



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 05:14 pm BST

PDB ID : 4V5T  
Title : X-ray structure of the Grapevine Fanleaf virus  
Authors : Schellenberger, P.; Sauter, C.; Lorber, B.; Bron, P.; Trapani, S.; Bergdoll, M.; Marmonier, A.; Schmitt-Keichinger, C.; Lemaire, O.; Demangeat, G.; Ritzenthaler, C.  
Deposited on : 2011-02-01  
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

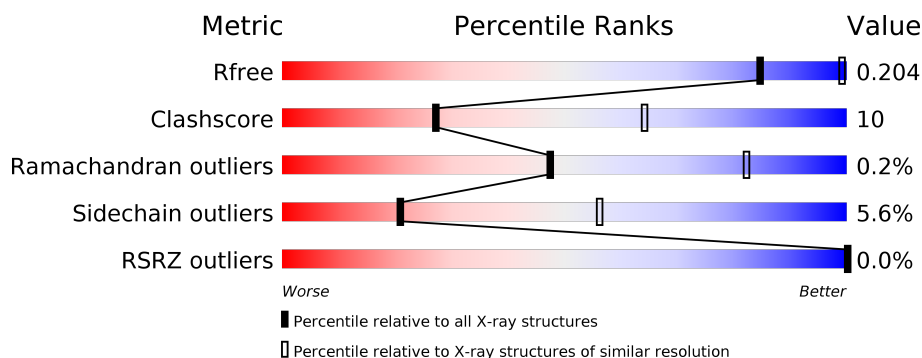
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	504	
1	AB	504	
1	AC	504	
1	AD	504	
1	AE	504	
1	AF	504	


























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Mol	Chain	Length	Quality of chain
1	AG	504	 80% 16% .
1	AH	504	 81% 16% .
1	AI	504	 81% 16% .
1	AJ	504	 82% 16% .
1	AK	504	 80% 18% .
1	AL	504	 81% 17% .
1	AM	504	 82% 16% .
1	AN	504	 79% 19% .
1	AO	504	 80% 18% .
1	AP	504	 81% 17% .
1	AQ	504	 82% 16% .
1	AR	504	 81% 16% .
1	AS	504	 81% 16% .
1	AT	504	 80% 18% .
1	BA	504	 81% 17% .
1	BB	504	 81% 16% .
1	BC	504	 80% 17% .
1	BD	504	 83% 15% .
1	BE	504	 82% 16% .
1	BF	504	 79% 18% .
1	BG	504	 80% 18% .
1	BH	504	 80% 18% .
1	BI	504	 80% 18% .
1	BJ	504	 81% 17% .
1	BK	504	 82% 16% .





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Mol	Chain	Length	Quality of chain
1	BL	504	 81% 16% .
1	BM	504	 81% 17% .
1	BN	504	 81% 16% .
1	BO	504	 80% 17% .
1	BP	504	 81% 16% .
1	BQ	504	 81% 17% .
1	BR	504	 81% 16% .
1	BS	504	 80% 18% .
1	BT	504	 80% 18% .
1	CA	504	 82% 15% .
1	CB	504	 81% 17% .
1	CC	504	 82% 15% .
1	CD	504	 81% 17% .
1	CE	504	 79% 19% .
1	CF	504	 80% 17% .
1	CG	504	 82% 16% .
1	CH	504	 80% 17% .
1	CI	504	 80% 17% .
1	CJ	504	 81% 17% .
1	CK	504	 81% 17% .
1	CL	504	 82% 16% .
1	CM	504	 79% 19% .
1	CN	504	 82% 16% .
1	CO	504	 80% 18% .
1	CP	504	 81% 16% .

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Mol	Chain	Length	Quality of chain
1	CQ	504	 82% 16% •
1	CR	504	 81% 17% •
1	CS	504	 81% 17% •
1	CT	504	 82% 16% •

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 237060 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AB	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AC	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AD	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AE	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AF	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AG	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AH	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AI	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AJ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AK	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AL	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AM	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AN	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AO	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AP	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AR	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AS	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	AT	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BA	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BB	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BC	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BD	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BE	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BF	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BG	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BH	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BI	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BJ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BK	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BL	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BM	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BN	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BO	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BP	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	BQ	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BR	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	BS	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	BT	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CA	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CB	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CC	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CD	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CE	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CF	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CG	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CH	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CI	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CJ	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CK	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CL	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CM	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CN	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CO	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CP	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CQ	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0
1	CR	504	Total 3951	C 2555	N 653	O 721	S 22	0	0	0

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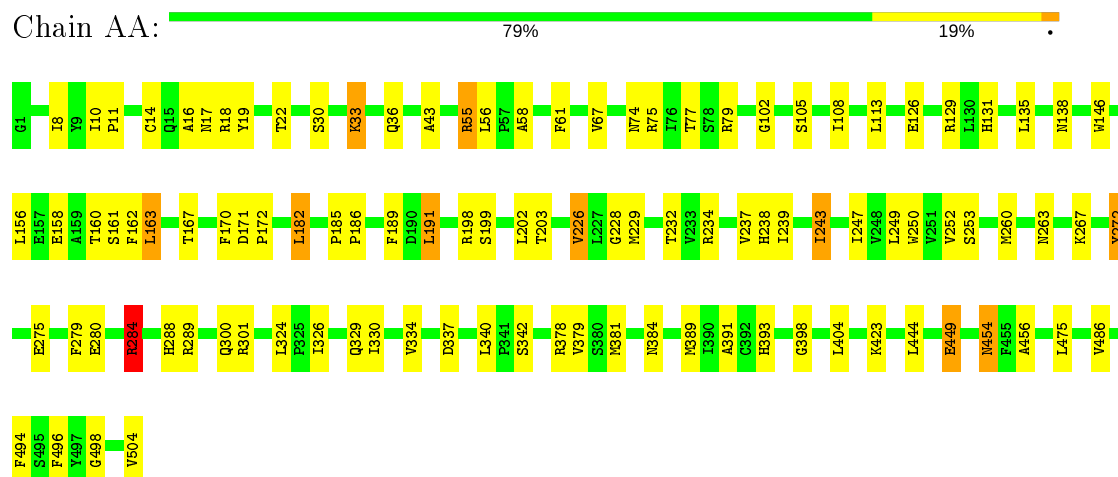
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CS	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			
1	CT	504	Total	C	N	O	S	0	0	0
			3951	2555	653	721	22			

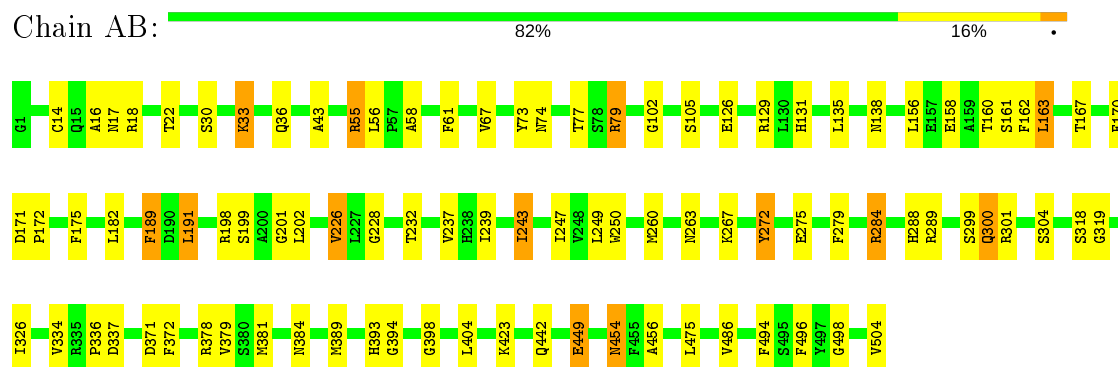
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

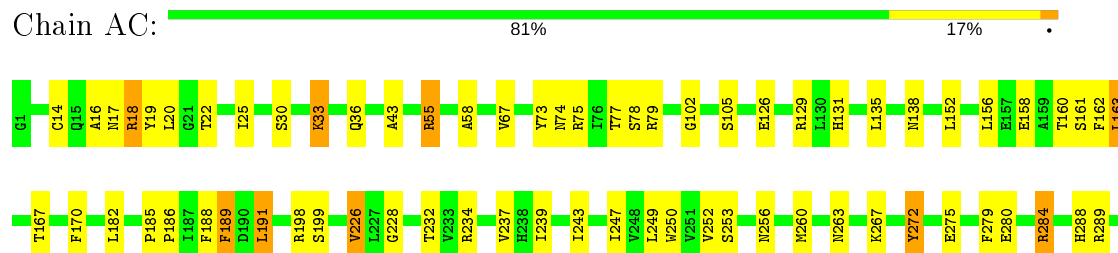
#### • Molecule 1: COAT PROTEIN



#### • Molecule 1: COAT PROTEIN



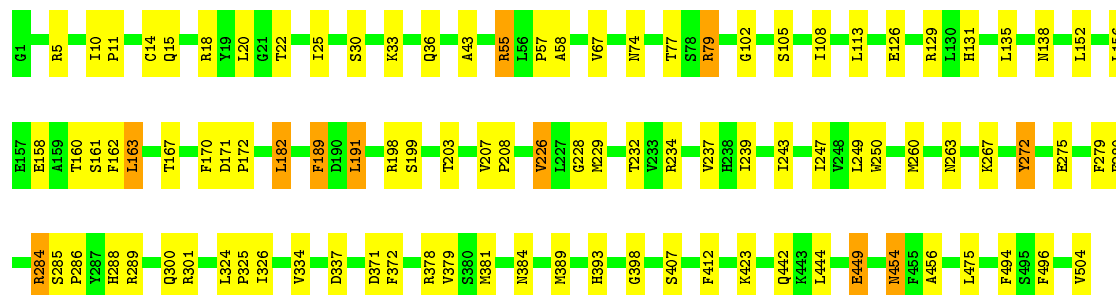
#### • Molecule 1: COAT PROTEIN





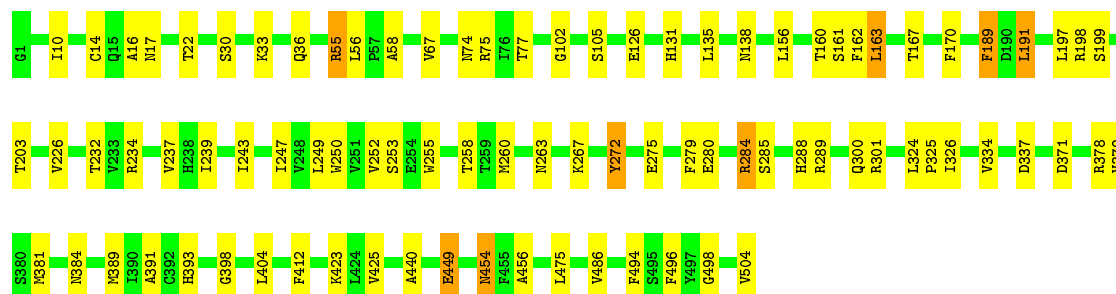
• Molecule 1: COAT PROTEIN

Chain AD: 80% 17% .



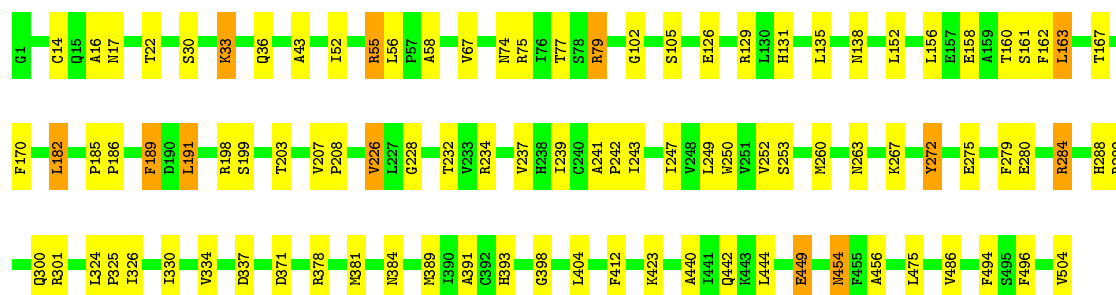
• Molecule 1: COAT PROTEIN

Chain AE: 83% 16% .



• Molecule 1: COAT PROTEIN

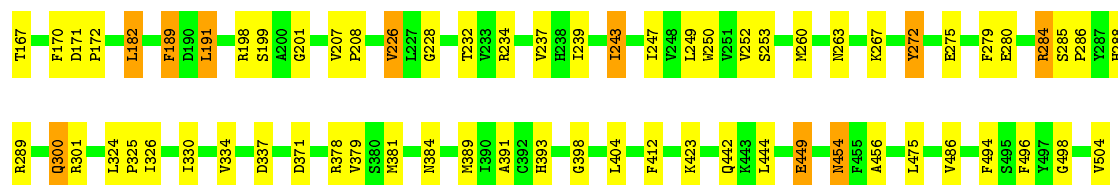
Chain AF: 81% 17% .



• Molecule 1: COAT PROTEIN

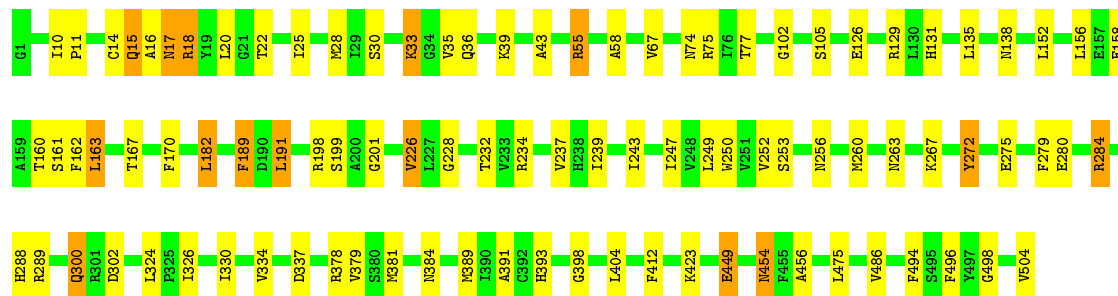
Chain AG: 80% 16% .





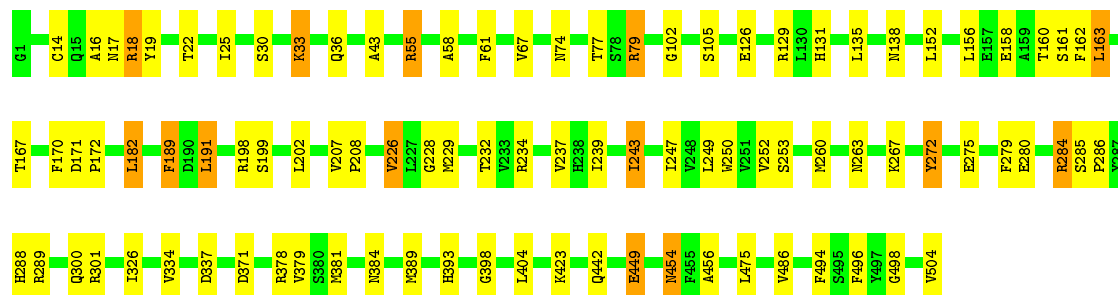
• Molecule 1: COAT PROTEIN

Chain AH: 81% 16% .



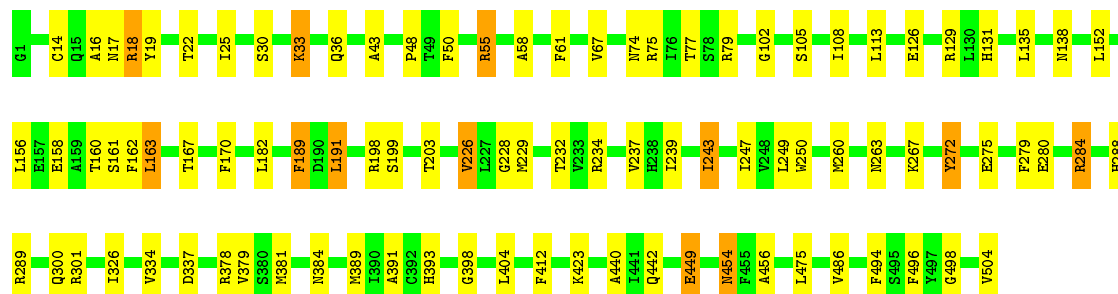
• Molecule 1: COAT PROTEIN

Chain AI: 81% 16% .



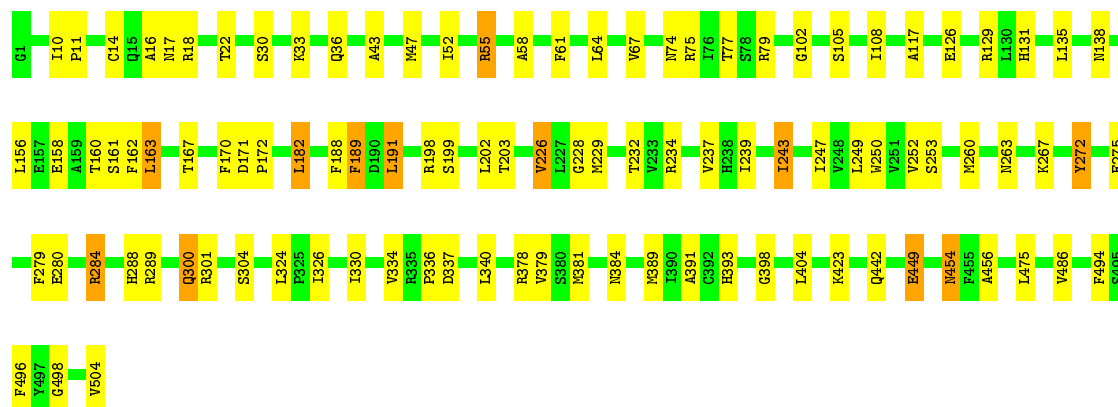
• Molecule 1: COAT PROTEIN

Chain AJ: 82% 16% .



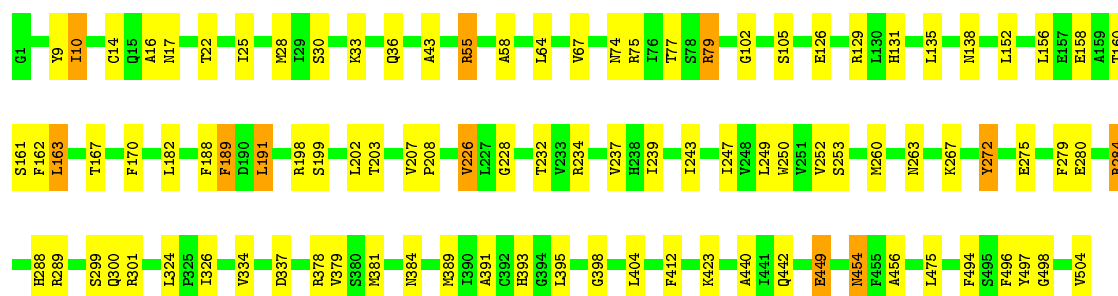
• Molecule 1: COAT PROTEIN

Chain AK: 80% 18% .



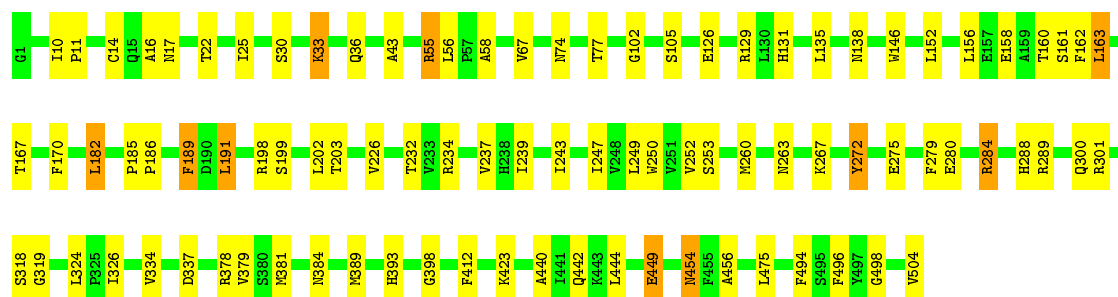
• Molecule 1: COAT PROTEIN

Chain AL: 81% 17% .



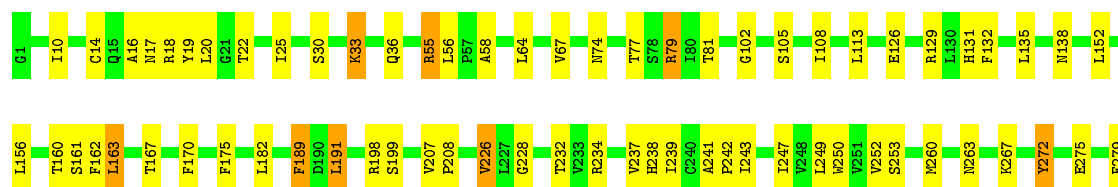
• Molecule 1: COAT PROTEIN

Chain AM: 82% 16% .



• Molecule 1: COAT PROTEIN

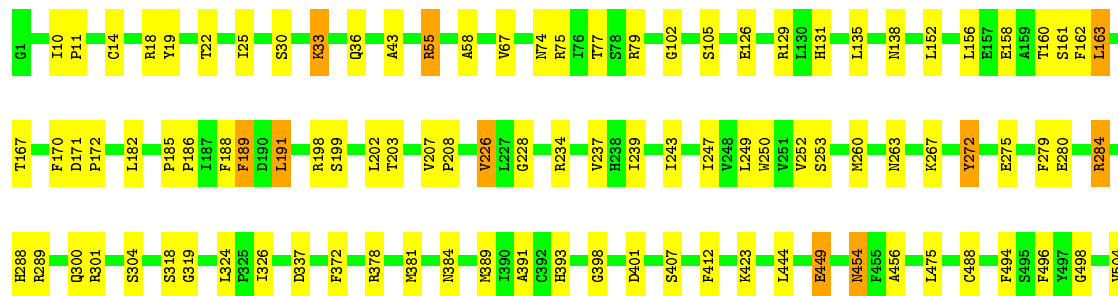
Chain AN: 79% 19% .





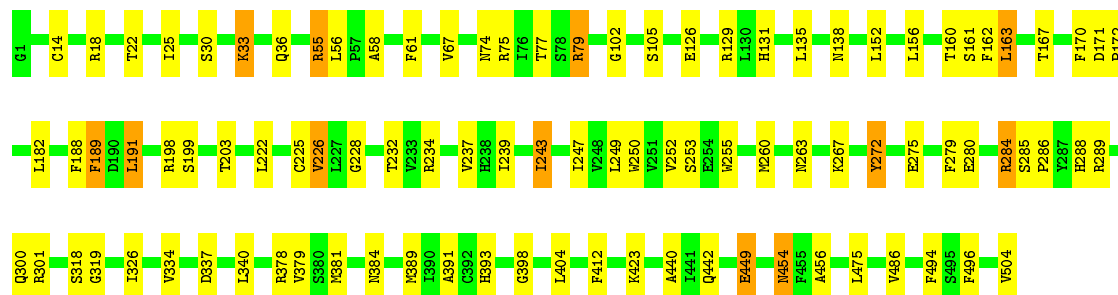
• Molecule 1: COAT PROTEIN

Chain AO: 80% 18% •



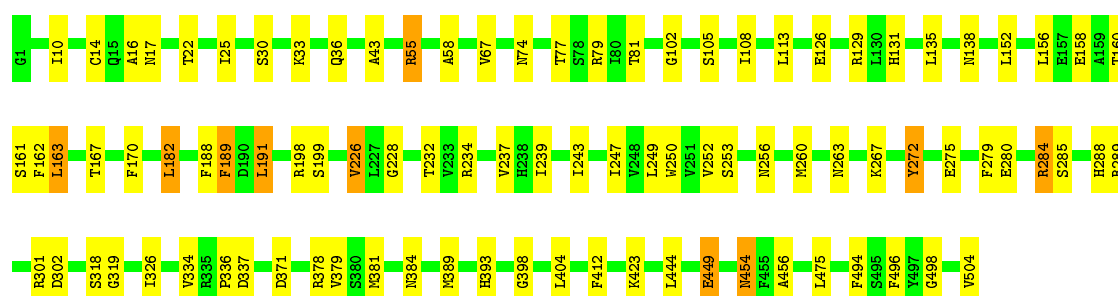
• Molecule 1: COAT PROTEIN

Chain AP: 81% 17% •



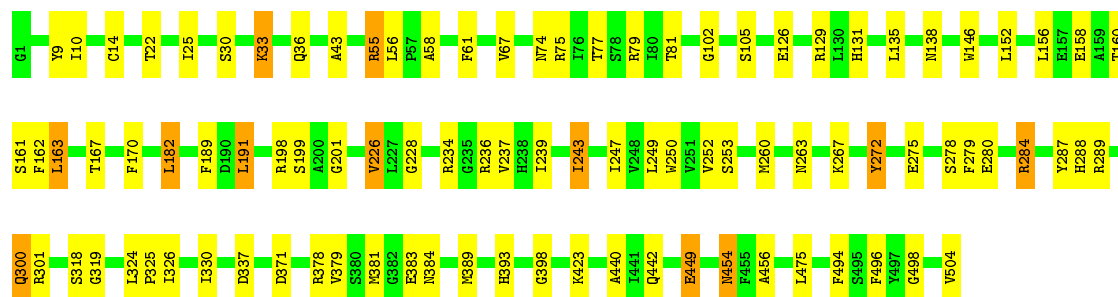
• Molecule 1: COAT PROTEIN

Chain AQ: 82% 16% •



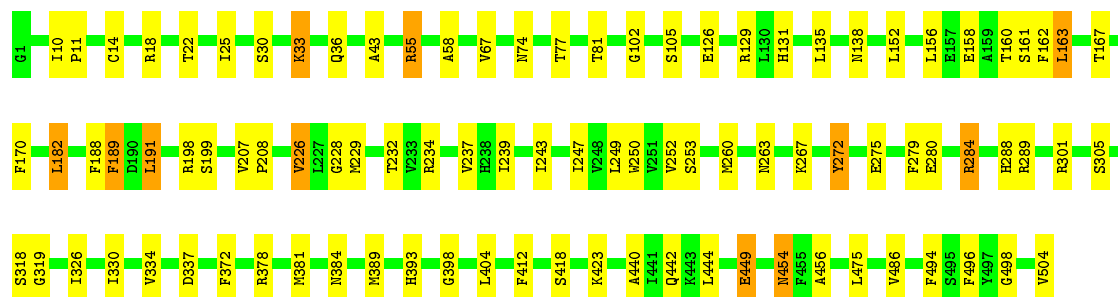
• Molecule 1: COAT PROTEIN

Chain AR: 81% 16% •



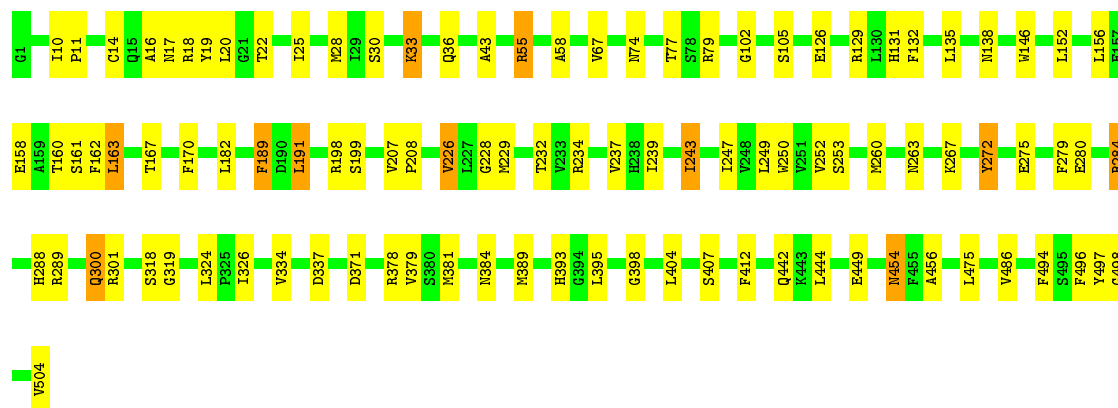
• Molecule 1: COAT PROTEIN

Chain AS: 81% 16% •



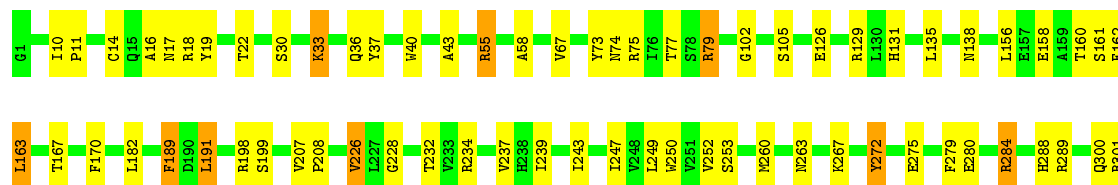
• Molecule 1: COAT PROTEIN

Chain AT: 80% 18% •



• Molecule 1: COAT PROTEIN

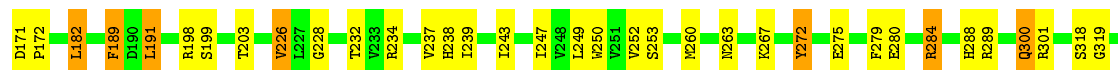
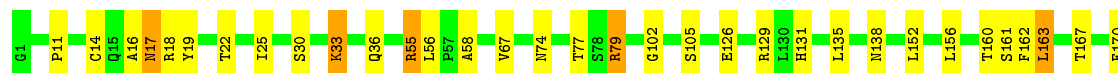
Chain BA: 81% 17% •





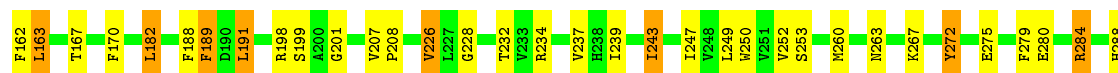
• Molecule 1: COAT PROTEIN

Chain BB: 81% 16% •



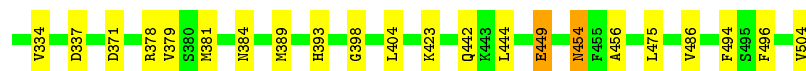
• Molecule 1: COAT PROTEIN

Chain BC: 80% 17% •



• Molecule 1: COAT PROTEIN

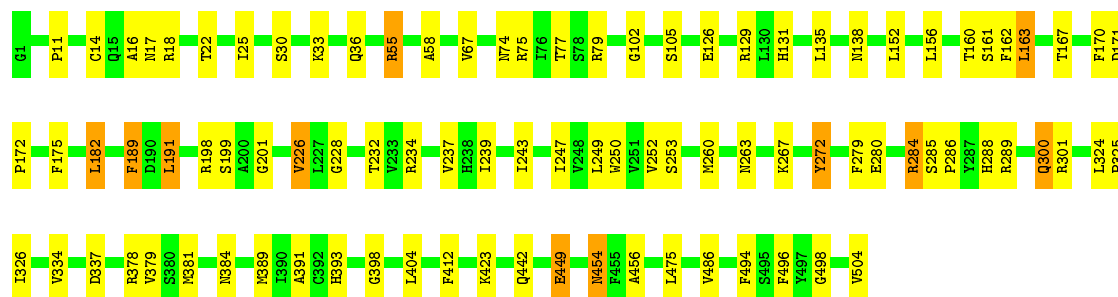
Chain BD: 83% 15% •



• Molecule 1: COAT PROTEIN

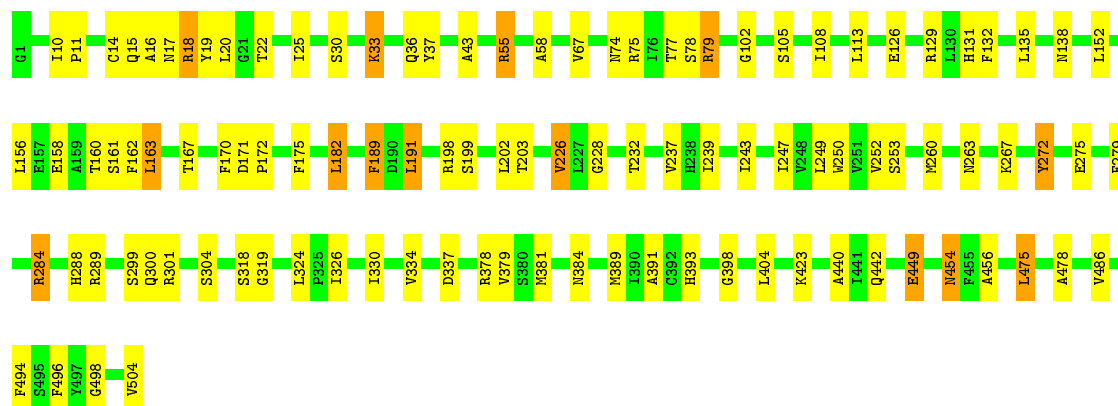
Chain BE: 82% 16% •





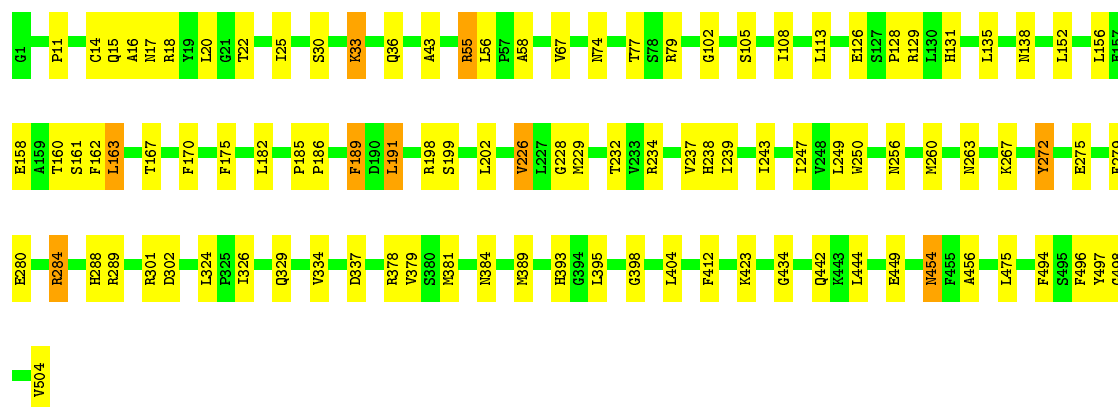
• Molecule 1: COAT PROTEIN

Chain BF: 79% 18%



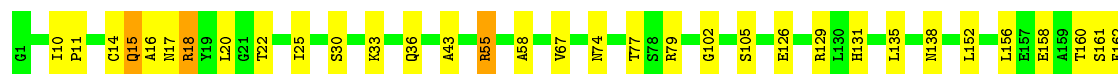
• Molecule 1: COAT PROTEIN

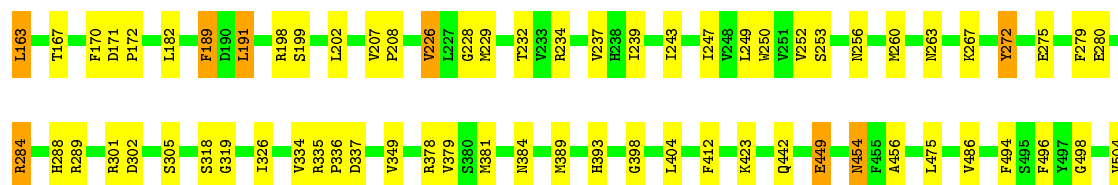
Chain BG: 80% 18%



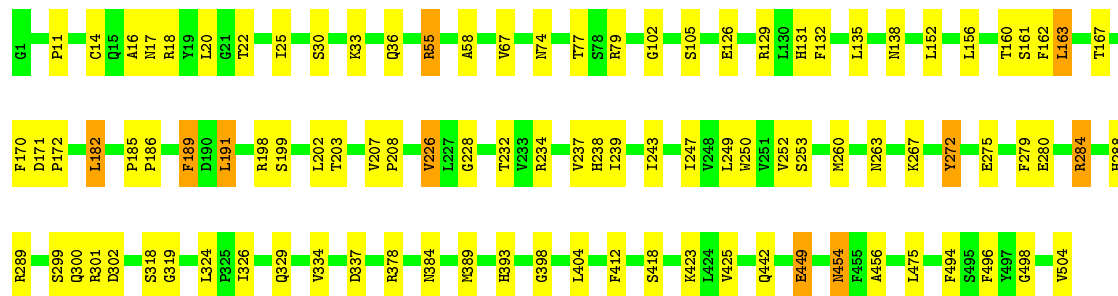
• Molecule 1: COAT PROTEIN

Chain BH: 80% 18%

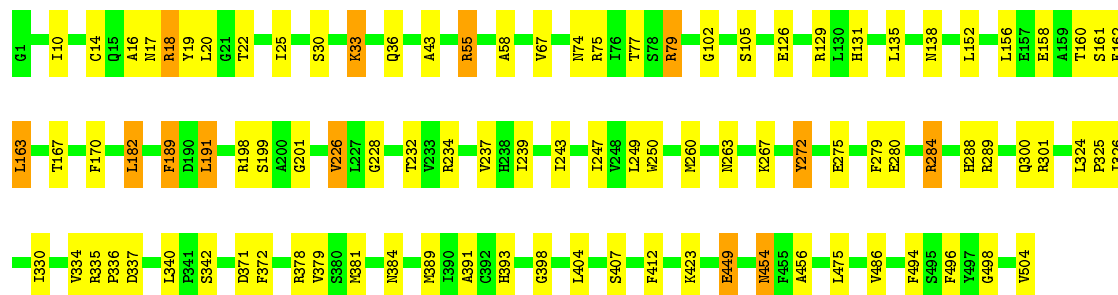
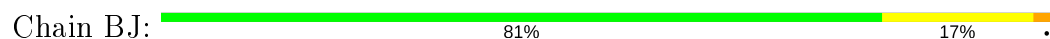




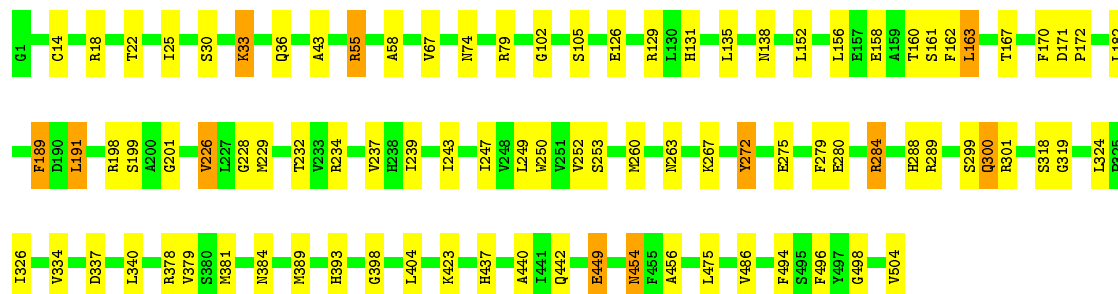
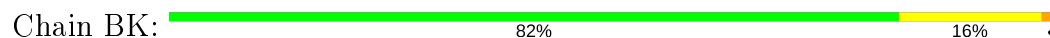
• Molecule 1: COAT PROTEIN



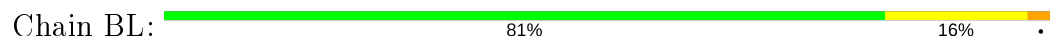
• Molecule 1: COAT PROTEIN

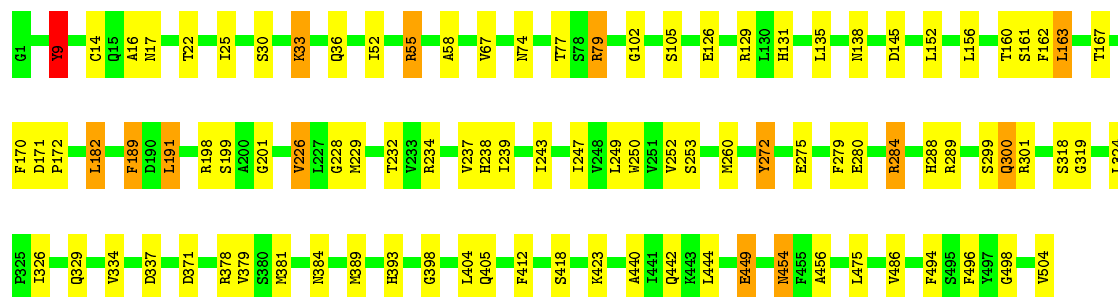


• Molecule 1: COAT PROTEIN



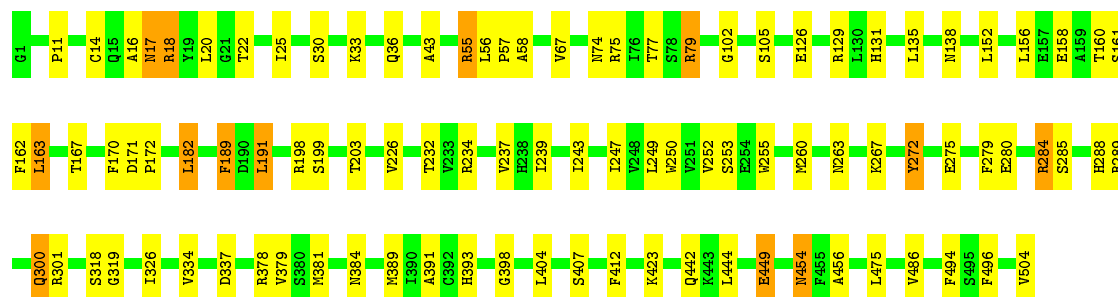
• Molecule 1: COAT PROTEIN





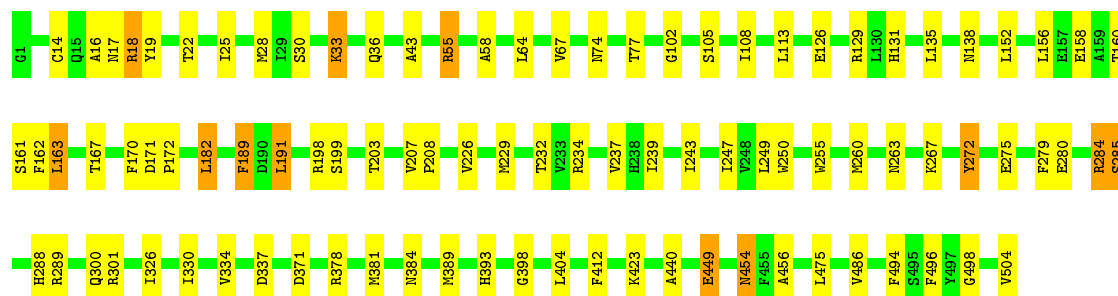
• Molecule 1: COAT PROTEIN

Chain BM: 81% 17%



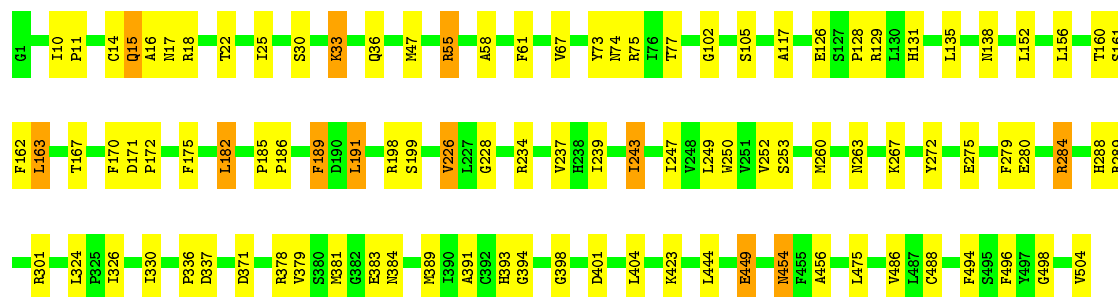
• Molecule 1: COAT PROTEIN

Chain BN: 81% 16%




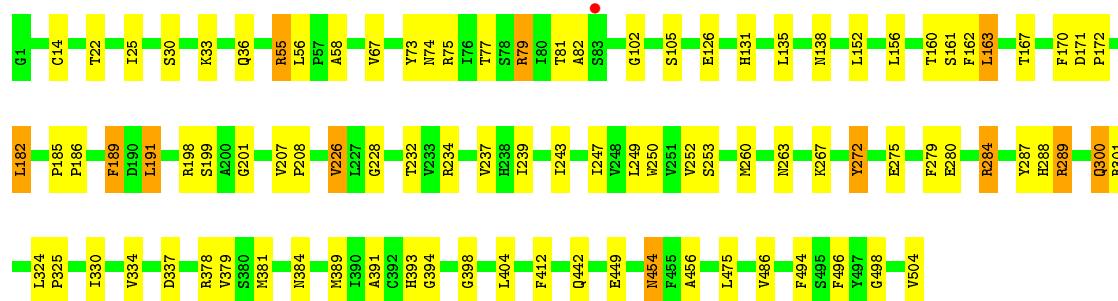
• Molecule 1: COAT PROTEIN

Chain BO: 80% 17%




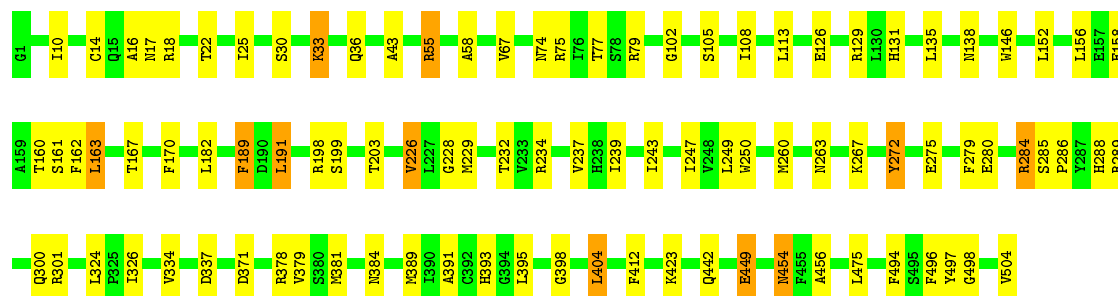
• Molecule 1: COAT PROTEIN

Chain BP:  81% 16%




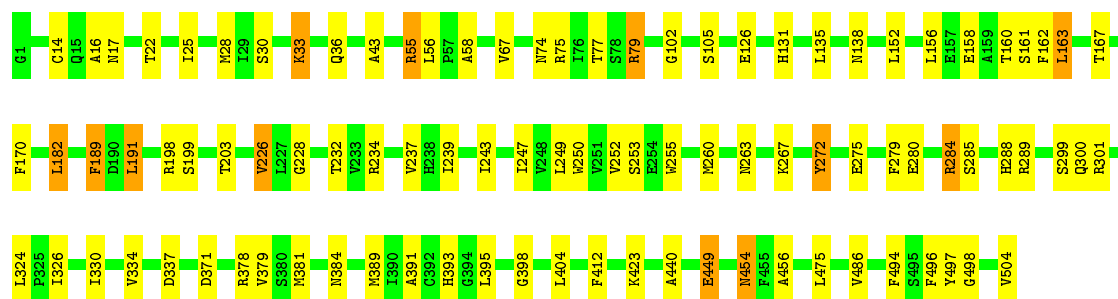
• Molecule 1: COAT PROTEIN

Chain BQ:  81% 17%




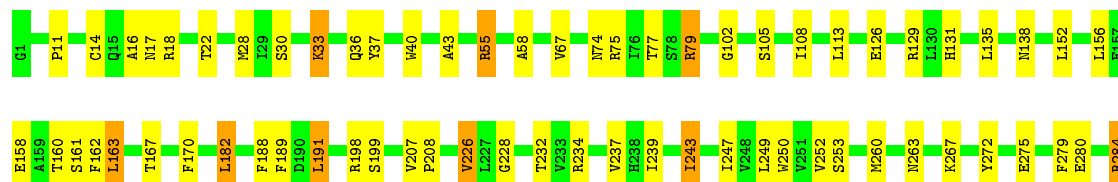
• Molecule 1: COAT PROTEIN

Chain BR:  81% 16%



• Molecule 1: COAT PROTEIN

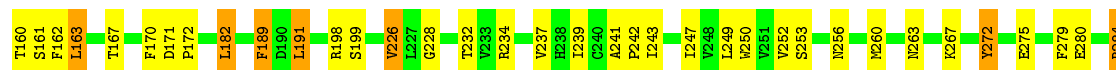
Chain BS:  80% 18%





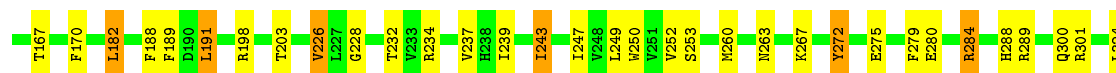
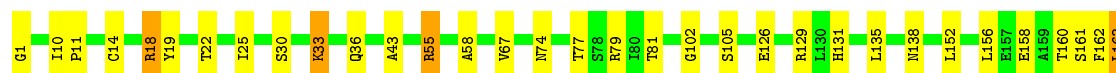
• Molecule 1: COAT PROTEIN

Chain BT: 80% 18% .



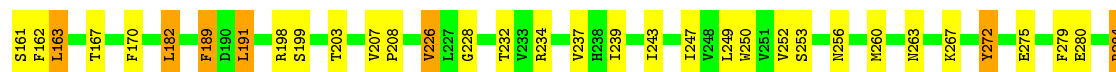
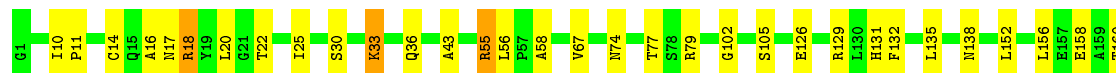
• Molecule 1: COAT PROTEIN

Chain CA: 82% 15% .



• Molecule 1: COAT PROTEIN

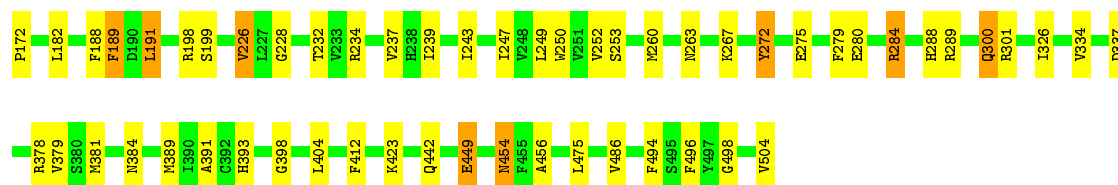
Chain CB: 81% 17% .



• Molecule 1: COAT PROTEIN

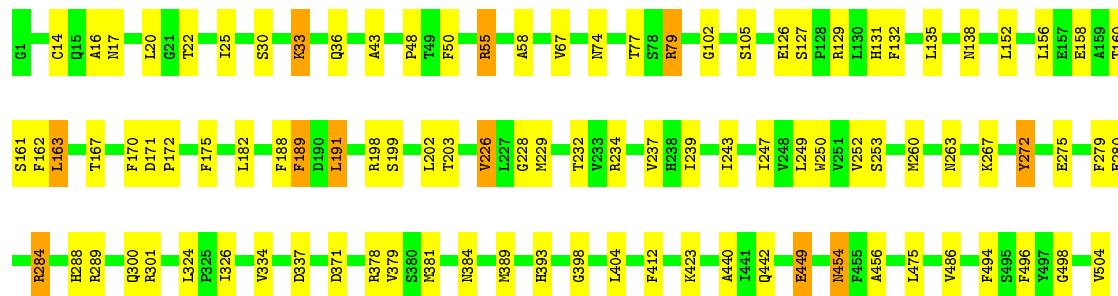
Chain CC: 82% 15% .





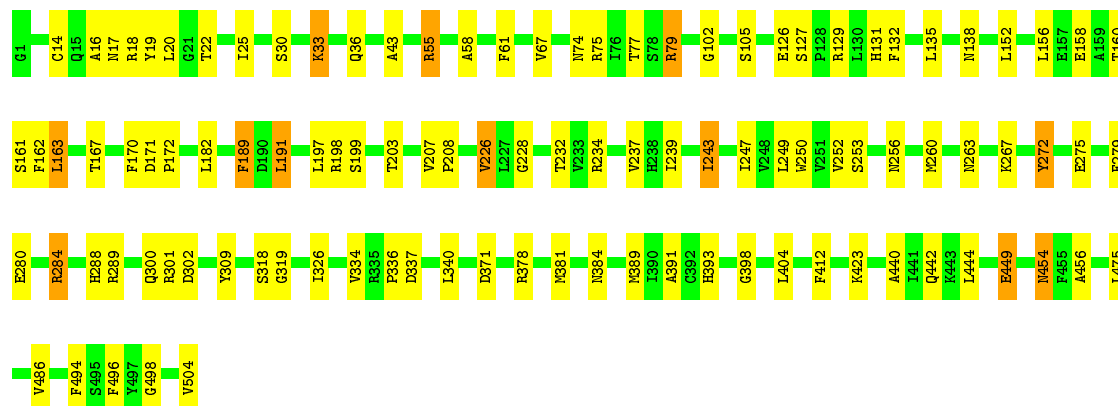
• Molecule 1: COAT PROTEIN

Chain CD: 81% 17% •



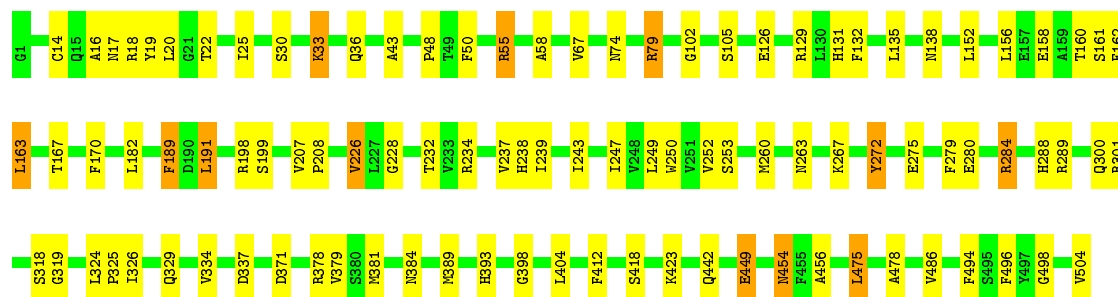
• Molecule 1: COAT PROTEIN

Chain CE: 79% 19% •




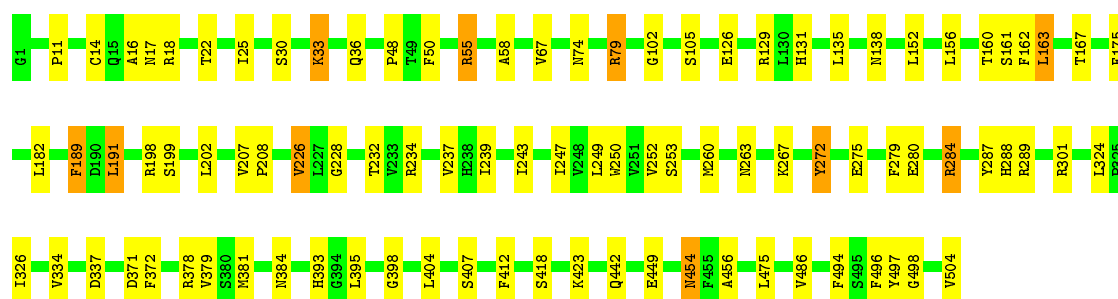
• Molecule 1: COAT PROTEIN

Chain CF: 80% 17% •



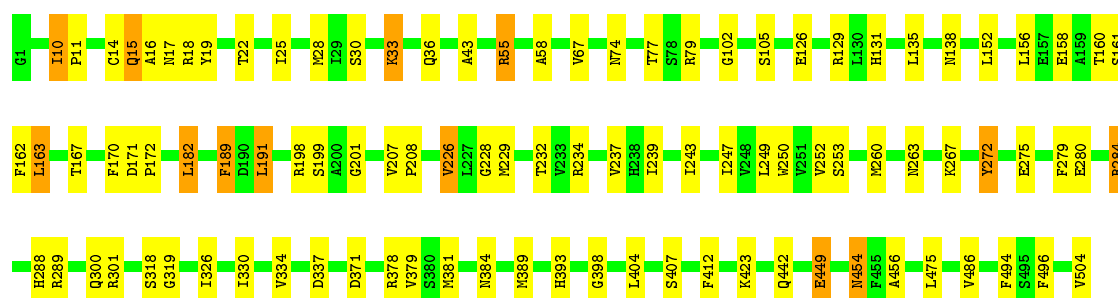
• Molecule 1: COAT PROTEIN

Chain CG:  82% 16%




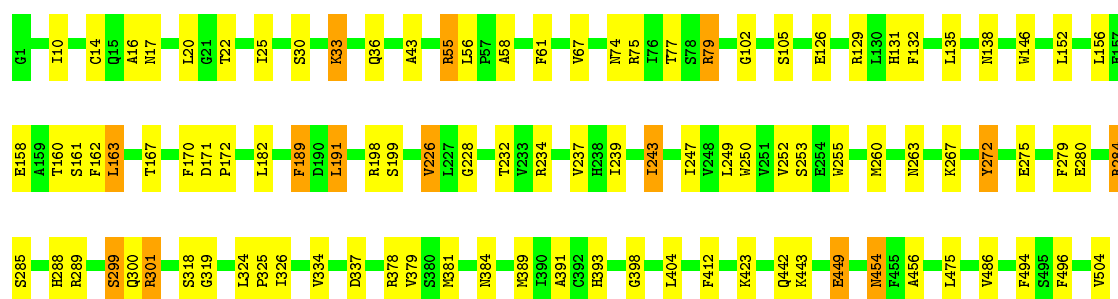
• Molecule 1: COAT PROTEIN

Chain CH:  80% 17%




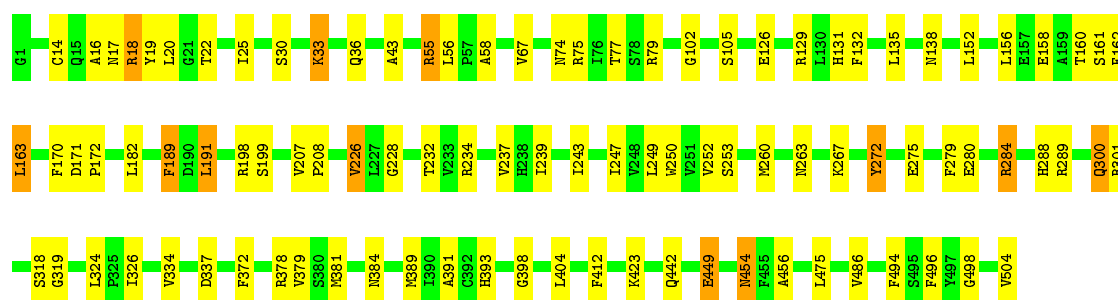
• Molecule 1: COAT PROTEIN

Chain CI:  80% 17%




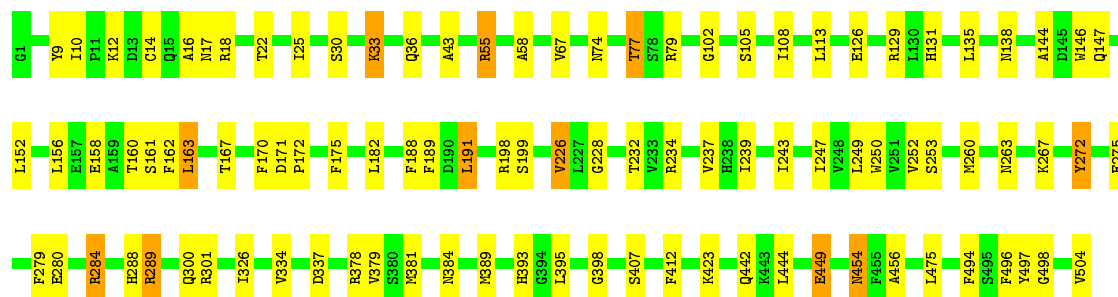
• Molecule 1: COAT PROTEIN

Chain CJ:  81% 17%




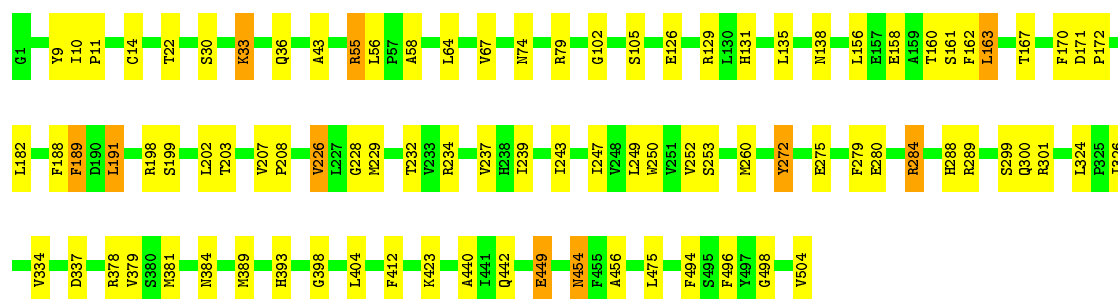
- Molecule 1: COAT PROTEIN

Chain CK:  81% 17%




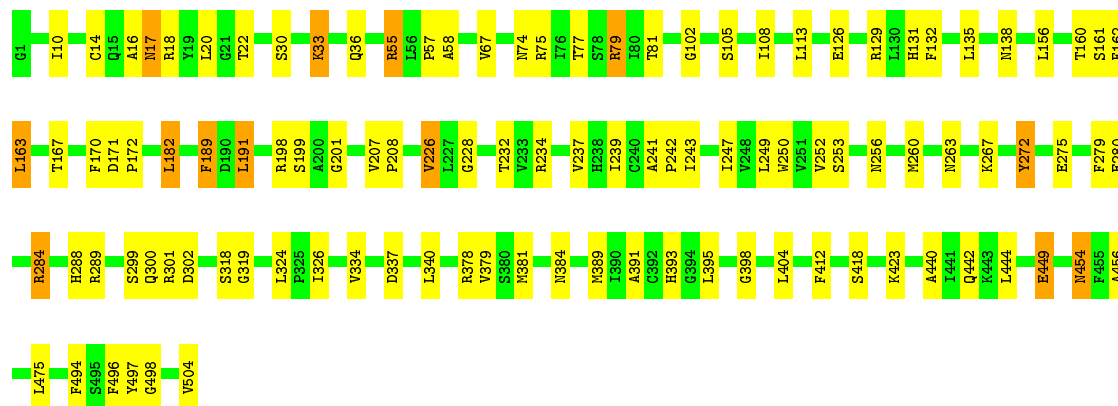
- Molecule 1: COAT PROTEIN

Chain CL:  82% 16%




- Molecule 1: COAT PROTEIN

Chain CM:  79% 19%

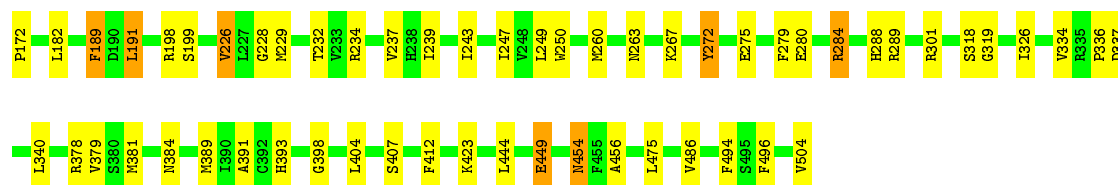


- Molecule 1: COAT PROTEIN

Chain CN:  82% 16%

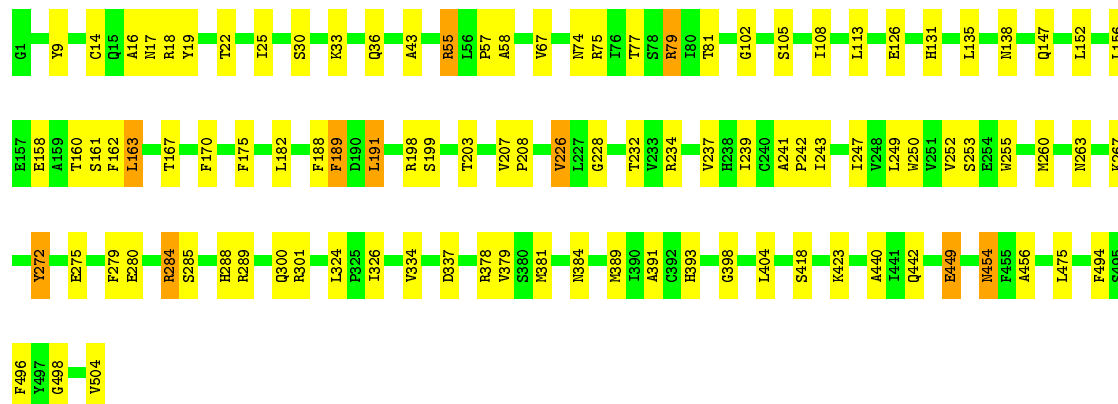






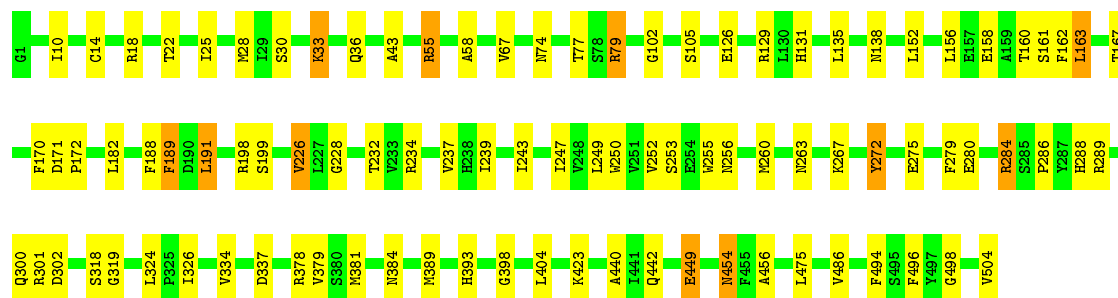
• Molecule 1: COAT PROTEIN

Chain CO: 80% 18% •



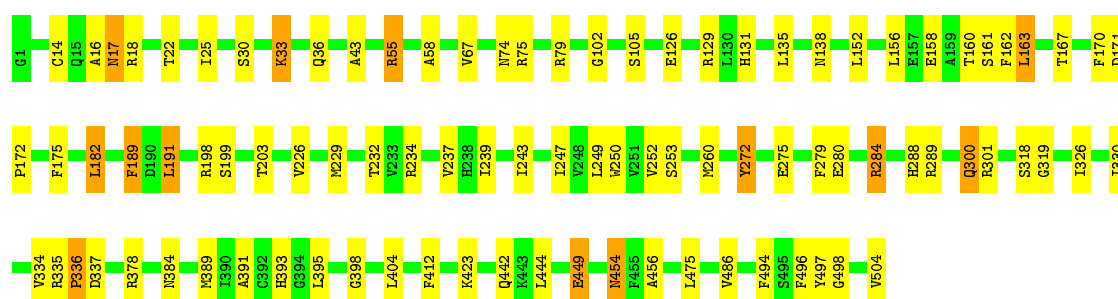
• Molecule 1: COAT PROTEIN

Chain CP: 81% 16% •




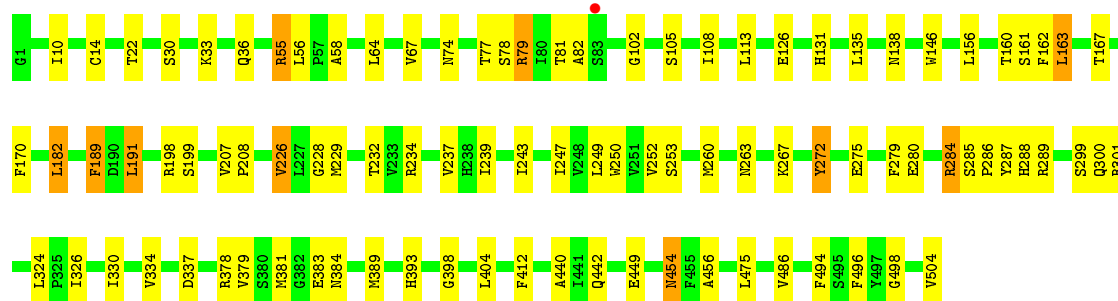
• Molecule 1: COAT PROTEIN

Chain CQ: 82% 16% •




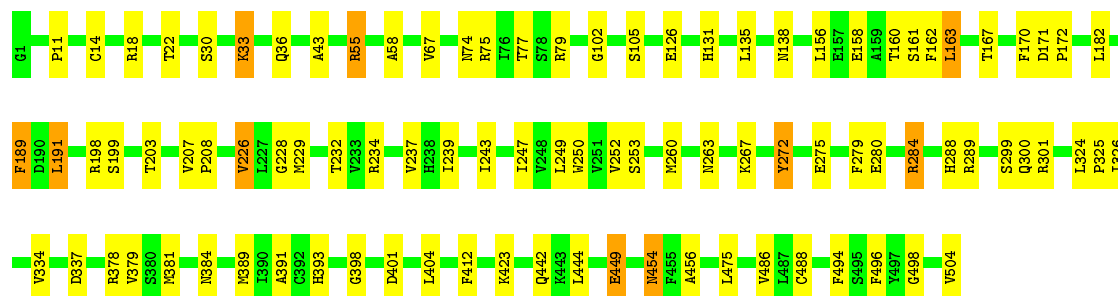
• Molecule 1: COAT PROTEIN

Chain CR:  81% 17%




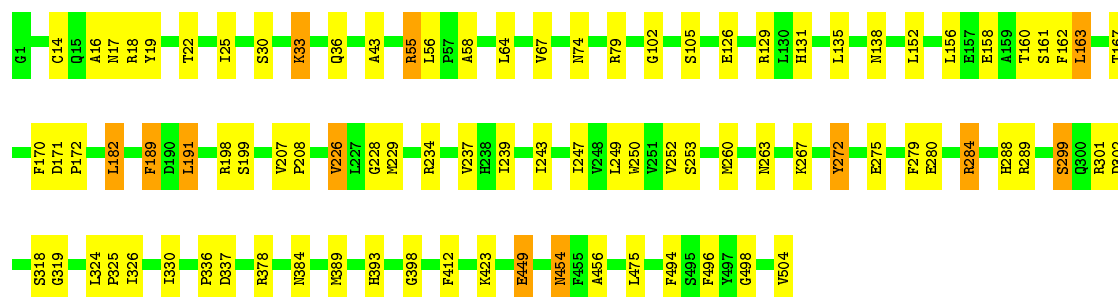
• Molecule 1: COAT PROTEIN

Chain CS:  81% 17%



• Molecule 1: COAT PROTEIN

Chain CT:  82% 16%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	279.40 Å   279.60 Å   293.30 Å 102.40°   116.40°   108.20°	Depositor
Resolution (Å)	135.43 – 3.00 135.43 – 3.00	Depositor EDS
% Data completeness (in resolution range)	88.3 (135.43-3.00) 96.3 (135.43-3.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.98 (at 3.01 Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.190 , 0.207 0.187 , 0.204	Depositor DCC
$R_{free}$ test set	66376 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.7	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for k,h,-h-k-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	237060	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	AA	0.50	0/4058	0.61	2/5517 (0.0%)
1	AB	0.50	2/4058 (0.0%)	0.62	1/5517 (0.0%)
1	AC	0.49	2/4058 (0.0%)	0.62	0/5517
1	AD	0.50	2/4058 (0.0%)	0.62	0/5517
1	AE	0.53	2/4058 (0.0%)	0.63	1/5517 (0.0%)
1	AF	0.49	1/4058 (0.0%)	0.62	1/5517 (0.0%)
1	AG	0.49	1/4058 (0.0%)	0.61	0/5517
1	AH	0.51	2/4058 (0.0%)	0.62	0/5517
1	AI	0.50	2/4058 (0.0%)	0.62	0/5517
1	AJ	0.49	1/4058 (0.0%)	0.62	0/5517
1	AK	0.48	2/4058 (0.0%)	0.61	0/5517
1	AL	0.53	2/4058 (0.0%)	0.64	0/5517
1	AM	0.51	2/4058 (0.0%)	0.62	1/5517 (0.0%)
1	AN	0.50	1/4058 (0.0%)	0.63	1/5517 (0.0%)
1	AO	0.52	2/4058 (0.0%)	0.63	0/5517
1	AP	0.51	2/4058 (0.0%)	0.63	1/5517 (0.0%)
1	AQ	0.50	1/4058 (0.0%)	0.61	0/5517
1	AR	0.52	2/4058 (0.0%)	0.63	1/5517 (0.0%)
1	AS	0.51	1/4058 (0.0%)	0.62	0/5517
1	AT	0.49	1/4058 (0.0%)	0.61	0/5517
1	BA	0.49	1/4058 (0.0%)	0.63	0/5517
1	BB	0.52	2/4058 (0.0%)	0.63	1/5517 (0.0%)
1	BC	0.49	1/4058 (0.0%)	0.62	0/5517
1	BD	0.48	2/4058 (0.0%)	0.62	0/5517
1	BE	0.50	2/4058 (0.0%)	0.63	0/5517
1	BF	0.51	2/4058 (0.0%)	0.62	0/5517
1	BG	0.50	2/4058 (0.0%)	0.62	1/5517 (0.0%)
1	BH	0.49	2/4058 (0.0%)	0.62	0/5517
1	BI	0.51	1/4058 (0.0%)	0.63	0/5517
1	BJ	0.49	1/4058 (0.0%)	0.62	0/5517
1	BK	0.49	2/4058 (0.0%)	0.61	0/5517
1	BL	0.52	3/4058 (0.1%)	0.62	0/5517
1	BM	0.53	3/4058 (0.1%)	0.64	1/5517 (0.0%)
1	BN	0.51	2/4058 (0.0%)	0.63	0/5517

