NE-CZ-NH2	9.01	124.81	120.30
2	3-B	379	TYR	CB-CG-CD2	-9.01	115.59	121.00
1	6-A	451	ARG	NE-CZ-NH2	-9.01	115.80	120.30
3	3-C	65	ARG	NE-CZ-NH1	9.01	124.80	120.30
3	4-D	341	ARG	NE-CZ-NH1	9.00	124.80	120.30
1	9-A	775	PHE	CB-CG-CD2	-9.00	114.50	120.80
3	1-D	272	PHE	CB-CG-CD2	-9.00	114.50	120.80
1	7-A	426	PHE	CB-CG-CD2	-8.99	114.51	120.80
1	7-A	372	ASP	CB-CG-OD2	8.99	126.39	118.30
1	8-A	204	ARG	NE-CZ-NH1	8.98	124.79	120.30
1	4-A	646	TYR	CB-CG-CD1	-8.98	115.61	121.00
1	8-A	193	TYR	CB-CG-CD1	8.97	126.38	121.00
3	5-D	192	ARG	NE-CZ-NH2	-8.96	115.82	120.30
3	9-D	162	TYR	CB-CG-CD2	-8.96	115.62	121.00
1	3-A	393	TYR	CB-CG-CD1	-8.96	115.63	121.00
2	3-B	609	ASP	CB-CG-OD2	-8.96	110.24	118.30
2	5-B	580	ARG	NE-CZ-NH2	-8.96	115.82	120.30
2	10-B	225	PHE	CB-CG-CD1	8.96	127.07	120.80
1	1-A	131	PHE	CB-CG-CD1	8.95	127.06	120.80
1	7-A	633	HIS	CA-CB-CG	8.95	128.81	113.60
2	8-B	641	PHE	CB-CG-CD2	-8.94	114.54	120.80
1	3-A	663	TYR	CB-CG-CD2	-8.94	115.64	121.00
3	4-D	394	PHE	CB-CG-CD2	-8.94	114.55	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	6-C	427	ARG	NE-CZ-NH2	-8.94	115.83	120.30
3	3-D	88	ASP	CB-CG-OD1	-8.93	110.26	118.30
1	5-A	438	PHE	CB-CG-CD1	8.93	127.05	120.80
1	4-A	614	TYR	CB-CG-CD2	8.92	126.35	121.00
3	3-D	84	ARG	NE-CZ-NH1	-8.91	115.85	120.30
2	7-B	342	TYR	CB-CG-CD2	8.90	126.34	121.00
1	8-A	296	TYR	CB-CG-CD2	-8.90	115.66	121.00
1	5-A	123	TYR	CD1-CE1-CZ	8.89	127.80	119.80
3	7-C	46	ARG	NE-CZ-NH1	8.88	124.74	120.30
3	7-D	247	TYR	CB-CG-CD2	-8.88	115.67	121.00
2	3-B	312	PHE	CB-CG-CD2	8.88	127.01	120.80
2	7-B	816	TYR	CB-CG-CD1	-8.88	115.67	121.00
2	3-B	816	TYR	CB-CG-CD2	-8.87	115.68	121.00
3	6-D	427	ARG	NE-CZ-NH2	-8.87	115.86	120.30
3	7-D	316	PHE	CB-CG-CD1	8.87	127.01	120.80
1	10-A	157	ARG	NE-CZ-NH1	8.87	124.73	120.30
3	1-C	87	PHE	CB-CG-CD1	8.86	127.00	120.80
2	9-B	839	PHE	CB-CG-CD2	-8.86	114.60	120.80
3	5-D	275	PHE	CB-CG-CD1	8.86	127.00	120.80
1	7-A	714	ARG	NE-CZ-NH1	8.86	124.73	120.30
1	9-A	413	TYR	CB-CG-CD1	8.85	126.31	121.00
2	10-B	580	ARG	NE-CZ-NH2	8.85	124.72	120.30
3	1-C	170	TYR	CB-CG-CD1	-8.84	115.70	121.00
1	8-A	108	ARG	NE-CZ-NH1	8.83	124.72	120.30
2	1-B	587	PHE	CB-CG-CD1	8.83	126.98	120.80
2	5-B	415	TYR	CB-CG-CD1	8.83	126.30	121.00
2	4-B	470	TYR	CG-CD1-CE1	8.82	128.36	121.30
3	4-D	362	TYR	CB-CG-CD1	8.82	126.29	121.00
3	5-D	173	PHE	CB-CG-CD2	8.82	126.97	120.80
1	6-A	704	TYR	CB-CG-CD2	-8.82	115.71	121.00
3	4-D	161	ARG	NE-CZ-NH2	-8.82	115.89	120.30
1	7-A	647	PHE	CB-CG-CD2	-8.82	114.63	120.80
2	10-B	335	PHE	CB-CG-CD1	-8.82	114.63	120.80
1	7-A	393	TYR	CB-CG-CD1	-8.81	115.71	121.00
1	5-A	360	SER	C-N-CA	8.81	143.73	121.70
3	7-C	54	PHE	CB-CG-CD1	-8.81	114.63	120.80
3	2-C	279	TYR	CB-CG-CD1	8.80	126.28	121.00
1	3-A	410	PHE	CB-CG-CD2	-8.81	114.64	120.80
3	2-D	41	ASP	CB-CG-OD1	-8.80	110.38	118.30
3	3-C	87	PHE	CB-CG-CD2	8.80	126.96	120.80
1	4-A	108	ARG	NE-CZ-NH1	8.80	124.70	120.30
1	2-A	623	ARG	NE-CZ-NH2	-8.80	115.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5-A	168	PHE	CB-CG-CD1	-8.79	114.65	120.80
1	6-A	400	ARG	NE-CZ-NH2	-8.78	115.91	120.30
1	6-A	663	TYR	CB-CG-CD2	-8.78	115.73	121.00
2	10-B	824	TYR	CB-CG-CD2	-8.77	115.74	121.00
3	6-C	292	TYR	CB-CG-CD1	8.77	126.26	121.00
3	6-D	267	PHE	CB-CG-CD1	8.76	126.94	120.80
3	3-C	358	ARG	NE-CZ-NH2	8.76	124.68	120.30
3	8-C	394	PHE	CB-CG-CD1	8.76	126.93	120.80
3	9-C	176	ARG	NE-CZ-NH1	8.76	124.68	120.30
1	7-A	198	ARG	NE-CZ-NH2	-8.75	115.93	120.30
1	2-A	372	ASP	CB-CG-OD1	-8.74	110.43	118.30
3	8-C	398	PHE	CB-CG-CD2	-8.74	114.68	120.80
1	10-A	168	PHE	CB-CG-CD1	8.74	126.92	120.80
2	10-B	380	HIS	CA-CB-CG	8.74	128.46	113.60
2	5-B	285	ARG	NE-CZ-NH2	-8.73	115.93	120.30
1	3-A	161	ASP	CB-CG-OD2	-8.73	110.44	118.30
2	1-B	666	ARG	NE-CZ-NH2	-8.73	115.94	120.30
3	6-D	315	TYR	CG-CD1-CE1	-8.73	114.32	121.30
3	1-D	65	ARG	NE-CZ-NH2	-8.73	115.94	120.30
2	5-B	585	ARG	NE-CZ-NH1	8.73	124.66	120.30
3	9-C	59	ARG	NE-CZ-NH1	8.73	124.66	120.30
1	5-A	413	TYR	CZ-CE2-CD2	-8.72	111.95	119.80
2	8-B	438	TYR	CG-CD1-CE1	-8.72	114.32	121.30
3	10-D	387	PHE	CB-CG-CD2	-8.72	114.69	120.80
1	7-A	395	ASP	CB-CG-OD1	8.71	126.14	118.30
3	7-C	87	PHE	CB-CG-CD2	-8.71	114.70	120.80
3	2-D	41	ASP	CB-CG-OD2	8.71	126.14	118.30
2	1-B	816	TYR	CB-CG-CD2	-8.71	115.78	121.00
3	3-D	292	TYR	CB-CG-CD1	-8.71	115.78	121.00
3	6-C	133	PHE	CB-CG-CD2	-8.70	114.71	120.80
1	7-A	102	PHE	CB-CG-CD1	8.70	126.89	120.80
3	7-C	109	TYR	CB-CG-CD1	-8.70	115.78	121.00
2	9-B	526	ARG	NE-CZ-NH2	8.70	124.65	120.30
3	1-C	341	ARG	NE-CZ-NH1	-8.69	115.95	120.30
2	5-B	526	ARG	NE-CZ-NH1	8.69	124.64	120.30
3	10-C	335	MET	CG-SD-CE	-8.69	86.30	100.20
1	6-A	296	TYR	CB-CG-CD1	-8.69	115.79	121.00
3	7-D	279	TYR	CB-CG-CD1	8.68	126.21	121.00
2	7-B	433	TYR	CB-CG-CD1	-8.68	115.79	121.00
2	7-B	583	TYR	CB-CG-CD1	8.68	126.21	121.00
3	6-C	243	ARG	NE-CZ-NH2	8.67	124.64	120.30
3	7-C	44	THR	CA-CB-CG2	-8.67	100.26	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	5-D	387	PHE	CB-CG-CD2	-8.67	114.73	120.80
2	1-B	580	ARG	NE-CZ-NH1	-8.66	115.97	120.30
1	6-A	588	TYR	CB-CG-CD2	-8.66	115.81	121.00
1	2-A	190	TYR	CB-CG-CD1	8.66	126.19	121.00
2	10-B	264	TYR	CD1-CE1-CZ	-8.66	112.01	119.80
1	8-A	703	VAL	CA-CB-CG2	8.65	123.88	110.90
2	1-B	345	TYR	CG-CD1-CE1	-8.65	114.38	121.30
1	5-A	150	TYR	CB-CG-CD1	-8.65	115.81	121.00
2	4-B	288	TYR	CB-CG-CD1	-8.65	115.81	121.00
2	7-B	776	TYR	CB-CG-CD1	8.65	126.19	121.00
1	4-A	123	TYR	CB-CG-CD2	8.64	126.18	121.00
1	6-A	140	TYR	CB-CG-CD2	-8.64	115.82	121.00
3	8-C	335	MET	CG-SD-CE	-8.64	86.38	100.20
2	9-B	343	TYR	CB-CG-CD1	8.63	126.18	121.00
1	5-A	413	TYR	CB-CG-CD2	8.63	126.18	121.00
2	7-B	231	TYR	CB-CG-CD1	-8.62	115.83	121.00
3	3-C	403	PHE	CB-CG-CD1	-8.62	114.77	120.80
3	9-C	319	TYR	CB-CG-CD2	-8.62	115.83	121.00
3	3-D	20	PHE	CB-CG-CD2	-8.62	114.77	120.80
3	5-D	249	TYR	CB-CG-CD1	-8.62	115.83	121.00
2	6-B	409	TYR	CB-CG-CD2	-8.62	115.83	121.00
1	8-A	284	TYR	CB-CG-CD1	-8.62	115.83	121.00
2	10-B	335	PHE	CB-CG-CD2	8.62	126.83	120.80
1	4-A	190	TYR	CB-CG-CD2	-8.61	115.83	121.00
2	2-B	776	TYR	CB-CG-CD2	-8.61	115.84	121.00
3	2-C	205	ASP	CB-CG-OD2	8.60	126.04	118.30
3	10-C	185	TYR	CB-CG-CD2	-8.60	115.84	121.00
1	9-A	646	TYR	CB-CG-CD2	8.60	126.16	121.00
3	10-C	68	MET	CG-SD-CE	-8.60	86.44	100.20
1	8-A	193	TYR	CB-CG-CD2	-8.59	115.85	121.00
1	2-A	663	TYR	CB-CG-CD2	8.58	126.15	121.00
2	5-B	319	PHE	CB-CG-CD2	-8.58	114.79	120.80
1	1-A	334	ASP	CB-CG-OD1	-8.58	110.58	118.30
1	5-A	413	TYR	CG-CD2-CE2	8.58	128.16	121.30
2	3-B	741	PHE	CB-CG-CD2	-8.57	114.80	120.80
2	1-B	661	PHE	CB-CG-CD2	-8.57	114.80	120.80
1	3-A	150	TYR	CZ-CE2-CD2	8.56	127.51	119.80
1	10-A	168	PHE	CB-CG-CD2	-8.56	114.81	120.80
2	10-B	612	ARG	NE-CZ-NH2	-8.54	116.03	120.30
1	9-A	794	TYR	CB-CG-CD2	-8.54	115.88	121.00
2	4-B	514	ARG	NE-CZ-NH1	8.53	124.56	120.30
1	5-A	458	TYR	CB-CG-CD2	-8.53	115.88	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	9-D	86	PHE	CB-CG-CD2	-8.53	114.83	120.80
3	7-D	329	ARG	NE-CZ-NH1	8.52	124.56	120.30
1	1-A	74	TYR	CB-CG-CD2	-8.52	115.89	121.00
1	8-A	137	ARG	NE-CZ-NH1	8.52	124.56	120.30
2	1-B	356	ARG	NE-CZ-NH2	-8.51	116.05	120.30
1	8-A	458	TYR	CB-CG-CD1	8.51	126.10	121.00
3	4-D	20	PHE	CB-CG-CD2	-8.50	114.85	120.80
3	4-D	136	PHE	CB-CG-CD1	8.50	126.75	120.80
3	8-D	421	ASP	CB-CG-OD2	8.50	125.95	118.30
3	9-C	437	TYR	CB-CG-CD1	-8.50	115.90	121.00
2	10-B	187	TYR	CB-CG-CD2	-8.50	115.90	121.00
1	2-A	190	TYR	CB-CG-CD2	-8.49	115.90	121.00
1	9-A	117	MET	CG-SD-CE	-8.49	86.61	100.20
2	5-B	816	TYR	CG-CD2-CE2	8.49	128.09	121.30
2	6-B	187	TYR	CB-CG-CD2	-8.49	115.91	121.00
1	9-A	393	TYR	CB-CG-CD2	-8.49	115.91	121.00
1	1-A	614	TYR	CG-CD1-CE1	8.48	128.09	121.30
1	1-A	410	PHE	CB-CG-CD2	-8.48	114.86	120.80
3	1-D	83	PHE	CB-CG-CD2	-8.48	114.86	120.80
2	4-B	471	ARG	NE-CZ-NH1	8.48	124.54	120.30
2	3-B	666	ARG	NE-CZ-NH1	8.48	124.54	120.30
3	6-C	362	TYR	CB-CG-CD1	8.48	126.09	121.00
1	8-A	182	VAL	CA-CB-CG2	8.48	123.62	110.90
3	9-D	423	PHE	CB-CG-CD2	8.48	126.73	120.80
1	6-A	336	ASP	CB-CG-OD1	8.47	125.93	118.30
3	7-D	359	ARG	NE-CZ-NH2	-8.47	116.06	120.30
1	7-A	251	PHE	CB-CG-CD1	8.47	126.73	120.80
3	5-C	109	TYR	CB-CG-CD2	-8.47	115.92	121.00
2	7-B	200	PHE	CB-CG-CD1	8.46	126.72	120.80
2	4-B	243	MET	CG-SD-CE	-8.46	86.66	100.20
3	6-D	249	TYR	CG-CD1-CE1	8.46	128.07	121.30
2	10-B	231	TYR	CB-CG-CD2	-8.46	115.92	121.00
3	6-C	341	ARG	NE-CZ-NH1	8.46	124.53	120.30
2	5-B	453	TYR	CB-CG-CD2	-8.45	115.93	121.00
3	10-D	223	ASP	CB-CG-OD2	-8.45	110.69	118.30
1	6-A	262	ARG	NE-CZ-NH2	-8.45	116.08	120.30
1	5-A	198	ARG	NE-CZ-NH1	8.44	124.52	120.30
3	7-D	403	PHE	CB-CG-CD1	-8.43	114.90	120.80
1	9-A	324	TYR	CB-CG-CD1	8.43	126.06	121.00
1	4-A	157	ARG	NE-CZ-NH2	-8.42	116.09	120.30
1	9-A	558	TYR	CB-CG-CD2	-8.42	115.95	121.00
3	4-C	309	ALA	N-CA-CB	8.42	121.89	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5-B	409	TYR	CG-CD1-CE1	8.42	128.03	121.30
2	1-B	471	ARG	NE-CZ-NH1	8.41	124.50	120.30
1	10-A	450	TYR	CB-CG-CD1	-8.41	115.95	121.00
1	9-A	657	TYR	CB-CG-CD1	8.40	126.04	121.00
2	10-B	285	ARG	NE-CZ-NH2	8.40	124.50	120.30
3	2-C	333	ARG	NE-CZ-NH1	8.40	124.50	120.30
3	5-C	292	TYR	CB-CG-CD2	-8.40	115.96	121.00
1	6-A	486	PHE	CB-CG-CD1	8.40	126.68	120.80
3	6-D	335	MET	CG-SD-CE	-8.40	86.76	100.20
1	8-A	647	PHE	CB-CG-CD1	8.40	126.68	120.80
3	5-D	55	ARG	NE-CZ-NH1	8.40	124.50	120.30
1	3-A	450	TYR	CB-CG-CD1	8.39	126.04	121.00
3	10-D	136	PHE	CB-CG-CD2	-8.39	114.92	120.80
2	3-B	526	ARG	NE-CZ-NH2	-8.39	116.10	120.30
3	6-C	325	ASN	N-CA-CB	8.39	125.70	110.60
1	2-A	349	ARG	NE-CZ-NH2	-8.38	116.11	120.30
1	4-A	111	ARG	NE-CZ-NH1	8.38	124.49	120.30
2	2-B	805	PHE	CB-CG-CD1	8.38	126.66	120.80
1	5-A	568	TYR	CG-CD1-CE1	-8.38	114.60	121.30
3	5-C	283	ASP	CB-CG-OD2	8.38	125.84	118.30
3	10-D	387	PHE	CB-CG-CD1	8.38	126.67	120.80
1	6-A	414	ASP	CB-CG-OD2	-8.38	110.76	118.30
3	10-D	333	ARG	NE-CZ-NH1	8.38	124.49	120.30
2	9-B	731	PHE	CB-CG-CD1	8.37	126.66	120.80
1	7-A	165	VAL	N-CA-C	-8.37	88.41	111.00
1	3-A	576	ARG	NE-CZ-NH2	-8.37	116.12	120.30
1	9-A	614	TYR	CB-CG-CD2	8.36	126.01	121.00
1	7-A	278	ASP	CB-CG-OD2	-8.35	110.78	118.30
1	9-A	198	ARG	NE-CZ-NH2	-8.35	116.12	120.30
3	5-C	39	LEU	CB-CG-CD1	8.34	125.18	111.00
1	8-A	78	PHE	CB-CG-CD1	8.34	126.64	120.80
2	5-B	362	PHE	CB-CG-CD1	-8.34	114.96	120.80
2	5-B	661	PHE	CB-CG-CD1	-8.33	114.97	120.80
2	2-B	393	PHE	CB-CG-CD1	8.33	126.63	120.80
3	2-C	387	PHE	CB-CG-CD1	-8.33	114.97	120.80
1	2-A	597	ARG	NE-CZ-NH1	8.32	124.46	120.30
2	6-B	824	TYR	CZ-CE2-CD2	-8.32	112.31	119.80
1	3-A	700	PHE	CB-CG-CD2	-8.32	114.98	120.80
1	10-A	663	TYR	CD1-CE1-CZ	8.32	127.29	119.80
2	8-B	612	ARG	NE-CZ-NH2	-8.32	116.14	120.30
1	9-A	150	TYR	CB-CG-CD2	8.32	125.99	121.00
1	9-A	157	ARG	NE-CZ-NH1	8.31	124.46	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2-C	193	ARG	NE-CZ-NH1	-8.31	116.14	120.30
2	1-B	400	TYR	CB-CG-CD2	8.31	125.98	121.00
3	1-D	267	PHE	CB-CG-CD2	-8.31	114.98	120.80
2	10-B	638	ARG	NE-CZ-NH2	-8.31	116.15	120.30
2	3-B	319	PHE	CB-CG-CD1	8.30	126.61	120.80
3	1-D	62	PHE	CB-CG-CD1	8.30	126.61	120.80
3	3-C	217	PHE	CB-CG-CD1	-8.29	114.99	120.80
2	2-B	816	TYR	CB-CG-CD1	-8.29	116.03	121.00
1	2-A	706	PHE	CB-CG-CD1	8.28	126.60	120.80
1	10-A	558	TYR	CB-CG-CD2	8.28	125.97	121.00
3	2-C	170	TYR	CB-CG-CD2	-8.28	116.03	121.00
2	10-B	312	PHE	CB-CG-CD2	-8.28	115.00	120.80
3	4-D	413	PHE	CB-CG-CD1	-8.28	115.01	120.80
1	7-A	793	PHE	CB-CG-CD1	8.28	126.59	120.80
2	5-B	297	TYR	CB-CG-CD1	-8.27	116.04	121.00
3	10-C	403	PHE	CB-CG-CD2	8.27	126.59	120.80
2	3-B	295	ARG	NE-CZ-NH1	8.27	124.43	120.30
2	8-B	393	PHE	CB-CG-CD2	-8.26	115.02	120.80
3	7-D	319	TYR	CB-CG-CD2	-8.26	116.04	121.00
3	8-D	315	TYR	CB-CG-CD1	-8.26	116.05	121.00
3	10-C	423	PHE	CB-CG-CD2	-8.26	115.02	120.80
2	10-B	641	PHE	CB-CG-CD2	-8.25	115.02	120.80
2	6-B	409	TYR	CB-CG-CD1	8.25	125.95	121.00
1	7-A	193	TYR	CB-CG-CD2	-8.25	116.05	121.00
3	5-C	83	PHE	CB-CG-CD1	-8.25	115.03	120.80
1	7-A	198	ARG	NE-CZ-NH1	8.25	124.42	120.30
2	7-B	415	TYR	CB-CG-CD1	-8.25	116.05	121.00
1	2-A	450	TYR	CB-CG-CD2	-8.25	116.05	121.00
1	2-A	451	ARG	NE-CZ-NH2	-8.24	116.18	120.30
2	1-B	190	TYR	CB-CG-CD2	-8.24	116.06	121.00
2	4-B	587	PHE	CB-CG-CD1	8.24	126.57	120.80
3	3-C	403	PHE	CB-CG-CD2	8.24	126.56	120.80
3	7-C	47	ASP	CB-CG-OD1	8.23	125.71	118.30
3	1-C	59	ARG	NE-CZ-NH2	-8.23	116.19	120.30
1	1-A	792	ASP	CB-CG-OD1	8.23	125.71	118.30
2	1-B	236	TYR	CB-CG-CD1	-8.23	116.06	121.00
2	6-B	400	TYR	CB-CG-CD1	8.23	125.94	121.00
2	8-B	580	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	4-A	143	ARG	NE-CZ-NH1	8.22	124.41	120.30
3	8-C	362	TYR	CB-CG-CD2	8.22	125.93	121.00
1	6-A	714	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	6-A	657	TYR	CB-CG-CD2	-8.21	116.07	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	7-A	302	TYR	CB-CG-CD1	8.21	125.92	121.00
1	6-A	644	MET	CG-SD-CE	-8.20	87.08	100.20
2	8-B	241	PHE	CB-CG-CD1	8.20	126.54	120.80
3	2-D	217	PHE	CB-CG-CD1	8.20	126.54	120.80
2	7-B	666	ARG	NE-CZ-NH1	8.20	124.40	120.30
3	10-D	162	TYR	CB-CG-CD2	-8.20	116.08	121.00
2	9-B	475	PHE	CB-CG-CD2	-8.19	115.06	120.80
2	2-B	587	PHE	CB-CG-CD2	-8.19	115.07	120.80
2	2-B	641	PHE	CB-CG-CD1	8.19	126.53	120.80
3	2-C	114	ARG	NE-CZ-NH1	8.19	124.39	120.30
3	2-D	329	ARG	NE-CZ-NH1	8.19	124.39	120.30
1	4-A	337	SER	N-CA-CB	8.18	122.78	110.50
1	7-A	111	ARG	NE-CZ-NH1	8.18	124.39	120.30
3	6-D	272	PHE	CB-CG-CD2	-8.18	115.08	120.80
3	4-D	438	VAL	CA-CB-CG2	8.17	123.16	110.90
3	10-C	105	TRP	CB-CG-CD1	-8.17	116.38	127.00
3	10-D	362	TYR	CB-CG-CD1	8.17	125.90	121.00
1	2-A	646	TYR	CB-CG-CD1	8.17	125.90	121.00
3	3-D	293	ASP	CB-CG-OD2	-8.17	110.95	118.30
2	5-B	612	ARG	NE-CZ-NH2	-8.16	116.22	120.30
2	5-B	343	TYR	CB-CG-CD2	-8.16	116.11	121.00
3	9-C	247	TYR	CB-CG-CD1	-8.16	116.11	121.00
3	9-D	70	ASP	CB-CG-OD2	-8.15	110.96	118.30
3	9-D	358	ARG	NE-CZ-NH1	8.15	124.38	120.30
2	10-B	429	TYR	CG-CD2-CE2	-8.15	114.78	121.30
2	10-B	231	TYR	CB-CG-CD1	8.14	125.89	121.00
3	5-C	243	ARG	NH1-CZ-NH2	-8.14	110.44	119.40
2	6-B	510	TYR	CB-CG-CD2	-8.14	116.12	121.00
3	7-D	316	PHE	CB-CG-CD2	-8.14	115.10	120.80
3	2-C	292	TYR	CB-CG-CD2	-8.14	116.12	121.00
1	6-A	657	TYR	CB-CG-CD1	8.13	125.88	121.00
3	7-D	53	PHE	CB-CG-CD2	-8.14	115.11	120.80
3	9-D	445	TYR	CB-CG-CD2	8.13	125.88	121.00
2	1-B	562	TYR	CB-CG-CD1	-8.13	116.12	121.00
1	5-A	76	ARG	NE-CZ-NH2	8.13	124.37	120.30
3	3-C	34	ASP	CB-CG-OD2	-8.13	110.98	118.30
2	8-B	827	ARG	NE-CZ-NH1	8.13	124.36	120.30
1	2-A	161	ASP	CB-CG-OD2	-8.12	110.99	118.30
2	5-B	264	TYR	CG-CD2-CE2	-8.12	114.80	121.30
1	9-A	105	PHE	CB-CG-CD1	8.12	126.48	120.80
2	10-B	297	TYR	CB-CG-CD1	8.12	125.87	121.00
3	4-C	427	ARG	NE-CZ-NH2	8.11	124.36	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2-B	599	PHE	CB-CG-CD2	-8.11	115.12	120.80
3	1-D	279	TYR	CB-CG-CD1	-8.11	116.14	121.00
2	9-B	633	ARG	NE-CZ-NH1	8.11	124.35	120.30
1	3-A	594	TYR	CB-CG-CD2	-8.10	116.14	121.00
3	7-C	160	ASP	CB-CG-OD2	-8.10	111.01	118.30
2	10-B	565	TYR	CB-CG-CD2	-8.09	116.14	121.00
3	4-D	279	TYR	CG-CD2-CE2	8.09	127.77	121.30
1	1-A	775	PHE	CB-CG-CD1	8.08	126.45	120.80
3	8-C	176	ARG	NE-CZ-NH2	-8.07	116.27	120.30
1	1-A	405	PHE	CB-CG-CD2	8.06	126.44	120.80
2	6-B	827	ARG	NE-CZ-NH1	8.06	124.33	120.30
1	1-A	116	TYR	CG-CD2-CE2	8.05	127.74	121.30
2	5-B	526	ARG	NE-CZ-NH2	-8.05	116.27	120.30
2	2-B	187	TYR	CB-CG-CD1	8.05	125.83	121.00
2	4-B	475	PHE	CB-CG-CD2	-8.05	115.16	120.80
2	5-B	562	TYR	CB-CG-CD2	8.05	125.83	121.00
1	4-A	62	ASP	CB-CG-OD1	8.04	125.54	118.30
3	3-C	333	ARG	NE-CZ-NH2	-8.04	116.28	120.30
1	7-A	262	ARG	NE-CZ-NH2	-8.04	116.28	120.30
3	7-D	279	TYR	CB-CG-CD2	-8.04	116.17	121.00
2	9-B	200	PHE	CB-CG-CD1	8.04	126.43	120.80
1	10-A	409	PHE	CB-CG-CD1	8.04	126.43	120.80
3	8-D	333	ARG	NE-CZ-NH1	8.04	124.32	120.30
2	9-B	297	TYR	CB-CG-CD2	-8.04	116.18	121.00
3	10-D	416	MET	CG-SD-CE	-8.03	87.34	100.20
2	10-B	429	TYR	CB-CG-CD2	-8.03	116.18	121.00
3	10-D	282	ASP	CB-CG-OD2	-8.03	111.07	118.30
1	7-A	410	PHE	CB-CG-CD1	8.03	126.42	120.80
2	4-B	578	PHE	CB-CG-CD1	8.03	126.42	120.80
1	5-A	160	ARG	NE-CZ-NH1	8.02	124.31	120.30
2	9-B	641	PHE	CB-CG-CD1	8.02	126.41	120.80
1	9-A	111	ARG	NE-CZ-NH1	8.02	124.31	120.30
2	9-B	758	TYR	CG-CD1-CE1	-8.02	114.89	121.30
3	9-D	44	THR	CA-CB-CG2	-8.02	101.18	112.40
2	10-B	446	PHE	CB-CG-CD2	-8.01	115.19	120.80
3	5-C	20	PHE	CB-CG-CD2	-8.01	115.19	120.80
1	2-A	74	TYR	CB-CG-CD1	8.00	125.80	121.00
2	1-B	822	ARG	NE-CZ-NH2	-8.00	116.30	120.30
2	3-B	242	ARG	NE-CZ-NH1	7.99	124.29	120.30
2	7-B	293	ARG	NE-CZ-NH2	7.99	124.29	120.30
2	7-B	359	TYR	CD1-CE1-CZ	7.99	126.99	119.80
2	3-B	741	PHE	CB-CG-CD1	7.98	126.39	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-D	403	PHE	CB-CG-CD2	-7.98	115.21	120.80
3	2-C	413	PHE	CB-CG-CD2	7.98	126.39	120.80
2	4-B	312	PHE	CB-CG-CD2	-7.98	115.22	120.80
3	6-C	358	ARG	NE-CZ-NH1	-7.98	116.31	120.30
3	1-D	352	MET	CG-SD-CE	-7.97	87.44	100.20
3	2-D	362	TYR	CB-CG-CD1	-7.97	116.22	121.00
3	6-D	204	PHE	CB-CG-CD1	-7.97	115.22	120.80
2	10-B	568	LEU	CB-CG-CD2	7.97	124.56	111.00
2	5-B	533	ARG	NE-CZ-NH1	7.97	124.29	120.30
1	7-A	204	ARG	NE-CZ-NH2	7.97	124.28	120.30
2	1-B	475	PHE	CB-CG-CD2	-7.97	115.22	120.80
2	3-B	638	ARG	NE-CZ-NH1	-7.97	116.32	120.30
2	4-B	312	PHE	CB-CG-CD1	7.96	126.38	120.80
1	5-A	145	PHE	CB-CG-CD2	7.96	126.38	120.80
1	1-A	663	TYR	CB-CG-CD1	-7.96	116.22	121.00
2	9-B	312	PHE	CB-CG-CD2	-7.96	115.23	120.80
1	5-A	157	ARG	NE-CZ-NH1	7.96	124.28	120.30
1	7-A	76	ARG	NE-CZ-NH1	7.96	124.28	120.30
2	2-B	389	ARG	NE-CZ-NH2	-7.95	116.32	120.30
1	4-A	197	PHE	CB-CG-CD2	-7.95	115.23	120.80
2	8-B	285	ARG	NE-CZ-NH1	-7.95	116.32	120.30
2	6-B	592	ARG	NE-CZ-NH2	-7.95	116.32	120.30
2	3-B	599	PHE	CB-CG-CD2	-7.95	115.24	120.80
2	4-B	299	ARG	NE-CZ-NH1	7.95	124.27	120.30
2	3-B	826	PHE	CB-CG-CD1	7.94	126.36	120.80
3	3-C	78	ASP	CB-CG-OD2	-7.94	111.15	118.30
3	1-C	208	SER	N-CA-CB	7.94	122.41	110.50
2	3-B	425	PHE	CB-CG-CD2	-7.94	115.24	120.80
3	6-D	170	TYR	CB-CG-CD1	7.94	125.76	121.00
3	1-C	54	PHE	CB-CG-CD2	-7.93	115.25	120.80
3	1-C	218	ARG	NE-CZ-NH1	7.93	124.27	120.30
3	3-C	434	MET	CG-SD-CE	-7.93	87.51	100.20
3	10-D	162	TYR	CG-CD2-CE2	-7.93	114.96	121.30
3	2-C	217	PHE	CB-CG-CD2	-7.92	115.25	120.80
1	4-A	558	TYR	CG-CD1-CE1	-7.92	114.96	121.30
2	1-B	343	TYR	CG-CD2-CE2	-7.92	114.96	121.30
1	1-A	451	ARG	NE-CZ-NH2	7.92	124.26	120.30
2	1-B	839	PHE	CB-CG-CD2	-7.92	115.26	120.80
3	1-C	87	PHE	CB-CG-CD2	-7.92	115.26	120.80
1	5-A	327	ARG	NE-CZ-NH2	-7.92	116.34	120.30
1	3-A	639	PHE	CB-CG-CD2	-7.91	115.26	120.80
3	3-D	48	ASP	CB-CG-OD2	7.91	125.42	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	5-D	293	ASP	CB-CG-OD1	7.91	125.42	118.30
3	5-C	341	ARG	NE-CZ-NH2	-7.91	116.35	120.30
3	7-D	315	TYR	CG-CD2-CE2	-7.91	114.97	121.30
1	8-A	704	TYR	CG-CD1-CE1	-7.91	114.98	121.30
2	9-B	328	ARG	NE-CZ-NH2	-7.90	116.35	120.30
3	5-C	87	PHE	CB-CG-CD1	7.90	126.33	120.80
2	3-B	585	ARG	NE-CZ-NH1	7.90	124.25	120.30
1	9-A	701	ASP	CB-CG-OD2	-7.90	111.19	118.30
2	4-B	822	ARG	NE-CZ-NH1	7.89	124.25	120.30
2	9-B	565	TYR	CB-CG-CD1	7.89	125.73	121.00
3	10-D	176	ARG	NE-CZ-NH1	7.88	124.24	120.30
3	10-D	41	ASP	CB-CG-OD1	-7.88	111.21	118.30
2	8-B	429	TYR	CB-CG-CD2	-7.88	116.27	121.00
1	1-A	646	TYR	CB-CG-CD2	-7.88	116.28	121.00
1	2-A	588	TYR	CB-CG-CD1	7.87	125.72	121.00
1	4-A	110	VAL	CA-CB-CG2	7.87	122.71	110.90
3	8-C	87	PHE	CB-CG-CD2	-7.87	115.29	120.80
2	9-B	379	TYR	CB-CG-CD1	-7.87	116.28	121.00
3	9-D	170	TYR	CB-CG-CD1	-7.87	116.28	121.00
3	6-D	173	PHE	CB-CG-CD1	7.86	126.30	120.80
1	10-A	198	ARG	NE-CZ-NH1	7.86	124.23	120.30
3	6-C	87	PHE	CB-CG-CD2	-7.86	115.30	120.80
2	2-B	652	TYR	CB-CG-CD1	7.85	125.71	121.00
3	3-D	247	TYR	CB-CG-CD1	-7.85	116.29	121.00
1	10-A	144	ARG	NE-CZ-NH2	-7.85	116.38	120.30
3	1-D	143	ALA	N-CA-CB	7.85	121.08	110.10
2	6-B	576	ARG	NE-CZ-NH1	7.84	124.22	120.30
1	6-A	486	PHE	CB-CG-CD2	-7.84	115.31	120.80
1	8-A	623	ARG	NE-CZ-NH2	-7.84	116.38	120.30
2	4-B	670	ARG	NE-CZ-NH2	7.84	124.22	120.30
2	5-B	243	MET	CG-SD-CE	-7.84	87.66	100.20
1	8-A	704	TYR	CB-CG-CD2	-7.83	116.30	121.00
3	5-D	190	ALA	CB-CA-C	-7.83	98.35	110.10
3	8-C	233	THR	CA-CB-CG2	-7.83	101.43	112.40
1	10-A	150	TYR	N-CA-CB	-7.83	96.50	110.60
2	8-B	468	PHE	CB-CG-CD2	-7.83	115.32	120.80
1	9-A	116	TYR	CB-CG-CD2	-7.83	116.30	121.00
2	7-B	319	PHE	CB-CG-CD2	-7.83	115.32	120.80
1	1-A	714	ARG	NE-CZ-NH1	-7.82	116.39	120.30
3	1-C	316	PHE	CB-CG-CD2	-7.82	115.32	120.80
1	6-A	591	VAL	CA-CB-CG2	-7.82	99.17	110.90
3	3-C	243	ARG	NE-CZ-NH2	-7.82	116.39	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	7-C	104	SER	N-CA-CB	7.81	122.22	110.50
1	3-A	203	ARG	NE-CZ-NH2	7.81	124.21	120.30
1	4-A	327	ARG	NE-CZ-NH2	-7.81	116.39	120.30
1	9-A	657	TYR	CB-CG-CD2	-7.81	116.31	121.00
2	5-B	338	MET	CG-SD-CE	-7.81	87.71	100.20
1	6-A	140	TYR	CB-CG-CD1	7.81	125.68	121.00
1	4-A	465	PHE	CB-CG-CD2	7.81	126.27	120.80
2	7-B	488	PHE	CB-CG-CD1	7.81	126.26	120.80
3	5-C	333	ARG	NE-CZ-NH2	-7.80	116.40	120.30
1	3-A	111	ARG	NE-CZ-NH1	-7.80	116.40	120.30
2	8-B	661	PHE	CB-CG-CD1	7.80	126.26	120.80
3	6-C	256	TYR	CB-CG-CD2	7.79	125.68	121.00
1	3-A	755	ASP	CB-CG-OD1	7.79	125.31	118.30
1	5-A	469	ARG	NE-CZ-NH1	7.79	124.19	120.30
2	5-B	470	TYR	CD1-CE1-CZ	7.79	126.81	119.80
1	7-A	190	TYR	CB-CG-CD2	-7.79	116.33	121.00
3	1-D	285	ALA	CB-CA-C	-7.79	98.42	110.10
1	4-A	714	ARG	NE-CZ-NH2	7.79	124.19	120.30
1	7-A	327	ARG	NE-CZ-NH2	-7.79	116.41	120.30
1	10-A	429	TYR	CB-CG-CD2	-7.79	116.33	121.00
3	2-C	83	PHE	CB-CG-CD2	-7.78	115.35	120.80
3	3-D	55	ARG	NE-CZ-NH1	7.78	124.19	120.30
2	4-B	404	MET	CG-SD-CE	-7.78	87.75	100.20
1	6-A	597	ARG	NE-CZ-NH1	7.78	124.19	120.30
2	6-B	510	TYR	CB-CG-CD1	7.78	125.67	121.00
1	9-A	663	TYR	CB-CG-CD1	7.78	125.67	121.00
2	9-B	439	ARG	NE-CZ-NH1	7.78	124.19	120.30
2	9-B	741	PHE	CB-CG-CD2	-7.78	115.36	120.80
1	9-A	587	ARG	NE-CZ-NH2	-7.78	116.41	120.30
2	2-B	846	ARG	NE-CZ-NH1	7.77	124.19	120.30
2	7-B	400	TYR	CG-CD1-CE1	-7.77	115.08	121.30
1	1-A	131	PHE	CB-CG-CD2	-7.77	115.36	120.80
2	3-B	592	ARG	NE-CZ-NH2	-7.77	116.42	120.30
3	4-C	34	ASP	CB-CG-OD2	-7.76	111.31	118.30
3	5-C	292	TYR	CA-CB-CG	7.76	128.15	113.40
3	10-D	278	ASP	CB-CG-OD2	-7.76	111.31	118.30
2	6-B	599	PHE	CB-CG-CD1	7.76	126.23	120.80
2	1-B	389	ARG	NE-CZ-NH2	-7.76	116.42	120.30
2	2-B	312	PHE	CB-CG-CD2	-7.76	115.37	120.80
2	5-B	249	MET	CG-SD-CE	-7.76	87.78	100.20
3	7-C	445	TYR	CB-CG-CD1	-7.76	116.34	121.00
1	8-A	279	TYR	CB-CG-CD1	-7.76	116.34	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2-D	192	ARG	NE-CZ-NH2	-7.76	116.42	120.30
2	7-B	638	ARG	NE-CZ-NH1	-7.76	116.42	120.30
1	7-A	267	PHE	CB-CG-CD1	7.75	126.23	120.80
2	10-B	468	PHE	CB-CG-CD2	-7.75	115.37	120.80
3	4-C	136	PHE	CB-CG-CD1	7.75	126.23	120.80
2	6-B	514	ARG	NE-CZ-NH1	7.75	124.18	120.30
1	2-A	393	TYR	CB-CG-CD1	7.75	125.65	121.00
3	8-C	65	ARG	NE-CZ-NH2	7.75	124.18	120.30
3	4-D	65	ARG	NE-CZ-NH2	-7.75	116.42	120.30
3	6-C	86	PHE	CB-CG-CD2	-7.75	115.38	120.80
3	7-C	176	ARG	NE-CZ-NH2	-7.75	116.43	120.30
3	10-D	407	TYR	CB-CG-CD1	7.75	125.65	121.00
3	2-D	384	VAL	CA-CB-CG1	7.74	122.51	110.90
1	5-A	630	ARG	NE-CZ-NH1	7.74	124.17	120.30
3	2-D	197	ASP	CB-CG-OD1	7.73	125.26	118.30
1	6-A	469	ARG	NE-CZ-NH2	-7.72	116.44	120.30
3	10-C	192	ARG	NE-CZ-NH1	-7.72	116.44	120.30
3	7-D	411	ASP	CB-CG-OD1	-7.72	111.35	118.30
2	1-B	293	ARG	NE-CZ-NH1	7.72	124.16	120.30
3	2-C	66	ALA	N-CA-CB	7.72	120.90	110.10
2	5-B	816	TYR	CB-CG-CD1	7.71	125.63	121.00
1	2-A	639	PHE	CB-CG-CD1	7.71	126.20	120.80
3	8-D	59	ARG	NE-CZ-NH1	-7.71	116.44	120.30
2	4-B	393	PHE	CB-CG-CD1	7.71	126.20	120.80
1	2-A	279	TYR	CB-CG-CD2	-7.71	116.38	121.00
1	8-A	325	PHE	CB-CG-CD1	7.71	126.19	120.80
2	2-B	524	SER	N-CA-CB	7.70	122.06	110.50
1	9-A	486	PHE	CB-CG-CD2	-7.70	115.41	120.80
2	8-B	345	TYR	CB-CG-CD1	7.70	125.62	121.00
2	10-B	664	MET	CG-SD-CE	-7.70	87.88	100.20
3	9-C	177	SER	N-CA-CB	7.70	122.05	110.50
2	4-B	297	TYR	CB-CG-CD2	-7.70	116.38	121.00
2	9-B	661	PHE	CB-CG-CD1	7.70	126.19	120.80
3	2-C	283	ASP	CB-CG-OD1	7.69	125.22	118.30
1	4-A	381	PHE	CB-CG-CD1	7.68	126.18	120.80
2	5-B	409	TYR	CB-CG-CD2	7.68	125.61	121.00
1	8-A	76	ARG	NE-CZ-NH1	-7.68	116.46	120.30
3	6-D	341	ARG	NE-CZ-NH2	-7.68	116.46	120.30
1	7-A	329	ASP	CB-CG-OD2	-7.68	111.39	118.30
2	4-B	470	TYR	CB-CG-CD1	7.68	125.61	121.00
3	6-C	316	PHE	CB-CG-CD2	-7.67	115.43	120.80
2	7-B	342	TYR	CA-CB-CG	-7.67	98.83	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	4-B	661	PHE	CB-CG-CD2	7.67	126.17	120.80
3	6-D	248	MET	CG-SD-CE	-7.67	87.93	100.20
1	9-A	121	ARG	NE-CZ-NH2	-7.67	116.47	120.30
3	6-D	247	TYR	CB-CG-CD2	-7.67	116.40	121.00
1	10-A	795	ASP	CB-CG-OD2	-7.67	111.40	118.30
3	8-C	333	ARG	NE-CZ-NH1	-7.67	116.47	120.30
1	10-A	193	TYR	CB-CG-CD1	7.67	125.60	121.00
2	8-B	312	PHE	CB-CG-CD2	-7.66	115.44	120.80
2	5-B	300	PHE	CB-CG-CD2	-7.66	115.44	120.80
1	3-A	393	TYR	CB-CG-CD2	-7.66	116.41	121.00
3	10-C	161	ARG	NE-CZ-NH1	7.66	124.13	120.30
2	3-B	819	PHE	CB-CG-CD1	7.66	126.16	120.80
1	9-A	568	TYR	CB-CG-CD1	-7.66	116.41	121.00
1	6-A	336	ASP	CB-CG-OD2	-7.65	111.41	118.30
3	8-D	247	TYR	CB-CG-CD2	-7.65	116.41	121.00
2	2-B	335	PHE	CB-CG-CD1	-7.65	115.45	120.80
3	5-C	423	PHE	CB-CG-CD2	-7.65	115.45	120.80
1	2-A	116	TYR	CB-CG-CD1	7.65	125.59	121.00
2	3-B	278	VAL	CA-CB-CG1	7.65	122.37	110.90
2	5-B	187	TYR	CB-CG-CD2	-7.64	116.41	121.00
2	6-B	231	TYR	CB-CG-CD1	-7.64	116.41	121.00
3	10-D	84	ARG	NE-CZ-NH1	7.64	124.12	120.30
3	3-D	158	LEU	CB-CG-CD1	7.64	123.99	111.00
3	6-C	333	ARG	NE-CZ-NH1	7.63	124.12	120.30
3	1-C	192	ARG	NE-CZ-NH2	-7.63	116.49	120.30
1	4-A	486	PHE	CB-CG-CD2	-7.63	115.46	120.80
2	2-B	356	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	3-A	664	ARG	NE-CZ-NH2	7.62	124.11	120.30
2	8-B	846	ARG	NE-CZ-NH2	7.62	124.11	120.30
2	2-B	431	VAL	CA-CB-CG2	-7.61	99.48	110.90
2	7-B	772	PHE	CB-CG-CD1	-7.61	115.47	120.80
2	8-B	514	ARG	NE-CZ-NH1	7.61	124.10	120.30
3	7-C	359	ARG	NE-CZ-NH2	-7.60	116.50	120.30
2	2-B	651	TYR	CG-CD2-CE2	-7.59	115.22	121.30
1	2-A	261	ASP	CB-CG-OD2	-7.59	111.47	118.30
3	6-C	118	ASP	CB-CG-OD1	-7.59	111.47	118.30
2	8-B	776	TYR	CA-CB-CG	7.59	127.82	113.40
3	3-D	293	ASP	CB-CG-OD1	7.58	125.13	118.30
3	10-D	86	PHE	CB-CG-CD2	7.58	126.11	120.80
3	4-D	247	TYR	CG-CD2-CE2	-7.58	115.24	121.30
3	6-D	90	ARG	NE-CZ-NH2	-7.58	116.51	120.30
3	8-D	413	PHE	CB-CG-CD2	7.58	126.11	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	102	PHE	CB-CG-CD2	-7.58	115.49	120.80
1	3-A	588	TYR	CG-CD1-CE1	-7.58	115.24	121.30
1	5-A	646	TYR	CB-CG-CD1	7.58	125.55	121.00
3	4-C	25	LEU	CB-CG-CD2	7.58	123.88	111.00
1	8-A	334	ASP	CB-CG-OD1	7.58	125.12	118.30
3	8-C	26	ALA	CB-CA-C	-7.58	98.73	110.10
1	10-A	161	ASP	CB-CG-OD1	7.58	125.12	118.30
1	8-A	647	PHE	CB-CG-CD2	-7.57	115.50	120.80
1	10-A	458	TYR	CB-CG-CD2	-7.57	116.45	121.00
1	8-A	143	ARG	NE-CZ-NH2	7.57	124.08	120.30
1	10-A	105	PHE	CB-CG-CD2	7.57	126.10	120.80
2	5-B	409	TYR	CB-CG-CD1	-7.56	116.46	121.00
1	7-A	349	ARG	NE-CZ-NH1	-7.56	116.52	120.30
1	2-A	262	ARG	NE-CZ-NH2	-7.55	116.52	120.30
2	8-B	483	MET	CG-SD-CE	-7.55	88.11	100.20
1	10-A	794	TYR	CB-CG-CD1	7.55	125.53	121.00
2	1-B	641	PHE	CB-CG-CD2	-7.55	115.51	120.80
1	4-A	558	TYR	CD1-CE1-CZ	7.55	126.59	119.80
3	4-C	20	PHE	CB-CG-CD1	7.55	126.08	120.80
3	6-C	93	TRP	CA-CB-CG	7.54	128.03	113.70
3	6-D	278	ASP	CB-CG-OD2	7.54	125.09	118.30
3	6-D	114	ARG	NE-CZ-NH1	-7.54	116.53	120.30
1	8-A	704	TYR	CD1-CE1-CZ	7.54	126.58	119.80
1	2-A	663	TYR	CB-CG-CD1	-7.54	116.48	121.00
1	6-A	161	ASP	CB-CG-OD1	7.54	125.08	118.30
2	8-B	485	LYS	N-CA-C	-7.54	90.65	111.00
1	9-A	358	ARG	NE-CZ-NH2	-7.53	116.53	120.30
2	8-B	359	TYR	CB-CG-CD2	7.53	125.52	121.00
1	8-A	279	TYR	CB-CG-CD2	7.53	125.52	121.00
2	7-B	844	SER	N-CA-CB	7.53	121.79	110.50
2	8-B	267	PHE	CB-CG-CD2	-7.52	115.53	120.80
3	10-C	162	TYR	CG-CD1-CE1	-7.52	115.28	121.30
2	1-B	571	VAL	CA-CB-CG2	-7.52	99.62	110.90
3	4-D	271	SER	N-CA-CB	7.52	121.78	110.50
3	5-C	376	MET	CG-SD-CE	-7.52	88.17	100.20
2	3-B	652	TYR	CB-CG-CD2	7.52	125.51	121.00
2	8-B	183	ASP	CB-CG-OD2	-7.52	111.53	118.30
3	9-C	272	PHE	CB-CG-CD2	7.52	126.06	120.80
3	1-D	90	ARG	NE-CZ-NH1	7.51	124.06	120.30
2	8-B	533	ARG	NE-CZ-NH1	7.51	124.06	120.30
3	1-C	176	ARG	NE-CZ-NH2	-7.50	116.55	120.30
2	5-B	409	TYR	CD1-CE1-CZ	-7.50	113.05	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2-A	299	PHE	CB-CG-CD2	-7.50	115.55	120.80
2	5-B	827	ARG	NE-CZ-NH2	-7.50	116.55	120.30
2	5-B	846	ARG	NE-CZ-NH1	7.50	124.05	120.30
2	9-B	285	ARG	NE-CZ-NH2	7.50	124.05	120.30
3	8-C	78	ASP	CB-CG-OD1	7.50	125.05	118.30
3	6-C	20	PHE	CB-CG-CD1	7.49	126.05	120.80
2	7-B	758	TYR	CG-CD2-CE2	-7.49	115.31	121.30
2	4-B	587	PHE	CB-CG-CD2	-7.49	115.56	120.80
3	7-C	87	PHE	CB-CG-CD1	7.49	126.04	120.80
3	7-C	109	TYR	CB-CG-CD2	7.49	125.49	121.00
3	4-C	348	SER	N-CA-CB	7.49	121.73	110.50
3	2-D	136	PHE	CG-CD1-CE1	7.48	129.03	120.80
3	9-C	423	PHE	CB-CG-CD1	-7.48	115.56	120.80
2	9-B	565	TYR	CG-CD1-CE1	-7.48	115.32	121.30
2	1-B	731	PHE	CB-CG-CD1	7.47	126.03	120.80
3	9-D	62	PHE	CB-CG-CD1	-7.47	115.57	120.80
2	1-B	403	PHE	CB-CG-CD1	-7.47	115.57	120.80
1	2-A	658	SER	CB-CA-C	-7.47	95.91	110.10
2	6-B	328	ARG	NH1-CZ-NH2	7.47	127.62	119.40
3	4-C	407	TYR	CG-CD2-CE2	-7.46	115.33	121.30
3	9-D	20	PHE	CB-CG-CD1	-7.46	115.58	120.80
3	10-C	279	TYR	CB-CG-CD1	7.46	125.48	121.00
3	6-C	437	TYR	CB-CG-CD1	7.46	125.48	121.00
1	2-A	286	TRP	CG-CD2-CE3	-7.46	127.19	133.90
1	2-A	137	ARG	NE-CZ-NH1	7.46	124.03	120.30
1	4-A	138	PHE	CB-CG-CD1	-7.46	115.58	120.80
2	5-B	612	ARG	NE-CZ-NH1	7.46	124.03	120.30
2	9-B	475	PHE	CB-CG-CD1	7.46	126.02	120.80
1	1-A	594	TYR	CG-CD2-CE2	7.45	127.26	121.30
1	3-A	121	ARG	NE-CZ-NH2	7.45	124.03	120.30
3	4-C	199	ASP	CB-CG-OD1	-7.45	111.59	118.30
2	2-B	464	LEU	CB-CG-CD2	7.45	123.66	111.00
2	4-B	236	TYR	CB-CG-CD1	7.45	125.47	121.00
3	1-D	83	PHE	CB-CG-CD1	7.45	126.01	120.80
3	2-C	131	ASP	CB-CG-OD2	-7.44	111.60	118.30
2	4-B	343	TYR	CA-CB-CG	7.44	127.54	113.40
3	10-D	218	ARG	NE-CZ-NH2	-7.44	116.58	120.30
2	4-B	633	ARG	NE-CZ-NH1	7.44	124.02	120.30
1	7-A	700	PHE	CB-CG-CD2	-7.44	115.59	120.80
2	2-B	770	TYR	CB-CG-CD1	-7.44	116.54	121.00
2	4-B	285	ARG	NH1-CZ-NH2	-7.44	111.22	119.40
2	4-B	728	HIS	CA-CB-CG	7.44	126.24	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5-B	598	TYR	CB-CG-CD1	7.44	125.46	121.00
3	7-D	315	TYR	CB-CG-CD1	-7.44	116.54	121.00
2	6-B	562	TYR	CB-CG-CD1	7.44	125.46	121.00
3	6-D	279	TYR	CB-CG-CD2	-7.43	116.54	121.00
1	4-A	171	ARG	NE-CZ-NH2	-7.43	116.58	120.30
3	5-D	66	ALA	CB-CA-C	-7.43	98.95	110.10
3	4-D	90	ARG	NE-CZ-NH1	-7.43	116.59	120.30
3	4-C	380	MET	CG-SD-CE	-7.42	88.32	100.20
1	4-A	775	PHE	CB-CG-CD2	-7.42	115.61	120.80
3	3-C	47	ASP	CB-CG-OD2	7.42	124.98	118.30
3	9-C	161	ARG	NE-CZ-NH2	-7.42	116.59	120.30
1	8-A	395	ASP	CB-CG-OD2	7.42	124.98	118.30
1	10-A	486	PHE	CB-CG-CD2	-7.42	115.61	120.80
3	6-D	413	PHE	CG-CD2-CE2	-7.41	112.64	120.80
1	7-A	102	PHE	CB-CG-CD2	-7.41	115.61	120.80
1	7-A	605	ASP	CB-CG-OD2	-7.41	111.63	118.30
2	7-B	839	PHE	CB-CG-CD1	-7.41	115.61	120.80
3	9-D	86	PHE	CB-CG-CD1	7.41	125.98	120.80
3	1-C	439	ALA	CB-CA-C	-7.41	98.99	110.10
3	1-D	249	TYR	CB-CG-CD1	7.40	125.44	121.00
1	1-A	251	PHE	CB-CG-CD1	7.40	125.98	120.80
3	8-C	423	PHE	CB-CG-CD2	-7.40	115.62	120.80
1	4-A	194	GLU	N-CA-CB	7.40	123.92	110.60
2	7-B	451	ASP	CB-CG-OD1	-7.40	111.64	118.30
2	3-B	293	ARG	NE-CZ-NH2	7.39	124.00	120.30
2	4-B	562	TYR	CG-CD1-CE1	-7.39	115.39	121.30
3	1-C	97	ASP	CB-CG-OD2	-7.39	111.65	118.30
3	3-D	20	PHE	CB-CG-CD1	7.39	125.97	120.80
1	4-A	172	GLU	OE1-CD-OE2	7.39	132.17	123.30
3	5-C	427	ARG	NE-CZ-NH1	7.39	124.00	120.30
1	8-A	160	ARG	NE-CZ-NH1	7.39	123.99	120.30
3	3-C	49	ASP	CB-CG-OD1	-7.39	111.65	118.30
1	6-A	684	MET	CA-CB-CG	7.38	125.85	113.30
3	4-D	275	PHE	CB-CG-CD2	-7.38	115.63	120.80
1	8-A	302	TYR	CD1-CE1-CZ	7.38	126.44	119.80
3	1-C	53	PHE	CB-CG-CD1	-7.38	115.64	120.80
2	6-B	648	MET	CG-SD-CE	-7.38	88.40	100.20
3	8-C	57	ASN	N-CA-CB	7.38	123.87	110.60
1	3-A	327	ARG	NE-CZ-NH1	7.37	123.99	120.30
1	7-A	706	PHE	CB-CG-CD2	-7.37	115.64	120.80
3	9-D	445	TYR	CB-CG-CD1	-7.37	116.58	121.00
2	1-B	776	TYR	CB-CG-CD2	-7.37	116.58	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4-A	150	TYR	CB-CG-CD2	-7.37	116.58	121.00
2	4-B	411	PHE	CB-CG-CD2	-7.37	115.64	120.80
3	9-C	244	PHE	CB-CG-CD1	7.37	125.96	120.80
1	2-A	171	ARG	NE-CZ-NH2	-7.37	116.62	120.30
3	3-C	68	MET	CA-CB-CG	7.37	125.83	113.30
3	3-D	292	TYR	CB-CG-CD2	7.37	125.42	121.00
1	10-A	302	TYR	CB-CG-CD2	-7.37	116.58	121.00
1	4-A	112	TYR	CB-CG-CD1	7.36	125.42	121.00
1	7-A	706	PHE	CB-CG-CD1	7.36	125.95	120.80
3	2-D	241	SER	N-CA-CB	7.36	121.54	110.50
3	4-C	48	ASP	CB-CG-OD2	-7.36	111.68	118.30
2	8-B	652	TYR	CB-CG-CD2	-7.36	116.58	121.00
1	8-A	636	MET	CG-SD-CE	-7.36	88.43	100.20
2	3-B	526	ARG	NE-CZ-NH1	7.35	123.98	120.30
2	5-B	452	GLN	N-CA-CB	7.35	123.83	110.60
3	8-D	65	ARG	NE-CZ-NH1	-7.35	116.63	120.30
1	2-A	775	PHE	CB-CG-CD2	7.35	125.94	120.80
3	4-C	375	MET	CG-SD-CE	-7.34	88.45	100.20
1	9-A	782	PHE	CB-CG-CD1	7.34	125.94	120.80
2	5-B	471	ARG	NE-CZ-NH1	7.33	123.97	120.30
2	10-B	508	PRO	CA-N-CD	-7.33	101.23	111.50
2	1-B	284	TYR	CB-CG-CD2	-7.33	116.60	121.00
1	2-A	624	ARG	NE-CZ-NH1	-7.33	116.64	120.30
3	4-C	319	TYR	CB-CG-CD2	7.33	125.40	121.00
1	8-A	426	PHE	CB-CG-CD1	7.33	125.93	120.80
1	2-A	321	ASP	CB-CG-OD1	7.33	124.89	118.30
1	7-A	157	ARG	NE-CZ-NH2	-7.32	116.64	120.30
3	2-C	87	PHE	CB-CG-CD1	-7.32	115.68	120.80
2	1-B	638	ARG	NE-CZ-NH2	-7.31	116.64	120.30
2	1-B	225	PHE	CB-CG-CD1	7.31	125.92	120.80
2	9-B	445	PHE	CB-CG-CD1	-7.31	115.68	120.80
2	9-B	644	PHE	CB-CG-CD1	-7.31	115.68	120.80
1	1-A	700	PHE	CB-CG-CD1	7.31	125.92	120.80
3	10-C	277	SER	N-CA-CB	7.31	121.46	110.50
3	7-C	75	VAL	CA-CB-CG2	7.31	121.86	110.90
3	3-C	62	PHE	CB-CG-CD2	7.31	125.91	120.80
3	10-D	439	ALA	CB-CA-C	-7.31	99.14	110.10
3	2-D	278	ASP	CB-CG-OD2	-7.30	111.72	118.30
3	8-C	65	ARG	NE-CZ-NH1	-7.30	116.65	120.30
2	1-B	299	ARG	NE-CZ-NH1	7.30	123.95	120.30
3	7-C	60	ASN	N-CA-CB	7.30	123.74	110.60
2	2-B	638	ARG	NE-CZ-NH2	-7.30	116.65	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3-B	285	ARG	NE-CZ-NH1	7.30	123.95	120.30
3	6-D	136	PHE	CB-CG-CD1	-7.30	115.69	120.80
2	1-B	510	TYR	CB-CG-CD1	-7.29	116.62	121.00
1	5-A	256	LEU	CB-CG-CD1	-7.29	98.60	111.00
2	6-B	242	ARG	NE-CZ-NH2	7.29	123.95	120.30
1	3-A	349	ARG	NE-CZ-NH2	-7.29	116.65	120.30
2	7-B	490	ASP	CB-CG-OD1	7.29	124.86	118.30
1	8-A	588	TYR	CB-CG-CD2	-7.29	116.62	121.00
3	10-C	292	TYR	CB-CG-CD2	-7.29	116.63	121.00
2	3-B	244	LEU	C-N-CA	7.29	139.91	121.70
1	2-A	786	LEU	N-CA-CB	7.28	124.97	110.40
2	3-B	445	PHE	CB-CG-CD2	7.28	125.90	120.80
1	5-A	329	ASP	CB-CG-OD1	-7.28	111.75	118.30
2	5-B	510	TYR	N-CA-CB	7.27	123.69	110.60
2	8-B	766	LEU	CB-CG-CD2	7.27	123.37	111.00
1	2-A	116	TYR	CA-CB-CG	7.27	127.22	113.40
1	5-A	646	TYR	CB-CG-CD2	-7.27	116.64	121.00
1	8-A	112	TYR	CB-CG-CD1	7.27	125.36	121.00
2	1-B	183	ASP	CB-CG-OD1	-7.26	111.76	118.30
2	2-B	470	TYR	CB-CG-CD1	7.26	125.36	121.00
3	3-C	271	SER	N-CA-CB	7.26	121.40	110.50
3	5-C	315	TYR	CB-CG-CD2	-7.26	116.65	121.00
2	8-B	558	PHE	CB-CG-CD2	-7.26	115.72	120.80
3	8-C	341	ARG	NE-CZ-NH1	7.25	123.93	120.30
2	10-B	827	ARG	NE-CZ-NH1	-7.25	116.67	120.30
2	5-B	391	PRO	N-CA-CB	7.25	112.00	103.30
3	1-C	161	ARG	NE-CZ-NH1	-7.25	116.68	120.30
3	5-C	333	ARG	NE-CZ-NH1	7.25	123.92	120.30
3	9-C	46	ARG	NE-CZ-NH1	-7.25	116.68	120.30
2	9-B	190	TYR	CB-CG-CD2	-7.24	116.66	121.00
3	6-C	285	ALA	CB-CA-C	-7.24	99.25	110.10
3	7-C	46	ARG	NE-CZ-NH2	-7.23	116.68	120.30
3	9-C	70	ASP	CB-CG-OD2	-7.23	111.79	118.30
2	10-B	385	PHE	CB-CG-CD1	7.23	125.86	120.80
2	2-B	529	MET	CG-SD-CE	-7.23	88.64	100.20
2	5-B	822	ARG	NE-CZ-NH2	7.23	123.91	120.30
2	7-B	324	ASP	CB-CG-OD1	-7.22	111.80	118.30
1	9-A	203	ARG	NE-CZ-NH1	7.22	123.91	120.30
3	1-C	217	PHE	CB-CG-CD1	7.22	125.86	120.80
2	2-B	405	ILE	CB-CA-C	-7.22	97.16	111.60
3	10-C	292	TYR	CA-CB-CG	7.22	127.11	113.40
3	7-D	243	ARG	NE-CZ-NH2	-7.21	116.69	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	7-A	144	ARG	NE-CZ-NH2	-7.21	116.69	120.30
2	10-B	644	PHE	CB-CG-CD2	7.21	125.85	120.80
2	7-B	429	TYR	CB-CG-CD2	-7.21	116.67	121.00
1	10-A	112	TYR	CG-CD2-CE2	-7.21	115.53	121.30
3	5-D	128	ASP	CB-CG-OD1	7.21	124.79	118.30
1	4-A	345	PHE	CB-CG-CD1	7.21	125.84	120.80
2	1-B	565	TYR	CG-CD1-CE1	-7.20	115.54	121.30
2	1-B	758	TYR	CB-CG-CD1	-7.20	116.68	121.00
3	1-C	279	TYR	CG-CD2-CE2	-7.20	115.54	121.30
1	10-A	327	ARG	NE-CZ-NH2	-7.20	116.70	120.30
3	1-C	307	SER	N-CA-CB	7.20	121.30	110.50
3	4-D	407	TYR	CG-CD2-CE2	-7.20	115.54	121.30
3	5-D	223	ASP	CB-CG-OD2	7.20	124.78	118.30
3	7-C	161	ARG	NE-CZ-NH2	-7.20	116.70	120.30
3	10-C	256	TYR	CD1-CE1-CZ	-7.19	113.33	119.80
1	4-A	95	ALA	N-CA-CB	7.19	120.17	110.10
1	7-A	58	LEU	CB-CG-CD1	7.19	123.23	111.00
2	4-B	661	PHE	CB-CG-CD1	-7.19	115.77	120.80
3	2-C	413	PHE	CB-CG-CD1	-7.19	115.77	120.80
3	5-D	443	ASP	CB-CG-OD2	-7.19	111.83	118.30
1	2-A	405	PHE	CB-CG-CD1	7.19	125.83	120.80
1	3-A	382	ALA	CB-CA-C	-7.19	99.32	110.10
3	2-D	46	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	1-A	623	ARG	NE-CZ-NH2	7.18	123.89	120.30
3	8-D	136	PHE	CB-CG-CD1	7.18	125.82	120.80
1	1-A	349	ARG	NE-CZ-NH2	-7.17	116.71	120.30
2	3-B	382	PRO	N-CA-CB	7.17	111.91	103.30
3	9-C	117	ASP	CB-CG-OD1	-7.17	111.84	118.30
1	10-A	410	PHE	CB-CG-CD2	-7.17	115.78	120.80
2	3-B	200	PHE	CB-CG-CD1	7.17	125.82	120.80
3	6-C	394	PHE	CB-CG-CD1	-7.17	115.78	120.80
1	6-A	98	MET	CG-SD-CE	-7.17	88.73	100.20
2	8-B	580	ARG	NE-CZ-NH1	7.16	123.88	120.30
3	8-C	267	PHE	CB-CG-CD2	7.16	125.81	120.80
3	10-C	272	PHE	CB-CG-CD2	-7.16	115.79	120.80
2	2-B	438	TYR	CB-CG-CD2	-7.16	116.70	121.00
3	3-D	436	ASP	CB-CG-OD2	-7.16	111.86	118.30
1	10-A	161	ASP	CB-CG-OD2	-7.15	111.86	118.30
2	10-B	772	PHE	CB-CG-CD2	-7.15	115.79	120.80
1	9-A	334	ASP	CB-CG-OD1	7.15	124.73	118.30
2	1-B	562	TYR	CG-CD1-CE1	-7.15	115.58	121.30
1	3-A	162	PHE	CB-CG-CD2	-7.15	115.80	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5-B	365	ALA	CB-CA-C	-7.15	99.38	110.10
3	7-C	84	ARG	NE-CZ-NH2	-7.15	116.73	120.30
3	2-C	188	ILE	CA-CB-CG1	7.14	124.58	111.00
1	5-A	78	PHE	CB-CG-CD2	7.14	125.80	120.80
1	5-A	435	VAL	CA-CB-CG2	7.14	121.61	110.90
1	1-A	582	TYR	CB-CG-CD2	-7.14	116.72	121.00
3	7-C	162	TYR	CB-CG-CD1	7.14	125.28	121.00
3	5-D	315	TYR	CB-CG-CD2	-7.14	116.72	121.00
3	5-C	402	ALA	N-CA-CB	7.13	120.09	110.10
3	6-C	387	PHE	CB-CG-CD1	-7.13	115.81	120.80
3	7-D	329	ARG	NE-CZ-NH2	-7.13	116.73	120.30
1	1-A	653	ASP	CB-CG-OD1	-7.13	111.88	118.30
2	2-B	589	PHE	CB-CG-CD2	-7.13	115.81	120.80
3	4-D	65	ARG	NE-CZ-NH1	7.13	123.87	120.30
3	5-D	299	LEU	CB-CG-CD2	7.13	123.12	111.00
1	3-A	395	ASP	CB-CG-OD2	-7.13	111.88	118.30
2	4-B	288	TYR	CB-CG-CD2	7.13	125.28	121.00
2	8-B	231	TYR	CB-CG-CD2	-7.13	116.72	121.00
3	6-D	362	TYR	CB-CG-CD2	-7.12	116.72	121.00
1	5-A	603	TRP	CB-CG-CD2	7.12	135.86	126.60
1	6-A	345	PHE	CB-CG-CD1	-7.12	115.81	120.80
3	4-C	315	TYR	CB-CG-CD1	7.12	125.27	121.00
2	3-B	565	TYR	CG-CD1-CE1	-7.12	115.60	121.30
1	9-A	62	ASP	CB-CG-OD1	7.12	124.71	118.30
2	5-B	664	MET	CG-SD-CE	-7.12	88.81	100.20
1	10-A	450	TYR	CB-CG-CD2	7.12	125.27	121.00
3	8-D	330	GLN	CA-CB-CG	7.11	129.05	113.40
3	7-C	70	ASP	N-CA-CB	7.10	123.39	110.60
3	7-D	222	ILE	CA-CB-CG2	-7.10	96.69	110.90
3	2-D	315	TYR	CB-CG-CD2	-7.10	116.74	121.00
3	5-C	133	PHE	CB-CG-CD1	7.10	125.77	120.80
2	9-B	651	TYR	CB-CG-CD1	-7.10	116.74	121.00
3	9-D	333	ARG	NE-CZ-NH2	-7.10	116.75	120.30
2	10-B	236	TYR	CB-CG-CD1	7.10	125.26	121.00
1	3-A	143	ARG	NE-CZ-NH2	-7.10	116.75	120.30
1	1-A	193	TYR	CB-CG-CD1	7.09	125.26	121.00
2	4-B	562	TYR	CB-CG-CD1	-7.09	116.74	121.00
3	6-C	247	TYR	CB-CG-CD1	7.09	125.26	121.00
1	3-A	795	ASP	CB-CG-OD1	7.09	124.68	118.30
1	7-A	127	SER	N-CA-CB	7.09	121.14	110.50
1	6-A	398	TYR	CZ-CE2-CD2	7.09	126.18	119.80
3	8-C	376	MET	CG-SD-CE	-7.09	88.86	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	111	ARG	NE-CZ-NH2	-7.09	116.76	120.30
2	1-B	300	PHE	CB-CG-CD2	-7.08	115.84	120.80
2	5-B	284	TYR	CG-CD1-CE1	-7.08	115.64	121.30
2	6-B	531	SER	CB-CA-C	7.08	123.56	110.10
1	1-A	400	ARG	NE-CZ-NH1	7.08	123.84	120.30
1	2-A	99	ASP	CB-CG-OD1	-7.08	111.93	118.30
1	5-A	568	TYR	CB-CG-CD1	-7.08	116.75	121.00
2	7-B	653	LEU	CB-CG-CD2	7.08	123.03	111.00
2	3-B	816	TYR	CB-CG-CD1	7.08	125.25	121.00
1	5-A	612	TRP	CB-CG-CD2	-7.08	117.40	126.60
1	10-A	642	THR	CA-CB-CG2	-7.08	102.50	112.40
1	2-A	123	TYR	CB-CG-CD2	-7.07	116.76	121.00
2	7-B	583	TYR	CB-CG-CD2	-7.07	116.76	121.00
3	8-C	20	PHE	CB-CG-CD2	-7.07	115.85	120.80
3	1-D	170	TYR	CB-CG-CD1	-7.07	116.76	121.00
2	5-B	216	PHE	CB-CG-CD1	-7.07	115.85	120.80
3	8-D	55	ARG	NE-CZ-NH2	-7.07	116.76	120.30
2	4-B	335	PHE	CB-CG-CD1	7.07	125.75	120.80
3	4-C	131	ASP	CB-CG-OD2	-7.07	111.94	118.30
3	8-D	422	GLU	OE1-CD-OE2	7.07	131.78	123.30
2	8-B	587	PHE	CB-CG-CD1	7.06	125.75	120.80
3	8-C	311	ASN	N-CA-CB	7.06	123.31	110.60
3	9-C	84	ARG	NE-CZ-NH2	-7.06	116.77	120.30
3	2-D	333	ARG	NE-CZ-NH1	7.06	123.83	120.30
2	3-B	470	TYR	CB-CG-CD2	7.06	125.24	121.00
1	6-A	157	ARG	NE-CZ-NH2	-7.06	116.77	120.30
2	10-B	319	PHE	CB-CG-CD1	7.06	125.74	120.80
3	1-C	398	PHE	CB-CG-CD2	-7.06	115.86	120.80
1	3-A	144	ARG	NH1-CZ-NH2	7.05	127.16	119.40
3	6-C	87	PHE	CB-CG-CD1	7.05	125.74	120.80
3	7-D	318	VAL	C-N-CA	7.05	139.34	121.70
1	3-A	337	SER	N-CA-CB	7.05	121.08	110.50
3	6-D	243	ARG	NE-CZ-NH1	7.05	123.83	120.30
3	8-C	252	MET	CG-SD-CE	-7.05	88.92	100.20
1	4-A	562	PHE	CB-CG-CD1	7.05	125.73	120.80
1	10-A	687	ARG	NE-CZ-NH2	-7.04	116.78	120.30
3	1-D	383	VAL	CA-CB-CG1	7.04	121.47	110.90
3	8-D	362	TYR	CG-CD1-CE1	-7.04	115.67	121.30
1	2-A	575	SER	C-N-CA	7.04	139.30	121.70
3	8-D	403	PHE	CB-CG-CD1	7.04	125.73	120.80
1	7-A	486	PHE	CB-CG-CD1	-7.04	115.87	120.80
3	8-D	279	TYR	CB-CG-CD2	7.04	125.22	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	10-B	225	PHE	CB-CG-CD2	-7.04	115.87	120.80
3	2-D	43	SER	N-CA-CB	7.04	121.05	110.50
3	6-C	411	ASP	CB-CG-OD1	-7.04	111.97	118.30
1	7-A	203	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	6-A	687	ARG	NE-CZ-NH1	7.03	123.82	120.30
2	8-B	450	ASN	N-CA-CB	7.03	123.26	110.60
2	4-B	612	ARG	NE-CZ-NH1	7.03	123.82	120.30
3	6-D	275	PHE	CB-CG-CD1	7.03	125.72	120.80
2	2-B	393	PHE	CB-CG-CD2	-7.02	115.88	120.80
3	8-C	308	THR	CA-CB-CG2	-7.02	102.57	112.40
2	6-B	505	ASP	CB-CG-OD1	7.02	124.62	118.30
3	10-C	86	PHE	CB-CG-CD1	7.01	125.71	120.80
2	4-B	839	PHE	CB-CG-CD2	-7.01	115.89	120.80
3	8-C	300	ASP	CB-CG-OD1	-7.01	111.99	118.30
3	10-C	204	PHE	CB-CG-CD2	7.01	125.71	120.80
3	1-D	387	PHE	CB-CG-CD1	7.01	125.70	120.80
2	5-B	264	TYR	CB-CG-CD1	-7.01	116.80	121.00
1	10-A	150	TYR	CB-CG-CD2	-7.01	116.80	121.00
1	7-A	186	MET	CG-SD-CE	-7.00	88.99	100.20
1	8-A	102	PHE	CB-CG-CD1	7.00	125.70	120.80
1	1-A	704	TYR	CB-CG-CD2	7.00	125.20	121.00
1	8-A	325	PHE	CB-CG-CD2	-7.00	115.90	120.80
2	5-B	514	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	2-A	633	HIS	CA-CB-CG	7.00	125.49	113.60
2	3-B	187	TYR	CG-CD1-CE1	-7.00	115.70	121.30
3	5-C	267	PHE	CB-CG-CD2	-7.00	115.90	120.80
1	9-A	267	PHE	N-CA-CB	7.00	123.19	110.60
1	2-A	299	PHE	CB-CG-CD1	6.99	125.69	120.80
1	9-A	624	ARG	NE-CZ-NH2	-6.99	116.80	120.30
1	8-A	791	PHE	CB-CG-CD2	6.99	125.69	120.80
2	10-B	758	TYR	CG-CD1-CE1	-6.99	115.71	121.30
2	1-B	244	LEU	N-CA-CB	6.99	124.38	110.40
2	5-B	285	ARG	NE-CZ-NH1	6.99	123.79	120.30
2	5-B	576	ARG	NE-CZ-NH1	6.99	123.79	120.30
2	2-B	433	TYR	CG-CD2-CE2	-6.99	115.71	121.30
1	10-A	368	SER	N-CA-CB	6.99	120.98	110.50
1	4-A	704	TYR	CB-CG-CD2	-6.98	116.81	121.00
3	6-C	75	VAL	CA-CB-CG2	-6.98	100.42	110.90
3	4-C	55	ARG	NE-CZ-NH1	-6.98	116.81	120.30
3	7-D	244	PHE	CB-CG-CD2	-6.98	115.92	120.80
1	8-A	334	ASP	CB-CG-OD2	-6.98	112.02	118.30
2	1-B	510	TYR	CB-CG-CD2	6.97	125.19	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-D	333	ARG	NE-CZ-NH1	-6.97	116.81	120.30
3	8-D	279	TYR	CG-CD1-CE1	6.97	126.88	121.30
2	7-B	816	TYR	CB-CG-CD2	6.97	125.18	121.00
1	1-A	671	ALA	N-CA-CB	6.97	119.86	110.10
2	1-B	612	ARG	NE-CZ-NH1	6.97	123.78	120.30
1	4-A	664	ARG	NE-CZ-NH2	6.97	123.78	120.30
3	4-D	300	ASP	CB-CG-OD1	-6.97	112.03	118.30
1	6-A	99	ASP	CB-CG-OD2	-6.97	112.03	118.30
2	6-B	631	LEU	CB-CG-CD2	6.97	122.84	111.00
1	1-A	410	PHE	CB-CG-CD1	6.96	125.67	120.80
1	2-A	558	TYR	CG-CD2-CE2	-6.96	115.73	121.30
3	9-C	427	ARG	NE-CZ-NH2	6.96	123.78	120.30
2	5-B	609	ASP	CB-CG-OD2	6.96	124.57	118.30
2	5-B	639	THR	CA-CB-CG2	-6.96	102.65	112.40
3	1-D	359	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	10-A	192	ILE	CA-CB-CG1	6.96	124.22	111.00
1	6-A	116	TYR	CB-CG-CD1	-6.96	116.83	121.00
1	2-A	373	ILE	CA-CB-CG1	6.96	124.22	111.00
1	6-A	107	ARG	NE-CZ-NH2	-6.96	116.82	120.30
2	6-B	591	TRP	CB-CG-CD1	6.95	136.03	127.00
2	3-B	297	TYR	CB-CG-CD1	-6.95	116.83	121.00
1	10-A	186	MET	CG-SD-CE	-6.95	89.08	100.20
3	6-C	46	ARG	NH1-CZ-NH2	6.95	127.04	119.40
3	7-D	197	ASP	CB-CG-OD1	-6.95	112.05	118.30
2	6-B	826	PHE	CB-CG-CD1	-6.94	115.94	120.80
1	9-A	293	ASN	CB-CA-C	-6.94	96.52	110.40
1	9-A	393	TYR	CG-CD1-CE1	-6.94	115.75	121.30
3	1-C	90	ARG	NE-CZ-NH1	6.94	123.77	120.30
1	1-A	687	ARG	NE-CZ-NH1	-6.93	116.83	120.30
2	1-B	547	ASP	CB-CG-OD2	-6.93	112.06	118.30
1	5-A	340	ASP	CB-CG-OD2	-6.93	112.06	118.30
3	5-C	358	ARG	NE-CZ-NH2	-6.93	116.83	120.30
1	4-A	600	ASP	CB-CG-OD1	-6.93	112.06	118.30
3	1-C	160	ASP	CB-CG-OD2	-6.93	112.07	118.30
1	2-A	413	TYR	CG-CD2-CE2	6.93	126.84	121.30
3	1-D	138	LEU	CB-CG-CD1	6.92	122.77	111.00
1	4-A	117	MET	CG-SD-CE	6.92	111.28	100.20
3	10-D	78	ASP	CB-CG-OD2	-6.92	112.07	118.30
2	1-B	488	PHE	CB-CG-CD2	6.92	125.64	120.80
3	3-C	335	MET	CA-CB-CG	6.92	125.07	113.30
1	4-A	709	PHE	CB-CG-CD2	-6.92	115.96	120.80
1	9-A	148	ASP	CB-CG-OD2	-6.92	112.08	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	4-B	295	ARG	NE-CZ-NH1	-6.91	116.84	120.30
3	3-C	199	ASP	CB-CG-OD1	-6.91	112.08	118.30
3	10-C	247	TYR	CG-CD2-CE2	-6.91	115.77	121.30
2	8-B	416	CYS	N-CA-C	-6.91	92.35	111.00
1	10-A	299	PHE	CB-CG-CD2	-6.91	115.97	120.80
3	10-D	384	VAL	CA-CB-CG1	-6.91	100.54	110.90
1	3-A	162	PHE	CB-CG-CD1	6.90	125.63	120.80
1	5-A	139	ALA	CB-CA-C	-6.90	99.75	110.10
3	8-C	275	PHE	CB-CG-CD2	-6.90	115.97	120.80
3	10-D	101	ALA	N-CA-CB	6.90	119.76	110.10
3	5-C	109	TYR	CG-CD2-CE2	-6.90	115.78	121.30
2	7-B	187	TYR	CB-CG-CD2	6.89	125.14	121.00
1	2-A	393	TYR	CB-CG-CD2	-6.89	116.86	121.00
1	1-A	132	GLY	N-CA-C	-6.89	95.88	113.10
1	1-A	689	LEU	CB-CG-CD2	6.89	122.71	111.00
3	10-D	362	TYR	CZ-CE2-CD2	-6.88	113.61	119.80
1	4-A	102	PHE	CB-CG-CD1	6.88	125.61	120.80
3	9-C	247	TYR	CB-CG-CD2	6.88	125.13	121.00
2	1-B	600	TYR	CZ-CE2-CD2	6.88	125.99	119.80
3	1-C	333	ARG	NE-CZ-NH1	-6.88	116.86	120.30
2	3-B	363	PHE	CB-CG-CD2	-6.88	115.99	120.80
2	4-B	187	TYR	CB-CG-CD2	-6.88	116.88	121.00
1	6-A	767	TYR	CB-CG-CD1	6.87	125.12	121.00
3	4-C	64	PRO	N-CA-CB	6.87	111.54	103.30
2	10-B	202	PHE	CB-CG-CD1	-6.87	115.99	120.80
1	3-A	324	TYR	CB-CG-CD2	6.87	125.12	121.00
2	4-B	439	ARG	NE-CZ-NH2	-6.87	116.87	120.30
3	4-C	66	ALA	N-CA-CB	6.87	119.71	110.10
1	10-A	588	TYR	CG-CD1-CE1	-6.87	115.81	121.30
3	7-C	434	MET	CA-CB-CG	6.86	124.97	113.30
2	7-B	593	PHE	CB-CG-CD1	6.86	125.60	120.80
3	1-C	407	TYR	CG-CD1-CE1	-6.86	115.81	121.30
2	1-B	343	TYR	CB-CG-CD2	-6.85	116.89	121.00
1	7-A	62	ASP	CB-CG-OD1	6.85	124.47	118.30
3	3-C	54	PHE	CB-CG-CD1	-6.85	116.00	120.80
3	4-C	319	TYR	CB-CG-CD1	-6.85	116.89	121.00
2	9-B	433	TYR	CG-CD1-CE1	6.85	126.78	121.30
3	2-C	268	LEU	CB-CG-CD1	6.85	122.64	111.00
2	5-B	328	ARG	NE-CZ-NH2	-6.84	116.88	120.30
2	5-B	543	ALA	CB-CA-C	-6.84	99.83	110.10
2	9-B	328	ARG	NE-CZ-NH1	6.84	123.72	120.30
2	7-B	555	TRP	CG-CD2-CE3	-6.84	127.74	133.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	9-B	385	PHE	CB-CG-CD1	6.84	125.59	120.80
3	3-C	359	ARG	NE-CZ-NH1	6.84	123.72	120.30
2	6-B	288	TYR	CB-CG-CD1	6.84	125.10	121.00
2	2-B	502	THR	CA-CB-CG2	-6.84	102.83	112.40
1	4-A	582	TYR	CB-CG-CD1	6.84	125.10	121.00
2	3-B	471	ARG	NE-CZ-NH2	-6.83	116.88	120.30
2	1-B	645	ASN	CB-CA-C	-6.83	96.73	110.40
2	2-B	294	LEU	CB-CG-CD2	-6.83	99.38	111.00
2	8-B	666	ARG	NE-CZ-NH1	6.83	123.72	120.30
2	10-B	776	TYR	CG-CD1-CE1	-6.83	115.83	121.30
1	4-A	624	ARG	NE-CZ-NH2	-6.83	116.88	120.30
3	10-D	329	ARG	NE-CZ-NH2	-6.83	116.89	120.30
1	5-A	623	ARG	NE-CZ-NH1	6.83	123.72	120.30
2	9-B	242	ARG	NE-CZ-NH1	6.83	123.71	120.30
2	9-B	459	HIS	CA-CB-CG	-6.83	101.99	113.60
2	7-B	453	TYR	CB-CG-CD1	-6.83	116.90	121.00
2	9-B	805	PHE	CB-CG-CD2	6.83	125.58	120.80
3	2-C	338	LEU	CB-CG-CD1	6.82	122.60	111.00
3	8-C	217	PHE	CB-CG-CD2	6.82	125.58	120.80
3	7-D	239	THR	CA-CB-CG2	-6.82	102.85	112.40
1	5-A	117	MET	CG-SD-CE	-6.82	89.29	100.20
3	5-C	362	TYR	CB-CG-CD2	6.82	125.09	121.00
2	6-B	472	ASP	CB-CG-OD1	6.82	124.44	118.30
2	8-B	453	TYR	CB-CG-CD1	6.82	125.09	121.00
3	8-D	55	ARG	NE-CZ-NH1	6.82	123.71	120.30
3	10-D	245	PRO	N-CA-CB	6.82	111.48	103.30
2	2-B	732	LEU	CB-CA-C	-6.82	97.25	110.20
1	5-A	193	TYR	CB-CG-CD2	-6.82	116.91	121.00
1	9-A	429	TYR	CB-CG-CD2	-6.82	116.91	121.00
1	7-A	576	ARG	NE-CZ-NH2	6.81	123.71	120.30
1	8-A	112	TYR	CG-CD2-CE2	6.81	126.75	121.30
1	8-A	190	TYR	CG-CD1-CE1	6.81	126.75	121.30
1	10-A	162	PHE	CB-CG-CD2	-6.81	116.03	120.80
3	4-D	92	THR	CA-CB-CG2	-6.81	102.87	112.40
3	9-D	133	PHE	CD1-CE1-CZ	6.81	128.27	120.10
2	5-B	651	TYR	CB-CG-CD1	6.81	125.08	121.00
3	10-C	407	TYR	CG-CD1-CE1	-6.81	115.86	121.30
1	5-A	182	VAL	CA-CB-CG2	-6.80	100.70	110.90
1	3-A	327	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	5-A	121	ARG	NE-CZ-NH2	6.80	123.70	120.30
2	6-B	468	PHE	CB-CG-CD1	-6.80	116.04	120.80
1	7-A	776	ARG	NE-CZ-NH1	-6.80	116.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	327	ARG	NE-CZ-NH2	-6.80	116.90	120.30
2	10-B	474	VAL	CA-CB-CG2	-6.80	100.70	110.90
1	8-A	123	TYR	CZ-CE2-CD2	6.80	125.92	119.80
2	9-B	591	TRP	CB-CG-CD2	-6.80	117.77	126.60
2	4-B	720	ASN	N-CA-CB	6.79	122.83	110.60
1	5-A	760	LEU	CB-CG-CD1	6.79	122.55	111.00
2	6-B	389	ARG	NE-CZ-NH2	-6.79	116.90	120.30
3	6-C	204	PHE	CB-CA-C	-6.79	96.81	110.40
1	6-A	358	ARG	NE-CZ-NH1	6.79	123.69	120.30
3	6-D	275	PHE	CG-CD2-CE2	6.79	128.27	120.80
1	2-A	587	ARG	NE-CZ-NH2	-6.79	116.91	120.30
2	4-B	305	GLU	N-CA-CB	6.79	122.82	110.60
1	5-A	334	ASP	CB-CG-OD1	-6.79	112.19	118.30
3	7-C	436	ASP	CB-CG-OD1	6.78	124.41	118.30
1	3-A	409	PHE	CB-CG-CD1	-6.78	116.05	120.80
2	7-B	362	PHE	CB-CG-CD1	6.78	125.55	120.80
1	8-A	117	MET	N-CA-CB	6.78	122.81	110.60
2	8-B	345	TYR	CB-CG-CD2	-6.78	116.93	121.00
3	8-D	319	TYR	CG-CD2-CE2	-6.78	115.88	121.30
1	1-A	110	VAL	CA-CB-CG1	6.78	121.07	110.90
2	2-B	200	PHE	CB-CG-CD1	-6.78	116.06	120.80
1	8-A	111	ARG	NE-CZ-NH2	6.77	123.69	120.30
3	9-D	218	ARG	NE-CZ-NH1	6.77	123.69	120.30
3	3-C	335	MET	CG-SD-CE	-6.76	89.38	100.20
3	7-D	100	SER	N-CA-CB	6.76	120.65	110.50
1	3-A	393	TYR	CG-CD1-CE1	-6.76	115.89	121.30
3	3-D	332	SER	N-CA-CB	6.76	120.64	110.50
1	5-A	261	ASP	CB-CG-OD1	6.76	124.38	118.30
1	6-A	630	ARG	NE-CZ-NH1	6.76	123.68	120.30
3	2-D	87	PHE	CB-CG-CD2	-6.76	116.07	120.80
3	2-D	117	ASP	CB-CG-OD2	-6.76	112.22	118.30
3	8-D	315	TYR	CB-CG-CD2	6.76	125.06	121.00
3	9-D	133	PHE	CB-CG-CD2	-6.76	116.07	120.80
3	10-D	25	LEU	CB-CG-CD2	6.75	122.48	111.00
2	10-B	471	ARG	NE-CZ-NH1	6.75	123.68	120.30
1	3-A	568	TYR	CB-CG-CD1	-6.75	116.95	121.00
1	6-A	755	ASP	CB-CG-OD1	-6.75	112.22	118.30
3	5-C	193	ARG	NE-CZ-NH2	-6.75	116.93	120.30
3	7-C	387	PHE	CB-CG-CD1	6.75	125.52	120.80
3	9-D	341	ARG	NE-CZ-NH2	-6.75	116.93	120.30
3	10-D	285	ALA	C-N-CA	6.75	138.57	121.70
3	1-C	249	TYR	CB-CG-CD2	6.75	125.05	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-C	437	TYR	CB-CG-CD1	6.75	125.05	121.00
3	6-D	192	ARG	NE-CZ-NH1	6.75	123.67	120.30
2	1-B	429	TYR	CD1-CG-CD2	6.74	125.32	117.90
2	4-B	359	TYR	CB-CG-CD1	6.74	125.05	121.00
3	10-C	58	CYS	CA-CB-SG	-6.74	101.86	114.00
2	4-B	319	PHE	CB-CG-CD2	-6.74	116.08	120.80
1	1-A	262	ARG	NE-CZ-NH2	-6.74	116.93	120.30
1	10-A	150	TYR	CG-CD2-CE2	-6.74	115.91	121.30
1	10-A	568	TYR	CB-CG-CD1	6.74	125.04	121.00
1	6-A	605	ASP	CB-CG-OD2	-6.74	112.24	118.30
1	10-A	393	TYR	CB-CG-CD2	-6.74	116.96	121.00
2	10-B	508	PRO	N-CA-CB	6.74	111.38	103.30
2	3-B	411	PHE	CB-CG-CD2	-6.73	116.09	120.80
3	9-C	113	THR	CA-CB-CG2	-6.73	102.97	112.40
1	1-A	278	ASP	CB-CG-OD2	6.73	124.36	118.30
3	5-C	319	TYR	CB-CG-CD2	-6.73	116.96	121.00
3	8-C	173	PHE	CB-CG-CD2	-6.73	116.09	120.80
2	1-B	593	PHE	CB-CG-CD1	6.73	125.51	120.80
3	5-D	398	PHE	CB-CG-CD1	-6.73	116.09	120.80
1	9-A	663	TYR	CB-CG-CD2	-6.73	116.96	121.00
2	10-B	599	PHE	CB-CG-CD2	-6.73	116.09	120.80
1	5-A	451	ARG	NE-CZ-NH1	-6.73	116.94	120.30
3	8-D	124	ASP	CB-CG-OD1	6.73	124.35	118.30
1	1-A	294	ASP	CB-CG-OD1	-6.72	112.25	118.30
1	6-A	633	HIS	CA-CB-CG	6.72	125.03	113.60
3	10-C	46	ARG	NE-CZ-NH2	-6.72	116.94	120.30
1	2-A	594	TYR	CG-CD2-CE2	6.72	126.68	121.30
2	3-B	446	PHE	CB-CG-CD1	6.72	125.50	120.80
2	10-B	181	GLU	CA-CB-CG	6.72	128.18	113.40
1	6-A	614	TYR	CB-CG-CD2	-6.72	116.97	121.00
2	5-B	385	PHE	CB-CG-CD2	-6.71	116.10	120.80
2	10-B	805	PHE	CB-CG-CD2	-6.71	116.10	120.80
3	1-D	249	TYR	CB-CG-CD2	-6.71	116.97	121.00
2	6-B	468	PHE	N-CA-CB	6.71	122.68	110.60
1	9-A	426	PHE	CB-CG-CD1	-6.71	116.11	120.80
1	7-A	478	MET	CG-SD-CE	-6.70	89.47	100.20
3	3-C	387	PHE	CB-CG-CD1	6.70	125.49	120.80
3	10-D	185	TYR	CB-CG-CD2	-6.70	116.98	121.00
2	4-B	821	ASP	CB-CG-OD1	6.70	124.33	118.30
1	3-A	112	TYR	CD1-CE1-CZ	-6.70	113.77	119.80
3	6-D	445	TYR	CG-CD1-CE1	-6.69	115.95	121.30
1	1-A	193	TYR	CG-CD2-CE2	6.69	126.65	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	4-B	729	ASN	N-CA-CB	6.69	122.64	110.60
3	6-C	275	PHE	CB-CG-CD2	-6.69	116.12	120.80
2	6-B	661	PHE	CB-CG-CD2	-6.69	116.12	120.80
2	7-B	805	PHE	CG-CD2-CE2	-6.69	113.44	120.80
1	8-A	332	LEU	CB-CG-CD1	6.69	122.37	111.00
1	3-A	558	TYR	CB-CG-CD1	6.68	125.01	121.00
2	6-B	293	ARG	NE-CZ-NH1	-6.68	116.96	120.30
3	8-D	87	PHE	CB-CG-CD2	6.68	125.48	120.80
2	1-B	409	TYR	CB-CG-CD1	-6.68	116.99	121.00
1	10-A	159	GLU	N-CA-CB	6.68	122.63	110.60
1	10-A	449	HIS	CA-CB-CG	6.68	124.96	113.60
2	2-B	580	ARG	NE-CZ-NH1	6.68	123.64	120.30
3	2-C	249	TYR	CB-CG-CD1	-6.68	116.99	121.00
1	4-A	299	PHE	CB-CG-CD1	6.67	125.47	120.80
2	4-B	409	TYR	CB-CG-CD1	-6.67	117.00	121.00
1	6-A	134	VAL	CG1-CB-CG2	6.67	121.58	110.90
1	5-A	627	ARG	NE-CZ-NH2	-6.67	116.96	120.30
1	6-A	647	PHE	CB-CG-CD1	6.67	125.47	120.80
3	9-C	445	TYR	CB-CG-CD2	6.67	125.00	121.00
3	3-D	48	ASP	CB-CG-OD1	-6.67	112.30	118.30
2	10-B	819	PHE	CB-CG-CD1	6.67	125.47	120.80
3	2-D	362	TYR	CB-CG-CD2	6.66	125.00	121.00
1	5-A	588	TYR	CB-CG-CD2	6.66	125.00	121.00
2	3-B	514	ARG	NE-CZ-NH2	6.66	123.63	120.30
2	10-B	293	ARG	NE-CZ-NH1	6.66	123.63	120.30
2	3-B	475	PHE	CB-CG-CD1	6.66	125.46	120.80
3	8-C	1	MET	CG-SD-CE	-6.66	89.55	100.20
2	4-B	591	TRP	CG-CD2-CE3	-6.66	127.91	133.90
3	10-C	176	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	6-A	380	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	7-A	624	ARG	NE-CZ-NH2	-6.66	116.97	120.30
3	9-D	443	ASP	CB-CG-OD2	-6.65	112.31	118.30
1	2-A	792	ASP	CB-CG-OD1	-6.65	112.31	118.30
2	3-B	236	TYR	CD1-CE1-CZ	-6.65	113.81	119.80
2	9-B	461	ASN	O-C-N	-6.65	112.06	122.70
1	3-A	121	ARG	NE-CZ-NH1	-6.65	116.97	120.30
3	5-D	101	ALA	N-CA-CB	6.65	119.41	110.10
1	9-A	566	ILE	CB-CA-C	-6.65	98.30	111.60
3	7-C	315	TYR	CB-CG-CD1	-6.64	117.01	121.00
2	10-B	394	ILE	N-CA-C	-6.64	93.06	111.00
1	7-A	591	VAL	CA-CB-CG1	-6.64	100.94	110.90
2	7-B	565	TYR	N-CA-C	-6.64	93.07	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2-D	279	TYR	CB-CG-CD2	6.64	124.98	121.00
2	9-B	648	MET	CG-SD-CE	-6.64	89.58	100.20
3	5-D	436	ASP	CB-CG-OD2	6.64	124.27	118.30
2	9-B	758	TYR	CB-CG-CD2	-6.63	117.02	121.00
2	10-B	328	ARG	NE-CZ-NH2	6.63	123.62	120.30
1	10-A	157	ARG	NE-CZ-NH2	-6.63	116.98	120.30
3	7-D	170	TYR	CB-CG-CD1	-6.63	117.02	121.00
2	10-B	342	TYR	CB-CG-CD2	-6.63	117.02	121.00
2	2-B	772	PHE	CB-CG-CD2	-6.63	116.16	120.80
1	7-A	304	ASP	CB-CG-OD2	-6.63	112.33	118.30
2	3-B	415	TYR	CB-CG-CD1	6.63	124.98	121.00
2	4-B	428	LYS	CB-CG-CD	6.62	128.81	111.60
2	4-B	460	THR	N-CA-CB	6.62	122.88	110.30
2	7-B	505	ASP	CB-CG-OD2	6.62	124.26	118.30
1	8-A	600	ASP	CB-CA-C	-6.62	97.16	110.40
3	8-D	352	MET	CA-CB-CG	6.62	124.56	113.30
2	3-B	242	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	5-A	340	ASP	N-CA-CB	6.62	122.52	110.60
3	3-D	65	ARG	NE-CZ-NH2	-6.62	116.99	120.30
3	6-D	47	ASP	CB-CG-OD2	-6.62	112.35	118.30
1	10-A	327	ARG	NE-CZ-NH1	6.62	123.61	120.30
2	7-B	357	ALA	N-CA-CB	6.61	119.36	110.10
3	2-C	315	TYR	CB-CG-CD2	-6.61	117.04	121.00
2	6-B	433	TYR	CB-CG-CD1	-6.61	117.04	121.00
1	2-A	800	ASP	CB-CG-OD1	-6.61	112.36	118.30
2	5-B	660	ASN	N-CA-CB	6.61	122.49	110.60
1	8-A	284	TYR	CB-CG-CD2	6.60	124.96	121.00
1	2-A	161	ASP	N-CA-CB	6.60	122.48	110.60
1	9-A	487	ASP	CB-CG-OD2	-6.60	112.36	118.30
2	10-B	501	ALA	N-CA-CB	6.60	119.34	110.10
1	1-A	664	ARG	NE-CZ-NH2	6.60	123.60	120.30
3	7-C	90	ARG	NE-CZ-NH1	6.60	123.60	120.30
1	8-A	150	TYR	CB-CG-CD1	-6.60	117.04	121.00
3	9-D	423	PHE	CB-CG-CD1	-6.59	116.18	120.80
3	10-D	72	GLU	CB-CA-C	-6.59	97.21	110.40
2	9-B	297	TYR	CB-CG-CD1	6.59	124.96	121.00
1	1-A	465	PHE	CB-CG-CD1	6.59	125.41	120.80
1	8-A	767	TYR	CG-CD2-CE2	6.59	126.57	121.30
3	5-C	292	TYR	N-CA-CB	6.59	122.46	110.60
1	7-A	568	TYR	N-CA-CB	6.59	122.46	110.60
1	2-A	267	PHE	CB-CG-CD2	-6.59	116.19	120.80
2	5-B	598	TYR	CZ-CE2-CD2	6.59	125.73	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	6-C	443	ASP	CB-CG-OD2	-6.59	112.37	118.30
3	7-D	87	PHE	CB-CG-CD2	-6.58	116.19	120.80
1	8-A	488	THR	CA-CB-CG2	-6.58	103.19	112.40
2	3-B	415	TYR	CB-CG-CD2	-6.58	117.05	121.00
1	4-A	80	ASP	CB-CG-OD1	6.58	124.22	118.30
1	8-A	140	TYR	CB-CG-CD1	-6.58	117.06	121.00
2	8-B	591	TRP	CE3-CZ3-CH2	-6.58	113.97	121.20
1	4-A	299	PHE	CB-CG-CD2	-6.57	116.20	120.80
1	1-A	793	PHE	CB-CG-CD2	-6.57	116.20	120.80
1	7-A	464	ASN	N-CA-CB	6.57	122.43	110.60
3	5-D	249	TYR	CZ-CE2-CD2	-6.57	113.89	119.80
3	8-D	54	PHE	CB-CG-CD2	-6.57	116.20	120.80
2	8-B	828	ALA	N-CA-CB	6.57	119.29	110.10
3	3-C	59	ARG	NE-CZ-NH2	-6.56	117.02	120.30
2	5-B	236	TYR	CB-CG-CD1	-6.56	117.06	121.00
1	3-A	334	ASP	CB-CG-OD1	6.56	124.20	118.30
1	4-A	76	ARG	NH1-CZ-NH2	-6.56	112.18	119.40
3	5-D	282	ASP	N-CA-CB	6.56	122.41	110.60
3	6-C	398	PHE	CB-CG-CD1	6.56	125.39	120.80
2	7-B	393	PHE	CB-CG-CD1	6.56	125.39	120.80
1	2-A	624	ARG	NE-CZ-NH2	6.56	123.58	120.30
2	9-B	670	ARG	NE-CZ-NH1	6.56	123.58	120.30
3	5-D	41	ASP	CB-CG-OD2	-6.55	112.40	118.30
3	7-D	65	ARG	NE-CZ-NH1	6.55	123.58	120.30
1	9-A	450	TYR	CG-CD1-CE1	-6.55	116.06	121.30
2	10-B	445	PHE	CD1-CE1-CZ	6.55	127.96	120.10
1	4-A	62	ASP	CB-CG-OD2	-6.55	112.40	118.30
3	10-C	427	ARG	NE-CZ-NH2	6.55	123.58	120.30
1	2-A	279	TYR	CB-CG-CD1	6.55	124.93	121.00
3	2-C	398	PHE	CG-CD1-CE1	6.55	128.00	120.80
2	3-B	236	TYR	CB-CG-CD2	6.55	124.93	121.00
1	7-A	157	ARG	NE-CZ-NH1	6.55	123.58	120.30
2	2-B	652	TYR	CB-CG-CD2	-6.55	117.07	121.00
2	9-B	585	ARG	NE-CZ-NH2	-6.55	117.03	120.30
3	2-C	173	PHE	CB-CG-CD2	-6.55	116.22	120.80
3	7-C	83	PHE	CB-CG-CD1	-6.55	116.22	120.80
1	10-A	700	PHE	CB-CG-CD2	-6.55	116.22	120.80
2	6-B	285	ARG	NE-CZ-NH2	-6.54	117.03	120.30
3	5-D	17	VAL	CA-CB-CG1	6.54	120.71	110.90
3	2-C	205	ASP	CB-CG-OD1	-6.54	112.41	118.30
3	6-C	169	THR	CA-CB-CG2	-6.54	103.24	112.40
1	8-A	302	TYR	CG-CD1-CE1	-6.54	116.07	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4-A	602	THR	CA-CB-CG2	-6.54	103.24	112.40
3	1-C	335	MET	CG-SD-CE	6.54	110.66	100.20
3	3-D	407	TYR	CG-CD2-CE2	-6.54	116.07	121.30
2	6-B	542	ASP	CB-CG-OD1	-6.54	112.42	118.30
2	4-B	267	PHE	CB-CG-CD2	-6.53	116.23	120.80
1	9-A	204	ARG	NE-CZ-NH2	6.53	123.57	120.30
2	2-B	646	SER	N-CA-CB	6.53	120.30	110.50
3	5-D	97	ASP	CB-CG-OD1	-6.53	112.42	118.30
3	5-C	185	TYR	CB-CG-CD2	6.53	124.92	121.00
2	3-B	824	TYR	CB-CG-CD1	6.53	124.92	121.00
2	8-B	453	TYR	CB-CG-CD2	-6.53	117.08	121.00
1	9-A	443	MET	CG-SD-CE	-6.53	89.76	100.20
1	2-A	657	TYR	CB-CG-CD2	-6.52	117.09	121.00
3	4-C	185	TYR	CB-CG-CD2	-6.52	117.09	121.00
3	5-C	8	LEU	CB-CG-CD2	6.52	122.09	111.00
2	5-B	562	TYR	CB-CG-CD1	-6.52	117.09	121.00
1	7-A	577	THR	CA-CB-CG2	6.52	121.53	112.40
2	3-B	379	TYR	CB-CG-CD1	6.52	124.91	121.00
3	4-C	34	ASP	CB-CG-OD1	6.51	124.16	118.30
2	2-B	472	ASP	CB-CG-OD2	-6.51	112.44	118.30
3	2-C	217	PHE	C-N-CA	6.51	137.98	121.70
2	5-B	770	TYR	CD1-CE1-CZ	6.51	125.66	119.80
2	9-B	431	VAL	CA-CB-CG2	-6.51	101.13	110.90
2	8-B	543	ALA	N-CA-CB	6.51	119.21	110.10
3	8-C	240	ASN	CB-CA-C	-6.51	97.39	110.40
1	2-A	296	TYR	CG-CD1-CE1	-6.50	116.10	121.30
2	6-B	421	TRP	CB-CG-CD2	-6.50	118.15	126.60
3	9-C	244	PHE	CB-CG-CD2	-6.50	116.25	120.80
2	1-B	510	TYR	CA-CB-CG	6.50	125.75	113.40
2	3-B	537	VAL	CG1-CB-CG2	6.50	121.30	110.90
2	5-B	393	PHE	CB-CG-CD2	-6.50	116.25	120.80
1	3-A	294	ASP	CB-CG-OD2	-6.50	112.45	118.30
3	4-D	223	ASP	CB-CG-OD1	6.50	124.15	118.30
1	5-A	400	ARG	NE-CZ-NH2	-6.50	117.05	120.30
3	1-C	347	TRP	N-CA-CB	6.49	122.29	110.60
3	9-C	316	PHE	CB-CG-CD2	-6.49	116.25	120.80
2	10-B	585	ARG	NE-CZ-NH2	-6.49	117.05	120.30
3	3-D	282	ASP	CB-CG-OD2	6.49	124.14	118.30
3	5-C	367	PRO	N-CA-CB	6.49	111.09	103.30
3	7-D	138	LEU	CB-CG-CD1	6.49	122.03	111.00
1	3-A	160	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	10-A	561	LYS	N-CA-CB	6.49	122.28	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-A	333	ARG	NE-CZ-NH2	-6.49	117.06	120.30
2	6-B	421	TRP	CH2-CZ2-CE2	6.49	123.89	117.40
3	2-C	403	PHE	CB-CG-CD2	-6.48	116.26	120.80
3	4-D	118	ASP	CB-CG-OD2	6.48	124.13	118.30
3	5-C	395	ASP	N-CA-CB	6.48	122.26	110.60
3	6-C	176	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	9-A	121	ARG	NE-CZ-NH1	6.48	123.54	120.30
3	2-C	432	SER	O-C-N	-6.48	112.34	122.70
1	3-A	286	TRP	CA-CB-CG	6.48	126.00	113.70
2	4-B	388	GLU	OE1-CD-OE2	-6.48	115.53	123.30
1	2-A	121	ARG	NE-CZ-NH2	-6.47	117.06	120.30
1	2-A	263	SER	N-CA-CB	6.47	120.21	110.50
2	6-B	565	TYR	CD1-CE1-CZ	6.47	125.63	119.80
3	5-C	394	PHE	CB-CG-CD1	6.47	125.33	120.80
1	6-A	78	PHE	CB-CG-CD1	-6.47	116.27	120.80
1	4-A	594	TYR	CB-CG-CD1	6.47	124.88	121.00
2	6-B	488	PHE	CB-CG-CD2	-6.47	116.27	120.80
3	8-D	41	ASP	CB-CG-OD2	-6.47	112.48	118.30
