



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:50 PM GMT

PDB ID : 4V7G  
Title : Crystal Structure of Lumazine Synthase from Bacillus Anthracis  
Authors : Morgunova, E.; Illarionov, B.; Saller, S.; Popov, A.; Sambaiah, T.; Bacher, A.;  
Cushman, M.; Fischer, M.; Ladenstein, R.  
Deposited on : 2009-09-16  
Resolution : 3.50 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  
<http://wwpdb.org/validation/2016/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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

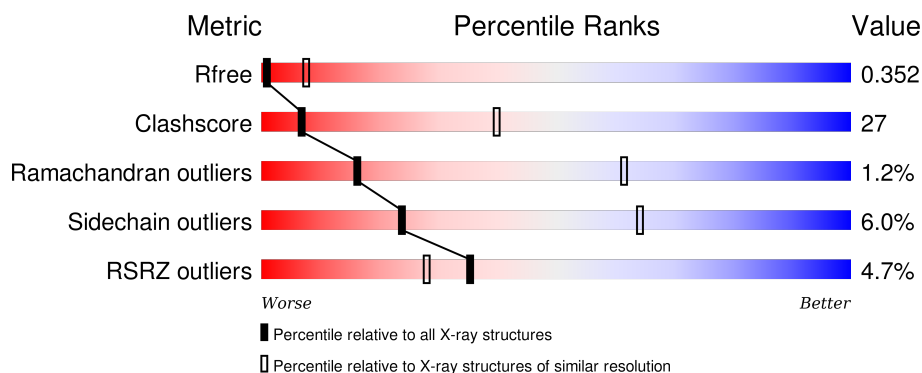
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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))
$R_{free}$	91344	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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. 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	A1	153	<div> <div>3%</div> <div>56%</div> <div>40%</div> <div>..</div> </div>
1	A2	153	<div> <div>2%</div> <div>58%</div> <div>38%</div> <div>..</div> </div>
1	A3	153	<div> <div>3%</div> <div>55%</div> <div>37%</div> <div>7%</div> <div>.</div> </div>
1	A4	153	<div> <div>3%</div> <div>56%</div> <div>37%</div> <div>6%</div> <div>.</div> </div>
1	AA	153	<div> <div>%</div> <div>61%</div> <div>35%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	AB	153	<div> <div>3%</div> <div>55%</div> <div>41%</div> <div>..</div> </div>
1	AC	153	<div> <div>2%</div> <div>56%</div> <div>41%</div> <div>..</div> </div>
1	AD	153	<div> <div>%</div> <div>52%</div> <div>41%</div> <div>7%</div> <div>.</div> </div>
1	AE	153	<div> <div>%</div> <div>55%</div> <div>39%</div> <div>6%</div> <div>.</div> </div>
1	AF	153	<div> <div>%</div> <div>59%</div> <div>37%</div> <div>..</div> </div>
1	AG	153	<div> <div>2%</div> <div>54%</div> <div>42%</div> <div>..</div> </div>
1	AH	153	<div> <div>2%</div> <div>58%</div> <div>38%</div> <div>..</div> </div>
1	AI	153	<div> <div>%</div> <div>53%</div> <div>40%</div> <div>7%</div> <div>.</div> </div>
1	AJ	153	<div> <div>2%</div> <div>55%</div> <div>39%</div> <div>6%</div> <div>.</div> </div>
1	AK	153	<div> <div>%</div> <div>58%</div> <div>37%</div> <div>..</div> </div>
1	AL	153	<div> <div>2%</div> <div>57%</div> <div>39%</div> <div>..</div> </div>
1	AM	153	<div> <div>%</div> <div>57%</div> <div>39%</div> <div>..</div> </div>
1	AN	153	<div> <div>%</div> <div>54%</div> <div>39%</div> <div>7%</div> <div>.</div> </div>
1	AO	153	<div> <div>2%</div> <div>55%</div> <div>39%</div> <div>6%</div> <div>.</div> </div>
1	AP	153	<div> <div>%</div> <div>58%</div> <div>37%</div> <div>..</div> </div>
1	AQ	153	<div> <div>%</div> <div>55%</div> <div>41%</div> <div>..</div> </div>
1	AR	153	<div> <div>2%</div> <div>56%</div> <div>41%</div> <div>..</div> </div>
1	AS	153	<div> <div>%</div> <div>54%</div> <div>39%</div> <div>7%</div> <div>.</div> </div>
1	AT	153	<div> <div>2%</div> <div>57%</div> <div>37%</div> <div>6%</div> <div>.</div> </div>
1	AU	153	<div> <div>%</div> <div>58%</div> <div>38%</div> <div>..</div> </div>
1	AV	153	<div> <div>3%</div> <div>56%</div> <div>40%</div> <div>..</div> </div>
1	AW	153	<div> <div>%</div> <div>57%</div> <div>39%</div> <div>..</div> </div>
1	AX	153	<div> <div>%</div> <div>55%</div> <div>39%</div> <div>6%</div> <div>.</div> </div>
1	AY	153	<div> <div>2%</div> <div>56%</div> <div>37%</div> <div>6%</div> <div>.</div> </div>
1	AZ	153	<div> <div>%</div> <div>61%</div> <div>35%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	B1	153	
1	B2	153	
1	B3	153	
1	B4	153	
1	BA	153	
1	BB	153	
1	BC	153	
1	BD	153	
1	BE	153	
1	BF	153	
1	BG	153	
1	BH	153	
1	BI	153	
1	BJ	153	
1	BK	153	
1	BL	153	
1	BM	153	
1	BN	153	
1	BO	153	
1	BP	153	
1	BQ	153	
1	BR	153	
1	BS	153	
1	BT	153	
1	BU	153	



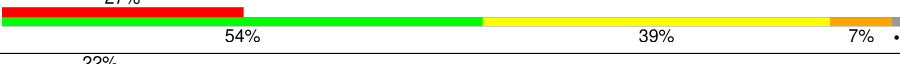
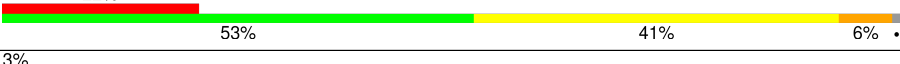


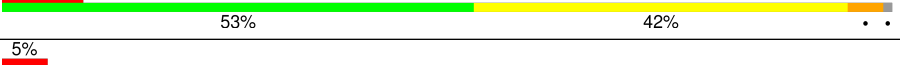


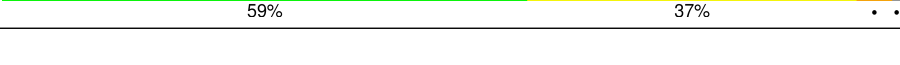
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Mol	Chain	Length	Quality of chain
1	BV	153	
1	BW	153	
1	BX	153	
1	BY	153	
1	BZ	153	
1	C1	153	
1	C2	153	
1	C3	153	
1	C4	153	
1	CA	153	
1	CB	153	
1	CC	153	
1	CD	153	
1	CE	153	
1	CF	153	
1	CG	153	
1	CH	153	
1	CI	153	
1	CJ	153	
1	CK	153	
1	CL	153	
1	CM	153	
1	CN	153	
1	CO	153	
1	CP	153	

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Mol	Chain	Length	Quality of chain
1	CQ	153	
1	CR	153	
1	CS	153	
1	CT	153	
1	CU	153	
1	CV	153	
1	CW	153	
1	CX	153	
1	CY	153	
1	CZ	153	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A2	1001	-	-	X	-
2	PO4	A4	1001	-	-	X	-
2	PO4	AC	1001	-	-	X	-
2	PO4	AE	1001	-	-	X	-
2	PO4	AH	1001	-	-	X	-
2	PO4	AJ	1001	-	-	X	-
2	PO4	AM	1001	-	-	X	-
2	PO4	AO	1001	-	-	X	-
2	PO4	AR	1001	-	-	X	-
2	PO4	AT	1001	-	-	X	-
2	PO4	AW	201	-	-	X	-
2	PO4	AY	1001	-	-	X	-
2	PO4	B2	1001	-	-	X	-
2	PO4	B4	1001	-	-	X	-
2	PO4	BC	1001	-	-	X	-
2	PO4	BE	1001	-	-	X	-
2	PO4	BH	1001	-	-	X	-
2	PO4	BJ	1001	-	-	X	-
2	PO4	BM	1001	-	-	X	-
2	PO4	BO	1001	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	BR	1001	-	-	X	-
2	PO4	BT	1001	-	-	X	-
2	PO4	BW	1001	-	-	X	-
2	PO4	BY	1001	-	-	X	-
2	PO4	C2	2201	-	-	X	-
2	PO4	C4	4201	-	-	X	-
2	PO4	CC	1001	-	-	X	-
2	PO4	CE	1001	-	-	X	-
2	PO4	CH	2201	-	-	X	-
2	PO4	CJ	4201	-	-	X	-
2	PO4	CM	2201	-	-	X	-
2	PO4	CO	4201	-	-	X	-
2	PO4	CR	2201	-	-	X	-
2	PO4	CT	4201	-	-	X	-
2	PO4	CW	2201	-	-	X	-
2	PO4	CY	4201	-	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 102534 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 6,7-dimethyl-8-ribityllumazine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AB	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AC	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AD	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AE	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AF	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AG	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AH	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AI	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AJ	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AK	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AL	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AM	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AN	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AO	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AP	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AR	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AS	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AT	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AU	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AV	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	AW	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AX	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AY	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	AZ	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	A1	152	Total	C	N	O	S	0	0	0
			1129	723	193	210	3			
1	A2	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	A3	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	A4	152	Total	C	N	O	S	0	0	0
			1132	724	193	212	3			
1	BA	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	BB	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	BC	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	BD	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	BE	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	BF	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	BG	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BH	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BI	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BJ	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BK	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BL	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BM	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BN	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BO	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BP	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BQ	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BR	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BS	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BT	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BU	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BV	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BW	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BX	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BY	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	BZ	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	B1	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	B2	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0

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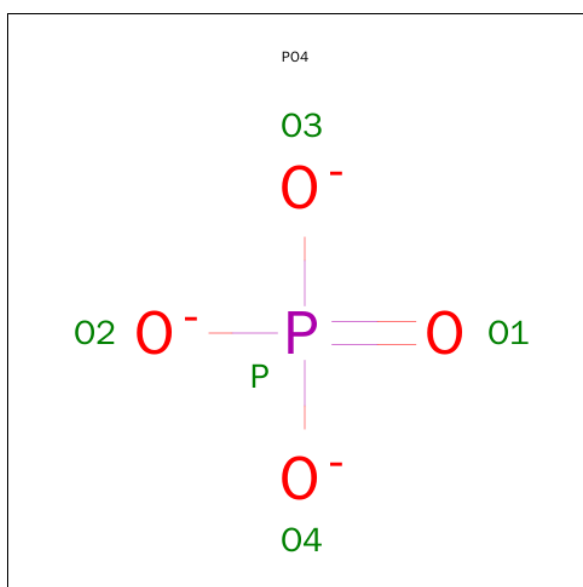
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B3	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	B4	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CA	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CB	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CC	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CD	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CE	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CF	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CG	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CH	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CI	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CJ	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CK	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CL	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CM	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CN	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CO	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CP	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CQ	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CR	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0
1	CS	152	Total 1136	C 726	N 193	O 214	S 3	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CT	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	CU	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	CV	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	CW	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	CX	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	CY	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	CZ	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	C1	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	C2	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	C3	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			
1	C4	152	Total	C	N	O	S	0	0	0
			1136	726	193	214	3			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AA	1	Total	O	P	0	0
			5	4	1		
2	AB	1	Total	O	P	0	0
			5	4	1		
2	AC	1	Total	O	P	0	0
			5	4	1		
2	AD	1	Total	O	P	0	0
			5	4	1		
2	AE	1	Total	O	P	0	0
			5	4	1		
2	AF	1	Total	O	P	0	0
			5	4	1		
2	AG	1	Total	O	P	0	0
			5	4	1		
2	AH	1	Total	O	P	0	0
			5	4	1		
2	AI	1	Total	O	P	0	0
			5	4	1		
2	AJ	1	Total	O	P	0	0
			5	4	1		
2	AK	1	Total	O	P	0	0
			5	4	1		
2	AL	1	Total	O	P	0	0
			5	4	1		
2	AM	1	Total	O	P	0	0
			5	4	1		
2	AN	1	Total	O	P	0	0
			5	4	1		
2	AO	1	Total	O	P	0	0
			5	4	1		
2	AP	1	Total	O	P	0	0
			5	4	1		
2	AQ	1	Total	O	P	0	0
			5	4	1		
2	AR	1	Total	O	P	0	0
			5	4	1		
2	AS	1	Total	O	P	0	0
			5	4	1		
2	AT	1	Total	O	P	0	0
			5	4	1		
2	AU	1	Total	O	P	0	0
			5	4	1		
2	AV	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AW	1	Total	O	P	0	0
			5	4	1		
2	AX	1	Total	O	P	0	0
			5	4	1		
2	AY	1	Total	O	P	0	0
			5	4	1		
2	AZ	1	Total	O	P	0	0
			5	4	1		
2	A1	1	Total	O	P	0	0
			5	4	1		
2	A2	1	Total	O	P	0	0
			5	4	1		
2	A3	1	Total	O	P	0	0
			5	4	1		
2	A4	1	Total	O	P	0	0
			5	4	1		
2	BA	1	Total	O	P	0	0
			5	4	1		
2	BB	1	Total	O	P	0	0
			5	4	1		
2	BC	1	Total	O	P	0	0
			5	4	1		
2	BD	1	Total	O	P	0	0
			5	4	1		
2	BE	1	Total	O	P	0	0
			5	4	1		
2	BF	1	Total	O	P	0	0
			5	4	1		
2	BG	1	Total	O	P	0	0
			5	4	1		
2	BH	1	Total	O	P	0	0
			5	4	1		
2	BI	1	Total	O	P	0	0
			5	4	1		
2	BJ	1	Total	O	P	0	0
			5	4	1		
2	BK	1	Total	O	P	0	0
			5	4	1		
2	BL	1	Total	O	P	0	0
			5	4	1		
2	BM	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	BN	1	Total	O	P	0	0
			5	4	1		
2	BO	1	Total	O	P	0	0
			5	4	1		
2	BP	1	Total	O	P	0	0
			5	4	1		
2	BQ	1	Total	O	P	0	0
			5	4	1		
2	BR	1	Total	O	P	0	0
			5	4	1		
2	BS	1	Total	O	P	0	0
			5	4	1		
2	BT	1	Total	O	P	0	0
			5	4	1		
2	BU	1	Total	O	P	0	0
			5	4	1		
2	BV	1	Total	O	P	0	0
			5	4	1		
2	BW	1	Total	O	P	0	0
			5	4	1		
2	BX	1	Total	O	P	0	0
			5	4	1		
2	BY	1	Total	O	P	0	0
			5	4	1		
2	BZ	1	Total	O	P	0	0
			5	4	1		
2	B1	1	Total	O	P	0	0
			5	4	1		
2	B2	1	Total	O	P	0	0
			5	4	1		
2	B3	1	Total	O	P	0	0
			5	4	1		
2	B4	1	Total	O	P	0	0
			5	4	1		
2	CA	1	Total	O	P	0	0
			5	4	1		
2	CB	1	Total	O	P	0	0
			5	4	1		
2	CC	1	Total	O	P	0	0
			5	4	1		
2	CD	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	CE	1	Total	O	P	0	0
			5	4	1		
2	CF	1	Total	O	P	0	0
			5	4	1		
2	CG	1	Total	O	P	0	0
			5	4	1		
2	CH	1	Total	O	P	0	0
			5	4	1		
2	CI	1	Total	O	P	0	0
			5	4	1		
2	CJ	1	Total	O	P	0	0
			5	4	1		
2	CK	1	Total	O	P	0	0
			5	4	1		
2	CL	1	Total	O	P	0	0
			5	4	1		
2	CM	1	Total	O	P	0	0
			5	4	1		
2	CN	1	Total	O	P	0	0
			5	4	1		
2	CO	1	Total	O	P	0	0
			5	4	1		
2	CP	1	Total	O	P	0	0
			5	4	1		
2	CQ	1	Total	O	P	0	0
			5	4	1		
2	CR	1	Total	O	P	0	0
			5	4	1		
2	CS	1	Total	O	P	0	0
			5	4	1		
2	CT	1	Total	O	P	0	0
			5	4	1		
2	CU	1	Total	O	P	0	0
			5	4	1		
2	CV	1	Total	O	P	0	0
			5	4	1		
2	CW	1	Total	O	P	0	0
			5	4	1		
2	CX	1	Total	O	P	0	0
			5	4	1		
2	CY	1	Total	O	P	0	0
			5	4	1		

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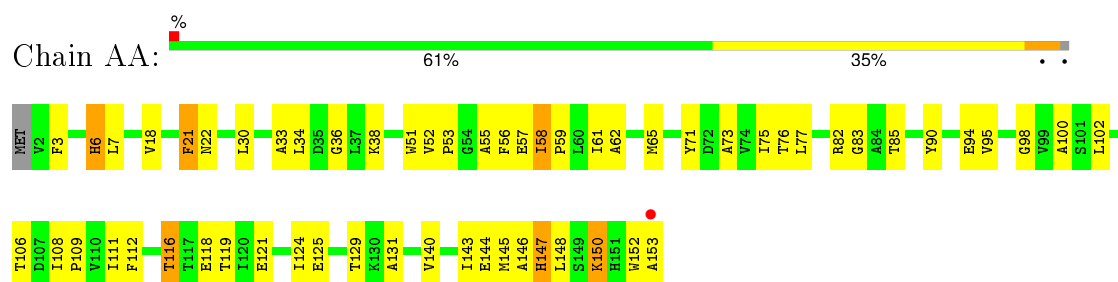
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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			5	4	1		
2	C1	1	Total	O	P	0	0
			5	4	1		
2	C2	1	Total	O	P	0	0
			5	4	1		
2	C3	1	Total	O	P	0	0
			5	4	1		
2	C4	1	Total	O	P	0	0
			5	4	1		

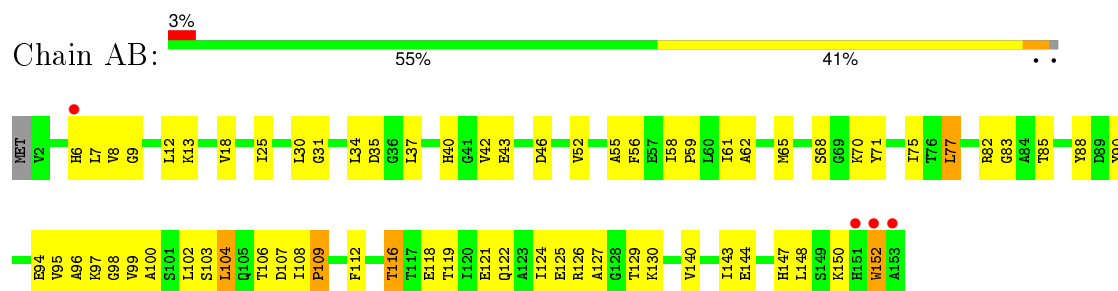
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

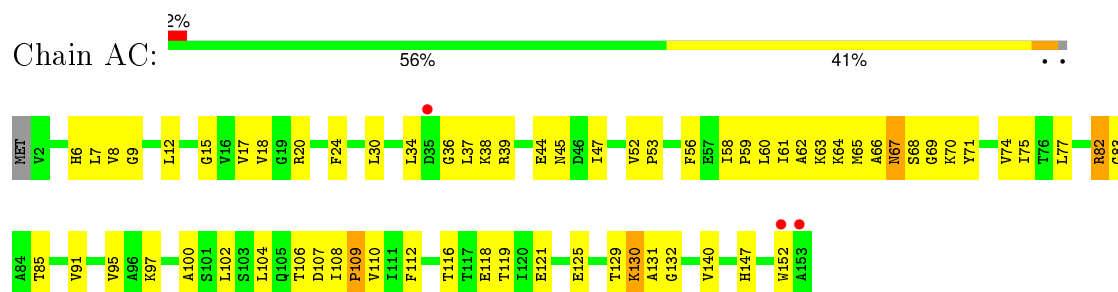
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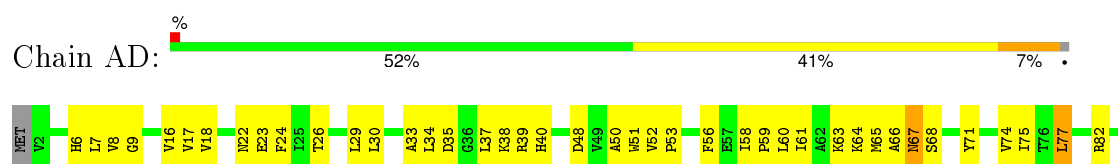
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

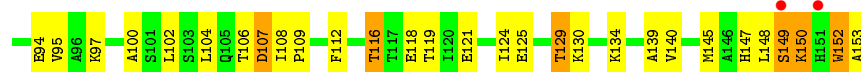
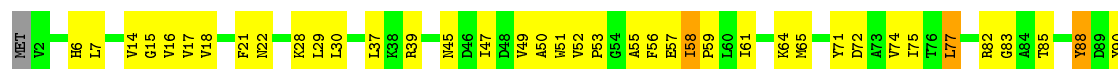


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

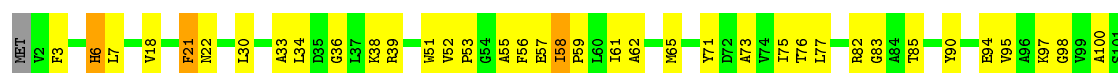




- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



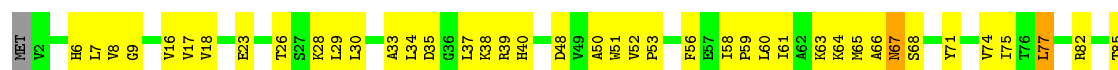
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

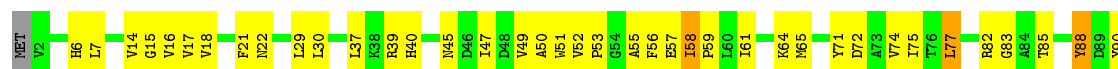


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

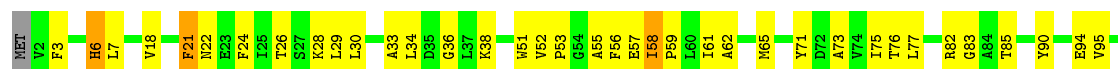




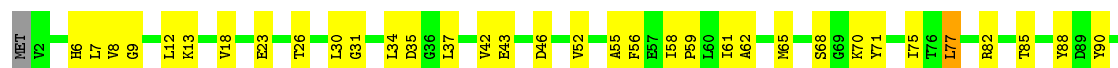
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



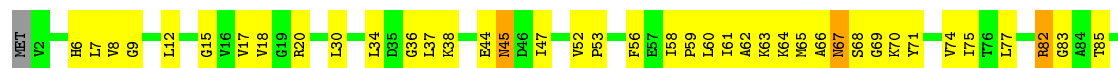
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

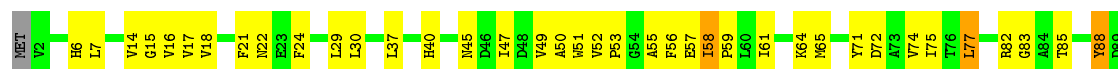


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

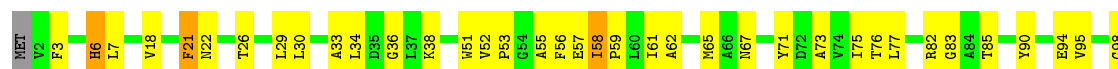




- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



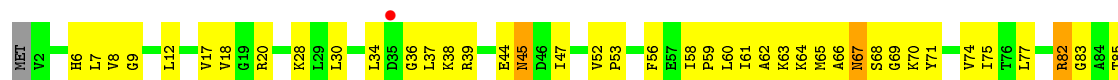
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

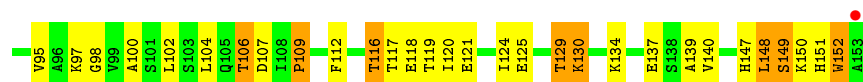


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

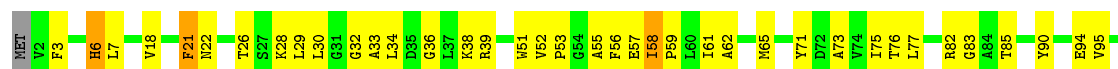




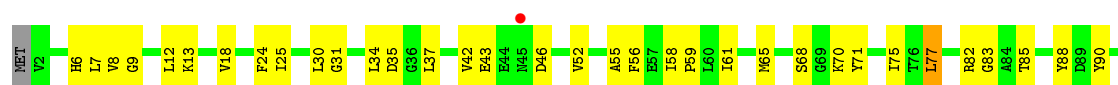
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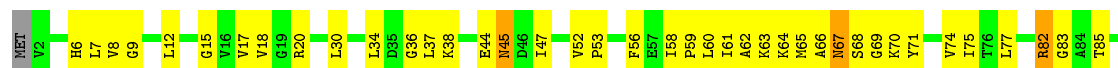
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



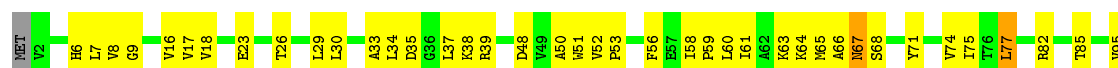
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

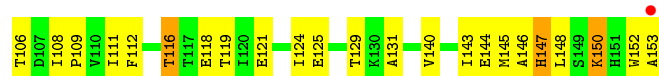




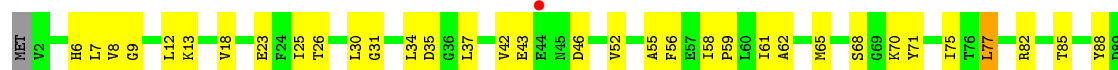
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



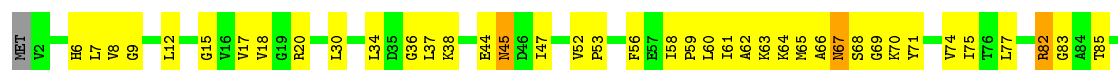
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



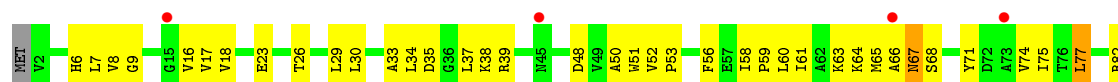
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

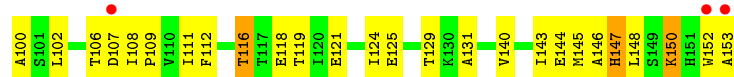
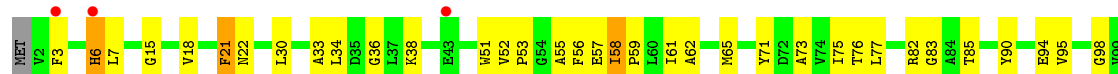




- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



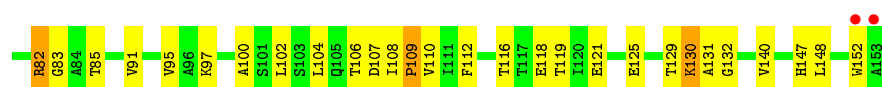
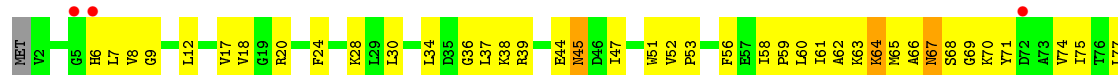
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



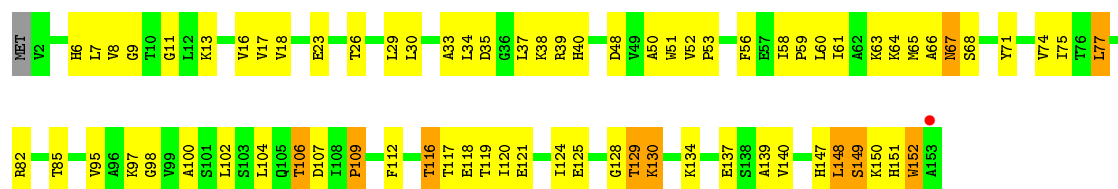
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



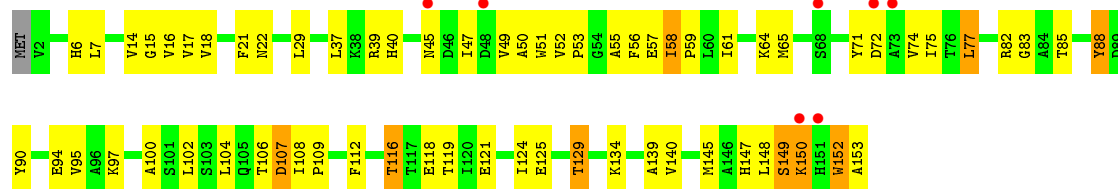
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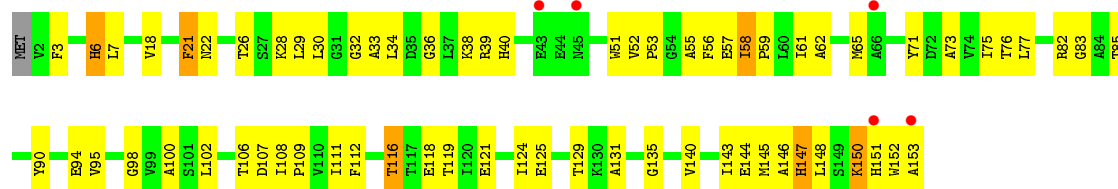




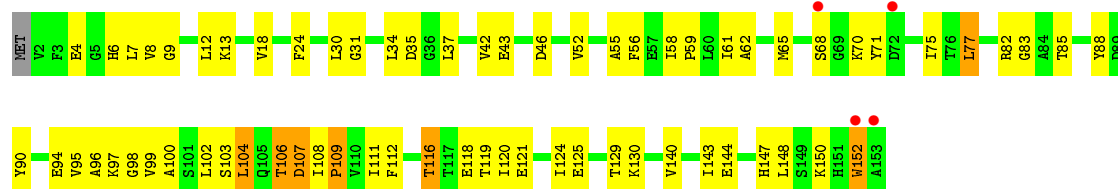
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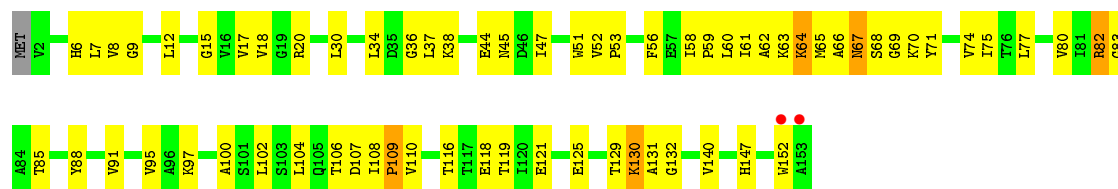
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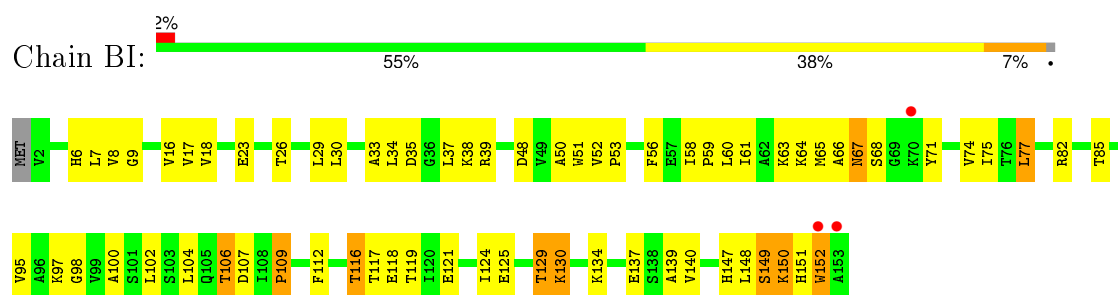
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



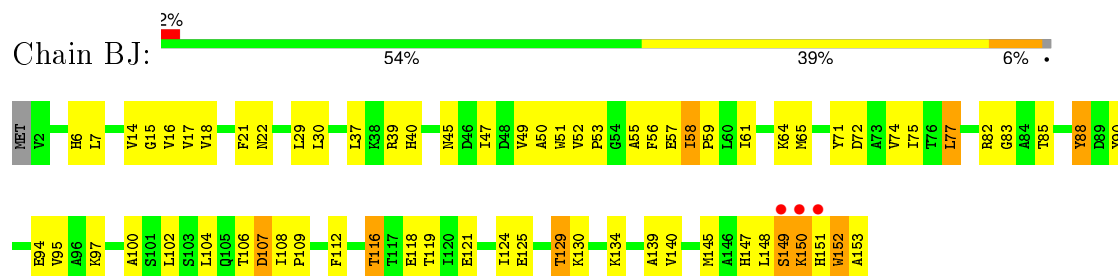
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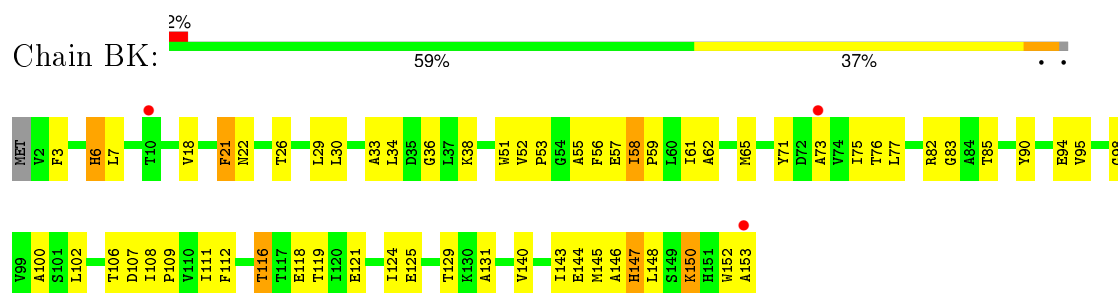
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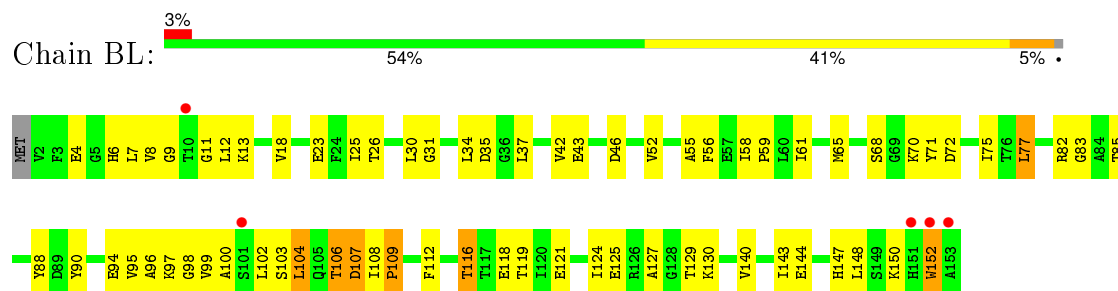
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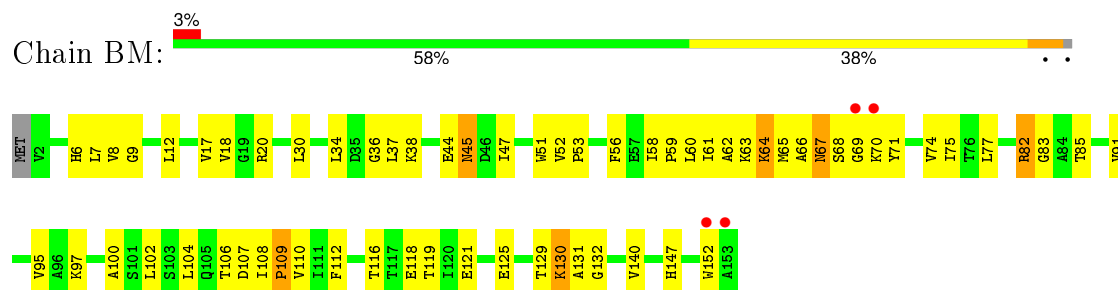
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



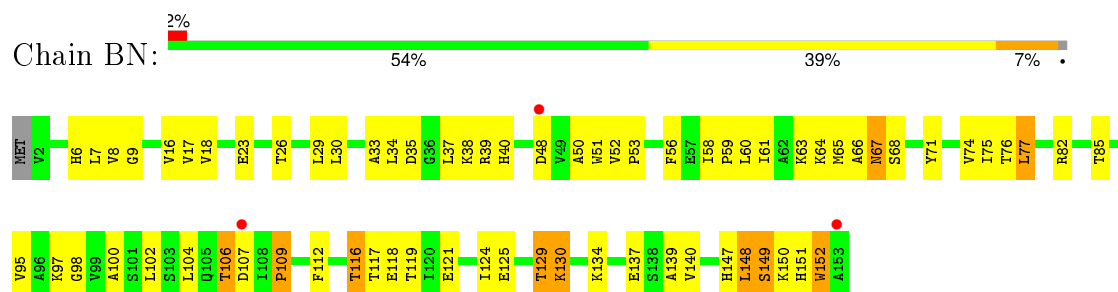
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



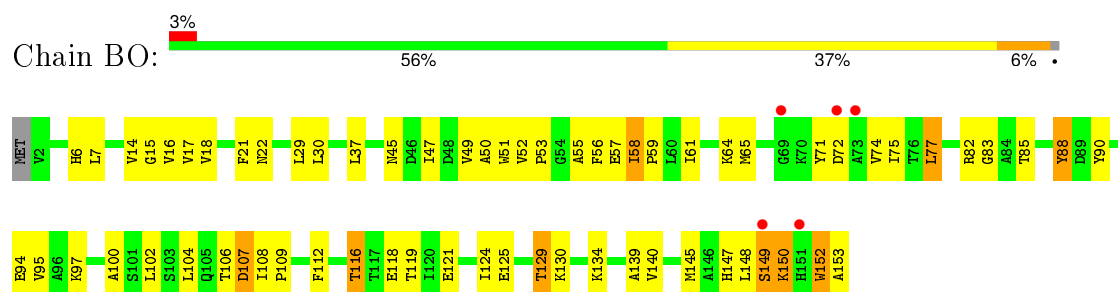
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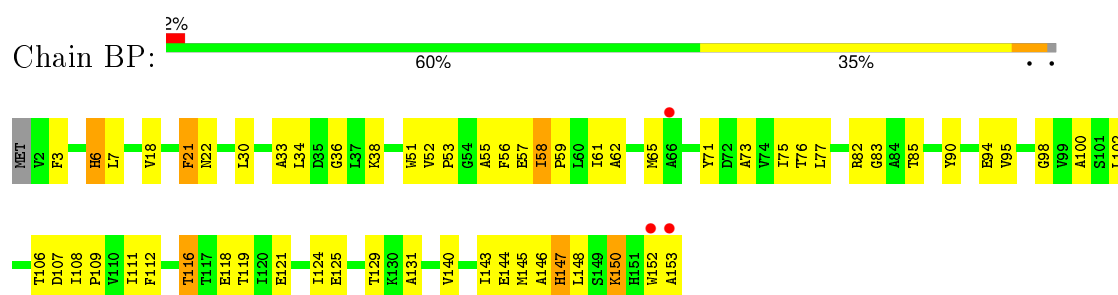
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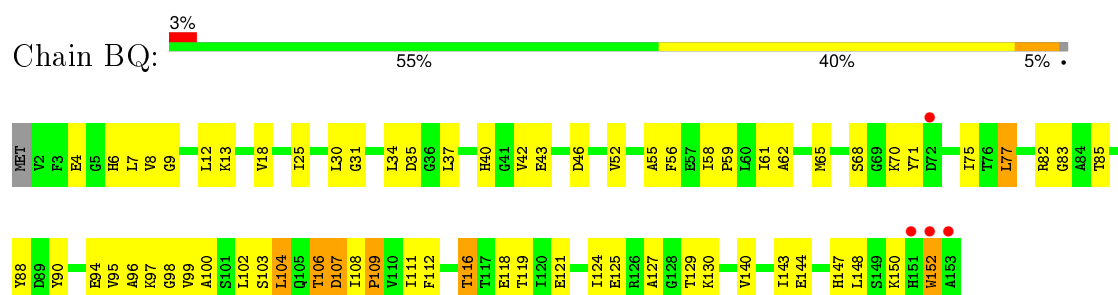
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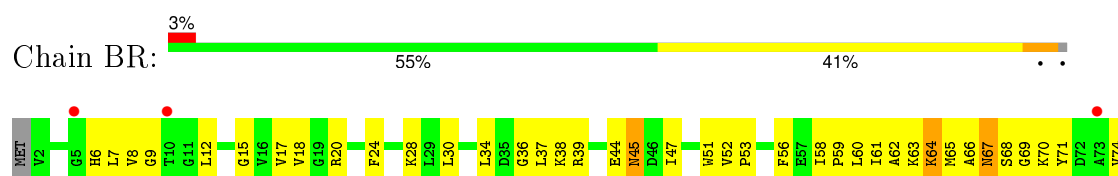
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



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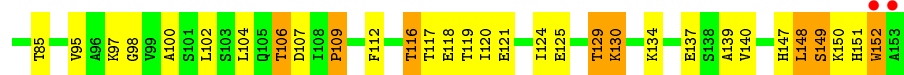
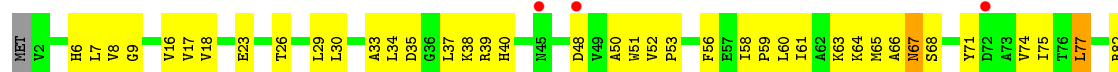


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

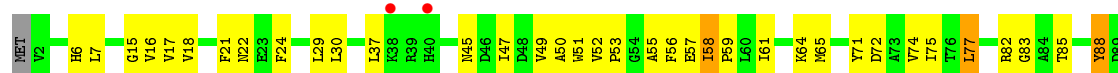




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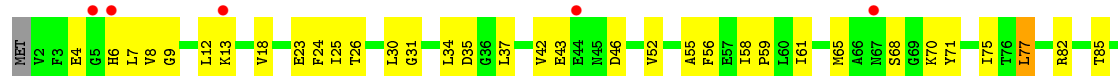
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- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

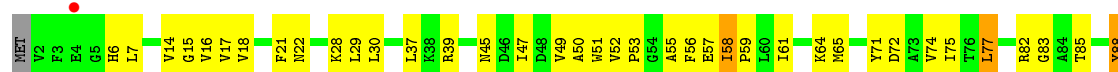




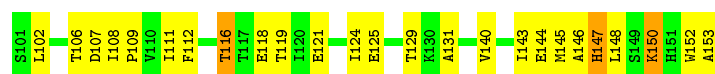
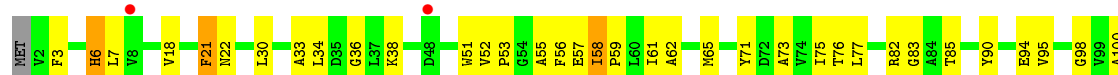
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- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



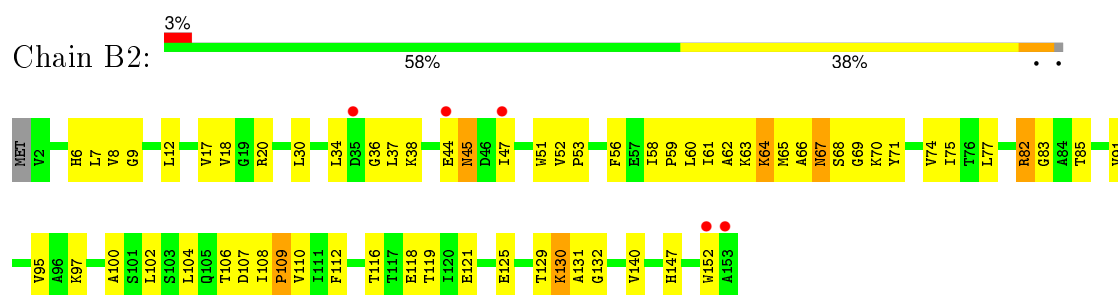
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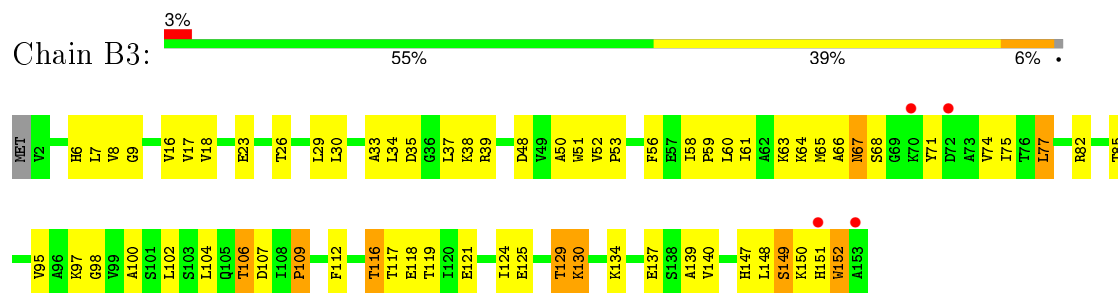
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



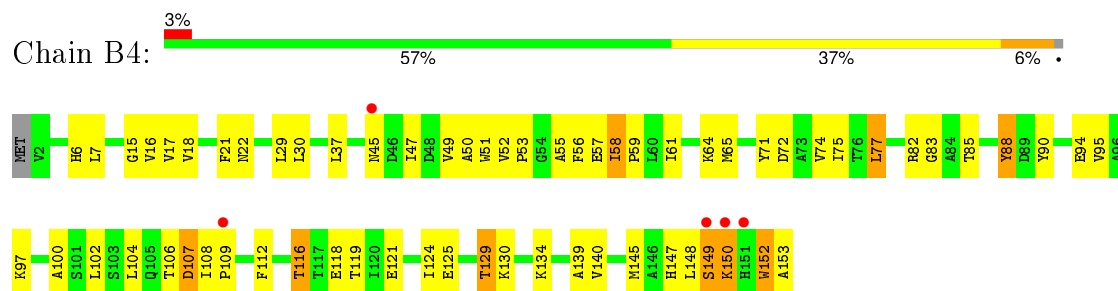
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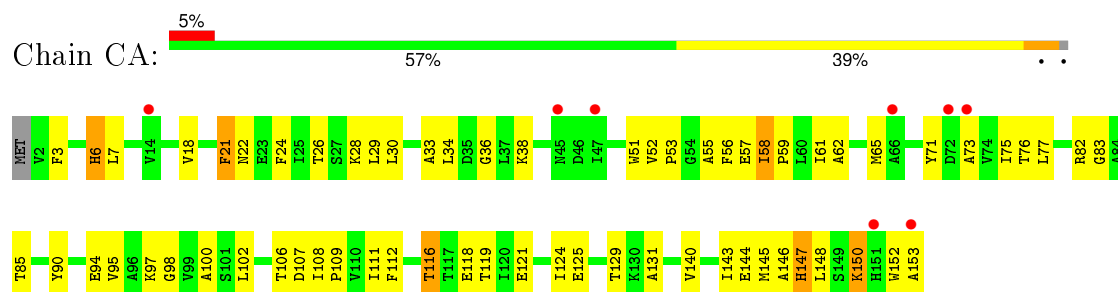
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



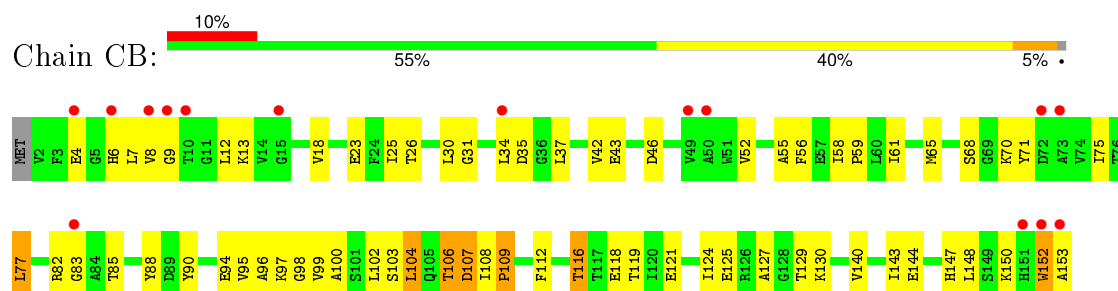
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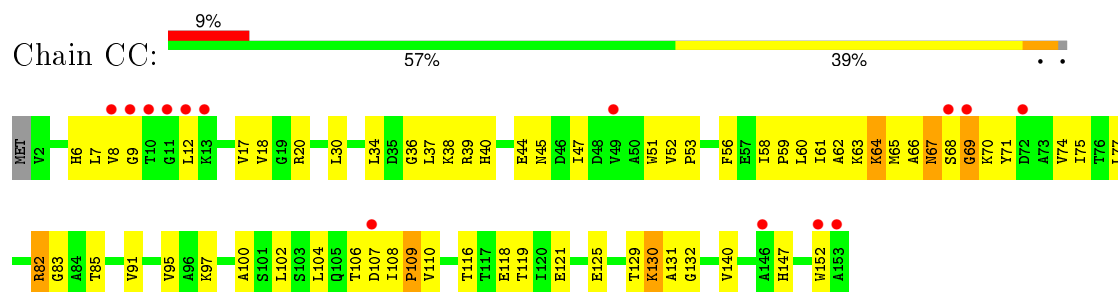
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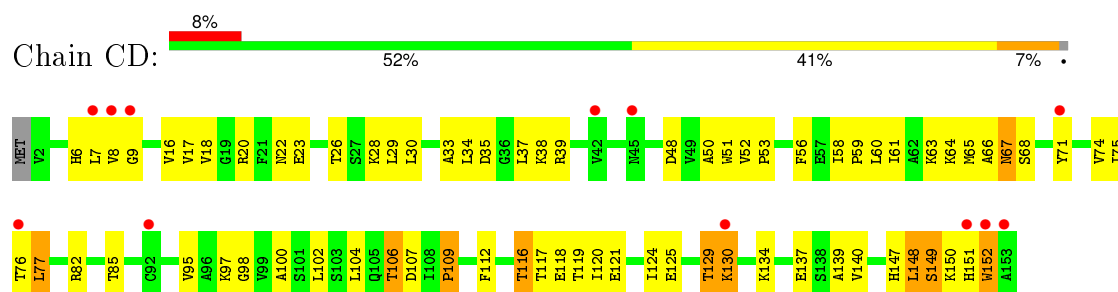
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



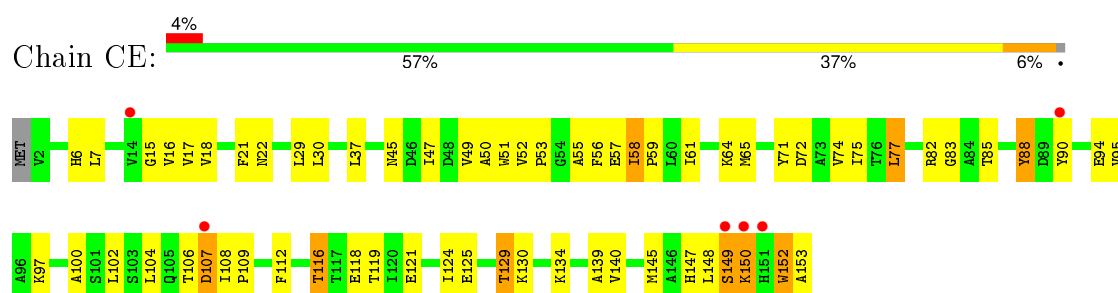
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



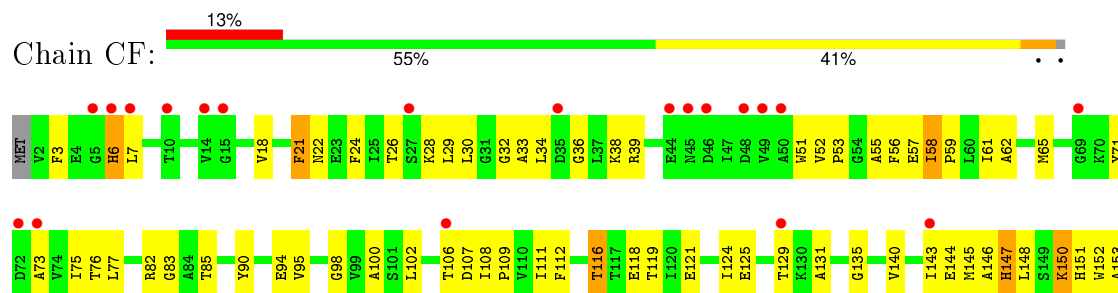
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



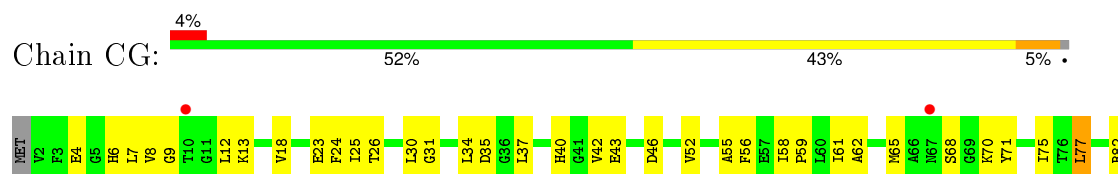
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

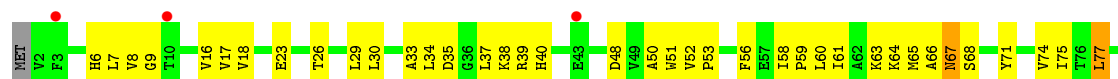




- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



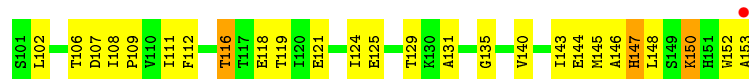
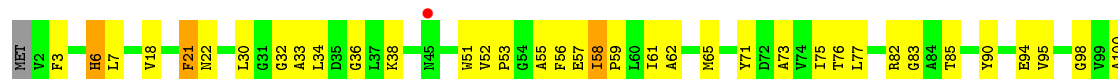
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



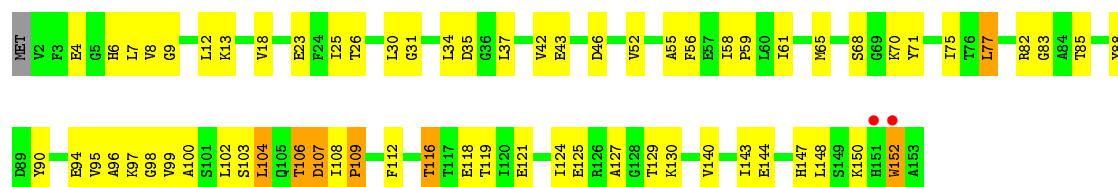
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



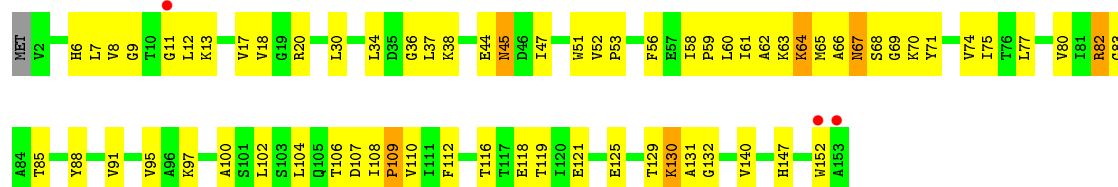
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