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	BO	0.51	3/4058 (0.1%)	0.63	0/5517
1	BP	0.53	2/4058 (0.0%)	0.65	1/5517 (0.0%)
1	BQ	0.51	2/4058 (0.0%)	0.62	0/5517
1	BR	0.51	2/4058 (0.0%)	0.62	1/5517 (0.0%)
1	BS	0.50	0/4058	0.62	0/5517
1	BT	0.48	1/4058 (0.0%)	0.62	0/5517
1	CA	0.51	1/4058 (0.0%)	0.62	0/5517
1	CB	0.51	2/4058 (0.0%)	0.62	1/5517 (0.0%)
1	CC	0.49	1/4058 (0.0%)	0.62	0/5517
1	CD	0.50	2/4058 (0.0%)	0.62	0/5517
1	CE	0.50	1/4058 (0.0%)	0.62	0/5517
1	CF	0.48	1/4058 (0.0%)	0.62	0/5517
1	CG	0.51	1/4058 (0.0%)	0.63	0/5517
1	CH	0.49	1/4058 (0.0%)	0.62	0/5517
1	CI	0.50	1/4058 (0.0%)	0.62	1/5517 (0.0%)
1	CJ	0.50	2/4058 (0.0%)	0.63	1/5517 (0.0%)
1	CK	0.48	0/4058	0.62	0/5517
1	CL	0.52	1/4058 (0.0%)	0.63	1/5517 (0.0%)
1	CM	0.51	1/4058 (0.0%)	0.62	0/5517
1	CN	0.51	1/4058 (0.0%)	0.63	0/5517
1	CO	0.51	2/4058 (0.0%)	0.63	0/5517
1	CP	0.52	2/4058 (0.0%)	0.62	0/5517
1	CQ	0.50	2/4058 (0.0%)	0.62	0/5517
1	CR	0.53	3/4058 (0.1%)	0.64	1/5517 (0.0%)
1	CS	0.52	2/4058 (0.0%)	0.63	0/5517
1	CT	0.50	1/4058 (0.0%)	0.62	1/5517 (0.0%)
All	All	0.50	95/243480 (0.0%)	0.62	20/331020 (0.0%)

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	AA	0	2
1	AB	0	2
1	AC	0	2
1	AD	0	1
1	AE	0	1
1	AF	0	2
1	AG	0	2
1	AH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	AI	0	2
1	AJ	0	2
1	AK	0	1
1	AL	0	1
1	AM	0	2
1	AN	0	2
1	AO	0	2
1	AP	0	2
1	AQ	0	1
1	AR	0	2
1	AS	0	2
1	AT	0	2
1	BA	0	2
1	BB	0	2
1	BC	0	1
1	BD	0	2
1	BE	0	1
1	BF	0	2
1	BG	0	2
1	BH	0	1
1	BI	0	1
1	BJ	0	2
1	BK	0	2
1	BL	0	2
1	BM	0	1
1	BN	0	2
1	BO	0	2
1	BP	0	1
1	BQ	0	2
1	BR	0	2
1	BS	0	2
1	BT	0	2
1	CA	0	2
1	CB	0	2
1	CC	0	2
1	CD	0	2
1	CE	0	2
1	CF	0	2
1	CG	0	2
1	CH	0	2
1	CI	0	2
1	CJ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	CK	0	2
1	CL	0	2
1	CM	0	2
1	CN	0	2
1	CO	0	1
1	CP	0	2
1	CQ	0	2
1	CR	0	1
1	CS	0	2
1	CT	0	2
All	All	0	107

All (95) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BM	189	PHE	CE1-CZ	-6.84	1.24	1.37
1	AL	189	PHE	CE1-CZ	-6.45	1.25	1.37
1	CJ	189	PHE	CE1-CZ	-6.29	1.25	1.37
1	BL	189	PHE	CE1-CZ	-6.29	1.25	1.37
1	BN	189	PHE	CE1-CZ	-6.23	1.25	1.37
1	BR	189	PHE	CE1-CZ	-6.22	1.25	1.37
1	CP	189	PHE	CE1-CZ	-6.21	1.25	1.37
1	CS	189	PHE	CE1-CZ	-6.20	1.25	1.37
1	BH	189	PHE	CE1-CZ	-6.17	1.25	1.37
1	AG	189	PHE	CE1-CZ	-6.12	1.25	1.37
1	BQ	189	PHE	CE1-CZ	-6.11	1.25	1.37
1	BR	189	PHE	CE2-CZ	-6.08	1.25	1.37
1	CA	1	GLY	N-CA	-6.08	1.36	1.46
1	AP	189	PHE	CE1-CZ	-6.03	1.25	1.37
1	BK	189	PHE	CE1-CZ	-6.03	1.25	1.37
1	AK	189	PHE	CE1-CZ	-6.01	1.25	1.37
1	BN	189	PHE	CE2-CZ	-5.99	1.25	1.37
1	AI	189	PHE	CE1-CZ	-5.99	1.25	1.37
1	AP	189	PHE	CE2-CZ	-5.95	1.26	1.37
1	BM	189	PHE	CE2-CZ	-5.93	1.26	1.37
1	CI	189	PHE	CE1-CZ	-5.92	1.26	1.37
1	CN	189	PHE	CE1-CZ	-5.92	1.26	1.37
1	AH	189	PHE	CE1-CZ	-5.88	1.26	1.37
1	CQ	189	PHE	CE1-CZ	-5.87	1.26	1.37
1	AM	189	PHE	CE1-CZ	-5.86	1.26	1.37
1	AE	189	PHE	CE1-CZ	-5.83	1.26	1.37
1	AD	189	PHE	CE1-CZ	-5.80	1.26	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BO	189	PHE	CE1-CZ	-5.78	1.26	1.37
1	CB	189	PHE	CE1-CZ	-5.78	1.26	1.37
1	AC	189	PHE	CE1-CZ	-5.77	1.26	1.37
1	BC	189	PHE	CE1-CZ	-5.73	1.26	1.37
1	BG	189	PHE	CE2-CZ	-5.72	1.26	1.37
1	BH	189	PHE	CE2-CZ	-5.70	1.26	1.37
1	BK	189	PHE	CE2-CZ	-5.68	1.26	1.37
1	CR	189	PHE	CE1-CZ	-5.68	1.26	1.37
1	AO	189	PHE	CE1-CZ	-5.67	1.26	1.37
1	AE	189	PHE	CE2-CZ	-5.66	1.26	1.37
1	AM	189	PHE	CE2-CZ	-5.63	1.26	1.37
1	BF	189	PHE	CE1-CZ	-5.60	1.26	1.37
1	BI	189	PHE	CE1-CZ	-5.59	1.26	1.37
1	CM	189	PHE	CE1-CZ	-5.59	1.26	1.37
1	AO	189	PHE	CE2-CZ	-5.58	1.26	1.37
1	CQ	189	PHE	CE2-CZ	-5.55	1.26	1.37
1	BG	189	PHE	CE1-CZ	-5.55	1.26	1.37
1	BL	9	TYR	CE2-CZ	5.53	1.45	1.38
1	BE	189	PHE	CE1-CZ	-5.50	1.26	1.37
1	AI	189	PHE	CE2-CZ	-5.49	1.26	1.37
1	AJ	189	PHE	CE1-CZ	-5.48	1.26	1.37
1	BB	189	PHE	CE1-CZ	-5.48	1.26	1.37
1	CP	189	PHE	CE2-CZ	-5.48	1.26	1.37
1	CH	189	PHE	CE1-CZ	-5.48	1.26	1.37
1	CT	189	PHE	CE1-CZ	-5.45	1.26	1.37
1	AB	189	PHE	CE1-CZ	-5.45	1.26	1.37
1	BJ	189	PHE	CE1-CZ	-5.44	1.27	1.37
1	CF	189	PHE	CE1-CZ	-5.43	1.27	1.37
1	BD	189	PHE	CE1-CZ	-5.42	1.27	1.37
1	BB	189	PHE	CE2-CZ	-5.42	1.27	1.37
1	AD	189	PHE	CE2-CZ	-5.37	1.27	1.37
1	AS	189	PHE	CE2-CZ	-5.37	1.27	1.37
1	AF	189	PHE	CE1-CZ	-5.35	1.27	1.37
1	AN	189	PHE	CE1-CZ	-5.35	1.27	1.37
1	BF	189	PHE	CE2-CZ	-5.33	1.27	1.37
1	CR	189	PHE	CE2-CZ	-5.33	1.27	1.37
1	BP	189	PHE	CE2-CZ	-5.33	1.27	1.37
1	AT	189	PHE	CE1-CZ	-5.32	1.27	1.37
1	CC	189	PHE	CE1-CZ	-5.30	1.27	1.37
1	AL	189	PHE	CE2-CZ	-5.30	1.27	1.37
1	CG	189	PHE	CE1-CZ	-5.30	1.27	1.37
1	CB	189	PHE	CE2-CZ	-5.30	1.27	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BP	189	PHE	CE1-CZ	-5.29	1.27	1.37
1	AB	189	PHE	CE2-CZ	-5.28	1.27	1.37
1	BL	189	PHE	CE2-CZ	-5.28	1.27	1.37
1	AC	189	PHE	CE2-CZ	-5.26	1.27	1.37
1	BE	189	PHE	CE2-CZ	-5.25	1.27	1.37
1	BM	189	PHE	CG-CD1	-5.25	1.30	1.38
1	BD	189	PHE	CE2-CZ	-5.24	1.27	1.37
1	CO	189	PHE	CE1-CZ	-5.23	1.27	1.37
1	BQ	189	PHE	CE2-CZ	-5.22	1.27	1.37
1	BA	189	PHE	CE1-CZ	-5.20	1.27	1.37
1	BO	383	GLU	CG-CD	5.18	1.59	1.51
1	AH	189	PHE	CE2-CZ	-5.13	1.27	1.37
1	CJ	189	PHE	CE2-CZ	-5.12	1.27	1.37
1	AQ	189	PHE	CE1-CZ	-5.10	1.27	1.37
1	CE	189	PHE	CE1-CZ	-5.10	1.27	1.37
1	CD	189	PHE	CE1-CZ	-5.10	1.27	1.37
1	BT	189	PHE	CE2-CZ	-5.09	1.27	1.37
1	CD	189	PHE	CE2-CZ	-5.09	1.27	1.37
1	BO	189	PHE	CE2-CZ	-5.09	1.27	1.37
1	CL	189	PHE	CE2-CZ	-5.08	1.27	1.37
1	CO	189	PHE	CE2-CZ	-5.08	1.27	1.37
1	AK	189	PHE	CE2-CZ	-5.06	1.27	1.37
1	CS	189	PHE	CE2-CZ	-5.06	1.27	1.37
1	AR	9	TYR	CD1-CE1	5.06	1.47	1.39
1	AR	383	GLU	CG-CD	5.04	1.59	1.51
1	CR	383	GLU	CG-CD	5.01	1.59	1.51

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	284	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	CJ	56	LEU	CA-CB-CG	5.46	127.86	115.30
1	AF	56	LEU	CA-CB-CG	5.34	127.57	115.30
1	CT	56	LEU	CA-CB-CG	5.29	127.46	115.30
1	AR	56	LEU	CA-CB-CG	5.25	127.36	115.30
1	BR	56	LEU	CA-CB-CG	5.24	127.36	115.30
1	CR	56	LEU	CA-CB-CG	5.24	127.34	115.30
1	AM	56	LEU	CA-CB-CG	5.24	127.34	115.30
1	BP	56	LEU	CA-CB-CG	5.23	127.33	115.30
1	BM	56	LEU	CA-CB-CG	5.23	127.32	115.30
1	AE	56	LEU	CA-CB-CG	5.20	127.27	115.30
1	CI	56	LEU	CA-CB-CG	5.20	127.27	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BB	56	LEU	CA-CB-CG	5.19	127.23	115.30
1	AB	56	LEU	CA-CB-CG	5.17	127.19	115.30
1	CL	56	LEU	CA-CB-CG	5.13	127.10	115.30
1	AP	56	LEU	CA-CB-CG	5.11	127.05	115.30
1	AA	56	LEU	CA-CB-CG	5.09	127.01	115.30
1	AN	56	LEU	CA-CB-CG	5.05	126.92	115.30
1	BG	56	LEU	CA-CB-CG	5.02	126.84	115.30
1	CB	56	LEU	CA-CB-CG	5.01	126.82	115.30

There are no chirality outliers.

All (107) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	33	LYS	Peptide
1	AA	55	ARG	Peptide
1	AB	33	LYS	Peptide
1	AB	55	ARG	Peptide
1	AC	33	LYS	Peptide
1	AC	55	ARG	Peptide
1	AD	55	ARG	Peptide
1	AE	55	ARG	Peptide
1	AF	33	LYS	Peptide
1	AF	55	ARG	Peptide
1	AG	33	LYS	Peptide
1	AG	55	ARG	Peptide
1	AH	33	LYS	Peptide
1	AH	55	ARG	Peptide
1	AI	33	LYS	Peptide
1	AI	55	ARG	Peptide
1	AJ	33	LYS	Peptide
1	AJ	55	ARG	Peptide
1	AK	55	ARG	Peptide
1	AL	55	ARG	Peptide
1	AM	33	LYS	Peptide
1	AM	55	ARG	Peptide
1	AN	33	LYS	Peptide
1	AN	55	ARG	Peptide
1	AO	33	LYS	Peptide
1	AO	55	ARG	Peptide
1	AP	33	LYS	Peptide
1	AP	55	ARG	Peptide
1	AQ	55	ARG	Peptide

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>Group</b>
1	AR	33	LYS	Peptide
1	AR	55	ARG	Peptide
1	AS	33	LYS	Peptide
1	AS	55	ARG	Peptide
1	AT	33	LYS	Peptide
1	AT	55	ARG	Peptide
1	BA	33	LYS	Peptide
1	BA	55	ARG	Peptide
1	BB	33	LYS	Peptide
1	BB	55	ARG	Peptide
1	BC	55	ARG	Peptide
1	BD	33	LYS	Peptide
1	BD	55	ARG	Peptide
1	BE	55	ARG	Peptide
1	BF	33	LYS	Peptide
1	BF	55	ARG	Peptide
1	BG	33	LYS	Peptide
1	BG	55	ARG	Peptide
1	BH	55	ARG	Peptide
1	BI	55	ARG	Peptide
1	BJ	33	LYS	Peptide
1	BJ	55	ARG	Peptide
1	BK	33	LYS	Peptide
1	BK	55	ARG	Peptide
1	BL	33	LYS	Peptide
1	BL	55	ARG	Peptide
1	BM	55	ARG	Peptide
1	BN	33	LYS	Peptide
1	BN	55	ARG	Peptide
1	BO	33	LYS	Peptide
1	BO	55	ARG	Peptide
1	BP	55	ARG	Peptide
1	BQ	33	LYS	Peptide
1	BQ	55	ARG	Peptide
1	BR	33	LYS	Peptide
1	BR	55	ARG	Peptide
1	BS	33	LYS	Peptide
1	BS	55	ARG	Peptide
1	BT	33	LYS	Peptide
1	BT	55	ARG	Peptide
1	CA	33	LYS	Peptide
1	CA	55	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	CB	33	LYS	Peptide
1	CB	55	ARG	Peptide
1	CC	33	LYS	Peptide
1	CC	55	ARG	Peptide
1	CD	33	LYS	Peptide
1	CD	55	ARG	Peptide
1	CE	33	LYS	Peptide
1	CE	55	ARG	Peptide
1	CF	33	LYS	Peptide
1	CF	55	ARG	Peptide
1	CG	33	LYS	Peptide
1	CG	55	ARG	Peptide
1	CH	33	LYS	Peptide
1	CH	55	ARG	Peptide
1	CI	33	LYS	Peptide
1	CI	55	ARG	Peptide
1	CJ	33	LYS	Peptide
1	CJ	55	ARG	Peptide
1	CK	33	LYS	Peptide
1	CK	55	ARG	Peptide
1	CL	33	LYS	Peptide
1	CL	55	ARG	Peptide
1	CM	33	LYS	Peptide
1	CM	55	ARG	Peptide
1	CN	33	LYS	Peptide
1	CN	55	ARG	Peptide
1	CO	55	ARG	Peptide
1	CP	33	LYS	Peptide
1	CP	55	ARG	Peptide
1	CQ	33	LYS	Peptide
1	CQ	55	ARG	Peptide
1	CR	55	ARG	Peptide
1	CS	33	LYS	Peptide
1	CS	55	ARG	Peptide
1	CT	33	LYS	Peptide
1	CT	55	ARG	Peptide

## 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	AA	3951	0	3909	91	0
1	AB	3951	0	3909	89	0
1	AC	3951	0	3909	87	0
1	AD	3951	0	3909	93	0
1	AE	3951	0	3909	86	0
1	AF	3951	0	3909	92	0
1	AG	3951	0	3909	91	0
1	AH	3951	0	3909	90	0
1	AI	3951	0	3909	88	0
1	AJ	3951	0	3909	86	0
1	AK	3951	0	3909	88	0
1	AL	3951	0	3909	87	0
1	AM	3951	0	3909	83	0
1	AN	3951	0	3909	104	0
1	AO	3951	0	3909	91	0
1	AP	3951	0	3909	87	0
1	AQ	3951	0	3909	85	0
1	AR	3951	0	3909	88	0
1	AS	3951	0	3909	89	0
1	AT	3951	0	3909	91	0
1	BA	3951	0	3909	93	0
1	BB	3951	0	3909	97	0
1	BC	3951	0	3909	85	0
1	BD	3951	0	3909	78	0
1	BE	3951	0	3909	86	0
1	BF	3951	0	3909	92	0
1	BG	3951	0	3909	92	0
1	BH	3951	0	3909	97	0
1	BI	3951	0	3909	89	0
1	BJ	3951	0	3909	93	0
1	BK	3951	0	3909	81	0
1	BL	3951	0	3909	89	0
1	BM	3951	0	3909	89	0
1	BN	3951	0	3909	80	0
1	BO	3951	0	3909	93	0
1	BP	3951	0	3909	93	0
1	BQ	3951	0	3909	83	0
1	BR	3951	0	3909	90	0
1	BS	3951	0	3909	87	0
1	BT	3951	0	3909	87	0
1	CA	3951	0	3909	81	0
1	CB	3951	0	3909	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CC	3951	0	3909	84	0
1	CD	3951	0	3909	89	0
1	CE	3951	0	3909	97	0
1	CF	3951	0	3909	94	0
1	CG	3951	0	3909	92	0
1	CH	3951	0	3909	91	0
1	CI	3951	0	3909	92	0
1	CJ	3951	0	3909	94	0
1	CK	3951	0	3909	84	0
1	CL	3951	0	3909	81	0
1	CM	3951	0	3909	93	0
1	CN	3951	0	3909	81	0
1	CO	3951	0	3909	96	0
1	CP	3951	0	3909	85	0
1	CQ	3951	0	3909	85	0
1	CR	3951	0	3909	86	0
1	CS	3951	0	3909	86	0
1	CT	3951	0	3909	76	0
All	All	237060	0	234540	4775	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 10.