1	10-A	623	ARG	NE-CZ-NH2	6.47	123.53	120.30
2	5-B	438	TYR	CB-CG-CD2	6.46	124.88	121.00
1	7-A	657	TYR	CB-CG-CD2	6.46	124.88	121.00
2	8-B	508	PRO	N-CD-CG	6.46	112.89	103.20
3	10-D	223	ASP	CB-CG-OD1	6.46	124.11	118.30
1	9-A	383	ASP	CB-CG-OD2	6.46	124.11	118.30
3	3-D	363	LEU	N-CA-C	-6.46	93.56	111.00
2	5-B	362	PHE	CB-CG-CD2	6.46	125.32	120.80
1	1-A	706	PHE	CB-CG-CD2	-6.46	116.28	120.80
1	3-A	576	ARG	NH1-CZ-NH2	6.46	126.50	119.40
2	3-B	583	TYR	CG-CD2-CE2	-6.46	116.14	121.30
3	4-C	8	LEU	N-CA-CB	6.46	123.31	110.40
1	3-A	262	ARG	NE-CZ-NH2	-6.45	117.07	120.30
3	6-C	386	VAL	CA-CB-CG1	-6.45	101.22	110.90
2	8-B	846	ARG	NE-CZ-NH1	-6.45	117.07	120.30
3	10-C	271	SER	N-CA-C	-6.45	93.58	111.00
3	2-D	223	ASP	CB-CG-OD1	-6.45	112.49	118.30
3	2-D	266	HIS	N-CA-CB	6.45	122.21	110.60
2	8-B	822	ARG	NE-CZ-NH2	-6.45	117.07	120.30
1	3-A	413	TYR	CB-CG-CD1	6.45	124.87	121.00
3	4-D	192	ARG	NE-CZ-NH1	6.45	123.52	120.30
1	7-A	451	ARG	NE-CZ-NH1	6.45	123.52	120.30
1	10-A	290	GLY	O-C-N	6.44	133.01	122.70
1	10-A	597	ARG	NE-CZ-NH1	6.44	123.52	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	10-C	315	TYR	CB-CG-CD1	-6.44	117.14	121.00
1	2-A	131	PHE	CB-CG-CD2	6.44	125.31	120.80
3	6-C	128	ASP	CB-CG-OD1	6.44	124.10	118.30
1	9-A	74	TYR	CG-CD1-CE1	-6.44	116.15	121.30
1	4-A	91	GLU	N-CA-CB	6.44	122.19	110.60
2	7-B	415	TYR	CB-CG-CD2	6.44	124.86	121.00
3	8-C	96	SER	N-CA-CB	6.44	120.16	110.50
2	5-B	359	TYR	CB-CG-CD2	-6.44	117.14	121.00
1	6-A	693	ILE	CA-C-N	6.44	135.12	117.10
3	7-D	249	TYR	CG-CD2-CE2	-6.43	116.15	121.30
3	3-D	437	TYR	CB-CG-CD2	6.43	124.86	121.00
2	5-B	345	TYR	CB-CG-CD1	-6.43	117.14	121.00
3	6-C	437	TYR	CB-CG-CD2	-6.43	117.14	121.00
1	8-A	576	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	8-A	612	TRP	CE2-CD2-CG	6.43	112.45	107.30
3	7-C	180	VAL	CA-CB-CG1	-6.43	101.25	110.90
2	5-B	297	TYR	CG-CD1-CE1	-6.43	116.16	121.30
3	8-C	244	PHE	CB-CG-CD2	-6.43	116.30	120.80
1	4-A	284	TYR	N-CA-CB	6.43	122.17	110.60
2	7-B	202	PHE	CB-CG-CD2	6.42	125.30	120.80
3	7-D	333	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	8-A	603	TRP	CE3-CZ3-CH2	-6.42	114.13	121.20
2	10-B	505	ASP	CB-CG-OD2	-6.42	112.52	118.30
1	1-A	704	TYR	CB-CG-CD1	-6.42	117.15	121.00
2	3-B	661	PHE	CB-CG-CD1	6.42	125.30	120.80
2	1-B	604	MET	CG-SD-CE	6.42	110.47	100.20
3	1-C	223	ASP	CB-CG-OD1	6.42	124.08	118.30
3	10-C	272	PHE	CD1-CE1-CZ	6.42	127.81	120.10
1	1-A	400	ARG	NE-CZ-NH2	-6.42	117.09	120.30
2	2-B	599	PHE	CB-CG-CD1	6.42	125.29	120.80
3	7-C	387	PHE	CB-CG-CD2	-6.42	116.31	120.80
2	1-B	532	PRO	C-N-CA	6.41	137.74	121.70
3	1-C	359	ARG	NE-CZ-NH1	6.41	123.51	120.30
2	6-B	562	TYR	CB-CG-CD2	-6.41	117.15	121.00
2	7-B	216	PHE	CB-CG-CD1	6.41	125.29	120.80
3	5-C	104	SER	N-CA-CB	6.41	120.12	110.50
3	8-D	12	GLN	C-N-CA	6.41	137.73	121.70
1	9-A	126	TRP	CG-CD2-CE3	-6.41	128.13	133.90
2	9-B	295	ARG	NE-CZ-NH2	-6.41	117.09	120.30
1	5-A	105	PHE	CB-CG-CD2	-6.41	116.31	120.80
2	5-B	637	LEU	CB-CA-C	-6.41	98.03	110.20
1	8-A	462	LEU	CB-CG-CD1	6.41	121.89	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	6-B	340	SER	N-CA-CB	6.40	120.10	110.50
3	1-D	407	TYR	CB-CG-CD2	-6.40	117.16	121.00
3	2-C	54	PHE	CB-CG-CD2	-6.40	116.32	120.80
3	2-D	105	TRP	CB-CG-CD1	6.40	135.32	127.00
3	7-D	59	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	5-A	332	LEU	CB-CG-CD2	6.40	121.87	111.00
3	6-C	195	ILE	CA-CB-CG1	6.40	123.15	111.00
2	6-B	194	ALA	N-CA-CB	6.39	119.05	110.10
2	7-B	665	THR	CA-CB-CG2	-6.39	103.45	112.40
2	1-B	409	TYR	CG-CD2-CE2	-6.39	116.19	121.30
2	1-B	433	TYR	CG-CD1-CE1	-6.39	116.19	121.30
2	1-B	816	TYR	CB-CG-CD1	6.39	124.83	121.00
1	2-A	405	PHE	CB-CG-CD2	-6.39	116.33	120.80
2	7-B	514	ARG	NE-CZ-NH1	6.39	123.50	120.30
3	7-D	248	MET	CG-SD-CE	-6.39	89.97	100.20
1	8-A	646	TYR	CB-CG-CD1	-6.39	117.17	121.00
2	9-B	592	ARG	NE-CZ-NH1	6.39	123.50	120.30
2	10-B	319	PHE	CB-CG-CD2	-6.39	116.33	120.80
2	3-B	515	VAL	CA-CB-CG2	6.39	120.49	110.90
3	3-D	185	TYR	CB-CG-CD1	-6.39	117.17	121.00
3	4-C	204	PHE	CB-CG-CD1	6.39	125.27	120.80
3	7-D	398	PHE	CB-CG-CD2	-6.39	116.33	120.80
3	6-D	243	ARG	NE-CZ-NH2	-6.39	117.11	120.30
3	7-C	294	VAL	CA-CB-CG2	6.39	120.48	110.90
1	5-A	74	TYR	CG-CD2-CE2	-6.39	116.19	121.30
1	3-A	334	ASP	CB-CG-OD2	-6.39	112.55	118.30
2	4-B	585	ARG	CD-NE-CZ	6.39	132.54	123.60
2	6-B	558	PHE	CB-CG-CD2	-6.39	116.33	120.80
1	10-A	303	ASP	CB-CG-OD1	-6.39	112.55	118.30
1	5-A	636	MET	CG-SD-CE	-6.38	89.98	100.20
1	8-A	296	TYR	CG-CD2-CE2	-6.38	116.19	121.30
1	10-A	162	PHE	CG-CD2-CE2	-6.38	113.78	120.80
3	5-C	271	SER	N-CA-C	-6.38	93.77	111.00
2	1-B	505	ASP	CB-CG-OD1	-6.38	112.56	118.30
1	4-A	587	ARG	NE-CZ-NH1	6.38	123.49	120.30
2	6-B	666	ARG	NE-CZ-NH1	6.38	123.49	120.30
3	6-C	73	PRO	N-CD-CG	6.38	112.76	103.20
3	8-D	443	ASP	N-CA-CB	6.38	122.08	110.60
3	7-D	337	LYS	CB-CA-C	-6.38	97.65	110.40
3	10-C	128	ASP	CB-CG-OD2	-6.38	112.56	118.30
2	3-B	236	TYR	CG-CD1-CE1	6.37	126.40	121.30
2	4-B	511	LYS	N-CA-CB	6.37	122.07	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	8-A	398	TYR	CB-CG-CD1	-6.37	117.18	121.00
3	2-C	185	TYR	CD1-CE1-CZ	-6.37	114.07	119.80
2	7-B	225	PHE	CA-CB-CG	6.37	129.18	113.90
2	3-B	385	PHE	CB-CG-CD1	6.37	125.26	120.80
1	8-A	393	TYR	CB-CG-CD2	6.37	124.82	121.00
1	9-A	603	TRP	O-C-N	-6.37	112.51	122.70
2	6-B	769	VAL	CA-CB-CG2	-6.37	101.35	110.90
2	7-B	324	ASP	CB-CG-OD2	6.37	124.03	118.30
2	2-B	819	PHE	CB-CG-CD2	-6.36	116.34	120.80
1	7-A	772	SER	N-CA-CB	6.36	120.05	110.50
1	8-A	394	VAL	CA-CB-CG1	6.36	120.44	110.90
1	3-A	430	GLN	N-CA-CB	6.36	122.05	110.60
2	9-B	644	PHE	CB-CG-CD2	6.36	125.25	120.80
2	6-B	585	ARG	NE-CZ-NH1	6.36	123.48	120.30
1	2-A	458	TYR	CG-CD2-CE2	6.36	126.39	121.30
2	4-B	418	GLU	CB-CA-C	6.36	123.12	110.40
2	10-B	580	ARG	NE-CZ-NH1	-6.36	117.12	120.30
3	7-D	54	PHE	CB-CG-CD2	-6.36	116.35	120.80
2	1-B	772	PHE	CB-CG-CD2	-6.35	116.35	120.80
1	5-A	638	HIS	CA-CB-CG	6.35	124.40	113.60
2	5-B	565	TYR	CB-CG-CD2	-6.35	117.19	121.00
3	5-C	97	ASP	CB-CG-OD1	6.35	124.02	118.30
2	6-B	652	TYR	CB-CG-CD2	-6.35	117.19	121.00
3	6-C	20	PHE	CB-CG-CD2	-6.35	116.35	120.80
3	8-C	362	TYR	CG-CD2-CE2	6.35	126.38	121.30
1	1-A	190	TYR	CB-CG-CD1	6.35	124.81	121.00
1	1-A	393	TYR	CA-CB-CG	-6.35	101.34	113.40
2	1-B	218	SER	N-CA-CB	6.35	120.02	110.50
1	6-A	771	ALA	CB-CA-C	-6.35	100.58	110.10
2	8-B	562	TYR	CD1-CE1-CZ	-6.35	114.08	119.80
1	9-A	77	TYR	CB-CG-CD1	-6.35	117.19	121.00
1	2-A	137	ARG	NE-CZ-NH2	-6.35	117.13	120.30
3	3-D	423	PHE	CB-CG-CD2	-6.35	116.36	120.80
3	4-C	352	MET	C-N-CA	6.35	137.57	121.70
2	9-B	661	PHE	CB-CG-CD2	-6.35	116.36	120.80
1	3-A	98	MET	CG-SD-CE	-6.35	90.05	100.20
3	5-D	400	LYS	C-N-CA	6.35	135.63	122.30
3	1-C	97	ASP	N-CA-CB	6.34	122.02	110.60
1	7-A	393	TYR	CB-CG-CD2	6.34	124.81	121.00
1	3-A	795	ASP	CB-CG-OD2	-6.34	112.59	118.30
1	1-A	158	LEU	N-CA-CB	6.34	123.08	110.40
1	2-A	300	MET	O-C-N	6.34	132.85	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	10-D	249	TYR	CA-CB-CG	-6.34	101.35	113.40
1	5-A	116	TYR	CB-CG-CD2	-6.34	117.20	121.00
2	5-B	356	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	8-A	262	ARG	NE-CZ-NH1	-6.34	117.13	120.30
2	9-B	453	TYR	CG-CD1-CE1	6.34	126.37	121.30
3	3-C	162	TYR	CB-CG-CD2	-6.34	117.20	121.00
1	8-A	700	PHE	CB-CG-CD2	-6.33	116.36	120.80
2	2-B	285	ARG	NE-CZ-NH1	-6.33	117.13	120.30
3	4-C	311	ASN	N-CA-C	-6.33	93.90	111.00
3	5-D	362	TYR	CG-CD1-CE1	-6.33	116.23	121.30
1	2-A	409	PHE	CB-CG-CD2	6.33	125.23	120.80
3	7-D	247	TYR	CG-CD2-CE2	-6.33	116.23	121.30
3	9-D	291	SER	CB-CA-C	-6.33	98.07	110.10
3	5-C	344	PHE	CB-CG-CD1	6.33	125.23	120.80
1	1-A	92	PHE	CB-CG-CD2	6.33	125.23	120.80
1	6-A	304	ASP	CB-CG-OD1	-6.33	112.60	118.30
1	9-A	131	PHE	CB-CG-CD1	6.33	125.23	120.80
2	4-B	829	ASP	CB-CG-OD2	-6.33	112.61	118.30
1	5-A	368	SER	N-CA-CB	6.33	119.99	110.50
2	7-B	425	PHE	CB-CG-CD2	-6.33	116.37	120.80
2	3-B	805	PHE	CB-CG-CD1	6.32	125.23	120.80
2	2-B	664	MET	CG-SD-CE	6.32	110.31	100.20
2	4-B	561	ASP	CB-CG-OD2	-6.32	112.61	118.30
2	8-B	438	TYR	CB-CG-CD2	-6.32	117.21	121.00
3	1-D	185	TYR	CB-CG-CD1	6.32	124.79	121.00
3	3-D	191	LEU	N-CA-CB	6.32	123.04	110.40
3	3-D	256	TYR	CB-CG-CD1	6.32	124.79	121.00
2	6-B	295	ARG	NE-CZ-NH2	-6.32	117.14	120.30
2	6-B	561	ASP	CB-CG-OD1	-6.32	112.61	118.30
2	2-B	839	PHE	CB-CG-CD2	-6.32	116.38	120.80
2	5-B	839	PHE	CB-CG-CD2	-6.32	116.38	120.80
1	3-A	128	ASP	CB-CG-OD1	-6.32	112.62	118.30
1	10-A	405	PHE	CB-CG-CD2	-6.32	116.38	120.80
1	4-A	700	PHE	CB-CG-CD1	6.31	125.22	120.80
3	1-C	95	ALA	N-CA-CB	6.31	118.94	110.10
1	3-A	325	PHE	CB-CG-CD2	6.31	125.22	120.80
1	8-A	438	PHE	CB-CG-CD2	-6.31	116.38	120.80
1	9-A	558	TYR	CD1-CG-CD2	6.31	124.84	117.90
2	5-B	598	TYR	CG-CD1-CE1	-6.31	116.25	121.30
1	1-A	714	ARG	NH1-CZ-NH2	6.30	126.33	119.40
1	9-A	347	MET	CG-SD-CE	-6.30	90.11	100.20
3	9-D	48	ASP	CB-CG-OD2	6.30	123.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	7-C	47	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	8-A	485	GLN	N-CA-CB	6.30	121.94	110.60
3	8-D	273	THR	O-C-N	-6.30	109.13	121.10
3	10-D	437	TYR	CD1-CE1-CZ	-6.30	114.13	119.80
2	2-B	598	TYR	CB-CG-CD1	-6.30	117.22	121.00
3	6-D	162	TYR	CB-CG-CD1	-6.30	117.22	121.00
3	2-D	367	PRO	N-CD-CG	6.29	112.64	103.20
1	6-A	296	TYR	CB-CG-CD2	6.29	124.78	121.00
3	6-D	292	TYR	CB-CG-CD1	6.29	124.78	121.00
1	1-A	414	ASP	CB-CG-OD2	-6.29	112.64	118.30
3	4-D	408	ASN	CB-CA-C	-6.29	97.81	110.40
2	5-B	265	THR	CA-CB-CG2	-6.29	103.59	112.40
1	8-A	204	ARG	NE-CZ-NH2	-6.29	117.15	120.30
2	2-B	359	TYR	CB-CG-CD1	6.29	124.77	121.00
3	4-D	299	LEU	CB-CG-CD2	6.29	121.69	111.00
1	10-A	646	TYR	CB-CG-CD1	-6.29	117.23	121.00
1	10-A	794	TYR	CB-CG-CD2	-6.29	117.23	121.00
3	4-C	244	PHE	CB-CG-CD2	-6.29	116.40	120.80
3	9-D	407	TYR	CG-CD2-CE2	-6.29	116.27	121.30
1	1-A	251	PHE	CB-CG-CD2	-6.28	116.40	120.80
3	1-C	199	ASP	CB-CG-OD2	-6.28	112.64	118.30
2	1-B	199	LEU	CB-CG-CD2	6.28	121.68	111.00
2	2-B	433	TYR	CZ-CE2-CD2	6.28	125.45	119.80
2	4-B	839	PHE	CB-CG-CD1	6.28	125.20	120.80
3	5-D	315	TYR	N-CA-CB	6.28	121.90	110.60
3	6-D	344	PHE	CB-CG-CD2	6.28	125.20	120.80
3	7-C	279	TYR	CG-CD2-CE2	6.28	126.32	121.30
2	4-B	416	CYS	N-CA-CB	6.28	121.90	110.60
3	1-C	20	PHE	CB-CG-CD1	6.28	125.19	120.80
2	2-B	822	ARG	NE-CZ-NH1	6.28	123.44	120.30
3	2-C	364	PRO	N-CA-CB	6.28	110.83	103.30
2	4-B	491	ALA	CB-CA-C	-6.28	100.69	110.10
3	7-D	443	ASP	CB-CG-OD2	6.28	123.95	118.30
3	8-C	160	ASP	CB-CG-OD1	6.28	123.95	118.30
1	10-A	111	ARG	NE-CZ-NH2	-6.28	117.16	120.30
2	10-B	587	PHE	CG-CD2-CE2	-6.28	113.90	120.80
2	2-B	666	ARG	NE-CZ-NH2	-6.27	117.16	120.30
2	3-B	200	PHE	CB-CG-CD2	-6.27	116.41	120.80
3	2-C	275	PHE	CB-CG-CD2	-6.27	116.41	120.80
3	7-C	436	ASP	CB-CG-OD2	-6.27	112.66	118.30
3	9-C	429	VAL	CA-CB-CG2	6.27	120.31	110.90
2	5-B	485	LYS	N-CA-CB	6.27	121.88	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	91	GLU	C-N-CA	6.27	137.37	121.70
1	9-A	345	PHE	CB-CG-CD2	-6.27	116.41	120.80
2	2-B	280	LEU	CB-CG-CD1	6.26	121.65	111.00
3	2-C	249	TYR	CD1-CE1-CZ	-6.26	114.16	119.80
2	10-B	468	PHE	N-CA-C	-6.26	94.08	111.00
1	4-A	684	MET	CG-SD-CE	-6.26	90.18	100.20
3	1-C	54	PHE	CB-CG-CD1	6.26	125.18	120.80
3	10-C	54	PHE	CB-CG-CD2	-6.26	116.42	120.80
1	9-A	591	VAL	CA-CB-CG2	6.26	120.29	110.90
3	1-D	23	SER	N-CA-CB	6.26	119.89	110.50
2	4-B	598	TYR	CG-CD2-CE2	6.25	126.30	121.30
3	9-C	193	ARG	NE-CZ-NH2	6.25	123.42	120.30
2	1-B	343	TYR	CZ-CE2-CD2	6.25	125.42	119.80
3	3-D	341	ARG	NE-CZ-NH2	-6.25	117.18	120.30
1	4-A	299	PHE	N-CA-C	-6.25	94.13	111.00
1	9-A	71	GLU	CA-CB-CG	6.25	127.14	113.40
1	1-A	363	ILE	N-CA-C	-6.24	94.14	111.00
3	2-D	124	ASP	CB-CG-OD1	6.24	123.92	118.30
1	9-A	383	ASP	CB-CG-OD1	-6.24	112.68	118.30
3	9-C	117	ASP	CB-CG-OD2	6.24	123.92	118.30
3	10-D	133	PHE	CB-CG-CD1	-6.24	116.43	120.80
2	2-B	776	TYR	CB-CG-CD1	6.24	124.75	121.00
1	6-A	299	PHE	CB-CG-CD2	6.24	125.17	120.80
3	2-C	407	TYR	CB-CG-CD1	-6.24	117.25	121.00
3	10-C	1	MET	CG-SD-CE	-6.24	90.22	100.20
2	1-B	578	PHE	CB-CG-CD1	6.24	125.17	120.80
3	1-C	90	ARG	NE-CZ-NH2	-6.24	117.18	120.30
3	4-D	223	ASP	CB-CG-OD2	-6.24	112.69	118.30
2	5-B	280	LEU	CB-CG-CD1	6.24	121.60	111.00
2	2-B	236	TYR	CB-CG-CD2	6.24	124.74	121.00
2	3-B	812	ILE	O-C-N	-6.24	112.72	122.70
3	3-C	93	TRP	CZ3-CH2-CZ2	-6.24	114.12	121.60
3	6-D	54	PHE	CB-CG-CD2	6.23	125.16	120.80
1	10-A	639	PHE	CB-CG-CD1	6.23	125.16	120.80
3	9-D	43	SER	N-CA-CB	6.23	119.85	110.50
2	10-B	476	ALA	N-CA-CB	6.23	118.83	110.10
1	3-A	764	LEU	CB-CG-CD2	6.23	121.59	111.00
1	6-A	676	LEU	CB-CG-CD2	6.23	121.59	111.00
2	5-B	574	VAL	C-N-CA	6.23	137.27	121.70
1	3-A	627	ARG	NE-CZ-NH2	-6.23	117.19	120.30
2	4-B	295	ARG	NE-CZ-NH2	6.23	123.41	120.30
3	7-C	207	ALA	CB-CA-C	-6.23	100.76	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3-B	653	LEU	CB-CG-CD2	-6.23	100.42	111.00
1	4-A	410	PHE	CB-CG-CD1	6.23	125.16	120.80
3	8-D	46	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	10-A	107	ARG	NE-CZ-NH2	6.23	123.41	120.30
2	2-B	438	TYR	CB-CG-CD1	6.22	124.73	121.00
3	6-D	272	PHE	CB-CG-CD1	6.22	125.16	120.80
2	7-B	365	ALA	N-CA-CB	6.22	118.81	110.10
3	8-D	21	LEU	CB-CG-CD1	6.22	121.58	111.00
3	10-C	192	ARG	NH1-CZ-NH2	6.22	126.25	119.40
3	7-D	220	PRO	O-C-N	6.22	132.66	122.70
2	9-B	194	ALA	N-CA-CB	6.22	118.81	110.10
1	3-A	198	ARG	NE-CZ-NH2	-6.22	117.19	120.30
3	4-D	65	ARG	CG-CD-NE	-6.22	98.74	111.80
3	1-D	170	TYR	CG-CD1-CE1	6.21	126.27	121.30
2	10-B	587	PHE	CZ-CE2-CD2	6.21	127.56	120.10
1	5-A	117	MET	CA-CB-CG	-6.21	102.74	113.30
3	4-C	248	MET	CA-CB-CG	6.21	123.86	113.30
2	7-B	827	ARG	NE-CZ-NH1	6.21	123.40	120.30
1	8-A	99	ASP	CB-CG-OD2	-6.21	112.71	118.30
2	9-B	571	VAL	N-CA-C	-6.20	94.25	111.00
3	3-D	114	ARG	NE-CZ-NH2	6.20	123.40	120.30
3	10-C	192	ARG	NE-CZ-NH2	-6.20	117.20	120.30
3	7-C	93	TRP	CG-CD2-CE3	-6.20	128.32	133.90
1	8-A	418	VAL	CA-CB-CG2	-6.20	101.60	110.90
3	3-C	300	ASP	CB-CG-OD2	6.20	123.88	118.30
3	6-D	100	SER	N-CA-CB	6.20	119.80	110.50
2	4-B	471	ARG	NH1-CZ-NH2	-6.20	112.58	119.40
3	6-C	143	ALA	N-CA-CB	6.20	118.78	110.10
2	1-B	415	TYR	CB-CG-CD1	6.20	124.72	121.00
2	9-B	599	PHE	CB-CG-CD1	6.20	125.14	120.80
1	1-A	403	GLU	CB-CA-C	-6.19	98.01	110.40
1	1-A	587	ARG	NE-CZ-NH2	-6.19	117.20	120.30
1	1-A	302	TYR	CG-CD2-CE2	-6.19	116.35	121.30
3	2-D	256	TYR	CG-CD1-CE1	-6.19	116.35	121.30
2	4-B	438	TYR	CG-CD1-CE1	-6.19	116.35	121.30
1	6-A	426	PHE	CB-CG-CD1	6.19	125.13	120.80
3	7-C	59	ARG	NE-CZ-NH1	-6.19	117.20	120.30
1	8-A	123	TYR	CB-CG-CD1	-6.19	117.29	121.00
2	8-B	379	TYR	CG-CD2-CE2	6.19	126.25	121.30
3	3-D	445	TYR	CG-CD1-CE1	6.19	126.25	121.30
1	6-A	179	GLU	N-CA-CB	6.18	121.73	110.60
3	6-C	118	ASP	CB-CG-OD2	6.18	123.87	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-A	767	TYR	CB-CG-CD1	6.18	124.71	121.00
2	3-B	543	ALA	N-CA-CB	6.18	118.75	110.10
1	8-A	386	GLU	N-CA-C	-6.18	94.31	111.00
2	4-B	530	ASN	N-CA-CB	6.18	121.72	110.60
2	10-B	598	TYR	CB-CG-CD2	6.18	124.71	121.00
3	10-C	319	TYR	CG-CD1-CE1	-6.18	116.36	121.30
2	3-B	772	PHE	CB-CG-CD2	-6.17	116.48	120.80
3	5-D	359	ARG	NE-CZ-NH2	6.17	123.39	120.30
1	7-A	78	PHE	CB-CG-CD1	6.17	125.12	120.80
3	10-D	161	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	5-A	429	TYR	CZ-CE2-CD2	6.17	125.35	119.80
1	7-A	627	ARG	N-CA-CB	6.17	121.71	110.60
1	9-A	714	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	3-A	700	PHE	CB-CG-CD1	6.17	125.12	120.80
2	8-B	267	PHE	CB-CG-CD1	6.17	125.12	120.80
3	3-C	20	PHE	CB-CG-CD2	-6.17	116.48	120.80
2	8-B	272	VAL	CG1-CB-CG2	6.17	120.77	110.90
1	9-A	321	ASP	CB-CG-OD1	6.17	123.85	118.30
3	9-C	95	ALA	N-CA-CB	6.17	118.73	110.10
3	10-D	1	MET	CG-SD-CE	-6.17	90.33	100.20
3	3-C	315	TYR	CB-CG-CD2	-6.17	117.30	121.00
1	7-A	73	THR	CA-CB-CG2	-6.17	103.77	112.40
1	7-A	150	TYR	CZ-CE2-CD2	-6.17	114.25	119.80
3	3-C	59	ARG	NE-CZ-NH1	6.16	123.38	120.30
3	3-D	49	ASP	CB-CG-OD1	-6.16	112.75	118.30
2	1-B	256	GLU	OE1-CD-OE2	-6.16	115.91	123.30
2	1-B	824	TYR	CB-CG-CD2	-6.16	117.30	121.00
1	3-A	158	LEU	CB-CG-CD1	6.16	121.47	111.00
3	7-C	55	ARG	NE-CZ-NH1	-6.16	117.22	120.30
3	8-D	362	TYR	CZ-CE2-CD2	-6.16	114.26	119.80
3	9-D	138	LEU	CB-CG-CD1	6.16	121.47	111.00
2	10-B	670	ARG	NE-CZ-NH1	6.16	123.38	120.30
3	3-D	427	ARG	NH1-CZ-NH2	-6.16	112.62	119.40
2	5-B	547	ASP	CB-CG-OD1	-6.16	112.76	118.30
3	6-D	21	LEU	CB-CG-CD2	6.16	121.47	111.00
3	6-D	68	MET	CG-SD-CE	-6.16	90.35	100.20
2	2-B	487	ASP	CB-CG-OD2	-6.15	112.76	118.30
2	4-B	241	PHE	CB-CG-CD2	6.15	125.11	120.80
3	5-D	92	THR	CA-CB-CG2	-6.15	103.79	112.40
2	3-B	488	PHE	CB-CG-CD1	6.15	125.11	120.80
2	7-B	526	ARG	NE-CZ-NH1	6.15	123.38	120.30
1	2-A	337	SER	N-CA-CB	6.15	119.72	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2-B	349	TRP	CB-CG-CD2	6.15	134.59	126.60
3	8-C	423	PHE	N-CA-CB	6.15	121.67	110.60
3	10-C	72	GLU	CA-C-N	6.15	134.32	117.10
1	2-A	398	TYR	CD1-CE1-CZ	6.14	125.33	119.80
3	2-C	192	ARG	NE-CZ-NH1	-6.14	117.23	120.30
3	5-D	328	PRO	N-CD-CG	6.14	112.42	103.20
3	3-D	162	TYR	CD1-CE1-CZ	6.14	125.33	119.80
2	4-B	342	TYR	CD1-CE1-CZ	-6.14	114.27	119.80
1	7-A	588	TYR	CG-CD1-CE1	6.14	126.21	121.30
3	9-C	256	TYR	CG-CD2-CE2	-6.14	116.39	121.30
3	10-C	86	PHE	CB-CG-CD2	-6.14	116.50	120.80
3	3-D	128	ASP	CB-CG-OD1	6.14	123.83	118.30
1	4-A	471	SER	N-CA-CB	6.14	119.71	110.50
1	2-A	165	VAL	N-CA-C	-6.14	94.43	111.00
3	9-D	46	ARG	NE-CZ-NH1	-6.14	117.23	120.30
3	10-C	347	TRP	CG-CD2-CE3	-6.14	128.37	133.90
2	9-B	742	ALA	N-CA-CB	6.14	118.69	110.10
3	9-C	437	TYR	CG-CD1-CE1	6.14	126.21	121.30
3	3-C	68	MET	CG-SD-CE	-6.13	90.39	100.20
3	9-D	20	PHE	CB-CG-CD2	6.13	125.09	120.80
1	3-A	588	TYR	CB-CG-CD1	-6.13	117.32	121.00
3	4-D	403	PHE	CB-CG-CD1	6.13	125.09	120.80
2	6-B	576	ARG	NE-CZ-NH2	-6.13	117.24	120.30
2	7-B	400	TYR	CB-CG-CD1	-6.13	117.32	121.00
3	10-C	70	ASP	CB-CG-OD2	-6.13	112.79	118.30
1	2-A	687	ARG	NE-CZ-NH2	-6.12	117.24	120.30
3	5-D	256	TYR	CB-CG-CD1	6.12	124.67	121.00
2	6-B	231	TYR	CZ-CE2-CD2	-6.12	114.29	119.80
3	4-C	307	SER	N-CA-CB	6.12	119.69	110.50
1	5-A	381	PHE	CB-CG-CD2	-6.12	116.51	120.80
2	6-B	222	HIS	CB-CA-C	-6.12	98.15	110.40
3	8-D	321	THR	CA-CB-CG2	-6.12	103.83	112.40
1	7-A	302	TYR	CG-CD2-CE2	6.12	126.20	121.30
2	8-B	822	ARG	CA-CB-CG	6.12	126.87	113.40
2	10-B	827	ARG	NE-CZ-NH2	6.12	123.36	120.30
1	7-A	714	ARG	CD-NE-CZ	-6.12	115.03	123.60
2	1-B	823	LEU	CB-CG-CD1	6.12	121.40	111.00
3	1-D	334	ALA	CB-CA-C	-6.12	100.92	110.10
3	5-D	41	ASP	CB-CG-OD1	6.12	123.81	118.30
1	3-A	667	THR	N-CA-C	-6.12	94.49	111.00
3	3-C	128	ASP	N-CA-CB	6.12	121.61	110.60
3	3-D	87	PHE	CG-CD1-CE1	6.12	127.53	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4-A	422	LEU	CB-CG-CD1	6.12	121.40	111.00
3	8-C	20	PHE	CB-CG-CD1	6.12	125.08	120.80
3	8-C	87	PHE	CB-CG-CD1	6.12	125.08	120.80
1	10-A	337	SER	N-CA-CB	6.12	119.67	110.50
2	10-B	471	ARG	NE-CZ-NH2	-6.12	117.24	120.30
3	10-D	296	LEU	CB-CG-CD2	6.11	121.39	111.00
2	9-B	300	PHE	CB-CG-CD2	-6.11	116.52	120.80
3	5-D	274	PRO	N-CD-CG	6.11	112.36	103.20
3	7-C	199	ASP	CB-CG-OD2	6.11	123.80	118.30
2	3-B	505	ASP	CB-CG-OD1	-6.10	112.81	118.30
1	10-A	627	ARG	CA-CB-CG	6.10	126.83	113.40
2	2-B	223	LEU	CB-CG-CD2	6.10	121.37	111.00
3	5-C	193	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	8-A	179	GLU	N-CA-CB	6.10	121.58	110.60
1	4-A	372	ASP	N-CA-CB	6.10	121.57	110.60
3	2-D	352	MET	N-CA-CB	6.10	121.57	110.60
1	1-A	165	VAL	N-CA-C	-6.09	94.55	111.00
3	4-C	161	ARG	NE-CZ-NH1	6.09	123.35	120.30
1	6-A	77	TYR	CB-CG-CD1	6.09	124.66	121.00
1	3-A	278	ASP	CB-CG-OD2	6.09	123.78	118.30
1	5-A	349	ARG	NE-CZ-NH2	-6.09	117.25	120.30
2	9-B	295	ARG	NE-CZ-NH1	6.09	123.35	120.30
2	9-B	514	ARG	NE-CZ-NH1	-6.09	117.25	120.30
1	7-A	369	ASN	N-CA-C	-6.09	94.56	111.00
1	2-A	756	ALA	CB-CA-C	-6.09	100.97	110.10
3	2-D	195	ILE	CA-CB-CG1	6.09	122.56	111.00
2	4-B	725	GLU	OE1-CD-OE2	6.09	130.60	123.30
3	5-C	218	ARG	NE-CZ-NH2	-6.09	117.26	120.30
3	7-D	192	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	3-A	429	TYR	CB-CG-CD2	-6.08	117.35	121.00
3	7-D	97	ASP	CB-CG-OD2	6.08	123.78	118.30
1	1-A	326	ILE	CA-CB-CG1	6.08	122.56	111.00
2	6-B	190	TYR	CB-CG-CD1	6.08	124.65	121.00
2	3-B	345	TYR	CB-CG-CD1	6.08	124.65	121.00
2	3-B	652	TYR	CB-CG-CD1	-6.08	117.35	121.00
3	3-C	336	THR	CA-CB-CG2	-6.08	103.89	112.40
1	4-A	169	SER	C-N-CA	6.08	136.90	121.70
1	10-A	770	ASN	N-CA-CB	6.08	121.54	110.60
2	1-B	350	LEU	CB-CA-C	-6.08	98.65	110.20
3	1-C	246	SER	N-CA-CB	6.08	119.61	110.50
3	6-C	59	ARG	NE-CZ-NH1	6.08	123.34	120.30
3	8-C	387	PHE	CB-CG-CD1	6.08	125.05	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	6-B	415	TYR	CB-CG-CD2	-6.07	117.36	121.00
3	9-D	171	SER	N-CA-CB	6.07	119.61	110.50
1	6-A	197	PHE	CB-CG-CD1	6.07	125.05	120.80
3	2-D	319	TYR	CA-CB-CG	-6.07	101.86	113.40
1	3-A	587	ARG	NH1-CZ-NH2	-6.07	112.72	119.40
2	4-B	846	ARG	NE-CZ-NH1	6.07	123.33	120.30
3	4-D	22	TRP	CH2-CZ2-CE2	-6.07	111.33	117.40
2	10-B	604	MET	CG-SD-CE	-6.07	90.49	100.20
2	6-B	515	VAL	CA-CB-CG2	-6.07	101.80	110.90
1	9-A	388	SER	CB-CA-C	-6.07	98.57	110.10
2	2-B	295	ARG	NE-CZ-NH1	-6.07	117.27	120.30
2	4-B	505	ASP	CB-CG-OD2	-6.07	112.84	118.30
1	5-A	150	TYR	CG-CD2-CE2	-6.07	116.45	121.30
3	5-C	90	ARG	NH1-CZ-NH2	-6.07	112.73	119.40
3	7-D	407	TYR	CG-CD1-CE1	-6.07	116.45	121.30
1	1-A	160	ARG	N-CA-CB	6.06	121.52	110.60
1	7-A	458	TYR	CG-CD1-CE1	-6.06	116.45	121.30
3	3-C	262	SER	N-CA-CB	6.06	119.59	110.50
1	4-A	675	GLU	O-C-N	-6.06	113.00	122.70
2	6-B	730	THR	CA-CB-CG2	-6.06	103.91	112.40
1	9-A	794	TYR	CB-CG-CD1	6.06	124.64	121.00
1	1-A	685	THR	CA-CB-CG2	-6.06	103.91	112.40
2	9-B	553	VAL	CA-CB-CG2	6.06	119.99	110.90
3	6-D	326	VAL	CA-CB-CG2	-6.06	101.81	110.90
3	9-C	335	MET	CG-SD-CE	-6.06	90.50	100.20
1	1-A	714	ARG	NE-CZ-NH2	-6.06	117.27	120.30
3	6-D	307	SER	C-N-CA	6.06	136.84	121.70
3	9-C	304	SER	N-CA-CB	6.06	119.58	110.50
1	1-A	383	ASP	N-CA-C	-6.05	94.65	111.00
2	3-B	328	ARG	NE-CZ-NH1	6.05	123.33	120.30
3	3-D	17	VAL	CA-CB-CG1	6.05	119.98	110.90
3	3-C	62	PHE	CB-CG-CD1	-6.05	116.56	120.80
3	7-C	296	LEU	CB-CA-C	-6.05	98.70	110.20
2	10-B	416	CYS	CA-CB-SG	6.05	124.89	114.00
3	5-D	272	PHE	CB-CG-CD1	6.05	125.03	120.80
1	9-A	588	TYR	CG-CD2-CE2	-6.05	116.46	121.30
3	3-C	395	ASP	CB-CG-OD2	6.04	123.74	118.30
3	1-C	224	LEU	CB-CG-CD2	6.04	121.27	111.00
3	5-C	176	ARG	NE-CZ-NH1	-6.04	117.28	120.30
2	6-B	225	PHE	CB-CG-CD1	6.04	125.03	120.80
2	8-B	411	PHE	CB-CG-CD2	6.04	125.03	120.80
2	8-B	555	TRP	CD2-CE3-CZ3	-6.04	110.94	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	9-C	173	PHE	CB-CG-CD1	-6.04	116.57	120.80
1	5-A	108	ARG	NE-CZ-NH1	-6.04	117.28	120.30
3	6-D	329	ARG	NH1-CZ-NH2	-6.04	112.76	119.40
2	7-B	652	TYR	CB-CG-CD2	-6.04	117.38	121.00
2	8-B	473	VAL	CG1-CB-CG2	-6.04	101.24	110.90
1	10-A	68	ILE	CA-CB-CG1	6.04	122.47	111.00
3	1-C	289	HIS	CA-CB-CG	6.04	123.86	113.60
3	10-C	90	ARG	NE-CZ-NH2	-6.04	117.28	120.30
2	9-B	249	MET	CG-SD-CE	-6.03	90.55	100.20
2	9-B	600	TYR	CB-CG-CD1	6.03	124.62	121.00
2	2-B	666	ARG	NE-CZ-NH1	6.03	123.32	120.30
1	4-A	159	GLU	CB-CG-CD	-6.03	97.91	114.20
2	4-B	758	TYR	CB-CG-CD2	-6.03	117.38	121.00
3	4-C	20	PHE	CB-CG-CD2	-6.03	116.58	120.80
3	7-C	249	TYR	CB-CG-CD2	6.03	124.62	121.00
1	9-A	287	LEU	CB-CG-CD2	6.03	121.25	111.00
1	5-A	704	TYR	CB-CG-CD1	-6.03	117.39	121.00
3	5-C	162	TYR	CB-CG-CD2	6.03	124.61	121.00
3	5-C	244	PHE	CB-CG-CD1	6.03	125.02	120.80
2	6-B	641	PHE	CB-CG-CD1	6.03	125.02	120.80
3	7-C	241	SER	CB-CA-C	-6.03	98.65	110.10
1	8-A	198	ARG	NE-CZ-NH1	-6.03	117.29	120.30
3	9-C	223	ASP	CB-CG-OD2	6.03	123.72	118.30
1	1-A	327	ARG	NE-CZ-NH1	6.02	123.31	120.30
2	1-B	350	LEU	CB-CG-CD2	6.02	121.24	111.00
3	1-C	204	PHE	CB-CG-CD2	-6.02	116.58	120.80
2	4-B	332	THR	CA-CB-CG2	-6.02	103.97	112.40
3	9-C	398	PHE	CB-CG-CD2	-6.02	116.58	120.80
3	10-D	88	ASP	CB-CG-OD2	-6.02	112.88	118.30
3	1-D	128	ASP	CB-CG-OD2	6.02	123.72	118.30
3	6-D	411	ASP	CB-CG-OD1	-6.02	112.88	118.30
2	1-B	527	HIS	CB-CA-C	-6.02	98.36	110.40
1	3-A	605	ASP	CB-CG-OD2	-6.02	112.88	118.30
3	3-C	12	GLN	C-N-CA	6.01	136.74	121.70
1	4-A	324	TYR	N-CA-CB	6.01	121.43	110.60
3	4-D	354	VAL	N-CA-C	-6.01	94.76	111.00
2	10-B	724	LEU	CB-CG-CD2	6.01	121.22	111.00
3	1-C	170	TYR	CA-CB-CG	-6.01	101.98	113.40
1	6-A	405	PHE	CB-CG-CD1	-6.01	116.59	120.80
3	7-D	117	ASP	CB-CG-OD2	-6.01	112.89	118.30
3	10-C	394	PHE	CB-CG-CD2	-6.01	116.59	120.80
3	10-D	136	PHE	CG-CD2-CE2	-6.01	114.19	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-C	272	PHE	CB-CG-CD1	-6.01	116.59	120.80
3	2-C	394	PHE	CG-CD2-CE2	-6.01	114.19	120.80
1	8-A	267	PHE	CB-CG-CD2	-6.01	116.59	120.80
1	8-A	393	TYR	CZ-CE2-CD2	-6.01	114.39	119.80
2	8-B	526	ARG	NE-CZ-NH2	-6.01	117.30	120.30
2	1-B	264	TYR	CB-CG-CD1	-6.01	117.40	121.00
3	2-C	243	ARG	NE-CZ-NH2	-6.01	117.30	120.30
1	9-A	150	TYR	CG-CD2-CE2	6.01	126.11	121.30
3	3-D	120	LEU	O-C-N	-6.00	113.09	122.70
2	6-B	598	TYR	CB-CG-CD2	6.00	124.60	121.00
3	10-D	351	ALA	N-CA-CB	6.00	118.50	110.10
1	1-A	691	ASP	CB-CG-OD2	-6.00	112.90	118.30
1	2-A	623	ARG	NE-CZ-NH1	6.00	123.30	120.30
2	7-B	729	ASN	N-CA-CB	6.00	121.40	110.60
3	4-C	105	TRP	CB-CG-CD1	6.00	134.80	127.00
1	8-A	301	THR	N-CA-C	-6.00	94.80	111.00
2	2-B	446	PHE	CB-CG-CD2	-6.00	116.60	120.80
2	4-B	445	PHE	CB-CG-CD2	-6.00	116.60	120.80
1	8-A	479	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	1-A	558	TYR	CD1-CE1-CZ	-6.00	114.40	119.80
3	1-D	437	TYR	CB-CG-CD2	-6.00	117.40	121.00
3	2-D	48	ASP	CB-CG-OD1	-6.00	112.90	118.30
2	4-B	425	PHE	CZ-CE2-CD2	-6.00	112.91	120.10
3	2-D	105	TRP	CB-CG-CD2	-6.00	118.81	126.60
3	4-D	236	SER	N-CA-CB	6.00	119.49	110.50
3	5-D	315	TYR	CB-CA-C	-5.99	98.41	110.40
3	6-C	398	PHE	N-CA-CB	5.99	121.39	110.60
3	9-C	347	TRP	C-N-CA	5.99	136.68	121.70
3	5-D	71	SER	N-CA-CB	5.99	119.49	110.50
3	10-C	244	PHE	CG-CD2-CE2	5.99	127.39	120.80
1	5-A	447	THR	CA-CB-CG2	-5.99	104.01	112.40
2	9-B	824	TYR	CB-CG-CD2	5.99	124.59	121.00
1	5-A	398	TYR	CG-CD1-CE1	-5.99	116.51	121.30
1	6-A	188	LEU	CB-CG-CD2	5.99	121.18	111.00
1	6-A	461	LEU	CB-CG-CD1	5.99	121.18	111.00
2	7-B	231	TYR	CB-CG-CD2	5.99	124.59	121.00
2	7-B	544	ARG	NE-CZ-NH1	-5.99	117.31	120.30
3	8-D	444	SER	N-CA-CB	5.99	119.48	110.50
3	4-C	271	SER	N-CA-CB	5.99	119.48	110.50
2	5-B	433	TYR	CB-CG-CD2	-5.99	117.41	121.00
2	8-B	343	TYR	CG-CD2-CE2	-5.99	116.51	121.30
3	8-C	193	ARG	NE-CZ-NH1	5.99	123.29	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	9-C	83	PHE	CB-CG-CD1	-5.99	116.61	120.80
3	10-D	440	ALA	N-CA-CB	5.99	118.48	110.10
2	1-B	545	VAL	N-CA-C	-5.98	94.84	111.00
1	6-A	288	THR	CA-CB-CG2	-5.98	104.02	112.40
2	10-B	288	TYR	CB-CG-CD1	-5.98	117.41	121.00
2	8-B	824	TYR	CB-CG-CD2	-5.98	117.41	121.00
3	10-C	422	GLU	N-CA-CB	5.98	121.37	110.60
3	4-C	407	TYR	CA-CB-CG	-5.98	102.04	113.40
3	1-C	93	TRP	CH2-CZ2-CE2	5.98	123.38	117.40
3	9-D	340	GLN	CA-CB-CG	5.98	126.55	113.40
1	2-A	324	TYR	CB-CG-CD1	-5.98	117.41	121.00
2	4-B	510	TYR	CZ-CE2-CD2	-5.98	114.42	119.80
3	1-C	276	THR	CA-CB-CG2	-5.98	104.03	112.40
2	4-B	510	TYR	CG-CD1-CE1	-5.97	116.52	121.30
1	6-A	112	TYR	CB-CG-CD1	-5.97	117.42	121.00
3	4-C	370	ASN	N-CA-CB	5.97	121.35	110.60
3	7-D	403	PHE	CB-CG-CD2	5.97	124.98	120.80
3	10-C	256	TYR	CG-CD1-CE1	5.97	126.08	121.30
1	1-A	203	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	3-A	450	TYR	CD1-CE1-CZ	5.97	125.17	119.80
1	3-A	475	ASN	N-CA-CB	5.97	121.35	110.60
2	1-B	555	TRP	CB-CG-CD2	-5.97	118.84	126.60
1	8-A	333	ARG	NE-CZ-NH1	-5.97	117.31	120.30
1	9-A	102	PHE	CB-CG-CD1	5.97	124.98	120.80
3	10-D	73	PRO	N-CA-CB	5.97	110.46	103.30
3	4-C	316	PHE	CB-CG-CD2	5.97	124.98	120.80
1	4-A	473	ASN	N-CA-CB	5.96	121.34	110.60
1	9-A	74	TYR	CB-CG-CD2	-5.96	117.42	121.00
3	5-D	84	ARG	NE-CZ-NH2	-5.96	117.32	120.30
3	7-D	443	ASP	CB-CG-OD1	-5.96	112.93	118.30
3	1-D	341	ARG	NE-CZ-NH1	-5.96	117.32	120.30
2	5-B	365	ALA	N-CA-CB	5.96	118.44	110.10
2	8-B	424	GLU	N-CA-CB	5.96	121.33	110.60
1	10-A	150	TYR	CZ-CE2-CD2	5.96	125.17	119.80
3	1-C	409	VAL	CA-CB-CG2	5.96	119.84	110.90
1	5-A	794	TYR	CB-CG-CD2	-5.96	117.42	121.00
2	8-B	460	THR	N-CA-CB	5.96	121.62	110.30
2	7-B	347	MET	CA-CB-CG	5.96	123.42	113.30
3	7-D	237	SER	O-C-N	-5.96	113.17	122.70
1	4-A	137	ARG	NE-CZ-NH1	5.95	123.28	120.30
2	4-B	591	TRP	CE2-CD2-CG	5.95	112.06	107.30
1	9-A	160	ARG	NE-CZ-NH2	5.95	123.28	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	10-D	362	TYR	CD1-CE1-CZ	5.95	125.16	119.80
1	3-A	148	ASP	CB-CG-OD1	-5.95	112.94	118.30
2	9-B	471	ARG	NE-CZ-NH2	-5.95	117.32	120.30
3	1-C	34	ASP	CB-CG-OD1	5.95	123.66	118.30
1	4-A	612	TRP	CE2-CD2-CE3	5.95	125.84	118.70
1	5-A	296	TYR	CB-CG-CD1	-5.95	117.43	121.00
2	6-B	471	ARG	NE-CZ-NH2	5.95	123.28	120.30
2	3-B	300	PHE	CB-CG-CD1	5.95	124.96	120.80
2	7-B	210	PRO	N-CA-C	-5.95	96.63	112.10
2	8-B	468	PHE	CB-CG-CD1	5.95	124.97	120.80
2	8-B	578	PHE	CB-CG-CD2	-5.95	116.64	120.80
1	4-A	627	ARG	NE-CZ-NH1	5.95	123.27	120.30
1	3-A	558	TYR	CB-CG-CD2	-5.95	117.43	121.00
3	4-D	272	PHE	CB-CG-CD2	5.95	124.96	120.80
1	7-A	296	TYR	CB-CG-CD2	-5.95	117.43	121.00
3	7-C	319	TYR	CB-CG-CD1	-5.95	117.43	121.00
3	10-D	85	GLY	O-C-N	-5.95	113.19	122.70
2	7-B	310	ASP	CB-CG-OD1	-5.94	112.95	118.30
3	8-D	362	TYR	CA-CB-CG	5.94	124.69	113.40
3	7-C	204	PHE	CB-CG-CD2	-5.94	116.64	120.80
2	9-B	846	ARG	NE-CZ-NH1	5.94	123.27	120.30
2	4-B	345	TYR	CB-CG-CD1	5.94	124.56	121.00
1	6-A	582	TYR	CB-CG-CD1	-5.94	117.44	121.00
1	8-A	165	VAL	N-CA-C	-5.94	94.97	111.00
1	1-A	92	PHE	CB-CG-CD1	-5.94	116.64	120.80
2	2-B	533	ARG	CD-NE-CZ	5.94	131.91	123.60
1	7-A	183	ASN	CB-CG-OD1	-5.94	109.73	121.60
1	5-A	714	ARG	NE-CZ-NH1	5.93	123.27	120.30
2	5-B	264	TYR	CD1-CG-CD2	5.93	124.43	117.90
2	5-B	439	ARG	NE-CZ-NH1	5.93	123.27	120.30
2	6-B	531	SER	CA-C-N	5.93	133.72	117.10
1	10-A	301	THR	CA-CB-CG2	-5.93	104.09	112.40
1	1-A	74	TYR	CA-CB-CG	5.93	124.67	113.40
2	6-B	433	TYR	CB-CG-CD2	5.93	124.56	121.00
1	9-A	150	TYR	CG-CD1-CE1	5.93	126.05	121.30
3	2-D	162	TYR	CB-CG-CD2	-5.93	117.44	121.00
3	3-D	279	TYR	CG-CD1-CE1	-5.93	116.56	121.30
1	1-A	793	PHE	CB-CG-CD1	5.93	124.95	120.80
1	7-A	612	TRP	CE2-CD2-CG	-5.93	102.56	107.30
2	10-B	576	ARG	NE-CZ-NH2	-5.93	117.33	120.30
3	1-C	118	ASP	CB-CA-C	-5.93	98.54	110.40
2	3-B	187	TYR	CB-CG-CD2	-5.93	117.44	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	5-D	55	ARG	NH1-CZ-NH2	-5.93	112.88	119.40
2	8-B	349	TRP	CG-CD2-CE3	-5.93	128.57	133.90
3	1-D	443	ASP	CB-CG-OD1	-5.92	112.97	118.30
1	7-A	700	PHE	CG-CD1-CE1	-5.92	114.28	120.80
2	7-B	272	VAL	CA-CB-CG1	5.92	119.79	110.90
3	7-C	117	ASP	CB-CG-OD1	-5.92	112.97	118.30
1	8-A	134	VAL	CG1-CB-CG2	-5.92	101.42	110.90
3	9-D	367	PRO	N-CD-CG	5.92	112.08	103.20
3	1-C	272	PHE	CB-CG-CD2	5.92	124.94	120.80
1	3-A	576	ARG	NE-CZ-NH1	-5.92	117.34	120.30
3	5-C	122	LYS	CB-CA-C	-5.92	98.56	110.40
2	10-B	266	ALA	N-CA-CB	5.92	118.39	110.10
1	7-A	150	TYR	CB-CG-CD2	-5.92	117.45	121.00
1	1-A	333	ARG	NE-CZ-NH1	5.92	123.26	120.30
2	1-B	299	ARG	NH1-CZ-NH2	-5.92	112.89	119.40
2	4-B	438	TYR	CB-CG-CD1	5.92	124.55	121.00
3	7-C	162	TYR	CG-CD2-CE2	-5.92	116.56	121.30
1	1-A	597	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	6-A	458	TYR	CB-CG-CD2	5.92	124.55	121.00
1	8-A	304	ASP	CB-CG-OD1	5.92	123.62	118.30
3	1-D	353	HIS	O-C-N	5.91	132.16	122.70
1	5-A	665	ASN	CB-CA-C	5.91	122.23	110.40
1	10-A	279	TYR	CZ-CE2-CD2	-5.91	114.48	119.80
2	2-B	446	PHE	CB-CG-CD1	5.91	124.94	120.80
1	8-A	280	CYS	CA-CB-SG	5.91	124.64	114.00
1	9-A	582	TYR	CZ-CE2-CD2	-5.91	114.48	119.80
2	9-B	587	PHE	CB-CG-CD2	-5.91	116.66	120.80
3	1-C	93	TRP	CZ3-CH2-CZ2	-5.91	114.51	121.60
3	1-C	269	SER	N-CA-CB	-5.91	101.64	110.50
2	2-B	588	ASN	N-CA-CB	5.91	121.23	110.60
3	4-C	349	SER	CB-CA-C	-5.91	98.87	110.10
3	10-C	427	ARG	NE-CZ-NH1	-5.91	117.35	120.30
2	1-B	429	TYR	CG-CD2-CE2	-5.91	116.57	121.30
2	5-B	242	ARG	NE-CZ-NH2	5.91	123.25	120.30
3	8-C	395	ASP	N-CA-CB	5.91	121.23	110.60
2	2-B	459	HIS	N-CA-CB	5.90	121.23	110.60
3	6-D	315	TYR	CD1-CE1-CZ	5.90	125.11	119.80
2	9-B	223	LEU	CA-CB-CG	5.90	128.88	115.30
3	1-C	362	TYR	CB-CA-C	-5.90	98.60	110.40
3	2-C	347	TRP	CB-CG-CD1	-5.90	119.33	127.00
3	6-D	183	GLN	N-CA-CB	5.90	121.22	110.60
1	7-A	612	TRP	CD1-CG-CD2	5.90	111.02	106.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6-A	706	PHE	CB-CG-CD1	5.90	124.93	120.80
1	8-A	160	ARG	NE-CZ-NH2	-5.90	117.35	120.30
2	8-B	325	LEU	CB-CA-C	-5.90	98.99	110.20
3	9-D	223	ASP	CB-CG-OD1	-5.90	112.99	118.30
2	10-B	253	LEU	CB-CG-CD2	5.90	121.03	111.00
2	1-B	565	TYR	CD1-CE1-CZ	5.90	125.11	119.80
3	9-D	54	PHE	CB-CG-CD2	-5.90	116.67	120.80
3	3-D	97	ASP	CB-CG-OD2	-5.89	113.00	118.30
2	4-B	819	PHE	CB-CG-CD2	-5.89	116.67	120.80
2	5-B	565	TYR	N-CA-C	-5.89	95.08	111.00
2	9-B	211	SER	C-N-CA	5.89	136.44	121.70
3	10-C	87	PHE	CB-CG-CD1	-5.89	116.67	120.80
3	10-D	247	TYR	CG-CD1-CE1	-5.89	116.58	121.30
3	4-C	329	ARG	NE-CZ-NH1	5.89	123.25	120.30
3	4-C	358	ARG	NE-CZ-NH1	5.89	123.25	120.30
2	6-B	819	PHE	CB-CG-CD1	-5.89	116.67	120.80
3	7-C	292	TYR	CG-CD2-CE2	-5.89	116.59	121.30
3	9-D	204	PHE	CB-CG-CD2	-5.89	116.68	120.80
1	10-A	469	ARG	NH1-CZ-NH2	-5.89	112.92	119.40
1	6-A	563	ASP	CB-CG-OD1	5.89	123.60	118.30
2	1-B	470	TYR	CB-CG-CD2	-5.89	117.47	121.00
2	2-B	773	VAL	CA-CB-CG1	5.89	119.73	110.90
2	5-B	242	ARG	NE-CZ-NH1	-5.89	117.36	120.30
3	6-D	176	ARG	NE-CZ-NH2	-5.89	117.36	120.30
2	2-B	730	THR	CA-CB-CG2	-5.88	104.16	112.40
3	4-C	84	ARG	NE-CZ-NH2	-5.88	117.36	120.30
3	4-C	249	TYR	CB-CG-CD1	5.88	124.53	121.00
2	5-B	846	ARG	NH1-CZ-NH2	-5.88	112.93	119.40
1	8-A	395	ASP	CB-CG-OD1	-5.88	113.00	118.30
1	8-A	769	SER	N-CA-CB	5.88	119.33	110.50
2	6-B	185	LEU	CB-CA-C	-5.88	99.03	110.20
3	8-C	55	ARG	NE-CZ-NH2	-5.88	117.36	120.30
2	7-B	445	PHE	CB-CG-CD1	-5.88	116.68	120.80
3	2-D	394	PHE	CB-CG-CD1	-5.88	116.69	120.80
3	1-D	265	LEU	CB-CG-CD2	5.88	120.99	111.00
2	2-B	641	PHE	CB-CA-C	-5.88	98.65	110.40
3	6-D	319	TYR	N-CA-C	-5.88	95.13	111.00
2	1-B	526	ARG	NE-CZ-NH1	-5.87	117.36	120.30
2	2-B	487	ASP	CB-CG-OD1	5.87	123.59	118.30
1	10-A	121	ARG	NH1-CZ-NH2	5.87	125.86	119.40
1	1-A	487	ASP	CB-CG-OD1	-5.87	113.02	118.30
1	2-A	98	MET	N-CA-CB	5.87	121.17	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5-A	776	ARG	NE-CZ-NH2	-5.87	117.36	120.30
1	7-A	108	ARG	NE-CZ-NH1	5.87	123.23	120.30
2	7-B	641	PHE	CB-CG-CD1	-5.87	116.69	120.80
2	8-B	297	TYR	CB-CG-CD1	-5.87	117.48	121.00
3	2-D	369	GLU	N-CA-C	-5.87	95.16	111.00
1	3-A	174	GLU	CB-CA-C	-5.87	98.66	110.40
2	7-B	431	VAL	CA-CB-CG2	-5.87	102.10	110.90
3	1-D	53	PHE	CB-CG-CD2	5.87	124.91	120.80
1	3-A	450	TYR	CG-CD1-CE1	-5.87	116.61	121.30
1	4-A	450	TYR	CG-CD1-CE1	-5.87	116.61	121.30
2	6-B	190	TYR	CG-CD2-CE2	-5.87	116.61	121.30
2	7-B	593	PHE	CB-CG-CD2	-5.87	116.69	120.80
3	8-C	136	PHE	CB-CA-C	-5.86	98.67	110.40
1	9-A	576	ARG	NH1-CZ-NH2	5.86	125.85	119.40
2	6-B	445	PHE	CG-CD2-CE2	5.86	127.25	120.80
2	9-B	218	SER	N-CA-CB	5.86	119.29	110.50
3	2-D	333	ARG	NE-CZ-NH2	-5.86	117.37	120.30
3	4-C	90	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	6-A	92	PHE	CB-CG-CD1	5.86	124.90	120.80
1	2-A	611	SER	N-CA-CB	5.86	119.29	110.50
3	3-D	157	ALA	CB-CA-C	-5.86	101.32	110.10
1	8-A	775	PHE	CB-CG-CD1	5.86	124.90	120.80
3	8-C	133	PHE	CB-CG-CD1	5.86	124.90	120.80
3	3-C	319	TYR	CB-CA-C	-5.85	98.69	110.40
3	6-D	136	PHE	CB-CG-CD2	5.85	124.90	120.80
2	1-B	501	ALA	N-CA-CB	5.85	118.29	110.10
1	2-A	562	PHE	CB-CG-CD2	-5.85	116.70	120.80
3	6-D	170	TYR	CG-CD1-CE1	-5.85	116.62	121.30
3	8-D	44	THR	CA-CB-CG2	-5.85	104.21	112.40
3	10-C	319	TYR	CA-CB-CG	5.85	124.52	113.40
2	9-B	416	CYS	N-CA-CB	5.85	121.13	110.60
1	4-A	267	PHE	CB-CG-CD1	5.85	124.89	120.80
3	5-C	165	LYS	N-CA-CB	5.85	121.12	110.60
1	7-A	193	TYR	CG-CD1-CE1	-5.85	116.62	121.30
3	7-D	296	LEU	CB-CA-C	-5.85	99.09	110.20
3	9-C	413	PHE	CB-CG-CD1	5.85	124.89	120.80
1	3-A	254	LYS	N-CA-CB	5.84	121.12	110.60
2	3-B	846	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	4-A	636	MET	CG-SD-CE	-5.84	90.85	100.20
1	4-A	693	ILE	CA-C-N	5.84	133.47	117.10
2	3-B	599	PHE	CB-CG-CD1	5.84	124.89	120.80
2	4-B	483	MET	CG-SD-CE	-5.84	90.85	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	7-A	451	ARG	NE-CZ-NH2	-5.84	117.38	120.30
3	10-C	40	PRO	N-CD-CG	5.84	111.96	103.20
3	4-D	204	PHE	CB-CG-CD1	5.84	124.89	120.80
2	5-B	467	LYS	O-C-N	-5.84	113.35	122.70
3	9-D	68	MET	CG-SD-CE	-5.84	90.85	100.20
3	10-D	54	PHE	CB-CG-CD2	-5.84	116.71	120.80
2	1-B	560	LEU	O-C-N	-5.84	113.36	122.70
3	3-C	269	SER	N-CA-C	-5.84	95.23	111.00
1	7-A	91	GLU	N-CA-C	-5.84	95.23	111.00
2	8-B	183	ASP	CB-CG-OD1	5.84	123.56	118.30
1	10-A	413	TYR	CB-CG-CD1	5.84	124.50	121.00
3	7-C	77	ALA	N-CA-CB	5.84	118.27	110.10
2	1-B	591	TRP	CB-CG-CD1	5.84	134.59	127.00
2	2-B	741	PHE	CB-CG-CD1	5.84	124.89	120.80
3	9-C	218	ARG	NE-CZ-NH2	-5.84	117.38	120.30
3	8-C	160	ASP	CB-CG-OD2	-5.83	113.05	118.30
1	1-A	687	ARG	NE-CZ-NH2	5.83	123.22	120.30
3	4-C	329	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	5-A	347	MET	CG-SD-CE	-5.83	90.87	100.20
2	5-B	772	PHE	CB-CA-C	-5.83	98.73	110.40
3	2-C	117	ASP	CB-CG-OD1	-5.83	113.05	118.30
2	4-B	826	PHE	CG-CD1-CE1	-5.83	114.39	120.80
2	5-B	310	ASP	CB-CG-OD1	-5.83	113.05	118.30
2	7-B	190	TYR	CD1-CG-CD2	5.83	124.31	117.90
2	9-B	359	TYR	CB-CG-CD2	-5.83	117.50	121.00
1	1-A	442	ASN	N-CA-CB	5.83	121.09	110.60
1	2-A	162	PHE	CB-CG-CD2	5.83	124.88	120.80
2	4-B	826	PHE	CD1-CE1-CZ	5.83	127.09	120.10
1	5-A	193	TYR	CB-CA-C	-5.83	98.74	110.40
2	8-B	203	ASP	CB-CG-OD1	5.83	123.55	118.30
1	10-A	482	LEU	CB-CG-CD1	5.83	120.91	111.00
3	3-D	49	ASP	CB-CG-OD2	5.83	123.54	118.30
1	5-A	479	ARG	NE-CZ-NH2	-5.83	117.39	120.30
2	2-B	394	ILE	N-CA-C	-5.82	95.28	111.00
3	3-D	93	TRP	CB-CG-CD1	5.82	134.57	127.00
1	4-A	405	PHE	CB-CG-CD1	5.82	124.88	120.80
3	4-C	403	PHE	CB-CG-CD2	-5.82	116.72	120.80
2	6-B	598	TYR	CG-CD2-CE2	5.82	125.96	121.30
3	8-D	23	SER	N-CA-CB	5.82	119.23	110.50
2	9-B	326	THR	CA-CB-CG2	-5.82	104.25	112.40
3	10-C	63	THR	N-CA-CB	5.82	121.36	110.30
1	3-A	255	ILE	CA-CB-CG1	5.82	122.06	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	4-B	577	PRO	N-CA-C	-5.82	96.97	112.10
3	5-D	75	VAL	CA-CB-CG2	-5.82	102.17	110.90
3	6-C	440	ALA	CB-CA-C	-5.82	101.37	110.10
1	2-A	398	TYR	CG-CD2-CE2	-5.82	116.64	121.30
1	5-A	286	TRP	CH2-CZ2-CE2	5.82	123.22	117.40
3	6-D	54	PHE	CB-CG-CD1	-5.82	116.73	120.80
2	8-B	652	TYR	CB-CG-CD1	5.82	124.49	121.00
3	9-C	88	ASP	N-CA-CB	5.82	121.07	110.60
1	6-A	630	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	6-A	634	ALA	N-CA-CB	5.82	118.24	110.10
3	4-D	279	TYR	CA-CB-CG	-5.81	102.35	113.40
2	5-B	293	ARG	NE-CZ-NH1	5.81	123.21	120.30
3	4-C	132	ASN	N-CA-CB	5.81	121.06	110.60
3	8-C	88	ASP	CB-CG-OD1	-5.81	113.07	118.30
2	10-B	541	LEU	CB-CG-CD2	5.81	120.88	111.00
3	10-C	307	SER	N-CA-CB	5.81	119.22	110.50
1	2-A	91	GLU	N-CA-CB	5.81	121.06	110.60
3	3-D	245	PRO	N-CD-CG	5.81	111.91	103.20
3	5-C	193	ARG	CB-CG-CD	5.81	126.70	111.60
1	2-A	487	ASP	N-CA-CB	5.81	121.05	110.60
1	7-A	704	TYR	CB-CG-CD1	-5.81	117.52	121.00
3	10-C	426	SER	CB-CA-C	-5.81	99.06	110.10
3	10-D	362	TYR	CG-CD1-CE1	-5.81	116.65	121.30
1	3-A	119	LEU	CB-CG-CD2	5.80	120.86	111.00
3	6-C	266	HIS	CA-CB-CG	5.80	123.47	113.60
3	1-D	407	TYR	CG-CD1-CE1	-5.80	116.66	121.30
3	3-C	221	ASN	N-CA-C	-5.80	95.33	111.00
2	10-B	415	TYR	CB-CG-CD2	-5.80	117.52	121.00
1	3-A	663	TYR	CB-CG-CD1	5.80	124.48	121.00
1	3-A	693	ILE	CA-C-N	5.80	133.34	117.10
2	6-B	216	PHE	CB-CG-CD2	-5.80	116.74	120.80
2	8-B	439	ARG	NE-CZ-NH2	-5.80	117.40	120.30
2	1-B	834	GLY	N-CA-C	-5.80	98.61	113.10
1	4-A	633	HIS	CA-CB-CG	5.80	123.45	113.60
3	9-D	33	THR	CA-CB-CG2	-5.80	104.28	112.40
2	10-B	264	TYR	CG-CD1-CE1	5.80	125.94	121.30
1	1-A	383	ASP	N-CA-CB	5.79	121.03	110.60
3	1-D	166	ILE	CA-CB-CG1	-5.79	99.99	111.00
3	3-C	445	TYR	CA-CB-CG	-5.79	102.39	113.40
2	4-B	813	VAL	CA-CB-CG1	-5.79	102.21	110.90
3	3-C	436	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	6-A	108	ARG	NE-CZ-NH2	-5.79	117.40	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	337	SER	N-CA-CB	5.79	119.19	110.50
2	7-B	510	TYR	CB-CG-CD1	-5.79	117.53	121.00
3	7-D	118	ASP	CB-CG-OD1	-5.79	113.09	118.30
1	9-A	775	PHE	CB-CG-CD1	5.79	124.85	120.80
3	6-D	78	ASP	CB-CG-OD1	5.79	123.51	118.30
3	8-D	198	SER	N-CA-CB	5.79	119.18	110.50
3	1-D	431	GLN	N-CA-CB	5.79	121.02	110.60
2	2-B	264	TYR	CG-CD1-CE1	-5.79	116.67	121.30
3	9-C	413	PHE	CB-CG-CD2	-5.79	116.75	120.80
2	3-B	363	PHE	CB-CG-CD1	5.79	124.85	120.80
2	5-B	284	TYR	CB-CG-CD1	5.79	124.47	121.00
1	2-A	582	TYR	CB-CG-CD2	-5.78	117.53	121.00
2	2-B	483	MET	CA-CB-CG	5.78	123.13	113.30
2	6-B	583	TYR	N-CA-CB	-5.78	100.19	110.60
1	1-A	393	TYR	CB-CG-CD2	-5.78	117.53	121.00
2	3-B	307	LEU	N-CA-C	-5.78	95.39	111.00
2	3-B	641	PHE	CG-CD2-CE2	-5.78	114.44	120.80
1	6-A	393	TYR	CD1-CE1-CZ	5.78	125.00	119.80
1	6-A	792	ASP	CB-CG-OD1	-5.78	113.10	118.30
2	5-B	200	PHE	CB-CG-CD2	-5.78	116.75	120.80
3	7-C	34	ASP	CB-CA-C	-5.78	98.84	110.40
3	10-C	105	TRP	CA-CB-CG	5.78	124.68	113.70
3	1-C	293	ASP	CB-CG-OD1	-5.78	113.10	118.30
1	4-A	794	TYR	CA-CB-CG	5.78	124.38	113.40
2	6-B	272	VAL	CA-CB-CG1	-5.78	102.24	110.90
2	8-B	475	PHE	CB-CG-CD2	-5.78	116.76	120.80
1	4-A	460	LYS	N-CA-CB	5.77	120.99	110.60
2	4-B	241	PHE	CB-CG-CD1	-5.77	116.76	120.80
1	5-A	342	ASN	N-CA-CB	5.77	120.99	110.60
3	6-C	136	PHE	CB-CG-CD1	-5.77	116.76	120.80
2	8-B	763	VAL	CG1-CB-CG2	-5.77	101.67	110.90
3	10-C	92	THR	CA-CB-CG2	-5.77	104.32	112.40
2	5-B	266	ALA	O-C-N	-5.77	113.47	122.70
3	10-D	247	TYR	CB-CG-CD1	-5.77	117.54	121.00
2	2-B	411	PHE	CB-CG-CD1	5.77	124.84	120.80
3	2-C	150	LEU	CB-CG-CD2	5.77	120.81	111.00
1	4-A	138	PHE	CB-CG-CD2	5.77	124.84	120.80
1	8-A	140	TYR	CZ-CE2-CD2	-5.77	114.61	119.80
1	9-A	568	TYR	CD1-CE1-CZ	5.77	124.99	119.80
2	10-B	312	PHE	CB-CG-CD1	5.77	124.84	120.80
1	8-A	591	VAL	CG1-CB-CG2	-5.77	101.67	110.90
2	2-B	556	ASP	O-C-N	-5.76	113.47	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8-C	143	ALA	N-CA-CB	5.76	118.17	110.10
2	9-B	236	TYR	CB-CG-CD1	5.76	124.46	121.00
3	10-C	195	ILE	CA-CB-CG1	5.76	121.95	111.00
3	8-C	185	TYR	CZ-CE2-CD2	-5.76	114.61	119.80
3	8-D	114	ARG	N-CA-CB	5.76	120.97	110.60
1	3-A	140	TYR	CG-CD2-CE2	-5.76	116.69	121.30
3	7-D	161	ARG	NE-CZ-NH2	-5.76	117.42	120.30
2	10-B	321	SER	N-CA-CB	5.76	119.14	110.50
1	1-A	676	LEU	CB-CG-CD1	5.76	120.79	111.00
2	5-B	776	TYR	CB-CG-CD1	-5.76	117.54	121.00
1	7-A	136	GLN	CB-CA-C	-5.76	98.88	110.40
2	3-B	243	MET	CG-SD-CE	-5.76	90.99	100.20
3	6-D	220	PRO	N-CA-CB	5.76	110.21	103.30
2	9-B	556	ASP	CB-CG-OD1	-5.76	113.12	118.30
1	7-A	278	ASP	CB-CG-OD1	5.76	123.48	118.30
3	8-C	344	PHE	CB-CG-CD2	-5.76	116.77	120.80
3	10-D	299	LEU	N-CA-CB	5.75	121.91	110.40
2	2-B	488	PHE	CB-CG-CD1	-5.75	116.77	120.80
1	9-A	165	VAL	N-CA-C	-5.75	95.47	111.00
3	3-C	129	SER	C-N-CA	5.75	136.08	121.70
3	4-D	218	ARG	CA-CB-CG	5.75	126.05	113.40
3	5-C	10	ALA	CB-CA-C	-5.75	101.47	110.10
2	6-B	764	LEU	CB-CG-CD2	5.75	120.78	111.00
1	8-A	112	TYR	CD1-CE1-CZ	-5.75	114.62	119.80
3	7-C	249	TYR	CG-CD2-CE2	5.75	125.90	121.30
3	8-D	359	ARG	NE-CZ-NH2	-5.75	117.43	120.30
3	9-C	249	TYR	CB-CG-CD1	-5.75	117.55	121.00
3	9-D	118	ASP	CB-CG-OD2	5.75	123.47	118.30
3	4-C	105	TRP	CB-CG-CD2	-5.75	119.13	126.60
1	4-A	163	ASN	CB-CA-C	-5.75	98.91	110.40
3	5-C	192	ARG	NE-CZ-NH2	-5.75	117.43	120.30
1	2-A	197	PHE	CB-CG-CD1	-5.74	116.78	120.80
3	5-D	68	MET	CG-SD-CE	-5.74	91.01	100.20
3	8-C	371	GLU	OE1-CD-OE2	5.74	130.19	123.30
3	3-C	320	ASN	N-CA-C	-5.74	95.50	111.00
2	6-B	424	GLU	CB-CA-C	-5.74	98.92	110.40
3	2-D	394	PHE	CG-CD2-CE2	-5.74	114.49	120.80
2	10-B	343	TYR	CB-CA-C	-5.74	98.92	110.40
1	3-A	266	MET	CB-CA-C	-5.74	98.92	110.40
2	3-B	431	VAL	CA-CB-CG1	5.74	119.51	110.90
3	3-D	329	ARG	CG-CD-NE	-5.74	99.75	111.80
3	4-D	99	ALA	N-CA-CB	5.74	118.13	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	6-D	335	MET	CA-CB-CG	5.74	123.06	113.30
3	7-C	437	TYR	CB-CG-CD1	-5.74	117.56	121.00
3	8-C	394	PHE	CB-CG-CD2	-5.74	116.78	120.80
2	9-B	493	ILE	CA-CB-CG1	5.74	121.90	111.00
1	2-A	329	ASP	CB-CG-OD1	5.74	123.46	118.30
3	2-C	20	PHE	CB-CG-CD2	-5.74	116.78	120.80
1	4-A	123	TYR	CG-CD2-CE2	-5.74	116.71	121.30
2	4-B	272	VAL	CG1-CB-CG2	-5.74	101.72	110.90
3	4-D	204	PHE	CB-CG-CD2	-5.74	116.79	120.80
2	6-B	216	PHE	CB-CG-CD1	5.74	124.81	120.80
3	10-D	344	PHE	CB-CG-CD1	-5.74	116.79	120.80
3	2-C	311	ASN	N-CA-CB	5.73	120.92	110.60
2	3-B	453	TYR	CB-CG-CD2	-5.73	117.56	121.00
1	4-A	473	ASN	CA-C-N	-5.73	101.05	117.10
2	1-B	576	ARG	NE-CZ-NH2	-5.73	117.43	120.30
3	1-C	54	PHE	N-CA-CB	5.73	120.92	110.60
1	3-A	624	ARG	NE-CZ-NH2	-5.73	117.43	120.30
3	3-C	424	ALA	CB-CA-C	-5.73	101.50	110.10
2	5-B	758	TYR	CZ-CE2-CD2	5.73	124.96	119.80
1	1-A	286	TRP	CA-CB-CG	5.73	124.59	113.70
3	2-D	268	LEU	CB-CA-C	-5.73	99.31	110.20
2	8-B	598	TYR	CB-CG-CD2	-5.73	117.56	121.00
3	1-D	295	MET	CG-SD-CE	-5.73	91.03	100.20
3	7-C	114	ARG	NE-CZ-NH2	-5.73	117.44	120.30
3	1-D	54	PHE	CB-CG-CD1	-5.73	116.79	120.80
3	2-C	344	PHE	CB-CG-CD2	-5.73	116.79	120.80
2	8-B	202	PHE	CB-CG-CD2	-5.73	116.79	120.80
3	5-D	54	PHE	N-CA-CB	5.73	120.91	110.60
1	10-A	587	ARG	CG-CD-NE	-5.73	99.78	111.80
3	3-D	253	SER	N-CA-CB	5.72	119.09	110.50
3	4-C	93	TRP	CB-CG-CD1	-5.72	119.56	127.00
3	7-D	363	LEU	CB-CA-C	-5.72	99.32	110.20
2	9-B	334	LEU	O-C-N	5.72	131.86	122.70
2	7-B	598	TYR	CB-CG-CD1	5.72	124.43	121.00
2	10-B	288	TYR	CB-CG-CD2	5.72	124.43	121.00
3	10-D	381	SER	N-CA-CB	-5.72	101.92	110.50
3	4-C	256	TYR	CB-CG-CD2	-5.72	117.57	121.00
3	2-C	66	ALA	CB-CA-C	-5.72	101.52	110.10
1	3-A	333	ARG	NE-CZ-NH2	5.72	123.16	120.30
3	7-C	17	VAL	CA-CB-CG2	5.72	119.48	110.90
3	9-D	161	ARG	NE-CZ-NH1	-5.72	117.44	120.30
3	3-C	77	ALA	N-CA-CB	5.72	118.11	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	6-B	578	PHE	CB-CG-CD2	-5.72	116.80	120.80
2	9-B	460	THR	N-CA-CB	5.72	121.16	110.30
3	7-C	117	ASP	CB-CG-OD2	5.72	123.44	118.30
3	9-C	275	PHE	O-C-N	-5.72	113.55	122.70
1	2-A	474	PRO	N-CD-CG	5.71	111.77	103.20
1	3-A	443	MET	C-N-CA	5.71	134.30	122.30
3	3-C	176	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	4-A	624	ARG	NE-CZ-NH1	5.71	123.16	120.30
2	4-B	308	SER	N-CA-CB	5.71	119.07	110.50
3	9-C	369	GLU	C-N-CA	5.71	135.99	121.70
2	10-B	826	PHE	CB-CG-CD1	-5.71	116.80	120.80
1	1-A	588	TYR	CG-CD2-CE2	-5.71	116.73	121.30
3	9-D	315	TYR	CA-CB-CG	-5.71	102.55	113.40
1	1-A	391	GLU	OE1-CD-OE2	5.71	130.15	123.30
3	2-C	289	HIS	CB-CA-C	-5.71	98.98	110.40
3	10-D	93	TRP	CB-CG-CD2	-5.71	119.17	126.60
3	2-D	436	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	4-A	250	ILE	N-CA-CB	5.71	123.93	110.80
2	7-B	288	TYR	CZ-CE2-CD2	5.71	124.94	119.80
2	8-B	834	GLY	N-CA-C	-5.71	98.83	113.10
3	1-D	47	ASP	O-C-N	5.71	131.83	122.70
2	6-B	470	TYR	CD1-CE1-CZ	5.71	124.94	119.80
1	7-A	150	TYR	CG-CD2-CE2	5.71	125.87	121.30
3	1-D	218	ARG	NE-CZ-NH2	-5.71	117.45	120.30
1	4-A	787	SER	N-CA-CB	5.70	119.06	110.50
3	4-C	221	ASN	N-CA-C	-5.70	95.60	111.00
3	4-C	314	THR	CA-CB-CG2	-5.70	104.42	112.40
3	6-C	302	SER	N-CA-CB	5.70	119.06	110.50
1	8-A	418	VAL	O-C-N	-5.70	113.58	122.70
1	6-A	755	ASP	CB-CG-OD2	5.70	123.43	118.30
2	8-B	495	LYS	O-C-N	-5.70	113.58	122.70
3	8-C	313	PRO	C-N-CA	5.70	135.95	121.70
2	2-B	839	PHE	CB-CG-CD1	5.70	124.79	120.80
3	2-C	192	ARG	NE-CZ-NH2	5.70	123.15	120.30
1	4-A	80	ASP	CB-CG-OD2	-5.70	113.17	118.30
3	10-D	19	LYS	N-CA-CB	5.70	120.86	110.60
2	2-B	585	ARG	NE-CZ-NH2	5.70	123.15	120.30
2	4-B	198	ALA	N-CA-CB	5.70	118.08	110.10
3	5-C	292	TYR	CD1-CE1-CZ	-5.70	114.67	119.80
2	9-B	577	PRO	N-CD-CG	5.70	111.75	103.20
3	9-D	341	ARG	NE-CZ-NH1	5.70	123.15	120.30
3	2-C	329	ARG	NE-CZ-NH1	5.70	123.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	6-D	376	MET	CG-SD-CE	-5.70	91.09	100.20
3	7-D	445	TYR	CB-CG-CD1	-5.70	117.58	121.00
3	10-C	432	SER	N-CA-CB	5.70	119.04	110.50
3	8-D	161	ARG	NE-CZ-NH1	-5.69	117.45	120.30
3	6-D	359	ARG	CA-C-O	5.69	132.05	120.10
2	7-B	772	PHE	CB-CG-CD2	5.69	124.78	120.80
2	10-B	258	SER	N-CA-CB	5.69	119.04	110.50
1	4-A	358	ARG	NE-CZ-NH2	-5.69	117.45	120.30
1	4-A	636	MET	CB-CA-C	-5.69	99.02	110.40
1	6-A	91	GLU	N-CA-CB	5.69	120.84	110.60
1	3-A	167	ASN	CA-CB-CG	-5.69	100.88	113.40
3	5-D	319	TYR	CB-CG-CD1	5.69	124.41	121.00
1	10-A	612	TRP	CD1-CG-CD2	-5.69	101.75	106.30
3	6-D	218	ARG	NE-CZ-NH1	-5.69	117.46	120.30
1	9-A	413	TYR	CB-CG-CD2	-5.69	117.59	121.00
2	10-B	379	TYR	CG-CD1-CE1	-5.69	116.75	121.30
3	5-D	78	ASP	CB-CG-OD2	5.68	123.42	118.30
2	7-B	758	TYR	CB-CG-CD2	5.68	124.41	121.00
1	9-A	324	TYR	CB-CG-CD2	-5.68	117.59	121.00
1	1-A	402	ASN	N-CA-CB	5.68	120.83	110.60
1	1-A	415	LEU	CB-CG-CD2	-5.68	101.34	111.00
3	1-D	416	MET	CG-SD-CE	-5.68	91.11	100.20
1	2-A	795	ASP	CB-CG-OD2	-5.68	113.19	118.30
3	4-C	93	TRP	CG-CD2-CE3	-5.68	128.78	133.90
2	5-B	758	TYR	CG-CD2-CE2	-5.68	116.75	121.30
2	1-B	415	TYR	CG-CD1-CE1	5.68	125.84	121.30
1	4-A	697	LEU	CB-CG-CD1	5.68	120.66	111.00
1	8-A	288	THR	CA-CB-CG2	-5.68	104.45	112.40
2	8-B	453	TYR	CZ-CE2-CD2	-5.68	114.69	119.80
3	1-D	185	TYR	CB-CG-CD2	-5.68	117.59	121.00
3	2-C	218	ARG	NE-CZ-NH2	5.68	123.14	120.30
3	5-C	335	MET	CG-SD-CE	-5.68	91.11	100.20
3	8-D	249	TYR	CD1-CE1-CZ	5.68	124.91	119.80
1	9-A	302	TYR	N-CA-CB	5.68	120.82	110.60
1	2-A	193	TYR	CB-CG-CD1	-5.68	117.59	121.00
3	2-D	70	ASP	CB-CG-OD1	5.68	123.41	118.30
3	4-C	70	ASP	CB-CG-OD1	5.68	123.41	118.30
3	4-C	247	TYR	CZ-CE2-CD2	-5.68	114.69	119.80
2	7-B	592	ARG	NE-CZ-NH1	5.68	123.14	120.30
3	7-C	44	THR	N-CA-CB	5.68	121.09	110.30
3	6-C	75	VAL	CA-CB-CG1	5.67	119.41	110.90
3	7-C	223	ASP	CB-CG-OD1	5.67	123.41	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	9-A	400	ARG	NE-CZ-NH1	5.67	123.14	120.30
3	4-C	93	TRP	CB-CG-CD2	5.67	133.97	126.60
1	7-A	635	LYS	CB-CA-C	-5.67	99.05	110.40
1	10-A	576	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	1-A	469	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	1-A	558	TYR	CG-CD1-CE1	5.67	125.84	121.30
2	2-B	335	PHE	CB-CG-CD2	5.67	124.77	120.80
3	4-C	445	TYR	CB-CG-CD2	5.67	124.40	121.00
2	10-B	501	ALA	CB-CA-C	-5.67	101.59	110.10
3	6-C	248	MET	CA-CB-CG	5.67	122.94	113.30
3	9-D	162	TYR	CB-CG-CD1	5.67	124.40	121.00
3	2-C	167	LEU	CB-CG-CD1	5.67	120.64	111.00
3	5-C	67	ILE	CA-CB-CG1	5.67	121.77	111.00
3	5-C	146	THR	CA-C-N	5.67	127.54	116.20
2	7-B	356	ARG	N-CA-C	-5.67	95.69	111.00
3	7-C	12	GLN	CA-CB-CG	5.67	125.87	113.40
3	7-D	333	ARG	NE-CZ-NH1	5.67	123.13	120.30
3	9-D	223	ASP	CB-CG-OD2	5.67	123.40	118.30
2	10-B	562	TYR	CZ-CE2-CD2	-5.67	114.70	119.80
1	1-A	418	VAL	CA-CB-CG2	5.66	119.40	110.90
2	5-B	532	PRO	N-CA-CB	5.66	110.09	103.30
1	7-A	123	TYR	CB-CG-CD1	-5.66	117.60	121.00
3	8-C	205	ASP	CB-CG-OD1	5.66	123.40	118.30
3	9-C	114	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	10-A	112	TYR	CB-CG-CD2	-5.66	117.60	121.00
2	4-B	400	TYR	CB-CG-CD2	-5.66	117.60	121.00
1	5-A	426	PHE	CB-CG-CD1	5.66	124.76	120.80
1	6-A	564	ILE	CA-CB-CG2	-5.66	99.58	110.90
2	8-B	734	ASN	CB-CA-C	-5.66	99.08	110.40
1	9-A	646	TYR	CB-CA-C	-5.66	99.08	110.40
2	10-B	661	PHE	CB-CG-CD2	-5.66	116.84	120.80
3	1-D	325	ASN	N-CA-CB	5.66	120.78	110.60
1	2-A	627	ARG	CD-NE-CZ	-5.66	115.68	123.60
3	3-D	47	ASP	CB-CG-OD2	-5.66	113.21	118.30
1	10-A	646	TYR	CG-CD1-CE1	-5.66	116.78	121.30
3	2-C	394	PHE	CZ-CE2-CD2	5.65	126.88	120.10
3	4-C	133	PHE	CB-CG-CD1	5.65	124.76	120.80
2	1-B	429	TYR	CG-CD1-CE1	-5.65	116.78	121.30
2	2-B	438	TYR	CG-CD1-CE1	5.65	125.82	121.30
1	3-A	400	ARG	NE-CZ-NH1	5.65	123.13	120.30
3	7-C	413	PHE	CB-CG-CD2	5.65	124.75	120.80
3	9-D	432	SER	N-CA-CB	5.65	118.98	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-C	416	MET	CB-CA-C	-5.65	99.10	110.40
1	9-A	558	TYR	CG-CD1-CE1	-5.65	116.78	121.30
3	1-C	53	PHE	CG-CD2-CE2	-5.65	114.59	120.80
1	3-A	266	MET	N-CA-CB	5.65	120.77	110.60
3	3-C	386	VAL	CG1-CB-CG2	5.65	119.94	110.90
3	7-C	282	ASP	CB-CG-OD2	5.65	123.38	118.30
2	9-B	188	VAL	CB-CA-C	5.65	122.13	111.40
1	2-A	128	ASP	C-N-CA	5.64	135.81	121.70
2	3-B	652	TYR	N-CA-CB	5.64	120.76	110.60
3	5-D	437	TYR	O-C-N	-5.64	113.67	122.70
3	7-C	344	PHE	CB-CG-CD1	5.64	124.75	120.80
1	8-A	657	TYR	CB-CG-CD2	-5.64	117.61	121.00
1	4-A	600	ASP	O-C-N	5.64	131.73	122.70
1	5-A	299	PHE	N-CA-CB	5.64	120.75	110.60
2	6-B	205	GLU	OE1-CD-OE2	5.64	130.07	123.30
1	2-A	667	THR	N-CA-CB	5.64	121.02	110.30
2	9-B	350	LEU	CB-CG-CD2	5.64	120.59	111.00
1	6-A	204	ARG	NE-CZ-NH1	5.64	123.12	120.30
2	7-B	758	TYR	CB-CG-CD1	-5.64	117.62	121.00
2	2-B	550	HIS	N-CA-CB	5.64	120.75	110.60
3	3-C	445	TYR	CB-CA-C	-5.64	99.13	110.40
2	8-B	741	PHE	CB-CG-CD2	-5.64	116.86	120.80
3	7-D	437	TYR	CB-CG-CD1	5.63	124.38	121.00
1	6-A	78	PHE	CG-CD2-CE2	-5.63	114.61	120.80
3	7-D	223	ASP	N-CA-CB	5.63	120.74	110.60
1	8-A	324	TYR	N-CA-CB	5.63	120.74	110.60
3	1-D	87	PHE	N-CA-C	-5.63	95.80	111.00
3	1-D	114	ARG	NE-CZ-NH1	5.63	123.11	120.30
2	2-B	190	TYR	CB-CG-CD1	-5.63	117.62	121.00
2	3-B	357	ALA	N-CA-CB	5.63	117.98	110.10
3	5-D	156	GLU	N-CA-CB	5.63	120.73	110.60
3	2-C	423	PHE	CB-CG-CD2	-5.62	116.86	120.80
1	6-A	629	THR	CA-CB-CG2	-5.62	104.53	112.40
2	7-B	802	LEU	N-CA-CB	5.62	121.65	110.40
3	4-C	266	HIS	N-CA-CB	5.62	120.72	110.60
3	8-D	170	TYR	CZ-CE2-CD2	5.62	124.86	119.80
3	9-D	267	PHE	CB-CG-CD2	-5.62	116.86	120.80
1	3-A	144	ARG	NE-CZ-NH1	-5.62	117.49	120.30
2	4-B	519	ALA	N-CA-CB	5.62	117.97	110.10
2	8-B	359	TYR	CB-CG-CD1	-5.62	117.63	121.00
3	1-C	275	PHE	CZ-CE2-CD2	5.62	126.84	120.10
3	4-D	181	VAL	CA-CB-CG2	5.62	119.33	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	7-B	190	TYR	CG-CD2-CE2	-5.62	116.81	121.30
2	7-B	222	HIS	CA-CB-CG	5.62	123.15	113.60
3	7-D	413	PHE	CB-CA-C	-5.62	99.16	110.40
1	8-A	481	LEU	CB-CG-CD1	5.62	120.55	111.00
2	8-B	354	LEU	CB-CG-CD2	5.62	120.55	111.00
3	10-D	92	THR	CA-CB-OG1	5.62	120.80	109.00
3	1-D	247	TYR	CZ-CE2-CD2	-5.62	114.75	119.80
2	4-B	529	MET	C-N-CA	5.62	135.74	121.70
2	5-B	187	TYR	CG-CD1-CE1	5.62	125.79	121.30
1	6-A	333	ARG	NE-CZ-NH1	-5.62	117.49	120.30
1	7-A	630	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	9-A	190	TYR	CB-CG-CD2	-5.62	117.63	121.00
2	2-B	824	TYR	CG-CD2-CE2	5.61	125.79	121.30
3	4-D	443	ASP	CB-CG-OD2	5.61	123.35	118.30
3	7-C	295	MET	CG-SD-CE	-5.61	91.22	100.20
3	8-C	192	ARG	NE-CZ-NH2	-5.61	117.49	120.30
3	9-D	404	LEU	CB-CG-CD2	5.61	120.54	111.00
1	5-A	110	VAL	CA-CB-CG1	5.61	119.32	110.90
1	5-A	597	ARG	CD-NE-CZ	5.61	131.46	123.60
2	5-B	475	PHE	CZ-CE2-CD2	-5.61	113.37	120.10
1	1-A	165	VAL	CA-CB-CG1	5.61	119.31	110.90
2	2-B	641	PHE	CB-CG-CD2	-5.61	116.87	120.80
2	6-B	559	THR	CA-CB-CG2	-5.61	104.55	112.40
2	6-B	652	TYR	CG-CD2-CE2	-5.61	116.81	121.30
2	7-B	188	VAL	CA-CB-CG1	-5.61	102.48	110.90
3	7-C	207	ALA	N-CA-CB	5.61	117.95	110.10
3	10-D	329	ARG	CD-NE-CZ	-5.61	115.75	123.60
2	2-B	644	PHE	CB-CG-CD2	5.61	124.73	120.80
3	3-C	248	MET	CG-SD-CE	-5.61	91.23	100.20
1	10-A	107	ARG	NE-CZ-NH1	-5.61	117.50	120.30
3	3-D	201	THR	CA-CB-CG2	5.61	120.25	112.40
3	4-D	329	ARG	NE-CZ-NH1	-5.61	117.50	120.30
2	5-B	349	TRP	N-CA-CB	-5.61	100.51	110.60
1	6-A	349	ARG	NH1-CZ-NH2	-5.61	113.23	119.40
1	9-A	183	ASN	N-CA-CB	5.61	120.69	110.60
1	5-A	203	ARG	N-CA-CB	5.60	120.69	110.60
2	8-B	435	SER	N-CA-CB	-5.60	102.09	110.50
2	3-B	241	PHE	CB-CG-CD1	5.60	124.72	120.80
3	9-D	259	LEU	CB-CG-CD1	5.60	120.52	111.00
2	2-B	566	PRO	CA-C-N	5.60	132.78	117.10
3	1-D	380	MET	C-N-CA	5.60	135.70	121.70
1	3-A	799	VAL	CA-CB-CG1	5.60	119.30	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	7-D	138	LEU	CB-CG-CD2	-5.60	101.48	111.00
1	1-A	579	MET	CB-CA-C	-5.60	99.20	110.40
3	3-C	170	TYR	CB-CG-CD1	-5.60	117.64	121.00
1	10-A	279	TYR	CA-CB-CG	-5.60	102.77	113.40
1	2-A	409	PHE	CA-CB-CG	-5.59	100.47	113.90
3	2-C	8	LEU	CB-CA-C	-5.59	99.57	110.20
1	4-A	413	TYR	CB-CG-CD1	-5.59	117.64	121.00
2	4-B	777	CYS	CB-CA-C	-5.59	99.21	110.40
1	7-A	262	ARG	NE-CZ-NH1	-5.59	117.50	120.30
2	8-B	571	VAL	CG1-CB-CG2	-5.59	101.95	110.90
3	3-C	247	TYR	CZ-CE2-CD2	-5.59	114.77	119.80
2	5-B	416	CYS	N-CA-CB	5.59	120.66	110.60
3	6-C	265	LEU	CB-CG-CD1	5.59	120.50	111.00
1	7-A	609	THR	CA-CB-CG2	-5.59	104.57	112.40
1	9-A	162	PHE	CA-CB-CG	-5.59	100.48	113.90
3	10-C	247	TYR	CB-CG-CD2	5.59	124.35	121.00
2	3-B	580	ARG	NE-CZ-NH1	5.59	123.09	120.30
2	6-B	362	PHE	CB-CG-CD1	5.59	124.71	120.80
1	8-A	469	ARG	NH1-CZ-NH2	-5.59	113.25	119.40
1	1-A	562	PHE	CB-CG-CD2	-5.59	116.89	120.80
2	6-B	526	ARG	NE-CZ-NH2	-5.59	117.51	120.30
3	8-C	162	TYR	CG-CD2-CE2	-5.59	116.83	121.30
3	8-C	197	ASP	CB-CG-OD2	-5.59	113.27	118.30
3	10-D	162	TYR	CZ-CE2-CD2	5.59	124.83	119.80
3	3-D	437	TYR	CA-CB-CG	-5.58	102.79	113.40
2	3-B	563	ILE	CA-CB-CG1	5.58	121.61	111.00
2	6-B	256	GLU	N-CA-CB	5.58	120.65	110.60
1	7-A	73	THR	C-N-CA	5.58	135.66	121.70
2	8-B	423	ASN	CB-CG-OD1	5.58	132.77	121.60
2	5-B	471	ARG	NE-CZ-NH2	-5.58	117.51	120.30
3	6-C	104	SER	N-CA-CB	5.58	118.87	110.50
1	8-A	458	TYR	CB-CG-CD2	-5.58	117.65	121.00
2	2-B	562	TYR	N-CA-C	-5.58	95.93	111.00
1	5-A	380	ASP	CB-CG-OD2	5.58	123.32	118.30
2	5-B	445	PHE	CB-CG-CD2	-5.58	116.89	120.80
2	6-B	480	ILE	CA-CB-CG1	5.58	121.60	111.00
2	10-B	286	GLU	CB-CA-C	-5.58	99.24	110.40
1	2-A	588	TYR	CB-CG-CD2	-5.58	117.65	121.00
3	2-D	387	PHE	CZ-CE2-CD2	-5.58	113.41	120.10
3	3-C	423	PHE	CB-CG-CD2	5.58	124.70	120.80
1	9-A	126	TRP	CE2-CD2-CE3	5.58	125.39	118.70
1	10-A	697	LEU	CB-CA-C	-5.58	99.60	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2-A	664	ARG	NE-CZ-NH1	-5.58	117.51	120.30
2	4-B	599	PHE	CB-CG-CD2	-5.58	116.90	120.80
3	4-C	85	GLY	N-CA-C	-5.58	99.16	113.10
3	3-C	169	THR	CA-CB-CG2	-5.58	104.59	112.40
3	9-D	437	TYR	CB-CG-CD2	-5.58	117.66	121.00
1	2-A	426	PHE	CB-CG-CD2	-5.57	116.90	120.80
3	4-C	65	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	7-A	358	ARG	NE-CZ-NH2	5.57	123.09	120.30
3	1-D	333	ARG	NE-CZ-NH1	5.57	123.09	120.30
3	4-D	437	TYR	CB-CG-CD1	-5.57	117.66	121.00
2	9-B	587	PHE	CB-CG-CD1	5.57	124.70	120.80
1	10-A	486	PHE	O-C-N	5.57	131.62	122.70
2	1-B	557	VAL	CA-CB-CG1	5.57	119.25	110.90
2	3-B	510	TYR	N-CA-CB	5.57	120.63	110.60
3	4-C	61	LYS	CB-CA-C	-5.57	99.26	110.40
1	5-A	778	CYS	CB-CA-C	-5.57	99.26	110.40
1	7-A	299	PHE	CB-CG-CD2	-5.57	116.90	120.80
3	7-D	176	ARG	NE-CZ-NH1	-5.57	117.52	120.30
3	1-C	437	TYR	CD1-CE1-CZ	-5.57	114.79	119.80
2	3-B	562	TYR	CB-CG-CD2	5.57	124.34	121.00
3	5-D	379	ASN	N-CA-CB	5.57	120.62	110.60
2	7-B	403	PHE	CG-CD1-CE1	-5.57	114.68	120.80
3	9-D	318	VAL	CB-CA-C	-5.57	100.82	111.40
1	6-A	262	ARG	NE-CZ-NH1	5.57	123.08	120.30
2	9-B	731	PHE	CB-CA-C	-5.57	99.27	110.40
1	1-A	366	ILE	N-CA-C	-5.56	95.98	111.00
3	1-D	398	PHE	CB-CG-CD2	-5.56	116.91	120.80
3	3-D	186	ASN	CB-CA-C	-5.56	99.28	110.40
3	7-C	114	ARG	CD-NE-CZ	-5.56	115.81	123.60
3	8-D	255	ILE	N-CA-CB	5.56	123.59	110.80
3	4-C	130	THR	CA-CB-CG2	-5.56	104.61	112.40
3	5-D	109	TYR	CB-CG-CD2	-5.56	117.66	121.00
3	5-D	411	ASP	CB-CG-OD2	5.56	123.31	118.30
3	6-C	124	ASP	CB-CG-OD2	5.56	123.31	118.30
1	8-A	775	PHE	O-C-N	-5.56	113.80	122.70
2	10-B	409	TYR	CB-CG-CD2	5.56	124.34	121.00
3	2-D	437	TYR	CB-CG-CD1	5.56	124.33	121.00
2	7-B	343	TYR	CB-CG-CD1	5.56	124.34	121.00
3	5-C	169	THR	CA-CB-CG2	-5.56	104.62	112.40
1	6-A	410	PHE	CB-CG-CD1	5.56	124.69	120.80
2	6-B	385	PHE	CB-CG-CD2	-5.56	116.91	120.80
2	6-B	453	TYR	CG-CD2-CE2	-5.56	116.85	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	8-A	624	ARG	NE-CZ-NH2	5.56	123.08	120.30
2	4-B	342	TYR	CA-CB-CG	-5.56	102.84	113.40
3	7-D	41	ASP	CB-CG-OD2	-5.56	113.30	118.30
2	1-B	326	THR	CA-CB-CG2	-5.55	104.62	112.40
3	4-C	83	PHE	CB-CG-CD1	5.55	124.69	120.80
3	4-C	315	TYR	CG-CD1-CE1	5.55	125.74	121.30
1	5-A	415	LEU	CB-CA-C	-5.55	99.65	110.20
2	5-B	798	SER	O-C-N	-5.55	113.81	122.70
2	6-B	839	PHE	CB-CG-CD2	5.55	124.69	120.80
2	8-B	487	ASP	CB-CG-OD2	-5.55	113.30	118.30
3	4-C	99	ALA	N-CA-CB	5.55	117.88	110.10
2	1-B	409	TYR	CD1-CG-CD2	5.55	124.01	117.90
3	5-D	240	ASN	N-CA-CB	5.55	120.59	110.60
3	6-C	54	PHE	CB-CG-CD2	-5.55	116.91	120.80
3	7-D	183	GLN	CA-CB-CG	5.55	125.61	113.40
3	8-D	393	THR	CA-CB-CG2	-5.55	104.63	112.40
2	3-B	600	TYR	CB-CA-C	5.55	121.50	110.40
1	6-A	67	LEU	CB-CA-C	-5.55	99.66	110.20
1	6-A	192	ILE	CA-CB-CG1	5.55	121.54	111.00
2	7-B	334	LEU	CB-CA-C	-5.55	99.66	110.20
2	9-B	488	PHE	CB-CG-CD1	-5.55	116.92	120.80
2	10-B	343	TYR	CB-CG-CD2	-5.55	117.67	121.00
2	6-B	231	TYR	CB-CG-CD2	5.55	124.33	121.00
3	8-D	406	ASN	C-N-CA	5.55	135.57	121.70
1	5-A	438	PHE	CB-CG-CD2	-5.55	116.92	120.80
2	5-B	233	SER	N-CA-CB	5.55	118.82	110.50
2	9-B	599	PHE	CB-CA-C	-5.54	99.31	110.40
3	3-D	30	ALA	N-CA-CB	5.54	117.86	110.10
1	4-A	406	LEU	CB-CG-CD2	5.54	120.42	111.00
3	4-C	199	ASP	CB-CA-C	-5.54	99.31	110.40
1	7-A	169	SER	C-N-CA	5.54	135.56	121.70
1	7-A	373	ILE	N-CA-CB	5.54	123.55	110.80
1	7-A	664	ARG	NE-CZ-NH2	-5.54	117.53	120.30
2	3-B	245	ASN	O-C-N	5.54	131.56	122.70
2	7-B	816	TYR	CG-CD1-CE1	5.54	125.73	121.30
3	6-C	20	PHE	CZ-CE2-CD2	5.54	126.75	120.10
3	9-C	345	PRO	CA-CB-CG	5.54	115.33	104.80
2	1-B	417	LYS	N-CA-CB	5.54	120.57	110.60
3	4-C	185	TYR	CG-CD1-CE1	-5.54	116.87	121.30
2	7-B	345	TYR	CB-CG-CD2	-5.54	117.68	121.00
2	7-B	428	LYS	C-N-CA	5.54	135.55	121.70
3	9-C	256	TYR	CZ-CE2-CD2	5.54	124.78	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3-A	612	TRP	CG-CD2-CE3	-5.54	128.92	133.90
2	4-B	757	PRO	N-CA-CB	5.54	109.94	103.30
3	5-D	100	SER	N-CA-CB	5.54	118.80	110.50
2	7-B	225	PHE	N-CA-CB	5.54	120.57	110.60
3	4-C	62	PHE	CB-CG-CD2	-5.53	116.93	120.80
1	6-A	693	ILE	CA-C-O	-5.53	108.48	120.10
2	7-B	285	ARG	NE-CZ-NH2	5.53	123.07	120.30
3	8-D	349	SER	N-CA-CB	5.53	118.80	110.50
1	9-A	203	ARG	NE-CZ-NH2	-5.53	117.53	120.30
3	2-C	315	TYR	CG-CD2-CE2	-5.53	116.87	121.30
1	5-A	691	ASP	CB-CG-OD1	5.53	123.28	118.30
3	5-D	430	VAL	CA-CB-CG2	5.53	119.20	110.90
1	7-A	74	TYR	CG-CD2-CE2	5.53	125.72	121.30
3	10-C	40	PRO	N-CA-CB	5.53	109.94	103.30
3	9-D	77	ALA	CB-CA-C	-5.53	101.81	110.10
3	9-D	329	ARG	CB-CA-C	-5.53	99.34	110.40
3	10-C	193	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	2-A	204	ARG	NE-CZ-NH2	5.53	123.06	120.30
3	4-D	434	MET	CG-SD-CE	-5.53	91.35	100.20
2	9-B	809	LEU	CB-CG-CD1	5.53	120.40	111.00
3	1-D	285	ALA	N-CA-CB	5.53	117.84	110.10
2	2-B	540	GLY	N-CA-C	5.53	126.92	113.10
3	2-C	61	LYS	N-CA-CB	5.53	120.55	110.60
1	4-A	612	TRP	CD1-CG-CD2	5.53	110.72	106.30
1	9-A	296	TYR	O-C-N	5.53	131.54	122.70
1	5-A	102	PHE	CA-C-O	-5.53	108.50	120.10