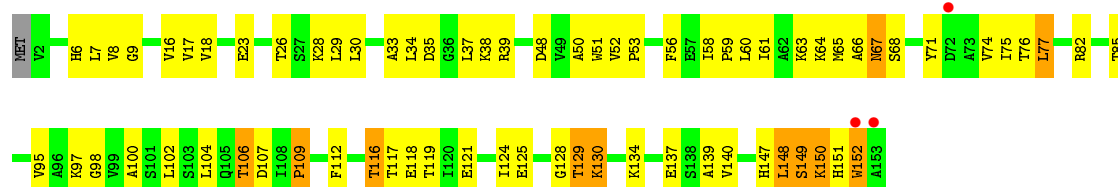




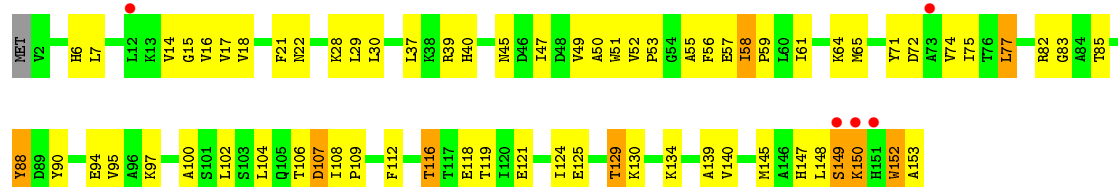
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



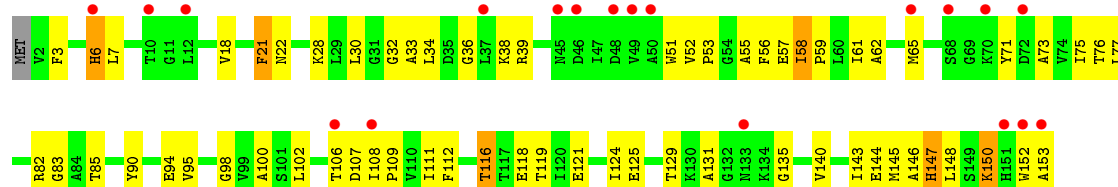
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



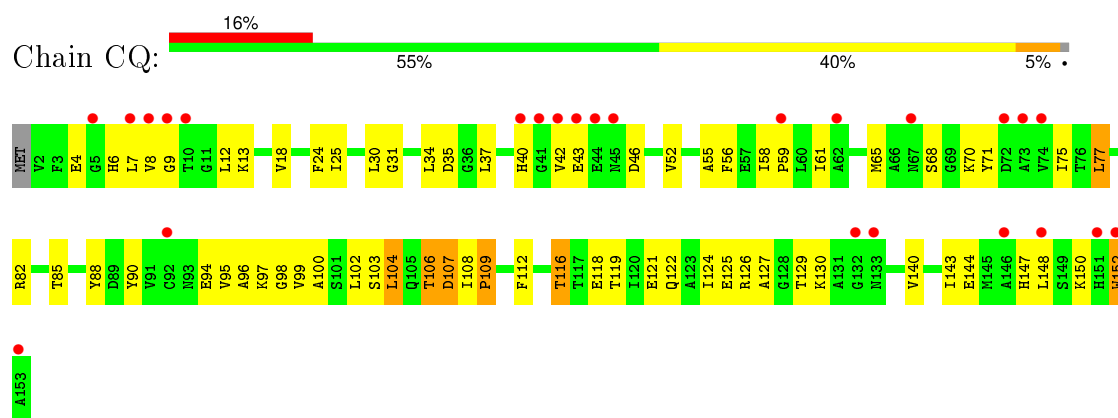
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



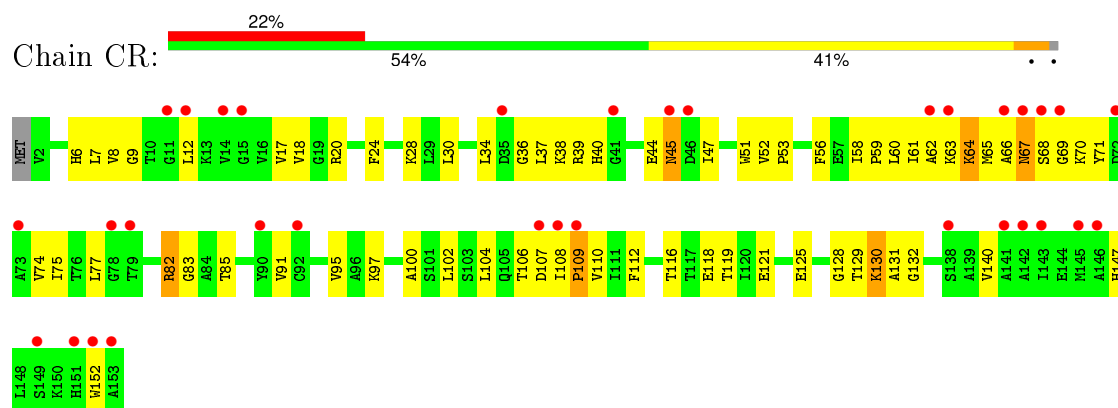
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



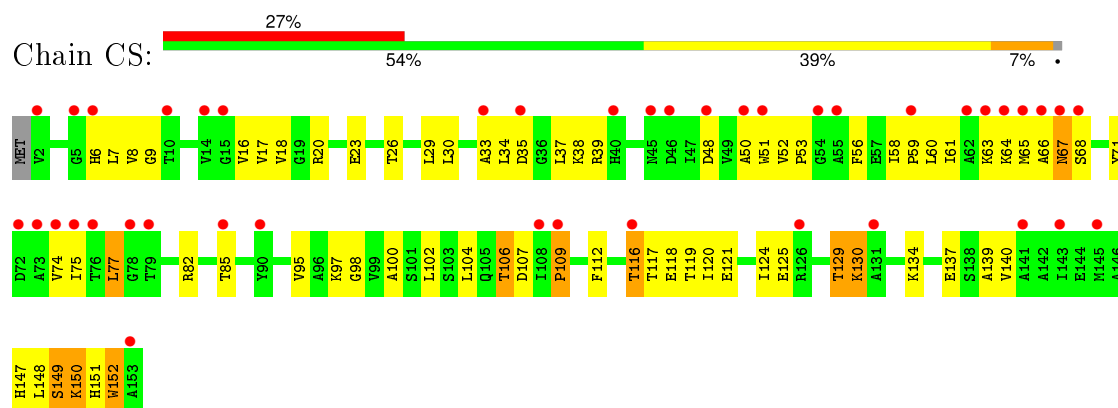
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



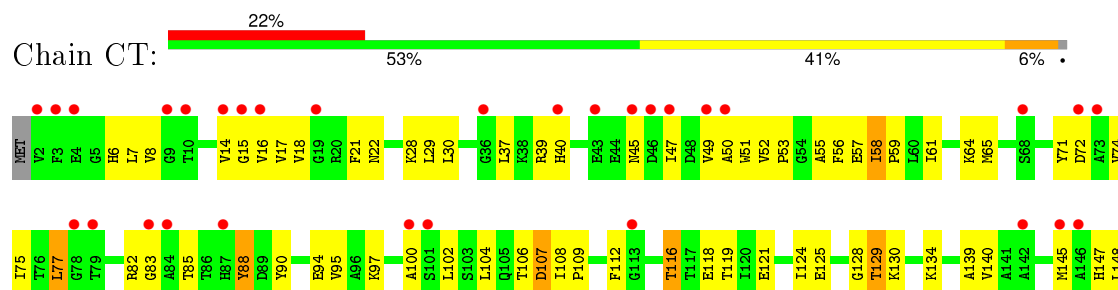
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

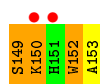


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

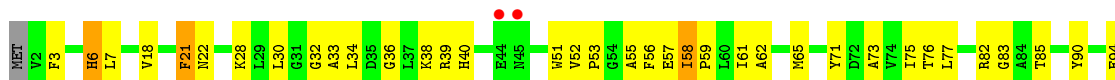


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

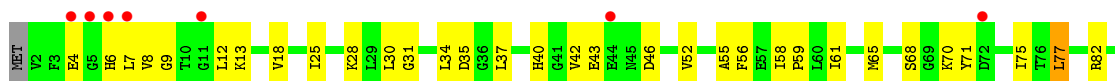




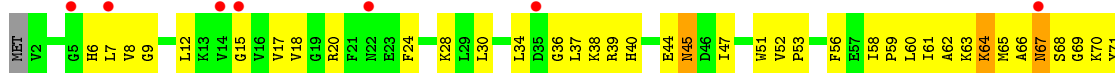
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



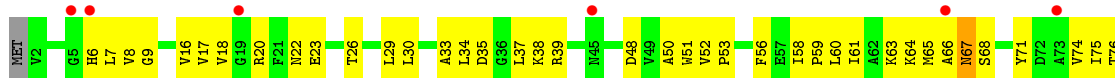
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

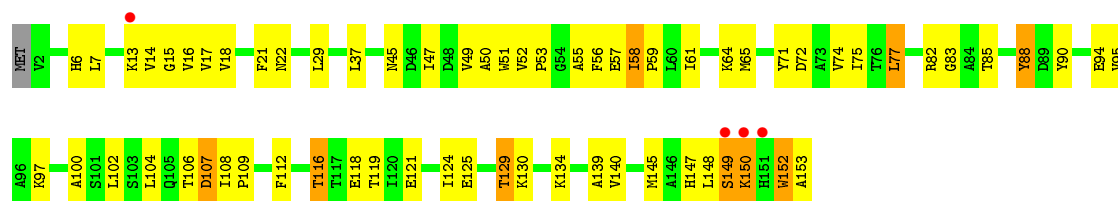


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

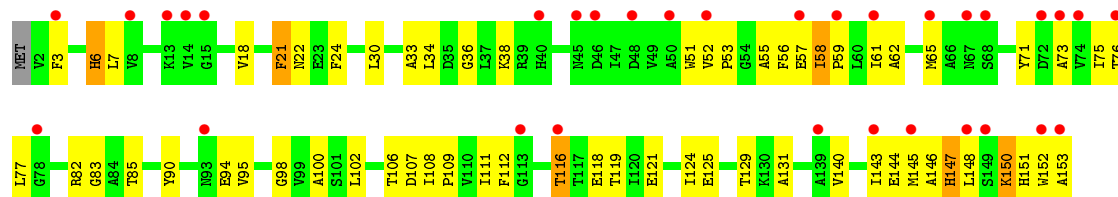


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

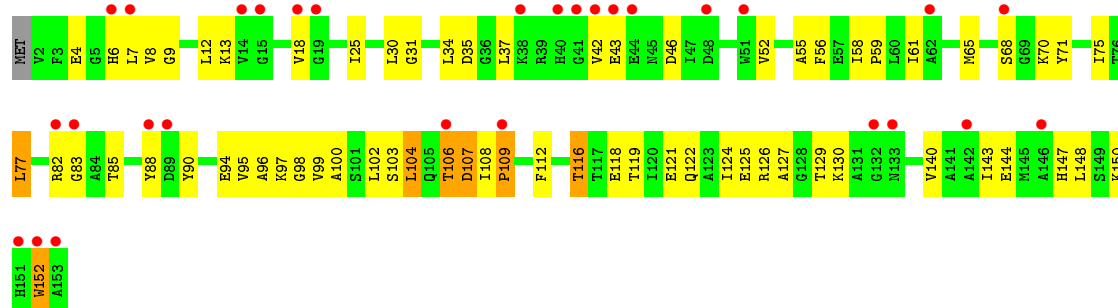




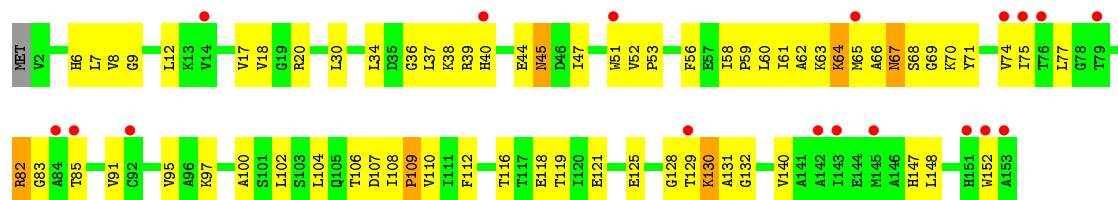
- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

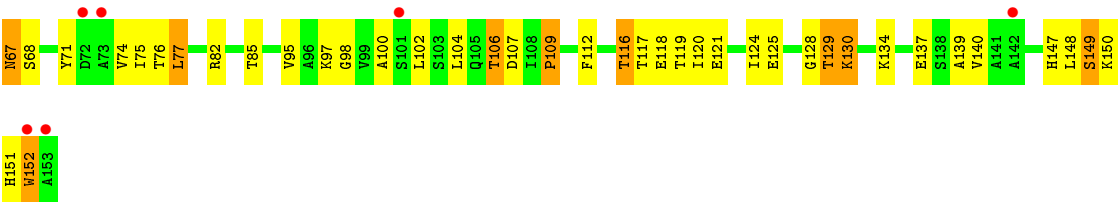


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase

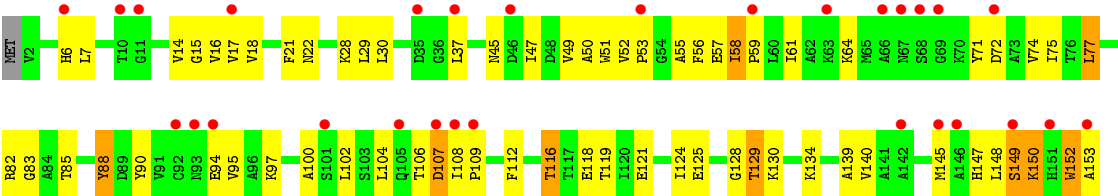


- Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase





• Molecule 1: 6,7-dimethyl-8-ribityllumazine synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.20Å 222.24Å 473.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.50 39.90 – 3.50	Depositor EDS
% Data completeness (in resolution range)	89.8 (15.00-3.50) 93.0 (39.90-3.50)	Depositor EDS
$R_{merge}$	0.29	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 3.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.235 , 0.286 0.346 , 0.352	Depositor DCC
$R_{free}$ test set	3841 reflections (2.05%)	DCC
Wilson B-factor (Å <sup>2</sup> )	67.0	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 79.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	1 of 194062 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.73	EDS
Total number of atoms	102534	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	A1	0.44	0/1149	0.71	2/1558 (0.1%)
1	A2	0.32	0/1152	0.62	1/1562 (0.1%)
1	A3	0.31	0/1152	0.85	5/1562 (0.3%)
1	A4	0.34	0/1152	0.58	1/1562 (0.1%)
1	AA	0.33	0/1149	0.49	1/1558 (0.1%)
1	AB	0.44	0/1149	0.71	2/1558 (0.1%)
1	AC	0.32	0/1152	0.62	1/1562 (0.1%)
1	AD	0.31	0/1152	0.85	5/1562 (0.3%)
1	AE	0.34	0/1152	0.58	1/1562 (0.1%)
1	AF	0.33	0/1149	0.49	1/1558 (0.1%)
1	AG	0.44	0/1149	0.71	2/1558 (0.1%)
1	AH	0.32	0/1152	0.63	1/1562 (0.1%)
1	AI	0.31	0/1152	0.85	5/1562 (0.3%)
1	AJ	0.34	0/1152	0.58	1/1562 (0.1%)
1	AK	0.33	0/1149	0.49	1/1558 (0.1%)
1	AL	0.44	0/1149	0.71	2/1558 (0.1%)
1	AM	0.32	0/1152	0.63	1/1562 (0.1%)
1	AN	0.31	0/1152	0.85	5/1562 (0.3%)
1	AO	0.34	0/1152	0.58	1/1562 (0.1%)
1	AP	0.33	0/1149	0.49	1/1558 (0.1%)
1	AQ	0.44	0/1149	0.71	2/1558 (0.1%)
1	AR	0.32	0/1152	0.62	1/1562 (0.1%)
1	AS	0.31	0/1152	0.85	5/1562 (0.3%)
1	AT	0.34	0/1152	0.58	1/1562 (0.1%)
1	AU	0.33	0/1149	0.49	1/1558 (0.1%)
1	AV	0.44	0/1149	0.71	2/1558 (0.1%)
1	AW	0.32	0/1152	0.63	1/1562 (0.1%)
1	AX	0.31	0/1152	0.85	5/1562 (0.3%)
1	AY	0.34	0/1152	0.58	1/1562 (0.1%)
1	AZ	0.33	0/1149	0.49	1/1558 (0.1%)
1	B1	0.44	0/1156	0.72	3/1567 (0.2%)
1	B2	0.32	0/1156	0.62	1/1567 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	B3	0.31	0/1156	0.85	5/1567 (0.3%)
1	B4	0.34	0/1156	0.58	1/1567 (0.1%)
1	BA	0.32	0/1156	0.51	2/1567 (0.1%)
1	BB	0.44	0/1156	0.72	3/1567 (0.2%)
1	BC	0.32	0/1156	0.62	1/1567 (0.1%)
1	BD	0.31	0/1156	0.85	5/1567 (0.3%)
1	BE	0.34	0/1156	0.58	1/1567 (0.1%)
1	BF	0.32	0/1156	0.51	2/1567 (0.1%)
1	BG	0.44	0/1156	0.72	3/1567 (0.2%)
1	BH	0.32	0/1156	0.62	1/1567 (0.1%)
1	BI	0.31	0/1156	0.85	5/1567 (0.3%)
1	BJ	0.34	0/1156	0.58	1/1567 (0.1%)
1	BK	0.32	0/1156	0.51	2/1567 (0.1%)
1	BL	0.44	0/1156	0.72	3/1567 (0.2%)
1	BM	0.32	0/1156	0.62	1/1567 (0.1%)
1	BN	0.31	0/1156	0.85	5/1567 (0.3%)
1	BO	0.34	0/1156	0.58	1/1567 (0.1%)
1	BP	0.33	0/1156	0.51	2/1567 (0.1%)
1	BQ	0.44	0/1156	0.72	3/1567 (0.2%)
1	BR	0.32	0/1156	0.62	1/1567 (0.1%)
1	BS	0.31	0/1156	0.85	5/1567 (0.3%)
1	BT	0.34	0/1156	0.58	1/1567 (0.1%)
1	BU	0.33	0/1156	0.51	2/1567 (0.1%)
1	BV	0.44	0/1156	0.72	3/1567 (0.2%)
1	BW	0.32	0/1156	0.62	1/1567 (0.1%)
1	BX	0.31	0/1156	0.85	5/1567 (0.3%)
1	BY	0.34	0/1156	0.58	1/1567 (0.1%)
1	BZ	0.33	0/1156	0.51	2/1567 (0.1%)
1	C1	0.44	0/1156	0.72	3/1567 (0.2%)
1	C2	0.32	0/1156	0.62	1/1567 (0.1%)
1	C3	0.31	0/1156	0.85	5/1567 (0.3%)
1	C4	0.34	0/1156	0.58	1/1567 (0.1%)
1	CA	0.33	0/1156	0.51	2/1567 (0.1%)
1	CB	0.44	0/1156	0.72	3/1567 (0.2%)
1	CC	0.32	0/1156	0.62	1/1567 (0.1%)
1	CD	0.31	0/1156	0.85	5/1567 (0.3%)
1	CE	0.34	0/1156	0.58	1/1567 (0.1%)
1	CF	0.33	0/1156	0.51	2/1567 (0.1%)
1	CG	0.44	0/1156	0.72	3/1567 (0.2%)
1	CH	0.32	0/1156	0.62	1/1567 (0.1%)
1	CI	0.31	0/1156	0.85	5/1567 (0.3%)
1	CJ	0.34	0/1156	0.58	1/1567 (0.1%)
1	CK	0.33	0/1156	0.51	2/1567 (0.1%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	CL	0.44	0/1156	0.72	3/1567 (0.2%)
1	CM	0.32	0/1156	0.62	1/1567 (0.1%)
1	CN	0.31	0/1156	0.85	5/1567 (0.3%)
1	CO	0.34	0/1156	0.58	1/1567 (0.1%)
1	CP	0.32	0/1156	0.51	2/1567 (0.1%)
1	CQ	0.44	0/1156	0.72	3/1567 (0.2%)
1	CR	0.32	0/1156	0.62	1/1567 (0.1%)
1	CS	0.31	0/1156	0.85	5/1567 (0.3%)
1	CT	0.34	0/1156	0.58	1/1567 (0.1%)
1	CU	0.33	0/1156	0.51	2/1567 (0.1%)
1	CV	0.44	0/1156	0.72	3/1567 (0.2%)
1	CW	0.32	0/1156	0.62	1/1567 (0.1%)
1	CX	0.31	0/1156	0.85	5/1567 (0.3%)
1	CY	0.34	0/1156	0.58	1/1567 (0.1%)
1	CZ	0.33	0/1156	0.51	2/1567 (0.1%)
All	All	0.35	0/103884	0.67	204/140832 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A1	0	1
1	AB	0	1
1	AG	0	1
1	AL	0	1
1	AQ	0	1
1	AV	0	1
1	B1	0	1
1	BB	0	1
1	BG	0	1
1	BL	0	1
1	BQ	0	1
1	BV	0	1
1	C1	0	1
1	CB	0	1
1	CG	0	1
1	CL	0	1
1	CQ	0	1
1	CV	0	1
All	All	0	18

There are no bond length outliers.

All (204) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BD	149	SER	CB-CA-C	-14.91	81.78	110.10
1	CD	149	SER	CB-CA-C	-14.90	81.79	110.10
1	C3	149	SER	CB-CA-C	-14.89	81.80	110.10
1	BI	149	SER	CB-CA-C	-14.89	81.81	110.10
1	CX	149	SER	CB-CA-C	-14.89	81.81	110.10
1	AS	149	SER	CB-CA-C	-14.88	81.82	110.10
1	AX	149	SER	CB-CA-C	-14.88	81.83	110.10
1	CS	149	SER	CB-CA-C	-14.88	81.83	110.10
1	AD	149	SER	CB-CA-C	-14.88	81.83	110.10
1	B3	149	SER	CB-CA-C	-14.88	81.83	110.10
1	AI	149	SER	CB-CA-C	-14.88	81.83	110.10
1	BX	149	SER	CB-CA-C	-14.88	81.84	110.10
1	CI	149	SER	CB-CA-C	-14.87	81.84	110.10
1	BN	149	SER	CB-CA-C	-14.87	81.85	110.10
1	BS	149	SER	CB-CA-C	-14.87	81.85	110.10
1	AN	149	SER	CB-CA-C	-14.86	81.86	110.10
1	A3	149	SER	CB-CA-C	-14.86	81.88	110.10
1	CN	149	SER	CB-CA-C	-14.86	81.88	110.10
1	CX	150	LYS	N-CA-CB	-13.59	86.14	110.60
1	BN	150	LYS	N-CA-CB	-13.59	86.14	110.60
1	C3	150	LYS	N-CA-CB	-13.59	86.14	110.60
1	BD	150	LYS	N-CA-CB	-13.58	86.15	110.60
1	AN	150	LYS	N-CA-CB	-13.58	86.16	110.60
1	CS	150	LYS	N-CA-CB	-13.58	86.16	110.60
1	BI	150	LYS	N-CA-CB	-13.57	86.16	110.60
1	CD	150	LYS	N-CA-CB	-13.57	86.17	110.60
1	AI	150	LYS	N-CA-CB	-13.57	86.18	110.60
1	AD	150	LYS	N-CA-CB	-13.56	86.19	110.60
1	AS	150	LYS	N-CA-CB	-13.56	86.19	110.60
1	A3	150	LYS	N-CA-CB	-13.56	86.20	110.60
1	BS	150	LYS	N-CA-CB	-13.55	86.20	110.60
1	B3	150	LYS	N-CA-CB	-13.55	86.21	110.60
1	CN	150	LYS	N-CA-CB	-13.55	86.21	110.60
1	AX	150	LYS	N-CA-CB	-13.54	86.22	110.60
1	CI	150	LYS	N-CA-CB	-13.54	86.22	110.60
1	BX	150	LYS	N-CA-CB	-13.53	86.24	110.60
1	CI	109	PRO	CA-N-CD	-12.47	94.04	111.50
1	B3	109	PRO	CA-N-CD	-12.46	94.05	111.50
1	BX	109	PRO	CA-N-CD	-12.46	94.06	111.50
1	A3	109	PRO	CA-N-CD	-12.45	94.07	111.50

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BD	109	PRO	CA-N-CD	-12.45	94.07	111.50
1	CS	109	PRO	CA-N-CD	-12.45	94.07	111.50
1	AD	109	PRO	CA-N-CD	-12.45	94.07	111.50
1	BS	109	PRO	CA-N-CD	-12.45	94.08	111.50
1	CD	109	PRO	CA-N-CD	-12.44	94.08	111.50
1	AN	109	PRO	CA-N-CD	-12.44	94.08	111.50
1	BN	109	PRO	CA-N-CD	-12.44	94.08	111.50
1	BI	109	PRO	CA-N-CD	-12.44	94.08	111.50
1	AI	109	PRO	CA-N-CD	-12.44	94.09	111.50
1	C3	109	PRO	CA-N-CD	-12.43	94.10	111.50
1	AX	109	PRO	CA-N-CD	-12.43	94.10	111.50
1	CX	109	PRO	CA-N-CD	-12.42	94.11	111.50
1	AS	109	PRO	CA-N-CD	-12.42	94.11	111.50
1	CN	109	PRO	CA-N-CD	-12.42	94.12	111.50
1	CG	109	PRO	CA-N-CD	-11.82	94.94	111.50
1	CV	109	PRO	CA-N-CD	-11.81	94.96	111.50
1	AG	109	PRO	CA-N-CD	-11.81	94.97	111.50
1	BL	109	PRO	CA-N-CD	-11.81	94.97	111.50
1	B1	109	PRO	CA-N-CD	-11.81	94.97	111.50
1	BG	109	PRO	CA-N-CD	-11.80	94.97	111.50
1	BB	109	PRO	CA-N-CD	-11.80	94.98	111.50
1	BQ	109	PRO	CA-N-CD	-11.80	94.98	111.50
1	AB	109	PRO	CA-N-CD	-11.79	94.99	111.50
1	AQ	109	PRO	CA-N-CD	-11.79	95.00	111.50
1	A1	109	PRO	CA-N-CD	-11.79	95.00	111.50
1	BV	109	PRO	CA-N-CD	-11.79	95.00	111.50
1	CQ	109	PRO	CA-N-CD	-11.79	95.00	111.50
1	CB	109	PRO	CA-N-CD	-11.79	95.00	111.50
1	AV	109	PRO	CA-N-CD	-11.77	95.02	111.50
1	CL	109	PRO	CA-N-CD	-11.77	95.02	111.50
1	AL	109	PRO	CA-N-CD	-11.77	95.03	111.50
1	C1	109	PRO	CA-N-CD	-11.77	95.03	111.50
1	AN	149	SER	N-CA-C	9.93	137.81	111.00
1	A3	149	SER	N-CA-C	9.91	137.76	111.00
1	AS	149	SER	N-CA-C	9.91	137.76	111.00
1	BS	149	SER	N-CA-C	9.91	137.76	111.00
1	CS	149	SER	N-CA-C	9.91	137.76	111.00
1	BN	149	SER	N-CA-C	9.91	137.75	111.00
1	AD	149	SER	N-CA-C	9.91	137.75	111.00
1	CI	149	SER	N-CA-C	9.91	137.75	111.00
1	B3	149	SER	N-CA-C	9.91	137.75	111.00
1	AI	149	SER	N-CA-C	9.90	137.74	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BD	149	SER	N-CA-C	9.90	137.75	111.00
1	AX	149	SER	N-CA-C	9.90	137.72	111.00
1	BI	149	SER	N-CA-C	9.90	137.72	111.00
1	CD	149	SER	N-CA-C	9.90	137.72	111.00
1	C3	149	SER	N-CA-C	9.90	137.72	111.00
1	BX	149	SER	N-CA-C	9.89	137.71	111.00
1	CN	149	SER	N-CA-C	9.89	137.71	111.00
1	CX	149	SER	N-CA-C	9.88	137.69	111.00
1	B2	109	PRO	CA-N-CD	-8.02	100.28	111.50
1	BR	109	PRO	CA-N-CD	-8.01	100.28	111.50
1	BM	109	PRO	CA-N-CD	-8.00	100.30	111.50
1	BW	109	PRO	CA-N-CD	-8.00	100.30	111.50
1	CR	109	PRO	CA-N-CD	-8.00	100.30	111.50
1	AH	109	PRO	CA-N-CD	-7.99	100.31	111.50
1	BH	109	PRO	CA-N-CD	-7.99	100.32	111.50
1	AC	109	PRO	CA-N-CD	-7.98	100.33	111.50
1	CW	109	PRO	CA-N-CD	-7.98	100.33	111.50
1	C2	109	PRO	CA-N-CD	-7.98	100.33	111.50
1	AM	109	PRO	CA-N-CD	-7.97	100.34	111.50
1	AW	109	PRO	CA-N-CD	-7.97	100.34	111.50
1	A2	109	PRO	CA-N-CD	-7.97	100.35	111.50
1	BC	109	PRO	CA-N-CD	-7.97	100.35	111.50
1	AR	109	PRO	CA-N-CD	-7.96	100.35	111.50
1	CH	109	PRO	CA-N-CD	-7.96	100.36	111.50
1	CM	109	PRO	CA-N-CD	-7.95	100.37	111.50
1	CC	109	PRO	CA-N-CD	-7.94	100.38	111.50
1	BS	148	LEU	N-CA-C	-5.84	95.23	111.00
1	AX	148	LEU	N-CA-C	-5.84	95.23	111.00
1	CS	148	LEU	N-CA-C	-5.84	95.24	111.00
1	B3	148	LEU	N-CA-C	-5.83	95.25	111.00
1	CI	148	LEU	N-CA-C	-5.83	95.25	111.00
1	A3	148	LEU	N-CA-C	-5.83	95.25	111.00
1	BD	148	LEU	N-CA-C	-5.83	95.25	111.00
1	AD	148	LEU	N-CA-C	-5.83	95.26	111.00
1	BX	148	LEU	N-CA-C	-5.83	95.27	111.00
1	AN	148	LEU	N-CA-C	-5.83	95.27	111.00
1	CN	148	LEU	N-CA-C	-5.83	95.27	111.00
1	CX	148	LEU	N-CA-C	-5.83	95.27	111.00
1	AI	148	LEU	N-CA-C	-5.82	95.28	111.00
1	BI	148	LEU	N-CA-C	-5.82	95.28	111.00
1	CD	148	LEU	N-CA-C	-5.82	95.28	111.00
1	AS	148	LEU	N-CA-C	-5.82	95.29	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C3	148	LEU	N-CA-C	-5.82	95.29	111.00
1	BN	148	LEU	N-CA-C	-5.82	95.30	111.00
1	B1	150	LYS	N-CA-C	-5.70	95.61	111.00
1	CB	150	LYS	N-CA-C	-5.70	95.61	111.00
1	CQ	150	LYS	N-CA-C	-5.69	95.63	111.00
1	CV	150	LYS	N-CA-C	-5.69	95.63	111.00
1	BQ	150	LYS	N-CA-C	-5.69	95.63	111.00
1	BV	150	LYS	N-CA-C	-5.69	95.64	111.00
1	CG	150	LYS	N-CA-C	-5.69	95.64	111.00
1	AQ	150	LYS	N-CA-C	-5.69	95.64	111.00
1	AB	150	LYS	N-CA-C	-5.69	95.64	111.00
1	AV	150	LYS	N-CA-C	-5.69	95.65	111.00
1	BL	150	LYS	N-CA-C	-5.69	95.65	111.00
1	CL	150	LYS	N-CA-C	-5.69	95.65	111.00
1	A1	150	LYS	N-CA-C	-5.68	95.66	111.00
1	BB	150	LYS	N-CA-C	-5.68	95.66	111.00
1	BG	150	LYS	N-CA-C	-5.68	95.66	111.00
1	AG	150	LYS	N-CA-C	-5.68	95.67	111.00
1	AL	150	LYS	N-CA-C	-5.68	95.67	111.00
1	C1	150	LYS	N-CA-C	-5.68	95.67	111.00
1	C4	58	ILE	CB-CA-C	-5.29	101.02	111.60
1	BE	58	ILE	CB-CA-C	-5.29	101.03	111.60
1	BY	58	ILE	CB-CA-C	-5.28	101.03	111.60
1	BJ	58	ILE	CB-CA-C	-5.28	101.04	111.60
1	CO	58	ILE	CB-CA-C	-5.28	101.04	111.60
1	AO	58	ILE	CB-CA-C	-5.28	101.05	111.60
1	B4	58	ILE	CB-CA-C	-5.27	101.06	111.60
1	CJ	58	ILE	CB-CA-C	-5.27	101.06	111.60
1	CY	58	ILE	CB-CA-C	-5.27	101.06	111.60
1	AY	58	ILE	CB-CA-C	-5.27	101.06	111.60
1	AE	58	ILE	CB-CA-C	-5.27	101.07	111.60
1	AT	58	ILE	CB-CA-C	-5.27	101.06	111.60
1	A4	58	ILE	CB-CA-C	-5.27	101.06	111.60
1	CT	58	ILE	CB-CA-C	-5.27	101.07	111.60
1	AJ	58	ILE	CB-CA-C	-5.26	101.07	111.60
1	BT	58	ILE	CB-CA-C	-5.26	101.08	111.60
1	CE	58	ILE	CB-CA-C	-5.26	101.09	111.60
1	BO	58	ILE	CB-CA-C	-5.24	101.12	111.60
1	BL	107	ASP	CB-CG-OD2	5.22	123.00	118.30
1	CZ	107	ASP	CB-CG-OD2	5.22	123.00	118.30
1	BA	107	ASP	CB-CG-OD2	5.22	123.00	118.30
1	BU	107	ASP	CB-CG-OD2	5.21	122.99	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BZ	107	ASP	CB-CG-OD2	5.21	122.99	118.30
1	CA	107	ASP	CB-CG-OD2	5.21	122.99	118.30
1	CP	107	ASP	CB-CG-OD2	5.21	122.99	118.30
1	BF	107	ASP	CB-CG-OD2	5.20	122.98	118.30
1	CU	107	ASP	CB-CG-OD2	5.20	122.98	118.30
1	CV	107	ASP	CB-CG-OD2	5.20	122.98	118.30
1	BQ	107	ASP	CB-CG-OD2	5.19	122.97	118.30
1	B1	107	ASP	CB-CG-OD2	5.19	122.97	118.30
1	CB	107	ASP	CB-CG-OD2	5.18	122.97	118.30
1	CL	107	ASP	CB-CG-OD2	5.18	122.96	118.30
1	BB	107	ASP	CB-CG-OD2	5.18	122.96	118.30
1	BP	107	ASP	CB-CG-OD2	5.17	122.95	118.30
1	CQ	107	ASP	CB-CG-OD2	5.17	122.95	118.30
1	CG	107	ASP	CB-CG-OD2	5.16	122.95	118.30
1	BK	107	ASP	CB-CG-OD2	5.16	122.94	118.30
1	CK	107	ASP	CB-CG-OD2	5.16	122.94	118.30
1	BV	107	ASP	CB-CG-OD2	5.16	122.94	118.30
1	BK	58	ILE	CB-CA-C	-5.15	101.29	111.60
1	C1	107	ASP	CB-CG-OD2	5.15	122.94	118.30
1	AP	58	ILE	CB-CA-C	-5.15	101.31	111.60
1	CA	58	ILE	CB-CA-C	-5.15	101.31	111.60
1	CU	58	ILE	CB-CA-C	-5.15	101.31	111.60
1	BA	58	ILE	CB-CA-C	-5.15	101.31	111.60
1	AK	58	ILE	CB-CA-C	-5.14	101.31	111.60
1	BZ	58	ILE	CB-CA-C	-5.14	101.31	111.60
1	CP	58	ILE	CB-CA-C	-5.14	101.31	111.60
1	BF	58	ILE	CB-CA-C	-5.14	101.32	111.60
1	AA	58	ILE	CB-CA-C	-5.14	101.32	111.60
1	BU	58	ILE	CB-CA-C	-5.14	101.32	111.60
1	CF	107	ASP	CB-CG-OD2	5.14	122.92	118.30
1	AF	58	ILE	CB-CA-C	-5.14	101.32	111.60
1	AU	58	ILE	CB-CA-C	-5.14	101.33	111.60
1	CZ	58	ILE	CB-CA-C	-5.14	101.33	111.60
1	CK	58	ILE	CB-CA-C	-5.13	101.33	111.60
1	BG	107	ASP	CB-CG-OD2	5.13	122.92	118.30
1	AZ	58	ILE	CB-CA-C	-5.12	101.36	111.60
1	BP	58	ILE	CB-CA-C	-5.12	101.36	111.60
1	CF	58	ILE	CB-CA-C	-5.11	101.38	111.60

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	99	VAL	Peptide
1	AB	99	VAL	Peptide
1	AG	99	VAL	Peptide
1	AL	99	VAL	Peptide
1	AQ	99	VAL	Peptide
1	AV	99	VAL	Peptide
1	B1	99	VAL	Peptide
1	BB	99	VAL	Peptide
1	BG	99	VAL	Peptide
1	BL	99	VAL	Peptide
1	BQ	99	VAL	Peptide
1	BV	99	VAL	Peptide
1	C1	99	VAL	Peptide
1	CB	99	VAL	Peptide
1	CG	99	VAL	Peptide
1	CL	99	VAL	Peptide
1	CQ	99	VAL	Peptide
1	CV	99	VAL	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	A1	1129	0	1143	68	0
1	A2	1132	0	1145	77	0
1	A3	1132	0	1145	64	0
1	A4	1132	0	1145	75	0
1	AA	1129	0	1143	52	0
1	AB	1129	0	1143	73	0
1	AC	1132	0	1145	81	0
1	AD	1132	0	1145	71	0
1	AE	1132	0	1145	82	0
1	AF	1129	0	1143	57	0
1	AG	1129	0	1143	68	2
1	AH	1132	0	1145	76	3
1	AI	1132	0	1145	70	0
1	AJ	1132	0	1145	81	0
1	AK	1129	0	1143	55	0
1	AL	1129	0	1143	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AM	1132	0	1145	78	0
1	AN	1132	0	1145	64	0
1	AO	1132	0	1145	80	0
1	AP	1129	0	1143	53	0
1	AQ	1129	0	1143	90	0
1	AR	1132	0	1145	85	0
1	AS	1132	0	1145	65	0
1	AT	1132	0	1145	75	0
1	AU	1129	0	1143	58	0
1	AV	1129	0	1143	67	0
1	AW	1132	0	1145	78	0
1	AX	1132	0	1145	62	0
1	AY	1132	0	1145	75	0
1	AZ	1129	0	1143	50	0
1	B1	1136	0	1149	73	0
1	B2	1136	0	1149	78	0
1	B3	1136	0	1149	60	0
1	B4	1136	0	1149	73	0
1	BA	1136	0	1149	49	0
1	BB	1136	0	1149	81	0
1	BC	1136	0	1149	88	0
1	BD	1136	0	1149	75	0
1	BE	1136	0	1149	74	0
1	BF	1136	0	1149	64	0
1	BG	1136	0	1149	76	0
1	BH	1136	0	1149	80	0
1	BI	1136	0	1149	63	0
1	BJ	1136	0	1149	78	1
1	BK	1136	0	1149	51	0
1	BL	1136	0	1149	74	3
1	BM	1136	0	1149	78	0
1	BN	1136	0	1149	65	0
1	BO	1136	0	1149	75	0
1	BP	1136	0	1149	49	0
1	BQ	1136	0	1149	81	0
1	BR	1136	0	1149	90	0
1	BS	1136	0	1149	67	0
1	BT	1136	0	1149	74	0
1	BU	1136	0	1149	77	0
1	BV	1136	0	1149	75	0
1	BW	1136	0	1149	80	0
1	BX	1136	0	1149	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BY	1136	0	1149	77	0
1	BZ	1136	0	1149	49	0
1	C1	1136	0	1149	74	0
1	C2	1136	0	1149	91	0
1	C3	1136	0	1149	76	0
1	C4	1136	0	1149	74	1
1	CA	1136	0	1149	55	0
1	CB	1136	0	1149	75	2
1	CC	1136	0	1149	96	2
1	CD	1136	0	1149	75	0
1	CE	1136	0	1149	76	0
1	CF	1136	0	1149	64	0
1	CG	1136	0	1149	84	3
1	CH	1136	0	1149	86	3
1	CI	1136	0	1149	68	0
1	CJ	1136	0	1149	77	0
1	CK	1136	0	1149	52	0
1	CL	1136	0	1149	74	0
1	CM	1136	0	1149	86	3
1	CN	1136	0	1149	68	0
1	CO	1136	0	1149	80	0
1	CP	1136	0	1149	59	0
1	CQ	1136	0	1149	81	0
1	CR	1136	0	1149	96	0
1	CS	1136	0	1149	71	0
1	CT	1136	0	1149	83	0
1	CU	1136	0	1149	61	0
1	CV	1136	0	1149	77	0
1	CW	1136	0	1149	92	0
1	CX	1136	0	1149	69	0
1	CY	1136	0	1149	73	1
1	CZ	1136	0	1149	52	1
2	A1	5	0	0	0	0
2	A2	5	0	0	3	0
2	A3	5	0	0	0	0
2	A4	5	0	0	2	0
2	AA	5	0	0	1	0
2	AB	5	0	0	1	0
2	AC	5	0	0	3	0
2	AD	5	0	0	0	0
2	AE	5	0	0	2	0
2	AF	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AG	5	0	0	1	0
2	AH	5	0	0	3	0
2	AI	5	0	0	0	0
2	AJ	5	0	0	2	0
2	AK	5	0	0	1	0
2	AL	5	0	0	0	0
2	AM	5	0	0	3	0
2	AN	5	0	0	0	0
2	AO	5	0	0	2	0
2	AP	5	0	0	1	0
2	AQ	5	0	0	1	0
2	AR	5	0	0	3	0
2	AS	5	0	0	0	0
2	AT	5	0	0	2	0
2	AU	5	0	0	1	0
2	AV	5	0	0	1	0
2	AW	5	0	0	3	0
2	AX	5	0	0	0	0
2	AY	5	0	0	2	0
2	AZ	5	0	0	1	0
2	B1	5	0	0	1	0
2	B2	5	0	0	3	0
2	B3	5	0	0	0	0
2	B4	5	0	0	2	0
2	BA	5	0	0	1	0
2	BB	5	0	0	1	0
2	BC	5	0	0	3	0
2	BD	5	0	0	0	0
2	BE	5	0	0	2	0
2	BF	5	0	0	1	0
2	BG	5	0	0	1	0
2	BH	5	0	0	3	0
2	BI	5	0	0	0	0
2	BJ	5	0	0	2	0
2	BK	5	0	0	1	0
2	BL	5	0	0	1	0
2	BM	5	0	0	3	0
2	BN	5	0	0	0	0
2	BO	5	0	0	2	0
2	BP	5	0	0	1	0
2	BQ	5	0	0	1	0
2	BR	5	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	BS	5	0	0	0	0
2	BT	5	0	0	2	0
2	BU	5	0	0	1	0
2	BV	5	0	0	0	0
2	BW	5	0	0	3	0
2	BX	5	0	0	0	0
2	BY	5	0	0	2	0
2	BZ	5	0	0	1	0
2	C1	5	0	0	1	0
2	C2	5	0	0	3	0
2	C3	5	0	0	0	0
2	C4	5	0	0	2	0
2	CA	5	0	0	1	0
2	CB	5	0	0	1	0
2	CC	5	0	0	3	0
2	CD	5	0	0	0	0
2	CE	5	0	0	2	0
2	CF	5	0	0	1	0
2	CG	5	0	0	1	0
2	CH	5	0	0	3	0
2	CI	5	0	0	0	0
2	CJ	5	0	0	2	0
2	CK	5	0	0	1	0
2	CL	5	0	0	1	0
2	CM	5	0	0	3	0
2	CN	5	0	0	0	0
2	CO	5	0	0	2	0
2	CP	5	0	0	1	0
2	CQ	5	0	0	0	0
2	CR	5	0	0	3	0
2	CS	5	0	0	0	0
2	CT	5	0	0	2	0
2	CU	5	0	0	1	0
2	CV	5	0	0	0	0
2	CW	5	0	0	3	0
2	CX	5	0	0	0	0
2	CY	5	0	0	2	0
2	CZ	5	0	0	1	0
All	All	102534	0	103266	5521	13

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 27.