All (4775) 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:CF:79:ARG:HG3	1:CF:79:ARG:HH11	1.18	1.07
1:CC:250:TRP:CZ3	1:CC:272:TYR:HE1	1.77	1.02
1:BO:250:TRP:CZ3	1:BO:272:TYR:HE1	1.83	0.97
1:BS:79:ARG:HG3	1:BS:79:ARG:HH11	1.31	0.96
1:BJ:250:TRP:CZ3	1:BJ:272:TYR:HE1	1.85	0.94
1:CC:250:TRP:CZ3	1:CC:272:TYR:CE1	2.54	0.94
1:BP:250:TRP:CZ3	1:BP:272:TYR:HE1	1.85	0.94
1:CD:79:ARG:HH11	1:CD:79:ARG:HG3	1.34	0.93
1:AS:250:TRP:CZ3	1:AS:272:TYR:HE1	1.87	0.92
1:BJ:191:LEU:HD23	1:BJ:191:LEU:H	1.34	0.92
1:BJ:250:TRP:CZ3	1:BJ:272:TYR:CE1	2.58	0.91
1:BO:250:TRP:CZ3	1:BO:272:TYR:CE1	2.58	0.91
1:BJ:79:ARG:HH11	1:BJ:79:ARG:HG3	1.35	0.91
1:AS:250:TRP:CZ3	1:AS:272:TYR:CE1	2.59	0.91
1:BE:191:LEU:HD23	1:BE:191:LEU:H	1.36	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:191:LEU:H	1:AJ:191:LEU:HD23	1.34	0.90
1:AL:191:LEU:H	1:AL:191:LEU:HD23	1.37	0.89
1:AP:191:LEU:H	1:AP:191:LEU:HD23	1.36	0.89
1:AC:191:LEU:HD23	1:AC:191:LEU:H	1.36	0.89
1:AM:191:LEU:H	1:AM:191:LEU:HD23	1.38	0.89
1:AR:191:LEU:HD23	1:AR:191:LEU:H	1.38	0.89
1:BP:250:TRP:CZ3	1:BP:272:TYR:CE1	2.60	0.89
1:AB:191:LEU:HD23	1:AB:191:LEU:H	1.37	0.89
1:AG:79:ARG:HG3	1:AG:79:ARG:HH11	1.36	0.89
1:AO:191:LEU:H	1:AO:191:LEU:HD23	1.37	0.89
1:BP:191:LEU:HD23	1:BP:191:LEU:H	1.37	0.89
1:AA:55:ARG:NE	1:CC:272:TYR:HE2	1.71	0.89
1:CC:191:LEU:H	1:CC:191:LEU:HD23	1.38	0.89
1:AN:79:ARG:HH11	1:AN:79:ARG:HG3	1.38	0.88
1:AG:191:LEU:H	1:AG:191:LEU:HD23	1.38	0.88
1:CP:191:LEU:H	1:CP:191:LEU:HD23	1.38	0.88
1:CE:191:LEU:H	1:CE:191:LEU:HD23	1.39	0.88
1:BH:15:GLN:HE21	1:BH:15:GLN:HA	1.38	0.88
1:AE:191:LEU:HD23	1:AE:191:LEU:H	1.39	0.88
1:BD:191:LEU:HD23	1:BD:191:LEU:H	1.39	0.88
1:CI:191:LEU:HD23	1:CI:191:LEU:H	1.37	0.88
1:BB:191:LEU:H	1:BB:191:LEU:HD23	1.39	0.88
1:BM:191:LEU:H	1:BM:191:LEU:HD23	1.38	0.88
1:CQ:191:LEU:H	1:CQ:191:LEU:HD23	1.37	0.87
1:AQ:191:LEU:HD23	1:AQ:191:LEU:H	1.39	0.87
1:CD:191:LEU:H	1:CD:191:LEU:HD23	1.39	0.87
1:CO:250:TRP:CZ3	1:CO:272:TYR:CE1	2.63	0.87
1:AL:79:ARG:HG3	1:AL:79:ARG:HH11	1.39	0.87
1:CB:191:LEU:HD23	1:CB:191:LEU:H	1.39	0.87
1:CL:191:LEU:H	1:CL:191:LEU:HD23	1.39	0.87
1:AA:191:LEU:HD23	1:AA:191:LEU:H	1.37	0.87
1:BQ:191:LEU:H	1:BQ:191:LEU:HD23	1.40	0.87
1:AA:55:ARG:NE	1:CC:272:TYR:CE2	2.42	0.87
1:BI:191:LEU:HD23	1:BI:191:LEU:H	1.39	0.87
1:BF:191:LEU:H	1:BF:191:LEU:HD23	1.40	0.87
1:BG:191:LEU:H	1:BG:191:LEU:HD23	1.39	0.87
1:BO:272:TYR:HE2	1:BR:55:ARG:NE	1.73	0.87
1:CM:191:LEU:H	1:CM:191:LEU:HD23	1.39	0.86
1:AO:250:TRP:CZ3	1:AO:272:TYR:CE1	2.63	0.86
1:BO:191:LEU:H	1:BO:191:LEU:HD23	1.38	0.86
1:BP:272:TYR:HE2	1:CE:55:ARG:NE	1.72	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:191:LEU:H	1:AK:191:LEU:HD23	1.38	0.86
1:CJ:250:TRP:CZ3	1:CJ:272:TYR:HE1	1.94	0.86
1:CK:191:LEU:HD23	1:CK:191:LEU:H	1.40	0.86
1:CF:191:LEU:HD23	1:CF:191:LEU:H	1.39	0.86
1:CR:191:LEU:H	1:CR:191:LEU:HD23	1.41	0.86
1:BC:191:LEU:H	1:BC:191:LEU:HD23	1.40	0.86
1:CQ:250:TRP:CZ3	1:CQ:272:TYR:CE1	2.64	0.86
1:AD:191:LEU:HD23	1:AD:191:LEU:H	1.40	0.86
1:BH:191:LEU:H	1:BH:191:LEU:HD23	1.40	0.86
1:BS:191:LEU:H	1:BS:191:LEU:HD23	1.40	0.86
1:BT:191:LEU:HD23	1:BT:191:LEU:H	1.40	0.86
1:CM:250:TRP:CZ3	1:CM:272:TYR:CE1	2.64	0.86
1:CN:189:PHE:HE1	1:CN:198:ARG:HG3	1.41	0.86
1:CJ:250:TRP:CZ3	1:CJ:272:TYR:CE1	2.63	0.86
1:AG:250:TRP:CZ3	1:AG:272:TYR:CE1	2.64	0.85
1:BJ:189:PHE:HE1	1:BJ:198:ARG:HG3	1.40	0.85
1:CH:191:LEU:H	1:CH:191:LEU:HD23	1.39	0.85
1:AF:79:ARG:HH11	1:AF:79:ARG:HG3	1.38	0.85
1:BK:191:LEU:HD23	1:BK:191:LEU:H	1.41	0.85
1:CO:191:LEU:HD23	1:CO:191:LEU:H	1.42	0.85
1:BR:191:LEU:HD23	1:BR:191:LEU:H	1.42	0.85
1:CP:250:TRP:CZ3	1:CP:272:TYR:CE1	2.65	0.85
1:CB:189:PHE:HE1	1:CB:198:ARG:CG	1.90	0.85
1:BP:272:TYR:CE2	1:CE:55:ARG:NE	2.44	0.85
1:CS:191:LEU:HD23	1:CS:191:LEU:H	1.42	0.85
1:CR:189:PHE:HE1	1:CR:198:ARG:CG	1.89	0.85
1:AT:191:LEU:H	1:AT:191:LEU:HD23	1.42	0.85
1:AT:250:TRP:CZ3	1:AT:272:TYR:CE1	2.65	0.85
1:CG:189:PHE:HE1	1:CG:198:ARG:CG	1.90	0.85
1:BT:250:TRP:CZ3	1:BT:272:TYR:CE1	2.65	0.84
1:AO:272:TYR:CE2	1:AR:55:ARG:NE	2.45	0.84
1:CN:191:LEU:H	1:CN:191:LEU:HD23	1.40	0.84
1:CO:250:TRP:CZ3	1:CO:272:TYR:HE1	1.95	0.84
1:AN:55:ARG:NE	1:AS:272:TYR:CE2	2.45	0.84
1:BN:189:PHE:HE1	1:BN:198:ARG:CG	1.91	0.84
1:BO:272:TYR:CE2	1:BR:55:ARG:NE	2.45	0.84
1:BA:191:LEU:H	1:BA:191:LEU:HD23	1.42	0.84
1:CG:191:LEU:H	1:CG:191:LEU:HD23	1.40	0.84
1:AN:189:PHE:HE1	1:AN:198:ARG:CG	1.91	0.84
1:CD:250:TRP:CZ3	1:CD:272:TYR:CE1	2.65	0.84
1:CM:189:PHE:HE1	1:CM:198:ARG:CG	1.91	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:191:LEU:HD23	1:AI:191:LEU:H	1.40	0.84
1:AF:189:PHE:HE1	1:AF:198:ARG:HG3	1.43	0.84
1:CJ:189:PHE:HE1	1:CJ:198:ARG:HG3	1.43	0.84
1:AM:454:ASN:HD22	1:AM:456:ALA:H	1.26	0.83
1:AN:191:LEU:HD23	1:AN:191:LEU:H	1.42	0.83
1:AR:189:PHE:HE1	1:AR:198:ARG:HG3	1.42	0.83
1:BP:79:ARG:HH11	1:BP:79:ARG:CG	1.90	0.83
1:AH:191:LEU:H	1:AH:191:LEU:HD23	1.43	0.83
1:AO:250:TRP:CZ3	1:AO:272:TYR:HE1	1.95	0.83
1:BB:454:ASN:HD22	1:BB:456:ALA:H	1.26	0.83
1:BN:191:LEU:HD23	1:BN:191:LEU:H	1.41	0.83
1:BO:15:GLN:HE21	1:BO:15:GLN:HA	1.43	0.83
1:CT:191:LEU:H	1:CT:191:LEU:HD23	1.41	0.83
1:AI:79:ARG:HG3	1:AI:79:ARG:HH11	1.43	0.83
1:CG:250:TRP:CZ3	1:CG:272:TYR:CE1	2.67	0.83
1:CQ:454:ASN:HD22	1:CQ:456:ALA:H	1.27	0.83
1:CA:191:LEU:HD23	1:CA:191:LEU:H	1.41	0.83
1:CF:250:TRP:CZ3	1:CF:272:TYR:CE1	2.66	0.83
1:AR:189:PHE:HE1	1:AR:198:ARG:CG	1.91	0.83
1:BA:79:ARG:HH11	1:BA:79:ARG:HG3	1.43	0.83
1:CC:250:TRP:CE3	1:CC:272:TYR:CE1	2.66	0.83
1:AB:250:TRP:CZ3	1:AB:272:TYR:CE1	2.66	0.83
1:AI:189:PHE:HE1	1:AI:198:ARG:CG	1.91	0.83
1:BA:250:TRP:CZ3	1:BA:272:TYR:CE1	2.67	0.83
1:CF:189:PHE:HE1	1:CF:198:ARG:CG	1.92	0.83
1:AS:191:LEU:H	1:AS:191:LEU:HD23	1.43	0.83
1:BE:189:PHE:HE1	1:BE:198:ARG:CG	1.91	0.82
1:BI:454:ASN:HD22	1:BI:456:ALA:H	1.26	0.82
1:CE:189:PHE:HE1	1:CE:198:ARG:HG3	1.44	0.82
1:BI:189:PHE:HE1	1:BI:198:ARG:HG3	1.44	0.82
1:AI:189:PHE:HE1	1:AI:198:ARG:HG3	1.42	0.82
1:AN:250:TRP:CZ3	1:AN:272:TYR:CE1	2.68	0.82
1:AR:250:TRP:CZ3	1:AR:272:TYR:CE1	2.67	0.82
1:CH:79:ARG:HH11	1:CH:79:ARG:HG3	1.45	0.82
1:CR:454:ASN:HD22	1:CR:456:ALA:H	1.27	0.82
1:AE:189:PHE:HE1	1:AE:198:ARG:HG3	1.42	0.82
1:AF:454:ASN:HD22	1:AF:456:ALA:H	1.27	0.82
1:BD:250:TRP:CZ3	1:BD:272:TYR:CE1	2.67	0.82
1:CG:189:PHE:HE1	1:CG:198:ARG:HG3	1.44	0.82
1:BB:189:PHE:HE1	1:BB:198:ARG:CG	1.92	0.82
1:BB:250:TRP:CZ3	1:BB:272:TYR:CE1	2.68	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:250:TRP:CZ3	1:BG:272:TYR:CE1	2.67	0.82
1:BL:191:LEU:HD23	1:BL:191:LEU:H	1.43	0.82
1:CH:250:TRP:CZ3	1:CH:272:TYR:CE1	2.68	0.82
1:CN:189:PHE:HE1	1:CN:198:ARG:CG	1.92	0.82
1:CR:250:TRP:CZ3	1:CR:272:TYR:CE1	2.68	0.82
1:AN:189:PHE:HE1	1:AN:198:ARG:HG3	1.44	0.82
1:AC:250:TRP:CZ3	1:AC:272:TYR:CE1	2.67	0.82
1:CJ:189:PHE:HE1	1:CJ:198:ARG:CG	1.92	0.82
1:AF:191:LEU:H	1:AF:191:LEU:HD23	1.43	0.81
1:AJ:189:PHE:HE1	1:AJ:198:ARG:CG	1.92	0.81
1:BH:189:PHE:HE1	1:BH:198:ARG:CG	1.92	0.81
1:CE:250:TRP:CZ3	1:CE:272:TYR:CE1	2.67	0.81
1:CF:454:ASN:HD22	1:CF:456:ALA:H	1.26	0.81
1:CB:189:PHE:HE1	1:CB:198:ARG:HG3	1.45	0.81
1:CK:250:TRP:CZ3	1:CK:272:TYR:CE1	2.68	0.81
1:AB:189:PHE:HE1	1:AB:198:ARG:CG	1.93	0.81
1:CF:79:ARG:CG	1:CF:79:ARG:HH11	1.91	0.81
1:CJ:191:LEU:H	1:CJ:191:LEU:HD23	1.42	0.81
1:BG:189:PHE:HE1	1:BG:198:ARG:HG3	1.45	0.81
1:CJ:272:TYR:CE2	1:CQ:55:ARG:NE	2.48	0.81
1:BN:250:TRP:CZ3	1:BN:272:TYR:CE1	2.69	0.81
1:BP:454:ASN:HD22	1:BP:456:ALA:H	1.27	0.81
1:CN:250:TRP:CZ3	1:CN:272:TYR:CE1	2.67	0.81
1:AH:189:PHE:HE1	1:AH:198:ARG:CG	1.93	0.81
1:AK:250:TRP:CZ3	1:AK:272:TYR:CE1	2.69	0.81
1:AH:250:TRP:CZ3	1:AH:272:TYR:CE1	2.68	0.81
1:CT:250:TRP:CZ3	1:CT:272:TYR:CE1	2.68	0.81
1:AE:250:TRP:CZ3	1:AE:272:TYR:CE1	2.69	0.81
1:AM:189:PHE:HE1	1:AM:198:ARG:CG	1.94	0.81
1:BI:250:TRP:CZ3	1:BI:272:TYR:CE1	2.69	0.81
1:BR:79:ARG:HH11	1:BR:79:ARG:HG3	1.45	0.81
1:CK:454:ASN:HD22	1:CK:456:ALA:H	1.28	0.81
1:AM:189:PHE:HE1	1:AM:198:ARG:HG3	1.45	0.80
1:AM:250:TRP:CZ3	1:AM:272:TYR:CE1	2.70	0.80
1:BK:250:TRP:CZ3	1:BK:272:TYR:CE1	2.68	0.80
1:BM:189:PHE:HE1	1:BM:198:ARG:CG	1.94	0.80
1:AL:250:TRP:CZ3	1:AL:272:TYR:CE1	2.69	0.80
1:BM:250:TRP:CZ3	1:BM:272:TYR:CE1	2.69	0.80
1:BB:189:PHE:HE1	1:BB:198:ARG:HG3	1.45	0.80
1:CS:454:ASN:HD22	1:CS:456:ALA:H	1.24	0.80
1:AR:454:ASN:HD22	1:AR:456:ALA:H	1.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:189:PHE:HE1	1:CF:198:ARG:HG3	1.46	0.80
1:CM:189:PHE:HE1	1:CM:198:ARG:HG3	1.45	0.80
1:CM:454:ASN:HD22	1:CM:456:ALA:H	1.29	0.80
1:CD:454:ASN:HD22	1:CD:456:ALA:H	1.30	0.80
1:BL:250:TRP:CZ3	1:BL:272:TYR:CE1	2.70	0.80
1:CI:189:PHE:HE1	1:CI:198:ARG:HG3	1.45	0.80
1:CL:454:ASN:HD22	1:CL:456:ALA:H	1.29	0.80
1:CS:250:TRP:CZ3	1:CS:272:TYR:CE1	2.69	0.80
1:AO:272:TYR:HE2	1:AR:55:ARG:NE	1.80	0.80
1:AL:454:ASN:HD22	1:AL:456:ALA:H	1.30	0.79
1:BF:189:PHE:HE1	1:BF:198:ARG:CG	1.95	0.79
1:CH:189:PHE:HE1	1:CH:198:ARG:CG	1.95	0.79
1:CI:250:TRP:CZ3	1:CI:272:TYR:CE1	2.69	0.79
1:AF:250:TRP:CZ3	1:AF:272:TYR:CE1	2.70	0.79
1:AG:189:PHE:HE1	1:AG:198:ARG:HG3	1.46	0.79
1:BK:454:ASN:HD22	1:BK:456:ALA:H	1.27	0.79
1:BO:250:TRP:CE3	1:BO:272:TYR:CE1	2.70	0.79
1:CN:454:ASN:HD22	1:CN:456:ALA:H	1.30	0.79
1:BF:250:TRP:CZ3	1:BF:272:TYR:CE1	2.70	0.79
1:BH:189:PHE:HE1	1:BH:198:ARG:HG3	1.45	0.79
1:BH:250:TRP:CZ3	1:BH:272:TYR:CE1	2.69	0.79
1:CP:250:TRP:CZ3	1:CP:272:TYR:HE1	2.01	0.79
1:BR:189:PHE:HE1	1:BR:198:ARG:HG3	1.46	0.79
1:BR:250:TRP:CZ3	1:BR:272:TYR:CE1	2.71	0.79
1:BT:454:ASN:HD22	1:BT:456:ALA:H	1.31	0.79
1:CA:250:TRP:CZ3	1:CA:272:TYR:CE1	2.71	0.79
1:CB:250:TRP:CZ3	1:CB:272:TYR:CE1	2.70	0.79
1:CL:250:TRP:CZ3	1:CL:272:TYR:CE1	2.70	0.79
1:BJ:272:TYR:CE2	1:BQ:55:ARG:NE	2.51	0.79
1:CR:189:PHE:HE1	1:CR:198:ARG:HG3	1.47	0.79
1:AJ:189:PHE:HE1	1:AJ:198:ARG:HG3	1.48	0.79
1:CI:189:PHE:HE1	1:CI:198:ARG:CG	1.96	0.79
1:BE:189:PHE:HE1	1:BE:198:ARG:HG3	1.46	0.78
1:BQ:250:TRP:CZ3	1:BQ:272:TYR:CE1	2.71	0.78
1:CO:272:TYR:CE2	1:CR:55:ARG:NE	2.51	0.78
1:AG:189:PHE:HE1	1:AG:198:ARG:CG	1.95	0.78
1:AQ:250:TRP:CZ3	1:AQ:272:TYR:CE1	2.71	0.78
1:AN:454:ASN:HD22	1:AN:456:ALA:H	1.30	0.78
1:BM:454:ASN:HD22	1:BM:456:ALA:H	1.31	0.78
1:BF:454:ASN:HD22	1:BF:456:ALA:H	1.30	0.78
1:AG:250:TRP:CZ3	1:AG:272:TYR:HE1	2.02	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:189:PHE:HE1	1:BJ:198:ARG:CG	1.96	0.78
1:CD:250:TRP:CZ3	1:CD:272:TYR:HE1	2.01	0.78
1:AE:454:ASN:HD22	1:AE:456:ALA:H	1.31	0.77
1:BJ:272:TYR:HE2	1:BQ:55:ARG:NE	1.82	0.77
1:BA:189:PHE:HE1	1:BA:198:ARG:HG3	1.49	0.77
1:BS:250:TRP:CZ3	1:BS:272:TYR:CE1	2.73	0.77
1:CJ:454:ASN:HD22	1:CJ:456:ALA:H	1.31	0.77
1:AA:454:ASN:HD22	1:AA:456:ALA:H	1.30	0.77
1:AD:454:ASN:HD22	1:AD:456:ALA:H	1.32	0.77
1:BG:189:PHE:HE1	1:BG:198:ARG:CG	1.96	0.77
1:AP:22:THR:OG1	1:AP:131:HIS:HD2	1.67	0.77
1:CH:189:PHE:HE1	1:CH:198:ARG:HG3	1.46	0.77
1:BC:454:ASN:HD22	1:BC:456:ALA:H	1.31	0.77
1:CO:79:ARG:HH11	1:CO:79:ARG:HG3	1.49	0.77
1:CT:454:ASN:HD22	1:CT:456:ALA:H	1.33	0.77
1:AA:250:TRP:CZ3	1:AA:272:TYR:CE1	2.72	0.77
1:AD:250:TRP:CZ3	1:AD:272:TYR:CE1	2.72	0.77
1:CE:189:PHE:HE1	1:CE:198:ARG:CG	1.98	0.77
1:AE:55:ARG:NE	1:CP:272:TYR:CE2	2.52	0.77
1:BL:454:ASN:HD22	1:BL:456:ALA:H	1.31	0.77
1:CD:22:THR:OG1	1:CD:131:HIS:HD2	1.68	0.77
1:BH:454:ASN:HD22	1:BH:456:ALA:H	1.30	0.77
1:BQ:284:ARG:HH11	1:BQ:284:ARG:CG	1.98	0.77
1:CO:189:PHE:HE1	1:CO:198:ARG:HG3	1.49	0.77
1:AK:55:ARG:NE	1:CF:272:TYR:CE2	2.53	0.76
1:CD:272:TYR:CE2	1:CS:55:ARG:NE	2.53	0.76
1:AK:454:ASN:HD22	1:AK:456:ALA:H	1.34	0.76
1:BA:454:ASN:HD22	1:BA:456:ALA:H	1.32	0.76
1:BQ:189:PHE:HE1	1:BQ:198:ARG:HG3	1.48	0.76
1:CE:250:TRP:CZ3	1:CE:272:TYR:HE1	2.03	0.76
1:BJ:250:TRP:CE3	1:BJ:272:TYR:CE1	2.73	0.76
1:BP:250:TRP:CE3	1:BP:272:TYR:CE1	2.73	0.76
1:AO:454:ASN:HD22	1:AO:456:ALA:H	1.33	0.76
1:AP:250:TRP:CZ3	1:AP:272:TYR:CE1	2.73	0.76
1:AB:189:PHE:HE1	1:AB:198:ARG:HG3	1.49	0.76
1:BF:79:ARG:HG3	1:BF:79:ARG:HH11	1.48	0.76
1:BL:189:PHE:HE1	1:BL:198:ARG:HG3	1.51	0.76
1:BP:189:PHE:HE1	1:BP:198:ARG:HG3	1.50	0.76
1:BD:272:TYR:CE2	1:BS:55:ARG:NE	2.54	0.76
1:BC:22:THR:OG1	1:BC:131:HIS:HD2	1.69	0.76
1:BP:22:THR:OG1	1:BP:131:HIS:HD2	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:33:LYS:HG2	1:AP:33:LYS:O	1.86	0.76
1:BE:250:TRP:CZ3	1:BE:272:TYR:CE1	2.73	0.76
1:CA:454:ASN:HD22	1:CA:456:ALA:H	1.34	0.76
1:AN:55:ARG:NE	1:AS:272:TYR:HE2	1.83	0.76
1:AG:55:ARG:NE	1:CG:272:TYR:CE2	2.53	0.75
1:BS:454:ASN:HD22	1:BS:456:ALA:H	1.30	0.75
1:CC:79:ARG:HH11	1:CC:79:ARG:HG3	1.51	0.75
1:AB:55:ARG:NE	1:BB:272:TYR:CE2	2.54	0.75
1:AF:189:PHE:HE1	1:AF:198:ARG:CG	1.98	0.75
1:AJ:454:ASN:HD22	1:AJ:456:ALA:H	1.35	0.75
1:AK:189:PHE:HE1	1:AK:198:ARG:HG3	1.51	0.75
1:AH:189:PHE:HE1	1:AH:198:ARG:HG3	1.49	0.75
1:BN:454:ASN:HD22	1:BN:456:ALA:H	1.33	0.75
1:BR:454:ASN:HD22	1:BR:456:ALA:H	1.31	0.75
1:CE:22:THR:OG1	1:CE:131:HIS:HD2	1.68	0.75
1:AO:272:TYR:HE2	1:AR:55:ARG:CD	2.00	0.75
1:BS:189:PHE:HE1	1:BS:198:ARG:HG3	1.52	0.75
1:CJ:22:THR:OG1	1:CJ:131:HIS:HD2	1.69	0.75
1:AR:22:THR:OG1	1:AR:131:HIS:HD2	1.70	0.75
1:BR:189:PHE:HE1	1:BR:198:ARG:CG	2.00	0.75
1:AC:454:ASN:HD22	1:AC:456:ALA:H	1.31	0.75
1:BN:189:PHE:HE1	1:BN:198:ARG:HG3	1.51	0.75
1:AF:22:THR:OG1	1:AF:131:HIS:HD2	1.70	0.75
1:AH:454:ASN:HD22	1:AH:456:ALA:H	1.35	0.75
1:BJ:454:ASN:HD22	1:BJ:456:ALA:H	1.32	0.75
1:BH:55:ARG:NE	1:BK:272:TYR:CE2	2.54	0.75
1:BG:272:TYR:CE2	1:CG:55:ARG:CD	2.68	0.75
1:AJ:250:TRP:CZ3	1:AJ:272:TYR:CE1	2.75	0.74
1:BA:74:ASN:HB3	1:BA:126:GLU:HG2	1.69	0.74
1:AE:22:THR:OG1	1:AE:131:HIS:HD2	1.69	0.74
1:AP:454:ASN:HD22	1:AP:456:ALA:H	1.32	0.74
1:BA:33:LYS:O	1:BA:33:LYS:HG2	1.87	0.74
1:BA:22:THR:OG1	1:BA:131:HIS:HD2	1.70	0.74
1:BG:74:ASN:HB3	1:BG:126:GLU:HG2	1.68	0.74
1:CL:33:LYS:O	1:CL:33:LYS:HG2	1.88	0.74
1:CB:454:ASN:HD22	1:CB:456:ALA:H	1.35	0.74
1:CL:189:PHE:HE1	1:CL:198:ARG:HG3	1.52	0.74
1:CI:74:ASN:HB3	1:CI:126:GLU:HG2	1.68	0.74
1:AS:454:ASN:HD22	1:AS:456:ALA:H	1.35	0.74
1:BB:33:LYS:HG2	1:BB:33:LYS:O	1.87	0.74
1:BG:33:LYS:O	1:BG:33:LYS:HG2	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:250:TRP:CE3	1:AS:272:TYR:CE1	2.75	0.74
1:BQ:36:GLN:NE2	1:BQ:156:LEU:H	1.85	0.74
1:AB:272:TYR:CE2	1:CB:55:ARG:NE	2.56	0.74
1:BC:250:TRP:CZ3	1:BC:272:TYR:CE1	2.76	0.74
1:BE:33:LYS:HG2	1:BE:33:LYS:O	1.88	0.74
1:BG:272:TYR:CE2	1:CG:55:ARG:HD3	2.23	0.74
1:BI:189:PHE:HE1	1:BI:198:ARG:CG	2.00	0.74
1:CH:454:ASN:HD22	1:CH:456:ALA:H	1.32	0.74
1:AE:189:PHE:HE1	1:AE:198:ARG:CG	1.98	0.74
1:BL:33:LYS:HG2	1:BL:33:LYS:O	1.87	0.74
1:BQ:284:ARG:HG2	1:BQ:284:ARG:HH11	1.52	0.74
1:BT:79:ARG:HG3	1:BT:79:ARG:HH11	1.51	0.74
1:AL:74:ASN:HB3	1:AL:126:GLU:HG2	1.70	0.73
1:AR:189:PHE:HE2	1:AR:249:LEU:HD21	1.53	0.73
1:CG:79:ARG:HH11	1:CG:79:ARG:HG3	1.52	0.73
1:CI:189:PHE:HE2	1:CI:249:LEU:HD21	1.53	0.73
1:AE:55:ARG:CD	1:CP:272:TYR:HE2	2.01	0.73
1:CO:454:ASN:HD22	1:CO:456:ALA:H	1.34	0.73
1:AD:55:ARG:NE	1:AN:272:TYR:CE2	2.56	0.73
1:AR:33:LYS:HG2	1:AR:33:LYS:O	1.88	0.73
1:AT:33:LYS:O	1:AT:33:LYS:HG2	1.88	0.73
1:BE:454:ASN:HD22	1:BE:456:ALA:H	1.35	0.73
1:BO:272:TYR:HE2	1:BR:55:ARG:CD	2.01	0.73
1:CC:454:ASN:HD22	1:CC:456:ALA:H	1.34	0.73
1:AF:33:LYS:O	1:AF:33:LYS:HG2	1.88	0.73
1:BS:74:ASN:HB3	1:BS:126:GLU:HG2	1.70	0.73
1:BA:14:CYS:H	1:BA:138:ASN:HD21	1.35	0.73
1:BM:284:ARG:CG	1:BM:284:ARG:HH11	2.02	0.73
1:CE:33:LYS:HG2	1:CE:33:LYS:O	1.89	0.73
1:BG:272:TYR:CE2	1:CG:55:ARG:NE	2.57	0.73
1:CL:284:ARG:CG	1:CL:284:ARG:HH11	2.01	0.73
1:CQ:250:TRP:CZ3	1:CQ:272:TYR:HE1	2.05	0.73
1:AM:284:ARG:CG	1:AM:284:ARG:HH11	2.01	0.73
1:BK:189:PHE:HE1	1:BK:198:ARG:HG3	1.52	0.73
1:CG:22:THR:OG1	1:CG:131:HIS:HD2	1.70	0.73
1:BB:284:ARG:HH11	1:BB:284:ARG:CG	2.02	0.73
1:BF:189:PHE:HE1	1:BF:198:ARG:HG3	1.52	0.73
1:BJ:189:PHE:CE1	1:BJ:198:ARG:HG3	2.23	0.73
1:BO:284:ARG:HH11	1:BO:284:ARG:HG2	1.54	0.73
1:CC:33:LYS:O	1:CC:33:LYS:HG2	1.88	0.73
1:CN:189:PHE:CE1	1:CN:198:ARG:HG3	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:22:THR:OG1	1:AN:131:HIS:HD2	1.72	0.73
1:BE:16:ALA:O	1:BE:17:ASN:HB2	1.89	0.73
1:BP:79:ARG:HH11	1:BP:79:ARG:HG3	1.52	0.73
1:CG:33:LYS:O	1:CG:33:LYS:HG2	1.88	0.73
1:CG:454:ASN:HD22	1:CG:456:ALA:H	1.34	0.73
1:AI:250:TRP:CZ3	1:AI:272:TYR:CE1	2.76	0.72
1:BD:250:TRP:CZ3	1:BD:272:TYR:HE1	2.06	0.72
1:BO:33:LYS:O	1:BO:33:LYS:HG2	1.87	0.72
1:CT:33:LYS:O	1:CT:33:LYS:HG2	1.88	0.72
1:AB:250:TRP:CZ3	1:AB:272:TYR:HE1	2.06	0.72
1:AC:284:ARG:HH11	1:AC:284:ARG:CG	2.02	0.72
1:AD:79:ARG:HG3	1:AD:79:ARG:HH11	1.54	0.72
1:BJ:191:LEU:CD2	1:BJ:191:LEU:H	2.02	0.72
1:CD:284:ARG:HH11	1:CD:284:ARG:HG2	1.55	0.72
1:CG:79:ARG:HH11	1:CG:79:ARG:CG	2.02	0.72
1:CO:272:TYR:HE2	1:CR:55:ARG:CD	2.03	0.72
1:BO:454:ASN:HD22	1:BO:456:ALA:H	1.37	0.72
1:CI:454:ASN:HD22	1:CI:456:ALA:H	1.35	0.72
1:AG:189:PHE:HE2	1:AG:249:LEU:HD21	1.54	0.72
1:AL:22:THR:OG1	1:AL:131:HIS:HD2	1.72	0.72
1:AM:22:THR:OG1	1:AM:131:HIS:HD2	1.72	0.72
1:AP:55:ARG:NE	1:BM:272:TYR:CE2	2.57	0.72
1:BD:33:LYS:O	1:BD:33:LYS:HG2	1.89	0.72
1:BK:33:LYS:O	1:BK:33:LYS:HG2	1.88	0.72
1:AK:55:ARG:CD	1:CF:272:TYR:CE2	2.71	0.72
1:CO:33:LYS:HG2	1:CO:33:LYS:O	1.89	0.72
1:AQ:74:ASN:HB3	1:AQ:126:GLU:HG2	1.72	0.72
1:AD:189:PHE:HE1	1:AD:198:ARG:HG3	1.54	0.72
1:AE:189:PHE:HE2	1:AE:249:LEU:HD21	1.55	0.72
1:AM:284:ARG:HG2	1:AM:284:ARG:HH11	1.51	0.72
1:AT:454:ASN:HD22	1:AT:456:ALA:H	1.36	0.72
1:BQ:33:LYS:O	1:BQ:33:LYS:HG2	1.89	0.72
1:CK:33:LYS:HG2	1:CK:33:LYS:O	1.90	0.72
1:AB:201:GLY:HA3	1:AB:300:GLN:HG2	1.70	0.72
1:BM:79:ARG:HH11	1:BM:79:ARG:HG3	1.55	0.72
1:AA:189:PHE:HE1	1:AA:198:ARG:HG3	1.53	0.72
1:AE:55:ARG:CD	1:CP:272:TYR:CE2	2.72	0.72
1:AK:55:ARG:CD	1:CF:272:TYR:HE2	2.03	0.72
1:AS:22:THR:OG1	1:AS:131:HIS:HD2	1.73	0.72
1:BH:33:LYS:HG2	1:BH:33:LYS:O	1.90	0.72
1:CP:79:ARG:HG3	1:CP:79:ARG:HH11	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:454:ASN:HD22	1:AQ:456:ALA:H	1.36	0.72
1:AT:55:ARG:NE	1:BA:272:TYR:CE2	2.57	0.72
1:BG:272:TYR:CD2	1:CG:55:ARG:HD3	2.24	0.72
1:AB:33:LYS:O	1:AB:33:LYS:HG2	1.90	0.72
1:AF:74:ASN:HB3	1:AF:126:GLU:HG2	1.72	0.72
1:AT:189:PHE:HE1	1:AT:198:ARG:HG3	1.53	0.72
1:AT:250:TRP:CZ3	1:AT:272:TYR:HE1	2.06	0.72
1:BL:74:ASN:HB3	1:BL:126:GLU:HG2	1.71	0.72
1:BM:189:PHE:HE2	1:BM:249:LEU:HD21	1.54	0.72
1:AC:250:TRP:CZ3	1:AC:272:TYR:HE1	2.08	0.71
1:BF:55:ARG:NE	1:CH:272:TYR:CE2	2.57	0.71
1:CL:74:ASN:HB3	1:CL:126:GLU:HG2	1.71	0.71
1:CN:36:GLN:NE2	1:CN:156:LEU:H	1.88	0.71
1:AB:454:ASN:HD22	1:AB:456:ALA:H	1.38	0.71
1:AC:33:LYS:O	1:AC:33:LYS:HG2	1.90	0.71
1:AM:33:LYS:O	1:AM:33:LYS:HG2	1.91	0.71
1:AN:55:ARG:CD	1:AS:272:TYR:HE2	2.03	0.71
1:BR:74:ASN:HB3	1:BR:126:GLU:HG2	1.72	0.71
1:CC:284:ARG:HG2	1:CC:284:ARG:HH11	1.55	0.71
1:CR:79:ARG:CG	1:CR:79:ARG:HH11	2.03	0.71
1:AC:55:ARG:NE	1:AT:272:TYR:CE2	2.58	0.71
1:AJ:33:LYS:HG2	1:AJ:33:LYS:O	1.90	0.71
1:AK:74:ASN:HB3	1:AK:126:GLU:HG2	1.72	0.71
1:BT:250:TRP:CZ3	1:BT:272:TYR:HE1	2.08	0.71
1:CC:55:ARG:NE	1:CT:272:TYR:CE2	2.58	0.71
1:AN:33:LYS:O	1:AN:33:LYS:HG2	1.90	0.71
1:AQ:33:LYS:HG2	1:AQ:33:LYS:O	1.89	0.71
1:BP:55:ARG:NE	1:CM:272:TYR:CE2	2.59	0.71
1:CJ:272:TYR:HE2	1:CQ:55:ARG:NE	1.86	0.71
1:AQ:22:THR:OG1	1:AQ:131:HIS:HD2	1.72	0.71
1:BH:22:THR:OG1	1:BH:131:HIS:HD2	1.73	0.71
1:CL:22:THR:OG1	1:CL:131:HIS:HD2	1.73	0.71
1:CM:250:TRP:CZ3	1:CM:272:TYR:HE1	2.06	0.71
1:AF:189:PHE:HE2	1:AF:249:LEU:HD21	1.55	0.71
1:AG:454:ASN:HD22	1:AG:456:ALA:H	1.36	0.71
1:BB:191:LEU:H	1:BB:191:LEU:CD2	2.03	0.71
1:BC:36:GLN:NE2	1:BC:156:LEU:H	1.89	0.71
1:BO:284:ARG:HH11	1:BO:284:ARG:CG	2.02	0.71
1:CH:36:GLN:NE2	1:CH:156:LEU:H	1.88	0.71
1:CS:74:ASN:HB3	1:CS:126:GLU:HG2	1.72	0.71
1:AJ:55:ARG:NE	1:BL:272:TYR:CE2	2.59	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:55:ARG:CD	1:AS:272:TYR:CE2	2.73	0.71
1:CK:36:GLN:NE2	1:CK:156:LEU:H	1.88	0.71
1:CE:272:TYR:CE2	1:CM:55:ARG:NE	2.58	0.71
1:AB:79:ARG:HG3	1:AB:79:ARG:HH11	1.56	0.71
1:AG:284:ARG:CG	1:AG:284:ARG:HH11	2.04	0.71
1:AR:250:TRP:CZ3	1:AR:272:TYR:HE1	2.06	0.71
1:AT:55:ARG:CD	1:BA:272:TYR:CE2	2.74	0.71
1:BS:22:THR:OG1	1:BS:131:HIS:HD2	1.74	0.71
1:BB:55:ARG:NE	1:CB:272:TYR:CE2	2.59	0.71
1:BG:272:TYR:HE2	1:CG:55:ARG:CD	2.03	0.71
1:CI:272:TYR:CE2	1:CO:55:ARG:NE	2.59	0.71
1:CN:55:ARG:NE	1:CS:272:TYR:CE2	2.59	0.71
1:CS:33:LYS:HG2	1:CS:33:LYS:O	1.91	0.71
1:AA:272:TYR:CE2	1:CT:55:ARG:NE	2.59	0.71
1:AB:284:ARG:HH11	1:AB:284:ARG:HG2	1.55	0.71
1:AC:272:TYR:CE2	1:BA:55:ARG:NE	2.58	0.71
1:BA:284:ARG:HH11	1:BA:284:ARG:CG	2.03	0.71
1:BC:189:PHE:HE1	1:BC:198:ARG:HG3	1.55	0.71
1:BI:33:LYS:HG2	1:BI:33:LYS:O	1.90	0.71
1:BN:22:THR:OG1	1:BN:131:HIS:HD2	1.74	0.71
1:BR:33:LYS:HG2	1:BR:33:LYS:O	1.90	0.71
1:CA:36:GLN:NE2	1:CA:156:LEU:H	1.89	0.71
1:CI:22:THR:OG1	1:CI:131:HIS:HD2	1.72	0.71
1:CJ:14:CYS:H	1:CJ:138:ASN:HD21	1.38	0.71
1:CJ:33:LYS:O	1:CJ:33:LYS:HG2	1.91	0.71
1:CN:74:ASN:HB3	1:CN:126:GLU:HG2	1.73	0.71
1:CR:33:LYS:HG2	1:CR:33:LYS:O	1.90	0.71
1:AE:272:TYR:CE2	1:AM:55:ARG:NE	2.59	0.71
1:BC:33:LYS:HG2	1:BC:33:LYS:O	1.91	0.71
1:BP:33:LYS:O	1:BP:33:LYS:HG2	1.90	0.71
1:BT:22:THR:OG1	1:BT:131:HIS:HD2	1.74	0.71
1:CF:22:THR:OG1	1:CF:131:HIS:HD2	1.73	0.71
1:BJ:74:ASN:HB3	1:BJ:126:GLU:HG2	1.73	0.70
1:BP:284:ARG:HG2	1:BP:284:ARG:HH11	1.56	0.70
1:BQ:272:TYR:CE2	1:CL:55:ARG:NE	2.58	0.70
1:CC:284:ARG:CG	1:CC:284:ARG:HH11	2.04	0.70
1:CP:189:PHE:HE1	1:CP:198:ARG:HG3	1.56	0.70
1:CT:74:ASN:HB3	1:CT:126:GLU:HG2	1.73	0.70
1:AB:191:LEU:CD2	1:AB:191:LEU:H	2.04	0.70
1:AK:14:CYS:H	1:AK:138:ASN:HD21	1.38	0.70
1:AN:74:ASN:HB3	1:AN:126:GLU:HG2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:272:TYR:CE2	1:BE:55:ARG:NE	2.59	0.70
1:BQ:454:ASN:HD22	1:BQ:456:ALA:H	1.37	0.70
1:BT:33:LYS:O	1:BT:33:LYS:HG2	1.90	0.70
1:CJ:189:PHE:CE1	1:CJ:198:ARG:HG3	2.26	0.70
1:CM:22:THR:OG1	1:CM:131:HIS:HD2	1.73	0.70
1:CJ:272:TYR:HE2	1:CQ:55:ARG:CD	2.04	0.70
1:AD:74:ASN:HB3	1:AD:126:GLU:HG2	1.73	0.70
1:AJ:79:ARG:HG3	1:AJ:79:ARG:HH11	1.56	0.70
1:BL:22:THR:OG1	1:BL:131:HIS:HD2	1.74	0.70
1:CB:22:THR:OG1	1:CB:131:HIS:HD2	1.73	0.70
1:CN:284:ARG:HH11	1:CN:284:ARG:HG2	1.57	0.70
1:AL:55:ARG:NE	1:CQ:272:TYR:CE2	2.59	0.70
1:AE:14:CYS:H	1:AE:138:ASN:HD21	1.39	0.70
1:AS:284:ARG:HH11	1:AS:284:ARG:CG	2.04	0.70
1:BI:284:ARG:CG	1:BI:284:ARG:HH11	2.04	0.70
1:CE:454:ASN:HD22	1:CE:456:ALA:H	1.37	0.70
1:CN:33:LYS:O	1:CN:33:LYS:HG2	1.91	0.70
1:CS:189:PHE:HE1	1:CS:198:ARG:HG3	1.56	0.70
1:CT:284:ARG:HH11	1:CT:284:ARG:CG	2.04	0.70
1:AF:189:PHE:CE1	1:AF:198:ARG:HG3	2.26	0.70
1:AF:272:TYR:CE2	1:BK:55:ARG:NE	2.59	0.70
1:AF:55:ARG:NE	1:BH:272:TYR:CE2	2.59	0.70
1:AG:284:ARG:HH11	1:AG:284:ARG:HG2	1.56	0.70
1:BA:250:TRP:CZ3	1:BA:272:TYR:HE1	2.10	0.70
1:BF:284:ARG:CG	1:BF:284:ARG:HH11	2.04	0.70
1:CA:33:LYS:HG2	1:CA:33:LYS:O	1.90	0.70
1:CB:74:ASN:HB3	1:CB:126:GLU:HG2	1.74	0.70
1:CQ:191:LEU:CD2	1:CQ:191:LEU:H	2.04	0.70
1:AA:33:LYS:O	1:AA:33:LYS:HG2	1.92	0.70
1:AP:191:LEU:H	1:AP:191:LEU:CD2	2.05	0.70
1:AS:33:LYS:HG2	1:AS:33:LYS:O	1.90	0.70
1:BT:189:PHE:HE1	1:BT:198:ARG:HG3	1.56	0.70
1:CD:55:ARG:NE	1:CN:272:TYR:CE2	2.59	0.70
1:CP:22:THR:OG1	1:CP:131:HIS:HD2	1.74	0.70
1:AL:284:ARG:CG	1:AL:284:ARG:HH11	2.05	0.70
1:CH:55:ARG:NE	1:CK:272:TYR:CE2	2.60	0.70
1:CT:284:ARG:HH11	1:CT:284:ARG:HG2	1.56	0.70
1:AI:22:THR:OG1	1:AI:131:HIS:HD2	1.75	0.70
1:BH:189:PHE:HE2	1:BH:249:LEU:HD21	1.56	0.70
1:BI:284:ARG:HH11	1:BI:284:ARG:HG2	1.57	0.70
1:BJ:22:THR:OG1	1:BJ:131:HIS:HD2	1.75	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:36:GLN:NE2	1:BJ:156:LEU:H	1.89	0.70
1:CB:79:ARG:HH11	1:CB:79:ARG:HG3	1.56	0.70
1:CE:189:PHE:CE1	1:CE:198:ARG:HG3	2.27	0.70
1:CJ:74:ASN:HB3	1:CJ:126:GLU:HG2	1.74	0.70
1:CJ:250:TRP:CE3	1:CJ:272:TYR:CE1	2.80	0.70
1:AN:189:PHE:HE2	1:AN:249:LEU:HD21	1.56	0.70
1:AO:191:LEU:H	1:AO:191:LEU:CD2	2.05	0.70
1:AR:189:PHE:CE1	1:AR:198:ARG:HG3	2.25	0.70
1:BD:272:TYR:HE2	1:BS:55:ARG:CD	2.04	0.70
1:BI:55:ARG:NE	1:BR:272:TYR:CE2	2.59	0.70
1:CO:272:TYR:HE2	1:CR:55:ARG:NE	1.88	0.70
1:CP:33:LYS:HG2	1:CP:33:LYS:O	1.89	0.70
1:CT:16:ALA:O	1:CT:17:ASN:HB2	1.91	0.70
1:AB:284:ARG:CG	1:AB:284:ARG:HH11	2.05	0.70
1:AH:189:PHE:HE2	1:AH:249:LEU:HD21	1.56	0.70
1:AH:33:LYS:HG2	1:AH:33:LYS:O	1.92	0.70
1:AI:33:LYS:HG2	1:AI:33:LYS:O	1.92	0.70
1:BD:284:ARG:CG	1:BD:284:ARG:HH11	2.05	0.70
1:BF:22:THR:OG1	1:BF:131:HIS:HD2	1.74	0.70
1:BH:284:ARG:HH11	1:BH:284:ARG:CG	2.04	0.70
1:BH:74:ASN:HB3	1:BH:126:GLU:HG2	1.74	0.70
1:BN:74:ASN:HB3	1:BN:126:GLU:HG2	1.74	0.70
1:AA:55:ARG:CD	1:CC:272:TYR:CE2	2.75	0.70
1:AE:189:PHE:CE1	1:AE:198:ARG:HG3	2.26	0.69
1:AE:33:LYS:O	1:AE:33:LYS:HG2	1.92	0.69
1:AK:191:LEU:CD2	1:AK:191:LEU:H	2.05	0.69
1:BD:191:LEU:CD2	1:BD:191:LEU:H	2.04	0.69
1:BL:79:ARG:HH11	1:BL:79:ARG:HG3	1.57	0.69
1:BM:189:PHE:HE1	1:BM:198:ARG:HG3	1.55	0.69
1:BS:33:LYS:HG2	1:BS:33:LYS:O	1.92	0.69
1:CA:22:THR:OG1	1:CA:131:HIS:HD2	1.75	0.69
1:CO:189:PHE:CE1	1:CO:198:ARG:HG3	2.26	0.69
1:AJ:191:LEU:H	1:AJ:191:LEU:CD2	2.04	0.69
1:AM:191:LEU:CD2	1:AM:191:LEU:H	2.05	0.69
1:AN:189:PHE:CE1	1:AN:198:ARG:HG3	2.26	0.69
1:AT:55:ARG:CD	1:BA:272:TYR:HE2	2.06	0.69
1:BO:22:THR:OG1	1:BO:131:HIS:HD2	1.75	0.69
1:AA:55:ARG:CD	1:CC:272:TYR:HE2	2.04	0.69
1:CD:284:ARG:HH11	1:CD:284:ARG:CG	2.04	0.69
1:AB:74:ASN:HB3	1:AB:126:GLU:HG2	1.73	0.69
1:AO:284:ARG:HH11	1:AO:284:ARG:HG2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:22:THR:OG1	1:BD:131:HIS:HD2	1.73	0.69
1:CE:272:TYR:HE2	1:CM:55:ARG:CD	2.05	0.69
1:AA:284:ARG:HH11	1:AA:284:ARG:CG	2.06	0.69
1:AE:74:ASN:HB3	1:AE:126:GLU:HG2	1.74	0.69
1:AG:33:LYS:HG2	1:AG:33:LYS:O	1.91	0.69
1:AK:33:LYS:O	1:AK:33:LYS:HG2	1.93	0.69
1:AL:191:LEU:H	1:AL:191:LEU:CD2	2.06	0.69
1:BB:284:ARG:HH11	1:BB:284:ARG:HG2	1.57	0.69
1:BC:55:ARG:NE	1:BT:272:TYR:CE2	2.60	0.69
1:CF:74:ASN:HB3	1:CF:126:GLU:HG2	1.73	0.69
1:AD:55:ARG:CD	1:AN:272:TYR:CE2	2.75	0.69
1:BN:33:LYS:HG2	1:BN:33:LYS:O	1.93	0.69
1:BT:74:ASN:HB3	1:BT:126:GLU:HG2	1.74	0.69
1:CB:33:LYS:HG2	1:CB:33:LYS:O	1.91	0.69
1:CL:189:PHE:CE1	1:CL:198:ARG:HG3	2.28	0.69
1:CO:284:ARG:HH11	1:CO:284:ARG:HG2	1.58	0.69
1:CQ:284:ARG:HH11	1:CQ:284:ARG:CG	2.06	0.69
1:AI:454:ASN:HD22	1:AI:456:ALA:H	1.39	0.69
1:BG:454:ASN:HD22	1:BG:456:ALA:H	1.39	0.69
1:BI:191:LEU:CD2	1:BI:191:LEU:H	2.05	0.69
1:BO:74:ASN:HB3	1:BO:126:GLU:HG2	1.73	0.69
1:CC:22:THR:OG1	1:CC:131:HIS:HD2	1.75	0.69
1:CI:284:ARG:CG	1:CI:284:ARG:HH11	2.06	0.69
1:CI:33:LYS:HG2	1:CI:33:LYS:O	1.90	0.69
1:CP:454:ASN:HD22	1:CP:456:ALA:H	1.40	0.69
1:AH:250:TRP:CZ3	1:AH:272:TYR:HE1	2.11	0.69
1:AT:22:THR:OG1	1:AT:131:HIS:HD2	1.76	0.69
1:AT:79:ARG:HH11	1:AT:79:ARG:HG3	1.58	0.69
1:BI:22:THR:OG1	1:BI:131:HIS:HD2	1.73	0.69
1:BO:191:LEU:CD2	1:BO:191:LEU:H	2.05	0.69
1:BP:191:LEU:CD2	1:BP:191:LEU:H	2.05	0.69
1:BT:191:LEU:H	1:BT:191:LEU:CD2	2.06	0.69
1:CG:189:PHE:HE2	1:CG:249:LEU:HD21	1.57	0.69
1:CG:189:PHE:CE1	1:CG:198:ARG:HG3	2.27	0.69
1:CT:14:CYS:H	1:CT:138:ASN:HD21	1.39	0.69
1:AA:22:THR:OG1	1:AA:131:HIS:HD2	1.74	0.69
1:BB:189:PHE:HE2	1:BB:249:LEU:HD21	1.56	0.69
1:BN:284:ARG:CG	1:BN:284:ARG:HH11	2.06	0.69
1:BP:189:PHE:CE1	1:BP:198:ARG:HG3	2.28	0.69
1:CH:15:GLN:HE21	1:CH:15:GLN:HA	1.57	0.69
1:AC:22:THR:OG1	1:AC:131:HIS:HD2	1.76	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:33:LYS:HG2	1:AD:33:LYS:O	1.93	0.69
1:AF:284:ARG:CG	1:AF:284:ARG:HH11	2.05	0.69
1:AI:189:PHE:CE1	1:AI:198:ARG:HG3	2.25	0.69
1:AM:189:PHE:HE2	1:AM:249:LEU:HD21	1.57	0.69
1:AN:250:TRP:CZ3	1:AN:272:TYR:HE1	2.10	0.69
1:AP:284:ARG:HH11	1:AP:284:ARG:CG	2.06	0.69
1:BH:55:ARG:CD	1:BK:272:TYR:CE2	2.76	0.69
1:CB:191:LEU:CD2	1:CB:191:LEU:H	2.06	0.69
1:CN:250:TRP:CZ3	1:CN:272:TYR:HE1	2.08	0.69
1:CN:284:ARG:CG	1:CN:284:ARG:HH11	2.06	0.69
1:CQ:74:ASN:HB3	1:CQ:126:GLU:HG2	1.74	0.69
1:AG:36:GLN:NE2	1:AG:156:LEU:H	1.91	0.69
1:AI:284:ARG:CG	1:AI:284:ARG:HH11	2.05	0.69
1:AJ:74:ASN:HB3	1:AJ:126:GLU:HG2	1.73	0.69
1:BD:189:PHE:HE1	1:BD:198:ARG:HG3	1.58	0.69
1:BJ:55:ARG:NE	1:CL:272:TYR:CE2	2.61	0.69
1:BK:284:ARG:HH11	1:BK:284:ARG:HG2	1.57	0.69
1:CB:189:PHE:CE1	1:CB:198:ARG:HG3	2.28	0.69
1:CF:250:TRP:CZ3	1:CF:272:TYR:HE1	2.09	0.69
1:AD:284:ARG:CG	1:AD:284:ARG:HH11	2.05	0.69
1:AL:189:PHE:HE1	1:AL:198:ARG:HG3	1.58	0.69
1:AR:284:ARG:HH11	1:AR:284:ARG:CG	2.06	0.69
1:BA:79:ARG:HH11	1:BA:79:ARG:CG	2.06	0.69
1:BB:55:ARG:CD	1:CB:272:TYR:CE2	2.76	0.69
1:CB:16:ALA:O	1:CB:17:ASN:HB2	1.93	0.69
1:AB:272:TYR:HE2	1:CB:55:ARG:CD	2.06	0.69
1:AH:284:ARG:CG	1:AH:284:ARG:HH11	2.06	0.68
1:AK:189:PHE:CE1	1:AK:198:ARG:HG3	2.28	0.68
1:AL:272:TYR:CE2	1:CJ:55:ARG:NE	2.61	0.68
1:AM:189:PHE:CE1	1:AM:198:ARG:HG3	2.28	0.68
1:AS:74:ASN:HB3	1:AS:126:GLU:HG2	1.74	0.68
1:BE:74:ASN:HB3	1:BE:126:GLU:HG2	1.74	0.68
1:CH:33:LYS:HG2	1:CH:33:LYS:O	1.91	0.68
1:CL:284:ARG:HH11	1:CL:284:ARG:HG2	1.56	0.68
1:CO:22:THR:OG1	1:CO:131:HIS:HD2	1.75	0.68
1:CS:22:THR:OG1	1:CS:131:HIS:HD2	1.76	0.68
1:CN:55:ARG:CD	1:CS:272:TYR:CE2	2.76	0.68
1:CT:189:PHE:HE1	1:CT:198:ARG:HG3	1.55	0.68
1:AL:33:LYS:HG2	1:AL:33:LYS:O	1.94	0.68
1:AR:191:LEU:H	1:AR:191:LEU:CD2	2.06	0.68
1:AO:272:TYR:CE2	1:AR:55:ARG:CD	2.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:191:LEU:H	1:BF:191:LEU:CD2	2.05	0.68
1:AQ:272:TYR:CE2	1:BL:55:ARG:NE	2.61	0.68
1:BM:16:ALA:O	1:BM:17:ASN:HB2	1.92	0.68
1:CM:189:PHE:HE2	1:CM:249:LEU:HD21	1.58	0.68
1:AA:36:GLN:NE2	1:AA:156:LEU:H	1.92	0.68
1:AC:74:ASN:HB3	1:AC:126:GLU:HG2	1.75	0.68
1:BG:284:ARG:CG	1:BG:284:ARG:HH11	2.07	0.68
1:CE:284:ARG:HH11	1:CE:284:ARG:CG	2.06	0.68
1:CG:189:PHE:CE1	1:CG:198:ARG:CG	2.77	0.68
1:CG:250:TRP:CZ3	1:CG:272:TYR:HE1	2.10	0.68
1:CI:189:PHE:CE1	1:CI:198:ARG:HG3	2.28	0.68
1:CI:191:LEU:CD2	1:CI:191:LEU:H	2.05	0.68
1:CN:191:LEU:H	1:CN:191:LEU:CD2	2.06	0.68
1:CR:189:PHE:HE2	1:CR:249:LEU:HD21	1.57	0.68
1:AA:191:LEU:CD2	1:AA:191:LEU:H	2.05	0.68
1:AH:15:GLN:HE21	1:AH:15:GLN:HA	1.57	0.68
1:AI:36:GLN:NE2	1:AI:156:LEU:H	1.92	0.68
1:AM:16:ALA:O	1:AM:17:ASN:HB2	1.92	0.68
1:AO:79:ARG:HH11	1:AO:79:ARG:HG3	1.56	0.68
1:AT:284:ARG:HH11	1:AT:284:ARG:HG2	1.59	0.68
1:BE:191:LEU:CD2	1:BE:191:LEU:H	2.06	0.68
1:BI:189:PHE:CE1	1:BI:198:ARG:HG3	2.28	0.68
1:BK:74:ASN:HB3	1:BK:126:GLU:HG2	1.74	0.68
1:BK:36:GLN:NE2	1:BK:156:LEU:H	1.89	0.68
1:CI:284:ARG:HH11	1:CI:284:ARG:HG2	1.57	0.68
1:CN:22:THR:OG1	1:CN:131:HIS:HD2	1.76	0.68
1:CN:189:PHE:HE2	1:CN:249:LEU:HD21	1.58	0.68
1:AO:284:ARG:HH11	1:AO:284:ARG:CG	2.05	0.68
1:BI:272:TYR:CE2	1:BO:55:ARG:NE	2.61	0.68
1:BO:272:TYR:CE2	1:BR:55:ARG:CD	2.77	0.68
1:BT:284:ARG:CG	1:BT:284:ARG:HH11	2.07	0.68
1:CB:250:TRP:CZ3	1:CB:272:TYR:HE1	2.11	0.68
1:CE:16:ALA:O	1:CE:17:ASN:HB2	1.92	0.68
1:CF:33:LYS:O	1:CF:33:LYS:HG2	1.94	0.68
1:CQ:33:LYS:O	1:CQ:33:LYS:HG2	1.93	0.68
1:BD:272:TYR:CE2	1:BS:55:ARG:CD	2.76	0.68
1:BR:284:ARG:CG	1:BR:284:ARG:HH11	2.07	0.68
1:AC:191:LEU:CD2	1:AC:191:LEU:H	2.06	0.68
1:AK:36:GLN:NE2	1:AK:156:LEU:H	1.92	0.68
1:AS:284:ARG:HH11	1:AS:284:ARG:HG2	1.58	0.68
1:BC:272:TYR:CE2	1:CA:55:ARG:NE	2.62	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:33:LYS:O	1:BJ:33:LYS:HG2	1.94	0.68
1:BM:191:LEU:H	1:BM:191:LEU:CD2	2.06	0.68
1:CM:191:LEU:CD2	1:CM:191:LEU:H	2.06	0.68
1:AB:189:PHE:HE2	1:AB:249:LEU:HD21	1.59	0.68
1:AC:284:ARG:HG2	1:AC:284:ARG:HH11	1.59	0.68
1:AL:14:CYS:H	1:AL:138:ASN:HD21	1.40	0.68
1:AT:74:ASN:HB3	1:AT:126:GLU:HG2	1.75	0.68
1:BL:284:ARG:CG	1:BL:284:ARG:HH11	2.07	0.68
1:CA:284:ARG:HG2	1:CA:284:ARG:HH11	1.57	0.68
1:CA:79:ARG:HH11	1:CA:79:ARG:HG3	1.58	0.68
1:CH:74:ASN:HB3	1:CH:126:GLU:HG2	1.75	0.68
1:CM:284:ARG:HH11	1:CM:284:ARG:CG	2.06	0.68
1:AG:22:THR:OG1	1:AG:131:HIS:HD2	1.77	0.68
1:AG:74:ASN:HB3	1:AG:126:GLU:HG2	1.75	0.68
1:AO:74:ASN:HB3	1:AO:126:GLU:HG2	1.75	0.68
1:AO:250:TRP:CE3	1:AO:272:TYR:CE1	2.81	0.68
1:BC:284:ARG:CG	1:BC:284:ARG:HH11	2.07	0.68
1:BG:189:PHE:HE2	1:BG:249:LEU:HD21	1.57	0.68
1:BM:22:THR:OG1	1:BM:131:HIS:HD2	1.76	0.68
1:BQ:284:ARG:NH1	1:BQ:284:ARG:HG2	2.09	0.68
1:CH:189:PHE:HE2	1:CH:249:LEU:HD21	1.59	0.68
1:CO:284:ARG:CG	1:CO:284:ARG:HH11	2.07	0.68
1:CP:74:ASN:HB3	1:CP:126:GLU:HG2	1.74	0.68
1:AK:284:ARG:CG	1:AK:284:ARG:HH11	2.06	0.68
1:BM:33:LYS:HG2	1:BM:33:LYS:O	1.93	0.68
1:CQ:22:THR:OG1	1:CQ:131:HIS:HD2	1.76	0.68
1:CH:250:TRP:CZ3	1:CH:272:TYR:HE1	2.12	0.67
1:CK:284:ARG:CG	1:CK:284:ARG:HH11	2.06	0.67
1:CM:33:LYS:O	1:CM:33:LYS:HG2	1.93	0.67
1:CP:191:LEU:H	1:CP:191:LEU:CD2	2.05	0.67
1:CR:22:THR:OG1	1:CR:131:HIS:HD2	1.76	0.67
1:CI:55:ARG:NE	1:CR:272:TYR:CE2	2.62	0.67
1:AA:284:ARG:HH11	1:AA:284:ARG:HG2	1.58	0.67
1:AG:191:LEU:H	1:AG:191:LEU:CD2	2.07	0.67
1:AI:191:LEU:CD2	1:AI:191:LEU:H	2.07	0.67
1:AD:272:TYR:CE2	1:AS:55:ARG:NE	2.63	0.67
1:BC:189:PHE:CE1	1:BC:198:ARG:HG3	2.30	0.67
1:BE:284:ARG:HH11	1:BE:284:ARG:CG	2.07	0.67
1:BR:284:ARG:HH11	1:BR:284:ARG:HG2	1.59	0.67
1:CC:189:PHE:HE1	1:CC:198:ARG:HG3	1.59	0.67
1:CD:272:TYR:CE2	1:CS:55:ARG:CD	2.78	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:74:ASN:HB3	1:CM:126:GLU:HG2	1.76	0.67
1:CN:55:ARG:CD	1:CS:272:TYR:HE2	2.07	0.67
1:AB:272:TYR:CE2	1:CB:55:ARG:CD	2.78	0.67
1:AD:284:ARG:HG2	1:AD:284:ARG:HH11	1.58	0.67
1:AI:74:ASN:HB3	1:AI:126:GLU:HG2	1.76	0.67
1:BB:250:TRP:CZ3	1:BB:272:TYR:HE1	2.11	0.67
1:BK:284:ARG:CG	1:BK:284:ARG:HH11	2.07	0.67
1:BM:11:PRO:HG2	1:BM:18:ARG:HD3	1.76	0.67
1:CJ:189:PHE:HE2	1:CJ:249:LEU:HD21	1.58	0.67
1:CM:189:PHE:CE1	1:CM:198:ARG:HG3	2.28	0.67
1:AF:272:TYR:CE2	1:BK:55:ARG:CD	2.77	0.67
1:AI:189:PHE:HE2	1:AI:249:LEU:HD21	1.58	0.67
1:AJ:22:THR:OG1	1:AJ:131:HIS:HD2	1.76	0.67
1:AT:36:GLN:NE2	1:AT:156:LEU:H	1.92	0.67
1:BE:189:PHE:HE2	1:BE:249:LEU:HD21	1.59	0.67
1:BF:284:ARG:HG2	1:BF:284:ARG:HH11	1.57	0.67
1:BH:189:PHE:CE1	1:BH:198:ARG:HG3	2.28	0.67
1:BM:284:ARG:HH11	1:BM:284:ARG:HG2	1.59	0.67
1:CA:191:LEU:CD2	1:CA:191:LEU:H	2.06	0.67
1:AH:272:TYR:CE2	1:CF:55:ARG:NE	2.63	0.67
1:CL:79:ARG:HH11	1:CL:79:ARG:HG3	1.59	0.67
1:AE:250:TRP:CZ3	1:AE:272:TYR:HE1	2.11	0.67
1:AN:284:ARG:HH11	1:AN:284:ARG:CG	2.08	0.67
1:BE:22:THR:OG1	1:BE:131:HIS:HD2	1.76	0.67
1:BH:191:LEU:H	1:BH:191:LEU:CD2	2.07	0.67
1:CL:191:LEU:H	1:CL:191:LEU:CD2	2.06	0.67
1:AD:14:CYS:H	1:AD:138:ASN:HD21	1.43	0.67
1:BC:284:ARG:HH11	1:BC:284:ARG:HG2	1.59	0.67
1:BK:22:THR:OG1	1:BK:131:HIS:HD2	1.76	0.67
1:BQ:191:LEU:H	1:BQ:191:LEU:CD2	2.07	0.67
1:CA:189:PHE:HE1	1:CA:198:ARG:HG3	1.58	0.67
1:CD:33:LYS:O	1:CD:33:LYS:HG2	1.95	0.67
1:CN:74:ASN:ND2	1:CN:77:THR:OG1	2.27	0.67
1:CO:250:TRP:CE3	1:CO:272:TYR:CE1	2.83	0.67
1:CO:272:TYR:CE2	1:CR:55:ARG:CD	2.78	0.67
1:CJ:272:TYR:CE2	1:CQ:55:ARG:CD	2.78	0.67
1:CT:22:THR:OG1	1:CT:131:HIS:HD2	1.78	0.67
1:AI:272:TYR:CE2	1:AO:55:ARG:CD	2.76	0.67
1:AI:284:ARG:HG2	1:AI:284:ARG:HH11	1.58	0.67
1:BB:16:ALA:O	1:BB:17:ASN:HB2	1.92	0.67
1:BC:191:LEU:CD2	1:BC:191:LEU:H	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:454:ASN:HD22	1:BD:456:ALA:H	1.43	0.67
1:CD:74:ASN:HB3	1:CD:126:GLU:HG2	1.77	0.67
1:CG:284:ARG:HH11	1:CG:284:ARG:CG	2.07	0.67
1:CT:191:LEU:H	1:CT:191:LEU:CD2	2.08	0.67
1:AI:272:TYR:CE2	1:AO:55:ARG:NE	2.63	0.67
1:AJ:189:PHE:HE2	1:AJ:249:LEU:HD21	1.59	0.67
1:AL:79:ARG:HH11	1:AL:79:ARG:CG	2.06	0.67
1:AR:284:ARG:HH11	1:AR:284:ARG:HG2	1.60	0.67
1:BD:55:ARG:NE	1:BN:272:TYR:CE2	2.63	0.67
1:BG:284:ARG:HG2	1:BG:284:ARG:HH11	1.60	0.67
1:BQ:189:PHE:CE1	1:BQ:198:ARG:HG3	2.29	0.67
1:BI:55:ARG:CD	1:BR:272:TYR:CE2	2.77	0.67
1:CC:191:LEU:CD2	1:CC:191:LEU:H	2.07	0.67
1:CR:189:PHE:CE1	1:CR:198:ARG:HG3	2.29	0.67
1:AD:191:LEU:H	1:AD:191:LEU:CD2	2.07	0.67
1:AE:36:GLN:NE2	1:AE:156:LEU:H	1.93	0.67
1:AS:189:PHE:HE1	1:AS:198:ARG:HG3	1.57	0.67
1:BQ:272:TYR:CE2	1:CL:55:ARG:CD	2.78	0.67
1:CC:74:ASN:HB3	1:CC:126:GLU:HG2	1.75	0.67
1:CE:74:ASN:HB3	1:CE:126:GLU:HG2	1.76	0.67
1:CF:189:PHE:HE2	1:CF:249:LEU:HD21	1.59	0.67
1:AB:55:ARG:CD	1:BB:272:TYR:CE2	2.78	0.66
1:AO:36:GLN:NE2	1:AO:156:LEU:H	1.92	0.66
1:AT:191:LEU:H	1:AT:191:LEU:CD2	2.08	0.66
1:BB:55:ARG:CD	1:CB:272:TYR:HE2	2.08	0.66
1:CB:284:ARG:HH11	1:CB:284:ARG:CG	2.08	0.66
1:CB:36:GLN:NE2	1:CB:156:LEU:H	1.93	0.66
1:AT:284:ARG:HH11	1:AT:284:ARG:CG	2.08	0.66
1:BB:189:PHE:CE1	1:BB:198:ARG:HG3	2.28	0.66
1:BI:189:PHE:HE2	1:BI:249:LEU:HD21	1.59	0.66
1:BS:191:LEU:H	1:BS:191:LEU:CD2	2.08	0.66
1:CE:189:PHE:HE2	1:CE:249:LEU:HD21	1.59	0.66
1:CM:16:ALA:O	1:CM:17:ASN:HB2	1.95	0.66
1:CG:191:LEU:H	1:CG:191:LEU:CD2	2.06	0.66
1:CK:191:LEU:CD2	1:CK:191:LEU:H	2.07	0.66
1:AA:272:TYR:CE2	1:CT:55:ARG:CD	2.79	0.66
1:AM:284:ARG:HG2	1:AM:284:ARG:NH1	2.09	0.66
1:BE:189:PHE:CE1	1:BE:198:ARG:HG3	2.29	0.66
1:BF:33:LYS:O	1:BF:33:LYS:HG2	1.96	0.66
1:BR:189:PHE:CE1	1:BR:198:ARG:HG3	2.29	0.66
1:CG:16:ALA:O	1:CG:17:ASN:HB2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:74:ASN:HB3	1:CO:126:GLU:HG2	1.77	0.66
1:CR:191:LEU:H	1:CR:191:LEU:CD2	2.08	0.66
1:AH:36:GLN:NE2	1:AH:156:LEU:H	1.93	0.66
1:AH:55:ARG:NE	1:AK:272:TYR:CE2	2.64	0.66
1:CE:79:ARG:HH11	1:CE:79:ARG:HG3	1.60	0.66
1:CF:191:LEU:H	1:CF:191:LEU:CD2	2.07	0.66
1:CH:284:ARG:HG2	1:CH:284:ARG:HH11	1.59	0.66
1:BA:189:PHE:CE1	1:BA:198:ARG:HG3	2.29	0.66
1:BB:189:PHE:CE1	1:BB:198:ARG:CG	2.78	0.66
1:BC:55:ARG:CD	1:BT:272:TYR:CE2	2.79	0.66
1:CD:36:GLN:NE2	1:CD:156:LEU:H	1.93	0.66
1:CE:191:LEU:CD2	1:CE:191:LEU:H	2.09	0.66
1:CN:14:CYS:H	1:CN:138:ASN:HD21	1.41	0.66
1:CP:284:ARG:HH11	1:CP:284:ARG:CG	2.07	0.66
1:CR:250:TRP:CZ3	1:CR:272:TYR:HE1	2.14	0.66
1:AO:33:LYS:HG2	1:AO:33:LYS:O	1.94	0.66
1:BA:191:LEU:H	1:BA:191:LEU:CD2	2.08	0.66
1:CE:272:TYR:CE2	1:CM:55:ARG:CD	2.79	0.66
1:CK:284:ARG:HG2	1:CK:284:ARG:HH11	1.59	0.66
1:CK:74:ASN:HB3	1:CK:126:GLU:HG2	1.76	0.66
1:CM:284:ARG:HH11	1:CM:284:ARG:HG2	1.60	0.66
1:AM:272:TYR:CE2	1:CP:55:ARG:NE	2.63	0.66
1:CQ:16:ALA:O	1:CQ:17:ASN:HB2	1.96	0.66
1:AE:55:ARG:HD3	1:CP:272:TYR:CD2	2.31	0.66
1:AR:14:CYS:H	1:AR:138:ASN:HD21	1.42	0.66
1:AT:55:ARG:HD3	1:BA:272:TYR:CD2	2.31	0.66
1:BC:74:ASN:HB3	1:BC:126:GLU:HG2	1.78	0.66
1:CS:284:ARG:CG	1:CS:284:ARG:HH11	2.09	0.66
1:CD:272:TYR:HE2	1:CS:55:ARG:CD	2.09	0.66
1:AI:14:CYS:H	1:AI:138:ASN:HD21	1.42	0.66
1:AN:189:PHE:HE2	1:AN:249:LEU:CD2	2.08	0.66
1:AP:74:ASN:HB3	1:AP:126:GLU:HG2	1.76	0.66
1:AQ:36:GLN:NE2	1:AQ:156:LEU:H	1.94	0.66
1:BH:55:ARG:CD	1:BK:272:TYR:HE2	2.09	0.66
1:BN:189:PHE:HE2	1:BN:249:LEU:HD21	1.61	0.66
1:BS:284:ARG:CG	1:BS:284:ARG:HH11	2.08	0.66
1:BP:272:TYR:CE2	1:CE:55:ARG:CZ	2.79	0.66
1:CI:272:TYR:CE2	1:CO:55:ARG:CD	2.79	0.66
1:CO:191:LEU:CD2	1:CO:191:LEU:H	2.07	0.66
1:AQ:189:PHE:HE1	1:AQ:198:ARG:HG3	1.60	0.66
1:AQ:272:TYR:CE2	1:BL:55:ARG:CD	2.79	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:250:TRP:CZ3	1:BK:272:TYR:HE1	2.13	0.66
1:AF:272:TYR:CD2	1:BK:55:ARG:HD3	2.31	0.65
1:AG:16:ALA:O	1:AG:17:ASN:HB2	1.94	0.65
1:AL:250:TRP:CZ3	1:AL:272:TYR:HE1	2.14	0.65
1:AL:284:ARG:HG2	1:AL:284:ARG:HH11	1.60	0.65
1:BO:189:PHE:HE1	1:BO:198:ARG:HG3	1.62	0.65
1:CD:191:LEU:H	1:CD:191:LEU:CD2	2.09	0.65
1:AK:55:ARG:HD3	1:CF:272:TYR:CD2	2.31	0.65
1:CH:191:LEU:H	1:CH:191:LEU:CD2	2.07	0.65
1:BE:272:TYR:CE2	1:BM:55:ARG:NE	2.65	0.65
1:BN:36:GLN:NE2	1:BN:156:LEU:H	1.94	0.65
1:AK:55:ARG:HD3	1:CF:272:TYR:CE2	2.31	0.65
1:CI:36:GLN:NE2	1:CI:156:LEU:H	1.94	0.65
1:CQ:284:ARG:HG2	1:CQ:284:ARG:HH11	1.62	0.65
1:AR:189:PHE:HE2	1:AR:249:LEU:CD2	2.09	0.65
1:BG:191:LEU:H	1:BG:191:LEU:CD2	2.08	0.65
1:AQ:272:TYR:CD2	1:BL:55:ARG:HD3	2.31	0.65
1:BT:55:ARG:NE	1:CA:272:TYR:CE2	2.64	0.65
1:CA:284:ARG:HH11	1:CA:284:ARG:CG	2.09	0.65
1:AM:74:ASN:HB3	1:AM:126:GLU:HG2	1.78	0.65
1:AN:191:LEU:CD2	1:AN:191:LEU:H	2.10	0.65
1:BJ:284:ARG:HH11	1:BJ:284:ARG:CG	2.08	0.65
1:BS:79:ARG:HH11	1:BS:79:ARG:CG	2.04	0.65
1:CB:284:ARG:HH11	1:CB:284:ARG:HG2	1.59	0.65
1:CH:284:ARG:CG	1:CH:284:ARG:HH11	2.08	0.65
1:CP:250:TRP:CE3	1:CP:272:TYR:CE1	2.84	0.65
1:AB:22:THR:OG1	1:AB:131:HIS:HD2	1.78	0.65
1:AP:284:ARG:HH11	1:AP:284:ARG:HG2	1.62	0.65
1:AB:55:ARG:CD	1:BB:272:TYR:HE2	2.10	0.65
1:BL:74:ASN:CB	1:BL:126:GLU:HG2	2.27	0.65
1:CF:189:PHE:CE1	1:CF:198:ARG:HG3	2.29	0.65
1:CQ:189:PHE:HE1	1:CQ:198:ARG:HG3	1.61	0.65
1:AP:55:ARG:CD	1:BM:272:TYR:HE2	2.10	0.65
1:AE:284:ARG:CG	1:AE:284:ARG:HH11	2.08	0.65
1:AF:189:PHE:HE2	1:AF:249:LEU:CD2	2.10	0.65
1:BD:74:ASN:HB3	1:BD:126:GLU:HG2	1.77	0.65
1:BL:191:LEU:CD2	1:BL:191:LEU:H	2.09	0.65
1:AJ:55:ARG:CD	1:BL:272:TYR:CE2	2.79	0.65
1:CH:22:THR:OG1	1:CH:131:HIS:HD2	1.78	0.65
1:CJ:191:LEU:H	1:CJ:191:LEU:CD2	2.10	0.65
1:CN:16:ALA:O	1:CN:17:ASN:HB2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:36:GLN:NE2	1:AB:156:LEU:H	1.94	0.65
1:AP:250:TRP:CZ3	1:AP:272:TYR:HE1	2.14	0.65
1:BS:189:PHE:CE1	1:BS:198:ARG:HG3	2.31	0.65
1:BJ:55:ARG:CD	1:CL:272:TYR:CE2	2.80	0.65
1:AA:74:ASN:HB3	1:AA:126:GLU:HG2	1.78	0.65
1:AD:36:GLN:NE2	1:AD:156:LEU:H	1.95	0.65
1:AF:284:ARG:HH11	1:AF:284:ARG:HG2	1.61	0.65
1:AS:189:PHE:CE1	1:AS:198:ARG:HG3	2.32	0.65
1:BB:14:CYS:H	1:BB:138:ASN:HD21	1.45	0.65
1:BB:239:ILE:HG12	1:BB:326:ILE:CD1	2.27	0.65
1:BI:74:ASN:HB3	1:BI:126:GLU:HG2	1.79	0.65
1:BN:250:TRP:CZ3	1:BN:272:TYR:HE1	2.15	0.65
1:CF:288:HIS:HD2	1:CF:337:ASP:OD2	1.79	0.65
1:CG:74:ASN:HB3	1:CG:126:GLU:HG2	1.78	0.65
1:CQ:14:CYS:H	1:CQ:138:ASN:HD21	1.43	0.65
1:BF:36:GLN:NE2	1:BF:156:LEU:H	1.94	0.65
1:BI:55:ARG:CD	1:BR:272:TYR:HE2	2.10	0.65
1:BK:189:PHE:CE1	1:BK:198:ARG:HG3	2.32	0.65
1:CB:189:PHE:HE2	1:CB:249:LEU:HD21	1.61	0.65
1:CD:272:TYR:CD2	1:CS:55:ARG:HD3	2.32	0.65
1:CG:284:ARG:HG2	1:CG:284:ARG:HH11	1.62	0.65
1:CK:189:PHE:HE1	1:CK:198:ARG:HG3	1.59	0.65
1:CM:189:PHE:CE1	1:CM:198:ARG:CG	2.79	0.65
1:CS:191:LEU:H	1:CS:191:LEU:CD2	2.10	0.65
1:AA:14:CYS:H	1:AA:138:ASN:HD21	1.45	0.64
1:AD:22:THR:OG1	1:AD:131:HIS:HD2	1.79	0.64
1:AH:189:PHE:CE1	1:AH:198:ARG:HG3	2.31	0.64
1:AJ:284:ARG:CG	1:AJ:284:ARG:HH11	2.10	0.64
1:BA:284:ARG:HH11	1:BA:284:ARG:HG2	1.61	0.64
1:BF:250:TRP:CZ3	1:BF:272:TYR:HE1	2.14	0.64
1:BH:250:TRP:CZ3	1:BH:272:TYR:HE1	2.15	0.64
1:BB:55:ARG:HD3	1:CB:272:TYR:CD2	2.32	0.64
1:AK:250:TRP:CZ3	1:AK:272:TYR:HE1	2.14	0.64
1:AD:55:ARG:HD3	1:AN:272:TYR:CD2	2.32	0.64
1:AT:189:PHE:CE1	1:AT:198:ARG:HG3	2.32	0.64
1:BE:272:TYR:CE2	1:BM:55:ARG:CD	2.80	0.64
1:AG:272:TYR:CE2	1:BG:55:ARG:NE	2.65	0.64
1:BJ:189:PHE:HE2	1:BJ:249:LEU:HD21	1.61	0.64
1:BJ:284:ARG:HH11	1:BJ:284:ARG:HG2	1.62	0.64
1:CJ:284:ARG:HH11	1:CJ:284:ARG:CG	2.10	0.64
1:CR:74:ASN:HB3	1:CR:126:GLU:HG2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:74:ASN:HB3	1:AH:126:GLU:HG2	1.79	0.64
1:AI:272:TYR:CD2	1:AO:55:ARG:HD3	2.32	0.64
1:AI:272:TYR:HE2	1:AO:55:ARG:CD	2.09	0.64
1:AP:55:ARG:CD	1:BM:272:TYR:CE2	2.80	0.64
1:BP:55:ARG:CD	1:CM:272:TYR:HE2	2.10	0.64
1:CC:189:PHE:CE1	1:CC:198:ARG:HG3	2.32	0.64
1:CI:74:ASN:CB	1:CI:126:GLU:HG2	2.26	0.64
1:CL:14:CYS:H	1:CL:138:ASN:HD21	1.45	0.64
1:BP:55:ARG:CD	1:CM:272:TYR:CE2	2.81	0.64
1:CR:189:PHE:CE1	1:CR:198:ARG:CG	2.78	0.64
1:AD:55:ARG:CD	1:AN:272:TYR:HE2	2.08	0.64
1:AN:55:ARG:HD3	1:AS:272:TYR:CD2	2.31	0.64
1:AS:36:GLN:NE2	1:AS:156:LEU:H	1.95	0.64
1:BE:189:PHE:CE1	1:BE:198:ARG:CG	2.78	0.64
1:BG:36:GLN:NE2	1:BG:156:LEU:H	1.96	0.64
1:BG:189:PHE:CE1	1:BG:198:ARG:HG3	2.29	0.64
1:BJ:189:PHE:CE1	1:BJ:198:ARG:CG	2.81	0.64
1:AN:16:ALA:O	1:AN:17:ASN:HB2	1.97	0.64
1:AT:55:ARG:HD3	1:BA:272:TYR:CE2	2.33	0.64
1:BM:189:PHE:HE2	1:BM:249:LEU:CD2	2.10	0.64
1:BN:284:ARG:HH11	1:BN:284:ARG:HG2	1.62	0.64
1:CF:284:ARG:CG	1:CF:284:ARG:HH11	2.10	0.64
1:BQ:272:TYR:HE2	1:CL:55:ARG:CD	2.10	0.64
1:AD:250:TRP:CZ3	1:AD:272:TYR:HE1	2.14	0.64
1:AE:191:LEU:CD2	1:AE:191:LEU:H	2.08	0.64
1:AF:250:TRP:CZ3	1:AF:272:TYR:HE1	2.15	0.64
1:AG:189:PHE:CE1	1:AG:198:ARG:HG3	2.29	0.64
1:AK:22:THR:OG1	1:AK:131:HIS:HD2	1.79	0.64
1:AL:36:GLN:NE2	1:AL:156:LEU:H	1.95	0.64
1:AQ:191:LEU:H	1:AQ:191:LEU:CD2	2.08	0.64
1:BF:272:TYR:CE2	1:CK:55:ARG:NE	2.66	0.64
1:BH:284:ARG:HG2	1:BH:284:ARG:HH11	1.61	0.64
1:CH:189:PHE:HE2	1:CH:249:LEU:CD2	2.10	0.64
1:CK:22:THR:OG1	1:CK:131:HIS:HD2	1.81	0.64
1:CK:250:TRP:CZ3	1:CK:272:TYR:HE1	2.13	0.64
1:CP:189:PHE:CE1	1:CP:198:ARG:HG3	2.33	0.64
1:CS:250:TRP:CZ3	1:CS:272:TYR:HE1	2.12	0.64
1:AO:189:PHE:HE1	1:AO:198:ARG:HG3	1.61	0.64
1:BB:22:THR:OG1	1:BB:131:HIS:HD2	1.80	0.64
1:BE:284:ARG:HH11	1:BE:284:ARG:HG2	1.61	0.64
1:BF:189:PHE:HE2	1:BF:249:LEU:HD21	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:55:ARG:HD3	1:BK:272:TYR:CD2	2.32	0.64
1:BR:189:PHE:HE2	1:BR:249:LEU:HD21	1.61	0.64
1:CK:14:CYS:H	1:CK:138:ASN:HD21	1.44	0.64
1:CN:55:ARG:HD3	1:CS:272:TYR:CE2	2.32	0.64
1:AB:189:PHE:CE1	1:AB:198:ARG:HG3	2.31	0.64
1:AQ:284:ARG:CG	1:AQ:284:ARG:HH11	2.11	0.64
1:BF:55:ARG:CD	1:CH:272:TYR:CE2	2.81	0.64
1:CI:272:TYR:HE2	1:CO:55:ARG:CD	2.11	0.64
1:AM:189:PHE:CE1	1:AM:198:ARG:CG	2.80	0.64
1:AM:250:TRP:CZ3	1:AM:272:TYR:HE1	2.16	0.64
1:AN:284:ARG:HH11	1:AN:284:ARG:HG2	1.63	0.64
1:AN:74:ASN:CB	1:AN:126:GLU:HG2	2.28	0.64
1:BG:79:ARG:HG3	1:BG:79:ARG:HH11	1.62	0.64
1:BH:36:GLN:NE2	1:BH:156:LEU:H	1.96	0.64
1:BL:189:PHE:CE1	1:BL:198:ARG:HG3	2.31	0.64
1:BN:55:ARG:NE	1:BS:272:TYR:CE2	2.65	0.64
1:BO:284:ARG:NH1	1:BO:284:ARG:HG2	2.12	0.64
1:BQ:22:THR:OG1	1:BQ:131:HIS:HD2	1.81	0.64
1:BS:74:ASN:CB	1:BS:126:GLU:HG2	2.28	0.64
1:CH:189:PHE:CE1	1:CH:198:ARG:HG3	2.30	0.64
1:AL:55:ARG:CD	1:CQ:272:TYR:CE2	2.81	0.64
1:AR:36:GLN:NE2	1:AR:156:LEU:H	1.95	0.64
1:BA:189:PHE:HE1	1:BA:198:ARG:CG	2.11	0.64
1:BF:67:VAL:HG23	1:BF:135:LEU:HB2	1.80	0.64
1:BO:36:GLN:NE2	1:BO:156:LEU:H	1.96	0.64
1:BQ:272:TYR:CD2	1:CL:55:ARG:HD3	2.33	0.64
1:BR:191:LEU:H	1:BR:191:LEU:CD2	2.09	0.64
1:CA:67:VAL:HG23	1:CA:135:LEU:HB2	1.79	0.64
1:CE:250:TRP:CE3	1:CE:272:TYR:CE1	2.86	0.64
1:CK:189:PHE:CE1	1:CK:198:ARG:HG3	2.33	0.64
1:AC:272:TYR:CE2	1:BA:55:ARG:CD	2.81	0.63
1:AC:55:ARG:CD	1:AT:272:TYR:CE2	2.81	0.63
1:AG:250:TRP:CE3	1:AG:272:TYR:CE1	2.86	0.63
1:AJ:189:PHE:CE1	1:AJ:198:ARG:HG3	2.30	0.63
1:AR:74:ASN:HB3	1:AR:126:GLU:HG2	1.80	0.63
1:AI:55:ARG:NE	1:AR:272:TYR:CE2	2.66	0.63
1:BN:55:ARG:CD	1:BS:272:TYR:CE2	2.80	0.63
1:BT:14:CYS:H	1:BT:138:ASN:HD21	1.46	0.63
1:AE:272:TYR:CE2	1:AM:55:ARG:CD	2.81	0.63
1:AF:55:ARG:CD	1:BH:272:TYR:CE2	2.81	0.63
1:BA:74:ASN:CB	1:BA:126:GLU:HG2	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:22:THR:OG1	1:BG:131:HIS:HD2	1.80	0.63
1:BG:250:TRP:CZ3	1:BG:272:TYR:HE1	2.13	0.63
1:BO:272:TYR:CE2	1:BR:55:ARG:CZ	2.81	0.63
1:CC:55:ARG:CD	1:CT:272:TYR:CE2	2.82	0.63
1:BF:55:ARG:CD	1:CH:272:TYR:HE2	2.10	0.63
1:CH:55:ARG:CD	1:CK:272:TYR:CE2	2.81	0.63
1:AA:55:ARG:CZ	1:CC:272:TYR:CE2	2.82	0.63
1:AL:272:TYR:CE2	1:CJ:55:ARG:CD	2.82	0.63
1:BE:36:GLN:NE2	1:BE:156:LEU:H	1.96	0.63
1:BH:189:PHE:CE1	1:BH:198:ARG:CG	2.80	0.63
1:CB:189:PHE:CE1	1:CB:198:ARG:CG	2.79	0.63
1:CN:18:ARG:HG3	1:CN:19:TYR:N	2.12	0.63
1:AD:189:PHE:CE1	1:AD:198:ARG:HG3	2.34	0.63
1:AE:55:ARG:HD3	1:CP:272:TYR:CE2	2.34	0.63
1:AG:284:ARG:HG2	1:AG:284:ARG:NH1	2.12	0.63
1:BB:74:ASN:HB3	1:BB:126:GLU:HG2	1.79	0.63
1:BN:189:PHE:CE1	1:BN:198:ARG:HG3	2.34	0.63
1:CD:250:TRP:CE3	1:CD:272:TYR:CE1	2.86	0.63
1:CE:189:PHE:CE1	1:CE:198:ARG:CG	2.81	0.63
1:BP:272:TYR:CD2	1:CE:55:ARG:CZ	2.82	0.63
1:CI:14:CYS:H	1:CI:138:ASN:HD21	1.47	0.63
1:AI:272:TYR:CE2	1:AO:55:ARG:HD3	2.34	0.63
1:BR:36:GLN:NE2	1:BR:156:LEU:H	1.97	0.63
1:CJ:189:PHE:CE1	1:CJ:198:ARG:CG	2.80	0.63
1:BF:272:TYR:CE2	1:CK:55:ARG:CD	2.81	0.63
1:CM:79:ARG:HG3	1:CM:79:ARG:HH11	1.64	0.63
1:AF:191:LEU:H	1:AF:191:LEU:CD2	2.11	0.63
1:AF:272:TYR:HE2	1:BK:55:ARG:CD	2.12	0.63
1:BL:284:ARG:HG2	1:BL:284:ARG:HH11	1.63	0.63
1:BN:189:PHE:CE1	1:BN:198:ARG:CG	2.79	0.63
1:BQ:74:ASN:HB3	1:BQ:126:GLU:HG2	1.81	0.63
1:CD:284:ARG:NH1	1:CD:284:ARG:HG2	2.12	0.63
1:AB:74:ASN:CB	1:AB:126:GLU:HG2	2.29	0.63
1:AL:189:PHE:CE1	1:AL:198:ARG:HG3	2.34	0.63
1:AR:189:PHE:CE1	1:AR:198:ARG:CG	2.79	0.63
1:AR:79:ARG:HG3	1:AR:79:ARG:HH11	1.63	0.63
1:BP:284:ARG:CG	1:BP:284:ARG:HH11	2.12	0.63
1:BP:74:ASN:HB3	1:BP:126:GLU:HG2	1.80	0.63
1:BJ:272:TYR:HE2	1:BQ:55:ARG:CD	2.10	0.63
1:CS:284:ARG:HG2	1:CS:284:ARG:HH11	1.63	0.63
1:AA:272:TYR:HE2	1:CT:55:ARG:CD	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:250:TRP:CZ3	1:BM:272:TYR:HE1	2.17	0.63
1:CA:74:ASN:HB3	1:CA:126:GLU:HG2	1.81	0.63
1:CF:284:ARG:HG2	1:CF:284:ARG:HH11	1.63	0.63
1:AO:203:THR:HB	1:AO:300:GLN:HG3	1.81	0.63
1:CA:250:TRP:CZ3	1:CA:272:TYR:HE1	2.14	0.63
1:CD:14:CYS:H	1:CD:138:ASN:HD21	1.46	0.63
1:CM:189:PHE:HE2	1:CM:249:LEU:CD2	2.11	0.63
1:CT:36:GLN:NE2	1:CT:156:LEU:H	1.97	0.63
1:AC:55:ARG:CD	1:AT:272:TYR:HE2	2.11	0.62
1:BB:79:ARG:HG3	1:BB:79:ARG:HH11	1.64	0.62
1:BC:74:ASN:ND2	1:BC:77:THR:OG1	2.32	0.62
1:BD:284:ARG:HG2	1:BD:284:ARG:HH11	1.64	0.62
1:BM:74:ASN:HB3	1:BM:126:GLU:HG2	1.80	0.62
1:CD:79:ARG:HH11	1:CD:79:ARG:CG	2.07	0.62
1:AA:189:PHE:CE1	1:AA:198:ARG:HG3	2.34	0.62
1:AG:79:ARG:NH1	1:AG:79:ARG:HG3	2.09	0.62
1:AM:272:TYR:CE2	1:CP:55:ARG:CD	2.82	0.62
1:AM:36:GLN:NE2	1:AM:156:LEU:H	1.97	0.62
1:BL:16:ALA:O	1:BL:17:ASN:HB2	1.98	0.62
1:BI:55:ARG:HD3	1:BR:272:TYR:CD2	2.33	0.62
1:BS:36:GLN:NE2	1:BS:156:LEU:H	1.95	0.62
1:BT:284:ARG:HG2	1:BT:284:ARG:HH11	1.63	0.62
1:AG:55:ARG:CD	1:CG:272:TYR:HE2	2.12	0.62
1:AL:272:TYR:HE2	1:CJ:55:ARG:CD	2.12	0.62
1:AN:36:GLN:NE2	1:AN:156:LEU:H	1.96	0.62
1:BB:36:GLN:NE2	1:BB:156:LEU:H	1.96	0.62
1:CE:36:GLN:NE2	1:CE:156:LEU:H	1.97	0.62
1:CN:55:ARG:HD3	1:CS:272:TYR:CD2	2.34	0.62
1:AH:284:ARG:HG2	1:AH:284:ARG:HH11	1.63	0.62
1:BE:79:ARG:HH11	1:BE:79:ARG:HG3	1.63	0.62
1:BI:189:PHE:HE2	1:BI:249:LEU:CD2	2.12	0.62
1:CG:189:PHE:HE2	1:CG:249:LEU:CD2	2.12	0.62
1:AC:284:ARG:HG2	1:AC:284:ARG:NH1	2.13	0.62
1:BD:272:TYR:CD2	1:BS:55:ARG:HD3	2.35	0.62
1:BJ:55:ARG:CD	1:CL:272:TYR:HE2	2.11	0.62
1:BL:239:ILE:HG12	1:BL:326:ILE:CD1	2.29	0.62
1:BP:14:CYS:H	1:BP:138:ASN:HD21	1.47	0.62
1:BT:74:ASN:CB	1:BT:126:GLU:HG2	2.28	0.62
1:CR:79:ARG:HH11	1:CR:79:ARG:HG2	1.64	0.62
1:CT:284:ARG:HG2	1:CT:284:ARG:NH1	2.14	0.62
1:AA:250:TRP:CZ3	1:AA:272:TYR:HE1	2.17	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:454:ASN:HD22	1:AM:456:ALA:N	1.97	0.62
1:BD:272:TYR:CE2	1:BS:55:ARG:HD3	2.34	0.62
1:BF:74:ASN:HB3	1:BF:126:GLU:HG2	1.80	0.62
1:BN:55:ARG:CD	1:BS:272:TYR:HE2	2.13	0.62
1:BS:284:ARG:HG2	1:BS:284:ARG:HH11	1.64	0.62
1:BC:55:ARG:CD	1:BT:272:TYR:HE2	2.12	0.62
1:CD:189:PHE:HE1	1:CD:198:ARG:HG3	1.64	0.62
1:AJ:36:GLN:NE2	1:AJ:156:LEU:H	1.96	0.62
1:BF:284:ARG:HG2	1:BF:284:ARG:NH1	2.13	0.62
1:BG:15:GLN:HA	1:BG:15:GLN:HE21	1.64	0.62
1:BI:272:TYR:HE2	1:BO:55:ARG:CD	2.13	0.62
1:BR:22:THR:OG1	1:BR:131:HIS:HD2	1.82	0.62
1:BC:55:ARG:HD3	1:BT:272:TYR:CD2	2.35	0.62
1:AC:189:PHE:HE1	1:AC:198:ARG:HG3	1.63	0.62
1:AH:272:TYR:CE2	1:CF:55:ARG:CD	2.83	0.62
1:AO:22:THR:OG1	1:AO:131:HIS:HD2	1.82	0.62
1:AO:272:TYR:CE2	1:AR:55:ARG:CZ	2.82	0.62
1:CA:189:PHE:CE1	1:CA:198:ARG:HG3	2.34	0.62
1:CF:454:ASN:HD22	1:CF:456:ALA:N	1.96	0.62
1:AR:201:GLY:HA3	1:AR:300:GLN:HG2	1.81	0.62
1:BB:288:HIS:HD2	1:BB:337:ASP:OD2	1.82	0.62
1:BK:191:LEU:H	1:BK:191:LEU:CD2	2.09	0.62
1:CL:36:GLN:NE2	1:CL:156:LEU:H	1.97	0.62
1:CQ:36:GLN:NE2	1:CQ:156:LEU:H	1.98	0.62
1:AE:272:TYR:HE2	1:AM:55:ARG:CD	2.13	0.62
1:AF:74:ASN:CB	1:AF:126:GLU:HG2	2.30	0.62
1:AH:22:THR:OG1	1:AH:131:HIS:HD2	1.81	0.62
1:AK:284:ARG:HH11	1:AK:284:ARG:HG2	1.64	0.62
1:AN:189:PHE:CE1	1:AN:198:ARG:CG	2.79	0.62
1:AS:191:LEU:CD2	1:AS:191:LEU:H	2.12	0.62
1:BB:55:ARG:HD3	1:CB:272:TYR:CE2	2.35	0.62
1:BH:14:CYS:H	1:BH:138:ASN:HD21	1.46	0.62
1:BI:272:TYR:CE2	1:BO:55:ARG:CD	2.82	0.62
1:CF:189:PHE:CE1	1:CF:198:ARG:CG	2.79	0.62
1:CL:250:TRP:CZ3	1:CL:272:TYR:HE1	2.14	0.62
1:CT:189:PHE:CE1	1:CT:198:ARG:HG3	2.33	0.62
1:AG:189:PHE:HE2	1:AG:249:LEU:CD2	2.12	0.61
1:AH:191:LEU:H	1:AH:191:LEU:CD2	2.10	0.61
1:AQ:79:ARG:HG3	1:AQ:79:ARG:HH11	1.64	0.61
1:BA:288:HIS:HD2	1:BA:337:ASP:OD2	1.83	0.61
1:BG:189:PHE:CE1	1:BG:198:ARG:CG	2.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:272:TYR:CE2	1:BQ:55:ARG:CD	2.83	0.61
1:CE:14:CYS:H	1:CE:138:ASN:HD21	1.45	0.61
1:CI:250:TRP:CZ3	1:CI:272:TYR:HE1	2.16	0.61
1:AL:55:ARG:CD	1:CQ:272:TYR:HE2	2.13	0.61
1:AH:67:VAL:HG23	1:AH:135:LEU:HB2	1.81	0.61
1:AK:74:ASN:CB	1:AK:126:GLU:HG2	2.29	0.61
1:AM:189:PHE:HE2	1:AM:249:LEU:CD2	2.13	0.61
1:BD:36:GLN:NE2	1:BD:156:LEU:H	1.98	0.61
1:BI:239:ILE:HG12	1:BI:326:ILE:CD1	2.30	0.61
1:BQ:250:TRP:CZ3	1:BQ:272:TYR:HE1	2.17	0.61
1:CJ:36:GLN:NE2	1:CJ:156:LEU:H	1.98	0.61
1:CS:189:PHE:CE1	1:CS:198:ARG:HG3	2.34	0.61
1:CS:454:ASN:ND2	1:CS:456:ALA:H	1.98	0.61
1:AL:16:ALA:O	1:AL:17:ASN:HB2	1.98	0.61
1:AP:36:GLN:NE2	1:AP:156:LEU:H	1.98	0.61
1:AR:284:ARG:NH1	1:AR:284:ARG:HG2	2.16	0.61
1:AT:250:TRP:CE3	1:AT:272:TYR:CE1	2.88	0.61
1:CB:74:ASN:CB	1:CB:126:GLU:HG2	2.30	0.61
1:CI:284:ARG:NH1	1:CI:284:ARG:HG2	2.15	0.61
1:CJ:74:ASN:CB	1:CJ:126:GLU:HG2	2.31	0.61
1:CT:250:TRP:CZ3	1:CT:272:TYR:HE1	2.14	0.61
1:AA:272:TYR:CD2	1:CT:55:ARG:HD3	2.36	0.61
1:AN:288:HIS:HD2	1:AN:337:ASP:OD2	1.83	0.61
1:BB:284:ARG:HG2	1:BB:284:ARG:NH1	2.14	0.61
1:CH:189:PHE:CE1	1:CH:198:ARG:CG	2.81	0.61
1:CR:284:ARG:HH11	1:CR:284:ARG:CG	2.12	0.61
1:AA:189:PHE:HE1	1:AA:198:ARG:CG	2.13	0.61
1:AI:284:ARG:HG2	1:AI:284:ARG:NH1	2.15	0.61
1:BC:74:ASN:CB	1:BC:126:GLU:HG2	2.30	0.61
1:BJ:79:ARG:CG	1:BJ:79:ARG:HH11	2.10	0.61
1:BR:250:TRP:CZ3	1:BR:272:TYR:HE1	2.15	0.61
1:BN:55:ARG:HD3	1:BS:272:TYR:CE2	2.35	0.61
1:CH:74:ASN:CB	1:CH:126:GLU:HG2	2.29	0.61
1:CI:189:PHE:HE2	1:CI:249:LEU:CD2	2.12	0.61
1:CH:55:ARG:CD	1:CK:272:TYR:HE2	2.13	0.61
1:CP:36:GLN:NE2	1:CP:156:LEU:H	1.98	0.61
1:CQ:250:TRP:CE3	1:CQ:272:TYR:CE1	2.89	0.61
1:AB:58:ALA:HB2	1:AB:102:GLY:HA3	1.83	0.61
1:AC:272:TYR:HE2	1:BA:55:ARG:CD	2.13	0.61
1:AF:36:GLN:NE2	1:AF:156:LEU:H	1.97	0.61
1:BD:250:TRP:CE3	1:BD:272:TYR:CE1	2.88	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:284:ARG:NH1	1:BM:284:ARG:HG2	2.15	0.61
1:CG:14:CYS:H	1:CG:138:ASN:HD21	1.48	0.61
1:CN:189:PHE:CE1	1:CN:198:ARG:CG	2.79	0.61
1:CS:454:ASN:HD22	1:CS:456:ALA:N	1.98	0.61
1:AE:74:ASN:CB	1:AE:126:GLU:HG2	2.31	0.61
1:AI:189:PHE:HE2	1:AI:249:LEU:CD2	2.14	0.61
1:AJ:284:ARG:HH11	1:AJ:284:ARG:HG2	1.65	0.61
1:AJ:203:THR:HB	1:AJ:300:GLN:HG3	1.82	0.61
1:AQ:250:TRP:CZ3	1:AQ:272:TYR:HE1	2.17	0.61
1:BB:189:PHE:HE2	1:BB:249:LEU:CD2	2.13	0.61
1:BC:272:TYR:CE2	1:CA:55:ARG:CD	2.84	0.61
1:BE:272:TYR:HE2	1:BM:55:ARG:CD	2.13	0.61
1:BE:74:ASN:CB	1:BE:126:GLU:HG2	2.30	0.61
1:CC:36:GLN:NE2	1:CC:156:LEU:H	1.98	0.61
1:AM:454:ASN:ND2	1:AM:456:ALA:H	1.96	0.61
1:BO:14:CYS:H	1:BO:138:ASN:HD21	1.48	0.61
1:CN:189:PHE:HE2	1:CN:249:LEU:CD2	2.12	0.61
1:CP:74:ASN:CB	1:CP:126:GLU:HG2	2.30	0.61
1:CR:284:ARG:HH11	1:CR:284:ARG:HG2	1.64	0.61
1:AC:36:GLN:NE2	1:AC:156:LEU:H	1.98	0.61
1:AO:67:VAL:HG23	1:AO:135:LEU:HB2	1.83	0.61
1:BI:250:TRP:CZ3	1:BI:272:TYR:HE1	2.16	0.61
1:CD:189:PHE:CE1	1:CD:198:ARG:HG3	2.36	0.61
1:AB:250:TRP:CE3	1:AB:272:TYR:CE1	2.89	0.61
1:BQ:74:ASN:ND2	1:BQ:77:THR:OG1	2.34	0.61
1:CM:74:ASN:CB	1:CM:126:GLU:HG2	2.31	0.61
1:AA:55:ARG:CZ	1:CC:272:TYR:CD2	2.84	0.60
1:BJ:189:PHE:HE2	1:BJ:249:LEU:CD2	2.14	0.60
1:BT:36:GLN:NE2	1:BT:156:LEU:H	1.99	0.60
1:BA:36:GLN:NE2	1:BA:156:LEU:H	1.99	0.60
1:BD:189:PHE:CE1	1:BD:198:ARG:HG3	2.34	0.60
1:BF:14:CYS:H	1:BF:138:ASN:HD21	1.47	0.60
1:BN:191:LEU:CD2	1:BN:191:LEU:H	2.10	0.60
1:CB:284:ARG:HG2	1:CB:284:ARG:NH1	2.16	0.60
1:CE:189:PHE:HE2	1:CE:249:LEU:CD2	2.13	0.60
1:CE:284:ARG:HH11	1:CE:284:ARG:HG2	1.66	0.60
1:CJ:284:ARG:HG2	1:CJ:284:ARG:HH11	1.66	0.60
1:AP:189:PHE:HE1	1:AP:198:ARG:HG3	1.66	0.60
1:AB:55:ARG:HD3	1:BB:272:TYR:CD2	2.35	0.60
1:BE:272:TYR:CE2	1:BM:55:ARG:HD3	2.35	0.60
1:BH:284:ARG:HG2	1:BH:284:ARG:NH1	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:74:ASN:CB	1:BH:126:GLU:HG2	2.31	0.60
1:CC:284:ARG:HG2	1:CC:284:ARG:NH1	2.12	0.60
1:CN:284:ARG:NH1	1:CN:284:ARG:HG2	2.15	0.60
1:CC:55:ARG:CD	1:CT:272:TYR:HE2	2.13	0.60
1:AD:272:TYR:CE2	1:AS:55:ARG:CD	2.85	0.60
1:BG:74:ASN:CB	1:BG:126:GLU:HG2	2.31	0.60
1:AF:55:ARG:CD	1:BH:272:TYR:HE2	2.13	0.60
1:AJ:55:ARG:HD3	1:BL:272:TYR:CD2	2.37	0.60
1:BO:74:ASN:CB	1:BO:126:GLU:HG2	2.31	0.60
1:BP:272:TYR:HE2	1:CE:55:ARG:CD	2.14	0.60
1:AM:272:TYR:HE2	1:CP:55:ARG:CD	2.14	0.60
1:CS:14:CYS:H	1:CS:138:ASN:HD21	1.49	0.60
1:AH:398:GLY:HA3	1:AH:494:PHE:CD2	2.37	0.60
1:AH:74:ASN:ND2	1:AH:77:THR:OG1	2.34	0.60
1:AO:272:TYR:CE2	1:AR:55:ARG:HD3	2.37	0.60
1:BG:189:PHE:HE2	1:BG:249:LEU:CD2	2.14	0.60
1:BC:272:TYR:HE2	1:CA:55:ARG:CD	2.14	0.60
1:AH:272:TYR:CD2	1:CF:55:ARG:HD3	2.36	0.60
1:CD:55:ARG:CD	1:CN:272:TYR:HE2	2.14	0.60
1:CQ:74:ASN:CB	1:CQ:126:GLU:HG2	2.31	0.60
1:AD:74:ASN:CB	1:AD:126:GLU:HG2	2.31	0.60
1:CM:284:ARG:NH1	1:CM:284:ARG:HG2	2.15	0.60
1:AB:189:PHE:CE1	1:AB:198:ARG:CG	2.81	0.60
1:AQ:74:ASN:CB	1:AQ:126:GLU:HG2	2.31	0.60
1:BE:272:TYR:CD2	1:BM:55:ARG:HD3	2.37	0.60
1:BO:16:ALA:O	1:BO:17:ASN:HB2	2.00	0.60
1:BT:250:TRP:CE3	1:BT:272:TYR:CE1	2.90	0.60
1:AF:189:PHE:CE1	1:AF:198:ARG:CG	2.82	0.60
1:AG:55:ARG:NE	1:CG:272:TYR:HE2	1.99	0.60
1:AS:284:ARG:NH1	1:AS:284:ARG:HG2	2.15	0.60
1:BF:189:PHE:CE1	1:BF:198:ARG:HG3	2.36	0.60
1:BF:272:TYR:HE2	1:CK:55:ARG:CD	2.14	0.60
1:CD:55:ARG:CD	1:CN:272:TYR:CE2	2.85	0.60
1:CL:284:ARG:NH1	1:CL:284:ARG:HG2	2.14	0.60
1:CL:74:ASN:CB	1:CL:126:GLU:HG2	2.32	0.60
1:CI:272:TYR:CD2	1:CO:55:ARG:HD3	2.36	0.60
1:AJ:191:LEU:N	1:AJ:191:LEU:HD23	2.12	0.60
1:AN:454:ASN:HD22	1:AN:456:ALA:N	2.00	0.60
1:AS:74:ASN:CB	1:AS:126:GLU:HG2	2.31	0.60
1:BR:74:ASN:CB	1:BR:126:GLU:HG2	2.31	0.60
1:CM:454:ASN:HD22	1:CM:456:ALA:N	1.99	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:14:CYS:H	1:AG:138:ASN:HD21	1.49	0.60
1:AK:284:ARG:NH1	1:AK:284:ARG:HG2	2.17	0.60
1:AC:272:TYR:CD2	1:BA:55:ARG:HD3	2.37	0.60
1:BR:284:ARG:HG2	1:BR:284:ARG:NH1	2.16	0.60
1:AF:79:ARG:HH11	1:AF:79:ARG:CG	2.10	0.59
1:AI:189:PHE:CE1	1:AI:198:ARG:CG	2.79	0.59
1:AO:454:ASN:HD22	1:AO:456:ALA:N	2.00	0.59
1:AT:74:ASN:CB	1:AT:126:GLU:HG2	2.31	0.59
1:BC:454:ASN:HD22	1:BC:456:ALA:N	2.00	0.59
1:BR:189:PHE:CE1	1:BR:198:ARG:CG	2.84	0.59
1:BI:55:ARG:HD3	1:BR:272:TYR:CE2	2.37	0.59
1:CE:74:ASN:ND2	1:CE:77:THR:OG1	2.35	0.59
1:CF:74:ASN:CB	1:CF:126:GLU:HG2	2.31	0.59
1:CG:36:GLN:NE2	1:CG:156:LEU:H	1.99	0.59
1:CQ:454:ASN:HD22	1:CQ:456:ALA:N	1.99	0.59
1:AB:189:PHE:HE2	1:AB:249:LEU:CD2	2.14	0.59
1:AL:284:ARG:HG2	1:AL:284:ARG:NH1	2.16	0.59
1:AL:74:ASN:CB	1:AL:126:GLU:HG2	2.32	0.59
1:BE:284:ARG:NH1	1:BE:284:ARG:HG2	2.17	0.59
1:AA:55:ARG:HD3	1:CC:272:TYR:CD2	2.38	0.59
1:CE:272:TYR:CE2	1:CM:55:ARG:HD3	2.37	0.59
1:CE:74:ASN:CB	1:CE:126:GLU:HG2	2.32	0.59
1:CF:189:PHE:HE2	1:CF:249:LEU:CD2	2.15	0.59
1:CK:284:ARG:HG2	1:CK:284:ARG:NH1	2.15	0.59
1:CQ:189:PHE:CE1	1:CQ:198:ARG:HG3	2.37	0.59
1:CQ:284:ARG:HG2	1:CQ:284:ARG:NH1	2.17	0.59
1:CT:74:ASN:CB	1:CT:126:GLU:HG2	2.31	0.59
1:AA:454:ASN:HD22	1:AA:456:ALA:N	1.99	0.59
1:AB:16:ALA:O	1:AB:17:ASN:HB2	2.02	0.59
1:AG:74:ASN:CB	1:AG:126:GLU:HG2	2.32	0.59
1:BG:284:ARG:HG2	1:BG:284:ARG:NH1	2.15	0.59
1:BI:454:ASN:HD22	1:BI:456:ALA:N	1.99	0.59
1:BL:189:PHE:HE1	1:BL:198:ARG:CG	2.14	0.59
1:CA:284:ARG:NH1	1:CA:284:ARG:HG2	2.15	0.59
1:AG:189:PHE:CE1	1:AG:198:ARG:CG	2.81	0.59
1:AO:284:ARG:NH1	1:AO:284:ARG:HG2	2.15	0.59
1:BB:454:ASN:HD22	1:BB:456:ALA:N	1.99	0.59
1:BE:250:TRP:CZ3	1:BE:272:TYR:HE1	2.18	0.59
1:BH:398:GLY:HA3	1:BH:494:PHE:CD2	2.36	0.59
1:BH:55:ARG:HD3	1:BK:272:TYR:CE2	2.38	0.59
1:BH:79:ARG:HG3	1:BH:79:ARG:HH11	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:74:ASN:CB	1:BK:126:GLU:HG2	2.32	0.59
1:BR:16:ALA:O	1:BR:17:ASN:HB2	2.02	0.59
1:CI:189:PHE:CE1	1:CI:198:ARG:CG	2.83	0.59
1:AA:272:TYR:CE2	1:CT:55:ARG:HD3	2.37	0.59
1:AE:203:THR:HB	1:AE:300:GLN:HG3	1.83	0.59
1:AG:55:ARG:CD	1:CG:272:TYR:CE2	2.86	0.59
1:AP:79:ARG:HH11	1:AP:79:ARG:HG3	1.66	0.59
1:BK:189:PHE:HE1	1:BK:198:ARG:CG	2.15	0.59
1:BK:284:ARG:NH1	1:BK:284:ARG:HG2	2.15	0.59
1:BM:239:ILE:HG12	1:BM:326:ILE:CD1	2.32	0.59
1:CD:454:ASN:HD22	1:CD:456:ALA:N	1.98	0.59
1:CD:74:ASN:CB	1:CD:126:GLU:HG2	2.32	0.59
1:CN:454:ASN:HD22	1:CN:456:ALA:N	2.00	0.59
1:CN:74:ASN:CB	1:CN:126:GLU:HG2	2.32	0.59
1:CR:189:PHE:HE2	1:CR:249:LEU:CD2	2.15	0.59
1:AD:55:ARG:HD3	1:AN:272:TYR:CE2	2.37	0.59
1:AJ:189:PHE:HE2	1:AJ:249:LEU:CD2	2.15	0.59
1:BI:284:ARG:NH1	1:BI:284:ARG:HG2	2.15	0.59
1:BK:14:CYS:H	1:BK:138:ASN:HD21	1.49	0.59
1:AJ:55:ARG:CD	1:BL:272:TYR:HE2	2.13	0.59
1:BQ:67:VAL:HG23	1:BQ:135:LEU:HB2	1.84	0.59
1:CF:250:TRP:CE3	1:CF:272:TYR:CE1	2.91	0.59
1:AJ:189:PHE:CE1	1:AJ:198:ARG:CG	2.79	0.59
1:AT:74:ASN:ND2	1:AT:77:THR:OG1	2.35	0.59
1:BC:239:ILE:HG12	1:BC:326:ILE:CD1	2.33	0.59
1:CF:250:TRP:HZ3	1:CF:272:TYR:CE1	2.20	0.59
1:CP:284:ARG:HH11	1:CP:284:ARG:HG2	1.66	0.59
1:AB:272:TYR:CE2	1:CB:55:ARG:HD3	2.38	0.59
1:AC:74:ASN:CB	1:AC:126:GLU:HG2	2.32	0.59
1:AF:284:ARG:HG2	1:AF:284:ARG:NH1	2.17	0.59
1:AJ:74:ASN:CB	1:AJ:126:GLU:HG2	2.32	0.59
1:AP:284:ARG:NH1	1:AP:284:ARG:HG2	2.17	0.59
1:BA:284:ARG:HG2	1:BA:284:ARG:NH1	2.15	0.59
1:BL:250:TRP:CZ3	1:BL:272:TYR:HE1	2.20	0.59
1:BN:16:ALA:O	1:BN:17:ASN:HB2	2.01	0.59
1:BQ:189:PHE:HE1	1:BQ:198:ARG:CG	2.13	0.59
1:BT:189:PHE:CE1	1:BT:198:ARG:HG3	2.36	0.59
1:CC:74:ASN:CB	1:CC:126:GLU:HG2	2.32	0.59
1:BJ:55:ARG:HD3	1:CL:272:TYR:CD2	2.38	0.59
1:AA:398:GLY:HA3	1:AA:494:PHE:CD2	2.38	0.59
1:AE:189:PHE:HE2	1:AE:249:LEU:CD2	2.14	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:284:ARG:HG2	1:AE:284:ARG:HH11	1.66	0.59
1:BS:250:TRP:CZ3	1:BS:272:TYR:HE1	2.19	0.59
1:CO:74:ASN:CB	1:CO:126:GLU:HG2	2.31	0.59
1:CS:288:HIS:HD2	1:CS:337:ASP:OD2	1.86	0.59
1:AC:250:TRP:CE3	1:AC:272:TYR:CE1	2.90	0.59
1:AH:189:PHE:HE2	1:AH:249:LEU:CD2	2.15	0.59
1:BF:74:ASN:CB	1:BF:126:GLU:HG2	2.33	0.59
1:BM:454:ASN:HD22	1:BM:456:ALA:N	2.00	0.59
1:AD:272:TYR:HE2	1:AS:55:ARG:CD	2.16	0.58
1:BD:55:ARG:CD	1:BN:272:TYR:CE2	2.86	0.58
1:BI:189:PHE:CE1	1:BI:198:ARG:CG	2.83	0.58
1:BM:189:PHE:CE1	1:BM:198:ARG:CG	2.82	0.58
1:BJ:55:ARG:HD3	1:CL:272:TYR:CE2	2.38	0.58
1:AL:55:ARG:HD3	1:CQ:272:TYR:CD2	2.37	0.58
1:AP:189:PHE:CE1	1:AP:198:ARG:HG3	2.38	0.58
1:BP:272:TYR:CE2	1:CE:55:ARG:CD	2.86	0.58
1:CG:250:TRP:CE3	1:CG:272:TYR:CE1	2.92	0.58
1:BF:272:TYR:CE2	1:CK:55:ARG:HD3	2.38	0.58
1:AO:239:ILE:HG12	1:AO:326:ILE:CD1	2.33	0.58
1:AJ:272:TYR:CE2	1:AQ:55:ARG:NE	2.71	0.58
1:AR:250:TRP:CE3	1:AR:272:TYR:CE1	2.91	0.58
1:BD:284:ARG:HG2	1:BD:284:ARG:NH1	2.18	0.58
1:AP:272:TYR:CE2	1:BE:55:ARG:CD	2.87	0.58
1:BG:16:ALA:O	1:BG:17:ASN:HB2	2.03	0.58
1:BI:74:ASN:CB	1:BI:126:GLU:HG2	2.32	0.58
1:CF:79:ARG:HG3	1:CF:79:ARG:NH1	2.00	0.58
1:CI:79:ARG:HH11	1:CI:79:ARG:HG3	1.68	0.58
1:AC:454:ASN:HD22	1:AC:456:ALA:N	2.00	0.58
1:AI:74:ASN:CB	1:AI:126:GLU:HG2	2.33	0.58
1:AE:272:TYR:CD2	1:AM:55:ARG:HD3	2.39	0.58
1:AQ:272:TYR:HE2	1:BL:55:ARG:CD	2.17	0.58
1:AQ:284:ARG:HH11	1:AQ:284:ARG:HG2	1.68	0.58
1:BA:189:PHE:CE1	1:BA:198:ARG:CG	2.86	0.58
1:BA:189:PHE:HE2	1:BA:249:LEU:HD21	1.67	0.58
1:BH:189:PHE:HE2	1:BH:249:LEU:CD2	2.16	0.58
1:BN:189:PHE:HE2	1:BN:249:LEU:CD2	2.16	0.58
1:BP:189:PHE:HE1	1:BP:198:ARG:CG	2.16	0.58
1:AA:74:ASN:ND2	1:AA:77:THR:OG1	2.36	0.58
1:AH:14:CYS:H	1:AH:138:ASN:HD21	1.50	0.58
1:BB:74:ASN:CB	1:BB:126:GLU:HG2	2.34	0.58
1:BJ:74:ASN:CB	1:BJ:126:GLU:HG2	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:43:ALA:HB1	1:BQ:158:GLU:HA	1.86	0.58
1:BS:189:PHE:HE1	1:BS:198:ARG:CG	2.16	0.58
1:CO:272:TYR:CE2	1:CR:55:ARG:HD3	2.38	0.58
1:AA:74:ASN:CB	1:AA:126:GLU:HG2	2.34	0.58
1:AB:272:TYR:CD2	1:CB:55:ARG:HD3	2.39	0.58
1:AB:284:ARG:NH1	1:AB:284:ARG:HG2	2.13	0.58
1:AP:74:ASN:CB	1:AP:126:GLU:HG2	2.34	0.58
1:BF:272:TYR:CD2	1:CK:55:ARG:HD3	2.39	0.58
1:BF:454:ASN:HD22	1:BF:456:ALA:N	2.00	0.58
1:BS:454:ASN:HD22	1:BS:456:ALA:N	2.01	0.58
1:CK:74:ASN:CB	1:CK:126:GLU:HG2	2.32	0.58
1:AA:189:PHE:CE1	1:AA:198:ARG:CG	2.87	0.58
1:AA:284:ARG:NH1	1:AA:284:ARG:HG2	2.15	0.58
1:AA:67:VAL:HG23	1:AA:135:LEU:HB2	1.85	0.58
1:AD:189:PHE:HE1	1:AD:198:ARG:CG	2.15	0.58
1:AF:203:THR:HB	1:AF:300:GLN:HG3	1.85	0.58
1:AP:58:ALA:HB2	1:AP:102:GLY:HA3	1.84	0.58
1:AR:454:ASN:HD22	1:AR:456:ALA:N	2.01	0.58
1:BC:284:ARG:NH1	1:BC:284:ARG:HG2	2.16	0.58
1:BC:55:ARG:HD3	1:BT:272:TYR:CE2	2.37	0.58
1:BO:398:GLY:HA3	1:BO:494:PHE:CD2	2.37	0.58
1:BS:14:CYS:H	1:BS:138:ASN:HD21	1.52	0.58
1:BT:55:ARG:CD	1:CA:272:TYR:CE2	2.86	0.58
1:CM:36:GLN:NE2	1:CM:156:LEU:H	2.02	0.58
1:CN:250:TRP:CE3	1:CN:272:TYR:CE1	2.91	0.58
1:AD:189:PHE:HE2	1:AD:249:LEU:CD2	2.17	0.58
1:AH:284:ARG:HG2	1:AH:284:ARG:NH1	2.17	0.58
1:AN:442:GLN:HE21	1:AO:412:PHE:HB2	1.68	0.58
1:AP:55:ARG:HD3	1:BM:272:TYR:CE2	2.39	0.58
1:BF:189:PHE:CE1	1:BF:198:ARG:CG	2.81	0.58
1:BN:454:ASN:HD22	1:BN:456:ALA:N	2.02	0.58
1:BN:67:VAL:HG23	1:BN:135:LEU:HB2	1.86	0.58
1:BP:55:ARG:HD3	1:CM:272:TYR:CD2	2.39	0.58
1:CI:454:ASN:HD22	1:CI:456:ALA:N	2.02	0.58
1:CM:250:TRP:CE3	1:CM:272:TYR:CE1	2.91	0.58
1:CR:36:GLN:NE2	1:CR:156:LEU:H	2.02	0.58
1:CS:74:ASN:CB	1:CS:126:GLU:HG2	2.32	0.58
1:AC:189:PHE:CE1	1:AC:198:ARG:HG3	2.39	0.58
1:AE:454:ASN:HD22	1:AE:456:ALA:N	2.01	0.58
1:AF:55:ARG:HD3	1:BH:272:TYR:CD2	2.39	0.58
1:AO:162:PHE:CD2	1:AO:163:LEU:HD13	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:74:ASN:ND2	1:AP:77:THR:OG1	2.37	0.58
1:AP:272:TYR:HE2	1:BE:55:ARG:CD	2.16	0.58
1:BP:284:ARG:HG2	1:BP:284:ARG:NH1	2.17	0.58
1:BD:272:TYR:HE2	1:BS:55:ARG:NE	2.02	0.58
1:CF:454:ASN:ND2	1:CF:456:ALA:H	2.00	0.58
1:CI:272:TYR:CE2	1:CO:55:ARG:HD3	2.39	0.58
1:CS:36:GLN:NE2	1:CS:156:LEU:H	2.01	0.58
1:AD:284:ARG:HG2	1:AD:284:ARG:NH1	2.14	0.58
1:AN:250:TRP:CE3	1:AN:272:TYR:CE1	2.92	0.58
1:AT:189:PHE:HE1	1:AT:198:ARG:CG	2.16	0.58
1:BA:189:PHE:HE2	1:BA:249:LEU:CD2	2.16	0.58
1:AG:272:TYR:CE2	1:BG:55:ARG:CD	2.87	0.58
1:BH:454:ASN:HD22	1:BH:456:ALA:N	2.02	0.58
1:AJ:55:ARG:HD3	1:BL:272:TYR:CE2	2.39	0.58
1:BL:284:ARG:HG2	1:BL:284:ARG:NH1	2.19	0.58
1:BM:250:TRP:HZ3	1:BM:272:TYR:CE1	2.20	0.58
1:CK:454:ASN:HD22	1:CK:456:ALA:N	1.98	0.58
1:CQ:250:TRP:HZ3	1:CQ:272:TYR:CE1	2.19	0.58
1:AM:398:GLY:HA3	1:AM:494:PHE:CD2	2.39	0.57
1:BA:250:TRP:HZ3	1:BA:272:TYR:CE1	2.22	0.57
1:BG:11:PRO:HG2	1:BG:18:ARG:HD2	1.85	0.57
1:BP:36:GLN:NE2	1:BP:156:LEU:H	2.02	0.57
1:BP:454:ASN:HD22	1:BP:456:ALA:N	1.99	0.57
1:BQ:272:TYR:CE2	1:CL:55:ARG:HD3	2.37	0.57
1:BQ:288:HIS:HD2	1:BQ:337:ASP:OD2	1.87	0.57
1:CG:454:ASN:HD22	1:CG:456:ALA:N	2.01	0.57
1:CH:79:ARG:HG3	1:CH:79:ARG:NH1	2.17	0.57
1:CJ:272:TYR:CD2	1:CQ:55:ARG:HD3	2.39	0.57
1:AH:272:TYR:HE2	1:CF:55:ARG:CD	2.18	0.57
1:AR:74:ASN:CB	1:AR:126:GLU:HG2	2.34	0.57
1:AT:189:PHE:CE1	1:AT:198:ARG:CG	2.87	0.57
1:BK:454:ASN:HD22	1:BK:456:ALA:N	1.99	0.57
1:BP:454:ASN:ND2	1:BP:456:ALA:H	2.00	0.57
1:BT:284:ARG:HG2	1:BT:284:ARG:NH1	2.18	0.57
1:CA:43:ALA:HB1	1:CA:158:GLU:HA	1.86	0.57
1:CG:284:ARG:NH1	1:CG:284:ARG:HG2	2.17	0.57
1:AJ:14:CYS:H	1:AJ:138:ASN:HD21	1.51	0.57
1:AN:284:ARG:HG2	1:AN:284:ARG:NH1	2.18	0.57
1:AN:55:ARG:CZ	1:AS:272:TYR:CD2	2.87	0.57
1:BB:454:ASN:ND2	1:BB:456:ALA:H	2.00	0.57
1:BO:15:GLN:HA	1:BO:15:GLN:NE2	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:189:PHE:CE1	1:BP:198:ARG:CG	2.88	0.57
1:CC:191:LEU:HD23	1:CC:191:LEU:N	2.16	0.57
1:AH:16:ALA:O	1:AH:17:ASN:HB2	2.04	0.57
1:BD:14:CYS:H	1:BD:138:ASN:HD21	1.50	0.57
1:BK:288:HIS:HD2	1:BK:337:ASP:OD2	1.86	0.57
1:BS:284:ARG:HG2	1:BS:284:ARG:NH1	2.19	0.57
1:CH:43:ALA:HB1	1:CH:158:GLU:HA	1.86	0.57
1:BL:189:PHE:CE1	1:BL:198:ARG:CG	2.87	0.57
1:BN:74:ASN:CB	1:BN:126:GLU:HG2	2.34	0.57
1:BO:189:PHE:CE1	1:BO:198:ARG:HG3	2.39	0.57
1:CK:74:ASN:ND2	1:CK:77:THR:OG1	2.38	0.57
1:BP:55:ARG:HD3	1:CM:272:TYR:CE2	2.39	0.57
1:AB:288:HIS:HD2	1:AB:337:ASP:OD2	1.86	0.57
1:AC:191:LEU:HD23	1:AC:191:LEU:N	2.15	0.57
1:AH:55:ARG:CD	1:AK:272:TYR:HE2	2.17	0.57
1:AT:284:ARG:NH1	1:AT:284:ARG:HG2	2.16	0.57
1:BC:14:CYS:H	1:BC:138:ASN:HD21	1.52	0.57
1:BL:250:TRP:HZ3	1:BL:272:TYR:CE1	2.22	0.57
1:BD:55:ARG:CD	1:BN:272:TYR:HE2	2.17	0.57
1:CO:14:CYS:H	1:CO:138:ASN:HD21	1.53	0.57
1:AM:272:TYR:CD2	1:CP:55:ARG:HD3	2.40	0.57
1:CS:284:ARG:HG2	1:CS:284:ARG:NH1	2.18	0.57
1:AL:272:TYR:CE2	1:CJ:55:ARG:HD3	2.40	0.57
1:BA:250:TRP:CE3	1:BA:272:TYR:CE1	2.93	0.57
1:BF:189:PHE:HE2	1:BF:249:LEU:CD2	2.17	0.57
1:BI:272:TYR:CE2	1:BO:55:ARG:HD3	2.40	0.57
1:BQ:14:CYS:H	1:BQ:138:ASN:HD21	1.53	0.57
1:BS:189:PHE:CE1	1:BS:198:ARG:CG	2.88	0.57
1:CB:189:PHE:HE2	1:CB:249:LEU:CD2	2.17	0.57
1:CL:189:PHE:CE1	1:CL:198:ARG:CG	2.88	0.57
1:CS:250:TRP:CE3	1:CS:272:TYR:CE1	2.93	0.57
1:AF:272:TYR:CE2	1:BK:55:ARG:HD3	2.40	0.57
1:AG:250:TRP:HZ3	1:AG:272:TYR:CE1	2.21	0.57
1:AN:239:ILE:HG12	1:AN:326:ILE:CD1	2.34	0.57
1:BK:189:PHE:HE2	1:BK:249:LEU:CD2	2.18	0.57
1:CR:14:CYS:H	1:CR:138:ASN:HD21	1.50	0.57
1:CR:189:PHE:HE1	1:CR:198:ARG:HG2	1.67	0.57
1:AB:14:CYS:H	1:AB:138:ASN:HD21	1.52	0.57
1:AN:14:CYS:H	1:AN:138:ASN:HD21	1.53	0.57
1:AQ:189:PHE:HE2	1:AQ:249:LEU:CD2	2.17	0.57
1:AS:398:GLY:HA3	1:AS:494:PHE:CD2	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:250:TRP:HZ3	1:BI:272:TYR:CE1	2.23	0.57
1:CC:250:TRP:CE3	1:CC:272:TYR:CD1	2.92	0.57
1:CF:284:ARG:NH1	1:CF:284:ARG:HG2	2.19	0.57
1:CH:284:ARG:HG2	1:CH:284:ARG:NH1	2.16	0.57
1:CM:14:CYS:H	1:CM:138:ASN:HD21	1.51	0.57
1:AH:189:PHE:CE1	1:AH:198:ARG:CG	2.81	0.57
1:AG:272:TYR:HE2	1:BG:55:ARG:CD	2.17	0.57
1:BK:454:ASN:ND2	1:BK:456:ALA:H	2.02	0.57
1:BP:74:ASN:CB	1:BP:126:GLU:HG2	2.35	0.57
1:BR:454:ASN:ND2	1:BR:456:ALA:H	2.03	0.57
1:CJ:18:ARG:HD2	1:CJ:19:TYR:O	2.05	0.57
1:CM:239:ILE:HG12	1:CM:326:ILE:CD1	2.35	0.57
1:CP:79:ARG:CG	1:CP:79:ARG:HH11	2.16	0.57
1:BB:250:TRP:CE3	1:BB:272:TYR:CE1	2.92	0.56
1:BT:288:HIS:HD2	1:BT:337:ASP:OD2	1.88	0.56
1:CJ:454:ASN:HD22	1:CJ:456:ALA:N	2.00	0.56
1:AB:55:ARG:HD3	1:BB:272:TYR:CE2	2.40	0.56
1:AH:250:TRP:CE3	1:AH:272:TYR:CE1	2.93	0.56
1:AJ:79:ARG:HG3	1:AJ:79:ARG:NH1	2.20	0.56
1:AQ:189:PHE:CE1	1:AQ:198:ARG:HG3	2.39	0.56
1:BA:14:CYS:H	1:BA:138:ASN:ND2	2.03	0.56
1:BB:191:LEU:N	1:BB:191:LEU:HD23	2.17	0.56
1:BE:74:ASN:ND2	1:BE:77:THR:OG1	2.38	0.56
1:BF:55:ARG:HD3	1:CH:272:TYR:CD2	2.40	0.56
1:BH:250:TRP:HZ3	1:BH:272:TYR:CE1	2.22	0.56
1:BM:14:CYS:H	1:BM:138:ASN:HD21	1.53	0.56
1:CF:239:ILE:HG12	1:CF:326:ILE:CD1	2.35	0.56
1:AH:75:ARG:NH2	1:AH:391:ALA:O	2.37	0.56
1:AI:454:ASN:HD22	1:AI:456:ALA:N	2.03	0.56
1:BA:454:ASN:HD22	1:BA:456:ALA:N	2.01	0.56
1:BM:36:GLN:NE2	1:BM:156:LEU:H	2.02	0.56
1:CE:272:TYR:CD2	1:CM:55:ARG:HD3	2.40	0.56
1:CF:36:GLN:NE2	1:CF:156:LEU:H	2.03	0.56
1:CG:250:TRP:HZ3	1:CG:272:TYR:CE1	2.23	0.56
1:CI:250:TRP:HZ3	1:CI:272:TYR:CE1	2.22	0.56
1:CO:284:ARG:HG2	1:CO:284:ARG:NH1	2.15	0.56
1:CT:14:CYS:H	1:CT:138:ASN:ND2	2.04	0.56
1:AF:79:ARG:NH1	1:AF:79:ARG:HG3	2.17	0.56
1:AH:55:ARG:CD	1:AK:272:TYR:CE2	2.88	0.56
1:AR:10:ILE:HG21	1:AR:146:TRP:CZ2	2.41	0.56
1:BJ:79:ARG:HG3	1:BJ:79:ARG:NH1	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:189:PHE:CE1	1:BN:198:ARG:HG2	2.41	0.56
1:CO:239:ILE:HG12	1:CO:326:ILE:CD1	2.34	0.56
1:AJ:272:TYR:CE2	1:AQ:55:ARG:CD	2.88	0.56
1:BE:454:ASN:HD22	1:BE:456:ALA:N	2.02	0.56
1:CS:398:GLY:HA3	1:CS:494:PHE:CD2	2.40	0.56
1:AA:189:PHE:HE2	1:AA:249:LEU:CD2	2.18	0.56
1:AQ:288:HIS:HD2	1:AQ:337:ASP:OD2	1.88	0.56
1:AT:454:ASN:HD22	1:AT:456:ALA:N	2.02	0.56
1:BM:398:GLY:HA3	1:BM:494:PHE:CD2	2.40	0.56
1:BN:284:ARG:HG2	1:BN:284:ARG:NH1	2.17	0.56
1:BR:189:PHE:HE2	1:BR:249:LEU:CD2	2.18	0.56
1:BS:58:ALA:HB2	1:BS:102:GLY:HA3	1.88	0.56
1:CM:250:TRP:HZ3	1:CM:272:TYR:CE1	2.18	0.56
1:CO:36:GLN:NE2	1:CO:156:LEU:H	2.03	0.56
1:AN:250:TRP:HZ3	1:AN:272:TYR:CE1	2.24	0.56
1:AC:55:ARG:HD3	1:AT:272:TYR:CD2	2.41	0.56
1:BH:15:GLN:NE2	1:BH:15:GLN:HA	2.15	0.56
1:BM:67:VAL:HG23	1:BM:135:LEU:HB2	1.88	0.56
1:BO:272:TYR:CD2	1:BR:55:ARG:CZ	2.88	0.56
1:BQ:189:PHE:CE1	1:BQ:198:ARG:CG	2.88	0.56
1:BR:454:ASN:HD22	1:BR:456:ALA:N	2.01	0.56
1:BT:189:PHE:HE1	1:BT:198:ARG:CG	2.18	0.56
1:BT:454:ASN:HD22	1:BT:456:ALA:N	2.01	0.56
1:CF:18:ARG:HG3	1:CF:19:TYR:N	2.19	0.56
1:CH:250:TRP:CE3	1:CH:272:TYR:CE1	2.93	0.56
1:CJ:189:PHE:HE2	1:CJ:249:LEU:CD2	2.19	0.56
1:CP:284:ARG:HG2	1:CP:284:ARG:NH1	2.20	0.56
1:AD:272:TYR:CD2	1:AS:55:ARG:HD3	2.41	0.56
1:AD:398:GLY:HA3	1:AD:494:PHE:CD2	2.40	0.56
1:AE:189:PHE:CE1	1:AE:198:ARG:CG	2.83	0.56
1:AE:250:TRP:CE3	1:AE:272:TYR:CE1	2.94	0.56
1:AP:250:TRP:CE3	1:AP:272:TYR:CE1	2.93	0.56
1:AQ:189:PHE:HE2	1:AQ:249:LEU:HD21	1.71	0.56
1:BJ:284:ARG:HG2	1:BJ:284:ARG:NH1	2.18	0.56
1:BK:398:GLY:HA3	1:BK:494:PHE:CD2	2.40	0.56
1:CH:191:LEU:N	1:CH:191:LEU:HD23	2.18	0.56
1:AM:74:ASN:CB	1:AM:126:GLU:HG2	2.35	0.56
1:CE:284:ARG:NH1	1:CE:284:ARG:HG2	2.21	0.56
1:CG:398:GLY:HA3	1:CG:494:PHE:CD2	2.41	0.56
1:CH:454:ASN:HD22	1:CH:456:ALA:N	2.02	0.56
1:CK:9:TYR:HE1	1:CK:147:GLN:HE21	1.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:284:ARG:HG2	1:AE:284:ARG:NH1	2.20	0.56
1:AL:288:HIS:HD2	1:AL:337:ASP:OD2	1.89	0.56
1:AM:288:HIS:HD2	1:AM:337:ASP:OD2	1.88	0.56
1:AT:288:HIS:HD2	1:AT:337:ASP:OD2	1.88	0.56
1:BD:67:VAL:HG23	1:BD:135:LEU:HB2	1.88	0.56
1:BF:74:ASN:ND2	1:BF:77:THR:OG1	2.38	0.56
1:BI:398:GLY:HA3	1:BI:494:PHE:CD2	2.41	0.56
1:BN:250:TRP:HZ3	1:BN:272:TYR:CE1	2.24	0.56
1:BS:79:ARG:HG3	1:BS:79:ARG:NH1	2.10	0.56
1:BT:55:ARG:CD	1:CA:272:TYR:HE2	2.19	0.56
1:CH:288:HIS:HD2	1:CH:337:ASP:OD2	1.88	0.56
1:CR:284:ARG:NH1	1:CR:284:ARG:HG2	2.20	0.56
1:CT:189:PHE:HE2	1:CT:249:LEU:CD2	2.19	0.56
1:AD:67:VAL:HG23	1:AD:135:LEU:HB2	1.88	0.56
1:AH:288:HIS:HD2	1:AH:337:ASP:OD2	1.88	0.56
1:AP:55:ARG:HD3	1:BM:272:TYR:CD2	2.41	0.56
1:BJ:18:ARG:HD2	1:BJ:19:TYR:O	2.06	0.56
1:CJ:272:TYR:CE2	1:CQ:55:ARG:CZ	2.89	0.56
1:CR:74:ASN:CB	1:CR:126:GLU:HG2	2.35	0.56
1:AN:79:ARG:HH11	1:AN:79:ARG:CG	2.11	0.55
1:AO:189:PHE:CE1	1:AO:198:ARG:HG3	2.40	0.55
1:BJ:454:ASN:HD22	1:BJ:456:ALA:N	2.02	0.55
1:BK:189:PHE:CE1	1:BK:198:ARG:CG	2.89	0.55
1:BK:250:TRP:CE3	1:BK:272:TYR:CE1	2.94	0.55