3	5-C	70	ASP	CB-CG-OD2	-5.53	113.33	118.30
3	6-D	182	VAL	CA-CB-CG2	5.53	119.19	110.90
1	7-A	755	ASP	CB-CG-OD1	5.53	123.27	118.30
3	2-C	398	PHE	CD1-CE1-CZ	-5.52	113.47	120.10
3	5-D	86	PHE	CB-CG-CD2	5.52	124.67	120.80
3	5-D	255	ILE	CA-CB-CG1	5.52	121.50	111.00
1	8-A	663	TYR	CB-CG-CD2	-5.52	117.69	121.00
3	3-C	424	ALA	N-CA-CB	5.52	117.83	110.10
3	6-D	309	ALA	N-CA-CB	5.52	117.83	110.10
2	9-B	570	LEU	CB-CG-CD1	5.52	120.39	111.00
1	10-A	693	ILE	CA-CB-CG1	5.52	121.49	111.00
3	1-C	245	PRO	O-C-N	5.52	131.53	122.70
2	5-B	446	PHE	CB-CG-CD1	-5.52	116.94	120.80
3	5-D	110	ASP	N-CA-CB	5.52	120.54	110.60
3	7-C	354	VAL	CA-CB-CG1	5.52	119.18	110.90
3	8-C	279	TYR	CB-CG-CD1	5.52	124.31	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3-A	360	SER	CB-CA-C	-5.52	99.61	110.10
1	4-A	623	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	8-A	477	LEU	CB-CG-CD2	-5.52	101.62	111.00
1	4-A	704	TYR	CG-CD2-CE2	-5.52	116.89	121.30
3	9-C	90	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	1-A	426	PHE	CB-CA-C	-5.52	99.37	110.40
2	5-B	756	GLN	CA-C-N	5.52	132.54	117.10
3	8-D	70	ASP	CB-CG-OD2	-5.52	113.34	118.30
2	2-B	471	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	4-A	785	GLU	CB-CA-C	5.51	121.43	110.40
2	5-B	526	ARG	N-CA-C	-5.51	96.11	111.00
1	7-A	60	VAL	CA-CB-CG1	5.51	119.17	110.90
1	8-A	324	TYR	CG-CD2-CE2	-5.51	116.89	121.30
1	3-A	112	TYR	CG-CD1-CE1	5.51	125.71	121.30
3	3-D	359	ARG	NE-CZ-NH1	5.51	123.06	120.30
3	6-C	369	GLU	N-CA-CB	5.51	120.52	110.60
1	8-A	477	LEU	CB-CG-CD1	5.51	120.37	111.00
2	3-B	588	ASN	CA-CB-CG	5.51	125.52	113.40
1	8-A	458	TYR	CA-CB-CG	-5.51	102.93	113.40
3	8-C	315	TYR	CB-CG-CD2	5.51	124.31	121.00
3	4-D	34	ASP	CB-CG-OD2	-5.51	113.34	118.30
3	7-C	344	PHE	CB-CG-CD2	-5.51	116.94	120.80
2	9-B	289	GLU	CA-CB-CG	5.51	125.52	113.40
2	1-B	741	PHE	CG-CD2-CE2	-5.51	114.74	120.80
2	9-B	285	ARG	NE-CZ-NH1	-5.51	117.55	120.30
1	5-A	454	ASN	O-C-N	5.51	131.51	122.70
1	7-A	568	TYR	CG-CD1-CE1	5.51	125.71	121.30
2	7-B	445	PHE	CB-CG-CD2	5.51	124.66	120.80
2	8-B	328	ARG	NH1-CZ-NH2	-5.51	113.34	119.40
3	8-D	110	ASP	CB-CG-OD2	-5.51	113.34	118.30
1	10-A	624	ARG	NE-CZ-NH2	5.51	123.05	120.30
3	10-D	314	THR	N-CA-C	-5.51	96.13	111.00
2	1-B	659	GLU	O-C-N	-5.50	113.89	122.70
1	1-A	108	ARG	CD-NE-CZ	5.50	131.31	123.60
3	2-C	77	ALA	N-CA-CB	5.50	117.80	110.10
1	6-A	80	ASP	CB-CG-OD2	5.50	123.25	118.30
1	7-A	358	ARG	NE-CZ-NH1	5.50	123.05	120.30
2	1-B	263	ASN	N-CA-CB	5.50	120.50	110.60
3	2-C	62	PHE	O-C-N	5.50	131.50	122.70
3	7-D	28	GLU	OE1-CD-OE2	5.50	129.90	123.30
2	8-B	565	TYR	CB-CG-CD2	-5.50	117.70	121.00
3	7-C	249	TYR	CZ-CE2-CD2	-5.50	114.85	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2-A	95	ALA	N-CA-CB	5.50	117.80	110.10
2	3-B	243	MET	N-CA-CB	5.50	120.50	110.60
3	5-C	140	HIS	C-N-CA	5.50	135.44	121.70
3	5-D	315	TYR	CB-CG-CD1	5.50	124.30	121.00
1	6-A	386	GLU	N-CA-CB	5.50	120.50	110.60
3	2-C	93	TRP	CD1-CG-CD2	-5.50	101.90	106.30
2	3-B	462	GLN	O-C-N	-5.50	113.91	122.70
1	5-A	278	ASP	N-CA-CB	5.50	120.49	110.60
3	8-C	292	TYR	CG-CD1-CE1	-5.50	116.90	121.30
2	2-B	760	THR	CA-CB-OG1	5.49	120.54	109.00
3	2-D	298	LEU	N-CA-CB	5.49	121.39	110.40
3	4-D	114	ARG	NE-CZ-NH1	5.49	123.05	120.30
3	4-D	218	ARG	NE-CZ-NH1	5.49	123.05	120.30
3	7-D	244	PHE	CG-CD1-CE1	5.49	126.84	120.80
2	10-B	425	PHE	CB-CG-CD1	5.49	124.64	120.80
1	4-A	394	VAL	N-CA-CB	5.49	123.58	111.50
2	6-B	433	TYR	CD1-CE1-CZ	5.49	124.74	119.80
2	8-B	671	THR	CA-CB-CG2	-5.49	104.71	112.40
3	8-D	110	ASP	CB-CG-OD1	5.49	123.24	118.30
3	9-D	307	SER	N-CA-CB	5.49	118.74	110.50
2	4-B	609	ASP	N-CA-C	-5.49	96.18	111.00
3	5-D	285	ALA	N-CA-CB	5.49	117.78	110.10
2	6-B	421	TRP	CD2-CE2-CZ2	-5.49	115.71	122.30
1	10-A	90	ILE	CA-CB-CG2	-5.49	99.92	110.90
2	10-B	453	TYR	CZ-CE2-CD2	-5.49	114.86	119.80
1	1-A	568	TYR	N-CA-C	-5.49	96.19	111.00
2	2-B	271	LEU	CB-CG-CD2	5.49	120.33	111.00
3	7-C	216	VAL	CA-CB-CG2	5.49	119.13	110.90
3	9-D	278	ASP	CB-CG-OD2	-5.49	113.36	118.30
2	3-B	489	MET	O-C-N	5.49	131.48	122.70
3	4-C	133	PHE	CB-CG-CD2	-5.49	116.96	120.80
1	6-A	358	ARG	N-CA-CB	5.49	120.47	110.60
2	8-B	643	GLN	CA-CB-CG	5.49	125.47	113.40
1	10-A	588	TYR	CB-CG-CD1	-5.49	117.71	121.00
3	2-D	407	TYR	CB-CG-CD1	-5.48	117.71	121.00
3	4-D	61	LYS	CA-CB-CG	5.48	125.46	113.40
1	5-A	282	MET	CG-SD-CE	-5.48	91.43	100.20
2	6-B	518	GLU	CB-CA-C	-5.48	99.44	110.40
3	7-C	169	THR	CA-CB-CG2	-5.48	104.73	112.40
3	7-D	236	SER	N-CA-CB	5.48	118.72	110.50
2	8-B	533	ARG	CD-NE-CZ	-5.48	115.93	123.60
3	4-D	70	ASP	N-CA-CB	5.48	120.46	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	7-C	341	ARG	NE-CZ-NH2	-5.48	117.56	120.30
3	8-D	405	ASN	CB-CG-OD1	-5.48	110.64	121.60
2	1-B	288	TYR	CB-CG-CD1	-5.48	117.71	121.00
1	2-A	302	TYR	CG-CD1-CE1	-5.48	116.92	121.30
1	3-A	143	ARG	NE-CZ-NH1	5.48	123.04	120.30
3	3-C	77	ALA	CB-CA-C	-5.48	101.88	110.10
1	4-A	358	ARG	O-C-N	5.48	131.46	122.70
3	4-D	246	SER	N-CA-CB	5.48	118.72	110.50
1	5-A	671	ALA	N-CA-CB	5.48	117.77	110.10
2	1-B	317	ASN	CA-CB-CG	-5.47	101.36	113.40
3	4-D	249	TYR	CB-CG-CD2	-5.47	117.72	121.00
1	5-A	297	GLN	N-CA-CB	5.47	120.46	110.60
1	5-A	680	LEU	O-C-N	-5.47	113.94	122.70
3	2-D	157	ALA	N-CA-CB	5.47	117.76	110.10
2	9-B	515	VAL	CA-CB-CG2	5.47	119.11	110.90
3	10-C	139	LEU	CB-CA-C	-5.47	99.81	110.20
3	1-C	445	TYR	CB-CG-CD2	-5.47	117.72	121.00
1	4-A	612	TRP	CG-CD2-CE3	-5.47	128.98	133.90
1	5-A	380	ASP	CB-CA-C	-5.47	99.46	110.40
1	7-A	285	GLU	O-C-N	5.47	131.45	122.70
1	7-A	646	TYR	CB-CG-CD2	5.47	124.28	121.00
2	9-B	187	TYR	CD1-CE1-CZ	-5.47	114.88	119.80
3	1-D	93	TRP	CG-CD2-CE3	-5.47	128.98	133.90
3	1-D	118	ASP	CB-CG-OD1	5.47	123.22	118.30
1	5-A	151	LEU	N-CA-CB	5.47	121.34	110.40
3	7-C	170	TYR	N-CA-C	-5.47	96.24	111.00
1	8-A	155	VAL	CA-CB-CG2	-5.47	102.70	110.90
2	4-B	659	GLU	OE1-CD-OE2	-5.47	116.74	123.30
3	1-D	55	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	7-A	609	THR	N-CA-C	5.46	125.75	111.00
2	10-B	288	TYR	CZ-CE2-CD2	5.46	124.72	119.80
3	3-C	217	PHE	CG-CD1-CE1	5.46	126.81	120.80
1	5-A	467	LEU	CB-CG-CD1	-5.46	101.72	111.00
3	6-D	190	ALA	CB-CA-C	-5.46	101.91	110.10
3	7-C	365	LEU	N-CA-C	-5.46	96.25	111.00
3	1-D	80	GLU	CG-CD-OE1	-5.46	107.38	118.30
2	2-B	589	PHE	CD1-CE1-CZ	5.46	126.65	120.10
3	2-C	84	ARG	NE-CZ-NH1	-5.46	117.57	120.30
3	4-D	76	ILE	CA-CB-CG1	5.46	121.38	111.00
3	10-C	170	TYR	CG-CD2-CE2	5.46	125.67	121.30
2	2-B	349	TRP	CA-CB-CG	5.46	124.07	113.70
2	3-B	612	ARG	CD-NE-CZ	5.46	131.24	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3-C	299	LEU	O-C-N	-5.46	113.97	122.70
1	7-A	623	ARG	CD-NE-CZ	-5.46	115.96	123.60
1	8-A	91	GLU	CA-CB-CG	5.46	125.41	113.40
3	9-D	2	GLY	C-N-CA	5.46	133.76	122.30
1	4-A	155	VAL	CA-CB-CG2	5.46	119.08	110.90
2	4-B	471	ARG	CA-C-O	5.46	131.56	120.10
3	4-C	179	GLU	OE1-CD-OE2	-5.46	116.75	123.30
2	5-B	198	ALA	N-CA-CB	5.46	117.74	110.10
1	9-A	611	SER	N-CA-CB	-5.46	102.32	110.50
3	5-C	301	PRO	N-CA-C	-5.45	97.92	112.10
1	9-A	713	MET	N-CA-CB	5.45	120.42	110.60
2	2-B	421	TRP	CD1-CG-CD2	5.45	110.66	106.30
3	10-D	124	ASP	CB-CG-OD1	5.45	123.21	118.30
3	1-D	427	ARG	NE-CZ-NH1	-5.45	117.58	120.30
2	5-B	846	ARG	NE-CZ-NH2	5.45	123.02	120.30
3	5-C	248	MET	CA-CB-CG	5.45	122.56	113.30
1	7-A	582	TYR	CD1-CE1-CZ	5.45	124.70	119.80
2	8-B	668	LEU	CB-CG-CD2	5.45	120.26	111.00
1	9-A	167	ASN	CA-CB-CG	-5.45	101.42	113.40
3	3-C	48	ASP	CB-CG-OD2	-5.45	113.40	118.30
3	4-D	319	TYR	CG-CD2-CE2	5.45	125.66	121.30
3	5-C	41	ASP	CB-CG-OD2	5.45	123.20	118.30
3	5-D	314	THR	CA-CB-OG1	5.45	120.44	109.00
3	7-C	443	ASP	CB-CA-C	-5.45	99.51	110.40
3	9-D	167	LEU	N-CA-C	-5.45	96.30	111.00
3	3-D	87	PHE	CD1-CG-CD2	-5.44	111.22	118.30
2	10-B	593	PHE	CZ-CE2-CD2	5.44	126.63	120.10
3	2-D	321	THR	CA-CB-CG2	-5.44	104.78	112.40
3	4-D	93	TRP	CA-CB-CG	5.44	124.04	113.70
3	2-C	333	ARG	NE-CZ-NH2	-5.44	117.58	120.30
2	3-B	385	PHE	CB-CG-CD2	-5.44	116.99	120.80
3	6-C	367	PRO	O-C-N	5.44	131.40	122.70
1	2-A	198	ARG	NE-CZ-NH2	-5.44	117.58	120.30
3	6-C	83	PHE	CB-CG-CD1	-5.44	116.99	120.80
3	6-D	124	ASP	CB-CG-OD2	-5.44	113.41	118.30
2	7-B	587	PHE	CB-CG-CD1	5.44	124.61	120.80
1	9-A	381	PHE	CB-CG-CD1	5.44	124.61	120.80
3	9-C	440	ALA	O-C-N	5.44	131.40	122.70
1	4-A	568	TYR	CB-CG-CD2	5.44	124.26	121.00
1	2-A	400	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	4-A	399	SER	CB-CA-C	-5.43	99.77	110.10
2	5-B	589	PHE	CB-CG-CD2	-5.43	117.00	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	7-B	201	PRO	N-CA-CB	5.43	109.82	103.30
2	7-B	300	PHE	CB-CG-CD2	5.43	124.60	120.80
3	2-C	145	GLY	CA-C-N	-5.43	105.25	117.20
2	3-B	300	PHE	CG-CD1-CE1	5.43	126.78	120.80
3	6-D	347	TRP	CH2-CZ2-CE2	5.43	122.83	117.40
1	7-A	770	ASN	N-CA-CB	5.43	120.38	110.60
2	8-B	334	LEU	CB-CG-CD1	5.43	120.23	111.00
1	9-A	706	PHE	CB-CG-CD2	-5.43	117.00	120.80
3	9-D	430	VAL	CA-CB-CG1	5.43	119.05	110.90
3	5-D	176	ARG	NE-CZ-NH2	-5.43	117.58	120.30
3	6-C	161	ARG	NE-CZ-NH1	5.43	123.02	120.30
2	1-B	394	ILE	N-CA-C	-5.43	96.34	111.00
3	1-D	165	LYS	N-CA-CB	5.43	120.38	110.60
1	4-A	126	TRP	CA-CB-CG	5.43	124.02	113.70
2	4-B	412	LEU	CB-CG-CD1	5.43	120.23	111.00
2	5-B	828	ALA	N-CA-CB	5.43	117.70	110.10
1	6-A	714	ARG	NH1-CZ-NH2	5.43	125.37	119.40
1	1-A	452	ASN	CB-CG-OD1	-5.43	110.74	121.60
2	4-B	734	ASN	CB-CG-OD1	-5.43	110.74	121.60
3	6-D	252	MET	N-CA-CB	5.43	120.37	110.60
2	7-B	578	PHE	CB-CG-CD1	-5.43	117.00	120.80
3	4-C	315	TYR	CD1-CG-CD2	-5.43	111.93	117.90
3	5-C	142	VAL	CA-CB-CG1	-5.43	102.76	110.90
1	10-A	161	ASP	N-CA-CB	5.43	120.37	110.60
1	1-A	126	TRP	CZ3-CH2-CZ2	-5.42	115.09	121.60
3	1-D	361	PRO	N-CD-CG	5.42	111.34	103.20
1	2-A	474	PRO	CA-N-CD	-5.42	103.91	111.50
3	5-C	118	ASP	N-CA-CB	5.42	120.36	110.60
2	6-B	758	TYR	CB-CG-CD1	-5.42	117.75	121.00
1	8-A	116	TYR	CA-CB-CG	5.42	123.71	113.40
1	8-A	792	ASP	CB-CG-OD1	-5.42	113.42	118.30
2	9-B	294	LEU	CB-CG-CD1	5.42	120.22	111.00
3	9-C	387	PHE	N-CA-CB	5.42	120.36	110.60
2	2-B	249	MET	CG-SD-CE	-5.42	91.52	100.20
1	10-A	587	ARG	NE-CZ-NH1	5.42	123.01	120.30
2	10-B	740	LEU	CB-CG-CD2	-5.42	101.78	111.00
2	10-B	765	LEU	CB-CA-C	-5.42	99.90	110.20
1	1-A	400	ARG	CD-NE-CZ	-5.42	116.01	123.60
3	2-C	150	LEU	CB-CG-CD1	-5.42	101.78	111.00
3	6-D	56	GLU	CB-CG-CD	-5.42	99.56	114.20
1	9-A	605	ASP	CB-CG-OD2	-5.42	113.42	118.30
3	4-C	110	ASP	CB-CG-OD2	5.42	123.18	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	5-D	344	PHE	CA-C-O	-5.42	108.72	120.10
1	6-A	99	ASP	N-CA-C	5.42	125.63	111.00
1	7-A	395	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	10-A	320	TRP	CB-CG-CD2	-5.42	119.56	126.60
2	1-B	431	VAL	CA-CB-CG2	-5.42	102.78	110.90
1	5-A	73	THR	OG1-CB-CG2	-5.42	97.54	110.00
3	7-C	4	GLU	N-CA-CB	5.42	120.35	110.60
1	6-A	161	ASP	CB-CG-OD2	-5.42	113.43	118.30
3	7-D	54	PHE	CB-CA-C	-5.42	99.57	110.40
1	10-A	190	TYR	CB-CG-CD1	5.42	124.25	121.00
2	1-B	439	ARG	NE-CZ-NH1	5.41	123.01	120.30
3	2-D	388	GLU	OE1-CD-OE2	5.41	129.79	123.30
3	9-D	367	PRO	N-CA-CB	5.41	109.80	103.30
3	2-D	114	ARG	NH1-CZ-NH2	-5.41	113.45	119.40
1	6-A	614	TYR	CB-CG-CD1	5.41	124.25	121.00
2	7-B	824	TYR	CB-CG-CD1	-5.41	117.75	121.00
3	1-C	137	GLN	N-CA-C	-5.41	96.39	111.00
1	3-A	134	VAL	CA-CB-CG1	-5.41	102.78	110.90
1	3-A	623	ARG	NE-CZ-NH1	5.41	123.00	120.30
3	3-C	127	ILE	N-CA-CB	5.41	123.24	110.80
3	3-C	397	VAL	CG1-CB-CG2	5.41	119.56	110.90
2	4-B	460	THR	CA-CB-CG2	-5.41	104.83	112.40
1	10-A	664	ARG	NE-CZ-NH1	5.41	123.00	120.30
3	10-C	85	GLY	N-CA-C	-5.41	99.57	113.10
3	10-C	311	ASN	N-CA-CB	5.41	120.34	110.60
1	1-A	77	TYR	CG-CD1-CE1	-5.41	116.97	121.30
3	1-D	113	THR	CA-CB-CG2	-5.41	104.83	112.40
2	2-B	453	TYR	CB-CG-CD1	5.41	124.25	121.00
1	1-A	272	LEU	CB-CG-CD1	5.41	120.19	111.00
2	3-B	822	ARG	NE-CZ-NH1	-5.41	117.60	120.30
3	4-C	383	VAL	CA-CB-CG1	-5.41	102.79	110.90
2	8-B	226	GLU	CG-CD-OE2	-5.41	107.49	118.30
3	9-C	216	VAL	CA-CB-CG1	-5.40	102.79	110.90
2	2-B	349	TRP	CD1-CG-CD2	-5.40	101.98	106.30
2	4-B	187	TYR	CD1-CE1-CZ	5.40	124.66	119.80
2	5-B	181	GLU	O-C-N	-5.40	114.06	122.70
3	6-C	136	PHE	CB-CG-CD2	5.40	124.58	120.80
3	6-D	300	ASP	CB-CG-OD2	-5.40	113.44	118.30
2	10-B	343	TYR	CA-CB-CG	5.40	123.67	113.40
3	2-C	271	SER	N-CA-CB	5.40	118.60	110.50
1	4-A	765	ILE	CG1-CB-CG2	-5.40	99.52	111.40
1	5-A	106	SER	N-CA-CB	5.40	118.60	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5-A	582	TYR	CG-CD1-CE1	-5.40	116.98	121.30
2	5-B	409	TYR	CG-CD2-CE2	-5.40	116.98	121.30
3	5-D	256	TYR	CG-CD1-CE1	5.40	125.62	121.30
1	6-A	611	SER	CB-CA-C	-5.40	99.84	110.10
2	7-B	256	GLU	OE1-CD-OE2	5.40	129.78	123.30
3	7-D	47	ASP	N-CA-CB	5.40	120.32	110.60
3	3-D	365	LEU	C-N-CA	5.40	135.20	121.70
2	8-B	548	LEU	C-N-CA	5.40	133.64	122.30
2	6-B	737	SER	N-CA-CB	5.40	118.59	110.50
1	9-A	90	ILE	CA-CB-CG1	5.40	121.26	111.00
3	9-C	49	ASP	CB-CA-C	-5.40	99.61	110.40
3	10-C	279	TYR	CD1-CE1-CZ	5.40	124.66	119.80
2	7-B	644	PHE	N-CA-CB	5.40	120.31	110.60
2	9-B	333	ASN	CA-CB-CG	-5.40	101.53	113.40
3	10-C	347	TRP	CB-CG-CD1	-5.40	119.98	127.00
3	6-C	319	TYR	CB-CG-CD1	-5.39	117.76	121.00
3	8-C	54	PHE	CD1-CE1-CZ	-5.39	113.63	120.10
1	9-A	767	TYR	CD1-CE1-CZ	-5.39	114.94	119.80
2	10-B	832	ASN	O-C-N	5.39	131.33	122.70
3	10-C	34	ASP	CB-CG-OD1	-5.39	113.44	118.30
3	4-C	362	TYR	CZ-CE2-CD2	-5.39	114.95	119.80
1	10-A	56	GLU	CA-CB-CG	5.39	125.26	113.40
1	6-A	374	THR	CA-CB-CG2	-5.39	104.85	112.40
3	9-D	84	ARG	NE-CZ-NH2	-5.39	117.61	120.30
3	1-D	63	THR	CA-CB-CG2	-5.39	104.86	112.40
1	3-A	345	PHE	CB-CG-CD1	5.39	124.57	120.80
2	3-B	641	PHE	CB-CG-CD1	-5.39	117.03	120.80
3	4-D	68	MET	CG-SD-CE	-5.39	91.58	100.20
3	7-D	387	PHE	CB-CG-CD1	5.39	124.57	120.80
1	3-A	439	LEU	N-CA-CB	5.39	121.17	110.40
1	7-A	445	GLU	OE1-CD-OE2	5.39	129.76	123.30
2	7-B	389	ARG	NE-CZ-NH2	5.39	122.99	120.30
2	8-B	285	ARG	NH1-CZ-NH2	5.39	125.33	119.40
1	9-A	299	PHE	CB-CG-CD1	5.39	124.57	120.80
3	1-C	136	PHE	CB-CA-C	-5.38	99.63	110.40
1	5-A	91	GLU	N-CA-CB	5.38	120.29	110.60
1	8-A	594	TYR	CB-CG-CD1	-5.38	117.77	121.00
3	1-D	16	HIS	N-CA-CB	5.38	120.29	110.60
1	2-A	794	TYR	CD1-CE1-CZ	5.38	124.64	119.80
1	8-A	420	LYS	CA-CB-CG	5.38	125.24	113.40
3	8-D	45	GLU	N-CA-CB	5.38	120.29	110.60
1	2-A	129	THR	N-CA-CB	5.38	120.52	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3-C	272	PHE	CB-CG-CD1	5.38	124.57	120.80
2	5-B	654	ASN	O-C-N	-5.38	114.09	122.70
3	5-C	143	ALA	CB-CA-C	-5.38	102.03	110.10
2	8-B	438	TYR	CD1-CE1-CZ	5.38	124.64	119.80
1	9-A	562	PHE	CB-CG-CD1	-5.38	117.03	120.80
2	9-B	593	PHE	CZ-CE2-CD2	5.38	126.56	120.10
3	10-D	243	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	1-A	190	TYR	CB-CG-CD2	-5.38	117.77	121.00
3	2-D	292	TYR	CD1-CE1-CZ	5.38	124.64	119.80
2	3-B	439	ARG	NE-CZ-NH1	5.38	122.99	120.30
3	8-D	329	ARG	N-CA-CB	5.38	120.28	110.60
1	1-A	193	TYR	CB-CA-C	-5.38	99.64	110.40
2	2-B	598	TYR	CG-CD1-CE1	-5.38	117.00	121.30
3	3-C	197	ASP	CB-CG-OD2	-5.38	113.46	118.30
3	4-D	6	ILE	N-CA-CB	5.38	123.17	110.80
2	7-B	359	TYR	CG-CD1-CE1	-5.38	117.00	121.30
2	7-B	562	TYR	CG-CD1-CE1	-5.38	117.00	121.30
1	1-A	638	HIS	CA-CB-CG	-5.38	104.46	113.60
3	1-C	373	SER	N-CA-CB	5.38	118.56	110.50
3	2-C	124	ASP	CB-CG-OD1	5.38	123.14	118.30
1	3-A	76	ARG	CD-NE-CZ	-5.38	116.07	123.60
3	4-D	131	ASP	CB-CG-OD2	5.38	123.14	118.30
1	5-A	791	PHE	CG-CD2-CE2	5.38	126.71	120.80
3	8-D	93	TRP	CA-CB-CG	5.38	123.92	113.70
3	9-D	363	LEU	CB-CG-CD1	5.38	120.14	111.00
3	10-C	403	PHE	N-CA-CB	5.38	120.28	110.60
2	4-B	419	VAL	N-CA-C	-5.38	96.49	111.00
3	8-C	271	SER	N-CA-CB	5.38	118.56	110.50
3	8-D	385	ASN	CB-CG-OD1	5.38	132.35	121.60
3	2-C	407	TYR	CD1-CG-CD2	5.37	123.81	117.90
3	3-C	162	TYR	CG-CD2-CE2	-5.37	117.00	121.30
3	3-D	133	PHE	CB-CG-CD2	-5.37	117.04	120.80
2	6-B	288	TYR	CD1-CE1-CZ	5.37	124.64	119.80
2	3-B	446	PHE	N-CA-CB	5.37	120.27	110.60
3	3-C	429	VAL	CA-CB-CG2	5.37	118.96	110.90
1	10-A	139	ALA	O-C-N	-5.37	114.11	122.70
3	1-C	109	TYR	CB-CG-CD1	-5.37	117.78	121.00
1	9-A	408	LEU	CB-CG-CD1	5.37	120.13	111.00
3	9-D	319	TYR	CB-CG-CD1	5.37	124.22	121.00
3	5-D	316	PHE	CB-CG-CD2	5.37	124.56	120.80
2	10-B	763	VAL	CA-CB-CG2	-5.37	102.85	110.90
2	7-B	633	ARG	NE-CZ-NH2	-5.37	117.62	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	10-C	218	ARG	N-CA-CB	5.37	120.26	110.60
1	1-A	768	ILE	CA-CB-CG2	5.37	121.63	110.90
3	1-C	430	VAL	CA-CB-CG1	5.37	118.95	110.90
2	3-B	510	TYR	CD1-CE1-CZ	-5.37	114.97	119.80
1	4-A	148	ASP	CB-CG-OD1	-5.37	113.47	118.30
3	10-C	416	MET	N-CA-CB	5.37	120.26	110.60
1	1-A	405	PHE	CB-CG-CD1	-5.36	117.05	120.80
3	1-C	250	SER	C-N-CA	5.36	135.11	121.70
2	9-B	772	PHE	CD1-CG-CD2	5.36	125.27	118.30
2	10-B	308	SER	N-CA-CB	5.36	118.54	110.50
1	3-A	614	TYR	CD1-CE1-CZ	5.36	124.63	119.80
3	8-D	408	ASN	CB-CA-C	-5.36	99.68	110.40
2	2-B	451	ASP	CB-CA-C	-5.36	99.68	110.40
2	3-B	311	THR	CA-CB-CG2	-5.36	104.90	112.40
3	5-D	158	LEU	CB-CG-CD2	5.36	120.11	111.00
1	7-A	190	TYR	CB-CG-CD1	5.36	124.22	121.00
3	8-D	173	PHE	CB-CG-CD2	5.36	124.55	120.80
2	1-B	284	TYR	CB-CG-CD1	5.36	124.22	121.00
3	2-C	293	ASP	CB-CG-OD1	5.36	123.12	118.30
3	4-C	41	ASP	CB-CG-OD2	-5.36	113.48	118.30
3	6-D	381	SER	N-CA-CB	5.36	118.54	110.50
3	9-D	185	TYR	CZ-CE2-CD2	5.36	124.62	119.80
2	1-B	264	TYR	CB-CG-CD2	5.36	124.21	121.00
1	2-A	321	ASP	CB-CG-OD2	-5.36	113.48	118.30
1	2-A	465	PHE	CB-CG-CD2	-5.36	117.05	120.80
1	3-A	691	ASP	O-C-N	-5.36	114.13	122.70
1	6-A	203	ARG	N-CA-CB	5.36	120.24	110.60
3	7-D	358	ARG	NH1-CZ-NH2	5.36	125.29	119.40
3	2-D	351	ALA	N-CA-CB	5.36	117.60	110.10
1	4-A	410	PHE	CB-CA-C	-5.36	99.69	110.40
1	5-A	358	ARG	NE-CZ-NH2	-5.36	117.62	120.30
2	9-B	486	SER	N-CA-CB	5.36	118.53	110.50
3	9-D	243	ARG	CB-CA-C	-5.36	99.69	110.40
2	6-B	600	TYR	CB-CG-CD2	-5.35	117.79	121.00
1	8-A	426	PHE	CB-CG-CD2	-5.35	117.05	120.80
3	8-D	72	GLU	O-C-N	-5.35	110.93	121.10
1	10-A	458	TYR	CB-CG-CD1	5.35	124.21	121.00
1	1-A	301	THR	CA-CB-CG2	-5.35	104.91	112.40
3	7-C	243	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	7-A	342	ASN	CA-CB-CG	5.35	125.17	113.40
1	1-A	289	GLN	CB-CA-C	-5.35	99.71	110.40
2	1-B	382	PRO	CA-N-CD	-5.35	104.01	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	7-B	193	LEU	C-N-CA	5.35	135.07	121.70
1	8-A	287	LEU	CB-CG-CD2	5.35	120.09	111.00
1	5-A	704	TYR	CB-CG-CD2	5.35	124.21	121.00
1	6-A	74	TYR	CD1-CE1-CZ	-5.35	114.99	119.80
1	10-A	70	LEU	N-CA-CB	5.35	121.09	110.40
3	2-D	54	PHE	CB-CG-CD2	-5.34	117.06	120.80
3	8-C	47	ASP	CB-CG-OD1	5.34	123.11	118.30
1	10-A	434	ASN	CB-CA-C	-5.34	99.71	110.40
1	2-A	108	ARG	CD-NE-CZ	-5.34	116.12	123.60
3	2-D	256	TYR	CD1-CE1-CZ	5.34	124.61	119.80
1	4-A	405	PHE	CB-CG-CD2	-5.34	117.06	120.80
1	5-A	409	PHE	CB-CG-CD2	-5.34	117.06	120.80
3	7-C	243	ARG	NE-CZ-NH1	5.34	122.97	120.30
3	7-C	310	MET	CG-SD-CE	5.34	108.75	100.20
3	7-D	411	ASP	CB-CG-OD2	5.34	123.11	118.30
3	1-D	180	VAL	N-CA-C	-5.34	96.58	111.00
3	5-C	95	ALA	N-CA-CB	5.34	117.58	110.10
3	8-D	437	TYR	N-CA-CB	5.34	120.21	110.60
3	9-D	249	TYR	CZ-CE2-CD2	5.34	124.61	119.80
3	3-C	186	ASN	CA-CB-CG	-5.34	101.66	113.40
1	5-A	465	PHE	CB-CG-CD1	5.34	124.54	120.80
3	5-D	359	ARG	CG-CD-NE	-5.34	100.59	111.80
1	8-A	257	GLU	OE1-CD-OE2	-5.34	116.89	123.30
1	10-A	575	SER	N-CA-CB	5.34	118.51	110.50
1	4-A	112	TYR	CB-CG-CD2	-5.34	117.80	121.00
3	4-C	86	PHE	CB-CA-C	-5.34	99.73	110.40
3	4-C	436	ASP	CB-CG-OD1	5.34	123.10	118.30
1	6-A	160	ARG	NE-CZ-NH2	5.34	122.97	120.30
1	7-A	337	SER	N-CA-CB	5.34	118.50	110.50
1	8-A	398	TYR	CZ-CE2-CD2	5.33	124.60	119.80
2	2-B	267	PHE	CB-CG-CD2	5.33	124.53	120.80
2	3-B	819	PHE	N-CA-CB	5.33	120.20	110.60
2	3-B	826	PHE	CZ-CE2-CD2	-5.33	113.70	120.10
2	6-B	638	ARG	CB-CG-CD	5.33	125.47	111.60
2	10-B	731	PHE	CB-CG-CD1	5.33	124.53	120.80
3	10-C	359	ARG	NH1-CZ-NH2	5.33	125.27	119.40
3	6-C	162	TYR	CD1-CE1-CZ	-5.33	115.00	119.80
3	10-C	279	TYR	CG-CD2-CE2	5.33	125.56	121.30
2	1-B	328	ARG	NE-CZ-NH2	-5.33	117.64	120.30
3	1-C	176	ARG	NE-CZ-NH1	5.33	122.96	120.30
3	4-D	272	PHE	CB-CG-CD1	-5.33	117.07	120.80
1	8-A	429	TYR	CG-CD1-CE1	-5.33	117.04	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	10-B	301	THR	N-CA-CB	5.33	120.43	110.30
2	1-B	531	SER	N-CA-C	-5.33	96.62	111.00
1	4-A	57	ALA	O-C-N	5.33	131.22	122.70
2	4-B	393	PHE	CB-CA-C	-5.33	99.75	110.40
1	8-A	612	TRP	CG-CD2-CE3	-5.33	129.11	133.90
3	9-D	192	ARG	NH1-CZ-NH2	-5.33	113.54	119.40
3	10-C	416	MET	CB-CA-C	-5.33	99.75	110.40
1	2-A	773	SER	CB-CA-C	-5.32	99.98	110.10
2	2-B	833	ASP	CA-CB-CG	-5.32	101.69	113.40
1	7-A	449	HIS	CA-CB-CG	-5.32	104.55	113.60
2	10-B	269	ASN	CB-CG-OD1	5.32	132.25	121.60
3	2-C	93	TRP	CE2-CD2-CG	5.32	111.56	107.30
2	3-B	583	TYR	CB-CA-C	-5.32	99.76	110.40
3	6-C	83	PHE	N-CA-CB	5.32	120.18	110.60
2	8-B	242	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	10-A	285	GLU	O-C-N	5.32	131.22	122.70
1	2-A	77	TYR	CD1-CE1-CZ	-5.32	115.01	119.80
3	9-D	41	ASP	CB-CG-OD1	5.32	123.09	118.30
3	9-D	211	ASN	C-N-CA	5.32	135.00	121.70
3	10-D	279	TYR	CB-CG-CD1	-5.32	117.81	121.00
3	1-C	217	PHE	CG-CD1-CE1	5.32	126.65	120.80
3	3-C	197	ASP	CB-CG-OD1	5.32	123.09	118.30
3	5-C	140	HIS	CB-CA-C	-5.32	99.76	110.40
2	9-B	840	LEU	CB-CG-CD1	5.32	120.04	111.00
3	10-D	394	PHE	CB-CG-CD1	-5.32	117.08	120.80
1	1-A	395	ASP	CB-CG-OD2	-5.32	113.52	118.30
3	3-C	87	PHE	CB-CG-CD1	-5.32	117.08	120.80
3	8-D	287	LYS	N-CA-C	-5.32	96.64	111.00
2	2-B	236	TYR	CB-CG-CD1	-5.32	117.81	121.00
1	3-A	108	ARG	NE-CZ-NH1	5.32	122.96	120.30
3	4-D	176	ARG	NE-CZ-NH2	-5.32	117.64	120.30
3	5-C	416	MET	CG-SD-CE	-5.32	91.69	100.20
3	8-C	441	GLU	O-C-N	5.32	131.20	122.70
1	10-A	642	THR	CA-CB-OG1	5.32	120.16	109.00
2	10-B	765	LEU	CB-CG-CD2	5.32	120.03	111.00
3	3-D	445	TYR	CB-CG-CD2	5.31	124.19	121.00
1	7-A	603	TRP	CE2-CD2-CG	-5.31	103.05	107.30
3	2-C	423	PHE	CB-CG-CD1	5.31	124.52	120.80
1	3-A	364	PRO	N-CA-CB	5.31	109.67	103.30
3	4-C	182	VAL	CG1-CB-CG2	5.31	119.40	110.90
1	7-A	145	PHE	CB-CG-CD1	-5.31	117.08	120.80
1	7-A	704	TYR	CG-CD1-CE1	5.31	125.55	121.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	7-C	54	PHE	CB-CG-CD2	5.31	124.52	120.80
3	9-C	428	GLU	OE1-CD-OE2	5.31	129.68	123.30
1	3-A	580	ILE	CA-CB-CG1	5.31	121.09	111.00
2	8-B	196	THR	CA-CB-CG2	-5.31	104.97	112.40
3	8-D	54	PHE	CG-CD1-CE1	-5.31	114.96	120.80
3	1-D	30	ALA	CB-CA-C	5.31	118.06	110.10
1	2-A	563	ASP	O-C-N	5.31	131.19	122.70
1	10-A	410	PHE	CB-CG-CD1	5.31	124.52	120.80
3	1-C	364	PRO	N-CD-CG	5.31	111.16	103.20
1	8-A	614	TYR	CD1-CE1-CZ	5.31	124.58	119.80
3	10-C	344	PHE	CB-CG-CD2	-5.31	117.08	120.80
3	2-C	354	VAL	N-CA-C	-5.31	96.67	111.00
3	9-C	256	TYR	CB-CG-CD1	-5.31	117.82	121.00
3	4-D	63	THR	N-CA-C	-5.30	96.68	111.00
1	6-A	684	MET	CB-CA-C	-5.30	99.79	110.40
2	7-B	538	ILE	CA-CB-CG1	5.30	121.08	111.00
3	7-D	70	ASP	CB-CG-OD2	-5.30	113.53	118.30
3	8-C	369	GLU	OE1-CD-OE2	-5.30	116.93	123.30
2	7-B	562	TYR	CA-CB-CG	-5.30	103.33	113.40
3	7-D	259	LEU	CB-CG-CD2	-5.30	101.98	111.00
1	1-A	171	ARG	NH1-CZ-NH2	5.30	125.23	119.40
2	1-B	322	HIS	C-N-CA	5.30	133.44	122.30
3	2-D	440	ALA	CB-CA-C	-5.30	102.15	110.10
1	4-A	74	TYR	CB-CG-CD2	-5.30	117.82	121.00
1	5-A	345	PHE	CB-CG-CD1	5.30	124.51	120.80
2	5-B	593	PHE	CB-CG-CD1	5.30	124.51	120.80
1	6-A	370	SER	CB-CA-C	-5.30	100.03	110.10
1	7-A	458	TYR	CB-CG-CD2	-5.30	117.82	121.00
2	8-B	349	TRP	CD1-CG-CD2	-5.30	102.06	106.30
2	9-B	278	VAL	CB-CA-C	-5.30	101.33	111.40
2	9-B	636	ILE	CA-CB-CG2	-5.30	100.30	110.90
3	4-D	109	TYR	CZ-CE2-CD2	-5.30	115.03	119.80
3	4-D	419	VAL	CA-CB-CG1	-5.30	102.95	110.90
1	5-A	695	LEU	CB-CG-CD2	5.30	120.01	111.00
2	6-B	275	GLY	C-N-CA	5.30	134.95	121.70
2	6-B	560	LEU	CB-CG-CD1	5.30	120.01	111.00
1	8-A	370	SER	N-CA-C	-5.30	96.69	111.00
2	6-B	580	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	8-A	102	PHE	CB-CG-CD2	-5.30	117.09	120.80
1	8-A	483	MET	CG-SD-CE	-5.30	91.72	100.20
3	1-D	22	TRP	CB-CG-CD2	5.30	133.49	126.60
1	2-A	151	LEU	CB-CA-C	5.30	120.26	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3-C	423	PHE	CB-CG-CD1	-5.30	117.09	120.80
3	7-D	394	PHE	CB-CG-CD1	5.30	124.51	120.80
1	10-A	136	GLN	N-CA-CB	5.30	120.14	110.60
1	3-A	100	PRO	C-N-CA	5.29	134.94	121.70
2	6-B	769	VAL	CG1-CB-CG2	-5.29	102.43	110.90
2	1-B	288	TYR	CG-CD2-CE2	-5.29	117.07	121.30
3	6-C	256	TYR	CG-CD1-CE1	5.29	125.53	121.30
3	7-D	93	TRP	NE1-CE2-CD2	5.29	112.59	107.30
1	8-A	710	ILE	CA-CB-CG2	-5.29	100.31	110.90
2	8-B	805	PHE	CA-CB-CG	5.29	126.60	113.90
3	9-C	343	LYS	N-CA-CB	5.29	120.13	110.60
1	5-A	356	VAL	CA-CB-CG1	-5.29	102.96	110.90
2	5-B	821	ASP	CB-CG-OD1	-5.29	113.54	118.30
2	3-B	295	ARG	NH1-CZ-NH2	-5.29	113.58	119.40
2	6-B	389	ARG	NE-CZ-NH1	5.29	122.94	120.30
2	6-B	441	ILE	CB-CA-C	-5.29	101.02	111.60
3	7-D	8	LEU	N-CA-C	-5.29	96.72	111.00
1	8-A	123	TYR	N-CA-CB	5.29	120.12	110.60
3	10-C	247	TYR	CZ-CE2-CD2	5.29	124.56	119.80
3	6-D	387	PHE	CG-CD2-CE2	5.29	126.62	120.80
2	10-B	505	ASP	CB-CG-OD1	5.29	123.06	118.30
2	2-B	822	ARG	CB-CA-C	-5.29	99.83	110.40
1	3-A	140	TYR	CZ-CE2-CD2	5.29	124.56	119.80
1	3-A	709	PHE	CB-CG-CD1	5.29	124.50	120.80
3	3-D	338	LEU	CB-CA-C	-5.29	100.16	110.20
2	6-B	612	ARG	NE-CZ-NH2	5.29	122.94	120.30
3	6-D	324	GLY	C-N-CA	5.29	134.91	121.70
1	10-A	558	TYR	CB-CG-CD1	-5.29	117.83	121.00
1	3-A	639	PHE	CB-CG-CD1	5.28	124.50	120.80
2	6-B	356	ARG	NE-CZ-NH1	-5.28	117.66	120.30
3	6-D	236	SER	N-CA-CB	5.28	118.43	110.50
1	3-A	393	TYR	CA-CB-CG	-5.28	103.36	113.40
1	5-A	198	ARG	NH1-CZ-NH2	-5.28	113.59	119.40
3	6-C	45	GLU	N-CA-CB	5.28	120.11	110.60
3	6-C	125	LYS	N-CA-CB	-5.28	101.09	110.60
2	8-B	299	ARG	NE-CZ-NH1	5.28	122.94	120.30
3	10-D	158	LEU	CB-CG-CD1	5.28	119.98	111.00
1	2-A	304	ASP	N-CA-C	-5.28	96.74	111.00
3	2-C	225	GLN	C-N-CA	5.28	134.90	121.70
3	2-D	248	MET	CG-SD-CE	-5.28	91.75	100.20
3	2-D	314	THR	N-CA-CB	5.28	120.33	110.30
2	3-B	207	ILE	CA-CB-CG1	5.28	121.03	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	4-B	451	ASP	CB-CA-C	-5.28	99.84	110.40
3	4-D	318	VAL	CA-CB-CG2	5.28	118.82	110.90
1	5-A	145	PHE	CG-CD2-CE2	5.28	126.61	120.80
2	8-B	289	GLU	N-CA-CB	-5.28	101.09	110.60
2	5-B	299	ARG	CD-NE-CZ	5.28	130.99	123.60
3	5-C	133	PHE	N-CA-CB	-5.28	101.10	110.60
3	7-C	318	VAL	CA-CB-CG2	5.28	118.82	110.90
2	4-B	539	ASN	C-N-CA	5.28	133.38	122.30
1	5-A	406	LEU	CB-CG-CD1	5.28	119.97	111.00
2	6-B	550	HIS	CB-CA-C	-5.28	99.84	110.40
2	6-B	569	SER	N-CA-CB	5.28	118.42	110.50
3	6-D	161	ARG	NE-CZ-NH1	5.28	122.94	120.30
2	7-B	300	PHE	CB-CG-CD1	-5.28	117.11	120.80
3	9-D	93	TRP	CE2-CD2-CG	-5.28	103.08	107.30
1	5-A	167	ASN	CA-CB-CG	-5.28	101.79	113.40
1	5-A	260	GLY	CA-C-O	-5.28	111.11	120.60
3	6-D	305	LEU	CB-CG-CD1	5.28	119.97	111.00
3	7-C	87	PHE	O-C-N	-5.28	114.26	122.70
2	8-B	558	PHE	CG-CD2-CE2	-5.28	115.00	120.80
3	10-C	429	VAL	CG1-CB-CG2	5.27	119.34	110.90
2	2-B	628	ILE	C-N-CA	5.27	134.88	121.70
2	4-B	451	ASP	CB-CG-OD2	-5.27	113.56	118.30
3	4-C	335	MET	CG-SD-CE	-5.27	91.77	100.20
2	1-B	367	ASN	N-CA-CB	5.27	120.09	110.60
3	1-D	204	PHE	CG-CD1-CE1	-5.27	115.00	120.80
3	6-C	25	LEU	N-CA-CB	5.27	120.94	110.40
3	2-C	51	LYS	N-CA-CB	5.27	120.08	110.60
2	3-B	630	LYS	C-N-CA	5.27	134.87	121.70
1	6-A	699	ILE	CA-CB-CG1	5.27	121.01	111.00
3	7-D	397	VAL	CA-CB-CG1	5.27	118.80	110.90
1	9-A	653	ASP	CB-CA-C	-5.27	99.86	110.40
2	10-B	349	TRP	CH2-CZ2-CE2	5.27	122.67	117.40
1	1-A	56	GLU	CA-CB-CG	5.27	124.99	113.40
1	1-A	137	ARG	NE-CZ-NH1	-5.27	117.67	120.30
2	1-B	563	ILE	C-N-CA	5.27	134.87	121.70
3	4-D	319	TYR	CG-CD1-CE1	-5.27	117.09	121.30
1	6-A	767	TYR	CB-CG-CD2	-5.27	117.84	121.00
3	6-C	176	ARG	O-C-N	-5.27	114.27	122.70
1	5-A	129	THR	CA-C-N	5.27	128.78	117.20
2	5-B	770	TYR	CG-CD1-CE1	-5.27	117.09	121.30
2	10-B	498	ASP	CB-CG-OD1	-5.27	113.56	118.30
3	1-D	59	ARG	NE-CZ-NH2	-5.26	117.67	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4-C	22	TRP	CE3-CZ3-CH2	-5.26	115.41	121.20
1	5-A	197	PHE	CD1-CG-CD2	5.26	125.14	118.30
1	6-A	623	ARG	NE-CZ-NH2	-5.26	117.67	120.30
2	6-B	471	ARG	C-N-CA	5.26	134.86	121.70
3	6-C	326	VAL	CB-CA-C	-5.26	101.40	111.40
1	10-A	429	TYR	CG-CD2-CE2	-5.26	117.09	121.30
2	6-B	445	PHE	CB-CG-CD1	-5.26	117.12	120.80
3	3-D	44	THR	CA-CB-CG2	5.26	119.77	112.40
1	4-A	593	GLN	CB-CA-C	-5.26	99.88	110.40
2	4-B	524	SER	N-CA-CB	5.26	118.39	110.50
1	7-A	394	VAL	CB-CA-C	-5.26	101.40	111.40
2	7-B	453	TYR	CG-CD1-CE1	-5.26	117.09	121.30
1	8-A	138	PHE	CB-CG-CD1	-5.26	117.12	120.80
2	8-B	498	ASP	CB-CG-OD1	5.26	123.03	118.30
3	4-C	246	SER	N-CA-CB	5.26	118.39	110.50
2	3-B	528	LEU	C-N-CA	5.26	134.84	121.70
1	5-A	302	TYR	CB-CG-CD2	-5.26	117.84	121.00
1	9-A	690	SER	CB-CA-C	-5.26	100.11	110.10
3	6-C	133	PHE	CG-CD2-CE2	-5.26	115.02	120.80
2	8-B	829	ASP	CB-CG-OD2	-5.26	113.57	118.30
3	8-D	55	ARG	CD-NE-CZ	-5.26	116.24	123.60
3	9-D	385	ASN	CB-CA-C	-5.26	99.89	110.40
1	10-A	279	TYR	CB-CG-CD2	-5.26	117.85	121.00
1	10-A	345	PHE	CB-CG-CD2	-5.26	117.12	120.80
3	4-D	173	PHE	CB-CG-CD1	-5.25	117.12	120.80
1	5-A	791	PHE	CB-CG-CD1	5.25	124.48	120.80
2	9-B	758	TYR	CA-CB-CG	-5.25	103.42	113.40
2	2-B	241	PHE	CG-CD1-CE1	-5.25	115.02	120.80
3	2-D	197	ASP	CB-CG-OD2	-5.25	113.57	118.30
3	4-C	114	ARG	N-CA-CB	5.25	120.06	110.60
3	4-D	413	PHE	CG-CD2-CE2	-5.25	115.02	120.80
3	5-C	319	TYR	CG-CD2-CE2	-5.25	117.10	121.30
3	5-D	47	ASP	CB-CG-OD2	-5.25	113.57	118.30
3	9-C	155	LEU	N-CA-CB	5.25	120.91	110.40
3	2-D	315	TYR	CG-CD2-CE2	-5.25	117.10	121.30
1	5-A	707	CYS	N-CA-CB	5.25	120.05	110.60
2	9-B	343	TYR	CG-CD2-CE2	-5.25	117.10	121.30
3	9-D	170	TYR	CB-CG-CD2	5.25	124.15	121.00
2	4-B	759	PRO	N-CA-CB	5.25	109.60	103.30
3	7-D	319	TYR	CD1-CE1-CZ	-5.25	115.08	119.80
1	9-A	405	PHE	CB-CA-C	-5.25	99.90	110.40
3	9-C	398	PHE	CB-CG-CD1	5.25	124.47	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	9-D	297	ASP	CB-CG-OD2	-5.25	113.58	118.30
1	1-A	465	PHE	CB-CG-CD2	-5.25	117.13	120.80
1	2-A	108	ARG	NH1-CZ-NH2	-5.25	113.63	119.40
3	2-D	318	VAL	CA-CB-CG1	5.25	118.77	110.90
2	5-B	319	PHE	CB-CG-CD1	5.25	124.47	120.80
3	5-D	162	TYR	CG-CD1-CE1	-5.25	117.10	121.30
1	4-A	593	GLN	N-CA-CB	5.25	120.04	110.60
3	7-D	295	MET	CB-CA-C	-5.25	99.91	110.40
2	9-B	826	PHE	N-CA-CB	-5.25	101.16	110.60
1	4-A	461	LEU	O-C-N	-5.24	114.31	122.70
3	4-C	389	ASN	CB-CG-OD1	5.24	132.09	121.60
3	9-D	344	PHE	N-CA-CB	5.24	120.04	110.60
2	10-B	488	PHE	CB-CG-CD2	-5.24	117.13	120.80
2	10-B	834	GLY	N-CA-C	-5.24	99.99	113.10
2	7-B	239	GLU	OE1-CD-OE2	5.24	129.59	123.30
3	8-C	437	TYR	CD1-CE1-CZ	5.24	124.52	119.80
1	9-A	413	TYR	CG-CD2-CE2	5.24	125.49	121.30
1	1-A	380	ASP	CB-CG-OD1	5.24	123.02	118.30
1	6-A	169	SER	C-N-CA	5.24	134.80	121.70
1	6-A	627	ARG	NE-CZ-NH1	-5.24	117.68	120.30
1	8-A	331	LEU	CB-CG-CD1	5.24	119.91	111.00
3	2-C	386	VAL	CA-CB-CG2	5.24	118.75	110.90
1	6-A	79	ASN	CB-CA-C	-5.24	99.93	110.40
1	9-A	585	ILE	N-CA-CB	5.24	122.84	110.80
2	9-B	187	TYR	CG-CD1-CE1	5.24	125.49	121.30
1	1-A	479	ARG	NE-CZ-NH2	-5.24	117.68	120.30
3	6-C	320	ASN	N-CA-C	-5.24	96.86	111.00
1	9-A	292	LEU	N-CA-CB	5.24	120.87	110.40
3	9-C	348	SER	N-CA-CB	-5.24	102.65	110.50
3	1-D	87	PHE	CB-CG-CD2	-5.23	117.14	120.80
1	8-A	624	ARG	NE-CZ-NH1	-5.23	117.68	120.30
3	5-C	70	ASP	CB-CG-OD1	5.23	123.01	118.30
2	6-B	243	MET	CG-SD-CE	-5.23	91.83	100.20
2	6-B	820	LYS	CA-CB-CG	5.23	124.91	113.40
1	7-A	429	TYR	CG-CD2-CE2	5.23	125.49	121.30
3	10-D	437	TYR	CB-CG-CD1	-5.23	117.86	121.00
1	1-A	602	THR	CA-CB-CG2	-5.23	105.08	112.40
3	3-C	90	ARG	NE-CZ-NH2	-5.23	117.69	120.30
3	5-D	103	ASN	CA-CB-CG	-5.23	101.90	113.40
2	1-B	338	MET	CG-SD-CE	-5.23	91.84	100.20
3	6-D	341	ARG	NE-CZ-NH1	5.23	122.91	120.30
3	10-D	52	PRO	N-CA-CB	5.23	109.57	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3-A	580	ILE	CA-CB-CG2	-5.23	100.45	110.90
3	10-D	10	ALA	N-CA-CB	5.23	117.42	110.10
1	1-A	413	TYR	CG-CD2-CE2	-5.22	117.12	121.30
1	1-A	691	ASP	C-N-CA	5.22	134.76	121.70
2	3-B	182	GLU	N-CA-CB	5.22	120.00	110.60
2	3-B	341	LEU	CB-CA-C	-5.22	100.27	110.20
1	4-A	140	TYR	CA-CB-CG	5.22	123.33	113.40
3	4-D	426	SER	N-CA-CB	5.22	118.34	110.50
1	5-A	421	HIS	O-C-N	5.22	131.06	122.70
3	5-C	275	PHE	N-CA-CB	5.22	120.00	110.60
3	5-C	277	SER	N-CA-C	-5.22	96.90	111.00
1	9-A	381	PHE	CB-CG-CD2	-5.22	117.14	120.80
3	9-D	241	SER	O-C-N	-5.22	114.34	122.70
3	9-D	279	TYR	C-N-CA	5.22	134.76	121.70
1	10-A	91	GLU	N-CA-CB	5.22	120.00	110.60
3	1-C	344	PHE	CB-CG-CD1	5.22	124.45	120.80
3	3-C	384	VAL	CA-CB-CG1	-5.22	103.07	110.90
3	3-D	90	ARG	NE-CZ-NH1	5.22	122.91	120.30
3	3-D	247	TYR	CG-CD2-CE2	-5.22	117.12	121.30
1	7-A	302	TYR	CZ-CE2-CD2	-5.22	115.10	119.80
1	7-A	633	HIS	N-CA-CB	-5.22	101.20	110.60
1	8-A	71	GLU	N-CA-CB	5.22	120.00	110.60
3	8-D	362	TYR	CG-CD2-CE2	5.22	125.47	121.30
2	9-B	425	PHE	O-C-N	5.22	131.05	122.70
1	10-A	74	TYR	CB-CG-CD1	-5.22	117.87	121.00
3	10-C	207	ALA	CB-CA-C	-5.22	102.27	110.10
2	7-B	411	PHE	CG-CD1-CE1	-5.22	115.06	120.80
1	8-A	779	LEU	CB-CA-C	-5.22	100.29	110.20
2	1-B	508	PRO	CA-N-CD	-5.22	104.20	111.50
3	1-C	217	PHE	CD1-CG-CD2	-5.22	111.52	118.30
3	6-D	83	PHE	CB-CG-CD2	5.22	124.45	120.80
3	7-D	394	PHE	CA-CB-CG	5.22	126.42	113.90
2	1-B	816	TYR	N-CA-CB	5.21	119.99	110.60
3	5-D	136	PHE	CB-CG-CD2	-5.21	117.15	120.80
2	7-B	394	ILE	N-CA-C	-5.21	96.92	111.00
3	8-C	413	PHE	CB-CA-C	-5.21	99.97	110.40
1	9-A	592	LEU	CB-CG-CD1	5.21	119.86	111.00
3	2-D	49	ASP	CB-CG-OD1	-5.21	113.61	118.30
1	10-A	426	PHE	N-CA-CB	5.21	119.98	110.60
3	10-D	247	TYR	CA-CB-CG	-5.21	103.50	113.40
2	1-B	312	PHE	CB-CG-CD2	-5.21	117.15	120.80
2	1-B	359	TYR	CD1-CE1-CZ	-5.21	115.11	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	4-B	194	ALA	N-CA-CB	5.21	117.40	110.10
1	5-A	253	GLN	OE1-CD-NE2	5.21	133.89	121.90
2	7-B	644	PHE	CB-CA-C	-5.21	99.98	110.40
3	7-C	73	PRO	N-CD-CG	5.21	111.02	103.20
3	9-D	247	TYR	CG-CD1-CE1	-5.21	117.13	121.30
1	2-A	413	TYR	CB-CG-CD1	5.21	124.13	121.00
1	7-A	286	TRP	CE2-CD2-CE3	5.21	124.95	118.70
1	8-A	595	HIS	CA-CB-CG	5.21	122.46	113.60
1	8-A	646	TYR	CB-CG-CD2	5.21	124.13	121.00
3	8-C	319	TYR	CZ-CE2-CD2	5.21	124.49	119.80
1	1-A	163	ASN	CA-CB-CG	5.21	124.86	113.40
2	1-B	670	ARG	NH1-CZ-NH2	5.21	125.13	119.40
2	2-B	729	ASN	N-CA-CB	5.21	119.98	110.60
3	2-D	247	TYR	CZ-CE2-CD2	5.21	124.49	119.80
3	4-C	116	GLN	CA-CB-CG	5.21	124.86	113.40
3	5-C	47	ASP	CB-CG-OD2	-5.21	113.61	118.30
2	7-B	411	PHE	CB-CG-CD1	-5.21	117.15	120.80
3	8-C	445	TYR	CG-CD1-CE1	-5.21	117.13	121.30
3	8-D	347	TRP	CH2-CZ2-CE2	-5.21	112.19	117.40
3	10-D	142	VAL	CG1-CB-CG2	5.21	119.23	110.90
1	3-A	414	ASP	CB-CG-OD1	5.21	122.98	118.30
3	7-D	223	ASP	CB-CG-OD1	5.21	122.98	118.30
3	10-D	267	PHE	CB-CG-CD1	5.21	124.44	120.80
3	2-D	407	TYR	CA-CB-CG	-5.21	103.51	113.40
2	5-B	835	ASP	CB-CG-OD1	-5.21	113.62	118.30
3	10-D	53	PHE	CG-CD1-CE1	-5.21	115.08	120.80
3	2-D	141	SER	CB-CA-C	-5.20	100.21	110.10
2	10-B	347	MET	CA-CB-CG	5.20	122.15	113.30
2	10-B	429	TYR	CD1-CG-CD2	5.20	123.62	117.90
2	3-B	223	LEU	CB-CA-C	-5.20	100.32	110.20
3	1-D	282	ASP	CB-CA-C	-5.20	100.00	110.40
3	3-C	69	MET	CG-SD-CE	-5.20	91.88	100.20
3	5-D	124	ASP	CB-CG-OD2	5.20	122.98	118.30
2	6-B	418	GLU	OE1-CD-OE2	-5.20	117.06	123.30
2	6-B	727	VAL	CG1-CB-CG2	5.20	119.22	110.90
1	7-A	568	TYR	CD1-CE1-CZ	-5.20	115.12	119.80
3	10-C	272	PHE	CG-CD1-CE1	-5.20	115.08	120.80
3	1-D	443	ASP	N-CA-CB	5.20	119.96	110.60
3	3-D	440	ALA	N-CA-CB	5.20	117.38	110.10
3	6-C	344	PHE	CA-C-N	5.20	131.66	117.10
1	1-A	76	ARG	NE-CZ-NH2	-5.20	117.70	120.30
2	1-B	801	LEU	CB-CA-C	-5.20	100.33	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3-D	362	TYR	CB-CG-CD1	5.20	124.12	121.00
3	7-C	111	ILE	CB-CA-C	5.20	122.00	111.60
1	2-A	397	CYS	N-CA-CB	5.20	119.95	110.60
2	3-B	264	TYR	CB-CG-CD2	5.20	124.12	121.00
2	5-B	599	PHE	CB-CG-CD2	-5.20	117.16	120.80
3	5-C	124	ASP	CB-CG-OD2	5.20	122.98	118.30
3	5-C	430	VAL	CA-CB-CG2	-5.20	103.11	110.90
1	6-A	105	PHE	CB-CG-CD1	5.20	124.44	120.80
1	7-A	77	TYR	CG-CD2-CE2	5.20	125.46	121.30
3	7-C	421	ASP	CB-CG-OD2	-5.20	113.62	118.30
2	8-B	312	PHE	CB-CG-CD1	5.20	124.44	120.80
3	9-D	427	ARG	NE-CZ-NH1	5.20	122.90	120.30
2	5-B	216	PHE	CB-CG-CD2	5.19	124.44	120.80
3	9-C	267	PHE	N-CA-C	-5.19	96.97	111.00
3	3-C	300	ASP	CB-CG-OD1	-5.19	113.63	118.30
3	6-D	413	PHE	CZ-CE2-CD2	5.19	126.33	120.10
3	7-D	101	ALA	N-CA-CB	5.19	117.37	110.10
3	8-C	162	TYR	CB-CG-CD2	-5.19	117.88	121.00
3	8-D	370	ASN	CA-CB-CG	-5.19	101.98	113.40
1	1-A	623	ARG	CA-CB-CG	5.19	124.82	113.40
2	1-B	231	TYR	CB-CG-CD2	5.19	124.11	121.00
3	1-D	124	ASP	CB-CG-OD2	-5.19	113.63	118.30
2	3-B	300	PHE	N-CA-CB	5.19	119.94	110.60
2	3-B	652	TYR	CD1-CE1-CZ	-5.19	115.13	119.80
2	3-B	829	ASP	CB-CG-OD1	-5.19	113.63	118.30
3	8-C	292	TYR	CB-CG-CD2	-5.19	117.89	121.00
2	9-B	510	TYR	N-CA-CB	5.19	119.94	110.60
3	3-D	423	PHE	CG-CD2-CE2	-5.19	115.09	120.80
1	7-A	155	VAL	CA-CB-CG2	5.19	118.68	110.90
1	8-A	256	LEU	CB-CG-CD1	5.19	119.82	111.00
1	10-A	290	GLY	CA-C-O	-5.19	111.26	120.60
2	10-B	266	ALA	CB-CA-C	-5.19	102.32	110.10
3	1-C	279	TYR	CD1-CG-CD2	5.19	123.61	117.90
3	5-C	294	VAL	CG1-CB-CG2	-5.19	102.60	110.90
1	6-A	558	TYR	CB-CG-CD1	-5.19	117.89	121.00
2	7-B	734	ASN	CB-CA-C	-5.19	100.03	110.40
3	7-D	42	SER	CB-CA-C	-5.19	100.25	110.10
1	9-A	693	ILE	CA-C-N	5.19	131.63	117.10
3	2-C	191	LEU	N-CA-CB	5.19	120.77	110.40
1	1-A	150	TYR	CB-CG-CD1	-5.18	117.89	121.00
3	1-C	436	ASP	CA-CB-CG	5.18	124.81	113.40
2	2-B	225	PHE	CG-CD2-CE2	5.18	126.50	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2-B	758	TYR	CB-CG-CD2	-5.18	117.89	121.00
3	4-D	193	ARG	NE-CZ-NH1	5.18	122.89	120.30
2	1-B	260	GLU	N-CA-CB	5.18	119.93	110.60
3	1-D	359	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	4-A	398	TYR	CB-CG-CD2	5.18	124.11	121.00
1	5-A	116	TYR	CB-CA-C	5.18	120.76	110.40
1	5-A	340	ASP	CB-CG-OD1	5.18	122.97	118.30
2	7-B	838	LEU	CB-CG-CD1	5.18	119.81	111.00
1	10-A	60	VAL	CG1-CB-CG2	5.18	119.19	110.90
2	8-B	489	MET	CB-CA-C	-5.18	100.04	110.40
1	9-A	794	TYR	CG-CD1-CE1	5.18	125.44	121.30
3	1-C	316	PHE	CG-CD1-CE1	-5.18	115.10	120.80
2	5-B	356	ARG	NH1-CZ-NH2	-5.18	113.70	119.40
3	5-D	70	ASP	N-CA-CB	5.18	119.92	110.60
2	9-B	208	GLN	N-CA-CB	5.18	119.92	110.60
2	2-B	212	LYS	N-CA-CB	5.18	119.92	110.60
2	6-B	279	SER	N-CA-CB	5.18	118.27	110.50
3	8-D	30	ALA	N-CA-CB	-5.18	102.85	110.10
3	2-D	168	THR	O-C-N	-5.18	114.42	122.70
1	3-A	771	ALA	CB-CA-C	-5.18	102.33	110.10
2	7-B	355	LEU	CB-CG-CD1	-5.18	102.20	111.00
3	10-D	441	GLU	O-C-N	-5.18	114.42	122.70
2	2-B	416	CYS	N-CA-C	-5.17	97.03	111.00
2	2-B	484	GLY	N-CA-C	-5.17	100.16	113.10
3	5-C	9	GLN	CB-CA-C	-5.17	100.05	110.40
1	10-A	78	PHE	CG-CD1-CE1	5.17	126.49	120.80
1	6-A	294	ASP	CA-CB-CG	-5.17	102.02	113.40
3	9-C	436	ASP	CB-CG-OD2	-5.17	113.64	118.30
1	3-A	266	MET	CG-SD-CE	5.17	108.48	100.20
2	3-B	194	ALA	N-CA-CB	5.17	117.34	110.10
2	5-B	482	LEU	CB-CG-CD2	5.17	119.79	111.00
3	6-D	69	MET	N-CA-CB	5.17	119.91	110.60
3	6-D	253	SER	O-C-N	5.17	130.98	122.70
1	7-A	479	ARG	CG-CD-NE	-5.17	100.94	111.80
3	7-D	316	PHE	N-CA-CB	5.17	119.91	110.60
3	8-D	99	ALA	C-N-CA	5.17	134.63	121.70
3	9-D	348	SER	CB-CA-C	-5.17	100.27	110.10
3	4-C	57	ASN	N-CA-CB	5.17	119.91	110.60
1	7-A	137	ARG	NE-CZ-NH1	5.17	122.89	120.30
3	8-D	203	VAL	CA-CB-CG1	5.17	118.66	110.90
1	9-A	154	LEU	CB-CG-CD2	-5.17	102.21	111.00
3	1-C	48	ASP	CB-CG-OD1	-5.17	113.65	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-D	94	VAL	N-CA-C	-5.17	97.04	111.00
3	3-C	78	ASP	CB-CG-OD1	5.17	122.95	118.30
2	5-B	279	SER	N-CA-CB	5.17	118.25	110.50
3	6-C	445	TYR	CD1-CE1-CZ	-5.17	115.15	119.80
1	7-A	784	GLN	CA-CB-CG	5.17	124.77	113.40
2	9-B	578	PHE	CB-CG-CD1	5.17	124.42	120.80
3	1-D	330	GLN	N-CA-CB	5.17	119.90	110.60
2	4-B	456	ILE	CA-CB-CG1	5.17	120.81	111.00
2	6-B	805	PHE	N-CA-CB	5.17	119.90	110.60
1	8-A	117	MET	CB-CA-C	-5.17	100.07	110.40
2	2-B	816	TYR	CA-CB-CG	-5.16	103.59	113.40
3	2-C	272	PHE	CG-CD1-CE1	-5.16	115.12	120.80
3	7-D	249	TYR	O-C-N	-5.16	114.44	122.70
1	10-A	700	PHE	CG-CD2-CE2	5.16	126.48	120.80
3	2-C	273	THR	N-CA-CB	5.16	120.11	110.30
1	3-A	792	ASP	CB-CG-OD2	-5.16	113.65	118.30
3	6-C	436	ASP	CB-CG-OD1	5.16	122.94	118.30
2	7-B	539	ASN	O-C-N	-5.16	114.43	123.20
3	7-C	365	LEU	CB-CG-CD1	5.16	119.77	111.00
3	8-C	321	THR	N-CA-C	-5.16	97.06	111.00
2	2-B	343	TYR	CB-CG-CD2	-5.16	117.91	121.00
1	3-A	792	ASP	CB-CG-OD1	5.16	122.94	118.30
2	3-B	470	TYR	CG-CD1-CE1	5.16	125.43	121.30
2	5-B	651	TYR	CG-CD1-CE1	-5.16	117.17	121.30
1	7-A	796	SER	N-CA-CB	5.16	118.24	110.50
2	10-B	218	SER	N-CA-CB	5.16	118.24	110.50
2	2-B	592	ARG	NE-CZ-NH2	5.16	122.88	120.30
1	5-A	77	TYR	CB-CG-CD1	5.16	124.09	121.00
2	8-B	343	TYR	CB-CG-CD1	-5.16	117.91	121.00
1	10-A	357	VAL	CA-CB-CG2	-5.16	103.17	110.90
2	1-B	589	PHE	CG-CD2-CE2	5.16	126.47	120.80
2	3-B	599	PHE	CG-CD2-CE2	-5.16	115.13	120.80
2	6-B	319	PHE	CB-CG-CD2	-5.16	117.19	120.80
1	7-A	91	GLU	N-CA-CB	5.16	119.88	110.60
3	7-D	93	TRP	CD1-NE1-CE2	-5.16	104.36	109.00
3	8-D	170	TYR	CB-CG-CD2	-5.16	117.91	121.00
3	1-C	170	TYR	CG-CD2-CE2	-5.15	117.18	121.30
3	4-D	70	ASP	N-CA-C	-5.15	97.08	111.00
3	6-C	246	SER	N-CA-CB	5.15	118.23	110.50
3	8-C	293	ASP	N-CA-CB	5.15	119.88	110.60
3	3-C	347	TRP	CD1-NE1-CE2	-5.15	104.36	109.00
3	5-D	99	ALA	C-N-CA	5.15	134.58	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	6-B	429	TYR	CB-CA-C	-5.15	100.10	110.40
3	7-C	105	TRP	CG-CD2-CE3	-5.15	129.26	133.90
3	9-D	41	ASP	CB-CG-OD2	-5.15	113.66	118.30
1	5-A	448	LYS	CA-CB-CG	5.15	124.73	113.40
3	7-C	299	LEU	CA-C-N	5.15	128.53	117.20
3	2-D	217	PHE	CB-CG-CD2	-5.15	117.20	120.80
3	3-D	72	GLU	N-CA-CB	5.15	119.87	110.60
3	1-D	45	GLU	OE1-CD-OE2	-5.15	117.12	123.30
1	5-A	787	SER	C-N-CA	5.15	134.57	121.70
2	5-B	488	PHE	CB-CG-CD1	5.15	124.40	120.80
3	5-D	294	VAL	CA-CB-CG1	5.15	118.62	110.90
1	3-A	255	ILE	N-CA-CB	5.15	122.64	110.80
2	6-B	187	TYR	CD1-CE1-CZ	-5.15	115.17	119.80
3	10-C	407	TYR	CB-CG-CD2	-5.15	117.91	121.00
3	1-D	118	ASP	N-CA-CB	5.14	119.86	110.60
3	2-C	84	ARG	NE-CZ-NH2	5.14	122.87	120.30
3	4-C	354	VAL	CA-CB-CG1	-5.14	103.18	110.90
3	4-D	417	GLN	N-CA-CB	5.14	119.86	110.60
1	8-A	710	ILE	N-CA-CB	5.14	122.63	110.80
2	1-B	470	TYR	CB-CG-CD1	5.14	124.08	121.00
1	5-A	628	ALA	N-CA-CB	5.14	117.30	110.10
3	6-C	169	THR	N-CA-CB	5.14	120.07	110.30
2	7-B	339	ILE	CA-CB-CG1	5.14	120.77	111.00
2	10-B	300	PHE	CB-CG-CD2	-5.14	117.20	120.80
1	1-A	781	ASN	N-CA-CB	5.14	119.86	110.60
3	2-D	281	HIS	N-CA-C	-5.14	97.12	111.00
2	7-B	537	VAL	CA-CB-CG2	-5.14	103.19	110.90
3	1-D	22	TRP	CB-CG-CD1	-5.14	120.32	127.00
2	3-B	468	PHE	O-C-N	-5.14	114.48	122.70
3	3-D	72	GLU	CA-C-N	5.14	131.49	117.10
1	5-A	424	GLN	N-CA-CB	5.14	119.85	110.60
2	6-B	551	GLY	C-N-CA	5.14	134.55	121.70
3	6-C	359	ARG	CD-NE-CZ	-5.14	116.41	123.60
3	7-C	321	THR	N-CA-C	-5.14	97.12	111.00
2	9-B	467	LYS	CB-CG-CD	5.14	124.97	111.60
3	10-D	163	PRO	CA-N-CD	-5.14	104.30	111.50
2	2-B	438	TYR	CZ-CE2-CD2	5.14	124.42	119.80
2	6-B	197	SER	CB-CA-C	-5.14	100.34	110.10
3	1-D	318	VAL	CG1-CB-CG2	5.14	119.12	110.90
1	3-A	104	THR	CA-CB-CG2	-5.14	105.21	112.40
1	5-A	197	PHE	CG-CD2-CE2	-5.14	115.15	120.80
3	8-D	295	MET	CG-SD-CE	-5.14	91.98	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	9-D	86	PHE	CD1-CE1-CZ	-5.14	113.94	120.10
3	10-C	182	VAL	CA-CB-CG1	-5.14	103.20	110.90
2	1-B	649	GLU	CA-CB-CG	5.13	124.70	113.40
3	1-C	340	GLN	CA-CB-CG	5.13	124.70	113.40
3	2-C	262	SER	N-CA-C	-5.13	97.14	111.00
3	2-D	377	LEU	CB-CG-CD1	5.13	119.73	111.00
3	3-C	309	ALA	CB-CA-C	5.13	117.80	110.10
1	6-A	358	ARG	CB-CA-C	-5.13	100.13	110.40
1	10-A	778	CYS	O-C-N	-5.13	114.48	122.70
1	2-A	158	LEU	CB-CG-CD2	-5.13	102.27	111.00
3	2-D	20	PHE	CB-CG-CD1	5.13	124.39	120.80
1	7-A	709	PHE	CD1-CE1-CZ	5.13	126.26	120.10
3	1-C	61	LYS	CD-CE-NZ	-5.13	99.90	111.70
3	4-D	15	ASN	CA-CB-CG	5.13	124.69	113.40
3	5-C	277	SER	N-CA-CB	5.13	118.20	110.50
3	6-C	312	ASN	CB-CA-C	-5.13	100.14	110.40
2	9-B	202	PHE	CB-CG-CD1	-5.13	117.21	120.80
1	2-A	703	VAL	CA-CB-CG2	-5.13	103.20	110.90
1	3-A	703	VAL	CB-CA-C	5.13	121.15	111.40
1	6-A	74	TYR	CG-CD1-CE1	5.13	125.40	121.30
2	7-B	504	SER	N-CA-CB	5.13	118.19	110.50
3	7-C	190	ALA	CB-CA-C	-5.13	102.41	110.10
3	7-D	6	ILE	O-C-N	5.13	130.91	122.70
2	10-B	243	MET	CA-CB-CG	5.13	122.02	113.30
1	1-A	429	TYR	CG-CD2-CE2	-5.13	117.20	121.30
3	5-D	335	MET	CA-CB-CG	5.13	122.02	113.30
1	6-A	322	THR	CA-CB-OG1	5.13	119.77	109.00
3	7-C	443	ASP	N-CA-CB	5.13	119.83	110.60
3	9-D	217	PHE	CB-CG-CD2	-5.13	117.21	120.80
2	1-B	335	PHE	CB-CG-CD2	-5.13	117.21	120.80
1	2-A	418	VAL	CA-CB-CG1	-5.13	103.21	110.90
3	3-D	385	ASN	O-C-N	5.13	130.90	122.70
2	6-B	731	PHE	CB-CG-CD2	-5.13	117.21	120.80
3	6-C	84	ARG	NH1-CZ-NH2	-5.13	113.76	119.40
1	7-A	365	THR	N-CA-CB	5.13	120.04	110.30
2	7-B	225	PHE	CB-CG-CD1	-5.13	117.21	120.80
3	3-D	133	PHE	CB-CG-CD1	5.12	124.39	120.80
3	3-D	243	ARG	NE-CZ-NH1	5.12	122.86	120.30
3	10-D	336	THR	CA-CB-CG2	-5.12	105.22	112.40
2	1-B	448	ILE	N-CA-CB	5.12	122.58	110.80
2	2-B	470	TYR	CZ-CE2-CD2	-5.12	115.19	119.80
1	3-A	776	ARG	NE-CZ-NH2	-5.12	117.74	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4-A	124	GLU	N-CA-CB	5.12	119.82	110.60
1	6-A	155	VAL	CA-CB-CG1	5.12	118.59	110.90
2	8-B	226	GLU	CG-CD-OE1	5.12	128.55	118.30
3	10-C	418	ASN	C-N-CA	5.12	134.51	121.70
3	10-D	321	THR	N-CA-CB	5.12	120.04	110.30
2	2-B	580	ARG	NE-CZ-NH2	-5.12	117.74	120.30
3	2-D	167	LEU	N-CA-CB	5.12	120.64	110.40
3	3-D	247	TYR	CA-CB-CG	-5.12	103.67	113.40
2	4-B	653	LEU	N-CA-CB	5.12	120.64	110.40
3	6-D	133	PHE	N-CA-CB	-5.12	101.38	110.60
2	7-B	285	ARG	NE-CZ-NH1	5.12	122.86	120.30
3	8-D	176	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	10-A	189	LEU	CB-CG-CD2	5.12	119.71	111.00
2	9-B	541	LEU	CB-CG-CD1	-5.12	102.30	111.00
1	10-A	400	ARG	CB-CA-C	-5.12	100.16	110.40
3	1-C	247	TYR	CD1-CE1-CZ	-5.12	115.19	119.80
1	4-A	426	PHE	CB-CG-CD1	5.12	124.38	120.80
2	4-B	562	TYR	N-CA-C	-5.12	97.18	111.00
1	6-A	171	ARG	NH1-CZ-NH2	-5.12	113.77	119.40
2	6-B	362	PHE	CB-CG-CD2	-5.12	117.22	120.80
2	7-B	337	SER	N-CA-CB	5.12	118.18	110.50
3	8-C	249	TYR	CG-CD2-CE2	-5.12	117.20	121.30
3	8-D	249	TYR	CB-CG-CD1	5.12	124.07	121.00
2	7-B	359	TYR	CB-CG-CD2	5.12	124.07	121.00
1	10-A	108	ARG	NE-CZ-NH1	-5.12	117.74	120.30
3	2-C	160	ASP	CB-CG-OD1	5.12	122.90	118.30
3	5-C	358	ARG	NE-CZ-NH1	5.12	122.86	120.30
3	6-D	172	VAL	CA-CB-CG1	-5.12	103.22	110.90
3	6-D	282	ASP	CB-CG-OD2	-5.12	113.70	118.30
3	7-D	193	ARG	NE-CZ-NH2	-5.12	117.74	120.30
3	8-C	104	SER	CB-CA-C	-5.12	100.38	110.10
2	9-B	335	PHE	CB-CG-CD2	-5.12	117.22	120.80
2	10-B	544	ARG	NE-CZ-NH2	-5.12	117.74	120.30
3	10-C	413	PHE	CB-CG-CD1	-5.12	117.22	120.80
3	1-C	173	PHE	CG-CD1-CE1	5.11	126.42	120.80
3	1-C	344	PHE	CB-CA-C	-5.11	100.17	110.40
1	3-A	554	LYS	CG-CD-CE	5.11	127.24	111.90
3	3-D	130	THR	CA-CB-CG2	5.11	119.56	112.40
3	4-D	269	SER	N-CA-CB	5.11	118.17	110.50
3	7-C	146	THR	CA-CB-OG1	5.11	119.74	109.00
3	7-D	46	ARG	NE-CZ-NH1	5.11	122.86	120.30
3	9-C	319	TYR	CA-CB-CG	5.11	123.11	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-A	126	TRP	CH2-CZ2-CE2	5.11	122.51	117.40
2	1-B	243	MET	CB-CA-C	-5.11	100.18	110.40
1	4-A	73	THR	CA-CB-OG1	5.11	119.73	109.00
2	6-B	438	TYR	CG-CD2-CE2	-5.11	117.21	121.30
2	9-B	742	ALA	CB-CA-C	-5.11	102.43	110.10
2	1-B	359	TYR	CD1-CG-CD2	5.11	123.52	117.90
3	2-D	68	MET	CG-SD-CE	-5.11	92.03	100.20
1	6-A	74	TYR	CD1-CG-CD2	-5.11	112.28	117.90
3	1-D	62	PHE	CB-CG-CD2	-5.11	117.22	120.80
3	3-D	68	MET	CG-SD-CE	-5.11	92.03	100.20
2	4-B	225	PHE	N-CA-CB	5.11	119.79	110.60
1	7-A	145	PHE	CB-CG-CD2	5.11	124.38	120.80
3	8-D	165	LYS	N-CA-CB	5.11	119.79	110.60
3	9-C	170	TYR	CZ-CE2-CD2	-5.11	115.20	119.80
2	2-B	187	TYR	CD1-CE1-CZ	-5.11	115.20	119.80
1	4-A	296	TYR	CG-CD2-CE2	-5.11	117.22	121.30
3	6-D	392	ASN	CB-CA-C	5.11	120.61	110.40
3	7-D	181	VAL	CA-CB-CG2	-5.11	103.24	110.90
3	8-C	296	LEU	CB-CG-CD1	-5.11	102.32	111.00
3	9-C	319	TYR	CB-CG-CD1	5.11	124.06	121.00
2	4-B	475	PHE	CA-CB-CG	-5.10	101.65	113.90
3	9-D	341	ARG	N-CA-CB	5.10	119.79	110.60
3	1-C	247	TYR	CG-CD1-CE1	5.10	125.38	121.30
2	2-B	641	PHE	N-CA-CB	5.10	119.78	110.60
2	2-B	757	PRO	N-CD-CG	5.10	110.85	103.20
3	2-D	117	ASP	CA-CB-CG	-5.10	102.17	113.40
3	8-C	372	VAL	N-CA-C	-5.10	97.22	111.00
2	9-B	526	ARG	NE-CZ-NH1	-5.10	117.75	120.30
3	10-C	354	VAL	N-CA-C	-5.10	97.22	111.00
3	4-C	46	ARG	NE-CZ-NH1	5.10	122.85	120.30
3	6-C	313	PRO	C-N-CA	5.10	134.45	121.70
3	1-D	300	ASP	CB-CG-OD2	-5.10	113.71	118.30
2	3-B	468	PHE	CB-CG-CD1	-5.10	117.23	120.80
1	4-A	205	THR	CA-CB-OG1	5.10	119.71	109.00
2	7-B	587	PHE	CG-CD1-CE1	5.10	126.41	120.80
3	8-C	244	PHE	CB-CG-CD1	5.10	124.37	120.80
1	10-A	299	PHE	N-CA-C	-5.10	97.23	111.00
1	1-A	709	PHE	N-CA-CB	5.10	119.77	110.60
3	1-D	279	TYR	CG-CD1-CE1	-5.10	117.22	121.30
1	4-A	127	SER	N-CA-CB	5.10	118.14	110.50
3	4-C	362	TYR	CG-CD2-CE2	5.10	125.38	121.30
2	5-B	533	ARG	NE-CZ-NH2	-5.10	117.75	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	8-C	50	THR	O-C-N	-5.10	114.54	122.70
3	10-D	258	THR	N-CA-CB	5.10	119.99	110.30
1	1-A	326	ILE	O-C-N	-5.10	114.55	122.70
1	2-A	76	ARG	NE-CZ-NH1	-5.10	117.75	120.30
2	4-B	356	ARG	O-C-N	5.10	130.85	122.70
2	9-B	390	VAL	CG1-CB-CG2	-5.10	102.75	110.90
2	10-B	772	PHE	CB-CG-CD1	5.10	124.37	120.80
1	1-A	345	PHE	CB-CG-CD1	5.09	124.37	120.80
3	1-D	86	PHE	CB-CG-CD2	-5.09	117.23	120.80
2	4-B	253	LEU	CB-CA-C	-5.09	100.52	110.20
2	5-B	340	SER	N-CA-CB	5.09	118.14	110.50
2	5-B	758	TYR	CA-C-O	-5.09	109.40	120.10
3	10-C	324	GLY	N-CA-C	-5.09	100.37	113.10
2	3-B	390	VAL	CA-CB-CG2	5.09	118.54	110.90
3	7-C	254	SER	N-CA-CB	5.09	118.14	110.50
2	5-B	470	TYR	CG-CD1-CE1	-5.09	117.23	121.30
1	7-A	670	VAL	CA-CB-CG1	-5.09	103.26	110.90
2	7-B	826	PHE	CB-CG-CD2	5.09	124.36	120.80
2	8-B	664	MET	CG-SD-CE	-5.09	92.05	100.20
1	9-A	266	MET	CA-CB-CG	5.09	121.96	113.30
1	3-A	597	ARG	NE-CZ-NH1	5.09	122.84	120.30
2	3-B	429	TYR	N-CA-CB	5.09	119.76	110.60
3	3-C	133	PHE	CG-CD2-CE2	-5.09	115.20	120.80
1	5-A	693	ILE	CA-C-N	5.09	131.35	117.10
3	5-C	259	LEU	CB-CG-CD1	5.09	119.65	111.00
2	7-B	533	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	10-A	605	ASP	CB-CG-OD2	-5.09	113.72	118.30
1	3-A	755	ASP	CB-CG-OD2	-5.09	113.72	118.30
3	3-C	358	ARG	NH1-CZ-NH2	-5.09	113.80	119.40
3	6-D	355	ASN	N-CA-C	-5.09	97.26	111.00
2	10-B	433	TYR	CG-CD1-CE1	-5.09	117.23	121.30
2	1-B	254	ILE	CB-CA-C	-5.09	101.43	111.60
1	2-A	663	TYR	CZ-CE2-CD2	-5.09	115.22	119.80
2	2-B	241	PHE	CD1-CG-CD2	5.09	124.91	118.30
3	2-C	4	GLU	O-C-N	5.09	130.84	122.70
3	6-C	68	MET	CG-SD-CE	-5.09	92.06	100.20
1	10-A	594	TYR	N-CA-CB	5.09	119.76	110.60
3	10-C	130	THR	CA-CB-CG2	-5.09	105.28	112.40
3	10-D	170	TYR	CZ-CE2-CD2	-5.09	115.22	119.80
1	5-A	647	PHE	CB-CG-CD1	5.08	124.36	120.80
1	6-A	273	ASN	CB-CG-OD1	-5.08	111.43	121.60
2	6-B	661	PHE	CB-CG-CD1	5.08	124.36	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	7-B	585	ARG	NE-CZ-NH1	5.08	122.84	120.30
2	1-B	200	PHE	CZ-CE2-CD2	-5.08	114.00	120.10
2	3-B	758	TYR	CB-CG-CD1	-5.08	117.95	121.00
3	5-C	223	ASP	CB-CG-OD2	5.08	122.88	118.30
3	6-D	16	HIS	CB-CA-C	-5.08	100.23	110.40
3	7-D	178	SER	CB-CA-C	-5.08	100.44	110.10
2	2-B	824	TYR	CB-CA-C	-5.08	100.23	110.40
3	2-C	125	LYS	O-C-N	-5.08	114.57	122.70
3	4-C	179	GLU	N-CA-CB	5.08	119.75	110.60
2	8-B	324	ASP	N-CA-CB	5.08	119.75	110.60
2	8-B	600	TYR	N-CA-CB	-5.08	101.45	110.60
2	7-B	382	PRO	N-CA-C	-5.08	98.89	112.10
3	1-D	205	ASP	CB-CG-OD1	-5.08	113.73	118.30
1	4-A	364	PRO	C-N-CA	5.08	134.40	121.70
1	8-A	684	MET	CG-SD-CE	-5.08	92.08	100.20
3	6-C	34	ASP	CB-CG-OD1	-5.08	113.73	118.30
1	8-A	398	TYR	CD1-CE1-CZ	-5.08	115.23	119.80
3	9-C	128	ASP	N-CA-CB	5.08	119.74	110.60
1	10-A	73	THR	CA-CB-CG2	-5.08	105.29	112.40
2	1-B	555	TRP	CB-CA-C	-5.08	100.25	110.40
1	4-A	394	VAL	CA-CB-CG1	-5.08	103.29	110.90
1	8-A	398	TYR	CG-CD2-CE2	-5.08	117.24	121.30
1	9-A	782	PHE	CB-CG-CD2	-5.08	117.25	120.80
1	2-A	413	TYR	C-N-CA	5.07	134.38	121.70
2	4-B	599	PHE	CB-CA-C	-5.07	100.25	110.40
3	4-D	87	PHE	N-CA-C	-5.07	97.30	111.00
3	8-C	173	PHE	CA-CB-CG	-5.07	101.72	113.90
1	1-A	157	ARG	O-C-N	-5.07	114.58	122.70
1	3-A	331	LEU	N-CA-C	5.07	124.69	111.00
3	4-C	101	ALA	N-CA-CB	5.07	117.20	110.10
2	5-B	656	ILE	CA-CB-CG1	5.07	120.63	111.00
3	5-D	279	TYR	CG-CD2-CE2	-5.07	117.24	121.30
1	7-A	434	ASN	CA-CB-CG	5.07	124.56	113.40
2	8-B	813	VAL	CA-CB-CG2	-5.07	103.29	110.90
1	10-A	762	GLN	N-CA-CB	5.07	119.73	110.60
2	10-B	223	LEU	CB-CA-C	-5.07	100.56	110.20
2	10-B	301	THR	CA-CB-CG2	-5.07	105.30	112.40
2	5-B	576	ARG	NE-CZ-NH2	-5.07	117.77	120.30
2	8-B	231	TYR	CB-CG-CD1	5.07	124.04	121.00
2	8-B	410	ILE	N-CA-CB	5.07	122.46	110.80
1	9-A	267	PHE	CB-CG-CD1	-5.07	117.25	120.80
1	9-A	380	ASP	N-CA-CB	5.07	119.72	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	9-C	6	ILE	CA-CB-CG1	5.07	120.63	111.00
3	2-D	310	MET	CA-CB-CG	5.07	121.91	113.30
1	4-A	341	LYS	CB-CA-C	-5.07	100.27	110.40
2	7-B	236	TYR	CB-CA-C	-5.07	100.26	110.40
2	7-B	598	TYR	CB-CG-CD2	-5.07	117.96	121.00
2	10-B	380	HIS	C-N-CA	5.07	134.37	121.70
3	10-D	77	ALA	N-CA-CB	5.07	117.19	110.10
3	2-D	427	ARG	NE-CZ-NH1	5.07	122.83	120.30
3	3-C	170	TYR	CA-CB-CG	-5.07	103.78	113.40
1	4-A	693	ILE	CA-C-O	-5.07	109.46	120.10
3	4-C	124	ASP	CB-CG-OD2	-5.07	113.74	118.30
1	8-A	453	ASP	CB-CG-OD2	-5.07	113.74	118.30
1	9-A	126	TRP	CD2-CE3-CZ3	-5.07	112.22	118.80
1	9-A	419	LEU	CB-CG-CD1	5.07	119.61	111.00
1	9-A	612	TRP	CB-CG-CD1	5.07	133.58	127.00
1	10-A	118	ILE	CA-CB-CG2	-5.07	100.77	110.90
2	4-B	446	PHE	CB-CG-CD1	5.06	124.34	120.80
1	8-A	665	ASN	CA-C-N	5.06	131.28	117.10
2	9-B	654	ASN	N-CA-CB	5.06	119.72	110.60
3	9-C	304	SER	N-CA-C	-5.06	97.33	111.00
1	1-A	321	ASP	CB-CG-OD2	-5.06	113.74	118.30
3	2-C	75	VAL	CA-CB-CG1	5.06	118.49	110.90
2	6-B	555	TRP	N-CA-CB	5.06	119.71	110.60
2	8-B	756	GLN	CA-C-O	-5.06	109.47	120.10
1	9-A	78	PHE	N-CA-C	-5.06	97.33	111.00
2	4-B	397	GLU	CA-CB-CG	5.06	124.53	113.40
3	6-C	54	PHE	CG-CD2-CE2	-5.06	115.23	120.80
2	3-B	583	TYR	CB-CG-CD1	-5.06	117.96	121.00
3	3-C	416	MET	C-N-CA	5.06	134.35	121.70
1	4-A	246	ALA	N-CA-CB	-5.06	103.02	110.10
3	5-C	362	TYR	N-CA-C	-5.06	97.34	111.00
3	7-C	179	GLU	CB-CA-C	5.06	120.52	110.40
1	10-A	644	MET	C-N-CA	5.06	134.35	121.70
2	1-B	591	TRP	CD1-CG-CD2	-5.06	102.25	106.30
3	1-D	71	SER	N-CA-CB	5.06	118.09	110.50
3	2-C	41	ASP	CB-CG-OD2	-5.06	113.75	118.30
3	3-D	407	TYR	CG-CD1-CE1	-5.06	117.25	121.30
1	4-A	200	ILE	CA-CB-CG2	5.06	121.01	110.90
3	5-D	324	GLY	C-N-CA	5.06	134.34	121.70
1	6-A	188	LEU	CB-CG-CD1	-5.06	102.40	111.00
1	6-A	666	PRO	N-CA-C	-5.06	98.95	112.10
3	6-D	363	LEU	CB-CG-CD1	-5.06	102.40	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	7-A	767	TYR	CA-CB-CG	-5.06	103.79	113.40
2	8-B	533	ARG	NE-CZ-NH2	-5.06	117.77	120.30
2	8-B	555	TRP	CG-CD2-CE3	-5.06	129.35	133.90
3	10-D	288	CYS	CA-CB-SG	-5.06	104.90	114.00
1	2-A	767	TYR	CB-CG-CD1	-5.06	117.97	121.00
2	5-B	356	ARG	NE-CZ-NH2	5.06	122.83	120.30
3	4-D	319	TYR	CZ-CE2-CD2	-5.05	115.25	119.80
3	6-D	73	PRO	N-CA-CB	5.05	109.37	103.30
1	7-A	358	ARG	NH1-CZ-NH2	-5.05	113.84	119.40
3	10-D	92	THR	CA-CB-CG2	-5.05	105.32	112.40
3	6-D	413	PHE	CB-CG-CD1	5.05	124.34	120.80
2	8-B	191	THR	CA-CB-OG1	5.05	119.61	109.00
1	1-A	687	ARG	N-CA-CB	5.05	119.69	110.60
3	3-C	132	ASN	N-CA-CB	5.05	119.69	110.60
3	5-C	84	ARG	CA-CB-CG	5.05	124.51	113.40
2	10-B	262	GLN	CA-C-O	5.05	130.71	120.10
3	2-D	136	PHE	CB-CG-CD2	5.05	124.33	120.80
3	2-D	288	CYS	N-CA-CB	5.05	119.69	110.60
1	4-A	128	ASP	N-CA-CB	5.05	119.69	110.60
2	5-B	297	TYR	CD1-CE1-CZ	5.05	124.34	119.80
3	5-C	58	CYS	CB-CA-C	-5.05	100.30	110.40
1	6-A	429	TYR	CG-CD2-CE2	-5.05	117.26	121.30
3	7-D	53	PHE	CB-CG-CD1	5.05	124.33	120.80
1	10-A	572	ILE	O-C-N	-5.05	114.62	122.70
3	10-D	170	TYR	CG-CD2-CE2	5.05	125.34	121.30
3	3-C	239	THR	CA-CB-CG2	-5.05	105.33	112.40
3	7-D	70	ASP	N-CA-CB	5.05	119.69	110.60
2	2-B	367	ASN	N-CA-CB	5.05	119.68	110.60
3	4-D	127	ILE	N-CA-CB	5.05	122.41	110.80
1	7-A	603	TRP	CH2-CZ2-CE2	5.05	122.45	117.40
1	10-A	199	GLU	OE1-CD-OE2	5.05	129.35	123.30
1	10-A	284	TYR	CG-CD1-CE1	-5.05	117.26	121.30
1	3-A	778	CYS	N-CA-CB	5.04	119.68	110.60
2	4-B	242	ARG	NE-CZ-NH2	5.04	122.82	120.30
2	5-B	731	PHE	N-CA-CB	5.04	119.68	110.60
1	6-A	671	ALA	CB-CA-C	-5.04	102.53	110.10
1	8-A	193	TYR	O-C-N	5.04	130.77	122.70
1	9-A	333	ARG	NE-CZ-NH1	5.04	122.82	120.30
2	9-B	555	TRP	CE2-CD2-CG	-5.04	103.26	107.30
3	2-D	387	PHE	CG-CD2-CE2	5.04	126.35	120.80
1	3-A	129	THR	CA-CB-CG2	-5.04	105.34	112.40
1	3-A	614	TYR	CB-CG-CD2	-5.04	117.97	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	4-A	116	TYR	N-CA-CB	5.04	119.68	110.60
1	4-A	277	GLN	CA-CB-CG	-5.04	102.31	113.40
3	5-D	319	TYR	CB-CA-C	-5.04	100.31	110.40
1	6-A	191	ASN	N-CA-CB	5.04	119.68	110.60
2	9-B	523	SER	O-C-N	-5.04	114.63	122.70
3	9-D	109	TYR	CA-CB-CG	-5.04	103.82	113.40
2	1-B	822	ARG	NE-CZ-NH1	5.04	122.82	120.30
3	3-D	407	TYR	CB-CG-CD2	-5.04	117.98	121.00
3	4-D	248	MET	O-C-N	5.04	130.77	122.70
1	5-A	668	LEU	CB-CA-C	-5.04	100.62	110.20
2	5-B	846	ARG	CB-CA-C	-5.04	100.32	110.40
2	7-B	289	GLU	OE1-CD-OE2	5.04	129.35	123.30
3	7-D	284	ILE	N-CA-C	-5.04	97.39	111.00
2	8-B	846	ARG	CB-CG-CD	5.04	124.71	111.60
2	9-B	416	CYS	C-N-CA	5.04	134.30	121.70
3	9-C	224	LEU	CB-CG-CD1	5.04	119.57	111.00
1	4-A	582	TYR	CB-CG-CD2	-5.04	117.98	121.00
3	8-D	175	ALA	CB-CA-C	-5.04	102.54	110.10
2	10-B	381	ILE	CA-CB-CG1	5.04	120.58	111.00
3	10-C	439	ALA	N-CA-CB	5.04	117.16	110.10
3	2-D	253	SER	CB-CA-C	-5.04	100.53	110.10
3	4-D	279	TYR	CB-CG-CD2	5.04	124.02	121.00
1	7-A	451	ARG	N-CA-CB	5.04	119.67	110.60
1	8-A	568	TYR	CB-CG-CD2	-5.04	117.98	121.00
3	2-D	255	ILE	O-C-N	5.04	130.76	122.70
1	4-A	286	TRP	CE3-CZ3-CH2	-5.04	115.66	121.20
1	6-A	293	ASN	N-CA-C	-5.04	97.40	111.00
3	9-D	176	ARG	CB-CG-CD	5.04	124.70	111.60
3	1-C	277	SER	N-CA-CB	5.04	118.05	110.50
3	1-D	272	PHE	CB-CG-CD1	5.04	124.33	120.80
3	3-C	319	TYR	CB-CG-CD2	-5.04	117.98	121.00
1	4-A	186	MET	CG-SD-CE	5.04	108.26	100.20
3	4-C	243	ARG	NE-CZ-NH1	5.04	122.82	120.30
2	8-B	583	TYR	N-CA-CB	5.04	119.66	110.60
1	10-A	288	THR	O-C-N	-5.04	114.64	122.70
3	10-C	344	PHE	CB-CA-C	5.04	120.47	110.40
3	4-D	170	TYR	CB-CG-CD2	5.03	124.02	121.00
3	5-C	219	ASN	O-C-N	-5.03	111.54	121.10
1	6-A	333	ARG	CG-CD-NE	-5.03	101.23	111.80
2	9-B	637	LEU	CB-CA-C	-5.03	100.64	110.20
3	9-C	75	VAL	CA-CB-CG2	-5.03	103.35	110.90
1	10-A	792	ASP	O-C-N	-5.03	114.65	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3-A	373	ILE	CA-CB-CG1	5.03	120.56	111.00
1	4-A	486	PHE	CB-CA-C	-5.03	100.34	110.40
3	6-C	57	ASN	C-N-CA	5.03	134.28	121.70
3	7-D	397	VAL	CA-CB-CG2	-5.03	103.35	110.90
3	5-C	243	ARG	CB-CA-C	-5.03	100.34	110.40
3	8-D	445	TYR	CZ-CE2-CD2	5.03	124.33	119.80
2	10-B	526	ARG	NE-CZ-NH1	-5.03	117.78	120.30
3	4-C	192	ARG	NE-CZ-NH1	-5.03	117.78	120.30
1	5-A	693	ILE	CA-C-O	-5.03	109.54	120.10
3	5-C	445	TYR	CZ-CE2-CD2	5.03	124.33	119.80
3	6-C	61	LYS	N-CA-CB	5.03	119.65	110.60
2	8-B	765	LEU	CB-CG-CD1	5.03	119.55	111.00
3	10-D	275	PHE	CB-CG-CD1	-5.03	117.28	120.80
1	2-A	75	ILE	CA-CB-CG1	5.03	120.55	111.00
2	2-B	225	PHE	CB-CG-CD1	5.03	124.32	120.80
2	2-B	342	TYR	CB-CG-CD2	-5.03	117.98	121.00
3	4-C	413	PHE	CB-CG-CD1	5.03	124.32	120.80
1	8-A	112	TYR	CG-CD1-CE1	5.03	125.32	121.30
2	8-B	271	LEU	CB-CG-CD2	-5.03	102.45	111.00
3	8-D	319	TYR	CB-CG-CD1	-5.03	117.98	121.00
1	9-A	429	TYR	CB-CG-CD1	5.03	124.02	121.00
1	10-A	563	ASP	CB-CG-OD2	5.03	122.82	118.30
3	10-C	363	LEU	CB-CA-C	-5.03	100.65	110.20
3	1-D	138	LEU	N-CA-CB	5.03	120.45	110.40
2	6-B	355	LEU	CB-CA-C	-5.03	100.65	110.20
1	8-A	581	LYS	CB-CA-C	-5.03	100.35	110.40
3	7-D	48	ASP	CB-CG-OD2	-5.02	113.78	118.30
2	8-B	428	LYS	N-CA-CB	5.02	119.64	110.60
1	9-A	487	ASP	CB-CG-OD1	5.02	122.82	118.30
3	2-C	95	ALA	N-CA-CB	5.02	117.13	110.10
3	5-C	375	MET	CG-SD-CE	-5.02	92.16	100.20
1	6-A	609	THR	CA-C-O	-5.02	109.55	120.10
2	6-B	824	TYR	CG-CD2-CE2	5.02	125.32	121.30
3	5-C	84	ARG	NE-CZ-NH1	5.02	122.81	120.30
3	2-D	393	THR	CA-CB-CG2	-5.02	105.37	112.40
3	6-C	396	LYS	O-C-N	5.02	130.73	122.70
1	8-A	706	PHE	CG-CD2-CE2	-5.02	115.28	120.80
2	9-B	493	ILE	N-CA-CB	5.02	122.34	110.80
1	10-A	436	LEU	CB-CG-CD1	5.02	119.53	111.00
3	3-C	83	PHE	CB-CG-CD2	-5.02	117.29	120.80
2	9-B	448	ILE	CA-CB-CG1	5.02	120.53	111.00
3	5-C	161	ARG	C-N-CA	5.02	134.24	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	3-B	411	PHE	CG-CD2-CE2	-5.01	115.28	120.80
1	4-A	604	MET	CG-SD-CE	-5.01	92.18	100.20
1	5-A	612	TRP	CE2-CD2-CG	-5.01	103.29	107.30
3	7-D	136	PHE	CB-CA-C	-5.01	100.37	110.40
1	10-A	610	PRO	N-CA-CB	5.01	109.32	103.30
1	2-A	158	LEU	CB-CG-CD1	5.01	119.52	111.00
2	6-B	222	HIS	N-CA-CB	5.01	119.62	110.60
3	6-C	217	PHE	CG-CD2-CE2	5.01	126.31	120.80
1	9-A	365	THR	N-CA-C	-5.01	97.47	111.00
1	10-A	349	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	2-A	123	TYR	N-CA-CB	5.01	119.62	110.60
1	4-A	794	TYR	CB-CG-CD2	-5.01	117.99	121.00
2	4-B	483	MET	C-N-CA	5.01	132.82	122.30
1	7-A	397	CYS	CA-CB-SG	-5.01	104.98	114.00
3	7-D	358	ARG	CB-CA-C	-5.01	100.38	110.40
2	9-B	801	LEU	CB-CG-CD2	5.01	119.52	111.00
3	10-C	21	LEU	CB-CG-CD2	5.01	119.52	111.00
3	10-C	109	TYR	CB-CG-CD2	-5.01	117.99	121.00
3	10-C	249	TYR	CB-CG-CD1	-5.01	117.99	121.00
2	3-B	403	PHE	CZ-CE2-CD2	-5.01	114.09	120.10
2	5-B	273	SER	N-CA-CB	5.01	118.01	110.50
2	5-B	608	ASN	CB-CA-C	-5.01	100.38	110.40
3	9-C	27	LYS	N-CA-CB	5.01	119.62	110.60
2	10-B	774	LYS	CB-CA-C	-5.01	100.38	110.40
3	9-C	47	ASP	CB-CG-OD1	5.01	122.81	118.30
3	10-C	205	ASP	CB-CG-OD2	-5.01	113.79	118.30
2	5-B	487	ASP	CB-CG-OD2	-5.01	113.79	118.30
3	8-C	316	PHE	N-CA-C	-5.01	97.48	111.00
3	1-D	47	ASP	CB-CG-OD1	5.00	122.81	118.30
2	3-B	420	GLN	C-N-CA	5.00	134.21	121.70
3	8-C	384	VAL	CA-CB-CG1	5.00	118.41	110.90
3	1-C	252	MET	CG-SD-CE	-5.00	92.19	100.20
3	2-C	310	MET	CA-CB-CG	-5.00	104.79	113.30
2	3-B	555	TRP	NE1-CE2-CZ2	5.00	135.90	130.40
1	4-A	393	TYR	CA-CB-CG	-5.00	103.89	113.40
1	6-A	562	PHE	CD1-CG-CD2	-5.00	111.80	118.30
3	6-C	168	THR	CA-CB-CG2	-5.00	105.39	112.40
2	7-B	555	TRP	CB-CG-CD2	5.00	133.11	126.60
1	8-A	612	TRP	CD1-CG-CD2	-5.00	102.30	106.30
1	9-A	100	PRO	N-CA-CB	5.00	109.30	103.30
1	3-A	413	TYR	CD1-CG-CD2	-5.00	112.40	117.90
3	4-D	437	TYR	CB-CG-CD2	5.00	124.00	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6-A	393	TYR	CB-CG-CD2	-5.00	118.00	121.00
1	6-A	597	ARG	CD-NE-CZ	5.00	130.60	123.60
1	9-A	92	PHE	CB-CA-C	-5.00	100.40	110.40
3	9-D	390	ALA	N-CA-CB	5.00	117.10	110.10