All (5521) 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:CT:53:PRO:CG	1:CT:57:GLU:HG3	1.49	1.43
1:CJ:53:PRO:CG	1:CJ:57:GLU:HG3	1.49	1.42
1:AE:53:PRO:CG	1:AE:57:GLU:HG3	1.49	1.42
1:B4:53:PRO:CG	1:B4:57:GLU:HG3	1.49	1.42
1:C4:53:PRO:CG	1:C4:57:GLU:HG3	1.49	1.42
1:CY:53:PRO:CG	1:CY:57:GLU:HG3	1.49	1.42
1:A4:53:PRO:CG	1:A4:57:GLU:HG3	1.49	1.42
1:AJ:53:PRO:CG	1:AJ:57:GLU:HG3	1.49	1.41
1:BJ:53:PRO:CG	1:BJ:57:GLU:HG3	1.49	1.41
1:AO:53:PRO:CG	1:AO:57:GLU:HG3	1.49	1.41
1:BO:53:PRO:CG	1:BO:57:GLU:HG3	1.49	1.41
1:AT:53:PRO:CG	1:AT:57:GLU:HG3	1.49	1.41
1:CE:53:PRO:CG	1:CE:57:GLU:HG3	1.49	1.40
1:BY:53:PRO:CG	1:BY:57:GLU:HG3	1.49	1.40
1:CO:53:PRO:CG	1:CO:57:GLU:HG3	1.49	1.40
1:AY:53:PRO:CG	1:AY:57:GLU:HG3	1.49	1.39
1:BT:53:PRO:CG	1:BT:57:GLU:HG3	1.49	1.39
1:BE:53:PRO:CG	1:BE:57:GLU:HG3	1.49	1.39
1:AQ:69:GLY:O	1:BU:10:THR:HG23	1.27	1.33
1:CE:53:PRO:HG2	1:CE:57:GLU:CG	1.59	1.32
1:CO:53:PRO:HG2	1:CO:57:GLU:CG	1.59	1.32
1:CT:53:PRO:HG2	1:CT:57:GLU:CG	1.59	1.32
1:AJ:53:PRO:HG2	1:AJ:57:GLU:CG	1.59	1.32
1:CY:53:PRO:HG2	1:CY:57:GLU:CG	1.59	1.32
1:AO:53:PRO:HG2	1:AO:57:GLU:CG	1.59	1.31
1:AE:53:PRO:HG2	1:AE:57:GLU:CG	1.59	1.31
1:CJ:53:PRO:HG2	1:CJ:57:GLU:CG	1.59	1.31
1:AT:53:PRO:HG2	1:AT:57:GLU:CG	1.59	1.31
1:BO:53:PRO:HG2	1:BO:57:GLU:CG	1.59	1.30
1:C4:53:PRO:HG2	1:C4:57:GLU:CG	1.59	1.30
1:B4:53:PRO:HG2	1:B4:57:GLU:CG	1.59	1.30
1:A4:53:PRO:HG2	1:A4:57:GLU:CG	1.59	1.30
1:BJ:53:PRO:HG2	1:BJ:57:GLU:CG	1.59	1.30
1:BY:53:PRO:HG2	1:BY:57:GLU:CG	1.59	1.30
1:BT:53:PRO:HG2	1:BT:57:GLU:CG	1.59	1.29
1:BE:53:PRO:HG2	1:BE:57:GLU:CG	1.59	1.29
1:AY:53:PRO:HG2	1:AY:57:GLU:CG	1.59	1.29
1:AR:129:THR:HG22	1:AR:130:LYS:H	1.05	1.20
1:BH:129:THR:HG22	1:BH:130:LYS:H	1.05	1.20
1:C2:129:THR:HG22	1:C2:130:LYS:H	1.05	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:129:THR:HG22	1:AC:130:LYS:H	1.05	1.17
1:CR:129:THR:HG22	1:CR:130:LYS:H	1.05	1.17
1:B2:129:THR:HG22	1:B2:130:LYS:H	1.05	1.16
1:BB:107:ASP:OD2	1:BC:64:LYS:NZ	1.76	1.15
1:BM:129:THR:HG22	1:BM:130:LYS:H	1.05	1.15
1:CM:129:THR:HG22	1:CM:130:LYS:H	1.05	1.15
1:CW:129:THR:HG22	1:CW:130:LYS:H	1.05	1.15
1:AM:129:THR:HG22	1:AM:130:LYS:H	1.05	1.15
1:C1:107:ASP:OD2	1:C2:64:LYS:NZ	1.76	1.14
1:AG:104:LEU:HD21	1:AH:60:LEU:HA	1.30	1.14
1:A2:129:THR:HG22	1:A2:130:LYS:H	1.05	1.14
1:BL:104:LEU:HD21	1:BM:60:LEU:HA	1.30	1.14
1:BG:104:LEU:HD21	1:BH:60:LEU:HA	1.30	1.13
1:A1:104:LEU:HD21	1:A2:60:LEU:HA	1.30	1.12
1:CL:104:LEU:HD21	1:CM:60:LEU:HA	1.30	1.12
1:CC:129:THR:HG22	1:CC:130:LYS:H	1.05	1.12
1:AL:104:LEU:HD21	1:AM:60:LEU:HA	1.30	1.12
1:BV:104:LEU:HD21	1:BW:60:LEU:HA	1.30	1.12
1:CV:107:ASP:OD2	1:CW:64:LYS:NZ	1.76	1.11
1:BW:129:THR:HG22	1:BW:130:LYS:H	1.05	1.11
1:BR:129:THR:HG22	1:BR:130:LYS:H	1.05	1.11
1:AW:129:THR:HG22	1:AW:130:LYS:H	1.05	1.11
1:AQ:13:LYS:NZ	1:BU:43:GLU:HG2	1.65	1.11
1:AH:129:THR:HG22	1:AH:130:LYS:H	1.05	1.11
1:CG:104:LEU:HD21	1:CH:60:LEU:HA	1.30	1.10
1:B1:107:ASP:OD2	1:B2:64:LYS:NZ	1.76	1.10
1:CV:104:LEU:HD21	1:CW:60:LEU:HA	1.30	1.10
1:CB:107:ASP:OD2	1:CC:64:LYS:NZ	1.76	1.09
1:AV:104:LEU:HD21	1:AW:60:LEU:HA	1.30	1.09
1:CB:104:LEU:HD21	1:CC:60:LEU:HA	1.30	1.09
1:CH:129:THR:HG22	1:CH:130:LYS:H	1.05	1.08
1:AQ:104:LEU:HD21	1:AR:60:LEU:HA	1.30	1.08
1:B1:104:LEU:HD21	1:B2:60:LEU:HA	1.30	1.07
1:BV:107:ASP:OD2	1:BW:64:LYS:NZ	1.76	1.07
1:CQ:107:ASP:OD2	1:CR:64:LYS:NZ	1.76	1.07
1:BC:129:THR:HG22	1:BC:130:LYS:H	1.05	1.07
1:BG:107:ASP:OD2	1:BH:64:LYS:NZ	1.76	1.07
1:AB:104:LEU:HD21	1:AC:60:LEU:HA	1.30	1.07
1:C1:104:LEU:HD21	1:C2:60:LEU:HA	1.30	1.06
1:BQ:104:LEU:HD21	1:BR:60:LEU:HA	1.30	1.06
1:AE:72:ASP:O	1:AE:150:LYS:HD3	1.56	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:72:ASP:O	1:AO:150:LYS:HD3	1.56	1.05
1:BB:104:LEU:HD21	1:BC:60:LEU:HA	1.30	1.05
1:BY:72:ASP:O	1:BY:150:LYS:HD3	1.56	1.05
1:CO:72:ASP:O	1:CO:150:LYS:HD3	1.56	1.05
1:CJ:72:ASP:O	1:CJ:150:LYS:HD3	1.56	1.05
1:CE:72:ASP:O	1:CE:150:LYS:HD3	1.56	1.05
1:BD:11:GLY:HA3	1:CM:11:GLY:HA3	1.38	1.05
1:CL:107:ASP:OD2	1:CM:64:LYS:NZ	1.76	1.05
1:AJ:72:ASP:O	1:AJ:150:LYS:HD3	1.56	1.04
1:BE:72:ASP:O	1:BE:150:LYS:HD3	1.56	1.04
1:CQ:104:LEU:HD21	1:CR:60:LEU:HA	1.30	1.04
1:BL:107:ASP:OD2	1:BM:64:LYS:NZ	1.76	1.04
1:A4:72:ASP:O	1:A4:150:LYS:HD3	1.56	1.04
1:BO:72:ASP:O	1:BO:150:LYS:HD3	1.56	1.04
1:AT:72:ASP:O	1:AT:150:LYS:HD3	1.56	1.04
1:AY:72:ASP:O	1:AY:150:LYS:HD3	1.56	1.03
1:CY:72:ASP:O	1:CY:150:LYS:HD3	1.56	1.03
1:B4:72:ASP:O	1:B4:150:LYS:HD3	1.56	1.03
1:BJ:72:ASP:O	1:BJ:150:LYS:HD3	1.56	1.03
1:BT:72:ASP:O	1:BT:150:LYS:HD3	1.56	1.03
1:C3:107:ASP:O	1:C3:107:ASP:OD1	1.77	1.02
1:BI:107:ASP:OD1	1:BI:107:ASP:O	1.77	1.02
1:CT:72:ASP:O	1:CT:150:LYS:HD3	1.56	1.02
1:AI:107:ASP:OD1	1:AI:107:ASP:O	1.77	1.02
1:CG:107:ASP:OD2	1:CH:64:LYS:NZ	1.76	1.02
1:BN:107:ASP:O	1:BN:107:ASP:OD1	1.77	1.02
1:C4:72:ASP:O	1:C4:150:LYS:HD3	1.56	1.02
1:AN:107:ASP:OD1	1:AN:107:ASP:O	1.77	1.01
1:CN:107:ASP:O	1:CN:107:ASP:OD1	1.77	1.01
1:CI:107:ASP:O	1:CI:107:ASP:OD1	1.77	1.01
1:A3:107:ASP:OD1	1:A3:107:ASP:O	1.77	1.01
1:AD:107:ASP:OD1	1:AD:107:ASP:O	1.77	1.01
1:BB:107:ASP:HB2	1:BB:152:TRP:CZ3	1.96	1.01
1:BL:107:ASP:HB2	1:BL:152:TRP:CZ3	1.96	1.01
1:B1:52:VAL:HG12	1:B1:61:ILE:HD12	1.43	1.01
1:AX:107:ASP:O	1:AX:107:ASP:OD1	1.77	1.01
1:CQ:107:ASP:HB2	1:CQ:152:TRP:CZ3	1.96	1.01
1:CX:107:ASP:OD1	1:CX:107:ASP:O	1.77	1.01
1:CV:107:ASP:HB2	1:CV:152:TRP:CZ3	1.96	1.00
1:CL:107:ASP:HB2	1:CL:152:TRP:CZ3	1.96	1.00
1:BV:52:VAL:HG12	1:BV:61:ILE:HD12	1.43	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CD:107:ASP:O	1:CD:107:ASP:OD1	1.77	1.00
1:AQ:52:VAL:HG12	1:AQ:61:ILE:HD12	1.43	1.00
1:CC:129:THR:HG21	1:CS:120:ILE:CD1	1.91	1.00
1:CB:107:ASP:HB2	1:CB:152:TRP:CZ3	1.96	1.00
1:BV:107:ASP:HB2	1:BV:152:TRP:CZ3	1.96	1.00
1:CS:107:ASP:OD1	1:CS:107:ASP:O	1.77	1.00
1:B1:107:ASP:HB2	1:B1:152:TRP:CZ3	1.96	1.00
1:BD:107:ASP:OD1	1:BD:107:ASP:O	1.77	1.00
1:CB:52:VAL:HG12	1:CB:61:ILE:HD12	1.43	1.00
1:AS:107:ASP:O	1:AS:107:ASP:OD1	1.77	1.00
1:AG:52:VAL:HG12	1:AG:61:ILE:HD12	1.43	1.00
1:BX:107:ASP:O	1:BX:107:ASP:OD1	1.77	1.00
1:BL:52:VAL:HG12	1:BL:61:ILE:HD12	1.43	1.00
1:BQ:107:ASP:OD2	1:BR:64:LYS:NZ	1.76	1.00
1:BG:107:ASP:HB2	1:BG:152:TRP:CZ3	1.96	0.99
1:B3:107:ASP:OD1	1:B3:107:ASP:O	1.77	0.99
1:AQ:69:GLY:O	1:BU:10:THR:CG2	2.08	0.99
1:BB:52:VAL:HG12	1:BB:61:ILE:HD12	1.43	0.99
1:BQ:107:ASP:HB2	1:BQ:152:TRP:CZ3	1.96	0.99
1:BS:107:ASP:O	1:BS:107:ASP:OD1	1.77	0.99
1:AL:52:VAL:HG12	1:AL:61:ILE:HD12	1.43	0.99
1:C1:107:ASP:HB2	1:C1:152:TRP:CZ3	1.96	0.99
1:CG:107:ASP:HB2	1:CG:152:TRP:CZ3	1.96	0.99
1:CQ:52:VAL:HG12	1:CQ:61:ILE:HD12	1.43	0.99
1:A1:52:VAL:HG12	1:A1:61:ILE:HD12	1.43	0.98
1:CL:52:VAL:HG12	1:CL:61:ILE:HD12	1.43	0.98
1:C1:52:VAL:HG12	1:C1:61:ILE:HD12	1.43	0.98
1:CV:52:VAL:HG12	1:CV:61:ILE:HD12	1.43	0.98
1:CG:52:VAL:HG12	1:CG:61:ILE:HD12	1.43	0.97
1:BG:52:VAL:HG12	1:BG:61:ILE:HD12	1.43	0.97
1:AB:52:VAL:HG12	1:AB:61:ILE:HD12	1.43	0.97
1:BQ:52:VAL:HG12	1:BQ:61:ILE:HD12	1.43	0.97
1:AV:52:VAL:HG12	1:AV:61:ILE:HD12	1.43	0.97
1:BB:96:ALA:C	1:BB:100:ALA:HB2	1.86	0.97
1:AV:96:ALA:C	1:AV:100:ALA:HB2	1.86	0.96
1:CB:96:ALA:C	1:CB:100:ALA:HB2	1.86	0.96
1:AG:96:ALA:C	1:AG:100:ALA:HB2	1.86	0.96
1:BL:96:ALA:C	1:BL:100:ALA:HB2	1.86	0.96
1:AL:96:ALA:C	1:AL:100:ALA:HB2	1.86	0.96
1:C1:96:ALA:C	1:C1:100:ALA:HB2	1.86	0.96
1:AQ:96:ALA:C	1:AQ:100:ALA:HB2	1.86	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:96:ALA:C	1:AB:100:ALA:HB2	1.86	0.96
1:B1:96:ALA:C	1:B1:100:ALA:HB2	1.86	0.96
1:CL:96:ALA:C	1:CL:100:ALA:HB2	1.86	0.95
1:CQ:96:ALA:C	1:CQ:100:ALA:HB2	1.86	0.95
1:BV:96:ALA:C	1:BV:100:ALA:HB2	1.86	0.95
1:BQ:96:ALA:C	1:BQ:100:ALA:HB2	1.86	0.95
1:BG:96:ALA:C	1:BG:100:ALA:HB2	1.86	0.95
1:CG:96:ALA:C	1:CG:100:ALA:HB2	1.86	0.95
1:CV:96:ALA:C	1:CV:100:ALA:HB2	1.86	0.95
1:AX:52:VAL:HG12	1:AX:61:ILE:HD12	1.49	0.94
1:A1:96:ALA:C	1:A1:100:ALA:HB2	1.86	0.94
1:AD:52:VAL:HG12	1:AD:61:ILE:HD12	1.49	0.94
1:AN:52:VAL:HG12	1:AN:61:ILE:HD12	1.49	0.94
1:B3:52:VAL:HG12	1:B3:61:ILE:HD12	1.49	0.94
1:CI:52:VAL:HG12	1:CI:61:ILE:HD12	1.49	0.94
1:BS:52:VAL:HG12	1:BS:61:ILE:HD12	1.49	0.94
1:BJ:52:VAL:HG12	1:BJ:61:ILE:HD12	1.50	0.94
1:BD:52:VAL:HG12	1:BD:61:ILE:HD12	1.49	0.94
1:BX:52:VAL:HG12	1:BX:61:ILE:HD12	1.49	0.93
1:BO:52:VAL:HG12	1:BO:61:ILE:HD12	1.50	0.93
1:C3:52:VAL:HG12	1:C3:61:ILE:HD12	1.49	0.93
1:AE:52:VAL:HG12	1:AE:61:ILE:HD12	1.51	0.93
1:AJ:52:VAL:HG12	1:AJ:61:ILE:HD12	1.51	0.93
1:AY:52:VAL:HG12	1:AY:61:ILE:HD12	1.50	0.93
1:BY:52:VAL:HG12	1:BY:61:ILE:HD12	1.51	0.93
1:C4:52:VAL:HG12	1:C4:61:ILE:HD12	1.51	0.93
1:B4:52:VAL:HG12	1:B4:61:ILE:HD12	1.51	0.93
1:AQ:13:LYS:HZ3	1:BU:43:GLU:HG2	1.19	0.93
1:AS:52:VAL:HG12	1:AS:61:ILE:HD12	1.49	0.93
1:A4:52:VAL:HG12	1:A4:61:ILE:HD12	1.51	0.93
1:AI:52:VAL:HG12	1:AI:61:ILE:HD12	1.49	0.93
1:AC:52:VAL:HG12	1:AC:61:ILE:HD12	1.51	0.93
1:CM:52:VAL:HG12	1:CM:61:ILE:HD12	1.51	0.93
1:A3:52:VAL:HG12	1:A3:61:ILE:HD12	1.50	0.93
1:CE:52:VAL:HG12	1:CE:61:ILE:HD12	1.51	0.93
1:BT:52:VAL:HG12	1:BT:61:ILE:HD12	1.50	0.93
1:BH:52:VAL:HG12	1:BH:61:ILE:HD12	1.51	0.93
1:BC:52:VAL:HG12	1:BC:61:ILE:HD12	1.51	0.92
1:AT:52:VAL:HG12	1:AT:61:ILE:HD12	1.51	0.92
1:BN:52:VAL:HG12	1:BN:61:ILE:HD12	1.49	0.92
1:CN:52:VAL:HG12	1:CN:61:ILE:HD12	1.49	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:52:VAL:HG12	1:AO:61:ILE:HD12	1.51	0.92
1:AH:52:VAL:HG12	1:AH:61:ILE:HD12	1.51	0.92
1:CR:52:VAL:HG12	1:CR:61:ILE:HD12	1.51	0.92
1:A2:52:VAL:HG12	1:A2:61:ILE:HD12	1.51	0.92
1:AM:52:VAL:HG12	1:AM:61:ILE:HD12	1.51	0.92
1:BE:52:VAL:HG12	1:BE:61:ILE:HD12	1.50	0.92
1:BR:52:VAL:HG12	1:BR:61:ILE:HD12	1.51	0.92
1:CC:52:VAL:HG12	1:CC:61:ILE:HD12	1.51	0.92
1:AW:52:VAL:HG12	1:AW:61:ILE:HD12	1.52	0.92
1:CS:52:VAL:HG12	1:CS:61:ILE:HD12	1.49	0.92
1:CJ:52:VAL:HG12	1:CJ:61:ILE:HD12	1.51	0.91
1:BI:52:VAL:HG12	1:BI:61:ILE:HD12	1.49	0.91
1:CH:52:VAL:HG12	1:CH:61:ILE:HD12	1.51	0.91
1:CX:52:VAL:HG12	1:CX:61:ILE:HD12	1.49	0.91
1:B2:52:VAL:HG12	1:B2:61:ILE:HD12	1.51	0.91
1:BM:52:VAL:HG12	1:BM:61:ILE:HD12	1.51	0.91
1:CD:52:VAL:HG12	1:CD:61:ILE:HD12	1.49	0.91
1:BW:52:VAL:HG12	1:BW:61:ILE:HD12	1.51	0.90
1:CO:52:VAL:HG12	1:CO:61:ILE:HD12	1.50	0.90
1:AR:52:VAL:HG12	1:AR:61:ILE:HD12	1.51	0.90
1:C2:52:VAL:HG12	1:C2:61:ILE:HD12	1.52	0.90
1:CY:52:VAL:HG12	1:CY:61:ILE:HD12	1.51	0.90
1:CW:52:VAL:HG12	1:CW:61:ILE:HD12	1.51	0.90
1:BP:52:VAL:HG12	1:BP:61:ILE:HD12	1.54	0.90
1:AP:52:VAL:HG12	1:AP:61:ILE:HD12	1.54	0.90
1:CK:52:VAL:HG12	1:CK:61:ILE:HD12	1.54	0.89
1:CT:52:VAL:HG12	1:CT:61:ILE:HD12	1.51	0.89
1:AU:52:VAL:HG12	1:AU:61:ILE:HD12	1.54	0.89
1:AF:52:VAL:HG12	1:AF:61:ILE:HD12	1.54	0.89
1:CU:52:VAL:HG12	1:CU:61:ILE:HD12	1.54	0.89
1:BO:52:VAL:HB	1:BO:53:PRO:HD2	1.55	0.89
1:CT:52:VAL:HB	1:CT:53:PRO:HD2	1.55	0.89
1:B4:52:VAL:HB	1:B4:53:PRO:HD2	1.55	0.89
1:CJ:52:VAL:HB	1:CJ:53:PRO:HD2	1.55	0.88
1:CR:129:THR:HG22	1:CR:130:LYS:N	1.88	0.88
1:AK:52:VAL:HG12	1:AK:61:ILE:HD12	1.54	0.88
1:BY:52:VAL:HB	1:BY:53:PRO:HD2	1.55	0.88
1:BT:52:VAL:HB	1:BT:53:PRO:HD2	1.55	0.88
1:CH:129:THR:HG22	1:CH:130:LYS:N	1.88	0.88
1:BK:52:VAL:HG12	1:BK:61:ILE:HD12	1.54	0.88
1:BF:52:VAL:HG12	1:BF:61:ILE:HD12	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:52:VAL:HB	1:AJ:53:PRO:HD2	1.55	0.88
1:AY:52:VAL:HB	1:AY:53:PRO:HD2	1.55	0.88
1:BW:129:THR:HG22	1:BW:130:LYS:N	1.89	0.88
1:BA:52:VAL:HG12	1:BA:61:ILE:HD12	1.54	0.88
1:A4:52:VAL:HB	1:A4:53:PRO:HD2	1.55	0.88
1:AO:52:VAL:HB	1:AO:53:PRO:HD2	1.55	0.88
1:BE:52:VAL:HB	1:BE:53:PRO:HD2	1.55	0.88
1:AR:129:THR:HG22	1:AR:130:LYS:N	1.88	0.88
1:CF:52:VAL:HG12	1:CF:61:ILE:HD12	1.54	0.88
1:CC:129:THR:HG22	1:CC:130:LYS:N	1.88	0.88
1:CA:52:VAL:HG12	1:CA:61:ILE:HD12	1.54	0.88
1:AT:52:VAL:HB	1:AT:53:PRO:HD2	1.55	0.87
1:C4:52:VAL:HB	1:C4:53:PRO:HD2	1.55	0.87
1:BH:129:THR:HG22	1:BH:130:LYS:N	1.89	0.87
1:CM:129:THR:HG22	1:CM:130:LYS:N	1.88	0.87
1:BR:129:THR:HG22	1:BR:130:LYS:N	1.89	0.87
1:CP:52:VAL:HG12	1:CP:61:ILE:HD12	1.54	0.87
1:BZ:52:VAL:HG12	1:BZ:61:ILE:HD12	1.54	0.87
1:B2:129:THR:HG22	1:B2:130:LYS:N	1.88	0.87
1:AH:129:THR:HG22	1:AH:130:LYS:N	1.89	0.87
1:CO:52:VAL:HB	1:CO:53:PRO:HD2	1.55	0.87
1:AW:129:THR:HG22	1:AW:130:LYS:N	1.88	0.87
1:CE:52:VAL:HB	1:CE:53:PRO:HD2	1.55	0.87
1:C2:129:THR:HG22	1:C2:130:LYS:N	1.88	0.87
1:AC:129:THR:HG22	1:AC:130:LYS:N	1.88	0.86
1:BC:129:THR:HG21	1:BS:120:ILE:CD1	2.05	0.86
1:A2:129:THR:HG22	1:A2:130:LYS:N	1.88	0.86
1:AW:129:THR:CG2	1:AW:130:LYS:H	1.89	0.86
1:BU:52:VAL:HG12	1:BU:61:ILE:HD12	1.54	0.86
1:AE:52:VAL:HB	1:AE:53:PRO:HD2	1.55	0.86
1:CY:52:VAL:HB	1:CY:53:PRO:HD2	1.55	0.86
1:BJ:52:VAL:HB	1:BJ:53:PRO:HD2	1.55	0.86
1:AA:52:VAL:HG12	1:AA:61:ILE:HD12	1.54	0.86
1:BM:129:THR:HG22	1:BM:130:LYS:N	1.88	0.86
1:AM:129:THR:HG22	1:AM:130:LYS:N	1.88	0.85
1:CZ:52:VAL:HG12	1:CZ:61:ILE:HD12	1.54	0.85
1:AZ:52:VAL:HG12	1:AZ:61:ILE:HD12	1.54	0.85
1:AQ:13:LYS:NZ	1:BU:43:GLU:CG	2.39	0.85
1:C1:55:ALA:HB1	1:C1:95:VAL:HG21	1.59	0.85
1:CQ:55:ALA:HB1	1:CQ:95:VAL:HG21	1.59	0.85
1:CV:55:ALA:HB1	1:CV:95:VAL:HG21	1.59	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:129:THR:CG2	1:BC:130:LYS:H	1.89	0.85
1:C2:129:THR:CG2	1:C2:130:LYS:H	1.89	0.85
1:AM:129:THR:CG2	1:AM:130:LYS:H	1.89	0.85
1:BG:55:ALA:HB1	1:BG:95:VAL:HG21	1.59	0.85
1:A1:55:ALA:HB1	1:A1:95:VAL:HG21	1.59	0.85
1:AB:55:ALA:HB1	1:AB:95:VAL:HG21	1.59	0.85
1:B1:55:ALA:HB1	1:B1:95:VAL:HG21	1.59	0.84
1:BC:129:THR:HG22	1:BC:130:LYS:N	1.88	0.84
1:BB:55:ALA:HB1	1:BB:95:VAL:HG21	1.59	0.84
1:CB:55:ALA:HB1	1:CB:95:VAL:HG21	1.59	0.84
1:AG:55:ALA:HB1	1:AG:95:VAL:HG21	1.59	0.84
1:CM:129:THR:CG2	1:CM:130:LYS:H	1.89	0.84
1:CH:129:THR:CG2	1:CH:130:LYS:H	1.89	0.84
1:BT:124:ILE:O	1:BT:129:THR:OG1	1.96	0.84
1:BV:55:ALA:HB1	1:BV:95:VAL:HG21	1.59	0.84
1:AO:124:ILE:O	1:AO:129:THR:OG1	1.96	0.84
1:BO:124:ILE:O	1:BO:129:THR:OG1	1.96	0.84
1:CT:124:ILE:O	1:CT:129:THR:OG1	1.96	0.83
1:AY:124:ILE:O	1:AY:129:THR:OG1	1.96	0.83
1:BY:124:ILE:O	1:BY:129:THR:OG1	1.96	0.83
1:A4:124:ILE:O	1:A4:129:THR:OG1	1.96	0.83
1:AV:55:ALA:HB1	1:AV:95:VAL:HG21	1.59	0.83
1:AJ:108:ILE:HG12	1:AJ:150:LYS:HE3	1.61	0.83
1:CO:124:ILE:O	1:CO:129:THR:OG1	1.96	0.83
1:CO:108:ILE:HG12	1:CO:150:LYS:HE3	1.61	0.83
1:BT:108:ILE:HG12	1:BT:150:LYS:HE3	1.61	0.83
1:CY:124:ILE:O	1:CY:129:THR:OG1	1.96	0.83
1:B2:129:THR:CG2	1:B2:130:LYS:H	1.89	0.83
1:BL:55:ALA:HB1	1:BL:95:VAL:HG21	1.59	0.83
1:AJ:124:ILE:O	1:AJ:129:THR:OG1	1.96	0.83
1:BE:124:ILE:O	1:BE:129:THR:OG1	1.96	0.83
1:BO:108:ILE:HG12	1:BO:150:LYS:HE3	1.61	0.83
1:BQ:55:ALA:HB1	1:BQ:95:VAL:HG21	1.59	0.83
1:BD:11:GLY:HA3	1:CM:11:GLY:CA	2.09	0.83
1:AT:108:ILE:HG12	1:AT:150:LYS:HE3	1.61	0.83
1:AQ:55:ALA:HB1	1:AQ:95:VAL:HG21	1.59	0.83
1:CL:55:ALA:HB1	1:CL:95:VAL:HG21	1.59	0.83
1:CG:55:ALA:HB1	1:CG:95:VAL:HG21	1.59	0.83
1:BJ:124:ILE:O	1:BJ:129:THR:OG1	1.96	0.83
1:CR:129:THR:CG2	1:CR:130:LYS:H	1.89	0.82
1:AE:108:ILE:HG12	1:AE:150:LYS:HE3	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:108:ILE:HG12	1:BE:150:LYS:HE3	1.61	0.82
1:AO:108:ILE:HG12	1:AO:150:LYS:HE3	1.61	0.82
1:CY:108:ILE:HG12	1:CY:150:LYS:HE3	1.61	0.82
1:CE:124:ILE:O	1:CE:129:THR:OG1	1.96	0.82
1:BJ:108:ILE:HG12	1:BJ:150:LYS:HE3	1.61	0.82
1:AL:55:ALA:HB1	1:AL:95:VAL:HG21	1.59	0.82
1:AE:124:ILE:O	1:AE:129:THR:OG1	1.96	0.82
1:AY:108:ILE:HG12	1:AY:150:LYS:HE3	1.61	0.82
1:B4:108:ILE:HG12	1:B4:150:LYS:HE3	1.61	0.82
1:CJ:124:ILE:O	1:CJ:129:THR:OG1	1.96	0.82
1:CW:129:THR:HG22	1:CW:130:LYS:N	1.88	0.82
1:B4:124:ILE:O	1:B4:129:THR:OG1	1.96	0.82
1:CJ:108:ILE:HG12	1:CJ:150:LYS:HE3	1.61	0.82
1:C4:124:ILE:O	1:C4:129:THR:OG1	1.96	0.82
1:AT:124:ILE:O	1:AT:129:THR:OG1	1.96	0.82
1:C4:108:ILE:HG12	1:C4:150:LYS:HE3	1.61	0.81
1:CE:108:ILE:HG12	1:CE:150:LYS:HE3	1.61	0.81
1:A4:108:ILE:HG12	1:A4:150:LYS:HE3	1.61	0.81
1:AR:129:THR:CG2	1:AR:130:LYS:H	1.89	0.81
1:AM:38:LYS:HZ2	1:AM:44:GLU:HG3	1.45	0.81
1:BY:108:ILE:HG12	1:BY:150:LYS:HE3	1.61	0.81
1:B2:7:LEU:HD11	1:B2:140:VAL:HG13	1.63	0.81
1:AQ:13:LYS:HZ3	1:BU:43:GLU:CG	1.94	0.81
1:AR:7:LEU:HD11	1:AR:140:VAL:HG13	1.63	0.81
1:CT:108:ILE:HG12	1:CT:150:LYS:HE3	1.61	0.81
1:BR:7:LEU:HD11	1:BR:140:VAL:HG13	1.63	0.81
1:BM:7:LEU:HD11	1:BM:140:VAL:HG13	1.63	0.81
1:CW:7:LEU:HD11	1:CW:140:VAL:HG13	1.63	0.80
1:BM:129:THR:CG2	1:BM:130:LYS:H	1.89	0.80
1:AQ:13:LYS:HZ1	1:BU:43:GLU:CB	1.94	0.80
1:BD:11:GLY:CA	1:CM:11:GLY:HA3	2.11	0.80
1:B3:18:VAL:HG12	1:B3:77:LEU:HB2	1.64	0.80
1:BN:18:VAL:HG12	1:BN:77:LEU:HB2	1.63	0.80
1:AD:18:VAL:HG12	1:AD:77:LEU:HB2	1.64	0.80
1:CD:28:LYS:NZ	1:CF:28:LYS:HZ2	1.79	0.80
1:CC:7:LEU:HD11	1:CC:140:VAL:HG13	1.63	0.80
1:AH:7:LEU:HD11	1:AH:140:VAL:HG13	1.63	0.80
1:AS:18:VAL:HG12	1:AS:77:LEU:HB2	1.64	0.80
1:AX:18:VAL:HG12	1:AX:77:LEU:HB2	1.63	0.80
1:BD:18:VAL:HG12	1:BD:77:LEU:HB2	1.64	0.80
1:AL:7:LEU:HD11	1:AL:140:VAL:HG13	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:7:LEU:HD11	1:AB:140:VAL:HG13	1.64	0.80
1:AC:7:LEU:HD11	1:AC:140:VAL:HG13	1.63	0.80
1:CM:7:LEU:HD11	1:CM:140:VAL:HG13	1.63	0.80
1:CR:7:LEU:HD11	1:CR:140:VAL:HG13	1.63	0.80
1:A2:7:LEU:HD11	1:A2:140:VAL:HG13	1.63	0.80
1:CB:7:LEU:HD11	1:CB:140:VAL:HG13	1.64	0.80
1:CW:129:THR:CG2	1:CW:130:LYS:H	1.89	0.80
1:CG:7:LEU:HD11	1:CG:140:VAL:HG13	1.64	0.79
1:CW:38:LYS:HZ2	1:CW:44:GLU:HG3	1.47	0.79
1:AO:72:ASP:C	1:AO:150:LYS:HD3	2.03	0.79
1:CQ:7:LEU:HD11	1:CQ:140:VAL:HG13	1.64	0.79
1:BX:18:VAL:HG12	1:BX:77:LEU:HB2	1.64	0.79
1:AW:7:LEU:HD11	1:AW:140:VAL:HG13	1.63	0.79
1:AT:72:ASP:C	1:AT:150:LYS:HD3	2.03	0.79
1:AY:72:ASP:C	1:AY:150:LYS:HD3	2.03	0.79
1:BB:7:LEU:HD11	1:BB:140:VAL:HG13	1.64	0.79
1:CL:7:LEU:HD11	1:CL:140:VAL:HG13	1.64	0.79
1:BI:18:VAL:HG12	1:BI:77:LEU:HB2	1.64	0.79
1:CE:72:ASP:C	1:CE:150:LYS:HD3	2.03	0.79
1:BH:7:LEU:HD11	1:BH:140:VAL:HG13	1.63	0.79
1:BW:7:LEU:HD11	1:BW:140:VAL:HG13	1.63	0.79
1:CI:18:VAL:HG12	1:CI:77:LEU:HB2	1.63	0.79
1:BO:72:ASP:C	1:BO:150:LYS:HD3	2.03	0.79
1:CJ:72:ASP:C	1:CJ:150:LYS:HD3	2.03	0.79
1:CX:18:VAL:HG12	1:CX:77:LEU:HB2	1.64	0.79
1:BH:129:THR:CG2	1:BH:130:LYS:H	1.89	0.79
1:AC:129:THR:CG2	1:AC:130:LYS:H	1.89	0.79
1:BD:120:ILE:CD1	1:BR:129:THR:HG21	2.12	0.79
1:CW:34:LEU:HD22	1:CW:38:LYS:HE2	1.65	0.79
1:CS:18:VAL:HG12	1:CS:77:LEU:HB2	1.63	0.79
1:C2:7:LEU:HD11	1:C2:140:VAL:HG13	1.63	0.79
1:CN:18:VAL:HG12	1:CN:77:LEU:HB2	1.64	0.79
1:BH:34:LEU:HD22	1:BH:38:LYS:HE2	1.65	0.79
1:BS:18:VAL:HG12	1:BS:77:LEU:HB2	1.63	0.79
1:CV:7:LEU:HD11	1:CV:140:VAL:HG13	1.64	0.79
1:C2:82:ARG:HH11	1:C2:82:ARG:HG3	1.49	0.79
1:AH:82:ARG:HG3	1:AH:82:ARG:HH11	1.48	0.78
1:BR:82:ARG:HH11	1:BR:82:ARG:HG3	1.48	0.78
1:B1:7:LEU:HD11	1:B1:140:VAL:HG13	1.64	0.78
1:B2:34:LEU:HD22	1:B2:38:LYS:HE2	1.65	0.78
1:AV:7:LEU:HD11	1:AV:140:VAL:HG13	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:82:ARG:HH11	1:CR:82:ARG:HG3	1.49	0.78
1:BW:119:THR:HG22	1:BW:121:GLU:H	1.49	0.78
1:BW:129:THR:CG2	1:BW:130:LYS:H	1.89	0.78
1:CT:72:ASP:C	1:CT:150:LYS:HD3	2.03	0.78
1:A3:18:VAL:HG12	1:A3:77:LEU:HB2	1.64	0.78
1:BH:82:ARG:HH11	1:BH:82:ARG:HG3	1.49	0.78
1:BC:7:LEU:HD11	1:BC:140:VAL:HG13	1.63	0.78
1:CD:18:VAL:HG12	1:CD:77:LEU:HB2	1.64	0.78
1:BC:82:ARG:HG3	1:BC:82:ARG:HH11	1.49	0.78
1:AR:34:LEU:HD22	1:AR:38:LYS:HE2	1.65	0.78
1:AN:18:VAL:HG12	1:AN:77:LEU:HB2	1.64	0.78
1:AW:82:ARG:HH11	1:AW:82:ARG:HG3	1.49	0.78
1:BW:82:ARG:HH11	1:BW:82:ARG:HG3	1.49	0.78
1:AD:120:ILE:CD1	1:AR:129:THR:HG21	2.14	0.78
1:BT:72:ASP:C	1:BT:150:LYS:HD3	2.03	0.78
1:BR:119:THR:HG22	1:BR:121:GLU:H	1.49	0.78
1:BE:72:ASP:C	1:BE:150:LYS:HD3	2.03	0.78
1:AC:34:LEU:HD22	1:AC:38:LYS:HE2	1.65	0.78
1:BM:119:THR:HG22	1:BM:121:GLU:H	1.49	0.78
1:AM:7:LEU:HD11	1:AM:140:VAL:HG13	1.63	0.78
1:BL:7:LEU:HD11	1:BL:140:VAL:HG13	1.64	0.78
1:A2:34:LEU:HD22	1:A2:38:LYS:HE2	1.65	0.78
1:B2:119:THR:HG22	1:B2:121:GLU:H	1.49	0.78
1:CM:119:THR:HG22	1:CM:121:GLU:H	1.49	0.78
1:BG:7:LEU:HD11	1:BG:140:VAL:HG13	1.64	0.78
1:C3:18:VAL:HG12	1:C3:77:LEU:HB2	1.64	0.78
1:CO:72:ASP:C	1:CO:150:LYS:HD3	2.03	0.78
1:BI:16:VAL:HG12	1:BI:75:ILE:HB	1.66	0.78
1:CW:82:ARG:HG3	1:CW:82:ARG:HH11	1.49	0.78
1:AI:18:VAL:HG12	1:AI:77:LEU:HB2	1.64	0.78
1:BC:119:THR:HG22	1:BC:121:GLU:H	1.49	0.78
1:CW:119:THR:HG22	1:CW:121:GLU:H	1.49	0.78
1:AR:119:THR:HG22	1:AR:121:GLU:H	1.49	0.78
1:BM:34:LEU:HD22	1:BM:38:LYS:HE2	1.65	0.78
1:A2:82:ARG:HG3	1:A2:82:ARG:HH11	1.48	0.78
1:C2:119:THR:HG22	1:C2:121:GLU:H	1.49	0.78
1:B4:72:ASP:C	1:B4:150:LYS:HD3	2.03	0.78
1:BR:34:LEU:HD22	1:BR:38:LYS:HE2	1.65	0.78
1:BC:34:LEU:HD22	1:BC:38:LYS:HE2	1.65	0.78
1:BM:82:ARG:HG3	1:BM:82:ARG:HH11	1.49	0.78
1:AW:119:THR:HG22	1:AW:121:GLU:H	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:34:LEU:HD22	1:CH:38:LYS:HE2	1.65	0.78
1:C4:72:ASP:C	1:C4:150:LYS:HD3	2.03	0.78
1:AX:16:VAL:HG12	1:AX:75:ILE:HB	1.66	0.78
1:BD:16:VAL:HG12	1:BD:75:ILE:HB	1.66	0.78
1:CX:16:VAL:HG12	1:CX:75:ILE:HB	1.66	0.78
1:C3:16:VAL:HG12	1:C3:75:ILE:HB	1.66	0.78
1:C1:7:LEU:HD11	1:C1:140:VAL:HG13	1.64	0.78
1:CR:38:LYS:HZ2	1:CR:44:GLU:HG3	1.48	0.78
1:AH:34:LEU:HD22	1:AH:38:LYS:HE2	1.65	0.78
1:AJ:72:ASP:C	1:AJ:150:LYS:HD3	2.03	0.77
1:CS:16:VAL:HG12	1:CS:75:ILE:HB	1.66	0.77
1:CH:7:LEU:HD11	1:CH:140:VAL:HG13	1.63	0.77
1:AM:119:THR:HG22	1:AM:121:GLU:H	1.49	0.77
1:CC:34:LEU:HD22	1:CC:38:LYS:HE2	1.65	0.77
1:CC:82:ARG:HH11	1:CC:82:ARG:HG3	1.48	0.77
1:CC:119:THR:HG22	1:CC:121:GLU:H	1.49	0.77
1:AE:72:ASP:C	1:AE:150:LYS:HD3	2.03	0.77
1:BJ:72:ASP:C	1:BJ:150:LYS:HD3	2.03	0.77
1:BQ:7:LEU:HD11	1:BQ:140:VAL:HG13	1.64	0.77
1:AN:16:VAL:HG12	1:AN:75:ILE:HB	1.66	0.77
1:CM:38:LYS:HZ2	1:CM:44:GLU:HG3	1.49	0.77
1:CR:34:LEU:HD22	1:CR:38:LYS:HE2	1.65	0.77
1:BY:18:VAL:HG12	1:BY:77:LEU:HB2	1.67	0.77
1:AY:18:VAL:HG12	1:AY:77:LEU:HB2	1.67	0.77
1:CY:18:VAL:HG12	1:CY:77:LEU:HB2	1.67	0.77
1:BO:18:VAL:HG12	1:BO:77:LEU:HB2	1.67	0.77
1:CY:72:ASP:C	1:CY:150:LYS:HD3	2.03	0.77
1:A3:16:VAL:HG12	1:A3:75:ILE:HB	1.66	0.77
1:AM:82:ARG:HG3	1:AM:82:ARG:HH11	1.49	0.77
1:BY:72:ASP:C	1:BY:150:LYS:HD3	2.03	0.77
1:A4:72:ASP:C	1:A4:150:LYS:HD3	2.03	0.77
1:AQ:7:LEU:HD11	1:AQ:140:VAL:HG13	1.64	0.77
1:BT:18:VAL:HG12	1:BT:77:LEU:HB2	1.67	0.77
1:AW:34:LEU:HD22	1:AW:38:LYS:HE2	1.65	0.77
1:BG:104:LEU:HD13	1:BH:102:LEU:HD22	1.67	0.77
1:AC:82:ARG:HG3	1:AC:82:ARG:HH11	1.49	0.77
1:AO:18:VAL:HG12	1:AO:77:LEU:HB2	1.67	0.77
1:CN:16:VAL:HG12	1:CN:75:ILE:HB	1.66	0.77
1:BW:34:LEU:HD22	1:BW:38:LYS:HE2	1.65	0.77
1:BV:104:LEU:HD13	1:BW:102:LEU:HD22	1.67	0.77
1:CB:104:LEU:HD13	1:CC:102:LEU:HD22	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:16:VAL:HG12	1:BX:75:ILE:HB	1.66	0.77
1:AC:119:THR:HG22	1:AC:121:GLU:H	1.49	0.77
1:BV:7:LEU:HD11	1:BV:140:VAL:HG13	1.64	0.77
1:CM:82:ARG:HH11	1:CM:82:ARG:HG3	1.49	0.77
1:C1:104:LEU:HD13	1:C2:102:LEU:HD22	1.67	0.77
1:BS:16:VAL:HG12	1:BS:75:ILE:HB	1.66	0.77
1:AE:18:VAL:HG12	1:AE:77:LEU:HB2	1.67	0.77
1:CV:104:LEU:HD13	1:CW:102:LEU:HD22	1.67	0.77
1:B1:104:LEU:HD13	1:B2:102:LEU:HD22	1.67	0.77
1:AD:16:VAL:HG12	1:AD:75:ILE:HB	1.66	0.77
1:AS:16:VAL:HG12	1:AS:75:ILE:HB	1.66	0.77
1:AJ:18:VAL:HG12	1:AJ:77:LEU:HB2	1.67	0.77
1:C2:34:LEU:HD22	1:C2:38:LYS:HE2	1.65	0.77
1:AH:129:THR:CG2	1:AH:130:LYS:H	1.89	0.76
1:CJ:109:PRO:HD2	1:CJ:150:LYS:HD2	1.67	0.76
1:CQ:104:LEU:HD13	1:CR:102:LEU:HD22	1.67	0.76
1:BO:109:PRO:HD2	1:BO:150:LYS:HD2	1.67	0.76
1:AM:34:LEU:HD22	1:AM:38:LYS:HE2	1.65	0.76
1:CC:7:LEU:HD23	1:CR:40:HIS:CE1	2.20	0.76
1:AH:119:THR:HG22	1:AH:121:GLU:H	1.49	0.76
1:A1:104:LEU:HD13	1:A2:102:LEU:HD22	1.67	0.76
1:AI:16:VAL:HG12	1:AI:75:ILE:HB	1.66	0.76
1:CM:34:LEU:HD22	1:CM:38:LYS:HE2	1.65	0.76
1:CO:18:VAL:HG12	1:CO:77:LEU:HB2	1.67	0.76
1:A2:119:THR:HG22	1:A2:121:GLU:H	1.49	0.76
1:AG:7:LEU:HD11	1:AG:140:VAL:HG13	1.64	0.76
1:B4:109:PRO:HD2	1:B4:150:LYS:HD2	1.68	0.76
1:A1:7:LEU:HD11	1:A1:140:VAL:HG13	1.64	0.76
1:AQ:104:LEU:HD13	1:AR:102:LEU:HD22	1.67	0.76
1:CY:109:PRO:HD2	1:CY:150:LYS:HD2	1.68	0.76
1:B3:16:VAL:HG12	1:B3:75:ILE:HB	1.66	0.76
1:CE:18:VAL:HG12	1:CE:77:LEU:HB2	1.67	0.76
1:CH:119:THR:HG22	1:CH:121:GLU:H	1.49	0.76
1:BB:104:LEU:HD13	1:BC:102:LEU:HD22	1.67	0.76
1:AJ:109:PRO:HD2	1:AJ:150:LYS:HD2	1.67	0.76
1:A4:109:PRO:HD2	1:A4:150:LYS:HD2	1.67	0.76
1:AR:68:SER:O	1:AR:70:LYS:HG2	1.86	0.76
1:AW:68:SER:O	1:AW:70:LYS:HG2	1.86	0.76
1:BE:18:VAL:HG12	1:BE:77:LEU:HB2	1.67	0.76
1:AO:109:PRO:HD2	1:AO:150:LYS:HD2	1.68	0.76
1:AH:68:SER:O	1:AH:70:LYS:HG2	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:104:LEU:HD13	1:AM:102:LEU:HD22	1.67	0.76
1:CC:129:THR:CG2	1:CC:130:LYS:H	1.89	0.76
1:BY:109:PRO:HD2	1:BY:150:LYS:HD2	1.67	0.76
1:CE:109:PRO:HD2	1:CE:150:LYS:HD2	1.68	0.76
1:BE:109:PRO:HD2	1:BE:150:LYS:HD2	1.67	0.76
1:CJ:18:VAL:HG12	1:CJ:77:LEU:HB2	1.67	0.76
1:BJ:18:VAL:HG12	1:BJ:77:LEU:HB2	1.67	0.76
1:BH:68:SER:O	1:BH:70:LYS:HG2	1.86	0.76
1:CC:68:SER:O	1:CC:70:LYS:HG2	1.86	0.76
1:A2:129:THR:CG2	1:A2:130:LYS:H	1.89	0.76
1:BJ:109:PRO:HD2	1:BJ:150:LYS:HD2	1.68	0.76
1:CH:38:LYS:HZ2	1:CH:44:GLU:HG3	1.50	0.76
1:AR:82:ARG:HH11	1:AR:82:ARG:HG3	1.48	0.76
1:AT:18:VAL:HG12	1:AT:77:LEU:HB2	1.67	0.76
1:CR:68:SER:O	1:CR:70:LYS:HG2	1.86	0.76
1:CK:55:ALA:HB1	1:CK:95:VAL:HG21	1.68	0.76
1:C4:18:VAL:HG12	1:C4:77:LEU:HB2	1.67	0.76
1:CF:125:GLU:HA	1:CF:129:THR:OG1	1.87	0.76
1:BH:119:THR:HG22	1:BH:121:GLU:H	1.49	0.76
1:CR:119:THR:HG22	1:CR:121:GLU:H	1.49	0.76
1:AB:104:LEU:HD13	1:AC:102:LEU:HD22	1.67	0.75
1:CO:109:PRO:HD2	1:CO:150:LYS:HD2	1.67	0.75
1:BN:16:VAL:HG12	1:BN:75:ILE:HB	1.66	0.75
1:B2:38:LYS:HZ2	1:B2:44:GLU:HG3	1.51	0.75
1:BP:125:GLU:HA	1:BP:129:THR:OG1	1.87	0.75
1:AA:55:ALA:HB1	1:AA:95:VAL:HG21	1.68	0.75
1:B2:68:SER:O	1:B2:70:LYS:HG2	1.86	0.75
1:BK:125:GLU:HA	1:BK:129:THR:OG1	1.87	0.75
1:CG:104:LEU:HD13	1:CH:102:LEU:HD22	1.67	0.75
1:CD:16:VAL:HG12	1:CD:75:ILE:HB	1.66	0.75
1:AU:55:ALA:HB1	1:AU:95:VAL:HG21	1.68	0.75
1:AU:125:GLU:HA	1:AU:129:THR:OG1	1.87	0.75
1:BM:68:SER:O	1:BM:70:LYS:HG2	1.86	0.75
1:B4:18:VAL:HG12	1:B4:77:LEU:HB2	1.67	0.75
1:BW:68:SER:O	1:BW:70:LYS:HG2	1.86	0.75
1:AE:109:PRO:HD2	1:AE:150:LYS:HD2	1.68	0.75
1:CI:16:VAL:HG12	1:CI:75:ILE:HB	1.66	0.75
1:CP:125:GLU:HA	1:CP:129:THR:OG1	1.87	0.75
1:B2:82:ARG:HG3	1:B2:82:ARG:HH11	1.49	0.75
1:CL:104:LEU:HD13	1:CM:102:LEU:HD22	1.67	0.75
1:BA:55:ALA:HB1	1:BA:95:VAL:HG21	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:125:GLU:HA	1:BA:129:THR:OG1	1.87	0.75
1:A4:18:VAL:HG12	1:A4:77:LEU:HB2	1.67	0.75
1:AV:104:LEU:HD13	1:AW:102:LEU:HD22	1.67	0.75
1:BA:119:THR:HG22	1:BA:121:GLU:H	1.52	0.75
1:BZ:125:GLU:HA	1:BZ:129:THR:OG1	1.87	0.75
1:CH:82:ARG:HG3	1:CH:82:ARG:HH11	1.48	0.75
1:CZ:55:ALA:HB1	1:CZ:95:VAL:HG21	1.68	0.75
1:A2:68:SER:O	1:A2:70:LYS:HG2	1.86	0.75
1:CT:119:THR:HG22	1:CT:121:GLU:H	1.52	0.75
1:BZ:55:ALA:HB1	1:BZ:95:VAL:HG21	1.68	0.75
1:AG:104:LEU:HD13	1:AH:102:LEU:HD22	1.67	0.75
1:AU:119:THR:HG22	1:AU:121:GLU:H	1.52	0.75
1:BC:68:SER:O	1:BC:70:LYS:HG2	1.86	0.75
1:BU:119:THR:HG22	1:BU:121:GLU:H	1.52	0.75
1:CM:68:SER:O	1:CM:70:LYS:HG2	1.86	0.75
1:CU:125:GLU:HA	1:CU:129:THR:OG1	1.86	0.75
1:BO:119:THR:HG22	1:BO:121:GLU:H	1.52	0.75
1:AM:68:SER:O	1:AM:70:LYS:HG2	1.86	0.75
1:BL:104:LEU:HD13	1:BM:102:LEU:HD22	1.67	0.75
1:CF:119:THR:HG22	1:CF:121:GLU:H	1.52	0.75
1:AZ:55:ALA:HB1	1:AZ:95:VAL:HG21	1.68	0.75
1:CO:119:THR:HG22	1:CO:121:GLU:H	1.52	0.75
1:BR:68:SER:O	1:BR:70:LYS:HG2	1.86	0.75
1:CH:68:SER:O	1:CH:70:LYS:HG2	1.86	0.75
1:CY:119:THR:HG22	1:CY:121:GLU:H	1.52	0.75
1:CA:125:GLU:HA	1:CA:129:THR:OG1	1.87	0.75
1:CZ:125:GLU:HA	1:CZ:129:THR:OG1	1.87	0.75
1:CT:18:VAL:HG12	1:CT:77:LEU:HB2	1.67	0.75
1:CK:119:THR:HG22	1:CK:121:GLU:H	1.52	0.75
1:CT:109:PRO:HD2	1:CT:150:LYS:HD2	1.68	0.74
1:BH:38:LYS:HZ2	1:BH:44:GLU:HG3	1.51	0.74
1:BZ:119:THR:HG22	1:BZ:121:GLU:H	1.52	0.74
1:AC:68:SER:O	1:AC:70:LYS:HG2	1.86	0.74
1:BU:55:ALA:HB1	1:BU:95:VAL:HG21	1.68	0.74
1:AF:125:GLU:HA	1:AF:129:THR:OG1	1.87	0.74
1:BP:119:THR:HG22	1:BP:121:GLU:H	1.52	0.74
1:CU:119:THR:HG22	1:CU:121:GLU:H	1.52	0.74
1:AA:119:THR:HG22	1:AA:121:GLU:H	1.52	0.74
1:CU:55:ALA:HB1	1:CU:95:VAL:HG21	1.68	0.74
1:BT:119:THR:HG22	1:BT:121:GLU:H	1.52	0.74
1:CW:68:SER:O	1:CW:70:LYS:HG2	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BF:125:GLU:HA	1:BF:129:THR:OG1	1.87	0.74
1:BA:76:THR:HG22	1:BA:111:ILE:O	1.88	0.74
1:AT:109:PRO:HD2	1:AT:150:LYS:HD2	1.67	0.74
1:AR:38:LYS:HZ2	1:AR:44:GLU:HG3	1.51	0.74
1:CZ:119:THR:HG22	1:CZ:121:GLU:H	1.52	0.74
1:AK:76:THR:HG22	1:AK:111:ILE:O	1.88	0.74
1:C2:68:SER:O	1:C2:70:LYS:HG2	1.86	0.74
1:CF:39:ARG:O	1:CQ:7:LEU:HB3	1.87	0.74
1:CZ:76:THR:HG22	1:CZ:111:ILE:O	1.88	0.74
1:BU:125:GLU:HA	1:BU:129:THR:OG1	1.87	0.74
1:CA:119:THR:HG22	1:CA:121:GLU:H	1.52	0.74
1:BJ:119:THR:HG22	1:BJ:121:GLU:H	1.52	0.74
1:AA:125:GLU:HA	1:AA:129:THR:OG1	1.87	0.74
1:AZ:125:GLU:HA	1:AZ:129:THR:OG1	1.87	0.74
1:C4:119:THR:HG22	1:C4:121:GLU:H	1.52	0.74
1:BF:76:THR:HG22	1:BF:111:ILE:O	1.88	0.74
1:BF:55:ALA:HB1	1:BF:95:VAL:HG21	1.68	0.74
1:BZ:76:THR:HG22	1:BZ:111:ILE:O	1.88	0.74
1:CU:76:THR:HG22	1:CU:111:ILE:O	1.88	0.74