1:CC:55:ARG:HD3	1:CT:272:TYR:CD2	2.40	0.55
1:CL:454:ASN:HD22	1:CL:456:ALA:N	2.01	0.55
1:AL:272:TYR:CD2	1:CJ:55:ARG:HD3	2.42	0.55
1:AM:272:TYR:CE2	1:CP:55:ARG:HD3	2.40	0.55
1:AR:58:ALA:HB2	1:AR:102:GLY:HA3	1.88	0.55
1:BE:288:HIS:HD2	1:BE:337:ASP:OD2	1.89	0.55
1:BP:75:ARG:NH2	1:BP:391:ALA:O	2.39	0.55
1:BF:55:ARG:HD3	1:CH:272:TYR:CE2	2.41	0.55
1:AH:11:PRO:HG2	1:AH:18:ARG:HD2	1.87	0.55
1:AL:250:TRP:HZ3	1:AL:272:TYR:CE1	2.22	0.55
1:AN:454:ASN:ND2	1:AN:456:ALA:H	2.03	0.55
1:BC:79:ARG:HG3	1:BC:79:ARG:HH11	1.70	0.55
1:BK:250:TRP:HZ3	1:BK:272:TYR:CE1	2.23	0.55
1:BL:288:HIS:HD2	1:BL:337:ASP:OD2	1.89	0.55
1:BP:77:THR:O	1:BP:81:THR:HG23	2.07	0.55
1:CB:454:ASN:HD22	1:CB:456:ALA:N	2.01	0.55
1:CB:67:VAL:HG23	1:CB:135:LEU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:454:ASN:HD22	1:CC:456:ALA:N	2.02	0.55
1:AL:55:ARG:HD3	1:CQ:272:TYR:CE2	2.41	0.55
1:CQ:288:HIS:HD2	1:CQ:337:ASP:OD2	1.89	0.55
1:AD:189:PHE:CE1	1:AD:198:ARG:CG	2.89	0.55
1:BB:11:PRO:HG2	1:BB:18:ARG:HD2	1.88	0.55
1:BI:191:LEU:N	1:BI:191:LEU:HD23	2.18	0.55
1:BJ:67:VAL:HG23	1:BJ:135:LEU:HB2	1.88	0.55
1:BQ:398:GLY:HA3	1:BQ:494:PHE:CD2	2.41	0.55
1:BT:55:ARG:HD3	1:CA:272:TYR:CD2	2.42	0.55
1:CJ:284:ARG:NH1	1:CJ:284:ARG:HG2	2.20	0.55
1:CJ:79:ARG:HG3	1:CJ:79:ARG:HH11	1.72	0.55
1:CO:189:PHE:CE1	1:CO:198:ARG:CG	2.90	0.55
1:CQ:454:ASN:ND2	1:CQ:456:ALA:H	2.00	0.55
1:CO:272:TYR:CD2	1:CR:55:ARG:HD3	2.41	0.55
1:AA:16:ALA:O	1:AA:17:ASN:HB2	2.07	0.55
1:AS:67:VAL:HG23	1:AS:135:LEU:HB2	1.88	0.55
1:BA:232:THR:HB	1:BA:334:VAL:HG23	1.87	0.55
1:BA:74:ASN:ND2	1:BA:77:THR:OG1	2.40	0.55
1:BB:67:VAL:HG23	1:BB:135:LEU:HB2	1.89	0.55
1:BB:74:ASN:ND2	1:BB:77:THR:OG1	2.39	0.55
1:BD:398:GLY:HA3	1:BD:494:PHE:CD2	2.40	0.55
1:BD:74:ASN:CB	1:BD:126:GLU:HG2	2.36	0.55
1:BM:74:ASN:CB	1:BM:126:GLU:HG2	2.36	0.55
1:CB:250:TRP:CE3	1:CB:272:TYR:CE1	2.93	0.55
1:CE:454:ASN:HD22	1:CE:456:ALA:N	2.03	0.55
1:CG:74:ASN:CB	1:CG:126:GLU:HG2	2.37	0.55
1:CH:55:ARG:HD3	1:CK:272:TYR:CD2	2.41	0.55
1:CM:75:ARG:NH2	1:CM:391:ALA:O	2.38	0.55
1:CD:272:TYR:HE2	1:CS:55:ARG:NE	2.01	0.55
1:AD:250:TRP:CE3	1:AD:272:TYR:CE1	2.95	0.55
1:AE:55:ARG:NE	1:CP:272:TYR:HE2	2.00	0.55
1:AG:55:ARG:CZ	1:CG:272:TYR:CE2	2.89	0.55
1:AR:398:GLY:HA3	1:AR:494:PHE:CD2	2.42	0.55
1:BF:250:TRP:CE3	1:BF:272:TYR:CE1	2.95	0.55
1:BN:55:ARG:HD3	1:BS:272:TYR:CD2	2.41	0.55
1:CA:74:ASN:CB	1:CA:126:GLU:HG2	2.37	0.55
1:CQ:189:PHE:HE2	1:CQ:249:LEU:CD2	2.20	0.55
1:CR:454:ASN:HD22	1:CR:456:ALA:N	2.02	0.55
1:CT:189:PHE:HE1	1:CT:198:ARG:CG	2.19	0.55
1:AB:191:LEU:HD23	1:AB:191:LEU:N	2.16	0.55
1:AF:14:CYS:H	1:AF:138:ASN:HD21	1.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:74:ASN:CB	1:AH:126:GLU:HG2	2.37	0.55
1:AQ:284:ARG:NH1	1:AQ:284:ARG:HG2	2.20	0.55
1:BC:16:ALA:O	1:BC:17:ASN:HB2	2.06	0.55
1:BO:250:TRP:CE3	1:BO:272:TYR:CD1	2.95	0.55
1:BQ:189:PHE:HE2	1:BQ:249:LEU:CD2	2.20	0.55
1:BS:189:PHE:HE2	1:BS:249:LEU:CD2	2.20	0.55
1:BS:288:HIS:HD2	1:BS:337:ASP:OD2	1.89	0.55
1:BS:454:ASN:ND2	1:BS:456:ALA:H	2.03	0.55
1:CS:203:THR:HB	1:CS:300:GLN:HG3	1.88	0.55
1:AQ:67:VAL:HG23	1:AQ:135:LEU:HB2	1.88	0.55
1:AS:250:TRP:HZ3	1:AS:272:TYR:CE1	2.23	0.55
1:BJ:272:TYR:CE2	1:BQ:55:ARG:CZ	2.90	0.55
1:BQ:74:ASN:CB	1:BQ:126:GLU:HG2	2.35	0.55
1:BT:189:PHE:HE2	1:BT:249:LEU:CD2	2.20	0.55
1:CE:288:HIS:HD2	1:CE:337:ASP:OD2	1.90	0.55
1:CN:250:TRP:HZ3	1:CN:272:TYR:CE1	2.23	0.55
1:AE:14:CYS:H	1:AE:138:ASN:ND2	2.05	0.55
1:AF:16:ALA:O	1:AF:17:ASN:HB2	2.07	0.55
1:AT:43:ALA:HB1	1:AT:158:GLU:HA	1.89	0.55
1:BI:454:ASN:ND2	1:BI:456:ALA:H	2.01	0.55
1:BJ:14:CYS:H	1:BJ:138:ASN:HD21	1.55	0.55
1:CK:250:TRP:CE3	1:CK:272:TYR:CE1	2.94	0.55
1:CR:250:TRP:CE3	1:CR:272:TYR:CE1	2.94	0.55
1:CS:189:PHE:CE1	1:CS:198:ARG:CG	2.90	0.55
1:AI:43:ALA:HB1	1:AI:158:GLU:HA	1.89	0.55
1:AJ:191:LEU:N	1:AJ:191:LEU:CD2	2.70	0.55
1:BE:189:PHE:HE2	1:BE:249:LEU:CD2	2.18	0.55
1:BG:250:TRP:CE3	1:BG:272:TYR:CE1	2.95	0.55
1:BG:67:VAL:HG23	1:BG:135:LEU:HB2	1.88	0.55
1:BM:189:PHE:CE1	1:BM:198:ARG:HG3	2.38	0.55
1:BQ:454:ASN:HD22	1:BQ:456:ALA:N	2.03	0.55
1:CH:11:PRO:HG2	1:CH:18:ARG:HD2	1.88	0.55
1:CI:288:HIS:HD2	1:CI:337:ASP:OD2	1.90	0.55
1:CT:454:ASN:HD22	1:CT:456:ALA:N	2.02	0.55
1:AB:250:TRP:HZ3	1:AB:272:TYR:CE1	2.23	0.54
1:AD:454:ASN:HD22	1:AD:456:ALA:N	2.02	0.54
1:AN:55:ARG:HD3	1:AS:272:TYR:CE2	2.42	0.54
1:AO:398:GLY:HA3	1:AO:494:PHE:CD2	2.42	0.54
1:BQ:189:PHE:HE2	1:BQ:249:LEU:HD21	1.72	0.54
1:BT:67:VAL:HG23	1:BT:135:LEU:HB2	1.89	0.54
1:CJ:58:ALA:HB2	1:CJ:102:GLY:HA3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:288:HIS:HD2	1:CM:337:ASP:OD2	1.90	0.54
1:AB:398:GLY:HA3	1:AB:494:PHE:CD2	2.43	0.54
1:AJ:284:ARG:NH1	1:AJ:284:ARG:HG2	2.21	0.54
1:AK:250:TRP:CE3	1:AK:272:TYR:CE1	2.96	0.54
1:AM:74:ASN:ND2	1:AM:77:THR:OG1	2.39	0.54
1:AQ:272:TYR:CE2	1:BL:55:ARG:HD3	2.42	0.54
1:AB:454:ASN:HD22	1:AB:456:ALA:N	2.04	0.54
1:AG:398:GLY:HA3	1:AG:494:PHE:CD2	2.43	0.54
1:AG:79:ARG:CG	1:AG:79:ARG:HH11	2.13	0.54
1:AH:43:ALA:HB1	1:AH:158:GLU:HA	1.88	0.54
1:AI:74:ASN:ND2	1:AI:77:THR:OG1	2.39	0.54
1:AK:454:ASN:HD22	1:AK:456:ALA:N	2.03	0.54
1:AO:272:TYR:CD2	1:AR:55:ARG:CZ	2.91	0.54
1:BA:398:GLY:HA3	1:BA:494:PHE:CD2	2.42	0.54
1:BD:288:HIS:HD2	1:BD:337:ASP:OD2	1.90	0.54
1:BH:288:HIS:HD2	1:BH:337:ASP:OD2	1.90	0.54
1:BL:36:GLN:NE2	1:BL:156:LEU:H	2.05	0.54
1:CP:288:HIS:HD2	1:CP:337:ASP:OD2	1.90	0.54
1:CS:189:PHE:HE1	1:CS:198:ARG:CG	2.19	0.54
1:AC:398:GLY:HA3	1:AC:494:PHE:CD2	2.42	0.54
1:AF:454:ASN:HD22	1:AF:456:ALA:N	1.99	0.54
1:AG:288:HIS:HD2	1:AG:337:ASP:OD2	1.89	0.54
1:AG:5:ARG:HD3	1:CG:263:ASN:HD22	1.73	0.54
1:AJ:250:TRP:CZ3	1:AJ:272:TYR:HE1	2.23	0.54
1:AP:454:ASN:HD22	1:AP:456:ALA:N	2.02	0.54
1:BI:14:CYS:H	1:BI:138:ASN:HD21	1.55	0.54
1:CD:272:TYR:CE2	1:CS:55:ARG:HD3	2.41	0.54
1:CH:67:VAL:HG23	1:CH:135:LEU:HB2	1.90	0.54
1:CL:250:TRP:CE3	1:CL:272:TYR:CE1	2.95	0.54
1:CD:55:ARG:HD3	1:CN:272:TYR:CD2	2.43	0.54
1:CS:189:PHE:HE2	1:CS:249:LEU:CD2	2.21	0.54
1:AI:250:TRP:CZ3	1:AI:272:TYR:HE1	2.22	0.54
1:AJ:67:VAL:HG23	1:AJ:135:LEU:HB2	1.90	0.54
1:AK:14:CYS:H	1:AK:138:ASN:ND2	2.05	0.54
1:BA:189:PHE:HD2	1:BA:247:ILE:HD11	1.72	0.54
1:BA:232:THR:HB	1:BA:334:VAL:CG2	2.37	0.54
1:BG:14:CYS:H	1:BG:138:ASN:HD21	1.54	0.54
1:BM:189:PHE:CE1	1:BM:198:ARG:HG2	2.43	0.54
1:BP:398:GLY:HA3	1:BP:494:PHE:CD2	2.43	0.54
1:BP:79:ARG:HH11	1:BP:79:ARG:HG2	1.70	0.54
1:CB:398:GLY:HA3	1:CB:494:PHE:CD2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:30:SER:O	1:CF:33:LYS:HB2	2.08	0.54
1:CR:398:GLY:HA3	1:CR:494:PHE:CD2	2.42	0.54
1:AC:67:VAL:HG23	1:AC:135:LEU:HB2	1.90	0.54
1:AD:454:ASN:ND2	1:AD:456:ALA:H	2.04	0.54
1:AR:454:ASN:HD21	1:AR:456:ALA:HB3	1.73	0.54
1:BD:454:ASN:HD22	1:BD:456:ALA:N	2.06	0.54
1:BG:454:ASN:HD22	1:BG:456:ALA:N	2.04	0.54
1:CF:79:ARG:NH1	1:CF:79:ARG:CG	2.60	0.54
1:CG:67:VAL:HG23	1:CG:135:LEU:HB2	1.90	0.54
1:CO:272:TYR:CE2	1:CR:55:ARG:CZ	2.91	0.54
1:CT:189:PHE:CE1	1:CT:198:ARG:CG	2.91	0.54
1:CT:250:TRP:CE3	1:CT:272:TYR:CE1	2.96	0.54
1:AA:58:ALA:HB2	1:AA:102:GLY:HA3	1.89	0.54
1:AL:14:CYS:H	1:AL:138:ASN:ND2	2.03	0.54
1:AQ:454:ASN:HD22	1:AQ:456:ALA:N	2.04	0.54
1:AR:189:PHE:CE2	1:AR:249:LEU:HD21	2.41	0.54
1:BC:398:GLY:HA3	1:BC:494:PHE:CD2	2.43	0.54
1:BG:250:TRP:HZ3	1:BG:272:TYR:CE1	2.20	0.54
1:BJ:74:ASN:ND2	1:BJ:77:THR:OG1	2.40	0.54
1:BP:189:PHE:HE2	1:BP:249:LEU:CD2	2.20	0.54
1:CA:250:TRP:CE3	1:CA:272:TYR:CE1	2.95	0.54
1:CB:14:CYS:H	1:CB:138:ASN:HD21	1.54	0.54
1:CC:67:VAL:HG23	1:CC:135:LEU:HB2	1.90	0.54
1:CD:67:VAL:HG23	1:CD:135:LEU:HB2	1.89	0.54
1:CT:250:TRP:HZ3	1:CT:272:TYR:CE1	2.23	0.54
1:AE:288:HIS:HD2	1:AE:337:ASP:OD2	1.90	0.54
1:AE:454:ASN:ND2	1:AE:456:ALA:H	2.03	0.54
1:AI:170:PHE:HD1	1:AI:389:MET:HE2	1.73	0.54
1:AM:67:VAL:HG23	1:AM:135:LEU:HB2	1.89	0.54
1:AP:14:CYS:H	1:AP:138:ASN:HD21	1.53	0.54
1:AO:272:TYR:CD2	1:AR:55:ARG:HD3	2.43	0.54
1:AT:14:CYS:H	1:AT:138:ASN:HD21	1.56	0.54
1:AT:189:PHE:HE2	1:AT:249:LEU:CD2	2.21	0.54
1:AT:11:PRO:HG2	1:AT:18:ARG:HD2	1.89	0.54
1:BR:398:GLY:HA3	1:BR:494:PHE:CD2	2.43	0.54
1:CE:454:ASN:HD21	1:CE:456:ALA:HB3	1.73	0.54
1:CH:14:CYS:H	1:CH:138:ASN:HD21	1.55	0.54
1:CI:74:ASN:ND2	1:CI:77:THR:OG1	2.40	0.54
1:CQ:454:ASN:HD21	1:CQ:456:ALA:HB3	1.72	0.54
1:CS:239:ILE:HG12	1:CS:326:ILE:CD1	2.37	0.54
1:CT:67:VAL:HG23	1:CT:135:LEU:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:288:HIS:HD2	1:AK:337:ASP:OD2	1.90	0.54
1:AO:288:HIS:HD2	1:AO:337:ASP:OD2	1.91	0.54
1:AT:398:GLY:HA3	1:AT:494:PHE:CD2	2.42	0.54
1:BD:189:PHE:HE2	1:BD:249:LEU:CD2	2.20	0.54
1:BQ:162:PHE:CD2	1:BQ:163:LEU:HD13	2.43	0.54
1:BR:250:TRP:CE3	1:BR:272:TYR:CE1	2.96	0.54
1:BO:272:TYR:CE2	1:BR:55:ARG:HD3	2.43	0.54
1:BS:79:ARG:CG	1:BS:79:ARG:NH1	2.66	0.54
1:CL:454:ASN:ND2	1:CL:456:ALA:H	2.03	0.54
1:CN:454:ASN:ND2	1:CN:456:ALA:H	2.02	0.54
1:CT:189:PHE:HD2	1:CT:247:ILE:HD11	1.73	0.54
1:AF:67:VAL:HG23	1:AF:135:LEU:HB2	1.90	0.54
1:AL:74:ASN:ND2	1:AL:77:THR:OG1	2.41	0.54
1:AM:250:TRP:CE3	1:AM:272:TYR:CE1	2.96	0.54
1:AR:288:HIS:HD2	1:AR:337:ASP:OD2	1.91	0.54
1:BB:30:SER:O	1:BB:33:LYS:HB2	2.08	0.54
1:BJ:191:LEU:HD23	1:BJ:191:LEU:N	2.13	0.54
1:BK:67:VAL:HG23	1:BK:135:LEU:HB2	1.90	0.54
1:BT:250:TRP:HZ3	1:BT:272:TYR:CE1	2.22	0.54
1:BT:170:PHE:HD1	1:BT:389:MET:HE2	1.72	0.54
1:CC:79:ARG:HG3	1:CC:79:ARG:NH1	2.21	0.54
1:CI:55:ARG:CD	1:CR:272:TYR:CE2	2.91	0.54
1:CK:67:VAL:HG23	1:CK:135:LEU:HB2	1.89	0.54
1:AC:55:ARG:HD3	1:AT:272:TYR:CE2	2.43	0.53
1:AI:67:VAL:HG23	1:AI:135:LEU:HB2	1.89	0.53
1:AO:74:ASN:CB	1:AO:126:GLU:HG2	2.37	0.53
1:AN:55:ARG:CZ	1:AS:272:TYR:CE2	2.91	0.53
1:CL:189:PHE:HE1	1:CL:198:ARG:CG	2.19	0.53
1:AG:454:ASN:HD22	1:AG:456:ALA:N	2.04	0.53
1:AH:250:TRP:HZ3	1:AH:272:TYR:CE1	2.24	0.53
1:BJ:272:TYR:N	1:BJ:272:TYR:HD1	2.06	0.53
1:BT:398:GLY:HA3	1:BT:494:PHE:CD2	2.43	0.53
1:BT:74:ASN:ND2	1:BT:77:THR:OG1	2.41	0.53
1:CE:203:THR:HB	1:CE:300:GLN:HG3	1.90	0.53
1:CJ:288:HIS:HD2	1:CJ:337:ASP:OD2	1.91	0.53
1:CO:67:VAL:HG23	1:CO:135:LEU:HB2	1.90	0.53
1:AA:189:PHE:HE2	1:AA:249:LEU:HD21	1.74	0.53
1:AF:288:HIS:HD2	1:AF:337:ASP:OD2	1.91	0.53
1:AO:75:ARG:NH2	1:AO:391:ALA:O	2.41	0.53
1:AS:454:ASN:HD22	1:AS:456:ALA:N	2.03	0.53
1:BM:25:ILE:HG23	1:BM:152:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:75:ARG:NH2	1:CC:391:ALA:O	2.41	0.53
1:CO:189:PHE:HE2	1:CO:249:LEU:CD2	2.22	0.53
1:AL:250:TRP:CE3	1:AL:272:TYR:CE1	2.95	0.53
1:AN:398:GLY:HA3	1:AN:494:PHE:CD2	2.43	0.53
1:AI:55:ARG:CD	1:AR:272:TYR:CE2	2.91	0.53
1:BJ:398:GLY:HA3	1:BJ:494:PHE:CD2	2.44	0.53
1:CR:189:PHE:CE1	1:CR:198:ARG:HG2	2.43	0.53
1:CS:75:ARG:NH2	1:CS:391:ALA:O	2.42	0.53
1:AD:272:TYR:CE2	1:AS:55:ARG:HD3	2.43	0.53
1:AQ:16:ALA:O	1:AQ:17:ASN:HB2	2.07	0.53
1:BD:55:ARG:HD3	1:BN:272:TYR:CD2	2.44	0.53
1:BR:43:ALA:HB1	1:BR:158:GLU:HA	1.91	0.53
1:BT:189:PHE:CE1	1:BT:198:ARG:CG	2.91	0.53
1:CA:11:PRO:HG2	1:CA:18:ARG:HD2	1.90	0.53
1:CB:288:HIS:HD2	1:CB:337:ASP:OD2	1.91	0.53
1:CC:288:HIS:HD2	1:CC:337:ASP:OD2	1.92	0.53
1:AG:272:TYR:HD1	1:AG:272:TYR:N	2.07	0.53
1:AK:191:LEU:N	1:AK:191:LEU:HD23	2.17	0.53
1:AK:74:ASN:ND2	1:AK:77:THR:OG1	2.42	0.53
1:BC:191:LEU:N	1:BC:191:LEU:HD23	2.19	0.53
1:BM:454:ASN:ND2	1:BM:456:ALA:H	2.04	0.53
1:BN:250:TRP:CE3	1:BN:272:TYR:CE1	2.96	0.53
1:BI:272:TYR:CD2	1:BO:55:ARG:HD3	2.43	0.53
1:CE:67:VAL:HG23	1:CE:135:LEU:HB2	1.91	0.53
1:CO:189:PHE:HE1	1:CO:198:ARG:CG	2.19	0.53
1:CR:67:VAL:HG23	1:CR:135:LEU:HB2	1.89	0.53
1:AC:239:ILE:HG12	1:AC:326:ILE:CD1	2.38	0.53
1:AG:58:ALA:HB2	1:AG:102:GLY:HA3	1.90	0.53
1:AH:162:PHE:CD2	1:AH:163:LEU:HD13	2.43	0.53
1:AJ:272:TYR:HE2	1:AQ:55:ARG:CD	2.22	0.53
1:AK:58:ALA:HB2	1:AK:102:GLY:HA3	1.89	0.53
1:AL:454:ASN:HD22	1:AL:456:ALA:N	2.01	0.53
1:AQ:250:TRP:CE3	1:AQ:272:TYR:CE1	2.97	0.53
1:AR:250:TRP:HZ3	1:AR:272:TYR:CE1	2.23	0.53
1:AI:55:ARG:CD	1:AR:272:TYR:HE2	2.21	0.53
1:BO:67:VAL:HG23	1:BO:135:LEU:HB2	1.90	0.53
1:BQ:250:TRP:CE3	1:BQ:272:TYR:CE1	2.97	0.53
1:BR:79:ARG:HH11	1:BR:79:ARG:CG	2.16	0.53
1:AA:239:ILE:HG12	1:AA:326:ILE:CD1	2.39	0.53
1:AF:454:ASN:ND2	1:AF:456:ALA:H	2.01	0.53
1:AO:191:LEU:N	1:AO:191:LEU:CD2	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:30:SER:O	1:AO:33:LYS:HB2	2.09	0.53
1:BB:162:PHE:CD2	1:BB:163:LEU:HD13	2.44	0.53
1:BE:189:PHE:CE1	1:BE:198:ARG:HG2	2.43	0.53
1:BG:191:LEU:HD23	1:BG:191:LEU:N	2.19	0.53
1:BJ:250:TRP:CE3	1:BJ:272:TYR:CD1	2.97	0.53
1:BM:288:HIS:HD2	1:BM:337:ASP:OD2	1.90	0.53
1:CG:189:PHE:CE1	1:CG:198:ARG:HG2	2.43	0.53
1:AA:288:HIS:HD2	1:AA:337:ASP:OD2	1.92	0.53
1:AC:250:TRP:HZ3	1:AC:272:TYR:CE1	2.26	0.53
1:AJ:272:TYR:CD2	1:AQ:55:ARG:HD3	2.44	0.53
1:AJ:454:ASN:HD22	1:AJ:456:ALA:N	2.03	0.53
1:BD:250:TRP:HZ3	1:BD:272:TYR:CE1	2.27	0.53
1:BF:191:LEU:N	1:BF:191:LEU:HD23	2.18	0.53
1:BN:18:ARG:HG3	1:BN:19:TYR:N	2.22	0.53
1:BP:250:TRP:CE3	1:BP:272:TYR:CD1	2.97	0.53
1:CP:189:PHE:HE2	1:CP:249:LEU:CD2	2.22	0.53
1:AA:454:ASN:ND2	1:AA:456:ALA:H	2.03	0.53
1:AC:272:TYR:CE2	1:BA:55:ARG:HD3	2.44	0.53
1:AK:398:GLY:HA3	1:AK:494:PHE:CD2	2.43	0.53
1:BC:272:TYR:CE2	1:CA:55:ARG:HD3	2.43	0.53
1:BK:189:PHE:HD2	1:BK:247:ILE:HD11	1.74	0.53
1:BM:203:THR:HB	1:BM:300:GLN:HG3	1.91	0.53
1:BN:454:ASN:ND2	1:BN:456:ALA:H	2.05	0.53
1:BP:58:ALA:HB2	1:BP:102:GLY:HA3	1.91	0.53
1:CK:454:ASN:ND2	1:CK:456:ALA:H	2.01	0.53
1:CO:79:ARG:CG	1:CO:79:ARG:HH11	2.20	0.53
1:AC:162:PHE:CD2	1:AC:163:LEU:HD13	2.44	0.52
1:AM:250:TRP:HZ3	1:AM:272:TYR:CE1	2.24	0.52
1:AO:43:ALA:HB1	1:AO:158:GLU:HA	1.91	0.52
1:AS:189:PHE:HE2	1:AS:249:LEU:CD2	2.22	0.52
1:BA:239:ILE:HG12	1:BA:326:ILE:CD1	2.39	0.52
1:BF:189:PHE:CE1	1:BF:198:ARG:HG2	2.43	0.52
1:BN:189:PHE:HE1	1:BN:198:ARG:HG2	1.68	0.52
1:BN:288:HIS:HD2	1:BN:337:ASP:OD2	1.92	0.52
1:BO:288:HIS:HD2	1:BO:337:ASP:OD2	1.92	0.52
1:CF:14:CYS:H	1:CF:138:ASN:HD21	1.57	0.52
1:CI:404:LEU:HD22	1:CI:486:VAL:HG22	1.91	0.52
1:CP:74:ASN:ND2	1:CP:77:THR:OG1	2.42	0.52
1:AD:288:HIS:HD2	1:AD:337:ASP:OD2	1.92	0.52
1:AK:189:PHE:CE1	1:AK:198:ARG:CG	2.92	0.52
1:BA:454:ASN:ND2	1:BA:456:ALA:H	2.05	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:250:TRP:CE3	1:BI:272:TYR:CE1	2.96	0.52
1:BI:36:GLN:NE2	1:BI:156:LEU:H	2.07	0.52
1:BM:79:ARG:HH11	1:BM:79:ARG:CG	2.22	0.52
1:CA:30:SER:O	1:CA:33:LYS:HB2	2.10	0.52
1:CC:55:ARG:HD3	1:CT:272:TYR:CE2	2.44	0.52
1:CE:226:VAL:HG13	1:CE:228:GLY:H	1.73	0.52
1:CH:250:TRP:HZ3	1:CH:272:TYR:CE1	2.22	0.52
1:AC:191:LEU:CD2	1:AC:191:LEU:N	2.73	0.52
1:AG:272:TYR:CD2	1:BG:55:ARG:HD3	2.44	0.52
1:AH:454:ASN:HD22	1:AH:456:ALA:N	2.03	0.52
1:AK:75:ARG:NH2	1:AK:391:ALA:O	2.42	0.52
1:AL:189:PHE:HE2	1:AL:249:LEU:CD2	2.22	0.52
1:AQ:189:PHE:HE1	1:AQ:198:ARG:CG	2.22	0.52
1:BF:30:SER:O	1:BF:33:LYS:HB2	2.09	0.52
1:BF:398:GLY:HA3	1:BF:494:PHE:CD2	2.45	0.52
1:BN:170:PHE:HD1	1:BN:389:MET:CE	2.21	0.52
1:BN:398:GLY:HA3	1:BN:494:PHE:CD2	2.45	0.52
1:BP:191:LEU:CD2	1:BP:191:LEU:N	2.73	0.52
1:BR:162:PHE:CD2	1:BR:163:LEU:HD13	2.44	0.52
1:CA:454:ASN:HD22	1:CA:456:ALA:N	2.04	0.52
1:CD:288:HIS:HD2	1:CD:337:ASP:OD2	1.92	0.52
1:CE:398:GLY:HA3	1:CE:494:PHE:CD2	2.44	0.52
1:CH:16:ALA:O	1:CH:17:ASN:HB2	2.08	0.52
1:CJ:454:ASN:ND2	1:CJ:456:ALA:H	2.04	0.52
1:CL:250:TRP:HZ3	1:CL:272:TYR:CE1	2.24	0.52
1:CM:67:VAL:HG23	1:CM:135:LEU:HB2	1.91	0.52
1:CO:398:GLY:HA3	1:CO:494:PHE:CD2	2.44	0.52
1:AF:250:TRP:CE3	1:AF:272:TYR:CE1	2.97	0.52
1:AM:203:THR:HB	1:AM:300:GLN:HG3	1.91	0.52
1:AQ:256:ASN:HD22	1:AQ:302:ASP:HA	1.73	0.52
1:BH:232:THR:HB	1:BH:334:VAL:CG2	2.40	0.52
1:BJ:30:SER:O	1:BJ:33:LYS:HB2	2.09	0.52
1:BM:43:ALA:HB1	1:BM:158:GLU:HA	1.92	0.52
1:CA:189:PHE:CE1	1:CA:198:ARG:CG	2.93	0.52
1:CF:398:GLY:HA3	1:CF:494:PHE:CD2	2.45	0.52
1:CI:250:TRP:CE3	1:CI:272:TYR:CE1	2.97	0.52
1:CL:398:GLY:HA3	1:CL:494:PHE:CD2	2.44	0.52
1:AA:250:TRP:CE3	1:AA:272:TYR:CE1	2.97	0.52
1:AB:191:LEU:CD2	1:AB:191:LEU:N	2.72	0.52
1:AS:288:HIS:HD2	1:AS:337:ASP:OD2	1.91	0.52
1:BE:189:PHE:HE1	1:BE:198:ARG:HG2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:288:HIS:HD2	1:BG:337:ASP:OD2	1.92	0.52
1:BJ:272:TYR:CD2	1:BQ:55:ARG:HD3	2.45	0.52
1:BS:250:TRP:HZ3	1:BS:272:TYR:CE1	2.27	0.52
1:BT:170:PHE:HD1	1:BT:389:MET:CE	2.22	0.52
1:CM:454:ASN:HD21	1:CM:456:ALA:HB3	1.73	0.52
1:CM:454:ASN:ND2	1:CM:456:ALA:H	2.02	0.52
1:CI:55:ARG:CD	1:CR:272:TYR:HE2	2.22	0.52
1:CS:67:VAL:HG23	1:CS:135:LEU:HB2	1.91	0.52
1:AJ:16:ALA:O	1:AJ:17:ASN:HB2	2.10	0.52
1:AL:189:PHE:CE1	1:AL:198:ARG:CG	2.92	0.52
1:AM:191:LEU:CD2	1:AM:191:LEU:N	2.73	0.52
1:AQ:239:ILE:HG12	1:AQ:326:ILE:CD1	2.40	0.52
1:BC:189:PHE:CE1	1:BC:198:ARG:CG	2.92	0.52
1:BC:288:HIS:HD2	1:BC:337:ASP:OD2	1.92	0.52
1:BE:58:ALA:HB2	1:BE:102:GLY:HA3	1.92	0.52
1:BJ:272:TYR:N	1:BJ:272:TYR:CD1	2.78	0.52
1:BJ:43:ALA:HB1	1:BJ:158:GLU:HA	1.92	0.52
1:BK:79:ARG:HH11	1:BK:79:ARG:HG3	1.75	0.52
1:CA:288:HIS:HD2	1:CA:337:ASP:OD2	1.92	0.52
1:CC:404:LEU:HD22	1:CC:486:VAL:HG22	1.92	0.52
1:CC:398:GLY:HA3	1:CC:494:PHE:CD2	2.44	0.52
1:CD:398:GLY:HA3	1:CD:494:PHE:CD2	2.45	0.52
1:AA:30:SER:O	1:AA:33:LYS:HB2	2.09	0.52
1:AL:79:ARG:NH1	1:AL:79:ARG:CG	2.71	0.52
1:BA:58:ALA:HB2	1:BA:102:GLY:HA3	1.90	0.52
1:BH:250:TRP:CE3	1:BH:272:TYR:CE1	2.97	0.52
1:BI:58:ALA:HB2	1:BI:102:GLY:HA3	1.92	0.52
1:BJ:454:ASN:HD21	1:BJ:456:ALA:HB3	1.73	0.52
1:CC:74:ASN:ND2	1:CC:77:THR:OG1	2.43	0.52
1:CT:43:ALA:HB1	1:CT:158:GLU:HA	1.90	0.52
1:AI:398:GLY:HA3	1:AI:494:PHE:CD2	2.45	0.52
1:AL:58:ALA:HB2	1:AL:102:GLY:HA3	1.92	0.52
1:BH:74:ASN:ND2	1:BH:77:THR:OG1	2.42	0.52
1:BQ:16:ALA:O	1:BQ:17:ASN:HB2	2.10	0.52
1:CA:74:ASN:ND2	1:CA:77:THR:OG1	2.43	0.52
1:CL:189:PHE:HE2	1:CL:249:LEU:CD2	2.22	0.52
1:CT:58:ALA:HB2	1:CT:102:GLY:HA3	1.92	0.52
1:AD:263:ASN:O	1:AD:267:LYS:HG3	2.10	0.52
1:AP:226:VAL:HG13	1:AP:228:GLY:H	1.75	0.52
1:AQ:25:ILE:HG23	1:AQ:152:LEU:HD11	1.92	0.52
1:BE:14:CYS:H	1:BE:138:ASN:HD21	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:288:HIS:HD2	1:BJ:337:ASP:OD2	1.91	0.52
1:BL:454:ASN:HD22	1:BL:456:ALA:N	2.03	0.52
1:BL:398:GLY:HA3	1:BL:494:PHE:CD2	2.44	0.52
1:BR:288:HIS:HD2	1:BR:337:ASP:OD2	1.93	0.52
1:BT:454:ASN:ND2	1:BT:456:ALA:H	2.03	0.52
1:BT:79:ARG:NH1	1:BT:79:ARG:HG3	2.21	0.52
1:CA:170:PHE:HD1	1:CA:389:MET:CE	2.23	0.52
1:CD:58:ALA:HB2	1:CD:102:GLY:HA3	1.91	0.52
1:CN:288:HIS:HD2	1:CN:337:ASP:OD2	1.92	0.52
1:CP:189:PHE:CE1	1:CP:198:ARG:CG	2.93	0.52
1:CR:250:TRP:HZ3	1:CR:272:TYR:CE1	2.23	0.52
1:CS:79:ARG:HH11	1:CS:79:ARG:HG3	1.73	0.52
1:AC:288:HIS:HD2	1:AC:337:ASP:OD2	1.92	0.52
1:AG:272:TYR:N	1:AG:272:TYR:CD1	2.77	0.52
1:AN:189:PHE:CE2	1:AN:249:LEU:HD21	2.42	0.52
1:AO:79:ARG:NH1	1:AO:79:ARG:HG3	2.24	0.52
1:BR:67:VAL:HG23	1:BR:135:LEU:HB2	1.91	0.52
1:CC:272:TYR:HD1	1:CC:272:TYR:N	2.07	0.52
1:CG:191:LEU:N	1:CG:191:LEU:HD23	2.19	0.52
1:CJ:272:TYR:CE2	1:CQ:55:ARG:HD3	2.45	0.52
1:CR:74:ASN:ND2	1:CR:77:THR:OG1	2.44	0.52
1:AA:8:ILE:HG22	1:AA:10:ILE:HD11	1.91	0.51
1:AO:189:PHE:HE2	1:AO:249:LEU:CD2	2.24	0.51
1:AQ:191:LEU:HD23	1:AQ:191:LEU:N	2.18	0.51
1:AR:67:VAL:HG23	1:AR:135:LEU:HB2	1.91	0.51
1:BF:379:VAL:HG11	1:BF:381:MET:HE1	1.92	0.51
1:BJ:250:TRP:HZ3	1:BJ:272:TYR:CE1	2.22	0.51
1:BL:250:TRP:CE3	1:BL:272:TYR:CE1	2.98	0.51
1:CK:288:HIS:HD2	1:CK:337:ASP:OD2	1.92	0.51
1:CN:170:PHE:HD1	1:CN:389:MET:CE	2.23	0.51
1:AC:454:ASN:HD21	1:AC:456:ALA:HB3	1.75	0.51
1:AJ:170:PHE:HD1	1:AJ:389:MET:HE2	1.76	0.51
1:AS:232:THR:HB	1:AS:334:VAL:HG23	1.92	0.51
1:AS:43:ALA:HB1	1:AS:158:GLU:HA	1.92	0.51
1:BQ:25:ILE:HG23	1:BQ:152:LEU:HD11	1.91	0.51
1:BO:272:TYR:CD2	1:BR:55:ARG:HD3	2.45	0.51
1:CA:189:PHE:HE2	1:CA:249:LEU:CD2	2.23	0.51
1:CH:55:ARG:HD3	1:CK:272:TYR:CE2	2.45	0.51
1:CR:288:HIS:HD2	1:CR:337:ASP:OD2	1.92	0.51
1:CT:191:LEU:HD23	1:CT:191:LEU:N	2.20	0.51
1:AH:272:TYR:CE2	1:CF:55:ARG:HD3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:288:HIS:HD2	1:AJ:337:ASP:OD2	1.93	0.51
1:AR:239:ILE:HG12	1:AR:326:ILE:CD1	2.41	0.51
1:AS:272:TYR:HD1	1:AS:272:TYR:N	2.08	0.51
1:BC:454:ASN:ND2	1:BC:456:ALA:H	2.03	0.51
1:BL:79:ARG:CG	1:BL:79:ARG:HH11	2.23	0.51
1:BD:55:ARG:HD3	1:BN:272:TYR:CE2	2.45	0.51
1:CG:162:PHE:CD2	1:CG:163:LEU:HD13	2.45	0.51
1:CH:398:GLY:HA3	1:CH:494:PHE:CD2	2.45	0.51
1:CI:191:LEU:CD2	1:CI:191:LEU:N	2.73	0.51
1:CJ:75:ARG:NH2	1:CJ:391:ALA:O	2.42	0.51
1:AD:170:PHE:HD1	1:AD:389:MET:CE	2.24	0.51
1:AD:454:ASN:HD21	1:AD:456:ALA:HB3	1.75	0.51
1:AF:58:ALA:HB2	1:AF:102:GLY:HA3	1.93	0.51
1:AH:454:ASN:HD21	1:AH:456:ALA:HB3	1.76	0.51
1:AI:14:CYS:H	1:AI:138:ASN:ND2	2.08	0.51
1:BA:189:PHE:CE2	1:BA:249:LEU:HD21	2.45	0.51
1:BC:58:ALA:HB2	1:BC:102:GLY:HA3	1.92	0.51
1:BE:162:PHE:CD2	1:BE:163:LEU:HD13	2.46	0.51
1:BE:250:TRP:CE3	1:BE:272:TYR:CE1	2.98	0.51
1:BJ:226:VAL:HG13	1:BJ:228:GLY:H	1.75	0.51
1:BQ:75:ARG:NH2	1:BQ:391:ALA:O	2.43	0.51
1:CG:239:ILE:HG12	1:CG:326:ILE:CD1	2.40	0.51
1:CJ:170:PHE:HD1	1:CJ:389:MET:CE	2.23	0.51
1:CN:43:ALA:HB1	1:CN:158:GLU:HA	1.93	0.51
1:AD:239:ILE:HG12	1:AD:326:ILE:CD1	2.41	0.51
1:AD:79:ARG:CG	1:AD:79:ARG:HH11	2.21	0.51
1:AJ:189:PHE:CE1	1:AJ:198:ARG:HG2	2.45	0.51
1:AL:189:PHE:HE2	1:AL:249:LEU:HD21	1.76	0.51
1:AR:379:VAL:HG11	1:AR:381:MET:HE1	1.91	0.51
1:BH:58:ALA:HB2	1:BH:102:GLY:HA3	1.92	0.51
1:BH:442:GLN:HE21	1:BI:412:PHE:HB2	1.76	0.51
1:BO:30:SER:O	1:BO:33:LYS:HB2	2.11	0.51
1:CF:67:VAL:HG23	1:CF:135:LEU:HB2	1.91	0.51
1:CK:454:ASN:HD21	1:CK:456:ALA:HB3	1.75	0.51
1:CP:189:PHE:HE1	1:CP:198:ARG:CG	2.23	0.51
1:CS:250:TRP:HZ3	1:CS:272:TYR:CE1	2.26	0.51
1:CT:288:HIS:HD2	1:CT:337:ASP:OD2	1.92	0.51
1:AE:58:ALA:HB2	1:AE:102:GLY:HA3	1.92	0.51
1:AO:226:VAL:HG13	1:AO:228:GLY:H	1.74	0.51
1:AQ:398:GLY:HA3	1:AQ:494:PHE:CD2	2.44	0.51
1:BD:30:SER:O	1:BD:33:LYS:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:191:LEU:N	1:BF:191:LEU:CD2	2.74	0.51
1:BO:272:TYR:N	1:BO:272:TYR:HD1	2.08	0.51
1:BQ:239:ILE:HG12	1:BQ:326:ILE:CD1	2.41	0.51
1:CB:43:ALA:HB1	1:CB:158:GLU:HA	1.92	0.51
1:CE:272:TYR:HD1	1:CE:272:TYR:N	2.08	0.51
1:CK:250:TRP:HZ3	1:CK:272:TYR:CE1	2.22	0.51
1:CS:191:LEU:HD23	1:CS:191:LEU:N	2.21	0.51
1:AB:272:TYR:N	1:AB:272:TYR:HD1	2.09	0.51
1:AJ:74:ASN:ND2	1:AJ:77:THR:OG1	2.44	0.51
1:AT:250:TRP:HZ3	1:AT:272:TYR:CE1	2.20	0.51
1:BD:18:ARG:HG3	1:BD:19:TYR:N	2.26	0.51
1:BF:43:ALA:HB1	1:BF:158:GLU:HA	1.92	0.51
1:BI:226:VAL:HG13	1:BI:228:GLY:H	1.76	0.51
1:BN:43:ALA:HB1	1:BN:158:GLU:HA	1.91	0.51
1:CB:232:THR:HB	1:CB:334:VAL:CG2	2.41	0.51
1:CB:74:ASN:ND2	1:CB:77:THR:OG1	2.44	0.51
1:CG:25:ILE:HG23	1:CG:152:LEU:HD11	1.93	0.51
1:BF:55:ARG:NE	1:CH:272:TYR:HE2	2.08	0.51
1:CK:412:PHE:HB2	1:CO:442:GLN:HE21	1.75	0.51
1:CQ:398:GLY:HA3	1:CQ:494:PHE:CD2	2.46	0.51
1:CS:11:PRO:HG2	1:CS:18:ARG:HD2	1.93	0.51
1:AB:79:ARG:CG	1:AB:79:ARG:HH11	2.22	0.51
1:AE:197:LEU:HD12	1:AE:198:ARG:N	2.26	0.51
1:AK:189:PHE:HE2	1:AK:249:LEU:CD2	2.23	0.51
1:AL:398:GLY:HA3	1:AL:494:PHE:CD2	2.46	0.51
1:AP:442:GLN:HE21	1:AQ:412:PHE:HB2	1.75	0.51
1:BB:18:ARG:HG3	1:BB:19:TYR:N	2.25	0.51
1:BB:250:TRP:HZ3	1:BB:272:TYR:CE1	2.23	0.51
1:BC:250:TRP:CZ3	1:BC:272:TYR:HE1	2.26	0.51
1:AP:272:TYR:CD2	1:BE:55:ARG:HD3	2.46	0.51
1:BF:170:PHE:HD1	1:BF:389:MET:CE	2.24	0.51
1:BH:284:ARG:NH1	1:BH:284:ARG:CG	2.69	0.51
1:BJ:272:TYR:CD2	1:BQ:55:ARG:CZ	2.94	0.51
1:BR:79:ARG:NH1	1:BR:79:ARG:HG3	2.22	0.51
1:BT:30:SER:O	1:BT:33:LYS:HB2	2.11	0.51
1:CA:250:TRP:HZ3	1:CA:272:TYR:CE1	2.26	0.51
1:CB:189:PHE:CE1	1:CB:198:ARG:HG2	2.46	0.51
1:CF:162:PHE:CD2	1:CF:163:LEU:HD13	2.45	0.51
1:CG:226:VAL:HG13	1:CG:228:GLY:H	1.75	0.51
1:CI:226:VAL:HG13	1:CI:228:GLY:H	1.76	0.51
1:CJ:191:LEU:N	1:CJ:191:LEU:HD23	2.21	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:75:ARG:NH2	1:CO:391:ALA:O	2.43	0.51
1:CP:191:LEU:N	1:CP:191:LEU:CD2	2.73	0.51
1:CQ:239:ILE:HG12	1:CQ:326:ILE:CD1	2.41	0.51
1:AE:67:VAL:HG23	1:AE:135:LEU:HB2	1.93	0.51
1:AF:239:ILE:HG12	1:AF:326:ILE:CD1	2.41	0.51
1:AI:170:PHE:HD1	1:AI:389:MET:CE	2.24	0.51
1:AQ:189:PHE:HD2	1:AQ:247:ILE:HD11	1.76	0.51
1:AQ:43:ALA:HB1	1:AQ:158:GLU:HA	1.91	0.51
1:AS:250:TRP:CE3	1:AS:272:TYR:CD1	2.99	0.51
1:AP:272:TYR:HE2	1:BE:55:ARG:NE	2.07	0.51
1:BI:288:HIS:HD2	1:BI:337:ASP:OD2	1.93	0.51
1:BL:9:TYR:HE2	1:BL:145:ASP:HB3	1.75	0.51
1:BS:250:TRP:CE3	1:BS:272:TYR:CE1	2.98	0.51
1:CI:284:ARG:CG	1:CI:284:ARG:NH1	2.71	0.51
1:CJ:272:TYR:HD1	1:CJ:272:TYR:N	2.07	0.51
1:CN:189:PHE:HD2	1:CN:247:ILE:CD1	2.24	0.51
1:AD:250:TRP:HZ3	1:AD:272:TYR:CE1	2.29	0.51
1:BA:16:ALA:O	1:BA:17:ASN:HB2	2.11	0.51
1:BB:189:PHE:HD2	1:BB:247:ILE:CD1	2.24	0.51
1:BH:232:THR:HB	1:BH:334:VAL:HG23	1.93	0.51
1:BI:30:SER:O	1:BI:33:LYS:HB2	2.10	0.51
1:BO:189:PHE:HE2	1:BO:249:LEU:CD2	2.24	0.51
1:CG:30:SER:O	1:CG:33:LYS:HB2	2.11	0.51
1:CM:191:LEU:CD2	1:CM:191:LEU:N	2.74	0.51
1:CO:250:TRP:HZ3	1:CO:272:TYR:CE1	2.23	0.51
1:AE:191:LEU:CD2	1:AE:191:LEU:N	2.74	0.50
1:AF:398:GLY:HA3	1:AF:494:PHE:CD2	2.46	0.50
1:AI:58:ALA:HB2	1:AI:102:GLY:HA3	1.92	0.50
1:AK:170:PHE:HD1	1:AK:389:MET:CE	2.24	0.50
1:AL:67:VAL:HG23	1:AL:135:LEU:HB2	1.94	0.50
1:AQ:189:PHE:CE1	1:AQ:198:ARG:CG	2.94	0.50
1:AQ:250:TRP:HZ3	1:AQ:272:TYR:CE1	2.26	0.50
1:BC:43:ALA:HB1	1:BC:158:GLU:HA	1.92	0.50
1:BH:170:PHE:HD1	1:BH:389:MET:CE	2.23	0.50
1:BK:239:ILE:HG12	1:BK:326:ILE:CD1	2.41	0.50
1:BL:189:PHE:HE2	1:BL:249:LEU:CD2	2.24	0.50
1:BQ:191:LEU:HD23	1:BQ:191:LEU:N	2.20	0.50
1:BS:162:PHE:CD2	1:BS:163:LEU:HD13	2.46	0.50
1:CD:454:ASN:ND2	1:CD:456:ALA:H	2.02	0.50
1:CH:191:LEU:N	1:CH:191:LEU:CD2	2.75	0.50
1:CJ:16:ALA:O	1:CJ:17:ASN:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:272:TYR:CD1	1:CJ:272:TYR:N	2.79	0.50
1:CJ:74:ASN:ND2	1:CJ:77:THR:OG1	2.44	0.50
1:CK:189:PHE:HE2	1:CK:249:LEU:CD2	2.24	0.50
1:CN:14:CYS:H	1:CN:138:ASN:ND2	2.09	0.50
1:AA:75:ARG:NH2	1:AA:391:ALA:O	2.45	0.50
1:AH:189:PHE:HE1	1:AH:198:ARG:HG2	1.75	0.50
1:AO:203:THR:CB	1:AO:300:GLN:HG3	2.40	0.50
1:AP:288:HIS:HD2	1:AP:337:ASP:OD2	1.94	0.50
1:AJ:272:TYR:CE2	1:AQ:55:ARG:HD3	2.46	0.50
1:BL:454:ASN:ND2	1:BL:456:ALA:H	2.05	0.50
1:BO:189:PHE:CE1	1:BO:198:ARG:CG	2.94	0.50
1:BT:234:ARG:HG2	1:BT:280:GLU:HG2	1.94	0.50
1:CB:454:ASN:ND2	1:CB:456:ALA:H	2.08	0.50
1:AA:55:ARG:HD3	1:CC:272:TYR:CE2	2.46	0.50
1:CF:16:ALA:O	1:CF:17:ASN:HB2	2.12	0.50
1:CK:14:CYS:H	1:CK:138:ASN:ND2	2.08	0.50
1:CT:263:ASN:O	1:CT:267:LYS:HG3	2.11	0.50
1:AB:272:TYR:CD1	1:AB:272:TYR:N	2.78	0.50
1:AC:79:ARG:HH11	1:AC:79:ARG:HG3	1.77	0.50
1:AF:250:TRP:HZ3	1:AF:272:TYR:CE1	2.25	0.50
1:AJ:189:PHE:HD2	1:AJ:247:ILE:CD1	2.25	0.50
1:AL:191:LEU:N	1:AL:191:LEU:CD2	2.72	0.50
1:AN:67:VAL:HG23	1:AN:135:LEU:HB2	1.94	0.50
1:AT:162:PHE:CD2	1:AT:163:LEU:HD13	2.47	0.50
1:BB:189:PHE:CE2	1:BB:249:LEU:HD21	2.43	0.50
1:BF:162:PHE:CD2	1:BF:163:LEU:HD13	2.47	0.50
1:BG:30:SER:O	1:BG:33:LYS:HB2	2.10	0.50
1:BI:67:VAL:HG23	1:BI:135:LEU:HB2	1.93	0.50
1:BI:79:ARG:HH11	1:BI:79:ARG:HG3	1.75	0.50
1:BM:250:TRP:CE3	1:BM:272:TYR:CE1	2.99	0.50
1:BS:74:ASN:ND2	1:BS:77:THR:OG1	2.44	0.50
1:CC:454:ASN:ND2	1:CC:456:ALA:H	2.06	0.50
1:CE:30:SER:O	1:CE:33:LYS:HB2	2.11	0.50
1:CH:18:ARG:HG3	1:CH:19:TYR:N	2.26	0.50
1:CO:16:ALA:O	1:CO:17:ASN:HB2	2.11	0.50
1:CO:77:THR:O	1:CO:81:THR:HG23	2.11	0.50
1:CS:30:SER:O	1:CS:33:LYS:HB2	2.12	0.50
1:AB:239:ILE:HG12	1:AB:326:ILE:CD1	2.41	0.50
1:AF:30:SER:O	1:AF:33:LYS:HB2	2.12	0.50
1:AG:79:ARG:NH1	1:AG:79:ARG:CG	2.72	0.50
1:AI:288:HIS:HD2	1:AI:337:ASP:OD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:170:PHE:HD1	1:AJ:389:MET:CE	2.24	0.50
1:AN:14:CYS:HB3	1:AN:64:LEU:HD21	1.94	0.50
1:AN:232:THR:HB	1:AN:334:VAL:CG2	2.40	0.50
1:AN:239:ILE:HG23	1:AN:324:LEU:HD21	1.93	0.50
1:AQ:239:ILE:HD12	1:AQ:275:GLU:HA	1.94	0.50
1:AR:162:PHE:CD2	1:AR:163:LEU:HD13	2.46	0.50
1:AS:162:PHE:CD2	1:AS:163:LEU:HD13	2.45	0.50
1:BA:75:ARG:NH2	1:BA:391:ALA:O	2.44	0.50
1:BC:250:TRP:HZ3	1:BC:272:TYR:CE1	2.28	0.50
1:BO:58:ALA:HB2	1:BO:102:GLY:HA3	1.93	0.50
1:CA:14:CYS:H	1:CA:138:ASN:HD21	1.57	0.50
1:CA:189:PHE:HE1	1:CA:198:ARG:CG	2.24	0.50
1:CD:250:TRP:HZ3	1:CD:272:TYR:CE1	2.26	0.50
1:CE:272:TYR:CD1	1:CE:272:TYR:N	2.80	0.50
1:CF:170:PHE:HD1	1:CF:389:MET:HE2	1.76	0.50
1:CP:189:PHE:HD2	1:CP:247:ILE:HD11	1.77	0.50
1:AD:14:CYS:H	1:AD:138:ASN:ND2	2.09	0.50
1:AD:191:LEU:N	1:AD:191:LEU:CD2	2.74	0.50
1:AG:191:LEU:CD2	1:AG:191:LEU:N	2.74	0.50
1:AG:75:ARG:NH2	1:AG:391:ALA:O	2.45	0.50
1:AF:412:PHE:HB2	1:AJ:442:GLN:HE21	1.76	0.50
1:AN:191:LEU:HD23	1:AN:191:LEU:N	2.20	0.50
1:AO:272:TYR:N	1:AO:272:TYR:HD1	2.10	0.50
1:BH:454:ASN:ND2	1:BH:456:ALA:H	2.04	0.50
1:BM:162:PHE:CD2	1:BM:163:LEU:HD13	2.46	0.50
1:CB:250:TRP:HZ3	1:CB:272:TYR:CE1	2.25	0.50
1:CM:189:PHE:CE1	1:CM:198:ARG:HG2	2.46	0.50
1:CR:454:ASN:ND2	1:CR:456:ALA:H	2.02	0.50
1:AD:442:GLN:HE21	1:AE:412:PHE:HB2	1.77	0.50
1:AF:191:LEU:HD23	1:AF:191:LEU:N	2.21	0.50
1:AI:191:LEU:N	1:AI:191:LEU:HD23	2.19	0.50
1:AI:226:VAL:HG13	1:AI:228:GLY:H	1.76	0.50
1:AO:189:PHE:CE1	1:AO:198:ARG:CG	2.95	0.50
1:BB:398:GLY:HA3	1:BB:494:PHE:CD2	2.47	0.50
1:AF:55:ARG:HD3	1:BH:272:TYR:CE2	2.46	0.50
1:BO:189:PHE:HE1	1:BO:198:ARG:CG	2.24	0.50
1:BS:170:PHE:HD1	1:BS:389:MET:CE	2.25	0.50
1:BS:398:GLY:HA3	1:BS:494:PHE:CD2	2.47	0.50
1:CE:18:ARG:HG3	1:CE:19:TYR:N	2.25	0.50
1:CI:398:GLY:HA3	1:CI:494:PHE:CD2	2.47	0.50
1:CJ:30:SER:O	1:CJ:33:LYS:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:239:ILE:HG12	1:CP:326:ILE:CD1	2.41	0.50
1:CQ:232:THR:HB	1:CQ:334:VAL:HG23	1.93	0.50
1:CR:58:ALA:HB2	1:CR:102:GLY:HA3	1.94	0.50
1:AC:58:ALA:HB2	1:AC:102:GLY:HA3	1.94	0.50
1:AH:170:PHE:HD1	1:AH:389:MET:HE2	1.76	0.50
1:AI:79:ARG:CG	1:AI:79:ARG:HH11	2.19	0.50
1:AM:58:ALA:HB2	1:AM:102:GLY:HA3	1.93	0.50
1:BI:189:PHE:HD2	1:BI:247:ILE:HD11	1.76	0.50
1:CC:250:TRP:HZ3	1:CC:272:TYR:CE1	2.20	0.50
1:CH:239:ILE:HG12	1:CH:326:ILE:CD1	2.42	0.50
1:CH:189:PHE:HD2	1:CH:247:ILE:CD1	2.25	0.50
1:CI:58:ALA:HB2	1:CI:102:GLY:HA3	1.93	0.50
1:CM:272:TYR:HD1	1:CM:272:TYR:N	2.09	0.50
1:CR:189:PHE:HD2	1:CR:247:ILE:CD1	2.25	0.50
1:AC:239:ILE:HD12	1:AC:275:GLU:HA	1.94	0.50
1:AE:250:TRP:HZ3	1:AE:272:TYR:CE1	2.28	0.50
1:AP:67:VAL:HG23	1:AP:135:LEU:HB2	1.93	0.50
1:BA:454:ASN:HD21	1:BA:456:ALA:HB3	1.77	0.50
1:BB:272:TYR:CD1	1:BB:272:TYR:N	2.79	0.50
1:BC:226:VAL:HG13	1:BC:228:GLY:H	1.76	0.50
1:BG:191:LEU:CD2	1:BG:191:LEU:N	2.75	0.50
1:BJ:239:ILE:HG12	1:BJ:326:ILE:CD1	2.41	0.50
1:BJ:404:LEU:HD22	1:BJ:486:VAL:HG22	1.93	0.50
1:BN:170:PHE:HD1	1:BN:389:MET:HE2	1.77	0.50
1:BP:67:VAL:HG23	1:BP:135:LEU:HB2	1.93	0.50
1:BQ:58:ALA:HB2	1:BQ:102:GLY:HA3	1.94	0.50
1:CB:454:ASN:HD21	1:CB:456:ALA:HB3	1.77	0.50
1:CJ:272:TYR:CD2	1:CQ:55:ARG:CZ	2.93	0.50
1:CK:43:ALA:HB1	1:CK:158:GLU:HA	1.93	0.50
1:CM:272:TYR:N	1:CM:272:TYR:CD1	2.79	0.50
1:CQ:14:CYS:H	1:CQ:138:ASN:ND2	2.09	0.50
1:AC:30:SER:O	1:AC:33:LYS:HB2	2.11	0.50
1:AD:189:PHE:HE2	1:AD:249:LEU:HD21	1.75	0.50
1:AE:272:TYR:CE2	1:AM:55:ARG:HD3	2.46	0.50
1:AK:43:ALA:HB1	1:AK:158:GLU:HA	1.93	0.50
1:AL:226:VAL:HG13	1:AL:228:GLY:H	1.77	0.50
1:AQ:170:PHE:HD1	1:AQ:389:MET:CE	2.25	0.50
1:AR:454:ASN:ND2	1:AR:456:ALA:H	2.03	0.50
1:AT:379:VAL:HG11	1:AT:381:MET:HE1	1.94	0.50
1:BB:58:ALA:HB2	1:BB:102:GLY:HA3	1.92	0.50
1:BB:189:PHE:CE1	1:BB:198:ARG:HG2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:170:PHE:HD1	1:BD:389:MET:CE	2.24	0.50
1:BG:398:GLY:HA3	1:BG:494:PHE:CD2	2.47	0.50
1:BK:454:ASN:HD21	1:BK:456:ALA:HB3	1.76	0.50
1:CJ:67:VAL:HG23	1:CJ:135:LEU:HB2	1.92	0.50
1:CK:189:PHE:CE1	1:CK:198:ARG:CG	2.94	0.50
1:CL:189:PHE:HD2	1:CL:247:ILE:HD11	1.76	0.50
1:CL:454:ASN:HD21	1:CL:456:ALA:HB3	1.77	0.50
1:CN:30:SER:O	1:CN:33:LYS:HB2	2.11	0.50
1:CP:454:ASN:HD22	1:CP:456:ALA:N	2.06	0.50
1:CQ:191:LEU:N	1:CQ:191:LEU:CD2	2.73	0.50
1:AD:170:PHE:HD1	1:AD:389:MET:HE2	1.77	0.49
1:AP:239:ILE:HG12	1:AP:326:ILE:CD1	2.42	0.49
1:AR:30:SER:O	1:AR:33:LYS:HB2	2.12	0.49
1:BD:170:PHE:HD1	1:BD:389:MET:HE2	1.76	0.49
1:BI:284:ARG:CG	1:BI:284:ARG:NH1	2.70	0.49
1:BJ:191:LEU:CD2	1:BJ:191:LEU:N	2.70	0.49
1:BM:189:PHE:HE1	1:BM:198:ARG:HG2	1.70	0.49
1:BS:189:PHE:HE2	1:BS:249:LEU:HD21	1.77	0.49
1:BT:189:PHE:HD2	1:BT:247:ILE:HD11	1.77	0.49
1:CB:232:THR:HB	1:CB:334:VAL:HG23	1.93	0.49
1:CF:170:PHE:HD1	1:CF:389:MET:CE	2.25	0.49
1:CE:272:TYR:HE2	1:CM:55:ARG:NE	2.03	0.49
1:CR:191:LEU:N	1:CR:191:LEU:CD2	2.75	0.49
1:AA:226:VAL:HG13	1:AA:228:GLY:H	1.77	0.49
1:AJ:404:LEU:HD22	1:AJ:486:VAL:HG22	1.94	0.49
1:AL:30:SER:O	1:AL:33:LYS:HB2	2.12	0.49
1:AO:189:PHE:HE1	1:AO:198:ARG:CG	2.25	0.49
1:AP:404:LEU:HD22	1:AP:486:VAL:HG22	1.94	0.49
1:AT:170:PHE:HD1	1:AT:389:MET:CE	2.25	0.49
1:BD:272:TYR:HD1	1:BD:272:TYR:N	2.11	0.49
1:BL:189:PHE:HD2	1:BL:247:ILE:HD11	1.76	0.49
1:BT:189:PHE:HE2	1:BT:249:LEU:HD21	1.76	0.49
1:CB:25:ILE:HG23	1:CB:152:LEU:HD11	1.94	0.49
1:CD:79:ARG:NH1	1:CD:79:ARG:CG	2.71	0.49
1:CG:189:PHE:CE2	1:CG:249:LEU:HD21	2.44	0.49
1:CL:67:VAL:HG23	1:CL:135:LEU:HB2	1.93	0.49
1:CR:30:SER:O	1:CR:33:LYS:HB2	2.12	0.49
1:AJ:203:THR:CB	1:AJ:300:GLN:HG3	2.42	0.49
1:AK:67:VAL:HG23	1:AK:135:LEU:HB2	1.92	0.49
1:AL:454:ASN:ND2	1:AL:456:ALA:H	2.05	0.49
1:AN:58:ALA:HB2	1:AN:102:GLY:HA3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:25:ILE:HG23	1:AO:152:LEU:HD11	1.93	0.49
1:BB:272:TYR:HD1	1:BB:272:TYR:N	2.11	0.49
1:BC:272:TYR:CD2	1:CA:55:ARG:HD3	2.47	0.49
1:BM:191:LEU:N	1:BM:191:LEU:CD2	2.74	0.49
1:BN:14:CYS:H	1:BN:138:ASN:HD21	1.58	0.49
1:BO:454:ASN:HD22	1:BO:456:ALA:N	2.06	0.49
1:CE:191:LEU:CD2	1:CE:191:LEU:N	2.76	0.49
1:CE:22:THR:OG1	1:CE:131:HIS:CD2	2.58	0.49
1:CI:189:PHE:HD2	1:CI:247:ILE:CD1	2.25	0.49
1:CL:288:HIS:HD2	1:CL:337:ASP:OD2	1.94	0.49
1:CM:189:PHE:HD2	1:CM:247:ILE:CD1	2.25	0.49
1:CN:67:VAL:HG23	1:CN:135:LEU:HB2	1.94	0.49
1:CQ:232:THR:HB	1:CQ:334:VAL:CG2	2.42	0.49
1:CQ:79:ARG:HH11	1:CQ:79:ARG:HG3	1.77	0.49
1:CR:404:LEU:HD22	1:CR:486:VAL:HG22	1.94	0.49
1:AD:284:ARG:CG	1:AD:284:ARG:NH1	2.70	0.49
1:AF:162:PHE:CD2	1:AF:163:LEU:HD13	2.47	0.49
1:AH:30:SER:O	1:AH:33:LYS:HB2	2.12	0.49
1:AJ:250:TRP:HZ3	1:AJ:272:TYR:CE1	2.28	0.49
1:AP:191:LEU:CD2	1:AP:191:LEU:N	2.72	0.49
1:BA:67:VAL:HG23	1:BA:135:LEU:HB2	1.94	0.49
1:BB:18:ARG:NH1	1:BB:18:ARG:HB2	2.27	0.49
1:BB:454:ASN:HD21	1:BB:456:ALA:HB3	1.77	0.49
1:BF:16:ALA:O	1:BF:17:ASN:HB2	2.11	0.49
1:BJ:79:ARG:CG	1:BJ:79:ARG:NH1	2.73	0.49
1:BK:189:PHE:HE2	1:BK:249:LEU:HD21	1.78	0.49
1:BN:263:ASN:O	1:BN:267:LYS:HG3	2.12	0.49
1:BO:75:ARG:NH2	1:BO:391:ALA:O	2.45	0.49
1:CE:189:PHE:CE2	1:CE:249:LEU:HD21	2.45	0.49
1:CL:14:CYS:HB3	1:CL:64:LEU:HD21	1.93	0.49
1:CO:288:HIS:HD2	1:CO:337:ASP:OD2	1.95	0.49
1:CO:454:ASN:HD22	1:CO:456:ALA:N	2.06	0.49
1:CP:28:MET:HE2	1:CP:152:LEU:HG	1.95	0.49
1:AB:30:SER:O	1:AB:33:LYS:HB2	2.12	0.49
1:AE:16:ALA:O	1:AE:17:ASN:HB2	2.11	0.49
1:AH:226:VAL:HG13	1:AH:228:GLY:H	1.77	0.49
1:AI:239:ILE:HG12	1:AI:326:ILE:CD1	2.42	0.49
1:AJ:239:ILE:HD12	1:AJ:275:GLU:HA	1.94	0.49
1:AJ:398:GLY:HA3	1:AJ:494:PHE:CD2	2.48	0.49
1:AQ:232:THR:HB	1:AQ:334:VAL:HG23	1.94	0.49
1:AS:189:PHE:CE1	1:AS:198:ARG:CG	2.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:284:ARG:NH1	1:BB:284:ARG:CG	2.67	0.49
1:BE:398:GLY:HA3	1:BE:494:PHE:CD2	2.48	0.49
1:BE:67:VAL:HG23	1:BE:135:LEU:HB2	1.94	0.49
1:BI:162:PHE:CD2	1:BI:163:LEU:HD13	2.47	0.49
1:BI:191:LEU:N	1:BI:191:LEU:CD2	2.74	0.49
1:BN:454:ASN:HD21	1:BN:456:ALA:HB3	1.78	0.49
1:BN:74:ASN:ND2	1:BN:77:THR:OG1	2.45	0.49
1:BO:272:TYR:N	1:BO:272:TYR:CD1	2.79	0.49
1:BQ:30:SER:O	1:BQ:33:LYS:HB2	2.11	0.49
1:CD:189:PHE:CE1	1:CD:198:ARG:CG	2.96	0.49
1:CF:58:ALA:HB2	1:CF:102:GLY:HA3	1.94	0.49
1:CG:288:HIS:HD2	1:CG:337:ASP:OD2	1.95	0.49
1:CK:239:ILE:HD12	1:CK:275:GLU:HA	1.94	0.49
1:CP:272:TYR:N	1:CP:272:TYR:HD1	2.10	0.49
1:AB:61:PHE:CD2	1:AB:243:ILE:HD11	2.47	0.49
1:AG:74:ASN:ND2	1:AG:77:THR:OG1	2.46	0.49
1:AI:191:LEU:N	1:AI:191:LEU:CD2	2.76	0.49
1:AK:16:ALA:O	1:AK:17:ASN:HB2	2.12	0.49
1:AL:189:PHE:HE1	1:AL:198:ARG:CG	2.24	0.49
1:BC:67:VAL:HG23	1:BC:135:LEU:HB2	1.94	0.49
1:BI:189:PHE:CE2	1:BI:249:LEU:HD21	2.45	0.49
1:BJ:170:PHE:HD1	1:BJ:389:MET:CE	2.25	0.49
1:BJ:58:ALA:HB2	1:BJ:102:GLY:HA3	1.94	0.49
1:BP:162:PHE:CD2	1:BP:163:LEU:HD13	2.47	0.49
1:CF:232:THR:HB	1:CF:334:VAL:CG2	2.43	0.49
1:CJ:239:ILE:HG12	1:CJ:326:ILE:CD1	2.43	0.49
1:CN:191:LEU:CD2	1:CN:191:LEU:N	2.75	0.49
1:CR:454:ASN:HD21	1:CR:456:ALA:HB3	1.77	0.49
1:AB:162:PHE:CD2	1:AB:163:LEU:HD13	2.48	0.49
1:AG:170:PHE:HD1	1:AG:389:MET:HE2	1.77	0.49
1:AI:263:ASN:O	1:AI:267:LYS:HG3	2.13	0.49
1:AK:79:ARG:HH11	1:AK:79:ARG:HG3	1.77	0.49
1:BA:191:LEU:N	1:BA:191:LEU:HD23	2.21	0.49
1:BD:43:ALA:HB1	1:BD:158:GLU:HA	1.94	0.49
1:BK:43:ALA:HB1	1:BK:158:GLU:HA	1.95	0.49
1:BO:74:ASN:ND2	1:BO:77:THR:OG1	2.45	0.49
1:BP:263:ASN:O	1:BP:267:LYS:HG3	2.13	0.49
1:BP:79:ARG:CG	1:BP:79:ARG:NH1	2.61	0.49
1:CA:239:ILE:HG12	1:CA:326:ILE:CD1	2.43	0.49
1:AB:272:TYR:CE2	1:CB:55:ARG:CZ	2.96	0.49
1:CD:170:PHE:HD1	1:CD:389:MET:CE	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:189:PHE:HD2	1:CF:247:ILE:CD1	2.26	0.49
1:CG:189:PHE:HD2	1:CG:247:ILE:HD11	1.77	0.49
1:CI:454:ASN:ND2	1:CI:456:ALA:H	2.08	0.49
1:CO:162:PHE:CD2	1:CO:163:LEU:HD13	2.47	0.49
1:CQ:189:PHE:HE2	1:CQ:249:LEU:HD21	1.77	0.49
1:AC:189:PHE:CE1	1:AC:198:ARG:CG	2.95	0.49
1:AE:398:GLY:HA3	1:AE:494:PHE:CD2	2.48	0.49
1:AM:191:LEU:HD23	1:AM:191:LEU:N	2.16	0.49
1:AO:454:ASN:ND2	1:AO:456:ALA:H	2.06	0.49
1:AP:454:ASN:HD21	1:AP:456:ALA:HB3	1.78	0.49
1:AS:189:PHE:HD2	1:AS:247:ILE:HD11	1.78	0.49
1:AT:58:ALA:HB2	1:AT:102:GLY:HA3	1.93	0.49
1:BA:272:TYR:N	1:BA:272:TYR:CD1	2.80	0.49
1:BE:170:PHE:HD1	1:BE:389:MET:HE2	1.77	0.49
1:AG:272:TYR:CE2	1:BG:55:ARG:HD3	2.47	0.49
1:BQ:191:LEU:CD2	1:BQ:191:LEU:N	2.76	0.49
1:CC:189:PHE:HE2	1:CC:249:LEU:CD2	2.26	0.49
1:CE:232:THR:HB	1:CE:334:VAL:HG23	1.95	0.49
1:CG:79:ARG:NH1	1:CG:79:ARG:CG	2.70	0.49
1:CK:239:ILE:HG12	1:CK:326:ILE:CD1	2.42	0.49
1:AH:55:ARG:HD3	1:AK:272:TYR:CD2	2.48	0.49
1:AL:284:ARG:CG	1:AL:284:ARG:NH1	2.70	0.49
1:AL:75:ARG:NH2	1:AL:391:ALA:O	2.46	0.49
1:AQ:14:CYS:H	1:AQ:138:ASN:HD21	1.58	0.49
1:AQ:454:ASN:HD21	1:AQ:456:ALA:HB3	1.78	0.49
1:AT:67:VAL:HG23	1:AT:135:LEU:HB2	1.93	0.49
1:BH:239:ILE:HG12	1:BH:326:ILE:CD1	2.42	0.49
1:BJ:16:ALA:O	1:BJ:17:ASN:HB2	2.11	0.49
1:BP:250:TRP:HZ3	1:BP:272:TYR:CE1	2.27	0.49
1:CC:58:ALA:HB2	1:CC:102:GLY:HA3	1.94	0.49
1:CD:272:TYR:HD1	1:CD:272:TYR:N	2.11	0.49
1:CE:284:ARG:NH1	1:CE:284:ARG:CG	2.71	0.49
1:CI:16:ALA:O	1:CI:17:ASN:HB2	2.13	0.49
1:CI:272:TYR:N	1:CI:272:TYR:CD1	2.81	0.49
1:CJ:189:PHE:HD2	1:CJ:247:ILE:CD1	2.26	0.49
1:CM:239:ILE:HD12	1:CM:275:GLU:HA	1.94	0.49
1:CT:398:GLY:HA3	1:CT:494:PHE:CD2	2.47	0.49
1:AG:55:ARG:CZ	1:CG:272:TYR:CD2	2.96	0.49
1:AH:55:ARG:HD3	1:AK:272:TYR:CE2	2.48	0.49
1:AK:272:TYR:N	1:AK:272:TYR:CD1	2.81	0.49
1:AR:442:GLN:HE21	1:AS:412:PHE:HB2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:30:SER:O	1:BA:33:LYS:HB2	2.13	0.49
1:BE:239:ILE:HG12	1:BE:326:ILE:CD1	2.42	0.49
1:BE:250:TRP:HZ3	1:BE:272:TYR:CE1	2.29	0.49
1:BK:284:ARG:CG	1:BK:284:ARG:NH1	2.72	0.49
1:BO:189:PHE:HD2	1:BO:247:ILE:HD11	1.77	0.49
1:BR:74:ASN:ND2	1:BR:77:THR:OG1	2.46	0.49
1:CB:263:ASN:O	1:CB:267:LYS:HG3	2.12	0.49
1:CC:30:SER:O	1:CC:33:LYS:HB2	2.13	0.49
1:CG:14:CYS:H	1:CG:138:ASN:ND2	2.10	0.49
1:CG:239:ILE:HD12	1:CG:275:GLU:HA	1.94	0.49
1:CQ:67:VAL:HG23	1:CQ:135:LEU:HB2	1.94	0.49
1:AB:189:PHE:HD2	1:AB:247:ILE:CD1	2.25	0.48
1:AG:189:PHE:HD2	1:AG:247:ILE:CD1	2.25	0.48
1:AN:79:ARG:NH1	1:AN:79:ARG:CG	2.74	0.48
1:AO:250:TRP:HZ3	1:AO:272:TYR:CE1	2.25	0.48
1:BA:284:ARG:NH1	1:BA:284:ARG:CG	2.68	0.48
1:BP:272:TYR:HD1	1:BP:272:TYR:N	2.11	0.48
1:BP:30:SER:O	1:BP:33:LYS:HB2	2.14	0.48
1:BR:191:LEU:N	1:BR:191:LEU:HD23	2.21	0.48
1:CA:284:ARG:NH1	1:CA:284:ARG:CG	2.74	0.48
1:CG:189:PHE:HE1	1:CG:198:ARG:HG2	1.75	0.48
1:CJ:14:CYS:H	1:CJ:138:ASN:ND2	2.07	0.48
1:CK:170:PHE:HD1	1:CK:389:MET:CE	2.26	0.48
1:CP:272:TYR:N	1:CP:272:TYR:CD1	2.81	0.48
1:CP:398:GLY:HA3	1:CP:494:PHE:CD2	2.48	0.48
1:CR:379:VAL:HG11	1:CR:381:MET:HE1	1.95	0.48
1:CT:299:SER:O	1:CT:302:ASP:HB2	2.13	0.48
1:AC:454:ASN:ND2	1:AC:456:ALA:H	2.06	0.48
1:AH:189:PHE:HD2	1:AH:247:ILE:CD1	2.26	0.48
1:AH:189:PHE:CE1	1:AH:198:ARG:HG2	2.48	0.48
1:AJ:250:TRP:CE3	1:AJ:272:TYR:CE1	3.01	0.48
1:AL:189:PHE:HD2	1:AL:247:ILE:HD11	1.78	0.48
1:AM:162:PHE:CD2	1:AM:163:LEU:HD13	2.48	0.48
1:AQ:234:ARG:HG2	1:AQ:280:GLU:HG2	1.94	0.48
1:AR:14:CYS:H	1:AR:138:ASN:ND2	2.07	0.48
1:AR:189:PHE:HD2	1:AR:247:ILE:CD1	2.25	0.48
1:AR:263:ASN:O	1:AR:267:LYS:HG3	2.13	0.48
1:AS:272:TYR:CD1	1:AS:272:TYR:N	2.80	0.48
1:AT:189:PHE:HD2	1:AT:247:ILE:HD11	1.78	0.48
1:BH:454:ASN:HD21	1:BH:456:ALA:HB3	1.78	0.48
1:BO:250:TRP:HZ3	1:BO:272:TYR:CE1	2.25	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:14:CYS:H	1:BP:138:ASN:ND2	2.11	0.48
1:CC:189:PHE:CE1	1:CC:198:ARG:CG	2.96	0.48
1:CF:189:PHE:CE1	1:CF:198:ARG:HG2	2.46	0.48
1:CI:189:PHE:CE2	1:CI:249:LEU:HD21	2.41	0.48
1:CO:18:ARG:HG3	1:CO:19:TYR:N	2.27	0.48
1:CR:237:VAL:HG23	1:CR:279:PHE:CD2	2.48	0.48
1:CS:74:ASN:ND2	1:CS:77:THR:OG1	2.46	0.48
1:AG:454:ASN:ND2	1:AG:456:ALA:H	2.08	0.48
1:AJ:30:SER:O	1:AJ:33:LYS:HB2	2.13	0.48
1:BC:252:VAL:HG22	1:BC:253:SER:N	2.28	0.48
1:BD:191:LEU:N	1:BD:191:LEU:CD2	2.73	0.48
1:BD:189:PHE:HD2	1:BD:247:ILE:HD11	1.78	0.48
1:BS:239:ILE:HG12	1:BS:326:ILE:CD1	2.44	0.48
1:BT:239:ILE:HG12	1:BT:326:ILE:CD1	2.43	0.48
1:CE:239:ILE:HG12	1:CE:326:ILE:CD1	2.44	0.48
1:CF:442:GLN:HE21	1:CG:412:PHE:HB2	1.78	0.48
1:CG:189:PHE:HD2	1:CG:247:ILE:CD1	2.26	0.48
1:CS:189:PHE:HE2	1:CS:249:LEU:HD21	1.77	0.48
1:CS:11:PRO:HG2	1:CS:18:ARG:CD	2.43	0.48
1:AB:442:GLN:HE21	1:AC:412:PHE:HB2	1.77	0.48
1:AG:189:PHE:CE2	1:AG:249:LEU:HD21	2.42	0.48
1:AK:189:PHE:HD2	1:AK:247:ILE:HD11	1.77	0.48
1:AN:232:THR:HB	1:AN:334:VAL:HG23	1.96	0.48
1:AT:191:LEU:N	1:AT:191:LEU:CD2	2.76	0.48
1:AT:454:ASN:ND2	1:AT:456:ALA:H	2.09	0.48
1:BC:189:PHE:HE2	1:BC:249:LEU:CD2	2.26	0.48
1:BD:201:GLY:HA3	1:BD:300:GLN:HG2	1.96	0.48
1:BG:189:PHE:CE2	1:BG:249:LEU:HD21	2.44	0.48
1:BI:454:ASN:HD21	1:BI:456:ALA:HB3	1.78	0.48
1:BO:239:ILE:HG12	1:BO:326:ILE:CD1	2.44	0.48
1:CD:191:LEU:CD2	1:CD:191:LEU:N	2.77	0.48
1:CM:398:GLY:HA3	1:CM:494:PHE:CD2	2.48	0.48
1:AH:189:PHE:CE2	1:AH:249:LEU:HD21	2.44	0.48
1:AI:250:TRP:CE3	1:AI:272:TYR:CE1	3.01	0.48
1:AJ:18:ARG:HD2	1:AJ:19:TYR:O	2.13	0.48
1:AO:18:ARG:HG3	1:AO:19:TYR:N	2.28	0.48
1:BA:43:ALA:HB1	1:BA:158:GLU:HA	1.95	0.48
1:BB:234:ARG:HG2	1:BB:280:GLU:HG2	1.95	0.48
1:BC:191:LEU:N	1:BC:191:LEU:CD2	2.76	0.48
1:BD:272:TYR:CD1	1:BD:272:TYR:N	2.81	0.48
1:BG:226:VAL:HG13	1:BG:228:GLY:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:272:TYR:N	1:BG:272:TYR:CD1	2.82	0.48
1:BH:189:PHE:CE1	1:BH:198:ARG:HG2	2.48	0.48
1:BJ:284:ARG:CG	1:BJ:284:ARG:NH1	2.73	0.48
1:AQ:272:TYR:HD2	1:BL:55:ARG:HD3	1.76	0.48
1:BM:272:TYR:N	1:BM:272:TYR:CD1	2.82	0.48
1:BQ:454:ASN:ND2	1:BQ:456:ALA:H	2.10	0.48
1:BS:454:ASN:HD21	1:BS:456:ALA:HB3	1.79	0.48
1:CD:55:ARG:HD3	1:CN:272:TYR:CE2	2.49	0.48
1:CN:10:ILE:HD13	1:CN:20:LEU:HD13	1.95	0.48
1:CO:393:HIS:CG	1:CO:496:PHE:HB3	2.48	0.48
1:CS:272:TYR:N	1:CS:272:TYR:CD1	2.81	0.48
1:AC:16:ALA:O	1:AC:17:ASN:HB2	2.13	0.48
1:AG:67:VAL:HG23	1:AG:135:LEU:HB2	1.96	0.48
1:AJ:189:PHE:CE2	1:AJ:249:LEU:HD21	2.46	0.48
1:AP:22:THR:OG1	1:AP:131:HIS:CD2	2.58	0.48
1:AR:272:TYR:N	1:AR:272:TYR:CD1	2.80	0.48
1:AR:272:TYR:N	1:AR:272:TYR:HD1	2.12	0.48
1:BF:250:TRP:HZ3	1:BF:272:TYR:CE1	2.26	0.48
1:CG:272:TYR:CD1	1:CG:272:TYR:N	2.82	0.48
1:CK:398:GLY:HA3	1:CK:494:PHE:CD2	2.48	0.48
1:CL:203:THR:HB	1:CL:300:GLN:HG3	1.94	0.48
1:CN:189:PHE:HD2	1:CN:247:ILE:HD11	1.77	0.48
1:CN:454:ASN:HD21	1:CN:456:ALA:HB3	1.77	0.48
1:CQ:189:PHE:CE1	1:CQ:198:ARG:CG	2.96	0.48
1:CS:234:ARG:HG2	1:CS:280:GLU:HG2	1.94	0.48
1:CS:272:TYR:N	1:CS:272:TYR:HD1	2.11	0.48
1:CT:189:PHE:HE2	1:CT:249:LEU:HD21	1.79	0.48
1:AA:252:VAL:HG22	1:AA:253:SER:N	2.28	0.48
1:AF:226:VAL:HG13	1:AF:228:GLY:H	1.78	0.48
1:AI:379:VAL:HG11	1:AI:381:MET:HE1	1.95	0.48
1:AQ:232:THR:HB	1:AQ:334:VAL:CG2	2.43	0.48
1:AR:189:PHE:HD2	1:AR:247:ILE:HD11	1.79	0.48
1:BF:454:ASN:HD21	1:BF:456:ALA:HB3	1.78	0.48
1:BG:58:ALA:HB2	1:BG:102:GLY:HA3	1.95	0.48
1:BH:43:ALA:HB1	1:BH:158:GLU:HA	1.95	0.48
1:BP:189:PHE:HE2	1:BP:249:LEU:HD21	1.79	0.48
1:CB:20:LEU:HB2	1:CB:132:PHE:O	2.14	0.48
1:CC:239:ILE:HG12	1:CC:326:ILE:CD1	2.44	0.48
1:CF:191:LEU:CD2	1:CF:191:LEU:N	2.75	0.48
1:CH:454:ASN:ND2	1:CH:456:ALA:H	2.06	0.48
1:CL:252:VAL:HG22	1:CL:253:SER:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:189:PHE:HD2	1:CO:247:ILE:HD11	1.78	0.48
1:CR:170:PHE:HD1	1:CR:389:MET:CE	2.25	0.48
1:CS:284:ARG:CG	1:CS:284:ARG:NH1	2.73	0.48
1:CT:272:TYR:CD1	1:CT:272:TYR:N	2.82	0.48
1:AH:25:ILE:HG23	1:AH:152:LEU:HD11	1.96	0.48
1:AP:454:ASN:ND2	1:AP:456:ALA:H	2.05	0.48
1:AP:55:ARG:CZ	1:BM:272:TYR:CE2	2.97	0.48
1:AS:232:THR:HB	1:AS:334:VAL:CG2	2.43	0.48
1:BB:239:ILE:HG23	1:BB:324:LEU:HD21	1.96	0.48
1:BC:404:LEU:HD22	1:BC:486:VAL:HG22	1.95	0.48
1:BF:239:ILE:HG12	1:BF:326:ILE:CD1	2.44	0.48
1:BN:239:ILE:HG12	1:BN:326:ILE:CD1	2.44	0.48
1:BR:75:ARG:NH2	1:BR:391:ALA:O	2.46	0.48
1:BT:189:PHE:CE2	1:BT:249:LEU:HD21	2.49	0.48
1:CD:22:THR:OG1	1:CD:131:HIS:CD2	2.58	0.48
1:CD:74:ASN:ND2	1:CD:77:THR:OG1	2.46	0.48
1:CQ:170:PHE:HD1	1:CQ:389:MET:CE	2.26	0.48
1:CR:10:ILE:HG21	1:CR:146:TRP:CZ2	2.49	0.48
1:AF:252:VAL:HG22	1:AF:253:SER:N	2.29	0.48
1:AF:272:TYR:HD2	1:BK:55:ARG:HD3	1.77	0.48
1:AK:250:TRP:HZ3	1:AK:272:TYR:CE1	2.23	0.48
1:AN:440:ALA:CB	1:AO:444:LEU:HD13	2.43	0.48
1:AO:14:CYS:H	1:AO:138:ASN:HD21	1.60	0.48
1:AR:22:THR:OG1	1:AR:131:HIS:CD2	2.60	0.48
1:BA:170:PHE:HD1	1:BA:389:MET:CE	2.26	0.48
1:BH:189:PHE:HD2	1:BH:247:ILE:CD1	2.27	0.48
1:BM:170:PHE:HD1	1:BM:389:MET:CE	2.27	0.48
1:BN:239:ILE:HD12	1:BN:275:GLU:HA	1.95	0.48
1:BR:263:ASN:O	1:BR:267:LYS:HG3	2.14	0.48
1:BS:189:PHE:HD2	1:BS:247:ILE:HD11	1.79	0.48
1:BT:16:ALA:O	1:BT:17:ASN:HB2	2.14	0.48
1:CB:30:SER:O	1:CB:33:LYS:HB2	2.14	0.48
1:CG:191:LEU:N	1:CG:191:LEU:CD2	2.75	0.48
1:CH:189:PHE:HD2	1:CH:247:ILE:HD11	1.79	0.48
1:CJ:43:ALA:HB1	1:CJ:158:GLU:HA	1.95	0.48
1:CO:191:LEU:HD23	1:CO:191:LEU:N	2.21	0.48
1:CO:79:ARG:NH1	1:CO:79:ARG:HG3	2.23	0.48
1:CP:162:PHE:CD2	1:CP:163:LEU:HD13	2.48	0.48
1:CR:239:ILE:HD12	1:CR:275:GLU:HA	1.96	0.48
1:AB:189:PHE:CE1	1:AB:198:ARG:HG2	2.49	0.48
1:AI:162:PHE:CD2	1:AI:163:LEU:HD13	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:454:ASN:ND2	1:AK:456:ALA:H	2.07	0.48
1:AS:239:ILE:HG12	1:AS:326:ILE:CD1	2.44	0.48
1:BD:189:PHE:CE1	1:BD:198:ARG:CG	2.95	0.48
1:AP:272:TYR:CE2	1:BE:55:ARG:HD3	2.49	0.48
1:BH:263:ASN:O	1:BH:267:LYS:HG3	2.14	0.48
1:BJ:393:HIS:CG	1:BJ:496:PHE:HB3	2.49	0.48
1:BJ:454:ASN:ND2	1:BJ:456:ALA:H	2.06	0.48
1:BL:440:ALA:CB	1:BM:444:LEU:HD13	2.44	0.48
1:BN:237:VAL:HG23	1:BN:279:PHE:CD2	2.49	0.48
1:BQ:442:GLN:HE21	1:BR:412:PHE:HB2	1.78	0.48
1:CC:162:PHE:CD2	1:CC:163:LEU:HD13	2.49	0.48
1:CD:393:HIS:CG	1:CD:496:PHE:HB3	2.48	0.48
1:CE:58:ALA:HB2	1:CE:102:GLY:HA3	1.96	0.48
1:CK:170:PHE:HD1	1:CK:389:MET:HE2	1.78	0.48
1:AA:250:TRP:HZ3	1:AA:272:TYR:CE1	2.28	0.47
1:AD:272:TYR:N	1:AD:272:TYR:HD1	2.12	0.47
1:AF:237:VAL:HG23	1:AF:279:PHE:CD2	2.49	0.47
1:AH:189:PHE:HD2	1:AH:247:ILE:HD11	1.79	0.47
1:AN:442:GLN:NE2	1:AO:412:PHE:HB2	2.29	0.47
1:AP:30:SER:O	1:AP:33:LYS:HB2	2.14	0.47
1:AS:234:ARG:HG2	1:AS:280:GLU:HG2	1.96	0.47
1:BH:191:LEU:N	1:BH:191:LEU:CD2	2.76	0.47
1:BR:239:ILE:HD12	1:BR:275:GLU:HA	1.95	0.47
1:CD:188:PHE:C	1:CD:189:PHE:HD1	2.17	0.47
1:CH:170:PHE:HD1	1:CH:389:MET:CE	2.27	0.47
1:CH:239:ILE:HD12	1:CH:275:GLU:HA	1.96	0.47
1:CK:16:ALA:O	1:CK:17:ASN:HB2	2.14	0.47
1:AB:67:VAL:HG23	1:AB:135:LEU:HB2	1.95	0.47
1:AI:30:SER:O	1:AI:33:LYS:HB2	2.14	0.47
1:AN:189:PHE:CE1	1:AN:198:ARG:HG2	2.49	0.47
1:BE:11:PRO:HG2	1:BE:18:ARG:HD3	1.95	0.47
1:BH:67:VAL:HG23	1:BH:135:LEU:HB2	1.96	0.47
1:BL:201:GLY:HA3	1:BL:300:GLN:HG2	1.96	0.47
1:BN:189:PHE:HD2	1:BN:247:ILE:CD1	2.26	0.47
1:BT:162:PHE:CD2	1:BT:163:LEU:HD13	2.48	0.47
1:CA:25:ILE:HG23	1:CA:152:LEU:HD11	1.96	0.47
1:CF:379:VAL:HG11	1:CF:381:MET:HE1	1.95	0.47
1:CH:58:ALA:HB2	1:CH:102:GLY:HA3	1.96	0.47
1:CJ:226:VAL:HG13	1:CJ:228:GLY:H	1.78	0.47
1:CK:191:LEU:CD2	1:CK:191:LEU:N	2.75	0.47
1:CK:234:ARG:HG2	1:CK:280:GLU:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:250:TRP:HZ3	1:CP:272:TYR:CE1	2.25	0.47
1:AF:189:PHE:HD2	1:AF:247:ILE:CD1	2.27	0.47
1:AH:201:GLY:HA3	1:AH:300:GLN:HG2	1.96	0.47
1:AJ:203:THR:HB	1:AJ:300:GLN:CG	2.45	0.47
1:AN:79:ARG:NH1	1:AN:79:ARG:HG3	2.18	0.47
1:AQ:393:HIS:CG	1:AQ:496:PHE:HB3	2.49	0.47
1:BI:272:TYR:N	1:BI:272:TYR:CD1	2.83	0.47
1:BT:256:ASN:HD22	1:BT:302:ASP:HA	1.79	0.47
1:CC:191:LEU:CD2	1:CC:191:LEU:N	2.74	0.47
1:CF:454:ASN:HD21	1:CF:456:ALA:HB3	1.78	0.47
1:CK:237:VAL:HG23	1:CK:279:PHE:CD2	2.49	0.47
1:CM:30:SER:O	1:CM:33:LYS:HB2	2.14	0.47
1:CO:203:THR:HB	1:CO:300:GLN:HG3	1.96	0.47
1:CP:30:SER:O	1:CP:33:LYS:HB2	2.14	0.47
1:CT:454:ASN:HD21	1:CT:456:ALA:HB3	1.79	0.47
1:AA:11:PRO:HG2	1:AA:18:ARG:HD2	1.96	0.47
1:AD:58:ALA:HB2	1:AD:102:GLY:HA3	1.96	0.47
1:AF:239:ILE:HD12	1:AF:275:GLU:HA	1.96	0.47
1:AG:55:ARG:HD3	1:CG:272:TYR:CE2	2.49	0.47
1:AM:234:ARG:HG2	1:AM:280:GLU:HG2	1.96	0.47
1:AM:252:VAL:HG22	1:AM:253:SER:N	2.29	0.47
1:AO:189:PHE:HD2	1:AO:247:ILE:HD11	1.79	0.47
1:AR:189:PHE:CE1	1:AR:198:ARG:HG2	2.49	0.47
1:BB:404:LEU:HD22	1:BB:486:VAL:HG22	1.95	0.47
1:BD:189:PHE:HE2	1:BD:249:LEU:HD21	1.79	0.47
1:BO:170:PHE:HD1	1:BO:389:MET:HE2	1.78	0.47
1:BS:232:THR:HB	1:BS:334:VAL:HG23	1.96	0.47
1:BT:55:ARG:HD3	1:CA:272:TYR:CE2	2.49	0.47
1:CC:379:VAL:HG11	1:CC:381:MET:HE1	1.96	0.47
1:CI:393:HIS:CG	1:CI:496:PHE:HB3	2.50	0.47
1:CO:272:TYR:CD2	1:CR:55:ARG:CZ	2.97	0.47
1:AA:272:TYR:CD1	1:AA:272:TYR:N	2.82	0.47
1:AD:272:TYR:CD1	1:AD:272:TYR:N	2.82	0.47
1:AE:189:PHE:CE2	1:AE:249:LEU:HD21	2.43	0.47
1:AN:189:PHE:HD2	1:AN:247:ILE:CD1	2.27	0.47
1:AS:191:LEU:N	1:AS:191:LEU:HD23	2.21	0.47
1:AS:58:ALA:HB2	1:AS:102:GLY:HA3	1.95	0.47
1:BF:189:PHE:HD2	1:BF:247:ILE:CD1	2.28	0.47
1:CB:11:PRO:HG2	1:CB:18:ARG:HD2	1.96	0.47
1:CH:162:PHE:CD2	1:CH:163:LEU:HD13	2.49	0.47
1:CI:61:PHE:CD2	1:CI:243:ILE:HD11	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:162:PHE:CD2	1:CJ:163:LEU:HD13	2.49	0.47
1:CJ:237:VAL:HG23	1:CJ:279:PHE:CD2	2.49	0.47
1:CJ:250:TRP:CE3	1:CJ:272:TYR:CD1	3.03	0.47
1:CO:30:SER:O	1:CO:33:LYS:HB2	2.15	0.47
1:AB:55:ARG:NE	1:BB:272:TYR:HE2	2.10	0.47
1:AD:30:SER:O	1:AD:33:LYS:HB2	2.13	0.47
1:AH:284:ARG:CG	1:AH:284:ARG:NH1	2.70	0.47
1:AL:170:PHE:HD1	1:AL:389:MET:CE	2.28	0.47
1:BD:239:ILE:HG12	1:BD:326:ILE:CD1	2.45	0.47
1:BJ:170:PHE:HD1	1:BJ:389:MET:HE2	1.80	0.47
1:BL:14:CYS:H	1:BL:138:ASN:HD21	1.62	0.47
1:BL:232:THR:HB	1:BL:334:VAL:CG2	2.45	0.47
1:BN:14:CYS:HB3	1:BN:64:LEU:HD21	1.97	0.47
1:BQ:79:ARG:HG3	1:BQ:79:ARG:HH11	1.79	0.47
1:BR:232:THR:HB	1:BR:334:VAL:HG23	1.96	0.47
1:BT:232:THR:HB	1:BT:334:VAL:CG2	2.44	0.47
1:CD:272:TYR:CD1	1:CD:272:TYR:N	2.82	0.47
1:CD:454:ASN:HD21	1:CD:456:ALA:HB3	1.79	0.47
1:CJ:250:TRP:HZ3	1:CJ:272:TYR:CE1	2.25	0.47
1:CK:191:LEU:HD23	1:CK:191:LEU:N	2.19	0.47
1:CS:191:LEU:CD2	1:CS:191:LEU:N	2.77	0.47
1:AD:74:ASN:ND2	1:AD:77:THR:OG1	2.48	0.47
1:AI:272:TYR:N	1:AI:272:TYR:CD1	2.83	0.47
1:AK:189:PHE:HE1	1:AK:198:ARG:CG	2.21	0.47
1:AN:440:ALA:HB3	1:AO:444:LEU:HD13	1.97	0.47
1:AO:272:TYR:N	1:AO:272:TYR:CD1	2.81	0.47
1:AQ:162:PHE:CD2	1:AQ:163:LEU:HD13	2.50	0.47
1:BB:189:PHE:HD2	1:BB:247:ILE:HD11	1.79	0.47
1:BG:239:ILE:HG12	1:BG:326:ILE:CD1	2.45	0.47
1:BK:58:ALA:HB2	1:BK:102:GLY:HA3	1.95	0.47
1:BQ:10:ILE:HG21	1:BQ:146:TRP:CZ2	2.50	0.47
1:BQ:189:PHE:HD2	1:BQ:247:ILE:HD11	1.79	0.47
1:BR:170:PHE:HD1	1:BR:389:MET:CE	2.27	0.47
1:CB:189:PHE:HD2	1:CB:247:ILE:CD1	2.27	0.47
1:CC:250:TRP:HE3	1:CC:272:TYR:CD1	2.33	0.47
1:CC:272:TYR:N	1:CC:272:TYR:CD1	2.78	0.47
1:CE:250:TRP:HZ3	1:CE:272:TYR:CE1	2.29	0.47
1:CG:58:ALA:HB2	1:CG:102:GLY:HA3	1.97	0.47
1:CH:379:VAL:HG11	1:CH:381:MET:HE1	1.97	0.47
1:CI:61:PHE:CE2	1:CI:243:ILE:HD11	2.50	0.47
1:CJ:398:GLY:HA3	1:CJ:494:PHE:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:239:ILE:HG12	1:CL:326:ILE:CD1	2.45	0.47
1:CM:393:HIS:CG	1:CM:496:PHE:HB3	2.50	0.47
1:CO:25:ILE:HG23	1:CO:152:LEU:HD11	1.97	0.47
1:CO:234:ARG:HG2	1:CO:280:GLU:HG2	1.97	0.47
1:CR:182:LEU:HG	1:CR:330:ILE:HB	1.97	0.47
1:AF:189:PHE:HD2	1:AF:247:ILE:HD11	1.80	0.47
1:AG:162:PHE:CD2	1:AG:163:LEU:HD13	2.48	0.47
1:AH:18:ARG:HG2	1:AH:20:LEU:HD23	1.96	0.47
1:AK:203:THR:HB	1:AK:300:GLN:HG3	1.97	0.47
1:AM:239:ILE:HD12	1:AM:275:GLU:HA	1.97	0.47
1:AN:25:ILE:HG23	1:AN:152:LEU:HD11	1.96	0.47
1:BD:162:PHE:CD2	1:BD:163:LEU:HD13	2.50	0.47
1:BD:379:VAL:HG11	1:BD:381:MET:HE1	1.97	0.47
1:BD:404:LEU:HD22	1:BD:486:VAL:HG22	1.96	0.47
1:BF:393:HIS:CG	1:BF:496:PHE:HB3	2.50	0.47
1:BF:55:ARG:CZ	1:CH:272:TYR:CE2	2.97	0.47
1:BH:256:ASN:HD22	1:BH:302:ASP:HA	1.80	0.47
1:BI:252:VAL:HG22	1:BI:253:SER:N	2.30	0.47
1:BI:393:HIS:CG	1:BI:496:PHE:HB3	2.50	0.47
1:BK:442:GLN:HE21	1:BL:412:PHE:HB2	1.80	0.47
1:BP:272:TYR:N	1:BP:272:TYR:CD1	2.83	0.47
1:BT:379:VAL:HG11	1:BT:381:MET:HE1	1.96	0.47
1:CB:162:PHE:CD2	1:CB:163:LEU:HD13	2.50	0.47
1:CB:239:ILE:HD12	1:CB:275:GLU:HA	1.97	0.47
1:CD:239:ILE:HG12	1:CD:326:ILE:CD1	2.45	0.47
1:CE:393:HIS:CG	1:CE:496:PHE:HB3	2.49	0.47
1:CL:170:PHE:HD1	1:CL:389:MET:CE	2.28	0.47
1:CN:58:ALA:HB2	1:CN:102:GLY:HA3	1.96	0.47
1:CP:189:PHE:HE2	1:CP:249:LEU:HD21	1.80	0.47
1:CS:189:PHE:HD2	1:CS:247:ILE:HD11	1.80	0.47
1:AA:191:LEU:CD2	1:AA:191:LEU:N	2.74	0.47
1:AB:226:VAL:HG13	1:AB:228:GLY:H	1.80	0.47
1:AG:226:VAL:HG13	1:AG:228:GLY:H	1.80	0.47
1:AG:61:PHE:CD2	1:AG:243:ILE:HD11	2.50	0.47
1:AK:162:PHE:CD2	1:AK:163:LEU:HD13	2.49	0.47
1:AM:189:PHE:CE2	1:AM:249:LEU:HD21	2.45	0.47
1:AP:398:GLY:HA3	1:AP:494:PHE:CD2	2.49	0.47
1:AP:55:ARG:NE	1:BM:272:TYR:HE2	2.10	0.47
1:AQ:189:PHE:CE2	1:AQ:249:LEU:HD21	2.49	0.47
1:BC:250:TRP:CE3	1:BC:272:TYR:CE1	3.02	0.47
1:BC:393:HIS:CG	1:BC:496:PHE:HB3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:226:VAL:HG13	1:BD:228:GLY:H	1.80	0.47
1:BF:288:HIS:HD2	1:BF:337:ASP:OD2	1.97	0.47
1:BH:16:ALA:O	1:BH:17:ASN:HB2	2.15	0.47
1:BH:379:VAL:HG11	1:BH:381:MET:HE1	1.97	0.47
1:BO:454:ASN:HD21	1:BO:456:ALA:HB3	1.80	0.47
1:CA:454:ASN:HD21	1:CA:456:ALA:HB3	1.79	0.47
1:CB:203:THR:HB	1:CB:300:GLN:HG3	1.97	0.47
1:CE:232:THR:HB	1:CE:334:VAL:CG2	2.45	0.47
1:CD:442:GLN:HE21	1:CE:412:PHE:HB2	1.79	0.47
1:CF:189:PHE:CE2	1:CF:249:LEU:HD21	2.46	0.47
1:CF:237:VAL:HG23	1:CF:279:PHE:CD2	2.50	0.47
1:CH:454:ASN:HD21	1:CH:456:ALA:HB3	1.79	0.47
1:CK:263:ASN:O	1:CK:267:LYS:HG3	2.15	0.47
1:CM:232:THR:HB	1:CM:334:VAL:CG2	2.45	0.47
1:CN:239:ILE:HD12	1:CN:275:GLU:HA	1.97	0.47
1:CN:75:ARG:NH2	1:CN:391:ALA:O	2.47	0.47
1:CO:379:VAL:HG11	1:CO:381:MET:HE1	1.95	0.47
1:AE:55:ARG:CZ	1:CP:272:TYR:CD2	2.98	0.47
1:CP:232:THR:HB	1:CP:334:VAL:CG2	2.45	0.47
1:CQ:189:PHE:CE2	1:CQ:249:LEU:HD21	2.50	0.47
1:AD:237:VAL:HG23	1:AD:279:PHE:CD2	2.50	0.47
1:AF:189:PHE:CE2	1:AF:249:LEU:HD21	2.42	0.47
1:AF:454:ASN:HD21	1:AF:456:ALA:HB3	1.80	0.47
1:AG:189:PHE:CE1	1:AG:198:ARG:HG2	2.50	0.47
1:AH:191:LEU:N	1:AH:191:LEU:CD2	2.77	0.47
1:AJ:189:PHE:HE1	1:AJ:198:ARG:HG2	1.74	0.47
1:AM:239:ILE:HG12	1:AM:326:ILE:CD1	2.44	0.47
1:AN:18:ARG:HG3	1:AN:19:TYR:N	2.30	0.47
1:AN:454:ASN:HD21	1:AN:456:ALA:HB3	1.80	0.47
1:AP:203:THR:HB	1:AP:300:GLN:HG3	1.97	0.47
1:AQ:30:SER:O	1:AQ:33:LYS:HB2	2.15	0.47
1:AS:170:PHE:HD1	1:AS:389:MET:HE2	1.79	0.47
1:BA:272:TYR:N	1:BA:272:TYR:HD1	2.12	0.47
1:BG:162:PHE:CD2	1:BG:163:LEU:HD13	2.50	0.47
1:BG:43:ALA:HB1	1:BG:158:GLU:HA	1.97	0.47
1:BH:162:PHE:CD2	1:BH:163:LEU:HD13	2.50	0.47
1:BL:393:HIS:CG	1:BL:496:PHE:HB3	2.50	0.47
1:BM:189:PHE:HD2	1:BM:247:ILE:CD1	2.28	0.47
1:BS:67:VAL:HG23	1:BS:135:LEU:HB2	1.95	0.47
1:CE:75:ARG:NH2	1:CE:391:ALA:O	2.48	0.47
1:CH:189:PHE:CE1	1:CH:198:ARG:HG2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:393:HIS:CG	1:CJ:496:PHE:HB3	2.50	0.47
1:CL:226:VAL:HG13	1:CL:228:GLY:H	1.79	0.47
1:CP:191:LEU:N	1:CP:191:LEU:HD23	2.17	0.47
1:AE:55:ARG:CZ	1:CP:272:TYR:CE2	2.97	0.47
1:CP:170:PHE:HD1	1:CP:389:MET:HE2	1.80	0.47
1:CS:379:VAL:HG11	1:CS:381:MET:HE1	1.96	0.47
1:AB:55:ARG:CZ	1:BB:272:TYR:CD2	2.97	0.47
1:AE:75:ARG:NH2	1:AE:391:ALA:O	2.47	0.47
1:AF:191:LEU:CD2	1:AF:191:LEU:N	2.78	0.47
1:AF:79:ARG:NH1	1:AF:79:ARG:CG	2.72	0.47
1:AI:234:ARG:HG2	1:AI:280:GLU:HG2	1.97	0.47
1:AJ:232:THR:HB	1:AJ:334:VAL:HG23	1.97	0.47
1:AJ:454:ASN:ND2	1:AJ:456:ALA:H	2.09	0.47
1:AN:189:PHE:HD2	1:AN:247:ILE:HD11	1.80	0.47
1:AP:79:ARG:CG	1:AP:79:ARG:HH11	2.27	0.47
1:AS:393:HIS:CG	1:AS:496:PHE:HB3	2.50	0.47
1:BB:25:ILE:HG23	1:BB:152:LEU:HD11	1.97	0.47
1:BD:16:ALA:O	1:BD:17:ASN:HB2	2.14	0.47
1:BE:30:SER:O	1:BE:33:LYS:HB2	2.15	0.47
1:BF:58:ALA:HB2	1:BF:102:GLY:HA3	1.97	0.47
1:BK:379:VAL:HG11	1:BK:381:MET:HE1	1.97	0.47
1:BL:237:VAL:HG23	1:BL:279:PHE:CD2	2.50	0.47
1:BM:189:PHE:HD2	1:BM:247:ILE:HD11	1.80	0.47
1:BP:73:TYR:CZ	1:BP:394:GLY:HA3	2.51	0.47
1:BQ:239:ILE:HD12	1:BQ:275:GLU:HA	1.97	0.47
1:CB:252:VAL:HG22	1:CB:253:SER:N	2.30	0.47
1:CE:79:ARG:HH11	1:CE:79:ARG:CG	2.28	0.47
1:CG:22:THR:OG1	1:CG:131:HIS:CD2	2.61	0.47
1:CI:162:PHE:CD2	1:CI:163:LEU:HD13	2.49	0.47
1:CJ:454:ASN:HD21	1:CJ:456:ALA:HB3	1.80	0.47
1:CK:30:SER:O	1:CK:33:LYS:HB2	2.15	0.47
1:CM:162:PHE:CD2	1:CM:163:LEU:HD13	2.50	0.47
1:CN:189:PHE:CE2	1:CN:249:LEU:HD21	2.45	0.47
1:AB:239:ILE:HD12	1:AB:275:GLU:HA	1.96	0.46
1:AQ:454:ASN:ND2	1:AQ:456:ALA:H	2.10	0.46
1:AT:263:ASN:O	1:AT:267:LYS:HG3	2.15	0.46
1:BA:393:HIS:CG	1:BA:496:PHE:HB3	2.50	0.46
1:BC:188:PHE:C	1:BC:189:PHE:HD1	2.17	0.46
1:BD:189:PHE:CE2	1:BD:249:LEU:HD21	2.50	0.46
1:BF:171:ASP:HA	1:BF:172:PRO:HD3	1.79	0.46
1:BG:25:ILE:HG23	1:BG:152:LEU:HD11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:232:THR:HB	1:BG:334:VAL:CG2	2.45	0.46
1:BL:232:THR:HB	1:BL:334:VAL:HG23	1.97	0.46
1:CA:234:ARG:HG2	1:CA:280:GLU:HG2	1.97	0.46
1:CA:398:GLY:HA3	1:CA:494:PHE:CD2	2.49	0.46
1:CC:442:GLN:HE21	1:CD:412:PHE:HB2	1.80	0.46
1:CE:189:PHE:HD2	1:CE:247:ILE:CD1	2.27	0.46
1:CG:263:ASN:O	1:CG:267:LYS:HG3	2.15	0.46
1:CG:272:TYR:HD1	1:CG:272:TYR:N	2.13	0.46
1:CL:162:PHE:CD2	1:CL:163:LEU:HD13	2.51	0.46
1:CN:171:ASP:HA	1:CN:172:PRO:HD3	1.78	0.46
1:CO:272:TYR:HD1	1:CO:272:TYR:N	2.13	0.46
1:CI:55:ARG:HD3	1:CR:272:TYR:CD2	2.50	0.46
1:AD:226:VAL:HG13	1:AD:228:GLY:H	1.80	0.46
1:AK:272:TYR:HD1	1:AK:272:TYR:N	2.13	0.46
1:AL:189:PHE:CE2	1:AL:249:LEU:HD21	2.50	0.46
1:AN:55:ARG:HD3	1:AS:272:TYR:HD2	1.77	0.46
1:AO:239:ILE:HD12	1:AO:275:GLU:HA	1.97	0.46
1:BF:404:LEU:HD22	1:BF:486:VAL:HG22	1.97	0.46
1:BH:30:SER:O	1:BH:33:LYS:HB2	2.14	0.46
1:BJ:189:PHE:CE2	1:BJ:249:LEU:HD21	2.47	0.46
1:BM:454:ASN:HD21	1:BM:456:ALA:HB3	1.80	0.46
1:BO:404:LEU:HD22	1:BO:486:VAL:HG22	1.96	0.46
1:BQ:232:THR:HB	1:BQ:334:VAL:HG23	1.96	0.46
1:BR:226:VAL:HG13	1:BR:228:GLY:H	1.80	0.46
1:CB:404:LEU:HD22	1:CB:486:VAL:HG22	1.96	0.46
1:CE:234:ARG:HG2	1:CE:280:GLU:HG2	1.97	0.46
1:AH:272:TYR:HD2	1:CF:55:ARG:HD3	1.80	0.46
1:CM:379:VAL:HG11	1:CM:381:MET:HE1	1.97	0.46
1:CN:232:THR:HB	1:CN:334:VAL:CG2	2.46	0.46
1:CR:284:ARG:NH1	1:CR:284:ARG:CG	2.76	0.46
1:CT:189:PHE:CE2	1:CT:249:LEU:HD21	2.50	0.46
1:AA:393:HIS:CG	1:AA:496:PHE:HB3	2.51	0.46
1:AB:263:ASN:O	1:AB:267:LYS:HG3	2.16	0.46
1:AD:189:PHE:HD2	1:AD:247:ILE:HD11	1.79	0.46
1:AE:162:PHE:CD2	1:AE:163:LEU:HD13	2.49	0.46
1:AE:203:THR:CB	1:AE:300:GLN:HG3	2.43	0.46
1:AG:30:SER:O	1:AG:33:LYS:HB2	2.14	0.46
1:AH:170:PHE:HD1	1:AH:389:MET:CE	2.27	0.46
1:AH:379:VAL:HG11	1:AH:381:MET:HE1	1.97	0.46
1:AH:454:ASN:ND2	1:AH:456:ALA:H	2.08	0.46
1:AI:55:ARG:HD3	1:AR:272:TYR:CD2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:234:ARG:HG2	1:AK:280:GLU:HG2	1.98	0.46
1:AM:232:THR:HB	1:AM:334:VAL:CG2	2.45	0.46
1:AN:239:ILE:HD12	1:AN:275:GLU:HA	1.97	0.46
1:AO:454:ASN:HD21	1:AO:456:ALA:HB3	1.80	0.46
1:AP:263:ASN:O	1:AP:267:LYS:HG3	2.15	0.46
1:AR:423:LYS:HE2	1:AR:449:GLU:O	2.15	0.46
1:AT:454:ASN:HD21	1:AT:456:ALA:HB3	1.80	0.46
1:BE:170:PHE:HD1	1:BE:389:MET:CE	2.28	0.46
1:BE:454:ASN:HD21	1:BE:456:ALA:HB3	1.79	0.46
1:BH:170:PHE:HD1	1:BH:389:MET:HE2	1.80	0.46
1:BN:30:SER:O	1:BN:33:LYS:HB2	2.15	0.46
1:BR:232:THR:HB	1:BR:334:VAL:CG2	2.45	0.46
1:BR:454:ASN:HD21	1:BR:456:ALA:HB3	1.80	0.46
1:BT:239:ILE:HD12	1:BT:275:GLU:HA	1.96	0.46
1:CA:189:PHE:HD2	1:CA:247:ILE:HD11	1.80	0.46
1:CJ:263:ASN:O	1:CJ:267:LYS:HG3	2.16	0.46
1:CL:14:CYS:H	1:CL:138:ASN:ND2	2.12	0.46
1:BQ:272:TYR:HD2	1:CL:55:ARG:HD3	1.81	0.46
1:CM:226:VAL:HG13	1:CM:228:GLY:H	1.80	0.46
1:CT:30:SER:O	1:CT:33:LYS:HB2	2.16	0.46
1:AA:162:PHE:CD2	1:AA:163:LEU:HD13	2.51	0.46
1:AB:232:THR:HB	1:AB:334:VAL:HG23	1.98	0.46
1:AB:454:ASN:ND2	1:AB:456:ALA:H	2.10	0.46
1:AG:55:ARG:HD3	1:CG:272:TYR:CD2	2.50	0.46
1:AJ:237:VAL:HG23	1:AJ:279:PHE:CD2	2.50	0.46
1:AK:239:ILE:HG12	1:AK:326:ILE:CD1	2.46	0.46
1:AK:263:ASN:O	1:AK:267:LYS:HG3	2.15	0.46
1:AO:239:ILE:HG23	1:AO:324:LEU:HD21	1.96	0.46
1:AR:191:LEU:N	1:AR:191:LEU:CD2	2.73	0.46
1:AS:226:VAL:HG13	1:AS:228:GLY:H	1.80	0.46
1:BB:423:LYS:HE2	1:BB:449:GLU:O	2.16	0.46
1:BC:30:SER:O	1:BC:33:LYS:HB2	2.15	0.46
1:BD:189:PHE:HE1	1:BD:198:ARG:CG	2.27	0.46
1:BH:239:ILE:HD12	1:BH:275:GLU:HA	1.96	0.46
1:BI:74:ASN:ND2	1:BI:77:THR:OG1	2.48	0.46
1:BO:170:PHE:HD1	1:BO:389:MET:CE	2.28	0.46
1:BS:232:THR:HB	1:BS:334:VAL:CG2	2.46	0.46
1:BS:393:HIS:CG	1:BS:496:PHE:HB3	2.50	0.46
1:CD:20:LEU:HB2	1:CD:132:PHE:O	2.16	0.46
1:CF:234:ARG:HG2	1:CF:280:GLU:HG2	1.98	0.46
1:CI:10:ILE:HG21	1:CI:146:TRP:CZ2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:263:ASN:O	1:CM:267:LYS:HG3	2.15	0.46
1:CS:58:ALA:HB2	1:CS:102:GLY:HA3	1.97	0.46
1:CS:454:ASN:HD21	1:CS:456:ALA:HB3	1.81	0.46
1:CT:454:ASN:ND2	1:CT:456:ALA:H	2.06	0.46
1:AA:239:ILE:HD12	1:AA:275:GLU:HA	1.96	0.46
1:AA:189:PHE:CE2	1:AA:249:LEU:HD21	2.51	0.46
1:AB:171:ASP:HA	1:AB:172:PRO:HD3	1.79	0.46
1:AB:55:ARG:CZ	1:BB:272:TYR:CE2	2.99	0.46
1:AD:162:PHE:CD2	1:AD:163:LEU:HD13	2.50	0.46
1:AG:393:HIS:CG	1:AG:496:PHE:HB3	2.51	0.46
1:AL:239:ILE:HD12	1:AL:275:GLU:HA	1.98	0.46
1:AL:442:GLN:HE21	1:AM:412:PHE:HB2	1.80	0.46
1:AN:393:HIS:CG	1:AN:496:PHE:HB3	2.50	0.46
1:AO:250:TRP:CE3	1:AO:272:TYR:CD1	3.04	0.46
1:AP:25:ILE:HG23	1:AP:152:LEU:HD11	1.97	0.46
1:AR:234:ARG:HG2	1:AR:280:GLU:HG2	1.98	0.46
1:AS:191:LEU:CD2	1:AS:191:LEU:N	2.79	0.46
1:AS:237:VAL:HG23	1:AS:279:PHE:CD2	2.50	0.46
1:AT:234:ARG:HG2	1:AT:280:GLU:HG2	1.97	0.46
1:BD:14:CYS:H	1:BD:138:ASN:ND2	2.14	0.46
1:BE:75:ARG:NH2	1:BE:391:ALA:O	2.49	0.46
1:BL:67:VAL:HG23	1:BL:135:LEU:HB2	1.98	0.46
1:BM:272:TYR:HD1	1:BM:272:TYR:N	2.14	0.46
1:BN:58:ALA:HB2	1:BN:102:GLY:HA3	1.96	0.46
1:BR:191:LEU:N	1:BR:191:LEU:CD2	2.77	0.46
1:BT:393:HIS:CG	1:BT:496:PHE:HB3	2.51	0.46
1:CC:300:GLN:HE21	1:CC:300:GLN:HB2	1.59	0.46
1:CI:272:TYR:HD1	1:CI:272:TYR:N	2.14	0.46
1:CO:189:PHE:HE2	1:CO:249:LEU:HD21	1.78	0.46
1:CP:58:ALA:HB2	1:CP:102:GLY:HA3	1.98	0.46
1:CQ:191:LEU:N	1:CQ:191:LEU:HD23	2.17	0.46
1:CT:14:CYS:HB3	1:CT:64:LEU:HD21	1.97	0.46
1:AC:43:ALA:HB1	1:AC:158:GLU:HA	1.98	0.46
1:AC:73:TYR:O	1:AC:75:ARG:HG2	2.16	0.46
1:AE:239:ILE:HG12	1:AE:326:ILE:CD1	2.45	0.46
1:AI:18:ARG:HG3	1:AI:19:TYR:O	2.16	0.46
1:AM:189:PHE:CE1	1:AM:198:ARG:HG2	2.50	0.46
1:AO:393:HIS:CG	1:AO:496:PHE:HB3	2.51	0.46
1:AS:189:PHE:HE2	1:AS:249:LEU:HD21	1.80	0.46
1:BC:263:ASN:O	1:BC:267:LYS:HG3	2.16	0.46
1:BH:15:GLN:HE21	1:BH:15:GLN:CA	2.09	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:30:SER:O	1:BK:33:LYS:HB2	2.15	0.46
1:BK:232:THR:HB	1:BK:334:VAL:HG23	1.97	0.46
1:BL:30:SER:O	1:BL:33:LYS:HB2	2.16	0.46
1:BL:454:ASN:HD21	1:BL:456:ALA:HB3	1.80	0.46
1:BL:9:TYR:CE2	1:BL:145:ASP:HB3	2.50	0.46
1:BP:287:TYR:HA	1:BT:162:PHE:CD1	2.50	0.46
1:CA:226:VAL:HG13	1:CA:228:GLY:H	1.79	0.46
1:CD:30:SER:O	1:CD:33:LYS:HB2	2.15	0.46
1:CE:14:CYS:H	1:CE:138:ASN:ND2	2.11	0.46
1:CE:197:LEU:HD13	1:CE:309:TYR:CZ	2.51	0.46
1:CK:272:TYR:CD1	1:CK:272:TYR:N	2.84	0.46
1:CL:272:TYR:CD1	1:CL:272:TYR:N	2.84	0.46
1:CO:170:PHE:HD1	1:CO:389:MET:CE	2.29	0.46
1:CP:393:HIS:CG	1:CP:496:PHE:HB3	2.51	0.46
1:CQ:30:SER:O	1:CQ:33:LYS:HB2	2.16	0.46
1:CR:207:VAL:HA	1:CR:208:PRO:HD3	1.84	0.46
1:AE:189:PHE:HD2	1:AE:247:ILE:CD1	2.28	0.46
1:AH:182:LEU:HG	1:AH:330:ILE:HB	1.98	0.46
1:AI:189:PHE:HD2	1:AI:247:ILE:CD1	2.28	0.46
1:AR:237:VAL:HG23	1:AR:279:PHE:CD2	2.51	0.46
1:AS:170:PHE:HD1	1:AS:389:MET:CE	2.28	0.46
1:AS:30:SER:O	1:AS:33:LYS:HB2	2.16	0.46
1:AT:239:ILE:HD12	1:AT:275:GLU:HA	1.98	0.46
1:BA:79:ARG:CG	1:BA:79:ARG:NH1	2.71	0.46
1:BE:300:GLN:HE21	1:BE:300:GLN:HB2	1.48	0.46
1:BH:234:ARG:HG2	1:BH:280:GLU:HG2	1.97	0.46
1:BI:189:PHE:HD2	1:BI:247:ILE:CD1	2.29	0.46
1:BM:234:ARG:HG2	1:BM:280:GLU:HG2	1.97	0.46
1:BM:379:VAL:HG11	1:BM:381:MET:HE1	1.97	0.46
1:BO:11:PRO:HG2	1:BO:18:ARG:CD	2.46	0.46
1:BO:191:LEU:CD2	1:BO:191:LEU:N	2.73	0.46
1:BO:234:ARG:HG2	1:BO:280:GLU:HG2	1.97	0.46
1:BN:440:ALA:CB	1:BO:444:LEU:HD13	2.45	0.46
1:BP:189:PHE:HD2	1:BP:247:ILE:HD11	1.80	0.46
1:BP:454:ASN:HD21	1:BP:456:ALA:HB3	1.81	0.46
1:BS:440:ALA:HB3	1:BT:444:LEU:HD13	1.98	0.46
1:BT:237:VAL:HG23	1:BT:279:PHE:CD2	2.51	0.46
1:CD:272:TYR:CD2	1:CS:55:ARG:CZ	2.98	0.46
1:CE:61:PHE:CD2	1:CE:243:ILE:HD11	2.50	0.46
1:CG:454:ASN:HD21	1:CG:456:ALA:HB3	1.81	0.46
1:CI:67:VAL:HG23	1:CI:135:LEU:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:189:PHE:HE2	1:CL:249:LEU:HD21	1.81	0.46
1:CN:189:PHE:CE1	1:CN:198:ARG:HG2	2.51	0.46
1:CO:79:ARG:CG	1:CO:79:ARG:NH1	2.79	0.46
1:CP:43:ALA:HB1	1:CP:158:GLU:HA	1.97	0.46
1:CR:263:ASN:O	1:CR:267:LYS:HG3	2.16	0.46
1:AC:237:VAL:HG23	1:AC:279:PHE:CD2	2.50	0.46
1:AH:393:HIS:CG	1:AH:496:PHE:HB3	2.50	0.46
1:AI:189:PHE:CE1	1:AI:198:ARG:HG2	2.51	0.46
1:AI:454:ASN:HD21	1:AI:456:ALA:HB3	1.80	0.46
1:AJ:234:ARG:HG2	1:AJ:280:GLU:HG2	1.98	0.46
1:AM:14:CYS:H	1:AM:138:ASN:HD21	1.64	0.46
1:AN:237:VAL:HG23	1:AN:279:PHE:CD2	2.51	0.46
1:AQ:74:ASN:ND2	1:AQ:77:THR:OG1	2.49	0.46
1:AT:189:PHE:HE2	1:AT:249:LEU:HD21	1.79	0.46
1:BA:22:THR:OG1	1:BA:131:HIS:CD2	2.61	0.46
1:BC:18:ARG:HG3	1:BC:19:TYR:N	2.31	0.46
1:BN:182:LEU:HG	1:BN:330:ILE:HB	1.97	0.46
1:BO:189:PHE:HE2	1:BO:249:LEU:HD21	1.79	0.46
1:BO:252:VAL:HG22	1:BO:253:SER:N	2.31	0.46
1:BT:43:ALA:HB1	1:BT:158:GLU:HA	1.97	0.46
1:BT:18:ARG:HG3	1:BT:19:TYR:N	2.31	0.46
1:BP:272:TYR:CD2	1:CE:55:ARG:HD3	2.51	0.46
1:CI:454:ASN:HD21	1:CI:456:ALA:HB3	1.81	0.46
1:CK:226:VAL:HG13	1:CK:228:GLY:H	1.81	0.46
1:CL:404:LEU:HD23	1:CL:404:LEU:N	2.31	0.46
1:CP:14:CYS:H	1:CP:138:ASN:HD21	1.62	0.46
1:CQ:393:HIS:CG	1:CQ:496:PHE:HB3	2.51	0.46
1:CP:440:ALA:CB	1:CQ:444:LEU:HD13	2.46	0.46
1:CQ:58:ALA:HB2	1:CQ:102:GLY:HA3	1.98	0.46
1:CR:189:PHE:CE2	1:CR:249:LEU:HD21	2.45	0.46
1:CS:324:LEU:HD23	1:CS:324:LEU:C	2.36	0.46
1:AA:55:ARG:NH1	1:CC:272:TYR:CD2	2.84	0.46
1:AF:232:THR:HB	1:AF:334:VAL:CG2	2.46	0.46
1:AF:272:TYR:CD1	1:AF:272:TYR:N	2.84	0.46
1:AF:442:GLN:HE21	1:AG:412:PHE:HB2	1.80	0.46
1:AI:18:ARG:NH1	1:AI:18:ARG:HB2	2.31	0.46
1:AJ:58:ALA:HB2	1:AJ:102:GLY:HA3	1.97	0.46
1:AL:393:HIS:CG	1:AL:496:PHE:HB3	2.50	0.46
1:AN:272:TYR:N	1:AN:272:TYR:CD1	2.83	0.46
1:AP:379:VAL:HG11	1:AP:381:MET:HE1	1.98	0.46
1:AS:263:ASN:O	1:AS:267:LYS:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:162:PHE:CD2	1:BA:163:LEU:HD13	2.50	0.46
1:BA:237:VAL:HG23	1:BA:279:PHE:CD2	2.51	0.46
1:BA:442:GLN:HE21	1:BB:412:PHE:HB2	1.79	0.46
1:BE:272:TYR:CD1	1:BE:272:TYR:N	2.84	0.46
1:BG:18:ARG:HG2	1:BG:20:LEU:HD23	1.98	0.46
1:BG:393:HIS:CG	1:BG:496:PHE:HB3	2.51	0.46
1:BH:272:TYR:CD1	1:BH:272:TYR:N	2.83	0.46
1:BJ:232:THR:HB	1:BJ:334:VAL:HG23	1.98	0.46
1:BL:25:ILE:HG23	1:BL:152:LEU:HD11	1.98	0.46
1:BJ:272:TYR:CE2	1:BQ:55:ARG:HD3	2.51	0.46
1:CA:232:THR:HB	1:CA:334:VAL:CG2	2.46	0.46
1:CB:58:ALA:HB2	1:CB:102:GLY:HA3	1.96	0.46
1:CD:14:CYS:H	1:CD:138:ASN:ND2	2.13	0.46
1:CF:232:THR:HB	1:CF:334:VAL:HG23	1.97	0.46
1:CH:189:PHE:CE2	1:CH:249:LEU:HD21	2.45	0.46
1:CK:379:VAL:HG11	1:CK:381:MET:HE1	1.98	0.46
1:CL:234:ARG:HG2	1:CL:280:GLU:HG2	1.97	0.46
1:CP:239:ILE:HD12	1:CP:275:GLU:HA	1.98	0.46
1:CQ:25:ILE:HG23	1:CQ:152:LEU:HD11	1.98	0.46
1:CT:171:ASP:HA	1:CT:172:PRO:HD3	1.79	0.46
1:CT:18:ARG:HG3	1:CT:19:TYR:N	2.30	0.46
1:CT:272:TYR:N	1:CT:272:TYR:HD1	2.14	0.46
1:AC:189:PHE:HE2	1:AC:249:LEU:CD2	2.28	0.46
1:AE:272:TYR:CD1	1:AE:272:TYR:N	2.84	0.46
1:AE:454:ASN:HD21	1:AE:456:ALA:HB3	1.80	0.46
1:AK:442:GLN:HE21	1:AL:412:PHE:HB2	1.81	0.46
1:AL:440:ALA:HB3	1:AM:444:LEU:HD13	1.98	0.46
1:AN:162:PHE:CD2	1:AN:163:LEU:HD13	2.51	0.46
1:AN:272:TYR:HD1	1:AN:272:TYR:N	2.14	0.46
1:BA:371:ASP:OD1	1:BA:381:MET:HG2	2.16	0.46
1:BB:79:ARG:CG	1:BB:79:ARG:HH11	2.26	0.46
1:BC:189:PHE:HD2	1:BC:247:ILE:HD11	1.80	0.46
1:BB:414:LYS:HA	1:BC:411:GLU:HB3	1.97	0.46
1:BI:16:ALA:O	1:BI:17:ASN:HB2	2.16	0.46
1:BH:55:ARG:HD3	1:BK:272:TYR:HD2	1.78	0.46
1:BL:191:LEU:CD2	1:BL:191:LEU:N	2.76	0.46
1:BS:16:ALA:O	1:BS:17:ASN:HB2	2.16	0.46
1:CE:318:SER:HA	1:CE:319:GLY:HA2	1.79	0.46
1:CF:263:ASN:O	1:CF:267:LYS:HG3	2.16	0.46
1:CH:30:SER:O	1:CH:33:LYS:HB2	2.16	0.46
1:CI:171:ASP:HA	1:CI:172:PRO:HD3	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:79:ARG:HH11	1:CK:79:ARG:HG3	1.80	0.46
1:CR:162:PHE:CD2	1:CR:163:LEU:HD13	2.51	0.46
1:CR:393:HIS:CG	1:CR:496:PHE:HB3	2.51	0.46
1:AB:61:PHE:CE2	1:AB:243:ILE:HD11	2.50	0.45
1:AE:170:PHE:HD1	1:AE:389:MET:CE	2.29	0.45
1:AE:232:THR:HB	1:AE:334:VAL:HG23	1.99	0.45
1:AE:189:PHE:HD2	1:AE:247:ILE:HD11	1.80	0.45
1:AE:30:SER:O	1:AE:33:LYS:HB2	2.16	0.45
1:AJ:43:ALA:HB1	1:AJ:158:GLU:HA	1.98	0.45
1:AL:263:ASN:O	1:AL:267:LYS:HG3	2.17	0.45
1:AM:30:SER:O	1:AM:33:LYS:HB2	2.16	0.45
1:AR:170:PHE:HD1	1:AR:389:MET:CE	2.29	0.45
1:AS:207:VAL:HA	1:AS:208:PRO:HD3	1.83	0.45
1:BB:237:VAL:HG23	1:BB:279:PHE:CD2	2.51	0.45
1:BC:237:VAL:HG23	1:BC:279:PHE:CD2	2.49	0.45
1:BD:237:VAL:HG23	1:BD:279:PHE:CD2	2.51	0.45
1:BE:189:PHE:CE2	1:BE:249:LEU:HD21	2.47	0.45
1:BI:25:ILE:HG23	1:BI:152:LEU:HD11	1.98	0.45
1:BJ:189:PHE:HD2	1:BJ:247:ILE:HD11	1.80	0.45
1:BN:255:TRP:CE3	1:BN:285:SER:HB2	2.51	0.45
1:BN:393:HIS:CG	1:BN:496:PHE:HB3	2.51	0.45
1:BP:237:VAL:HG23	1:BP:279:PHE:CD2	2.51	0.45
1:BP:250:TRP:CZ3	1:BP:272:TYR:CD1	3.05	0.45
1:BR:250:TRP:HZ3	1:BR:272:TYR:CE1	2.27	0.45
1:BS:30:SER:O	1:BS:33:LYS:HB2	2.16	0.45
1:CB:239:ILE:HG12	1:CB:326:ILE:CD1	2.46	0.45
1:CD:203:THR:HB	1:CD:300:GLN:HG3	1.98	0.45
1:CG:232:THR:HB	1:CG:334:VAL:HG23	1.97	0.45
1:CH:371:ASP:OD1	1:CH:381:MET:HG2	2.16	0.45
1:CK:189:PHE:HD2	1:CK:247:ILE:HD11	1.80	0.45
1:CN:232:THR:HB	1:CN:334:VAL:HG23	1.99	0.45
1:CO:272:TYR:N	1:CO:272:TYR:CD1	2.84	0.45
1:CP:237:VAL:HG23	1:CP:279:PHE:CD2	2.51	0.45
1:CQ:75:ARG:NH2	1:CQ:391:ALA:O	2.48	0.45
1:CS:263:ASN:O	1:CS:267:LYS:HG3	2.17	0.45
1:AB:189:PHE:CE2	1:AB:249:LEU:HD21	2.46	0.45
1:AC:393:HIS:CG	1:AC:496:PHE:HB3	2.51	0.45
1:AF:284:ARG:CG	1:AF:284:ARG:NH1	2.70	0.45
1:AH:272:TYR:CD1	1:AH:272:TYR:N	2.85	0.45
1:AI:79:ARG:HG3	1:AI:79:ARG:NH1	2.18	0.45
1:AM:454:ASN:HD21	1:AM:456:ALA:HB3	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:61:PHE:CD2	1:AP:243:ILE:HD11	2.51	0.45
1:AS:189:PHE:CE2	1:AS:249:LEU:HD21	2.51	0.45
1:AT:395:LEU:HB2	1:AT:497:TYR:HB2	1.98	0.45
1:BC:22:THR:OG1	1:BC:131:HIS:CD2	2.59	0.45
1:BE:234:ARG:HG2	1:BE:280:GLU:HG2	1.98	0.45
1:BG:442:GLN:HE21	1:BH:412:PHE:HB2	1.82	0.45
1:BL:252:VAL:HG22	1:BL:253:SER:N	2.31	0.45
1:BM:30:SER:O	1:BM:33:LYS:HB2	2.15	0.45
1:CC:170:PHE:HD1	1:CC:389:MET:CE	2.30	0.45
1:CC:188:PHE:C	1:CC:189:PHE:HD1	2.19	0.45
1:CE:454:ASN:ND2	1:CE:456:ALA:H	2.11	0.45
1:CG:234:ARG:HG2	1:CG:280:GLU:HG2	1.97	0.45
1:CH:226:VAL:HG13	1:CH:228:GLY:H	1.82	0.45
1:CJ:189:PHE:CE1	1:CJ:198:ARG:HG2	2.52	0.45
1:CO:191:LEU:N	1:CO:191:LEU:CD2	2.76	0.45
1:CQ:171:ASP:HA	1:CQ:172:PRO:HD3	1.78	0.45
1:CT:226:VAL:HG13	1:CT:228:GLY:H	1.81	0.45
1:AD:189:PHE:CE2	1:AD:249:LEU:HD21	2.51	0.45
1:AG:170:PHE:HD1	1:AG:389:MET:CE	2.29	0.45
1:AJ:379:VAL:HG11	1:AJ:381:MET:HE1	1.99	0.45
1:AJ:454:ASN:HD21	1:AJ:456:ALA:HB3	1.81	0.45
1:AK:182:LEU:HG	1:AK:330:ILE:HB	1.98	0.45
1:AQ:379:VAL:HG11	1:AQ:381:MET:HE1	1.98	0.45
1:AT:404:LEU:HD22	1:AT:486:VAL:HG22	1.97	0.45
1:BB:318:SER:HA	1:BB:319:GLY:HA2	1.78	0.45
1:BB:393:HIS:CG	1:BB:496:PHE:HB3	2.51	0.45
1:BE:25:ILE:HG23	1:BE:152:LEU:HD11	1.98	0.45
1:BF:202:LEU:HB2	1:BF:304:SER:O	2.17	0.45
1:BK:189:PHE:CE2	1:BK:249:LEU:HD21	2.51	0.45
1:BM:252:VAL:HG22	1:BM:253:SER:N	2.31	0.45
1:BQ:263:ASN:O	1:BQ:267:LYS:HG3	2.17	0.45
1:BR:14:CYS:H	1:BR:138:ASN:HD21	1.65	0.45
1:CB:79:ARG:NH1	1:CB:79:ARG:HG3	2.30	0.45
1:CE:189:PHE:HD2	1:CE:247:ILE:HD11	1.81	0.45
1:CH:237:VAL:HG23	1:CH:279:PHE:CD2	2.51	0.45
1:CI:170:PHE:HD1	1:CI:389:MET:CE	2.29	0.45
1:CI:43:ALA:HB1	1:CI:158:GLU:HA	1.97	0.45
1:CJ:20:LEU:HB2	1:CJ:132:PHE:O	2.16	0.45
1:CO:252:VAL:HG22	1:CO:253:SER:N	2.32	0.45
1:CS:423:LYS:HE2	1:CS:449:GLU:O	2.17	0.45
1:CT:239:ILE:HG12	1:CT:326:ILE:CD1	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:442:GLN:HE21	1:CT:412:PHE:HB2	1.81	0.45
1:AA:189:PHE:HD2	1:AA:247:ILE:HD11	1.81	0.45
1:AE:239:ILE:HD12	1:AE:275:GLU:HA	1.98	0.45
1:AG:171:ASP:HA	1:AG:172:PRO:HD3	1.80	0.45
1:AG:189:PHE:HD2	1:AG:247:ILE:HD11	1.81	0.45
1:AI:284:ARG:CG	1:AI:284:ARG:NH1	2.70	0.45
1:AK:226:VAL:HG13	1:AK:228:GLY:H	1.81	0.45
1:AK:393:HIS:CG	1:AK:496:PHE:HB3	2.52	0.45
1:AL:25:ILE:HG23	1:AL:152:LEU:HD11	1.97	0.45
1:AM:272:TYR:N	1:AM:272:TYR:CD1	2.85	0.45
1:AM:170:PHE:HD1	1:AM:389:MET:HE2	1.81	0.45
1:AN:234:ARG:HG2	1:AN:280:GLU:HG2	1.99	0.45
1:AS:25:ILE:HG23	1:AS:152:LEU:HD11	1.98	0.45
1:BB:163:LEU:HA	1:BB:163:LEU:HD12	1.83	0.45
1:BE:189:PHE:HD2	1:BE:247:ILE:CD1	2.30	0.45
1:BE:237:VAL:HG23	1:BE:279:PHE:CD2	2.51	0.45