There are no chirality outliers.

All (717) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	112	TYR	Sidechain
1	1-A	116	TYR	Sidechain
1	1-A	123	TYR	Sidechain
1	1-A	157	ARG	Sidechain
1	1-A	183	ASN	Mainchain
1	1-A	299	PHE	Sidechain
1	1-A	393	TYR	Sidechain
1	1-A	413	TYR	Sidechain
1	1-A	426	PHE	Sidechain
1	1-A	429	TYR	Sidechain
1	1-A	451	ARG	Sidechain
1	1-A	469	ARG	Sidechain
1	1-A	562	PHE	Sidechain
1	1-A	587	ARG	Sidechain
1	1-A	588	TYR	Sidechain
1	1-A	594	TYR	Sidechain
1	1-A	627	ARG	Sidechain
1	1-A	646	TYR	Sidechain
1	1-A	664	ARG	Sidechain
1	1-A	665	ASN	Mainchain
1	1-A	706	PHE	Sidechain
1	1-A	767	TYR	Sidechain
1	1-A	77	TYR	Sidechain
1	1-A	78	PHE	Sidechain
1	1-A	794	TYR	Sidechain
2	1-B	200	PHE	Sidechain
2	1-B	204	HIS	Sidechain
2	1-B	225	PHE	Sidechain
2	1-B	231	TYR	Sidechain
2	1-B	285	ARG	Sidechain
2	1-B	297	TYR	Sidechain
2	1-B	299	ARG	Sidechain
2	1-B	328	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	1-B	345	TYR	Sidechain
2	1-B	393	PHE	Sidechain
2	1-B	430	HIS	Sidechain
2	1-B	433	TYR	Sidechain
2	1-B	438	TYR	Sidechain
2	1-B	446	PHE	Sidechain
2	1-B	459	HIS	Sidechain
2	1-B	565	TYR	Sidechain
2	1-B	583	TYR	Sidechain
2	1-B	585	ARG	Sidechain
2	1-B	587	PHE	Sidechain
2	1-B	598	TYR	Sidechain
2	1-B	599	PHE	Sidechain
2	1-B	612	ARG	Sidechain
2	1-B	651	TYR	Sidechain
2	1-B	652	TYR	Sidechain
2	1-B	741	PHE	Sidechain
2	1-B	770	TYR	Sidechain
2	1-B	816	TYR	Sidechain
3	1-C	109	TYR	Sidechain
3	1-C	185	TYR	Sidechain
3	1-C	20	PHE	Sidechain
3	1-C	204	PHE	Sidechain
3	1-C	218	ARG	Sidechain
3	1-C	247	TYR	Sidechain
3	1-C	279	TYR	Sidechain
3	1-C	292	TYR	Sidechain
3	1-C	315	TYR	Sidechain
3	1-C	319	TYR	Sidechain
3	1-C	362	TYR	Sidechain
3	1-C	374	GLY	Mainchain
3	1-C	387	PHE	Sidechain
3	1-C	53	PHE	Sidechain
3	1-C	84	ARG	Sidechain
3	1-C	90	ARG	Sidechain
3	1-D	170	TYR	Sidechain
3	1-D	182	VAL	Mainchain
3	1-D	185	TYR	Sidechain
3	1-D	204	PHE	Sidechain
3	1-D	205	ASP	Mainchain
3	1-D	249	TYR	Sidechain
3	1-D	315	TYR	Sidechain