1:AZ:119:THR:HG22	1:AZ:121:GLU:H	1.52	0.74
1:CE:119:THR:HG22	1:CE:121:GLU:H	1.52	0.74
1:BP:76:THR:HG22	1:BP:111:ILE:O	1.88	0.74
1:CA:76:THR:HG22	1:CA:111:ILE:O	1.88	0.74
1:AK:55:ALA:HB1	1:AK:95:VAL:HG21	1.68	0.74
1:CF:76:THR:HG22	1:CF:111:ILE:O	1.88	0.74
1:BK:76:THR:HG22	1:BK:111:ILE:O	1.88	0.74
1:BK:55:ALA:HB1	1:BK:95:VAL:HG21	1.68	0.74
1:AP:55:ALA:HB1	1:AP:95:VAL:HG21	1.68	0.74
1:AP:125:GLU:HA	1:AP:129:THR:OG1	1.87	0.74
1:BQ:104:LEU:HD13	1:BR:102:LEU:HD22	1.67	0.74
1:BT:109:PRO:HD2	1:BT:150:LYS:HD2	1.67	0.74
1:AT:119:THR:HG22	1:AT:121:GLU:H	1.52	0.74
1:AE:119:THR:HG22	1:AE:121:GLU:H	1.52	0.74
1:AY:119:THR:HG22	1:AY:121:GLU:H	1.52	0.74
1:AY:109:PRO:HD2	1:AY:150:LYS:HD2	1.68	0.74
1:AZ:76:THR:HG22	1:AZ:111:ILE:O	1.88	0.74
1:BU:76:THR:HG22	1:BU:111:ILE:O	1.88	0.74
1:CA:55:ALA:HB1	1:CA:95:VAL:HG21	1.68	0.74
1:CP:76:THR:HG22	1:CP:111:ILE:O	1.88	0.74
1:AF:76:THR:HG22	1:AF:111:ILE:O	1.88	0.74
1:CT:40:HIS:CE1	1:C3:7:LEU:HD23	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:125:GLU:HA	1:AK:129:THR:OG1	1.87	0.73
1:B4:119:THR:HG22	1:B4:121:GLU:H	1.52	0.73
1:C4:109:PRO:HD2	1:C4:150:LYS:HD2	1.68	0.73
1:A4:119:THR:HG22	1:A4:121:GLU:H	1.52	0.73
1:CK:76:THR:HG22	1:CK:111:ILE:O	1.88	0.73
1:CP:119:THR:HG22	1:CP:121:GLU:H	1.52	0.73
1:CK:125:GLU:HA	1:CK:129:THR:OG1	1.87	0.73
1:BF:119:THR:HG22	1:BF:121:GLU:H	1.52	0.73
1:CF:55:ALA:HB1	1:CF:95:VAL:HG21	1.68	0.73
1:CP:55:ALA:HB1	1:CP:95:VAL:HG21	1.68	0.73
1:AA:76:THR:HG22	1:AA:111:ILE:O	1.88	0.73
1:AJ:119:THR:HG22	1:AJ:121:GLU:H	1.52	0.73
1:AF:119:THR:HG22	1:AF:121:GLU:H	1.52	0.73
1:AK:119:THR:HG22	1:AK:121:GLU:H	1.52	0.73
1:BP:55:ALA:HB1	1:BP:95:VAL:HG21	1.68	0.73
1:BE:119:THR:HG22	1:BE:121:GLU:H	1.52	0.73
1:CG:40:HIS:CE1	1:CU:7:LEU:HD23	2.23	0.73
1:BB:7:LEU:HB3	1:BU:39:ARG:O	1.89	0.72
1:BW:38:LYS:HZ2	1:BW:44:GLU:HG3	1.53	0.72
1:AF:55:ALA:HB1	1:AF:95:VAL:HG21	1.68	0.72
1:CJ:119:THR:HG22	1:CJ:121:GLU:H	1.52	0.72
1:BK:119:THR:HG22	1:BK:121:GLU:H	1.52	0.72
1:AU:76:THR:HG22	1:AU:111:ILE:O	1.88	0.72
1:BB:40:HIS:CE1	1:BU:7:LEU:HD23	2.23	0.72
1:BY:119:THR:HG22	1:BY:121:GLU:H	1.52	0.72
1:AP:76:THR:HG22	1:AP:111:ILE:O	1.88	0.72
1:AP:119:THR:HG22	1:AP:121:GLU:H	1.52	0.72
1:AO:119:THR:HG22	1:AO:121:GLU:H	1.52	0.72
1:AB:104:LEU:CD2	1:AC:60:LEU:HA	2.17	0.72
1:CC:129:THR:HG21	1:CS:120:ILE:HD13	1.72	0.71
1:B1:104:LEU:CD2	1:B2:60:LEU:HA	2.17	0.71
1:AX:149:SER:O	1:AX:152:TRP:CZ2	2.43	0.71
1:BN:149:SER:O	1:BN:152:TRP:CZ2	2.43	0.71
1:AI:149:SER:O	1:AI:152:TRP:CZ2	2.43	0.71
1:A1:119:THR:HG22	1:A1:121:GLU:H	1.55	0.71
1:BG:119:THR:HG22	1:BG:121:GLU:H	1.55	0.71
1:BQ:119:THR:HG22	1:BQ:121:GLU:H	1.55	0.71
1:BX:149:SER:O	1:BX:152:TRP:CZ2	2.43	0.71
1:CN:149:SER:O	1:CN:152:TRP:CZ2	2.43	0.71
1:AV:119:THR:HG22	1:AV:121:GLU:H	1.55	0.71
1:A3:149:SER:O	1:A3:152:TRP:CZ2	2.43	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:104:LEU:CD2	1:AR:60:LEU:HA	2.17	0.71
1:BM:38:LYS:HZ2	1:BM:44:GLU:HG3	1.54	0.71
1:CC:38:LYS:HZ2	1:CC:44:GLU:HG3	1.55	0.71
1:AS:149:SER:O	1:AS:152:TRP:CZ2	2.43	0.71
1:BD:149:SER:O	1:BD:152:TRP:CZ2	2.43	0.71
1:C3:149:SER:O	1:C3:152:TRP:CZ2	2.43	0.71
1:CQ:119:THR:HG22	1:CQ:121:GLU:H	1.55	0.71
1:CL:119:THR:HG22	1:CL:121:GLU:H	1.55	0.71
1:BS:149:SER:O	1:BS:152:TRP:CZ2	2.43	0.71
1:BB:119:THR:HG22	1:BB:121:GLU:H	1.55	0.71
1:CD:107:ASP:CG	1:CD:107:ASP:O	2.29	0.71
1:B3:149:SER:O	1:B3:152:TRP:CZ2	2.43	0.71
1:BI:149:SER:O	1:BI:152:TRP:CZ2	2.43	0.71
1:CB:119:THR:HG22	1:CB:121:GLU:H	1.55	0.71
1:BV:119:THR:HG22	1:BV:121:GLU:H	1.55	0.71
1:AN:149:SER:O	1:AN:152:TRP:CZ2	2.43	0.71
1:CV:119:THR:HG22	1:CV:121:GLU:H	1.55	0.71
1:BC:129:THR:HG21	1:BS:120:ILE:HD11	1.73	0.71
1:C3:107:ASP:O	1:C3:107:ASP:CG	2.29	0.71
1:AN:107:ASP:CG	1:AN:107:ASP:O	2.29	0.71
1:CI:149:SER:O	1:CI:152:TRP:CZ2	2.43	0.71
1:AD:149:SER:O	1:AD:152:TRP:CZ2	2.43	0.71
1:CS:149:SER:O	1:CS:152:TRP:CZ2	2.43	0.71
1:AX:107:ASP:CG	1:AX:107:ASP:O	2.29	0.71
1:AL:119:THR:HG22	1:AL:121:GLU:H	1.55	0.71
1:BF:7:LEU:HD23	1:BQ:40:HIS:CE1	2.26	0.71
1:AI:107:ASP:CG	1:AI:107:ASP:O	2.29	0.71
1:CN:107:ASP:CG	1:CN:107:ASP:O	2.29	0.71
1:AB:119:THR:HG22	1:AB:121:GLU:H	1.55	0.71
1:BN:107:ASP:CG	1:BN:107:ASP:O	2.29	0.71
1:BS:107:ASP:O	1:BS:107:ASP:CG	2.29	0.71
1:C2:38:LYS:HZ2	1:C2:44:GLU:HG3	1.54	0.71
1:AD:107:ASP:CG	1:AD:107:ASP:O	2.29	0.70
1:A2:38:LYS:HZ2	1:A2:44:GLU:HG3	1.56	0.70
1:BR:38:LYS:HZ2	1:BR:44:GLU:HG3	1.56	0.70
1:B3:107:ASP:CG	1:B3:107:ASP:O	2.29	0.70
1:CX:149:SER:O	1:CX:152:TRP:CZ2	2.43	0.70
1:BL:119:THR:HG22	1:BL:121:GLU:H	1.55	0.70
1:AL:104:LEU:CD2	1:AM:60:LEU:HA	2.17	0.70
1:CD:149:SER:O	1:CD:152:TRP:CZ2	2.43	0.70
1:AG:119:THR:HG22	1:AG:121:GLU:H	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:107:ASP:CG	1:BI:107:ASP:O	2.29	0.70
1:CG:104:LEU:CD2	1:CH:60:LEU:HA	2.17	0.70
1:CI:107:ASP:O	1:CI:107:ASP:CG	2.29	0.70
1:BX:107:ASP:CG	1:BX:107:ASP:O	2.29	0.70
1:CQ:104:LEU:CD2	1:CR:60:LEU:HA	2.17	0.70
1:BU:124:ILE:O	1:BU:129:THR:OG1	2.10	0.70
1:CG:119:THR:HG22	1:CG:121:GLU:H	1.55	0.70
1:BL:104:LEU:CD2	1:BM:60:LEU:HA	2.17	0.69
1:BG:104:LEU:CD2	1:BH:60:LEU:HA	2.17	0.69
1:A1:104:LEU:CD2	1:A2:60:LEU:HA	2.17	0.69
1:CX:107:ASP:CG	1:CX:107:ASP:O	2.29	0.69
1:CE:16:VAL:HG12	1:CE:75:ILE:HB	1.74	0.69
1:BE:16:VAL:HG12	1:BE:75:ILE:HB	1.74	0.69
1:BB:104:LEU:CD2	1:BC:60:LEU:HA	2.17	0.69
1:A3:107:ASP:CG	1:A3:107:ASP:O	2.29	0.69
1:AE:16:VAL:HG12	1:AE:75:ILE:HB	1.75	0.69
1:AJ:16:VAL:HG12	1:AJ:75:ILE:HB	1.75	0.69
1:A4:16:VAL:HG12	1:A4:75:ILE:HB	1.74	0.69
1:AQ:119:THR:HG22	1:AQ:121:GLU:H	1.55	0.69
1:BB:144:GLU:CD	1:BU:39:ARG:HH22	1.95	0.69
1:CY:16:VAL:HG12	1:CY:75:ILE:HB	1.74	0.69
1:CZ:124:ILE:O	1:CZ:129:THR:OG1	2.10	0.69
1:C1:119:THR:HG22	1:C1:121:GLU:H	1.55	0.69
1:BD:107:ASP:O	1:BD:107:ASP:CG	2.29	0.69
1:CU:124:ILE:O	1:CU:129:THR:OG1	2.10	0.69
1:CA:124:ILE:O	1:CA:129:THR:OG1	2.10	0.69
1:AS:107:ASP:O	1:AS:107:ASP:CG	2.29	0.69
1:CT:16:VAL:HG12	1:CT:75:ILE:HB	1.74	0.69
1:B1:119:THR:HG22	1:B1:121:GLU:H	1.55	0.69
1:BR:129:THR:CG2	1:BR:130:LYS:H	1.89	0.69
1:AC:38:LYS:HZ2	1:AC:44:GLU:HG3	1.58	0.69
1:BY:16:VAL:HG12	1:BY:75:ILE:HB	1.75	0.69
1:B4:16:VAL:HG12	1:B4:75:ILE:HB	1.74	0.69
1:BY:109:PRO:HG3	1:BY:149:SER:OG	1.93	0.69
1:CJ:16:VAL:HG12	1:CJ:75:ILE:HB	1.75	0.69
1:CR:106:THR:O	1:CR:107:ASP:CB	2.41	0.69
1:AM:106:THR:O	1:AM:107:ASP:CB	2.41	0.69
1:AO:109:PRO:HG3	1:AO:149:SER:OG	1.93	0.69
1:CY:109:PRO:HG3	1:CY:149:SER:OG	1.93	0.69
1:BJ:109:PRO:HG3	1:BJ:149:SER:OG	1.93	0.69
1:CG:144:GLU:CD	1:CU:39:ARG:HH22	1.96	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:106:THR:O	1:CC:107:ASP:CB	2.41	0.69
1:CJ:109:PRO:HG3	1:CJ:149:SER:OG	1.93	0.69
1:BO:16:VAL:HG12	1:BO:75:ILE:HB	1.75	0.69
1:BT:16:VAL:HG12	1:BT:75:ILE:HB	1.75	0.69
1:BR:106:THR:O	1:BR:107:ASP:CB	2.41	0.69
1:BJ:16:VAL:HG12	1:BJ:75:ILE:HB	1.75	0.69
1:C2:106:THR:O	1:C2:107:ASP:CB	2.41	0.69
1:CS:107:ASP:CG	1:CS:107:ASP:O	2.29	0.68
1:AY:16:VAL:HG12	1:AY:75:ILE:HB	1.75	0.68
1:BW:106:THR:O	1:BW:107:ASP:CB	2.41	0.68
1:CO:109:PRO:HG3	1:CO:149:SER:OG	1.93	0.68
1:A4:109:PRO:HG3	1:A4:149:SER:OG	1.93	0.68
1:BT:109:PRO:HG3	1:BT:149:SER:OG	1.93	0.68
1:C4:109:PRO:HG3	1:C4:149:SER:OG	1.93	0.68
1:AO:16:VAL:HG12	1:AO:75:ILE:HB	1.74	0.68
1:BV:104:LEU:CD2	1:BW:60:LEU:HA	2.17	0.68
1:CE:109:PRO:HG3	1:CE:149:SER:OG	1.93	0.68
1:BO:109:PRO:HG3	1:BO:149:SER:OG	1.93	0.68
1:AW:106:THR:O	1:AW:107:ASP:CB	2.41	0.68
1:AY:109:PRO:HG3	1:AY:149:SER:OG	1.93	0.68
1:BA:124:ILE:O	1:BA:129:THR:OG1	2.10	0.68
1:AF:124:ILE:O	1:AF:129:THR:OG1	2.10	0.68
1:BE:109:PRO:HG3	1:BE:149:SER:OG	1.93	0.68
1:AT:109:PRO:HG3	1:AT:149:SER:OG	1.93	0.68
1:AH:38:LYS:HZ2	1:AH:44:GLU:HG3	1.59	0.68
1:B2:106:THR:O	1:B2:107:ASP:CB	2.41	0.68
1:AJ:109:PRO:HG3	1:AJ:149:SER:OG	1.93	0.68
1:A4:17:VAL:HG12	1:A4:50:ALA:HB3	1.76	0.68
1:BU:56:PHE:CZ	1:BY:100:ALA:HB2	2.29	0.68
1:CU:56:PHE:CZ	1:CY:100:ALA:HB2	2.29	0.68
1:CZ:152:TRP:CG	1:CZ:153:ALA:N	2.62	0.68
1:BK:56:PHE:CZ	1:BO:100:ALA:HB2	2.29	0.68
1:CK:124:ILE:O	1:CK:129:THR:OG1	2.10	0.68
1:AN:17:VAL:HG12	1:AN:50:ALA:HB3	1.76	0.68
1:AT:17:VAL:HG12	1:AT:50:ALA:HB3	1.76	0.68
1:BP:56:PHE:CZ	1:BT:100:ALA:HB2	2.29	0.68
1:B4:17:VAL:HG12	1:B4:50:ALA:HB3	1.76	0.68
1:CM:106:THR:O	1:CM:107:ASP:CB	2.41	0.68
1:CQ:30:LEU:HA	1:CQ:77:LEU:HD23	1.76	0.68
1:AT:16:VAL:HG12	1:AT:75:ILE:HB	1.75	0.68
1:C4:16:VAL:HG12	1:C4:75:ILE:HB	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:17:VAL:HG12	1:AE:50:ALA:HB3	1.76	0.68
1:AP:152:TRP:CG	1:AP:153:ALA:N	2.62	0.68
1:CJ:17:VAL:HG12	1:CJ:50:ALA:HB3	1.76	0.68
1:CN:17:VAL:HG12	1:CN:50:ALA:HB3	1.76	0.68
1:C3:17:VAL:HG12	1:C3:50:ALA:HB3	1.76	0.68
1:CZ:56:PHE:CZ	1:C4:100:ALA:HB2	2.29	0.68
1:AE:109:PRO:HG3	1:AE:149:SER:OG	1.93	0.68
1:B4:109:PRO:HG3	1:B4:149:SER:OG	1.93	0.68
1:BG:30:LEU:HA	1:BG:77:LEU:HD23	1.76	0.68
1:AP:56:PHE:CZ	1:AT:100:ALA:HB2	2.29	0.68
1:BJ:17:VAL:HG12	1:BJ:50:ALA:HB3	1.76	0.68
1:BF:152:TRP:CG	1:BF:153:ALA:N	2.62	0.68
1:BP:152:TRP:CG	1:BP:153:ALA:N	2.62	0.68
1:CF:152:TRP:CG	1:CF:153:ALA:N	2.62	0.68
1:B1:30:LEU:HA	1:B1:77:LEU:HD23	1.76	0.68
1:CL:30:LEU:HA	1:CL:77:LEU:HD23	1.76	0.68
1:AU:152:TRP:CG	1:AU:153:ALA:N	2.62	0.68
1:BZ:56:PHE:CZ	1:B4:100:ALA:HB2	2.29	0.68
1:BQ:104:LEU:CD2	1:BR:60:LEU:HA	2.17	0.68
1:CT:109:PRO:HG3	1:CT:149:SER:OG	1.93	0.68
1:AB:96:ALA:C	1:AB:100:ALA:CB	2.62	0.68
1:AQ:30:LEU:HA	1:AQ:77:LEU:HD23	1.76	0.68
1:AK:56:PHE:CZ	1:AO:100:ALA:HB2	2.29	0.68
1:BD:17:VAL:HG12	1:BD:50:ALA:HB3	1.76	0.68
1:AF:56:PHE:CZ	1:AJ:100:ALA:HB2	2.29	0.68
1:C1:30:LEU:HA	1:C1:77:LEU:HD23	1.76	0.68
1:CO:17:VAL:HG12	1:CO:50:ALA:HB3	1.76	0.68
1:C4:17:VAL:HG12	1:C4:50:ALA:HB3	1.76	0.68
1:BE:37:LEU:HG	1:BE:139:ALA:HB1	1.77	0.68
1:BU:152:TRP:CG	1:BU:153:ALA:N	2.62	0.68
1:AG:96:ALA:C	1:AG:100:ALA:CB	2.62	0.67
1:BG:96:ALA:C	1:BG:100:ALA:CB	2.62	0.67
1:CP:124:ILE:O	1:CP:129:THR:OG1	2.10	0.67
1:AP:124:ILE:O	1:AP:129:THR:OG1	2.10	0.67
1:AX:151:HIS:CB	1:AY:64:LYS:HB3	2.25	0.67
1:BB:30:LEU:HA	1:BB:77:LEU:HD23	1.76	0.67
1:AX:17:VAL:HG12	1:AX:50:ALA:HB3	1.76	0.67
1:CA:56:PHE:CZ	1:CE:100:ALA:HB2	2.29	0.67
1:CK:56:PHE:CZ	1:CO:100:ALA:HB2	2.29	0.67
1:AG:104:LEU:CD2	1:AH:60:LEU:HA	2.17	0.67
1:BQ:96:ALA:C	1:BQ:100:ALA:CB	2.62	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:124:ILE:O	1:BK:129:THR:OG1	2.10	0.67
1:AF:152:TRP:CG	1:AF:153:ALA:N	2.62	0.67
1:BF:56:PHE:CZ	1:BJ:100:ALA:HB2	2.29	0.67
1:CF:56:PHE:CZ	1:CJ:100:ALA:HB2	2.29	0.67
1:AO:37:LEU:HG	1:AO:139:ALA:HB1	1.77	0.67
1:AF:7:LEU:HD23	1:AQ:40:HIS:CE1	2.28	0.67
1:BI:151:HIS:CB	1:BJ:64:LYS:HB3	2.25	0.67
1:BS:151:HIS:CB	1:BT:64:LYS:HB3	2.25	0.67
1:AU:56:PHE:CZ	1:AY:100:ALA:HB2	2.29	0.67
1:AR:106:THR:O	1:AR:107:ASP:CB	2.41	0.67
1:A1:96:ALA:C	1:A1:100:ALA:CB	2.62	0.67
1:BB:124:ILE:HD11	1:BV:24:PHE:CE2	2.29	0.67
1:BD:151:HIS:CB	1:BE:64:LYS:HB3	2.25	0.67
1:CT:17:VAL:HG12	1:CT:50:ALA:HB3	1.76	0.67
1:CX:151:HIS:CB	1:CY:64:LYS:HB3	2.25	0.67
1:CS:151:HIS:CB	1:CT:64:LYS:HB3	2.25	0.67
1:C3:151:HIS:CB	1:C4:64:LYS:HB3	2.25	0.67
1:AB:30:LEU:HA	1:AB:77:LEU:HD23	1.76	0.67
1:BY:17:VAL:HG12	1:BY:50:ALA:HB3	1.76	0.67
1:B3:151:HIS:CB	1:B4:64:LYS:HB3	2.25	0.67
1:AA:152:TRP:CG	1:AA:153:ALA:N	2.62	0.67
1:AT:37:LEU:HG	1:AT:139:ALA:HB1	1.77	0.67
1:CB:104:LEU:CD2	1:CC:60:LEU:HA	2.17	0.67
1:BZ:124:ILE:O	1:BZ:129:THR:OG1	2.10	0.67
1:AI:151:HIS:CB	1:AJ:64:LYS:HB3	2.25	0.67
1:AD:151:HIS:CB	1:AE:64:LYS:HB3	2.25	0.67
1:BM:106:THR:O	1:BM:107:ASP:CB	2.41	0.67
1:CP:56:PHE:CZ	1:CT:100:ALA:HB2	2.29	0.67
1:CG:30:LEU:HA	1:CG:77:LEU:HD23	1.76	0.67
1:A3:151:HIS:CB	1:A4:64:LYS:HB3	2.25	0.67
1:BO:17:VAL:HG12	1:BO:50:ALA:HB3	1.76	0.67
1:B4:37:LEU:HG	1:B4:139:ALA:HB1	1.77	0.67
1:BX:151:HIS:CB	1:BY:64:LYS:HB3	2.25	0.67
1:A1:30:LEU:HA	1:A1:77:LEU:HD23	1.76	0.67
1:BN:151:HIS:CB	1:BO:64:LYS:HB3	2.25	0.67
1:BC:106:THR:O	1:BC:107:ASP:CB	2.41	0.67
1:CW:106:THR:O	1:CW:107:ASP:CB	2.41	0.67
1:CL:104:LEU:CD2	1:CM:60:LEU:HA	2.17	0.67
1:C1:96:ALA:C	1:C1:100:ALA:CB	2.62	0.67
1:CV:96:ALA:C	1:CV:100:ALA:CB	2.63	0.67
1:CN:151:HIS:CB	1:CO:64:LYS:HB3	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:152:TRP:CG	1:AK:153:ALA:N	2.62	0.67
1:AA:56:PHE:CZ	1:AE:100:ALA:HB2	2.29	0.67
1:AD:17:VAL:HG12	1:AD:50:ALA:HB3	1.76	0.67
1:BO:37:LEU:HG	1:BO:139:ALA:HB1	1.77	0.67
1:BV:30:LEU:HA	1:BV:77:LEU:HD23	1.76	0.67
1:AE:37:LEU:HG	1:AE:139:ALA:HB1	1.77	0.67
1:AV:96:ALA:C	1:AV:100:ALA:CB	2.62	0.67
1:CB:96:ALA:C	1:CB:100:ALA:CB	2.63	0.67
1:CW:7:LEU:HB3	1:C2:39:ARG:O	1.94	0.67
1:AW:38:LYS:HZ2	1:AW:44:GLU:HG3	1.60	0.67
1:BA:56:PHE:CZ	1:BE:100:ALA:HB2	2.29	0.67
1:AC:106:THR:O	1:AC:107:ASP:CB	2.41	0.67
1:BZ:152:TRP:CG	1:BZ:153:ALA:N	2.62	0.67
1:AJ:17:VAL:HG12	1:AJ:50:ALA:HB3	1.76	0.67
1:AG:30:LEU:HA	1:AG:77:LEU:HD23	1.76	0.67
1:CK:152:TRP:CG	1:CK:153:ALA:N	2.62	0.67
1:AS:151:HIS:CB	1:AT:64:LYS:HB3	2.25	0.67
1:A1:148:LEU:HD13	1:A2:61:ILE:CD1	2.25	0.67
1:AZ:152:TRP:CG	1:AZ:153:ALA:N	2.62	0.67
1:CT:37:LEU:HG	1:CT:139:ALA:HB1	1.77	0.67
1:A3:17:VAL:HG12	1:A3:50:ALA:HB3	1.76	0.67
1:CY:37:LEU:HG	1:CY:139:ALA:HB1	1.77	0.67
1:BX:17:VAL:HG12	1:BX:50:ALA:HB3	1.76	0.67
1:C1:104:LEU:CD2	1:C2:60:LEU:HA	2.17	0.67
1:CQ:148:LEU:HD13	1:CR:61:ILE:CD1	2.25	0.67
1:BL:30:LEU:HA	1:BL:77:LEU:HD23	1.76	0.67
1:AN:151:HIS:CB	1:AO:64:LYS:HB3	2.25	0.67
1:BT:55:ALA:HB1	1:BT:95:VAL:HG21	1.77	0.67
1:BL:96:ALA:C	1:BL:100:ALA:CB	2.63	0.66
1:AG:148:LEU:HD13	1:AH:61:ILE:CD1	2.25	0.66
1:CO:16:VAL:HG12	1:CO:75:ILE:HB	1.74	0.66
1:BM:106:THR:O	1:BM:107:ASP:HB3	1.96	0.66
1:B4:55:ALA:HB1	1:B4:95:VAL:HG21	1.77	0.66
1:A2:106:THR:O	1:A2:107:ASP:CB	2.41	0.66
1:CD:151:HIS:CB	1:CE:64:LYS:HB3	2.25	0.66
1:CB:148:LEU:HD13	1:CC:61:ILE:CD1	2.25	0.66
1:AV:148:LEU:HD13	1:AW:61:ILE:CD1	2.26	0.66
1:BL:148:LEU:HD13	1:BM:61:ILE:CD1	2.25	0.66
1:AZ:56:PHE:CZ	1:A4:100:ALA:HB2	2.29	0.66
1:AL:30:LEU:HA	1:AL:77:LEU:HD23	1.76	0.66
1:BB:148:LEU:HD13	1:BC:61:ILE:CD1	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:148:LEU:HD13	1:CW:61:ILE:CD1	2.26	0.66
1:AU:124:ILE:O	1:AU:129:THR:OG1	2.10	0.66
1:AM:106:THR:O	1:AM:107:ASP:HB3	1.96	0.66
1:BW:106:THR:O	1:BW:107:ASP:HB3	1.96	0.66
1:B2:106:THR:O	1:B2:107:ASP:HB3	1.96	0.66
1:AY:55:ALA:HB1	1:AY:95:VAL:HG21	1.77	0.66
1:CS:17:VAL:HG12	1:CS:50:ALA:HB3	1.76	0.66
1:BA:152:TRP:CG	1:BA:153:ALA:N	2.62	0.66
1:CI:17:VAL:HG12	1:CI:50:ALA:HB3	1.76	0.66
1:CV:30:LEU:HA	1:CV:77:LEU:HD23	1.76	0.66
1:CG:96:ALA:C	1:CG:100:ALA:CB	2.63	0.66
1:BG:148:LEU:HD13	1:BH:61:ILE:CD1	2.25	0.66
1:B1:148:LEU:HD13	1:B2:61:ILE:CD1	2.25	0.66
1:C1:148:LEU:HD13	1:C2:61:ILE:CD1	2.25	0.66
1:AZ:124:ILE:O	1:AZ:129:THR:OG1	2.10	0.66
1:CM:106:THR:O	1:CM:107:ASP:HB3	1.96	0.66
1:AT:55:ALA:HB1	1:AT:95:VAL:HG21	1.77	0.66
1:CD:17:VAL:HG12	1:CD:50:ALA:HB3	1.76	0.66
1:AV:104:LEU:CD2	1:AW:60:LEU:HA	2.17	0.66
1:BR:106:THR:O	1:BR:107:ASP:HB3	1.96	0.66
1:AC:106:THR:O	1:AC:107:ASP:HB3	1.96	0.66
1:BS:17:VAL:HG12	1:BS:50:ALA:HB3	1.76	0.66
1:C4:37:LEU:HG	1:C4:139:ALA:HB1	1.77	0.66
1:A4:55:ALA:HB1	1:A4:95:VAL:HG21	1.77	0.66
1:AE:55:ALA:HB1	1:AE:95:VAL:HG21	1.77	0.66
1:CT:55:ALA:HB1	1:CT:95:VAL:HG21	1.78	0.66
1:AR:106:THR:O	1:AR:107:ASP:HB3	1.96	0.66
1:BH:106:THR:O	1:BH:107:ASP:CB	2.41	0.66
1:AS:17:VAL:HG12	1:AS:50:ALA:HB3	1.76	0.66
1:BI:17:VAL:HG12	1:BI:50:ALA:HB3	1.76	0.66
1:BT:17:VAL:HG12	1:BT:50:ALA:HB3	1.76	0.66
1:AY:37:LEU:HG	1:AY:139:ALA:HB1	1.77	0.66
1:CE:17:VAL:HG12	1:CE:50:ALA:HB3	1.76	0.66
1:AD:120:ILE:HD11	1:AR:129:THR:HG21	1.76	0.66
1:AL:96:ALA:C	1:AL:100:ALA:CB	2.62	0.66
1:B1:96:ALA:C	1:B1:100:ALA:CB	2.62	0.66
1:BQ:148:LEU:HD13	1:BR:61:ILE:CD1	2.25	0.66
1:AC:7:LEU:HB3	1:AR:39:ARG:O	1.96	0.66
1:CW:106:THR:O	1:CW:107:ASP:HB3	1.96	0.66
1:BE:17:VAL:HG12	1:BE:50:ALA:HB3	1.76	0.66
1:CG:148:LEU:HD13	1:CH:61:ILE:CD1	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B2:38:LYS:NZ	1:B2:44:GLU:HG3	2.11	0.66
1:AV:30:LEU:HA	1:AV:77:LEU:HD23	1.76	0.66
1:A4:37:LEU:HG	1:A4:139:ALA:HB1	1.77	0.66
1:CJ:55:ALA:HB1	1:CJ:95:VAL:HG21	1.77	0.66
1:CI:151:HIS:CB	1:CJ:64:LYS:HB3	2.25	0.66
1:CA:152:TRP:CG	1:CA:153:ALA:N	2.62	0.66
1:CV:104:LEU:CD2	1:CW:60:LEU:HA	2.17	0.66
1:CL:148:LEU:HD13	1:CM:61:ILE:CD1	2.26	0.66
1:BM:38:LYS:NZ	1:BM:44:GLU:HG3	2.11	0.66
1:BR:38:LYS:NZ	1:BR:44:GLU:HG3	2.11	0.66
1:BC:38:LYS:NZ	1:BC:44:GLU:HG3	2.11	0.66
1:BW:38:LYS:NZ	1:BW:44:GLU:HG3	2.11	0.66
1:AE:75:ILE:HG22	1:AE:77:LEU:HD13	1.78	0.66
1:BP:124:ILE:O	1:BP:129:THR:OG1	2.10	0.66
1:AK:124:ILE:O	1:AK:129:THR:OG1	2.10	0.66
1:CW:128:GLY:O	1:C3:22:ASN:HA	1.96	0.66
1:CH:106:THR:O	1:CH:107:ASP:CB	2.41	0.66
1:AJ:55:ALA:HB1	1:AJ:95:VAL:HG21	1.77	0.66
1:AO:58:ILE:HG22	1:AO:58:ILE:O	1.96	0.66
1:BK:152:TRP:CG	1:BK:153:ALA:N	2.62	0.66
1:AG:96:ALA:O	1:AG:100:ALA:CB	2.44	0.66
1:AB:148:LEU:HD13	1:AC:61:ILE:CD1	2.25	0.66
1:CW:38:LYS:NZ	1:CW:44:GLU:HG3	2.11	0.66
1:CC:38:LYS:NZ	1:CC:44:GLU:HG3	2.11	0.66
1:CJ:75:ILE:HG22	1:CJ:77:LEU:HD13	1.78	0.66
1:C4:75:ILE:HG22	1:C4:77:LEU:HD13	1.78	0.66
1:AA:124:ILE:O	1:AA:129:THR:OG1	2.10	0.66
1:CR:106:THR:O	1:CR:107:ASP:HB3	1.96	0.66
1:BH:106:THR:O	1:BH:107:ASP:HB3	1.96	0.66
1:BQ:4:GLU:HG2	1:BR:51:TRP:HD1	1.61	0.66
1:BT:37:LEU:HG	1:BT:139:ALA:HB1	1.77	0.66
1:CO:58:ILE:O	1:CO:58:ILE:HG22	1.96	0.66
1:BL:96:ALA:O	1:BL:100:ALA:CB	2.45	0.65
1:BT:75:ILE:HG22	1:BT:77:LEU:HD13	1.78	0.65
1:AW:38:LYS:NZ	1:AW:44:GLU:HG3	2.11	0.65
1:CF:124:ILE:O	1:CF:129:THR:OG1	2.10	0.65
1:B3:17:VAL:HG12	1:B3:50:ALA:HB3	1.76	0.65
1:CO:37:LEU:HG	1:CO:139:ALA:HB1	1.77	0.65
1:BV:4:GLU:HG2	1:BW:51:TRP:HD1	1.61	0.65
1:CY:17:VAL:HG12	1:CY:50:ALA:HB3	1.76	0.65
1:AY:17:VAL:HG12	1:AY:50:ALA:HB3	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:37:LEU:HG	1:AJ:139:ALA:HB1	1.77	0.65
1:AH:106:THR:O	1:AH:107:ASP:HB3	1.96	0.65
1:BB:96:ALA:C	1:BB:100:ALA:CB	2.62	0.65
1:AQ:96:ALA:O	1:AQ:100:ALA:CB	2.45	0.65
1:BG:96:ALA:O	1:BG:100:ALA:CB	2.44	0.65
1:CF:39:ARG:HH22	1:CQ:144:GLU:CD	2.00	0.65
1:AL:148:LEU:HD13	1:AM:61:ILE:CD1	2.26	0.65
1:AK:53:PRO:HD2	1:AK:57:GLU:HB2	1.79	0.65
1:BA:53:PRO:HD2	1:BA:57:GLU:HB2	1.79	0.65
1:AO:75:ILE:HG22	1:AO:77:LEU:HD13	1.78	0.65
1:B4:75:ILE:HG22	1:B4:77:LEU:HD13	1.78	0.65
1:BJ:58:ILE:HG22	1:BJ:58:ILE:O	1.96	0.65
1:BY:55:ALA:HB1	1:BY:95:VAL:HG21	1.77	0.65
1:BE:55:ALA:HB1	1:BE:95:VAL:HG21	1.77	0.65
1:CP:152:TRP:CG	1:CP:153:ALA:N	2.62	0.65
1:CX:17:VAL:HG12	1:CX:50:ALA:HB3	1.76	0.65
1:BB:96:ALA:O	1:BB:100:ALA:CB	2.45	0.65
1:CP:39:ARG:O	1:CV:7:LEU:HB3	1.96	0.65
1:AR:38:LYS:NZ	1:AR:44:GLU:HG3	2.11	0.65
1:AC:38:LYS:NZ	1:AC:44:GLU:HG3	2.11	0.65
1:AH:38:LYS:NZ	1:AH:44:GLU:HG3	2.11	0.65
1:AT:58:ILE:HG22	1:AT:58:ILE:O	1.96	0.65
1:AO:17:VAL:HG12	1:AO:50:ALA:HB3	1.76	0.65
1:AI:17:VAL:HG12	1:AI:50:ALA:HB3	1.76	0.65
1:AL:96:ALA:O	1:AL:100:ALA:CB	2.45	0.65
1:BQ:96:ALA:O	1:BQ:100:ALA:CB	2.45	0.65
1:CG:96:ALA:O	1:CG:100:ALA:CB	2.45	0.65
1:AQ:148:LEU:HD13	1:AR:61:ILE:CD1	2.26	0.65
1:CY:75:ILE:HG22	1:CY:77:LEU:HD13	1.78	0.65
1:A4:75:ILE:HG22	1:A4:77:LEU:HD13	1.78	0.65
1:A2:106:THR:O	1:A2:107:ASP:HB3	1.96	0.65
1:CU:152:TRP:CG	1:CU:153:ALA:N	2.62	0.65
1:BN:17:VAL:HG12	1:BN:50:ALA:HB3	1.76	0.65
1:CO:55:ALA:HB1	1:CO:95:VAL:HG21	1.77	0.65
1:BJ:55:ALA:HB1	1:BJ:95:VAL:HG21	1.77	0.65
1:CL:4:GLU:HG2	1:CM:51:TRP:HD1	1.61	0.65
1:CE:37:LEU:HG	1:CE:139:ALA:HB1	1.77	0.65
1:BL:100:ALA:HA	1:BM:56:PHE:HZ	1.62	0.65
1:C1:96:ALA:O	1:C1:100:ALA:CB	2.44	0.65
1:BV:96:ALA:O	1:BV:100:ALA:CB	2.45	0.65
1:A1:96:ALA:O	1:A1:100:ALA:CB	2.45	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:148:LEU:HD13	1:BW:61:ILE:CD1	2.26	0.65
1:CU:53:PRO:HD2	1:CU:57:GLU:HB2	1.79	0.65
1:AZ:53:PRO:HD2	1:AZ:57:GLU:HB2	1.79	0.65
1:C2:106:THR:O	1:C2:107:ASP:HB3	1.96	0.65
1:BQ:4:GLU:HG2	1:BR:51:TRP:CD1	2.32	0.65
1:C1:4:GLU:HG2	1:C2:51:TRP:HD1	1.61	0.65
1:CB:30:LEU:HA	1:CB:77:LEU:HD23	1.76	0.65
1:BO:58:ILE:HG22	1:BO:58:ILE:O	1.96	0.65
1:CE:107:ASP:CG	1:CE:107:ASP:O	2.35	0.65
1:C4:55:ALA:HB1	1:C4:95:VAL:HG21	1.77	0.65
1:AC:129:THR:HG21	1:AS:120:ILE:CD1	2.27	0.65
1:CQ:96:ALA:C	1:CQ:100:ALA:CB	2.63	0.65
1:CQ:96:ALA:O	1:CQ:100:ALA:CB	2.45	0.65
1:AB:7:LEU:HB3	1:AU:39:ARG:O	1.97	0.65
1:BF:53:PRO:HD2	1:BF:57:GLU:HB2	1.79	0.65
1:CZ:53:PRO:HD2	1:CZ:57:GLU:HB2	1.79	0.65
1:AM:38:LYS:NZ	1:AM:44:GLU:HG3	2.11	0.65
1:CC:40:HIS:CE1	1:CR:7:LEU:HD23	2.32	0.65
1:CT:75:ILE:HG22	1:CT:77:LEU:HD13	1.78	0.65
1:C1:4:GLU:HG2	1:C2:51:TRP:CD1	2.32	0.65
1:BJ:37:LEU:HG	1:BJ:139:ALA:HB1	1.77	0.65
1:BY:37:LEU:HG	1:BY:139:ALA:HB1	1.77	0.65
1:BK:7:LEU:HD11	1:BK:140:VAL:HG13	1.79	0.65
1:AE:107:ASP:CG	1:AE:107:ASP:O	2.35	0.65
1:B1:96:ALA:O	1:B1:100:ALA:CB	2.45	0.65
1:AU:53:PRO:HD2	1:AU:57:GLU:HB2	1.79	0.65
1:BJ:75:ILE:HG22	1:BJ:77:LEU:HD13	1.78	0.65
1:CU:7:LEU:HD11	1:CU:140:VAL:HG13	1.79	0.65
1:CJ:37:LEU:HG	1:CJ:139:ALA:HB1	1.77	0.65
1:CE:55:ALA:HB1	1:CE:95:VAL:HG21	1.77	0.65
1:BA:7:LEU:HD11	1:BA:140:VAL:HG13	1.79	0.65
1:BL:4:GLU:HG2	1:BM:51:TRP:HD1	1.61	0.65
1:CB:4:GLU:HG2	1:CC:51:TRP:HD1	1.61	0.65
1:AP:7:LEU:HD11	1:AP:140:VAL:HG13	1.79	0.65
1:BB:100:ALA:HA	1:BC:56:PHE:HZ	1.62	0.65
1:CB:96:ALA:O	1:CB:100:ALA:CB	2.45	0.65
1:CV:96:ALA:O	1:CV:100:ALA:CB	2.45	0.65
1:BO:75:ILE:HG22	1:BO:77:LEU:HD13	1.78	0.65
1:AW:106:THR:O	1:AW:107:ASP:HB3	1.96	0.65
1:BL:4:GLU:HG2	1:BM:51:TRP:CD1	2.32	0.65
1:CF:7:LEU:HD11	1:CF:140:VAL:HG13	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:4:GLU:HG2	1:BC:51:TRP:HD1	1.61	0.65
1:BZ:7:LEU:HD11	1:BZ:140:VAL:HG13	1.79	0.65
1:BQ:30:LEU:HA	1:BQ:77:LEU:HD23	1.76	0.65
1:CX:120:ILE:CD1	1:C2:129:THR:HG21	2.27	0.65
1:BV:107:ASP:HB2	1:BV:152:TRP:HZ3	1.62	0.65
1:AB:100:ALA:HA	1:AC:56:PHE:HZ	1.62	0.65
1:CK:53:PRO:HD2	1:CK:57:GLU:HB2	1.79	0.65
1:CD:28:LYS:NZ	1:CF:28:LYS:NZ	2.43	0.65
1:BE:75:ILE:HG22	1:BE:77:LEU:HD13	1.78	0.65
1:CL:4:GLU:HG2	1:CM:51:TRP:CD1	2.32	0.65
1:CQ:4:GLU:HG2	1:CR:51:TRP:HD1	1.62	0.65
1:BT:107:ASP:O	1:BT:107:ASP:CG	2.35	0.65
1:CT:58:ILE:O	1:CT:58:ILE:HG22	1.96	0.65
1:CT:107:ASP:CG	1:CT:107:ASP:O	2.35	0.65
1:CE:58:ILE:HG22	1:CE:58:ILE:O	1.96	0.65
1:BY:107:ASP:CG	1:BY:107:ASP:O	2.35	0.65
1:CB:107:ASP:HB2	1:CB:152:TRP:HZ3	1.61	0.65
1:CB:100:ALA:HA	1:CC:56:PHE:HZ	1.62	0.65
1:AG:100:ALA:HA	1:AH:56:PHE:HZ	1.62	0.65
1:C1:100:ALA:HA	1:C2:56:PHE:HZ	1.62	0.65
1:B1:100:ALA:HA	1:B2:56:PHE:HZ	1.62	0.65
1:CL:96:ALA:O	1:CL:100:ALA:CB	2.45	0.65
1:CQ:100:ALA:HA	1:CR:56:PHE:HZ	1.62	0.65
1:BU:53:PRO:HD2	1:BU:57:GLU:HB2	1.79	0.65
1:BF:124:ILE:O	1:BF:129:THR:OG1	2.10	0.65
1:BC:106:THR:O	1:BC:107:ASP:HB3	1.96	0.65
1:BO:55:ALA:HB1	1:BO:95:VAL:HG21	1.77	0.65
1:AK:7:LEU:HD11	1:AK:140:VAL:HG13	1.79	0.65
1:BJ:107:ASP:CG	1:BJ:107:ASP:O	2.35	0.65
1:BS:100:ALA:HB2	1:BT:56:PHE:CZ	2.32	0.65
1:CY:55:ALA:HB1	1:CY:95:VAL:HG21	1.77	0.65
1:CV:4:GLU:HG2	1:CW:51:TRP:CD1	2.32	0.65
1:CN:100:ALA:HB2	1:CO:56:PHE:CZ	2.32	0.65
1:BG:4:GLU:HG2	1:BH:51:TRP:CD1	2.32	0.65
1:BY:58:ILE:O	1:BY:58:ILE:HG22	1.96	0.65
1:AV:100:ALA:HA	1:AW:56:PHE:HZ	1.62	0.64
1:A1:96:ALA:HB2	1:A1:112:PHE:CZ	2.33	0.64
1:BY:75:ILE:HG22	1:BY:77:LEU:HD13	1.78	0.64
1:BU:7:LEU:HD11	1:BU:140:VAL:HG13	1.79	0.64
1:BX:149:SER:O	1:BX:152:TRP:CE2	2.51	0.64
1:B3:149:SER:O	1:B3:152:TRP:CE2	2.50	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:149:SER:O	1:BI:152:TRP:CE2	2.50	0.64
1:CS:149:SER:O	1:CS:152:TRP:CE2	2.51	0.64
1:BI:100:ALA:HB2	1:BJ:56:PHE:CZ	2.32	0.64
1:AD:100:ALA:HB2	1:AE:56:PHE:CZ	2.32	0.64
1:AN:100:ALA:HB2	1:AO:56:PHE:CZ	2.32	0.64
1:BN:100:ALA:HB2	1:BO:56:PHE:CZ	2.33	0.64
1:C3:100:ALA:HB2	1:C4:56:PHE:CZ	2.33	0.64
1:BG:96:ALA:HB2	1:BG:112:PHE:CZ	2.33	0.64
1:CG:96:ALA:HB2	1:CG:112:PHE:CZ	2.33	0.64
1:AP:53:PRO:HD2	1:AP:57:GLU:HB2	1.79	0.64
1:BH:38:LYS:NZ	1:BH:44:GLU:HG3	2.11	0.64
1:CR:38:LYS:NZ	1:CR:44:GLU:HG3	2.11	0.64
1:AY:75:ILE:HG22	1:AY:77:LEU:HD13	1.78	0.64
1:BD:149:SER:O	1:BD:152:TRP:CE2	2.50	0.64
1:AH:106:THR:O	1:AH:107:ASP:CB	2.41	0.64
1:BB:4:GLU:HG2	1:BC:51:TRP:CD1	2.32	0.64
1:AA:7:LEU:HD11	1:AA:140:VAL:HG13	1.79	0.64
1:CY:107:ASP:O	1:CY:107:ASP:CG	2.35	0.64
1:CI:100:ALA:HB2	1:CJ:56:PHE:CZ	2.32	0.64
1:A4:107:ASP:O	1:A4:107:ASP:CG	2.35	0.64
1:CD:100:ALA:HB2	1:CE:56:PHE:CZ	2.33	0.64
1:CC:129:THR:HG21	1:CS:120:ILE:CG1	2.27	0.64
1:BD:120:ILE:HD11	1:BR:129:THR:HG21	1.79	0.64
1:BB:98:GLY:HA2	1:BB:102:LEU:HD23	1.80	0.64
1:AV:96:ALA:O	1:AV:100:ALA:CB	2.45	0.64
1:C1:96:ALA:HB2	1:C1:112:PHE:CZ	2.33	0.64
1:BV:96:ALA:HB2	1:BV:112:PHE:CZ	2.33	0.64
1:BV:96:ALA:C	1:BV:100:ALA:CB	2.63	0.64
1:BQ:96:ALA:HB2	1:BQ:112:PHE:CZ	2.33	0.64
1:CG:98:GLY:HA2	1:CG:102:LEU:HD23	1.80	0.64
1:BP:53:PRO:HD2	1:BP:57:GLU:HB2	1.79	0.64
1:BK:53:PRO:HD2	1:BK:57:GLU:HB2	1.79	0.64
1:CH:38:LYS:NZ	1:CH:44:GLU:HG3	2.11	0.64
1:CM:38:LYS:NZ	1:CM:44:GLU:HG3	2.11	0.64
1:AJ:75:ILE:HG22	1:AJ:77:LEU:HD13	1.78	0.64
1:CO:75:ILE:HG22	1:CO:77:LEU:HD13	1.78	0.64
1:CE:75:ILE:HG22	1:CE:77:LEU:HD13	1.78	0.64
1:AT:75:ILE:HG22	1:AT:77:LEU:HD13	1.78	0.64
1:AN:149:SER:O	1:AN:152:TRP:CE2	2.51	0.64
1:CC:106:THR:O	1:CC:107:ASP:HB3	1.96	0.64
1:CH:106:THR:O	1:CH:107:ASP:HB3	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:7:LEU:HD23	1:CQ:40:HIS:CE1	2.32	0.64
1:CY:58:ILE:O	1:CY:58:ILE:HG22	1.96	0.64
1:CG:4:GLU:HG2	1:CH:51:TRP:CD1	2.32	0.64
1:AX:100:ALA:HB2	1:AY:56:PHE:CZ	2.33	0.64
1:BE:58:ILE:HG22	1:BE:58:ILE:O	1.96	0.64
1:BD:119:THR:HG22	1:BD:121:GLU:H	1.63	0.64
1:CC:129:THR:HG21	1:CS:120:ILE:HD11	1.75	0.64
1:AQ:100:ALA:HA	1:AR:56:PHE:HZ	1.62	0.64
1:CL:98:GLY:O	1:CL:102:LEU:HB3	1.98	0.64
1:CL:100:ALA:HA	1:CM:56:PHE:HZ	1.62	0.64
1:AA:53:PRO:HD2	1:AA:57:GLU:HB2	1.79	0.64
1:A2:38:LYS:NZ	1:A2:44:GLU:HG3	2.11	0.64
1:CI:149:SER:O	1:CI:152:TRP:CE2	2.50	0.64
1:C3:119:THR:HG22	1:C3:121:GLU:H	1.63	0.64
1:CX:119:THR:HG22	1:CX:121:GLU:H	1.63	0.64
1:CS:100:ALA:HB2	1:CT:56:PHE:CZ	2.32	0.64
1:C4:107:ASP:O	1:C4:107:ASP:CG	2.35	0.64
1:BL:98:GLY:O	1:BL:102:LEU:HB3	1.98	0.64
1:B1:96:ALA:HB2	1:B1:112:PHE:CZ	2.33	0.64
1:CQ:98:GLY:O	1:CQ:102:LEU:HB3	1.98	0.64
1:AI:149:SER:O	1:AI:152:TRP:CE2	2.51	0.64
1:BF:7:LEU:HD11	1:BF:140:VAL:HG13	1.79	0.64
1:BQ:18:VAL:HG22	1:BQ:77:LEU:HB2	1.80	0.64
1:BX:119:THR:HG22	1:BX:121:GLU:H	1.63	0.64
1:BI:119:THR:HG22	1:BI:121:GLU:H	1.63	0.64
1:B1:4:GLU:HG2	1:B2:51:TRP:HD1	1.61	0.64
1:CI:119:THR:HG22	1:CI:121:GLU:H	1.63	0.64
1:AE:58:ILE:HG22	1:AE:58:ILE:O	1.96	0.64
1:B3:100:ALA:HB2	1:B4:56:PHE:CZ	2.33	0.64
1:B4:58:ILE:O	1:B4:58:ILE:HG22	1.96	0.64
1:BX:100:ALA:HB2	1:BY:56:PHE:CZ	2.32	0.64
1:AX:119:THR:HG22	1:AX:121:GLU:H	1.63	0.64
1:BB:98:GLY:O	1:BB:102:LEU:HB3	1.98	0.64
1:AG:98:GLY:O	1:AG:102:LEU:HB3	1.98	0.64
1:AL:98:GLY:O	1:AL:102:LEU:HB3	1.98	0.64
1:AB:98:GLY:O	1:AB:102:LEU:HB3	1.98	0.64
1:BG:98:GLY:O	1:BG:102:LEU:HB3	1.98	0.64
1:BG:100:ALA:HA	1:BH:56:PHE:HZ	1.62	0.64
1:CG:100:ALA:HA	1:CH:56:PHE:HZ	1.62	0.64
1:CV:96:ALA:HB2	1:CV:112:PHE:CZ	2.33	0.64
1:A3:149:SER:O	1:A3:152:TRP:CE2	2.51	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:4:GLU:HG2	1:CC:51:TRP:CD1	2.32	0.64
1:CV:4:GLU:HG2	1:CW:51:TRP:HD1	1.61	0.64
1:CB:98:GLY:O	1:CB:102:LEU:HB3	1.98	0.64
1:C1:98:GLY:O	1:C1:102:LEU:HB3	1.98	0.64
1:CL:98:GLY:HA2	1:CL:102:LEU:HD23	1.80	0.64
1:BV:98:GLY:O	1:BV:102:LEU:HB3	1.98	0.64
1:BV:100:ALA:HA	1:BW:56:PHE:HZ	1.62	0.64
1:BN:149:SER:O	1:BN:152:TRP:CE2	2.51	0.64
1:AS:149:SER:O	1:AS:152:TRP:CE2	2.51	0.64
1:C3:149:SER:O	1:C3:152:TRP:CE2	2.50	0.64
1:AD:149:SER:O	1:AD:152:TRP:CE2	2.51	0.64
1:BB:18:VAL:HG22	1:BB:77:LEU:HB2	1.80	0.64
1:CQ:4:GLU:HG2	1:CR:51:TRP:CD1	2.32	0.64
1:CG:4:GLU:HG2	1:CH:51:TRP:HD1	1.61	0.64
1:AO:107:ASP:CG	1:AO:107:ASP:O	2.35	0.64
1:AY:58:ILE:HG22	1:AY:58:ILE:O	1.96	0.64
1:AV:96:ALA:HB2	1:AV:112:PHE:CZ	2.33	0.64
1:CB:96:ALA:HB2	1:CB:112:PHE:CZ	2.33	0.64
1:AG:96:ALA:HB2	1:AG:112:PHE:CZ	2.33	0.64
1:BL:96:ALA:HB2	1:BL:112:PHE:CZ	2.33	0.64
1:AL:96:ALA:HB2	1:AL:112:PHE:CZ	2.33	0.64
1:AB:96:ALA:O	1:AB:100:ALA:CB	2.45	0.64
1:B1:98:GLY:HA2	1:B1:102:LEU:HD23	1.80	0.64
1:BQ:100:ALA:HA	1:BR:56:PHE:HZ	1.62	0.64
1:CV:98:GLY:O	1:CV:102:LEU:HB3	1.98	0.64
1:BR:82:ARG:HH11	1:BR:82:ARG:CG	2.11	0.64
1:BV:4:GLU:HG2	1:BW:51:TRP:CD1	2.32	0.64
1:AJ:107:ASP:CG	1:AJ:107:ASP:O	2.35	0.64
1:AI:100:ALA:HB2	1:AJ:56:PHE:CZ	2.32	0.64
1:AL:100:ALA:HA	1:AM:56:PHE:HZ	1.62	0.64
1:CV:98:GLY:HA2	1:CV:102:LEU:HD23	1.80	0.64
1:CP:53:PRO:HD2	1:CP:57:GLU:HB2	1.79	0.64
1:CX:149:SER:O	1:CX:152:TRP:CE2	2.51	0.64
1:C1:18:VAL:HG22	1:C1:77:LEU:HB2	1.80	0.64
1:AF:7:LEU:HD11	1:AF:140:VAL:HG13	1.79	0.64
1:AJ:58:ILE:HG22	1:AJ:58:ILE:O	1.96	0.64
1:CX:100:ALA:HB2	1:CY:56:PHE:CZ	2.32	0.64
1:AS:100:ALA:HB2	1:AT:56:PHE:CZ	2.33	0.64
1:CT:7:LEU:HB3	1:C3:39:ARG:O	1.98	0.64
1:C1:98:GLY:HA2	1:C1:102:LEU:HD23	1.80	0.64
1:AF:53:PRO:HD2	1:AF:57:GLU:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:53:PRO:HD2	1:CF:57:GLU:HB2	1.79	0.64
1:BZ:53:PRO:HD2	1:BZ:57:GLU:HB2	1.79	0.64
1:C2:38:LYS:NZ	1:C2:44:GLU:HG3	2.11	0.64
1:CQ:18:VAL:HG22	1:CQ:77:LEU:HB2	1.80	0.64
1:B1:18:VAL:HG22	1:B1:77:LEU:HB2	1.80	0.64
1:AQ:18:VAL:HG22	1:AQ:77:LEU:HB2	1.80	0.64