1:BF:25:ILE:HG23	1:BF:152:LEU:HD11	1.99	0.45
1:BF:454:ASN:ND2	1:BF:456:ALA:H	2.05	0.45
1:BG:189:PHE:HD2	1:BG:247:ILE:HD11	1.82	0.45
1:BH:189:PHE:CE2	1:BH:249:LEU:HD21	2.44	0.45
1:BJ:263:ASN:O	1:BJ:267:LYS:HG3	2.16	0.45
1:BL:162:PHE:CD2	1:BL:163:LEU:HD13	2.51	0.45
1:BL:239:ILE:HD12	1:BL:275:GLU:HA	1.97	0.45
1:BO:15:GLN:HE21	1:BO:15:GLN:CA	2.22	0.45
1:BO:162:PHE:CD2	1:BO:163:LEU:HD13	2.51	0.45
1:BO:250:TRP:CZ3	1:BO:272:TYR:CD1	3.04	0.45
1:BQ:232:THR:HB	1:BQ:334:VAL:CG2	2.46	0.45
1:BT:12:LYS:HB3	1:BT:144:ALA:C	2.37	0.45
1:CA:442:GLN:HE21	1:CB:412:PHE:HB2	1.81	0.45
1:CB:191:LEU:CD2	1:CB:191:LEU:N	2.74	0.45
1:CC:252:VAL:HG22	1:CC:253:SER:N	2.31	0.45
1:CE:170:PHE:HD1	1:CE:389:MET:CE	2.29	0.45
1:CJ:239:ILE:HD12	1:CJ:275:GLU:HA	1.98	0.45
1:CJ:234:ARG:HG2	1:CJ:280:GLU:HG2	1.98	0.45
1:CK:423:LYS:HE2	1:CK:449:GLU:O	2.16	0.45
1:CK:58:ALA:HB2	1:CK:102:GLY:HA3	1.99	0.45
1:CL:237:VAL:HG23	1:CL:279:PHE:CD2	2.52	0.45
1:CL:324:LEU:HD23	1:CL:324:LEU:C	2.37	0.45
1:CP:170:PHE:HD1	1:CP:389:MET:CE	2.30	0.45
1:AB:379:VAL:HG11	1:AB:381:MET:HE1	1.98	0.45
1:AC:189:PHE:HD2	1:AC:247:ILE:HD11	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:272:TYR:CD1	1:AC:272:TYR:N	2.85	0.45
1:AE:284:ARG:CG	1:AE:284:ARG:NH1	2.72	0.45
1:AL:162:PHE:CD2	1:AL:163:LEU:HD13	2.51	0.45
1:AL:234:ARG:HG2	1:AL:280:GLU:HG2	1.99	0.45
1:AM:232:THR:HB	1:AM:334:VAL:HG23	1.98	0.45
1:AO:189:PHE:HE2	1:AO:249:LEU:HD21	1.82	0.45
1:AO:234:ARG:HG2	1:AO:280:GLU:HG2	1.99	0.45
1:AP:189:PHE:CE1	1:AP:198:ARG:CG	2.99	0.45
1:AP:272:TYR:N	1:AP:272:TYR:HD1	2.15	0.45
1:AR:393:HIS:CG	1:AR:496:PHE:HB3	2.52	0.45
1:AS:442:GLN:HE21	1:AT:412:PHE:HB2	1.81	0.45
1:AC:272:TYR:HE2	1:BA:55:ARG:NE	2.10	0.45
1:BE:226:VAL:HG13	1:BE:228:GLY:H	1.81	0.45
1:BE:454:ASN:ND2	1:BE:456:ALA:H	2.08	0.45
1:BL:191:LEU:HD23	1:BL:191:LEU:N	2.21	0.45
1:BL:404:LEU:HD22	1:BL:486:VAL:HG22	1.99	0.45
1:BL:440:ALA:HB3	1:BM:444:LEU:HD13	1.98	0.45
1:BP:226:VAL:HG13	1:BP:228:GLY:H	1.82	0.45
1:BR:30:SER:O	1:BR:33:LYS:HB2	2.15	0.45
1:CA:191:LEU:CD2	1:CA:191:LEU:N	2.74	0.45
1:CB:170:PHE:HD1	1:CB:389:MET:CE	2.28	0.45
1:CI:189:PHE:HD2	1:CI:247:ILE:HD11	1.81	0.45
1:CJ:79:ARG:HH11	1:CJ:79:ARG:CG	2.29	0.45
1:CN:398:GLY:HA3	1:CN:494:PHE:CD2	2.52	0.45
1:CO:226:VAL:HG13	1:CO:228:GLY:H	1.81	0.45
1:CT:170:PHE:HD1	1:CT:389:MET:CE	2.30	0.45
1:AA:237:VAL:HG23	1:AA:279:PHE:CD2	2.51	0.45
1:AC:404:LEU:HD22	1:AC:486:VAL:HG22	1.99	0.45
1:AF:393:HIS:CG	1:AF:496:PHE:HB3	2.52	0.45
1:AI:272:TYR:HD1	1:AI:272:TYR:N	2.15	0.45
1:AJ:162:PHE:CD2	1:AJ:163:LEU:HD13	2.52	0.45
1:AT:226:VAL:HG13	1:AT:228:GLY:H	1.81	0.45
1:AT:79:ARG:HH11	1:AT:79:ARG:CG	2.29	0.45
1:BA:239:ILE:HD12	1:BA:275:GLU:HA	1.98	0.45
1:BD:393:HIS:CG	1:BD:496:PHE:HB3	2.52	0.45
1:BE:232:THR:HB	1:BE:334:VAL:CG2	2.47	0.45
1:BF:14:CYS:H	1:BF:138:ASN:ND2	2.14	0.45
1:BG:189:PHE:CE1	1:BG:198:ARG:HG2	2.51	0.45
1:BK:234:ARG:HG2	1:BK:280:GLU:HG2	1.99	0.45
1:BL:74:ASN:ND2	1:BL:77:THR:OG1	2.50	0.45
1:BM:75:ARG:NH2	1:BM:391:ALA:O	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:191:LEU:CD2	1:BN:191:LEU:N	2.77	0.45
1:BO:263:ASN:O	1:BO:267:LYS:HG3	2.17	0.45
1:BP:189:PHE:CE2	1:BP:249:LEU:HD21	2.52	0.45
1:BP:288:HIS:HD2	1:BP:337:ASP:OD2	2.00	0.45
1:BP:79:ARG:HG3	1:BP:79:ARG:NH1	2.26	0.45
1:BQ:237:VAL:HG23	1:BQ:279:PHE:CD2	2.52	0.45
1:CE:263:ASN:O	1:CE:267:LYS:HG3	2.16	0.45
1:CF:272:TYR:CD1	1:CF:272:TYR:N	2.85	0.45
1:CK:162:PHE:CD2	1:CK:163:LEU:HD13	2.51	0.45
1:CM:77:THR:O	1:CM:81:THR:HG23	2.16	0.45
1:CO:207:VAL:HA	1:CO:208:PRO:HD3	1.83	0.45
1:CP:18:ARG:HG3	1:CP:18:ARG:HH11	1.82	0.45
1:AD:191:LEU:HD23	1:AD:191:LEU:N	2.18	0.45
1:AF:75:ARG:NH2	1:AF:391:ALA:O	2.49	0.45
1:AH:232:THR:HB	1:AH:334:VAL:HG23	1.99	0.45
1:AI:207:VAL:HA	1:AI:208:PRO:HD3	1.84	0.45
1:AL:14:CYS:HB3	1:AL:64:LEU:HD21	1.98	0.45
1:AP:18:ARG:HH11	1:AP:18:ARG:CG	2.29	0.45
1:BA:234:ARG:HG2	1:BA:280:GLU:HG2	1.97	0.45
1:BG:263:ASN:O	1:BG:267:LYS:HG3	2.17	0.45
1:BH:25:ILE:HG23	1:BH:152:LEU:HD11	1.98	0.45
1:BH:423:LYS:HE2	1:BH:449:GLU:O	2.16	0.45
1:BK:232:THR:HB	1:BK:334:VAL:CG2	2.47	0.45
1:BK:393:HIS:CG	1:BK:496:PHE:HB3	2.52	0.45
1:BO:239:ILE:HD12	1:BO:275:GLU:HA	1.99	0.45
1:BQ:272:TYR:CD1	1:BQ:272:TYR:N	2.84	0.45
1:BR:272:TYR:N	1:BR:272:TYR:CD1	2.85	0.45
1:CF:393:HIS:CG	1:CF:496:PHE:HB3	2.52	0.45
1:CH:74:ASN:ND2	1:CH:77:THR:OG1	2.50	0.45
1:CJ:232:THR:HB	1:CJ:334:VAL:HG23	1.99	0.45
1:CK:25:ILE:HG23	1:CK:152:LEU:HD11	1.99	0.45
1:BP:55:ARG:NE	1:CM:272:TYR:HE2	2.10	0.45
1:CM:234:ARG:HG2	1:CM:280:GLU:HG2	1.99	0.45
1:CP:379:VAL:HG11	1:CP:381:MET:HE1	1.98	0.45
1:CQ:170:PHE:HD1	1:CQ:389:MET:HE2	1.81	0.45
1:AB:393:HIS:CG	1:AB:496:PHE:HB3	2.51	0.45
1:AD:234:ARG:HG2	1:AD:280:GLU:HG2	1.98	0.45
1:AG:234:ARG:HG2	1:AG:280:GLU:HG2	1.98	0.45
1:AM:43:ALA:HB1	1:AM:158:GLU:HA	1.99	0.45
1:AN:263:ASN:O	1:AN:267:LYS:HG3	2.17	0.45
1:AP:318:SER:HA	1:AP:319:GLY:HA2	1.76	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:454:ASN:ND2	1:AS:456:ALA:H	2.09	0.45
1:BE:393:HIS:CG	1:BE:496:PHE:HB3	2.51	0.45
1:BF:239:ILE:HD12	1:BF:275:GLU:HA	1.99	0.45
1:BI:239:ILE:HD12	1:BI:275:GLU:HA	1.98	0.45
1:BP:171:ASP:HA	1:BP:172:PRO:HD3	1.79	0.45
1:BQ:170:PHE:HD1	1:BQ:389:MET:CE	2.30	0.45
1:BS:170:PHE:HD1	1:BS:389:MET:HE2	1.82	0.45
1:BT:171:ASP:HA	1:BT:172:PRO:HD3	1.81	0.45
1:BT:191:LEU:N	1:BT:191:LEU:CD2	2.74	0.45
1:CC:18:ARG:HG3	1:CC:19:TYR:N	2.30	0.45
1:CE:423:LYS:HE2	1:CE:449:GLU:O	2.17	0.45
1:CH:10:ILE:HA	1:CH:11:PRO:HD3	1.86	0.45
1:CH:442:GLN:HE21	1:CI:412:PHE:HB2	1.81	0.45
1:CJ:207:VAL:HA	1:CJ:208:PRO:HD3	1.83	0.45
1:CP:440:ALA:HB3	1:CQ:444:LEU:HD13	1.97	0.45
1:AD:203:THR:HB	1:AD:300:GLN:HG3	1.99	0.45
1:AD:55:ARG:CZ	1:AN:272:TYR:CD2	3.00	0.45
1:AH:232:THR:HB	1:AH:334:VAL:CG2	2.47	0.45
1:AH:239:ILE:HG12	1:AH:326:ILE:CD1	2.46	0.45
1:AI:250:TRP:HZ3	1:AI:272:TYR:CE1	2.31	0.45
1:AK:55:ARG:HD3	1:CF:272:TYR:HD2	1.81	0.45
1:AQ:191:LEU:N	1:AQ:191:LEU:CD2	2.75	0.45
1:BB:425:VAL:HG11	1:BC:342:SER:HB2	1.98	0.45
1:BC:440:ALA:CB	1:BD:444:LEU:HD13	2.47	0.45
1:BJ:75:ARG:NH2	1:BJ:391:ALA:O	2.49	0.45
1:BL:442:GLN:HE21	1:BM:412:PHE:HB2	1.81	0.45
1:BR:237:VAL:HG23	1:BR:279:PHE:CD2	2.52	0.45
1:CI:14:CYS:H	1:CI:138:ASN:ND2	2.15	0.45
1:CJ:22:THR:OG1	1:CJ:131:HIS:CD2	2.60	0.45
1:CJ:284:ARG:NH1	1:CJ:284:ARG:CG	2.74	0.45
1:CK:393:HIS:CG	1:CK:496:PHE:HB3	2.52	0.45
1:CL:191:LEU:N	1:CL:191:LEU:HD23	2.19	0.45
1:CQ:43:ALA:HB1	1:CQ:158:GLU:HA	1.99	0.45
1:CS:162:PHE:CD2	1:CS:163:LEU:HD13	2.52	0.45
1:AB:74:ASN:ND2	1:AB:77:THR:OG1	2.50	0.45
1:AF:263:ASN:O	1:AF:267:LYS:HG3	2.17	0.45
1:AG:371:ASP:OD1	1:AG:381:MET:HG2	2.17	0.45
1:AG:423:LYS:HE2	1:AG:449:GLU:O	2.17	0.45
1:AH:237:VAL:HG23	1:AH:279:PHE:CD2	2.52	0.45
1:AJ:381:MET:HE2	1:AJ:381:MET:HB2	1.82	0.45
1:AK:232:THR:HB	1:AK:334:VAL:HG23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:170:PHE:HD1	1:AP:389:MET:CE	2.30	0.45
1:AS:188:PHE:C	1:AS:189:PHE:HD1	2.20	0.45
1:BC:239:ILE:HD12	1:BC:275:GLU:HA	1.98	0.45
1:BG:272:TYR:N	1:BG:272:TYR:HD1	2.14	0.45
1:BH:10:ILE:HD13	1:BH:20:LEU:HD13	1.99	0.45
1:BJ:232:THR:HB	1:BJ:334:VAL:CG2	2.47	0.45
1:BJ:250:TRP:CZ3	1:BJ:272:TYR:CD1	3.04	0.45
1:BL:58:ALA:HB2	1:BL:102:GLY:HA3	1.98	0.45
1:BP:182:LEU:HG	1:BP:330:ILE:HB	1.99	0.45
1:BQ:203:THR:HB	1:BQ:300:GLN:HG3	1.99	0.45
1:BR:189:PHE:HD2	1:BR:247:ILE:HD11	1.81	0.45
1:CA:162:PHE:CD2	1:CA:163:LEU:HD13	2.51	0.45
1:CA:272:TYR:N	1:CA:272:TYR:CD1	2.85	0.45
1:CA:393:HIS:CG	1:CA:496:PHE:HB3	2.52	0.45
1:CB:324:LEU:C	1:CB:324:LEU:HD23	2.38	0.45
1:CB:371:ASP:OD1	1:CB:381:MET:HG2	2.16	0.45
1:CB:170:PHE:HD1	1:CB:389:MET:HE2	1.82	0.45
1:CE:162:PHE:CD2	1:CE:163:LEU:HD13	2.52	0.45
1:CK:189:PHE:HE1	1:CK:198:ARG:CG	2.27	0.45
1:CO:170:PHE:HD1	1:CO:389:MET:HE2	1.81	0.45
1:CR:191:LEU:N	1:CR:191:LEU:HD23	2.19	0.45
1:CR:234:ARG:HG2	1:CR:280:GLU:HG2	1.97	0.45
1:CS:171:ASP:HA	1:CS:172:PRO:HD3	1.78	0.45
1:CT:207:VAL:HA	1:CT:208:PRO:HD3	1.84	0.45
1:AA:272:TYR:HD1	1:AA:272:TYR:N	2.15	0.44
1:AF:234:ARG:HG2	1:AF:280:GLU:HG2	1.99	0.44
1:AF:324:LEU:C	1:AF:324:LEU:HD23	2.36	0.44
1:AH:234:ARG:HG2	1:AH:280:GLU:HG2	1.98	0.44
1:AH:239:ILE:HD12	1:AH:275:GLU:HA	1.98	0.44
1:AI:393:HIS:CG	1:AI:496:PHE:HB3	2.52	0.44
1:AJ:393:HIS:CG	1:AJ:496:PHE:HB3	2.51	0.44
1:AS:14:CYS:H	1:AS:138:ASN:HD21	1.64	0.44
1:AT:189:PHE:CE2	1:AT:249:LEU:HD21	2.52	0.44
1:BA:404:LEU:HD22	1:BA:486:VAL:HG22	1.98	0.44
1:BD:272:TYR:CE2	1:BS:55:ARG:CZ	2.99	0.44
1:BF:203:THR:HB	1:BF:300:GLN:HG3	1.99	0.44
1:BG:79:ARG:HG3	1:BG:79:ARG:NH1	2.30	0.44
1:BI:170:PHE:HD1	1:BI:389:MET:CE	2.30	0.44
1:BI:234:ARG:HG2	1:BI:280:GLU:HG2	1.98	0.44
1:BK:272:TYR:CD1	1:BK:272:TYR:N	2.85	0.44
1:BN:234:ARG:HG2	1:BN:280:GLU:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:189:PHE:HD2	1:BR:247:ILE:CD1	2.30	0.44
1:BT:423:LYS:HE2	1:BT:449:GLU:O	2.16	0.44
1:CA:454:ASN:ND2	1:CA:456:ALA:H	2.08	0.44
1:CC:232:THR:HB	1:CC:334:VAL:HG23	1.99	0.44
1:CD:16:ALA:O	1:CD:17:ASN:HB2	2.17	0.44
1:CF:189:PHE:HD2	1:CF:247:ILE:HD11	1.81	0.44
1:CH:201:GLY:HA3	1:CH:300:GLN:HG2	1.98	0.44
1:CH:263:ASN:O	1:CH:267:LYS:HG3	2.17	0.44
1:CJ:189:PHE:CE2	1:CJ:249:LEU:HD21	2.47	0.44
1:CL:30:SER:O	1:CL:33:LYS:HB2	2.17	0.44
1:CP:232:THR:HB	1:CP:334:VAL:HG23	1.98	0.44
1:CP:454:ASN:ND2	1:CP:456:ALA:H	2.13	0.44
1:CQ:272:TYR:CD1	1:CQ:272:TYR:N	2.83	0.44
1:CR:14:CYS:H	1:CR:138:ASN:ND2	2.15	0.44
1:AG:379:VAL:HG11	1:AG:381:MET:HE1	1.99	0.44
1:AH:252:VAL:HG22	1:AH:253:SER:N	2.32	0.44
1:AJ:239:ILE:HG12	1:AJ:326:ILE:CD1	2.48	0.44
1:AP:393:HIS:CG	1:AP:496:PHE:HB3	2.51	0.44
1:AR:25:ILE:HG23	1:AR:152:LEU:HD11	1.99	0.44
1:AP:272:TYR:CD2	1:BE:55:ARG:CZ	3.00	0.44
1:BQ:272:TYR:HD1	1:BQ:272:TYR:N	2.15	0.44
1:BS:237:VAL:HG23	1:BS:279:PHE:CD2	2.52	0.44
1:CA:189:PHE:HE2	1:CA:249:LEU:HD21	1.82	0.44
1:CC:454:ASN:HD21	1:CC:456:ALA:HB3	1.83	0.44
1:CF:238:HIS:HE1	1:CF:329:GLN:OE1	2.00	0.44
1:CJ:232:THR:HB	1:CJ:334:VAL:CG2	2.47	0.44
1:CL:393:HIS:CG	1:CL:496:PHE:HB3	2.52	0.44
1:CM:171:ASP:HA	1:CM:172:PRO:HD3	1.79	0.44
1:CE:272:TYR:CE2	1:CM:55:ARG:CZ	3.00	0.44
1:CO:58:ALA:HB2	1:CO:102:GLY:HA3	1.99	0.44
1:CO:454:ASN:HD21	1:CO:456:ALA:HB3	1.82	0.44
1:CQ:162:PHE:CD2	1:CQ:163:LEU:HD13	2.52	0.44
1:AA:263:ASN:O	1:AA:267:LYS:HG3	2.17	0.44
1:AG:252:VAL:HG22	1:AG:253:SER:N	2.33	0.44
1:AJ:232:THR:HB	1:AJ:334:VAL:CG2	2.47	0.44
1:AL:203:THR:HB	1:AL:300:GLN:HG3	1.98	0.44
1:AP:18:ARG:HG3	1:AP:18:ARG:HH11	1.81	0.44
1:AQ:252:VAL:HG22	1:AQ:253:SER:N	2.32	0.44
1:AR:10:ILE:HG21	1:AR:146:TRP:CE2	2.52	0.44
1:AS:454:ASN:HD21	1:AS:456:ALA:HB3	1.82	0.44
1:BF:272:TYR:CD1	1:BF:272:TYR:N	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:237:VAL:HG23	1:BJ:279:PHE:CD2	2.51	0.44
1:BM:232:THR:HB	1:BM:334:VAL:CG2	2.47	0.44
1:BM:232:THR:HB	1:BM:334:VAL:HG23	2.00	0.44
1:BM:263:ASN:O	1:BM:267:LYS:HG3	2.17	0.44
1:BN:28:MET:HE2	1:BN:152:LEU:HG	1.98	0.44
1:BQ:189:PHE:CE2	1:BQ:249:LEU:HD21	2.52	0.44
1:BS:191:LEU:CD2	1:BS:191:LEU:N	2.75	0.44
1:CB:272:TYR:N	1:CB:272:TYR:CD1	2.85	0.44
1:CC:250:TRP:CZ3	1:CC:272:TYR:CD1	3.03	0.44
1:CG:393:HIS:CG	1:CG:496:PHE:HB3	2.52	0.44
1:CJ:300:GLN:HE21	1:CJ:300:GLN:HB2	1.59	0.44
1:CT:79:ARG:HG3	1:CT:79:ARG:HH11	1.83	0.44
1:AC:226:VAL:HG13	1:AC:228:GLY:H	1.83	0.44
1:AC:423:LYS:HE2	1:AC:449:GLU:O	2.17	0.44
1:AE:170:PHE:HD1	1:AE:389:MET:HE2	1.82	0.44
1:AF:170:PHE:HD1	1:AF:389:MET:CE	2.30	0.44
1:AF:404:LEU:HD22	1:AF:486:VAL:HG22	2.00	0.44
1:AJ:75:ARG:NH2	1:AJ:391:ALA:O	2.47	0.44
1:AN:191:LEU:CD2	1:AN:191:LEU:N	2.77	0.44
1:AN:379:VAL:HG11	1:AN:381:MET:HE1	1.99	0.44
1:AP:272:TYR:CD1	1:AP:272:TYR:N	2.85	0.44
1:AQ:226:VAL:HG13	1:AQ:228:GLY:H	1.83	0.44
1:AR:61:PHE:CD2	1:AR:243:ILE:HD11	2.52	0.44
1:AS:404:LEU:HD22	1:AS:486:VAL:HG22	1.98	0.44
1:BC:272:TYR:CD1	1:BC:272:TYR:N	2.85	0.44
1:BD:423:LYS:HE2	1:BD:449:GLU:O	2.18	0.44
1:BE:191:LEU:CD2	1:BE:191:LEU:N	2.74	0.44
1:BH:393:HIS:CG	1:BH:496:PHE:HB3	2.51	0.44
1:BN:162:PHE:CD2	1:BN:163:LEU:HD13	2.52	0.44
1:CC:234:ARG:HG2	1:CC:280:GLU:HG2	1.99	0.44
1:CD:234:ARG:HG2	1:CD:280:GLU:HG2	1.99	0.44
1:CI:191:LEU:HD23	1:CI:191:LEU:N	2.17	0.44
1:CJ:318:SER:HA	1:CJ:319:GLY:HA2	1.81	0.44
1:CM:395:LEU:HB2	1:CM:497:TYR:HB2	1.99	0.44
1:CP:189:PHE:CE2	1:CP:249:LEU:HD21	2.53	0.44
1:CQ:189:PHE:HD2	1:CQ:247:ILE:HD11	1.81	0.44
1:CR:232:THR:HB	1:CR:334:VAL:HG23	1.99	0.44
1:AA:43:ALA:HB1	1:AA:158:GLU:HA	2.00	0.44
1:AE:232:THR:HB	1:AE:334:VAL:CG2	2.48	0.44
1:AE:404:LEU:HD22	1:AE:486:VAL:HG22	1.98	0.44
1:AG:263:ASN:O	1:AG:267:LYS:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:25:ILE:HG23	1:AI:152:LEU:HD11	1.98	0.44
1:AM:423:LYS:HE2	1:AM:449:GLU:O	2.18	0.44
1:AN:170:PHE:HD1	1:AN:389:MET:CE	2.30	0.44
1:AQ:272:TYR:CD1	1:AQ:272:TYR:N	2.85	0.44
1:AS:182:LEU:C	1:AS:182:LEU:HD12	2.37	0.44
1:AT:232:THR:HB	1:AT:334:VAL:HG23	1.98	0.44
1:BC:162:PHE:CD2	1:BC:163:LEU:HD13	2.52	0.44
1:BC:61:PHE:CD2	1:BC:243:ILE:HD11	2.53	0.44
1:BC:454:ASN:HD21	1:BC:456:ALA:HB3	1.82	0.44
1:BF:423:LYS:HE2	1:BF:449:GLU:O	2.17	0.44
1:BG:404:LEU:N	1:BG:404:LEU:HD23	2.32	0.44
1:BM:18:ARG:HG2	1:BM:20:LEU:HD23	2.00	0.44
1:BM:237:VAL:HG23	1:BM:279:PHE:CD2	2.52	0.44
1:BM:404:LEU:HD22	1:BM:486:VAL:HG22	2.00	0.44
1:BM:74:ASN:ND2	1:BM:77:THR:OG1	2.51	0.44
1:BN:232:THR:HB	1:BN:334:VAL:CG2	2.47	0.44
1:BO:189:PHE:CE2	1:BO:249:LEU:HD21	2.52	0.44
1:BP:22:THR:OG1	1:BP:131:HIS:CD2	2.58	0.44
1:BP:379:VAL:HG11	1:BP:381:MET:HE1	1.99	0.44
1:BS:189:PHE:CE2	1:BS:249:LEU:HD21	2.53	0.44
1:BS:75:ARG:NH2	1:BS:391:ALA:O	2.50	0.44
1:CA:188:PHE:C	1:CA:189:PHE:HD1	2.21	0.44
1:CD:232:THR:HB	1:CD:334:VAL:CG2	2.48	0.44
1:CD:237:VAL:HG23	1:CD:279:PHE:CD2	2.53	0.44
1:CE:43:ALA:HB1	1:CE:158:GLU:HA	2.00	0.44
1:CF:404:LEU:HD22	1:CF:486:VAL:HG22	1.98	0.44
1:CG:232:THR:HB	1:CG:334:VAL:CG2	2.48	0.44
1:CL:171:ASP:HA	1:CL:172:PRO:HD3	1.80	0.44
1:CN:15:GLN:HA	1:CN:15:GLN:OE1	2.17	0.44
1:CN:423:LYS:HE2	1:CN:449:GLU:O	2.17	0.44
1:CQ:189:PHE:HE1	1:CQ:198:ARG:CG	2.29	0.44
1:CT:162:PHE:CD2	1:CT:163:LEU:HD13	2.53	0.44
1:AB:189:PHE:HD2	1:AB:247:ILE:HD11	1.83	0.44
1:AC:188:PHE:C	1:AC:189:PHE:HD1	2.20	0.44
1:AC:442:GLN:HE21	1:AD:412:PHE:HB2	1.83	0.44
1:AE:272:TYR:N	1:AE:272:TYR:HD1	2.15	0.44
1:AE:55:ARG:HD3	1:CP:272:TYR:HD2	1.79	0.44
1:AH:35:VAL:O	1:AH:39:LYS:HG3	2.18	0.44
1:AI:16:ALA:O	1:AI:17:ASN:HB2	2.17	0.44
1:AJ:189:PHE:HD2	1:AJ:247:ILE:HD11	1.82	0.44
1:AK:30:SER:O	1:AK:33:LYS:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:237:VAL:HG23	1:AL:279:PHE:CD2	2.52	0.44
1:AO:237:VAL:HG23	1:AO:279:PHE:CD2	2.53	0.44
1:AO:284:ARG:NH1	1:AO:284:ARG:CG	2.71	0.44
1:BA:263:ASN:O	1:BA:267:LYS:HG3	2.17	0.44
1:BB:232:THR:HB	1:BB:334:VAL:CG2	2.47	0.44
1:BB:371:ASP:OD1	1:BB:381:MET:HG2	2.17	0.44
1:BD:454:ASN:HD21	1:BD:456:ALA:HB3	1.82	0.44
1:BE:16:ALA:O	1:BE:17:ASN:CB	2.64	0.44
1:BE:404:LEU:HD22	1:BE:486:VAL:HG22	2.00	0.44
1:BF:11:PRO:HG2	1:BF:18:ARG:CD	2.48	0.44
1:BF:318:SER:HA	1:BF:319:GLY:HA2	1.84	0.44
1:BG:234:ARG:HG2	1:BG:280:GLU:HG2	1.99	0.44
1:BH:404:LEU:HD22	1:BH:486:VAL:HG22	1.99	0.44
1:BK:239:ILE:HD12	1:BK:275:GLU:HA	2.00	0.44
1:BK:318:SER:HA	1:BK:319:GLY:HA2	1.80	0.44
1:BK:404:LEU:HD22	1:BK:486:VAL:HG22	1.99	0.44
1:BO:14:CYS:H	1:BO:138:ASN:ND2	2.14	0.44
1:BP:324:LEU:HA	1:BP:325:PRO:HD3	1.84	0.44
1:BQ:234:ARG:HG2	1:BQ:280:GLU:HG2	2.00	0.44
1:BT:58:ALA:HB2	1:BT:102:GLY:HA3	2.00	0.44
1:CC:43:ALA:HB1	1:CC:158:GLU:HA	1.99	0.44
1:CD:239:ILE:HD12	1:CD:275:GLU:HA	1.99	0.44
1:CA:444:LEU:HD13	1:CE:440:ALA:CB	2.48	0.44
1:CG:379:VAL:HG11	1:CG:381:MET:HE1	1.99	0.44
1:CH:232:THR:HB	1:CH:334:VAL:HG23	1.99	0.44
1:CI:300:GLN:HE21	1:CI:300:GLN:HB2	1.70	0.44
1:CK:272:TYR:HD1	1:CK:272:TYR:N	2.16	0.44
1:CM:241:ALA:HB1	1:CM:242:PRO:HD2	1.99	0.44
1:CM:189:PHE:CE2	1:CM:249:LEU:HD21	2.45	0.44
1:CM:232:THR:HB	1:CM:334:VAL:HG23	2.00	0.44
1:CP:67:VAL:HG23	1:CP:135:LEU:HB2	1.98	0.44
1:AA:18:ARG:HG3	1:AA:19:TYR:N	2.32	0.44
1:AD:171:ASP:HA	1:AD:172:PRO:HD3	1.79	0.44
1:AD:232:THR:HB	1:AD:334:VAL:HG23	2.00	0.44
1:AE:237:VAL:HG23	1:AE:279:PHE:CD2	2.52	0.44
1:AH:272:TYR:HD1	1:AH:272:TYR:N	2.16	0.44
1:AH:404:LEU:HD22	1:AH:486:VAL:HG22	2.00	0.44
1:AJ:226:VAL:HG13	1:AJ:228:GLY:H	1.82	0.44
1:AS:250:TRP:CZ3	1:AS:272:TYR:CD1	3.05	0.44
1:BA:300:GLN:HE21	1:BA:300:GLN:HB2	1.55	0.44
1:BF:189:PHE:HD2	1:BF:247:ILE:HD11	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:252:VAL:HG22	1:BF:253:SER:N	2.33	0.44
1:BJ:189:PHE:HD2	1:BJ:247:ILE:CD1	2.30	0.44
1:BM:239:ILE:HD12	1:BM:275:GLU:HA	1.99	0.44
1:BP:300:GLN:HE21	1:BP:300:GLN:HB2	1.58	0.44
1:BP:289:ARG:NH1	1:BP:337:ASP:OD1	2.51	0.44
1:BQ:423:LYS:HE2	1:BQ:449:GLU:O	2.18	0.44
1:BS:440:ALA:CB	1:BT:444:LEU:HD13	2.48	0.44
1:BT:226:VAL:HG13	1:BT:228:GLY:H	1.83	0.44
1:CA:58:ALA:HB2	1:CA:102:GLY:HA3	2.00	0.44
1:CA:237:VAL:HG23	1:CA:279:PHE:CD2	2.53	0.44
1:CD:171:ASP:HA	1:CD:172:PRO:HD3	1.79	0.44
1:CD:404:LEU:HD22	1:CD:486:VAL:HG22	2.00	0.44
1:CM:207:VAL:HA	1:CM:208:PRO:HD3	1.85	0.44
1:CN:263:ASN:O	1:CN:267:LYS:HG3	2.18	0.44
1:CQ:239:ILE:HD12	1:CQ:275:GLU:HA	1.99	0.44
1:CQ:252:VAL:HG22	1:CQ:253:SER:N	2.33	0.44
1:CQ:237:VAL:HG23	1:CQ:279:PHE:CD2	2.52	0.44
1:CR:77:THR:O	1:CR:81:THR:HG23	2.17	0.44
1:CD:272:TYR:HD2	1:CS:55:ARG:HD3	1.77	0.44
1:CT:191:LEU:CD2	1:CT:191:LEU:N	2.76	0.44
1:CT:393:HIS:CG	1:CT:496:PHE:HB3	2.51	0.44
1:AB:404:LEU:HD22	1:AB:486:VAL:HG22	2.00	0.44
1:AG:404:LEU:HD22	1:AG:486:VAL:HG22	1.98	0.44
1:AI:237:VAL:HG23	1:AI:279:PHE:CD2	2.52	0.44
1:AJ:25:ILE:HG23	1:AJ:152:LEU:HD11	1.99	0.44
1:AK:191:LEU:CD2	1:AK:191:LEU:N	2.74	0.44
1:AL:324:LEU:C	1:AL:324:LEU:HD23	2.38	0.44
1:AL:170:PHE:HD1	1:AL:389:MET:HE2	1.83	0.44
1:AP:272:TYR:CE2	1:BE:55:ARG:CZ	3.00	0.44
1:AS:423:LYS:HE2	1:AS:449:GLU:O	2.18	0.44
1:AT:272:TYR:N	1:AT:272:TYR:CD1	2.83	0.44
1:AT:272:TYR:HD1	1:AT:272:TYR:N	2.14	0.44
1:BH:252:VAL:HG22	1:BH:253:SER:N	2.33	0.44
1:BI:272:TYR:N	1:BI:272:TYR:HD1	2.16	0.44
1:BK:162:PHE:CD2	1:BK:163:LEU:HD13	2.53	0.44
1:BM:423:LYS:HE2	1:BM:449:GLU:O	2.17	0.44
1:BO:10:ILE:HA	1:BO:11:PRO:HD3	1.86	0.44
1:BQ:250:TRP:HZ3	1:BQ:272:TYR:CE1	2.27	0.44
1:BS:263:ASN:O	1:BS:267:LYS:HG3	2.18	0.44
1:BT:25:ILE:HG23	1:BT:152:LEU:HD11	1.99	0.44
1:CD:162:PHE:CD2	1:CD:163:LEU:HD13	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:379:VAL:HG11	1:CD:381:MET:HE1	1.99	0.44
1:CH:423:LYS:HE2	1:CH:449:GLU:O	2.18	0.44
1:CN:170:PHE:HD1	1:CN:389:MET:HE2	1.82	0.44
1:CP:442:GLN:HE21	1:CQ:412:PHE:HB2	1.81	0.44
1:CR:272:TYR:CD1	1:CR:272:TYR:N	2.86	0.44
1:CS:207:VAL:HA	1:CS:208:PRO:HD3	1.83	0.44
1:CS:393:HIS:CG	1:CS:496:PHE:HB3	2.53	0.44
1:CT:237:VAL:HG23	1:CT:279:PHE:CD2	2.53	0.44
1:AA:14:CYS:H	1:AA:138:ASN:ND2	2.12	0.44
1:AC:189:PHE:HE1	1:AC:198:ARG:CG	2.27	0.44
1:AC:18:ARG:HG2	1:AC:20:LEU:HD23	1.98	0.44
1:AC:272:TYR:N	1:AC:272:TYR:HD1	2.16	0.44
1:AD:207:VAL:HA	1:AD:208:PRO:HD3	1.83	0.44
1:AI:232:THR:HB	1:AI:334:VAL:HG23	1.98	0.44
1:AJ:108:ILE:HG23	1:AJ:113:LEU:HD12	2.00	0.44
1:AM:442:GLN:HE21	1:AN:412:PHE:HB2	1.83	0.44
1:BG:239:ILE:HD12	1:BG:275:GLU:HA	1.99	0.44
1:AG:272:TYR:HE2	1:BG:55:ARG:NE	2.13	0.44
1:BI:203:THR:HB	1:BI:300:GLN:HG3	2.00	0.44
1:BJ:182:LEU:HG	1:BJ:330:ILE:HB	1.99	0.44
1:BM:189:PHE:CE2	1:BM:249:LEU:HD21	2.42	0.44
1:BP:74:ASN:ND2	1:BP:77:THR:OG1	2.50	0.44
1:BQ:36:GLN:HE22	1:BQ:156:LEU:H	1.63	0.44
1:BR:203:THR:HB	1:BR:300:GLN:HG3	1.99	0.44
1:BR:79:ARG:NH1	1:BR:79:ARG:CG	2.77	0.44
1:BR:440:ALA:CB	1:BS:444:LEU:HD13	2.48	0.44
1:CA:232:THR:HB	1:CA:334:VAL:HG23	1.99	0.44
1:CA:170:PHE:HD1	1:CA:389:MET:HE2	1.82	0.44
1:CC:25:ILE:HG23	1:CC:152:LEU:HD11	1.99	0.44
1:CE:252:VAL:HG22	1:CE:253:SER:N	2.33	0.44
1:CE:239:ILE:HD12	1:CE:275:GLU:HA	2.00	0.44
1:CI:379:VAL:HG11	1:CI:381:MET:HE1	1.98	0.44
1:CJ:404:LEU:HD22	1:CJ:486:VAL:HG22	1.99	0.44
1:CO:74:ASN:ND2	1:CO:77:THR:OG1	2.51	0.44
1:CD:272:TYR:CE2	1:CS:55:ARG:CZ	3.01	0.44
1:AA:170:PHE:HD1	1:AA:389:MET:CE	2.31	0.43
1:AA:423:LYS:HE2	1:AA:449:GLU:O	2.18	0.43
1:AB:454:ASN:HD21	1:AB:456:ALA:HB3	1.82	0.43
1:AC:75:ARG:NH2	1:AC:391:ALA:O	2.51	0.43
1:AD:379:VAL:HG12	1:AD:381:MET:HE2	2.00	0.43
1:AE:393:HIS:CG	1:AE:496:PHE:HB3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:423:LYS:HE2	1:AF:449:GLU:O	2.18	0.43
1:AH:324:LEU:HD23	1:AH:324:LEU:C	2.38	0.43
1:AH:423:LYS:HE2	1:AH:449:GLU:O	2.18	0.43
1:AK:379:VAL:HG11	1:AK:381:MET:HE1	2.00	0.43
1:AO:300:GLN:HE21	1:AO:300:GLN:HB2	1.64	0.43
1:AP:189:PHE:HD2	1:AP:247:ILE:HD11	1.83	0.43
1:AQ:108:ILE:HG23	1:AQ:113:LEU:HD12	2.00	0.43
1:AT:239:ILE:HG12	1:AT:326:ILE:CD1	2.48	0.43
1:AT:393:HIS:CG	1:AT:496:PHE:HB3	2.52	0.43
1:BG:15:GLN:NE2	1:BG:15:GLN:HA	2.30	0.43
1:BH:171:ASP:HA	1:BH:172:PRO:HD3	1.78	0.43
1:BL:423:LYS:HE2	1:BL:449:GLU:O	2.18	0.43
1:BO:61:PHE:CE2	1:BO:243:ILE:HD11	2.53	0.43
1:BQ:393:HIS:CG	1:BQ:496:PHE:HB3	2.53	0.43
1:BR:170:PHE:HD1	1:BR:389:MET:HE2	1.83	0.43
1:BT:454:ASN:HD21	1:BT:456:ALA:HB3	1.82	0.43
1:BP:272:TYR:CD2	1:CE:55:ARG:NH1	2.86	0.43
1:CF:239:ILE:HD12	1:CF:275:GLU:HA	1.99	0.43
1:CF:371:ASP:OD1	1:CF:381:MET:HG2	2.17	0.43
1:CG:11:PRO:HG2	1:CG:18:ARG:HD2	2.00	0.43
1:CG:237:VAL:HG23	1:CG:279:PHE:CD2	2.53	0.43
1:CH:272:TYR:N	1:CH:272:TYR:CD1	2.86	0.43
1:CH:393:HIS:CG	1:CH:496:PHE:HB3	2.53	0.43
1:CK:442:GLN:HE21	1:CL:412:PHE:HB2	1.82	0.43
1:CM:318:SER:HA	1:CM:319:GLY:HA2	1.77	0.43
1:CP:226:VAL:HG13	1:CP:228:GLY:H	1.82	0.43
1:AA:79:ARG:HH11	1:AA:79:ARG:HG3	1.82	0.43
1:AB:43:ALA:HB1	1:AB:158:GLU:HA	2.00	0.43
1:AI:232:THR:HB	1:AI:334:VAL:CG2	2.48	0.43
1:AL:272:TYR:N	1:AL:272:TYR:CD1	2.86	0.43
1:AM:189:PHE:HD2	1:AM:247:ILE:CD1	2.30	0.43
1:BC:18:ARG:HB2	1:BC:18:ARG:NH1	2.34	0.43
1:BE:11:PRO:HG2	1:BE:18:ARG:CD	2.48	0.43
1:BH:189:PHE:HD2	1:BH:247:ILE:HD11	1.83	0.43
1:BH:11:PRO:HG2	1:BH:18:ARG:HD2	1.99	0.43
1:BI:11:PRO:HG2	1:BI:18:ARG:HD2	2.00	0.43
1:BH:442:GLN:NE2	1:BI:412:PHE:HB2	2.33	0.43
1:BK:252:VAL:HG22	1:BK:253:SER:N	2.33	0.43
1:BL:418:SER:HB3	1:BM:407:SER:HB3	2.00	0.43
1:BM:58:ALA:HB2	1:BM:102:GLY:HA3	1.99	0.43
1:BO:237:VAL:HG23	1:BO:279:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:404:LEU:HD22	1:BP:486:VAL:HG22	2.00	0.43
1:BO:272:TYR:CD2	1:BR:55:ARG:NH1	2.86	0.43
1:CD:189:PHE:HE2	1:CD:249:LEU:CD2	2.31	0.43
1:CH:252:VAL:HG22	1:CH:253:SER:N	2.33	0.43
1:CI:239:ILE:HG12	1:CI:326:ILE:CD1	2.48	0.43
1:CF:412:PHE:HB2	1:CJ:442:GLN:HE21	1.83	0.43
1:CL:188:PHE:C	1:CL:189:PHE:HD1	2.22	0.43
1:CL:423:LYS:HE2	1:CL:449:GLU:O	2.18	0.43
1:CM:22:THR:OG1	1:CM:131:HIS:CD2	2.63	0.43
1:CS:237:VAL:HG23	1:CS:279:PHE:CD2	2.53	0.43
1:AC:234:ARG:HG2	1:AC:280:GLU:HG2	1.99	0.43
1:AE:379:VAL:HG11	1:AE:381:MET:HE1	1.99	0.43
1:AG:237:VAL:HG23	1:AG:279:PHE:CD2	2.54	0.43
1:AK:61:PHE:CD2	1:AK:243:ILE:HD11	2.54	0.43
1:AO:189:PHE:CE2	1:AO:249:LEU:HD21	2.53	0.43
1:AO:318:SER:HA	1:AO:319:GLY:HA2	1.79	0.43
1:AR:189:PHE:HE1	1:AR:198:ARG:HG2	1.78	0.43
1:AR:252:VAL:HG22	1:AR:253:SER:N	2.33	0.43
1:AS:318:SER:HA	1:AS:319:GLY:HA2	1.79	0.43
1:BA:379:VAL:HG11	1:BA:381:MET:HE1	2.01	0.43
1:BA:73:TYR:CE2	1:BA:394:GLY:HA3	2.54	0.43
1:BB:263:ASN:O	1:BB:267:LYS:HG3	2.18	0.43
1:BD:234:ARG:HG2	1:BD:280:GLU:HG2	1.99	0.43
1:BH:226:VAL:HG13	1:BH:228:GLY:H	1.82	0.43
1:BM:393:HIS:CG	1:BM:496:PHE:HB3	2.53	0.43
1:BT:232:THR:HB	1:BT:334:VAL:HG23	2.00	0.43
1:CC:423:LYS:HE2	1:CC:449:GLU:O	2.18	0.43
1:CD:189:PHE:HD2	1:CD:247:ILE:HD11	1.83	0.43
1:CH:232:THR:HB	1:CH:334:VAL:CG2	2.49	0.43
1:CI:237:VAL:HG23	1:CI:279:PHE:CD2	2.53	0.43
1:CI:263:ASN:O	1:CI:267:LYS:HG3	2.18	0.43
1:CO:182:LEU:C	1:CO:182:LEU:HD12	2.38	0.43
1:CO:239:ILE:HG23	1:CO:324:LEU:HD21	2.01	0.43
1:CO:404:LEU:N	1:CO:404:LEU:HD23	2.32	0.43
1:CQ:272:TYR:N	1:CQ:272:TYR:HD1	2.15	0.43
1:CT:423:LYS:HE2	1:CT:449:GLU:O	2.18	0.43
1:AC:232:THR:HB	1:AC:334:VAL:CG2	2.49	0.43
1:AC:440:ALA:HB3	1:AD:444:LEU:HD13	1.99	0.43
1:AD:11:PRO:HG2	1:AD:18:ARG:CD	2.48	0.43
1:AD:79:ARG:CG	1:AD:79:ARG:NH1	2.81	0.43
1:AE:255:TRP:CE3	1:AE:285:SER:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:272:TYR:N	1:AF:272:TYR:HD1	2.16	0.43
1:AG:10:ILE:HA	1:AG:11:PRO:HD3	1.81	0.43
1:AG:201:GLY:HA3	1:AG:300:GLN:HG2	1.99	0.43
1:AI:404:LEU:HD22	1:AI:486:VAL:HG22	1.99	0.43
1:AI:55:ARG:NE	1:AR:272:TYR:HE2	2.16	0.43
1:AJ:272:TYR:CD1	1:AJ:272:TYR:N	2.86	0.43
1:AK:423:LYS:HE2	1:AK:449:GLU:O	2.18	0.43
1:AK:404:LEU:HD22	1:AK:486:VAL:HG22	2.00	0.43
1:AP:162:PHE:CD2	1:AP:163:LEU:HD13	2.53	0.43
1:AP:171:ASP:HA	1:AP:172:PRO:HD3	1.79	0.43
1:AS:74:ASN:ND2	1:AS:77:THR:OG1	2.52	0.43
1:AT:232:THR:HB	1:AT:334:VAL:CG2	2.48	0.43
1:BB:189:PHE:HE1	1:BB:198:ARG:HG2	1.76	0.43
1:BC:234:ARG:HG2	1:BC:280:GLU:HG2	2.00	0.43
1:BI:163:LEU:HD12	1:BI:163:LEU:HA	1.87	0.43
1:BI:207:VAL:HA	1:BI:208:PRO:HD3	1.84	0.43
1:BJ:423:LYS:HE2	1:BJ:449:GLU:O	2.18	0.43
1:BK:300:GLN:HB2	1:BK:300:GLN:HE21	1.60	0.43
1:BK:170:PHE:HD1	1:BK:389:MET:HE2	1.83	0.43
1:BL:171:ASP:HA	1:BL:172:PRO:HD3	1.76	0.43
1:BM:171:ASP:HA	1:BM:172:PRO:HD3	1.79	0.43
1:BN:272:TYR:CD1	1:BN:272:TYR:N	2.86	0.43
1:BN:404:LEU:HD22	1:BN:486:VAL:HG22	2.01	0.43
1:BO:393:HIS:CG	1:BO:496:PHE:HB3	2.52	0.43
1:CA:423:LYS:HE2	1:CA:449:GLU:O	2.19	0.43
1:CA:79:ARG:HG3	1:CA:79:ARG:NH1	2.29	0.43
1:CC:393:HIS:CG	1:CC:496:PHE:HB3	2.52	0.43
1:CD:226:VAL:HG13	1:CD:228:GLY:H	1.82	0.43
1:CG:423:LYS:HE2	1:CG:449:GLU:O	2.17	0.43
1:CH:404:LEU:HD22	1:CH:486:VAL:HG22	1.99	0.43
1:CI:324:LEU:HD23	1:CI:324:LEU:C	2.38	0.43
1:CK:188:PHE:C	1:CK:189:PHE:HD1	2.21	0.43
1:CK:252:VAL:HG22	1:CK:253:SER:N	2.33	0.43
1:CO:232:THR:HB	1:CO:334:VAL:CG2	2.49	0.43
1:CS:189:PHE:CE2	1:CS:249:LEU:HD21	2.53	0.43
1:AD:393:HIS:CG	1:AD:496:PHE:HB3	2.52	0.43
1:AD:55:ARG:HD3	1:AN:272:TYR:HD2	1.78	0.43
1:AJ:263:ASN:O	1:AJ:267:LYS:HG3	2.18	0.43
1:AK:252:VAL:HG22	1:AK:253:SER:N	2.33	0.43
1:AM:25:ILE:HG23	1:AM:152:LEU:HD11	2.00	0.43
1:AM:237:VAL:HG23	1:AM:279:PHE:CD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:379:VAL:HG11	1:AM:381:MET:HE1	2.00	0.43
1:AR:250:TRP:HZ3	1:AR:272:TYR:HE1	1.61	0.43
1:BB:239:ILE:HD12	1:BB:275:GLU:HA	2.00	0.43
1:BB:55:ARG:HD3	1:CB:272:TYR:HD2	1.81	0.43
1:BC:11:PRO:HG2	1:BC:18:ARG:HD2	2.00	0.43
1:BE:232:THR:HB	1:BE:334:VAL:HG23	1.99	0.43
1:BE:379:VAL:HG11	1:BE:381:MET:HE1	1.99	0.43
1:BG:232:THR:HB	1:BG:334:VAL:HG23	2.00	0.43
1:BH:55:ARG:NE	1:BK:272:TYR:HE2	2.12	0.43
1:BL:238:HIS:HE1	1:BL:329:GLN:OE1	2.01	0.43
1:BM:16:ALA:O	1:BM:17:ASN:CB	2.65	0.43
1:BN:108:ILE:HG23	1:BN:113:LEU:HD12	2.00	0.43
1:BN:189:PHE:CE2	1:BN:249:LEU:HD21	2.48	0.43
1:BO:61:PHE:CD2	1:BO:243:ILE:HD11	2.53	0.43
1:BP:239:ILE:HD12	1:BP:275:GLU:HA	2.00	0.43
1:BP:442:GLN:HE21	1:BQ:412:PHE:HB2	1.82	0.43
1:BQ:324:LEU:HD23	1:BQ:324:LEU:C	2.39	0.43
1:BT:371:ASP:OD1	1:BT:381:MET:HG2	2.19	0.43
1:CA:189:PHE:CE2	1:CA:249:LEU:HD21	2.53	0.43
1:BC:272:TYR:CE2	1:CA:55:ARG:CZ	3.00	0.43
1:CJ:189:PHE:HD2	1:CJ:247:ILE:HD11	1.83	0.43
1:CL:58:ALA:HB2	1:CL:102:GLY:HA3	2.00	0.43
1:CO:188:PHE:C	1:CO:189:PHE:HD1	2.22	0.43
1:CI:55:ARG:CZ	1:CR:272:TYR:CD2	3.02	0.43
1:CS:239:ILE:HD12	1:CS:275:GLU:HA	1.99	0.43
1:AC:232:THR:HB	1:AC:334:VAL:HG23	2.00	0.43
1:AC:252:VAL:HG22	1:AC:253:SER:N	2.33	0.43
1:AC:300:GLN:HE21	1:AC:300:GLN:HB2	1.53	0.43
1:AK:232:THR:HB	1:AK:334:VAL:CG2	2.49	0.43
1:AM:170:PHE:HD1	1:AM:389:MET:CE	2.32	0.43
1:AM:454:ASN:C	1:AM:454:ASN:HD22	2.22	0.43
1:AO:191:LEU:HD23	1:AO:191:LEU:N	2.16	0.43
1:AO:263:ASN:O	1:AO:267:LYS:HG3	2.17	0.43
1:AR:77:THR:O	1:AR:81:THR:HG23	2.18	0.43
1:BC:423:LYS:HE2	1:BC:449:GLU:O	2.19	0.43
1:BG:379:VAL:HG12	1:BG:381:MET:HE2	2.01	0.43
1:BI:202:LEU:HD23	1:BI:202:LEU:HA	1.87	0.43
1:BJ:239:ILE:HD12	1:BJ:275:GLU:HA	2.00	0.43
1:BL:170:PHE:HD1	1:BL:389:MET:HE2	1.83	0.43
1:BO:175:PHE:O	1:BO:175:PHE:CD2	2.72	0.43
1:BO:22:THR:OG1	1:BO:131:HIS:CD2	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:201:GLY:HA3	1:BP:300:GLN:HG2	1.99	0.43
1:BP:232:THR:HB	1:BP:334:VAL:CG2	2.47	0.43
1:BR:163:LEU:HA	1:BR:163:LEU:HD12	1.87	0.43
1:CA:234:ARG:CG	1:CA:280:GLU:HG2	2.49	0.43
1:CB:237:VAL:HG23	1:CB:279:PHE:CD2	2.53	0.43
1:CC:189:PHE:HD2	1:CC:247:ILE:HD11	1.83	0.43
1:CD:202:LEU:HD23	1:CD:202:LEU:HA	1.89	0.43
1:CE:237:VAL:HG23	1:CE:279:PHE:CD2	2.54	0.43
1:CF:284:ARG:CG	1:CF:284:ARG:NH1	2.74	0.43
1:CI:234:ARG:HG2	1:CI:280:GLU:HG2	1.99	0.43
1:CI:30:SER:O	1:CI:33:LYS:HB2	2.18	0.43
1:CN:239:ILE:HG12	1:CN:326:ILE:CD1	2.47	0.43
1:CP:454:ASN:HD21	1:CP:456:ALA:HB3	1.84	0.43
1:CT:239:ILE:HD12	1:CT:275:GLU:HA	2.01	0.43
1:AC:170:PHE:HD1	1:AC:389:MET:CE	2.31	0.43
1:AE:234:ARG:HG2	1:AE:280:GLU:HG2	1.99	0.43
1:AK:189:PHE:HE2	1:AK:249:LEU:HD21	1.84	0.43
1:AM:10:ILE:HG21	1:AM:146:TRP:CZ2	2.54	0.43
1:AN:14:CYS:H	1:AN:138:ASN:ND2	2.17	0.43
1:AP:442:GLN:NE2	1:AQ:412:PHE:HB2	2.34	0.43
1:AT:170:PHE:HD1	1:AT:389:MET:HE2	1.84	0.43
1:AT:237:VAL:HG23	1:AT:279:PHE:CD2	2.54	0.43
1:BB:418:SER:HB3	1:BC:407:SER:HB3	2.00	0.43
1:BC:55:ARG:HD3	1:BT:272:TYR:HD2	1.84	0.43
1:BD:58:ALA:HB2	1:BD:102:GLY:HA3	1.99	0.43
1:BE:272:TYR:HD1	1:BE:272:TYR:N	2.16	0.43
1:BG:74:ASN:ND2	1:BG:77:THR:OG1	2.51	0.43
1:BI:234:ARG:CG	1:BI:280:GLU:HG2	2.49	0.43
1:BL:226:VAL:HG13	1:BL:228:GLY:H	1.83	0.43
1:CB:272:TYR:N	1:CB:272:TYR:HD1	2.16	0.43
1:AB:272:TYR:HE2	1:CB:55:ARG:NE	2.06	0.43
1:CE:371:ASP:OD1	1:CE:381:MET:HG2	2.18	0.43
1:CF:418:SER:HB3	1:CG:407:SER:HB3	2.01	0.43
1:CG:252:VAL:HG22	1:CG:253:SER:N	2.34	0.43
1:BG:272:TYR:HD2	1:CG:55:ARG:HD3	1.78	0.43
1:CK:108:ILE:HG23	1:CK:113:LEU:HD12	2.01	0.43
1:CR:285:SER:HA	1:CR:286:PRO:HD3	1.91	0.43
1:AC:272:TYR:CD2	1:BA:55:ARG:CZ	3.01	0.43
1:AK:237:VAL:HG23	1:AK:279:PHE:CD2	2.54	0.43
1:AM:189:PHE:HD2	1:AM:247:ILE:HD11	1.83	0.43
1:AM:202:LEU:HA	1:AM:202:LEU:HD23	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:5:ARG:HD3	1:AN:263:ASN:HD22	1.84	0.43
1:AN:318:SER:HA	1:AN:319:GLY:HA2	1.78	0.43
1:AP:188:PHE:C	1:AP:189:PHE:HD1	2.22	0.43
1:AQ:371:ASP:OD1	1:AQ:381:MET:HG2	2.18	0.43
1:BE:171:ASP:HA	1:BE:172:PRO:HD3	1.78	0.43
1:BK:171:ASP:HA	1:BK:172:PRO:HD3	1.81	0.43
1:BM:442:GLN:HE21	1:BN:412:PHE:HB2	1.83	0.43
1:BP:170:PHE:HD1	1:BP:389:MET:CE	2.32	0.43
1:BP:232:THR:HB	1:BP:334:VAL:HG23	2.01	0.43
1:BP:234:ARG:HG2	1:BP:280:GLU:HG2	2.00	0.43
1:BS:11:PRO:HG2	1:BS:18:ARG:HD2	2.01	0.43
1:BS:239:ILE:HD12	1:BS:275:GLU:HA	2.01	0.43
1:BT:272:TYR:CD1	1:BT:272:TYR:N	2.86	0.43
1:CC:33:LYS:HE2	1:CC:33:LYS:HB2	1.94	0.43
1:CF:324:LEU:C	1:CF:324:LEU:HD23	2.39	0.43
1:CJ:191:LEU:N	1:CJ:191:LEU:CD2	2.78	0.43
1:CK:232:THR:HB	1:CK:334:VAL:CG2	2.49	0.43
1:CO:239:ILE:HD12	1:CO:275:GLU:HA	2.00	0.43
1:CO:189:PHE:CE2	1:CO:249:LEU:HD21	2.53	0.43
1:CO:263:ASN:O	1:CO:267:LYS:HG3	2.19	0.43
1:CC:55:ARG:CZ	1:CT:272:TYR:CE2	3.01	0.43
1:AA:10:ILE:HG21	1:AA:146:TRP:CZ2	2.54	0.43
1:AB:371:ASP:OD1	1:AB:381:MET:HG2	2.19	0.43
1:AG:232:THR:HB	1:AG:334:VAL:HG23	2.01	0.43
1:AK:239:ILE:HD12	1:AK:275:GLU:HA	2.00	0.43
1:AL:379:VAL:HG11	1:AL:381:MET:HE1	2.00	0.43
1:AL:454:ASN:HD21	1:AL:456:ALA:HB3	1.84	0.43
1:AM:182:LEU:C	1:AM:182:LEU:HD12	2.39	0.43
1:AN:238:HIS:HE1	1:AN:329:GLN:OE1	2.00	0.43
1:AN:423:LYS:HE2	1:AN:449:GLU:O	2.19	0.43
1:AP:423:LYS:HE2	1:AP:449:GLU:O	2.19	0.43
1:AQ:237:VAL:HG23	1:AQ:279:PHE:CD2	2.54	0.43
1:BC:108:ILE:HG23	1:BC:113:LEU:HD12	2.00	0.43
1:BC:182:LEU:HG	1:BC:330:ILE:HB	1.99	0.43
1:BE:263:ASN:O	1:BE:267:LYS:HG3	2.18	0.43
1:BH:272:TYR:HD1	1:BH:272:TYR:N	2.15	0.43
1:BI:272:TYR:CE2	1:BO:55:ARG:CZ	3.02	0.43
1:BR:395:LEU:HB2	1:BR:497:TYR:HB2	2.01	0.43
1:CA:263:ASN:O	1:CA:267:LYS:HG3	2.18	0.43
1:CI:239:ILE:HD12	1:CI:275:GLU:HA	2.00	0.43
1:CM:79:ARG:HH11	1:CM:79:ARG:CG	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:232:THR:HB	1:CR:334:VAL:CG2	2.49	0.43
1:AA:232:THR:HB	1:AA:334:VAL:HG23	2.01	0.43
1:AB:202:LEU:HB2	1:AB:304:SER:O	2.19	0.43
1:AB:55:ARG:HD3	1:BB:272:TYR:HD2	1.81	0.43
1:AC:25:ILE:HG23	1:AC:152:LEU:HD11	2.01	0.43
1:AF:444:LEU:HD13	1:AJ:440:ALA:CB	2.49	0.43
1:AK:454:ASN:HD21	1:AK:456:ALA:HB3	1.83	0.43
1:AO:58:ALA:HB2	1:AO:102:GLY:HA3	2.01	0.43
1:AI:272:TYR:HD2	1:AO:55:ARG:HD3	1.83	0.43
1:AP:33:LYS:CG	1:AP:33:LYS:O	2.58	0.43
1:AQ:404:LEU:N	1:AQ:404:LEU:HD23	2.34	0.43
1:AS:440:ALA:HB3	1:AT:444:LEU:HD13	2.01	0.43
1:AT:318:SER:HA	1:AT:319:GLY:HA2	1.78	0.43
1:BB:234:ARG:CG	1:BB:280:GLU:HG2	2.48	0.43
1:BC:170:PHE:HD1	1:BC:389:MET:HE2	1.84	0.43
1:BD:263:ASN:O	1:BD:267:LYS:HG3	2.19	0.43
1:BT:314:PRO:HB3	1:BT:324:LEU:HD13	2.00	0.43
1:CA:239:ILE:HD12	1:CA:275:GLU:HA	2.00	0.43
1:CA:272:TYR:N	1:CA:272:TYR:HD1	2.17	0.43
1:AB:272:TYR:CD2	1:CB:55:ARG:CZ	3.01	0.43
1:CC:237:VAL:HG23	1:CC:279:PHE:CD2	2.54	0.43
1:CB:442:GLN:HE21	1:CC:412:PHE:HB2	1.84	0.43
1:CF:43:ALA:HB1	1:CF:158:GLU:HA	2.01	0.43
1:CL:10:ILE:HA	1:CL:11:PRO:HD3	1.88	0.43
1:CR:300:GLN:HB2	1:CR:300:GLN:HE21	1.71	0.43
1:CS:170:PHE:HD1	1:CS:389:MET:CE	2.31	0.43
1:AA:8:ILE:HG22	1:AA:10:ILE:CD1	2.49	0.42
1:AB:79:ARG:CG	1:AB:79:ARG:NH1	2.82	0.42
1:AD:232:THR:HB	1:AD:334:VAL:CG2	2.49	0.42
1:AK:324:LEU:HD23	1:AK:324:LEU:C	2.40	0.42
1:AN:22:THR:OG1	1:AN:131:HIS:CD2	2.63	0.42
1:AN:300:GLN:HB2	1:AN:300:GLN:HE21	1.60	0.42
1:AR:300:GLN:HE21	1:AR:300:GLN:HB2	1.54	0.42
1:AR:74:ASN:ND2	1:AR:77:THR:OG1	2.52	0.42
1:AT:25:ILE:HG23	1:AT:152:LEU:HD11	2.01	0.42
1:BA:252:VAL:HG22	1:BA:253:SER:N	2.34	0.42
1:AC:272:TYR:HD2	1:BA:55:ARG:HD3	1.82	0.42
1:BB:14:CYS:H	1:BB:138:ASN:ND2	2.12	0.42
1:BC:239:ILE:HG23	1:BC:324:LEU:HD21	2.00	0.42
1:BC:170:PHE:HD1	1:BC:389:MET:CE	2.32	0.42
1:BF:226:VAL:HG13	1:BF:228:GLY:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:237:VAL:HG23	1:BF:279:PHE:CD2	2.54	0.42
1:BG:189:PHE:HD2	1:BG:247:ILE:CD1	2.31	0.42
1:BI:404:LEU:N	1:BI:404:LEU:HD23	2.33	0.42
1:BJ:10:ILE:CD1	1:BJ:20:LEU:HD13	2.49	0.42
1:BJ:25:ILE:HG23	1:BJ:152:LEU:HD11	2.01	0.42
1:BN:232:THR:HB	1:BN:334:VAL:HG23	2.00	0.42
1:CA:18:ARG:HG3	1:CA:19:TYR:N	2.32	0.42
1:CB:393:HIS:CG	1:CB:496:PHE:HB3	2.53	0.42
1:CD:43:ALA:HB1	1:CD:158:GLU:HA	2.00	0.42
1:CD:250:TRP:CE3	1:CD:272:TYR:CD1	3.07	0.42
1:CI:299:SER:OG	1:CI:301:ARG:HG2	2.18	0.42
1:CI:442:GLN:HE21	1:CJ:412:PHE:HB2	1.83	0.42
1:CL:189:PHE:CE2	1:CL:249:LEU:HD21	2.54	0.42
1:CN:237:VAL:HG23	1:CN:279:PHE:CD2	2.54	0.42
1:CM:442:GLN:HE21	1:CN:412:PHE:HB2	1.84	0.42
1:CP:234:ARG:HG2	1:CP:280:GLU:HG2	1.99	0.42
1:CR:226:VAL:HG13	1:CR:228:GLY:H	1.83	0.42
1:AA:454:ASN:HD21	1:AA:456:ALA:HB3	1.84	0.42
1:AB:232:THR:HB	1:AB:334:VAL:CG2	2.49	0.42
1:AB:404:LEU:HD23	1:AB:404:LEU:N	2.34	0.42
1:AC:440:ALA:CB	1:AD:444:LEU:HD13	2.49	0.42
1:AI:239:ILE:HD12	1:AI:275:GLU:HA	2.01	0.42
1:AI:423:LYS:HE2	1:AI:449:GLU:O	2.18	0.42
1:AL:272:TYR:CE2	1:CJ:55:ARG:CZ	3.02	0.42
1:AL:232:THR:HB	1:AL:334:VAL:HG23	2.01	0.42
1:AQ:162:PHE:CD1	1:AR:287:TYR:HA	2.54	0.42
1:AR:324:LEU:HA	1:AR:325:PRO:HD3	1.85	0.42
1:AT:30:SER:O	1:AT:33:LYS:HB2	2.19	0.42
1:BC:55:ARG:CZ	1:BT:272:TYR:CD2	3.02	0.42
1:BD:188:PHE:C	1:BD:189:PHE:HD1	2.23	0.42
1:BE:189:PHE:HD2	1:BE:247:ILE:HD11	1.83	0.42
1:BF:79:ARG:CG	1:BF:79:ARG:HH11	2.19	0.42
1:BI:318:SER:HA	1:BI:319:GLY:HA2	1.78	0.42
1:BK:25:ILE:HG23	1:BK:152:LEU:HD11	2.01	0.42
1:BO:11:PRO:HG2	1:BO:18:ARG:HD2	2.01	0.42
1:BS:395:LEU:HB2	1:BS:497:TYR:HB2	2.00	0.42
1:CC:239:ILE:HD12	1:CC:275:GLU:HA	2.01	0.42
1:CE:20:LEU:HB2	1:CE:132:PHE:O	2.19	0.42
1:CI:79:ARG:CG	1:CI:79:ARG:HH11	2.33	0.42
1:CJ:163:LEU:HA	1:CJ:163:LEU:HD12	1.85	0.42
1:CJ:324:LEU:HD23	1:CJ:324:LEU:C	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:79:ARG:HH11	1:CL:79:ARG:CG	2.28	0.42
1:CM:423:LYS:HE2	1:CM:449:GLU:O	2.19	0.42
1:CN:234:ARG:HG2	1:CN:280:GLU:HG2	2.01	0.42
1:CK:444:LEU:HD13	1:CO:440:ALA:HB3	2.01	0.42
1:CQ:395:LEU:HB2	1:CQ:497:TYR:HB2	2.01	0.42
1:CQ:423:LYS:HE2	1:CQ:449:GLU:O	2.19	0.42
1:AB:250:TRP:HZ3	1:AB:272:TYR:HE1	1.61	0.42
1:AD:239:ILE:HD12	1:AD:275:GLU:HA	2.01	0.42
1:AG:239:ILE:HG12	1:AG:326:ILE:CD1	2.50	0.42
1:AH:14:CYS:H	1:AH:138:ASN:ND2	2.16	0.42
1:AK:170:PHE:HD1	1:AK:389:MET:HE2	1.83	0.42
1:AL:423:LYS:HE2	1:AL:449:GLU:O	2.19	0.42
1:AN:30:SER:O	1:AN:33:LYS:HB2	2.19	0.42
1:AO:401:ASP:O	1:AO:488:CYS:HA	2.19	0.42
1:AO:423:LYS:HE2	1:AO:449:GLU:O	2.18	0.42
1:AP:239:ILE:HD12	1:AP:275:GLU:HA	2.00	0.42
1:AP:255:TRP:CE3	1:AP:285:SER:HB2	2.54	0.42
1:AP:440:ALA:HB3	1:AQ:444:LEU:HD13	2.01	0.42
1:AT:252:VAL:HG22	1:AT:253:SER:N	2.35	0.42
1:BA:18:ARG:HG3	1:BA:19:TYR:N	2.34	0.42
1:BA:226:VAL:HG13	1:BA:228:GLY:H	1.84	0.42
1:BB:203:THR:HB	1:BB:300:GLN:HG3	2.01	0.42
1:BG:237:VAL:HG23	1:BG:279:PHE:CD2	2.54	0.42
1:BK:226:VAL:HG13	1:BK:228:GLY:H	1.83	0.42
1:BK:423:LYS:HE2	1:BK:449:GLU:O	2.20	0.42
1:BM:182:LEU:HD12	1:BM:182:LEU:C	2.39	0.42
1:BP:393:HIS:CG	1:BP:496:PHE:HB3	2.54	0.42
1:BQ:300:GLN:HB2	1:BQ:300:GLN:HE21	1.60	0.42
1:BR:234:ARG:HG2	1:BR:280:GLU:HG2	2.01	0.42
1:CB:189:PHE:HD2	1:CB:247:ILE:HD11	1.83	0.42
1:CF:25:ILE:HG23	1:CF:152:LEU:HD11	2.01	0.42
1:CG:324:LEU:C	1:CG:324:LEU:HD23	2.40	0.42
1:CI:55:ARG:CZ	1:CR:272:TYR:CE2	3.02	0.42
1:CL:272:TYR:N	1:CL:272:TYR:HD1	2.16	0.42
1:CL:440:ALA:CB	1:CM:444:LEU:HD13	2.49	0.42
1:CP:256:ASN:HD22	1:CP:302:ASP:HA	1.84	0.42
1:CP:404:LEU:HD22	1:CP:486:VAL:HG22	1.99	0.42
1:CQ:175:PHE:O	1:CQ:175:PHE:CD2	2.73	0.42
1:CR:239:ILE:HG12	1:CR:326:ILE:CD1	2.48	0.42
1:AF:185:PRO:HA	1:AF:186:PRO:HD3	1.90	0.42
1:AG:442:GLN:HE21	1:AH:412:PHE:HB2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:14:CYS:HB3	1:AK:64:LEU:HD21	2.01	0.42
1:AM:318:SER:HA	1:AM:319:GLY:HA2	1.80	0.42
1:AQ:263:ASN:O	1:AQ:267:LYS:HG3	2.19	0.42
1:AQ:318:SER:HA	1:AQ:319:GLY:HA2	1.80	0.42
1:BD:371:ASP:OD1	1:BD:381:MET:HG2	2.20	0.42
1:BF:232:THR:HB	1:BF:334:VAL:HG23	2.00	0.42
1:BF:442:GLN:HE21	1:BG:412:PHE:HB2	1.84	0.42
1:BJ:371:ASP:OD1	1:BJ:381:MET:HG2	2.19	0.42
1:BN:423:LYS:HE2	1:BN:449:GLU:O	2.19	0.42
1:BO:171:ASP:HA	1:BO:172:PRO:HD3	1.79	0.42
1:BO:423:LYS:HE2	1:BO:449:GLU:O	2.19	0.42
1:BP:324:LEU:C	1:BP:324:LEU:HD23	2.40	0.42
1:BR:25:ILE:HG23	1:BR:152:LEU:HD11	2.00	0.42
1:CB:207:VAL:HA	1:CB:208:PRO:HD3	1.82	0.42
1:CB:189:PHE:CE2	1:CB:249:LEU:HD21	2.49	0.42
1:CH:207:VAL:HA	1:CH:208:PRO:HD3	1.84	0.42
1:CH:25:ILE:HG23	1:CH:152:LEU:HD11	2.01	0.42
1:CH:318:SER:HA	1:CH:319:GLY:HA2	1.76	0.42
1:CL:442:GLN:HE21	1:CM:412:PHE:HB2	1.85	0.42
1:CN:272:TYR:CD1	1:CN:272:TYR:N	2.87	0.42
1:CN:404:LEU:HD22	1:CN:486:VAL:HG22	2.00	0.42
1:CP:324:LEU:C	1:CP:324:LEU:HD23	2.40	0.42
1:AA:239:ILE:HG23	1:AA:324:LEU:HD21	2.01	0.42
1:AA:379:VAL:HG11	1:AA:381:MET:HE1	2.02	0.42
1:AA:404:LEU:HD22	1:AA:486:VAL:HG22	2.00	0.42
1:AG:234:ARG:CG	1:AG:280:GLU:HG2	2.49	0.42
1:AI:404:LEU:HD23	1:AI:404:LEU:N	2.34	0.42
1:AL:395:LEU:HB2	1:AL:497:TYR:HB2	2.01	0.42
1:AM:324:LEU:C	1:AM:324:LEU:HD23	2.40	0.42
1:AO:252:VAL:HG22	1:AO:253:SER:N	2.33	0.42
1:BA:207:VAL:HA	1:BA:208:PRO:HD3	1.86	0.42
1:BB:191:LEU:N	1:BB:191:LEU:CD2	2.73	0.42
1:BF:272:TYR:HD1	1:BF:272:TYR:N	2.17	0.42
1:BI:232:THR:HB	1:BI:334:VAL:CG2	2.49	0.42
1:BI:237:VAL:HG23	1:BI:279:PHE:CD2	2.54	0.42
1:BI:170:PHE:HD1	1:BI:389:MET:HE2	1.84	0.42
1:BK:272:TYR:HD1	1:BK:272:TYR:N	2.17	0.42
1:BK:437:HIS:CE1	1:BL:405:GLN:NE2	2.88	0.42
1:BL:239:ILE:HG23	1:BL:324:LEU:HD21	2.01	0.42
1:BQ:454:ASN:HD21	1:BQ:456:ALA:HB3	1.85	0.42
1:BR:404:LEU:HD22	1:BR:486:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:340:LEU:HA	1:BS:340:LEU:HD23	1.88	0.42
1:BT:182:LEU:HD12	1:BT:182:LEU:C	2.39	0.42
1:BT:252:VAL:HG22	1:BT:253:SER:N	2.33	0.42
1:CB:234:ARG:HG2	1:CB:280:GLU:HG2	2.00	0.42
1:CD:25:ILE:HG23	1:CD:152:LEU:HD11	2.00	0.42
1:CH:234:ARG:HG2	1:CH:280:GLU:HG2	2.00	0.42
1:CH:79:ARG:CG	1:CH:79:ARG:NH1	2.77	0.42
1:CK:171:ASP:HA	1:CK:172:PRO:HD3	1.79	0.42
1:CL:22:THR:OG1	1:CL:131:HIS:CD2	2.63	0.42
1:BP:55:ARG:CZ	1:CM:272:TYR:CE2	3.03	0.42
1:CR:14:CYS:HB3	1:CR:64:LEU:HD21	2.01	0.42
1:CT:234:ARG:HG2	1:CT:280:GLU:HG2	2.02	0.42
1:AC:74:ASN:ND2	1:AC:77:THR:OG1	2.53	0.42
1:AE:263:ASN:O	1:AE:267:LYS:HG3	2.19	0.42
1:AD:442:GLN:NE2	1:AE:412:PHE:HB2	2.34	0.42
1:AF:55:ARG:CZ	1:BH:272:TYR:CE2	3.02	0.42
1:AJ:61:PHE:CD2	1:AJ:243:ILE:HD11	2.55	0.42
1:AN:418:SER:HB3	1:AO:407:SER:HB3	2.01	0.42
1:AP:285:SER:HA	1:AP:286:PRO:HD3	1.91	0.42
1:AQ:234:ARG:CG	1:AQ:280:GLU:HG2	2.49	0.42
1:AR:182:LEU:HG	1:AR:330:ILE:HB	2.02	0.42
1:AT:79:ARG:NH1	1:AT:79:ARG:HG3	2.31	0.42
1:BA:189:PHE:HD2	1:BA:247:ILE:CD1	2.33	0.42
1:BA:324:LEU:HD23	1:BA:324:LEU:C	2.39	0.42
1:BC:232:THR:HB	1:BC:334:VAL:HG23	2.02	0.42
1:BC:430:MET:CE	1:BD:296:ALA:HA	2.49	0.42
1:BG:423:LYS:HE2	1:BG:449:GLU:O	2.18	0.42
1:BH:14:CYS:H	1:BH:138:ASN:ND2	2.14	0.42
1:BH:237:VAL:HG23	1:BH:279:PHE:CD2	2.54	0.42
1:BI:171:ASP:HA	1:BI:172:PRO:HD3	1.79	0.42
1:BM:203:THR:CB	1:BM:300:GLN:HG3	2.49	0.42
1:BM:381:MET:HE2	1:BM:381:MET:HB2	1.84	0.42
1:BO:182:LEU:HG	1:BO:330:ILE:HB	2.02	0.42
1:BS:423:LYS:HE2	1:BS:449:GLU:O	2.20	0.42
1:BT:14:CYS:H	1:BT:138:ASN:ND2	2.14	0.42
1:CC:18:ARG:HG2	1:CC:20:LEU:HD23	2.01	0.42
1:CF:20:LEU:HB2	1:CF:132:PHE:O	2.19	0.42
1:AK:55:ARG:CZ	1:CF:272:TYR:CE2	3.02	0.42
1:CH:272:TYR:N	1:CH:272:TYR:HD1	2.17	0.42
1:CJ:25:ILE:HG23	1:CJ:152:LEU:HD11	2.01	0.42
1:CL:191:LEU:N	1:CL:191:LEU:CD2	2.75	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:418:SER:HB3	1:CN:407:SER:HB3	2.01	0.42
1:CN:379:VAL:HG11	1:CN:381:MET:HE1	2.02	0.42
1:CQ:442:GLN:HE21	1:CR:412:PHE:HB2	1.84	0.42
1:AI:442:GLN:HE21	1:AJ:412:PHE:HB2	1.84	0.42
1:AK:10:ILE:HA	1:AK:11:PRO:HD3	1.88	0.42
1:AN:252:VAL:HG22	1:AN:253:SER:N	2.34	0.42
1:AM:440:ALA:HB3	1:AN:444:LEU:HD13	2.00	0.42
1:AR:55:ARG:HH11	1:AR:55:ARG:HG2	1.83	0.42
1:BA:191:LEU:N	1:BA:191:LEU:CD2	2.77	0.42
1:BA:33:LYS:O	1:BA:33:LYS:CG	2.59	0.42
1:BB:226:VAL:HG13	1:BB:228:GLY:H	1.84	0.42
1:BE:182:LEU:C	1:BE:182:LEU:HD12	2.40	0.42
1:BF:300:GLN:HB2	1:BF:300:GLN:HE21	1.58	0.42
1:BI:182:LEU:C	1:BI:182:LEU:HD12	2.40	0.42
1:BJ:162:PHE:CD2	1:BJ:163:LEU:HD13	2.55	0.42
1:BJ:201:GLY:HA3	1:BJ:300:GLN:HG2	2.00	0.42
1:BK:263:ASN:O	1:BK:267:LYS:HG3	2.20	0.42
1:BL:272:TYR:N	1:BL:272:TYR:CD1	2.85	0.42
1:BO:250:TRP:HE3	1:BO:272:TYR:CD1	2.37	0.42
1:CB:226:VAL:HG13	1:CB:228:GLY:H	1.84	0.42
1:CD:440:ALA:CB	1:CE:444:LEU:HD13	2.50	0.42
1:CG:418:SER:HB3	1:CH:407:SER:HB3	2.02	0.42
1:CJ:379:VAL:HG11	1:CJ:381:MET:HE1	2.02	0.42
1:CJ:404:LEU:HD23	1:CJ:404:LEU:N	2.35	0.42
1:CM:182:LEU:C	1:CM:182:LEU:HD12	2.40	0.42
1:CM:252:VAL:HG22	1:CM:253:SER:N	2.35	0.42
1:CR:324:LEU:HD23	1:CR:324:LEU:C	2.40	0.42
1:AC:18:ARG:HG3	1:AC:19:TYR:N	2.34	0.42
1:AC:256:ASN:HD22	1:AC:302:ASP:HA	1.85	0.42
1:AD:423:LYS:HE2	1:AD:449:GLU:O	2.19	0.42
1:AE:252:VAL:HG22	1:AE:253:SER:N	2.35	0.42
1:AF:232:THR:HB	1:AF:334:VAL:HG23	2.01	0.42
1:AF:412:PHE:HB2	1:AJ:442:GLN:NE2	2.35	0.42
1:AF:43:ALA:HB1	1:AF:158:GLU:HA	2.02	0.42
1:AJ:234:ARG:CG	1:AJ:280:GLU:HG2	2.50	0.42
1:AL:239:ILE:HG12	1:AL:326:ILE:CD1	2.50	0.42
1:AO:10:ILE:HA	1:AO:11:PRO:HD3	1.90	0.42
1:AQ:423:LYS:HE2	1:AQ:449:GLU:O	2.20	0.42
1:AT:163:LEU:HD12	1:AT:163:LEU:HA	1.84	0.42
1:AT:207:VAL:HA	1:AT:208:PRO:HD3	1.85	0.42
1:BB:232:THR:HB	1:BB:334:VAL:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:238:HIS:HE1	1:BB:329:GLN:OE1	2.02	0.42
1:BC:18:ARG:HG2	1:BC:20:LEU:HD23	2.01	0.42
1:BC:318:SER:HA	1:BC:319:GLY:HA2	1.78	0.42
1:BF:15:GLN:HE21	1:BF:15:GLN:HA	1.84	0.42
1:BF:75:ARG:NH2	1:BF:391:ALA:O	2.49	0.42
1:BK:340:LEU:HD23	1:BK:340:LEU:HA	1.89	0.42
1:BR:182:LEU:HG	1:BR:330:ILE:HB	2.01	0.42
1:BR:272:TYR:N	1:BR:272:TYR:HD1	2.18	0.42
1:BR:28:MET:CE	1:BR:152:LEU:HG	2.50	0.42
1:BR:371:ASP:OD1	1:BR:381:MET:HG2	2.20	0.42
1:BS:239:ILE:HG23	1:BS:324:LEU:HD21	2.02	0.42
1:CA:379:VAL:HG11	1:CA:381:MET:HE1	2.00	0.42
1:CB:182:LEU:C	1:CB:182:LEU:HD12	2.40	0.42
1:CC:226:VAL:HG13	1:CC:228:GLY:H	1.85	0.42
1:CE:189:PHE:CE1	1:CE:198:ARG:HG2	2.53	0.42
1:CI:232:THR:HB	1:CI:334:VAL:CG2	2.50	0.42
1:CO:234:ARG:CG	1:CO:280:GLU:HG2	2.50	0.42
1:CO:250:TRP:CE3	1:CO:272:TYR:CD1	3.07	0.42
1:CO:33:LYS:HE2	1:CO:33:LYS:HB2	1.96	0.42
1:CP:423:LYS:HE2	1:CP:449:GLU:O	2.20	0.42
1:AA:232:THR:HB	1:AA:334:VAL:CG2	2.50	0.42
1:AE:197:LEU:HD21	1:AE:258:THR:HG21	2.02	0.42
1:AH:55:ARG:CZ	1:AK:272:TYR:CE2	3.03	0.42
1:AH:58:ALA:HB2	1:AH:102:GLY:HA3	2.02	0.42
1:AN:207:VAL:HA	1:AN:208:PRO:HD3	1.83	0.42
1:AN:285:SER:HA	1:AN:286:PRO:HD3	1.93	0.42
1:AQ:182:LEU:HD12	1:AQ:182:LEU:C	2.40	0.42
1:AQ:79:ARG:HG3	1:AQ:79:ARG:NH1	2.32	0.42
1:AT:16:ALA:O	1:AT:17:ASN:HB2	2.20	0.42
1:AT:55:ARG:HD3	1:BA:272:TYR:HD2	1.80	0.42
1:BI:324:LEU:HD23	1:BI:324:LEU:C	2.40	0.42
1:BJ:163:LEU:HD12	1:BJ:163:LEU:HA	1.84	0.42
1:BJ:189:PHE:CE1	1:BJ:198:ARG:HG2	2.55	0.42
1:BK:170:PHE:HD1	1:BK:389:MET:CE	2.32	0.42
1:BO:234:ARG:CG	1:BO:280:GLU:HG2	2.50	0.42
1:BT:272:TYR:HD1	1:BT:272:TYR:N	2.18	0.42
1:BT:324:LEU:HA	1:BT:325:PRO:HD3	1.88	0.42
1:CB:318:SER:HA	1:CB:319:GLY:HA2	1.76	0.42
1:CD:423:LYS:HE2	1:CD:449:GLU:O	2.19	0.42
1:AK:55:ARG:CZ	1:CF:272:TYR:CD2	3.02	0.42
1:CN:393:HIS:CG	1:CN:496:PHE:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:25:ILE:HG23	1:CP:152:LEU:HD11	2.01	0.42
1:CQ:162:PHE:CD1	1:CR:287:TYR:HA	2.55	0.42
1:CS:203:THR:CB	1:CS:300:GLN:HG3	2.49	0.42
1:AA:185:PRO:HA	1:AA:186:PRO:HD3	1.93	0.42
1:AE:272:TYR:CD2	1:AM:55:ARG:CZ	3.03	0.42
1:AG:324:LEU:HA	1:AG:325:PRO:HD3	1.89	0.42
1:AH:191:LEU:N	1:AH:191:LEU:HD23	2.22	0.42
1:AM:263:ASN:O	1:AM:267:LYS:HG3	2.20	0.42
1:AO:188:PHE:C	1:AO:189:PHE:HD1	2.23	0.42
1:AP:189:PHE:HE2	1:AP:249:LEU:CD2	2.33	0.42
1:AP:237:VAL:HG23	1:AP:279:PHE:CD2	2.55	0.42
1:AT:18:ARG:HG3	1:AT:19:TYR:N	2.35	0.42
1:BA:163:LEU:HD21	1:BA:458:ALA:HB2	2.01	0.42
1:BD:324:LEU:C	1:BD:324:LEU:HD23	2.40	0.42
1:BG:175:PHE:CD2	1:BG:175:PHE:O	2.73	0.42
1:BH:202:LEU:HA	1:BH:202:LEU:HD23	1.85	0.42
1:BH:318:SER:HA	1:BH:319:GLY:HA2	1.78	0.42
1:BL:234:ARG:HG2	1:BL:280:GLU:HG2	2.00	0.42
1:BL:300:GLN:HE21	1:BL:300:GLN:HB2	1.58	0.42
1:BN:25:ILE:HG23	1:BN:152:LEU:HD11	2.01	0.42
1:BO:25:ILE:HG23	1:BO:152:LEU:HD11	2.02	0.42
1:BQ:371:ASP:OD1	1:BQ:381:MET:HG2	2.20	0.42
1:BS:272:TYR:N	1:BS:272:TYR:CD1	2.88	0.42
1:CB:423:LYS:HE2	1:CB:449:GLU:O	2.20	0.42
1:CC:263:ASN:O	1:CC:267:LYS:HG3	2.19	0.42
1:CD:250:TRP:CZ3	1:CD:272:TYR:CD1	3.08	0.42
1:CD:232:THR:HB	1:CD:334:VAL:HG23	2.02	0.42
1:CE:25:ILE:HG23	1:CE:152:LEU:HD11	2.01	0.42
1:CE:234:ARG:CG	1:CE:280:GLU:HG2	2.50	0.42
1:CE:256:ASN:HD22	1:CE:302:ASP:HA	1.84	0.42
1:CF:226:VAL:HG13	1:CF:228:GLY:H	1.85	0.42
1:CI:25:ILE:HG23	1:CI:152:LEU:HD11	2.01	0.42
1:CI:324:LEU:HA	1:CI:325:PRO:HD3	1.88	0.42
1:CO:237:VAL:HG23	1:CO:279:PHE:CD2	2.55	0.42
1:CO:250:TRP:CZ3	1:CO:272:TYR:CD1	3.08	0.42
1:CS:14:CYS:H	1:CS:138:ASN:ND2	2.17	0.42
1:CS:226:VAL:HG13	1:CS:228:GLY:H	1.85	0.42
1:CS:252:VAL:HG22	1:CS:253:SER:N	2.35	0.42
1:AB:170:PHE:HD1	1:AB:389:MET:CE	2.33	0.41
1:AC:263:ASN:O	1:AC:267:LYS:HG3	2.20	0.41
1:AC:404:LEU:HD23	1:AC:404:LEU:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:10:ILE:CD1	1:AD:20:LEU:HD13	2.49	0.41
1:AF:371:ASP:OD1	1:AF:381:MET:HG2	2.20	0.41
1:AI:189:PHE:HD2	1:AI:247:ILE:HD11	1.85	0.41
1:AJ:48:PRO:HG2	1:AJ:50:PHE:CZ	2.55	0.41
1:AJ:55:ARG:CZ	1:BL:272:TYR:CE2	3.02	0.41
1:AL:381:MET:HB2	1:AL:381:MET:HE2	1.88	0.41
1:AL:55:ARG:CZ	1:CQ:272:TYR:CD2	3.03	0.41
1:AE:272:TYR:HD2	1:AM:55:ARG:HD3	1.82	0.41
1:AN:226:VAL:HG13	1:AN:228:GLY:H	1.85	0.41
1:AD:55:ARG:CZ	1:AN:272:TYR:CE2	3.02	0.41
1:AP:191:LEU:HD23	1:AP:191:LEU:N	2.15	0.41
1:AQ:272:TYR:CD2	1:BL:55:ARG:CD	3.02	0.41
1:AT:300:GLN:HE21	1:AT:300:GLN:HB2	1.55	0.41
1:BD:25:ILE:HG23	1:BD:152:LEU:HD11	2.02	0.41
1:BE:175:PHE:O	1:BE:175:PHE:CD2	2.73	0.41
1:BE:252:VAL:HG22	1:BE:253:SER:N	2.36	0.41
1:BG:324:LEU:HD23	1:BG:324:LEU:C	2.40	0.41
1:BH:55:ARG:CZ	1:BK:272:TYR:CD2	3.03	0.41
1:BI:20:LEU:HB2	1:BI:132:PHE:O	2.20	0.41
1:BM:255:TRP:CE3	1:BM:285:SER:HB2	2.55	0.41
1:CB:379:VAL:HG11	1:CB:381:MET:HE1	2.02	0.41
1:CC:189:PHE:HE2	1:CC:249:LEU:HD21	1.85	0.41
1:CC:55:ARG:CZ	1:CT:272:TYR:CD2	3.03	0.41
1:CD:48:PRO:HG2	1:CD:50:PHE:CZ	2.55	0.41
1:CD:79:ARG:NH1	1:CD:79:ARG:HG3	2.14	0.41
1:CL:232:THR:HB	1:CL:334:VAL:HG23	2.01	0.41
1:CM:58:ALA:HB2	1:CM:102:GLY:HA3	2.02	0.41
1:CQ:234:ARG:HG2	1:CQ:280:GLU:HG2	2.02	0.41
1:AF:440:ALA:HB3	1:AG:444:LEU:HD13	2.02	0.41
1:AF:74:ASN:ND2	1:AF:77:THR:OG1	2.53	0.41
1:AG:207:VAL:HA	1:AG:208:PRO:HD3	1.81	0.41
1:AK:61:PHE:CE2	1:AK:243:ILE:HD11	2.54	0.41
1:AM:272:TYR:HD1	1:AM:272:TYR:N	2.18	0.41
1:AN:379:VAL:HG12	1:AN:381:MET:HE2	2.02	0.41
1:AN:55:ARG:NE	1:AS:272:TYR:CD2	2.88	0.41
1:AN:77:THR:O	1:AN:81:THR:HG23	2.20	0.41
1:AP:234:ARG:HG2	1:AP:280:GLU:HG2	2.01	0.41
1:AQ:58:ALA:HB2	1:AQ:102:GLY:HA3	2.02	0.41
1:AR:318:SER:HA	1:AR:319:GLY:HA2	1.75	0.41
1:BB:16:ALA:O	1:BB:17:ASN:CB	2.64	0.41
1:BB:170:PHE:HD1	1:BB:389:MET:CE	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:252:VAL:HG22	1:BB:253:SER:N	2.35	0.41
1:BG:379:VAL:HG11	1:BG:381:MET:HE1	2.01	0.41
1:BK:191:LEU:CD2	1:BK:191:LEU:N	2.76	0.41
1:BK:440:ALA:HB3	1:BL:444:LEU:HD13	2.02	0.41
1:BO:226:VAL:HG13	1:BO:228:GLY:H	1.85	0.41
1:CA:19:TYR:CZ	1:CA:81:THR:HG22	2.55	0.41
1:CB:14:CYS:H	1:CB:138:ASN:ND2	2.18	0.41
1:CC:16:ALA:O	1:CC:17:ASN:HB2	2.20	0.41
1:CD:252:VAL:HG22	1:CD:253:SER:N	2.35	0.41
1:CD:371:ASP:OD1	1:CD:381:MET:HG2	2.20	0.41
1:CJ:379:VAL:HG12	1:CJ:381:MET:HE2	2.02	0.41
1:CK:189:PHE:CE2	1:CK:249:LEU:HD21	2.55	0.41
1:CN:14:CYS:HB3	1:CN:64:LEU:HD21	2.01	0.41
1:AA:238:HIS:HE1	1:AA:329:GLN:OE1	2.03	0.41
1:AB:300:GLN:HB2	1:AB:300:GLN:HE21	1.46	0.41
1:AC:185:PRO:HA	1:AC:186:PRO:HD3	1.93	0.41
1:AF:207:VAL:HA	1:AF:208:PRO:HD3	1.86	0.41
1:AG:36:GLN:HE22	1:AG:156:LEU:H	1.66	0.41
1:AK:188:PHE:C	1:AK:189:PHE:HD1	2.24	0.41
1:AL:232:THR:HB	1:AL:334:VAL:CG2	2.50	0.41
1:BA:423:LYS:HE2	1:BA:449:GLU:O	2.20	0.41
1:BC:372:PHE:H	1:BC:381:MET:HE1	1.85	0.41
1:BE:324:LEU:HA	1:BE:325:PRO:HD3	1.87	0.41
1:BF:189:PHE:CE2	1:BF:249:LEU:HD21	2.49	0.41
1:BP:272:TYR:CE2	1:CE:55:ARG:HD3	2.55	0.41
1:BQ:379:VAL:HG11	1:BQ:381:MET:HE1	2.02	0.41
1:BS:182:LEU:HD12	1:BS:182:LEU:C	2.41	0.41
1:BT:285:SER:HA	1:BT:286:PRO:HD3	1.92	0.41
1:CC:232:THR:HB	1:CC:334:VAL:CG2	2.49	0.41
1:CF:272:TYR:HD1	1:CF:272:TYR:N	2.16	0.41
1:CG:202:LEU:HD23	1:CG:202:LEU:HA	1.93	0.41
1:CG:404:LEU:HD22	1:CG:486:VAL:HG22	2.02	0.41
1:CH:182:LEU:HD12	1:CH:182:LEU:C	2.40	0.41
1:CI:189:PHE:CE1	1:CI:198:ARG:HG2	2.55	0.41
1:CI:379:VAL:HG12	1:CI:381:MET:HE2	2.01	0.41
1:CJ:171:ASP:HA	1:CJ:172:PRO:HD3	1.78	0.41
1:CL:239:ILE:HD12	1:CL:275:GLU:HA	2.01	0.41
1:CM:237:VAL:HG23	1:CM:279:PHE:CD2	2.55	0.41
1:CP:188:PHE:C	1:CP:189:PHE:HD1	2.24	0.41
1:CN:55:ARG:CZ	1:CS:272:TYR:CE2	3.03	0.41
1:CT:318:SER:HA	1:CT:319:GLY:HA2	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:324:LEU:C	1:AD:324:LEU:HD23	2.41	0.41
1:AF:22:THR:OG1	1:AF:131:HIS:CD2	2.60	0.41
1:AG:14:CYS:H	1:AG:138:ASN:ND2	2.15	0.41
1:AH:234:ARG:CG	1:AH:280:GLU:HG2	2.50	0.41
1:AK:47:MET:HG2	1:AK:117:ALA:HB2	2.03	0.41
1:AK:189:PHE:CE2	1:AK:249:LEU:HD21	2.55	0.41
1:AL:404:LEU:N	1:AL:404:LEU:HD23	2.34	0.41
1:AM:440:ALA:CB	1:AN:444:LEU:HD13	2.50	0.41
1:AO:372:PHE:H	1:AO:381:MET:HE1	1.85	0.41
1:AP:14:CYS:H	1:AP:138:ASN:ND2	2.18	0.41
1:AQ:272:TYR:HD1	1:AQ:272:TYR:N	2.17	0.41
1:AS:22:THR:OG1	1:AS:131:HIS:CD2	2.63	0.41
1:BF:55:ARG:CZ	1:CH:272:TYR:CD2	3.04	0.41
1:BH:22:THR:OG1	1:BH:131:HIS:CD2	2.64	0.41
1:BH:55:ARG:CZ	1:BK:272:TYR:CE2	3.04	0.41
1:BS:300:GLN:HB2	1:BS:300:GLN:HE21	1.57	0.41
1:BS:379:VAL:HG11	1:BS:381:MET:HE1	2.02	0.41
1:CD:163:LEU:HA	1:CD:163:LEU:HD12	1.85	0.41
1:CE:207:VAL:HA	1:CE:208:PRO:HD3	1.83	0.41
1:CE:272:TYR:CD2	1:CM:55:ARG:CZ	3.03	0.41
1:CF:207:VAL:HA	1:CF:208:PRO:HD3	1.83	0.41
1:CF:239:ILE:HG23	1:CF:324:LEU:HD21	2.02	0.41
1:CG:175:PHE:O	1:CG:175:PHE:CD2	2.74	0.41
1:CG:239:ILE:HG23	1:CG:324:LEU:HD21	2.02	0.41
1:CJ:423:LYS:HE2	1:CJ:449:GLU:O	2.20	0.41
1:CL:379:VAL:HG11	1:CL:381:MET:HE1	2.01	0.41
1:CT:182:LEU:HG	1:CT:330:ILE:HB	2.02	0.41
1:AA:202:LEU:HD23	1:AA:202:LEU:HA	1.91	0.41
1:AE:300:GLN:HB2	1:AE:300:GLN:HE21	1.72	0.41
1:AG:25:ILE:HG23	1:AG:152:LEU:HD11	2.03	0.41
1:AG:285:SER:HA	1:AG:286:PRO:HD3	1.94	0.41
1:AH:163:LEU:HA	1:AH:163:LEU:HD12	1.90	0.41
1:AK:52:ILE:HD11	1:AK:108:ILE:HD12	2.03	0.41
1:AK:202:LEU:HB2	1:AK:304:SER:O	2.21	0.41
1:AN:20:LEU:HB2	1:AN:132:PHE:O	2.21	0.41
1:AO:250:TRP:CZ3	1:AO:272:TYR:CD1	3.06	0.41
1:AO:79:ARG:CG	1:AO:79:ARG:NH1	2.84	0.41
1:AR:43:ALA:HB1	1:AR:158:GLU:HA	2.02	0.41
1:AS:239:ILE:HD12	1:AS:275:GLU:HA	2.02	0.41
1:AS:252:VAL:HG22	1:AS:253:SER:N	2.35	0.41
1:AT:379:VAL:CG1	1:AT:381:MET:CE	2.98	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:239:ILE:HD12	1:BD:275:GLU:HA	2.02	0.41
1:BD:442:GLN:HE21	1:BE:412:PHE:HB2	1.86	0.41
1:BG:170:PHE:HD1	1:BG:389:MET:CE	2.33	0.41
1:BL:170:PHE:HD1	1:BL:389:MET:CE	2.33	0.41
1:BO:379:VAL:HG11	1:BO:381:MET:HE1	2.01	0.41
1:BR:252:VAL:HG22	1:BR:253:SER:N	2.36	0.41
1:BT:234:ARG:CG	1:BT:280:GLU:HG2	2.50	0.41
1:BP:412:PHE:HB2	1:BT:442:GLN:HE21	1.86	0.41
1:CA:412:PHE:HB2	1:CE:442:GLN:HE21	1.85	0.41
1:CE:163:LEU:HA	1:CE:163:LEU:HD12	1.88	0.41
1:CE:171:ASP:HA	1:CE:172:PRO:HD3	1.80	0.41
1:CF:252:VAL:HG22	1:CF:253:SER:N	2.36	0.41
1:CF:423:LYS:HE2	1:CF:449:GLU:O	2.19	0.41
1:CI:232:THR:HB	1:CI:334:VAL:HG23	2.03	0.41
1:CM:20:LEU:HB2	1:CM:132:PHE:O	2.21	0.41
1:CP:28:MET:CE	1:CP:152:LEU:HG	2.51	0.41
1:CP:250:TRP:CE3	1:CP:272:TYR:CD1	3.08	0.41
1:CP:252:VAL:HG22	1:CP:253:SER:N	2.35	0.41
1:CP:255:TRP:CG	1:CP:286:PRO:HD3	2.56	0.41
1:CQ:318:SER:HA	1:CQ:319:GLY:HA2	1.76	0.41
1:CS:232:THR:HB	1:CS:334:VAL:CG2	2.51	0.41
1:CT:324:LEU:HD23	1:CT:324:LEU:C	2.41	0.41
1:CT:324:LEU:HA	1:CT:325:PRO:HD3	1.87	0.41
1:AA:171:ASP:HA	1:AA:172:PRO:HD3	1.83	0.41
1:AE:324:LEU:C	1:AE:324:LEU:HD23	2.41	0.41
1:AE:371:ASP:OD1	1:AE:381:MET:HG2	2.20	0.41
1:AG:182:LEU:HG	1:AG:330:ILE:HB	2.03	0.41
1:AH:28:MET:HE2	1:AH:152:LEU:HG	2.03	0.41
1:AH:55:ARG:NE	1:AK:272:TYR:HE2	2.14	0.41
1:AI:182:LEU:C	1:AI:182:LEU:HD12	2.41	0.41
1:AI:61:PHE:CD2	1:AI:243:ILE:HD11	2.55	0.41
1:AI:285:SER:HA	1:AI:286:PRO:HD3	1.93	0.41
1:AO:202:LEU:HB2	1:AO:304:SER:O	2.21	0.41
1:AR:239:ILE:HD12	1:AR:275:GLU:HA	2.02	0.41
1:AS:182:LEU:HG	1:AS:330:ILE:HB	2.03	0.41
1:AS:11:PRO:HG2	1:AS:18:ARG:CD	2.51	0.41
1:BB:300:GLN:HB2	1:BB:300:GLN:HE21	1.67	0.41
1:BE:201:GLY:HA3	1:BE:300:GLN:HG2	2.02	0.41
1:BF:108:ILE:HG23	1:BF:113:LEU:HD12	2.02	0.41
1:BH:163:LEU:HD12	1:BH:163:LEU:HA	1.85	0.41
1:BI:263:ASN:O	1:BI:267:LYS:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:425:VAL:HG11	1:BJ:342:SER:HB2	2.01	0.41
1:BL:52:ILE:HG12	1:BL:152:LEU:CD2	2.51	0.41
1:BM:170:PHE:HD1	1:BM:389:MET:HE2	1.85	0.41
1:BN:171:ASP:HA	1:BN:172:PRO:HD3	1.79	0.41
1:BN:189:PHE:HD2	1:BN:247:ILE:HD11	1.86	0.41
1:BN:300:GLN:HE21	1:BN:300:GLN:HB2	1.53	0.41
1:BQ:226:VAL:HG13	1:BQ:228:GLY:H	1.86	0.41
1:BR:255:TRP:CE3	1:BR:285:SER:HB2	2.56	0.41
1:BS:234:ARG:HG2	1:BS:280:GLU:HG2	2.03	0.41
1:CB:79:ARG:CG	1:CB:79:ARG:HH11	2.27	0.41
1:CC:171:ASP:HA	1:CC:172:PRO:HD3	1.79	0.41
1:CC:22:THR:OG1	1:CC:131:HIS:CD2	2.66	0.41
1:CD:175:PHE:O	1:CD:175:PHE:CD2	2.74	0.41
1:CG:454:ASN:ND2	1:CG:456:ALA:H	2.08	0.41
1:CH:28:MET:HE2	1:CH:152:LEU:HG	2.02	0.41
1:CI:318:SER:HA	1:CI:319:GLY:HA2	1.78	0.41
1:CL:440:ALA:HB3	1:CM:444:LEU:HD13	2.02	0.41
1:CN:162:PHE:CD2	1:CN:163:LEU:HD13	2.55	0.41
1:CN:226:VAL:HG13	1:CN:228:GLY:H	1.85	0.41
1:CO:232:THR:HB	1:CO:334:VAL:HG23	2.02	0.41
1:CQ:182:LEU:HD12	1:CQ:182:LEU:C	2.41	0.41
1:CQ:404:LEU:HD22	1:CQ:486:VAL:HG22	2.03	0.41
1:CR:272:TYR:N	1:CR:272:TYR:HD1	2.18	0.41
1:AA:272:TYR:CE2	1:CT:55:ARG:CZ	3.04	0.41
1:AC:189:PHE:CE2	1:AC:249:LEU:HD21	2.56	0.41
1:AE:74:ASN:ND2	1:AE:77:THR:OG1	2.53	0.41
1:AF:324:LEU:HA	1:AF:325:PRO:HD3	1.85	0.41
1:AI:454:ASN:ND2	1:AI:456:ALA:H	2.12	0.41
1:AI:170:PHE:HB2	1:AI:496:PHE:HE1	1.86	0.41
1:AK:340:LEU:HA	1:AK:340:LEU:HD23	1.89	0.41
1:AL:202:LEU:HA	1:AL:202:LEU:HD23	1.86	0.41
1:AO:170:PHE:HD1	1:AO:389:MET:CE	2.33	0.41
1:AP:232:THR:HB	1:AP:334:VAL:CG2	2.51	0.41
1:AQ:188:PHE:C	1:AQ:189:PHE:HD1	2.24	0.41
1:AQ:170:PHE:HB2	1:AQ:496:PHE:HE1	1.85	0.41
1:AR:226:VAL:HG13	1:AR:228:GLY:H	1.85	0.41
1:AT:28:MET:CE	1:AT:152:LEU:HG	2.51	0.41
1:BD:33:LYS:HB2	1:BD:33:LYS:HE2	1.96	0.41
1:BG:454:ASN:HD21	1:BG:456:ALA:HB3	1.84	0.41
1:BK:14:CYS:H	1:BK:138:ASN:ND2	2.15	0.41
1:BN:203:THR:HB	1:BN:300:GLN:OE1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:324:LEU:HD23	1:BO:324:LEU:C	2.41	0.41
1:BO:73:TYR:CE2	1:BO:394:GLY:HA3	2.56	0.41
1:BP:25:ILE:HG23	1:BP:152:LEU:HD11	2.01	0.41
1:BQ:404:LEU:HD23	1:BQ:404:LEU:N	2.36	0.41
1:BS:108:ILE:HG23	1:BS:113:LEU:HD12	2.02	0.41
1:BS:252:VAL:HG22	1:BS:253:SER:N	2.36	0.41
1:CD:263:ASN:O	1:CD:267:LYS:HG3	2.21	0.41
1:CD:272:TYR:CD2	1:CS:55:ARG:CD	3.02	0.41
1:CE:404:LEU:HD22	1:CE:486:VAL:HG22	2.03	0.41
1:CF:14:CYS:H	1:CF:138:ASN:ND2	2.18	0.41
1:CK:10:ILE:HG21	1:CK:146:TRP:CZ2	2.56	0.41
1:CK:12:LYS:HB3	1:CK:144:ALA:C	2.41	0.41
1:CK:300:GLN:HB2	1:CK:300:GLN:HE21	1.58	0.41
1:CK:395:LEU:HB2	1:CK:497:TYR:HB2	2.02	0.41
1:CK:9:TYR:HE1	1:CK:147:GLN:NE2	2.17	0.41
1:CM:239:ILE:HG23	1:CM:324:LEU:HD21	2.02	0.41
1:CO:454:ASN:ND2	1:CO:456:ALA:H	2.09	0.41
1:CP:171:ASP:HA	1:CP:172:PRO:HD3	1.76	0.41
1:CP:263:ASN:O	1:CP:267:LYS:HG3	2.20	0.41
1:CP:33:LYS:HE2	1:CP:33:LYS:HB2	1.93	0.41
1:CJ:272:TYR:HD2	1:CQ:55:ARG:HD3	1.85	0.41
1:CR:108:ILE:HG23	1:CR:113:LEU:HD12	2.03	0.41
1:CS:324:LEU:HA	1:CS:325:PRO:HD3	1.84	0.41
1:CS:401:ASP:O	1:CS:488:CYS:HA	2.21	0.41
1:AA:182:LEU:HG	1:AA:330:ILE:HB	2.02	0.41
1:AA:61:PHE:CD2	1:AA:243:ILE:HD11	2.56	0.41
1:AB:237:VAL:HG23	1:AB:279:PHE:CD2	2.55	0.41
1:AE:423:LYS:HE2	1:AE:449:GLU:O	2.21	0.41
1:AF:241:ALA:HB1	1:AF:242:PRO:HD2	2.02	0.41
1:AG:182:LEU:C	1:AG:182:LEU:HD12	2.40	0.41
1:AL:188:PHE:C	1:AL:189:PHE:HD1	2.24	0.41
1:AQ:33:LYS:HB2	1:AQ:33:LYS:HE2	1.95	0.41
1:AT:28:MET:HE2	1:AT:152:LEU:HG	2.02	0.41
1:BE:404:LEU:N	1:BE:404:LEU:HD23	2.36	0.41
1:BF:324:LEU:HD23	1:BF:324:LEU:C	2.41	0.41
1:BF:232:THR:HB	1:BF:334:VAL:CG2	2.50	0.41
1:BF:475:LEU:HB3	1:BF:478:ALA:HB2	2.03	0.41
1:BG:11:PRO:HG2	1:BG:18:ARG:CD	2.49	0.41
1:BG:185:PRO:HA	1:BG:186:PRO:HD3	1.92	0.41
1:BG:202:LEU:HA	1:BG:202:LEU:HD23	1.93	0.41
1:BI:442:GLN:HE21	1:BJ:412:PHE:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:340:LEU:HA	1:BJ:340:LEU:HD23	1.90	0.41
1:BJ:372:PHE:H	1:BJ:381:MET:HE1	1.85	0.41
1:BN:182:LEU:HD12	1:BN:182:LEU:C	2.41	0.41
1:BO:185:PRO:HA	1:BO:186:PRO:HD3	1.95	0.41
1:BO:47:MET:HG2	1:BO:117:ALA:HB2	2.03	0.41
1:BP:185:PRO:HA	1:BP:186:PRO:HD3	1.95	0.41
1:BQ:272:TYR:CE2	1:CL:55:ARG:CZ	3.04	0.41
1:BR:324:LEU:C	1:BR:324:LEU:HD23	2.41	0.41
1:BR:170:PHE:HB2	1:BR:496:PHE:HE1	1.86	0.41
1:BS:243:ILE:N	1:BS:243:ILE:HD12	2.36	0.41
1:CF:379:VAL:CG1	1:CF:381:MET:CE	2.98	0.41
1:CH:14:CYS:H	1:CH:138:ASN:ND2	2.18	0.41
1:CJ:252:VAL:HG22	1:CJ:253:SER:N	2.35	0.41
1:CK:232:THR:HB	1:CK:334:VAL:HG23	2.02	0.41
1:CK:407:SER:HB3	1:CO:418:SER:HB3	2.02	0.41
1:CL:207:VAL:HA	1:CL:208:PRO:HD3	1.85	0.41
1:CM:189:PHE:HD2	1:CM:247:ILE:HD11	1.84	0.41
1:CP:318:SER:HA	1:CP:319:GLY:HA2	1.75	0.41
1:AA:108:ILE:HG23	1:AA:113:LEU:HD12	2.02	0.41
1:AA:11:PRO:HG2	1:AA:18:ARG:CD	2.51	0.41
1:AA:234:ARG:HG2	1:AA:280:GLU:HG2	2.01	0.41
1:AC:324:LEU:HA	1:AC:325:PRO:HD3	1.86	0.41
1:AD:108:ILE:HG23	1:AD:113:LEU:HD12	2.03	0.41
1:AD:25:ILE:HG23	1:AD:152:LEU:HD11	2.03	0.41
1:AF:182:LEU:HD12	1:AF:182:LEU:C	2.42	0.41
1:AF:182:LEU:HG	1:AF:330:ILE:HB	2.02	0.41
1:AH:256:ASN:HD22	1:AH:302:ASP:HA	1.86	0.41
1:AI:252:VAL:HG22	1:AI:253:SER:N	2.36	0.41
1:AL:10:ILE:HG12	1:AL:10:ILE:H	1.76	0.41
1:AM:185:PRO:HA	1:AM:186:PRO:HD3	1.91	0.41
1:AR:371:ASP:OD1	1:AR:381:MET:HG2	2.21	0.41
1:AR:440:ALA:CB	1:AS:444:LEU:HD13	2.50	0.41
1:AP:412:PHE:HB2	1:AT:442:GLN:HE21	1.85	0.41
1:BC:379:VAL:HG11	1:BC:381:MET:HE1	2.02	0.41
1:BF:79:ARG:CG	1:BF:79:ARG:NH1	2.80	0.41
1:BI:22:THR:OG1	1:BI:131:HIS:CD2	2.63	0.41
1:BI:55:ARG:HD3	1:BR:272:TYR:HD2	1.81	0.41
1:BL:272:TYR:N	1:BL:272:TYR:HD1	2.19	0.41
1:BN:207:VAL:HA	1:BN:208:PRO:HD3	1.83	0.41
1:BO:371:ASP:OD1	1:BO:381:MET:HG2	2.21	0.41
1:BP:250:TRP:HE3	1:BP:272:TYR:CD1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:423:LYS:HE2	1:BR:449:GLU:O	2.21	0.41
1:BR:58:ALA:HB2	1:BR:102:GLY:HA3	2.03	0.41
1:BT:263:ASN:O	1:BT:267:LYS:HG3	2.20	0.41
1:BT:20:LEU:HD11	1:BT:66:TRP:CD1	2.56	0.41
1:CA:324:LEU:C	1:CA:324:LEU:HD23	2.41	0.41
1:CD:126:GLU:HG3	1:CD:127:SER:H	1.86	0.41
1:CG:395:LEU:HB2	1:CG:497:TYR:HB2	2.02	0.41
1:CG:48:PRO:HG2	1:CG:50:PHE:CZ	2.56	0.41
1:CM:108:ILE:HG23	1:CM:113:LEU:HD12	2.02	0.41
1:CM:256:ASN:HD22	1:CM:302:ASP:HA	1.86	0.41
1:CN:404:LEU:HD23	1:CN:404:LEU:N	2.35	0.41
1:CO:9:TYR:HE1	1:CO:147:GLN:HE21	1.69	0.41
1:AA:203:THR:HB	1:AA:300:GLN:HG3	2.01	0.41
1:AB:372:PHE:H	1:AB:381:MET:HE1	1.86	0.41
1:AC:14:CYS:H	1:AC:138:ASN:HD21	1.68	0.41
1:AC:454:ASN:ND2	1:AC:456:ALA:HB3	2.36	0.41
1:AH:263:ASN:O	1:AH:267:LYS:HG3	2.21	0.41
1:AL:43:ALA:HB1	1:AL:158:GLU:HA	2.03	0.41
1:AL:207:VAL:HA	1:AL:208:PRO:HD3	1.83	0.41
1:AL:252:VAL:HG22	1:AL:253:SER:N	2.36	0.41
1:AO:171:ASP:HA	1:AO:172:PRO:HD3	1.81	0.41
1:AO:185:PRO:HA	1:AO:186:PRO:HD3	1.92	0.41
1:AP:252:VAL:HG22	1:AP:253:SER:N	2.36	0.41
1:AP:340:LEU:HD23	1:AP:340:LEU:HA	1.91	0.41
1:AS:372:PHE:H	1:AS:381:MET:HE1	1.86	0.41
1:AR:440:ALA:HB3	1:AS:444:LEU:HD13	2.03	0.41
1:AS:77:THR:O	1:AS:81:THR:HG23	2.21	0.41
1:AC:55:ARG:CZ	1:AT:272:TYR:CE2	3.03	0.41
1:AT:371:ASP:OD1	1:AT:381:MET:HG2	2.21	0.41
1:BG:25:ILE:HD12	1:BG:128:PRO:HB2	2.03	0.41
1:BJ:324:LEU:HA	1:BJ:325:PRO:HD3	1.84	0.41
1:BL:189:PHE:HE2	1:BL:249:LEU:HD21	1.86	0.41
1:BR:28:MET:HE2	1:BR:152:LEU:HG	2.03	0.41
1:CF:475:LEU:HB3	1:CF:478:ALA:HB2	2.02	0.41
1:CI:170:PHE:HD1	1:CI:389:MET:HE2	1.86	0.41
1:CI:252:VAL:HG22	1:CI:253:SER:N	2.36	0.41
1:CI:443:LYS:HD3	1:CI:443:LYS:HA	1.93	0.41
1:CJ:372:PHE:H	1:CJ:381:MET:HE1	1.85	0.41
1:CM:201:GLY:HA3	1:CM:300:GLN:HG2	2.02	0.41
1:CM:170:PHE:HD1	1:CM:389:MET:CE	2.34	0.41
1:CN:318:SER:HA	1:CN:319:GLY:HA2	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CN:340:LEU:HA	1:CN:340:LEU:HD23	1.88	0.41
1:CM:440:ALA:HB3	1:CN:444:LEU:HD13	2.03	0.41
1:CO:43:ALA:HB1	1:CO:158:GLU:HA	2.03	0.41
1:CR:189:PHE:HD2	1:CR:247:ILE:HD11	1.86	0.41
1:CI:55:ARG:HD3	1:CR:272:TYR:CE2	2.55	0.41
1:CR:440:ALA:CB	1:CS:444:LEU:HD13	2.51	0.41
1:AD:285:SER:HA	1:AD:286:PRO:HD3	1.92	0.41
1:AD:371:ASP:OD1	1:AD:381:MET:HG2	2.20	0.41
1:AE:36:GLN:HE22	1:AE:156:LEU:H	1.69	0.41
1:AA:444:LEU:HD13	1:AE:440:ALA:CB	2.51	0.41
1:AL:28:MET:CE	1:AL:152:LEU:HG	2.51	0.41
1:AL:250:TRP:HZ3	1:AL:272:TYR:HE1	1.64	0.41
1:AM:33:LYS:HE2	1:AM:33:LYS:HB2	1.95	0.41
1:AL:442:GLN:NE2	1:AM:412:PHE:HB2	2.35	0.41
1:AN:175:PHE:CD2	1:AN:175:PHE:O	2.74	0.41
1:AT:324:LEU:HD23	1:AT:324:LEU:C	2.40	0.41
1:BA:37:TYR:O	1:BA:40:TRP:HB3	2.21	0.41
1:BE:285:SER:HA	1:BE:286:PRO:HD3	1.93	0.41
1:BF:263:ASN:O	1:BF:267:LYS:HG3	2.21	0.41
1:BK:239:ILE:HG23	1:BK:324:LEU:HD21	2.02	0.41
1:BL:371:ASP:OD1	1:BL:381:MET:HG2	2.21	0.41
1:BO:25:ILE:HD12	1:BO:128:PRO:HB2	2.01	0.41
1:BO:401:ASP:O	1:BO:488:CYS:HA	2.22	0.41
1:BP:207:VAL:HA	1:BP:208:PRO:HD3	1.83	0.41
1:BR:239:ILE:HG12	1:BR:326:ILE:CD1	2.50	0.41
1:BR:379:VAL:HG11	1:BR:381:MET:HE1	2.02	0.41
1:BR:379:VAL:HG12	1:BR:381:MET:HE2	2.03	0.41
1:BT:20:LEU:HB2	1:BT:132:PHE:O	2.21	0.41
1:CA:252:VAL:HG22	1:CA:253:SER:N	2.36	0.41
1:CA:182:LEU:HG	1:CA:330:ILE:HB	2.03	0.41
1:CD:324:LEU:HD23	1:CD:324:LEU:C	2.40	0.41
1:CA:444:LEU:HD13	1:CE:440:ALA:HB3	2.02	0.41
1:CF:162:PHE:CD1	1:CG:287:TYR:HA	2.56	0.41
1:CF:324:LEU:HA	1:CF:325:PRO:HD3	1.85	0.41
1:CF:48:PRO:HG2	1:CF:50:PHE:CZ	2.56	0.41
1:CI:20:LEU:HB2	1:CI:132:PHE:O	2.21	0.41
1:CK:175:PHE:CD2	1:CK:175:PHE:O	2.74	0.41
1:CM:163:LEU:HA	1:CM:163:LEU:HD12	1.87	0.41
1:CK:412:PHE:HB2	1:CO:442:GLN:NE2	2.35	0.41
1:CQ:182:LEU:HG	1:CQ:330:ILE:HB	2.03	0.41
1:AB:175:PHE:O	1:AB:175:PHE:CD2	2.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:18:ARG:HB2	1:AB:18:ARG:NH1	2.36	0.40
1:AC:234:ARG:CG	1:AC:280:GLU:HG2	2.51	0.40
1:AG:239:ILE:HD12	1:AG:275:GLU:HA	2.04	0.40
1:AH:10:ILE:HA	1:AH:11:PRO:HD3	1.95	0.40
1:AH:182:LEU:HD12	1:AH:182:LEU:C	2.41	0.40
1:AI:171:ASP:HA	1:AI:172:PRO:HD3	1.77	0.40
1:AI:379:VAL:CG1	1:AI:381:MET:CE	2.99	0.40
1:AM:393:HIS:CG	1:AM:496:PHE:HB3	2.56	0.40
1:AN:241:ALA:HB1	1:AN:242:PRO:HD2	2.03	0.40
1:AO:203:THR:HB	1:AO:300:GLN:CG	2.49	0.40
1:AO:74:ASN:ND2	1:AO:77:THR:OG1	2.55	0.40
1:AP:75:ARG:NH2	1:AP:391:ALA:O	2.53	0.40
1:AR:379:VAL:CG1	1:AR:381:MET:CE	2.99	0.40
1:BF:379:VAL:CG1	1:BF:381:MET:CE	2.99	0.40
1:BG:108:ILE:HG23	1:BG:113:LEU:HD12	2.04	0.40
1:BH:18:ARG:HG2	1:BH:20:LEU:HD23	2.03	0.40
1:BH:207:VAL:HA	1:BH:208:PRO:HD3	1.81	0.40
1:BH:234:ARG:CG	1:BH:280:GLU:HG2	2.51	0.40
1:BG:434:GLY:O	1:BH:349:VAL:HG23	2.21	0.40
1:BK:237:VAL:HG23	1:BK:279:PHE:CD2	2.55	0.40
1:BK:442:GLN:NE2	1:BL:412:PHE:HB2	2.36	0.40
1:BM:170:PHE:HB2	1:BM:496:PHE:HE1	1.86	0.40
1:BS:379:VAL:HG12	1:BS:381:MET:HE2	2.03	0.40
1:CA:203:THR:HB	1:CA:300:GLN:HG3	2.03	0.40
1:CA:340:LEU:HA	1:CA:340:LEU:HD23	1.88	0.40
1:CB:10:ILE:HA	1:CB:11:PRO:HD3	1.94	0.40
1:CC:189:PHE:CE2	1:CC:249:LEU:HD21	2.56	0.40
1:CE:340:LEU:HD23	1:CE:340:LEU:HA	1.88	0.40
1:CF:318:SER:HA	1:CF:319:GLY:HA2	1.76	0.40
1:CG:163:LEU:HA	1:CG:163:LEU:HD12	1.89	0.40
1:CG:207:VAL:HA	1:CG:208:PRO:HD3	1.82	0.40
1:CG:33:LYS:HB2	1:CG:33:LYS:HE2	1.93	0.40
1:CG:442:GLN:HE21	1:CH:412:PHE:HB2	1.86	0.40
1:CI:272:TYR:CE2	1:CO:55:ARG:CZ	3.04	0.40
1:CL:202:LEU:HD23	1:CL:202:LEU:HA	1.93	0.40
1:BQ:272:TYR:CD2	1:CL:55:ARG:CZ	3.04	0.40
1:CQ:203:THR:HB	1:CQ:300:GLN:HG3	2.03	0.40
1:CQ:170:PHE:HB2	1:CQ:496:PHE:HE1	1.85	0.40
1:CT:252:VAL:HG22	1:CT:253:SER:N	2.35	0.40
1:AB:423:LYS:HE2	1:AB:449:GLU:O	2.20	0.40
1:AD:43:ALA:HB1	1:AD:158:GLU:HA	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:234:ARG:CG	1:AD:280:GLU:HG2	2.50	0.40
1:AD:379:VAL:CG1	1:AD:381:MET:HE2	2.51	0.40
1:AI:371:ASP:OD1	1:AI:381:MET:HG2	2.21	0.40
1:AJ:423:LYS:HE2	1:AJ:449:GLU:O	2.20	0.40
1:AP:222:LEU:O	1:AP:225:CYS:HB2	2.21	0.40
1:BB:324:LEU:HD23	1:BB:324:LEU:C	2.42	0.40
1:BB:340:LEU:HD23	1:BB:340:LEU:HA	1.89	0.40
1:BF:175:PHE:O	1:BF:175:PHE:CD2	2.75	0.40
1:BF:182:LEU:HG	1:BF:330:ILE:HB	2.02	0.40
1:BG:284:ARG:CG	1:BG:284:ARG:NH1	2.71	0.40
1:BI:238:HIS:HE1	1:BI:329:GLN:OE1	2.04	0.40
1:BI:423:LYS:HE2	1:BI:449:GLU:O	2.21	0.40
1:BJ:324:LEU:HD23	1:BJ:324:LEU:C	2.42	0.40
1:BK:201:GLY:HA3	1:BK:300:GLN:HG2	2.03	0.40
1:BL:318:SER:HA	1:BL:319:GLY:HA2	1.77	0.40
1:BQ:108:ILE:HG23	1:BQ:113:LEU:HD12	2.03	0.40
1:BS:43:ALA:HB1	1:BS:158:GLU:HA	2.03	0.40
1:CA:243:ILE:HD12	1:CA:243:ILE:N	2.37	0.40
1:CG:371:ASP:OD1	1:CG:381:MET:HG2	2.21	0.40
1:CH:182:LEU:HG	1:CH:330:ILE:HB	2.02	0.40
1:CI:234:ARG:CG	1:CI:280:GLU:HG2	2.51	0.40
1:CI:255:TRP:CE3	1:CI:285:SER:HB2	2.56	0.40
1:CI:75:ARG:NH2	1:CI:391:ALA:O	2.53	0.40
1:CJ:170:PHE:HD1	1:CJ:389:MET:HE2	1.86	0.40
1:CH:55:ARG:CZ	1:CK:272:TYR:CD2	3.05	0.40
1:CL:232:THR:HB	1:CL:334:VAL:CG2	2.50	0.40
1:CM:14:CYS:H	1:CM:138:ASN:ND2	2.18	0.40
1:CM:404:LEU:HD23	1:CM:404:LEU:N	2.36	0.40
1:CO:175:PHE:O	1:CO:175:PHE:CD2	2.75	0.40
1:CS:43:ALA:HB1	1:CS:158:GLU:HA	2.02	0.40
1:CS:404:LEU:HD22	1:CS:486:VAL:HG22	2.04	0.40
1:AA:36:GLN:HE22	1:AA:156:LEU:H	1.67	0.40
1:AB:73:TYR:CE2	1:AB:394:GLY:HA3	2.57	0.40
1:AD:182:LEU:C	1:AD:182:LEU:HD12	2.42	0.40
1:AD:272:TYR:CE2	1:AS:55:ARG:CZ	3.04	0.40
1:AA:342:SER:HB2	1:AE:425:VAL:HG11	2.02	0.40
1:AF:440:ALA:CB	1:AG:444:LEU:HD13	2.52	0.40
1:AH:272:TYR:CD2	1:CF:55:ARG:CZ	3.05	0.40
1:AI:202:LEU:HD23	1:AI:202:LEU:HA	1.87	0.40
1:AJ:22:THR:OG1	1:AJ:131:HIS:CD2	2.66	0.40
1:AS:440:ALA:CB	1:AT:444:LEU:HD13	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:20:LEU:HB2	1:AT:132:PHE:O	2.21	0.40
1:BA:11:PRO:HG2	1:BA:18:ARG:CD	2.51	0.40
1:BB:182:LEU:C	1:BB:182:LEU:HD12	2.42	0.40
1:BB:33:LYS:HE2	1:BB:33:LYS:HB2	1.95	0.40
1:BC:207:VAL:HA	1:BC:208:PRO:HD3	1.84	0.40
1:BC:232:THR:HB	1:BC:334:VAL:CG2	2.52	0.40
1:BE:423:LYS:HE2	1:BE:449:GLU:O	2.20	0.40
1:BF:18:ARG:HG3	1:BF:19:TYR:N	2.36	0.40
1:BG:238:HIS:HE1	1:BG:329:GLN:OE1	2.03	0.40
1:BG:256:ASN:HD22	1:BG:302:ASP:HA	1.87	0.40
1:BH:15:GLN:NE2	1:BH:15:GLN:CA	2.81	0.40
1:BH:335:ARG:N	1:BH:336:PRO:HD3	2.36	0.40
1:BM:234:ARG:CG	1:BM:280:GLU:HG2	2.52	0.40
1:BN:371:ASP:OD1	1:BN:381:MET:HG2	2.21	0.40
1:BP:182:LEU:C	1:BP:182:LEU:HD12	2.42	0.40
1:BP:73:TYR:CE2	1:BP:394:GLY:HA3	2.56	0.40
1:BQ:395:LEU:HB2	1:BQ:497:TYR:HB2	2.03	0.40
1:BS:285:SER:HA	1:BS:286:PRO:HD3	1.95	0.40
1:BS:37:TYR:O	1:BS:40:TRP:HB3	2.21	0.40
1:BD:272:TYR:HD2	1:BS:55:ARG:HD3	1.85	0.40
1:CB:256:ASN:HD22	1:CB:302:ASP:HA	1.85	0.40
1:CI:423:LYS:HE2	1:CI:449:GLU:O	2.21	0.40
1:CK:289:ARG:HD3	1:CK:289:ARG:HH11	1.76	0.40
1:CL:43:ALA:HB1	1:CL:158:GLU:HA	2.02	0.40
1:CM:340:LEU:HD23	1:CM:340:LEU:HA	1.92	0.40
1:CD:55:ARG:CZ	1:CN:272:TYR:CE2	3.03	0.40
1:CN:272:TYR:N	1:CN:272:TYR:HD1	2.18	0.40
1:CO:108:ILE:HG23	1:CO:113:LEU:HD12	2.02	0.40
1:CO:255:TRP:CE3	1:CO:285:SER:HB2	2.57	0.40
1:CO:423:LYS:HE2	1:CO:449:GLU:O	2.21	0.40
1:CQ:335:ARG:N	1:CQ:336:PRO:HD3	2.36	0.40
1:CQ:404:LEU:HD23	1:CQ:404:LEU:N	2.37	0.40
1:AA:340:LEU:HA	1:AA:340:LEU:HD23	1.92	0.40
1:AC:272:TYR:CE2	1:BA:55:ARG:CZ	3.04	0.40
1:AC:324:LEU:HD23	1:AC:324:LEU:C	2.42	0.40
1:AF:52:ILE:HG12	1:AF:152:LEU:CD2	2.51	0.40
1:AF:189:PHE:CE1	1:AF:198:ARG:HG2	2.55	0.40
1:AF:55:ARG:HD3	1:BH:272:TYR:HD2	1.84	0.40
1:AK:170:PHE:HB2	1:AK:496:PHE:HE1	1.87	0.40
1:AK:171:ASP:HA	1:AK:172:PRO:HD3	1.79	0.40
1:AN:308:PHE:CZ	1:AN:328:VAL:HG21	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:207:VAL:HA	1:AO:208:PRO:HD3	1.86	0.40
1:AP:61:PHE:CE2	1:AP:243:ILE:HD11	2.57	0.40
1:AP:33:LYS:HE2	1:AP:33:LYS:HB2	1.97	0.40
1:AP:440:ALA:CB	1:AQ:444:LEU:HD13	2.51	0.40
1:AR:33:LYS:HE2	1:AR:33:LYS:HB2	1.97	0.40
1:AT:10:ILE:HG21	1:AT:146:TRP:CZ2	2.57	0.40
1:AT:379:VAL:HG12	1:AT:381:MET:HE2	2.03	0.40
1:BA:10:ILE:HA	1:BA:11:PRO:HD3	1.89	0.40
1:AT:55:ARG:CZ	1:BA:272:TYR:CE2	3.05	0.40
1:BA:379:VAL:HG12	1:BA:381:MET:HE2	2.03	0.40
1:BA:73:TYR:CZ	1:BA:394:GLY:HA3	2.55	0.40
1:BB:250:TRP:HZ3	1:BB:272:TYR:HE1	1.63	0.40
1:BC:201:GLY:HA3	1:BC:300:GLN:HG2	2.03	0.40
1:BC:55:ARG:CZ	1:BT:272:TYR:CE2	3.04	0.40
1:BD:175:PHE:O	1:BD:175:PHE:CD2	2.74	0.40
1:BD:232:THR:HB	1:BD:334:VAL:CG2	2.51	0.40
1:BD:318:SER:HA	1:BD:319:GLY:HA2	1.81	0.40
1:BE:33:LYS:HE2	1:BE:33:LYS:HB2	1.97	0.40
1:BF:20:LEU:HB2	1:BF:132:PHE:O	2.22	0.40
1:BF:30:SER:HA	1:BF:37:TYR:CD1	2.57	0.40
1:BG:234:ARG:CG	1:BG:280:GLU:HG2	2.52	0.40
1:BG:33:LYS:HB2	1:BG:33:LYS:HE2	1.98	0.40
1:BG:395:LEU:HB2	1:BG:497:TYR:HB2	2.03	0.40
1:BF:440:ALA:CB	1:BG:444:LEU:HD13	2.51	0.40
1:AF:55:ARG:CZ	1:BH:272:TYR:CD2	3.05	0.40
1:BJ:234:ARG:HG2	1:BJ:280:GLU:HG2	2.03	0.40
1:BJ:335:ARG:N	1:BJ:336:PRO:HD3	2.37	0.40
1:BJ:379:VAL:HG11	1:BJ:381:MET:HE1	2.03	0.40
1:BL:182:LEU:HD12	1:BL:182:LEU:C	2.42	0.40
1:BL:379:VAL:HG11	1:BL:381:MET:HE1	2.03	0.40
1:BD:55:ARG:CZ	1:BN:272:TYR:CE2	3.04	0.40
1:BO:182:LEU:HD12	1:BO:182:LEU:C	2.42	0.40
1:BQ:285:SER:HA	1:BQ:286:PRO:HD3	1.93	0.40
1:BR:454:ASN:C	1:BR:454:ASN:HD22	2.25	0.40
1:BS:207:VAL:HA	1:BS:208:PRO:HD3	1.85	0.40
1:BS:226:VAL:HG13	1:BS:228:GLY:H	1.87	0.40
1:BS:28:MET:CE	1:BS:152:LEU:HG	2.52	0.40
1:CH:171:ASP:HA	1:CH:172:PRO:HD3	1.79	0.40
1:CH:55:ARG:CZ	1:CK:272:TYR:CE2	3.04	0.40
1:CN:33:LYS:HE2	1:CN:33:LYS:HB2	1.96	0.40
1:CO:241:ALA:HB1	1:CO:242:PRO:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CO:324:LEU:C	1:CO:324:LEU:HD23	2.42	0.40
1:CR:252:VAL:HG22	1:CR:253:SER:N	2.36	0.40
1:CR:442:GLN:HE21	1:CS:412:PHE:HB2	1.86	0.40
1:CS:234:ARG:CG	1:CS:280:GLU:HG2	2.51	0.40
1:CS:33:LYS:HE2	1:CS:33:LYS:HB2	1.95	0.40
1:AA:272:TYR:CD2	1:CT:55:ARG:CZ	3.05	0.40
1:AB:318:SER:HA	1:AB:319:GLY:HA2	1.78	0.40
1:AD:324:LEU:HA	1:AD:325:PRO:HD3	1.86	0.40
1:AD:372:PHE:H	1:AD:381:MET:HE1	1.87	0.40
1:AC:418:SER:HB3	1:AD:407:SER:HB3	2.04	0.40
1:AE:324:LEU:HA	1:AE:325:PRO:HD3	1.84	0.40
1:AI:189:PHE:CE2	1:AI:249:LEU:HD21	2.45	0.40
1:AI:79:ARG:CG	1:AI:79:ARG:NH1	2.80	0.40
1:AJ:284:ARG:CG	1:AJ:284:ARG:NH1	2.75	0.40
1:AN:108:ILE:HG23	1:AN:113:LEU:HD12	2.03	0.40
1:AN:33:LYS:HB2	1:AN:33:LYS:HE2	1.93	0.40
1:AN:55:ARG:CD	1:AS:272:TYR:CD2	2.98	0.40
1:AQ:77:THR:O	1:AQ:81:THR:HG23	2.20	0.40
1:AR:236:ARG:HA	1:AR:278:SER:HA	2.04	0.40
1:AS:234:ARG:CG	1:AS:280:GLU:HG2	2.51	0.40
1:AT:243:ILE:HD12	1:AT:243:ILE:N	2.37	0.40
1:AS:418:SER:HB3	1:AT:407:SER:HB3	2.02	0.40
1:BA:412:PHE:HB2	1:BE:442:GLN:HE21	1.86	0.40
1:BB:171:ASP:HA	1:BB:172:PRO:HD3	1.80	0.40
1:BD:454:ASN:ND2	1:BD:456:ALA:H	2.14	0.40
1:BE:324:LEU:HD23	1:BE:324:LEU:C	2.42	0.40
1:BG:454:ASN:ND2	1:BG:456:ALA:H	2.11	0.40
1:BI:185:PRO:HA	1:BI:186:PRO:HD3	1.93	0.40
1:BI:299:SER:O	1:BI:302:ASP:HB2	2.22	0.40
1:BI:33:LYS:HB2	1:BI:33:LYS:HE2	1.97	0.40
1:BI:418:SER:HB3	1:BJ:407:SER:HB3	2.02	0.40
1:BL:22:THR:OG1	1:BL:131:HIS:CD2	2.63	0.40
1:AQ:272:TYR:CD2	1:BL:55:ARG:CZ	3.04	0.40
1:BM:318:SER:HA	1:BM:319:GLY:HA2	1.78	0.40
1:BN:272:TYR:HD1	1:BN:272:TYR:N	2.18	0.40
1:BP:252:VAL:HG22	1:BP:253:SER:N	2.36	0.40
1:BR:393:HIS:CG	1:BR:496:PHE:HB3	2.57	0.40
1:BS:188:PHE:C	1:BS:189:PHE:HD1	2.25	0.40
1:BT:241:ALA:HB1	1:BT:242:PRO:HD2	2.03	0.40
1:CE:126:GLU:HG3	1:CE:127:SER:H	1.87	0.40
1:CF:163:LEU:HD12	1:CF:163:LEU:HA	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:372:PHE:H	1:CG:381:MET:HE1	1.85	0.40
1:CJ:250:TRP:CZ3	1:CJ:272:TYR:CD1	3.08	0.40
1:BJ:55:ARG:CZ	1:CL:272:TYR:CE2	3.05	0.40
1:CT:25:ILE:HG23	1:CT:152:LEU:HD11	2.03	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 X-ray entries followed by that with respect to entries of similar resolution.