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Mol	Chain	Res	Type	Group
3	1-D	341	ARG	Sidechain
3	1-D	353	HIS	Sidechain
3	1-D	359	ARG	Sidechain
3	1-D	362	TYR	Sidechain
3	1-D	55	ARG	Sidechain
3	1-D	90	ARG	Sidechain
1	10-A	107	ARG	Sidechain
1	10-A	111	ARG	Sidechain
1	10-A	121	ARG	Sidechain
1	10-A	157	ARG	Sidechain
1	10-A	171	ARG	Sidechain
1	10-A	279	TYR	Sidechain
1	10-A	296	TYR	Sidechain
1	10-A	302	TYR	Sidechain
1	10-A	334	ASP	Mainchain
1	10-A	349	ARG	Sidechain
1	10-A	393	TYR	Sidechain
1	10-A	429	TYR	Sidechain
1	10-A	465	PHE	Sidechain
1	10-A	469	ARG	Sidechain
1	10-A	594	TYR	Sidechain
1	10-A	614	TYR	Sidechain
1	10-A	646	TYR	Sidechain
1	10-A	663	TYR	Sidechain
1	10-A	706	PHE	Sidechain
2	10-B	222	HIS	Sidechain
2	10-B	231	TYR	Sidechain
2	10-B	285	ARG	Sidechain
2	10-B	288	TYR	Sidechain
2	10-B	293	ARG	Sidechain
2	10-B	343	TYR	Sidechain
2	10-B	363	PHE	Sidechain
2	10-B	389	ARG	Sidechain
2	10-B	411	PHE	Sidechain
2	10-B	429	TYR	Sidechain
2	10-B	459	HIS	Sidechain
2	10-B	470	TYR	Sidechain
2	10-B	510	TYR	Sidechain
2	10-B	558	PHE	Mainchain
2	10-B	562	TYR	Sidechain
2	10-B	580	ARG	Sidechain
2	10-B	599	PHE	Sidechain