1:CG:18:VAL:HG22	1:CG:77:LEU:HB2	1.80	0.64
1:AL:18:VAL:HG22	1:AL:77:LEU:HB2	1.80	0.64
1:AV:18:VAL:HG22	1:AV:77:LEU:HB2	1.80	0.64
1:AT:107:ASP:CG	1:AT:107:ASP:O	2.35	0.64
1:CU:34:LEU:HD11	1:CU:38:LYS:HD2	1.80	0.64
1:B4:107:ASP:O	1:B4:107:ASP:CG	2.35	0.64
1:AQ:96:ALA:C	1:AQ:100:ALA:CB	2.63	0.63
1:CQ:96:ALA:HB2	1:CQ:112:PHE:CZ	2.33	0.63
1:AC:82:ARG:CG	1:AC:82:ARG:HH11	2.11	0.63
1:CN:149:SER:O	1:CN:152:TRP:CE2	2.50	0.63
1:AG:18:VAL:HG22	1:AG:77:LEU:HB2	1.80	0.63
1:CN:119:THR:HG22	1:CN:121:GLU:H	1.63	0.63
1:AU:34:LEU:HD11	1:AU:38:LYS:HD2	1.80	0.63
1:AI:119:THR:HG22	1:AI:121:GLU:H	1.63	0.63
1:A3:100:ALA:HB2	1:A4:56:PHE:CZ	2.33	0.63
1:BT:58:ILE:O	1:BT:58:ILE:HG22	1.96	0.63
1:BS:119:THR:HG22	1:BS:121:GLU:H	1.63	0.63
1:BP:34:LEU:HD11	1:BP:38:LYS:HD2	1.80	0.63
1:CZ:34:LEU:HD11	1:CZ:38:LYS:HD2	1.80	0.63
1:BB:96:ALA:HB2	1:BB:112:PHE:CZ	2.33	0.63
1:AB:96:ALA:HB2	1:AB:112:PHE:CZ	2.33	0.63
1:BQ:98:GLY:HA2	1:BQ:102:LEU:HD23	1.80	0.63
1:A1:100:ALA:HA	1:A2:56:PHE:HZ	1.62	0.63
1:BC:82:ARG:HH11	1:BC:82:ARG:CG	2.11	0.63
1:AW:82:ARG:HH11	1:AW:82:ARG:CG	2.11	0.63
1:CL:18:VAL:HG22	1:CL:77:LEU:HB2	1.80	0.63
1:A4:58:ILE:O	1:A4:58:ILE:HG22	1.96	0.63
1:CA:7:LEU:HD11	1:CA:140:VAL:HG13	1.79	0.63
1:CJ:107:ASP:CG	1:CJ:107:ASP:O	2.35	0.63
1:CK:7:LEU:HD11	1:CK:140:VAL:HG13	1.79	0.63
1:AO:55:ALA:HB1	1:AO:95:VAL:HG21	1.77	0.63
1:BD:100:ALA:HB2	1:BE:56:PHE:CZ	2.32	0.63
1:AI:39:ARG:O	1:AO:7:LEU:HB3	1.99	0.63
1:AQ:96:ALA:HB2	1:AQ:112:PHE:CZ	2.33	0.63
1:CQ:98:GLY:HA2	1:CQ:102:LEU:HD23	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CV:100:ALA:HA	1:CW:56:PHE:HZ	1.62	0.63
1:AX:149:SER:O	1:AX:152:TRP:CE2	2.51	0.63
1:AB:18:VAL:HG22	1:AB:77:LEU:HB2	1.80	0.63
1:BV:18:VAL:HG22	1:BV:77:LEU:HB2	1.80	0.63
1:B1:4:GLU:HG2	1:B2:51:TRP:CD1	2.32	0.63
1:BF:34:LEU:HD11	1:BF:38:LYS:HD2	1.80	0.63
1:CA:34:LEU:HD11	1:CA:38:LYS:HD2	1.80	0.63
1:AZ:7:LEU:HD11	1:AZ:140:VAL:HG13	1.79	0.63
1:BE:107:ASP:CG	1:BE:107:ASP:O	2.35	0.63
1:CO:107:ASP:CG	1:CO:107:ASP:O	2.35	0.63
1:AQ:98:GLY:HA2	1:AQ:102:LEU:HD23	1.80	0.63
1:CL:96:ALA:HB2	1:CL:112:PHE:CZ	2.33	0.63
1:BG:98:GLY:HA2	1:BG:102:LEU:HD23	1.80	0.63
1:A1:98:GLY:O	1:A1:102:LEU:HB3	1.98	0.63
1:A1:98:GLY:HA2	1:A1:102:LEU:HD23	1.80	0.63
1:CA:53:PRO:HD2	1:CA:57:GLU:HB2	1.79	0.63
1:CC:82:ARG:HH11	1:CC:82:ARG:CG	2.11	0.63
1:BS:149:SER:O	1:BS:152:TRP:CE2	2.50	0.63
1:CD:149:SER:O	1:CD:152:TRP:CE2	2.51	0.63
1:BG:4:GLU:HG2	1:BH:51:TRP:HD1	1.61	0.63
1:AY:107:ASP:O	1:AY:107:ASP:CG	2.35	0.63
1:BO:107:ASP:O	1:BO:107:ASP:CG	2.35	0.63
1:C4:58:ILE:O	1:C4:58:ILE:HG22	1.96	0.63
1:BQ:98:GLY:O	1:BQ:102:LEU:HB3	1.98	0.63
1:CG:7:LEU:HB3	1:CU:39:ARG:O	1.98	0.63
1:AF:39:ARG:HH22	1:AQ:144:GLU:CD	2.02	0.63
1:CW:82:ARG:HH11	1:CW:82:ARG:CG	2.11	0.63
1:A2:82:ARG:CG	1:A2:82:ARG:HH11	2.11	0.63
1:BA:34:LEU:HD11	1:BA:38:LYS:HD2	1.80	0.63
1:CZ:7:LEU:HD11	1:CZ:140:VAL:HG13	1.79	0.63
1:BP:7:LEU:HD11	1:BP:140:VAL:HG13	1.79	0.63
1:CJ:58:ILE:O	1:CJ:58:ILE:HG22	1.96	0.63
1:CP:7:LEU:HD11	1:CP:140:VAL:HG13	1.79	0.63
1:AZ:34:LEU:HD11	1:AZ:38:LYS:HD2	1.80	0.63
1:A3:119:THR:HG22	1:A3:121:GLU:H	1.63	0.63
1:CD:119:THR:HG22	1:CD:121:GLU:H	1.63	0.63
1:AV:98:GLY:O	1:AV:102:LEU:HB3	1.98	0.63
1:AQ:98:GLY:O	1:AQ:102:LEU:HB3	1.98	0.63
1:BV:98:GLY:HA2	1:BV:102:LEU:HD23	1.80	0.63
1:AF:34:LEU:HD11	1:AF:38:LYS:HD2	1.80	0.63
1:AG:98:GLY:HA2	1:AG:102:LEU:HD23	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B1:98:GLY:O	1:B1:102:LEU:HB3	1.98	0.63
1:AM:82:ARG:CG	1:AM:82:ARG:HH11	2.11	0.63
1:CM:82:ARG:HH11	1:CM:82:ARG:CG	2.11	0.63
1:BD:40:HIS:CE1	1:BJ:7:LEU:HD23	2.34	0.63
1:AV:58:ILE:N	1:AV:59:PRO:HD2	2.14	0.63
1:AR:82:ARG:HH11	1:AR:82:ARG:CG	2.11	0.63
1:BB:107:ASP:HB2	1:BB:152:TRP:HZ3	1.62	0.63
1:BB:58:ILE:N	1:BB:59:PRO:HD2	2.14	0.63
1:BL:98:GLY:HA2	1:BL:102:LEU:HD23	1.80	0.63
1:CL:96:ALA:C	1:CL:100:ALA:CB	2.63	0.63
1:BG:58:ILE:N	1:BG:59:PRO:HD2	2.14	0.63
1:CV:58:ILE:N	1:CV:59:PRO:HD2	2.14	0.63
1:A1:58:ILE:N	1:A1:59:PRO:HD2	2.14	0.63
1:CR:82:ARG:HH11	1:CR:82:ARG:CG	2.11	0.63
1:AF:58:ILE:N	1:AF:59:PRO:HD2	2.14	0.63
1:CB:18:VAL:HG22	1:CB:77:LEU:HB2	1.80	0.63
1:BD:7:LEU:HD23	1:BJ:40:HIS:CE1	2.34	0.63
1:CP:34:LEU:HD11	1:CP:38:LYS:HD2	1.80	0.63
1:AQ:13:LYS:HZ1	1:BU:43:GLU:CG	2.10	0.62
1:AL:98:GLY:HA2	1:AL:102:LEU:HD23	1.80	0.62
1:C1:58:ILE:N	1:C1:59:PRO:HD2	2.14	0.62
1:CH:82:ARG:HH11	1:CH:82:ARG:CG	2.11	0.62
1:CU:58:ILE:N	1:CU:59:PRO:HD2	2.14	0.62
1:A1:18:VAL:HG22	1:A1:77:LEU:HB2	1.80	0.62
1:BK:34:LEU:HD11	1:BK:38:LYS:HD2	1.80	0.62
1:AN:119:THR:HG22	1:AN:121:GLU:H	1.63	0.62
1:BZ:34:LEU:HD11	1:BZ:38:LYS:HD2	1.80	0.62
1:B3:119:THR:HG22	1:B3:121:GLU:H	1.63	0.62
1:AW:97:LYS:HG3	1:AX:97:LYS:HZ3	1.65	0.62
1:BL:58:ILE:N	1:BL:59:PRO:HD2	2.14	0.62
1:AQ:58:ILE:N	1:AQ:59:PRO:HD2	2.14	0.62
1:AB:98:GLY:HA2	1:AB:102:LEU:HD23	1.80	0.62
1:BL:18:VAL:HG22	1:BL:77:LEU:HB2	1.80	0.62
1:CT:7:LEU:HD23	1:C3:40:HIS:CE1	2.34	0.62
1:BG:18:VAL:HG22	1:BG:77:LEU:HB2	1.80	0.62
1:BX:151:HIS:HB3	1:BY:64:LYS:HB3	1.82	0.62
1:CN:151:HIS:HB3	1:CO:64:LYS:HB3	1.82	0.62
1:CS:119:THR:HG22	1:CS:121:GLU:H	1.63	0.62
1:CF:34:LEU:HD11	1:CF:38:LYS:HD2	1.80	0.62
1:BN:119:THR:HG22	1:BN:121:GLU:H	1.63	0.62
1:CD:120:ILE:CD1	1:CR:129:THR:HG21	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:58:ILE:N	1:CB:59:PRO:HD2	2.14	0.62
1:AB:58:ILE:N	1:AB:59:PRO:HD2	2.14	0.62
1:C2:82:ARG:CG	1:C2:82:ARG:HH11	2.11	0.62
1:AK:58:ILE:N	1:AK:59:PRO:HD2	2.14	0.62
1:BP:58:ILE:N	1:BP:59:PRO:HD2	2.14	0.62
1:CF:58:ILE:N	1:CF:59:PRO:HD2	2.14	0.62
1:BK:58:ILE:N	1:BK:59:PRO:HD2	2.14	0.62
1:CD:151:HIS:HB3	1:CE:64:LYS:HB3	1.82	0.62
1:AU:7:LEU:HD11	1:AU:140:VAL:HG13	1.79	0.62
1:AG:58:ILE:N	1:AG:59:PRO:HD2	2.14	0.62
1:BH:82:ARG:HH11	1:BH:82:ARG:CG	2.11	0.62
1:CK:58:ILE:N	1:CK:59:PRO:HD2	2.15	0.62
1:AP:58:ILE:N	1:AP:59:PRO:HD2	2.14	0.62
1:AS:151:HIS:HB3	1:AT:64:LYS:HB3	1.81	0.62
1:B4:152:TRP:HE3	1:B4:153:ALA:H	1.48	0.62
1:C4:152:TRP:HE3	1:C4:153:ALA:H	1.47	0.62
1:AT:152:TRP:HE3	1:AT:153:ALA:H	1.48	0.62
1:CX:22:ASN:HA	1:C2:128:GLY:O	2.00	0.62
1:CQ:58:ILE:N	1:CQ:59:PRO:HD2	2.14	0.62
1:CG:98:GLY:O	1:CG:102:LEU:HB3	1.98	0.62
1:B2:82:ARG:CG	1:B2:82:ARG:HH11	2.11	0.62
1:CS:151:HIS:HB3	1:CT:64:LYS:HB3	1.82	0.62
1:A3:151:HIS:HB3	1:A4:64:LYS:HB3	1.82	0.62
1:BN:151:HIS:HB3	1:BO:64:LYS:HB3	1.82	0.62
1:CV:18:VAL:HG22	1:CV:77:LEU:HB2	1.80	0.62
1:BU:34:LEU:HD11	1:BU:38:LYS:HD2	1.80	0.62
1:CK:34:LEU:HD11	1:CK:38:LYS:HD2	1.80	0.62
1:AD:119:THR:HG22	1:AD:121:GLU:H	1.63	0.62
1:AK:34:LEU:HD11	1:AK:38:LYS:HD2	1.80	0.62
1:C1:107:ASP:HB2	1:C1:152:TRP:HZ3	1.62	0.62
1:CB:98:GLY:HA2	1:CB:102:LEU:HD23	1.80	0.62
1:CG:58:ILE:N	1:CG:59:PRO:HD2	2.14	0.62
1:AH:82:ARG:CG	1:AH:82:ARG:HH11	2.11	0.62
1:BC:38:LYS:HZ2	1:BC:44:GLU:HG3	1.64	0.62
1:AI:151:HIS:HB3	1:AJ:64:LYS:HB3	1.82	0.62
1:CE:152:TRP:HE3	1:CE:153:ALA:H	1.48	0.62
1:CC:8:VAL:HG13	1:CR:8:VAL:HG21	1.81	0.62
1:AV:98:GLY:HA2	1:AV:102:LEU:HD23	1.80	0.62
1:CT:58:ILE:N	1:CT:59:PRO:HD2	2.15	0.62
1:A4:58:ILE:N	1:A4:59:PRO:HD2	2.15	0.62
1:BQ:58:ILE:N	1:BQ:59:PRO:HD2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CP:58:ILE:N	1:CP:59:PRO:HD2	2.14	0.62
1:BD:151:HIS:HB3	1:BE:64:LYS:HB3	1.82	0.62
1:BJ:152:TRP:HE3	1:BJ:153:ALA:H	1.47	0.62
1:CC:129:THR:O	1:CC:132:GLY:N	2.25	0.62
1:BU:58:ILE:N	1:BU:59:PRO:HD2	2.14	0.62
1:B4:58:ILE:N	1:B4:59:PRO:HD2	2.15	0.62
1:BT:152:TRP:HE3	1:BT:153:ALA:H	1.48	0.62
1:AU:58:ILE:N	1:AU:59:PRO:HD2	2.14	0.61
1:CZ:58:ILE:N	1:CZ:59:PRO:HD2	2.14	0.61
1:AZ:58:ILE:N	1:AZ:59:PRO:HD2	2.14	0.61
1:BI:151:HIS:HB3	1:BJ:64:LYS:HB3	1.82	0.61
1:AY:58:ILE:N	1:AY:59:PRO:HD2	2.15	0.61
1:BO:152:TRP:HE3	1:BO:153:ALA:H	1.48	0.61
1:CR:129:THR:O	1:CR:132:GLY:N	2.25	0.61
1:AA:58:ILE:N	1:AA:59:PRO:HD2	2.14	0.61
1:BF:58:ILE:N	1:BF:59:PRO:HD2	2.14	0.61
1:AD:151:HIS:HB3	1:AE:64:LYS:HB3	1.82	0.61
1:CI:151:HIS:HB3	1:CJ:64:LYS:HB3	1.81	0.61
1:AE:58:ILE:N	1:AE:59:PRO:HD2	2.15	0.61
1:AA:34:LEU:HD11	1:AA:38:LYS:HD2	1.80	0.61
1:BT:58:ILE:N	1:BT:59:PRO:HD2	2.15	0.61
1:B2:6:HIS:HE1	1:B2:8:VAL:HB	1.66	0.61
1:BL:97:LYS:HE3	1:BM:97:LYS:HZ3	1.64	0.61
1:A1:148:LEU:HD13	1:A2:61:ILE:HD11	1.83	0.61
1:BA:58:ILE:N	1:BA:59:PRO:HD2	2.14	0.61
1:AX:151:HIS:HB3	1:AY:64:LYS:HB3	1.82	0.61
1:CE:58:ILE:N	1:CE:59:PRO:HD2	2.15	0.61
1:C4:58:ILE:N	1:C4:59:PRO:HD2	2.15	0.61
1:CJ:58:ILE:N	1:CJ:59:PRO:HD2	2.15	0.61
1:AA:34:LEU:HD12	1:AA:38:LYS:HB2	1.83	0.61
1:CW:100:ALA:HB2	1:CX:56:PHE:CZ	2.36	0.61
1:AE:152:TRP:HE3	1:AE:153:ALA:H	1.48	0.61
1:B1:58:ILE:N	1:B1:59:PRO:HD2	2.14	0.61
1:CL:58:ILE:N	1:CL:59:PRO:HD2	2.14	0.61
1:BS:151:HIS:HB3	1:BT:64:LYS:HB3	1.82	0.61
1:BJ:58:ILE:N	1:BJ:59:PRO:HD2	2.15	0.61
1:AJ:58:ILE:N	1:AJ:59:PRO:HD2	2.15	0.61
1:CZ:34:LEU:HD12	1:CZ:38:LYS:HB2	1.83	0.61
1:CC:6:HIS:HE1	1:CC:8:VAL:HB	1.66	0.61
1:AS:119:THR:HG22	1:AS:121:GLU:H	1.63	0.61
1:AR:6:HIS:HE1	1:AR:8:VAL:HB	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B2:100:ALA:HB2	1:B3:56:PHE:CZ	2.36	0.61
1:CT:152:TRP:HE3	1:CT:153:ALA:H	1.47	0.61
1:CO:53:PRO:CD	1:CO:57:GLU:HG3	2.29	0.61
1:AW:129:THR:O	1:AW:132:GLY:N	2.25	0.61
1:BV:58:ILE:N	1:BV:59:PRO:HD2	2.14	0.61
1:CQ:148:LEU:HD13	1:CR:61:ILE:HD11	1.83	0.61
1:BQ:148:LEU:HD13	1:BR:61:ILE:HD11	1.83	0.61
1:AQ:148:LEU:HD13	1:AR:61:ILE:HD11	1.83	0.61
1:CA:58:ILE:N	1:CA:59:PRO:HD2	2.14	0.61
1:B3:151:HIS:HB3	1:B4:64:LYS:HB3	1.82	0.61
1:BP:34:LEU:HD12	1:BP:38:LYS:HB2	1.83	0.61
1:BF:34:LEU:HD12	1:BF:38:LYS:HB2	1.83	0.61
1:BA:34:LEU:HD12	1:BA:38:LYS:HB2	1.83	0.61
1:BU:34:LEU:HD12	1:BU:38:LYS:HB2	1.83	0.61
1:AR:100:ALA:HB2	1:AS:56:PHE:CZ	2.36	0.61
1:BM:100:ALA:HB2	1:BN:56:PHE:CZ	2.36	0.61
1:AW:6:HIS:HE1	1:AW:8:VAL:HB	1.66	0.61
1:BW:100:ALA:HB2	1:BX:56:PHE:CZ	2.36	0.61
1:CM:6:HIS:HE1	1:CM:8:VAL:HB	1.66	0.61
1:BV:148:LEU:HD13	1:BW:61:ILE:HD11	1.83	0.61
1:CG:24:PHE:CE2	1:CQ:124:ILE:HD11	2.35	0.61
1:CO:58:ILE:N	1:CO:59:PRO:HD2	2.15	0.61
1:AT:58:ILE:N	1:AT:59:PRO:HD2	2.15	0.61
1:BO:58:ILE:N	1:BO:59:PRO:HD2	2.15	0.61
1:AU:34:LEU:HD12	1:AU:38:LYS:HB2	1.83	0.61
1:CH:100:ALA:HB2	1:CI:56:PHE:CZ	2.36	0.61
1:A2:100:ALA:HB2	1:A3:56:PHE:CZ	2.36	0.61
1:AW:100:ALA:HB2	1:AX:56:PHE:CZ	2.36	0.61
1:AP:34:LEU:HD11	1:AP:38:LYS:HD2	1.80	0.61
1:AY:53:PRO:CD	1:AY:57:GLU:HG3	2.29	0.61
1:BH:129:THR:O	1:BH:132:GLY:N	2.25	0.61
1:C1:148:LEU:HD13	1:C2:61:ILE:HD11	1.83	0.61
1:BW:82:ARG:HH11	1:BW:82:ARG:CG	2.11	0.61
1:BR:63:LYS:O	1:BR:67:ASN:HB2	2.01	0.61
1:AO:58:ILE:N	1:AO:59:PRO:HD2	2.15	0.61
1:AP:34:LEU:HD12	1:AP:38:LYS:HB2	1.83	0.61
1:CH:6:HIS:HE1	1:CH:8:VAL:HB	1.66	0.61
1:B2:63:LYS:O	1:B2:67:ASN:HB2	2.01	0.61
1:B4:53:PRO:CD	1:B4:57:GLU:HG3	2.29	0.61
1:CH:129:THR:O	1:CH:132:GLY:N	2.25	0.61
1:B2:97:LYS:HG3	1:B3:97:LYS:HZ3	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:148:LEU:HD13	1:AC:61:ILE:HD11	1.83	0.61
1:AG:148:LEU:HD13	1:AH:61:ILE:HD11	1.83	0.61
1:AV:148:LEU:HD13	1:AW:61:ILE:HD11	1.83	0.61
1:B1:148:LEU:HD13	1:B2:61:ILE:HD11	1.83	0.61
1:CV:148:LEU:HD13	1:CW:61:ILE:HD11	1.83	0.61
1:AW:63:LYS:O	1:AW:67:ASN:HB2	2.01	0.61
1:BM:63:LYS:O	1:BM:67:ASN:HB2	2.01	0.61
1:CM:63:LYS:O	1:CM:67:ASN:HB2	2.01	0.61
1:CH:63:LYS:O	1:CH:67:ASN:HB2	2.01	0.61
1:BE:58:ILE:N	1:BE:59:PRO:HD2	2.15	0.61
1:BZ:34:LEU:HD12	1:BZ:38:LYS:HB2	1.83	0.61
1:AC:100:ALA:HB2	1:AD:56:PHE:CZ	2.36	0.61
1:AM:6:HIS:HE1	1:AM:8:VAL:HB	1.66	0.61
1:BC:6:HIS:HE1	1:BC:8:VAL:HB	1.66	0.61
1:CI:124:ILE:O	1:CI:129:THR:OG1	2.16	0.61
1:BN:124:ILE:O	1:BN:129:THR:OG1	2.16	0.61
1:CY:152:TRP:HE3	1:CY:153:ALA:H	1.48	0.61
1:AL:58:ILE:N	1:AL:59:PRO:HD2	2.14	0.61
1:BG:148:LEU:HD13	1:BH:61:ILE:HD11	1.83	0.61
1:CB:148:LEU:HD13	1:CC:61:ILE:HD11	1.83	0.61
1:AF:39:ARG:O	1:AQ:7:LEU:HB3	2.01	0.61
1:BZ:58:ILE:N	1:BZ:59:PRO:HD2	2.14	0.61
1:C3:151:HIS:HB3	1:C4:64:LYS:HB3	1.82	0.61
1:AN:151:HIS:HB3	1:AO:64:LYS:HB3	1.82	0.61
1:CY:58:ILE:N	1:CY:59:PRO:HD2	2.15	0.61
1:AZ:34:LEU:HD12	1:AZ:38:LYS:HB2	1.83	0.61
1:CK:34:LEU:HD12	1:CK:38:LYS:HB2	1.83	0.61
1:BH:100:ALA:HB2	1:BI:56:PHE:CZ	2.36	0.61
1:C2:6:HIS:HE1	1:C2:8:VAL:HB	1.66	0.61
1:AD:124:ILE:O	1:AD:129:THR:OG1	2.16	0.61
1:BW:6:HIS:HE1	1:BW:8:VAL:HB	1.66	0.61
1:AH:100:ALA:HB2	1:AI:56:PHE:CZ	2.36	0.61
1:AJ:152:TRP:HE3	1:AJ:153:ALA:H	1.48	0.61
1:BM:82:ARG:CG	1:BM:82:ARG:HH11	2.11	0.60
1:AK:34:LEU:HD12	1:AK:38:LYS:HB2	1.83	0.60
1:A2:6:HIS:HE1	1:A2:8:VAL:HB	1.66	0.60
1:CM:100:ALA:HB2	1:CN:56:PHE:CZ	2.36	0.60
1:CR:97:LYS:HG3	1:CS:97:LYS:HZ1	1.66	0.60
1:BR:20:ARG:HG3	1:BR:52:VAL:O	2.01	0.60
1:AR:63:LYS:O	1:AR:67:ASN:HB2	2.01	0.60
1:C2:63:LYS:O	1:C2:67:ASN:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:58:ILE:N	1:BY:59:PRO:HD2	2.15	0.60
1:CA:34:LEU:HD12	1:CA:38:LYS:HB2	1.83	0.60
1:CP:34:LEU:HD12	1:CP:38:LYS:HB2	1.83	0.60
1:C2:100:ALA:HB2	1:C3:56:PHE:CZ	2.36	0.60
1:CD:124:ILE:O	1:CD:129:THR:OG1	2.16	0.60
1:CW:129:THR:O	1:CW:132:GLY:N	2.25	0.60
1:BC:20:ARG:HG3	1:BC:52:VAL:O	2.01	0.60
1:CX:151:HIS:HB3	1:CX:64:LYS:HB3	1.82	0.60
1:AF:34:LEU:HD12	1:AF:38:LYS:HB2	1.83	0.60
1:BC:63:LYS:O	1:BC:67:ASN:HB2	2.01	0.60
1:AM:100:ALA:HB2	1:AN:56:PHE:CZ	2.36	0.60
1:CP:28:LYS:HD2	1:CW:24:PHE:CD1	2.36	0.60
1:BH:6:HIS:HE1	1:BH:8:VAL:HB	1.66	0.60
1:CR:20:ARG:HG3	1:CR:52:VAL:O	2.02	0.60
1:CC:20:ARG:HG3	1:CC:52:VAL:O	2.01	0.60
1:CW:63:LYS:O	1:CW:67:ASN:HB2	2.01	0.60
1:BR:6:HIS:HE1	1:BR:8:VAL:HB	1.66	0.60
1:CO:152:TRP:HE3	1:CO:153:ALA:H	1.47	0.60
1:CY:53:PRO:CD	1:CY:57:GLU:HG3	2.29	0.60
1:AH:63:LYS:O	1:AH:67:ASN:HB2	2.01	0.60
1:BE:152:TRP:HE3	1:BE:153:ALA:H	1.48	0.60
1:CR:100:ALA:HB2	1:CS:56:PHE:CZ	2.36	0.60
1:CC:100:ALA:HB2	1:CD:56:PHE:CZ	2.36	0.60
1:BM:6:HIS:HE1	1:BM:8:VAL:HB	1.66	0.60
1:CJ:152:TRP:HE3	1:CJ:153:ALA:H	1.47	0.60
1:AM:63:LYS:O	1:AM:67:ASN:HB2	2.01	0.60
1:AC:63:LYS:O	1:AC:67:ASN:HB2	2.01	0.60
1:BC:100:ALA:HB2	1:BD:56:PHE:CZ	2.36	0.60
1:CW:6:HIS:HE1	1:CW:8:VAL:HB	1.66	0.60
1:AH:20:ARG:HG3	1:AH:52:VAL:O	2.02	0.60
1:AW:20:ARG:HG3	1:AW:52:VAL:O	2.01	0.60
1:C2:20:ARG:HG3	1:C2:52:VAL:O	2.01	0.60
1:BH:63:LYS:O	1:BH:67:ASN:HB2	2.01	0.60
1:CK:95:VAL:HG12	1:CK:112:PHE:HE1	1.67	0.60
1:AP:95:VAL:HG12	1:AP:112:PHE:HE1	1.67	0.60
1:BK:34:LEU:HD12	1:BK:38:LYS:HB2	1.83	0.60
1:BD:124:ILE:O	1:BD:129:THR:OG1	2.16	0.60
1:BH:20:ARG:HG3	1:BH:52:VAL:O	2.01	0.60
1:CW:20:ARG:HG3	1:CW:52:VAL:O	2.01	0.60
1:BA:95:VAL:HG12	1:BA:112:PHE:HE1	1.67	0.60
1:A2:63:LYS:O	1:A2:67:ASN:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:95:VAL:HG12	1:BZ:112:PHE:HE1	1.67	0.60
1:A4:152:TRP:HE3	1:A4:153:ALA:H	1.48	0.60
1:AN:124:ILE:O	1:AN:129:THR:OG1	2.16	0.60
1:AH:6:HIS:HE1	1:AH:8:VAL:HB	1.66	0.60
1:BF:39:ARG:HH22	1:BQ:144:GLU:CD	2.05	0.60
1:CC:63:LYS:O	1:CC:67:ASN:HB2	2.01	0.60
1:AM:20:ARG:HG3	1:AM:52:VAL:O	2.02	0.60
1:AL:148:LEU:HD13	1:AM:61:ILE:HD11	1.83	0.60
1:BW:20:ARG:HG3	1:BW:52:VAL:O	2.01	0.60
1:AR:20:ARG:HG3	1:AR:52:VAL:O	2.01	0.60
1:CA:95:VAL:HG12	1:CA:112:PHE:HE1	1.67	0.60
1:BK:95:VAL:HG12	1:BK:112:PHE:HE1	1.67	0.60
1:BR:100:ALA:HB2	1:BS:56:PHE:CZ	2.36	0.60
1:AC:6:HIS:HE1	1:AC:8:VAL:HB	1.66	0.60
1:AT:53:PRO:CD	1:AT:57:GLU:HG3	2.29	0.59
1:AG:97:LYS:HE3	1:AH:97:LYS:NZ	2.17	0.59
1:CL:97:LYS:HE3	1:CM:97:LYS:HZ3	1.67	0.59
1:BQ:97:LYS:HE3	1:BR:97:LYS:NZ	2.17	0.59
1:CG:148:LEU:HD13	1:CH:61:ILE:HD11	1.83	0.59
1:CZ:95:VAL:HG12	1:CZ:112:PHE:HE1	1.67	0.59
1:BA:58:ILE:O	1:BA:58:ILE:CG2	2.50	0.59
1:CF:95:VAL:HG12	1:CF:112:PHE:HE1	1.67	0.59
1:AE:58:ILE:CG2	1:AE:58:ILE:O	2.50	0.59
1:CR:63:LYS:O	1:CR:67:ASN:HB2	2.01	0.59
1:BY:152:TRP:HE3	1:BY:153:ALA:H	1.48	0.59
1:BW:63:LYS:O	1:BW:67:ASN:HB2	2.01	0.59
1:B3:124:ILE:O	1:B3:129:THR:OG1	2.16	0.59
1:AL:97:LYS:HE3	1:AM:97:LYS:NZ	2.17	0.59
1:AQ:97:LYS:HE3	1:AR:97:LYS:NZ	2.17	0.59
1:A1:97:LYS:HE3	1:A2:97:LYS:NZ	2.18	0.59
1:B2:20:ARG:HG3	1:B2:52:VAL:O	2.01	0.59
1:BM:20:ARG:HG3	1:BM:52:VAL:O	2.02	0.59
1:CW:39:ARG:O	1:C2:7:LEU:HB3	2.02	0.59
1:AA:95:VAL:HG12	1:AA:112:PHE:HE1	1.67	0.59
1:AO:58:ILE:O	1:AO:58:ILE:CG2	2.51	0.59
1:CP:83:GLY:HA3	2:CP:201:PO4:O2	2.03	0.59
1:BD:33:ALA:O	1:BD:37:LEU:HB2	2.03	0.59
1:AP:83:GLY:HA3	2:AP:1001:PO4:O2	2.03	0.59
1:CU:83:GLY:HA3	2:CU:201:PO4:O2	2.02	0.59
1:AF:83:GLY:HA3	2:AF:1001:PO4:O2	2.03	0.59
1:AZ:83:GLY:HA3	2:AZ:1001:PO4:O2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:33:ALA:O	1:AS:37:LEU:HB2	2.03	0.59
1:AU:83:GLY:HA3	2:AU:1001:PO4:O2	2.03	0.59
1:C1:97:LYS:HE3	1:C2:97:LYS:NZ	2.18	0.59
1:AB:97:LYS:HE3	1:AC:97:LYS:NZ	2.18	0.59
1:BV:97:LYS:HE3	1:BW:97:LYS:NZ	2.18	0.59
1:BH:97:LYS:HG3	1:BI:97:LYS:HZ3	1.66	0.59
1:AF:95:VAL:HG12	1:AF:112:PHE:HE1	1.67	0.59
1:AO:152:TRP:HE3	1:AO:153:ALA:H	1.48	0.59
1:AB:107:ASP:CB	1:AB:152:TRP:CZ3	2.86	0.59
1:AY:152:TRP:HE3	1:AY:153:ALA:H	1.48	0.59
1:AN:33:ALA:O	1:AN:37:LEU:HB2	2.03	0.59
1:B1:6:HIS:HE1	1:B1:8:VAL:HB	1.68	0.59
1:AV:107:ASP:CB	1:AV:152:TRP:CZ3	2.86	0.59
1:BZ:83:GLY:HA3	2:BZ:1001:PO4:O2	2.02	0.59
1:CV:97:LYS:HE3	1:CW:97:LYS:NZ	2.18	0.59
1:CH:20:ARG:HG3	1:CH:52:VAL:O	2.02	0.59
1:CK:58:ILE:CG2	1:CK:58:ILE:O	2.50	0.59
1:AZ:148:LEU:HD23	1:AZ:148:LEU:O	2.03	0.59
1:AL:6:HIS:HE1	1:AL:8:VAL:HB	1.68	0.59
1:BP:148:LEU:O	1:BP:148:LEU:HD23	2.03	0.59
1:CA:83:GLY:HA3	2:CA:1001:PO4:O2	2.03	0.59
1:AQ:107:ASP:CB	1:AQ:152:TRP:CZ3	2.86	0.59
1:CN:33:ALA:O	1:CN:37:LEU:HB2	2.03	0.59
1:AU:148:LEU:HD23	1:AU:148:LEU:O	2.03	0.59
1:AI:33:ALA:O	1:AI:37:LEU:HB2	2.03	0.59
1:BK:148:LEU:HD23	1:BK:148:LEU:O	2.03	0.59
1:AL:107:ASP:CB	1:AL:152:TRP:CZ3	2.86	0.59
1:BG:107:ASP:HB2	1:BG:152:TRP:HZ3	1.62	0.59
1:BG:97:LYS:HE3	1:BH:97:LYS:NZ	2.18	0.59
1:CM:20:ARG:HG3	1:CM:52:VAL:O	2.01	0.59
1:BB:148:LEU:HD13	1:BC:61:ILE:HD11	1.83	0.59
1:A2:20:ARG:HG3	1:A2:52:VAL:O	2.01	0.59
1:AK:95:VAL:HG12	1:AK:112:PHE:HE1	1.67	0.59
1:CO:58:ILE:CG2	1:CO:58:ILE:O	2.51	0.59
1:BX:33:ALA:O	1:BX:37:LEU:HB2	2.03	0.59
1:AK:148:LEU:HD23	1:AK:148:LEU:O	2.03	0.59
1:AG:107:ASP:CB	1:AG:152:TRP:CZ3	2.86	0.59
1:CA:148:LEU:O	1:CA:148:LEU:HD23	2.03	0.59
1:BP:83:GLY:HA3	2:BP:1001:PO4:O2	2.03	0.59
1:CK:148:LEU:HD23	1:CK:148:LEU:O	2.03	0.59
1:BJ:53:PRO:CD	1:BJ:57:GLU:HG3	2.29	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:53:PRO:CD	1:AO:57:GLU:HG3	2.29	0.59
1:AH:97:LYS:HG3	1:AI:97:LYS:HZ1	1.67	0.59
1:B1:97:LYS:HE3	1:B2:97:LYS:NZ	2.17	0.59
1:AC:20:ARG:HG3	1:AC:52:VAL:O	2.01	0.59
1:AZ:95:VAL:HG12	1:AZ:112:PHE:HE1	1.67	0.59
1:CR:6:HIS:HE1	1:CR:8:VAL:HB	1.66	0.59
1:BU:83:GLY:HA3	2:BU:1001:PO4:O2	2.03	0.59
1:CD:33:ALA:O	1:CD:37:LEU:HB2	2.03	0.59
1:BU:148:LEU:HD23	1:BU:148:LEU:O	2.03	0.59
1:CL:148:LEU:HD13	1:CM:61:ILE:HD11	1.83	0.59
1:CC:65:MET:HE3	1:CC:71:TYR:CE1	2.38	0.59
1:AA:58:ILE:CG2	1:AA:58:ILE:O	2.50	0.59
1:AK:83:GLY:HA3	2:AK:1001:PO4:O2	2.03	0.59
1:AP:148:LEU:O	1:AP:148:LEU:HD23	2.03	0.59
1:AB:6:HIS:HE1	1:AB:8:VAL:HB	1.68	0.59
1:CB:6:HIS:HE1	1:CB:8:VAL:HB	1.68	0.59
1:BF:83:GLY:HA3	2:BF:1001:PO4:O2	2.03	0.59
1:A1:107:ASP:CB	1:A1:152:TRP:CZ3	2.86	0.59
1:AM:129:THR:O	1:AM:132:GLY:N	2.25	0.59
1:BR:129:THR:O	1:BR:132:GLY:N	2.25	0.59
1:CB:97:LYS:HE3	1:CC:97:LYS:NZ	2.18	0.59
1:BL:148:LEU:HD13	1:BM:61:ILE:HD11	1.83	0.59
1:CM:65:MET:HE3	1:CM:71:TYR:CE1	2.38	0.59
1:BY:58:ILE:O	1:BY:58:ILE:CG2	2.51	0.59
1:AX:33:ALA:O	1:AX:37:LEU:HB2	2.03	0.59
1:B3:33:ALA:O	1:B3:37:LEU:HB2	2.03	0.59
1:AW:116:THR:O	1:AX:85:THR:HB	2.03	0.59
1:CX:33:ALA:O	1:CX:37:LEU:HB2	2.03	0.59
1:BI:33:ALA:O	1:BI:37:LEU:HB2	2.03	0.59
1:B2:129:THR:O	1:B2:132:GLY:N	2.25	0.59
1:CQ:97:LYS:HE3	1:CR:97:LYS:NZ	2.18	0.59
1:BU:95:VAL:HG12	1:BU:112:PHE:HE1	1.67	0.59
1:BP:95:VAL:HG12	1:BP:112:PHE:HE1	1.67	0.59
1:BE:58:ILE:CG2	1:BE:58:ILE:O	2.50	0.59
1:CF:34:LEU:HD12	1:CF:38:LYS:HB2	1.83	0.59
1:CQ:6:HIS:HE1	1:CQ:8:VAL:HB	1.68	0.59
1:CZ:148:LEU:HD23	1:CZ:148:LEU:O	2.03	0.59
1:A3:33:ALA:O	1:A3:37:LEU:HB2	2.03	0.59
1:BH:116:THR:O	1:BI:85:THR:HB	2.03	0.59
1:BZ:148:LEU:O	1:BZ:148:LEU:HD23	2.03	0.59
1:CK:83:GLY:HA3	2:CK:201:PO4:O2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:116:THR:O	1:CI:85:THR:HB	2.03	0.59
1:AQ:6:HIS:HE1	1:AQ:8:VAL:HB	1.68	0.59
1:BV:6:HIS:HE1	1:BV:8:VAL:HB	1.68	0.59
1:CW:65:MET:HE3	1:CW:71:TYR:CE1	2.38	0.59
1:CU:34:LEU:HD12	1:CU:38:LYS:HB2	1.83	0.59
1:BF:148:LEU:O	1:BF:148:LEU:HD23	2.03	0.59
1:CF:148:LEU:HD23	1:CF:148:LEU:O	2.03	0.59
1:CL:6:HIS:HE1	1:CL:8:VAL:HB	1.68	0.59
1:C3:33:ALA:O	1:C3:37:LEU:HB2	2.03	0.59
1:BA:148:LEU:HD23	1:BA:148:LEU:O	2.03	0.59
1:B2:116:THR:O	1:B3:85:THR:HB	2.03	0.59
1:CC:116:THR:O	1:CD:85:THR:HB	2.03	0.59
1:BW:116:THR:O	1:BX:85:THR:HB	2.03	0.59
1:BG:6:HIS:HE1	1:BG:8:VAL:HB	1.68	0.59
1:BL:97:LYS:HE3	1:BM:97:LYS:NZ	2.17	0.58
1:CG:97:LYS:HE3	1:CH:97:LYS:NZ	2.18	0.58
1:AR:65:MET:HE3	1:AR:71:TYR:CE1	2.38	0.58
1:AU:95:VAL:HG12	1:AU:112:PHE:HE1	1.67	0.58
1:CY:58:ILE:O	1:CY:58:ILE:CG2	2.50	0.58
1:C2:116:THR:O	1:C3:85:THR:HB	2.03	0.58
1:AI:124:ILE:O	1:AI:129:THR:OG1	2.16	0.58
1:CS:33:ALA:O	1:CS:37:LEU:HB2	2.02	0.58
1:CP:148:LEU:O	1:CP:148:LEU:HD23	2.03	0.58
1:BN:33:ALA:O	1:BN:37:LEU:HB2	2.03	0.58
1:BM:116:THR:O	1:BN:85:THR:HB	2.03	0.58
1:CV:6:HIS:HE1	1:CV:8:VAL:HB	1.68	0.58
1:AM:116:THR:O	1:AN:85:THR:HB	2.03	0.58
1:AH:116:THR:O	1:AI:85:THR:HB	2.03	0.58
1:BU:58:ILE:O	1:BU:58:ILE:CG2	2.50	0.58
1:BF:95:VAL:HG12	1:BF:112:PHE:HE1	1.67	0.58
1:BD:39:ARG:O	1:BJ:7:LEU:HB3	2.02	0.58
1:AF:148:LEU:HD23	1:AF:148:LEU:O	2.03	0.58
1:AD:33:ALA:O	1:AD:37:LEU:HB2	2.03	0.58
1:CJ:53:PRO:CD	1:CJ:57:GLU:HG3	2.29	0.58
1:AE:53:PRO:CD	1:AE:57:GLU:HG3	2.29	0.58
1:BB:97:LYS:HE3	1:BC:97:LYS:NZ	2.17	0.58
1:AV:97:LYS:HE3	1:AW:97:LYS:NZ	2.18	0.58
1:BM:65:MET:HE3	1:BM:71:TYR:CE1	2.38	0.58
1:BJ:58:ILE:CG2	1:BJ:58:ILE:O	2.51	0.58
1:CT:58:ILE:O	1:CT:58:ILE:CG2	2.50	0.58
1:BA:83:GLY:HA3	2:BA:1001:PO4:O2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:83:GLY:HA3	2:CF:201:PO4:O2	2.03	0.58
1:A1:6:HIS:HE1	1:A1:8:VAL:HB	1.68	0.58
1:BR:116:THR:O	1:BS:85:THR:HB	2.03	0.58
1:BC:97:LYS:HG3	1:BD:97:LYS:HZ3	1.68	0.58
1:CD:28:LYS:HZ3	1:CF:28:LYS:NZ	2.00	0.58
1:AZ:58:ILE:O	1:AZ:58:ILE:CG2	2.50	0.58
1:CP:95:VAL:HG12	1:CP:112:PHE:HE1	1.67	0.58
1:C3:124:ILE:O	1:C3:129:THR:OG1	2.16	0.58
1:CI:33:ALA:O	1:CI:37:LEU:HB2	2.03	0.58
1:C1:6:HIS:HE1	1:C1:8:VAL:HB	1.68	0.58
1:BK:83:GLY:HA3	2:BK:1001:PO4:O2	2.03	0.58
1:A2:116:THR:O	1:A3:85:THR:HB	2.03	0.58
1:CM:116:THR:O	1:CN:85:THR:HB	2.03	0.58
1:CM:129:THR:O	1:CM:132:GLY:N	2.25	0.58
1:CZ:58:ILE:O	1:CZ:58:ILE:CG2	2.50	0.58
1:AM:65:MET:HE3	1:AM:71:TYR:CE1	2.39	0.58
1:B4:58:ILE:O	1:B4:58:ILE:CG2	2.51	0.58
1:CZ:83:GLY:HA3	2:CZ:201:PO4:O2	2.03	0.58
1:BQ:6:HIS:HE1	1:BQ:8:VAL:HB	1.68	0.58
1:A4:53:PRO:CD	1:A4:57:GLU:HG3	2.29	0.58
1:CC:129:THR:HG21	1:CS:120:ILE:HG12	1.85	0.58
1:CL:97:LYS:HE3	1:CM:97:LYS:NZ	2.17	0.58
1:CU:95:VAL:HG12	1:CU:112:PHE:HE1	1.67	0.58
1:BO:58:ILE:CG2	1:BO:58:ILE:O	2.51	0.58
1:CE:58:ILE:O	1:CE:58:ILE:CG2	2.50	0.58
1:C4:58:ILE:O	1:C4:58:ILE:CG2	2.50	0.58
1:BB:6:HIS:HE1	1:BB:8:VAL:HB	1.68	0.58
1:BC:116:THR:O	1:BD:85:THR:HB	2.03	0.58
1:CL:107:ASP:HB2	1:CL:152:TRP:HZ3	1.62	0.58
1:BL:107:ASP:HB2	1:BL:152:TRP:HZ3	1.62	0.58
1:CG:107:ASP:HB2	1:CG:152:TRP:HZ3	1.62	0.58
1:CF:58:ILE:CG2	1:CF:58:ILE:O	2.50	0.58
1:AT:58:ILE:CG2	1:AT:58:ILE:O	2.51	0.58
1:AJ:58:ILE:CG2	1:AJ:58:ILE:O	2.50	0.58
1:CJ:58:ILE:O	1:CJ:58:ILE:CG2	2.50	0.58
1:CU:148:LEU:O	1:CU:148:LEU:HD23	2.03	0.58
1:CG:6:HIS:HE1	1:CG:8:VAL:HB	1.68	0.58
1:CD:20:ARG:CZ	1:CR:39:ARG:CZ	2.81	0.58
1:CW:116:THR:O	1:CX:85:THR:HB	2.03	0.58
1:BO:53:PRO:CD	1:BO:57:GLU:HG3	2.29	0.58
1:AQ:13:LYS:HZ1	1:BU:43:GLU:HG2	1.63	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:40:HIS:CE1	1:C2:7:LEU:HD23	2.39	0.58
1:AF:125:GLU:O	1:AF:131:ALA:HB3	2.04	0.58
1:AA:125:GLU:O	1:AA:131:ALA:HB3	2.04	0.58
1:AF:58:ILE:CG2	1:AF:58:ILE:O	2.50	0.58
1:CL:121:GLU:O	1:CL:124:ILE:HG22	2.04	0.58
1:BT:53:PRO:HG2	1:BT:57:GLU:HG3	0.65	0.58
1:AU:125:GLU:O	1:AU:131:ALA:HB3	2.04	0.58
1:BZ:125:GLU:O	1:BZ:131:ALA:HB3	2.04	0.58
1:AC:65:MET:HE3	1:AC:71:TYR:CE1	2.39	0.58
1:AY:58:ILE:CG2	1:AY:58:ILE:O	2.50	0.58
1:BS:33:ALA:O	1:BS:37:LEU:HB2	2.03	0.58
1:AA:83:GLY:HA3	2:AA:1001:PO4:O2	2.03	0.58
1:AA:148:LEU:O	1:AA:148:LEU:HD23	2.03	0.58
1:CT:53:PRO:CD	1:CT:57:GLU:HG3	2.29	0.58
1:CP:125:GLU:O	1:CP:131:ALA:HB3	2.04	0.58
1:CU:125:GLU:O	1:CU:131:ALA:HB3	2.04	0.58
1:CA:125:GLU:O	1:CA:131:ALA:HB3	2.04	0.58
1:A1:121:GLU:O	1:A1:124:ILE:HG22	2.04	0.58
1:BG:121:GLU:O	1:BG:124:ILE:HG22	2.04	0.58
1:BQ:121:GLU:O	1:BQ:124:ILE:HG22	2.04	0.58
1:B1:121:GLU:O	1:B1:124:ILE:HG22	2.04	0.58
1:AR:116:THR:O	1:AS:85:THR:HB	2.03	0.58
1:AC:116:THR:O	1:AD:85:THR:HB	2.03	0.58
1:CU:102:LEU:HD22	1:CY:104:LEU:HD13	1.86	0.58
1:CQ:107:ASP:HB2	1:CQ:152:TRP:HZ3	1.62	0.57
1:AH:65:MET:HE3	1:AH:71:TYR:CE1	2.38	0.57
1:CF:125:GLU:O	1:CF:131:ALA:HB3	2.04	0.57
1:BU:125:GLU:O	1:BU:131:ALA:HB3	2.04	0.57
1:CK:125:GLU:O	1:CK:131:ALA:HB3	2.04	0.57
1:AZ:125:GLU:O	1:AZ:131:ALA:HB3	2.04	0.57
1:CP:58:ILE:CG2	1:CP:58:ILE:O	2.50	0.57
1:AK:125:GLU:O	1:AK:131:ALA:HB3	2.04	0.57
1:AG:121:GLU:O	1:AG:124:ILE:HG22	2.04	0.57
1:BA:102:LEU:HD22	1:BE:104:LEU:HD13	1.86	0.57
1:AV:6:HIS:HE1	1:AV:8:VAL:HB	1.68	0.57
1:C4:53:PRO:HG2	1:C4:57:GLU:HG3	0.65	0.57
1:BZ:58:ILE:CG2	1:BZ:58:ILE:O	2.50	0.57
1:BS:7:LEU:HB3	1:BY:39:ARG:O	2.04	0.57
1:AG:6:HIS:HE1	1:AG:8:VAL:HB	1.68	0.57
1:BK:125:GLU:O	1:BK:131:ALA:HB3	2.04	0.57
1:BF:125:GLU:O	1:BF:131:ALA:HB3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:58:ILE:O	1:A4:58:ILE:CG2	2.50	0.57
1:BZ:102:LEU:HD22	1:B4:104:LEU:HD13	1.86	0.57
1:CP:102:LEU:HD22	1:CT:104:LEU:HD13	1.87	0.57
1:BL:6:HIS:HE1	1:BL:8:VAL:HB	1.68	0.57
1:CR:116:THR:O	1:CS:85:THR:HB	2.03	0.57
1:AF:102:LEU:HD22	1:AJ:104:LEU:HD13	1.86	0.57
1:BK:58:ILE:O	1:BK:58:ILE:CG2	2.50	0.57
1:CQ:121:GLU:O	1:CQ:124:ILE:HG22	2.04	0.57
1:CB:121:GLU:O	1:CB:124:ILE:HG22	2.04	0.57
1:AF:73:ALA:HB2	1:AF:146:ALA:HB2	1.87	0.57
1:CZ:102:LEU:HD22	1:C4:104:LEU:HD13	1.86	0.57
1:AI:48:ASP:HB2	1:AI:71:TYR:HE1	1.70	0.57
1:CK:102:LEU:HD22	1:CO:104:LEU:HD13	1.86	0.57
1:AK:58:ILE:O	1:AK:58:ILE:CG2	2.50	0.57
1:BB:121:GLU:O	1:BB:124:ILE:HG22	2.04	0.57
1:CV:121:GLU:O	1:CV:124:ILE:HG22	2.04	0.57
1:CG:121:GLU:O	1:CG:124:ILE:HG22	2.04	0.57
1:CD:48:ASP:HB2	1:CD:71:TYR:HE1	1.70	0.57
1:CD:63:LYS:O	1:CD:67:ASN:HB2	2.05	0.57
1:AP:73:ALA:HB2	1:AP:146:ALA:HB2	1.87	0.57
1:BP:102:LEU:HD22	1:BT:104:LEU:HD13	1.86	0.57
1:AC:24:PHE:CE1	1:AU:28:LYS:HD2	2.40	0.57
1:A2:65:MET:HE3	1:A2:71:TYR:CE1	2.39	0.57
1:CZ:125:GLU:O	1:CZ:131:ALA:HB3	2.04	0.57
1:C2:65:MET:HE3	1:C2:71:TYR:CE1	2.38	0.57
1:AP:125:GLU:O	1:AP:131:ALA:HB3	2.04	0.57
1:BT:58:ILE:O	1:BT:58:ILE:CG2	2.50	0.57
1:AA:102:LEU:HD22	1:AE:104:LEU:HD13	1.86	0.57
1:AN:63:LYS:O	1:AN:67:ASN:HB2	2.05	0.57
1:CP:73:ALA:HB2	1:CP:146:ALA:HB2	1.87	0.57
1:CW:58:ILE:N	1:CW:59:PRO:HD2	2.20	0.57
1:CA:102:LEU:HD22	1:CE:104:LEU:HD13	1.87	0.57
1:C4:53:PRO:CD	1:C4:57:GLU:HG3	2.29	0.57
1:CY:53:PRO:HG2	1:CY:57:GLU:HG3	0.65	0.57
1:BW:129:THR:O	1:BW:132:GLY:N	2.25	0.57
1:BA:125:GLU:O	1:BA:131:ALA:HB3	2.04	0.57
1:BL:121:GLU:O	1:BL:124:ILE:HG22	2.04	0.57
1:CC:8:VAL:HG21	1:CR:8:VAL:HG13	1.86	0.57
1:BR:58:ILE:N	1:BR:59:PRO:HD2	2.20	0.57
1:CZ:73:ALA:HB2	1:CZ:146:ALA:HB2	1.87	0.57
1:AU:102:LEU:HD22	1:AY:104:LEU:HD13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:124:ILE:O	1:BS:129:THR:OG1	2.16	0.57
1:CA:73:ALA:HB2	1:CA:146:ALA:HB2	1.87	0.57
1:CU:73:ALA:HB2	1:CU:146:ALA:HB2	1.87	0.57
1:BM:58:ILE:N	1:BM:59:PRO:HD2	2.20	0.57
1:BU:73:ALA:HB2	1:BU:146:ALA:HB2	1.87	0.57
1:CS:48:ASP:HB2	1:CS:71:TYR:HE1	1.70	0.57
1:C2:129:THR:O	1:C2:132:GLY:N	2.25	0.57
1:BV:97:LYS:HE3	1:BW:97:LYS:HZ3	1.69	0.57
1:CP:39:ARG:HH22	1:CV:144:GLU:CD	2.08	0.57
1:BP:125:GLU:O	1:BP:131:ALA:HB3	2.04	0.57
1:BR:65:MET:HE3	1:BR:71:TYR:CE1	2.40	0.57
1:AV:121:GLU:O	1:AV:124:ILE:HG22	2.04	0.57
1:CX:63:LYS:O	1:CX:67:ASN:HB2	2.05	0.57
1:BI:63:LYS:O	1:BI:67:ASN:HB2	2.05	0.57
1:A2:58:ILE:N	1:A2:59:PRO:HD2	2.20	0.57
1:CN:48:ASP:HB2	1:CN:71:TYR:HE1	1.70	0.57
1:CF:102:LEU:HD22	1:CJ:104:LEU:HD13	1.86	0.57
1:BH:58:ILE:N	1:BH:59:PRO:HD2	2.20	0.57
1:AJ:53:PRO:CD	1:AJ:57:GLU:HG3	2.29	0.57
1:BW:97:LYS:HG3	1:BX:97:LYS:HZ1	1.70	0.57
1:BF:39:ARG:O	1:BQ:7:LEU:HB3	2.04	0.57
1:BN:48:ASP:HB2	1:BN:71:TYR:HE1	1.70	0.57
1:AP:102:LEU:HD22	1:AT:104:LEU:HD13	1.86	0.57
1:BS:63:LYS:O	1:BS:67:ASN:HB2	2.05	0.57
1:AK:73:ALA:HB2	1:AK:146:ALA:HB2	1.87	0.57
1:CX:7:LEU:HD11	1:CX:140:VAL:HG22	1.87	0.57
1:BM:37:LEU:HD12	1:BM:47:ILE:HD13	1.87	0.57
1:AM:58:ILE:N	1:AM:59:PRO:HD2	2.20	0.57
1:AX:63:LYS:O	1:AX:67:ASN:HB2	2.05	0.57
1:B3:63:LYS:O	1:B3:67:ASN:HB2	2.05	0.57
1:CC:8:VAL:HG13	1:CR:8:VAL:CG2	2.34	0.57
1:BR:6:HIS:CE1	1:BR:8:VAL:HB	2.40	0.57
1:BC:58:ILE:N	1:BC:59:PRO:HD2	2.20	0.57
1:CS:63:LYS:O	1:CS:67:ASN:HB2	2.05	0.57
1:BX:48:ASP:HB2	1:BX:71:TYR:HE1	1.70	0.57
1:CT:52:VAL:CB	1:CT:53:PRO:HD2	2.34	0.56
1:B4:53:PRO:HG2	1:B4:57:GLU:HG3	0.65	0.56
1:BF:58:ILE:O	1:BF:58:ILE:CG2	2.50	0.56
1:CA:58:ILE:O	1:CA:58:ILE:CG2	2.50	0.56
1:AL:121:GLU:O	1:AL:124:ILE:HG22	2.04	0.56
1:AB:121:GLU:O	1:AB:124:ILE:HG22	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:121:GLU:O	1:AQ:124:ILE:HG22	2.04	0.56