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	AA	502/504 (100%)	478 (95%)	23 (5%)	1 (0%)	47	82
1	AB	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	AC	502/504 (100%)	480 (96%)	20 (4%)	2 (0%)	34	72
1	AD	502/504 (100%)	482 (96%)	20 (4%)	0	100	100
1	AE	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	AF	502/504 (100%)	482 (96%)	20 (4%)	0	100	100
1	AG	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	34	72
1	AH	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	34	72
1	AI	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	AJ	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	AK	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	AL	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	AM	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	AN	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	AO	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	AP	502/504 (100%)	483 (96%)	19 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AQ	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	AR	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	47	82
1	AS	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	AT	502/504 (100%)	484 (96%)	17 (3%)	1 (0%)	47	82
1	BA	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	BB	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	34	72
1	BC	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	BD	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	BE	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	BF	502/504 (100%)	481 (96%)	19 (4%)	2 (0%)	34	72
1	BG	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	BH	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	47	82
1	BI	502/504 (100%)	479 (95%)	22 (4%)	1 (0%)	47	82
1	BJ	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	BK	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	47	82
1	BL	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	BM	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	BN	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	BO	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	BP	502/504 (100%)	479 (95%)	21 (4%)	2 (0%)	34	72
1	BQ	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	BR	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	BS	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	BT	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	CA	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	CB	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	CC	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	CD	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	CE	502/504 (100%)	483 (96%)	18 (4%)	1 (0%)	47	82
1	CF	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	CG	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CH	502/504 (100%)	481 (96%)	21 (4%)	0	100	100
1	CI	502/504 (100%)	482 (96%)	20 (4%)	0	100	100
1	CJ	502/504 (100%)	484 (96%)	17 (3%)	1 (0%)	47	82
1	CK	502/504 (100%)	482 (96%)	19 (4%)	1 (0%)	47	82
1	CL	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	CM	502/504 (100%)	480 (96%)	20 (4%)	2 (0%)	34	72
1	CN	502/504 (100%)	482 (96%)	20 (4%)	0	100	100
1	CO	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	CP	502/504 (100%)	480 (96%)	21 (4%)	1 (0%)	47	82
1	CQ	502/504 (100%)	482 (96%)	18 (4%)	2 (0%)	34	72
1	CR	502/504 (100%)	478 (95%)	22 (4%)	2 (0%)	34	72
1	CS	502/504 (100%)	481 (96%)	20 (4%)	1 (0%)	47	82
1	CT	502/504 (100%)	479 (95%)	22 (4%)	1 (0%)	47	82
All	All	30120/30240 (100%)	28870 (96%)	1187 (4%)	63 (0%)	47	82