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Mol	Chain	Res	Type	Group
2	10-B	600	TYR	Sidechain
2	10-B	651	TYR	Sidechain
2	10-B	661	PHE	Sidechain
2	10-B	666	ARG	Sidechain
2	10-B	728	HIS	Sidechain
2	10-B	770	TYR	Sidechain
2	10-B	776	TYR	Sidechain
2	10-B	819	PHE	Sidechain
3	10-C	109	TYR	Sidechain
3	10-C	161	ARG	Sidechain
3	10-C	185	TYR	Sidechain
3	10-C	192	ARG	Sidechain
3	10-C	218	ARG	Sidechain
3	10-C	249	TYR	Sidechain
3	10-C	256	TYR	Sidechain
3	10-C	329	ARG	Sidechain
3	10-C	362	TYR	Sidechain
3	10-C	394	PHE	Sidechain
3	10-C	398	PHE	Sidechain
3	10-C	423	PHE	Sidechain
3	10-C	55	ARG	Sidechain
3	10-D	114	ARG	Sidechain
3	10-D	192	ARG	Sidechain
3	10-D	193	ARG	Sidechain
3	10-D	218	ARG	Sidechain
3	10-D	279	TYR	Sidechain
3	10-D	292	TYR	Sidechain
3	10-D	319	TYR	Sidechain
3	10-D	423	PHE	Sidechain
3	10-D	59	ARG	Sidechain
3	10-D	65	ARG	Sidechain
1	2-A	111	ARG	Sidechain
1	2-A	116	TYR	Sidechain
1	2-A	150	TYR	Sidechain
1	2-A	324	TYR	Sidechain
1	2-A	325	PHE	Sidechain
1	2-A	349	ARG	Sidechain
1	2-A	450	TYR	Sidechain
1	2-A	479	ARG	Sidechain
1	2-A	576	ARG	Sidechain
1	2-A	587	ARG	Sidechain
1	2-A	594	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	2-A	614	TYR	Sidechain
1	2-A	623	ARG	Sidechain
1	2-A	624	ARG	Sidechain
1	2-A	646	TYR	Sidechain
1	2-A	664	ARG	Sidechain
1	2-A	700	PHE	Sidechain
1	2-A	706	PHE	Sidechain
1	2-A	714	ARG	Sidechain
1	2-A	794	TYR	Sidechain
2	2-B	231	TYR	Sidechain
2	2-B	236	TYR	Sidechain
2	2-B	242	ARG	Sidechain
2	2-B	297	TYR	Sidechain
2	2-B	342	TYR	Sidechain
2	2-B	363	PHE	Sidechain
2	2-B	409	TYR	Sidechain
2	2-B	415	TYR	Sidechain
2	2-B	438	TYR	Sidechain
2	2-B	453	TYR	Sidechain
2	2-B	468	PHE	Sidechain
2	2-B	488	PHE	Sidechain
2	2-B	514	ARG	Sidechain
2	2-B	526	ARG	Sidechain
2	2-B	533	ARG	Sidechain
2	2-B	540	GLY	Mainchain
2	2-B	580	ARG	Sidechain
2	2-B	741	PHE	Sidechain
2	2-B	824	TYR	Sidechain
2	2-B	826	PHE	Sidechain
2	2-B	827	ARG	Sidechain
3	2-C	173	PHE	Sidechain
3	2-C	218	ARG	Sidechain
3	2-C	247	TYR	Sidechain
3	2-C	249	TYR	Sidechain
3	2-C	256	TYR	Sidechain
3	2-C	279	TYR	Sidechain
3	2-C	292	TYR	Sidechain
3	2-C	319	TYR	Sidechain
3	2-C	341	ARG	Sidechain
3	2-C	427	ARG	Sidechain
3	2-C	46	ARG	Sidechain
3	2-D	162	TYR	Sidechain

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Mol	Chain	Res	Type	Group
3	2-D	218	ARG	Sidechain
3	2-D	249	TYR	Sidechain
3	2-D	289	HIS	Sidechain
3	2-D	292	TYR	Sidechain
3	2-D	315	TYR	Sidechain
3	2-D	344	PHE	Sidechain
3	2-D	394	PHE	Sidechain
3	2-D	407	TYR	Sidechain
3	2-D	437	TYR	Sidechain
3	2-D	445	TYR	Sidechain
3	2-D	53	PHE	Sidechain
1	3-A	138	PHE	Sidechain
1	3-A	143	ARG	Sidechain
1	3-A	162	PHE	Sidechain
1	3-A	193	TYR	Sidechain
1	3-A	198	ARG	Sidechain
1	3-A	203	ARG	Sidechain
1	3-A	267	PHE	Sidechain
1	3-A	296	TYR	Sidechain
1	3-A	299	PHE	Sidechain
1	3-A	324	TYR	Sidechain
1	3-A	349	ARG	Sidechain
1	3-A	358	ARG	Sidechain
1	3-A	393	TYR	Sidechain
1	3-A	400	ARG	Sidechain
1	3-A	576	ARG	Sidechain
1	3-A	587	ARG	Sidechain
1	3-A	594	TYR	Sidechain
1	3-A	597	ARG	Sidechain
1	3-A	664	ARG	Sidechain
1	3-A	700	PHE	Sidechain
1	3-A	706	PHE	Sidechain
1	3-A	714	ARG	Sidechain
2	3-B	190	TYR	Sidechain
2	3-B	231	TYR	Sidechain
2	3-B	236	TYR	Sidechain
2	3-B	284	TYR	Sidechain
2	3-B	288	TYR	Sidechain
2	3-B	312	PHE	Sidechain
2	3-B	359	TYR	Sidechain
2	3-B	400	TYR	Sidechain
2	3-B	403	PHE	Sidechain

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Mol	Chain	Res	Type	Group
2	3-B	409	TYR	Sidechain
2	3-B	429	TYR	Sidechain
2	3-B	439	ARG	Sidechain
2	3-B	510	TYR	Sidechain
2	3-B	526	ARG	Sidechain
2	3-B	533	ARG	Sidechain
2	3-B	558	PHE	Sidechain
2	3-B	565	TYR	Sidechain
2	3-B	580	ARG	Sidechain
2	3-B	599	PHE	Sidechain
2	3-B	641	PHE	Sidechain
2	3-B	652	TYR	Sidechain
2	3-B	661	PHE	Sidechain
2	3-B	670	ARG	Sidechain
2	3-B	728	HIS	Sidechain
2	3-B	758	TYR	Sidechain
2	3-B	824	TYR	Sidechain
2	3-B	827	ARG	Sidechain
2	3-B	846	ARG	Sidechain
3	3-C	109	TYR	Sidechain
3	3-C	204	PHE	Sidechain
3	3-C	244	PHE	Sidechain
3	3-C	333	ARG	Sidechain
3	3-C	359	ARG	Sidechain
3	3-C	407	TYR	Sidechain
3	3-C	423	PHE	Sidechain
3	3-C	46	ARG	Sidechain
3	3-C	59	ARG	Sidechain
3	3-D	267	PHE	Sidechain
3	3-D	292	TYR	Sidechain
3	3-D	329	ARG	Sidechain
3	3-D	362	TYR	Sidechain
3	3-D	413	PHE	Sidechain
3	3-D	55	ARG	Sidechain
3	3-D	93	TRP	Mainchain
1	4-A	102	PHE	Sidechain
1	4-A	112	TYR	Sidechain
1	4-A	116	TYR	Sidechain
1	4-A	131	PHE	Sidechain
1	4-A	138	PHE	Sidechain
1	4-A	140	TYR	Sidechain
1	4-A	150	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	4-A	157	ARG	Sidechain
1	4-A	190	TYR	Sidechain
1	4-A	193	TYR	Sidechain
1	4-A	279	TYR	Sidechain
1	4-A	284	TYR	Sidechain
1	4-A	302	TYR	Sidechain
1	4-A	333	ARG	Sidechain
1	4-A	413	TYR	Sidechain
1	4-A	429	TYR	Sidechain
1	4-A	450	TYR	Sidechain
1	4-A	451	ARG	Sidechain
1	4-A	473	ASN	Mainchain,Peptide
1	4-A	568	TYR	Sidechain
1	4-A	646	TYR	Sidechain
1	4-A	657	TYR	Sidechain
1	4-A	663	TYR	Sidechain
1	4-A	92	PHE	Mainchain
2	4-B	225	PHE	Sidechain
2	4-B	231	TYR	Sidechain
2	4-B	264	TYR	Sidechain
2	4-B	284	TYR	Sidechain
2	4-B	293	ARG	Sidechain
2	4-B	299	ARG	Sidechain
2	4-B	328	ARG	Sidechain
2	4-B	342	TYR	Sidechain
2	4-B	359	TYR	Sidechain
2	4-B	403	PHE	Sidechain
2	4-B	411	PHE	Sidechain
2	4-B	415	TYR	Sidechain
2	4-B	433	TYR	Sidechain
2	4-B	439	ARG	Sidechain
2	4-B	445	PHE	Sidechain
2	4-B	468	PHE	Sidechain
2	4-B	510	TYR	Sidechain
2	4-B	565	TYR	Sidechain
2	4-B	580	ARG	Sidechain
2	4-B	592	ARG	Sidechain
2	4-B	598	TYR	Sidechain
2	4-B	600	TYR	Sidechain
2	4-B	772	PHE	Sidechain
3	4-C	109	TYR	Sidechain
3	4-C	136	PHE	Sidechain

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Mol	Chain	Res	Type	Group
3	4-C	170	TYR	Sidechain
3	4-C	185	TYR	Sidechain
3	4-C	192	ARG	Sidechain
3	4-C	218	ARG	Sidechain
3	4-C	243	ARG	Sidechain
3	4-C	249	TYR	Sidechain
3	4-C	279	TYR	Sidechain
3	4-C	319	TYR	Sidechain
3	4-C	358	ARG	Sidechain
3	4-C	407	TYR	Sidechain
3	4-C	423	PHE	Sidechain
3	4-C	427	ARG	Sidechain
3	4-C	46	ARG	Sidechain
3	4-D	176	ARG	Sidechain
3	4-D	192	ARG	Sidechain
3	4-D	193	ARG	Sidechain
3	4-D	218	ARG	Sidechain
3	4-D	267	PHE	Sidechain
3	4-D	341	ARG	Sidechain
3	4-D	344	PHE	Sidechain
3	4-D	362	TYR	Sidechain
3	4-D	413	PHE	Sidechain
3	4-D	423	PHE	Sidechain
3	4-D	445	TYR	Sidechain
3	4-D	54	PHE	Sidechain
3	4-D	65	ARG	Sidechain
3	4-D	90	ARG	Sidechain
1	5-A	105	PHE	Sidechain
1	5-A	111	ARG	Sidechain
1	5-A	112	TYR	Sidechain
1	5-A	131	PHE	Sidechain
1	5-A	144	ARG	Sidechain
1	5-A	150	TYR	Sidechain
1	5-A	162	PHE	Sidechain
1	5-A	183	ASN	Mainchain
1	5-A	204	ARG	Sidechain
1	5-A	302	TYR	Sidechain
1	5-A	349	ARG	Sidechain
1	5-A	393	TYR	Sidechain
1	5-A	398	TYR	Sidechain
1	5-A	413	TYR	Sidechain
1	5-A	450	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	5-A	451	ARG	Sidechain
1	5-A	465	PHE	Sidechain
1	5-A	568	TYR	Sidechain
1	5-A	588	TYR	Sidechain
1	5-A	597	ARG	Sidechain
1	5-A	624	ARG	Sidechain
1	5-A	647	PHE	Sidechain
1	5-A	663	TYR	Sidechain
1	5-A	665	ASN	Mainchain
1	5-A	74	TYR	Sidechain
1	5-A	77	TYR	Sidechain
1	5-A	776	ARG	Sidechain
2	5-B	288	TYR	Sidechain
2	5-B	328	ARG	Sidechain
2	5-B	359	TYR	Sidechain
2	5-B	379	TYR	Sidechain
2	5-B	385	PHE	Sidechain
2	5-B	389	ARG	Mainchain
2	5-B	409	TYR	Sidechain
2	5-B	415	TYR	Sidechain
2	5-B	510	TYR	Sidechain
2	5-B	562	TYR	Sidechain
2	5-B	565	TYR	Sidechain
2	5-B	576	ARG	Sidechain
2	5-B	580	ARG	Sidechain
2	5-B	583	TYR	Sidechain
2	5-B	598	TYR	Sidechain
2	5-B	600	TYR	Sidechain
2	5-B	612	ARG	Sidechain
2	5-B	651	TYR	Sidechain
2	5-B	742	ALA	Peptide
2	5-B	770	TYR	Sidechain
2	5-B	816	TYR	Sidechain
2	5-B	827	ARG	Sidechain
3	5-C	114	ARG	Sidechain
3	5-C	170	TYR	Sidechain
3	5-C	193	ARG	Sidechain
3	5-C	244	PHE	Sidechain
3	5-C	249	TYR	Sidechain
3	5-C	279	TYR	Sidechain
3	5-C	292	TYR	Sidechain
3	5-C	319	TYR	Sidechain

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Mol	Chain	Res	Type	Group
3	5-C	387	PHE	Sidechain
3	5-C	407	TYR	Sidechain
3	5-C	427	ARG	Sidechain
3	5-C	445	TYR	Sidechain
3	5-C	83	PHE	Sidechain
3	5-C	86	PHE	Sidechain
3	5-D	176	ARG	Sidechain
3	5-D	182	VAL	Mainchain
3	5-D	185	TYR	Sidechain
3	5-D	192	ARG	Sidechain
3	5-D	193	ARG	Sidechain
3	5-D	217	PHE	Sidechain
3	5-D	218	ARG	Sidechain
3	5-D	256	TYR	Sidechain
3	5-D	292	TYR	Sidechain
3	5-D	315	TYR	Sidechain
3	5-D	319	TYR	Sidechain
3	5-D	333	ARG	Sidechain
3	5-D	362	TYR	Sidechain
3	5-D	387	PHE	Sidechain
3	5-D	394	PHE	Sidechain
3	5-D	423	PHE	Sidechain
3	5-D	84	ARG	Sidechain
1	6-A	108	ARG	Sidechain
1	6-A	112	TYR	Sidechain
1	6-A	131	PHE	Sidechain
1	6-A	140	TYR	Sidechain
1	6-A	143	ARG	Sidechain
1	6-A	150	TYR	Sidechain
1	6-A	160	ARG	Sidechain
1	6-A	198	ARG	Sidechain
1	6-A	279	TYR	Sidechain
1	6-A	302	TYR	Sidechain
1	6-A	324	TYR	Sidechain
1	6-A	345	PHE	Sidechain
1	6-A	409	PHE	Sidechain
1	6-A	588	TYR	Sidechain
1	6-A	624	ARG	Sidechain
1	6-A	630	ARG	Sidechain
1	6-A	646	TYR	Sidechain
1	6-A	78	PHE	Sidechain
2	6-B	261	LEU	Mainchain

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Mol	Chain	Res	Type	Group
2	6-B	288	TYR	Sidechain
2	6-B	297	TYR	Sidechain
2	6-B	319	PHE	Sidechain
2	6-B	328	ARG	Sidechain
2	6-B	342	TYR	Sidechain
2	6-B	359	TYR	Sidechain
2	6-B	379	TYR	Sidechain
2	6-B	393	PHE	Sidechain
2	6-B	411	PHE	Sidechain
2	6-B	429	TYR	Sidechain
2	6-B	433	TYR	Sidechain
2	6-B	438	TYR	Sidechain
2	6-B	468	PHE	Sidechain
2	6-B	471	ARG	Sidechain
2	6-B	507	LEU	Mainchain
2	6-B	510	TYR	Sidechain
2	6-B	558	PHE	Sidechain
2	6-B	587	PHE	Sidechain
2	6-B	598	TYR	Sidechain
2	6-B	633	ARG	Sidechain
2	6-B	651	TYR	Sidechain
2	6-B	776	TYR	Sidechain
3	6-C	140	HIS	Mainchain
3	6-C	218	ARG	Sidechain
3	6-C	243	ARG	Sidechain
3	6-C	247	TYR	Sidechain
3	6-C	256	TYR	Sidechain
3	6-C	292	TYR	Sidechain
3	6-C	315	TYR	Sidechain
3	6-C	358	ARG	Sidechain
3	6-C	403	PHE	Sidechain
3	6-C	407	TYR	Sidechain
3	6-C	423	PHE	Sidechain
3	6-C	437	TYR	Sidechain
3	6-C	445	TYR	Sidechain
3	6-C	53	PHE	Sidechain
3	6-C	59	ARG	Sidechain
3	6-C	83	PHE	Sidechain
3	6-D	109	TYR	Sidechain
3	6-D	176	ARG	Sidechain
3	6-D	247	TYR	Sidechain
3	6-D	249	TYR	Sidechain

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Mol	Chain	Res	Type	Group
3	6-D	275	PHE	Sidechain
3	6-D	292	TYR	Sidechain
3	6-D	315	TYR	Sidechain
3	6-D	362	TYR	Sidechain
3	6-D	427	ARG	Sidechain
3	6-D	437	TYR	Sidechain
3	6-D	445	TYR	Sidechain
3	6-D	46	ARG	Sidechain
1	7-A	112	TYR	Sidechain
1	7-A	123	TYR	Sidechain
1	7-A	144	ARG	Sidechain
1	7-A	145	PHE	Sidechain
1	7-A	160	ARG	Sidechain
1	7-A	171	ARG	Sidechain
1	7-A	190	TYR	Sidechain
1	7-A	203	ARG	Sidechain
1	7-A	251	PHE	Sidechain
1	7-A	279	TYR	Sidechain
1	7-A	393	TYR	Sidechain
1	7-A	398	TYR	Sidechain
1	7-A	405	PHE	Sidechain
1	7-A	426	PHE	Sidechain
1	7-A	558	TYR	Sidechain
1	7-A	568	TYR	Sidechain
1	7-A	582	TYR	Sidechain
1	7-A	588	TYR	Sidechain
1	7-A	597	ARG	Sidechain
1	7-A	614	TYR	Sidechain
1	7-A	624	ARG	Sidechain
1	7-A	646	TYR	Sidechain
1	7-A	647	PHE	Sidechain
1	7-A	663	TYR	Sidechain
1	7-A	704	TYR	Sidechain
1	7-A	776	ARG	Sidechain
2	7-B	285	ARG	Sidechain
2	7-B	293	ARG	Sidechain,Mainchain
2	7-B	345	TYR	Sidechain
2	7-B	356	ARG	Sidechain
2	7-B	403	PHE	Sidechain
2	7-B	409	TYR	Sidechain
2	7-B	411	PHE	Sidechain
2	7-B	429	TYR	Sidechain

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Mol	Chain	Res	Type	Group
2	7-B	433	TYR	Sidechain
2	7-B	438	TYR	Sidechain
2	7-B	469	HIS	Sidechain
2	7-B	470	TYR	Sidechain
2	7-B	562	TYR	Sidechain
2	7-B	565	TYR	Sidechain
2	7-B	600	TYR	Sidechain
2	7-B	612	ARG	Sidechain
2	7-B	728	HIS	Sidechain
2	7-B	772	PHE	Sidechain
2	7-B	776	TYR	Sidechain
3	7-C	114	ARG	Sidechain
3	7-C	193	ARG	Sidechain
3	7-C	20	PHE	Sidechain
3	7-C	243	ARG	Sidechain
3	7-C	247	TYR	Sidechain
3	7-C	275	PHE	Sidechain
3	7-C	292	TYR	Sidechain
3	7-C	316	PHE	Mainchain
3	7-C	359	ARG	Sidechain
3	7-C	46	ARG	Sidechain
3	7-C	55	ARG	Sidechain
3	7-C	62	PHE	Sidechain
3	7-C	84	ARG	Sidechain
3	7-D	109	TYR	Sidechain
3	7-D	161	ARG	Sidechain
3	7-D	162	TYR	Sidechain
3	7-D	182	VAL	Mainchain
3	7-D	217	PHE	Sidechain
3	7-D	256	TYR	Sidechain
3	7-D	266	HIS	Sidechain
3	7-D	267	PHE	Sidechain
3	7-D	272	PHE	Sidechain
3	7-D	292	TYR	Sidechain
3	7-D	359	ARG	Sidechain
3	7-D	413	PHE	Sidechain
3	7-D	86	PHE	Sidechain
1	8-A	108	ARG	Sidechain
1	8-A	111	ARG	Sidechain
1	8-A	116	TYR	Sidechain
1	8-A	123	TYR	Sidechain
1	8-A	138	PHE	Sidechain

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Mol	Chain	Res	Type	Group
1	8-A	150	TYR	Sidechain
1	8-A	157	ARG	Sidechain
1	8-A	203	ARG	Sidechain
1	8-A	262	ARG	Sidechain
1	8-A	302	TYR	Sidechain
1	8-A	405	PHE	Sidechain
1	8-A	409	PHE	Sidechain
1	8-A	458	TYR	Sidechain
1	8-A	558	TYR	Sidechain
1	8-A	559	HIS	Sidechain
1	8-A	614	TYR	Sidechain
1	8-A	623	ARG	Sidechain
1	8-A	633	HIS	Sidechain
1	8-A	92	PHE	Sidechain
2	8-B	190	TYR	Sidechain
2	8-B	236	TYR	Sidechain
2	8-B	241	PHE	Sidechain
2	8-B	242	ARG	Sidechain
2	8-B	264	TYR	Sidechain
2	8-B	295	ARG	Sidechain
2	8-B	303	HIS	Sidechain
2	8-B	343	TYR	Sidechain
2	8-B	345	TYR	Sidechain
2	8-B	409	TYR	Sidechain
2	8-B	425	PHE	Sidechain
2	8-B	429	TYR	Sidechain
2	8-B	438	TYR	Sidechain
2	8-B	562	TYR	Sidechain
2	8-B	576	ARG	Sidechain
2	8-B	600	TYR	Sidechain
2	8-B	652	TYR	Sidechain
2	8-B	741	PHE	Sidechain
2	8-B	839	PHE	Sidechain
3	8-C	162	TYR	Sidechain
3	8-C	176	ARG	Sidechain
3	8-C	204	PHE	Sidechain
3	8-C	243	ARG	Sidechain
3	8-C	292	TYR	Sidechain
3	8-C	296	LEU	Mainchain
3	8-C	315	TYR	Sidechain
3	8-C	319	TYR	Sidechain
3	8-C	358	ARG	Sidechain

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Mol	Chain	Res	Type	Group
3	8-C	398	PHE	Sidechain
3	8-C	407	TYR	Sidechain
3	8-C	86	PHE	Sidechain
3	8-D	162	TYR	Sidechain
3	8-D	170	TYR	Sidechain
3	8-D	243	ARG	Sidechain
3	8-D	256	TYR	Sidechain
3	8-D	292	TYR	Sidechain
3	8-D	329	ARG	Sidechain
3	8-D	437	TYR	Sidechain
3	8-D	445	TYR	Sidechain
3	8-D	46	ARG	Sidechain
3	8-D	55	ARG	Sidechain
3	8-D	59	ARG	Sidechain
3	8-D	65	ARG	Sidechain
3	8-D	90	ARG	Sidechain
1	9-A	102	PHE	Sidechain
1	9-A	105	PHE	Sidechain
1	9-A	108	ARG	Sidechain
1	9-A	112	TYR	Sidechain
1	9-A	116	TYR	Sidechain
1	9-A	123	TYR	Sidechain
1	9-A	144	ARG	Sidechain
1	9-A	157	ARG	Sidechain
1	9-A	160	ARG	Sidechain
1	9-A	197	PHE	Sidechain
1	9-A	251	PHE	Sidechain
1	9-A	302	TYR	Sidechain
1	9-A	333	ARG	Sidechain
1	9-A	363	ILE	Mainchain
1	9-A	409	PHE	Sidechain
1	9-A	413	TYR	Sidechain
1	9-A	450	TYR	Sidechain
1	9-A	458	TYR	Sidechain
1	9-A	469	ARG	Sidechain
1	9-A	562	PHE	Sidechain
1	9-A	568	TYR	Sidechain
1	9-A	576	ARG	Sidechain
1	9-A	614	TYR	Sidechain
1	9-A	630	ARG	Sidechain
1	9-A	646	TYR	Sidechain
1	9-A	657	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	9-A	687	ARG	Sidechain
1	9-A	78	PHE	Mainchain
1	9-A	794	TYR	Sidechain
2	9-B	190	TYR	Sidechain
2	9-B	231	TYR	Sidechain
2	9-B	295	ARG	Sidechain
2	9-B	328	ARG	Sidechain
2	9-B	342	TYR	Sidechain
2	9-B	345	TYR	Sidechain
2	9-B	415	TYR	Sidechain
2	9-B	422	THR	Peptide
2	9-B	423	ASN	Peptide
2	9-B	424	GLU	Peptide
2	9-B	425	PHE	Peptide
2	9-B	426	SER	Peptide
2	9-B	433	TYR	Sidechain
2	9-B	470	TYR	Sidechain
2	9-B	471	ARG	Sidechain
2	9-B	488	PHE	Sidechain
2	9-B	510	TYR	Sidechain
2	9-B	526	ARG	Sidechain
2	9-B	558	PHE	Sidechain
2	9-B	578	PHE	Sidechain
2	9-B	585	ARG	Sidechain
2	9-B	599	PHE	Sidechain
2	9-B	644	PHE	Sidechain
2	9-B	651	TYR	Sidechain
2	9-B	670	ARG	Sidechain
2	9-B	758	TYR	Sidechain
2	9-B	770	TYR	Sidechain
2	9-B	778	ASN	Peptide
3	9-C	136	PHE	Sidechain
3	9-C	162	TYR	Sidechain
3	9-C	170	TYR	Sidechain
3	9-C	292	TYR	Sidechain
3	9-C	316	PHE	Sidechain
3	9-C	445	TYR	Sidechain
3	9-D	161	ARG	Sidechain
3	9-D	170	TYR	Sidechain
3	9-D	217	PHE	Sidechain
3	9-D	226	HIS	Sidechain
3	9-D	256	TYR	Sidechain