1:BW:6:HIS:CE1	1:BW:8:VAL:HB	2.40	0.56
1:AM:37:LEU:HD12	1:AM:47:ILE:HD13	1.87	0.56
1:AC:58:ILE:N	1:AC:59:PRO:HD2	2.20	0.56
1:AS:124:ILE:O	1:AS:129:THR:OG1	2.16	0.56
1:BP:73:ALA:HB2	1:BP:146:ALA:HB2	1.87	0.56
1:CC:37:LEU:HD12	1:CC:47:ILE:HD13	1.87	0.56
1:BK:73:ALA:HB2	1:BK:146:ALA:HB2	1.87	0.56
1:CK:73:ALA:HB2	1:CK:146:ALA:HB2	1.87	0.56
1:AR:58:ILE:N	1:AR:59:PRO:HD2	2.20	0.56
1:BF:73:ALA:HB2	1:BF:146:ALA:HB2	1.87	0.56
1:AP:82:ARG:HG3	1:AP:118:GLU:OE2	2.06	0.56
1:BQ:107:ASP:HB2	1:BQ:152:TRP:HZ3	1.62	0.56
1:AP:58:ILE:CG2	1:AP:58:ILE:O	2.50	0.56
1:CH:6:HIS:CE1	1:CH:8:VAL:HB	2.40	0.56
1:BC:6:HIS:CE1	1:BC:8:VAL:HB	2.41	0.56
1:BS:48:ASP:HB2	1:BS:71:TYR:HE1	1.70	0.56
1:CF:82:ARG:HG3	1:CF:118:GLU:OE2	2.06	0.56
1:BC:37:LEU:HD12	1:BC:47:ILE:HD13	1.87	0.56
1:BZ:82:ARG:HG3	1:BZ:118:GLU:OE2	2.05	0.56
1:AD:48:ASP:HB2	1:AD:71:TYR:HE1	1.70	0.56
1:BZ:73:ALA:HB2	1:BZ:146:ALA:HB2	1.87	0.56
1:B2:58:ILE:N	1:B2:59:PRO:HD2	2.20	0.56
1:CA:82:ARG:HG3	1:CA:118:GLU:OE2	2.06	0.56
1:BW:58:ILE:N	1:BW:59:PRO:HD2	2.20	0.56
1:BU:102:LEU:HD22	1:BY:104:LEU:HD13	1.86	0.56
1:AY:53:PRO:CG	1:AY:57:GLU:CG	2.46	0.56
1:AW:6:HIS:CE1	1:AW:8:VAL:HB	2.41	0.56
1:C2:6:HIS:CE1	1:C2:8:VAL:HB	2.41	0.56
1:CH:58:ILE:N	1:CH:59:PRO:HD2	2.20	0.56
1:AU:100:ALA:HB2	1:AV:56:PHE:CZ	2.41	0.56
1:BK:100:ALA:HB2	1:BL:56:PHE:CZ	2.41	0.56
1:AA:73:ALA:HB2	1:AA:146:ALA:HB2	1.87	0.56
1:CM:58:ILE:N	1:CM:59:PRO:HD2	2.20	0.56
1:CE:83:GLY:HA3	2:CE:1001:PO4:P	2.46	0.56
1:AR:37:LEU:HD12	1:AR:47:ILE:HD13	1.87	0.56
1:AX:48:ASP:HB2	1:AX:71:TYR:HE1	1.70	0.56
1:AH:58:ILE:N	1:AH:59:PRO:HD2	2.20	0.56
1:AN:7:LEU:HD11	1:AN:140:VAL:HG22	1.87	0.56
1:AS:48:ASP:HB2	1:AS:71:TYR:HE1	1.70	0.56
1:CI:48:ASP:HB2	1:CI:71:TYR:HE1	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:82:ARG:HG3	1:AA:118:GLU:OE2	2.06	0.56
1:CC:58:ILE:N	1:CC:59:PRO:HD2	2.20	0.56
1:AK:82:ARG:HG3	1:AK:118:GLU:OE2	2.06	0.56
1:CZ:82:ARG:HG3	1:CZ:118:GLU:OE2	2.06	0.56
1:BD:48:ASP:HB2	1:BD:71:TYR:HE1	1.70	0.56
1:BA:82:ARG:HG3	1:BA:118:GLU:OE2	2.06	0.56
1:C2:58:ILE:N	1:C2:59:PRO:HD2	2.20	0.56
1:BE:83:GLY:HA3	2:BE:1001:PO4:P	2.46	0.56
1:C3:48:ASP:HB2	1:C3:71:TYR:HE1	1.70	0.56
1:AE:53:PRO:HG2	1:AE:57:GLU:HG3	0.65	0.56
1:CG:96:ALA:O	1:CG:100:ALA:HB2	2.06	0.56
1:BV:121:GLU:O	1:BV:124:ILE:HG22	2.04	0.56
1:CM:6:HIS:CE1	1:CM:8:VAL:HB	2.40	0.56
1:A3:63:LYS:O	1:A3:67:ASN:HB2	2.05	0.56
1:CZ:100:ALA:HB2	1:C1:56:PHE:CZ	2.41	0.56
1:CX:48:ASP:HB2	1:CX:71:TYR:HE1	1.70	0.56
1:AZ:100:ALA:HB2	1:A1:56:PHE:CZ	2.40	0.56
1:BI:48:ASP:HB2	1:BI:71:TYR:HE1	1.70	0.56
1:CW:37:LEU:HD12	1:CW:47:ILE:HD13	1.87	0.56
1:CU:100:ALA:HB2	1:CV:56:PHE:CZ	2.41	0.56
1:BN:7:LEU:HD11	1:BN:140:VAL:HG22	1.87	0.56
1:AU:82:ARG:HG3	1:AU:118:GLU:OE2	2.05	0.56
1:CJ:53:PRO:CG	1:CJ:57:GLU:CG	2.46	0.56
1:BJ:53:PRO:HG2	1:BJ:57:GLU:HG3	0.65	0.56
1:AV:96:ALA:O	1:AV:100:ALA:HB2	2.06	0.56
1:BG:97:LYS:HE3	1:BH:97:LYS:HZ3	1.70	0.56
1:BC:39:ARG:O	1:BR:7:LEU:HB3	2.06	0.56
1:BM:6:HIS:CE1	1:BM:8:VAL:HB	2.40	0.56
1:AS:63:LYS:O	1:AS:67:ASN:HB2	2.05	0.56
1:CI:63:LYS:O	1:CI:67:ASN:HB2	2.05	0.56
1:CS:7:LEU:HD11	1:CS:140:VAL:HG22	1.87	0.56
1:BJ:83:GLY:HA3	2:BJ:1001:PO4:P	2.46	0.56
1:CS:124:ILE:O	1:CS:129:THR:OG1	2.16	0.56
1:BN:63:LYS:O	1:BN:67:ASN:HB2	2.05	0.56
1:AE:83:GLY:HA3	2:AE:1001:PO4:P	2.46	0.56
1:AQ:70:LYS:HE3	1:BU:43:GLU:OE2	2.05	0.56
1:AV:97:LYS:HE3	1:AW:97:LYS:HZ3	1.70	0.56
1:C1:121:GLU:O	1:C1:124:ILE:HG22	2.04	0.56
1:AH:6:HIS:CE1	1:AH:8:VAL:HB	2.41	0.56
1:CP:100:ALA:HB2	1:CQ:56:PHE:CZ	2.41	0.56
1:AK:100:ALA:HB2	1:AL:56:PHE:CZ	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:73:ALA:HB2	1:AZ:146:ALA:HB2	1.87	0.56
1:CY:83:GLY:HA3	2:CY:4201:PO4:P	2.46	0.56
1:A3:48:ASP:HB2	1:A3:71:TYR:HE1	1.70	0.56
1:CA:100:ALA:HB2	1:CB:56:PHE:CZ	2.41	0.56
1:BK:82:ARG:HG3	1:BK:118:GLU:OE2	2.06	0.56
1:AU:73:ALA:HB2	1:AU:146:ALA:HB2	1.87	0.56
1:AD:63:LYS:O	1:AD:67:ASN:HB2	2.05	0.56
1:A3:7:LEU:HD11	1:A3:140:VAL:HG22	1.87	0.56
1:AX:7:LEU:HD11	1:AX:140:VAL:HG22	1.87	0.56
1:AF:100:ALA:HB2	1:AG:56:PHE:CZ	2.41	0.56
1:BU:100:ALA:HB2	1:BV:56:PHE:CZ	2.41	0.56
1:BM:129:THR:O	1:BM:132:GLY:N	2.25	0.56
1:CU:58:ILE:O	1:CU:58:ILE:CG2	2.50	0.56
1:C3:7:LEU:HD11	1:C3:140:VAL:HG22	1.87	0.56
1:C4:83:GLY:HA3	2:C4:4201:PO4:P	2.46	0.56
1:AY:83:GLY:HA3	2:AY:1001:PO4:P	2.46	0.56
1:BH:37:LEU:HD12	1:BH:47:ILE:HD13	1.87	0.56
1:AO:83:GLY:HA3	2:AO:1001:PO4:P	2.46	0.56
1:C3:63:LYS:O	1:C3:67:ASN:HB2	2.05	0.56
1:CJ:52:VAL:CB	1:CJ:53:PRO:HD2	2.34	0.56
1:AJ:53:PRO:HG2	1:AJ:57:GLU:HG3	0.65	0.56
1:BC:38:LYS:HZ2	1:BC:44:GLU:HA	1.69	0.56
1:CR:6:HIS:CE1	1:CR:8:VAL:HB	2.40	0.56
1:CW:6:HIS:CE1	1:CW:8:VAL:HB	2.41	0.56
1:AI:63:LYS:O	1:AI:67:ASN:HB2	2.05	0.56
1:BI:7:LEU:HD11	1:BI:140:VAL:HG22	1.87	0.56
1:AA:100:ALA:HB2	1:AB:56:PHE:CZ	2.41	0.56
1:CO:83:GLY:HA3	2:CO:4201:PO4:P	2.46	0.56
1:AK:102:LEU:HD22	1:AO:104:LEU:HD13	1.86	0.56
1:CR:58:ILE:N	1:CR:59:PRO:HD2	2.20	0.56
1:AD:7:LEU:HD11	1:AD:140:VAL:HG22	1.87	0.56
1:C2:37:LEU:HD12	1:C2:47:ILE:HD13	1.87	0.56
1:BO:83:GLY:HA3	2:BO:1001:PO4:P	2.46	0.56
1:AI:7:LEU:HD11	1:AI:140:VAL:HG22	1.87	0.56
1:CV:96:ALA:O	1:CV:100:ALA:HB2	2.06	0.56
1:AU:58:ILE:CG2	1:AU:58:ILE:O	2.50	0.56
1:BP:58:ILE:CG2	1:BP:58:ILE:O	2.50	0.56
1:BF:102:LEU:HD22	1:BJ:104:LEU:HD13	1.86	0.56
1:BY:83:GLY:HA3	2:BY:1001:PO4:P	2.46	0.56
1:B2:37:LEU:HD12	1:B2:47:ILE:HD13	1.87	0.56
1:BZ:100:ALA:HB2	1:B1:56:PHE:CZ	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:82:ARG:HG3	1:CK:118:GLU:OE2	2.06	0.56
1:B3:48:ASP:HB2	1:B3:71:TYR:HE1	1.70	0.56
1:A3:95:VAL:HG12	1:A3:112:PHE:HE1	1.71	0.56
1:AF:82:ARG:HG3	1:AF:118:GLU:OE2	2.06	0.56
1:AJ:53:PRO:CG	1:AJ:57:GLU:CG	2.46	0.56
1:BJ:52:VAL:CB	1:BJ:53:PRO:HD2	2.34	0.56
1:BD:151:HIS:HB2	1:BE:64:LYS:HB3	1.88	0.56
1:CS:151:HIS:HB2	1:CT:64:LYS:HB3	1.88	0.56
1:AD:151:HIS:HB2	1:AE:64:LYS:HB3	1.88	0.56
1:AO:107:ASP:OD1	1:AO:107:ASP:O	2.24	0.56
1:B2:6:HIS:CE1	1:B2:8:VAL:HB	2.41	0.56
1:CD:7:LEU:HD11	1:CD:140:VAL:HG22	1.87	0.56
1:CR:37:LEU:HD12	1:CR:47:ILE:HD13	1.87	0.56
1:CP:82:ARG:HG3	1:CP:118:GLU:OE2	2.06	0.56
1:BA:100:ALA:HB2	1:BB:56:PHE:CZ	2.41	0.56
1:AW:58:ILE:N	1:AW:59:PRO:HD2	2.20	0.56
1:AZ:102:LEU:HD22	1:A4:104:LEU:HD13	1.87	0.56
1:BA:73:ALA:HB2	1:BA:146:ALA:HB2	1.87	0.56
1:CJ:83:GLY:HA3	2:CJ:4201:PO4:P	2.46	0.56
1:AP:100:ALA:HB2	1:AQ:56:PHE:CZ	2.41	0.56
1:AE:53:PRO:CG	1:AE:57:GLU:CG	2.46	0.55
1:CY:53:PRO:CG	1:CY:57:GLU:CG	2.46	0.55
1:AV:95:VAL:HG12	1:AV:112:PHE:HE1	1.72	0.55
1:AI:151:HIS:HB2	1:AJ:64:LYS:HB3	1.88	0.55
1:AS:151:HIS:HB2	1:AT:64:LYS:HB3	1.89	0.55
1:CT:107:ASP:OD1	1:CT:107:ASP:O	2.24	0.55
1:C4:107:ASP:O	1:C4:107:ASP:OD1	2.24	0.55
1:BF:85:THR:HB	1:BJ:116:THR:O	2.07	0.55
1:CM:37:LEU:HD12	1:CM:47:ILE:HD13	1.87	0.55
1:CK:100:ALA:HB2	1:CL:56:PHE:CZ	2.41	0.55
1:AN:48:ASP:HB2	1:AN:71:TYR:HE1	1.70	0.55
1:BD:63:LYS:O	1:BD:67:ASN:HB2	2.05	0.55
1:CU:82:ARG:HG3	1:CU:118:GLU:OE2	2.06	0.55
1:BF:100:ALA:HB2	1:BG:56:PHE:CZ	2.40	0.55
1:A4:83:GLY:HA3	2:A4:1001:PO4:P	2.46	0.55
1:CH:37:LEU:HD12	1:CH:47:ILE:HD13	1.87	0.55
1:BX:124:ILE:O	1:BX:129:THR:OG1	2.16	0.55
1:AR:129:THR:O	1:AR:132:GLY:N	2.25	0.55
1:BB:95:VAL:HG12	1:BB:112:PHE:HE1	1.72	0.55
1:CB:96:ALA:O	1:CB:100:ALA:HB2	2.06	0.55
1:AC:97:LYS:HE3	1:AD:97:LYS:HZ3	1.69	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:7:LEU:HD11	1:BS:140:VAL:HG22	1.87	0.55
1:BF:82:ARG:HG3	1:BF:118:GLU:OE2	2.06	0.55
1:CN:124:ILE:O	1:CN:129:THR:OG1	2.16	0.55
1:BP:82:ARG:HG3	1:BP:118:GLU:OE2	2.05	0.55
1:CF:85:THR:HB	1:CJ:116:THR:O	2.07	0.55
1:CF:73:ALA:HB2	1:CF:146:ALA:HB2	1.87	0.55
1:AK:85:THR:HB	1:AO:116:THR:O	2.07	0.55
1:BW:37:LEU:HD12	1:BW:47:ILE:HD13	1.87	0.55
1:BA:85:THR:HB	1:BE:116:THR:O	2.07	0.55
1:CT:83:GLY:HA3	2:CT:4201:PO4:P	2.46	0.55
1:BK:102:LEU:HD22	1:BO:104:LEU:HD13	1.86	0.55
1:CQ:96:ALA:O	1:CQ:100:ALA:HB2	2.06	0.55
1:CQ:100:ALA:HA	1:CR:56:PHE:CZ	2.42	0.55
1:CV:95:VAL:HG12	1:CV:112:PHE:HE1	1.72	0.55
1:CV:97:LYS:O	1:CV:102:LEU:HB2	2.07	0.55
1:AX:151:HIS:HB2	1:AY:64:LYS:HB3	1.88	0.55
1:BN:151:HIS:HB2	1:BO:64:LYS:HB3	1.88	0.55
1:BE:107:ASP:OD1	1:BE:107:ASP:O	2.24	0.55
1:CC:6:HIS:CE1	1:CC:8:VAL:HB	2.41	0.55
1:AR:6:HIS:CE1	1:AR:8:VAL:HB	2.40	0.55
1:AM:6:HIS:CE1	1:AM:8:VAL:HB	2.41	0.55
1:A2:6:HIS:CE1	1:A2:8:VAL:HB	2.40	0.55
1:CH:152:TRP:HD1	1:CI:68:SER:HB2	1.72	0.55
1:AZ:85:THR:HB	1:A4:116:THR:O	2.07	0.55
1:BU:85:THR:HB	1:BY:116:THR:O	2.07	0.55
1:CF:100:ALA:HB2	1:CG:56:PHE:CZ	2.41	0.55
1:AP:85:THR:HB	1:AT:116:THR:O	2.07	0.55
1:CO:53:PRO:HG2	1:CO:57:GLU:HG3	0.65	0.55
1:CV:107:ASP:HB2	1:CV:152:TRP:HZ3	1.62	0.55
1:AQ:100:ALA:HA	1:AR:56:PHE:CZ	2.42	0.55
1:BV:96:ALA:O	1:BV:100:ALA:HB2	2.06	0.55
1:BV:97:LYS:O	1:BV:102:LEU:HB2	2.07	0.55
1:AW:38:LYS:HZ2	1:AW:44:GLU:HA	1.71	0.55
1:CY:107:ASP:O	1:CY:107:ASP:OD1	2.24	0.55
1:AC:6:HIS:CE1	1:AC:8:VAL:HB	2.40	0.55
1:B3:95:VAL:HG12	1:B3:112:PHE:HE1	1.71	0.55
1:CU:3:PHE:CD2	1:CU:150:LYS:HE2	2.42	0.55
1:AZ:3:PHE:CD2	1:AZ:150:LYS:HE2	2.42	0.55
1:CF:3:PHE:CD2	1:CF:150:LYS:HE2	2.42	0.55
1:CZ:85:THR:HB	1:C4:116:THR:O	2.07	0.55
1:CR:152:TRP:HD1	1:CS:68:SER:HB2	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:3:PHE:CD2	1:CK:150:LYS:HE2	2.42	0.55
1:CI:7:LEU:HD11	1:CI:140:VAL:HG22	1.87	0.55
1:AC:152:TRP:HD1	1:AD:68:SER:HB2	1.72	0.55
1:BX:63:LYS:O	1:BX:67:ASN:HB2	2.05	0.55
1:BR:37:LEU:HD12	1:BR:47:ILE:HD13	1.87	0.55
1:BY:53:PRO:CD	1:BY:57:GLU:HG3	2.29	0.55
1:AY:53:PRO:HG2	1:AY:57:GLU:HG3	0.65	0.55
1:AL:96:ALA:O	1:AL:100:ALA:HB2	2.06	0.55
1:AL:97:LYS:O	1:AL:102:LEU:HB2	2.07	0.55
1:B1:100:ALA:HA	1:B2:56:PHE:CZ	2.42	0.55
1:BQ:96:ALA:O	1:BQ:100:ALA:HB2	2.06	0.55
1:CG:97:LYS:O	1:CG:102:LEU:HB2	2.07	0.55
1:BH:6:HIS:CE1	1:BH:8:VAL:HB	2.41	0.55
1:CW:152:TRP:HD1	1:CX:68:SER:HB2	1.72	0.55
1:CX:124:ILE:O	1:CX:129:THR:OG1	2.16	0.55
1:AA:85:THR:HB	1:AE:116:THR:O	2.07	0.55
1:BU:3:PHE:CD2	1:BU:150:LYS:HE2	2.42	0.55
1:AT:83:GLY:HA3	2:AT:1001:PO4:P	2.46	0.55
1:BK:85:THR:HB	1:BO:116:THR:O	2.07	0.55
1:A3:124:ILE:O	1:A3:129:THR:OG1	2.16	0.55
1:AA:3:PHE:CD2	1:AA:150:LYS:HE2	2.42	0.55
1:BP:100:ALA:HB2	1:BQ:56:PHE:CZ	2.41	0.55
1:CN:63:LYS:O	1:CN:67:ASN:HB2	2.05	0.55
1:CM:152:TRP:HD1	1:CN:68:SER:HB2	1.72	0.55
1:AJ:83:GLY:HA3	2:AJ:1001:PO4:P	2.46	0.55
1:CC:97:LYS:HG3	1:CD:97:LYS:HZ3	1.71	0.55
1:C1:95:VAL:HG12	1:C1:112:PHE:HE1	1.72	0.55
1:B1:95:VAL:HG12	1:B1:112:PHE:HE1	1.72	0.55
1:CG:95:VAL:HG12	1:CG:112:PHE:HE1	1.72	0.55
1:A1:97:LYS:O	1:A1:102:LEU:HB2	2.07	0.55
1:CO:107:ASP:OD1	1:CO:107:ASP:O	2.25	0.55
1:AZ:82:ARG:HG3	1:AZ:118:GLU:OE2	2.06	0.55
1:BH:152:TRP:HD1	1:BI:68:SER:HB2	1.72	0.55
1:CN:95:VAL:HG12	1:CN:112:PHE:HE1	1.71	0.55
1:BZ:85:THR:HB	1:B4:116:THR:O	2.07	0.55
1:BP:3:PHE:CD2	1:BP:150:LYS:HE2	2.42	0.55
1:BP:85:THR:HB	1:BT:116:THR:O	2.07	0.55
1:AH:37:LEU:HD12	1:AH:47:ILE:HD13	1.87	0.55
1:CI:95:VAL:HG12	1:CI:112:PHE:HE1	1.71	0.55
1:AK:3:PHE:CD2	1:AK:150:LYS:HE2	2.42	0.55
1:CZ:3:PHE:CD2	1:CZ:150:LYS:HE2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B4:83:GLY:HA3	2:B4:1001:PO4:P	2.46	0.55
1:AD:95:VAL:HG12	1:AD:112:PHE:HE1	1.71	0.55
1:BK:3:PHE:CD2	1:BK:150:LYS:HE2	2.42	0.55
1:CP:3:PHE:CD2	1:CP:150:LYS:HE2	2.42	0.55
1:AX:95:VAL:HG12	1:AX:112:PHE:HE1	1.71	0.55
1:CQ:95:VAL:HG12	1:CQ:112:PHE:HE1	1.72	0.55
1:BQ:97:LYS:O	1:BQ:102:LEU:HB2	2.07	0.55
1:CW:39:ARG:CZ	1:C3:20:ARG:NH1	2.69	0.55
1:AN:151:HIS:HB2	1:AO:64:LYS:HB3	1.88	0.55
1:AE:107:ASP:OD1	1:AE:107:ASP:O	2.24	0.55
1:AC:37:LEU:HD12	1:AC:47:ILE:HD13	1.87	0.55
1:CN:7:LEU:HD11	1:CN:140:VAL:HG22	1.87	0.55
1:AS:95:VAL:HG12	1:AS:112:PHE:HE1	1.71	0.55
1:BM:152:TRP:HD1	1:BN:68:SER:HB2	1.72	0.55
1:AG:129:THR:HG22	1:AG:130:LYS:H	1.72	0.55
1:CE:53:PRO:HG2	1:CE:57:GLU:HG3	0.65	0.55
1:CB:97:LYS:O	1:CB:102:LEU:HB2	2.07	0.55
1:AQ:96:ALA:O	1:AQ:100:ALA:HB2	2.06	0.55
1:CL:95:VAL:HG12	1:CL:112:PHE:HE1	1.72	0.55
1:CV:100:ALA:HA	1:CW:56:PHE:CZ	2.42	0.55
1:CE:107:ASP:OD1	1:CE:107:ASP:O	2.25	0.55
1:BY:107:ASP:OD1	1:BY:107:ASP:O	2.24	0.55
1:BJ:107:ASP:OD1	1:BJ:107:ASP:O	2.24	0.55
1:CV:129:THR:HG22	1:CV:130:LYS:H	1.72	0.55
1:AW:37:LEU:HD12	1:AW:47:ILE:HD13	1.87	0.55
1:BC:152:TRP:HD1	1:BD:68:SER:HB2	1.72	0.55
1:CS:95:VAL:HG12	1:CS:112:PHE:HE1	1.71	0.55
1:CA:3:PHE:CD2	1:CA:150:LYS:HE2	2.42	0.55
1:BD:95:VAL:HG12	1:BD:112:PHE:HE1	1.71	0.55
1:CT:53:PRO:HG2	1:CT:57:GLU:HG3	0.65	0.55
1:BL:97:LYS:O	1:BL:102:LEU:HB2	2.07	0.55
1:BM:97:LYS:HG3	1:BN:97:LYS:HZ3	1.71	0.55
1:BG:100:ALA:HA	1:BH:56:PHE:CZ	2.42	0.55
1:BE:18:VAL:HG12	1:BE:77:LEU:CB	2.37	0.55
1:CH:65:MET:HE3	1:CH:71:TYR:CE1	2.41	0.55
1:AT:107:ASP:OD1	1:AT:107:ASP:O	2.25	0.55
1:AS:7:LEU:HD11	1:AS:140:VAL:HG22	1.87	0.55
1:C3:95:VAL:HG12	1:C3:112:PHE:HE1	1.71	0.55
1:A2:37:LEU:HD12	1:A2:47:ILE:HD13	1.87	0.55
1:B3:7:LEU:HD11	1:B3:140:VAL:HG22	1.87	0.55
1:AW:152:TRP:HD1	1:AX:68:SER:HB2	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:82:ARG:HG3	1:BU:118:GLU:OE2	2.06	0.55
1:BL:129:THR:HG22	1:BL:130:LYS:H	1.72	0.55
1:AU:3:PHE:CD2	1:AU:150:LYS:HE2	2.42	0.55
1:CB:129:THR:HG22	1:CB:130:LYS:H	1.72	0.55
1:CT:52:VAL:HB	1:CT:53:PRO:CD	2.35	0.55
1:BE:53:PRO:HG2	1:BE:57:GLU:HG3	0.65	0.55
1:A2:129:THR:O	1:A2:132:GLY:N	2.25	0.55
1:AG:95:VAL:HG12	1:AG:112:PHE:HE1	1.72	0.55
1:AQ:95:VAL:HG12	1:AQ:112:PHE:HE1	1.72	0.55
1:BG:95:VAL:HG12	1:BG:112:PHE:HE1	1.72	0.55
1:AY:18:VAL:HG12	1:AY:77:LEU:CB	2.37	0.55
1:BI:151:HIS:HB2	1:BJ:64:LYS:HB3	1.88	0.55
1:BO:107:ASP:O	1:BO:107:ASP:OD1	2.24	0.55
1:BD:7:LEU:HD11	1:BD:140:VAL:HG22	1.87	0.55
1:BC:18:VAL:HG21	1:BC:30:LEU:HD13	1.89	0.55
1:BX:7:LEU:HD11	1:BX:140:VAL:HG22	1.87	0.55
1:CX:95:VAL:HG12	1:CX:112:PHE:HE1	1.71	0.55
1:CQ:129:THR:HG22	1:CQ:130:LYS:H	1.72	0.55
1:BI:95:VAL:HG12	1:BI:112:PHE:HE1	1.71	0.55
1:BZ:75:ILE:HG22	1:BZ:77:LEU:HD13	1.90	0.55
1:AV:129:THR:HG22	1:AV:130:LYS:H	1.72	0.55
1:AO:52:VAL:CB	1:AO:53:PRO:HD2	2.34	0.54
1:BB:97:LYS:O	1:BB:102:LEU:HB2	2.07	0.54
1:CB:95:VAL:HG12	1:CB:112:PHE:HE1	1.72	0.54
1:C1:96:ALA:O	1:C1:100:ALA:HB2	2.06	0.54
1:BQ:95:VAL:HG12	1:BQ:112:PHE:HE1	1.72	0.54
1:C4:18:VAL:HG12	1:C4:77:LEU:CB	2.37	0.54
1:BX:151:HIS:HB2	1:BY:64:LYS:HB3	1.88	0.54
1:CI:151:HIS:HB2	1:CJ:64:LYS:HB3	1.88	0.54
1:AE:39:ARG:O	1:AN:7:LEU:HB3	2.05	0.54
1:BX:95:VAL:HG12	1:BX:112:PHE:HE1	1.71	0.54
1:BZ:3:PHE:CD2	1:BZ:150:LYS:HE2	2.42	0.54
1:CP:85:THR:HB	1:CT:116:THR:O	2.07	0.54
1:CT:128:GLY:O	1:C4:22:ASN:HA	2.07	0.54
1:CK:85:THR:HB	1:CO:116:THR:O	2.07	0.54
1:AG:97:LYS:O	1:AG:102:LEU:HB2	2.07	0.54
1:CW:97:LYS:HE3	1:CX:97:LYS:HZ1	1.73	0.54
1:CW:7:LEU:HD23	1:C2:40:HIS:CE1	2.42	0.54
1:AH:38:LYS:HZ2	1:AH:44:GLU:HA	1.72	0.54
1:BS:151:HIS:HB2	1:BT:64:LYS:HB3	1.88	0.54
1:BG:129:THR:HG22	1:BG:130:LYS:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:83:GLY:HA3	2:BT:1001:PO4:P	2.46	0.54
1:BR:18:VAL:HG21	1:BR:30:LEU:HD13	1.89	0.54
1:AI:95:VAL:HG12	1:AI:112:PHE:HE1	1.71	0.54
1:BH:18:VAL:HG21	1:BH:30:LEU:HD13	1.89	0.54
1:BR:152:TRP:HD1	1:BS:68:SER:HB2	1.72	0.54
1:BW:18:VAL:HG21	1:BW:30:LEU:HD13	1.89	0.54
1:AF:85:THR:HB	1:AJ:116:THR:O	2.07	0.54
1:CM:18:VAL:HG21	1:CM:30:LEU:HD13	1.89	0.54
1:A4:53:PRO:HG2	1:A4:57:GLU:HG3	0.65	0.54
1:B1:107:ASP:HB2	1:B1:152:TRP:HZ3	1.62	0.54
1:AB:97:LYS:O	1:AB:102:LEU:HB2	2.07	0.54
1:BV:95:VAL:HG12	1:BV:112:PHE:HE1	1.72	0.54
1:BG:97:LYS:O	1:BG:102:LEU:HB2	2.07	0.54
1:AJ:18:VAL:HG12	1:AJ:77:LEU:CB	2.37	0.54
1:A4:107:ASP:OD1	1:A4:107:ASP:O	2.24	0.54
1:CJ:107:ASP:OD1	1:CJ:107:ASP:O	2.25	0.54
1:A1:129:THR:HG22	1:A1:130:LYS:H	1.72	0.54
1:C2:18:VAL:HG21	1:C2:30:LEU:HD13	1.89	0.54
1:BP:75:ILE:HG22	1:BP:77:LEU:HD13	1.90	0.54
1:BB:129:THR:HG22	1:BB:130:LYS:H	1.72	0.54
1:AA:75:ILE:HG22	1:AA:77:LEU:HD13	1.90	0.54
1:CC:152:TRP:HD1	1:CD:68:SER:HB2	1.72	0.54
1:AU:85:THR:HB	1:AY:116:THR:O	2.07	0.54
1:CJ:52:VAL:HB	1:CJ:53:PRO:CD	2.35	0.54
1:BJ:52:VAL:HB	1:BJ:53:PRO:CD	2.35	0.54
1:AT:52:VAL:HB	1:AT:53:PRO:CD	2.35	0.54
1:AC:129:THR:O	1:AC:132:GLY:N	2.25	0.54
1:CL:100:ALA:HA	1:CM:56:PHE:CZ	2.42	0.54
1:C1:75:ILE:HG22	1:C1:77:LEU:HD13	1.90	0.54
1:C3:151:HIS:HB2	1:C4:64:LYS:HB3	1.88	0.54
1:AR:18:VAL:HG21	1:AR:30:LEU:HD13	1.89	0.54
1:AF:3:PHE:CD2	1:AF:150:LYS:HE2	2.42	0.54
1:AW:18:VAL:HG21	1:AW:30:LEU:HD13	1.89	0.54
1:AP:75:ILE:HG22	1:AP:77:LEU:HD13	1.89	0.54
1:AC:18:VAL:HG21	1:AC:30:LEU:HD13	1.89	0.54
1:AZ:75:ILE:HG22	1:AZ:77:LEU:HD13	1.90	0.54
1:CP:75:ILE:HG22	1:CP:77:LEU:HD13	1.90	0.54
1:B2:18:VAL:HG21	1:B2:30:LEU:HD13	1.89	0.54
1:CJ:53:PRO:HG2	1:CJ:57:GLU:HG3	0.65	0.54
1:A4:52:VAL:CB	1:A4:53:PRO:HD2	2.33	0.54
1:BN:18:VAL:HG12	1:BN:77:LEU:CB	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CL:75:ILE:HG22	1:CL:77:LEU:HD13	1.90	0.54
1:B3:151:HIS:HB2	1:B4:64:LYS:HB3	1.88	0.54
1:CD:151:HIS:HB2	1:CE:64:LYS:HB3	1.88	0.54
1:AM:18:VAL:HG21	1:AM:30:LEU:HD13	1.89	0.54
1:AU:75:ILE:HG22	1:AU:77:LEU:HD13	1.89	0.54
1:AP:3:PHE:CD2	1:AP:150:LYS:HE2	2.42	0.54
1:BF:3:PHE:CD2	1:BF:150:LYS:HE2	2.42	0.54
1:C4:53:PRO:CG	1:C4:57:GLU:CG	2.46	0.54
1:CL:97:LYS:O	1:CL:102:LEU:HB2	2.07	0.54
1:BQ:100:ALA:HA	1:BR:56:PHE:CZ	2.42	0.54
1:B3:18:VAL:HG12	1:B3:77:LEU:CB	2.37	0.54
1:AO:18:VAL:HG12	1:AO:77:LEU:CB	2.37	0.54
1:BH:65:MET:HE3	1:BH:71:TYR:CE1	2.42	0.54
1:A3:151:HIS:HB2	1:A4:64:LYS:HB3	1.88	0.54
1:CW:18:VAL:HG21	1:CW:30:LEU:HD13	1.89	0.54
1:AH:152:TRP:HD1	1:AI:68:SER:HB2	1.72	0.54
1:AQ:129:THR:HG22	1:AQ:130:LYS:H	1.72	0.54
1:CD:95:VAL:HG12	1:CD:112:PHE:HE1	1.71	0.54
1:BS:39:ARG:O	1:BY:7:LEU:HB3	2.07	0.54
1:CZ:75:ILE:HG22	1:CZ:77:LEU:HD13	1.90	0.54
1:BL:95:VAL:HG12	1:BL:112:PHE:HE1	1.72	0.54
1:AL:100:ALA:HA	1:AM:56:PHE:CZ	2.42	0.54
1:B1:97:LYS:O	1:B1:102:LEU:HB2	2.07	0.54
1:CH:97:LYS:HE3	1:CI:97:LYS:HZ3	1.73	0.54
1:BT:107:ASP:OD1	1:BT:107:ASP:O	2.24	0.54
1:CA:75:ILE:HG22	1:CA:77:LEU:HD13	1.90	0.54
1:AM:152:TRP:HD1	1:AN:68:SER:HB2	1.72	0.54
1:CI:39:ARG:O	1:CO:7:LEU:HB3	2.08	0.54
1:CD:22:ASN:HA	1:CR:128:GLY:O	2.07	0.54
1:BN:95:VAL:HG12	1:BN:112:PHE:HE1	1.71	0.54
1:BE:53:PRO:CD	1:BE:57:GLU:HG3	2.29	0.54
1:AC:129:THR:HG21	1:AS:120:ILE:HD11	1.89	0.54
1:AV:97:LYS:O	1:AV:102:LEU:HB2	2.07	0.54
1:CQ:97:LYS:O	1:CQ:102:LEU:HB2	2.07	0.54
1:CG:100:ALA:HA	1:CH:56:PHE:CZ	2.42	0.54
1:AI:18:VAL:HG12	1:AI:77:LEU:CB	2.37	0.54
1:CN:151:HIS:HB2	1:CO:64:LYS:HB3	1.88	0.54
1:BV:75:ILE:HG22	1:BV:77:LEU:HD13	1.90	0.54
1:BA:3:PHE:CD2	1:BA:150:LYS:HE2	2.42	0.54
1:AL:129:THR:HG22	1:AL:130:LYS:H	1.72	0.54
1:BF:75:ILE:HG22	1:BF:77:LEU:HD13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:95:VAL:HG12	1:BS:112:PHE:HE1	1.71	0.54
1:AB:129:THR:HG22	1:AB:130:LYS:H	1.72	0.54
1:C2:152:TRP:HD1	1:C3:68:SER:HB2	1.72	0.54
1:BE:52:VAL:HB	1:BE:53:PRO:CD	2.35	0.54
1:C1:100:ALA:HA	1:C2:56:PHE:CZ	2.42	0.54
1:A1:100:ALA:HA	1:A2:56:PHE:CZ	2.42	0.54
1:BW:70:LYS:HB2	1:BW:71:TYR:CE1	2.43	0.54
1:CX:151:HIS:HB2	1:CY:64:LYS:HB3	1.88	0.54
1:AJ:107:ASP:OD1	1:AJ:107:ASP:O	2.25	0.54
1:AY:107:ASP:O	1:AY:107:ASP:OD1	2.24	0.54
1:CR:18:VAL:HG21	1:CR:30:LEU:HD13	1.89	0.54
1:BK:75:ILE:HG22	1:BK:77:LEU:HD13	1.90	0.54
1:AN:95:VAL:HG12	1:AN:112:PHE:HE1	1.71	0.54
1:BV:129:THR:HG22	1:BV:130:LYS:H	1.72	0.54
1:BA:75:ILE:HG22	1:BA:77:LEU:HD13	1.90	0.54
1:BE:53:PRO:CG	1:BE:57:GLU:CG	2.46	0.54
1:AQ:13:LYS:HZ1	1:BU:43:GLU:HB2	1.72	0.54
1:AQ:97:LYS:O	1:AQ:102:LEU:HB2	2.07	0.54
1:A2:70:LYS:HB2	1:A2:71:TYR:CE1	2.43	0.54
1:BG:75:ILE:HG22	1:BG:77:LEU:HD13	1.90	0.54
1:AQ:75:ILE:HG22	1:AQ:77:LEU:HD13	1.90	0.54
1:CI:7:LEU:HB3	1:CO:39:ARG:O	2.08	0.54
1:CH:18:VAL:HG21	1:CH:30:LEU:HD13	1.89	0.54
1:BM:18:VAL:HG21	1:BM:30:LEU:HD13	1.89	0.54
1:CK:75:ILE:HG22	1:CK:77:LEU:HD13	1.90	0.54
1:CP:22:ASN:HA	1:C3:128:GLY:O	2.08	0.54
1:C1:97:LYS:O	1:C1:102:LEU:HB2	2.07	0.53
1:AB:100:ALA:HA	1:AC:56:PHE:CZ	2.42	0.53
1:CH:70:LYS:HB2	1:CH:71:TYR:CE1	2.43	0.53
1:AH:18:VAL:HG21	1:AH:30:LEU:HD13	1.89	0.53
1:A2:152:TRP:HD1	1:A3:68:SER:HB2	1.72	0.53
1:CZ:143:ILE:O	1:CZ:147:HIS:HB2	2.09	0.53
1:AX:124:ILE:O	1:AX:129:THR:OG1	2.16	0.53
1:BW:152:TRP:HD1	1:BX:68:SER:HB2	1.72	0.53
1:CU:85:THR:HB	1:CY:116:THR:O	2.07	0.53
1:BY:53:PRO:CG	1:BY:57:GLU:CG	2.46	0.53
1:BY:53:PRO:HG2	1:BY:57:GLU:HG3	0.65	0.53
1:AY:52:VAL:HB	1:AY:53:PRO:CD	2.35	0.53
1:BT:52:VAL:HB	1:BT:53:PRO:CD	2.35	0.53
1:AL:95:VAL:HG12	1:AL:112:PHE:HE1	1.72	0.53
1:AB:95:VAL:HG12	1:AB:112:PHE:HE1	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:70:LYS:HB2	1:CR:71:TYR:CE1	2.43	0.53
1:CM:70:LYS:HB2	1:CM:71:TYR:CE1	2.43	0.53
1:BQ:129:THR:HG22	1:BQ:130:LYS:H	1.72	0.53
1:BQ:75:ILE:HG22	1:BQ:77:LEU:HD13	1.90	0.53
1:CO:152:TRP:HE3	1:CO:153:ALA:N	2.07	0.53
1:CJ:152:TRP:HE3	1:CJ:153:ALA:N	2.07	0.53
1:AI:7:LEU:HD23	1:AO:40:HIS:CE1	2.43	0.53
1:AA:6:HIS:HB2	1:AA:147:HIS:ND1	2.24	0.53
1:B1:129:THR:HG22	1:B1:130:LYS:H	1.72	0.53
1:B2:152:TRP:HD1	1:B3:68:SER:HB2	1.72	0.53
1:BF:6:HIS:HB2	1:BF:147:HIS:ND1	2.24	0.53
1:CF:75:ILE:HG22	1:CF:77:LEU:HD13	1.90	0.53
1:BU:6:HIS:HB2	1:BU:147:HIS:ND1	2.23	0.53
1:CY:52:VAL:HB	1:CY:53:PRO:CD	2.35	0.53
1:AJ:52:VAL:CB	1:AJ:53:PRO:HD2	2.34	0.53
1:CG:97:LYS:HE3	1:CH:97:LYS:HZ3	1.71	0.53
1:AW:70:LYS:HB2	1:AW:71:TYR:CE1	2.43	0.53
1:B4:18:VAL:HG12	1:B4:77:LEU:CB	2.37	0.53
1:BG:121:GLU:O	1:BG:125:GLU:HG3	2.09	0.53
1:BV:121:GLU:O	1:BV:125:GLU:HG3	2.09	0.53
1:AY:152:TRP:HE3	1:AY:153:ALA:N	2.07	0.53
1:BP:3:PHE:HD2	1:BP:150:LYS:HE2	1.74	0.53
1:AK:6:HIS:HB2	1:AK:147:HIS:ND1	2.23	0.53
1:CP:6:HIS:HB2	1:CP:147:HIS:ND1	2.24	0.53
1:AK:75:ILE:HG22	1:AK:77:LEU:HD13	1.90	0.53
1:CA:143:ILE:O	1:CA:147:HIS:HB2	2.09	0.53
1:CU:75:ILE:HG22	1:CU:77:LEU:HD13	1.89	0.53
1:C3:104:LEU:HD13	1:C4:102:LEU:HG	1.91	0.53
1:CN:104:LEU:HD13	1:CO:102:LEU:HG	1.91	0.53
1:AO:52:VAL:HB	1:AO:53:PRO:CD	2.35	0.53
1:AR:97:LYS:HE3	1:AS:97:LYS:HZ1	1.74	0.53
1:AR:70:LYS:HB2	1:AR:71:TYR:CE1	2.43	0.53
1:B4:107:ASP:O	1:B4:107:ASP:OD1	2.24	0.53
1:AJ:152:TRP:HE3	1:AJ:153:ALA:N	2.07	0.53
1:CK:3:PHE:HD2	1:CK:150:LYS:HE2	1.74	0.53
1:AF:143:ILE:O	1:AF:147:HIS:HB2	2.09	0.53
1:CI:104:LEU:HD13	1:CJ:102:LEU:HG	1.91	0.53
1:BK:143:ILE:O	1:BK:147:HIS:HB2	2.09	0.53
1:CK:6:HIS:HB2	1:CK:147:HIS:ND1	2.24	0.53
1:BV:100:ALA:HA	1:BW:56:PHE:CZ	2.42	0.53
1:CF:28:LYS:HZ1	1:CR:28:LYS:HZ3	1.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:18:VAL:HG12	1:BT:77:LEU:CB	2.37	0.53
1:CT:18:VAL:HG12	1:CT:77:LEU:CB	2.37	0.53
1:C2:70:LYS:HB2	1:C2:71:TYR:CE1	2.43	0.53
1:CL:121:GLU:O	1:CL:125:GLU:HG3	2.09	0.53
1:AL:121:GLU:O	1:AL:125:GLU:HG3	2.09	0.53
1:AB:124:ILE:HD11	1:AV:24:PHE:CE2	2.43	0.53
1:B1:75:ILE:HG22	1:B1:77:LEU:HD13	1.90	0.53
1:BL:75:ILE:HG22	1:BL:77:LEU:HD13	1.90	0.53
1:CV:75:ILE:HG22	1:CV:77:LEU:HD13	1.90	0.53
1:C4:152:TRP:HE3	1:C4:153:ALA:N	2.07	0.53
1:CF:3:PHE:HD2	1:CF:150:LYS:HE2	1.74	0.53
1:CA:3:PHE:HD2	1:CA:150:LYS:HE2	1.74	0.53
1:BA:6:HIS:HB2	1:BA:147:HIS:ND1	2.24	0.53
1:AU:6:HIS:HB2	1:AU:147:HIS:ND1	2.24	0.53
1:BD:128:GLY:O	1:BF:22:ASN:HA	2.09	0.53
1:BL:100:ALA:HA	1:BM:56:PHE:CZ	2.42	0.53
1:BR:97:LYS:HG3	1:BS:97:LYS:HZ1	1.74	0.53
1:A1:95:VAL:HG12	1:A1:112:PHE:HE1	1.72	0.53
1:CC:70:LYS:HB2	1:CC:71:TYR:CE1	2.43	0.53
1:A4:18:VAL:HG12	1:A4:77:LEU:CB	2.37	0.53
1:B1:121:GLU:O	1:B1:125:GLU:HG3	2.09	0.53
1:AG:75:ILE:HG22	1:AG:77:LEU:HD13	1.90	0.53
1:CZ:3:PHE:HD2	1:CZ:150:LYS:HE2	1.74	0.53
1:AU:3:PHE:HD2	1:AU:150:LYS:HE2	1.74	0.53
1:BA:3:PHE:HD2	1:BA:150:LYS:HE2	1.74	0.53
1:BA:143:ILE:O	1:BA:147:HIS:HB2	2.09	0.53
1:AR:152:TRP:HD1	1:AS:68:SER:HB2	1.72	0.53
1:CG:129:THR:HG22	1:CG:130:LYS:H	1.72	0.53
1:C1:129:THR:HG22	1:C1:130:LYS:H	1.72	0.53
1:CD:104:LEU:HD13	1:CE:102:LEU:HG	1.91	0.53
1:CD:28:LYS:HZ3	1:CF:28:LYS:HZ2	1.55	0.53
1:BR:70:LYS:HB2	1:BR:71:TYR:CE1	2.43	0.53
1:AG:121:GLU:O	1:AG:125:GLU:HG3	2.09	0.53
1:A1:75:ILE:HG22	1:A1:77:LEU:HD13	1.90	0.53
1:BE:152:TRP:HE3	1:BE:153:ALA:N	2.07	0.53
1:CD:20:ARG:NH1	1:CR:39:ARG:CZ	2.72	0.53
1:AF:75:ILE:HG22	1:AF:77:LEU:HD13	1.90	0.53
1:AZ:6:HIS:HB2	1:AZ:147:HIS:ND1	2.24	0.53
1:BP:143:ILE:O	1:BP:147:HIS:HB2	2.09	0.53
1:A2:18:VAL:HG21	1:A2:30:LEU:HD13	1.89	0.53
1:AE:52:VAL:HB	1:AE:53:PRO:CD	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:100:ALA:HA	1:AH:56:PHE:CZ	2.42	0.53
1:C2:97:LYS:HG3	1:C3:97:LYS:HZ3	1.74	0.53
1:A2:97:LYS:HG3	1:A3:97:LYS:HZ1	1.74	0.53
1:CS:18:VAL:HG12	1:CS:77:LEU:CB	2.37	0.53
1:BO:18:VAL:HG12	1:BO:77:LEU:CB	2.37	0.53
1:AM:70:LYS:HB2	1:AM:71:TYR:CE1	2.43	0.53
1:A1:121:GLU:O	1:A1:125:GLU:HG3	2.09	0.53
1:CB:121:GLU:O	1:CB:125:GLU:HG3	2.09	0.53
1:BE:37:LEU:HD12	1:BE:47:ILE:HD11	1.91	0.53
1:BB:75:ILE:HG22	1:BB:77:LEU:HD13	1.90	0.53
1:AV:75:ILE:HG22	1:AV:77:LEU:HD13	1.90	0.53
1:CT:152:TRP:HE3	1:CT:153:ALA:N	2.07	0.53
1:CU:3:PHE:HD2	1:CU:150:LYS:HE2	1.74	0.53
1:BZ:3:PHE:HD2	1:BZ:150:LYS:HE2	1.74	0.53
1:CA:6:HIS:HB2	1:CA:147:HIS:ND1	2.24	0.53
1:BK:6:HIS:HB2	1:BK:147:HIS:ND1	2.23	0.53
1:AU:143:ILE:O	1:AU:147:HIS:HB2	2.09	0.53
1:CU:6:HIS:HB2	1:CU:147:HIS:ND1	2.24	0.53
1:CX:104:LEU:HD13	1:CX:102:LEU:HG	1.91	0.53
1:AD:104:LEU:HD13	1:AE:102:LEU:HG	1.91	0.53
1:B4:52:VAL:HB	1:B4:53:PRO:CD	2.35	0.53
1:C4:52:VAL:CB	1:C4:53:PRO:HD2	2.34	0.53
1:AT:53:PRO:HG2	1:AT:57:GLU:HG3	0.65	0.53
1:BB:100:ALA:HA	1:BC:56:PHE:CZ	2.42	0.53
1:AV:100:ALA:HA	1:AW:56:PHE:CZ	2.42	0.53
1:AC:38:LYS:HZ2	1:AC:44:GLU:HA	1.73	0.53
1:B2:70:LYS:HB2	1:B2:71:TYR:CE1	2.43	0.53
1:CQ:121:GLU:O	1:CQ:125:GLU:HG3	2.09	0.53
1:C1:121:GLU:O	1:C1:125:GLU:HG3	2.09	0.53
1:AB:40:HIS:CE1	1:AU:7:LEU:HD23	2.44	0.53
1:BV:6:HIS:CE1	1:BV:8:VAL:HB	2.44	0.53
1:AK:3:PHE:HD2	1:AK:150:LYS:HE2	1.74	0.53
1:CU:143:ILE:O	1:CU:147:HIS:HB2	2.09	0.53
1:CA:85:THR:HB	1:CE:116:THR:O	2.07	0.53
1:AX:104:LEU:HD13	1:AY:102:LEU:HG	1.91	0.53
1:C2:97:LYS:HG3	1:C3:97:LYS:NZ	2.24	0.53
1:A2:38:LYS:HZ2	1:A2:44:GLU:HA	1.74	0.53
1:BR:38:LYS:HZ2	1:BR:44:GLU:HA	1.74	0.53
1:AC:70:LYS:HB2	1:AC:71:TYR:CE1	2.43	0.53
1:BL:121:GLU:O	1:BL:125:GLU:HG3	2.09	0.53
1:CP:3:PHE:HD2	1:CP:150:LYS:HE2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:104:LEU:HD13	1:AO:102:LEU:HG	1.91	0.53
1:AT:52:VAL:CB	1:AT:53:PRO:HD2	2.34	0.52
1:BT:53:PRO:CD	1:BT:57:GLU:HG3	2.29	0.52
1:AM:97:LYS:HG3	1:AN:97:LYS:NZ	2.24	0.52
1:BB:144:GLU:CD	1:BU:39:ARG:NH2	2.61	0.52
1:BY:18:VAL:HG12	1:BY:77:LEU:CB	2.37	0.52
1:BM:70:LYS:HB2	1:BM:71:TYR:CE1	2.43	0.52
1:AQ:121:GLU:O	1:AQ:125:GLU:HG3	2.09	0.52
1:AO:37:LEU:HD12	1:AO:47:ILE:HD11	1.91	0.52
1:A4:37:LEU:HD12	1:A4:47:ILE:HD11	1.91	0.52
1:AT:152:TRP:HE3	1:AT:153:ALA:N	2.07	0.52
1:BT:152:TRP:HE3	1:BT:153:ALA:N	2.07	0.52
1:BR:6:HIS:HB3	1:BR:147:HIS:CG	2.45	0.52
1:BF:143:ILE:O	1:BF:147:HIS:HB2	2.09	0.52
1:AK:143:ILE:O	1:AK:147:HIS:HB2	2.09	0.52
1:CP:143:ILE:O	1:CP:147:HIS:HB2	2.09	0.52
1:BU:75:ILE:HG22	1:BU:77:LEU:HD13	1.90	0.52
1:BZ:6:HIS:HB2	1:BZ:147:HIS:ND1	2.24	0.52
1:BF:28:LYS:CE	1:BR:28:LYS:HZ3	2.22	0.52
1:BW:97:LYS:HG3	1:BX:97:LYS:NZ	2.24	0.52
1:A2:97:LYS:HG3	1:A3:97:LYS:NZ	2.24	0.52
1:BJ:18:VAL:HG12	1:BJ:77:LEU:CB	2.37	0.52
1:BK:125:GLU:CA	1:BK:129:THR:OG1	2.57	0.52
1:CU:125:GLU:CA	1:CU:129:THR:OG1	2.57	0.52
1:CW:70:LYS:HB2	1:CW:71:TYR:CE1	2.43	0.52
1:AK:125:GLU:CA	1:AK:129:THR:OG1	2.57	0.52
1:AB:121:GLU:O	1:AB:125:GLU:HG3	2.09	0.52
1:CG:121:GLU:O	1:CG:125:GLU:HG3	2.09	0.52
1:CQ:75:ILE:HG22	1:CQ:77:LEU:HD13	1.90	0.52
1:AB:75:ILE:HG22	1:AB:77:LEU:HD13	1.90	0.52
1:AL:75:ILE:HG22	1:AL:77:LEU:HD13	1.90	0.52
1:AY:37:LEU:HD12	1:AY:47:ILE:HD11	1.91	0.52
1:BJ:37:LEU:HD12	1:BJ:47:ILE:HD11	1.91	0.52
1:BY:37:LEU:HD12	1:BY:47:ILE:HD11	1.91	0.52
1:BM:6:HIS:HB3	1:BM:147:HIS:CG	2.45	0.52
1:AA:3:PHE:HD2	1:AA:150:LYS:HE2	1.74	0.52
1:BU:143:ILE:O	1:BU:147:HIS:HB2	2.09	0.52
1:AP:143:ILE:O	1:AP:147:HIS:HB2	2.09	0.52
1:A3:104:LEU:HD13	1:A4:102:LEU:HG	1.91	0.52
1:CS:104:LEU:HD13	1:CT:102:LEU:HG	1.91	0.52
1:CU:109:PRO:HB3	1:CU:145:MET:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:18:VAL:HG21	1:CC:30:LEU:HD13	1.89	0.52
1:CF:143:ILE:O	1:CF:147:HIS:HB2	2.09	0.52
1:CE:53:PRO:CD	1:CE:57:GLU:HG3	2.29	0.52
1:BC:129:THR:O	1:BC:132:GLY:N	2.25	0.52
1:AH:97:LYS:HG3	1:AI:97:LYS:NZ	2.24	0.52
1:AR:97:LYS:HG3	1:AS:97:LYS:NZ	2.24	0.52
1:AC:97:LYS:HG3	1:AD:97:LYS:NZ	2.24	0.52
1:BR:97:LYS:HG3	1:BS:97:LYS:NZ	2.24	0.52
1:CH:97:LYS:HG3	1:CI:97:LYS:NZ	2.24	0.52
1:BS:18:VAL:HG12	1:BS:77:LEU:CB	2.37	0.52
1:BC:7:LEU:HB3	1:BR:39:ARG:O	2.09	0.52
1:AH:70:LYS:HB2	1:AH:71:TYR:CE1	2.43	0.52
1:BC:70:LYS:HB2	1:BC:71:TYR:CE1	2.43	0.52
1:BQ:121:GLU:O	1:BQ:125:GLU:HG3	2.09	0.52
1:BB:121:GLU:O	1:BB:125:GLU:HG3	2.09	0.52
1:CC:6:HIS:HB3	1:CC:147:HIS:CG	2.45	0.52
1:AM:6:HIS:HB3	1:AM:147:HIS:CG	2.45	0.52
1:AC:6:HIS:HB3	1:AC:147:HIS:CG	2.45	0.52
1:AQ:6:HIS:CE1	1:AQ:8:VAL:HB	2.45	0.52
1:BG:6:HIS:CE1	1:BG:8:VAL:HB	2.45	0.52
1:BU:3:PHE:HD2	1:BU:150:LYS:HE2	1.74	0.52
1:BK:3:PHE:HD2	1:BK:150:LYS:HE2	1.74	0.52
1:AZ:143:ILE:O	1:AZ:147:HIS:HB2	2.09	0.52
1:CF:6:HIS:HB2	1:CF:147:HIS:ND1	2.24	0.52
1:AX:35:ASP:O	1:AX:39:ARG:HG3	2.10	0.52
1:CK:109:PRO:HB3	1:CK:145:MET:HB3	1.91	0.52
1:CT:53:PRO:CG	1:CT:57:GLU:CG	2.46	0.52
1:CM:97:LYS:HG3	1:CN:97:LYS:HZ1	1.73	0.52
1:CM:97:LYS:HG3	1:CN:97:LYS:NZ	2.24	0.52
1:AD:18:VAL:HG12	1:AD:77:LEU:CB	2.37	0.52