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BP	82	ALA
1	CR	82	ALA
1	BM	17	ASN
1	AC	78	SER
1	BB	17	ASN
1	BD	17	ASN
1	BF	78	SER
1	CM	17	ASN
1	AH	17	ASN
1	BA	498	GLY
1	CQ	17	ASN
1	AG	17	ASN
1	AN	498	GLY
1	AT	498	GLY
1	BG	498	GLY
1	BP	498	GLY
1	BT	498	GLY
1	CF	498	GLY
1	CG	498	GLY

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Mol	Chain	Res	Type
1	CT	498	GLY
1	AE	498	GLY
1	AQ	498	GLY
1	BF	498	GLY
1	BK	498	GLY
1	BL	498	GLY
1	CK	498	GLY
1	CL	498	GLY
1	CM	498	GLY
1	CR	498	GLY
1	AA	498	GLY
1	AG	498	GLY
1	AK	498	GLY
1	AM	498	GLY
1	BC	498	GLY
1	BE	498	GLY
1	BJ	498	GLY
1	BN	498	GLY
1	BO	498	GLY
1	CD	498	GLY
1	CO	498	GLY
1	AJ	498	GLY
1	AS	498	GLY
1	BH	498	GLY
1	BR	498	GLY
1	BS	498	GLY
1	CB	498	GLY
1	CE	498	GLY
1	CP	498	GLY
1	CS	498	GLY
1	AH	498	GLY
1	AI	498	GLY
1	AO	498	GLY
1	AR	498	GLY
1	BB	498	GLY
1	CA	498	GLY
1	CJ	498	GLY
1	CQ	498	GLY
1	AB	498	GLY
1	AC	498	GLY
1	AL	498	GLY
1	BI	498	GLY