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Mol	Chain	Res	Type	Group
3	9-D	275	PHE	Sidechain
3	9-D	29	HIS	Sidechain
3	9-D	292	TYR	Sidechain
3	9-D	315	TYR	Sidechain
3	9-D	319	TYR	Sidechain
3	9-D	329	ARG	Sidechain
3	9-D	341	ARG	Sidechain
3	9-D	423	PHE	Sidechain
3	9-D	437	TYR	Sidechain
3	9-D	53	PHE	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	4831	0	4863	62	0
1	2-A	4831	0	4863	79	0
1	3-A	4831	0	4863	77	0
1	4-A	4831	0	4863	61	0
1	5-A	4831	0	4863	105	0
1	6-A	4831	0	4863	97	0
1	7-A	4831	0	4863	99	0
1	8-A	4831	0	4863	120	0
1	9-A	4831	0	4863	76	0
1	10-A	4831	0	4863	112	0
2	1-B	4701	0	4731	92	0
2	2-B	4701	0	4731	93	0
2	3-B	4701	0	4731	61	0
2	4-B	4701	0	4731	100	0
2	5-B	4701	0	4731	84	0
2	6-B	4701	0	4731	86	0
2	7-B	4701	0	4731	80	0
2	8-B	4701	0	4730	105	0
2	9-B	4701	0	4731	128	0
2	10-B	4701	0	4731	100	0
3	1-C	3485	0	3342	62	0
3	1-D	3485	0	3342	41	0
3	2-C	3485	0	3340	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	2-D	3485	0	3342	43	0
3	3-C	3485	0	3341	68	0
3	3-D	3485	0	3342	74	0
3	4-C	3485	0	3342	38	0
3	4-D	3485	0	3342	43	0
3	5-C	3485	0	3342	60	0
3	5-D	3485	0	3342	34	0
3	6-C	3485	0	3342	32	0
3	6-D	3485	0	3342	68	0
3	7-C	3485	0	3340	61	0
3	7-D	3485	0	3341	59	0
3	8-C	3485	0	3340	31	0
3	8-D	3485	0	3341	28	0
3	9-C	3485	0	3342	32	0
3	9-D	3485	0	3342	35	0
3	10-C	3485	0	3342	46	0
3	10-D	3485	0	3342	53	0
4	1-E	220	0	46	0	0
4	1-F	220	0	46	0	0
4	2-E	220	0	46	0	0
4	2-F	220	0	46	0	0
4	3-E	220	0	46	0	0
4	3-F	220	0	46	0	0
4	4-E	220	0	46	0	0
4	4-F	220	0	46	0	0
4	5-E	220	0	46	0	0
4	5-F	220	0	46	0	0
4	6-E	220	0	46	0	0
4	6-F	220	0	46	0	0
4	7-E	220	0	46	0	0
4	7-F	220	0	46	0	0
4	8-E	220	0	46	0	0
4	8-F	220	0	46	1	0
4	9-E	220	0	46	0	0
4	9-F	220	0	46	0	0
4	10-E	220	0	46	0	0
4	10-F	220	0	46	0	0
All	All	169420	0	163690	2439	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (2439) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:ARG:HH22	2:B:292:ILE:CD1	1.12	1.60
1:A:585:ILE:CD1	1:A:683:ILE:HD13	1.26	1.56
1:A:70:LEU:CD2	2:B:216:PHE:CG	1.87	1.53
3:C:59:ARG:HG3	3:D:280:ILE:CD1	1.40	1.51
1:A:143:ARG:CZ	2:B:292:ILE:HD11	1.38	1.49
2:B:405:ILE:CD1	2:B:456:ILE:HD13	1.47	1.45
1:A:137:ARG:NH2	2:B:328:ARG:HH12	1.07	1.44
1:A:143:ARG:NH2	2:B:292:ILE:HD11	1.13	1.44
1:A:585:ILE:CD1	1:A:683:ILE:CD1	1.96	1.43
3:C:59:ARG:HH21	3:D:285:ALA:CB	1.28	1.43
1:A:143:ARG:NH2	2:B:288:TYR:HD2	1.08	1.42
1:A:137:ARG:NH2	2:B:328:ARG:HH22	1.14	1.40
1:A:143:ARG:NH2	2:B:292:ILE:HD11	1.09	1.39
3:C:188:ILE:HD13	3:C:394:PHE:CD1	1.59	1.38
2:B:405:ILE:CD1	2:B:456:ILE:CD1	2.03	1.36
1:A:585:ILE:HD12	1:A:683:ILE:CD1	1.51	1.36
1:A:137:ARG:NH2	2:B:328:ARG:NH1	1.73	1.36
1:A:137:ARG:HH21	2:B:328:ARG:NH2	1.23	1.34
1:A:143:ARG:NH2	2:B:288:TYR:CD2	1.95	1.34
2:B:480:ILE:CD1	2:B:541:LEU:HD11	1.56	1.34
1:A:143:ARG:CZ	2:B:288:TYR:HE2	1.41	1.33
3:C:59:ARG:NH2	3:D:285:ALA:HB2	1.43	1.33
2:B:405:ILE:HG13	2:B:456:ILE:CD1	1.58	1.32
3:C:58:CYS:SG	3:D:286:HIS:C	2.08	1.32
1:A:458:TYR:CD1	1:A:484:ILE:HD12	1.64	1.32
1:A:138:PHE:CE2	1:A:275:ILE:HD11	1.65	1.31
1:A:599:LEU:CD1	1:A:640:ILE:CD1	2.07	1.30
1:A:138:PHE:CZ	1:A:275:ILE:HD11	1.65	1.30
2:B:438:TYR:CD2	2:B:441:ILE:HD12	1.62	1.30
3:C:59:ARG:CG	3:D:280:ILE:HD11	1.61	1.30
1:A:143:ARG:NE	2:B:288:TYR:CE2	1.99	1.30
3:D:17:VAL:CB	3:D:231:ILE:HD11	1.62	1.29
1:A:118:ILE:HD12	1:A:190:TYR:CZ	1.66	1.28
1:A:70:LEU:HD22	2:B:216:PHE:CD1	1.24	1.27
3:D:188:ILE:CD1	3:D:394:PHE:HB2	1.62	1.27
3:C:188:ILE:CD1	3:C:394:PHE:CD1	2.17	1.27
1:A:296:TYR:CG	2:B:322:HIS:HE1	1.54	1.26
1:A:73:THR:HG22	2:B:215:ASN:ND2	1.48	1.25
2:B:213:ILE:HD11	2:B:221:LEU:CD1	1.64	1.25
3:D:280:ILE:HD11	3:D:371:GLU:OE1	1.36	1.25
3:D:188:ILE:CD1	3:D:394:PHE:HB2	1.67	1.24
2:B:180:PRO:N	2:B:184:ILE:HD12	1.53	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:533:ARG:N	2:B:538:ILE:HD12	1.50	1.23
3:C:58:CYS:HB3	3:D:286:HIS:O	1.30	1.23
2:B:257:ILE:CD1	2:B:297:TYR:CD2	2.22	1.23
2:B:405:ILE:HG13	2:B:456:ILE:CD1	1.69	1.23
3:C:59:ARG:CG	3:D:280:ILE:CD1	2.15	1.23
2:B:257:ILE:HD12	2:B:297:TYR:CD2	1.73	1.22
3:C:188:ILE:HD13	3:C:394:PHE:CD2	1.73	1.22
1:A:140:TYR:CZ	2:B:324:ASP:OD1	1.91	1.22
3:D:188:ILE:CD1	3:D:394:PHE:HB2	1.68	1.22
1:A:426:PHE:CZ	1:A:564:ILE:CD1	2.23	1.21
1:A:72:GLY:O	2:B:215:ASN:CG	1.78	1.21
2:B:445:PHE:CE1	2:B:449:ILE:HD11	1.75	1.21
1:A:143:ARG:CZ	2:B:288:TYR:CE2	2.24	1.21
3:D:5:ILE:HD12	3:D:53:PHE:CE2	1.76	1.21
3:D:5:ILE:HD12	3:D:53:PHE:CZ	1.76	1.21
3:D:188:ILE:HD12	3:D:394:PHE:CD1	1.75	1.21
1:A:143:ARG:NH2	2:B:292:ILE:CD1	2.02	1.20
1:A:625:ILE:HD11	1:A:761:ILE:CD1	1.70	1.20
3:C:258:THR:HG21	3:C:356:ILE:CD1	1.71	1.20
1:A:599:LEU:CD1	1:A:640:ILE:HD13	1.70	1.20
3:C:59:ARG:NH2	3:D:285:ALA:CB	1.97	1.20
3:C:59:ARG:NH2	3:D:279:TYR:HB3	1.55	1.20
1:A:72:GLY:O	2:B:215:ASN:CB	1.89	1.20
3:D:188:ILE:HD11	3:D:394:PHE:CB	1.72	1.20
2:B:339:ILE:CD1	2:B:439:ARG:HB2	1.69	1.19
1:A:625:ILE:CD1	1:A:761:ILE:HG21	1.70	1.19
2:B:296:ILE:HD13	2:B:319:PHE:CZ	1.76	1.19
1:A:140:TYR:CE2	2:B:324:ASP:OD1	1.94	1.19
1:A:72:GLY:CA	2:B:215:ASN:HB2	1.72	1.19
2:B:355:LEU:HB2	2:B:364:ILE:CD1	1.72	1.18
1:A:118:ILE:HD12	1:A:190:TYR:OH	1.41	1.18
2:B:405:ILE:CG1	2:B:456:ILE:CD1	2.21	1.18
2:B:296:ILE:CD1	2:B:327:ILE:HD12	1.72	1.18
3:C:188:ILE:HD12	3:C:394:PHE:CD1	1.77	1.18
1:A:151:LEU:HD12	2:B:285:ARG:HD3	1.26	1.17
3:C:59:ARG:NE	3:D:285:ALA:HB3	1.59	1.17
1:A:774:ILE:HD12	1:A:796:SER:CB	1.73	1.16
3:C:188:ILE:CD1	3:C:394:PHE:CD2	2.29	1.16
1:A:143:ARG:CZ	2:B:292:ILE:CD1	2.22	1.16
1:A:137:ARG:CZ	2:B:325:LEU:HD22	1.76	1.16
1:A:363:ILE:HD11	1:A:366:ILE:HB	1.21	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:533:ARG:HA	2:B:538:ILE:CD1	1.74	1.15
1:A:426:PHE:CE2	1:A:564:ILE:CD1	2.30	1.15
1:A:296:TYR:CG	2:B:322:HIS:CE1	2.35	1.14
3:D:188:ILE:HD11	3:D:394:PHE:HB3	1.25	1.14
2:B:296:ILE:CD1	2:B:319:PHE:CE1	2.28	1.14
2:B:405:ILE:HD13	2:B:456:ILE:CD1	1.78	1.14
1:A:625:ILE:CD1	1:A:761:ILE:HG23	1.77	1.14
1:A:143:ARG:NE	2:B:288:TYR:HE2	1.46	1.14
2:B:213:ILE:CD1	2:B:221:LEU:HD11	1.78	1.14
1:A:426:PHE:CZ	1:A:564:ILE:HD11	1.80	1.13
2:B:526:ARG:O	2:B:538:ILE:HD12	1.48	1.13
2:B:586:ILE:HD11	2:B:732:LEU:HD13	1.17	1.13
1:A:625:ILE:HD12	1:A:761:ILE:CG2	1.79	1.13
2:B:731:PHE:CE1	2:B:735:ILE:HD11	1.83	1.13
1:A:70:LEU:HD22	2:B:216:PHE:CG	1.67	1.13
2:B:533:ARG:HA	2:B:538:ILE:HD12	1.17	1.13
3:C:188:ILE:HD13	3:C:394:PHE:CE2	1.84	1.13
2:B:405:ILE:HG13	2:B:456:ILE:HD12	1.29	1.13
1:A:134:VAL:HG13	1:A:275:ILE:HD13	1.29	1.13
3:D:188:ILE:HD11	3:D:394:PHE:HA	1.18	1.12
1:A:357:VAL:HB	1:A:363:ILE:HD12	1.29	1.12
1:A:137:ARG:NH1	2:B:325:LEU:HD22	1.62	1.12
3:C:322:ILE:HD13	3:C:358:ARG:NH2	1.64	1.12
2:B:586:ILE:HD11	2:B:732:LEU:CD1	1.80	1.12
3:C:322:ILE:HD13	3:C:358:ARG:HH21	1.09	1.12
1:A:151:LEU:HD13	2:B:286:GLU:OE2	1.49	1.11
3:C:188:ILE:CD1	3:C:394:PHE:CD2	2.33	1.11
1:A:458:TYR:CE1	1:A:484:ILE:HD12	1.84	1.11
1:A:151:LEU:HD12	2:B:285:ARG:CD	1.79	1.11
3:C:59:ARG:HE	3:D:285:ALA:HB3	1.07	1.11
3:C:123:ILE:HD11	3:C:154:LEU:HD11	1.15	1.11
1:A:625:ILE:CD1	1:A:761:ILE:CG2	2.28	1.11
2:B:405:ILE:CG1	2:B:456:ILE:HD11	1.80	1.11
1:A:143:ARG:NE	2:B:288:TYR:CE2	2.18	1.11
1:A:774:ILE:HD12	1:A:796:SER:OG	1.48	1.11
1:A:70:LEU:CD2	2:B:216:PHE:CD1	1.99	1.11
3:C:258:THR:OG1	3:C:356:ILE:HD11	1.48	1.10
1:A:625:ILE:HD12	1:A:761:ILE:HG21	1.26	1.10
2:B:525:LEU:HD22	2:B:538:ILE:HD12	1.32	1.10
2:B:355:LEU:CB	2:B:364:ILE:HD12	1.81	1.10
1:A:151:LEU:CD1	2:B:286:GLU:OE2	1.99	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:339:ILE:HD13	2:B:439:ARG:HB2	1.12	1.10
2:B:180:PRO:N	2:B:184:ILE:CD1	2.14	1.10
1:A:606:LEU:HD11	1:A:710:ILE:HD11	1.33	1.10
1:A:625:ILE:HD11	1:A:761:ILE:HD12	1.29	1.10
1:A:695:LEU:HD21	1:A:774:ILE:HD12	1.20	1.09
1:A:639:PHE:CZ	1:A:643:ILE:HD11	1.87	1.09
3:D:258:THR:HG21	3:D:356:ILE:HD12	1.20	1.09
1:A:72:GLY:HA2	2:B:215:ASN:CB	1.81	1.09
2:B:405:ILE:HD12	2:B:453:TYR:CD1	1.86	1.09
1:A:706:PHE:HZ	1:A:710:ILE:HD12	1.12	1.09
2:B:480:ILE:HD13	2:B:537:VAL:HG11	1.33	1.09
2:B:445:PHE:CE2	2:B:449:ILE:HD11	1.85	1.09
3:C:188:ILE:HD11	3:C:394:PHE:CE1	1.86	1.09
2:B:213:ILE:HD11	2:B:221:LEU:HD11	1.16	1.09
3:D:280:ILE:CD1	3:D:371:GLU:OE1	2.01	1.09
1:A:151:LEU:HD11	2:B:282:SER:CB	1.82	1.09
3:D:188:ILE:HD11	3:D:394:PHE:HB2	1.09	1.08
1:A:706:PHE:CZ	1:A:710:ILE:HD12	1.86	1.08
1:A:458:TYR:CD1	1:A:484:ILE:CD1	2.34	1.08
3:C:59:ARG:NH1	3:D:283:ASP:OD2	1.86	1.08
1:A:599:LEU:HD12	1:A:640:ILE:HD13	1.21	1.08
1:A:147:GLU:HG3	2:B:285:ARG:HG3	1.35	1.08
2:B:355:LEU:HB2	2:B:364:ILE:HD12	1.21	1.08
2:B:772:PHE:HE1	2:B:812:ILE:HD13	1.19	1.08
3:C:258:THR:HG21	3:C:356:ILE:HD11	1.09	1.08
1:A:137:ARG:NH2	2:B:328:ARG:NH2	1.83	1.08
2:B:586:ILE:HD11	2:B:732:LEU:CG	1.84	1.08
1:A:458:TYR:CE1	1:A:484:ILE:HD12	1.87	1.08
3:C:58:CYS:SG	3:D:286:HIS:N	2.25	1.07
2:B:405:ILE:CD1	2:B:452:GLN:OE1	2.03	1.07
3:C:242:ILE:HD11	3:C:252:MET:SD	1.94	1.07
1:A:72:GLY:HA2	2:B:215:ASN:HB2	1.20	1.07
3:C:123:ILE:HD11	3:C:154:LEU:HD11	1.35	1.07
3:D:119:ILE:CD1	3:D:154:LEU:HD13	1.85	1.07
1:A:557:ILE:CD1	1:A:594:TYR:OH	2.03	1.06
3:D:212:ILE:HD12	3:D:303:ASN:ND2	1.69	1.06
2:B:430:HIS:CG	2:B:448:ILE:HD13	1.89	1.06
2:B:364:ILE:CD1	2:B:383:ILE:HD11	1.86	1.06
1:A:105:PHE:CZ	1:A:109:ILE:HD11	1.90	1.06
3:D:188:ILE:HD11	3:D:394:PHE:HB2	1.13	1.06
1:A:68:ILE:CD1	2:B:281:LYS:HD3	1.85	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:625:ILE:HD11	1:A:761:ILE:HG23	1.11	1.06
1:A:585:ILE:HD11	1:A:683:ILE:HD13	1.26	1.06
3:C:188:ILE:HD13	3:C:394:PHE:CD2	1.88	1.06
2:B:405:ILE:HG23	2:B:456:ILE:HD12	1.37	1.05
1:A:698:GLN:OE1	1:A:774:ILE:CD1	2.04	1.05
3:D:17:VAL:HG22	3:D:231:ILE:HD12	1.35	1.05
1:A:128:ASP:OD1	2:B:299:ARG:NH2	1.87	1.05
2:B:209:ILE:HD13	2:B:213:ILE:HD12	1.37	1.05
1:A:143:ARG:NH1	2:B:292:ILE:CD1	2.19	1.05
1:A:151:LEU:HG	2:B:285:ARG:NE	1.63	1.05
3:C:59:ARG:HG3	3:D:280:ILE:HD13	1.39	1.05
2:B:209:ILE:CD1	2:B:213:ILE:HD12	1.86	1.05
1:A:409:PHE:CE1	1:A:573:ILE:CD1	2.40	1.05
3:D:188:ILE:HD11	3:D:394:PHE:HB2	1.09	1.04
3:C:59:ARG:HG3	3:D:280:ILE:HD11	1.06	1.04
3:C:166:ILE:HD13	3:C:256:TYR:CD2	1.92	1.04
1:A:695:LEU:CD2	1:A:774:ILE:HD12	1.86	1.04
2:B:480:ILE:HD13	2:B:537:VAL:CG1	1.86	1.04
2:B:364:ILE:HD11	2:B:383:ILE:CD1	1.88	1.04
3:C:188:ILE:CD1	3:C:394:PHE:CD2	2.39	1.04
3:C:255:ILE:HD11	3:C:358:ARG:HH11	1.16	1.04
1:A:138:PHE:CE2	1:A:275:ILE:CD1	2.40	1.04
3:C:204:PHE:CD2	3:C:231:ILE:HD11	1.91	1.04
1:A:108:ARG:HH21	1:A:177:ILE:HD12	1.22	1.04
3:C:276:THR:OG1	3:C:284:ILE:CD1	2.05	1.04
3:C:188:ILE:HD11	3:C:394:PHE:CB	1.86	1.04
2:B:257:ILE:CD1	2:B:297:TYR:CE2	2.41	1.03
1:A:567:PRO:HD2	1:A:574:ILE:HD11	1.35	1.03
2:B:533:ARG:CA	2:B:538:ILE:HD12	1.86	1.03
2:B:241:PHE:HB3	2:B:254:ILE:CD1	1.87	1.03
1:A:357:VAL:HB	1:A:363:ILE:CD1	1.89	1.03
3:D:212:ILE:HD11	3:D:302:SER:O	1.56	1.03
3:C:258:THR:CG2	3:C:356:ILE:CD1	2.36	1.03
1:A:409:PHE:CE1	1:A:573:ILE:HD11	1.94	1.03
2:B:405:ILE:HD11	2:B:456:ILE:HD13	1.04	1.02
1:A:699:ILE:CD1	1:A:775:PHE:CE1	2.42	1.02
1:A:566:ILE:HG13	1:A:574:ILE:CD1	1.89	1.02
2:B:241:PHE:HB3	2:B:254:ILE:HD11	1.39	1.02
2:B:296:ILE:HD11	2:B:319:PHE:CE1	1.93	1.02
2:B:405:ILE:HD12	2:B:456:ILE:HD11	1.40	1.02
2:B:339:ILE:CD1	2:B:439:ARG:CB	2.37	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:THR:CG2	2:B:215:ASN:HD21	1.71	1.02
1:A:774:ILE:CD1	1:A:796:SER:HB2	1.89	1.02
2:B:586:ILE:HD11	2:B:732:LEU:HD22	1.37	1.02
2:B:405:ILE:CD1	2:B:456:ILE:HD11	1.90	1.02
2:B:480:ILE:CD1	2:B:541:LEU:CD1	2.37	1.01
2:B:296:ILE:HD11	2:B:327:ILE:CD1	1.88	1.01
1:A:143:ARG:HH12	2:B:292:ILE:HD12	1.23	1.01
3:C:58:CYS:CB	3:D:286:HIS:O	2.08	1.01
3:D:213:SER:HB3	3:D:222:ILE:HD11	1.42	1.01
1:A:425:ILE:HD13	1:A:564:ILE:HD12	1.37	1.01
3:C:188:ILE:HD11	3:C:394:PHE:CG	1.95	1.01
3:D:188:ILE:HD11	3:D:394:PHE:CB	1.89	1.01
2:B:405:ILE:HD12	2:B:456:ILE:CD1	1.85	1.01
2:B:499:ILE:HD11	2:B:508:PRO:HG3	1.40	1.01
2:B:405:ILE:CD1	2:B:456:ILE:HD11	1.91	1.01
3:D:21:LEU:HD12	3:D:235:ILE:HD13	1.40	1.01
1:A:599:LEU:HD22	1:A:640:ILE:HD11	1.38	1.01
2:B:405:ILE:HG23	2:B:456:ILE:HD12	1.02	1.01
2:B:634:ILE:HD12	2:B:772:PHE:CE1	1.95	1.01
1:A:151:LEU:HD11	2:B:282:SER:OG	1.60	1.00
3:C:188:ILE:HD12	3:C:394:PHE:CG	1.96	1.00
1:A:698:GLN:OE1	1:A:774:ILE:HD13	1.61	1.00
3:D:256:TYR:CE1	3:D:260:ILE:HD12	1.95	1.00
3:D:188:ILE:HD11	3:D:394:PHE:CA	1.91	1.00
3:C:258:THR:HG21	3:C:356:ILE:CD1	1.91	1.00
1:A:625:ILE:HG13	1:A:765:ILE:CD1	1.91	1.00
1:A:425:ILE:CD1	1:A:564:ILE:HD12	1.91	1.00
3:C:212:ILE:HD11	3:C:302:SER:O	1.61	1.00
2:B:405:ILE:HG13	2:B:456:ILE:HD11	1.02	1.00
2:B:586:ILE:HD11	2:B:732:LEU:HG	1.44	1.00
3:C:199:ASP:O	3:C:260:ILE:CD1	2.10	1.00
1:A:151:LEU:CD1	2:B:285:ARG:HD3	1.92	1.00
2:B:405:ILE:HD11	2:B:456:ILE:HG13	1.41	1.00
1:A:202:GLU:O	1:A:205:THR:O	1.80	1.00
1:A:585:ILE:HD11	1:A:683:ILE:CG2	1.91	0.99
1:A:357:VAL:CB	1:A:363:ILE:HD12	1.91	0.99
2:B:402:ILE:CG2	2:B:449:ILE:HD12	1.92	0.99
1:A:143:ARG:HH22	2:B:292:ILE:CD1	1.69	0.99
3:D:17:VAL:HB	3:D:231:ILE:CD1	1.91	0.99
3:C:59:ARG:NE	3:D:280:ILE:HD11	1.77	0.99
3:C:127:ILE:CD1	3:C:162:TYR:CZ	2.45	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:405:ILE:HD13	2:B:456:ILE:HD11	0.99	0.99
1:A:137:ARG:HH22	2:B:328:ARG:NH1	1.54	0.98
1:A:130:SER:OG	2:B:322:HIS:NE2	1.95	0.98
1:A:643:ILE:HD13	1:A:696:GLN:HE22	1.28	0.98
3:C:123:ILE:HD13	3:C:158:LEU:HD21	1.43	0.98
1:A:138:PHE:CZ	1:A:275:ILE:CD1	2.46	0.98
3:D:119:ILE:HD12	3:D:154:LEU:CD1	1.93	0.98
3:C:188:ILE:CD1	3:C:394:PHE:CG	2.46	0.98
2:B:405:ILE:CG2	2:B:456:ILE:HD12	1.94	0.97
1:A:426:PHE:CE2	1:A:564:ILE:HD13	1.98	0.97
1:A:695:LEU:CD2	1:A:774:ILE:CD1	2.42	0.97
1:A:458:TYR:CD1	1:A:484:ILE:CD1	2.46	0.97
1:A:625:ILE:CD1	1:A:761:ILE:HG21	1.95	0.97
1:A:625:ILE:CD1	1:A:761:ILE:CG2	2.42	0.97
1:A:118:ILE:CD1	1:A:190:TYR:CZ	2.46	0.97
2:B:731:PHE:CE1	2:B:735:ILE:CD1	2.48	0.97
3:D:258:THR:HG21	3:D:356:ILE:CD1	1.93	0.97
1:A:699:ILE:HD11	1:A:775:PHE:CE1	2.00	0.97
2:B:533:ARG:HA	2:B:538:ILE:CD1	1.95	0.97
1:A:606:LEU:CD1	1:A:710:ILE:HD11	1.94	0.96
3:C:166:ILE:CD1	3:C:256:TYR:CD2	2.46	0.96
1:A:143:ARG:NH1	2:B:292:ILE:HD12	1.78	0.96
1:A:138:PHE:HB3	1:A:275:ILE:HD11	1.44	0.96
3:C:59:ARG:NH1	3:D:283:ASP:OD1	1.97	0.96
3:C:58:CYS:SG	3:D:286:HIS:CA	1.13	0.96
1:A:606:LEU:CD1	1:A:710:ILE:CD1	2.44	0.96
2:B:241:PHE:HB3	2:B:254:ILE:CD1	1.95	0.96
1:A:625:ILE:HD13	1:A:761:ILE:HG12	1.44	0.96
3:C:59:ARG:HH21	3:D:285:ALA:HB2	0.96	0.96
3:C:255:ILE:CD1	3:C:358:ARG:HH11	1.78	0.96
3:D:188:ILE:HD11	3:D:394:PHE:HA	1.48	0.96
3:C:188:ILE:CD1	3:C:394:PHE:CE1	2.45	0.96
1:A:151:LEU:HD22	2:B:285:ARG:HG3	1.44	0.96
1:A:585:ILE:HD11	1:A:683:ILE:HG21	1.48	0.96
3:D:188:ILE:CD1	3:D:394:PHE:HA	1.96	0.96
1:A:585:ILE:HD13	1:A:683:ILE:HG12	1.45	0.95
3:C:188:ILE:CD1	3:C:394:PHE:CG	2.48	0.95
2:B:586:ILE:HD13	2:B:732:LEU:HB2	1.45	0.95
1:A:599:LEU:HD13	1:A:640:ILE:CD1	1.95	0.95
3:D:258:THR:CG2	3:D:356:ILE:HD12	1.95	0.95
1:A:138:PHE:CE1	1:A:275:ILE:HD11	2.01	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:59:ARG:CD	3:D:280:ILE:HD11	1.96	0.95
1:A:643:ILE:CD1	1:A:696:GLN:NE2	2.30	0.95
1:A:135:LEU:HD13	1:A:247:ILE:HD13	1.46	0.95
3:C:127:ILE:HD13	3:C:162:TYR:CZ	2.02	0.95
3:D:188:ILE:CD1	3:D:394:PHE:HB3	1.96	0.95
1:A:625:ILE:HD13	1:A:761:ILE:CG2	1.93	0.95
2:B:398:LEU:CG	2:B:449:ILE:HD12	1.96	0.95
1:A:72:GLY:O	2:B:215:ASN:HB3	1.67	0.94
2:B:346:LEU:HD11	2:B:402:ILE:HD13	1.48	0.94
2:B:656:ILE:HD11	2:B:738:HIS:CD2	2.02	0.94
3:D:255:ILE:HD12	3:D:358:ARG:CZ	1.97	0.94
1:A:151:LEU:CG	2:B:285:ARG:NE	2.12	0.94
2:B:398:LEU:HG	2:B:449:ILE:CD1	1.97	0.94
1:A:138:PHE:CD2	1:A:275:ILE:HD11	2.00	0.94
1:A:557:ILE:HD13	1:A:594:TYR:OH	1.67	0.94
2:B:493:ILE:HD12	2:B:598:TYR:CB	1.97	0.94
1:A:147:GLU:CG	2:B:285:ARG:HG3	1.97	0.94
2:B:293:ARG:HE	2:B:330:ILE:HD11	1.30	0.94
1:A:151:LEU:HD22	2:B:285:ARG:HB3	1.45	0.94
1:A:585:ILE:CD1	1:A:683:ILE:CG1	2.44	0.94
3:C:123:ILE:CD1	3:C:154:LEU:HD11	1.96	0.94
1:A:566:ILE:HG13	1:A:574:ILE:HD13	1.48	0.94
2:B:480:ILE:HD11	2:B:541:LEU:CD1	1.98	0.94
3:C:276:THR:CB	3:C:284:ILE:HD12	1.96	0.94
3:D:17:VAL:CG2	3:D:231:ILE:HD12	1.98	0.94
2:B:430:HIS:CG	2:B:448:ILE:CD1	2.51	0.94
2:B:297:TYR:OH	2:B:330:ILE:HD13	1.68	0.94
3:C:188:ILE:CD1	3:C:394:PHE:CB	2.44	0.94
2:B:480:ILE:HD12	2:B:541:LEU:HD11	1.48	0.94
2:B:241:PHE:CB	2:B:254:ILE:CD1	2.46	0.94
3:C:58:CYS:HB3	3:D:286:HIS:C	1.88	0.94
2:B:241:PHE:HB3	2:B:254:ILE:HD11	1.47	0.94
1:A:138:PHE:HE2	1:A:275:ILE:CD1	1.80	0.94
1:A:625:ILE:HD11	1:A:761:ILE:CG2	1.98	0.93
3:C:204:PHE:CG	3:C:231:ILE:HD11	2.03	0.93
1:A:375:ILE:HD13	1:A:396:LYS:HE3	1.50	0.93
3:D:119:ILE:HD12	3:D:154:LEU:HD13	1.49	0.93
3:C:59:ARG:CG	3:D:280:ILE:HD13	1.96	0.93
1:A:108:ARG:NH2	1:A:177:ILE:HD12	1.82	0.93
3:C:199:ASP:O	3:C:260:ILE:HD13	1.68	0.93
2:B:525:LEU:HD22	2:B:538:ILE:CD1	1.98	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:526:ARG:O	2:B:538:ILE:CD1	2.16	0.93
3:D:213:SER:HB3	3:D:222:ILE:CD1	1.99	0.93
1:A:599:LEU:HD12	1:A:640:ILE:CD1	1.85	0.93
1:A:458:TYR:CE1	1:A:484:ILE:CD1	2.50	0.93
3:C:240:ASN:OD1	3:C:322:ILE:HD11	1.69	0.93
2:B:296:ILE:HD11	2:B:327:ILE:HD12	0.95	0.92
2:B:405:ILE:HG23	2:B:456:ILE:CD1	1.95	0.92
3:C:127:ILE:CD1	3:C:162:TYR:CE2	2.51	0.92
2:B:438:TYR:CD2	2:B:441:ILE:CD1	2.51	0.92
2:B:586:ILE:HD11	2:B:732:LEU:CD2	1.99	0.92
1:A:72:GLY:CA	2:B:215:ASN:CB	2.44	0.92
2:B:586:ILE:CD1	2:B:732:LEU:HD12	1.98	0.92
1:A:409:PHE:CZ	1:A:573:ILE:HD13	2.04	0.92
1:A:68:ILE:CD1	2:B:281:LYS:CD	2.46	0.92
3:C:258:THR:CG2	3:C:356:ILE:HD11	1.99	0.92
1:A:143:ARG:HH22	2:B:292:ILE:HD11	1.15	0.92
3:D:17:VAL:HB	3:D:231:ILE:HD11	0.94	0.92
2:B:499:ILE:HD11	2:B:508:PRO:HD3	1.49	0.92
1:A:143:ARG:HH22	2:B:292:ILE:CG1	1.83	0.92
3:C:188:ILE:CD1	3:C:394:PHE:HB2	2.00	0.92
2:B:209:ILE:CD1	2:B:213:ILE:CD1	2.47	0.92
2:B:339:ILE:HD12	2:B:439:ARG:CB	2.00	0.91
1:A:625:ILE:HD13	1:A:761:ILE:CB	1.99	0.91
2:B:296:ILE:CD1	2:B:319:PHE:CZ	2.51	0.91
1:A:320:TRP:O	1:A:572:ILE:HD12	1.70	0.91
1:A:585:ILE:HD13	1:A:683:ILE:CG1	2.00	0.91
3:D:242:ILE:HD11	3:D:252:MET:HB2	1.52	0.91
3:D:188:ILE:HD11	3:D:394:PHE:CB	1.99	0.91
1:A:143:ARG:CZ	2:B:288:TYR:CE2	2.53	0.91
2:B:480:ILE:HD11	2:B:541:LEU:HD11	1.53	0.91
2:B:405:ILE:CG1	2:B:456:ILE:CD1	2.43	0.91
3:C:258:THR:CG2	3:C:356:ILE:HD11	1.99	0.91
1:A:143:ARG:CZ	2:B:288:TYR:CD2	2.52	0.91
2:B:241:PHE:HB3	2:B:254:ILE:HD11	1.51	0.91
1:A:699:ILE:CD1	1:A:775:PHE:CE2	2.54	0.91
1:A:606:LEU:HG	1:A:710:ILE:HD13	1.51	0.91
2:B:739:LYS:O	2:B:743:THR:O	1.89	0.91
3:C:188:ILE:HD12	3:C:394:PHE:CD2	2.02	0.91
3:C:59:ARG:CZ	3:D:285:ALA:HB3	2.00	0.91
1:A:774:ILE:CD1	1:A:796:SER:CB	2.45	0.91
3:D:213:SER:HB3	3:D:222:ILE:HD12	1.49	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:482:LEU:HD12	2:B:657:ILE:HD12	1.54	0.91
3:C:59:ARG:HH21	3:D:285:ALA:CA	1.84	0.91
3:C:280:ILE:HD13	3:C:284:ILE:HG12	1.53	0.91
1:A:699:ILE:HD13	1:A:775:PHE:CE1	2.05	0.90
2:B:257:ILE:HD13	2:B:297:TYR:CE2	2.06	0.90
1:A:147:GLU:HB3	2:B:285:ARG:HD3	1.52	0.90
2:B:634:ILE:HD12	2:B:772:PHE:HE1	1.33	0.90
3:D:258:THR:OG1	3:D:356:ILE:HD11	1.71	0.90
2:B:533:ARG:CA	2:B:538:ILE:HD12	2.02	0.90
3:C:58:CYS:HB3	3:D:286:HIS:O	1.70	0.90
3:D:188:ILE:CD1	3:D:394:PHE:HA	1.99	0.90
1:A:567:PRO:HD2	1:A:574:ILE:CD1	2.01	0.90
2:B:533:ARG:O	2:B:538:ILE:HD12	1.72	0.90
1:A:137:ARG:NH1	2:B:325:LEU:CD2	2.35	0.90
2:B:188:VAL:HG13	2:B:224:ILE:HD11	1.51	0.90
3:D:212:ILE:CD1	3:D:303:ASN:CG	2.40	0.90
1:A:143:ARG:CZ	2:B:292:ILE:HD11	2.00	0.90
1:A:426:PHE:HZ	1:A:564:ILE:HD11	1.31	0.90
1:A:147:GLU:HG2	2:B:285:ARG:HG2	1.52	0.90
1:A:151:LEU:HG	2:B:285:ARG:HE	1.32	0.90
1:A:296:TYR:CD1	2:B:322:HIS:CE1	2.59	0.89
1:A:133:MET:HE1	2:B:323:GLY:H	1.33	0.89
1:A:585:ILE:HD12	1:A:683:ILE:HD13	0.91	0.89
3:C:58:CYS:H	3:D:287:LYS:HG3	1.35	0.89
2:B:493:ILE:CD1	2:B:598:TYR:HB2	2.01	0.89
1:A:137:ARG:HH21	2:B:328:ARG:NH1	1.46	0.89
3:C:58:CYS:HG	3:D:286:HIS:HA	1.07	0.89
3:C:6:ILE:HD13	3:C:126:GLU:HB3	1.53	0.89
3:D:166:ILE:HD12	3:D:256:TYR:CG	2.07	0.89
1:A:625:ILE:HD12	1:A:761:ILE:HG23	1.53	0.89
2:B:209:ILE:HD11	2:B:213:ILE:CD1	2.02	0.89
1:A:320:TRP:O	1:A:572:ILE:CD1	2.21	0.88
1:A:639:PHE:CE1	1:A:643:ILE:HD11	2.07	0.88
1:A:581:LYS:HB3	1:A:683:ILE:HD13	1.54	0.88
3:C:58:CYS:O	3:D:285:ALA:HA	1.72	0.88
1:A:138:PHE:CE1	1:A:275:ILE:HD11	2.08	0.88
2:B:607:SER:HB3	2:B:634:ILE:HD13	1.56	0.88
1:A:557:ILE:CD1	1:A:594:TYR:CZ	2.57	0.88
2:B:405:ILE:HD11	2:B:452:GLN:OE1	1.73	0.88
2:B:586:ILE:CD1	2:B:732:LEU:HB2	2.04	0.88
3:D:256:TYR:HE1	3:D:260:ILE:HD12	1.34	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:445:PHE:HE1	2:B:449:ILE:HD11	1.25	0.88
1:A:375:ILE:HD11	1:A:396:LYS:HG2	1.54	0.88
1:A:409:PHE:CE1	1:A:573:ILE:HD13	2.09	0.88
1:A:366:ILE:HD11	1:A:371:SER:HB3	1.54	0.87
1:A:409:PHE:CZ	1:A:573:ILE:HD11	2.09	0.87
1:A:128:ASP:HB3	2:B:299:ARG:HH22	1.38	0.87
3:D:276:THR:OG1	3:D:284:ILE:HD13	1.73	0.87
1:A:421:HIS:CE1	1:A:425:ILE:HD11	2.09	0.87
3:C:123:ILE:HD11	3:C:154:LEU:CD1	2.01	0.87
1:A:138:PHE:HE2	1:A:192:ILE:HD12	1.38	0.87
3:C:58:CYS:SG	3:D:284:ILE:O	2.32	0.87
2:B:586:ILE:HD11	2:B:732:LEU:CD1	2.03	0.87
2:B:398:LEU:HG	2:B:449:ILE:HD12	1.55	0.87
3:C:123:ILE:CD1	3:C:154:LEU:HD11	2.03	0.87
2:B:364:ILE:HD13	2:B:403:PHE:HD1	1.38	0.87
3:D:212:ILE:CD1	3:D:303:ASN:ND2	2.37	0.87
2:B:586:ILE:HD11	2:B:732:LEU:HD12	1.54	0.87
1:A:566:ILE:CG1	1:A:574:ILE:HD12	2.04	0.87
1:A:585:ILE:HD13	1:A:683:ILE:HD13	1.57	0.87
3:C:255:ILE:HD11	3:C:358:ARG:NH1	1.88	0.87
3:C:59:ARG:NH2	3:D:278:ASP:O	2.07	0.87
2:B:241:PHE:HB2	2:B:254:ILE:HD13	1.57	0.86
3:C:241:SER:OG	3:C:322:ILE:CD1	2.23	0.86
2:B:181:GLU:OE1	2:B:184:ILE:HD11	1.75	0.86
2:B:445:PHE:CE2	2:B:449:ILE:CD1	2.58	0.86
2:B:339:ILE:HD12	2:B:439:ARG:HB3	1.56	0.86
2:B:296:ILE:HD13	2:B:319:PHE:CE1	2.05	0.86
2:B:533:ARG:CA	2:B:538:ILE:CD1	2.53	0.86
3:C:255:ILE:CD1	3:C:358:ARG:NH1	2.37	0.86
3:C:188:ILE:CD1	3:C:394:PHE:CG	2.59	0.86
2:B:402:ILE:HG12	2:B:449:ILE:HD13	1.57	0.86
3:C:280:ILE:CD1	3:C:284:ILE:HD11	2.05	0.86
3:D:212:ILE:HD11	3:D:302:SER:O	1.74	0.86
1:A:625:ILE:CG2	1:A:765:ILE:HD13	2.04	0.86
3:C:212:ILE:CD1	3:C:302:SER:O	2.24	0.86
3:D:166:ILE:HD12	3:D:252:MET:HE2	1.55	0.86
1:A:71:GLU:HA	1:A:75:ILE:HD13	1.58	0.86
2:B:213:ILE:HD11	2:B:221:LEU:HD12	1.55	0.86
2:B:398:LEU:CD1	2:B:449:ILE:HD12	2.06	0.86
1:A:426:PHE:HE2	1:A:564:ILE:HD13	1.41	0.86
2:B:493:ILE:HD12	2:B:598:TYR:CG	2.11	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:SER:OG	1:A:404:ILE:HD11	1.76	0.86
1:A:147:GLU:CG	2:B:285:ARG:CG	2.53	0.86
2:B:405:ILE:HD13	2:B:452:GLN:OE1	1.74	0.85
3:C:256:TYR:CD1	3:C:260:ILE:HD12	2.10	0.85
2:B:398:LEU:CD2	2:B:449:ILE:HD12	2.07	0.85
1:A:557:ILE:HD13	1:A:594:TYR:OH	1.75	0.85
3:C:56:GLU:OE1	3:D:286:HIS:CE1	2.29	0.85
2:B:355:LEU:HG	2:B:364:ILE:HD12	1.57	0.85
1:A:426:PHE:CE2	1:A:564:ILE:HD12	2.09	0.85
2:B:731:PHE:CZ	2:B:735:ILE:HD11	2.10	0.85
2:B:586:ILE:HD12	2:B:735:ILE:CD1	2.06	0.85
3:D:139:LEU:HD21	3:D:235:ILE:CD1	2.07	0.85
2:B:533:ARG:HD3	2:B:538:ILE:HD13	1.57	0.85
1:A:68:ILE:HD12	2:B:281:LYS:CD	2.07	0.85
3:D:17:VAL:CB	3:D:231:ILE:CD1	2.51	0.85
3:C:188:ILE:HD12	3:C:394:PHE:CD2	2.11	0.85
2:B:241:PHE:CB	2:B:254:ILE:CD1	2.54	0.84
1:A:118:ILE:CD1	1:A:190:TYR:CE1	2.60	0.84
2:B:293:ARG:NE	2:B:330:ILE:HD11	1.90	0.84
2:B:445:PHE:CE1	2:B:449:ILE:CD1	2.59	0.84
2:B:405:ILE:HD12	2:B:453:TYR:HD1	1.40	0.84
3:D:119:ILE:HD11	3:D:154:LEU:HD13	1.58	0.84
3:C:56:GLU:HB2	3:D:286:HIS:CD2	2.12	0.84
3:C:188:ILE:HD11	3:C:394:PHE:CD1	2.12	0.84
3:C:188:ILE:HD11	3:C:394:PHE:CB	2.07	0.84
3:C:276:THR:HB	3:C:284:ILE:HD12	1.58	0.84
1:A:663:TYR:HD1	1:A:672:ILE:HD13	1.43	0.84
3:C:57:ASN:HB2	3:D:285:ALA:HA	1.59	0.84
2:B:772:PHE:CE1	2:B:812:ILE:HD13	2.11	0.84
3:D:216:VAL:O	3:D:280:ILE:HD12	1.78	0.84
3:D:188:ILE:CD1	3:D:394:PHE:CB	2.53	0.84
3:C:188:ILE:CD1	3:C:394:PHE:CD1	2.60	0.84
1:A:74:TYR:HB3	2:B:215:ASN:HD22	1.41	0.84
1:A:118:ILE:HD13	1:A:190:TYR:CE1	2.12	0.84
1:A:425:ILE:HD13	1:A:482:LEU:HD13	1.58	0.84
2:B:526:ARG:NH2	2:B:538:ILE:HD11	1.93	0.84
1:A:363:ILE:HD11	1:A:408:LEU:HD11	1.57	0.84
3:D:242:ILE:HD11	3:D:252:MET:SD	2.17	0.84
3:D:127:ILE:CD1	3:D:162:TYR:CZ	2.61	0.84
2:B:480:ILE:HD13	2:B:541:LEU:HD11	1.60	0.84
1:A:643:ILE:HD13	1:A:692:LEU:HD21	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:123:ILE:HD13	3:C:158:LEU:HD21	1.57	0.84
2:B:405:ILE:CD1	2:B:456:ILE:CD1	2.52	0.84
3:D:188:ILE:HD11	3:D:394:PHE:CB	2.08	0.84
1:A:366:ILE:HD12	1:A:404:ILE:HD11	1.60	0.83
3:C:188:ILE:CD1	3:C:394:PHE:CD1	2.60	0.83
2:B:533:ARG:N	2:B:538:ILE:CD1	2.37	0.83
1:A:625:ILE:CD1	1:A:761:ILE:CB	2.56	0.83
3:C:188:ILE:CD1	3:C:394:PHE:HD2	1.85	0.83
2:B:241:PHE:HB2	2:B:254:ILE:HD13	1.58	0.83
2:B:493:ILE:CD1	2:B:598:TYR:CB	2.55	0.83
3:D:127:ILE:HD13	3:D:162:TYR:CZ	2.13	0.83
3:D:188:ILE:HD12	3:D:394:PHE:CB	2.09	0.83
2:B:438:TYR:CE2	2:B:441:ILE:HD12	2.14	0.83
2:B:257:ILE:HD12	2:B:297:TYR:CG	2.14	0.83
2:B:533:ARG:HA	2:B:538:ILE:HD13	1.58	0.83
1:A:73:THR:H	2:B:215:ASN:ND2	1.75	0.83
2:B:653:LEU:HD23	2:B:657:ILE:HD12	1.59	0.83
1:A:557:ILE:CD1	1:A:594:TYR:OH	2.27	0.83
1:A:128:ASP:HB3	2:B:299:ARG:NH2	1.94	0.83
3:C:276:THR:OG1	3:C:284:ILE:HD11	1.76	0.83
2:B:611:ILE:HD13	2:B:777:CYS:SG	2.18	0.83
1:A:625:ILE:HD12	1:A:761:ILE:HG21	1.53	0.83
3:D:139:LEU:HD21	3:D:235:ILE:HD13	1.61	0.83
2:B:430:HIS:ND1	2:B:448:ILE:HD11	1.92	0.82
1:A:143:ARG:HH12	2:B:292:ILE:CD1	1.89	0.82
1:A:70:LEU:HD22	2:B:220:LEU:HD21	1.60	0.82
2:B:398:LEU:HD11	2:B:449:ILE:HD12	1.60	0.82
3:D:216:VAL:O	3:D:280:ILE:CD1	2.27	0.82
3:C:166:ILE:HD13	3:C:256:TYR:CE2	2.13	0.82
1:A:143:ARG:NH2	2:B:292:ILE:CD1	1.90	0.82
2:B:241:PHE:CB	2:B:254:ILE:HD13	2.09	0.82
2:B:364:ILE:HD11	2:B:383:ILE:HD11	0.92	0.82
2:B:405:ILE:CG1	2:B:456:ILE:HD11	2.08	0.82
1:A:126:TRP:CZ2	1:A:192:ILE:HD13	2.14	0.82
3:C:188:ILE:HD11	3:C:394:PHE:CE1	2.15	0.82
3:C:58:CYS:SG	3:D:286:HIS:HA	0.24	0.82
2:B:493:ILE:HD12	2:B:598:TYR:HB2	1.60	0.82
1:A:458:TYR:CD1	1:A:484:ILE:HD12	2.09	0.82
3:D:188:ILE:CD1	3:D:394:PHE:CD1	2.61	0.82
1:A:192:ILE:HD13	1:A:254:LYS:HG3	1.61	0.82
3:C:58:CYS:CB	3:D:286:HIS:C	2.30	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:241:PHE:CB	2:B:254:ILE:HD11	2.08	0.82
1:A:425:ILE:HD13	1:A:564:ILE:CD1	2.10	0.82
1:A:296:TYR:CB	2:B:322:HIS:HE1	1.92	0.82
3:C:188:ILE:HD13	3:C:394:PHE:CG	2.15	0.82
1:A:134:VAL:HG13	1:A:275:ILE:HD13	1.62	0.82
1:A:599:LEU:CD1	1:A:640:ILE:HD12	2.09	0.81
1:A:625:ILE:HD13	1:A:761:ILE:HB	1.60	0.81
1:A:699:ILE:HD11	1:A:775:PHE:CE2	2.14	0.81
3:D:127:ILE:HD13	3:D:162:TYR:CZ	2.15	0.81
2:B:257:ILE:HD12	2:B:297:TYR:CD2	2.15	0.81
2:B:586:ILE:CD1	2:B:732:LEU:CD1	2.58	0.81
1:A:557:ILE:HD13	1:A:594:TYR:CZ	2.15	0.81
1:A:68:ILE:HD11	2:B:281:LYS:CD	2.10	0.81
1:A:366:ILE:HD12	1:A:404:ILE:CD1	2.11	0.81
3:C:59:ARG:HE	3:D:280:ILE:HD11	1.42	0.81
3:C:255:ILE:HD11	3:C:358:ARG:HH11	1.46	0.81
1:A:585:ILE:HD13	1:A:683:ILE:CD1	2.10	0.81
1:A:409:PHE:HE1	1:A:573:ILE:HD11	1.40	0.81
3:C:59:ARG:NH2	3:D:279:TYR:CB	2.41	0.81
1:A:585:ILE:CD1	1:A:683:ILE:HG21	2.11	0.81
3:D:166:ILE:HD12	3:D:252:MET:CE	2.10	0.81
1:A:74:TYR:HB3	2:B:215:ASN:ND2	1.95	0.81
1:A:625:ILE:CD1	1:A:761:ILE:HD13	2.11	0.81
3:D:188:ILE:HD11	3:D:394:PHE:CA	2.10	0.81
2:B:355:LEU:HB2	2:B:364:ILE:HD11	1.61	0.81
3:C:188:ILE:HD13	3:C:394:PHE:CD2	2.14	0.81
3:D:188:ILE:CD1	3:D:394:PHE:CB	2.41	0.81
1:A:151:LEU:HD11	2:B:282:SER:HB2	1.60	0.81
1:A:566:ILE:CG1	1:A:574:ILE:CD1	2.57	0.80
1:A:72:GLY:C	2:B:215:ASN:CB	2.48	0.80
3:D:241:SER:OG	3:D:322:ILE:HD12	1.81	0.80
2:B:480:ILE:CD1	2:B:537:VAL:HG13	2.11	0.80
2:B:335:PHE:CE2	2:B:339:ILE:HD11	2.16	0.80
1:A:138:PHE:HD1	1:A:275:ILE:HD11	1.45	0.80
2:B:241:PHE:CB	2:B:254:ILE:HD13	2.11	0.80
1:A:321:ASP:HB3	1:A:572:ILE:HD11	1.60	0.80
1:A:484:ILE:HD11	1:A:560:LEU:HD11	1.63	0.80
1:A:625:ILE:HD11	1:A:761:ILE:HD13	1.63	0.80
1:A:585:ILE:HD12	1:A:683:ILE:HD11	1.58	0.80
3:D:98:GLY:O	3:D:111:ILE:HD13	1.81	0.80
2:B:257:ILE:HD12	2:B:297:TYR:CE2	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:643:ILE:CD1	1:A:696:GLN:HE22	1.89	0.80
1:A:255:ILE:CD1	1:A:272:LEU:HD22	2.12	0.80
3:D:166:ILE:HD12	3:D:256:TYR:CD1	2.16	0.80
1:A:699:ILE:HD13	1:A:775:PHE:CE2	2.14	0.80
2:B:405:ILE:HD11	2:B:456:ILE:CG1	2.11	0.80
2:B:480:ILE:CD1	2:B:537:VAL:CG1	2.59	0.80
1:A:147:GLU:HG2	2:B:285:ARG:CG	2.10	0.80
1:A:699:ILE:HD13	1:A:775:PHE:HE2	1.47	0.80
3:C:123:ILE:HD11	3:C:154:LEU:HD11	1.64	0.80
1:A:613:LYS:HD3	1:A:614:TYR:O	1.81	0.80
1:A:147:GLU:HG3	2:B:285:ARG:CG	2.11	0.80
1:A:375:ILE:CD1	1:A:396:LYS:HG2	2.11	0.80
1:A:557:ILE:HD13	1:A:594:TYR:OH	1.80	0.80
1:A:138:PHE:CE2	1:A:192:ILE:HD12	2.16	0.80
1:A:130:SER:CB	2:B:322:HIS:NE2	2.44	0.80
3:C:58:CYS:CB	3:D:286:HIS:O	2.30	0.80
3:C:188:ILE:CD1	3:C:394:PHE:HB3	2.11	0.79
3:D:188:ILE:HD12	3:D:394:PHE:HB2	1.60	0.79
3:C:59:ARG:CZ	3:D:285:ALA:CB	2.57	0.79
3:C:188:ILE:HD11	3:C:394:PHE:HB2	1.56	0.79
2:B:533:ARG:O	2:B:538:ILE:CD1	2.31	0.79
3:D:280:ILE:HD13	3:D:371:GLU:CD	2.03	0.79
3:C:188:ILE:HD12	3:C:394:PHE:CG	2.16	0.79
3:C:59:ARG:NH2	3:D:371:GLU:OE2	2.16	0.79
2:B:586:ILE:HD13	2:B:732:LEU:HD22	1.61	0.79
2:B:257:ILE:HD11	2:B:297:TYR:CD2	2.18	0.79
1:A:68:ILE:HD12	2:B:281:LYS:HD3	1.64	0.79
3:C:188:ILE:HD11	3:C:394:PHE:CD1	2.04	0.79
1:A:73:THR:HG22	2:B:215:ASN:HD21	1.46	0.79
3:D:139:LEU:HD21	3:D:235:ILE:CD1	2.12	0.79
1:A:74:TYR:H	2:B:215:ASN:HD21	1.31	0.79
3:C:241:SER:OG	3:C:322:ILE:HD11	1.82	0.79
1:A:425:ILE:HD13	1:A:482:LEU:HD11	1.65	0.78
2:B:257:ILE:HD12	2:B:297:TYR:CE2	2.17	0.78
3:C:127:ILE:HD12	3:C:162:TYR:CZ	2.18	0.78
3:C:60:ASN:H	3:D:286:HIS:CE1	2.01	0.78
3:C:242:ILE:CD1	3:C:252:MET:SD	2.71	0.78
3:D:119:ILE:HD13	3:D:154:LEU:HD22	1.66	0.78
3:D:255:ILE:HD13	3:D:358:ARG:NH2	1.98	0.78
1:A:774:ILE:CD1	1:A:796:SER:OG	2.30	0.78
2:B:250:LYS:HD3	2:B:254:ILE:HD11	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:58:CYS:HB3	3:D:286:HIS:C	2.01	0.78
1:A:625:ILE:CD1	1:A:761:ILE:HG23	2.12	0.78
1:A:566:ILE:HG13	1:A:574:ILE:HD12	1.63	0.78
1:A:68:ILE:HD11	2:B:281:LYS:HD3	1.64	0.78
1:A:70:LEU:HD11	2:B:216:PHE:O	1.83	0.78
3:D:188:ILE:CD1	3:D:394:PHE:CB	2.61	0.78
3:C:258:THR:HG21	3:C:356:ILE:HD13	1.64	0.78
2:B:493:ILE:CD1	2:B:598:TYR:CG	2.67	0.78
3:C:188:ILE:HD11	3:C:394:PHE:HB3	1.65	0.78
1:A:73:THR:CG2	2:B:215:ASN:ND2	2.47	0.78
3:D:127:ILE:HD13	3:D:162:TYR:HE2	1.49	0.78
1:A:143:ARG:NH1	2:B:292:ILE:HD11	1.86	0.78
3:D:139:LEU:HD21	3:D:235:ILE:HD11	1.66	0.78
2:B:499:ILE:HD12	2:B:511:LYS:HD3	1.66	0.78
3:D:5:ILE:CD1	3:D:53:PHE:CE2	2.64	0.78
1:A:599:LEU:HD11	1:A:640:ILE:CD1	2.12	0.78
3:D:280:ILE:HD13	3:D:371:GLU:HG3	1.65	0.77
1:A:599:LEU:HD13	1:A:640:ILE:HD12	1.64	0.77
2:B:634:ILE:CD1	2:B:772:PHE:CE1	2.67	0.77
2:B:772:PHE:HE1	2:B:812:ILE:CD1	1.96	0.77
3:C:127:ILE:CD1	3:C:162:TYR:CE2	2.68	0.77
1:A:663:TYR:CD1	1:A:672:ILE:HD13	2.18	0.77
2:B:402:ILE:CG2	2:B:449:ILE:HD13	2.14	0.77
3:C:59:ARG:HH21	3:D:279:TYR:HB3	1.49	0.77
2:B:209:ILE:HD11	2:B:213:ILE:HD11	1.64	0.77
3:D:212:ILE:HD12	3:D:303:ASN:HD21	1.48	0.77
1:A:118:ILE:CD1	1:A:190:TYR:OH	2.29	0.77
1:A:138:PHE:CD1	1:A:275:ILE:HD11	2.20	0.77
2:B:209:ILE:HD13	2:B:213:ILE:CD1	2.13	0.77
3:C:210:LEU:HG	3:C:222:ILE:HD11	1.64	0.77
3:D:255:ILE:CD1	3:D:358:ARG:NH2	2.48	0.77
2:B:296:ILE:CD1	2:B:319:PHE:HE1	1.90	0.77
1:A:643:ILE:HD13	1:A:696:GLN:NE2	1.97	0.77
2:B:213:ILE:HD11	2:B:221:LEU:HD22	1.66	0.77
3:D:188:ILE:HD11	3:D:427:ARG:NH2	1.99	0.77
1:A:421:HIS:CE1	1:A:425:ILE:CD1	2.68	0.77
2:B:367:ASN:O	2:B:384:GLU:OE2	2.03	0.77
3:D:212:ILE:HD12	3:D:303:ASN:ND2	1.99	0.77
1:A:296:TYR:CB	2:B:322:HIS:CE1	2.68	0.76
3:C:123:ILE:HD13	3:C:158:LEU:HD21	1.67	0.76
1:A:73:THR:HG22	2:B:215:ASN:ND2	1.99	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:188:ILE:CD1	3:C:394:PHE:CB	2.63	0.76
1:A:151:LEU:HD11	2:B:288:TYR:HE2	1.49	0.76
1:A:128:ASP:HB3	2:B:299:ARG:NH2	1.99	0.76
2:B:405:ILE:HG23	2:B:456:ILE:CD1	2.16	0.76
3:D:188:ILE:HD11	3:D:394:PHE:N	2.00	0.76
1:A:797:SER:O	1:A:800:ASP:O	2.02	0.76
3:C:188:ILE:CD1	3:C:394:PHE:CB	2.63	0.76
1:A:625:ILE:HD11	1:A:758:LEU:CD1	2.16	0.76
1:A:151:LEU:HD11	2:B:281:LYS:HE2	1.65	0.76
1:A:70:LEU:O	2:B:216:PHE:CE2	2.38	0.76
2:B:482:LEU:HB3	2:B:657:ILE:HD11	1.66	0.76
1:A:625:ILE:HD13	1:A:761:ILE:HD13	1.66	0.76
1:A:143:ARG:NH2	2:B:288:TYR:CE2	2.54	0.76
1:A:625:ILE:HD11	1:A:758:LEU:HD12	1.68	0.76
2:B:209:ILE:HD12	2:B:213:ILE:CD1	2.16	0.76
1:A:195:GLU:HG3	1:A:250:ILE:HD13	1.67	0.76
3:C:204:PHE:CB	3:C:231:ILE:HD11	2.16	0.76
3:C:322:ILE:CD1	3:C:358:ARG:NH2	2.46	0.75
2:B:631:LEU:H	2:B:631:LEU:HD12	1.50	0.75
2:B:586:ILE:CD1	2:B:732:LEU:CD2	2.64	0.75
1:A:625:ILE:CD1	1:A:761:ILE:CD1	2.60	0.75
3:D:280:ILE:HD13	3:D:371:GLU:CG	2.16	0.75
2:B:241:PHE:CB	2:B:254:ILE:HD11	2.16	0.75
1:A:557:ILE:HD11	1:A:594:TYR:CZ	2.20	0.75
1:A:133:MET:HE1	2:B:323:GLY:N	2.02	0.75
2:B:612:ARG:O	2:B:776:TYR:CD2	2.38	0.75
3:C:188:ILE:HD11	3:C:394:PHE:HB2	1.68	0.75
3:C:58:CYS:HB2	3:D:284:ILE:HB	1.67	0.75
2:B:499:ILE:HD13	2:B:508:PRO:HA	1.69	0.75
1:A:585:ILE:HD11	1:A:683:ILE:HG21	1.67	0.75
2:B:743:THR:O	2:B:756:GLN:HA	1.85	0.75
2:B:525:LEU:HB2	2:B:538:ILE:HD12	1.69	0.75
3:D:188:ILE:HD13	3:D:394:PHE:HB2	1.69	0.74
2:B:656:ILE:HD13	2:B:738:HIS:CD2	2.22	0.74
2:B:772:PHE:HE1	2:B:812:ILE:CD1	1.99	0.74
2:B:493:ILE:HD13	2:B:598:TYR:CB	2.17	0.74
2:B:739:LYS:O	2:B:743:THR:O	2.05	0.74
1:A:151:LEU:HB3	2:B:285:ARG:CZ	2.17	0.74
2:B:843:LYS:O	2:B:846:ARG:O	2.04	0.74
2:B:250:LYS:HD2	2:B:254:ILE:HD12	1.66	0.74
3:D:123:ILE:HD11	3:D:154:LEU:HD11	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:625:ILE:CD1	1:A:761:ILE:CD1	2.65	0.74
3:D:212:ILE:HD13	3:D:275:PHE:CE2	2.22	0.74
1:A:409:PHE:HZ	1:A:573:ILE:HD11	1.52	0.74
2:B:445:PHE:CZ	2:B:449:ILE:HD11	2.21	0.74
3:C:188:ILE:CD1	3:C:394:PHE:HB2	2.17	0.74
3:D:127:ILE:CD1	3:D:162:TYR:CE2	2.71	0.74
3:C:188:ILE:CD1	3:C:394:PHE:CD1	2.70	0.74
3:C:188:ILE:HD12	3:C:394:PHE:CB	2.17	0.74
1:A:321:ASP:CB	1:A:572:ILE:HD11	2.17	0.74
2:B:405:ILE:CG2	2:B:456:ILE:HD12	2.17	0.74
1:A:625:ILE:HD13	1:A:761:ILE:CG1	2.18	0.74
1:A:133:MET:SD	2:B:322:HIS:HA	2.28	0.74
1:A:625:ILE:CG2	1:A:765:ILE:CD1	2.65	0.74
1:A:118:ILE:HD12	1:A:189:LEU:HD11	1.68	0.74
3:D:127:ILE:CD1	3:D:162:TYR:CZ	2.70	0.74
2:B:402:ILE:HG22	2:B:449:ILE:HD12	1.70	0.73
1:A:143:ARG:HH21	2:B:288:TYR:HD2	0.75	0.73
1:A:371:SER:OG	1:A:404:ILE:CD1	2.36	0.73
3:D:212:ILE:CD1	3:D:302:SER:O	2.35	0.73
3:D:188:ILE:CD1	3:D:394:PHE:CB	2.65	0.73
2:B:586:ILE:CD1	2:B:735:ILE:CD1	2.66	0.73
3:C:188:ILE:HD12	3:C:394:PHE:CD1	2.23	0.73
1:A:375:ILE:CD1	1:A:396:LYS:CE	2.66	0.73
3:C:188:ILE:HD12	3:C:394:PHE:CG	2.24	0.73
3:D:212:ILE:HD13	3:D:303:ASN:ND2	2.03	0.73
1:A:128:ASP:HB3	2:B:299:ARG:HH12	1.52	0.73
1:A:625:ILE:HG21	1:A:765:ILE:CD1	2.18	0.73
1:A:108:ARG:HH21	1:A:177:ILE:CD1	1.97	0.73
3:C:258:THR:CG2	3:C:356:ILE:HD12	2.19	0.73
2:B:526:ARG:NH2	2:B:538:ILE:CD1	2.50	0.73
3:C:188:ILE:CD1	3:C:394:PHE:CG	2.71	0.73
3:C:255:ILE:CD1	3:C:358:ARG:NH1	2.52	0.73
2:B:349:TRP:CZ3	2:B:364:ILE:HD11	2.23	0.73
2:B:493:ILE:HD13	2:B:598:TYR:HB3	1.69	0.73
3:D:188:ILE:HD12	3:D:394:PHE:HB3	1.70	0.73
1:A:80:ASP:O	1:A:90:ILE:N	2.22	0.73
1:A:108:ARG:HH11	1:A:177:ILE:HD12	1.54	0.73
1:A:142:ILE:HD13	1:A:189:LEU:CD1	2.19	0.73
2:B:739:LYS:O	2:B:743:THR:O	2.05	0.73
3:D:17:VAL:CG2	3:D:231:ILE:HD11	2.19	0.73
1:A:363:ILE:HD11	1:A:366:ILE:CB	2.12	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:210:LEU:CD1	3:C:222:ILE:HD13	2.19	0.72
1:A:134:VAL:HG13	1:A:275:ILE:CD1	2.15	0.72
2:B:493:ILE:HD12	2:B:598:TYR:CB	2.18	0.72
3:C:5:ILE:HD11	3:C:252:MET:CE	2.18	0.72
1:A:138:PHE:HE2	1:A:192:ILE:CD1	2.02	0.72
1:A:599:LEU:CD1	1:A:640:ILE:HD11	2.15	0.72
2:B:525:LEU:O	2:B:538:ILE:CD1	2.37	0.72
1:A:147:GLU:OE2	2:B:288:TYR:CE2	2.42	0.72
1:A:143:ARG:HD2	2:B:288:TYR:OH	1.89	0.72
3:C:212:ILE:HD11	3:C:300:ASP:O	1.87	0.72
1:A:71:GLU:HA	2:B:216:PHE:CZ	2.24	0.72
1:A:72:GLY:O	2:B:215:ASN:OD1	2.06	0.72
3:D:284:ILE:HG22	3:D:370:ASN:H	1.54	0.72
1:A:133:MET:SD	2:B:323:GLY:HA3	2.28	0.72
3:C:280:ILE:HD11	3:C:284:ILE:HD11	1.72	0.72
1:A:797:SER:O	1:A:800:ASP:O	2.06	0.72
2:B:533:ARG:CD	2:B:538:ILE:HD13	2.18	0.72
2:B:822:ARG:NH1	2:B:825:ILE:HD12	2.04	0.72
2:B:405:ILE:HG13	2:B:456:ILE:HD11	1.69	0.72
3:D:222:ILE:HD11	3:D:227:THR:OG1	1.89	0.72
3:C:188:ILE:CD1	3:C:394:PHE:HD2	1.97	0.72
3:C:127:ILE:HD12	3:C:162:TYR:HE2	1.55	0.72
1:A:356:VAL:HG13	1:A:572:ILE:HD12	1.71	0.72
2:B:241:PHE:HB3	2:B:254:ILE:HD13	1.71	0.72
1:A:70:LEU:HD12	2:B:216:PHE:CE2	2.25	0.72
2:B:250:LYS:HD2	2:B:254:ILE:CD1	2.20	0.72
3:D:188:ILE:HD11	3:D:427:ARG:HH21	1.54	0.72
3:C:56:GLU:CB	3:D:286:HIS:CD2	2.73	0.71
2:B:499:ILE:HD11	2:B:508:PRO:CD	2.19	0.71
2:B:564:LEU:HD13	2:B:564:LEU:H	1.55	0.71
2:B:398:LEU:HD21	2:B:449:ILE:HD11	1.73	0.71
2:B:512:LEU:HA	2:B:515:VAL:HG22	1.73	0.71
3:D:255:ILE:HD11	3:D:320:ASN:ND2	2.06	0.71
2:B:441:ILE:HD12	2:B:443:THR:HG22	1.71	0.71
3:D:188:ILE:HD11	3:D:394:PHE:CD2	2.25	0.71
2:B:364:ILE:HD13	2:B:403:PHE:CD1	2.25	0.71
1:A:375:ILE:CD1	1:A:396:LYS:HE3	2.20	0.71
3:D:213:SER:HB3	3:D:222:ILE:CD1	2.20	0.71
1:A:599:LEU:CD2	1:A:640:ILE:HD11	2.17	0.71
2:B:405:ILE:CD1	2:B:456:ILE:CG1	2.68	0.71
3:D:127:ILE:CD1	3:D:162:TYR:OH	2.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:195:ILE:HD11	3:D:423:PHE:HE1	1.56	0.71
1:A:625:ILE:HG13	1:A:765:ILE:HD11	1.71	0.71
1:A:143:ARG:NH2	2:B:288:TYR:CD2	2.59	0.71
1:A:557:ILE:HD11	1:A:594:TYR:OH	1.90	0.71
1:A:695:LEU:HD23	1:A:774:ILE:HD11	1.73	0.71
2:B:499:ILE:HD12	2:B:512:LEU:HD22	1.71	0.70
1:A:73:THR:HG22	2:B:215:ASN:ND2	2.06	0.70
3:C:322:ILE:HD13	3:C:358:ARG:HH21	1.54	0.70
2:B:250:LYS:CD	2:B:254:ILE:CD1	2.69	0.70
1:A:133:MET:SD	2:B:323:GLY:N	2.64	0.70
1:A:699:ILE:HD12	1:A:775:PHE:CZ	2.26	0.70
1:A:136:GLN:HE22	2:B:324:ASP:HB2	1.55	0.70
1:A:70:LEU:HD22	2:B:216:PHE:O	1.90	0.70
3:D:5:ILE:CD1	3:D:53:PHE:CZ	2.67	0.70
1:A:151:LEU:HD22	2:B:285:ARG:CB	2.21	0.70
2:B:499:ILE:CD1	2:B:508:PRO:HA	2.20	0.70
3:D:188:ILE:HD12	3:D:394:PHE:HB2	1.70	0.70
1:A:661:LYS:HG2	1:A:664:ARG:HH21	1.57	0.70
2:B:628:ILE:HG12	2:B:629:ASN:H	1.57	0.70
3:D:188:ILE:HD12	3:D:394:PHE:CG	2.27	0.70
1:A:375:ILE:HD13	1:A:393:TYR:HA	1.74	0.70
1:A:557:ILE:HD13	1:A:594:TYR:CE2	2.27	0.70
2:B:480:ILE:HD11	2:B:541:LEU:HD13	1.74	0.70
3:C:188:ILE:HD11	3:C:391:CYS:HA	1.74	0.70
2:B:586:ILE:HD12	2:B:732:LEU:HD12	1.73	0.70
1:A:625:ILE:HD12	1:A:761:ILE:CD1	2.21	0.70
2:B:567:PRO:HG2	2:B:721:ILE:HD12	1.72	0.70
3:D:188:ILE:HD12	3:D:394:PHE:HB2	1.74	0.70
2:B:412:LEU:CD1	2:B:463:ILE:HD13	2.22	0.70
1:A:585:ILE:HD11	1:A:683:ILE:HG23	1.74	0.70
3:C:59:ARG:HH22	3:D:279:TYR:HB3	1.53	0.70
1:A:148:ASP:OD1	2:B:288:TYR:OH	2.10	0.70
1:A:138:PHE:CE2	1:A:275:ILE:HD11	2.27	0.70
3:C:127:ILE:HD13	3:C:162:TYR:CE2	2.26	0.69
3:D:188:ILE:CD1	3:D:394:PHE:HB3	2.22	0.69
1:A:567:PRO:CD	1:A:574:ILE:HD11	2.18	0.69
1:A:625:ILE:HD11	1:A:765:ILE:HG13	1.72	0.69
3:C:188:ILE:HD11	3:C:394:PHE:HD2	1.56	0.69
3:C:258:THR:HG23	3:C:356:ILE:HD11	1.74	0.69
1:A:599:LEU:HD22	1:A:640:ILE:HD13	1.74	0.69
1:A:585:ILE:HD13	1:A:683:ILE:CD1	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:445:PHE:HE1	2:B:449:ILE:CD1	2.00	0.69
1:A:695:LEU:CD2	1:A:774:ILE:HD11	2.22	0.69
2:B:586:ILE:CD1	2:B:732:LEU:HD22	2.18	0.69
1:A:606:LEU:CG	1:A:710:ILE:HD13	2.21	0.69
3:C:280:ILE:CD1	3:C:284:ILE:CG1	2.70	0.69
2:B:349:TRP:CH2	2:B:383:ILE:HD13	2.27	0.69
3:D:139:LEU:HD21	3:D:235:ILE:HD11	1.74	0.69
3:D:188:ILE:HD13	3:D:394:PHE:CD1	2.27	0.69
3:C:123:ILE:HD11	3:C:154:LEU:HD11	1.73	0.69
1:A:421:HIS:HE1	1:A:425:ILE:HD11	1.55	0.69
3:D:188:ILE:CD1	3:D:394:PHE:CG	2.74	0.69
1:A:625:ILE:CG1	1:A:765:ILE:CD1	2.70	0.69
3:C:280:ILE:CD1	3:C:284:ILE:CD1	2.70	0.69
3:C:123:ILE:HD11	3:C:154:LEU:CD1	2.23	0.69
3:D:212:ILE:HD11	3:D:302:SER:C	2.12	0.69
3:C:127:ILE:CD1	3:C:162:TYR:HE2	2.05	0.69
1:A:375:ILE:HD12	1:A:396:LYS:HE2	1.73	0.69
3:D:195:ILE:CD1	3:D:423:PHE:HE1	2.05	0.69
3:C:255:ILE:HD11	3:C:358:ARG:NH1	2.06	0.69
2:B:365:ALA:HB2	2:B:389:ARG:HH22	1.56	0.69
2:B:405:ILE:CD1	2:B:456:ILE:HG13	2.21	0.69
1:A:425:ILE:HD11	1:A:478:MET:HA	1.75	0.69
3:C:280:ILE:HD13	3:C:284:ILE:CG1	2.22	0.69
1:A:774:ILE:HD13	1:A:796:SER:HB2	1.74	0.69
2:B:612:ARG:O	2:B:776:TYR:CE2	2.45	0.69
3:C:188:ILE:HD13	3:C:394:PHE:CD1	2.28	0.69
2:B:398:LEU:CD2	2:B:449:ILE:HD11	2.22	0.69
1:A:136:GLN:NE2	2:B:324:ASP:HB2	2.07	0.69
3:C:258:THR:HG1	3:C:356:ILE:HD11	1.57	0.69
3:D:242:ILE:CD1	3:D:252:MET:HB2	2.23	0.69
3:D:258:THR:OG1	3:D:356:ILE:CD1	2.40	0.69
2:B:234:LEU:CD2	2:B:257:ILE:HD11	2.22	0.68
3:D:280:ILE:CD1	3:D:371:GLU:CD	2.59	0.68
3:C:188:ILE:HD12	3:C:394:PHE:HB2	1.74	0.68
1:A:74:TYR:CB	2:B:215:ASN:ND2	2.56	0.68
1:A:606:LEU:HD12	1:A:710:ILE:CD1	2.21	0.68
1:A:774:ILE:HD12	1:A:796:SER:HB2	1.51	0.68
2:B:234:LEU:HD23	2:B:257:ILE:HD11	1.74	0.68
2:B:430:HIS:ND1	2:B:448:ILE:CD1	2.56	0.68
3:C:8:LEU:CD2	3:C:67:ILE:HD12	2.23	0.68
3:C:127:ILE:HD12	3:C:162:TYR:OH	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:LEU:HD13	2:B:216:PHE:HA	1.74	0.68
3:D:98:GLY:CA	3:D:111:ILE:HD12	2.23	0.68
2:B:656:ILE:CD1	2:B:738:HIS:CD2	2.76	0.68
1:A:375:ILE:HD13	1:A:396:LYS:CE	2.24	0.68
3:D:127:ILE:HD12	3:D:162:TYR:OH	1.94	0.68
3:D:119:ILE:CD1	3:D:154:LEU:HD22	2.23	0.68
2:B:213:ILE:CD1	2:B:221:LEU:HD22	2.23	0.68
2:B:257:ILE:HD12	2:B:297:TYR:CD2	2.29	0.68
1:A:625:ILE:HD12	1:A:761:ILE:CG2	2.07	0.68
1:A:73:THR:HG22	2:B:215:ASN:HD21	0.75	0.68
1:A:73:THR:CG2	2:B:215:ASN:ND2	2.43	0.68
1:A:357:VAL:CG2	1:A:363:ILE:HD12	2.23	0.68
1:A:105:PHE:CZ	1:A:109:ILE:CD1	2.73	0.68
2:B:438:TYR:CG	2:B:441:ILE:HD12	2.28	0.68
1:A:138:PHE:CE1	1:A:275:ILE:CD1	2.74	0.68
3:C:59:ARG:HE	3:D:280:ILE:CD1	2.05	0.68
3:C:188:ILE:HD11	3:C:394:PHE:HB2	1.75	0.68
3:C:258:THR:HG21	3:C:356:ILE:HD13	1.77	0.68
1:A:366:ILE:CD1	1:A:404:ILE:HD13	2.24	0.68
1:A:643:ILE:HD11	1:A:696:GLN:NE2	2.09	0.67
3:C:58:CYS:N	3:D:287:LYS:HG3	2.09	0.67
1:A:151:LEU:HD21	2:B:282:SER:HB2	1.75	0.67
1:A:599:LEU:HD11	1:A:640:ILE:HD13	1.73	0.67
1:A:143:ARG:CZ	2:B:288:TYR:HE2	1.97	0.67
3:C:188:ILE:HD11	3:C:394:PHE:HB3	1.73	0.67
1:A:70:LEU:CD2	2:B:220:LEU:HD21	2.24	0.67
2:B:398:LEU:HD21	2:B:449:ILE:CD1	2.25	0.67
1:A:426:PHE:CZ	1:A:564:ILE:HD12	2.24	0.67
2:B:430:HIS:CG	2:B:448:ILE:HD12	2.29	0.67
2:B:402:ILE:CG2	2:B:449:ILE:CD1	2.70	0.67
3:C:123:ILE:HD11	3:C:154:LEU:CD1	2.21	0.67
1:A:151:LEU:CD2	2:B:285:ARG:HG3	2.23	0.67
1:A:641:LYS:HG2	3:C:356:ILE:HD13	1.77	0.67
1:A:105:PHE:CE1	1:A:109:ILE:HD11	2.28	0.67
1:A:68:ILE:CD1	2:B:281:LYS:HD2	2.24	0.67
2:B:739:LYS:O	2:B:743:THR:O	2.13	0.67
1:A:460:LYS:HZ2	2:B:833:ASP:CG	1.97	0.67
2:B:287:ILE:HG12	2:B:290:ASN:HD21	1.59	0.67
2:B:493:ILE:HD13	2:B:598:TYR:HB3	1.77	0.67
2:B:402:ILE:HD11	2:B:449:ILE:HD11	1.77	0.67
2:B:402:ILE:CG2	2:B:449:ILE:CD1	2.73	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:188:ILE:CD1	3:D:394:PHE:CG	2.78	0.67
2:B:296:ILE:HD13	2:B:319:PHE:HZ	1.54	0.67
2:B:772:PHE:CD2	2:B:812:ILE:HD13	2.30	0.67
3:C:59:ARG:NH2	3:D:285:ALA:HB3	1.95	0.67
1:A:133:MET:SD	2:B:323:GLY:CA	2.83	0.67
1:A:143:ARG:HH21	2:B:288:TYR:HD2	1.42	0.66
3:D:213:SER:HB3	3:D:222:ILE:HD11	1.76	0.66
3:C:204:PHE:CD2	3:C:231:ILE:CD1	2.76	0.66
1:A:639:PHE:CZ	1:A:643:ILE:CD1	2.71	0.66
3:C:258:THR:OG1	3:C:356:ILE:HD11	1.95	0.66
1:A:321:ASP:CG	1:A:572:ILE:HD11	2.16	0.66
1:A:557:ILE:CD1	1:A:594:TYR:CZ	2.78	0.66
2:B:779:LEU:HG	2:B:780:ASN:O	1.96	0.66
1:A:557:ILE:HD11	1:A:594:TYR:CZ	2.31	0.66
3:D:255:ILE:HD12	3:D:358:ARG:NE	2.10	0.66
2:B:293:ARG:HG3	2:B:330:ILE:CD1	2.26	0.66
1:A:202:GLU:HA	1:A:205:THR:O	1.95	0.66
1:A:625:ILE:HG22	1:A:765:ILE:HD13	1.76	0.66
2:B:349:TRP:CH2	2:B:383:ILE:CD1	2.79	0.66
3:C:59:ARG:HG2	3:D:280:ILE:CD1	2.23	0.66
2:B:586:ILE:CD1	2:B:732:LEU:HG	2.24	0.66
3:C:188:ILE:CD1	3:C:394:PHE:CE2	2.67	0.66
2:B:349:TRP:HH2	2:B:383:ILE:HD13	1.61	0.66
2:B:540:GLY:HA3	2:B:563:ILE:HD13	1.77	0.66
1:A:460:LYS:NZ	2:B:833:ASP:CG	2.49	0.66
2:B:493:ILE:CD1	2:B:598:TYR:CB	2.73	0.66
2:B:843:LYS:O	2:B:846:ARG:O	2.13	0.66
2:B:546:LEU:HB2	2:B:550:HIS:CE1	2.31	0.65
1:A:356:VAL:CG1	1:A:572:ILE:HD12	2.26	0.65
3:D:328:PRO:HB2	3:D:331:ILE:HD12	1.78	0.65
2:B:772:PHE:CE1	2:B:812:ILE:HD13	2.30	0.65
2:B:772:PHE:CE1	2:B:812:ILE:CD1	2.78	0.65
2:B:355:LEU:HB3	2:B:364:ILE:HD12	1.73	0.65
3:D:209:LEU:HD21	3:D:231:ILE:HD11	1.77	0.65
1:A:137:ARG:HH21	2:B:328:ARG:HH12	0.67	0.65
3:D:320:ASN:HD22	3:D:356:ILE:HB	1.62	0.65
2:B:586:ILE:HD12	2:B:735:ILE:HD12	1.75	0.65
1:A:134:VAL:HG13	1:A:275:ILE:HD13	1.79	0.65
2:B:402:ILE:HG12	2:B:449:ILE:CD1	2.27	0.65
2:B:527:HIS:CE1	2:B:538:ILE:HD11	2.31	0.65
2:B:628:ILE:HG12	2:B:629:ASN:H	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:TYR:CZ	1:A:177:ILE:HD13	2.32	0.65
1:A:137:ARG:HA	2:B:324:ASP:OD1	1.96	0.65
3:C:280:ILE:CD1	3:C:284:ILE:HG12	2.26	0.65
1:A:72:GLY:C	2:B:215:ASN:HB2	2.12	0.65
1:A:296:TYR:HB2	2:B:322:HIS:CE1	2.31	0.65
3:D:84:ARG:HE	3:D:84:ARG:H	1.45	0.65
3:D:119:ILE:CD1	3:D:154:LEU:CD1	2.59	0.65
3:D:213:SER:HB3	3:D:222:ILE:CD1	2.24	0.65
1:A:698:GLN:OE1	1:A:774:ILE:HD11	1.96	0.65
1:A:137:ARG:HH22	2:B:328:ARG:HH12	1.43	0.65
3:D:98:GLY:O	3:D:111:ILE:CD1	2.45	0.65
1:A:458:TYR:CD1	1:A:484:ILE:HD13	2.32	0.65
1:A:70:LEU:O	2:B:216:PHE:CD2	2.50	0.65
1:A:63:LEU:HG	1:A:170:ILE:HD11	1.79	0.65
2:B:499:ILE:HD11	2:B:508:PRO:CG	2.24	0.65
2:B:822:ARG:HH11	2:B:825:ILE:HD12	1.62	0.65
1:A:625:ILE:CG1	1:A:765:ILE:HD11	2.26	0.65
2:B:220:LEU:HD13	2:B:224:ILE:HD12	1.79	0.64
3:C:258:THR:OG1	3:C:356:ILE:CD1	2.37	0.64
1:A:151:LEU:HD12	2:B:285:ARG:CG	2.27	0.64
3:D:255:ILE:CD1	3:D:358:ARG:CZ	2.71	0.64
3:D:328:PRO:HB2	3:D:331:ILE:HD12	1.79	0.64
3:C:8:LEU:HD21	3:C:67:ILE:HD12	1.80	0.64
1:A:142:ILE:HD13	1:A:189:LEU:HD13	1.79	0.64
3:C:276:THR:CB	3:C:284:ILE:CD1	2.67	0.64
3:D:98:GLY:N	3:D:111:ILE:HD12	2.13	0.64
1:A:255:ILE:HD13	1:A:272:LEU:HD22	1.78	0.64
1:A:699:ILE:HD12	1:A:775:PHE:HZ	1.61	0.64
2:B:293:ARG:HD3	2:B:330:ILE:CD1	2.28	0.64
3:C:127:ILE:HD12	3:C:162:TYR:CE2	2.33	0.64
2:B:567:PRO:CG	2:B:721:ILE:HD12	2.27	0.64
3:C:58:CYS:HG	3:D:286:HIS:CA	1.73	0.64
1:A:73:THR:CG2	2:B:215:ASN:HD21	2.09	0.64
1:A:372:ASP:HB3	1:A:375:ILE:HD12	1.80	0.64
1:A:128:ASP:CG	2:B:299:ARG:HH22	1.99	0.64
2:B:586:ILE:CD1	2:B:732:LEU:CG	2.72	0.64
1:A:128:ASP:CB	2:B:299:ARG:NH2	2.61	0.63
3:D:97:ASP:HB2	3:D:111:ILE:HD11	1.80	0.63
1:A:695:LEU:HD21	1:A:774:ILE:CD1	2.04	0.63
1:A:699:ILE:HD13	1:A:775:PHE:CZ	2.33	0.63
2:B:586:ILE:HD11	2:B:735:ILE:HD12	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:443:ASP:HB3	3:D:445:TYR:O	1.98	0.63
3:C:188:ILE:HD12	3:C:394:PHE:CB	2.28	0.63
2:B:772:PHE:CE2	2:B:812:ILE:HD13	2.34	0.63
1:A:625:ILE:HG21	1:A:765:ILE:HD12	1.80	0.63
2:B:202:PHE:CD1	2:B:207:ILE:HD11	2.33	0.63
2:B:405:ILE:CD1	2:B:456:ILE:HD13	2.28	0.63
1:A:643:ILE:HD13	1:A:692:LEU:HD13	1.81	0.63
2:B:250:LYS:CD	2:B:254:ILE:HD11	2.28	0.63
1:A:137:ARG:HH12	2:B:325:LEU:CD2	2.09	0.63
1:A:151:LEU:HG	2:B:282:SER:HA	1.80	0.63
1:A:643:ILE:HD11	1:A:696:GLN:HE21	1.62	0.63
2:B:493:ILE:HD12	2:B:598:TYR:HB2	1.80	0.63
2:B:493:ILE:HD11	2:B:598:TYR:CD1	2.33	0.63
2:B:430:HIS:HB3	2:B:448:ILE:HD13	1.81	0.63
3:C:280:ILE:HD12	3:C:284:ILE:HD11	1.81	0.63
1:A:366:ILE:CD1	1:A:404:ILE:CD1	2.77	0.63
3:C:188:ILE:CD1	3:C:394:PHE:HB2	2.29	0.63
1:A:625:ILE:CD1	1:A:761:ILE:HG12	2.26	0.63
1:A:474:PRO:HB3	2:B:670:ARG:HH22	1.64	0.63
2:B:213:ILE:CD1	2:B:221:LEU:CD1	2.49	0.63
3:C:265:LEU:HD22	3:C:317:ASN:HD22	1.64	0.63
3:C:241:SER:OG	3:C:322:ILE:HD12	1.99	0.63
2:B:342:TYR:CE2	2:B:394:ILE:HD12	2.34	0.63
3:C:204:PHE:HB3	3:C:231:ILE:HD11	1.81	0.63
3:D:412:LEU:H	3:D:412:LEU:HD22	1.62	0.62
2:B:296:ILE:CD1	2:B:327:ILE:CD1	2.63	0.62
1:A:71:GLU:HA	2:B:216:PHE:CE2	2.34	0.62
3:C:256:TYR:CD1	3:C:260:ILE:HD12	2.34	0.62
3:D:72:GLU:HG3	3:D:76:ILE:HD12	1.80	0.62
3:C:17:VAL:HG22	3:C:228:ASN:HB3	1.80	0.62
2:B:601:GLN:HE22	2:B:605:LEU:HD11	1.65	0.62
3:C:292:TYR:CE1	3:C:296:LEU:HD21	2.34	0.62
2:B:250:LYS:HD3	2:B:254:ILE:CD1	2.30	0.62
2:B:296:ILE:HD11	2:B:319:PHE:HE1	1.57	0.62
3:C:188:ILE:HD13	3:C:394:PHE:HD1	1.54	0.62
2:B:405:ILE:CD1	2:B:456:ILE:CD1	2.76	0.62
3:C:241:SER:HG	3:C:322:ILE:HD11	1.62	0.62
3:D:139:LEU:HD21	3:D:235:ILE:HD11	1.82	0.62
3:D:212:ILE:HD12	3:D:303:ASN:ND2	2.14	0.62
2:B:207:ILE:HD13	2:B:221:LEU:HD22	1.81	0.62
1:A:366:ILE:HD11	1:A:371:SER:CB	2.27	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:ASP:CB	2:B:299:ARG:HH22	2.12	0.62
3:D:6:ILE:HD13	3:D:126:GLU:HB3	1.82	0.62
2:B:349:TRP:CZ3	2:B:383:ILE:CD1	2.82	0.62
1:A:484:ILE:CD1	1:A:560:LEU:HD11	2.30	0.62
3:D:241:SER:OG	3:D:255:ILE:HD11	1.97	0.62
1:A:285:GLU:HB3	1:A:291:ILE:HG23	1.82	0.62
2:B:250:LYS:HE2	2:B:254:ILE:HD12	1.81	0.62
3:C:258:THR:HG21	3:C:356:ILE:HD12	1.71	0.62
1:A:68:ILE:HD12	2:B:281:LYS:HD2	1.82	0.62
2:B:250:LYS:CD	2:B:254:ILE:HD12	2.30	0.62
2:B:181:GLU:HB3	2:B:184:ILE:HD12	1.82	0.61
1:A:599:LEU:HD13	1:A:640:ILE:HD11	1.80	0.61
1:A:375:ILE:HD11	1:A:396:LYS:CG	2.29	0.61
3:D:241:SER:OG	3:D:322:ILE:CD1	2.48	0.61
1:A:585:ILE:CD1	1:A:683:ILE:CG2	2.73	0.61
2:B:188:VAL:CG1	2:B:224:ILE:HD11	2.28	0.61
1:A:151:LEU:CD1	2:B:288:TYR:HE2	2.11	0.61
3:D:212:ILE:CD1	3:D:303:ASN:HA	2.30	0.61
2:B:405:ILE:HD13	2:B:452:GLN:CD	2.20	0.61
2:B:493:ILE:HD12	2:B:598:TYR:CG	2.36	0.61
1:A:128:ASP:OD1	2:B:295:ARG:CZ	2.47	0.61
1:A:581:LYS:HB3	1:A:683:ILE:CD1	2.27	0.61
2:B:405:ILE:CG1	2:B:456:ILE:HD13	2.07	0.61
1:A:368:SER:HA	1:A:373:ILE:HD13	1.81	0.61
1:A:421:HIS:NE2	1:A:425:ILE:HD12	2.15	0.61
1:A:625:ILE:HG13	1:A:765:ILE:HD13	1.77	0.61
2:B:241:PHE:HB3	2:B:254:ILE:CD1	2.30	0.61
1:A:606:LEU:HD11	1:A:710:ILE:CD1	2.30	0.61
3:C:322:ILE:HD13	3:C:358:ARG:CZ	2.30	0.61
1:A:141:GLU:HG3	1:A:144:ARG:HH21	1.66	0.61
1:A:425:ILE:CD1	1:A:482:LEU:HD13	2.31	0.61
2:B:634:ILE:HD11	2:B:772:PHE:CD1	2.35	0.61
3:D:98:GLY:HA2	3:D:111:ILE:HD12	1.82	0.61
1:A:367:PRO:HG3	1:A:373:ILE:HD13	1.82	0.61
3:C:322:ILE:HD13	3:C:358:ARG:NH2	2.16	0.61
2:B:349:TRP:CZ3	2:B:364:ILE:CD1	2.84	0.61
3:D:258:THR:CG2	3:D:356:ILE:CD1	2.68	0.61
1:A:122:ALA:HB1	1:A:126:TRP:CZ2	2.36	0.61
3:D:212:ILE:HD12	3:D:303:ASN:HA	1.82	0.61
2:B:402:ILE:HD11	2:B:449:ILE:HD13	1.83	0.61
2:B:612:ARG:O	2:B:776:TYR:CD2	2.53	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:127:ILE:CD1	3:D:162:TYR:OH	2.48	0.61
2:B:607:SER:CB	2:B:634:ILE:HD13	2.28	0.61
2:B:207:ILE:HD11	2:B:225:PHE:HA	1.82	0.61
2:B:493:ILE:CD1	2:B:598:TYR:HB2	2.31	0.61
2:B:478:LYS:HA	2:B:482:LEU:HD23	1.80	0.61
3:C:234:ILE:HD11	3:C:303:ASN:ND2	2.16	0.60
2:B:257:ILE:CD1	2:B:297:TYR:CD2	2.83	0.60
3:D:97:ASP:O	3:D:111:ILE:HD13	2.00	0.60
2:B:339:ILE:HD11	2:B:439:ARG:HD3	1.82	0.60
3:D:97:ASP:CB	3:D:111:ILE:HD11	2.31	0.60
3:C:4:GLU:HG3	3:C:131:ASP:H	1.67	0.60
3:D:17:VAL:CG2	3:D:231:ILE:CD1	2.79	0.60
3:C:57:ASN:O	3:D:286:HIS:ND1	2.24	0.60
3:C:188:ILE:CD1	3:C:394:PHE:HD2	2.11	0.60
3:C:296:LEU:HD13	3:C:376:MET:HB2	1.83	0.60
3:D:127:ILE:HD12	3:D:162:TYR:OH	2.02	0.60
1:A:126:TRP:HH2	1:A:192:ILE:HD13	1.66	0.60
3:C:210:LEU:CG	3:C:222:ILE:HD11	2.30	0.60
3:C:188:ILE:HD13	3:C:394:PHE:CG	2.34	0.60
1:A:557:ILE:CD1	1:A:594:TYR:OH	2.49	0.60
2:B:297:TYR:OH	2:B:330:ILE:HD12	2.02	0.60
1:A:625:ILE:HD12	1:A:761:ILE:HD11	1.84	0.60
1:A:613:LYS:HG3	1:A:614:TYR:O	2.00	0.60
1:A:630:ARG:HA	1:A:633:HIS:CD2	2.36	0.60
1:A:606:LEU:CD1	1:A:710:ILE:HD13	2.31	0.60
1:A:375:ILE:CD1	1:A:396:LYS:HB3	2.31	0.60
2:B:402:ILE:HG23	2:B:449:ILE:HD13	1.82	0.60
2:B:525:LEU:CD2	2:B:538:ILE:HD12	2.21	0.60
3:D:212:ILE:HD13	3:D:303:ASN:CG	2.21	0.60
1:A:699:ILE:HD11	1:A:775:PHE:HE1	1.60	0.60
3:C:59:ARG:HG2	3:D:280:ILE:HD13	1.80	0.60
3:D:98:GLY:HA3	3:D:111:ILE:HD13	1.84	0.60
2:B:346:LEU:HD11	2:B:402:ILE:HD13	1.84	0.60
3:C:7:THR:HG23	3:C:139:LEU:HD13	1.84	0.59
2:B:430:HIS:CB	2:B:448:ILE:HD13	2.32	0.59
2:B:731:PHE:CE1	2:B:735:ILE:HD12	2.34	0.59
1:A:566:ILE:HD12	1:A:576:ARG:HG2	1.83	0.59
2:B:209:ILE:HD12	2:B:213:ILE:HD13	1.83	0.59
3:C:72:GLU:HB2	3:C:76:ILE:HD11	1.83	0.59
1:A:70:LEU:HD12	2:B:216:PHE:CD2	2.36	0.59
3:D:188:ILE:HD11	3:D:393:THR:C	2.22	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:188:ILE:CD1	3:D:394:PHE:CD1	2.85	0.59
1:A:151:LEU:HD11	2:B:282:SER:OG	2.02	0.59
1:A:72:GLY:HA2	2:B:215:ASN:HB3	1.78	0.59
3:C:59:ARG:HH21	3:D:285:ALA:N	2.01	0.59
3:C:395:ASP:HA	3:C:398:PHE:CE2	2.37	0.59
1:A:143:ARG:HH22	2:B:292:ILE:HD13	1.46	0.59
3:C:127:ILE:HD12	3:C:162:TYR:CE2	2.34	0.59
3:C:59:ARG:HE	3:D:280:ILE:CG1	2.14	0.59
3:C:127:ILE:HD11	3:C:162:TYR:CE2	2.36	0.59
1:A:201:GLU:HA	1:A:204:ARG:HE	1.67	0.59
3:D:5:ILE:HD12	3:D:53:PHE:HE2	1.61	0.59
3:C:31:ILE:HD12	3:C:35:GLY:HA2	1.83	0.59
2:B:412:LEU:HD11	2:B:463:ILE:HD13	1.83	0.59
1:A:409:PHE:CE1	1:A:573:ILE:HD11	2.38	0.59
3:D:258:THR:OG1	3:D:356:ILE:HD11	2.03	0.59
1:A:625:ILE:CD1	1:A:761:ILE:HD13	2.33	0.59
1:A:157:ARG:HH11	1:A:173:LEU:HD22	1.67	0.59
2:B:607:SER:CB	2:B:634:ILE:CD1	2.81	0.59
3:C:412:LEU:HD22	3:C:412:LEU:H	1.68	0.59
3:D:17:VAL:HG21	3:D:231:ILE:CD1	2.33	0.59
1:A:147:GLU:CB	2:B:285:ARG:HD3	2.29	0.59
3:D:119:ILE:HD13	3:D:154:LEU:HD11	1.84	0.59
3:D:127:ILE:HD11	3:D:162:TYR:CE2	2.38	0.59
1:A:414:ASP:O	1:A:418:VAL:HG23	2.02	0.58
1:A:699:ILE:CD1	1:A:775:PHE:CZ	2.86	0.58
1:A:625:ILE:CD1	1:A:758:LEU:HD12	2.32	0.58
1:A:606:LEU:HD21	1:A:710:ILE:HD13	1.84	0.58
3:C:258:THR:CG2	3:C:356:ILE:CD1	2.81	0.58
1:A:699:ILE:HD11	1:A:775:PHE:CE2	2.38	0.58
2:B:246:ILE:HG12	2:B:247:SER:H	1.68	0.58
1:A:128:ASP:OD1	2:B:299:ARG:NH2	2.35	0.58
3:C:204:PHE:HB3	3:C:231:ILE:CD1	2.33	0.58
1:A:774:ILE:HD11	1:A:796:SER:CB	2.33	0.58
3:D:130:THR:HG21	3:D:133:PHE:HB2	1.85	0.58
2:B:607:SER:HB3	2:B:634:ILE:CD1	2.32	0.58
2:B:402:ILE:HG22	2:B:449:ILE:HD13	1.85	0.58
2:B:290:ASN:H	2:B:290:ASN:HD22	1.52	0.58
1:A:375:ILE:CD1	1:A:396:LYS:CG	2.81	0.58
1:A:458:TYR:CG	1:A:484:ILE:CD1	2.86	0.58
1:A:409:PHE:CZ	1:A:573:ILE:CD1	2.84	0.58
2:B:297:TYR:OH	2:B:330:ILE:CD1	2.48	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:127:ILE:HD13	3:C:162:TYR:CZ	2.38	0.58
1:A:339:GLU:H	1:A:339:GLU:CD	2.07	0.58
2:B:398:LEU:CD2	2:B:449:ILE:CD1	2.82	0.58
1:A:196:ILE:HD11	1:A:250:ILE:HD13	1.86	0.58
1:A:137:ARG:NH2	2:B:325:LEU:HD22	2.17	0.58
2:B:499:ILE:HD12	2:B:512:LEU:HD23	1.86	0.58
2:B:250:LYS:HE2	2:B:254:ILE:CD1	2.33	0.58
1:A:695:LEU:CG	1:A:774:ILE:CD1	2.81	0.58
3:C:59:ARG:NH2	3:D:284:ILE:C	2.57	0.58
3:D:119:ILE:HD12	3:D:154:LEU:HD11	1.82	0.58
2:B:293:ARG:CD	2:B:330:ILE:HD11	2.33	0.58
2:B:339:ILE:HD13	2:B:343:TYR:OH	2.04	0.58
2:B:586:ILE:CD1	2:B:732:LEU:HD23	2.33	0.58
2:B:771:GLU:OE1	2:B:812:ILE:HD11	2.04	0.58
3:C:127:ILE:HD13	3:C:162:TYR:OH	2.03	0.58
2:B:207:ILE:CD1	2:B:221:LEU:HD22	2.34	0.58
3:C:250:SER:O	3:C:255:ILE:HD12	2.04	0.58
1:A:126:TRP:CE2	1:A:192:ILE:HD13	2.39	0.58
2:B:241:PHE:CB	2:B:254:ILE:HD11	2.25	0.58
1:A:73:THR:HG22	2:B:215:ASN:CG	2.24	0.57
3:D:139:LEU:HD21	3:D:235:ILE:HD13	1.85	0.57
3:D:412:LEU:H	3:D:412:LEU:HD22	1.69	0.57
2:B:405:ILE:CD1	2:B:452:GLN:CD	2.72	0.57
2:B:480:ILE:HD11	2:B:537:VAL:HG13	1.83	0.57
1:A:151:LEU:HD12	2:B:286:GLU:OE2	1.99	0.57
1:A:151:LEU:HD11	2:B:282:SER:OG	2.04	0.57
3:C:5:ILE:HD11	3:C:252:MET:HE1	1.85	0.57
1:A:151:LEU:HD22	2:B:285:ARG:CG	2.29	0.57
2:B:319:PHE:CE1	2:B:327:ILE:HD11	2.39	0.57
3:C:58:CYS:HB3	3:D:287:LYS:N	2.20	0.57
1:A:566:ILE:HG12	1:A:574:ILE:HD12	1.82	0.57
1:A:638:HIS:CE1	3:C:355:ASN:H	2.23	0.57
3:D:188:ILE:HD13	3:D:394:PHE:HA	1.86	0.57
3:D:188:ILE:CD1	3:D:394:PHE:CG	2.87	0.57
3:C:57:ASN:O	3:D:286:HIS:CG	2.58	0.57
3:C:58:CYS:O	3:D:286:HIS:CB	2.52	0.57
3:C:221:ASN:O	3:C:226:HIS:CE1	2.57	0.57
1:A:70:LEU:HG	2:B:216:PHE:CB	2.34	0.57
2:B:532:PRO:C	2:B:538:ILE:HD12	2.21	0.57
1:A:105:PHE:CD1	1:A:170:ILE:HD11	2.39	0.57
1:A:699:ILE:HD13	1:A:793:PHE:HZ	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:695:LEU:HG	1:A:774:ILE:CD1	2.35	0.57
2:B:489:MET:CE	2:B:493:ILE:HD11	2.34	0.57
1:A:375:ILE:CD1	1:A:396:LYS:HE2	2.34	0.57
1:A:699:ILE:HD11	1:A:775:PHE:CZ	2.38	0.57
3:C:119:ILE:HD11	3:C:154:LEU:HD22	1.86	0.57
2:B:548:LEU:O	2:B:550:HIS:CD2	2.58	0.56
3:D:222:ILE:CD1	3:D:227:THR:OG1	2.53	0.56
3:C:188:ILE:HD12	3:C:394:PHE:CB	2.31	0.56
2:B:812:ILE:HG23	2:B:816:TYR:CE2	2.39	0.56
3:D:283:ASP:HA	3:D:370:ASN:HB2	1.87	0.56
3:D:139:LEU:CD2	3:D:235:ILE:HD11	2.35	0.56
1:A:699:ILE:HD13	1:A:793:PHE:CZ	2.41	0.56
2:B:525:LEU:HD11	2:B:538:ILE:HG13	1.86	0.56
2:B:526:ARG:HH22	2:B:538:ILE:CD1	2.18	0.56
1:A:585:ILE:HD13	1:A:683:ILE:HG21	1.88	0.56
3:C:46:ARG:HH12	3:C:365:LEU:H	1.52	0.56
2:B:402:ILE:HD11	2:B:449:ILE:HD13	1.87	0.56
3:D:67:ILE:HD11	3:D:122:LYS:HB2	1.87	0.56
1:A:699:ILE:CD1	1:A:775:PHE:HE1	2.09	0.56
2:B:405:ILE:CG1	2:B:456:ILE:HD13	2.34	0.56
3:D:17:VAL:CG1	3:D:231:ILE:HD11	2.34	0.56
1:A:261:ASP:O	1:A:265:VAL:HG23	2.05	0.56
3:C:188:ILE:HD12	3:C:394:PHE:HD1	1.55	0.56
3:C:188:ILE:HD13	3:C:394:PHE:CG	2.41	0.56
2:B:364:ILE:CD1	2:B:403:PHE:HD1	2.14	0.56
2:B:527:HIS:CD2	2:B:538:ILE:HD11	2.40	0.56
2:B:825:ILE:HG22	2:B:837:GLU:HB2	1.88	0.56
1:A:625:ILE:CD1	1:A:758:LEU:CD1	2.83	0.56
3:C:130:THR:HG21	3:C:133:PHE:HB2	1.87	0.56
3:D:188:ILE:HD11	3:D:394:PHE:CG	2.41	0.56
3:D:17:VAL:HG21	3:D:231:ILE:HD13	1.86	0.56
1:A:138:PHE:CE2	1:A:275:ILE:CD1	2.86	0.56
3:D:326:VAL:HG21	3:D:370:ASN:HD22	1.70	0.55
1:A:599:LEU:HD12	1:A:640:ILE:CD1	2.36	0.55
1:A:78:PHE:HB2	1:A:91:GLU:H	1.71	0.55
3:C:188:ILE:HD12	3:C:394:PHE:HB2	1.87	0.55
3:C:240:ASN:OD1	3:C:322:ILE:CD1	2.49	0.55
3:C:56:GLU:HB2	3:D:286:HIS:NE2	2.22	0.55
1:A:151:LEU:HG	2:B:285:ARG:CD	2.34	0.55
2:B:818:ASN:HB3	2:B:822:ARG:HH12	1.71	0.55
1:A:599:LEU:HD12	1:A:640:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:599:LEU:HD13	1:A:640:ILE:CD1	2.36	0.55
2:B:430:HIS:CB	2:B:448:ILE:CD1	2.84	0.55
2:B:430:HIS:CG	2:B:448:ILE:HD11	2.34	0.55
1:A:72:GLY:HA2	2:B:215:ASN:HB3	1.88	0.55
2:B:546:LEU:H	2:B:550:HIS:CE1	2.24	0.55
1:A:420:LYS:HA	1:A:423:GLN:HE21	1.72	0.55
2:B:463:ILE:HA	2:B:467:LYS:HG2	1.89	0.55
1:A:169:SER:HA	1:A:171:ARG:HH21	1.71	0.55
1:A:603:TRP:CE2	1:A:633:HIS:HB2	2.41	0.55
1:A:284:TYR:O	1:A:288:THR:HG22	2.05	0.55
2:B:349:TRP:HE1	2:B:403:PHE:HA	1.71	0.55
2:B:430:HIS:CG	2:B:448:ILE:HD13	2.41	0.55
1:A:479:ARG:HG3	1:A:480:GLN:HE21	1.72	0.55
3:D:391:CYS:HA	3:D:394:PHE:CD2	2.41	0.55
2:B:349:TRP:CZ3	2:B:383:ILE:HD11	2.41	0.55
3:D:391:CYS:HA	3:D:394:PHE:CD2	2.42	0.55
3:C:322:ILE:CD1	3:C:358:ARG:HH21	2.01	0.55
1:A:328:LYS:H	1:A:328:LYS:HD2	1.72	0.55
3:D:31:ILE:HG22	3:D:37:SER:HA	1.89	0.55
1:A:603:TRP:CE2	1:A:633:HIS:HB2	2.42	0.55
1:A:109:ILE:HD11	1:A:170:ILE:HD13	1.87	0.55
3:D:105:TRP:CH2	3:D:109:TYR:CD2	2.94	0.55
2:B:289:GLU:CD	2:B:289:GLU:H	2.10	0.55
2:B:413:GLU:OE2	2:B:419:VAL:HG11	2.07	0.55
2:B:402:ILE:HD11	2:B:449:ILE:CD1	2.36	0.55
2:B:533:ARG:CA	2:B:538:ILE:HD12	2.36	0.55
2:B:489:MET:HE2	2:B:493:ILE:HD11	1.88	0.55
1:A:557:ILE:HD11	1:A:594:TYR:OH	1.97	0.55
1:A:138:PHE:CE2	1:A:142:ILE:CD1	2.90	0.55
1:A:142:ILE:CD1	1:A:189:LEU:HD13	2.36	0.55
2:B:207:ILE:HG12	2:B:209:ILE:H	1.72	0.55
2:B:220:LEU:HD11	2:B:224:ILE:HD11	1.88	0.55
1:A:706:PHE:CD1	1:A:768:ILE:HD13	2.41	0.55
1:A:120:THR:HA	1:A:123:TYR:CZ	2.42	0.55
3:D:412:LEU:HD22	3:D:412:LEU:H	1.71	0.55
2:B:437:SER:HB2	2:B:441:ILE:HD11	1.87	0.55
2:B:412:LEU:HD13	2:B:463:ILE:HD13	1.88	0.55
3:D:127:ILE:HD13	3:D:162:TYR:CE2	2.41	0.55
3:D:173:PHE:CD1	3:D:203:VAL:HG13	2.41	0.55
3:C:276:THR:HG1	3:C:284:ILE:HD11	1.72	0.55
3:C:210:LEU:CD1	3:C:222:ILE:HD11	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:123:ILE:HD13	3:D:158:LEU:HD21	1.88	0.55
3:D:188:ILE:HD12	3:D:394:PHE:CE1	2.39	0.55
1:A:151:LEU:HD12	2:B:285:ARG:HD3	1.88	0.55
2:B:364:ILE:CD1	2:B:403:PHE:CD1	2.90	0.54
2:B:574:VAL:HG23	2:B:576:ARG:H	1.72	0.54
2:B:349:TRP:CE3	2:B:364:ILE:HD11	2.42	0.54
1:A:625:ILE:CD1	1:A:761:ILE:HB	2.28	0.54
2:B:493:ILE:HD12	2:B:598:TYR:HB3	1.88	0.54
1:A:363:ILE:HD11	1:A:412:GLY:O	2.07	0.54
1:A:140:TYR:OH	2:B:324:ASP:OD1	2.24	0.54
3:D:97:ASP:O	3:D:111:ILE:CD1	2.55	0.54
1:A:606:LEU:HD11	1:A:710:ILE:HD12	1.89	0.54
1:A:462:LEU:HD22	1:A:484:ILE:HG22	1.89	0.54
1:A:375:ILE:CD1	1:A:396:LYS:CB	2.85	0.54
3:D:292:TYR:CZ	3:D:296:LEU:HD11	2.42	0.54
1:A:699:ILE:HD11	1:A:775:PHE:CD1	2.43	0.54
3:D:258:THR:CG2	3:D:356:ILE:HD13	2.38	0.54
3:D:67:ILE:HD11	3:D:122:LYS:CB	2.38	0.54
1:A:567:PRO:HD3	1:A:574:ILE:CD1	2.37	0.54
1:A:137:ARG:NH2	2:B:328:ARG:HH12	2.05	0.54
1:A:280:CYS:HB3	1:A:380:ASP:HA	1.89	0.54
3:D:17:VAL:CG2	3:D:231:ILE:CD1	2.82	0.54
3:C:6:ILE:HD13	3:C:126:GLU:HB3	1.88	0.54
2:B:346:LEU:HD23	2:B:445:PHE:CZ	2.43	0.54
1:A:585:ILE:HD11	1:A:683:ILE:HG23	1.83	0.54
1:A:357:VAL:CG2	1:A:363:ILE:CD1	2.86	0.54
3:D:243:ARG:HH12	3:D:363:LEU:HD21	1.71	0.54
3:C:17:VAL:HG22	3:C:228:ASN:HB3	1.90	0.54
1:A:564:ILE:HD13	1:A:579:MET:HG3	1.89	0.54
1:A:625:ILE:CD1	1:A:761:ILE:CG1	2.86	0.54
3:C:188:ILE:HD12	3:C:394:PHE:HD2	1.62	0.54
2:B:354:LEU:HD21	2:B:410:ILE:CD1	2.37	0.54
1:A:328:LYS:HD2	1:A:328:LYS:H	1.71	0.54
3:C:188:ILE:HD11	3:C:394:PHE:CD2	2.39	0.54
2:B:181:GLU:OE1	2:B:184:ILE:CD1	2.53	0.54
3:D:105:TRP:CZ2	3:D:109:TYR:CD2	2.96	0.54
2:B:354:LEU:CD2	2:B:410:ILE:HD12	2.38	0.54
3:D:124:ASP:HA	3:D:127:ILE:HG12	1.90	0.54
3:C:358:ARG:HA	3:C:358:ARG:HE	1.72	0.54
2:B:657:ILE:HG22	2:B:735:ILE:HD11	1.89	0.54
3:D:119:ILE:CD1	3:D:154:LEU:HD21	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:124:ASP:HA	3:D:127:ILE:HG12	1.90	0.54
3:C:17:VAL:HG21	3:C:231:ILE:HG23	1.89	0.54
1:A:114:LYS:HE3	1:A:118:ILE:HD11	1.90	0.54
3:C:212:ILE:HD11	3:C:300:ASP:C	2.29	0.54
2:B:653:LEU:CD2	2:B:657:ILE:HD12	2.35	0.54
1:A:138:PHE:HB2	1:A:275:ILE:HD11	1.89	0.54
2:B:527:HIS:CE1	2:B:538:ILE:HG23	2.42	0.54
1:A:625:ILE:CD1	1:A:765:ILE:HD11	2.37	0.54
3:C:119:ILE:HD13	3:C:154:LEU:HD13	1.89	0.54
2:B:489:MET:O	2:B:493:ILE:HG13	2.08	0.53
1:A:323:GLN:HG2	1:A:324:TYR:H	1.73	0.53
3:C:188:ILE:HD11	3:C:427:ARG:HH22	1.73	0.53
1:A:75:ILE:HG12	1:A:94:ILE:HG22	1.90	0.53
2:B:426:SER:O	2:B:430:HIS:CG	2.61	0.53
2:B:525:LEU:O	2:B:538:ILE:HD13	2.08	0.53
3:C:10:ALA:HB1	3:C:147:GLY:HA2	1.89	0.53
1:A:56:GLU:CD	1:A:56:GLU:H	2.11	0.53
2:B:282:SER:HA	2:B:285:ARG:HE	1.74	0.53
3:D:318:VAL:HG22	3:D:319:TYR:N	2.23	0.53
2:B:611:ILE:HD13	2:B:777:CYS:CB	2.38	0.53
2:B:507:LEU:HB2	2:B:508:PRO:HD3	1.90	0.53
1:A:72:GLY:HA3	2:B:215:ASN:ND2	2.24	0.53
3:C:123:ILE:HG22	3:C:127:ILE:CD1	2.38	0.53
1:A:138:PHE:HE2	1:A:275:ILE:HD12	1.70	0.53
3:C:292:TYR:CZ	3:C:296:LEU:HD11	2.42	0.53
2:B:555:TRP:CE3	2:B:595:LYS:HD2	2.43	0.53
3:C:258:THR:HG21	3:C:356:ILE:CD1	2.37	0.53
2:B:586:ILE:CD1	2:B:735:ILE:HD11	2.39	0.53
1:A:126:TRP:CH2	1:A:192:ILE:HD13	2.44	0.53
3:C:59:ARG:HA	3:D:281:HIS:CE1	2.43	0.53
1:A:129:THR:H	1:A:130:SER:HA	1.74	0.53
3:D:193:ARG:HH12	3:D:419:VAL:HG11	1.72	0.53
1:A:132:GLY:HA3	1:A:135:LEU:HD13	1.90	0.53
3:C:78:ASP:HB3	3:C:87:PHE:CE2	2.44	0.53
3:D:242:ILE:CD1	3:D:252:MET:CE	2.87	0.53
3:C:188:ILE:HD12	3:C:394:PHE:HB2	1.91	0.53
1:A:458:TYR:CE1	1:A:484:ILE:CD1	2.73	0.53
1:A:567:PRO:CD	1:A:574:ILE:CD1	2.86	0.53
2:B:719:LEU:HD23	2:B:720:ASN:H	1.73	0.53
2:B:405:ILE:HD11	2:B:456:ILE:HD13	1.90	0.53
1:A:151:LEU:CD1	2:B:285:ARG:CD	2.64	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:241:PHE:CB	2:B:254:ILE:CD1	2.86	0.53
2:B:390:VAL:HG23	2:B:396:LYS:HD2	1.91	0.53
1:A:63:LEU:HG	1:A:170:ILE:HD11	1.91	0.53
1:A:774:ILE:HD11	1:A:796:SER:HB2	1.90	0.53
2:B:355:LEU:CB	2:B:364:ILE:CD1	2.55	0.53
1:A:137:ARG:HD2	2:B:324:ASP:HA	1.90	0.53
1:A:625:ILE:CD1	1:A:761:ILE:HD11	2.36	0.53
2:B:480:ILE:HD11	2:B:537:VAL:HG22	1.91	0.53
2:B:563:ILE:HD13	2:B:565:TYR:OH	2.09	0.53
3:C:166:ILE:HD11	3:C:256:TYR:CD2	2.42	0.53
3:D:212:ILE:HD11	3:D:302:SER:O	2.09	0.53
1:A:189:LEU:O	1:A:192:ILE:HG12	2.08	0.53
1:A:372:ASP:HB3	1:A:375:ILE:CD1	2.38	0.53
1:A:151:LEU:HD11	2:B:282:SER:HB2	1.91	0.53
1:A:142:ILE:HD13	1:A:188:LEU:HD13	1.89	0.52
1:A:361:LEU:HG	1:A:365:THR:H	1.74	0.52
3:D:123:ILE:HD12	3:D:161:ARG:HH12	1.74	0.52
3:C:59:ARG:CZ	3:D:286:HIS:ND1	2.72	0.52
2:B:445:PHE:CE2	2:B:449:ILE:HD11	2.44	0.52
3:D:213:SER:HB3	3:D:222:ILE:HD11	1.86	0.52
1:A:625:ILE:CB	1:A:765:ILE:HD13	2.39	0.52
3:D:21:LEU:HD12	3:D:235:ILE:CD1	2.26	0.52
1:A:133:MET:HE3	2:B:323:GLY:H	1.74	0.52
1:A:624:ARG:HE	1:A:624:ARG:H	1.56	0.52
3:C:210:LEU:HD11	3:C:222:ILE:HD13	1.89	0.52
1:A:126:TRP:CD2	1:A:135:LEU:HB3	2.45	0.52
3:C:8:LEU:HD22	3:C:67:ILE:HD11	1.91	0.52
2:B:586:ILE:HD11	2:B:735:ILE:HD11	1.91	0.52
3:D:127:ILE:HD13	3:D:162:TYR:CE2	2.38	0.52
1:A:137:ARG:NH2	2:B:328:ARG:CZ	2.69	0.52
3:D:258:THR:HG21	3:D:356:ILE:HD13	1.91	0.52
1:A:151:LEU:CD1	2:B:282:SER:OG	2.46	0.52
1:A:695:LEU:HD23	1:A:774:ILE:CD1	2.27	0.52
1:A:599:LEU:HG	1:A:640:ILE:HD11	1.90	0.52
2:B:335:PHE:CE2	2:B:339:ILE:HD11	2.44	0.52
3:D:188:ILE:HD13	3:D:394:PHE:CG	2.44	0.52
3:C:188:ILE:CD1	3:C:394:PHE:CG	2.92	0.52
2:B:402:ILE:HG22	2:B:449:ILE:CD1	2.40	0.52
2:B:288:TYR:O	2:B:291:ILE:HG12	2.09	0.52
2:B:546:LEU:H	2:B:550:HIS:HE1	1.55	0.52
3:C:22:TRP:CZ2	3:C:66:ALA:HB2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:599:LEU:HG	1:A:640:ILE:CD1	2.40	0.52
1:A:625:ILE:HD13	1:A:761:ILE:HD13	1.92	0.52
3:C:67:ILE:HD11	3:C:126:GLU:HG3	1.92	0.52
2:B:568:LEU:HD23	2:B:721:ILE:HD11	1.91	0.52
2:B:402:ILE:HG23	2:B:449:ILE:HD12	1.86	0.52
3:C:380:MET:HG3	3:C:382:THR:HG22	1.92	0.52
1:A:183:ASN:HD22	1:A:183:ASN:H	1.58	0.52
1:A:624:ARG:HG2	1:A:627:ARG:HH21	1.74	0.52
3:C:258:THR:HG21	3:C:356:ILE:HD11	1.92	0.52
3:C:234:ILE:HD11	3:C:303:ASN:ND2	2.25	0.52
2:B:220:LEU:HD13	2:B:224:ILE:CD1	2.40	0.52
3:C:398:PHE:HA	3:C:404:LEU:HD21	1.92	0.52
3:C:111:ILE:HA	3:C:114:ARG:HE	1.75	0.52
3:C:5:ILE:HD12	3:C:53:PHE:CZ	2.45	0.52
4:F:41:UNK:O	4:F:44:UNK:O	2.27	0.52
3:C:21:LEU:HD13	3:C:235:ILE:HG23	1.92	0.52
2:B:247:SER:HA	2:B:359:TYR:CE2	2.45	0.52
2:B:455:GLU:O	2:B:459:HIS:CD2	2.63	0.52
1:A:466:GLU:HG3	1:A:479:ARG:HH21	1.75	0.52
1:A:138:PHE:CE2	1:A:142:ILE:HD12	2.45	0.52
3:D:212:ILE:CD1	3:D:303:ASN:ND2	2.59	0.52
2:B:206:GLN:HG2	2:B:207:ILE:H	1.75	0.52
2:B:533:ARG:HD3	2:B:538:ILE:CD1	2.37	0.52
3:D:4:GLU:HB2	3:D:130:THR:HG23	1.92	0.52
3:C:234:ILE:HG12	3:C:272:PHE:CD2	2.45	0.52
3:C:59:ARG:NH2	3:D:284:ILE:HG21	2.24	0.52
1:A:68:ILE:HD11	2:B:281:LYS:HD2	1.91	0.51
2:B:222:HIS:HA	2:B:225:PHE:CE2	2.45	0.51
1:A:143:ARG:NE	2:B:288:TYR:CD2	2.70	0.51
1:A:625:ILE:HD11	1:A:765:ILE:HD11	1.92	0.51
1:A:72:GLY:HA3	2:B:215:ASN:HB3	1.92	0.51
2:B:220:LEU:CD1	2:B:224:ILE:CD1	2.88	0.51
2:B:532:PRO:HB2	2:B:538:ILE:HD11	1.92	0.51
3:C:195:ILE:HD12	3:C:423:PHE:HZ	1.75	0.51
1:A:421:HIS:NE2	1:A:425:ILE:CD1	2.74	0.51
3:D:188:ILE:HD13	3:D:394:PHE:HB2	1.91	0.51
3:D:17:VAL:HG21	3:D:231:ILE:HD12	1.92	0.51
3:D:320:ASN:ND2	3:D:356:ILE:HD12	2.25	0.51
1:A:105:PHE:O	1:A:109:ILE:HG13	2.11	0.51
1:A:585:ILE:HD11	1:A:683:ILE:CG2	2.39	0.51
3:D:231:ILE:O	3:D:235:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:493:ILE:HD13	2:B:598:TYR:CB	2.40	0.51
3:D:256:TYR:CZ	3:D:260:ILE:HD11	2.45	0.51
1:A:285:GLU:HB3	1:A:291:ILE:HG23	1.92	0.51
3:D:70:ASP:CG	3:D:71:SER:H	2.12	0.51
3:C:188:ILE:HD12	3:C:394:PHE:CG	2.46	0.51
3:D:4:GLU:HB2	3:D:130:THR:HG23	1.92	0.51
1:A:425:ILE:CD1	1:A:478:MET:HA	2.40	0.51
2:B:532:PRO:C	2:B:538:ILE:CD1	2.78	0.51
2:B:182:GLU:CD	2:B:182:GLU:H	2.14	0.51
2:B:405:ILE:HG13	2:B:456:ILE:CD1	2.41	0.51
1:A:294:ASP:HB3	1:A:297:GLN:HA	1.93	0.51
3:C:59:ARG:NH2	3:D:285:ALA:N	2.58	0.51
3:C:201:THR:HG22	3:C:266:HIS:CD2	2.45	0.51
1:A:606:LEU:CD1	1:A:710:ILE:HD12	2.40	0.51
3:C:338:LEU:HA	3:C:341:ARG:HE	1.75	0.51
2:B:181:GLU:H	2:B:184:ILE:HD12	1.76	0.51
1:A:451:ARG:H	1:A:454:ASN:HB2	1.75	0.51
2:B:319:PHE:CE1	2:B:327:ILE:HG23	2.46	0.51
1:A:155:VAL:HG21	2:B:278:VAL:CG2	2.41	0.51
1:A:371:SER:HG	1:A:404:ILE:HD11	1.76	0.51
1:A:630:ARG:HE	1:A:633:HIS:CE1	2.29	0.51
3:C:188:ILE:HD11	3:C:394:PHE:CB	2.33	0.51
3:C:395:ASP:HA	3:C:398:PHE:CZ	2.46	0.51
2:B:366:GLU:CD	2:B:367:ASN:O	2.49	0.51
1:A:626:VAL:O	1:A:629:THR:HG22	2.11	0.51
1:A:566:ILE:HG22	1:A:574:ILE:HD11	1.93	0.51
1:A:366:ILE:HD11	1:A:404:ILE:HD13	1.91	0.51
3:D:256:TYR:HE1	3:D:260:ILE:CD1	2.16	0.51
1:A:109:ILE:HA	1:A:112:TYR:CD2	2.46	0.51
1:A:320:TRP:O	1:A:572:ILE:HD11	2.10	0.51
2:B:181:GLU:OE1	2:B:184:ILE:HD11	2.11	0.51
2:B:606:LYS:HE2	2:B:773:VAL:HG11	1.92	0.51
1:A:606:LEU:CG	1:A:710:ILE:CD1	2.87	0.51
3:D:105:TRP:CE3	3:D:189:LEU:HD23	2.46	0.50
2:B:405:ILE:HD13	2:B:452:GLN:NE2	2.25	0.50
3:D:188:ILE:CD1	3:D:394:PHE:HB2	2.41	0.50
1:A:625:ILE:CD1	1:A:761:ILE:HD13	2.34	0.50
2:B:285:ARG:HH21	2:B:286:GLU:HB2	1.76	0.50
1:A:625:ILE:HD11	1:A:758:LEU:HD11	1.89	0.50
1:A:655:GLU:O	1:A:659:LEU:HD13	2.10	0.50
2:B:843:LYS:O	2:B:846:ARG:O	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:72:GLU:HB2	3:C:76:ILE:CD1	2.40	0.50
2:B:402:ILE:HG21	2:B:449:ILE:CD1	2.42	0.50
1:A:321:ASP:OD2	1:A:572:ILE:HD12	2.11	0.50
2:B:430:HIS:HB3	2:B:448:ILE:CD1	2.39	0.50
2:B:355:LEU:HD12	2:B:362:PHE:CD2	2.46	0.50
3:D:215:LYS:HG3	3:D:216:VAL:HG23	1.94	0.50
1:A:151:LEU:CG	2:B:282:SER:HA	2.39	0.50
3:C:289:HIS:CE1	3:C:331:ILE:HG22	2.47	0.50
1:A:625:ILE:CD1	1:A:765:ILE:CD1	2.89	0.50
3:D:258:THR:HG1	3:D:356:ILE:HD11	1.72	0.50
2:B:634:ILE:CD1	2:B:772:PHE:CD1	2.93	0.50
3:D:17:VAL:HG21	3:D:231:ILE:HD12	1.91	0.50
2:B:293:ARG:HD3	2:B:330:ILE:HD12	1.93	0.50
1:A:142:ILE:CD1	1:A:188:LEU:HD13	2.42	0.50
3:D:17:VAL:CG1	3:D:231:ILE:CD1	2.89	0.50
2:B:779:LEU:HG	2:B:780:ASN:H	1.76	0.50
3:D:403:PHE:CZ	3:D:406:ASN:HB2	2.46	0.50
3:D:288:CYS:H	3:D:291:SER:HB2	1.75	0.50
1:A:425:ILE:HD11	1:A:564:ILE:HD12	1.88	0.50
2:B:603:GLU:OE1	2:B:770:TYR:HA	2.12	0.50
3:C:322:ILE:CD1	3:C:358:ARG:HH21	2.21	0.50
1:A:133:MET:CE	2:B:323:GLY:H	2.25	0.50
3:D:16:HIS:CG	3:D:228:ASN:HD21	2.30	0.50
1:A:335:CYS:HA	1:A:340:ASP:HB3	1.93	0.50
3:C:191:LEU:HD13	3:C:191:LEU:O	2.11	0.50
2:B:572:LEU:HG	2:B:580:ARG:HE	1.77	0.50
1:A:706:PHE:HD1	1:A:768:ILE:HD13	1.77	0.50
2:B:200:PHE:CD1	2:B:200:PHE:N	2.79	0.50
3:D:166:ILE:CD1	3:D:252:MET:CE	2.85	0.50
1:A:368:SER:OG	1:A:373:ILE:CD1	2.59	0.50
2:B:430:HIS:HB3	2:B:448:ILE:HD12	1.94	0.50
2:B:422:THR:HA	2:B:425:PHE:CD2	2.47	0.50
2:B:421:TRP:O	2:B:424:GLU:HG2	2.12	0.50
2:B:515:VAL:HA	2:B:518:GLU:HG3	1.92	0.50
3:C:72:GLU:HB2	3:C:76:ILE:HD12	1.94	0.50
2:B:405:ILE:HD11	2:B:453:TYR:HB2	1.93	0.50
3:C:195:ILE:HD11	3:C:423:PHE:HE1	1.76	0.50
1:A:450:TYR:HA	1:A:488:THR:HG21	1.92	0.50
1:A:74:TYR:H	2:B:215:ASN:ND2	2.04	0.50
1:A:713:MET:SD	1:A:714:ARG:O	2.69	0.50
3:D:97:ASP:O	3:D:111:ILE:HD13	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:633:ARG:NH1	3:D:445:TYR:O	2.45	0.50
1:A:151:LEU:HD11	2:B:282:SER:CB	2.41	0.50
1:A:73:THR:HG22	2:B:215:ASN:OD1	2.12	0.50
2:B:220:LEU:CD1	2:B:224:ILE:HD12	2.42	0.50
3:C:188:ILE:HD13	3:C:394:PHE:CE2	2.38	0.50
3:D:6:ILE:HD13	3:D:126:GLU:HB2	1.92	0.50
1:A:286:TRP:CZ2	1:A:351:GLY:HA3	2.46	0.49
1:A:466:GLU:CG	1:A:479:ARG:HH21	2.25	0.49
3:C:12:GLN:HE22	3:C:144:GLY:HA2	1.76	0.49
1:A:72:GLY:HA3	2:B:215:ASN:HB3	1.94	0.49
3:D:56:GLU:HG2	3:D:62:PHE:CE1	2.46	0.49
1:A:246:ALA:O	1:A:250:ILE:HG13	2.12	0.49
2:B:434:GLN:HA	2:B:439:ARG:HH22	1.75	0.49
1:A:357:VAL:HG23	1:A:363:ILE:HD12	1.94	0.49
3:C:97:ASP:O	3:C:111:ILE:HD13	2.11	0.49
2:B:398:LEU:HD23	2:B:449:ILE:HD12	1.92	0.49
2:B:326:THR:O	2:B:330:ILE:HG13	2.12	0.49
1:A:564:ILE:CD1	1:A:579:MET:HG3	2.41	0.49
3:D:105:TRP:CH2	3:D:109:TYR:CD1	3.01	0.49
2:B:430:HIS:HD1	2:B:448:ILE:HD11	1.76	0.49
1:A:173:LEU:H	1:A:173:LEU:HD12	1.76	0.49
3:C:56:GLU:OE1	3:D:286:HIS:HE1	1.88	0.49
3:C:7:THR:CG2	3:C:139:LEU:HD13	2.42	0.49
2:B:567:PRO:HG2	2:B:721:ILE:CD1	2.42	0.49
3:C:256:TYR:CD2	3:C:260:ILE:HD12	2.47	0.49
1:A:146:LEU:HD22	1:A:150:TYR:OH	2.12	0.49
3:D:242:ILE:HD12	3:D:252:MET:HE1	1.93	0.49
1:A:613:LYS:HG3	1:A:614:TYR:O	2.10	0.49
1:A:625:ILE:HD13	1:A:761:ILE:HG21	1.89	0.49
2:B:346:LEU:HD11	2:B:402:ILE:HD13	1.95	0.49
3:D:120:LEU:HD22	3:D:161:ARG:HH11	1.78	0.49
1:A:625:ILE:HB	1:A:765:ILE:HD13	1.95	0.49
3:C:256:TYR:CE1	3:C:260:ILE:HD11	2.47	0.49
2:B:402:ILE:HD11	2:B:449:ILE:CD1	2.42	0.49
1:A:632:LEU:HD21	1:A:768:ILE:HG23	1.95	0.49
2:B:493:ILE:HD11	2:B:598:TYR:CG	2.46	0.49
3:C:78:ASP:HB3	3:C:87:PHE:CZ	2.47	0.49
3:D:180:VAL:HG12	3:D:181:VAL:H	1.78	0.49
1:A:113:GLY:HA2	1:A:116:TYR:CD2	2.47	0.49
3:C:258:THR:CG2	3:C:356:ILE:HD11	2.43	0.49
3:D:255:ILE:CD1	3:D:320:ASN:ND2	2.74	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:24:GLN:HE22	3:C:233:THR:HA	1.78	0.49
2:B:812:ILE:HB	2:B:816:TYR:CZ	2.48	0.49
2:B:289:GLU:CD	2:B:289:GLU:H	2.16	0.49
1:A:451:ARG:HA	1:A:451:ARG:HE	1.78	0.49
3:C:39:LEU:H	3:C:40:PRO:CD	2.25	0.49
3:D:213:SER:HB2	3:D:222:ILE:HD11	1.95	0.49
2:B:465:ASN:O	2:B:469:HIS:HA	2.13	0.49
2:B:482:LEU:HA	2:B:590:LEU:CD1	2.43	0.48
3:C:315:TYR:CG	3:C:438:VAL:HG13	2.48	0.48
1:A:570:LEU:HD22	1:A:570:LEU:H	1.77	0.48
2:B:283:LEU:O	2:B:287:ILE:HG12	2.13	0.48
3:D:258:THR:OG1	3:D:356:ILE:CD1	2.61	0.48
3:D:188:ILE:CD1	3:D:427:ARG:HH21	2.23	0.48
2:B:527:HIS:NE2	2:B:538:ILE:HD11	2.28	0.48
2:B:765:LEU:O	2:B:769:VAL:HG23	2.12	0.48
3:C:56:GLU:HB3	3:D:286:HIS:CD2	2.48	0.48
2:B:207:ILE:HD12	2:B:221:LEU:HD11	1.95	0.48
1:A:638:HIS:CG	3:C:354:VAL:HG13	2.48	0.48
3:C:363:LEU:HD12	3:C:366:GLN:HB3	1.94	0.48
1:A:138:PHE:CD1	1:A:275:ILE:HD11	2.45	0.48
2:B:499:ILE:HD12	2:B:507:LEU:CD2	2.43	0.48
1:A:359:ALA:C	1:A:361:LEU:H	2.16	0.48
3:D:124:ASP:HA	3:D:127:ILE:HG12	1.95	0.48
1:A:651:VAL:HG13	1:A:686:ASN:HD21	1.76	0.48
1:A:135:LEU:HB2	1:A:247:ILE:HD13	1.94	0.48
3:C:212:ILE:HD13	3:C:275:PHE:CE1	2.48	0.48
1:A:789:GLU:HB3	1:A:793:PHE:CZ	2.48	0.48
1:A:375:ILE:HD13	1:A:396:LYS:HG2	1.96	0.48
2:B:534:ASN:HD22	2:B:534:ASN:H	1.60	0.48
1:A:591:VAL:HA	1:A:594:TYR:CE2	2.48	0.48
3:D:205:ASP:HB3	3:D:305:LEU:H	1.78	0.48
3:C:59:ARG:HH22	3:D:279:TYR:CB	2.18	0.48
2:B:441:ILE:HG22	2:B:444:ASN:H	1.79	0.48
3:C:289:HIS:H	3:C:289:HIS:CD2	2.30	0.48
3:C:59:ARG:HH12	3:D:283:ASP:CG	2.14	0.48
3:C:256:TYR:CE1	3:C:260:ILE:HD12	2.46	0.48
2:B:639:THR:HG21	3:D:261:PRO:HA	1.95	0.48
3:C:234:ILE:HD13	3:C:303:ASN:OD1	2.13	0.48
1:A:73:THR:HG23	2:B:215:ASN:ND2	2.28	0.48
3:D:6:ILE:HD13	3:D:126:GLU:HB3	1.94	0.48
1:A:108:ARG:HH22	1:A:112:TYR:HB2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:ASN:HD22	1:A:488:THR:HG21	1.78	0.48
3:C:255:ILE:HD13	3:C:358:ARG:NH1	2.27	0.48
2:B:499:ILE:HD11	2:B:508:PRO:HA	1.96	0.48
2:B:657:ILE:HG22	2:B:735:ILE:CD1	2.44	0.48
3:C:292:TYR:CE1	3:C:296:LEU:HD11	2.48	0.48
3:D:119:ILE:CD1	3:D:154:LEU:CD2	2.92	0.48
1:A:108:ARG:HH12	1:A:112:TYR:HB2	1.78	0.48
2:B:204:HIS:CG	2:B:204:HIS:O	2.66	0.48
3:C:120:LEU:HA	3:C:161:ARG:HH12	1.79	0.48
1:A:138:PHE:CE2	1:A:142:ILE:HD11	2.49	0.48
1:A:133:MET:CE	2:B:323:GLY:N	2.75	0.48
3:D:212:ILE:CD1	3:D:302:SER:O	2.46	0.48
1:A:390:LEU:O	1:A:394:VAL:HG23	2.14	0.48
3:C:123:ILE:HD13	3:C:158:LEU:CD2	2.29	0.48
1:A:115:GLN:NE2	1:A:118:ILE:HD11	2.29	0.48
3:D:75:VAL:HG21	3:D:94:VAL:HG12	1.96	0.48
3:D:234:ILE:HD13	3:D:303:ASN:CG	2.34	0.48
2:B:586:ILE:CD1	2:B:732:LEU:HD13	2.12	0.48
2:B:366:GLU:OE1	2:B:367:ASN:O	2.32	0.48
2:B:390:VAL:HB	2:B:391:PRO:HD2	1.96	0.48
1:A:72:GLY:CA	2:B:215:ASN:HB3	2.44	0.48
1:A:602:THR:HG21	1:A:707:CYS:SG	2.54	0.48
3:D:98:GLY:N	3:D:111:ILE:CD1	2.76	0.48
2:B:571:VAL:HA	2:B:575:ASN:HD22	1.78	0.48
2:B:201:PRO:HB2	2:B:208:GLN:H	1.79	0.48
2:B:241:PHE:HB3	2:B:254:ILE:CD1	2.34	0.48
2:B:592:ARG:HA	2:B:592:ARG:HE	1.79	0.48
2:B:469:HIS:O	2:B:473:VAL:HG23	2.14	0.48
1:A:142:ILE:HD11	1:A:188:LEU:CD1	2.44	0.48
2:B:430:HIS:CD2	2:B:448:ILE:HD13	2.45	0.48
2:B:441:ILE:HD12	2:B:443:THR:CG2	2.40	0.48
2:B:335:PHE:CD2	2:B:339:ILE:HD11	2.48	0.48
1:A:151:LEU:HD21	2:B:282:SER:CA	2.44	0.48
3:D:188:ILE:CD1	3:D:394:PHE:HB2	2.42	0.48
1:A:672:ILE:O	1:A:675:GLU:HG2	2.14	0.48
3:D:188:ILE:HD11	3:D:394:PHE:HB3	1.81	0.48
3:C:60:ASN:N	3:D:286:HIS:CE1	2.78	0.48
1:A:585:ILE:HD11	1:A:683:ILE:HG23	1.95	0.47
1:A:781:ASN:HD21	1:A:787:SER:HB2	1.77	0.47
3:C:322:ILE:HD13	3:C:358:ARG:CZ	2.40	0.47
3:D:209:LEU:HD21	3:D:231:ILE:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:799:VAL:HG12	1:A:800:ASP:O	2.14	0.47
1:A:196:ILE:CD1	1:A:250:ILE:HD13	2.43	0.47
1:A:410:PHE:O	1:A:414:ASP:HA	2.12	0.47
2:B:489:MET:HG2	2:B:594:LYS:HG2	1.95	0.47
1:A:126:TRP:HH2	1:A:192:ILE:HD13	1.78	0.47
2:B:491:ALA:HB1	2:B:522:LEU:HD23	1.95	0.47
3:C:5:ILE:HD12	3:C:53:PHE:CZ	2.49	0.47
2:B:442:SER:HA	2:B:445:PHE:CD2	2.50	0.47
2:B:366:GLU:OE2	2:B:367:ASN:O	2.31	0.47
1:A:142:ILE:HD11	1:A:186:MET:HB3	1.96	0.47
1:A:781:ASN:HD22	1:A:790:LYS:HG3	1.79	0.47
3:D:6:ILE:HD13	3:D:126:GLU:CB	2.44	0.47
3:D:212:ILE:HD11	3:D:302:SER:N	2.29	0.47
2:B:582:GLU:O	2:B:585:ARG:HG2	2.15	0.47
2:B:772:PHE:HE1	2:B:812:ILE:HD12	1.74	0.47
2:B:284:TYR:OH	2:B:291:ILE:CD1	2.62	0.47
1:A:425:ILE:HD13	1:A:481:LEU:HD21	1.96	0.47
1:A:151:LEU:CD1	2:B:285:ARG:CG	2.93	0.47
1:A:433:HIS:CE1	3:C:242:ILE:O	2.67	0.47
3:D:188:ILE:HD11	3:D:394:PHE:CG	2.41	0.47
3:C:81:ASN:C	3:C:83:PHE:H	2.18	0.47
3:C:10:ALA:HB1	3:C:147:GLY:HA2	1.97	0.47
2:B:405:ILE:HG13	2:B:456:ILE:HD13	1.76	0.47
2:B:480:ILE:HD12	2:B:541:LEU:CD1	2.25	0.47
3:C:29:HIS:HE1	3:C:243:ARG:HH11	1.61	0.47
1:A:466:GLU:HA	1:A:479:ARG:HE	1.79	0.47
2:B:320:LYS:O	2:B:328:ARG:HG3	2.15	0.47
2:B:612:ARG:O	2:B:779:LEU:HD11	2.15	0.47
2:B:556:ASP:HA	2:B:592:ARG:HH22	1.78	0.47
3:D:93:TRP:HE1	3:D:118:ASP:HB3	1.79	0.47
1:A:133:MET:CE	2:B:323:GLY:N	2.77	0.47
3:C:221:ASN:O	3:C:226:HIS:HE1	1.98	0.47
1:A:134:VAL:HA	1:A:137:ARG:HH11	1.79	0.47
1:A:562:PHE:H	1:A:583:GLN:HG3	1.79	0.47
3:D:323:ILE:HB	3:D:359:ARG:HA	1.95	0.47
2:B:202:PHE:CD1	2:B:207:ILE:CD1	2.97	0.47
1:A:774:ILE:HD11	1:A:796:SER:HB3	1.96	0.47
3:D:240:ASN:HA	3:D:243:ARG:HE	1.79	0.47
2:B:759:PRO:O	2:B:763:VAL:HG23	2.14	0.47
3:D:124:ASP:HA	3:D:127:ILE:HG12	1.96	0.47
3:C:250:SER:HA	3:C:255:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:292:TYR:CE1	3:C:374:GLY:HA3	2.50	0.47
1:A:361:LEU:HD12	1:A:364:PRO:HA	1.97	0.47
2:B:412:LEU:HD13	2:B:463:ILE:CD1	2.45	0.47
2:B:480:ILE:HG23	2:B:481:LEU:N	2.30	0.47
3:D:212:ILE:HD12	3:D:303:ASN:OD1	2.15	0.47
2:B:664:MET:HG2	2:B:727:VAL:HG22	1.97	0.47
2:B:405:ILE:HG12	2:B:453:TYR:CD1	2.49	0.47
2:B:526:ARG:HH21	2:B:538:ILE:HD11	1.75	0.47
3:C:204:PHE:CB	3:C:231:ILE:CD1	2.90	0.47
2:B:365:ALA:HB2	2:B:386:ASN:HB2	1.96	0.47
1:A:183:ASN:H	1:A:183:ASN:ND2	2.12	0.47
1:A:183:ASN:HA	1:A:186:MET:SD	2.55	0.47
1:A:391:GLU:HA	1:A:394:VAL:HG22	1.95	0.47
1:A:73:THR:HG22	2:B:215:ASN:CG	2.30	0.47
2:B:362:PHE:CE2	2:B:364:ILE:HD12	2.50	0.47
3:D:213:SER:CB	3:D:222:ILE:CD1	2.84	0.47
2:B:827:ARG:HH22	3:D:353:HIS:CD2	2.33	0.47
1:A:557:ILE:HD13	1:A:594:TYR:CZ	2.45	0.47
2:B:629:ASN:H	2:B:629:ASN:HD22	1.63	0.47
2:B:385:PHE:CZ	2:B:390:VAL:HG11	2.49	0.47
3:D:193:ARG:HH12	3:D:419:VAL:CG1	2.28	0.47
3:D:166:ILE:HD12	3:D:252:MET:HE3	1.95	0.47
1:A:136:GLN:HE22	2:B:324:ASP:N	2.12	0.47
3:C:176:ARG:HG3	3:C:176:ARG:HH11	1.80	0.47
3:C:292:TYR:CZ	3:C:374:GLY:HA3	2.49	0.47
2:B:181:GLU:CD	2:B:181:GLU:H	2.18	0.47
2:B:319:PHE:HA	2:B:322:HIS:CD2	2.49	0.47
3:D:139:LEU:CD2	3:D:235:ILE:CD1	2.85	0.47
1:A:437:LYS:HE2	3:C:2:GLY:H	1.80	0.47
3:C:57:ASN:O	3:D:286:HIS:ND1	2.47	0.47
2:B:355:LEU:HD13	2:B:356:ARG:N	2.30	0.47
1:A:567:PRO:CD	1:A:574:ILE:HD12	2.44	0.47
3:C:322:ILE:HG12	3:C:358:ARG:HE	1.79	0.47
1:A:67:LEU:HD21	1:A:113:GLY:HA3	1.96	0.47
3:C:36:LEU:H	3:C:36:LEU:HD12	1.80	0.47
1:A:609:THR:HG23	1:A:610:PRO:HD3	1.97	0.47
3:C:59:ARG:HH21	3:D:284:ILE:HG21	1.79	0.47
3:D:188:ILE:HD11	3:D:394:PHE:CB	2.42	0.47
2:B:526:ARG:NH2	2:B:538:ILE:HD13	2.30	0.46
1:A:774:ILE:HB	1:A:793:PHE:CD2	2.50	0.46
1:A:73:THR:HG22	2:B:215:ASN:ND2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:499:ILE:CD1	2:B:511:LYS:HD3	2.40	0.46
1:A:128:ASP:OD1	2:B:299:ARG:NH2	2.47	0.46
3:D:89:PRO:HD2	3:D:90:ARG:HH11	1.80	0.46
1:A:774:ILE:HD12	1:A:796:SER:HG	1.71	0.46
3:D:244:PHE:CE1	3:D:363:LEU:HD21	2.50	0.46
1:A:557:ILE:HD13	1:A:594:TYR:HH	1.77	0.46
2:B:349:TRP:CH2	2:B:383:ILE:HD11	2.49	0.46
2:B:802:LEU:HA	2:B:805:PHE:CD2	2.50	0.46
2:B:772:PHE:CZ	2:B:812:ILE:HD13	2.50	0.46
1:A:582:TYR:CZ	1:A:680:LEU:HD21	2.49	0.46
1:A:699:ILE:CD1	1:A:775:PHE:CE1	2.99	0.46
2:B:464:LEU:HD23	2:B:468:PHE:CZ	2.49	0.46
1:A:123:TYR:CD1	1:A:139:ALA:HB1	2.50	0.46
2:B:424:GLU:HG2	2:B:425:PHE:CD1	2.51	0.46
2:B:527:HIS:O	2:B:532:PRO:HA	2.16	0.46
3:D:412:LEU:HD22	3:D:412:LEU:H	1.79	0.46
1:A:105:PHE:CD1	1:A:170:ILE:CD1	2.98	0.46
3:C:6:ILE:HD13	3:C:126:GLU:HB3	1.98	0.46
1:A:151:LEU:HB2	2:B:285:ARG:HH11	1.79	0.46
1:A:402:ASN:O	1:A:406:LEU:HD23	2.16	0.46
2:B:336:ASN:O	2:B:339:ILE:HG22	2.15	0.46
3:C:152:SER:HB3	3:C:193:ARG:HG3	1.98	0.46
1:A:286:TRP:HB2	1:A:292:LEU:HD22	1.97	0.46
3:D:289:HIS:CE1	3:D:331:ILE:HG22	2.50	0.46
3:D:213:SER:HB3	3:D:222:ILE:HD13	1.95	0.46
2:B:349:TRP:CE2	2:B:364:ILE:CD1	2.99	0.46
2:B:633:ARG:HH12	3:D:444:SER:H	1.64	0.46
1:A:335:CYS:HB2	1:A:344:LEU:HD22	1.97	0.46
3:D:21:LEU:CD1	3:D:235:ILE:HD13	2.29	0.46
2:B:533:ARG:N	2:B:538:ILE:HD12	2.31	0.46
1:A:105:PHE:HD1	1:A:170:ILE:HD11	1.81	0.46
3:C:105:TRP:CH2	3:C:109:TYR:CD2	3.03	0.46
2:B:314:ILE:O	2:B:318:ILE:HG13	2.15	0.46
2:B:533:ARG:HH21	2:B:534:ASN:HD21	1.62	0.46
3:D:4:GLU:HB2	3:D:130:THR:HG23	1.98	0.46
2:B:586:ILE:CD1	2:B:732:LEU:CB	2.87	0.46
2:B:604:MET:HB3	2:B:638:ARG:HE	1.80	0.46
1:A:72:GLY:CA	2:B:215:ASN:HB3	2.46	0.46
3:D:119:ILE:O	3:D:123:ILE:HG13	2.15	0.46
1:A:151:LEU:HD21	2:B:282:SER:CB	2.43	0.46
3:D:320:ASN:HD21	3:D:358:ARG:HE	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:630:ARG:HA	1:A:633:HIS:CD2	2.51	0.46
2:B:349:TRP:CZ2	2:B:364:ILE:HD13	2.51	0.46
2:B:526:ARG:HH22	2:B:538:ILE:HD13	1.81	0.46
3:D:213:SER:CB	3:D:222:ILE:HD11	2.45	0.46
1:A:557:ILE:HD13	1:A:594:TYR:CE1	2.51	0.46
2:B:526:ARG:HH21	2:B:538:ILE:CD1	2.29	0.46
3:D:16:HIS:HB3	3:D:228:ASN:HD21	1.81	0.46
3:C:57:ASN:CG	3:C:58:CYS:H	2.19	0.46
3:D:256:TYR:CE2	3:D:260:ILE:HD11	2.51	0.46
1:A:109:ILE:HD11	1:A:170:ILE:HD11	1.97	0.46
1:A:297:GLN:HG2	1:A:327:ARG:HH21	1.80	0.46
2:B:181:GLU:N	2:B:184:ILE:HD12	2.30	0.46
2:B:293:ARG:CD	2:B:330:ILE:CD1	2.94	0.46
3:C:356:ILE:HG22	3:C:357:GLY:N	2.31	0.46
3:C:212:ILE:HD11	3:C:300:ASP:O	2.16	0.46
3:C:317:ASN:HB3	3:C:379:ASN:HB3	1.98	0.46
3:D:90:ARG:HB3	3:D:125:LYS:HE2	1.98	0.46
2:B:527:HIS:CG	2:B:538:ILE:HD11	2.51	0.46
1:A:251:PHE:CE2	1:A:275:ILE:HD13	2.51	0.46
2:B:317:ASN:HB3	2:B:335:PHE:CE2	2.51	0.46
3:C:205:ASP:CB	3:C:305:LEU:H	2.28	0.46
3:C:68:MET:HB3	3:C:92:THR:HG23	1.98	0.46
3:D:263:PRO:O	3:D:266:HIS:CD2	2.68	0.46
3:D:287:LYS:HB2	3:D:291:SER:CB	2.46	0.46
1:A:423:GLN:O	1:A:427:LEU:HB3	2.15	0.46
2:B:308:SER:O	2:B:311:THR:HG22	2.16	0.46
1:A:78:PHE:CD2	1:A:90:ILE:HD12	2.51	0.46
2:B:656:ILE:CD1	2:B:738:HIS:CG	2.99	0.46
3:D:17:VAL:HG11	3:D:231:ILE:HD13	1.97	0.46
2:B:422:THR:HA	2:B:425:PHE:CD2	2.51	0.46
3:D:435:GLU:O	3:D:438:VAL:HG12	2.16	0.46
3:C:391:CYS:HA	3:C:394:PHE:CD2	2.51	0.46
1:A:418:VAL:HA	1:A:421:HIS:CD2	2.51	0.45
1:A:451:ARG:HG3	1:A:451:ARG:HH11	1.81	0.45
1:A:557:ILE:CD1	1:A:594:TYR:OH	2.54	0.45
3:C:105:TRP:HB2	3:C:186:ASN:HD22	1.81	0.45
3:D:290:SER:HA	3:D:335:MET:HG3	1.98	0.45
3:D:74:SER:O	3:D:77:ALA:HB3	2.16	0.45
2:B:353:GLY:HA3	2:B:410:ILE:HG23	1.98	0.45
3:D:17:VAL:HG11	3:D:231:ILE:CD1	2.46	0.45
1:A:288:THR:HG23	1:A:289:GLN:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:188:ILE:HD12	3:C:394:PHE:CB	2.28	0.45
3:D:119:ILE:HD12	3:D:154:LEU:HD21	1.96	0.45
3:D:188:ILE:HD13	3:D:394:PHE:CB	2.44	0.45
1:A:799:VAL:HG22	1:A:800:ASP:O	2.16	0.45
2:B:809:LEU:O	2:B:813:VAL:HG23	2.16	0.45
1:A:387:GLY:H	1:A:390:LEU:HG	1.81	0.45
1:A:580:ILE:O	1:A:584:ILE:HG13	2.17	0.45
3:D:363:LEU:HD12	3:D:365:LEU:O	2.16	0.45
2:B:419:VAL:C	2:B:421:TRP:H	2.19	0.45
3:C:292:TYR:CZ	3:C:374:GLY:HA3	2.52	0.45
2:B:442:SER:HA	2:B:445:PHE:CE2	2.51	0.45
3:C:29:HIS:CE1	3:C:243:ARG:HH11	2.34	0.45
3:D:212:ILE:HD12	3:D:303:ASN:CG	2.33	0.45
3:C:192:ARG:HH11	3:C:423:PHE:HB2	1.80	0.45
2:B:445:PHE:CD2	2:B:449:ILE:CD1	2.99	0.45
3:D:369:GLU:HG3	3:D:371:GLU:H	1.81	0.45
3:D:437:TYR:HA	3:D:442:GLN:HB2	1.98	0.45
1:A:353:LEU:HD22	1:A:401:ALA:HB1	1.98	0.45
2:B:420:GLN:HB3	2:B:423:ASN:HD22	1.80	0.45
3:D:21:LEU:HD22	3:D:235:ILE:HG21	1.99	0.45
1:A:569:PRO:O	1:A:572:ILE:HG12	2.16	0.45
3:C:212:ILE:HD11	3:C:300:ASP:O	2.16	0.45
3:D:240:ASN:HB2	3:D:358:ARG:HH12	1.81	0.45
1:A:143:ARG:CD	2:B:288:TYR:CE2	2.95	0.45
3:D:347:TRP:CE2	3:D:353:HIS:HA	2.52	0.45
1:A:488:THR:HG21	1:A:559:HIS:CD2	2.51	0.45
3:D:184:SER:O	3:D:188:ILE:HG13	2.17	0.45
1:A:323:GLN:HG2	1:A:324:TYR:H	1.82	0.45
2:B:364:ILE:HD11	2:B:403:PHE:HB2	1.98	0.45
2:B:349:TRP:CE2	2:B:406:GLY:HA3	2.52	0.45
1:A:258:ASN:HD22	1:A:264:SER:HB2	1.81	0.45
3:C:210:LEU:CD1	3:C:222:ILE:CD1	2.93	0.45
1:A:370:SER:C	1:A:372:ASP:H	2.19	0.45
1:A:143:ARG:HH22	2:B:292:ILE:HG13	1.76	0.45
1:A:138:PHE:HD1	1:A:275:ILE:HD11	1.81	0.45
2:B:280:LEU:HD23	2:B:280:LEU:C	2.37	0.45
2:B:430:HIS:CG	2:B:448:ILE:HD12	2.51	0.45
2:B:499:ILE:HD12	2:B:512:LEU:CD2	2.47	0.45
1:A:557:ILE:CD1	1:A:594:TYR:CE2	2.98	0.45
1:A:72:GLY:C	2:B:215:ASN:HB3	2.28	0.45
3:D:93:TRP:HB2	3:D:122:LYS:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:339:GLN:HA	3:D:342:ILE:HG22	1.97	0.45
3:C:424:ALA:HA	3:C:427:ARG:HH21	1.81	0.45
1:A:143:ARG:NE	2:B:288:TYR:CD2	2.76	0.45
2:B:533:ARG:CA	2:B:538:ILE:CD1	2.94	0.45
3:D:185:TYR:CZ	3:D:397:VAL:HG13	2.51	0.45
1:A:643:ILE:CD1	1:A:692:LEU:HD13	2.47	0.45
2:B:366:GLU:HA	2:B:383:ILE:HG22	1.97	0.45
2:B:653:LEU:HD12	2:B:657:ILE:HD12	1.98	0.45
3:C:31:ILE:CG2	3:C:35:GLY:HA2	2.46	0.45
2:B:430:HIS:CB	2:B:448:ILE:HD13	2.44	0.45
3:D:258:THR:CB	3:D:356:ILE:CD1	2.94	0.45
3:D:212:ILE:HD11	3:D:303:ASN:CA	2.46	0.45
1:A:118:ILE:HD13	1:A:193:TYR:CE2	2.51	0.45
3:C:166:ILE:HD11	3:C:256:TYR:CG	2.52	0.45
2:B:628:ILE:HG23	2:B:630:LYS:H	1.82	0.45
1:A:113:GLY:HA2	1:A:116:TYR:CD2	2.51	0.45
1:A:603:TRP:CE3	1:A:633:HIS:HB2	2.51	0.45
2:B:775:VAL:HG11	2:B:805:PHE:CD1	2.51	0.45
1:A:706:PHE:CZ	1:A:710:ILE:CD1	2.78	0.45
1:A:581:LYS:CB	1:A:683:ILE:CD1	2.95	0.45
3:C:213:SER:HB2	3:C:222:ILE:HD11	1.97	0.45
2:B:405:ILE:CD1	2:B:456:ILE:HD11	2.41	0.45
3:D:293:ASP:HB2	3:D:335:MET:HE1	1.99	0.45
3:D:234:ILE:HD13	3:D:303:ASN:CG	2.37	0.45
3:D:166:ILE:CD1	3:D:252:MET:HE2	2.37	0.45
1:A:150:TYR:CE2	2:B:281:LYS:HE2	2.52	0.45
3:D:191:LEU:HB3	3:D:423:PHE:CZ	2.52	0.45
1:A:624:ARG:HD3	1:A:624:ARG:H	1.82	0.45
3:C:188:ILE:HD12	3:C:394:PHE:CD1	2.52	0.45
1:A:264:SER:HA	1:A:267:PHE:CE2	2.52	0.45
2:B:219:GLY:O	2:B:222:HIS:HB2	2.16	0.45
1:A:196:ILE:HD13	1:A:250:ILE:CD1	2.47	0.45
1:A:375:ILE:HD13	1:A:396:LYS:CG	2.47	0.45
1:A:695:LEU:HD13	1:A:794:TYR:HA	1.99	0.45
3:C:188:ILE:HD12	3:C:394:PHE:HB3	1.97	0.45
3:C:212:ILE:HA	3:C:215:LYS:HZ3	1.82	0.45
2:B:511:LYS:O	2:B:515:VAL:HG13	2.17	0.45
2:B:293:ARG:CG	2:B:330:ILE:CD1	2.93	0.45
2:B:398:LEU:HG	2:B:449:ILE:HD13	1.92	0.45
2:B:398:LEU:CD2	2:B:449:ILE:HD12	2.47	0.45
1:A:425:ILE:HD11	1:A:478:MET:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:GLU:HA	1:A:75:ILE:CD1	2.39	0.45
3:D:242:ILE:HD12	3:D:252:MET:CE	2.46	0.45
1:A:151:LEU:HD11	2:B:282:SER:CB	2.47	0.45
3:C:17:VAL:HG13	3:C:139:LEU:HD23	1.98	0.45
3:C:123:ILE:CD1	3:C:158:LEU:HD21	2.44	0.45
3:D:119:ILE:HD12	3:D:154:LEU:CD2	2.46	0.45
1:A:141:GLU:HG2	1:A:144:ARG:NH2	2.32	0.45
3:D:272:PHE:HB2	3:D:303:ASN:HD21	1.82	0.45
3:C:239:THR:HB	3:C:243:ARG:HE	1.82	0.45
1:A:699:ILE:HD12	1:A:775:PHE:CE1	2.52	0.45
1:A:151:LEU:HB2	2:B:285:ARG:HB2	1.99	0.45
1:A:430:GLN:HA	3:C:246:SER:H	1.82	0.45
3:C:58:CYS:O	3:D:286:HIS:HB3	2.16	0.45
3:D:119:ILE:HD12	3:D:154:LEU:CD2	2.46	0.45
1:A:134:VAL:CG1	1:A:275:ILE:HD13	2.42	0.45
1:A:339:GLU:CD	1:A:339:GLU:H	2.20	0.44
3:D:289:HIS:H	3:D:289:HIS:CD2	2.34	0.44
2:B:493:ILE:CD1	2:B:598:TYR:HB3	2.44	0.44
2:B:807:THR:O	2:B:811:GLU:HG3	2.17	0.44
1:A:372:ASP:O	1:A:375:ILE:HG22	2.16	0.44
2:B:222:HIS:HA	2:B:225:PHE:CD2	2.52	0.44
3:D:391:CYS:HA	3:D:394:PHE:CE2	2.52	0.44
1:A:128:ASP:OD1	2:B:295:ARG:NE	2.50	0.44
1:A:140:TYR:OH	2:B:325:LEU:HD22	2.16	0.44
2:B:412:LEU:HD13	2:B:463:ILE:HD13	1.99	0.44
3:D:239:THR:O	3:D:242:ILE:HG12	2.17	0.44
3:D:240:ASN:HA	3:D:243:ARG:HE	1.82	0.44
2:B:482:LEU:HA	2:B:590:LEU:HD13	1.99	0.44
2:B:610:ILE:O	2:B:610:ILE:HG12	2.16	0.44
2:B:465:ASN:O	2:B:469:HIS:HA	2.17	0.44
2:B:533:ARG:O	2:B:538:ILE:HD13	2.15	0.44
1:A:567:PRO:CD	1:A:574:ILE:HD11	2.47	0.44
1:A:567:PRO:HD3	1:A:574:ILE:HD12	1.98	0.44
3:D:258:THR:CG2	3:D:356:ILE:CD1	2.94	0.44
3:C:127:ILE:CD1	3:C:162:TYR:OH	2.65	0.44
3:D:381:SER:O	3:D:384:VAL:HG12	2.17	0.44
1:A:112:TYR:CE2	1:A:177:ILE:HD11	2.52	0.44
2:B:596:ASN:HA	2:B:599:PHE:CD2	2.53	0.44
1:A:303:ASP:OD1	1:A:304:ASP:O	2.36	0.44
3:C:300:ASP:HB3	3:C:301:PRO:HD3	1.99	0.44
2:B:612:ARG:HB3	2:B:776:TYR:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:127:ILE:HD13	3:C:162:TYR:CE1	2.52	0.44
1:A:423:GLN:O	1:A:427:LEU:HB2	2.17	0.44
3:C:329:ARG:HH11	3:C:359:ARG:HH11	1.64	0.44
3:D:7:THR:HG21	3:D:22:TRP:CH2	2.52	0.44
3:C:210:LEU:HD12	3:C:222:ILE:CD1	2.48	0.44
3:D:212:ILE:CD1	3:D:303:ASN:CA	2.95	0.44
2:B:383:ILE:H	2:B:407:LYS:NZ	2.16	0.44
3:C:315:TYR:CD2	3:C:348:SER:HA	2.53	0.44
1:A:128:ASP:OD2	2:B:295:ARG:NH2	2.50	0.44
2:B:441:ILE:HG12	2:B:444:ASN:H	1.82	0.44
3:C:342:ILE:HD12	3:C:344:PHE:HE1	1.82	0.44
2:B:398:LEU:HD21	2:B:446:PHE:CD1	2.53	0.44
1:A:123:TYR:HD1	1:A:139:ALA:HB1	1.83	0.44
2:B:493:ILE:HG21	2:B:598:TYR:CD2	2.53	0.44
1:A:134:VAL:HG13	1:A:275:ILE:HG21	2.00	0.44
1:A:435:VAL:O	1:A:439:LEU:HD23	2.18	0.44
3:D:426:SER:O	3:D:430:VAL:HG23	2.17	0.44
1:A:151:LEU:CD2	2:B:285:ARG:HB3	2.32	0.44
3:D:9:GLN:HE21	3:D:15:ASN:HA	1.83	0.44
1:A:585:ILE:CD1	1:A:683:ILE:HG23	2.44	0.44
2:B:241:PHE:HB3	2:B:254:ILE:HD11	2.00	0.44
2:B:367:ASN:O	2:B:381:ILE:HD11	2.17	0.44
3:D:14:GLY:HA2	3:D:139:LEU:HG	1.98	0.44
1:A:476:ASN:ND2	1:A:479:ARG:HE	2.16	0.44
1:A:562:PHE:HB2	1:A:587:ARG:HH22	1.83	0.44
3:C:26:ALA:HA	3:C:31:ILE:HD12	1.99	0.44
3:D:256:TYR:CE2	3:D:260:ILE:CD1	3.01	0.44
1:A:74:TYR:CE1	2:B:216:PHE:CZ	3.05	0.44
2:B:656:ILE:HD13	2:B:738:HIS:CG	2.52	0.44
1:A:630:ARG:HE	1:A:633:HIS:HE1	1.64	0.44
1:A:155:VAL:HG21	2:B:278:VAL:HG22	2.00	0.44
3:D:289:HIS:CD2	3:D:332:SER:HA	2.53	0.44
1:A:625:ILE:HB	1:A:765:ILE:CD1	2.48	0.44
3:C:31:ILE:HD13	3:C:62:PHE:CD2	2.53	0.44
2:B:202:PHE:CE1	2:B:206:GLN:HA	2.53	0.44
2:B:533:ARG:HA	2:B:538:ILE:CD1	2.48	0.44
1:A:366:ILE:CD1	1:A:371:SER:CB	2.95	0.44
3:D:93:TRP:HE1	3:D:118:ASP:HB3	1.83	0.44
3:D:284:ILE:HG12	3:D:370:ASN:H	1.82	0.44
1:A:277:GLN:HE22	1:A:381:PHE:HA	1.82	0.44
1:A:300:MET:CE	1:A:327:ARG:HH21	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:LEU:CD1	2:B:285:ARG:HB2	2.47	0.44
1:A:112:TYR:CE2	1:A:177:ILE:CD1	3.01	0.44
2:B:438:TYR:CG	2:B:441:ILE:CD1	2.96	0.44
3:D:212:ILE:HD11	3:D:302:SER:H	1.82	0.44
3:C:212:ILE:HD11	3:C:301:PRO:HA	2.00	0.44
3:C:381:SER:O	3:C:384:VAL:HG22	2.18	0.44
1:A:567:PRO:HD2	1:A:574:ILE:CD1	2.47	0.44
2:B:499:ILE:CD1	2:B:507:LEU:CD2	2.96	0.44
2:B:499:ILE:CD1	2:B:508:PRO:HD3	2.35	0.44
2:B:349:TRP:CE3	2:B:353:GLY:HA2	2.52	0.44
2:B:234:LEU:HD22	2:B:257:ILE:HD11	2.00	0.44
2:B:560:LEU:HA	2:B:560:LEU:HD23	1.88	0.44
1:A:295:PRO:HG3	2:B:321:SER:CB	2.48	0.44
3:C:306:VAL:HG13	3:C:386:VAL:HG23	1.98	0.44
1:A:363:ILE:HG12	1:A:365:THR:H	1.82	0.44
2:B:499:ILE:HD13	2:B:508:PRO:HB3	2.00	0.44
3:D:166:ILE:CD1	3:D:252:MET:HE3	2.48	0.44
1:A:109:ILE:HD11	1:A:170:ILE:CD1	2.48	0.44
3:C:53:PHE:HB2	3:C:54:PHE:CD1	2.53	0.44
3:C:56:GLU:OE1	3:D:286:HIS:NE2	2.51	0.44
2:B:405:ILE:CG2	2:B:456:ILE:CD1	2.89	0.43
3:D:176:ARG:HA	3:D:176:ARG:HE	1.83	0.43
2:B:419:VAL:HG23	2:B:421:TRP:NE1	2.32	0.43
3:C:93:TRP:CZ3	3:C:95:ALA:HB2	2.52	0.43
1:A:473:ASN:HB2	1:A:474:PRO:HD2	1.99	0.43
2:B:339:ILE:CD1	2:B:439:ARG:HD3	2.48	0.43
3:D:29:HIS:HD1	3:D:47:ASP:HA	1.83	0.43
2:B:426:SER:HA	2:B:429:TYR:CE2	2.53	0.43
2:B:544:ARG:HE	2:B:545:VAL:H	1.65	0.43
2:B:586:ILE:HD11	2:B:732:LEU:HD13	1.99	0.43
1:A:281:THR:HA	1:A:284:TYR:CD2	2.53	0.43
1:A:375:ILE:HD13	1:A:396:LYS:HB3	1.99	0.43
3:D:212:ILE:HD11	3:D:303:ASN:CG	2.33	0.43
3:D:176:ARG:CD	3:D:386:VAL:HG22	2.48	0.43
1:A:280:CYS:HB2	1:A:380:ASP:CG	2.39	0.43
2:B:296:ILE:CD1	2:B:327:ILE:HD12	2.49	0.43
1:A:142:ILE:HD11	1:A:188:LEU:HD13	1.99	0.43
3:C:105:TRP:CZ2	3:C:109:TYR:CD1	3.06	0.43
1:A:585:ILE:HD11	1:A:683:ILE:CD1	2.05	0.43
1:A:202:GLU:C	1:A:205:THR:O	2.52	0.43
1:A:138:PHE:CD2	1:A:275:ILE:CD1	2.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:GLU:HG3	1:A:389:ASN:H	1.83	0.43
1:A:133:MET:HG2	2:B:322:HIS:CE1	2.54	0.43
1:A:142:ILE:HD13	1:A:189:LEU:HD11	1.96	0.43
3:D:255:ILE:HG21	3:D:255:ILE:HD13	1.87	0.43
1:A:613:LYS:HG2	1:A:614:TYR:H	1.83	0.43
2:B:284:TYR:OH	2:B:291:ILE:HD12	2.18	0.43
3:D:397:VAL:HG11	3:D:420:GLN:HE22	1.82	0.43
1:A:186:MET:HA	1:A:189:LEU:HD12	1.99	0.43
1:A:625:ILE:HD11	1:A:761:ILE:CG1	2.43	0.43
2:B:316:LEU:HG	2:B:335:PHE:CE2	2.53	0.43
1:A:774:ILE:HG22	1:A:793:PHE:HB2	2.01	0.43
1:A:137:ARG:O	1:A:137:ARG:HD2	2.18	0.43
2:B:493:ILE:CD1	2:B:598:TYR:CG	3.01	0.43
3:C:139:LEU:HD12	3:C:139:LEU:N	2.33	0.43
3:C:212:ILE:O	3:C:216:VAL:HG22	2.18	0.43
1:A:458:TYR:CD1	1:A:484:ILE:HD13	2.40	0.43
2:B:628:ILE:HG23	2:B:629:ASN:N	2.34	0.43
3:D:258:THR:HG23	3:D:356:ILE:CD1	2.48	0.43
1:A:370:SER:HB3	1:A:400:ARG:HG3	2.00	0.43
2:B:187:TYR:HA	2:B:190:TYR:CD2	2.53	0.43
3:D:279:TYR:CG	3:D:280:ILE:N	2.87	0.43
2:B:285:ARG:O	2:B:288:TYR:HB2	2.19	0.43
2:B:827:ARG:HH22	3:D:353:HIS:CG	2.36	0.43
3:C:212:ILE:CD1	3:C:300:ASP:O	2.63	0.43
1:A:375:ILE:CD1	1:A:393:TYR:HA	2.45	0.43
2:B:251:LYS:O	2:B:255:ILE:HG13	2.18	0.43
1:A:135:LEU:HB2	1:A:247:ILE:CD1	2.49	0.43
3:C:292:TYR:CZ	3:C:374:GLY:HA3	2.53	0.43
3:D:354:VAL:O	3:D:354:VAL:HG22	2.19	0.43
1:A:64:LEU:HD22	1:A:167:ASN:HD22	1.84	0.43
1:A:323:GLN:HG2	1:A:324:TYR:H	1.83	0.43
1:A:80:ASP:HA	1:A:121:ARG:HH12	1.82	0.43
3:C:119:ILE:HD12	3:C:154:LEU:HD23	2.00	0.43
3:D:166:ILE:CD1	3:D:256:TYR:CD1	2.96	0.43
3:D:255:ILE:O	3:D:259:LEU:HG	2.18	0.43
2:B:843:LYS:O	2:B:846:ARG:O	2.36	0.43
3:C:105:TRP:HB2	3:C:186:ASN:HD22	1.83	0.43
3:C:188:ILE:HD11	3:C:394:PHE:HD2	1.80	0.43
2:B:731:PHE:HE1	2:B:735:ILE:CD1	2.17	0.43
1:A:485:GLN:HG3	1:A:561:LYS:HB2	2.01	0.43
1:A:296:TYR:CD2	2:B:322:HIS:HE1	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:578:PHE:C	2:B:580:ARG:H	2.20	0.43
3:C:416:MET:CG	3:C:417:GLN:H	2.32	0.43
3:D:195:ILE:HD11	3:D:430:VAL:HG21	2.01	0.43
3:C:123:ILE:HD12	3:C:161:ARG:HH12	1.83	0.43
3:C:292:TYR:CE1	3:C:374:GLY:HA3	2.53	0.43
3:C:230:LEU:O	3:C:234:ILE:HG13	2.18	0.43
1:A:137:ARG:HH22	2:B:328:ARG:HH11	1.53	0.43
1:A:458:TYR:CE1	1:A:484:ILE:HD11	2.49	0.43
1:A:251:PHE:HE2	1:A:275:ILE:HD13	1.84	0.43
3:C:136:PHE:CD1	3:C:167:LEU:HD13	2.54	0.43
3:C:188:ILE:HD11	3:C:427:ARG:HE	1.84	0.43
1:A:425:ILE:HD11	1:A:482:LEU:HD13	2.01	0.43
1:A:425:ILE:CD1	1:A:481:LEU:HD21	2.49	0.43
3:D:212:ILE:CD1	3:D:303:ASN:ND2	2.82	0.43
2:B:517:GLN:O	2:B:520:VAL:HG22	2.19	0.43
3:D:52:PRO:O	3:D:65:ARG:HD2	2.18	0.43
1:A:587:ARG:O	1:A:591:VAL:HG23	2.18	0.43
1:A:294:ASP:HA	1:A:298:GLU:H	1.84	0.43
3:D:212:ILE:CD1	3:D:303:ASN:OD1	2.65	0.43
2:B:664:MET:HG3	2:B:727:VAL:HG13	2.00	0.43
3:C:10:ALA:HB1	3:C:147:GLY:HA2	2.01	0.43
3:D:333:ARG:HH21	3:D:334:ALA:HA	1.84	0.43
1:A:357:VAL:CB	1:A:363:ILE:CD1	2.69	0.43
2:B:365:ALA:HB2	2:B:389:ARG:HH22	1.84	0.43
1:A:585:ILE:HD12	1:A:683:ILE:HG21	2.00	0.43
1:A:606:LEU:HD11	1:A:710:ILE:CD1	2.11	0.43
3:D:97:ASP:C	3:D:111:ILE:CD1	2.88	0.43
1:A:109:ILE:HD13	1:A:109:ILE:HG21	1.82	0.43
3:C:364:PRO:HD2	3:C:365:LEU:HD22	2.01	0.43
1:A:384:LEU:N	1:A:384:LEU:HD22	2.33	0.43
2:B:556:ASP:HA	2:B:592:ARG:NH2	2.34	0.43
2:B:196:THR:HA	2:B:202:PHE:HB2	2.01	0.43
2:B:325:LEU:H	2:B:325:LEU:CD2	2.32	0.43
3:D:234:ILE:HD13	3:D:303:ASN:OD1	2.19	0.43
1:A:67:LEU:CD2	1:A:113:GLY:HA3	2.49	0.43
1:A:128:ASP:CG	2:B:295:ARG:CZ	2.87	0.43
2:B:493:ILE:HD12	2:B:598:TYR:CB	2.49	0.43
1:A:571:ASN:HA	1:A:574:ILE:HD12	2.01	0.43
1:A:252:GLN:HE21	1:A:252:GLN:HA	1.84	0.43
1:A:557:ILE:HD13	1:A:594:TYR:HH	1.81	0.43
3:D:212:ILE:HD12	3:D:303:ASN:CG	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:591:VAL:O	1:A:595:HIS:CD2	2.72	0.43
2:B:222:HIS:HA	2:B:225:PHE:CD2	2.53	0.43
2:B:284:TYR:CZ	2:B:291:ILE:CD1	3.02	0.43
2:B:493:ILE:HD13	2:B:493:ILE:HG21	1.91	0.43
2:B:499:ILE:HD11	2:B:508:PRO:CA	2.48	0.43
3:C:179:GLU:H	3:C:179:GLU:CD	2.21	0.43
1:A:300:MET:HB3	1:A:332:LEU:H	1.84	0.43
1:A:697:LEU:HD22	1:A:697:LEU:HA	1.92	0.43
2:B:357:ALA:O	2:B:358:THR:HG22	2.19	0.43
3:C:256:TYR:CE2	3:C:260:ILE:HD12	2.54	0.43
2:B:470:TYR:CE1	2:B:565:TYR:CE2	3.07	0.43
2:B:601:GLN:HE22	2:B:605:LEU:CD1	2.31	0.42
3:C:195:ILE:HA	3:C:266:HIS:CE1	2.54	0.42
1:A:660:GLU:HA	1:A:663:TYR:CD2	2.54	0.42
3:C:234:ILE:HD11	3:C:303:ASN:CG	2.40	0.42
1:A:409:PHE:CZ	1:A:573:ILE:HD11	2.54	0.42
3:C:356:ILE:HG12	3:C:357:GLY:N	2.34	0.42
1:A:143:ARG:HD2	2:B:288:TYR:CZ	2.54	0.42
1:A:114:LYS:HG3	1:A:118:ILE:HD12	2.01	0.42
2:B:398:LEU:HD21	2:B:449:ILE:HD13	2.01	0.42
2:B:532:PRO:C	2:B:538:ILE:HD11	2.39	0.42
2:B:643:GLN:HE21	3:D:354:VAL:HG11	1.83	0.42
1:A:327:ARG:HD3	1:A:330:VAL:HG23	2.00	0.42
3:C:57:ASN:O	3:D:286:HIS:HB3	2.19	0.42
3:D:431:GLN:O	3:D:435:GLU:HG2	2.19	0.42
3:C:280:ILE:HG23	3:C:282:ASP:H	1.83	0.42
3:C:306:VAL:HG11	3:C:383:VAL:HA	2.00	0.42
2:B:725:GLU:HA	2:B:728:HIS:CD2	2.53	0.42
3:D:13:CYS:O	3:D:17:VAL:HG23	2.19	0.42
3:D:281:HIS:CG	3:D:282:ASP:N	2.87	0.42
1:A:781:ASN:HD22	1:A:790:LYS:H	1.66	0.42
2:B:201:PRO:HG2	2:B:208:GLN:HE21	1.83	0.42
3:D:17:VAL:HG23	3:D:231:ILE:HG23	2.00	0.42
2:B:611:ILE:HG21	2:B:777:CYS:SG	2.60	0.42
3:C:251:SER:O	3:C:255:ILE:HG13	2.19	0.42
3:D:105:TRP:CD2	3:D:189:LEU:HB3	2.54	0.42
1:A:292:LEU:HD22	1:A:299:PHE:CE2	2.54	0.42
3:D:6:ILE:HD13	3:D:126:GLU:HB2	2.00	0.42
1:A:482:LEU:HA	1:A:564:ILE:HG22	2.02	0.42
3:D:127:ILE:HD11	3:D:162:TYR:CE2	2.54	0.42
1:A:679:GLY:O	1:A:683:ILE:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:119:ILE:HD12	3:D:154:LEU:HD21	2.00	0.42
3:D:212:ILE:CD1	3:D:302:SER:O	2.67	0.42
3:C:138:LEU:HB3	3:C:169:THR:HG22	2.01	0.42
1:A:357:VAL:HG22	1:A:408:LEU:HD22	2.00	0.42
3:D:251:SER:O	3:D:255:ILE:HG13	2.18	0.42
3:D:9:GLN:HE21	3:D:15:ASN:HA	1.83	0.42
1:A:285:GLU:HB3	1:A:291:ILE:HB	2.00	0.42
1:A:450:TYR:O	1:A:451:ARG:HG2	2.19	0.42
3:C:34:ASP:HB3	3:C:85:GLY:HA3	2.01	0.42
2:B:220:LEU:O	2:B:224:ILE:HG13	2.19	0.42
1:A:296:TYR:HB2	2:B:322:HIS:ND1	2.35	0.42
2:B:453:TYR:O	2:B:456:ILE:HG22	2.19	0.42
2:B:743:THR:HA	2:B:759:PRO:HD3	2.02	0.42
2:B:430:HIS:CG	2:B:448:ILE:HD13	2.53	0.42
1:A:358:ARG:HH21	1:A:363:ILE:HG23	1.84	0.42
1:A:564:ILE:HD11	1:A:579:MET:HB2	2.01	0.42
1:A:638:HIS:CE1	3:C:355:ASN:H	2.37	0.42
3:D:306:VAL:HG12	3:D:382:THR:HG21	2.01	0.42
2:B:387:GLN:H	2:B:387:GLN:CD	2.22	0.42
3:C:131:ASP:O	3:C:132:ASN:HB2	2.19	0.42
3:D:123:ILE:HG22	3:D:127:ILE:HD12	2.01	0.42
1:A:557:ILE:HD12	1:A:594:TYR:OH	2.10	0.42
2:B:280:LEU:O	2:B:284:TYR:CD2	2.73	0.42
3:D:234:ILE:O	3:D:238:VAL:HG23	2.19	0.42
1:A:196:ILE:CD1	1:A:250:ILE:CD1	2.98	0.42
1:A:624:ARG:CZ	1:A:627:ARG:HH12	2.31	0.42
1:A:128:ASP:OD1	2:B:295:ARG:NH1	2.53	0.42
3:C:37:SER:H	3:C:61:LYS:HD2	1.84	0.42
1:A:481:LEU:HA	1:A:565:ASN:HD22	1.84	0.42
2:B:207:ILE:HG22	2:B:225:PHE:CD1	2.54	0.42
3:C:240:ASN:HA	3:C:243:ARG:HE	1.84	0.42
2:B:207:ILE:CD1	2:B:221:LEU:HD11	2.49	0.42
1:A:578:CYS:SG	1:A:680:LEU:HD21	2.60	0.42
1:A:606:LEU:HD11	1:A:710:ILE:HD11	2.01	0.42
1:A:99:ASP:HB3	1:A:102:PHE:CD2	2.54	0.42
2:B:441:ILE:HD13	2:B:444:ASN:HB2	2.01	0.42
3:C:102:GLY:HA3	3:C:107:ASN:HD22	1.85	0.42
1:A:630:ARG:HD2	3:C:261:PRO:O	2.19	0.42
3:D:340:GLN:HE22	3:D:341:ARG:HE	1.68	0.42
2:B:220:LEU:H	2:B:220:LEU:HD22	1.84	0.42
2:B:430:HIS:HB3	2:B:448:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:320:ASN:HB3	3:D:358:ARG:HH21	1.83	0.42
1:A:609:THR:HB	1:A:610:PRO:HD3	2.01	0.42
2:B:300:PHE:O	2:B:304:LEU:HB2	2.19	0.42
2:B:241:PHE:HB2	2:B:254:ILE:CD1	2.49	0.42
3:C:267:PHE:HB2	3:C:383:VAL:HG11	2.00	0.42
2:B:307:LEU:HD23	2:B:307:LEU:HA	1.86	0.42
1:A:706:PHE:O	1:A:710:ILE:HG13	2.20	0.42
3:C:123:ILE:O	3:C:127:ILE:HG13	2.20	0.42
3:C:176:ARG:H	3:C:207:ALA:HB2	1.85	0.42
3:C:176:ARG:HE	3:C:210:LEU:HD23	1.84	0.42
2:B:405:ILE:CD1	2:B:452:GLN:NE2	2.83	0.42
2:B:533:ARG:NH1	2:B:538:ILE:HD11	2.35	0.42
2:B:766:LEU:O	2:B:769:VAL:HG12	2.20	0.42
2:B:829:ASP:HA	2:B:835:ASP:HB2	2.02	0.42
3:D:3:GLY:HA2	3:D:132:ASN:O	2.20	0.42
1:A:142:ILE:HG12	1:A:146:LEU:HD22	2.00	0.42
1:A:595:HIS:HB3	1:A:700:PHE:CD1	2.55	0.42
1:A:613:LYS:HD3	1:A:614:TYR:O	2.20	0.42
2:B:482:LEU:CB	2:B:657:ILE:HD11	2.42	0.42
3:D:363:LEU:H	3:D:363:LEU:HD23	1.85	0.42
1:A:72:GLY:CA	2:B:215:ASN:HB3	2.37	0.42
1:A:70:LEU:HD11	2:B:216:PHE:HA	2.02	0.42
1:A:151:LEU:CB	2:B:285:ARG:NE	2.76	0.42
2:B:363:PHE:HA	2:B:389:ARG:HE	1.84	0.42
3:D:435:GLU:O	3:D:438:VAL:HG22	2.20	0.42
1:A:68:ILE:HG22	1:A:70:LEU:HG	2.01	0.42
2:B:429:TYR:HB3	2:B:433:TYR:CZ	2.54	0.42
2:B:366:GLU:OE2	2:B:381:ILE:HD11	2.19	0.42
2:B:445:PHE:CD2	2:B:449:ILE:HD12	2.55	0.42
3:D:212:ILE:HD11	3:D:300:ASP:O	2.20	0.42
3:C:140:HIS:CE1	3:C:142:VAL:HG12	2.55	0.42
2:B:636:ILE:HG22	3:D:261:PRO:HB2	2.02	0.42
1:A:581:LYS:CB	1:A:683:ILE:HD13	2.38	0.42
3:D:328:PRO:HB2	3:D:331:ILE:CD1	2.48	0.42
2:B:405:ILE:HD13	2:B:452:GLN:HE22	1.84	0.42
3:D:359:ARG:H	3:D:359:ARG:NE	2.17	0.42
3:C:188:ILE:CD1	3:C:394:PHE:CB	2.85	0.42
1:A:149:VAL:O	1:A:153:THR:HG23	2.20	0.42
2:B:239:GLU:HA	2:B:242:ARG:HH21	1.84	0.42
1:A:557:ILE:CD1	1:A:595:HIS:HE1	2.33	0.42
3:D:154:LEU:O	3:D:158:LEU:HG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:325:ASN:H	3:D:359:ARG:HH22	1.68	0.42
1:A:577:THR:O	1:A:580:ILE:HG12	2.19	0.42
3:D:195:ILE:HD11	3:D:423:PHE:CE1	2.44	0.42
3:D:188:ILE:HG21	3:D:188:ILE:HD13	1.80	0.42
3:C:206:ASN:HA	3:C:209:LEU:HB2	2.02	0.42
3:C:59:ARG:NH1	3:C:60:ASN:HD22	2.18	0.42
1:A:63:LEU:CG	1:A:170:ILE:HD11	2.48	0.42
3:C:205:ASP:HB3	3:C:305:LEU:H	1.84	0.42
1:A:363:ILE:HG21	1:A:363:ILE:HD13	1.88	0.42
2:B:493:ILE:HG21	2:B:598:TYR:HB3	2.02	0.42
2:B:641:PHE:CZ	2:B:765:LEU:HD22	2.54	0.42
3:C:322:ILE:HA	3:C:358:ARG:HB3	2.01	0.42
3:C:6:ILE:CD1	3:C:126:GLU:HB3	2.49	0.42
3:D:183:GLN:HE22	3:D:393:THR:HG21	1.84	0.42
3:D:384:VAL:HB	3:D:434:MET:SD	2.60	0.42
1:A:449:HIS:CD2	1:A:449:HIS:H	2.37	0.42
1:A:697:LEU:HD22	1:A:697:LEU:HA	1.93	0.42
3:C:8:LEU:HD23	3:C:67:ILE:HB	2.02	0.42
1:A:187:GLU:HG2	1:A:190:TYR:CZ	2.55	0.42
2:B:304:LEU:HA	2:B:307:LEU:O	2.20	0.42
2:B:476:ALA:O	2:B:480:ILE:HG22	2.19	0.42
3:D:127:ILE:CD1	3:D:162:TYR:CE2	3.02	0.42
1:A:634:ALA:HB2	3:C:261:PRO:HB3	2.02	0.42
1:A:70:LEU:HG	2:B:216:PHE:HB3	2.02	0.41
2:B:604:MET:HG3	2:B:638:ARG:HG2	2.01	0.41
2:B:586:ILE:HD12	2:B:732:LEU:HD22	2.02	0.41
3:C:284:ILE:HG21	3:C:284:ILE:HD13	1.85	0.41
3:D:212:ILE:HD13	3:D:275:PHE:CD2	2.55	0.41
1:A:292:LEU:HA	1:A:292:LEU:HD23	1.79	0.41
3:C:299:LEU:HA	3:C:299:LEU:HD13	1.87	0.41
1:A:143:ARG:HH11	1:A:147:GLU:HG3	1.84	0.41
2:B:180:PRO:HD2	2:B:185:LEU:HD21	2.02	0.41
2:B:446:PHE:HA	2:B:449:ILE:HG12	2.02	0.41
3:D:209:LEU:HD22	3:D:230:LEU:HD12	2.02	0.41
1:A:64:LEU:HD13	1:A:64:LEU:C	2.40	0.41
3:C:325:ASN:HB3	3:C:372:VAL:HA	2.02	0.41
2:B:356:ARG:HE	2:B:358:THR:H	1.67	0.41
2:B:187:TYR:HA	2:B:190:TYR:CD2	2.55	0.41
2:B:339:ILE:HD13	2:B:339:ILE:HG21	1.87	0.41
3:D:231:ILE:O	3:D:235:ILE:HG13	2.20	0.41
2:B:813:VAL:HG11	3:D:445:TYR:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:499:ILE:HD13	2:B:511:LYS:HZ3	1.85	0.41
1:A:128:ASP:OD1	2:B:299:ARG:NH1	2.53	0.41
2:B:320:LYS:HA	2:B:328:ARG:HA	2.01	0.41
2:B:578:PHE:HA	2:B:581:LYS:HB2	2.01	0.41
3:C:123:ILE:CD1	3:C:161:ARG:HH12	2.33	0.41
3:D:173:PHE:CD1	3:D:203:VAL:HG13	2.54	0.41
3:D:270:PRO:HA	3:D:376:MET:O	2.20	0.41
3:C:330:GLN:H	3:C:330:GLN:CD	2.23	0.41
2:B:339:ILE:HD13	2:B:343:TYR:OH	2.20	0.41
2:B:346:LEU:CD1	2:B:402:ILE:HD13	2.51	0.41
2:B:538:ILE:HG21	2:B:538:ILE:HD13	1.85	0.41
3:C:279:TYR:CE1	3:C:281:HIS:CE1	3.09	0.41
2:B:363:PHE:HA	2:B:389:ARG:HE	1.85	0.41
2:B:499:ILE:HD13	2:B:499:ILE:HG21	1.89	0.41
3:C:344:PHE:HB3	3:C:345:PRO:HD3	2.01	0.41
3:D:433:LEU:HD12	3:D:433:LEU:HA	1.84	0.41
1:A:146:LEU:CD2	1:A:183:ASN:HD22	2.33	0.41
1:A:151:LEU:CD1	2:B:285:ARG:CB	2.99	0.41
2:B:773:VAL:HG12	2:B:777:CYS:HG	1.84	0.41
1:A:375:ILE:HD12	1:A:396:LYS:HG2	1.96	0.41
3:C:59:ARG:HH22	3:D:371:GLU:HG3	1.85	0.41
2:B:607:SER:CB	2:B:634:ILE:HD11	2.50	0.41
3:C:188:ILE:HD12	3:C:394:PHE:CD1	2.55	0.41
3:C:93:TRP:CH2	3:C:95:ALA:HB2	2.56	0.41
3:C:20:PHE:O	3:C:24:GLN:HG3	2.20	0.41
3:C:322:ILE:HD11	3:C:377:LEU:HD12	2.03	0.41
3:D:217:PHE:CE1	3:D:226:HIS:CD2	3.09	0.41
1:A:151:LEU:HD12	2:B:285:ARG:CG	2.51	0.41
3:C:17:VAL:HG22	3:C:228:ASN:CB	2.49	0.41
2:B:402:ILE:CG1	2:B:449:ILE:HD13	2.41	0.41
3:D:105:TRP:CZ2	3:D:109:TYR:CD2	3.09	0.41
2:B:349:TRP:HE1	2:B:403:PHE:HA	1.85	0.41
3:C:46:ARG:HD2	3:C:365:LEU:HB2	2.02	0.41
1:A:567:PRO:HD2	1:A:574:ILE:HD11	2.02	0.41
3:C:64:PRO:HD3	3:C:86:PHE:CD1	2.55	0.41
2:B:427:LYS:HB2	2:B:448:ILE:HD12	2.02	0.41
3:D:70:ASP:HB2	3:D:71:SER:H	1.71	0.41
2:B:438:TYR:HB2	2:B:441:ILE:HD11	2.01	0.41
1:A:693:ILE:HD13	1:A:693:ILE:HG21	1.81	0.41
3:D:188:ILE:HD11	3:D:394:PHE:HB3	1.99	0.41
1:A:79:ASN:O	1:A:80:ASP:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ARG:HH22	1:A:164:LYS:HD2	1.86	0.41
1:A:172:GLU:H	1:A:172:GLU:CD	2.24	0.41
1:A:400:ARG:O	1:A:404:ILE:HG13	2.21	0.41
1:A:568:TYR:CD1	1:A:569:PRO:HA	2.55	0.41
2:B:381:ILE:HB	2:B:570:LEU:HD21	2.02	0.41
3:D:5:ILE:HD11	3:D:252:MET:HG2	2.01	0.41
2:B:427:LYS:CB	2:B:448:ILE:HD12	2.51	0.41
3:C:188:ILE:HG21	3:C:188:ILE:HD13	1.84	0.41
3:D:67:ILE:HG23	3:D:122:LYS:HD3	2.03	0.41
1:A:142:ILE:HD11	1:A:271:LEU:HG	2.02	0.41
3:D:67:ILE:HD11	3:D:122:LYS:HB2	2.02	0.41
1:A:674:ASN:HD22	1:A:674:ASN:HA	1.72	0.41
2:B:234:LEU:O	2:B:238:VAL:HG23	2.20	0.41
2:B:244:LEU:HD13	2:B:244:LEU:HA	2.00	0.41
2:B:532:PRO:HA	2:B:535:SER:HB3	2.03	0.41
3:C:68:MET:SD	3:C:75:VAL:HG22	2.61	0.41
3:D:318:VAL:CG2	3:D:319:TYR:N	2.84	0.41
3:C:212:ILE:HD12	3:C:302:SER:O	2.15	0.41
3:D:210:LEU:HA	3:D:210:LEU:HD23	1.95	0.41
2:B:728:HIS:O	2:B:732:LEU:HG	2.20	0.41
2:B:402:ILE:HD13	2:B:402:ILE:HG21	1.75	0.41
2:B:213:ILE:HD11	2:B:221:LEU:HD12	2.01	0.41
2:B:434:GLN:HE22	2:B:444:ASN:HB3	1.86	0.41
2:B:560:LEU:HD13	2:B:561:ASP:N	2.35	0.41
3:C:188:ILE:HD12	3:C:394:PHE:HB3	1.86	0.41
3:C:31:ILE:HG21	3:C:35:GLY:HA2	2.03	0.41
3:D:234:ILE:HD13	3:D:303:ASN:OD1	2.21	0.41
1:A:409:PHE:CZ	1:A:573:ILE:CD1	2.80	0.41
1:A:693:ILE:HG23	1:A:694:PRO:HD3	2.03	0.41
2:B:451:ASP:O	2:B:455:GLU:HG3	2.20	0.41
1:A:384:LEU:HA	1:A:384:LEU:HD12	1.90	0.41
2:B:238:VAL:O	2:B:242:ARG:HG3	2.20	0.41
2:B:412:LEU:HD13	2:B:463:ILE:CD1	2.50	0.41
2:B:339:ILE:HG12	2:B:343:TYR:CE1	2.56	0.41
3:C:266:HIS:CE1	3:C:267:PHE:CZ	3.08	0.41
3:C:271:SER:CB	3:C:296:LEU:HB3	2.50	0.41
2:B:529:MET:SD	2:B:531:SER:HB2	2.61	0.41
3:C:36:LEU:HD12	3:C:36:LEU:H	1.85	0.41
1:A:59:VAL:HB	1:A:102:PHE:CE2	2.55	0.41
1:A:560:LEU:HD12	1:A:560:LEU:HA	1.82	0.41
1:A:599:LEU:HD22	1:A:703:VAL:HG11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:426:SER:HA	2:B:429:TYR:CD2	2.56	0.41
3:D:318:VAL:HG23	3:D:354:VAL:HG12	2.03	0.41
1:A:378:ILE:HG21	1:A:378:ILE:HD13	1.85	0.41
3:C:24:GLN:HE22	3:C:232:SER:HB2	1.85	0.41
3:C:271:SER:HA	3:C:302:SER:HA	2.02	0.41
3:C:122:LYS:O	3:C:125:LYS:HG2	2.20	0.41
1:A:75:ILE:HD11	1:A:92:PHE:HB3	2.02	0.41
3:C:255:ILE:HD13	3:C:358:ARG:NH1	2.33	0.41
3:D:217:PHE:HA	3:D:280:ILE:HD12	2.02	0.41
3:D:271:SER:HB3	3:D:376:MET:HB3	2.01	0.41
1:A:391:GLU:HA	1:A:394:VAL:HG22	2.03	0.41
2:B:202:PHE:CE1	2:B:207:ILE:HD11	2.56	0.41
2:B:296:ILE:HD12	2:B:327:ILE:HD12	2.03	0.41
1:A:321:ASP:HB3	1:A:572:ILE:CD1	2.42	0.41
1:A:55:GLN:HB3	1:A:56:GLU:H	1.68	0.41
2:B:499:ILE:CD1	2:B:507:LEU:HD23	2.50	0.41
2:B:826:PHE:O	2:B:829:ASP:HB3	2.21	0.41
3:C:188:ILE:HD12	3:C:394:PHE:CD1	2.50	0.41
3:D:318:VAL:HG22	3:D:319:TYR:N	2.35	0.41
2:B:220:LEU:HD21	2:B:280:LEU:HB3	2.03	0.41
2:B:544:ARG:HB2	2:B:561:ASP:HB2	2.02	0.41
1:A:189:LEU:HB3	1:A:193:TYR:CZ	2.56	0.41
1:A:357:VAL:HB	1:A:363:ILE:HD11	1.91	0.41
1:A:609:THR:CG2	1:A:610:PRO:HD3	2.51	0.41
2:B:264:TYR:O	2:B:268:VAL:HG23	2.21	0.41
1:A:150:TYR:HE2	2:B:281:LYS:HE2	1.86	0.41
2:B:363:PHE:CD2	2:B:390:VAL:HG22	2.56	0.41
3:C:394:PHE:CE2	3:C:424:ALA:HB2	2.56	0.41
3:C:256:TYR:CE1	3:C:260:ILE:HD12	2.56	0.41
2:B:480:ILE:HG21	2:B:480:ILE:HD13	1.93	0.41
1:A:643:ILE:CD1	1:A:692:LEU:HD21	2.38	0.41
3:C:170:TYR:CD2	3:C:235:ILE:HG22	2.55	0.41
1:A:669:ALA:O	1:A:672:ILE:HG12	2.21	0.41
2:B:464:LEU:HD23	2:B:468:PHE:CE2	2.56	0.41
3:C:286:HIS:CD2	3:C:371:GLU:HB3	2.56	0.41
3:D:105:TRP:CH2	3:D:109:TYR:CD2	3.09	0.41
1:A:637:ASN:HA	1:A:640:ILE:HG12	2.03	0.41
2:B:544:ARG:HA	2:B:544:ARG:NE	2.36	0.41
2:B:493:ILE:CD1	2:B:595:LYS:HA	2.51	0.41
3:C:280:ILE:HD11	3:C:284:ILE:CD1	2.41	0.41
1:A:135:LEU:CD1	1:A:247:ILE:HD13	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:ARG:O	1:A:263:SER:HB2	2.20	0.40
1:A:268:LEU:O	1:A:268:LEU:HD23	2.21	0.40
1:A:280:CYS:HB3	1:A:380:ASP:HA	2.02	0.40
1:A:481:LEU:HB3	1:A:564:ILE:HG23	2.03	0.40
1:A:606:LEU:HA	1:A:606:LEU:HD23	1.82	0.40
1:A:781:ASN:ND2	1:A:790:LYS:H	2.19	0.40
2:B:738:HIS:N	2:B:738:HIS:CD2	2.84	0.40
3:C:206:ASN:HA	3:C:209:LEU:HD12	2.03	0.40
2:B:330:ILE:HG21	2:B:330:ILE:HD13	1.88	0.40
2:B:508:PRO:O	2:B:512:LEU:HD23	2.20	0.40
3:C:127:ILE:HD13	3:C:127:ILE:HG21	1.91	0.40
1:A:484:ILE:HD13	1:A:484:ILE:HG21	1.85	0.40
3:C:8:LEU:HB2	3:C:138:LEU:HD12	2.03	0.40
2:B:363:PHE:CG	2:B:390:VAL:HG22	2.56	0.40
1:A:361:LEU:O	1:A:361:LEU:HD23	2.21	0.40
3:C:67:ILE:HD13	3:C:67:ILE:HG21	1.93	0.40
2:B:642:GLN:HE22	3:D:257:SER:HB2	1.87	0.40
1:A:126:TRP:CG	1:A:135:LEU:HB3	2.57	0.40
3:C:75:VAL:HG13	3:C:92:THR:CG2	2.51	0.40
1:A:252:GLN:HE22	1:A:272:LEU:HD11	1.85	0.40
1:A:599:LEU:HD11	1:A:640:ILE:HD11	1.89	0.40
1:A:599:LEU:HD13	1:A:640:ILE:HD11	1.92	0.40
3:C:72:GLU:HB2	3:C:76:ILE:CD1	2.50	0.40
3:C:72:GLU:HA	3:C:75:VAL:HG12	2.03	0.40
1:A:176:ILE:HG21	1:A:176:ILE:HD13	1.93	0.40
1:A:423:GLN:HA	1:A:427:LEU:HB2	2.03	0.40
3:C:67:ILE:HD13	3:C:67:ILE:HG21	1.87	0.40
3:C:195:ILE:HD11	3:C:423:PHE:CE1	2.56	0.40
3:C:210:LEU:HD12	3:C:227:THR:HG21	2.02	0.40
3:D:219:ASN:HB2	3:D:279:TYR:CE2	2.57	0.40
1:A:359:ALA:C	1:A:361:LEU:H	2.24	0.40
1:A:594:TYR:CZ	1:A:595:HIS:CE1	3.10	0.40
3:D:176:ARG:HE	3:D:389:ASN:HB2	1.86	0.40
1:A:139:ALA:CB	1:A:143:ARG:HH21	2.34	0.40
3:D:105:TRP:CE2	3:D:189:LEU:HB3	2.56	0.40
1:A:606:LEU:HD21	1:A:710:ILE:CD1	2.50	0.40
2:B:276:THR:HG23	2:B:278:VAL:HG12	2.02	0.40
2:B:505:ASP:H	2:B:508:PRO:HG2	1.86	0.40
3:D:247:TYR:CE1	3:D:361:PRO:HD2	2.57	0.40
1:A:59:VAL:HG11	1:A:102:PHE:CE1	2.57	0.40
2:B:725:GLU:HA	2:B:728:HIS:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:VAL:CG1	1:A:275:ILE:HD13	2.22	0.40
2:B:207:ILE:HD13	2:B:221:LEU:HD21	2.02	0.40
2:B:660:ASN:HB3	2:B:731:PHE:CD1	2.56	0.40
1:A:331:LEU:HD12	1:A:332:LEU:H	1.87	0.40
3:D:242:ILE:CD1	3:D:252:MET:HE2	2.51	0.40
1:A:425:ILE:HD13	1:A:478:MET:O	2.21	0.40
1:A:779:LEU:HD13	1:A:779:LEU:C	2.42	0.40
2:B:349:TRP:CE2	2:B:364:ILE:HD11	2.57	0.40
3:C:250:SER:O	3:C:255:ILE:CD1	2.69	0.40
1:A:59:VAL:HG11	1:A:102:PHE:CZ	2.56	0.40
3:D:164:LYS:HG2	3:D:164:LYS:O	2.21	0.40
2:B:743:THR:O	2:B:756:GLN:CA	2.63	0.40
3:C:84:ARG:H	3:C:84:ARG:HG2	1.69	0.40
2:B:843:LYS:HD2	2:B:846:ARG:HB2	2.03	0.40
2:B:250:LYS:O	2:B:254:ILE:HG13	2.21	0.40
1:A:363:ILE:HG22	1:A:365:THR:H	1.86	0.40
3:C:412:LEU:HD12	3:C:412:LEU:H	1.87	0.40
3:D:119:ILE:HD13	3:D:154:LEU:HD21	2.03	0.40
2:B:199:LEU:HD23	2:B:199:LEU:H	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-A	561/823 (68%)	526 (94%)	21 (4%)	14 (2%)	7	46
1	2-A	561/823 (68%)	524 (93%)	19 (3%)	18 (3%)	5	41
1	3-A	561/823 (68%)	521 (93%)	24 (4%)	16 (3%)	6	43
1	4-A	561/823 (68%)	523 (93%)	25 (4%)	13 (2%)	8	48
1	5-A	561/823 (68%)	524 (93%)	23 (4%)	14 (2%)	7	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	6-A	561/823 (68%)	525 (94%)	26 (5%)	10 (2%)	11	53
1	7-A	561/823 (68%)	519 (92%)	27 (5%)	15 (3%)	6	45
1	8-A	561/823 (68%)	519 (92%)	26 (5%)	16 (3%)	6	43
1	9-A	561/823 (68%)	526 (94%)	23 (4%)	12 (2%)	9	50
1	10-A	561/823 (68%)	528 (94%)	19 (3%)	14 (2%)	7	46
2	1-B	553/846 (65%)	512 (93%)	26 (5%)	15 (3%)	6	45
2	2-B	553/846 (65%)	505 (91%)	41 (7%)	7 (1%)	15	60
2	3-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	9	51
2	4-B	553/846 (65%)	503 (91%)	32 (6%)	18 (3%)	5	40
2	5-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	9	51
2	6-B	553/846 (65%)	502 (91%)	36 (6%)	15 (3%)	6	45
2	7-B	553/846 (65%)	515 (93%)	24 (4%)	14 (2%)	7	46
2	8-B	553/846 (65%)	516 (93%)	29 (5%)	8 (1%)	14	58
2	9-B	553/846 (65%)	505 (91%)	24 (4%)	24 (4%)	3	34
2	10-B	553/846 (65%)	512 (93%)	30 (5%)	11 (2%)	9	51
3	1-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
3	1-D	443/473 (94%)	395 (89%)	37 (8%)	11 (2%)	7	46
3	2-C	443/473 (94%)	395 (89%)	29 (6%)	19 (4%)	3	34
3	2-D	443/473 (94%)	390 (88%)	33 (7%)	20 (4%)	3	33
3	3-C	443/473 (94%)	396 (89%)	33 (7%)	14 (3%)	5	41
3	3-D	443/473 (94%)	393 (89%)	33 (7%)	17 (4%)	4	37
3	4-C	443/473 (94%)	401 (90%)	29 (6%)	13 (3%)	6	43
3	4-D	443/473 (94%)	402 (91%)	29 (6%)	12 (3%)	6	45
3	5-C	443/473 (94%)	400 (90%)	27 (6%)	16 (4%)	4	38
3	5-D	443/473 (94%)	401 (90%)	28 (6%)	14 (3%)	5	41
3	6-C	443/473 (94%)	397 (90%)	34 (8%)	12 (3%)	6	45
3	6-D	443/473 (94%)	396 (89%)	32 (7%)	15 (3%)	5	40
3	7-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
3	7-D	443/473 (94%)	389 (88%)	33 (7%)	21 (5%)	3	32
3	8-C	443/473 (94%)	391 (88%)	29 (6%)	23 (5%)	2	30
3	8-D	443/473 (94%)	408 (92%)	26 (6%)	9 (2%)	9	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	9-C	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
3	9-D	443/473 (94%)	401 (90%)	29 (6%)	13 (3%)	6	43
3	10-C	443/473 (94%)	396 (89%)	29 (6%)	18 (4%)	3	35
3	10-D	443/473 (94%)	403 (91%)	29 (6%)	11 (2%)	7	46
All	All	20000/26150 (76%)	18292 (92%)	1141 (6%)	567 (3%)	10	44