1:AE:18:VAL:HG12	1:AE:77:LEU:CB	2.37	0.52
1:CJ:18:VAL:HG12	1:CJ:77:LEU:CB	2.37	0.52
1:BP:125:GLU:CA	1:BP:129:THR:OG1	2.57	0.52
1:AW:6:HIS:HB3	1:AW:147:HIS:CG	2.45	0.52
1:CY:152:TRP:HE3	1:CY:153:ALA:N	2.07	0.52
1:BW:6:HIS:HB3	1:BW:147:HIS:CG	2.45	0.52
1:BS:35:ASP:O	1:BS:39:ARG:HG3	2.10	0.52
1:CZ:6:HIS:HB2	1:CZ:147:HIS:ND1	2.24	0.52
1:AA:143:ILE:O	1:AA:147:HIS:HB2	2.09	0.52
1:BZ:109:PRO:HB3	1:BZ:145:MET:HB3	1.91	0.52
1:CZ:109:PRO:HB3	1:CZ:145:MET:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:124:ILE:O	1:BI:129:THR:OG1	2.16	0.52
1:BD:104:LEU:HD13	1:BE:102:LEU:HG	1.91	0.52
1:CY:52:VAL:CB	1:CY:53:PRO:HD2	2.34	0.52
1:CO:18:VAL:HG12	1:CO:77:LEU:CB	2.37	0.52
1:CE:18:VAL:HG12	1:CE:77:LEU:CB	2.37	0.52
1:AT:18:VAL:HG12	1:AT:77:LEU:CB	2.37	0.52
1:AA:125:GLU:CA	1:AA:129:THR:OG1	2.57	0.52
1:AV:121:GLU:O	1:AV:125:GLU:HG3	2.09	0.52
1:CY:37:LEU:HD12	1:CY:47:ILE:HD11	1.91	0.52
1:CB:75:ILE:HG22	1:CB:77:LEU:HD13	1.90	0.52
1:B4:152:TRP:HE3	1:B4:153:ALA:N	2.07	0.52
1:BO:152:TRP:HE3	1:BO:153:ALA:N	2.07	0.52
1:B2:6:HIS:HB3	1:B2:147:HIS:CG	2.45	0.52
1:BC:6:HIS:HB3	1:BC:147:HIS:CG	2.45	0.52
1:BY:152:TRP:HE3	1:BY:153:ALA:N	2.07	0.52
1:AG:6:HIS:CE1	1:AG:8:VAL:HB	2.44	0.52
1:AI:104:LEU:HD13	1:AJ:102:LEU:HG	1.91	0.52
1:BX:35:ASP:O	1:BX:39:ARG:HG3	2.10	0.52
1:AS:6:HIS:HE1	1:AS:8:VAL:HB	1.75	0.52
1:BJ:53:PRO:CG	1:BJ:57:GLU:CG	2.46	0.52
1:BD:11:GLY:HA3	1:CM:11:GLY:N	2.25	0.52
1:A1:96:ALA:O	1:A1:100:ALA:HB2	2.06	0.52
1:BG:120:ILE:HD11	1:BQ:130:LYS:HG3	1.91	0.52
1:CE:37:LEU:HD12	1:CE:47:ILE:HD11	1.91	0.52
1:AR:6:HIS:HB3	1:AR:147:HIS:CG	2.45	0.52
1:C2:6:HIS:HB3	1:C2:147:HIS:CG	2.45	0.52
1:CW:6:HIS:HB3	1:CW:147:HIS:CG	2.45	0.52
1:B1:6:HIS:CE1	1:B1:8:VAL:HB	2.44	0.52
1:AF:6:HIS:HB2	1:AF:147:HIS:ND1	2.24	0.52
1:CK:143:ILE:O	1:CK:147:HIS:HB2	2.09	0.52
1:BP:6:HIS:HB2	1:BP:147:HIS:ND1	2.24	0.52
1:AP:6:HIS:HB2	1:AP:147:HIS:ND1	2.24	0.52
1:CD:35:ASP:O	1:CD:39:ARG:HG3	2.10	0.52
1:BV:82:ARG:HG3	1:BV:118:GLU:OE2	2.10	0.52
1:BO:52:VAL:HB	1:BO:53:PRO:CD	2.35	0.52
1:CE:52:VAL:CB	1:CE:53:PRO:HD2	2.34	0.52
1:BY:52:VAL:CB	1:BY:53:PRO:HD2	2.34	0.52
1:AM:97:LYS:HE3	1:AN:97:LYS:HZ1	1.75	0.52
1:AD:97:LYS:HG3	1:AE:97:LYS:NZ	2.25	0.52
1:CN:97:LYS:HG3	1:CO:97:LYS:NZ	2.25	0.52
1:CG:144:GLU:CD	1:CU:39:ARG:NH2	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:6:HIS:HB3	1:CH:147:HIS:CG	2.45	0.52
1:AV:6:HIS:CE1	1:AV:8:VAL:HB	2.45	0.52
1:AZ:3:PHE:HD2	1:AZ:150:LYS:HE2	1.74	0.52
1:B3:6:HIS:HE1	1:B3:8:VAL:HB	1.75	0.52
1:AI:28:LYS:HG3	1:AK:24:PHE:CD1	2.44	0.52
1:BD:97:LYS:HG3	1:BE:97:LYS:NZ	2.25	0.52
1:AX:97:LYS:HG3	1:AY:97:LYS:NZ	2.25	0.52
1:CB:100:ALA:HA	1:CC:56:PHE:CZ	2.42	0.52
1:CC:97:LYS:HG3	1:CD:97:LYS:NZ	2.24	0.52
1:CW:97:LYS:HG3	1:CX:97:LYS:NZ	2.24	0.52
1:CC:38:LYS:HZ2	1:CC:44:GLU:HA	1.75	0.52
1:BH:70:LYS:HB2	1:BH:71:TYR:CE1	2.43	0.52
1:AT:37:LEU:HD12	1:AT:47:ILE:HD11	1.91	0.52
1:B4:37:LEU:HD12	1:B4:47:ILE:HD11	1.91	0.52
1:BO:37:LEU:HD12	1:BO:47:ILE:HD11	1.91	0.52
1:AE:152:TRP:HE3	1:AE:153:ALA:N	2.07	0.52
1:A4:152:TRP:HE3	1:A4:153:ALA:N	2.07	0.52
1:AF:3:PHE:HD2	1:AF:150:LYS:HE2	1.74	0.52
1:CI:35:ASP:O	1:CI:39:ARG:HG3	2.10	0.52
1:AF:109:PRO:HB3	1:AF:145:MET:HB3	1.91	0.52
1:AP:109:PRO:HB3	1:AP:145:MET:HB3	1.91	0.52
1:CL:129:THR:HG22	1:CL:130:LYS:H	1.72	0.52
1:C1:82:ARG:HG3	1:C1:118:GLU:OE2	2.10	0.52
1:CL:82:ARG:HG3	1:CL:118:GLU:OE2	2.10	0.52
1:BO:52:VAL:CB	1:BO:53:PRO:HD2	2.34	0.52
1:AQ:13:LYS:CE	1:BU:43:GLU:HG2	2.40	0.52
1:AH:129:THR:O	1:AH:132:GLY:N	2.25	0.52
1:BC:97:LYS:HG3	1:BD:97:LYS:NZ	2.24	0.52
1:AR:97:LYS:HG3	1:AS:97:LYS:HZ1	1.75	0.52
1:CY:18:VAL:HG12	1:CY:77:LEU:CB	2.37	0.52
1:CV:121:GLU:O	1:CV:125:GLU:HG3	2.09	0.52
1:C4:37:LEU:HD12	1:C4:47:ILE:HD11	1.91	0.52
1:CE:152:TRP:HE3	1:CE:153:ALA:N	2.07	0.52
1:AO:152:TRP:HE3	1:AO:153:ALA:N	2.07	0.52
1:A1:6:HIS:CE1	1:A1:8:VAL:HB	2.45	0.52
1:AP:3:PHE:HD2	1:AP:150:LYS:HE2	1.74	0.52
1:BZ:143:ILE:O	1:BZ:147:HIS:HB2	2.09	0.52
1:BL:82:ARG:HG3	1:BL:118:GLU:OE2	2.10	0.52
1:BI:104:LEU:HD13	1:BJ:102:LEU:HG	1.91	0.52
1:BG:82:ARG:HG3	1:BG:118:GLU:OE2	2.10	0.52
1:AK:109:PRO:HB3	1:AK:145:MET:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:104:LEU:HD13	1:BT:102:LEU:HG	1.91	0.52
1:AN:35:ASP:O	1:AN:39:ARG:HG3	2.10	0.52
1:CP:109:PRO:HB3	1:CP:145:MET:HB3	1.91	0.52
1:AN:6:HIS:HE1	1:AN:8:VAL:HB	1.75	0.52
1:BX:104:LEU:HD13	1:BY:102:LEU:HG	1.91	0.52
1:CC:129:THR:CG2	1:CS:120:ILE:CD1	2.78	0.52
1:AT:109:PRO:HB3	1:AT:145:MET:HB3	1.92	0.52
1:CD:97:LYS:HG3	1:CE:97:LYS:NZ	2.25	0.52
1:AI:97:LYS:HG3	1:AJ:97:LYS:NZ	2.25	0.52
1:AJ:37:LEU:HD12	1:AJ:47:ILE:HD11	1.91	0.52
1:BD:7:LEU:HB3	1:BJ:39:ARG:O	2.10	0.52
1:CV:6:HIS:CE1	1:CV:8:VAL:HB	2.44	0.52
1:BA:109:PRO:HB3	1:BA:145:MET:HB3	1.91	0.52
1:A3:35:ASP:O	1:A3:39:ARG:HG3	2.10	0.52
1:BS:6:HIS:HE1	1:BS:8:VAL:HB	1.75	0.52
1:CS:6:HIS:HE1	1:CS:8:VAL:HB	1.75	0.52
1:CW:129:THR:HG21	1:C3:120:ILE:CD1	2.40	0.51
1:AJ:109:PRO:HB3	1:AJ:145:MET:HB3	1.92	0.51
1:BM:97:LYS:HG3	1:BN:97:LYS:NZ	2.24	0.51
1:AN:97:LYS:HG3	1:AO:97:LYS:NZ	2.25	0.51
1:C2:97:LYS:HE3	1:C3:97:LYS:HZ3	1.75	0.51
1:AS:97:LYS:HG3	1:AT:97:LYS:NZ	2.25	0.51
1:BR:97:LYS:HE3	1:BS:97:LYS:HZ1	1.75	0.51
1:CX:18:VAL:HG12	1:CX:77:LEU:CB	2.37	0.51
1:CG:75:ILE:HG22	1:CG:77:LEU:HD13	1.90	0.51
1:BT:37:LEU:HD12	1:BT:47:ILE:HD11	1.91	0.51
1:CO:37:LEU:HD12	1:CO:47:ILE:HD11	1.91	0.51
1:AI:35:ASP:O	1:AI:39:ARG:HG3	2.10	0.51
1:BD:35:ASP:O	1:BD:39:ARG:HG3	2.10	0.51
1:CL:6:HIS:CE1	1:CL:8:VAL:HB	2.45	0.51
1:BN:104:LEU:HD13	1:BO:102:LEU:HG	1.91	0.51
1:CV:82:ARG:HG3	1:CV:118:GLU:OE2	2.10	0.51
1:AL:82:ARG:HG3	1:AL:118:GLU:OE2	2.10	0.51
1:CE:53:PRO:CG	1:CE:57:GLU:CG	2.46	0.51
1:B2:97:LYS:HG3	1:B3:97:LYS:NZ	2.24	0.51
1:BI:97:LYS:HG3	1:BJ:97:LYS:NZ	2.25	0.51
1:AB:144:GLU:CD	1:AU:39:ARG:HH22	2.13	0.51
1:BI:18:VAL:HG12	1:BI:77:LEU:CB	2.37	0.51
1:AU:125:GLU:CA	1:AU:129:THR:OG1	2.57	0.51
1:BU:125:GLU:CA	1:BU:129:THR:OG1	2.57	0.51
1:CT:37:LEU:HD12	1:CT:47:ILE:HD11	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CJ:37:LEU:HD12	1:CJ:47:ILE:HD11	1.91	0.51
1:AL:6:HIS:CE1	1:AL:8:VAL:HB	2.44	0.51
1:BQ:82:ARG:HG3	1:BQ:118:GLU:OE2	2.10	0.51
1:BN:35:ASP:O	1:BN:39:ARG:HG3	2.10	0.51
1:BK:109:PRO:HB3	1:BK:145:MET:HB3	1.91	0.51
1:B3:104:LEU:HD13	1:B4:102:LEU:HG	1.91	0.51
1:BS:97:LYS:HG3	1:BT:97:LYS:NZ	2.25	0.51
1:BH:97:LYS:HG3	1:BI:97:LYS:NZ	2.24	0.51
1:A3:97:LYS:HG3	1:A4:97:LYS:NZ	2.25	0.51
1:CF:39:ARG:NH2	1:CQ:144:GLU:CD	2.63	0.51
1:A3:18:VAL:HG12	1:A3:77:LEU:CB	2.37	0.51
1:BA:125:GLU:CA	1:BA:129:THR:OG1	2.57	0.51
1:AE:37:LEU:HD12	1:AE:47:ILE:HD11	1.91	0.51
1:A2:6:HIS:HB3	1:A2:147:HIS:CG	2.45	0.51
1:CP:28:LYS:HD2	1:CW:24:PHE:CE1	2.45	0.51
1:CB:6:HIS:CE1	1:CB:8:VAL:HB	2.45	0.51
1:A1:82:ARG:HG3	1:A1:118:GLU:OE2	2.10	0.51
1:BX:6:HIS:HE1	1:BX:8:VAL:HB	1.75	0.51
1:AT:53:PRO:CG	1:AT:57:GLU:CG	2.46	0.51
1:B4:109:PRO:HB3	1:B4:145:MET:HB3	1.92	0.51
1:C3:97:LYS:HG3	1:C4:97:LYS:NZ	2.25	0.51
1:CR:97:LYS:HG3	1:CS:97:LYS:NZ	2.24	0.51
1:CD:18:VAL:HG12	1:CD:77:LEU:CB	2.37	0.51
1:CM:6:HIS:HB3	1:CM:147:HIS:CG	2.45	0.51
1:AH:6:HIS:HB3	1:AH:147:HIS:CG	2.45	0.51
1:BQ:6:HIS:CE1	1:BQ:8:VAL:HB	2.45	0.51
1:BL:6:HIS:CE1	1:BL:8:VAL:HB	2.44	0.51
1:AD:23:GLU:HA	1:AD:26:THR:OG1	2.11	0.51
1:CS:23:GLU:HA	1:CS:26:THR:OG1	2.11	0.51
1:BI:6:HIS:HE1	1:BI:8:VAL:HB	1.75	0.51
1:A3:23:GLU:HA	1:A3:26:THR:OG1	2.11	0.51
1:AD:35:ASP:O	1:AD:39:ARG:HG3	2.10	0.51
1:AU:109:PRO:HB3	1:AU:145:MET:HB3	1.91	0.51
1:AZ:109:PRO:HB3	1:AZ:145:MET:HB3	1.92	0.51
1:A4:109:PRO:HB3	1:A4:145:MET:HB3	1.92	0.51
1:BJ:109:PRO:HB3	1:BJ:145:MET:HB3	1.92	0.51
1:BN:97:LYS:HG3	1:BO:97:LYS:NZ	2.25	0.51
1:C2:82:ARG:CG	1:C2:82:ARG:NH1	2.73	0.51
1:BR:82:ARG:CG	1:BR:82:ARG:NH1	2.73	0.51
1:AM:82:ARG:CG	1:AM:82:ARG:NH1	2.73	0.51
1:AR:82:ARG:CG	1:AR:82:ARG:NH1	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B2:82:ARG:NH1	1:B2:82:ARG:CG	2.73	0.51
1:BB:6:HIS:CE1	1:BB:8:VAL:HB	2.45	0.51
1:AA:109:PRO:HB3	1:AA:145:MET:HB3	1.91	0.51
1:CD:23:GLU:HA	1:CD:26:THR:OG1	2.11	0.51
1:CQ:82:ARG:HG3	1:CQ:118:GLU:OE2	2.10	0.51
1:B3:35:ASP:O	1:B3:39:ARG:HG3	2.10	0.51
1:BD:6:HIS:HE1	1:BD:8:VAL:HB	1.75	0.51
1:CA:109:PRO:HB3	1:CA:145:MET:HB3	1.91	0.51
1:CN:6:HIS:HE1	1:CN:8:VAL:HB	1.75	0.51
1:BP:109:PRO:HB3	1:BP:145:MET:HB3	1.91	0.51
1:B4:52:VAL:CB	1:B4:53:PRO:HD2	2.34	0.51
1:BT:109:PRO:HB3	1:BT:145:MET:HB3	1.92	0.51
1:CS:97:LYS:HG3	1:CT:97:LYS:NZ	2.25	0.51
1:CX:97:LYS:HG3	1:CY:97:LYS:NZ	2.25	0.51
1:A2:97:LYS:HE3	1:A3:97:LYS:HZ1	1.75	0.51
1:BM:38:LYS:HZ2	1:BM:44:GLU:HA	1.75	0.51
1:C3:35:ASP:O	1:C3:39:ARG:HG3	2.10	0.51
1:BH:6:HIS:HB3	1:BH:147:HIS:CG	2.45	0.51
1:AC:24:PHE:CD1	1:AU:28:LYS:HD2	2.46	0.51
1:AX:6:HIS:HE1	1:AX:8:VAL:HB	1.75	0.51
1:BN:23:GLU:HA	1:BN:26:THR:OG1	2.11	0.51
1:BX:23:GLU:HA	1:BX:26:THR:OG1	2.11	0.51
1:CB:82:ARG:HG3	1:CB:118:GLU:OE2	2.10	0.51
1:C3:6:HIS:HE1	1:C3:8:VAL:HB	1.75	0.51
1:BI:35:ASP:O	1:BI:39:ARG:HG3	2.10	0.51
1:CI:23:GLU:HA	1:CI:26:THR:OG1	2.11	0.51
1:BO:53:PRO:CG	1:BO:57:GLU:CG	2.46	0.51
1:CE:109:PRO:HB3	1:CE:145:MET:HB3	1.92	0.51
1:AY:109:PRO:HB3	1:AY:145:MET:HB3	1.92	0.51
1:AM:97:LYS:HG3	1:AN:97:LYS:HZ1	1.74	0.51
1:CR:6:HIS:HB3	1:CR:147:HIS:CG	2.45	0.51
1:BB:82:ARG:HG3	1:BB:118:GLU:OE2	2.10	0.51
1:AD:6:HIS:HE1	1:AD:8:VAL:HB	1.75	0.51
1:C3:23:GLU:HA	1:C3:26:THR:OG1	2.11	0.51
1:B1:82:ARG:HG3	1:B1:118:GLU:OE2	2.10	0.51
1:AS:35:ASP:O	1:AS:39:ARG:HG3	2.10	0.51
1:CX:6:HIS:HE1	1:CX:8:VAL:HB	1.75	0.51
1:CY:53:PRO:HD2	1:CY:57:GLU:HB2	1.93	0.51
1:BC:129:THR:HG21	1:BS:120:ILE:HD13	1.89	0.51
1:C4:109:PRO:HB3	1:C4:145:MET:HB3	1.92	0.51
1:AQ:97:LYS:HE3	1:AR:97:LYS:HZ3	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B3:97:LYS:HG3	1:B4:97:LYS:NZ	2.25	0.51
1:AW:65:MET:HE2	1:AW:71:TYR:CE1	2.46	0.51
1:BG:24:PHE:CE2	1:BQ:124:ILE:HD11	2.46	0.51
1:CQ:6:HIS:CE1	1:CQ:8:VAL:HB	2.44	0.51
1:BF:3:PHE:HD2	1:BF:150:LYS:HE2	1.74	0.51
1:AX:39:ARG:O	1:A4:7:LEU:HB3	2.11	0.51
1:AB:82:ARG:HG3	1:AB:118:GLU:OE2	2.10	0.51
1:A3:6:HIS:HE1	1:A3:8:VAL:HB	1.75	0.51
1:CE:7:LEU:HB3	1:CN:39:ARG:O	2.10	0.51
1:CX:23:GLU:HA	1:CX:26:THR:OG1	2.11	0.51
1:CJ:53:PRO:HD2	1:CJ:57:GLU:HB2	1.93	0.51
1:BY:52:VAL:HB	1:BY:53:PRO:CD	2.35	0.51
1:A4:71:TYR:C	1:A4:150:LYS:HZ3	2.15	0.51
1:BO:109:PRO:HB3	1:BO:145:MET:HB3	1.92	0.51
1:B4:71:TYR:C	1:B4:150:LYS:HZ3	2.15	0.51
1:AW:97:LYS:HG3	1:AX:97:LYS:NZ	2.24	0.51
1:CM:97:LYS:HE3	1:CN:97:LYS:HZ1	1.76	0.51
1:C1:6:HIS:CE1	1:C1:8:VAL:HB	2.45	0.51
1:AS:104:LEU:HD13	1:AT:102:LEU:HG	1.91	0.51
1:AQ:82:ARG:HG3	1:AQ:118:GLU:OE2	2.10	0.51
1:CG:82:ARG:HG3	1:CG:118:GLU:OE2	2.10	0.51
1:AN:23:GLU:HA	1:AN:26:THR:OG1	2.11	0.51
1:BF:109:PRO:HB3	1:BF:145:MET:HB3	1.91	0.51
1:B4:53:PRO:HD2	1:B4:57:GLU:HB2	1.93	0.51
1:A4:52:VAL:HB	1:A4:53:PRO:CD	2.35	0.51
1:A4:53:PRO:HD2	1:A4:57:GLU:HB2	1.93	0.51
1:AO:53:PRO:HG2	1:AO:57:GLU:HG3	0.65	0.51
1:AY:53:PRO:HD2	1:AY:57:GLU:HB2	1.93	0.51
1:CI:97:LYS:HG3	1:CJ:97:LYS:NZ	2.25	0.51
1:CV:97:LYS:HE3	1:CW:97:LYS:HZ3	1.74	0.51
1:CI:18:VAL:HG12	1:CI:77:LEU:CB	2.37	0.51
1:BW:82:ARG:NH1	1:BW:82:ARG:CG	2.73	0.51
1:AC:82:ARG:CG	1:AC:82:ARG:NH1	2.73	0.51
1:C2:38:LYS:HZ2	1:C2:44:GLU:HA	1.75	0.51
1:AE:107:ASP:C	1:AE:107:ASP:OD1	2.50	0.51
1:BJ:152:TRP:HE3	1:BJ:153:ALA:N	2.07	0.51
1:AB:6:HIS:CE1	1:AB:8:VAL:HB	2.45	0.51
1:CN:35:ASP:O	1:CN:39:ARG:HG3	2.10	0.51
1:CF:109:PRO:HB3	1:CF:145:MET:HB3	1.91	0.51
1:CX:35:ASP:O	1:CX:39:ARG:HG3	2.10	0.51
1:AO:53:PRO:CG	1:AO:57:GLU:CG	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:97:LYS:HG3	1:BY:97:LYS:NZ	2.25	0.50
1:CC:52:VAL:CG1	1:CC:61:ILE:HD12	2.35	0.50
1:AW:52:VAL:CG1	1:AW:61:ILE:HD12	2.35	0.50
1:AC:39:ARG:O	1:AR:7:LEU:HB3	2.11	0.50
1:BW:38:LYS:HZ2	1:BW:44:GLU:HA	1.76	0.50
1:CA:58:ILE:O	1:CA:58:ILE:HG22	2.11	0.50
1:CS:35:ASP:O	1:CS:39:ARG:HG3	2.10	0.50
1:BD:23:GLU:HA	1:BD:26:THR:OG1	2.11	0.50
1:AG:82:ARG:HG3	1:AG:118:GLU:OE2	2.10	0.50
1:C4:53:PRO:HD2	1:C4:57:GLU:HB2	1.93	0.50
1:CO:52:VAL:HB	1:CO:53:PRO:CD	2.35	0.50
1:AE:71:TYR:C	1:AE:150:LYS:HZ3	2.15	0.50
1:CJ:109:PRO:HB3	1:CJ:145:MET:HB3	1.92	0.50
1:BE:109:PRO:HB3	1:BE:145:MET:HB3	1.92	0.50
1:BB:125:GLU:HG2	1:BV:120:ILE:CD1	2.41	0.50
1:AA:102:LEU:CD2	1:AE:104:LEU:HD13	2.42	0.50
1:AU:102:LEU:CD2	1:AY:104:LEU:HD13	2.42	0.50
1:AP:102:LEU:CD2	1:AT:104:LEU:HD13	2.42	0.50
1:AV:82:ARG:HG3	1:AV:118:GLU:OE2	2.10	0.50
1:CD:6:HIS:HE1	1:CD:8:VAL:HB	1.75	0.50
1:BJ:53:PRO:HD2	1:BJ:57:GLU:HB2	1.93	0.50
1:AT:53:PRO:HD2	1:AT:57:GLU:HB2	1.93	0.50
1:BJ:71:TYR:C	1:BJ:150:LYS:HZ3	2.15	0.50
1:AS:18:VAL:HG12	1:AS:77:LEU:CB	2.37	0.50
1:C3:18:VAL:HG12	1:C3:77:LEU:CB	2.37	0.50
1:CW:82:ARG:NH1	1:CW:82:ARG:CG	2.73	0.50
1:CP:125:GLU:CA	1:CP:129:THR:OG1	2.57	0.50
1:AY:107:ASP:OD1	1:AY:107:ASP:C	2.50	0.50
1:CG:6:HIS:CE1	1:CG:8:VAL:HB	2.44	0.50
1:BZ:102:LEU:CD2	1:B4:104:LEU:HD13	2.42	0.50
1:AZ:102:LEU:CD2	1:A4:104:LEU:HD13	2.42	0.50
1:AI:6:HIS:HE1	1:AI:8:VAL:HB	1.75	0.50
1:BY:53:PRO:HD2	1:BY:57:GLU:HB2	1.93	0.50
1:CO:53:PRO:HD2	1:CO:57:GLU:HB2	1.93	0.50
1:CN:18:VAL:HG12	1:CN:77:LEU:CB	2.37	0.50
1:BJ:107:ASP:OD1	1:BJ:107:ASP:C	2.50	0.50
1:AJ:107:ASP:OD1	1:AJ:107:ASP:C	2.50	0.50
1:CJ:107:ASP:OD1	1:CJ:107:ASP:C	2.50	0.50
1:AJ:53:PRO:HD2	1:AJ:57:GLU:HB2	1.93	0.50
1:BB:152:TRP:C	1:BB:152:TRP:CD1	2.85	0.50
1:B1:152:TRP:CD1	1:B1:152:TRP:C	2.85	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:109:PRO:HB3	1:AE:145:MET:HB3	1.92	0.50
1:AO:109:PRO:HB3	1:AO:145:MET:HB3	1.92	0.50
1:CO:109:PRO:HB3	1:CO:145:MET:HB3	1.92	0.50
1:CY:109:PRO:HB3	1:CY:145:MET:HB3	1.92	0.50
1:C1:97:LYS:HE3	1:C2:97:LYS:HZ3	1.75	0.50
1:CX:20:ARG:NH1	1:C2:39:ARG:CZ	2.74	0.50
1:AA:58:ILE:HG22	1:AA:58:ILE:O	2.11	0.50
1:CP:58:ILE:HG22	1:CP:58:ILE:O	2.11	0.50
1:BE:107:ASP:OD1	1:BE:107:ASP:C	2.50	0.50
1:CP:102:LEU:CD2	1:CT:104:LEU:HD13	2.42	0.50
1:BU:109:PRO:HB3	1:BU:145:MET:HB3	1.91	0.50
1:AT:71:TYR:C	1:AT:150:LYS:HZ3	2.15	0.50
1:AG:96:ALA:O	1:AG:100:ALA:HB2	2.06	0.50
1:BO:16:VAL:HG22	1:BO:49:VAL:HG22	1.94	0.50
1:CE:16:VAL:HG22	1:CE:49:VAL:HG22	1.94	0.50
1:A4:107:ASP:C	1:A4:107:ASP:OD1	2.50	0.50
1:AO:107:ASP:OD1	1:AO:107:ASP:C	2.50	0.50
1:CZ:102:LEU:CD2	1:C4:104:LEU:HD13	2.42	0.50
1:BK:18:VAL:HG21	1:BK:30:LEU:HD13	1.94	0.50
1:AI:23:GLU:HA	1:AI:26:THR:OG1	2.11	0.50
1:AS:23:GLU:HA	1:AS:26:THR:OG1	2.11	0.50
1:CS:116:THR:O	1:CT:85:THR:HB	2.12	0.50
1:BT:53:PRO:HD2	1:BT:57:GLU:HB2	1.93	0.50
1:BE:52:VAL:CB	1:BE:53:PRO:HD2	2.34	0.50
1:CB:152:TRP:C	1:CB:152:TRP:CD1	2.85	0.50
1:BY:109:PRO:HB3	1:BY:145:MET:HB3	1.92	0.50
1:CH:97:LYS:HG3	1:CI:97:LYS:HZ3	1.76	0.50
1:BF:125:GLU:CA	1:BF:129:THR:OG1	2.57	0.50
1:AZ:125:GLU:CA	1:AZ:129:THR:OG1	2.57	0.50
1:CC:8:VAL:HG22	1:CR:8:VAL:HG22	1.93	0.50
1:A1:152:TRP:CD1	1:A1:152:TRP:C	2.85	0.50
1:CO:82:ARG:HG3	1:CO:118:GLU:OE2	2.12	0.50
1:AX:23:GLU:HA	1:AX:26:THR:OG1	2.11	0.50
1:BN:6:HIS:HE1	1:BN:8:VAL:HB	1.75	0.50
1:AE:82:ARG:HG3	1:AE:118:GLU:OE2	2.12	0.50
1:BI:23:GLU:HA	1:BI:26:THR:OG1	2.11	0.50
1:BS:23:GLU:HA	1:BS:26:THR:OG1	2.11	0.50
1:CG:152:TRP:CD1	1:CG:152:TRP:C	2.85	0.50
1:BG:96:ALA:O	1:BG:100:ALA:HB2	2.06	0.50
1:AH:82:ARG:CG	1:AH:82:ARG:NH1	2.73	0.50
1:AO:16:VAL:HG22	1:AO:49:VAL:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:125:GLU:CA	1:AF:129:THR:OG1	2.57	0.50
1:BA:58:ILE:O	1:BA:58:ILE:HG22	2.11	0.50
1:B4:107:ASP:C	1:B4:107:ASP:OD1	2.50	0.50
1:AF:102:LEU:CD2	1:AJ:104:LEU:HD13	2.42	0.50
1:AZ:18:VAL:HG21	1:AZ:30:LEU:HD13	1.94	0.50
1:CA:18:VAL:HG21	1:CA:30:LEU:HD13	1.94	0.50
1:BU:18:VAL:HG21	1:BU:30:LEU:HD13	1.94	0.50
1:AI:28:LYS:NZ	1:AK:28:LYS:NZ	2.59	0.50
1:BC:28:LYS:HZ3	1:BU:28:LYS:CE	2.25	0.50
1:BT:82:ARG:HG3	1:BT:118:GLU:OE2	2.12	0.50
1:CN:23:GLU:HA	1:CN:26:THR:OG1	2.11	0.50
1:BX:116:THR:O	1:BY:85:THR:HB	2.12	0.50
1:BD:116:THR:O	1:BE:85:THR:HB	2.12	0.50
1:BT:53:PRO:CG	1:BT:57:GLU:CG	2.46	0.50
1:BE:53:PRO:HD2	1:BE:57:GLU:HB2	1.93	0.50
1:BV:152:TRP:CD1	1:BV:152:TRP:C	2.85	0.50
1:CW:52:VAL:CG1	1:CW:61:ILE:HD12	2.35	0.50
1:CR:82:ARG:CG	1:CR:82:ARG:NH1	2.73	0.50
1:AE:16:VAL:HG22	1:AE:49:VAL:HG22	1.94	0.50
1:AT:16:VAL:HG22	1:AT:49:VAL:HG22	1.94	0.50
1:CA:125:GLU:CA	1:CA:129:THR:OG1	2.57	0.50
1:CY:107:ASP:C	1:CY:107:ASP:OD1	2.50	0.50
1:AV:152:TRP:CD1	1:AV:152:TRP:C	2.85	0.50
1:CP:18:VAL:HG21	1:CP:30:LEU:HD13	1.94	0.50
1:AD:6:HIS:CE1	1:AD:8:VAL:HB	2.47	0.50
1:AX:116:THR:O	1:AY:85:THR:HB	2.12	0.50
1:CX:116:THR:O	1:CY:85:THR:HB	2.12	0.50
1:C4:82:ARG:HG3	1:C4:118:GLU:OE2	2.12	0.50
1:AJ:82:ARG:HG3	1:AJ:118:GLU:OE2	2.12	0.50
1:AE:53:PRO:HD2	1:AE:57:GLU:HB2	1.93	0.49
1:B4:53:PRO:CG	1:B4:57:GLU:CG	2.46	0.49
1:AO:53:PRO:HD2	1:AO:57:GLU:HB2	1.93	0.49
1:CQ:152:TRP:CD1	1:CQ:152:TRP:C	2.85	0.49
1:BG:152:TRP:C	1:BG:152:TRP:CD1	2.85	0.49
1:CL:152:TRP:CD1	1:CL:152:TRP:C	2.85	0.49
1:AJ:71:TYR:C	1:AJ:150:LYS:HZ3	2.15	0.49
1:BY:16:VAL:HG22	1:BY:49:VAL:HG22	1.94	0.49
1:BJ:16:VAL:HG22	1:BJ:49:VAL:HG22	1.94	0.49
1:CE:107:ASP:OD1	1:CE:107:ASP:C	2.50	0.49
1:AL:152:TRP:C	1:AL:152:TRP:CD1	2.85	0.49
1:BA:102:LEU:CD2	1:BE:104:LEU:HD13	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BU:102:LEU:CD2	1:BY:104:LEU:HD13	2.42	0.49
1:CZ:18:VAL:HG21	1:CZ:30:LEU:HD13	1.94	0.49
1:C3:6:HIS:CE1	1:C3:8:VAL:HB	2.47	0.49
1:CJ:24:PHE:CD1	1:CO:28:LYS:HG3	2.46	0.49
1:CI:6:HIS:HE1	1:CI:8:VAL:HB	1.75	0.49
1:AO:82:ARG:HG3	1:AO:118:GLU:OE2	2.12	0.49
1:AN:116:THR:O	1:AO:85:THR:HB	2.12	0.49
1:CT:109:PRO:HB3	1:CT:145:MET:HB3	1.92	0.49
1:BK:58:ILE:HG22	1:BK:58:ILE:O	2.11	0.49
1:AA:18:VAL:HG21	1:AA:30:LEU:HD13	1.94	0.49
1:AF:18:VAL:HG21	1:AF:30:LEU:HD13	1.94	0.49
1:AI:6:HIS:CE1	1:AI:8:VAL:HB	2.47	0.49
1:C2:17:VAL:HG21	1:C2:62:ALA:HA	1.94	0.49
1:B3:23:GLU:HA	1:B3:26:THR:OG1	2.11	0.49
1:CT:82:ARG:HG3	1:CT:118:GLU:OE2	2.12	0.49
1:BE:7:LEU:HD23	1:BN:40:HIS:CE1	2.46	0.49
1:C3:116:THR:O	1:C4:85:THR:HB	2.12	0.49
1:AJ:52:VAL:HB	1:AJ:53:PRO:CD	2.35	0.49
1:C1:152:TRP:C	1:C1:152:TRP:CD1	2.85	0.49
1:B2:52:VAL:CG1	1:B2:61:ILE:HD12	2.35	0.49
1:B4:16:VAL:HG22	1:B4:49:VAL:HG22	1.94	0.49
1:BY:107:ASP:C	1:BY:107:ASP:OD1	2.50	0.49
1:C4:107:ASP:C	1:C4:107:ASP:OD1	2.50	0.49
1:C2:18:VAL:HG22	1:C2:77:LEU:HB2	1.94	0.49
1:BF:18:VAL:HG21	1:BF:30:LEU:HD13	1.94	0.49
1:BI:6:HIS:CE1	1:BI:8:VAL:HB	2.47	0.49
1:CX:6:HIS:CE1	1:CX:8:VAL:HB	2.47	0.49
1:B2:17:VAL:HG21	1:B2:62:ALA:HA	1.94	0.49
1:BO:71:TYR:C	1:BO:150:LYS:HZ3	2.15	0.49
1:BQ:97:LYS:HE3	1:BR:97:LYS:HZ3	1.77	0.49
1:BG:58:ILE:HG22	1:BG:58:ILE:O	2.13	0.49
1:BJ:18:VAL:HG23	1:BJ:51:TRP:CE3	2.48	0.49
1:CT:16:VAL:HG22	1:CT:49:VAL:HG22	1.94	0.49
1:BT:107:ASP:C	1:BT:107:ASP:OD1	2.50	0.49
1:BO:107:ASP:OD1	1:BO:107:ASP:C	2.50	0.49
1:AP:18:VAL:HG21	1:AP:30:LEU:HD13	1.94	0.49
1:AM:18:VAL:HG22	1:AM:77:LEU:HB2	1.94	0.49
1:CH:18:VAL:HG22	1:CH:77:LEU:HB2	1.94	0.49
1:AK:18:VAL:HG21	1:AK:30:LEU:HD13	1.94	0.49
1:AN:6:HIS:CE1	1:AN:8:VAL:HB	2.47	0.49
1:AY:82:ARG:HG3	1:AY:118:GLU:OE2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:116:THR:O	1:AE:85:THR:HB	2.12	0.49
1:B3:116:THR:O	1:B4:85:THR:HB	2.12	0.49
1:CW:17:VAL:HG21	1:CW:62:ALA:HA	1.95	0.49
1:BB:96:ALA:O	1:BB:100:ALA:HB2	2.06	0.49
1:AB:58:ILE:HG22	1:AB:58:ILE:O	2.13	0.49
1:AY:16:VAL:HG22	1:AY:49:VAL:HG22	1.94	0.49
1:CY:16:VAL:HG22	1:CY:49:VAL:HG22	1.94	0.49
1:BT:16:VAL:HG22	1:BT:49:VAL:HG22	1.94	0.49
1:CE:18:VAL:HG23	1:CE:51:TRP:CE3	2.48	0.49
1:BE:18:VAL:HG23	1:BE:51:TRP:CE3	2.48	0.49
1:AQ:152:TRP:C	1:AQ:152:TRP:CD1	2.85	0.49
1:BF:102:LEU:CD2	1:BJ:104:LEU:HD13	2.42	0.49
1:CB:12:LEU:HD11	1:CB:143:ILE:HG23	1.95	0.49
1:BI:116:THR:O	1:BJ:85:THR:HB	2.12	0.49
1:BE:82:ARG:HG3	1:BE:118:GLU:OE2	2.12	0.49
1:CR:17:VAL:HG21	1:CR:62:ALA:HA	1.95	0.49
1:AY:71:TYR:C	1:AY:150:LYS:HZ3	2.15	0.49
1:AI:106:THR:O	1:AI:107:ASP:HB3	2.13	0.49
1:BL:96:ALA:O	1:BL:100:ALA:HB2	2.06	0.49
1:BL:58:ILE:O	1:BL:58:ILE:HG22	2.13	0.49
1:BO:18:VAL:HG23	1:BO:51:TRP:CE3	2.48	0.49
1:AE:18:VAL:HG23	1:AE:51:TRP:CE3	2.48	0.49
1:A4:16:VAL:HG22	1:A4:49:VAL:HG22	1.94	0.49
1:A4:18:VAL:HG23	1:A4:51:TRP:CE3	2.48	0.49
1:CK:125:GLU:CA	1:CK:129:THR:OG1	2.57	0.49
1:AB:152:TRP:C	1:AB:152:TRP:CD1	2.85	0.49
1:CA:102:LEU:CD2	1:CE:104:LEU:HD13	2.42	0.49
1:AK:102:LEU:CD2	1:AO:104:LEU:HD13	2.42	0.49
1:BZ:18:VAL:HG21	1:BZ:30:LEU:HD13	1.94	0.49
1:AH:18:VAL:HG22	1:AH:77:LEU:HB2	1.94	0.49
1:BX:6:HIS:CE1	1:BX:8:VAL:HB	2.47	0.49
1:AI:116:THR:O	1:AJ:85:THR:HB	2.12	0.49
1:CV:12:LEU:HD11	1:CV:143:ILE:HG23	1.95	0.49
1:BQ:12:LEU:HD11	1:BQ:143:ILE:HG23	1.95	0.49
1:A4:82:ARG:HG3	1:A4:118:GLU:OE2	2.12	0.49
1:CT:53:PRO:HD2	1:CT:57:GLU:HB2	1.93	0.49
1:CE:53:PRO:HD2	1:CE:57:GLU:HB2	1.93	0.49
1:CC:129:THR:CG2	1:CS:120:ILE:HD11	2.40	0.49
1:BT:18:VAL:HG23	1:BT:51:TRP:CE3	2.48	0.49
1:CM:82:ARG:CG	1:CM:82:ARG:NH1	2.73	0.49
1:AP:58:ILE:HG22	1:AP:58:ILE:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:102:LEU:CD2	1:CJ:104:LEU:HD13	2.42	0.49
1:BK:102:LEU:CD2	1:BO:104:LEU:HD13	2.42	0.49
1:CK:18:VAL:HG21	1:CK:30:LEU:HD13	1.94	0.49
1:CU:18:VAL:HG21	1:CU:30:LEU:HD13	1.94	0.49
1:A2:17:VAL:HG21	1:A2:62:ALA:HA	1.95	0.49
1:CC:17:VAL:HG21	1:CC:62:ALA:HA	1.95	0.49
1:A1:12:LEU:HD11	1:A1:143:ILE:HG23	1.95	0.49
1:A3:116:THR:O	1:A4:85:THR:HB	2.12	0.49
1:AV:12:LEU:HD11	1:AV:143:ILE:HG23	1.95	0.49
1:CN:106:THR:O	1:CN:107:ASP:HB3	2.13	0.49
1:CD:106:THR:O	1:CD:107:ASP:HB3	2.13	0.49
1:BQ:152:TRP:CD1	1:BQ:152:TRP:C	2.85	0.49
1:AG:58:ILE:O	1:AG:58:ILE:HG22	2.13	0.49
1:CD:28:LYS:HZ1	1:CF:28:LYS:HZ2	1.57	0.49
1:AY:18:VAL:HG23	1:AY:51:TRP:CE3	2.48	0.49
1:CJ:16:VAL:HG22	1:CJ:49:VAL:HG22	1.94	0.49
1:C4:16:VAL:HG22	1:C4:49:VAL:HG22	1.94	0.49
1:CT:107:ASP:C	1:CT:107:ASP:OD1	2.50	0.49
1:AT:107:ASP:C	1:AT:107:ASP:OD1	2.50	0.49
1:CK:102:LEU:CD2	1:CO:104:LEU:HD13	2.42	0.49
1:BP:102:LEU:CD2	1:BT:104:LEU:HD13	2.42	0.49
1:CM:18:VAL:HG22	1:CM:77:LEU:HB2	1.94	0.49
1:CW:18:VAL:HG22	1:CW:77:LEU:HB2	1.94	0.49
1:CD:6:HIS:CE1	1:CD:8:VAL:HB	2.47	0.49
1:BN:6:HIS:CE1	1:BN:8:VAL:HB	2.47	0.49
1:BT:24:PHE:CD1	1:BY:28:LYS:HG3	2.48	0.49
1:CE:82:ARG:HG3	1:CE:118:GLU:OE2	2.12	0.49
1:AL:65:MET:O	1:AL:68:SER:HB3	2.13	0.49
1:BB:12:LEU:HD11	1:BB:143:ILE:HG23	1.95	0.49
1:BO:53:PRO:HG2	1:BO:57:GLU:HG3	0.65	0.49
1:AY:52:VAL:CB	1:AY:53:PRO:HD2	2.33	0.49
1:CV:152:TRP:CD1	1:CV:152:TRP:C	2.85	0.49
1:BE:71:TYR:C	1:BE:150:LYS:HZ3	2.16	0.49
1:C4:71:TYR:C	1:C4:150:LYS:HZ3	2.16	0.49
1:CY:18:VAL:HG23	1:CY:51:TRP:CE3	2.48	0.49
1:CO:18:VAL:HG23	1:CO:51:TRP:CE3	2.48	0.49
1:BP:58:ILE:HG22	1:BP:58:ILE:O	2.12	0.49
1:CO:107:ASP:OD1	1:CO:107:ASP:C	2.50	0.49
1:BC:18:VAL:HG22	1:BC:77:LEU:HB2	1.95	0.49
1:AC:18:VAL:HG22	1:AC:77:LEU:HB2	1.94	0.49
1:AU:18:VAL:HG21	1:AU:30:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:6:HIS:CE1	1:AS:8:VAL:HB	2.47	0.49
1:CS:6:HIS:CE1	1:CS:8:VAL:HB	2.47	0.49
1:BY:82:ARG:HG3	1:BY:118:GLU:OE2	2.12	0.49
1:CN:98:GLY:O	1:CN:102:LEU:HB2	2.13	0.49
1:CH:17:VAL:HG21	1:CH:62:ALA:HA	1.95	0.49
1:CY:82:ARG:HG3	1:CY:118:GLU:OE2	2.12	0.49
1:B1:65:MET:O	1:B1:68:SER:HB3	2.13	0.49
1:AL:12:LEU:HD11	1:AL:143:ILE:HG23	1.95	0.49
1:A4:53:PRO:CG	1:A4:57:GLU:CG	2.46	0.49
1:BT:52:VAL:CB	1:BT:53:PRO:HD2	2.33	0.49
1:CJ:71:TYR:C	1:CJ:150:LYS:HZ3	2.15	0.49
1:BI:106:THR:O	1:BI:107:ASP:HB3	2.13	0.49
1:AX:106:THR:O	1:AX:107:ASP:HB3	2.13	0.49
1:B3:106:THR:O	1:B3:107:ASP:HB3	2.13	0.49
1:B2:38:LYS:HZ2	1:B2:44:GLU:HA	1.78	0.49
1:AR:38:LYS:HZ2	1:AR:44:GLU:HA	1.78	0.49
1:C4:18:VAL:HG23	1:C4:51:TRP:CE3	2.48	0.49
1:CT:18:VAL:HG23	1:CT:51:TRP:CE3	2.48	0.49
1:AW:18:VAL:HG22	1:AW:77:LEU:HB2	1.94	0.49
1:BS:6:HIS:CE1	1:BS:8:VAL:HB	2.47	0.49
1:AR:17:VAL:HG21	1:AR:62:ALA:HA	1.95	0.49
1:BR:17:VAL:HG21	1:BR:62:ALA:HA	1.95	0.49
1:CI:116:THR:O	1:CJ:85:THR:HB	2.12	0.49
1:AS:98:GLY:O	1:AS:102:LEU:HB2	2.13	0.49
1:AT:82:ARG:HG3	1:AT:118:GLU:OE2	2.12	0.49
1:BK:65:MET:HE3	1:BK:71:TYR:CE2	2.48	0.49
1:CD:116:THR:O	1:CE:85:THR:HB	2.12	0.49
1:BG:12:LEU:HD11	1:BG:143:ILE:HG23	1.95	0.49
1:AQ:65:MET:O	1:AQ:68:SER:HB3	2.13	0.49
1:BV:12:LEU:HD11	1:BV:143:ILE:HG23	1.95	0.49
1:BY:71:TYR:C	1:BY:150:LYS:HZ3	2.16	0.48
1:BL:152:TRP:C	1:BL:152:TRP:CD1	2.85	0.48
1:BN:106:THR:O	1:BN:107:ASP:HB3	2.13	0.48
1:AN:106:THR:O	1:AN:107:ASP:HB3	2.13	0.48
1:CI:106:THR:O	1:CI:107:ASP:HB3	2.13	0.48
1:BH:38:LYS:HZ2	1:BH:44:GLU:HA	1.78	0.48
1:BH:82:ARG:CG	1:BH:82:ARG:NH1	2.73	0.48
1:AT:18:VAL:HG23	1:AT:51:TRP:CE3	2.48	0.48
1:CT:39:ARG:O	1:C3:7:LEU:HB3	2.13	0.48
1:CU:102:LEU:CD2	1:CY:104:LEU:HD13	2.42	0.48
1:BM:18:VAL:HG22	1:BM:77:LEU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B3:6:HIS:CE1	1:B3:8:VAL:HB	2.47	0.48
1:CN:6:HIS:CE1	1:CN:8:VAL:HB	2.47	0.48
1:CI:6:HIS:CE1	1:CI:8:VAL:HB	2.47	0.48
1:AG:12:LEU:HD11	1:AG:143:ILE:HG23	1.95	0.48
1:A1:65:MET:O	1:A1:68:SER:HB3	2.13	0.48
1:CN:116:THR:O	1:CO:85:THR:HB	2.12	0.48
1:BS:106:THR:O	1:BS:107:ASP:HB3	2.13	0.48
1:BB:58:ILE:O	1:BB:58:ILE:HG22	2.13	0.48
1:CB:58:ILE:HG22	1:CB:58:ILE:O	2.13	0.48
1:AX:18:VAL:HG12	1:AX:77:LEU:CB	2.37	0.48
1:AJ:16:VAL:HG22	1:AJ:49:VAL:HG22	1.94	0.48
1:CO:16:VAL:HG22	1:CO:49:VAL:HG22	1.94	0.48
1:AP:125:GLU:CA	1:AP:129:THR:OG1	2.57	0.48
1:A3:6:HIS:CE1	1:A3:8:VAL:HB	2.47	0.48
1:C1:12:LEU:HD11	1:C1:143:ILE:HG23	1.95	0.48
1:CQ:65:MET:O	1:CQ:68:SER:HB3	2.13	0.48
1:AD:98:GLY:O	1:AD:102:LEU:HB2	2.13	0.48
1:AX:98:GLY:O	1:AX:102:LEU:HB2	2.13	0.48
1:BN:98:GLY:O	1:BN:102:LEU:HB2	2.13	0.48
1:CE:71:TYR:C	1:CE:150:LYS:HZ3	2.15	0.48
1:AJ:71:TYR:O	1:AJ:150:LYS:NZ	2.44	0.48
1:AD:106:THR:O	1:AD:107:ASP:HB3	2.13	0.48
1:CS:106:THR:O	1:CS:107:ASP:HB3	2.13	0.48
1:CW:97:LYS:HG3	1:CX:97:LYS:HZ1	1.76	0.48
1:BD:18:VAL:HG12	1:BD:77:LEU:CB	2.37	0.48
1:A2:82:ARG:CG	1:A2:82:ARG:NH1	2.73	0.48
1:AG:152:TRP:C	1:AG:152:TRP:CD1	2.85	0.48
1:AX:6:HIS:CE1	1:AX:8:VAL:HB	2.47	0.48
1:BN:116:THR:O	1:BO:85:THR:HB	2.12	0.48
1:AC:17:VAL:HG21	1:AC:62:ALA:HA	1.95	0.48
1:AH:17:VAL:HG21	1:AH:62:ALA:HA	1.95	0.48
1:CJ:82:ARG:HG3	1:CJ:118:GLU:OE2	2.12	0.48
1:CD:98:GLY:O	1:CD:102:LEU:HB2	2.13	0.48
1:CV:65:MET:O	1:CV:68:SER:HB3	2.13	0.48
1:BO:53:PRO:HD2	1:BO:57:GLU:HB2	1.93	0.48
1:CE:52:VAL:HB	1:CE:53:PRO:CD	2.35	0.48
1:AO:71:TYR:C	1:AO:150:LYS:HZ3	2.15	0.48
1:AS:106:THR:O	1:AS:107:ASP:HB3	2.13	0.48
1:AB:97:LYS:HE3	1:AC:97:LYS:HZ3	1.75	0.48
1:BI:52:VAL:CG1	1:BI:61:ILE:HD12	2.35	0.48
1:BE:16:VAL:HG22	1:BE:49:VAL:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BZ:58:ILE:HG22	1:BZ:58:ILE:O	2.11	0.48
1:B2:18:VAL:HG22	1:B2:77:LEU:HB2	1.95	0.48
1:A2:18:VAL:HG22	1:A2:77:LEU:HB2	1.94	0.48
1:AD:39:ARG:O	1:AJ:7:LEU:HB3	2.13	0.48
1:CS:66:ALA:HB2	1:CS:74:VAL:HG21	1.96	0.48
1:AB:12:LEU:HD11	1:AB:143:ILE:HG23	1.95	0.48
1:CG:65:MET:O	1:CG:68:SER:HB3	2.13	0.48
1:C1:65:MET:O	1:C1:68:SER:HB3	2.13	0.48
1:AN:66:ALA:HB2	1:AN:74:VAL:HG21	1.96	0.48
1:BD:66:ALA:HB2	1:BD:74:VAL:HG21	1.96	0.48
1:AX:66:ALA:HB2	1:AX:74:VAL:HG21	1.96	0.48
1:AG:65:MET:O	1:AG:68:SER:HB3	2.13	0.48
1:BG:65:MET:O	1:BG:68:SER:HB3	2.13	0.48
1:AI:98:GLY:O	1:AI:102:LEU:HB2	2.13	0.48
1:CO:71:TYR:O	1:CO:150:LYS:NZ	2.44	0.48
1:BT:71:TYR:C	1:BT:150:LYS:HZ3	2.15	0.48
1:CN:30:LEU:HA	1:CN:77:LEU:HD23	1.96	0.48
1:BY:18:VAL:HG23	1:BY:51:TRP:CE3	2.48	0.48
1:CJ:18:VAL:HG23	1:CJ:51:TRP:CE3	2.48	0.48
1:B4:18:VAL:HG23	1:B4:51:TRP:CE3	2.48	0.48
1:CO:121:GLU:O	1:CO:125:GLU:HB2	2.14	0.48
1:BT:121:GLU:O	1:BT:125:GLU:HB2	2.14	0.48
1:BF:58:ILE:O	1:BF:58:ILE:HG22	2.11	0.48
1:AS:149:SER:HB3	1:AS:152:TRP:CZ2	2.49	0.48
1:CR:18:VAL:HG22	1:CR:77:LEU:HB2	1.95	0.48
1:BA:18:VAL:HG21	1:BA:30:LEU:HD13	1.94	0.48
1:BV:12:LEU:HB2	1:BV:42:VAL:HG13	1.96	0.48
1:BS:98:GLY:O	1:BS:102:LEU:HB2	2.13	0.48
1:BJ:82:ARG:HG3	1:BJ:118:GLU:OE2	2.12	0.48
1:BC:17:VAL:HG21	1:BC:62:ALA:HA	1.95	0.48
1:C3:66:ALA:HB2	1:C3:74:VAL:HG21	1.96	0.48
1:AE:52:VAL:CB	1:AE:53:PRO:HD2	2.34	0.48
1:CC:97:LYS:HE3	1:CD:97:LYS:HZ3	1.78	0.48
1:AC:97:LYS:HG3	1:AD:97:LYS:HZ3	1.79	0.48
1:B1:58:ILE:HG22	1:B1:58:ILE:O	2.13	0.48
1:CS:52:VAL:CG1	1:CS:61:ILE:HD12	2.35	0.48
1:BM:52:VAL:CG1	1:BM:61:ILE:HD12	2.35	0.48
1:CF:58:ILE:HG22	1:CF:58:ILE:O	2.11	0.48
1:AF:58:ILE:HG22	1:AF:58:ILE:O	2.12	0.48
1:B4:121:GLU:O	1:B4:125:GLU:HB2	2.14	0.48
1:BE:121:GLU:O	1:BE:125:GLU:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:149:SER:HB3	1:BN:152:TRP:CZ2	2.49	0.48
1:CX:149:SER:HB3	1:CX:152:TRP:CZ2	2.49	0.48
1:BR:106:THR:HG23	1:BR:108:ILE:H	1.79	0.48
1:CF:18:VAL:HG21	1:CF:30:LEU:HD13	1.94	0.48
1:BF:28:LYS:CE	1:BR:28:LYS:NZ	2.76	0.48
1:BD:6:HIS:CE1	1:BD:8:VAL:HB	2.47	0.48
1:CL:12:LEU:HD11	1:CL:143:ILE:HG23	1.95	0.48
1:BQ:65:MET:O	1:BQ:68:SER:HB3	2.13	0.48
1:BO:82:ARG:HG3	1:BO:118:GLU:OE2	2.12	0.48
1:AS:66:ALA:HB2	1:AS:74:VAL:HG21	1.96	0.48
1:B3:66:ALA:HB2	1:B3:74:VAL:HG21	1.96	0.48
1:AQ:12:LEU:HB2	1:AQ:42:VAL:HG13	1.96	0.48
1:A3:149:SER:HB3	1:A3:152:TRP:CZ2	2.49	0.48
1:CI:149:SER:HB3	1:CI:152:TRP:CZ2	2.49	0.48
1:BI:39:ARG:O	1:BO:7:LEU:HB3	2.14	0.48
1:CM:17:VAL:HG21	1:CM:62:ALA:HA	1.95	0.48
1:AV:65:MET:O	1:AV:68:SER:HB3	2.13	0.48
1:BI:98:GLY:O	1:BI:102:LEU:HB2	2.13	0.48
1:AV:116:THR:O	1:AW:85:THR:HB	2.14	0.48
1:BL:65:MET:O	1:BL:68:SER:HB3	2.13	0.48
1:AN:98:GLY:O	1:AN:102:LEU:HB2	2.13	0.48
1:AL:116:THR:O	1:AM:85:THR:HB	2.14	0.48