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Mol	Chain	Res	Type
1	BQ	498	GLY
1	CC	498	GLY

### 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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	AB	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	AC	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	AD	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	AE	430/430 (100%)	409 (95%)	21 (5%)	25	61
1	AF	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	AG	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	AH	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	AI	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	AJ	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	AK	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	AL	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	AM	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	AN	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	AO	430/430 (100%)	408 (95%)	22 (5%)	24	60
1	AP	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	AQ	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	AR	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	AS	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	AT	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	BA	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	BB	430/430 (100%)	405 (94%)	25 (6%)	20	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BC	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	BD	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	BE	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	BF	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	BG	430/430 (100%)	408 (95%)	22 (5%)	24	60
1	BH	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	BI	430/430 (100%)	408 (95%)	22 (5%)	24	60
1	BJ	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	BK	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	BL	430/430 (100%)	403 (94%)	27 (6%)	18	51
1	BM	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	BN	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	BO	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	BP	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	BQ	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	BR	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	BS	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	BT	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	CA	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	CB	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	CC	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	CD	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	CE	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	CF	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	CG	430/430 (100%)	408 (95%)	22 (5%)	24	60
1	CH	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	CI	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	CJ	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	CK	430/430 (100%)	406 (94%)	24 (6%)	21	56
1	CL	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	CM	430/430 (100%)	403 (94%)	27 (6%)	18	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CN	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	CO	430/430 (100%)	408 (95%)	22 (5%)	24	60
1	CP	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	CQ	430/430 (100%)	404 (94%)	26 (6%)	19	53
1	CR	430/430 (100%)	405 (94%)	25 (6%)	20	55
1	CS	430/430 (100%)	407 (95%)	23 (5%)	22	58
1	CT	430/430 (100%)	405 (94%)	25 (6%)	20	55
All	All	25800/25800 (100%)	24352 (94%)	1448 (6%)	21	56

All (1448) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	105	SER
1	AA	129	ARG
1	AA	160	THR
1	AA	161	SER
1	AA	163	LEU
1	AA	167	THR
1	AA	182	LEU
1	AA	191	LEU
1	AA	199	SER
1	AA	226	VAL
1	AA	229	MET
1	AA	243	ILE
1	AA	260	MET
1	AA	272	TYR
1	AA	284	ARG
1	AA	289	ARG
1	AA	301	ARG
1	AA	378	ARG
1	AA	384	ASN
1	AA	449	GLU
1	AA	454	ASN
1	AA	475	LEU
1	AA	504	VAL
1	AB	79	ARG
1	AB	105	SER
1	AB	129	ARG
1	AB	160	THR
1	AB	161	SER

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Mol	Chain	Res	Type
1	AB	163	LEU
1	AB	167	THR
1	AB	182	LEU
1	AB	191	LEU
1	AB	199	SER
1	AB	226	VAL
1	AB	243	ILE
1	AB	260	MET
1	AB	272	TYR
1	AB	284	ARG
1	AB	289	ARG
1	AB	299	SER
1	AB	300	GLN
1	AB	301	ARG
1	AB	336	PRO
1	AB	378	ARG
1	AB	384	ASN
1	AB	449	GLU
1	AB	454	ASN
1	AB	475	LEU
1	AB	504	VAL
1	AC	18	ARG
1	AC	105	SER
1	AC	129	ARG
1	AC	160	THR
1	AC	161	SER
1	AC	163	LEU
1	AC	167	THR
1	AC	182	LEU
1	AC	191	LEU
1	AC	199	SER
1	AC	226	VAL
1	AC	243	ILE
1	AC	260	MET
1	AC	272	TYR
1	AC	284	ARG
1	AC	289	ARG
1	AC	300	GLN
1	AC	301	ARG
1	AC	378	ARG
1	AC	384	ASN
1	AC	449	GLU

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Mol	Chain	Res	Type
1	AC	454	ASN
1	AC	475	LEU
1	AC	504	VAL
1	AD	15	GLN
1	AD	57	PRO
1	AD	79	ARG
1	AD	105	SER
1	AD	129	ARG
1	AD	160	THR
1	AD	161	SER
1	AD	163	LEU
1	AD	167	THR
1	AD	182	LEU
1	AD	191	LEU
1	AD	199	SER
1	AD	226	VAL
1	AD	229	MET
1	AD	243	ILE
1	AD	260	MET
1	AD	272	TYR
1	AD	284	ARG
1	AD	289	ARG
1	AD	301	ARG
1	AD	378	ARG
1	AD	384	ASN
1	AD	449	GLU
1	AD	454	ASN
1	AD	475	LEU
1	AD	504	VAL
1	AE	10	ILE
1	AE	105	SER
1	AE	160	THR
1	AE	161	SER
1	AE	163	LEU
1	AE	167	THR
1	AE	191	LEU
1	AE	199	SER
1	AE	226	VAL
1	AE	243	ILE
1	AE	260	MET
1	AE	272	TYR
1	AE	284	ARG

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Mol	Chain	Res	Type
1	AE	289	ARG
1	AE	301	ARG
1	AE	378	ARG
1	AE	384	ASN
1	AE	449	GLU
1	AE	454	ASN
1	AE	475	LEU
1	AE	504	VAL
1	AF	79	ARG
1	AF	105	SER
1	AF	129	ARG
1	AF	160	THR
1	AF	161	SER
1	AF	163	LEU
1	AF	167	THR
1	AF	182	LEU
1	AF	191	LEU
1	AF	199	SER
1	AF	226	VAL
1	AF	243	ILE
1	AF	260	MET
1	AF	272	TYR
1	AF	284	ARG
1	AF	289	ARG
1	AF	301	ARG
1	AF	378	ARG
1	AF	384	ASN
1	AF	449	GLU
1	AF	454	ASN
1	AF	475	LEU
1	AF	504	VAL
1	AG	10	ILE
1	AG	79	ARG
1	AG	105	SER
1	AG	129	ARG
1	AG	160	THR
1	AG	161	SER
1	AG	163	LEU
1	AG	167	THR
1	AG	182	LEU
1	AG	191	LEU
1	AG	199	SER

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Mol	Chain	Res	Type
1	AG	226	VAL
1	AG	243	ILE
1	AG	260	MET
1	AG	272	TYR
1	AG	284	ARG
1	AG	289	ARG
1	AG	300	GLN
1	AG	301	ARG
1	AG	378	ARG
1	AG	384	ASN
1	AG	449	GLU
1	AG	454	ASN
1	AG	475	LEU
1	AG	504	VAL
1	AH	15	GLN
1	AH	18	ARG
1	AH	105	SER
1	AH	129	ARG
1	AH	160	THR
1	AH	161	SER
1	AH	163	LEU
1	AH	167	THR
1	AH	182	LEU
1	AH	191	LEU
1	AH	199	SER
1	AH	226	VAL
1	AH	243	ILE
1	AH	260	MET
1	AH	272	TYR
1	AH	284	ARG
1	AH	289	ARG
1	AH	300	GLN
1	AH	378	ARG
1	AH	384	ASN
1	AH	449	GLU
1	AH	454	ASN
1	AH	475	LEU
1	AH	504	VAL
1	AI	18	ARG
1	AI	79	ARG
1	AI	105	SER
1	AI	129	ARG

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Mol	Chain	Res	Type
1	AI	160	THR
1	AI	161	SER
1	AI	163	LEU
1	AI	167	THR
1	AI	182	LEU
1	AI	191	LEU
1	AI	199	SER
1	AI	226	VAL
1	AI	229	MET
1	AI	243	ILE
1	AI	260	MET
1	AI	272	TYR
1	AI	284	ARG
1	AI	289	ARG
1	AI	300	GLN
1	AI	301	ARG
1	AI	378	ARG
1	AI	384	ASN
1	AI	449	GLU
1	AI	454	ASN
1	AI	475	LEU
1	AI	504	VAL
1	AJ	18	ARG
1	AJ	105	SER
1	AJ	129	ARG
1	AJ	160	THR
1	AJ	161	SER
1	AJ	163	LEU
1	AJ	167	THR
1	AJ	182	LEU
1	AJ	191	LEU
1	AJ	199	SER
1	AJ	226	VAL
1	AJ	229	MET
1	AJ	243	ILE
1	AJ	260	MET
1	AJ	272	TYR
1	AJ	284	ARG
1	AJ	289	ARG
1	AJ	301	ARG
1	AJ	378	ARG
1	AJ	384	ASN

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Mol	Chain	Res	Type
1	AJ	449	GLU
1	AJ	454	ASN
1	AJ	475	LEU
1	AJ	504	VAL
1	AK	18	ARG
1	AK	105	SER
1	AK	129	ARG
1	AK	160	THR
1	AK	161	SER
1	AK	163	LEU
1	AK	167	THR
1	AK	182	LEU
1	AK	191	LEU
1	AK	199	SER
1	AK	226	VAL
1	AK	229	MET
1	AK	243	ILE
1	AK	260	MET
1	AK	272	TYR
1	AK	284	ARG
1	AK	289	ARG
1	AK	300	GLN
1	AK	301	ARG
1	AK	336	PRO
1	AK	378	ARG
1	AK	384	ASN
1	AK	449	GLU
1	AK	454	ASN
1	AK	475	LEU
1	AK	504	VAL
1	AL	9	TYR
1	AL	10	ILE
1	AL	79	ARG
1	AL	105	SER
1	AL	129	ARG
1	AL	160	THR
1	AL	161	SER
1	AL	163	LEU
1	AL	167	THR
1	AL	182	LEU
1	AL	191	LEU
1	AL	199	SER

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Mol	Chain	Res	Type
1	AL	226	VAL
1	AL	243	ILE
1	AL	260	MET
1	AL	272	TYR
1	AL	284	ARG
1	AL	289	ARG
1	AL	299	SER
1	AL	301	ARG
1	AL	378	ARG
1	AL	384	ASN
1	AL	449	GLU
1	AL	454	ASN
1	AL	475	LEU
1	AL	504	VAL
1	AM	11	PRO
1	AM	105	SER
1	AM	129	ARG
1	AM	160	THR
1	AM	161	SER
1	AM	163	LEU
1	AM	167	THR
1	AM	182	LEU
1	AM	191	LEU
1	AM	199	SER
1	AM	226	VAL
1	AM	243	ILE
1	AM	260	MET
1	AM	272	TYR
1	AM	284	ARG
1	AM	289	ARG
1	AM	301	ARG
1	AM	378	ARG
1	AM	384	ASN
1	AM	449	GLU
1	AM	454	ASN
1	AM	475	LEU
1	AM	504	VAL
1	AN	10	ILE
1	AN	79	ARG
1	AN	105	SER
1	AN	129	ARG
1	AN	160	THR

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Mol	Chain	Res	Type
1	AN	161	SER
1	AN	163	LEU
1	AN	167	THR
1	AN	182	LEU
1	AN	191	LEU
1	AN	199	SER
1	AN	226	VAL
1	AN	243	ILE
1	AN	260	MET
1	AN	272	TYR
1	AN	284	ARG
1	AN	289	ARG
1	AN	301	ARG
1	AN	378	ARG
1	AN	384	ASN
1	AN	449	GLU
1	AN	454	ASN
1	AN	475	LEU
1	AN	504	VAL
1	AO	105	SER
1	AO	129	ARG
1	AO	160	THR
1	AO	161	SER
1	AO	163	LEU
1	AO	167	THR
1	AO	182	LEU
1	AO	191	LEU
1	AO	199	SER
1	AO	226	VAL
1	AO	243	ILE
1	AO	260	MET
1	AO	272	TYR
1	AO	284	ARG
1	AO	289	ARG
1	AO	301	ARG
1	AO	378	ARG
1	AO	384	ASN
1	AO	449	GLU
1	AO	454	ASN
1	AO	475	LEU
1	AO	504	VAL
1	AP	79	ARG

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Mol	Chain	Res	Type
1	AP	105	SER
1	AP	129	ARG
1	AP	160	THR
1	AP	161	SER
1	AP	163	LEU
1	AP	167	THR
1	AP	182	LEU
1	AP	191	LEU
1	AP	199	SER
1	AP	226	VAL
1	AP	243	ILE
1	AP	260	MET
1	AP	272	TYR
1	AP	284	ARG
1	AP	289	ARG
1	AP	301	ARG
1	AP	378	ARG
1	AP	384	ASN
1	AP	449	GLU
1	AP	454	ASN
1	AP	475	LEU
1	AP	504	VAL
1	AQ	10	ILE
1	AQ	105	SER
1	AQ	129	ARG
1	AQ	160	THR
1	AQ	161	SER
1	AQ	163	LEU
1	AQ	167	THR
1	AQ	182	LEU
1	AQ	191	LEU
1	AQ	199	SER
1	AQ	226	VAL
1	AQ	243	ILE
1	AQ	260	MET
1	AQ	272	TYR
1	AQ	284	ARG
1	AQ	285	SER
1	AQ	289	ARG
1	AQ	301	ARG
1	AQ	336	PRO
1	AQ	378	ARG

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Mol	Chain	Res	Type
1	AQ	384	ASN
1	AQ	449	GLU
1	AQ	454	ASN
1	AQ	475	LEU
1	AQ	504	VAL
1	AR	75	ARG
1	AR	105	SER
1	AR	129	ARG
1	AR	160	THR
1	AR	161	SER
1	AR	163	LEU
1	AR	167	THR
1	AR	182	LEU
1	AR	191	LEU
1	AR	199	SER
1	AR	226	VAL
1	AR	243	ILE
1	AR	260	MET
1	AR	272	TYR
1	AR	284	ARG
1	AR	289	ARG
1	AR	300	GLN
1	AR	301	ARG
1	AR	378	ARG
1	AR	384	ASN
1	AR	449	GLU
1	AR	454	ASN
1	AR	475	LEU
1	AR	504	VAL
1	AS	10	ILE
1	AS	105	SER
1	AS	129	ARG
1	AS	160	THR
1	AS	161	SER
1	AS	163	LEU
1	AS	167	THR
1	AS	182	LEU
1	AS	191	LEU
1	AS	199	SER
1	AS	226	VAL
1	AS	229	MET
1	AS	243	ILE

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Mol	Chain	Res	Type
1	AS	260	MET
1	AS	272	TYR
1	AS	284	ARG
1	AS	289	ARG
1	AS	301	ARG
1	AS	305	SER
1	AS	378	ARG
1	AS	384	ASN
1	AS	449	GLU
1	AS	454	ASN
1	AS	475	LEU
1	AS	504	VAL
1	AT	105	SER
1	AT	129	ARG
1	AT	160	THR
1	AT	161	SER
1	AT	163	LEU
1	AT	167	THR
1	AT	182	LEU
1	AT	191	LEU
1	AT	199	SER
1	AT	226	VAL
1	AT	229	MET
1	AT	243	ILE
1	AT	260	MET
1	AT	272	TYR
1	AT	284	ARG
1	AT	289	ARG
1	AT	300	GLN
1	AT	301	ARG
1	AT	378	ARG
1	AT	384	ASN
1	AT	449	GLU
1	AT	454	ASN
1	AT	475	LEU
1	AT	504	VAL
1	BA	79	ARG
1	BA	105	SER
1	BA	129	ARG
1	BA	160	THR
1	BA	161	SER
1	BA	163	LEU

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Mol	Chain	Res	Type
1	BA	167	THR
1	BA	182	LEU
1	BA	191	LEU
1	BA	199	SER
1	BA	226	VAL
1	BA	243	ILE
1	BA	260	MET
1	BA	272	TYR
1	BA	284	ARG
1	BA	289	ARG
1	BA	301	ARG
1	BA	378	ARG
1	BA	384	ASN
1	BA	449	GLU
1	BA	454	ASN
1	BA	475	LEU
1	BA	504	VAL
1	BB	79	ARG
1	BB	105	SER
1	BB	129	ARG
1	BB	160	THR
1	BB	161	SER
1	BB	163	LEU
1	BB	167	THR
1	BB	182	LEU
1	BB	191	LEU
1	BB	199	SER
1	BB	226	VAL
1	BB	243	ILE
1	BB	260	MET
1	BB	272	TYR
1	BB	284	ARG
1	BB	289	ARG
1	BB	300	GLN
1	BB	301	ARG
1	BB	336	PRO
1	BB	378	ARG
1	BB	384	ASN
1	BB	449	GLU
1	BB	454	ASN
1	BB	475	LEU
1	BB	504	VAL

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Mol	Chain	Res	Type
1	BC	18	ARG
1	BC	105	SER
1	BC	129	ARG
1	BC	160	THR
1	BC	161	SER
1	BC	163	LEU
1	BC	167	THR
1	BC	182	LEU
1	BC	191	LEU
1	BC	199	SER
1	BC	226	VAL
1	BC	243	ILE
1	BC	260	MET
1	BC	272	TYR
1	BC	284	ARG
1	BC	289	ARG
1	BC	301	ARG
1	BC	378	ARG
1	BC	384	ASN
1	BC	449	GLU
1	BC	454	ASN
1	BC	475	LEU
1	BC	504	VAL
1	BD	105	SER
1	BD	129	ARG
1	BD	160	THR
1	BD	161	SER
1	BD	163	LEU
1	BD	167	THR
1	BD	182	LEU
1	BD	191	LEU
1	BD	199	SER
1	BD	226	VAL
1	BD	243	ILE
1	BD	260	MET
1	BD	272	TYR
1	BD	284	ARG
1	BD	289	ARG
1	BD	300	GLN
1	BD	301	ARG
1	BD	378	ARG
1	BD	384	ASN

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Mol	Chain	Res	Type
1	BD	449	GLU
1	BD	454	ASN
1	BD	475	LEU
1	BD	504	VAL
1	BE	105	SER
1	BE	129	ARG
1	BE	160	THR
1	BE	161	SER
1	BE	163	LEU
1	BE	167	THR
1	BE	182	LEU
1	BE	191	LEU
1	BE	199	SER
1	BE	226	VAL
1	BE	243	ILE
1	BE	260	MET
1	BE	272	TYR
1	BE	284	ARG
1	BE	289	ARG
1	BE	300	GLN
1	BE	301	ARG
1	BE	378	ARG
1	BE	384	ASN
1	BE	449	GLU
1	BE	454	ASN
1	BE	475	LEU
1	BE	504	VAL
1	BF	10	ILE
1	BF	18	ARG
1	BF	79	ARG
1	BF	105	SER
1	BF	129	ARG
1	BF	160	THR
1	BF	161	SER
1	BF	163	LEU
1	BF	167	THR
1	BF	182	LEU
1	BF	191	LEU
1	BF	199	SER
1	BF	226	VAL
1	BF	243	ILE
1	BF	260	MET

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Mol	Chain	Res	Type
1	BF	272	TYR
1	BF	284	ARG
1	BF	289	ARG
1	BF	299	SER
1	BF	301	ARG
1	BF	378	ARG
1	BF	384	ASN
1	BF	449	GLU
1	BF	454	ASN
1	BF	475	LEU
1	BF	504	VAL
1	BG	105	SER
1	BG	129	ARG
1	BG	160	THR
1	BG	161	SER
1	BG	163	LEU
1	BG	167	THR
1	BG	182	LEU
1	BG	191	LEU
1	BG	199	SER
1	BG	226	VAL
1	BG	229	MET
1	BG	243	ILE
1	BG	260	MET
1	BG	272	TYR
1	BG	284	ARG
1	BG	289	ARG
1	BG	301	ARG
1	BG	378	ARG
1	BG	384	ASN
1	BG	454	ASN
1	BG	475	LEU
1	BG	504	VAL
1	BH	15	GLN
1	BH	18	ARG
1	BH	105	SER
1	BH	129	ARG
1	BH	160	THR
1	BH	161	SER
1	BH	163	LEU
1	BH	167	THR
1	BH	182	LEU

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Mol	Chain	Res	Type
1	BH	191	LEU
1	BH	199	SER
1	BH	226	VAL
1	BH	229	MET
1	BH	243	ILE
1	BH	260	MET
1	BH	272	TYR
1	BH	284	ARG
1	BH	289	ARG
1	BH	301	ARG
1	BH	305	SER
1	BH	378	ARG
1	BH	384	ASN
1	BH	449	GLU
1	BH	454	ASN
1	BH	475	LEU
1	BH	504	VAL
1	BI	105	SER
1	BI	129	ARG
1	BI	160	THR
1	BI	161	SER
1	BI	163	LEU
1	BI	167	THR
1	BI	182	LEU
1	BI	191	LEU
1	BI	199	SER
1	BI	226	VAL
1	BI	243	ILE
1	BI	260	MET
1	BI	272	TYR
1	BI	284	ARG
1	BI	289	ARG
1	BI	301	ARG
1	BI	378	ARG
1	BI	384	ASN
1	BI	449	GLU
1	BI	454	ASN
1	BI	475	LEU
1	BI	504	VAL
1	BJ	18	ARG
1	BJ	79	ARG
1	BJ	105	SER

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Mol	Chain	Res	Type
1	BJ	129	ARG
1	BJ	160	THR
1	BJ	161	SER
1	BJ	163	LEU
1	BJ	167	THR
1	BJ	182	LEU
1	BJ	191	LEU
1	BJ	199	SER
1	BJ	226	VAL
1	BJ	243	ILE
1	BJ	260	MET
1	BJ	272	TYR
1	BJ	284	ARG
1	BJ	289	ARG
1	BJ	301	ARG
1	BJ	378	ARG
1	BJ	384	ASN
1	BJ	449	GLU
1	BJ	454	ASN
1	BJ	475	LEU
1	BJ	504	VAL
1	BK	18	ARG
1	BK	105	SER
1	BK	129	ARG
1	BK	160	THR
1	BK	161	SER
1	BK	163	LEU
1	BK	167	THR
1	BK	182	LEU
1	BK	191	LEU
1	BK	199	SER
1	BK	226	VAL
1	BK	229	MET
1	BK	243	ILE
1	BK	260	MET
1	BK	272	TYR
1	BK	284	ARG
1	BK	289	ARG
1	BK	299	SER
1	BK	300	GLN
1	BK	301	ARG
1	BK	378	ARG

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Mol	Chain	Res	Type
1	BK	384	ASN
1	BK	449	GLU
1	BK	454	ASN
1	BK	475	LEU
1	BK	504	VAL
1	BL	9	TYR
1	BL	79	ARG
1	BL	105	SER
1	BL	129	ARG
1	BL	160	THR
1	BL	161	SER
1	BL	163	LEU
1	BL	167	THR
1	BL	182	LEU
1	BL	191	LEU
1	BL	199	SER
1	BL	226	VAL
1	BL	229	MET
1	BL	243	ILE
1	BL	260	MET
1	BL	272	TYR
1	BL	284	ARG
1	BL	289	ARG
1	BL	299	SER
1	BL	300	GLN
1	BL	301	ARG
1	BL	378	ARG
1	BL	384	ASN
1	BL	449	GLU
1	BL	454	ASN
1	BL	475	LEU
1	BL	504	VAL
1	BM	18	ARG
1	BM	57	PRO
1	BM	79	ARG
1	BM	105	SER
1	BM	129	ARG
1	BM	160	THR
1	BM	161	SER
1	BM	163	LEU
1	BM	167	THR
1	BM	182	LEU

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Mol	Chain	Res	Type
1	BM	191	LEU
1	BM	199	SER
1	BM	226	VAL
1	BM	243	ILE
1	BM	260	MET
1	BM	272	TYR
1	BM	284	ARG
1	BM	289	ARG
1	BM	300	GLN
1	BM	301	ARG
1	BM	378	ARG
1	BM	384	ASN
1	BM	449	GLU
1	BM	454	ASN
1	BM	475	LEU
1	BM	504	VAL
1	BN	18	ARG
1	BN	105	SER
1	BN	129	ARG
1	BN	160	THR
1	BN	161	SER
1	BN	163	LEU
1	BN	167	THR
1	BN	182	LEU
1	BN	191	LEU
1	BN	199	SER
1	BN	226	VAL
1	BN	229	MET
1	BN	243	ILE
1	BN	260	MET
1	BN	272	TYR
1	BN	284	ARG
1	BN	285	SER
1	BN	289	ARG
1	BN	301	ARG
1	BN	378	ARG
1	BN	384	ASN
1	BN	449	GLU
1	BN	454	ASN
1	BN	475	LEU
1	BN	504	VAL
1	BO	15	GLN

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Mol	Chain	Res	Type
1	BO	105	SER
1	BO	129	ARG
1	BO	160	THR
1	BO	161	SER
1	BO	163	LEU
1	BO	167	THR
1	BO	182	LEU
1	BO	191	LEU
1	BO	199	SER
1	BO	226	VAL
1	BO	243	ILE
1	BO	260	MET
1	BO	284	ARG
1	BO	289	ARG
1	BO	301	ARG
1	BO	336	PRO
1	BO	378	ARG
1	BO	384	ASN
1	BO	449	GLU
1	BO	454	ASN
1	BO	475	LEU
1	BO	504	VAL
1	BP	79	ARG
1	BP	105	SER
1	BP	160	THR
1	BP	161	SER
1	BP	163	LEU
1	BP	167	THR
1	BP	182	LEU
1	BP	191	LEU
1	BP	199	SER
1	BP	226	VAL
1	BP	243	ILE
1	BP	260	MET
1	BP	272	TYR
1	BP	284	ARG
1	BP	289	ARG
1	BP	300	GLN
1	BP	301	ARG
1	BP	378	ARG
1	BP	384	ASN
1	BP	449	GLU

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Mol	Chain	Res	Type
1	BP	454	ASN
1	BP	475	LEU
1	BP	504	VAL
1	BQ	18	ARG
1	BQ	105	SER
1	BQ	129	ARG
1	BQ	160	THR
1	BQ	161	SER
1	BQ	163	LEU
1	BQ	167	THR
1	BQ	182	LEU
1	BQ	191	LEU
1	BQ	199	SER
1	BQ	226	VAL
1	BQ	229	MET
1	BQ	243	ILE
1	BQ	260	MET
1	BQ	272	TYR
1	BQ	284	ARG
1	BQ	289	ARG
1	BQ	301	ARG
1	BQ	378	ARG
1	BQ	384	ASN
1	BQ	404	LEU
1	BQ	449	GLU
1	BQ	454	ASN
1	BQ	475	LEU
1	BQ	504	VAL
1	BR	79	ARG
1	BR	105	SER
1	BR	160	THR
1	BR	161	SER
1	BR	163	LEU
1	BR	167	THR
1	BR	182	LEU
1	BR	191	LEU
1	BR	199	SER
1	BR	226	VAL
1	BR	243	ILE
1	BR	260	MET
1	BR	272	TYR
1	BR	284	ARG

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Mol	Chain	Res	Type
1	BR	289	ARG
1	BR	299	SER
1	BR	301	ARG
1	BR	378	ARG
1	BR	384	ASN
1	BR	449	GLU
1	BR	454	ASN
1	BR	475	LEU
1	BR	504	VAL
1	BS	79	ARG
1	BS	105	SER
1	BS	129	ARG
1	BS	160	THR
1	BS	161	SER
1	BS	163	LEU
1	BS	167	THR
1	BS	182	LEU
1	BS	191	LEU
1	BS	199	SER
1	BS	226	VAL
1	BS	243	ILE
1	BS	260	MET
1	BS	284	ARG
1	BS	289	ARG
1	BS	299	SER
1	BS	301	ARG
1	BS	336	PRO
1	BS	378	ARG
1	BS	384	ASN
1	BS	449	GLU
1	BS	454	ASN
1	BS	475	LEU
1	BS	504	VAL
1	BT	105	SER
1	BT	129	ARG
1	BT	160	THR
1	BT	161	SER
1	BT	163	LEU
1	BT	167	THR
1	BT	182	LEU
1	BT	191	LEU
1	BT	199	SER

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Mol	Chain	Res	Type
1	BT	226	VAL
1	BT	243	ILE
1	BT	260	MET
1	BT	272	TYR
1	BT	284	ARG
1	BT	289	ARG
1	BT	299	SER
1	BT	300	GLN
1	BT	301	ARG
1	BT	378	ARG
1	BT	384	ASN
1	BT	449	GLU
1	BT	454	ASN
1	BT	475	LEU
1	BT	504	VAL
1	CA	10	ILE
1	CA	18	ARG
1	CA	105	SER
1	CA	129	ARG
1	CA	160	THR
1	CA	161	SER
1	CA	163	LEU
1	CA	167	THR
1	CA	182	LEU
1	CA	191	LEU
1	CA	226	VAL
1	CA	243	ILE
1	CA	260	MET
1	CA	272	TYR
1	CA	284	ARG
1	CA	289	ARG
1	CA	301	ARG
1	CA	378	ARG
1	CA	384	ASN
1	CA	449	GLU
1	CA	454	ASN
1	CA	475	LEU
1	CA	504	VAL
1	CB	18	ARG
1	CB	105	SER
1	CB	129	ARG
1	CB	160	THR

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Mol	Chain	Res	Type
1	CB	161	SER
1	CB	163	LEU
1	CB	167	THR
1	CB	182	LEU
1	CB	191	LEU
1	CB	199	SER
1	CB	226	VAL
1	CB	243	ILE
1	CB	260	MET
1	CB	272	TYR
1	CB	284	ARG
1	CB	289	ARG
1	CB	300	GLN
1	CB	301	ARG
1	CB	378	ARG
1	CB	384	ASN
1	CB	449	GLU
1	CB	454	ASN
1	CB	475	LEU
1	CB	504	VAL
1	CC	105	SER
1	CC	129	ARG
1	CC	160	THR
1	CC	161	SER
1	CC	163	LEU
1	CC	167	THR
1	CC	182	LEU
1	CC	191	LEU
1	CC	199	SER
1	CC	226	VAL
1	CC	243	ILE
1	CC	260	MET
1	CC	272	TYR
1	CC	284	ARG
1	CC	289	ARG
1	CC	300	GLN
1	CC	301	ARG
1	CC	378	ARG
1	CC	384	ASN
1	CC	449	GLU
1	CC	454	ASN
1	CC	475	LEU

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Mol	Chain	Res	Type
1	CC	504	VAL
1	CD	79	ARG
1	CD	105	SER
1	CD	129	ARG
1	CD	160	THR
1	CD	161	SER
1	CD	163	LEU
1	CD	167	THR
1	CD	182	LEU
1	CD	191	LEU
1	CD	199	SER
1	CD	226	VAL
1	CD	229	MET
1	CD	243	ILE
1	CD	260	MET
1	CD	272	TYR
1	CD	284	ARG
1	CD	289	ARG
1	CD	301	ARG
1	CD	378	ARG
1	CD	384	ASN
1	CD	449	GLU
1	CD	454	ASN
1	CD	475	LEU
1	CD	504	VAL
1	CE	79	ARG
1	CE	105	SER
1	CE	129	ARG
1	CE	160	THR
1	CE	161	SER
1	CE	163	LEU
1	CE	167	THR
1	CE	182	LEU
1	CE	191	LEU
1	CE	199	SER
1	CE	226	VAL
1	CE	243	ILE
1	CE	260	MET
1	CE	272	TYR
1	CE	284	ARG
1	CE	289	ARG
1	CE	301	ARG

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Mol	Chain	Res	Type
1	CE	336	PRO
1	CE	378	ARG
1	CE	384	ASN
1	CE	449	GLU
1	CE	454	ASN
1	CE	475	LEU
1	CE	504	VAL
1	CF	79	ARG
1	CF	105	SER
1	CF	129	ARG
1	CF	160	THR
1	CF	161	SER
1	CF	163	LEU
1	CF	167	THR
1	CF	182	LEU
1	CF	191	LEU
1	CF	199	SER
1	CF	226	VAL
1	CF	243	ILE
1	CF	260	MET
1	CF	272	TYR
1	CF	284	ARG
1	CF	289	ARG
1	CF	300	GLN
1	CF	301	ARG
1	CF	378	ARG
1	CF	384	ASN
1	CF	449	GLU
1	CF	454	ASN
1	CF	475	LEU
1	CF	504	VAL
1	CG	79	ARG
1	CG	105	SER
1	CG	129	ARG
1	CG	160	THR
1	CG	161	SER
1	CG	163	LEU
1	CG	167	THR
1	CG	182	LEU
1	CG	191	LEU
1	CG	199	SER
1	CG	226	VAL

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Mol	Chain	Res	Type
1	CG	243	ILE
1	CG	260	MET
1	CG	272	TYR
1	CG	284	ARG
1	CG	289	ARG
1	CG	301	ARG
1	CG	378	ARG
1	CG	384	ASN
1	CG	454	ASN
1	CG	475	LEU
1	CG	504	VAL
1	CH	10	ILE
1	CH	15	GLN
1	CH	105	SER
1	CH	129	ARG
1	CH	160	THR
1	CH	161	SER
1	CH	163	LEU
1	CH	167	THR
1	CH	182	LEU
1	CH	191	LEU
1	CH	199	SER
1	CH	226	VAL
1	CH	229	MET
1	CH	243	ILE
1	CH	260	MET
1	CH	272	TYR
1	CH	284	ARG
1	CH	289	ARG
1	CH	301	ARG
1	CH	378	ARG
1	CH	384	ASN
1	CH	449	GLU
1	CH	454	ASN
1	CH	475	LEU
1	CH	504	VAL
1	CI	79	ARG
1	CI	105	SER
1	CI	129	ARG
1	CI	160	THR
1	CI	161	SER
1	CI	163	LEU

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Mol	Chain	Res	Type
1	CI	167	THR
1	CI	182	LEU
1	CI	191	LEU
1	CI	199	SER
1	CI	226	VAL
1	CI	243	ILE
1	CI	260	MET
1	CI	272	TYR
1	CI	284	ARG
1	CI	289	ARG
1	CI	299	SER
1	CI	301	ARG
1	CI	378	ARG
1	CI	384	ASN
1	CI	449	GLU
1	CI	454	ASN
1	CI	475	LEU
1	CI	504	VAL
1	CJ	18	ARG
1	CJ	105	SER
1	CJ	129	ARG
1	CJ	160	THR
1	CJ	161	SER
1	CJ	163	LEU
1	CJ	182	LEU
1	CJ	191	LEU
1	CJ	199	SER
1	CJ	226	VAL
1	CJ	243	ILE
1	CJ	260	MET
1	CJ	272	TYR
1	CJ	284	ARG
1	CJ	289	ARG
1	CJ	300	GLN
1	CJ	301	ARG
1	CJ	378	ARG
1	CJ	384	ASN
1	CJ	449	GLU
1	CJ	454	ASN
1	CJ	475	LEU
1	CJ	504	VAL
1	CK	18	ARG

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Mol	Chain	Res	Type
1	CK	77	THR
1	CK	105	SER
1	CK	129	ARG
1	CK	160	THR
1	CK	161	SER
1	CK	163	LEU
1	CK	167	THR
1	CK	182	LEU
1	CK	191	LEU
1	CK	199	SER
1	CK	226	VAL
1	CK	243	ILE
1	CK	260	MET
1	CK	272	TYR
1	CK	284	ARG
1	CK	289	ARG
1	CK	301	ARG
1	CK	378	ARG
1	CK	384	ASN
1	CK	449	GLU
1	CK	454	ASN
1	CK	475	LEU
1	CK	504	VAL
1	CL	9	TYR
1	CL	105	SER
1	CL	129	ARG
1	CL	160	THR
1	CL	161	SER
1	CL	163	LEU
1	CL	167	THR
1	CL	182	LEU
1	CL	191	LEU
1	CL	199	SER
1	CL	226	VAL
1	CL	229	MET
1	CL	243	ILE
1	CL	260	MET
1	CL	272	TYR
1	CL	284	ARG
1	CL	289	ARG
1	CL	299	SER
1	CL	301	ARG

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Mol	Chain	Res	Type
1	CL	378	ARG
1	CL	384	ASN
1	CL	449	GLU
1	CL	454	ASN
1	CL	475	LEU
1	CL	504	VAL
1	CM	10	ILE
1	CM	18	ARG
1	CM	57	PRO
1	CM	79	ARG
1	CM	105	SER
1	CM	129	ARG
1	CM	160	THR
1	CM	161	SER
1	CM	163	LEU
1	CM	167	THR
1	CM	182	LEU
1	CM	191	LEU
1	CM	199	SER
1	CM	226	VAL
1	CM	243	ILE
1	CM	260	MET
1	CM	272	TYR
1	CM	284	ARG
1	CM	289	ARG
1	CM	299	SER
1	CM	301	ARG
1	CM	378	ARG
1	CM	384	ASN
1	CM	449	GLU
1	CM	454	ASN
1	CM	475	LEU
1	CM	504	VAL
1	CN	105	SER
1	CN	160	THR
1	CN	161	SER
1	CN	163	LEU
1	CN	167	THR
1	CN	182	LEU
1	CN	191	LEU
1	CN	199	SER
1	CN	226	VAL

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Mol	Chain	Res	Type
1	CN	229	MET
1	CN	243	ILE
1	CN	260	MET
1	CN	272	TYR
1	CN	284	ARG
1	CN	289	ARG
1	CN	301	ARG
1	CN	336	PRO
1	CN	378	ARG
1	CN	384	ASN
1	CN	449	GLU
1	CN	454	ASN
1	CN	475	LEU
1	CN	504	VAL
1	CO	57	PRO
1	CO	79	ARG
1	CO	105	SER
1	CO	160	THR
1	CO	161	SER
1	CO	163	LEU
1	CO	167	THR
1	CO	191	LEU
1	CO	199	SER
1	CO	226	VAL
1	CO	243	ILE
1	CO	260	MET
1	CO	272	TYR
1	CO	284	ARG
1	CO	289	ARG
1	CO	301	ARG
1	CO	378	ARG
1	CO	384	ASN
1	CO	449	GLU
1	CO	454	ASN
1	CO	475	LEU
1	CO	504	VAL
1	CP	10	ILE
1	CP	79	ARG
1	CP	105	SER
1	CP	129	ARG
1	CP	160	THR
1	CP	161	SER

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Mol	Chain	Res	Type
1	CP	163	LEU
1	CP	167	THR
1	CP	182	LEU
1	CP	191	LEU
1	CP	199	SER
1	CP	226	VAL
1	CP	243	ILE
1	CP	260	MET
1	CP	272	TYR
1	CP	284	ARG
1	CP	289	ARG
1	CP	300	GLN
1	CP	301	ARG
1	CP	378	ARG
1	CP	384	ASN
1	CP	449	GLU
1	CP	454	ASN
1	CP	475	LEU
1	CP	504	VAL
1	CQ	18	ARG
1	CQ	105	SER
1	CQ	129	ARG
1	CQ	160	THR
1	CQ	161	SER
1	CQ	163	LEU
1	CQ	167	THR
1	CQ	182	LEU
1	CQ	191	LEU
1	CQ	199	SER
1	CQ	226	VAL
1	CQ	229	MET
1	CQ	243	ILE
1	CQ	260	MET
1	CQ	272	TYR
1	CQ	284	ARG
1	CQ	289	ARG
1	CQ	300	GLN
1	CQ	301	ARG
1	CQ	336	PRO
1	CQ	378	ARG
1	CQ	384	ASN
1	CQ	449	GLU

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Mol	Chain	Res	Type
1	CQ	454	ASN
1	CQ	475	LEU
1	CQ	504	VAL
1	CR	78	SER
1	CR	79	ARG
1	CR	105	SER
1	CR	160	THR
1	CR	161	SER
1	CR	163	LEU
1	CR	167	THR
1	CR	182	LEU
1	CR	191	LEU
1	CR	199	SER
1	CR	226	VAL
1	CR	229	MET
1	CR	243	ILE
1	CR	260	MET
1	CR	272	TYR
1	CR	284	ARG
1	CR	289	ARG
1	CR	299	SER
1	CR	301	ARG
1	CR	378	ARG
1	CR	384	ASN
1	CR	449	GLU
1	CR	454	ASN
1	CR	475	LEU
1	CR	504	VAL
1	CS	105	SER
1	CS	160	THR
1	CS	161	SER
1	CS	163	LEU
1	CS	167	THR
1	CS	182	LEU
1	CS	191	LEU
1	CS	199	SER
1	CS	226	VAL
1	CS	229	MET
1	CS	243	ILE
1	CS	260	MET
1	CS	272	TYR
1	CS	284	ARG

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Mol	Chain	Res	Type
1	CS	289	ARG
1	CS	299	SER
1	CS	301	ARG
1	CS	378	ARG
1	CS	384	ASN
1	CS	449	GLU
1	CS	454	ASN
1	CS	475	LEU
1	CS	504	VAL
1	CT	105	SER
1	CT	129	ARG
1	CT	160	THR
1	CT	161	SER
1	CT	163	LEU
1	CT	167	THR
1	CT	182	LEU
1	CT	191	LEU
1	CT	199	SER
1	CT	226	VAL
1	CT	229	MET
1	CT	243	ILE
1	CT	260	MET
1	CT	272	TYR
1	CT	284	ARG
1	CT	289	ARG
1	CT	299	SER
1	CT	301	ARG
1	CT	336	PRO
1	CT	378	ARG
1	CT	384	ASN
1	CT	449	GLU
1	CT	454	ASN
1	CT	475	LEU
1	CT	504	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (662) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	36	GLN
1	AA	74	ASN
1	AA	131	HIS
1	AA	138	ASN

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Mol	Chain	Res	Type
1	AA	238	HIS
1	AA	256	ASN
1	AA	263	ASN
1	AA	288	HIS
1	AA	300	GLN
1	AA	437	HIS
1	AA	454	ASN
1	AB	36	GLN
1	AB	74	ASN
1	AB	131	HIS
1	AB	138	ASN
1	AB	147	GLN
1	AB	238	HIS
1	AB	256	ASN
1	AB	263	ASN
1	AB	288	HIS
1	AB	300	GLN
1	AB	454	ASN
1	AC	36	GLN
1	AC	74	ASN
1	AC	131	HIS
1	AC	138	ASN
1	AC	147	GLN
1	AC	238	HIS
1	AC	256	ASN
1	AC	263	ASN
1	AC	288	HIS
1	AC	300	GLN
1	AC	437	HIS
1	AC	454	ASN
1	AD	36	GLN
1	AD	74	ASN
1	AD	131	HIS
1	AD	138	ASN
1	AD	147	GLN
1	AD	238	HIS
1	AD	256	ASN
1	AD	263	ASN
1	AD	288	HIS
1	AD	454	ASN
1	AE	36	GLN
1	AE	74	ASN

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Mol	Chain	Res	Type
1	AE	131	HIS
1	AE	138	ASN
1	AE	147	GLN
1	AE	238	HIS
1	AE	256	ASN
1	AE	263	ASN
1	AE	288	HIS
1	AE	454	ASN
1	AF	15	GLN
1	AF	36	GLN
1	AF	74	ASN
1	AF	131	HIS
1	AF	138	ASN
1	AF	147	GLN
1	AF	238	HIS
1	AF	256	ASN
1	AF	263	ASN
1	AF	288	HIS
1	AF	300	GLN
1	AF	454	ASN
1	AG	15	GLN
1	AG	36	GLN
1	AG	74	ASN
1	AG	131	HIS
1	AG	138	ASN
1	AG	238	HIS
1	AG	256	ASN
1	AG	263	ASN
1	AG	288	HIS
1	AG	300	GLN
1	AG	454	ASN
1	AH	15	GLN
1	AH	36	GLN
1	AH	74	ASN
1	AH	131	HIS
1	AH	138	ASN
1	AH	238	HIS
1	AH	256	ASN
1	AH	263	ASN
1	AH	288	HIS
1	AH	300	GLN
1	AH	454	ASN

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Mol	Chain	Res	Type
1	AI	36	GLN
1	AI	74	ASN
1	AI	131	HIS
1	AI	138	ASN
1	AI	238	HIS
1	AI	256	ASN
1	AI	263	ASN
1	AI	288	HIS
1	AI	300	GLN
1	AI	454	ASN
1	AJ	15	GLN
1	AJ	36	GLN
1	AJ	74	ASN
1	AJ	131	HIS
1	AJ	138	ASN
1	AJ	147	GLN
1	AJ	238	HIS
1	AJ	256	ASN
1	AJ	263	ASN
1	AJ	288	HIS
1	AJ	454	ASN
1	AK	36	GLN
1	AK	74	ASN
1	AK	131	HIS
1	AK	138	ASN
1	AK	147	GLN
1	AK	238	HIS
1	AK	256	ASN
1	AK	263	ASN
1	AK	288	HIS
1	AK	300	GLN
1	AK	437	HIS
1	AK	454	ASN
1	AL	36	GLN
1	AL	74	ASN
1	AL	131	HIS
1	AL	138	ASN
1	AL	147	GLN
1	AL	238	HIS
1	AL	256	ASN
1	AL	263	ASN
1	AL	288	HIS

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Mol	Chain	Res	Type
1	AL	454	ASN
1	AM	36	GLN
1	AM	74	ASN
1	AM	131	HIS
1	AM	138	ASN
1	AM	238	HIS
1	AM	256	ASN
1	AM	263	ASN
1	AM	288	HIS
1	AM	454	ASN
1	AN	36	GLN
1	AN	74	ASN
1	AN	131	HIS
1	AN	138	ASN
1	AN	147	GLN
1	AN	238	HIS
1	AN	256	ASN
1	AN	263	ASN
1	AN	288	HIS
1	AN	300	GLN
1	AN	454	ASN
1	AO	36	GLN
1	AO	74	ASN
1	AO	131	HIS
1	AO	138	ASN
1	AO	147	GLN
1	AO	238	HIS
1	AO	256	ASN
1	AO	263	ASN
1	AO	288	HIS
1	AO	300	GLN
1	AO	437	HIS
1	AO	454	ASN
1	AP	36	GLN
1	AP	74	ASN
1	AP	131	HIS
1	AP	138	ASN
1	AP	147	GLN
1	AP	238	HIS
1	AP	256	ASN
1	AP	263	ASN
1	AP	288	HIS

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Mol	Chain	Res	Type
1	AP	300	GLN
1	AP	437	HIS
1	AP	454	ASN
1	AQ	36	GLN
1	AQ	74	ASN
1	AQ	131	HIS
1	AQ	138	ASN
1	AQ	147	GLN
1	AQ	238	HIS
1	AQ	256	ASN
1	AQ	263	ASN
1	AQ	288	HIS
1	AQ	300	GLN
1	AQ	454	ASN
1	AR	36	GLN
1	AR	74	ASN
1	AR	131	HIS
1	AR	138	ASN
1	AR	147	GLN
1	AR	238	HIS
1	AR	256	ASN
1	AR	263	ASN
1	AR	288	HIS
1	AR	300	GLN
1	AR	454	ASN
1	AS	36	GLN
1	AS	74	ASN
1	AS	131	HIS
1	AS	138	ASN
1	AS	147	GLN
1	AS	238	HIS
1	AS	256	ASN
1	AS	263	ASN
1	AS	288	HIS
1	AS	300	GLN
1	AS	437	HIS
1	AS	454	ASN
1	AT	36	GLN
1	AT	74	ASN
1	AT	131	HIS
1	AT	138	ASN
1	AT	147	GLN

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Mol	Chain	Res	Type
1	AT	238	HIS
1	AT	256	ASN
1	AT	263	ASN
1	AT	288	HIS
1	AT	300	GLN
1	AT	454	ASN
1	BA	36	GLN
1	BA	74	ASN
1	BA	131	HIS
1	BA	138	ASN
1	BA	147	GLN
1	BA	238	HIS
1	BA	256	ASN
1	BA	263	ASN
1	BA	288	HIS
1	BA	300	GLN
1	BA	454	ASN
1	BB	36	GLN
1	BB	74	ASN
1	BB	131	HIS
1	BB	138	ASN
1	BB	147	GLN
1	BB	238	HIS
1	BB	256	ASN
1	BB	263	ASN
1	BB	288	HIS
1	BB	300	GLN
1	BB	437	HIS
1	BB	454	ASN
1	BC	36	GLN
1	BC	74	ASN
1	BC	131	HIS
1	BC	138	ASN
1	BC	147	GLN
1	BC	238	HIS
1	BC	256	ASN
1	BC	263	ASN
1	BC	288	HIS
1	BC	300	GLN
1	BC	437	HIS
1	BC	454	ASN
1	BD	36	GLN

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Mol	Chain	Res	Type
1	BD	74	ASN
1	BD	131	HIS
1	BD	138	ASN
1	BD	147	GLN
1	BD	238	HIS
1	BD	256	ASN
1	BD	263	ASN
1	BD	288	HIS
1	BD	300	GLN
1	BD	454	ASN
1	BE	36	GLN
1	BE	74	ASN
1	BE	131	HIS
1	BE	138	ASN
1	BE	147	GLN
1	BE	238	HIS
1	BE	256	ASN
1	BE	263	ASN
1	BE	288	HIS
1	BE	300	GLN
1	BE	454	ASN
1	BF	15	GLN
1	BF	36	GLN
1	BF	74	ASN
1	BF	131	HIS
1	BF	138	ASN
1	BF	147	GLN
1	BF	238	HIS
1	BF	256	ASN
1	BF	263	ASN
1	BF	288	HIS
1	BF	300	GLN
1	BF	437	HIS
1	BF	454	ASN
1	BG	15	GLN
1	BG	36	GLN
1	BG	74	ASN
1	BG	131	HIS
1	BG	138	ASN
1	BG	147	GLN
1	BG	238	HIS
1	BG	256	ASN

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Mol	Chain	Res	Type
1	BG	263	ASN
1	BG	288	HIS
1	BG	300	GLN
1	BG	454	ASN
1	BH	15	GLN
1	BH	36	GLN
1	BH	74	ASN
1	BH	131	HIS
1	BH	138	ASN
1	BH	147	GLN
1	BH	238	HIS
1	BH	256	ASN
1	BH	263	ASN
1	BH	288	HIS
1	BH	454	ASN
1	BI	36	GLN
1	BI	74	ASN
1	BI	131	HIS
1	BI	138	ASN
1	BI	147	GLN
1	BI	238	HIS
1	BI	256	ASN
1	BI	263	ASN
1	BI	288	HIS
1	BI	300	GLN
1	BI	454	ASN
1	BJ	36	GLN
1	BJ	74	ASN
1	BJ	131	HIS
1	BJ	138	ASN
1	BJ	238	HIS
1	BJ	256	ASN
1	BJ	263	ASN
1	BJ	288	HIS
1	BJ	300	GLN
1	BJ	437	HIS
1	BJ	454	ASN
1	BK	36	GLN
1	BK	74	ASN
1	BK	131	HIS
1	BK	138	ASN
1	BK	147	GLN

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Mol	Chain	Res	Type
1	BK	238	HIS
1	BK	256	ASN
1	BK	263	ASN
1	BK	288	HIS
1	BK	454	ASN
1	BL	36	GLN
1	BL	74	ASN
1	BL	131	HIS
1	BL	138	ASN
1	BL	147	GLN
1	BL	238	HIS
1	BL	256	ASN
1	BL	263	ASN
1	BL	288	HIS
1	BL	300	GLN
1	BL	437	HIS
1	BL	454	ASN
1	BM	36	GLN
1	BM	74	ASN
1	BM	131	HIS
1	BM	138	ASN
1	BM	147	GLN
1	BM	238	HIS
1	BM	256	ASN
1	BM	263	ASN
1	BM	288	HIS
1	BM	300	GLN
1	BM	437	HIS
1	BM	454	ASN
1	BN	36	GLN
1	BN	74	ASN
1	BN	131	HIS
1	BN	138	ASN
1	BN	238	HIS
1	BN	256	ASN
1	BN	263	ASN
1	BN	288	HIS
1	BN	454	ASN
1	BO	15	GLN
1	BO	36	GLN
1	BO	74	ASN
1	BO	131	HIS

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Mol	Chain	Res	Type
1	BO	138	ASN
1	BO	147	GLN
1	BO	238	HIS
1	BO	256	ASN
1	BO	263	ASN
1	BO	288	HIS
1	BO	300	GLN
1	BO	454	ASN
1	BP	36	GLN
1	BP	74	ASN
1	BP	131	HIS
1	BP	138	ASN
1	BP	147	GLN
1	BP	238	HIS
1	BP	256	ASN
1	BP	263	ASN
1	BP	288	HIS
1	BP	300	GLN
1	BP	437	HIS
1	BP	454	ASN
1	BQ	36	GLN
1	BQ	74	ASN
1	BQ	131	HIS
1	BQ	138	ASN
1	BQ	147	GLN
1	BQ	238	HIS
1	BQ	256	ASN
1	BQ	263	ASN
1	BQ	288	HIS
1	BQ	454	ASN
1	BR	36	GLN
1	BR	74	ASN
1	BR	131	HIS
1	BR	138	ASN
1	BR	147	GLN
1	BR	238	HIS
1	BR	256	ASN
1	BR	263	ASN
1	BR	288	HIS
1	BR	300	GLN
1	BR	437	HIS
1	BR	454	ASN

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Mol	Chain	Res	Type
1	BS	36	GLN
1	BS	74	ASN
1	BS	131	HIS
1	BS	138	ASN
1	BS	147	GLN
1	BS	238	HIS
1	BS	256	ASN
1	BS	263	ASN
1	BS	288	HIS
1	BS	300	GLN
1	BS	454	ASN
1	BT	36	GLN
1	BT	74	ASN
1	BT	131	HIS
1	BT	138	ASN
1	BT	147	GLN
1	BT	238	HIS
1	BT	256	ASN
1	BT	263	ASN
1	BT	288	HIS
1	BT	300	GLN
1	BT	454	ASN
1	CA	36	GLN
1	CA	74	ASN
1	CA	131	HIS
1	CA	138	ASN
1	CA	238	HIS
1	CA	256	ASN
1	CA	263	ASN
1	CA	288	HIS
1	CA	454	ASN
1	CB	36	GLN
1	CB	74	ASN
1	CB	131	HIS
1	CB	138	ASN
1	CB	238	HIS
1	CB	256	ASN
1	CB	263	ASN
1	CB	288	HIS
1	CB	300	GLN
1	CB	454	ASN
1	CC	36	GLN

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Mol	Chain	Res	Type
1	CC	74	ASN
1	CC	131	HIS
1	CC	147	GLN
1	CC	238	HIS
1	CC	256	ASN
1	CC	263	ASN
1	CC	288	HIS
1	CC	300	GLN
1	CC	454	ASN
1	CD	36	GLN
1	CD	74	ASN
1	CD	131	HIS
1	CD	138	ASN
1	CD	147	GLN
1	CD	238	HIS
1	CD	256	ASN
1	CD	263	ASN
1	CD	288	HIS
1	CD	454	ASN
1	CE	36	GLN
1	CE	74	ASN
1	CE	131	HIS
1	CE	138	ASN
1	CE	147	GLN
1	CE	238	HIS
1	CE	256	ASN
1	CE	263	ASN
1	CE	288	HIS
1	CE	454	ASN
1	CF	36	GLN
1	CF	74	ASN
1	CF	131	HIS
1	CF	138	ASN
1	CF	147	GLN
1	CF	238	HIS
1	CF	256	ASN
1	CF	263	ASN
1	CF	288	HIS
1	CF	300	GLN
1	CF	454	ASN
1	CG	36	GLN
1	CG	74	ASN

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Mol	Chain	Res	Type
1	CG	131	HIS
1	CG	138	ASN
1	CG	147	GLN
1	CG	238	HIS
1	CG	256	ASN
1	CG	263	ASN
1	CG	288	HIS
1	CG	300	GLN
1	CG	437	HIS
1	CG	454	ASN
1	CH	15	GLN
1	CH	36	GLN
1	CH	74	ASN
1	CH	131	HIS
1	CH	138	ASN
1	CH	238	HIS
1	CH	256	ASN
1	CH	263	ASN
1	CH	288	HIS
1	CH	437	HIS
1	CH	454	ASN
1	CI	36	GLN
1	CI	74	ASN
1	CI	131	HIS
1	CI	138	ASN
1	CI	147	GLN
1	CI	238	HIS
1	CI	256	ASN
1	CI	263	ASN
1	CI	288	HIS
1	CI	300	GLN
1	CI	437	HIS
1	CI	454	ASN
1	CJ	15	GLN
1	CJ	36	GLN
1	CJ	74	ASN
1	CJ	131	HIS
1	CJ	138	ASN
1	CJ	238	HIS
1	CJ	256	ASN
1	CJ	263	ASN
1	CJ	288	HIS

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Mol	Chain	Res	Type
1	CJ	300	GLN
1	CJ	454	ASN
1	CK	36	GLN
1	CK	74	ASN
1	CK	131	HIS
1	CK	138	ASN
1	CK	147	GLN
1	CK	238	HIS
1	CK	256	ASN
1	CK	263	ASN
1	CK	288	HIS
1	CK	454	ASN
1	CL	36	GLN
1	CL	74	ASN
1	CL	131	HIS
1	CL	138	ASN
1	CL	147	GLN
1	CL	238	HIS
1	CL	256	ASN
1	CL	263	ASN
1	CL	288	HIS
1	CL	454	ASN
1	CM	36	GLN
1	CM	74	ASN
1	CM	131	HIS
1	CM	138	ASN
1	CM	147	GLN
1	CM	238	HIS
1	CM	256	ASN
1	CM	263	ASN
1	CM	288	HIS
1	CM	454	ASN
1	CN	36	GLN
1	CN	74	ASN
1	CN	131	HIS
1	CN	138	ASN
1	CN	147	GLN
1	CN	238	HIS
1	CN	256	ASN
1	CN	263	ASN
1	CN	288	HIS
1	CN	300	GLN

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Mol	Chain	Res	Type
1	CN	437	HIS
1	CN	454	ASN
1	CO	36	GLN
1	CO	74	ASN
1	CO	131	HIS
1	CO	138	ASN
1	CO	147	GLN
1	CO	238	HIS
1	CO	256	ASN
1	CO	263	ASN
1	CO	288	HIS
1	CO	300	GLN
1	CO	454	ASN
1	CP	36	GLN
1	CP	74	ASN
1	CP	131	HIS
1	CP	138	ASN
1	CP	147	GLN
1	CP	238	HIS
1	CP	256	ASN
1	CP	263	ASN
1	CP	288	HIS
1	CP	300	GLN
1	CP	454	ASN
1	CQ	36	GLN
1	CQ	74	ASN
1	CQ	131	HIS
1	CQ	138	ASN
1	CQ	147	GLN
1	CQ	238	HIS
1	CQ	256	ASN
1	CQ	263	ASN
1	CQ	288	HIS
1	CQ	300	GLN
1	CQ	454	ASN
1	CR	36	GLN
1	CR	74	ASN
1	CR	131	HIS
1	CR	138	ASN
1	CR	147	GLN
1	CR	238	HIS
1	CR	256	ASN

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Mol	Chain	Res	Type
1	CR	263	ASN
1	CR	288	HIS
1	CR	300	GLN
1	CR	437	HIS
1	CR	454	ASN
1	CS	36	GLN
1	CS	74	ASN
1	CS	131	HIS
1	CS	138	ASN
1	CS	147	GLN
1	CS	238	HIS
1	CS	256	ASN
1	CS	263	ASN
1	CS	288	HIS
1	CS	437	HIS
1	CS	454	ASN
1	CT	15	GLN
1	CT	36	GLN
1	CT	74	ASN
1	CT	131	HIS
1	CT	138	ASN
1	CT	238	HIS
1	CT	256	ASN
1	CT	263	ASN
1	CT	288	HIS
1	CT	300	GLN
1	CT	437	HIS
1	CT	454	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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	AA	504/504 (100%)	-0.59	0	100 100	23, 33, 53, 78	0
1	AB	504/504 (100%)	-0.62	0	100 100	22, 34, 54, 78	0
1	AC	504/504 (100%)	-0.58	0	100 100	23, 34, 54, 78	0
1	AD	504/504 (100%)	-0.59	0	100 100	22, 33, 52, 78	0
1	AE	504/504 (100%)	-0.53	0	100 100	17, 31, 52, 77	0
1	AF	504/504 (100%)	-0.63	0	100 100	24, 34, 54, 80	0
1	AG	504/504 (100%)	-0.62	0	100 100	23, 34, 55, 80	0
1	AH	504/504 (100%)	-0.62	0	100 100	24, 35, 56, 79	0
1	AI	504/504 (100%)	-0.61	0	100 100	23, 34, 55, 80	0
1	AJ	504/504 (100%)	-0.57	0	100 100	22, 34, 54, 80	0
1	AK	504/504 (100%)	-0.61	0	100 100	23, 34, 55, 79	0
1	AL	504/504 (100%)	-0.57	0	100 100	23, 33, 54, 77	0
1	AM	504/504 (100%)	-0.58	0	100 100	21, 32, 52, 77	0
1	AN	504/504 (100%)	-0.55	0	100 100	22, 33, 54, 78	0
1	AO	504/504 (100%)	-0.53	0	100 100	21, 33, 54, 80	0
1	AP	504/504 (100%)	-0.55	0	100 100	19, 32, 53, 79	0
1	AQ	504/504 (100%)	-0.61	0	100 100	23, 33, 54, 77	0
1	AR	504/504 (100%)	-0.57	0	100 100	21, 32, 52, 77	0
1	AS	504/504 (100%)	-0.59	0	100 100	23, 33, 54, 80	0
1	AT	504/504 (100%)	-0.55	0	100 100	22, 33, 54, 77	0
1	BA	504/504 (100%)	-0.59	0	100 100	23, 33, 54, 79	0
1	BB	504/504 (100%)	-0.59	0	100 100	23, 34, 55, 77	0
1	BC	504/504 (100%)	-0.60	0	100 100	23, 34, 54, 78	0
1	BD	504/504 (100%)	-0.57	0	100 100	23, 34, 54, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
1	BE	504/504 (100%)	-0.58	0	100	100	23, 33, 54, 77	0
1	BF	504/504 (100%)	-0.54	0	100	100	22, 35, 56, 80	0
1	BG	504/504 (100%)	-0.62	0	100	100	22, 34, 54, 79	0
1	BH	504/504 (100%)	-0.61	0	100	100	21, 33, 54, 75	0
1	BI	504/504 (100%)	-0.53	0	100	100	22, 32, 54, 78	0
1	BJ	504/504 (100%)	-0.60	0	100	100	22, 34, 54, 79	0
1	BK	504/504 (100%)	-0.61	0	100	100	22, 33, 53, 77	0
1	BL	504/504 (100%)	-0.57	0	100	100	21, 32, 52, 75	0
1	BM	504/504 (100%)	-0.51	0	100	100	21, 32, 52, 77	0
1	BN	504/504 (100%)	-0.57	0	100	100	20, 33, 53, 76	0
1	BO	504/504 (100%)	-0.58	0	100	100	22, 33, 53, 80	0
1	BP	504/504 (100%)	-0.50	1 (0%)	95	87	21, 32, 53, 76	0
1	BQ	504/504 (100%)	-0.57	0	100	100	22, 33, 54, 80	0
1	BR	504/504 (100%)	-0.60	0	100	100	22, 33, 54, 79	0
1	BS	504/504 (100%)	-0.57	0	100	100	22, 33, 54, 80	0
1	BT	504/504 (100%)	-0.61	0	100	100	22, 34, 53, 77	0
1	CA	504/504 (100%)	-0.61	0	100	100	23, 35, 56, 80	0
1	CB	504/504 (100%)	-0.64	0	100	100	23, 34, 54, 77	0
1	CC	504/504 (100%)	-0.61	0	100	100	23, 34, 54, 81	0
1	CD	504/504 (100%)	-0.60	0	100	100	23, 34, 54, 79	0
1	CE	504/504 (100%)	-0.61	0	100	100	23, 33, 54, 78	0
1	CF	504/504 (100%)	-0.61	0	100	100	23, 34, 55, 80	0
1	CG	504/504 (100%)	-0.58	0	100	100	24, 34, 55, 81	0
1	CH	504/504 (100%)	-0.60	0	100	100	24, 34, 55, 79	0
1	CI	504/504 (100%)	-0.59	0	100	100	23, 33, 53, 79	0
1	CJ	504/504 (100%)	-0.57	0	100	100	24, 33, 54, 79	0
1	CK	504/504 (100%)	-0.54	0	100	100	21, 34, 54, 79	0
1	CL	504/504 (100%)	-0.61	0	100	100	22, 33, 54, 77	0
1	CM	504/504 (100%)	-0.57	0	100	100	22, 32, 53, 79	0
1	CN	504/504 (100%)	-0.57	0	100	100	22, 32, 54, 79	0
1	CO	504/504 (100%)	-0.56	0	100	100	23, 32, 54, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	CP	504/504 (100%)	-0.55	0 100 100	21, 31, 53, 78	0
1	CQ	504/504 (100%)	-0.56	0 100 100	21, 32, 53, 79	0
1	CR	504/504 (100%)	-0.47	1 (0%) 95 87	17, 31, 53, 75	0
1	CS	504/504 (100%)	-0.58	0 100 100	22, 32, 53, 78	0
1	CT	504/504 (100%)	-0.60	0 100 100	21, 32, 52, 77	0
All	All	30240/30240 (100%)	-0.58	2 (0%) 100 100	17, 33, 54, 81	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	CR	83	SER	2.5
1	BP	83	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.