All (567) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	91	GLU
1	1-A	97	LYS
1	1-A	130	SER
1	1-A	785	GLU
2	1-B	247	SER
2	1-B	533	ARG
2	1-B	564	LEU
2	1-B	610	ILE
3	1-C	246	SER
3	1-C	325	ASN
3	1-D	143	ALA
3	1-D	262	SER
3	1-D	274	PRO
3	1-D	354	VAL
1	2-A	91	GLU
1	2-A	97	LYS
1	2-A	337	SER
1	2-A	432	GLY
1	2-A	569	PRO
2	2-B	441	ILE
2	2-B	577	PRO
3	2-C	132	ASN
3	2-C	163	PRO
3	2-C	218	ARG
3	2-C	223	ASP
3	2-C	315	TYR
3	2-D	37	SER
3	2-D	43	SER
3	2-D	70	ASP
3	2-D	86	PHE
3	2-D	266	HIS
3	2-D	288	CYS

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Mol	Chain	Res	Type
1	3-A	91	GLU
1	3-A	331	LEU
2	3-B	245	ASN
2	3-B	469	HIS
3	3-C	44	THR
3	3-C	132	ASN
3	3-C	325	ASN
1	4-A	91	GLU
1	4-A	97	LYS
1	4-A	299	PHE
1	4-A	322	THR
1	4-A	365	THR
1	4-A	474	PRO
1	4-A	787	SER
2	4-B	380	HIS
2	4-B	416	CYS
2	4-B	530	ASN
3	4-C	132	ASN
3	4-C	261	PRO
3	4-C	278	ASP
3	4-C	325	ASN
3	4-C	416	MET
3	4-D	100	SER
3	4-D	328	PRO
1	5-A	91	GLU
1	5-A	337	SER
1	5-A	361	LEU
1	5-A	384	LEU
1	5-A	567	PRO
2	5-B	546	LEU
2	5-B	575	ASN
3	5-C	70	ASP
3	5-C	174	PRO
3	5-C	218	ARG
3	5-C	248	MET
3	5-D	45	GLU
3	5-D	131	ASP
3	5-D	163	PRO
3	5-D	325	ASN
1	6-A	91	GLU
2	6-B	196	THR
2	6-B	210	PRO

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Mol	Chain	Res	Type
2	6-B	244	LEU
2	6-B	419	VAL
2	6-B	531	SER
3	6-C	132	ASN
3	6-C	174	PRO
3	6-C	285	ALA
3	6-D	314	THR
3	6-D	325	ASN
1	7-A	91	GLU
1	7-A	129	THR
1	7-A	331	LEU
1	7-A	337	SER
2	7-B	573	ASN
3	7-C	132	ASN
3	7-C	280	ILE
3	7-D	49	ASP
3	7-D	163	PRO
3	7-D	179	GLU
3	7-D	261	PRO
3	7-D	266	HIS
3	7-D	287	LYS
3	7-D	328	PRO
3	7-D	416	MET
1	8-A	91	GLU
1	8-A	331	LEU
1	8-A	364	PRO
2	8-B	206	GLN
2	8-B	416	CYS
3	8-C	45	GLU
3	8-C	59	ARG
3	8-C	285	ALA
3	8-C	325	ASN
3	8-D	59	ARG
3	8-D	266	HIS
3	8-D	274	PRO
1	9-A	91	GLU
2	9-B	194	ALA
2	9-B	206	GLN
2	9-B	212	LYS
2	9-B	416	CYS
2	9-B	417	LYS
2	9-B	427	LYS

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Mol	Chain	Res	Type
2	9-B	572	LEU
2	9-B	610	ILE
3	9-C	304	SER
3	9-D	43	SER
3	9-D	163	PRO
3	9-D	325	ASN
1	10-A	91	GLU
1	10-A	97	LYS
1	10-A	331	LEU
1	10-A	337	SER
1	10-A	567	PRO
2	10-B	416	CYS
3	10-C	174	PRO
3	10-C	277	SER
3	10-C	307	SER
3	10-C	325	ASN
3	10-D	286	HIS
3	10-D	327	GLU
3	10-D	371	GLU
1	1-A	337	SER
1	1-A	360	SER
1	1-A	383	ASP
2	1-B	324	ASP
3	1-C	70	ASP
3	1-C	266	HIS
3	1-C	277	SER
3	1-C	361	PRO
3	1-D	70	ASP
3	1-D	174	PRO
3	1-D	307	SER
3	1-D	325	ASN
1	2-A	129	THR
1	2-A	263	SER
1	2-A	414	ASP
1	2-A	613	LYS
1	2-A	785	GLU
2	2-B	416	CYS
3	2-C	174	PRO
3	2-C	251	SER
3	2-D	163	PRO
1	3-A	295	PRO
1	3-A	335	CYS

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Mol	Chain	Res	Type
1	3-A	608	LYS
1	3-A	666	PRO
1	3-A	799	VAL
2	3-B	420	GLN
2	3-B	529	MET
3	3-C	248	MET
3	3-C	274	PRO
3	3-C	369	GLU
3	3-D	70	ASP
3	3-D	74	SER
3	3-D	277	SER
3	3-D	365	LEU
1	4-A	334	ASP
1	4-A	337	SER
1	4-A	360	SER
2	4-B	273	SER
2	4-B	552	SER
2	4-B	577	PRO
2	4-B	610	ILE
3	4-C	70	ASP
3	4-C	248	MET
3	4-D	70	ASP
3	4-D	163	PRO
3	4-D	282	ASP
3	4-D	325	ASN
1	5-A	131	PHE
1	5-A	299	PHE
1	5-A	608	LYS
1	5-A	666	PRO
2	5-B	198	ALA
3	5-C	132	ASN
3	5-C	266	HIS
3	5-D	70	ASP
1	6-A	666	PRO
2	6-B	570	LEU
2	6-B	611	ILE
3	6-C	70	ASP
3	6-C	314	THR
3	6-C	325	ASN
3	6-D	70	ASP
3	6-D	266	HIS
1	7-A	364	PRO

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Mol	Chain	Res	Type
1	7-A	365	THR
1	7-A	386	GLU
1	7-A	432	GLY
1	7-A	449	HIS
1	7-A	489	GLU
2	7-B	416	CYS
2	7-B	531	SER
2	7-B	834	GLY
2	7-B	845	LEU
3	7-C	70	ASP
3	7-C	178	SER
3	7-C	251	SER
3	7-C	281	HIS
3	7-C	310	MET
3	7-D	70	ASP
3	7-D	181	VAL
1	8-A	97	LYS
1	8-A	263	SER
1	8-A	432	GLY
1	8-A	450	TYR
3	8-C	96	SER
3	8-C	163	PRO
3	8-C	286	HIS
3	8-C	314	THR
3	8-C	362	TYR
3	8-D	70	ASP
1	9-A	297	GLN
1	9-A	414	ASP
1	9-A	489	GLU
1	9-A	786	LEU
2	9-B	424	GLU
2	9-B	574	VAL
3	9-C	70	ASP
3	9-C	248	MET
3	9-C	261	PRO
3	9-C	348	SER
3	9-C	361	PRO
3	9-D	280	ILE
3	9-D	361	PRO
1	10-A	470	GLN
2	10-B	210	PRO
2	10-B	533	ARG

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Mol	Chain	Res	Type
3	10-C	248	MET
3	10-C	348	SER
3	10-C	351	ALA
3	10-C	353	HIS
3	10-C	368	ASN
3	10-D	70	ASP
3	10-D	96	SER
3	10-D	343	LYS
3	10-D	349	SER
2	1-B	194	ALA
2	1-B	382	PRO
2	1-B	577	PRO
2	1-B	833	ASP
3	1-C	248	MET
3	1-C	251	SER
3	1-C	261	PRO
3	1-D	266	HIS
1	2-A	331	LEU
1	2-A	471	SER
2	2-B	324	ASP
3	2-C	45	GLU
3	2-C	59	ARG
3	2-C	70	ASP
3	2-C	261	PRO
3	2-C	328	PRO
3	2-C	353	HIS
3	2-C	361	PRO
3	2-C	416	MET
3	2-D	33	THR
3	2-D	57	ASN
3	2-D	103	ASN
3	2-D	261	PRO
3	2-D	278	ASP
3	2-D	311	ASN
1	3-A	96	LYS
1	3-A	322	THR
1	3-A	361	LEU
1	3-A	370	SER
1	3-A	482	LEU
2	3-B	779	LEU
3	3-C	47	ASP
3	3-C	70	ASP

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Mol	Chain	Res	Type
3	3-C	261	PRO
3	3-C	275	PHE
3	3-C	309	ALA
3	3-C	361	PRO
3	3-D	71	SER
3	3-D	84	ARG
3	3-D	221	ASN
3	3-D	288	CYS
1	4-A	331	LEU
1	4-A	666	PRO
2	4-B	194	ALA
3	4-C	96	SER
3	4-D	98	GLY
3	4-D	174	PRO
1	5-A	97	LYS
1	5-A	98	MET
1	5-A	259	LEU
2	5-B	278	VAL
2	5-B	324	ASP
2	5-B	382	PRO
2	5-B	577	PRO
3	5-C	57	ASN
3	5-C	99	ALA
3	5-C	280	ILE
3	5-C	307	SER
3	5-D	41	ASP
3	5-D	98	GLY
3	5-D	100	SER
3	5-D	164	LYS
1	6-A	334	ASP
1	6-A	370	SER
2	6-B	416	CYS
2	6-B	550	HIS
3	6-C	59	ARG
3	6-C	307	SER
3	6-C	370	ASN
3	6-D	174	PRO
3	6-D	246	SER
1	7-A	98	MET
2	7-B	381	ILE
2	7-B	540	GLY
2	7-B	563	ILE

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Mol	Chain	Res	Type
2	7-B	577	PRO
3	7-C	98	GLY
3	7-C	261	PRO
3	7-C	367	PRO
3	7-D	283	ASP
3	7-D	325	ASN
1	8-A	470	GLN
1	8-A	613	LYS
1	8-A	785	GLU
3	8-C	70	ASP
3	8-C	261	PRO
3	8-C	266	HIS
3	8-C	311	ASN
3	8-C	367	PRO
3	8-D	348	SER
1	9-A	322	THR
1	9-A	331	LEU
1	9-A	337	SER
2	9-B	197	SER
2	9-B	540	GLY
3	9-C	96	SER
3	9-D	70	ASP
3	9-D	132	ASN
1	10-A	128	ASP
1	10-A	129	THR
1	10-A	414	ASP
1	10-A	488	THR
1	10-A	785	GLU
3	10-C	70	ASP
3	10-C	315	TYR
3	10-D	98	GLY
3	10-D	325	ASN
1	1-A	296	TYR
2	1-B	201	PRO
2	1-B	206	GLN
2	1-B	358	THR
2	1-B	438	TYR
3	1-D	313	PRO
1	2-A	364	PRO
1	2-A	608	LYS
1	2-A	786	LEU
2	2-B	278	VAL

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Mol	Chain	Res	Type
2	2-B	358	THR
3	2-C	43	SER
1	3-A	128	ASP
1	3-A	337	SER
1	3-A	369	ASN
1	3-A	470	GLN
2	3-B	247	SER
2	3-B	574	VAL
3	3-D	42	SER
3	3-D	102	GLY
3	3-D	103	ASN
2	4-B	209	ILE
2	4-B	247	SER
2	4-B	417	LYS
2	4-B	529	MET
3	4-C	266	HIS
3	4-C	309	ALA
3	4-D	87	PHE
3	4-D	101	ALA
3	4-D	266	HIS
1	5-A	99	ASP
2	5-B	247	SER
2	5-B	527	HIS
3	5-C	251	SER
3	5-C	313	PRO
3	5-D	58	CYS
3	5-D	246	SER
1	6-A	99	ASP
1	6-A	295	PRO
1	6-A	667	THR
2	6-B	211	SER
2	6-B	547	ASP
2	6-B	845	LEU
3	6-C	246	SER
3	6-C	266	HIS
3	6-D	59	ARG
3	6-D	179	GLU
3	6-D	312	ASN
1	7-A	367	PRO
2	7-B	324	ASP
3	7-D	45	GLU
3	7-D	285	ALA

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Mol	Chain	Res	Type
3	7-D	311	ASN
3	7-D	312	ASN
1	8-A	300	MET
1	8-A	360	SER
1	8-A	608	LYS
1	8-A	666	PRO
2	8-B	247	SER
2	8-B	357	ALA
2	8-B	395	PRO
3	8-C	179	GLU
3	8-C	276	THR
3	8-D	163	PRO
1	9-A	785	GLU
2	9-B	247	SER
2	9-B	395	PRO
2	9-B	485	LYS
3	9-C	45	GLU
3	9-C	218	ARG
3	9-C	415	SER
3	9-D	174	PRO
3	9-D	309	ALA
3	9-D	312	ASN
3	9-D	343	LYS
3	9-D	345	PRO
2	10-B	381	ILE
2	10-B	395	PRO
3	10-C	96	SER
3	10-C	312	ASN
3	10-D	163	PRO
1	1-A	322	THR
1	1-A	567	PRO
1	1-A	666	PRO
1	1-A	786	LEU
2	1-B	531	SER
3	1-D	328	PRO
1	2-A	361	LEU
1	2-A	365	THR
3	2-D	218	ARG
3	2-D	274	PRO
3	2-D	277	SER
3	2-D	361	PRO
3	2-D	415	SER

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Mol	Chain	Res	Type
2	3-B	243	MET
2	3-B	274	SER
3	3-C	368	ASN
3	3-D	131	ASP
2	4-B	324	ASP
2	4-B	358	THR
3	4-C	348	SER
1	5-A	360	SER
3	5-C	278	ASP
2	6-B	548	LEU
3	6-D	42	SER
3	6-D	45	GLU
1	7-A	785	GLU
3	7-C	163	PRO
3	7-D	310	MET
3	7-D	345	PRO
2	8-B	274	SER
3	8-C	58	CYS
3	8-C	248	MET
3	8-C	278	ASP
3	8-C	315	TYR
3	8-D	58	CYS
3	8-D	444	SER
1	9-A	333	ARG
1	9-A	666	PRO
2	9-B	244	LEU
2	9-B	324	ASP
2	9-B	358	THR
2	9-B	381	ILE
2	9-B	426	SER
2	9-B	535	SER
2	9-B	564	LEU
3	9-D	262	SER
1	10-A	360	SER
2	10-B	215	ASN
2	10-B	552	SER
2	10-B	577	PRO
3	10-C	48	ASP
3	10-C	261	PRO
3	10-C	361	PRO
3	10-D	175	ALA
1	1-A	297	GLN

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Mol	Chain	Res	Type
1	1-A	613	LYS
2	1-B	213	ILE
3	2-C	97	ASP
2	3-B	201	PRO
3	3-C	218	ARG
3	3-D	39	LEU
3	3-D	40	PRO
3	3-D	176	ARG
1	4-A	567	PRO
2	4-B	576	ARG
3	4-C	282	ASP
3	4-C	443	ASP
3	4-D	58	CYS
2	5-B	205	GLU
3	5-C	361	PRO
3	5-D	221	ASN
1	6-A	383	ASP
2	6-B	382	PRO
3	6-D	37	SER
3	6-D	315	TYR
1	7-A	666	PRO
2	7-B	548	LEU
2	7-B	779	LEU
3	7-D	41	ASP
3	7-D	245	PRO
1	8-A	667	THR
2	8-B	524	SER
3	8-C	284	ILE
3	8-C	370	ASN
3	8-D	276	THR
3	9-C	39	LEU
1	10-A	372	ASP
1	10-A	489	GLU
2	10-B	247	SER
2	10-B	438	TYR
3	10-C	309	ALA
3	1-C	163	PRO
3	1-C	345	PRO
1	2-A	666	PRO
2	2-B	247	SER
3	2-C	2	GLY
2	3-B	503	PRO

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Mol	Chain	Res	Type
3	5-C	261	PRO
3	6-D	163	PRO
1	7-A	166	PRO
2	7-B	551	GLY
3	8-C	306	VAL
2	9-B	565	TYR
2	10-B	382	PRO
3	2-D	174	PRO
3	2-D	301	PRO
3	5-D	364	PRO
3	6-D	261	PRO
2	7-B	391	PRO
1	9-A	364	PRO
2	9-B	201	PRO
3	10-C	220	PRO
3	2-C	280	ILE
3	3-D	328	PRO
2	4-B	532	PRO
2	5-B	532	PRO
3	7-D	174	PRO
2	4-B	391	PRO
3	5-D	361	PRO
1	6-A	364	PRO
1	6-A	473	ASN
2	6-B	395	PRO
3	6-C	361	PRO
2	8-B	210	PRO
2	4-B	214	PRO
3	5-C	245	PRO
1	8-A	367	PRO
3	3-D	274	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	1-A	542/766 (71%)	498 (92%)	44 (8%)	15	49	
1	2-A	542/766 (71%)	502 (93%)	40 (7%)	17	54	
1	3-A	542/766 (71%)	510 (94%)	32 (6%)	24	61	
1	4-A	542/766 (71%)	499 (92%)	43 (8%)	15	51	
1	5-A	542/766 (71%)	508 (94%)	34 (6%)	22	59	
1	6-A	542/766 (71%)	487 (90%)	55 (10%)	9	38	
1	7-A	542/766 (71%)	501 (92%)	41 (8%)	16	53	
1	8-A	542/766 (71%)	497 (92%)	45 (8%)	14	48	
1	9-A	542/766 (71%)	505 (93%)	37 (7%)	20	57	
1	10-A	542/766 (71%)	497 (92%)	45 (8%)	14	48	
2	1-B	528/787 (67%)	492 (93%)	36 (7%)	20	57	
2	2-B	528/787 (67%)	492 (93%)	36 (7%)	20	57	
2	3-B	528/787 (67%)	490 (93%)	38 (7%)	18	55	
2	4-B	528/787 (67%)	482 (91%)	46 (9%)	13	45	
2	5-B	528/787 (67%)	493 (93%)	35 (7%)	21	57	
2	6-B	528/787 (67%)	479 (91%)	49 (9%)	11	42	
2	7-B	528/787 (67%)	487 (92%)	41 (8%)	16	51	
2	8-B	528/787 (67%)	491 (93%)	37 (7%)	19	56	
2	9-B	528/787 (67%)	486 (92%)	42 (8%)	15	50	
2	10-B	528/787 (67%)	475 (90%)	53 (10%)	9	38	
3	1-C	396/421 (94%)	369 (93%)	27 (7%)	20	57	
3	1-D	396/421 (94%)	375 (95%)	21 (5%)	28	64	
3	2-C	396/421 (94%)	371 (94%)	25 (6%)	22	59	
3	2-D	396/421 (94%)	373 (94%)	23 (6%)	25	61	
3	3-C	396/421 (94%)	374 (94%)	22 (6%)	26	62	
3	3-D	396/421 (94%)	371 (94%)	25 (6%)	22	59	
3	4-C	396/421 (94%)	375 (95%)	21 (5%)	28	64	
3	4-D	396/421 (94%)	366 (92%)	30 (8%)	16	53	
3	5-C	396/421 (94%)	375 (95%)	21 (5%)	28	64	
3	5-D	396/421 (94%)	369 (93%)	27 (7%)	20	57	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	6-C	396/421 (94%)	375 (95%)	21 (5%)	28	64
3	6-D	396/421 (94%)	376 (95%)	20 (5%)	29	66
3	7-C	396/421 (94%)	380 (96%)	16 (4%)	38	71
3	7-D	396/421 (94%)	379 (96%)	17 (4%)	35	70
3	8-C	396/421 (94%)	376 (95%)	20 (5%)	29	66
3	8-D	396/421 (94%)	375 (95%)	21 (5%)	28	64
3	9-C	396/421 (94%)	372 (94%)	24 (6%)	23	60
3	9-D	396/421 (94%)	377 (95%)	19 (5%)	31	67
3	10-C	396/421 (94%)	368 (93%)	28 (7%)	18	55
3	10-D	396/421 (94%)	366 (92%)	30 (8%)	16	53
All	All	18620/23950 (78%)	17333 (93%)	1287 (7%)	24	56

All (1287) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-A	55	GLN
1	1-A	56	GLU
1	1-A	74	TYR
1	1-A	100	PRO
1	1-A	108	ARG
1	1-A	110	VAL
1	1-A	116	TYR
1	1-A	130	SER
1	1-A	146	LEU
1	1-A	152	LYS
1	1-A	153	THR
1	1-A	159	GLU
1	1-A	160	ARG
1	1-A	168	PHE
1	1-A	174	GLU
1	1-A	251	PHE
1	1-A	252	GLN
1	1-A	288	THR
1	1-A	296	TYR
1	1-A	298	GLU
1	1-A	325	PHE
1	1-A	331	LEU
1	1-A	332	LEU

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Mol	Chain	Res	Type
1	1-A	337	SER
1	1-A	339	GLU
1	1-A	358	ARG
1	1-A	385	MET
1	1-A	386	GLU
1	1-A	413	TYR
1	1-A	424	GLN
1	1-A	481	LEU
1	1-A	623	ARG
1	1-A	633	HIS
1	1-A	637	ASN
1	1-A	646	TYR
1	1-A	648	ASN
1	1-A	661	LYS
1	1-A	667	THR
1	1-A	681	THR
1	1-A	691	ASP
1	1-A	785	GLU
1	1-A	793	PHE
1	1-A	794	TYR
1	1-A	799	VAL
2	1-B	182	GLU
2	1-B	225	PHE
2	1-B	231	TYR
2	1-B	250	LYS
2	1-B	273	SER
2	1-B	290	ASN
2	1-B	335	PHE
2	1-B	347	MET
2	1-B	385	PHE
2	1-B	397	GLU
2	1-B	403	PHE
2	1-B	410	ILE
2	1-B	414	LYS
2	1-B	438	TYR
2	1-B	439	ARG
2	1-B	468	PHE
2	1-B	492	LEU
2	1-B	508	PRO
2	1-B	510	TYR
2	1-B	522	LEU
2	1-B	528	LEU

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Mol	Chain	Res	Type
2	1-B	576	ARG
2	1-B	585	ARG
2	1-B	600	TYR
2	1-B	604	MET
2	1-B	641	PHE
2	1-B	649	GLU
2	1-B	659	GLU
2	1-B	728	HIS
2	1-B	731	PHE
2	1-B	741	PHE
2	1-B	758	TYR
2	1-B	764	LEU
2	1-B	772	PHE
2	1-B	776	TYR
2	1-B	811	GLU
3	1-C	96	SER
3	1-C	104	SER
3	1-C	120	LEU
3	1-C	126	GLU
3	1-C	141	SER
3	1-C	148	SER
3	1-C	150	LEU
3	1-C	189	LEU
3	1-C	232	SER
3	1-C	248	MET
3	1-C	253	SER
3	1-C	261	PRO
3	1-C	282	ASP
3	1-C	305	LEU
3	1-C	307	SER
3	1-C	325	ASN
3	1-C	329	ARG
3	1-C	333	ARG
3	1-C	340	GLN
3	1-C	359	ARG
3	1-C	366	GLN
3	1-C	375	MET
3	1-C	391	CYS
3	1-C	416	MET
3	1-C	420	GLN
3	1-C	435	GLU
3	1-C	443	ASP

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Mol	Chain	Res	Type
3	1-D	38	GLN
3	1-D	41	ASP
3	1-D	69	MET
3	1-D	71	SER
3	1-D	76	ILE
3	1-D	140	HIS
3	1-D	158	LEU
3	1-D	176	ARG
3	1-D	183	GLN
3	1-D	218	ARG
3	1-D	249	TYR
3	1-D	287	LYS
3	1-D	313	PRO
3	1-D	340	GLN
3	1-D	341	ARG
3	1-D	354	VAL
3	1-D	366	GLN
3	1-D	369	GLU
3	1-D	376	MET
3	1-D	393	THR
3	1-D	425	GLU
1	2-A	56	GLU
1	2-A	59	VAL
1	2-A	75	ILE
1	2-A	98	MET
1	2-A	111	ARG
1	2-A	133	MET
1	2-A	136	GLN
1	2-A	140	TYR
1	2-A	147	GLU
1	2-A	156	GLU
1	2-A	158	LEU
1	2-A	163	ASN
1	2-A	166	PRO
1	2-A	168	PHE
1	2-A	171	ARG
1	2-A	173	LEU
1	2-A	181	GLU
1	2-A	195	GLU
1	2-A	198	ARG
1	2-A	199	GLU
1	2-A	262	ARG

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Mol	Chain	Res	Type
1	2-A	285	GLU
1	2-A	296	TYR
1	2-A	327	ARG
1	2-A	328	LYS
1	2-A	344	LEU
1	2-A	376	GLN
1	2-A	393	TYR
1	2-A	429	TYR
1	2-A	472	GLU
1	2-A	569	PRO
1	2-A	598	LEU
1	2-A	633	HIS
1	2-A	637	ASN
1	2-A	651	VAL
1	2-A	654	LYS
1	2-A	673	GLN
1	2-A	677	GLU
1	2-A	714	ARG
1	2-A	794	TYR
2	2-B	183	ASP
2	2-B	201	PRO
2	2-B	205	GLU
2	2-B	206	GLN
2	2-B	229	LEU
2	2-B	240	LYS
2	2-B	262	GLN
2	2-B	280	LEU
2	2-B	289	GLU
2	2-B	328	ARG
2	2-B	349	TRP
2	2-B	351	THR
2	2-B	356	ARG
2	2-B	386	ASN
2	2-B	387	GLN
2	2-B	400	TYR
2	2-B	439	ARG
2	2-B	450	ASN
2	2-B	462	GLN
2	2-B	470	TYR
2	2-B	488	PHE
2	2-B	498	ASP
2	2-B	503	PRO

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Mol	Chain	Res	Type
2	2-B	508	PRO
2	2-B	555	TRP
2	2-B	562	TYR
2	2-B	564	LEU
2	2-B	601	GLN
2	2-B	609	ASP
2	2-B	649	GLU
2	2-B	719	LEU
2	2-B	728	HIS
2	2-B	731	PHE
2	2-B	780	ASN
2	2-B	808	ASN
2	2-B	839	PHE
3	2-C	12	GLN
3	2-C	23	SER
3	2-C	46	ARG
3	2-C	59	ARG
3	2-C	89	PRO
3	2-C	94	VAL
3	2-C	113	THR
3	2-C	115	ASN
3	2-C	140	HIS
3	2-C	248	MET
3	2-C	267	PHE
3	2-C	289	HIS
3	2-C	292	TYR
3	2-C	301	PRO
3	2-C	315	TYR
3	2-C	328	PRO
3	2-C	335	MET
3	2-C	352	MET
3	2-C	363	LEU
3	2-C	366	GLN
3	2-C	406	ASN
3	2-C	428	GLU
3	2-C	435	GLU
3	2-C	436	ASP
3	2-C	442	GLN
3	2-D	46	ARG
3	2-D	78	ASP
3	2-D	87	PHE
3	2-D	121	ASN

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Mol	Chain	Res	Type
3	2-D	140	HIS
3	2-D	153	ASN
3	2-D	165	LYS
3	2-D	174	PRO
3	2-D	176	ARG
3	2-D	183	GLN
3	2-D	188	ILE
3	2-D	218	ARG
3	2-D	222	ILE
3	2-D	243	ARG
3	2-D	287	LYS
3	2-D	315	TYR
3	2-D	317	ASN
3	2-D	318	VAL
3	2-D	319	TYR
3	2-D	330	GLN
3	2-D	340	GLN
3	2-D	411	ASP
3	2-D	435	GLU
1	3-A	103	LYS
1	3-A	140	TYR
1	3-A	165	VAL
1	3-A	168	PHE
1	3-A	175	GLN
1	3-A	186	MET
1	3-A	195	GLU
1	3-A	198	ARG
1	3-A	300	MET
1	3-A	324	TYR
1	3-A	328	LYS
1	3-A	339	GLU
1	3-A	345	PHE
1	3-A	346	LYS
1	3-A	358	ARG
1	3-A	361	LEU
1	3-A	374	THR
1	3-A	405	PHE
1	3-A	431	SER
1	3-A	443	MET
1	3-A	449	HIS
1	3-A	469	ARG
1	3-A	478	MET

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Mol	Chain	Res	Type
1	3-A	485	GLN
1	3-A	593	GLN
1	3-A	603	TRP
1	3-A	644	MET
1	3-A	655	GLU
1	3-A	663	TYR
1	3-A	677	GLU
1	3-A	714	ARG
1	3-A	761	ILE
2	3-B	181	GLU
2	3-B	195	THR
2	3-B	231	TYR
2	3-B	244	LEU
2	3-B	250	LYS
2	3-B	285	ARG
2	3-B	316	LEU
2	3-B	346	LEU
2	3-B	387	GLN
2	3-B	396	LYS
2	3-B	398	LEU
2	3-B	421	TRP
2	3-B	423	ASN
2	3-B	427	LYS
2	3-B	431	VAL
2	3-B	438	TYR
2	3-B	446	PHE
2	3-B	469	HIS
2	3-B	508	PRO
2	3-B	515	VAL
2	3-B	559	THR
2	3-B	564	LEU
2	3-B	570	LEU
2	3-B	574	VAL
2	3-B	576	ARG
2	3-B	585	ARG
2	3-B	588	ASN
2	3-B	595	LYS
2	3-B	600	TYR
2	3-B	669	GLN
2	3-B	728	HIS
2	3-B	756	GLN
2	3-B	772	PHE

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Mol	Chain	Res	Type
2	3-B	774	LYS
2	3-B	804	LYS
2	3-B	810	LYS
2	3-B	822	ARG
2	3-B	826	PHE
3	3-C	12	GLN
3	3-C	21	LEU
3	3-C	48	ASP
3	3-C	51	LYS
3	3-C	97	ASP
3	3-C	122	LYS
3	3-C	126	GLU
3	3-C	140	HIS
3	3-C	222	ILE
3	3-C	248	MET
3	3-C	274	PRO
3	3-C	275	PHE
3	3-C	292	TYR
3	3-C	297	ASP
3	3-C	335	MET
3	3-C	389	ASN
3	3-C	394	PHE
3	3-C	396	LYS
3	3-C	412	LEU
3	3-C	418	ASN
3	3-C	427	ARG
3	3-C	442	GLN
3	3-D	12	GLN
3	3-D	38	GLN
3	3-D	54	PHE
3	3-D	69	MET
3	3-D	125	LYS
3	3-D	130	THR
3	3-D	134	GLU
3	3-D	140	HIS
3	3-D	156	GLU
3	3-D	158	LEU
3	3-D	192	ARG
3	3-D	198	SER
3	3-D	239	THR
3	3-D	292	TYR
3	3-D	293	ASP

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Mol	Chain	Res	Type
3	3-D	318	VAL
3	3-D	326	VAL
3	3-D	340	GLN
3	3-D	352	MET
3	3-D	354	VAL
3	3-D	355	ASN
3	3-D	359	ARG
3	3-D	369	GLU
3	3-D	394	PHE
3	3-D	412	LEU
1	4-A	56	GLU
1	4-A	79	ASN
1	4-A	93	LYS
1	4-A	99	ASP
1	4-A	103	LYS
1	4-A	107	ARG
1	4-A	112	TYR
1	4-A	133	MET
1	4-A	137	ARG
1	4-A	140	TYR
1	4-A	162	PHE
1	4-A	168	PHE
1	4-A	177	ILE
1	4-A	249	LYS
1	4-A	266	MET
1	4-A	297	GLN
1	4-A	324	TYR
1	4-A	334	ASP
1	4-A	354	LEU
1	4-A	365	THR
1	4-A	375	ILE
1	4-A	380	ASP
1	4-A	405	PHE
1	4-A	425	ILE
1	4-A	448	LYS
1	4-A	451	ARG
1	4-A	474	PRO
1	4-A	583	GLN
1	4-A	594	TYR
1	4-A	597	ARG
1	4-A	624	ARG
1	4-A	635	LYS

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Mol	Chain	Res	Type
1	4-A	653	ASP
1	4-A	663	TYR
1	4-A	684	MET
1	4-A	692	LEU
1	4-A	705	LYS
1	4-A	708	LYS
1	4-A	714	ARG
1	4-A	763	LYS
1	4-A	776	ARG
1	4-A	778	CYS
1	4-A	794	TYR
2	4-B	210	PRO
2	4-B	222	HIS
2	4-B	231	TYR
2	4-B	248	PRO
2	4-B	264	TYR
2	4-B	276	THR
2	4-B	289	GLU
2	4-B	298	CYS
2	4-B	306	GLU
2	4-B	335	PHE
2	4-B	351	THR
2	4-B	356	ARG
2	4-B	358	THR
2	4-B	400	TYR
2	4-B	415	TYR
2	4-B	418	GLU
2	4-B	428	LYS
2	4-B	447	GLU
2	4-B	453	TYR
2	4-B	470	TYR
2	4-B	472	ASP
2	4-B	489	MET
2	4-B	526	ARG
2	4-B	559	THR
2	4-B	564	LEU
2	4-B	566	PRO
2	4-B	585	ARG
2	4-B	598	TYR
2	4-B	600	TYR
2	4-B	612	ARG
2	4-B	641	PHE

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Mol	Chain	Res	Type
2	4-B	643	GLN
2	4-B	660	ASN
2	4-B	663	GLU
2	4-B	670	ARG
2	4-B	719	LEU
2	4-B	722	ASP
2	4-B	728	HIS
2	4-B	729	ASN
2	4-B	731	PHE
2	4-B	732	LEU
2	4-B	737	SER
2	4-B	741	PHE
2	4-B	773	VAL
2	4-B	780	ASN
2	4-B	846	ARG
3	4-C	8	LEU
3	4-C	12	GLN
3	4-C	46	ARG
3	4-C	49	ASP
3	4-C	73	PRO
3	4-C	114	ARG
3	4-C	150	LEU
3	4-C	153	ASN
3	4-C	188	ILE
3	4-C	248	MET
3	4-C	271	SER
3	4-C	292	TYR
3	4-C	293	ASP
3	4-C	325	ASN
3	4-C	329	ARG
3	4-C	333	ARG
3	4-C	358	ARG
3	4-C	371	GLU
3	4-C	418	ASN
3	4-C	428	GLU
3	4-C	437	TYR
3	4-D	27	LYS
3	4-D	40	PRO
3	4-D	45	GLU
3	4-D	49	ASP
3	4-D	52	PRO
3	4-D	61	LYS

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Mol	Chain	Res	Type
3	4-D	69	MET
3	4-D	75	VAL
3	4-D	111	ILE
3	4-D	125	LYS
3	4-D	140	HIS
3	4-D	193	ARG
3	4-D	217	PHE
3	4-D	218	ARG
3	4-D	220	PRO
3	4-D	328	PRO
3	4-D	335	MET
3	4-D	339	GLN
3	4-D	355	ASN
3	4-D	359	ARG
3	4-D	363	LEU
3	4-D	372	VAL
3	4-D	380	MET
3	4-D	385	ASN
3	4-D	394	PHE
3	4-D	396	LYS
3	4-D	409	VAL
3	4-D	416	MET
3	4-D	435	GLU
3	4-D	437	TYR
1	5-A	55	GLN
1	5-A	56	GLU
1	5-A	76	ARG
1	5-A	107	ARG
1	5-A	116	TYR
1	5-A	129	THR
1	5-A	160	ARG
1	5-A	162	PHE
1	5-A	165	VAL
1	5-A	179	GLU
1	5-A	186	MET
1	5-A	194	GLU
1	5-A	198	ARG
1	5-A	284	TYR
1	5-A	288	THR
1	5-A	299	PHE
1	5-A	354	LEU
1	5-A	355	LYS

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Mol	Chain	Res	Type
1	5-A	372	ASP
1	5-A	385	MET
1	5-A	405	PHE
1	5-A	438	PHE
1	5-A	451	ARG
1	5-A	469	ARG
1	5-A	473	ASN
1	5-A	486	PHE
1	5-A	576	ARG
1	5-A	603	TRP
1	5-A	624	ARG
1	5-A	663	TYR
1	5-A	673	GLN
1	5-A	689	LEU
1	5-A	714	ARG
1	5-A	760	LEU
2	5-B	181	GLU
2	5-B	234	LEU
2	5-B	239	GLU
2	5-B	264	TYR
2	5-B	304	LEU
2	5-B	316	LEU
2	5-B	327	ILE
2	5-B	335	PHE
2	5-B	351	THR
2	5-B	358	THR
2	5-B	362	PHE
2	5-B	387	GLN
2	5-B	401	LYS
2	5-B	415	TYR
2	5-B	421	TRP
2	5-B	427	LYS
2	5-B	428	LYS
2	5-B	438	TYR
2	5-B	462	GLN
2	5-B	468	PHE
2	5-B	483	MET
2	5-B	504	SER
2	5-B	529	MET
2	5-B	533	ARG
2	5-B	545	VAL
2	5-B	553	VAL

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Mol	Chain	Res	Type
2	5-B	577	PRO
2	5-B	581	LYS
2	5-B	638	ARG
2	5-B	649	GLU
2	5-B	666	ARG
2	5-B	722	ASP
2	5-B	727	VAL
2	5-B	728	HIS
2	5-B	764	LEU
3	5-C	12	GLN
3	5-C	46	ARG
3	5-C	59	ARG
3	5-C	81	ASN
3	5-C	84	ARG
3	5-C	86	PHE
3	5-C	90	ARG
3	5-C	94	VAL
3	5-C	139	LEU
3	5-C	140	HIS
3	5-C	158	LEU
3	5-C	180	VAL
3	5-C	183	GLN
3	5-C	219	ASN
3	5-C	318	VAL
3	5-C	353	HIS
3	5-C	359	ARG
3	5-C	382	THR
3	5-C	385	ASN
3	5-C	396	LYS
3	5-C	431	GLN
3	5-D	19	LYS
3	5-D	41	ASP
3	5-D	46	ARG
3	5-D	58	CYS
3	5-D	120	LEU
3	5-D	140	HIS
3	5-D	148	SER
3	5-D	154	LEU
3	5-D	192	ARG
3	5-D	225	GLN
3	5-D	231	ILE
3	5-D	273	THR

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Mol	Chain	Res	Type
3	5-D	292	TYR
3	5-D	296	LEU
3	5-D	329	ARG
3	5-D	340	GLN
3	5-D	341	ARG
3	5-D	347	TRP
3	5-D	359	ARG
3	5-D	360	SER
3	5-D	366	GLN
3	5-D	388	GLU
3	5-D	393	THR
3	5-D	394	PHE
3	5-D	416	MET
3	5-D	435	GLU
3	5-D	437	TYR
1	6-A	74	TYR
1	6-A	91	GLU
1	6-A	97	LYS
1	6-A	107	ARG
1	6-A	108	ARG
1	6-A	114	LYS
1	6-A	116	TYR
1	6-A	126	TRP
1	6-A	140	TYR
1	6-A	143	ARG
1	6-A	155	VAL
1	6-A	156	GLU
1	6-A	165	VAL
1	6-A	175	GLN
1	6-A	181	GLU
1	6-A	183	ASN
1	6-A	186	MET
1	6-A	187	GLU
1	6-A	262	ARG
1	6-A	263	SER
1	6-A	273	ASN
1	6-A	274	ASN
1	6-A	300	MET
1	6-A	333	ARG
1	6-A	358	ARG
1	6-A	361	LEU
1	6-A	364	PRO

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Mol	Chain	Res	Type
1	6-A	369	ASN
1	6-A	371	SER
1	6-A	393	TYR
1	6-A	402	ASN
1	6-A	406	LEU
1	6-A	427	LEU
1	6-A	438	PHE
1	6-A	439	LEU
1	6-A	451	ARG
1	6-A	461	LEU
1	6-A	472	GLU
1	6-A	478	MET
1	6-A	481	LEU
1	6-A	485	GLN
1	6-A	486	PHE
1	6-A	589	GLN
1	6-A	594	TYR
1	6-A	632	LEU
1	6-A	663	TYR
1	6-A	676	LEU
1	6-A	697	LEU
1	6-A	704	TYR
1	6-A	706	PHE
1	6-A	770	ASN
1	6-A	779	LEU
1	6-A	793	PHE
1	6-A	797	SER
1	6-A	799	VAL
2	6-B	181	GLU
2	6-B	202	PHE
2	6-B	207	ILE
2	6-B	221	LEU
2	6-B	225	PHE
2	6-B	230	LEU
2	6-B	240	LYS
2	6-B	243	MET
2	6-B	249	MET
2	6-B	250	LYS
2	6-B	262	GLN
2	6-B	281	LYS
2	6-B	283	LEU
2	6-B	289	GLU

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Mol	Chain	Res	Type
2	6-B	304	LEU
2	6-B	307	LEU
2	6-B	310	ASP
2	6-B	335	PHE
2	6-B	346	LEU
2	6-B	362	PHE
2	6-B	384	GLU
2	6-B	385	PHE
2	6-B	398	LEU
2	6-B	409	TYR
2	6-B	411	PHE
2	6-B	423	ASN
2	6-B	439	ARG
2	6-B	447	GLU
2	6-B	456	ILE
2	6-B	462	GLN
2	6-B	512	LEU
2	6-B	516	LEU
2	6-B	532	PRO
2	6-B	555	TRP
2	6-B	560	LEU
2	6-B	566	PRO
2	6-B	580	ARG
2	6-B	609	ASP
2	6-B	629	ASN
2	6-B	652	TYR
2	6-B	654	ASN
2	6-B	664	MET
2	6-B	722	ASP
2	6-B	731	PHE
2	6-B	757	PRO
2	6-B	770	TYR
2	6-B	771	GLU
2	6-B	806	ASN
2	6-B	836	GLU
3	6-C	21	LEU
3	6-C	41	ASP
3	6-C	46	ARG
3	6-C	47	ASP
3	6-C	86	PHE
3	6-C	100	SER
3	6-C	130	THR

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Mol	Chain	Res	Type
3	6-C	148	SER
3	6-C	165	LYS
3	6-C	183	GLN
3	6-C	206	ASN
3	6-C	219	ASN
3	6-C	248	MET
3	6-C	266	HIS
3	6-C	273	THR
3	6-C	293	ASP
3	6-C	295	MET
3	6-C	310	MET
3	6-C	335	MET
3	6-C	347	TRP
3	6-C	431	GLN
3	6-D	1	MET
3	6-D	47	ASP
3	6-D	51	LYS
3	6-D	126	GLU
3	6-D	140	HIS
3	6-D	183	GLN
3	6-D	193	ARG
3	6-D	206	ASN
3	6-D	228	ASN
3	6-D	247	TYR
3	6-D	256	TYR
3	6-D	275	PHE
3	6-D	289	HIS
3	6-D	292	TYR
3	6-D	306	VAL
3	6-D	333	ARG
3	6-D	341	ARG
3	6-D	358	ARG
3	6-D	380	MET
3	6-D	418	ASN
1	7-A	63	LEU
1	7-A	108	ARG
1	7-A	129	THR
1	7-A	136	GLN
1	7-A	166	PRO
1	7-A	167	ASN
1	7-A	168	PHE
1	7-A	171	ARG

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Mol	Chain	Res	Type
1	7-A	175	GLN
1	7-A	186	MET
1	7-A	249	LYS
1	7-A	266	MET
1	7-A	284	TYR
1	7-A	289	GLN
1	7-A	294	ASP
1	7-A	300	MET
1	7-A	342	ASN
1	7-A	361	LEU
1	7-A	369	ASN
1	7-A	385	MET
1	7-A	386	GLU
1	7-A	400	ARG
1	7-A	415	LEU
1	7-A	429	TYR
1	7-A	451	ARG
1	7-A	458	TYR
1	7-A	464	ASN
1	7-A	485	GLN
1	7-A	597	ARG
1	7-A	633	HIS
1	7-A	676	LEU
1	7-A	684	MET
1	7-A	697	LEU
1	7-A	700	PHE
1	7-A	714	ARG
1	7-A	755	ASP
1	7-A	775	PHE
1	7-A	776	ARG
1	7-A	781	ASN
1	7-A	783	THR
1	7-A	786	LEU
2	7-B	180	PRO
2	7-B	182	GLU
2	7-B	200	PHE
2	7-B	203	ASP
2	7-B	206	GLN
2	7-B	232	GLN
2	7-B	245	ASN
2	7-B	289	GLU
2	7-B	304	LEU

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Mol	Chain	Res	Type
2	7-B	306	GLU
2	7-B	347	MET
2	7-B	354	LEU
2	7-B	362	PHE
2	7-B	384	GLU
2	7-B	387	GLN
2	7-B	390	VAL
2	7-B	405	ILE
2	7-B	415	TYR
2	7-B	418	GLU
2	7-B	427	LYS
2	7-B	446	PHE
2	7-B	467	LYS
2	7-B	477	LEU
2	7-B	478	LYS
2	7-B	486	SER
2	7-B	494	GLU
2	7-B	510	TYR
2	7-B	545	VAL
2	7-B	559	THR
2	7-B	565	TYR
2	7-B	573	ASN
2	7-B	594	LYS
2	7-B	601	GLN
2	7-B	604	MET
2	7-B	612	ARG
2	7-B	660	ASN
2	7-B	666	ARG
2	7-B	723	GLU
2	7-B	725	GLU
2	7-B	731	PHE
2	7-B	774	LYS
3	7-C	12	GLN
3	7-C	45	GLU
3	7-C	69	MET
3	7-C	165	LYS
3	7-C	217	PHE
3	7-C	329	ARG
3	7-C	335	MET
3	7-C	352	MET
3	7-C	359	ARG
3	7-C	369	GLU

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Mol	Chain	Res	Type
3	7-C	394	PHE
3	7-C	396	LYS
3	7-C	404	LEU
3	7-C	427	ARG
3	7-C	441	GLU
3	7-C	442	GLN
3	7-D	46	ARG
3	7-D	55	ARG
3	7-D	84	ARG
3	7-D	122	LYS
3	7-D	140	HIS
3	7-D	183	GLN
3	7-D	248	MET
3	7-D	273	THR
3	7-D	284	ILE
3	7-D	286	HIS
3	7-D	308	THR
3	7-D	325	ASN
3	7-D	392	ASN
3	7-D	394	PHE
3	7-D	412	LEU
3	7-D	433	LEU
3	7-D	434	MET
1	8-A	56	GLU
1	8-A	91	GLU
1	8-A	108	ARG
1	8-A	115	GLN
1	8-A	116	TYR
1	8-A	126	TRP
1	8-A	140	TYR
1	8-A	156	GLU
1	8-A	161	ASP
1	8-A	162	PHE
1	8-A	163	ASN
1	8-A	167	ASN
1	8-A	171	ARG
1	8-A	174	GLU
1	8-A	175	GLN
1	8-A	199	GLU
1	8-A	269	LYS
1	8-A	300	MET
1	8-A	332	LEU

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Mol	Chain	Res	Type
1	8-A	358	ARG
1	8-A	379	ASN
1	8-A	408	LEU
1	8-A	409	PHE
1	8-A	411	GLN
1	8-A	422	LEU
1	8-A	429	TYR
1	8-A	438	PHE
1	8-A	439	LEU
1	8-A	473	ASN
1	8-A	485	GLN
1	8-A	563	ASP
1	8-A	593	GLN
1	8-A	594	TYR
1	8-A	599	LEU
1	8-A	604	MET
1	8-A	661	LYS
1	8-A	666	PRO
1	8-A	667	THR
1	8-A	674	ASN
1	8-A	692	LEU
1	8-A	697	LEU
1	8-A	707	CYS
1	8-A	708	LYS
1	8-A	775	PHE
1	8-A	776	ARG
2	8-B	202	PHE
2	8-B	216	PHE
2	8-B	231	TYR
2	8-B	261	LEU
2	8-B	280	LEU
2	8-B	286	GLU
2	8-B	307	LEU
2	8-B	317	ASN
2	8-B	326	THR
2	8-B	335	PHE
2	8-B	354	LEU
2	8-B	384	GLU
2	8-B	400	TYR
2	8-B	416	CYS
2	8-B	434	GLN
2	8-B	453	TYR

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Mol	Chain	Res	Type
2	8-B	461	ASN
2	8-B	481	LEU
2	8-B	488	PHE
2	8-B	507	LEU
2	8-B	510	TYR
2	8-B	512	LEU
2	8-B	537	VAL
2	8-B	544	ARG
2	8-B	555	TRP
2	8-B	559	THR
2	8-B	562	TYR
2	8-B	601	GLN
2	8-B	608	ASN
2	8-B	629	ASN
2	8-B	630	LYS
2	8-B	662	LYS
2	8-B	668	LEU
2	8-B	739	LYS
2	8-B	772	PHE
2	8-B	805	PHE
2	8-B	846	ARG
3	8-C	9	GLN
3	8-C	12	GLN
3	8-C	47	ASP
3	8-C	48	ASP
3	8-C	55	ARG
3	8-C	59	ARG
3	8-C	84	ARG
3	8-C	88	ASP
3	8-C	213	SER
3	8-C	248	MET
3	8-C	266	HIS
3	8-C	269	SER
3	8-C	293	ASP
3	8-C	299	LEU
3	8-C	318	VAL
3	8-C	340	GLN
3	8-C	371	GLU
3	8-C	377	LEU
3	8-C	412	LEU
3	8-C	443	ASP
3	8-D	5	ILE

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Mol	Chain	Res	Type
3	8-D	27	LYS
3	8-D	75	VAL
3	8-D	93	TRP
3	8-D	94	VAL
3	8-D	125	LYS
3	8-D	140	HIS
3	8-D	176	ARG
3	8-D	198	SER
3	8-D	248	MET
3	8-D	250	SER
3	8-D	258	THR
3	8-D	299	LEU
3	8-D	329	ARG
3	8-D	341	ARG
3	8-D	365	LEU
3	8-D	380	MET
3	8-D	394	PHE
3	8-D	412	LEU
3	8-D	435	GLU
3	8-D	437	TYR
1	9-A	98	MET
1	9-A	141	GLU
1	9-A	146	LEU
1	9-A	160	ARG
1	9-A	168	PHE
1	9-A	171	ARG
1	9-A	194	GLU
1	9-A	198	ARG
1	9-A	262	ARG
1	9-A	292	LEU
1	9-A	300	MET
1	9-A	323	GLN
1	9-A	332	LEU
1	9-A	361	LEU
1	9-A	374	THR
1	9-A	409	PHE
1	9-A	453	ASP
1	9-A	455	ASN
1	9-A	457	ASN
1	9-A	458	TYR
1	9-A	467	LEU
1	9-A	485	GLN

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Mol	Chain	Res	Type
1	9-A	562	PHE
1	9-A	569	PRO
1	9-A	576	ARG
1	9-A	609	THR
1	9-A	633	HIS
1	9-A	636	MET
1	9-A	641	LYS
1	9-A	651	VAL
1	9-A	655	GLU
1	9-A	661	LYS
1	9-A	664	ARG
1	9-A	707	CYS
1	9-A	775	PHE
1	9-A	792	ASP
1	9-A	800	ASP
2	9-B	196	THR
2	9-B	197	SER
2	9-B	225	PHE
2	9-B	231	TYR
2	9-B	237	LYS
2	9-B	251	LYS
2	9-B	283	LEU
2	9-B	285	ARG
2	9-B	289	GLU
2	9-B	291	ILE
2	9-B	303	HIS
2	9-B	316	LEU
2	9-B	335	PHE
2	9-B	352	LYS
2	9-B	355	LEU
2	9-B	384	GLU
2	9-B	388	GLU
2	9-B	404	MET
2	9-B	418	GLU
2	9-B	425	PHE
2	9-B	428	LYS
2	9-B	432	LEU
2	9-B	451	ASP
2	9-B	467	LYS
2	9-B	489	MET
2	9-B	495	LYS
2	9-B	539	ASN

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Mol	Chain	Res	Type
2	9-B	546	LEU
2	9-B	553	VAL
2	9-B	569	SER
2	9-B	574	VAL
2	9-B	580	ARG
2	9-B	600	TYR
2	9-B	605	LEU
2	9-B	641	PHE
2	9-B	654	ASN
2	9-B	728	HIS
2	9-B	765	LEU
2	9-B	771	GLU
2	9-B	772	PHE
2	9-B	810	LYS
2	9-B	839	PHE
3	9-C	21	LEU
3	9-C	46	ARG
3	9-C	51	LYS
3	9-C	86	PHE
3	9-C	107	ASN
3	9-C	122	LYS
3	9-C	124	ASP
3	9-C	158	LEU
3	9-C	176	ARG
3	9-C	179	GLU
3	9-C	180	VAL
3	9-C	240	ASN
3	9-C	245	PRO
3	9-C	262	SER
3	9-C	266	HIS
3	9-C	287	LYS
3	9-C	292	TYR
3	9-C	295	MET
3	9-C	301	PRO
3	9-C	333	ARG
3	9-C	354	VAL
3	9-C	359	ARG
3	9-C	379	ASN
3	9-C	394	PHE
3	9-D	55	ARG
3	9-D	84	ARG
3	9-D	88	ASP

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Mol	Chain	Res	Type
3	9-D	116	GLN
3	9-D	121	ASN
3	9-D	133	PHE
3	9-D	140	HIS
3	9-D	160	ASP
3	9-D	181	VAL
3	9-D	193	ARG
3	9-D	209	LEU
3	9-D	248	MET
3	9-D	287	LYS
3	9-D	292	TYR
3	9-D	359	ARG
3	9-D	376	MET
3	9-D	394	PHE
3	9-D	398	PHE
3	9-D	435	GLU
1	10-A	55	GLN
1	10-A	67	LEU
1	10-A	93	LYS
1	10-A	97	LYS
1	10-A	108	ARG
1	10-A	129	THR
1	10-A	141	GLU
1	10-A	146	LEU
1	10-A	156	GLU
1	10-A	171	ARG
1	10-A	173	LEU
1	10-A	179	GLU
1	10-A	181	GLU
1	10-A	183	ASN
1	10-A	186	MET
1	10-A	253	GLN
1	10-A	278	ASP
1	10-A	284	TYR
1	10-A	288	THR
1	10-A	354	LEU
1	10-A	360	SER
1	10-A	365	THR
1	10-A	368	SER
1	10-A	384	LEU
1	10-A	385	MET
1	10-A	424	GLN

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Mol	Chain	Res	Type
1	10-A	481	LEU
1	10-A	486	PHE
1	10-A	562	PHE
1	10-A	580	ILE
1	10-A	587	ARG
1	10-A	598	LEU
1	10-A	603	TRP
1	10-A	606	LEU
1	10-A	624	ARG
1	10-A	630	ARG
1	10-A	661	LYS
1	10-A	663	TYR
1	10-A	696	GLN
1	10-A	700	PHE
1	10-A	711	LYS
1	10-A	761	ILE
1	10-A	776	ARG
1	10-A	792	ASP
1	10-A	793	PHE
2	10-B	182	GLU
2	10-B	199	LEU
2	10-B	213	ILE
2	10-B	225	PHE
2	10-B	229	LEU
2	10-B	231	TYR
2	10-B	243	MET
2	10-B	250	LYS
2	10-B	270	ASN
2	10-B	271	LEU
2	10-B	285	ARG
2	10-B	289	GLU
2	10-B	294	LEU
2	10-B	315	GLU
2	10-B	326	THR
2	10-B	334	LEU
2	10-B	338	MET
2	10-B	347	MET
2	10-B	385	PHE
2	10-B	398	LEU
2	10-B	400	TYR
2	10-B	415	TYR
2	10-B	425	PHE

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Mol	Chain	Res	Type
2	10-B	427	LYS
2	10-B	445	PHE
2	10-B	462	GLN
2	10-B	466	GLN
2	10-B	471	ARG
2	10-B	481	LEU
2	10-B	489	MET
2	10-B	494	GLU
2	10-B	526	ARG
2	10-B	544	ARG
2	10-B	559	THR
2	10-B	564	LEU
2	10-B	568	LEU
2	10-B	572	LEU
2	10-B	580	ARG
2	10-B	592	ARG
2	10-B	599	PHE
2	10-B	612	ARG
2	10-B	641	PHE
2	10-B	723	GLU
2	10-B	725	GLU
2	10-B	728	HIS
2	10-B	764	LEU
2	10-B	770	TYR
2	10-B	780	ASN
2	10-B	802	LEU
2	10-B	826	PHE
2	10-B	827	ARG
2	10-B	843	LYS
2	10-B	846	ARG
3	10-C	8	LEU
3	10-C	12	GLN
3	10-C	36	LEU
3	10-C	46	ARG
3	10-C	59	ARG
3	10-C	86	PHE
3	10-C	125	LYS
3	10-C	126	GLU
3	10-C	140	HIS
3	10-C	150	LEU
3	10-C	178	SER
3	10-C	179	GLU

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Mol	Chain	Res	Type
3	10-C	183	GLN
3	10-C	243	ARG
3	10-C	248	MET
3	10-C	260	ILE
3	10-C	282	ASP
3	10-C	310	MET
3	10-C	316	PHE
3	10-C	319	TYR
3	10-C	322	ILE
3	10-C	325	ASN
3	10-C	333	ARG
3	10-C	347	TRP
3	10-C	358	ARG
3	10-C	359	ARG
3	10-C	379	ASN
3	10-C	427	ARG
3	10-D	12	GLN
3	10-D	31	ILE
3	10-D	42	SER
3	10-D	49	ASP
3	10-D	61	LYS
3	10-D	130	THR
3	10-D	140	HIS
3	10-D	163	PRO
3	10-D	180	VAL
3	10-D	182	VAL
3	10-D	183	GLN
3	10-D	188	ILE
3	10-D	211	ASN
3	10-D	256	TYR
3	10-D	266	HIS
3	10-D	296	LEU
3	10-D	311	ASN
3	10-D	314	THR
3	10-D	331	ILE
3	10-D	335	MET
3	10-D	341	ARG
3	10-D	358	ARG
3	10-D	359	ARG
3	10-D	362	TYR
3	10-D	363	LEU
3	10-D	379	ASN

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Mol	Chain	Res	Type
3	10-D	380	MET
3	10-D	391	CYS
3	10-D	393	THR
3	10-D	435	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (310) such sidechains are listed below:

Mol	Chain	Res	Type
1	1-A	55	GLN
1	1-A	252	GLN
1	1-A	258	ASN
1	1-A	277	GLN
1	1-A	411	GLN
1	1-A	421	HIS
1	1-A	423	GLN
1	1-A	442	ASN
1	1-A	454	ASN
1	1-A	473	ASN
1	1-A	476	ASN
1	1-A	480	GLN
1	1-A	589	GLN
1	1-A	770	ASN
2	1-B	290	ASN
2	1-B	322	HIS
2	1-B	466	GLN
2	1-B	527	HIS
2	1-B	539	ASN
2	1-B	573	ASN
2	1-B	832	ASN
3	1-C	12	GLN
3	1-C	15	ASN
3	1-C	29	HIS
3	1-C	153	ASN
3	1-C	266	HIS
3	1-C	392	ASN
3	1-D	29	HIS
3	1-D	266	HIS
3	1-D	303	ASN
3	1-D	312	ASN
3	1-D	320	ASN
3	1-D	325	ASN
3	1-D	418	ASN

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Mol	Chain	Res	Type
1	2-A	136	GLN
1	2-A	277	GLN
1	2-A	379	ASN
1	2-A	455	ASN
1	2-A	595	HIS
1	2-A	781	ASN
1	2-A	784	GLN
2	2-B	206	GLN
2	2-B	215	ASN
2	2-B	380	HIS
2	2-B	386	ASN
2	2-B	452	GLN
2	2-B	534	ASN
2	2-B	738	HIS
2	2-B	767	ASN
3	2-C	81	ASN
3	2-C	91	ASN
3	2-C	116	GLN
3	2-C	286	HIS
3	2-C	289	HIS
3	2-C	303	ASN
3	2-C	312	ASN
3	2-C	366	GLN
3	2-C	418	ASN
3	2-D	229	GLN
3	2-D	312	ASN
3	2-D	320	ASN
3	2-D	355	ASN
3	2-D	417	GLN
1	3-A	389	ASN
1	3-A	421	HIS
1	3-A	454	ASN
1	3-A	455	ASN
1	3-A	633	HIS
1	3-A	665	ASN
1	3-A	686	ASN
2	3-B	420	GLN
2	3-B	423	ASN
2	3-B	434	GLN
2	3-B	465	ASN
2	3-B	469	HIS
2	3-B	527	HIS

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Mol	Chain	Res	Type
2	3-B	608	ASN
2	3-B	642	GLN
2	3-B	654	ASN
2	3-B	669	GLN
2	3-B	738	HIS
2	3-B	808	ASN
3	3-C	116	GLN
3	3-C	140	HIS
3	3-C	266	HIS
3	3-C	289	HIS
3	3-C	312	ASN
3	3-C	392	ASN
3	3-D	60	ASN
3	3-D	228	ASN
3	3-D	320	ASN
3	3-D	353	HIS
3	3-D	355	ASN
3	3-D	370	ASN
3	3-D	389	ASN
1	4-A	79	ASN
1	4-A	167	ASN
1	4-A	389	ASN
1	4-A	449	HIS
1	4-A	480	GLN
1	4-A	595	HIS
1	4-A	607	ASN
1	4-A	633	HIS
1	4-A	638	HIS
2	4-B	204	HIS
2	4-B	206	GLN
2	4-B	215	ASN
2	4-B	643	GLN
2	4-B	660	ASN
2	4-B	780	ASN
3	4-C	12	GLN
3	4-C	16	HIS
3	4-C	29	HIS
3	4-C	103	ASN
3	4-C	121	ASN
3	4-C	137	GLN
3	4-C	186	ASN
3	4-C	211	ASN

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Mol	Chain	Res	Type
3	4-C	408	ASN
3	4-C	418	ASN
3	4-D	153	ASN
3	4-D	281	HIS
3	4-D	312	ASN
3	4-D	325	ASN
3	4-D	370	ASN
1	5-A	167	ASN
1	5-A	175	GLN
1	5-A	297	GLN
1	5-A	455	ASN
1	5-A	485	GLN
1	5-A	559	HIS
1	5-A	595	HIS
1	5-A	607	ASN
1	5-A	665	ASN
1	5-A	673	GLN
1	5-A	696	GLN
2	5-B	430	HIS
2	5-B	550	HIS
2	5-B	669	GLN
3	5-C	15	ASN
3	5-C	24	GLN
3	5-C	115	ASN
3	5-C	219	ASN
3	5-C	289	HIS
3	5-C	355	ASN
3	5-D	12	GLN
3	5-D	38	GLN
3	5-D	320	ASN
3	5-D	325	ASN
3	5-D	370	ASN
3	5-D	385	ASN
1	6-A	183	ASN
1	6-A	369	ASN
1	6-A	421	HIS
1	6-A	423	GLN
1	6-A	430	GLN
1	6-A	454	ASN
1	6-A	559	HIS
1	6-A	607	ASN
1	6-A	637	ASN

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Mol	Chain	Res	Type
1	6-A	638	HIS
1	6-A	770	ASN
2	6-B	348	ASN
2	6-B	380	HIS
2	6-B	386	ASN
2	6-B	430	HIS
2	6-B	629	ASN
2	6-B	756	GLN
2	6-B	767	ASN
3	6-C	9	GLN
3	6-C	15	ASN
3	6-C	16	HIS
3	6-C	206	ASN
3	6-C	340	GLN
3	6-C	353	HIS
3	6-D	9	GLN
3	6-D	115	ASN
3	6-D	183	GLN
3	6-D	289	HIS
3	6-D	303	ASN
3	6-D	320	ASN
3	6-D	368	ASN
3	6-D	431	GLN
1	7-A	55	GLN
1	7-A	136	GLN
1	7-A	277	GLN
1	7-A	454	ASN
1	7-A	455	ASN
1	7-A	470	GLN
1	7-A	559	HIS
1	7-A	589	GLN
1	7-A	633	HIS
1	7-A	638	HIS
1	7-A	650	ASN
1	7-A	698	GLN
1	7-A	781	ASN
2	7-B	206	GLN
2	7-B	215	ASN
2	7-B	290	ASN
2	7-B	303	HIS
2	7-B	461	ASN
2	7-B	466	GLN

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Mol	Chain	Res	Type
2	7-B	573	ASN
2	7-B	608	ASN
2	7-B	654	ASN
2	7-B	660	ASN
2	7-B	728	HIS
3	7-C	186	ASN
3	7-C	226	HIS
3	7-C	286	HIS
3	7-C	311	ASN
3	7-C	317	ASN
3	7-C	406	ASN
3	7-D	91	ASN
3	7-D	281	HIS
3	7-D	312	ASN
3	7-D	392	ASN
1	8-A	273	ASN
1	8-A	293	ASN
1	8-A	421	HIS
1	8-A	452	ASN
1	8-A	565	ASN
1	8-A	638	HIS
1	8-A	674	ASN
1	8-A	686	ASN
1	8-A	781	ASN
2	8-B	208	GLN
2	8-B	420	GLN
2	8-B	534	ASN
2	8-B	550	HIS
2	8-B	601	GLN
2	8-B	629	ASN
2	8-B	642	GLN
2	8-B	808	ASN
3	8-C	12	GLN
3	8-C	16	HIS
3	8-C	266	HIS
3	8-C	289	HIS
3	8-C	317	ASN
3	8-C	368	ASN
3	8-C	379	ASN
3	8-D	15	ASN
3	8-D	16	HIS
3	8-D	153	ASN

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Mol	Chain	Res	Type
3	8-D	228	ASN
3	8-D	320	ASN
3	8-D	353	HIS
3	8-D	370	ASN
3	8-D	414	GLN
1	9-A	252	GLN
1	9-A	323	GLN
1	9-A	376	GLN
1	9-A	559	HIS
2	9-B	206	GLN
2	9-B	215	ASN
2	9-B	386	ASN
2	9-B	387	GLN
2	9-B	430	HIS
2	9-B	434	GLN
2	9-B	588	ASN
2	9-B	597	ASN
2	9-B	642	GLN
2	9-B	643	GLN
2	9-B	645	ASN
2	9-B	815	GLN
3	9-C	16	HIS
3	9-C	29	HIS
3	9-C	107	ASN
3	9-C	226	HIS
3	9-C	317	ASN
3	9-C	385	ASN
3	9-D	9	GLN
3	9-D	16	HIS
3	9-D	266	HIS
3	9-D	303	ASN
3	9-D	339	GLN
3	9-D	353	HIS
3	9-D	368	ASN
3	9-D	420	GLN
1	10-A	115	GLN
1	10-A	274	ASN
1	10-A	379	ASN
1	10-A	442	ASN
1	10-A	633	HIS
1	10-A	638	HIS
2	10-B	322	HIS

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Mol	Chain	Res	Type
2	10-B	459	HIS
2	10-B	461	ASN
2	10-B	462	GLN
2	10-B	469	HIS
2	10-B	479	ASN
2	10-B	669	GLN
2	10-B	780	ASN
2	10-B	799	ASN
2	10-B	806	ASN
2	10-B	832	ASN
3	10-C	16	HIS
3	10-C	24	GLN
3	10-C	91	ASN
3	10-C	153	ASN
3	10-C	186	ASN
3	10-C	206	ASN
3	10-C	266	HIS
3	10-C	312	ASN
3	10-C	405	ASN
3	10-D	225	GLN
3	10-D	226	HIS
3	10-D	281	HIS
3	10-D	289	HIS
3	10-D	312	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.