1:CV:116:THR:O	1:CW:85:THR:HB	2.14	0.48
1:BX:66:ALA:HB2	1:BX:74:VAL:HG21	1.96	0.48
1:BD:106:THR:O	1:BD:107:ASP:HB3	2.13	0.48
1:CB:97:LYS:HE3	1:CC:97:LYS:HZ3	1.79	0.48
1:A1:58:ILE:O	1:A1:58:ILE:HG22	2.13	0.48
1:BO:121:GLU:O	1:BO:125:GLU:HB2	2.14	0.48
1:A4:121:GLU:O	1:A4:125:GLU:HB2	2.14	0.48
1:AJ:121:GLU:O	1:AJ:125:GLU:HB2	2.14	0.48
1:BX:149:SER:HB3	1:BX:152:TRP:CZ2	2.49	0.48
1:BS:149:SER:HB3	1:BS:152:TRP:CZ2	2.49	0.48
1:AN:149:SER:HB3	1:AN:152:TRP:CZ2	2.49	0.48
1:BR:18:VAL:HG22	1:BR:77:LEU:HB2	1.94	0.48
1:BH:18:VAL:HG22	1:BH:77:LEU:HB2	1.94	0.48
1:BW:18:VAL:HG22	1:BW:77:LEU:HB2	1.94	0.48
1:CB:12:LEU:HB2	1:CB:42:VAL:HG13	1.96	0.48
1:BX:98:GLY:O	1:BX:102:LEU:HB2	2.13	0.48
1:BW:17:VAL:HG21	1:BW:62:ALA:HA	1.95	0.48
1:AW:17:VAL:HG21	1:AW:62:ALA:HA	1.95	0.48
1:BS:66:ALA:HB2	1:BS:74:VAL:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:65:MET:O	1:AB:68:SER:HB3	2.13	0.48
1:BS:116:THR:O	1:BT:85:THR:HB	2.12	0.48
1:CB:65:MET:O	1:CB:68:SER:HB3	2.13	0.48
1:CH:24:PHE:CE1	1:CU:28:LYS:HD2	2.49	0.48
1:BX:106:THR:O	1:BX:107:ASP:HB3	2.13	0.48
1:AB:144:GLU:OE2	1:AC:20:ARG:HD2	2.14	0.48
1:A1:144:GLU:OE2	1:A2:20:ARG:HD2	2.14	0.48
1:AO:18:VAL:HG23	1:AO:51:TRP:CE3	2.48	0.48
1:AJ:18:VAL:HG23	1:AJ:51:TRP:CE3	2.48	0.48
1:C4:121:GLU:O	1:C4:125:GLU:HB2	2.14	0.48
1:B3:149:SER:HB3	1:B3:152:TRP:CZ2	2.49	0.48
1:BI:149:SER:HB3	1:BI:152:TRP:CZ2	2.49	0.48
1:AM:106:THR:HG23	1:AM:108:ILE:H	1.79	0.48
1:BS:137:GLU:O	1:BS:140:VAL:HG12	2.14	0.48
1:CR:152:TRP:HE1	1:CS:64:LYS:C	2.18	0.48
1:BP:18:VAL:HG21	1:BP:30:LEU:HD13	1.94	0.48
1:AR:152:TRP:HE1	1:AS:64:LYS:C	2.17	0.48
1:CN:66:ALA:HB2	1:CN:74:VAL:HG21	1.96	0.48
1:B1:12:LEU:HB2	1:B1:42:VAL:HG13	1.96	0.48
1:AB:116:THR:O	1:AC:85:THR:HB	2.14	0.48
1:AM:17:VAL:HG21	1:AM:62:ALA:HA	1.95	0.48
1:BM:45:ASN:HA	1:BM:45:ASN:HD22	1.64	0.48
1:BV:65:MET:O	1:BV:68:SER:HB3	2.13	0.48
1:BB:116:THR:O	1:BC:85:THR:HB	2.14	0.48
1:C4:52:VAL:HB	1:C4:53:PRO:CD	2.35	0.48
1:CO:52:VAL:CB	1:CO:53:PRO:HD2	2.34	0.48
1:C3:106:THR:O	1:C3:107:ASP:HB3	2.13	0.48
1:BM:97:LYS:HE3	1:BN:97:LYS:HZ3	1.78	0.48
1:AL:58:ILE:HG22	1:AL:58:ILE:O	2.13	0.48
1:CC:39:ARG:O	1:CR:7:LEU:HB3	2.14	0.48
1:CR:106:THR:HG23	1:CR:108:ILE:H	1.79	0.48
1:B2:106:THR:HG23	1:B2:108:ILE:H	1.79	0.48
1:BH:106:THR:HG23	1:BH:108:ILE:H	1.79	0.48
1:A3:137:GLU:O	1:A3:140:VAL:HG12	2.14	0.48
1:AX:137:GLU:O	1:AX:140:VAL:HG12	2.14	0.48
1:CW:152:TRP:HE1	1:CX:64:LYS:C	2.18	0.48
1:BC:152:TRP:HE1	1:BD:64:LYS:C	2.18	0.48
1:AR:18:VAL:HG22	1:AR:77:LEU:HB2	1.94	0.48
1:BG:12:LEU:HB2	1:BG:42:VAL:HG13	1.96	0.48
1:AQ:12:LEU:HD11	1:AQ:143:ILE:HG23	1.95	0.48
1:BG:116:THR:O	1:BH:85:THR:HB	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B4:82:ARG:HG3	1:B4:118:GLU:OE2	2.12	0.48
1:BL:116:THR:O	1:BM:85:THR:HB	2.14	0.48
1:CP:65:MET:HE3	1:CP:71:TYR:CE2	2.48	0.48
1:CV:13:LYS:HD2	1:CV:46:ASP:OD2	2.14	0.48
1:BL:13:LYS:HD2	1:BL:46:ASP:OD2	2.14	0.48
1:BM:17:VAL:HG21	1:BM:62:ALA:HA	1.95	0.48
1:CG:12:LEU:HD11	1:CG:143:ILE:HG23	1.95	0.48
1:A3:66:ALA:HB2	1:A3:74:VAL:HG21	1.96	0.48
1:B3:98:GLY:O	1:B3:102:LEU:HB2	2.13	0.48
1:CQ:90:TYR:O	1:CQ:94:GLU:HG2	2.14	0.48
1:CO:71:TYR:C	1:CO:150:LYS:HZ3	2.15	0.47
1:CL:58:ILE:O	1:CL:58:ILE:HG22	2.13	0.47
1:BV:144:GLU:OE2	1:BW:20:ARG:HD2	2.14	0.47
1:BX:30:LEU:HA	1:BX:77:LEU:HD23	1.96	0.47
1:AN:30:LEU:HA	1:AN:77:LEU:HD23	1.96	0.47
1:CA:121:GLU:O	1:CA:125:GLU:HG3	2.14	0.47
1:BW:106:THR:HG23	1:BW:108:ILE:H	1.79	0.47
1:AH:106:THR:HG23	1:AH:108:ILE:H	1.79	0.47
1:AI:137:GLU:O	1:AI:140:VAL:HG12	2.14	0.47
1:CD:137:GLU:O	1:CD:140:VAL:HG12	2.14	0.47
1:AW:152:TRP:HE1	1:AX:64:LYS:C	2.18	0.47
1:BX:137:GLU:O	1:BX:140:VAL:HG12	2.14	0.47
1:CC:152:TRP:HE1	1:CD:64:LYS:C	2.18	0.47
1:AG:12:LEU:HB2	1:AG:42:VAL:HG13	1.96	0.47
1:B1:12:LEU:HD11	1:B1:143:ILE:HG23	1.95	0.47
1:BD:98:GLY:O	1:BD:102:LEU:HB2	2.13	0.47
1:AS:116:THR:O	1:AT:85:THR:HB	2.12	0.47
1:BI:66:ALA:HB2	1:BI:74:VAL:HG21	1.96	0.47
1:BB:65:MET:O	1:BB:68:SER:HB3	2.13	0.47
1:AD:82:ARG:HG3	1:AD:118:GLU:OE2	2.14	0.47
1:AB:13:LYS:HD2	1:AB:46:ASP:OD2	2.14	0.47
1:AD:66:ALA:HB2	1:AD:74:VAL:HG21	1.96	0.47
1:BB:152:TRP:O	1:BB:152:TRP:CD1	2.67	0.47
1:A3:106:THR:O	1:A3:107:ASP:HB3	2.13	0.47
1:CX:106:THR:O	1:CX:107:ASP:HB3	2.13	0.47
1:AG:97:LYS:HE3	1:AH:97:LYS:HZ3	1.79	0.47
1:AX:52:VAL:CG1	1:AX:61:ILE:HD12	2.35	0.47
1:BG:144:GLU:OE2	1:BH:20:ARG:HD2	2.14	0.47
1:CS:30:LEU:HA	1:CS:77:LEU:HD23	1.96	0.47
1:AI:30:LEU:HA	1:AI:77:LEU:HD23	1.96	0.47
1:BP:121:GLU:O	1:BP:125:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CH:82:ARG:CG	1:CH:82:ARG:NH1	2.73	0.47
1:AY:121:GLU:O	1:AY:125:GLU:HB2	2.14	0.47
1:C2:106:THR:HG23	1:C2:108:ILE:H	1.79	0.47
1:CM:152:TRP:HE1	1:CN:64:LYS:C	2.17	0.47
1:BM:152:TRP:HE1	1:BN:64:LYS:C	2.17	0.47
1:CC:18:VAL:HG22	1:CC:77:LEU:HB2	1.94	0.47
1:AE:7:LEU:HB3	1:AN:39:ARG:O	2.13	0.47
1:AV:12:LEU:HB2	1:AV:42:VAL:HG13	1.96	0.47
1:CL:13:LYS:HD2	1:CL:46:ASP:OD2	2.14	0.47
1:BB:13:LYS:HD2	1:BB:46:ASP:OD2	2.15	0.47
1:CB:13:LYS:HD2	1:CB:46:ASP:OD2	2.14	0.47
1:BV:116:THR:O	1:BW:85:THR:HB	2.14	0.47
1:C3:98:GLY:O	1:C3:102:LEU:HB2	2.13	0.47
1:CQ:12:LEU:HB2	1:CQ:42:VAL:HG13	1.96	0.47
1:BG:13:LYS:HD2	1:BG:46:ASP:OD2	2.14	0.47
1:BL:152:TRP:O	1:BL:152:TRP:CD1	2.67	0.47
1:CG:152:TRP:CD1	1:CG:152:TRP:O	2.67	0.47
1:CB:55:ALA:HB1	1:CB:95:VAL:CG2	2.40	0.47
1:AI:52:VAL:CG1	1:AI:61:ILE:HD12	2.35	0.47
1:CV:144:GLU:OE2	1:CW:20:ARG:HD2	2.14	0.47
1:AS:30:LEU:HA	1:AS:77:LEU:HD23	1.96	0.47
1:AN:18:VAL:HG12	1:AN:77:LEU:CB	2.37	0.47
1:C3:30:LEU:HA	1:C3:77:LEU:HD23	1.96	0.47
1:AH:70:LYS:HB2	1:AH:71:TYR:CD1	2.50	0.47
1:BK:121:GLU:O	1:BK:125:GLU:HG3	2.14	0.47
1:BZ:125:GLU:CA	1:BZ:129:THR:OG1	2.57	0.47
1:CY:121:GLU:O	1:CY:125:GLU:HB2	2.14	0.47
1:AE:121:GLU:O	1:AE:125:GLU:HB2	2.14	0.47
1:AX:149:SER:HB3	1:AX:152:TRP:CZ2	2.49	0.47
1:BM:106:THR:HG23	1:BM:108:ILE:H	1.79	0.47
1:AL:152:TRP:O	1:AL:152:TRP:CD1	2.68	0.47
1:CO:83:GLY:HA3	2:CO:4201:PO4:O2	2.15	0.47
1:AJ:83:GLY:HA3	2:AJ:1001:PO4:O2	2.14	0.47
1:C2:152:TRP:HE1	1:C3:64:LYS:C	2.18	0.47
1:B2:152:TRP:HE1	1:B3:64:LYS:C	2.17	0.47
1:AL:12:LEU:HB2	1:AL:42:VAL:HG13	1.96	0.47
1:CQ:12:LEU:HD11	1:CQ:143:ILE:HG23	1.95	0.47
1:BH:17:VAL:HG21	1:BH:62:ALA:HA	1.94	0.47
1:CS:98:GLY:O	1:CS:102:LEU:HB2	2.13	0.47
1:AG:13:LYS:HD2	1:AG:46:ASP:OD2	2.15	0.47
1:CQ:13:LYS:HD2	1:CQ:46:ASP:OD2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:128:GLY:O	1:AK:22:ASN:HA	2.14	0.47
1:CX:120:ILE:HG12	1:C2:129:THR:HG21	1.97	0.47
1:C1:152:TRP:CD1	1:C1:152:TRP:O	2.67	0.47
1:CB:152:TRP:O	1:CB:152:TRP:CD1	2.68	0.47
1:BG:152:TRP:O	1:BG:152:TRP:CD1	2.68	0.47
1:AQ:58:ILE:HG22	1:AQ:58:ILE:O	2.13	0.47
1:BW:97:LYS:HE3	1:BX:97:LYS:HZ1	1.79	0.47
1:AQ:144:GLU:OE2	1:AR:20:ARG:HD2	2.14	0.47
1:CW:70:LYS:HB2	1:CW:71:TYR:CD1	2.50	0.47
1:AT:121:GLU:O	1:AT:125:GLU:HB2	2.14	0.47
1:AD:149:SER:HB3	1:AD:152:TRP:CZ2	2.49	0.47
1:CC:106:THR:HG23	1:CC:108:ILE:H	1.79	0.47
1:AW:106:THR:HG23	1:AW:108:ILE:H	1.79	0.47
1:AB:152:TRP:O	1:AB:152:TRP:CD1	2.68	0.47
1:AQ:152:TRP:O	1:AQ:152:TRP:CD1	2.68	0.47
1:AO:83:GLY:HA3	2:AO:1001:PO4:O2	2.15	0.47
1:CJ:83:GLY:HA3	2:CJ:4201:PO4:O2	2.15	0.47
1:A4:83:GLY:HA3	2:A4:1001:PO4:O2	2.15	0.47
1:BR:152:TRP:HE1	1:BS:64:LYS:C	2.18	0.47
1:CV:12:LEU:HB2	1:CV:42:VAL:HG13	1.96	0.47
1:C1:12:LEU:HB2	1:C1:42:VAL:HG13	1.96	0.47
1:BL:12:LEU:HD11	1:BL:143:ILE:HG23	1.95	0.47
1:AL:13:LYS:HD2	1:AL:46:ASP:OD2	2.14	0.47
1:CI:98:GLY:O	1:CI:102:LEU:HB2	2.13	0.47
1:AQ:90:TYR:O	1:AQ:94:GLU:HG2	2.14	0.47
1:AK:65:MET:HE3	1:AK:71:TYR:CE2	2.50	0.47
1:BI:82:ARG:HG3	1:BI:118:GLU:OE2	2.14	0.47
1:BA:65:MET:HE3	1:BA:71:TYR:CE2	2.49	0.47
1:A3:98:GLY:O	1:A3:102:LEU:HB2	2.13	0.47
1:A3:82:ARG:HG3	1:A3:118:GLU:OE2	2.15	0.47
1:BL:90:TYR:O	1:BL:94:GLU:HG2	2.14	0.47
1:CL:90:TYR:O	1:CL:94:GLU:HG2	2.14	0.47
1:C1:106:THR:O	1:C1:107:ASP:HB3	2.15	0.47
1:CV:152:TRP:CD1	1:CV:152:TRP:O	2.68	0.47
1:CV:58:ILE:O	1:CV:58:ILE:HG22	2.13	0.47
1:CL:144:GLU:OE2	1:CM:20:ARG:HD2	2.14	0.47
1:CQ:144:GLU:OE2	1:CR:20:ARG:HD2	2.14	0.47
1:CF:121:GLU:O	1:CF:125:GLU:HG3	2.14	0.47
1:CF:125:GLU:CA	1:CF:129:THR:OG1	2.57	0.47
1:B2:70:LYS:HB2	1:B2:71:TYR:CD1	2.50	0.47
1:AU:121:GLU:O	1:AU:125:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BM:70:LYS:HB2	1:BM:71:TYR:CD1	2.50	0.47
1:BC:70:LYS:HB2	1:BC:71:TYR:CD1	2.50	0.47
1:CU:121:GLU:O	1:CU:125:GLU:HG3	2.14	0.47
1:AM:70:LYS:HB2	1:AM:71:TYR:CD1	2.50	0.47
1:BR:70:LYS:HB2	1:BR:71:TYR:CD1	2.50	0.47
1:CW:106:THR:HG23	1:CW:108:ILE:H	1.79	0.47
1:AG:152:TRP:O	1:AG:152:TRP:CD1	2.68	0.47
1:AE:83:GLY:HA3	2:AE:1001:PO4:O2	2.15	0.47
1:CI:137:GLU:O	1:CI:140:VAL:HG12	2.14	0.47
1:BR:30:LEU:HA	1:BR:77:LEU:HD23	1.97	0.47
1:CG:130:LYS:HG3	1:CV:120:ILE:HD11	1.95	0.47
1:CB:37:LEU:O	1:CB:42:VAL:HG23	2.15	0.47
1:AL:37:LEU:O	1:AL:42:VAL:HG23	2.15	0.47
1:CV:90:TYR:O	1:CV:94:GLU:HG2	2.14	0.47
1:CN:82:ARG:HG3	1:CN:118:GLU:OE2	2.14	0.47
1:BG:90:TYR:O	1:BG:94:GLU:HG2	2.14	0.47
1:C1:13:LYS:HD2	1:C1:46:ASP:OD2	2.14	0.47
1:BS:82:ARG:HG3	1:BS:118:GLU:OE2	2.14	0.47
1:CL:65:MET:O	1:CL:68:SER:HB3	2.13	0.47
1:B3:82:ARG:HG3	1:B3:118:GLU:OE2	2.14	0.47
1:BP:65:MET:HE3	1:BP:71:TYR:CE2	2.49	0.47
1:CL:116:THR:O	1:CM:85:THR:HB	2.14	0.47
1:AQ:13:LYS:HD2	1:AQ:46:ASP:OD2	2.14	0.47
1:BL:106:THR:O	1:BL:107:ASP:HB3	2.15	0.47
1:BQ:58:ILE:O	1:BQ:58:ILE:HG22	2.13	0.47
1:CG:58:ILE:HG22	1:CG:58:ILE:O	2.13	0.47
1:CX:52:VAL:CG1	1:CX:61:ILE:HD12	2.35	0.47
1:B3:30:LEU:HA	1:B3:77:LEU:HD23	1.96	0.47
1:AD:30:LEU:HA	1:AD:77:LEU:HD23	1.96	0.47
1:BD:30:LEU:HA	1:BD:77:LEU:HD23	1.96	0.47
1:CI:30:LEU:HA	1:CI:77:LEU:HD23	1.96	0.47
1:AH:63:LYS:C	1:AH:65:MET:H	2.18	0.47
1:CR:70:LYS:HB2	1:CR:71:TYR:CD1	2.50	0.47
1:BW:70:LYS:HB2	1:BW:71:TYR:CD1	2.50	0.47
1:AK:58:ILE:O	1:AK:58:ILE:HG22	2.11	0.47
1:BY:121:GLU:O	1:BY:125:GLU:HB2	2.14	0.47
1:CD:149:SER:HB3	1:CD:152:TRP:CZ2	2.49	0.47
1:BW:63:LYS:C	1:BW:65:MET:H	2.18	0.47
1:CV:129:THR:CG2	1:CV:130:LYS:H	2.28	0.47
1:B3:137:GLU:O	1:B3:140:VAL:HG12	2.14	0.47
1:BT:83:GLY:HA3	2:BT:1001:PO4:O2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:75:ILE:HG22	1:CM:77:LEU:HD13	1.97	0.47
1:AW:30:LEU:HA	1:AW:77:LEU:HD23	1.97	0.47
1:AM:152:TRP:HE1	1:AN:64:LYS:C	2.18	0.47
1:BW:152:TRP:HE1	1:BX:64:LYS:C	2.18	0.47
1:B1:129:THR:CG2	1:B1:130:LYS:H	2.28	0.47
1:CL:12:LEU:HB2	1:CL:42:VAL:HG13	1.96	0.47
1:AQ:37:LEU:O	1:AQ:42:VAL:HG23	2.15	0.47
1:AI:66:ALA:HB2	1:AI:74:VAL:HG21	1.96	0.47
1:A1:116:THR:O	1:A2:85:THR:HB	2.14	0.47
1:AL:90:TYR:O	1:AL:94:GLU:HG2	2.14	0.47
1:BB:90:TYR:O	1:BB:94:GLU:HG2	2.14	0.47
1:AV:90:TYR:O	1:AV:94:GLU:HG2	2.14	0.47
1:B1:116:THR:O	1:B2:85:THR:HB	2.14	0.47
1:AP:65:MET:HE3	1:AP:71:TYR:CE2	2.50	0.47
1:AG:116:THR:O	1:AH:85:THR:HB	2.14	0.47
1:CB:106:THR:O	1:CB:107:ASP:HB3	2.15	0.47
1:CL:106:THR:O	1:CL:107:ASP:HB3	2.15	0.47
1:CY:71:TYR:C	1:CY:150:LYS:HZ3	2.18	0.47
1:BB:144:GLU:OE2	1:BC:20:ARG:HD2	2.14	0.47
1:BQ:144:GLU:OE2	1:BR:20:ARG:HD2	2.14	0.47
1:AW:82:ARG:CG	1:AW:82:ARG:NH1	2.73	0.47
1:CR:38:LYS:HZ2	1:CR:44:GLU:HA	1.80	0.47
1:AR:70:LYS:HB2	1:AR:71:TYR:CD1	2.50	0.47
1:AW:70:LYS:HB2	1:AW:71:TYR:CD1	2.50	0.47
1:CC:70:LYS:HB2	1:CC:71:TYR:CD1	2.50	0.47
1:BU:121:GLU:O	1:BU:125:GLU:HG3	2.14	0.47
1:AZ:58:ILE:O	1:AZ:58:ILE:HG22	2.12	0.47
1:BR:63:LYS:C	1:BR:65:MET:H	2.18	0.47
1:CH:63:LYS:C	1:CH:65:MET:H	2.18	0.47
1:C2:70:LYS:HB2	1:C2:71:TYR:CD1	2.50	0.47
1:BJ:121:GLU:O	1:BJ:125:GLU:HB2	2.14	0.47
1:AZ:121:GLU:O	1:AZ:125:GLU:HG3	2.14	0.47
1:CE:121:GLU:O	1:CE:125:GLU:HB2	2.14	0.47
1:CJ:121:GLU:O	1:CJ:125:GLU:HB2	2.14	0.47
1:BD:149:SER:HB3	1:BD:152:TRP:CZ2	2.49	0.47
1:A2:106:THR:HG23	1:A2:108:ILE:H	1.79	0.47
1:CH:106:THR:HG23	1:CH:108:ILE:H	1.79	0.47
1:CT:7:LEU:CB	1:C3:39:ARG:O	2.63	0.47
1:CR:63:LYS:C	1:CR:65:MET:H	2.18	0.47
1:AN:137:GLU:O	1:AN:140:VAL:HG12	2.14	0.47
1:BE:83:GLY:HA3	2:BE:1001:PO4:O2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:137:GLU:O	1:BN:140:VAL:HG12	2.14	0.47
1:CY:83:GLY:HA3	2:CY:4201:PO4:O2	2.15	0.47
1:BI:137:GLU:O	1:BI:140:VAL:HG12	2.14	0.47
1:AC:152:TRP:HE1	1:AD:64:LYS:C	2.17	0.47
1:AT:83:GLY:HA3	2:AT:1001:PO4:O2	2.15	0.47
1:B4:83:GLY:HA3	2:B4:1001:PO4:O2	2.15	0.47
1:BC:30:LEU:HA	1:BC:77:LEU:HD23	1.97	0.47
1:BH:30:LEU:HA	1:BH:77:LEU:HD23	1.97	0.47
1:AR:75:ILE:HG22	1:AR:77:LEU:HD13	1.97	0.47
1:CR:75:ILE:HG22	1:CR:77:LEU:HD13	1.97	0.47
1:CC:30:LEU:HA	1:CC:77:LEU:HD23	1.97	0.47
1:AV:37:LEU:O	1:AV:42:VAL:HG23	2.15	0.47
1:BV:37:LEU:O	1:BV:42:VAL:HG23	2.15	0.47
1:C1:37:LEU:O	1:C1:42:VAL:HG23	2.15	0.47
1:BL:12:LEU:HB2	1:BL:42:VAL:HG13	1.96	0.47
1:BX:82:ARG:HG3	1:BX:118:GLU:OE2	2.15	0.47
1:BV:13:LYS:HD2	1:BV:46:ASP:OD2	2.14	0.47
1:CX:82:ARG:HG3	1:CX:118:GLU:OE2	2.14	0.47
1:CB:116:THR:O	1:CC:85:THR:HB	2.14	0.47
1:CX:98:GLY:O	1:CX:102:LEU:HB2	2.13	0.47
1:C1:116:THR:O	1:C2:85:THR:HB	2.14	0.47
1:CI:66:ALA:HB2	1:CI:74:VAL:HG21	1.96	0.47
1:CG:116:THR:O	1:CH:85:THR:HB	2.14	0.47
1:AB:90:TYR:O	1:AB:94:GLU:HG2	2.14	0.47
1:BN:66:ALA:HB2	1:BN:74:VAL:HG21	1.96	0.47
1:CG:106:THR:O	1:CG:107:ASP:HB3	2.15	0.47
1:BQ:106:THR:O	1:BQ:107:ASP:HB3	2.15	0.47
1:AV:58:ILE:O	1:AV:58:ILE:HG22	2.13	0.47
1:AG:144:GLU:OE2	1:AH:20:ARG:HD2	2.14	0.47
1:CB:144:GLU:OE2	1:CC:20:ARG:HD2	2.14	0.47
1:BL:144:GLU:OE2	1:BM:20:ARG:HD2	2.14	0.47
1:BN:30:LEU:HA	1:BN:77:LEU:HD23	1.96	0.47
1:CH:38:LYS:HZ2	1:CH:44:GLU:HA	1.79	0.47
1:CP:121:GLU:O	1:CP:125:GLU:HG3	2.14	0.47
1:AR:106:THR:HG23	1:AR:108:ILE:H	1.79	0.47
1:AC:106:THR:HG23	1:AC:108:ILE:H	1.79	0.47
1:AV:152:TRP:CD1	1:AV:152:TRP:O	2.67	0.47
1:A1:152:TRP:CD1	1:A1:152:TRP:O	2.67	0.47
1:AY:83:GLY:HA3	2:AY:1001:PO4:O2	2.15	0.47
1:BO:83:GLY:HA3	2:BO:1001:PO4:O2	2.15	0.47
1:CT:83:GLY:HA3	2:CT:4201:PO4:O2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:75:ILE:HG22	1:BR:77:LEU:HD13	1.97	0.47
1:AC:75:ILE:HG22	1:AC:77:LEU:HD13	1.97	0.47
1:CI:40:HIS:CE1	1:CO:7:LEU:HD23	2.50	0.47
1:BD:117:THR:HG22	1:BE:85:THR:HG21	1.97	0.47
1:C3:117:THR:HG22	1:C4:85:THR:HG21	1.97	0.47
1:BB:12:LEU:HB2	1:BB:42:VAL:HG13	1.96	0.47
1:BB:37:LEU:O	1:BB:42:VAL:HG23	2.15	0.47
1:CG:37:LEU:O	1:CG:42:VAL:HG23	2.15	0.47
1:AG:90:TYR:O	1:AG:94:GLU:HG2	2.14	0.47
1:AH:45:ASN:HA	1:AH:45:ASN:HD22	1.64	0.47
1:AR:148:LEU:HD23	1:AR:148:LEU:HA	1.79	0.47
1:AN:82:ARG:HG3	1:AN:118:GLU:OE2	2.14	0.47
1:CK:65:MET:HE3	1:CK:71:TYR:CE2	2.49	0.47
1:CD:82:ARG:HG3	1:CD:118:GLU:OE2	2.14	0.47
1:B1:152:TRP:CD1	1:B1:152:TRP:O	2.68	0.47
1:CQ:152:TRP:O	1:CQ:152:TRP:CD1	2.68	0.47
1:AE:71:TYR:O	1:AE:150:LYS:NZ	2.44	0.47
1:CJ:71:TYR:O	1:CJ:150:LYS:NZ	2.44	0.47
1:CL:152:TRP:CD1	1:CL:152:TRP:O	2.67	0.47
1:AL:100:ALA:CA	1:AM:56:PHE:HZ	2.28	0.47
1:C1:58:ILE:HG22	1:C1:58:ILE:O	2.13	0.47
1:AX:30:LEU:HA	1:AX:77:LEU:HD23	1.96	0.47
1:A3:30:LEU:HA	1:A3:77:LEU:HD23	1.96	0.47
1:BM:82:ARG:NH1	1:BM:82:ARG:CG	2.73	0.47
1:AR:63:LYS:C	1:AR:65:MET:H	2.18	0.47
1:BM:63:LYS:C	1:BM:65:MET:H	2.18	0.47
1:AA:121:GLU:O	1:AA:125:GLU:HG3	2.14	0.47
1:BF:121:GLU:O	1:BF:125:GLU:HG3	2.14	0.47
1:CP:58:ILE:H	1:CP:59:PRO:HD2	1.80	0.47
1:AI:149:SER:HB3	1:AI:152:TRP:CZ2	2.49	0.47
1:CX:137:GLU:O	1:CX:140:VAL:HG12	2.14	0.47
1:BH:152:TRP:HE1	1:BI:64:LYS:C	2.17	0.47
1:A2:75:ILE:HG22	1:A2:77:LEU:HD13	1.97	0.47
1:AX:117:THR:HG22	1:AY:85:THR:HG21	1.97	0.47
1:AN:117:THR:HG22	1:AO:85:THR:HG21	1.97	0.47
1:CI:117:THR:HG22	1:CJ:85:THR:HG21	1.97	0.47
1:BG:37:LEU:O	1:BG:42:VAL:HG23	2.15	0.47
1:BQ:13:LYS:HD2	1:BQ:46:ASP:OD2	2.14	0.47
1:BQ:116:THR:O	1:BR:85:THR:HB	2.14	0.47
1:CG:90:TYR:O	1:CG:94:GLU:HG2	2.14	0.47
1:AY:29:LEU:HD11	1:AY:134:LYS:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:29:LEU:HD11	1:AE:134:LYS:HB3	1.97	0.47
1:A1:13:LYS:HD2	1:A1:46:ASP:OD2	2.14	0.47
1:BE:29:LEU:HD11	1:BE:134:LYS:HB3	1.97	0.47
1:BB:106:THR:O	1:BB:107:ASP:HB3	2.15	0.47
1:BG:106:THR:O	1:BG:107:ASP:HB3	2.15	0.47
1:BJ:71:TYR:O	1:BJ:150:LYS:NZ	2.44	0.47
1:B1:97:LYS:HE3	1:B2:97:LYS:HZ3	1.78	0.47
1:CQ:100:ALA:CA	1:CR:56:PHE:HZ	2.28	0.47
1:BV:58:ILE:HG22	1:BV:58:ILE:O	2.13	0.47
1:AW:63:LYS:C	1:AW:65:MET:H	2.18	0.47
1:A2:63:LYS:C	1:A2:65:MET:H	2.18	0.47
1:CT:121:GLU:O	1:CT:125:GLU:HB2	2.14	0.47
1:AM:63:LYS:C	1:AM:65:MET:H	2.18	0.47
1:CK:121:GLU:O	1:CK:125:GLU:HG3	2.14	0.47
1:AC:63:LYS:C	1:AC:65:MET:H	2.18	0.47
1:AF:121:GLU:O	1:AF:125:GLU:HG3	2.14	0.47
1:C3:137:GLU:O	1:C3:140:VAL:HG12	2.14	0.47
1:AO:121:GLU:O	1:AO:125:GLU:HB2	2.14	0.47
1:CS:149:SER:HB3	1:CS:152:TRP:CZ2	2.49	0.47
1:BD:137:GLU:O	1:BD:140:VAL:HG12	2.14	0.47
1:BS:48:ASP:HB2	1:BS:71:TYR:CE1	2.50	0.47
1:CX:48:ASP:HB2	1:CX:71:TYR:CE1	2.50	0.47
1:AS:137:GLU:O	1:AS:140:VAL:HG12	2.14	0.47
1:AW:75:ILE:HG22	1:AW:77:LEU:HD13	1.97	0.47
1:AM:30:LEU:HA	1:AM:77:LEU:HD23	1.97	0.47
1:A2:152:TRP:HE1	1:A3:64:LYS:C	2.18	0.47
1:BX:117:THR:HG22	1:BY:85:THR:HG21	1.97	0.47
1:AS:117:THR:HG22	1:AT:85:THR:HG21	1.97	0.47
1:AV:13:LYS:HD2	1:AV:46:ASP:OD2	2.14	0.47
1:CX:66:ALA:HB2	1:CX:74:VAL:HG21	1.96	0.47
1:CO:29:LEU:HD11	1:CO:134:LYS:HB3	1.97	0.47
1:B1:13:LYS:HD2	1:B1:46:ASP:OD2	2.14	0.47
1:CZ:65:MET:HE3	1:CZ:71:TYR:CE2	2.50	0.47
1:BO:29:LEU:HD11	1:BO:134:LYS:HB3	1.97	0.47
1:CS:82:ARG:HG3	1:CS:118:GLU:OE2	2.14	0.47
1:CI:82:ARG:HG3	1:CI:118:GLU:OE2	2.14	0.47
1:CD:66:ALA:HB2	1:CD:74:VAL:HG21	1.96	0.47
1:CW:9:GLY:HA3	1:CW:12:LEU:HD12	1.97	0.47
1:C1:90:TYR:O	1:C1:94:GLU:HG2	2.14	0.47
1:CV:106:THR:O	1:CV:107:ASP:HB3	2.15	0.46
1:BV:106:THR:O	1:BV:107:ASP:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BT:71:TYR:O	1:BT:150:LYS:NZ	2.44	0.46
1:BQ:152:TRP:O	1:BQ:152:TRP:CD1	2.68	0.46
1:AM:52:VAL:CG1	1:AM:61:ILE:HD12	2.35	0.46
1:CM:38:LYS:HZ2	1:CM:44:GLU:HA	1.80	0.46
1:BZ:121:GLU:O	1:BZ:125:GLU:HG3	2.14	0.46
1:C3:149:SER:HB3	1:C3:152:TRP:CZ2	2.49	0.46
1:CM:106:THR:HG23	1:CM:108:ILE:H	1.79	0.46
1:B2:63:LYS:C	1:B2:65:MET:H	2.18	0.46
1:CS:137:GLU:O	1:CS:140:VAL:HG12	2.14	0.46
1:BJ:83:GLY:HA3	2:BJ:1001:PO4:O2	2.15	0.46
1:BY:83:GLY:HA3	2:BY:1001:PO4:O2	2.15	0.46
1:C2:30:LEU:HA	1:C2:77:LEU:HD23	1.97	0.46
1:BV:129:THR:CG2	1:BV:130:LYS:H	2.28	0.46
1:AH:30:LEU:HA	1:AH:77:LEU:HD23	1.97	0.46
1:CS:117:THR:HG22	1:CT:85:THR:HG21	1.97	0.46
1:CV:37:LEU:O	1:CV:42:VAL:HG23	2.15	0.46
1:BQ:12:LEU:HB2	1:BQ:42:VAL:HG13	1.96	0.46
1:AG:37:LEU:O	1:AG:42:VAL:HG23	2.15	0.46
1:CN:117:THR:HG22	1:CO:85:THR:HG21	1.97	0.46
1:AB:12:LEU:HB2	1:AB:42:VAL:HG13	1.96	0.46
1:AB:65:MET:HE3	1:AB:71:TYR:CZ	2.51	0.46
1:CH:104:LEU:HD13	1:CI:102:LEU:HG	1.98	0.46
1:BY:29:LEU:HD11	1:BY:134:LYS:HB3	1.97	0.46
1:AQ:116:THR:O	1:AR:85:THR:HB	2.14	0.46
1:B1:90:TYR:O	1:B1:94:GLU:HG2	2.14	0.46
1:C1:100:ALA:CA	1:C2:56:PHE:HZ	2.28	0.46
1:AB:100:ALA:CA	1:AC:56:PHE:HZ	2.28	0.46
1:CQ:58:ILE:O	1:CQ:58:ILE:HG22	2.13	0.46
1:AV:144:GLU:OE2	1:AW:20:ARG:HD2	2.14	0.46
1:CZ:125:GLU:CA	1:CZ:129:THR:OG1	2.57	0.46
1:CW:63:LYS:C	1:CW:65:MET:H	2.18	0.46
1:CN:149:SER:HB3	1:CN:152:TRP:CZ2	2.49	0.46
1:BC:106:THR:HG23	1:BC:108:ILE:H	1.79	0.46
1:C4:83:GLY:HA3	2:C4:4201:PO4:O2	2.15	0.46
1:CH:152:TRP:HE1	1:CI:64:LYS:C	2.18	0.46
1:CN:137:GLU:O	1:CN:140:VAL:HG12	2.14	0.46
1:AG:129:THR:CG2	1:AG:130:LYS:H	2.28	0.46
1:CH:75:ILE:HG22	1:CH:77:LEU:HD13	1.97	0.46
1:A1:12:LEU:HB2	1:A1:42:VAL:HG13	1.96	0.46
1:BN:117:THR:HG22	1:BO:85:THR:HG21	1.97	0.46
1:B2:104:LEU:HD13	1:B3:102:LEU:HG	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:9:GLY:HA3	1:CC:12:LEU:HD12	1.97	0.46
1:AS:82:ARG:HG3	1:AS:118:GLU:OE2	2.14	0.46
1:CW:45:ASN:HD22	1:CW:45:ASN:HA	1.64	0.46
1:BT:29:LEU:HD11	1:BT:134:LYS:HB3	1.97	0.46
1:BV:90:TYR:O	1:BV:94:GLU:HG2	2.14	0.46
1:B1:96:ALA:O	1:B1:100:ALA:HB2	2.06	0.46
1:A1:100:ALA:CA	1:A2:56:PHE:HZ	2.28	0.46
1:BH:52:VAL:CG1	1:BH:61:ILE:HD12	2.35	0.46
1:B1:144:GLU:OE2	1:B2:20:ARG:HD2	2.14	0.46
1:BH:70:LYS:HB2	1:BH:71:TYR:CD1	2.50	0.46
1:CC:63:LYS:C	1:CC:65:MET:H	2.18	0.46
1:A2:70:LYS:HB2	1:A2:71:TYR:CD1	2.50	0.46
1:CM:63:LYS:C	1:CM:65:MET:H	2.18	0.46
1:CH:70:LYS:HB2	1:CH:71:TYR:CD1	2.50	0.46
1:CF:58:ILE:H	1:CF:59:PRO:HD2	1.80	0.46
1:BC:63:LYS:C	1:BC:65:MET:H	2.18	0.46
1:BC:65:MET:HE2	1:BC:65:MET:HB3	1.51	0.46
1:B2:75:ILE:HG22	1:B2:77:LEU:HD13	1.97	0.46
1:CW:75:ILE:HG22	1:CW:77:LEU:HD13	1.97	0.46
1:AQ:129:THR:CG2	1:AQ:130:LYS:H	2.28	0.46
1:AL:129:THR:CG2	1:AL:130:LYS:H	2.28	0.46
1:CH:30:LEU:HA	1:CH:77:LEU:HD23	1.97	0.46
1:B3:117:THR:HG22	1:B4:85:THR:HG21	1.97	0.46
1:BI:117:THR:HG22	1:BJ:85:THR:HG21	1.97	0.46
1:A3:117:THR:HG22	1:A4:85:THR:HG21	1.97	0.46
1:C2:104:LEU:HD13	1:C3:102:LEU:HG	1.98	0.46
1:CQ:37:LEU:O	1:CQ:42:VAL:HG23	2.15	0.46
1:BL:37:LEU:O	1:BL:42:VAL:HG23	2.15	0.46
1:CQ:116:THR:O	1:CR:85:THR:HB	2.14	0.46
1:BQ:90:TYR:O	1:BQ:94:GLU:HG2	2.14	0.46
1:AT:29:LEU:HD11	1:AT:134:LYS:HB3	1.97	0.46
1:BV:152:TRP:O	1:BV:152:TRP:CD1	2.67	0.46
1:CQ:106:THR:O	1:CQ:107:ASP:HB3	2.15	0.46
1:AL:144:GLU:OE2	1:AM:20:ARG:HD2	2.14	0.46
1:CG:144:GLU:OE2	1:CH:20:ARG:HD2	2.14	0.46
1:C1:144:GLU:OE2	1:C2:20:ARG:HD2	2.14	0.46
1:CP:39:ARG:NH2	1:CV:144:GLU:CD	2.68	0.46
1:BX:18:VAL:HG12	1:BX:77:LEU:CB	2.37	0.46
1:CD:30:LEU:HA	1:CD:77:LEU:HD23	1.96	0.46
1:CM:70:LYS:HB2	1:CM:71:TYR:CD1	2.50	0.46
1:AC:70:LYS:HB2	1:AC:71:TYR:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:121:GLU:O	1:AP:125:GLU:HG3	2.14	0.46
1:AK:121:GLU:O	1:AK:125:GLU:HG3	2.14	0.46
1:BM:30:LEU:HA	1:BM:77:LEU:HD23	1.97	0.46
1:AC:104:LEU:HD13	1:AD:102:LEU:HG	1.98	0.46
1:AG:65:MET:HE3	1:AG:71:TYR:CZ	2.51	0.46
1:CG:13:LYS:HD2	1:CG:46:ASP:OD2	2.14	0.46
1:BJ:29:LEU:HD11	1:BJ:134:LYS:HB3	1.97	0.46
1:CX:120:ILE:HD11	1:C2:129:THR:HG21	1.97	0.46
1:CH:52:VAL:CG1	1:CH:61:ILE:HD12	2.35	0.46
1:AX:75:ILE:HG22	1:AX:77:LEU:HD13	1.98	0.46
1:BI:30:LEU:HA	1:BI:77:LEU:HD23	1.96	0.46
1:CX:75:ILE:HG22	1:CX:77:LEU:HD13	1.98	0.46
1:A3:18:VAL:HG11	1:A3:30:LEU:HD13	1.98	0.46
1:AN:75:ILE:HG22	1:AN:77:LEU:HD13	1.98	0.46
1:C3:75:ILE:HG22	1:C3:77:LEU:HD13	1.98	0.46
1:CK:58:ILE:H	1:CK:59:PRO:HD2	1.80	0.46
1:CZ:121:GLU:O	1:CZ:125:GLU:HG3	2.14	0.46
1:CE:83:GLY:HA3	2:CE:1001:PO4:O2	2.15	0.46
1:AD:137:GLU:O	1:AD:140:VAL:HG12	2.14	0.46
1:BC:75:ILE:HG22	1:BC:77:LEU:HD13	1.97	0.46
1:CM:30:LEU:HA	1:CM:77:LEU:HD23	1.97	0.46
1:AC:30:LEU:HA	1:AC:77:LEU:HD23	1.97	0.46
1:BM:75:ILE:HG22	1:BM:77:LEU:HD13	1.97	0.46
1:A1:37:LEU:O	1:A1:42:VAL:HG23	2.15	0.46
1:A1:65:MET:HE3	1:A1:71:TYR:CZ	2.50	0.46
1:B1:37:LEU:O	1:B1:42:VAL:HG23	2.15	0.46
1:AI:82:ARG:HG3	1:AI:118:GLU:OE2	2.14	0.46
1:BD:13:LYS:NZ	1:CM:13:LYS:HD3	2.30	0.46
1:CT:29:LEU:HD11	1:CT:134:LYS:HB3	1.97	0.46
1:C2:45:ASN:HA	1:C2:45:ASN:HD22	1.63	0.46
1:BF:65:MET:HE3	1:BF:71:TYR:CE2	2.50	0.46
1:AX:82:ARG:HG3	1:AX:118:GLU:OE2	2.15	0.46
1:AO:29:LEU:HD11	1:AO:134:LYS:HB3	1.97	0.46
1:BN:82:ARG:HG3	1:BN:118:GLU:OE2	2.14	0.46
1:BX:18:VAL:HG11	1:BX:30:LEU:HD13	1.98	0.46
1:BS:30:LEU:HA	1:BS:77:LEU:HD23	1.96	0.46
1:AA:58:ILE:O	1:AA:62:ALA:CB	2.64	0.46
1:BA:121:GLU:O	1:BA:125:GLU:HG3	2.14	0.46
1:AZ:58:ILE:H	1:AZ:59:PRO:HD2	1.80	0.46
1:CP:7:LEU:HD23	1:CV:40:HIS:CE1	2.51	0.46
1:BE:39:ARG:O	1:BN:7:LEU:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:129:THR:CG2	1:BB:130:LYS:H	2.28	0.46
1:B2:30:LEU:HA	1:B2:77:LEU:HD23	1.97	0.46
1:AM:75:ILE:HG22	1:AM:77:LEU:HD13	1.97	0.46
1:BD:9:GLY:HA2	1:BD:147:HIS:HE1	1.81	0.46
1:CD:117:THR:HG22	1:CE:85:THR:HG21	1.97	0.46
1:CQ:65:MET:HE3	1:CQ:71:TYR:CZ	2.51	0.46
1:BS:117:THR:HG22	1:BT:85:THR:HG21	1.97	0.46
1:CG:12:LEU:HB2	1:CG:42:VAL:HG13	1.96	0.46
1:A2:104:LEU:HD13	1:A3:102:LEU:HG	1.98	0.46
1:C3:82:ARG:HG3	1:C3:118:GLU:OE2	2.15	0.46
1:BW:9:GLY:HA3	1:BW:12:LEU:HD12	1.98	0.46
1:CM:9:GLY:HA3	1:CM:12:LEU:HD12	1.97	0.46
1:A1:90:TYR:O	1:A1:94:GLU:HG2	2.14	0.46
1:BD:82:ARG:HG3	1:BD:118:GLU:OE2	2.14	0.46
1:A4:71:TYR:O	1:A4:150:LYS:NZ	2.44	0.46
1:B3:18:VAL:HG11	1:B3:30:LEU:HD13	1.98	0.46
1:BX:75:ILE:HG22	1:BX:77:LEU:HD13	1.98	0.46
1:BI:18:VAL:HG11	1:BI:30:LEU:HD13	1.98	0.46
1:BI:75:ILE:HG22	1:BI:77:LEU:HD13	1.98	0.46
1:BS:75:ILE:HG22	1:BS:77:LEU:HD13	1.98	0.46
1:CD:75:ILE:HG22	1:CD:77:LEU:HD13	1.98	0.46
1:CK:58:ILE:O	1:CK:62:ALA:CB	2.64	0.46
1:BZ:58:ILE:O	1:BZ:62:ALA:CB	2.64	0.46
1:AK:58:ILE:O	1:AK:62:ALA:CB	2.64	0.46
1:BW:75:ILE:HG22	1:BW:77:LEU:HD13	1.97	0.46
1:AH:152:TRP:HE1	1:AI:64:LYS:C	2.17	0.46
1:CR:30:LEU:HA	1:CR:77:LEU:HD23	1.97	0.46
1:CC:75:ILE:HG22	1:CC:77:LEU:HD13	1.97	0.46
1:CN:9:GLY:HA2	1:CN:147:HIS:HE1	1.81	0.46
1:AX:9:GLY:HA2	1:AX:147:HIS:HE1	1.81	0.46
1:CX:9:GLY:HA2	1:CX:147:HIS:HE1	1.81	0.46
1:CF:65:MET:HE3	1:CF:71:TYR:CE2	2.51	0.46
1:AJ:29:LEU:HD11	1:AJ:134:LYS:HB3	1.97	0.46
1:CJ:29:LEU:HD11	1:CJ:134:LYS:HB3	1.97	0.46
1:A4:29:LEU:HD11	1:A4:134:LYS:HB3	1.97	0.46
1:AR:9:GLY:HA3	1:AR:12:LEU:HD12	1.98	0.46
1:AM:9:GLY:HA3	1:AM:12:LEU:HD12	1.97	0.46
1:BD:120:ILE:HD13	1:BR:129:THR:HG21	1.96	0.46
1:B4:71:TYR:O	1:B4:150:LYS:NZ	2.44	0.46
1:BB:97:LYS:HE3	1:BC:97:LYS:HZ3	1.78	0.46
1:CM:52:VAL:CG1	1:CM:61:ILE:HD12	2.35	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:30:LEU:HA	1:CX:77:LEU:HD23	1.96	0.46
1:C3:18:VAL:HG11	1:C3:30:LEU:HD13	1.98	0.46
1:CZ:58:ILE:O	1:CZ:58:ILE:HG22	2.11	0.46
1:CZ:58:ILE:O	1:CZ:62:ALA:CB	2.64	0.46
1:C2:63:LYS:C	1:C2:65:MET:H	2.18	0.46
1:AF:58:ILE:H	1:AF:59:PRO:HD2	1.80	0.46
1:AI:40:HIS:CE1	1:AO:7:LEU:HD23	2.51	0.46
1:BD:48:ASP:HB2	1:BD:71:TYR:CE1	2.50	0.46
1:B3:48:ASP:HB2	1:B3:71:TYR:CE1	2.50	0.46
1:CQ:129:THR:CG2	1:CQ:130:LYS:H	2.28	0.46
1:AH:75:ILE:HG22	1:AH:77:LEU:HD13	1.97	0.46
1:BX:9:GLY:HA2	1:BX:147:HIS:HE1	1.81	0.46
1:AD:9:GLY:HA2	1:AD:147:HIS:HE1	1.81	0.46
1:AR:104:LEU:HD13	1:AS:102:LEU:HG	1.98	0.46
1:AB:37:LEU:O	1:AB:42:VAL:HG23	2.15	0.46
1:AV:65:MET:HE3	1:AV:71:TYR:CZ	2.51	0.46
1:BW:104:LEU:HD13	1:BX:102:LEU:HG	1.97	0.46
1:B4:29:LEU:HD11	1:B4:134:LYS:HB3	1.97	0.46
1:A2:45:ASN:HD22	1:A2:45:ASN:HA	1.64	0.46
1:C4:29:LEU:HD11	1:C4:134:LYS:HB3	1.97	0.46
1:CH:9:GLY:HA3	1:CH:12:LEU:HD12	1.98	0.46
1:BQ:100:ALA:CA	1:BR:56:PHE:HZ	2.28	0.46
1:BD:75:ILE:HG22	1:BD:77:LEU:HD13	1.98	0.46
1:CS:75:ILE:HG22	1:CS:77:LEU:HD13	1.98	0.46
1:A3:75:ILE:HG22	1:A3:77:LEU:HD13	1.98	0.46
1:CK:58:ILE:HG22	1:CK:58:ILE:O	2.11	0.46
1:AZ:58:ILE:O	1:AZ:62:ALA:CB	2.64	0.46
1:BR:67:ASN:HA	1:BR:67:ASN:HD22	1.59	0.46
1:BX:48:ASP:HB2	1:BX:71:TYR:CE1	2.50	0.46
1:AX:7:LEU:HB3	1:A4:39:ARG:O	2.16	0.46
1:B3:9:GLY:HA2	1:B3:147:HIS:HE1	1.81	0.46
1:AI:117:THR:HG22	1:AJ:85:THR:HG21	1.97	0.46
1:CV:65:MET:HE3	1:CV:71:TYR:CZ	2.51	0.46
1:CW:104:LEU:HD13	1:CX:102:LEU:HG	1.98	0.46
1:CY:29:LEU:HD11	1:CY:134:LYS:HB3	1.97	0.46
1:BD:148:LEU:HA	1:BD:148:LEU:HD23	1.82	0.46
1:CB:90:TYR:O	1:CB:94:GLU:HG2	2.14	0.46
1:BO:109:PRO:HG3	1:BO:149:SER:CB	2.46	0.46
1:BO:71:TYR:O	1:BO:150:LYS:NZ	2.44	0.46
1:BV:100:ALA:CA	1:BW:56:PHE:HZ	2.28	0.46
1:A1:97:LYS:N	1:A1:100:ALA:HB2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:39:ARG:NH2	1:AQ:144:GLU:CD	2.68	0.46
1:CI:75:ILE:HG22	1:CI:77:LEU:HD13	1.98	0.46
1:CN:18:VAL:HG11	1:CN:30:LEU:HD13	1.98	0.46
1:CN:75:ILE:HG22	1:CN:77:LEU:HD13	1.98	0.46
1:AI:75:ILE:HG22	1:AI:77:LEU:HD13	1.98	0.46
1:BH:63:LYS:C	1:BH:65:MET:H	2.18	0.46
1:CU:58:ILE:O	1:CU:58:ILE:HG22	2.11	0.46
1:CU:58:ILE:O	1:CU:62:ALA:CB	2.64	0.46
1:BA:58:ILE:O	1:BA:62:ALA:CB	2.64	0.46
1:BP:58:ILE:H	1:BP:59:PRO:HD2	1.80	0.46
1:CF:58:ILE:O	1:CF:62:ALA:CB	2.64	0.46
1:CD:20:ARG:CZ	1:CR:39:ARG:NE	2.78	0.46
1:AB:129:THR:CG2	1:AB:130:LYS:H	2.28	0.46
1:BQ:37:LEU:O	1:BQ:42:VAL:HG23	2.15	0.46
1:AQ:65:MET:HE3	1:AQ:71:TYR:CZ	2.51	0.46
1:AC:83:GLY:HA3	2:AC:1001:PO4:O4	2.16	0.46
1:AH:9:GLY:HA3	1:AH:12:LEU:HD12	1.97	0.46
1:CR:83:GLY:HA3	2:CR:2201:PO4:O4	2.16	0.46
1:BJ:109:PRO:HG3	1:BJ:149:SER:CB	2.46	0.45
1:CB:100:ALA:CA	1:CC:56:PHE:HZ	2.28	0.45
1:BL:100:ALA:CA	1:BM:56:PHE:HZ	2.28	0.45
1:BN:75:ILE:HG22	1:BN:77:LEU:HD13	1.98	0.45
1:AD:48:ASP:HB2	1:AD:71:TYR:CE1	2.50	0.45
1:BH:75:ILE:HG22	1:BH:77:LEU:HD13	1.97	0.45
1:BW:30:LEU:HA	1:BW:77:LEU:HD23	1.97	0.45
1:A2:30:LEU:HA	1:A2:77:LEU:HD23	1.97	0.45
1:AL:65:MET:HE3	1:AL:71:TYR:CZ	2.52	0.45
1:CL:37:LEU:O	1:CL:42:VAL:HG23	2.15	0.45
1:CQ:70:LYS:O	1:CQ:70:LYS:HG2	2.17	0.45
1:CM:83:GLY:HA3	2:CM:2201:PO4:O4	2.16	0.45
1:C2:9:GLY:HA3	1:C2:12:LEU:HD12	1.98	0.45
1:AT:109:PRO:HG3	1:AT:149:SER:CB	2.46	0.45
1:BQ:97:LYS:N	1:BQ:100:ALA:HB2	2.31	0.45
1:BD:18:VAL:HG11	1:BD:30:LEU:HD13	1.98	0.45
1:BU:58:ILE:O	1:BU:58:ILE:HG22	2.11	0.45
1:BF:58:ILE:H	1:BF:59:PRO:HD2	1.80	0.45
1:CP:58:ILE:O	1:CP:62:ALA:CB	2.64	0.45
1:AM:108:ILE:O	1:AM:110:VAL:HG23	2.17	0.45
1:BC:108:ILE:O	1:BC:110:VAL:HG23	2.17	0.45
1:B1:4:GLU:CG	1:B2:51:TRP:HD1	2.29	0.45
1:AZ:7:LEU:HD12	1:AZ:7:LEU:HA	1.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:65:MET:HB3	1:BW:65:MET:HE2	1.51	0.45
1:CS:48:ASP:HB2	1:CS:71:TYR:CE1	2.50	0.45
1:CN:48:ASP:HB2	1:CN:71:TYR:CE1	2.50	0.45
1:BG:65:MET:HE3	1:BG:71:TYR:CZ	2.51	0.45
1:AH:104:LEU:HD13	1:AI:102:LEU:HG	1.98	0.45
1:AD:24:PHE:CD1	1:AR:28:LYS:HG3	2.52	0.45
1:CH:148:LEU:HA	1:CH:148:LEU:HD23	1.80	0.45
1:BR:45:ASN:HD22	1:BR:45:ASN:HA	1.63	0.45
1:C2:83:GLY:HA3	2:C2:2201:PO4:O4	2.16	0.45
1:AO:109:PRO:HG3	1:AO:149:SER:CB	2.46	0.45
1:CE:109:PRO:HG3	1:CE:149:SER:CB	2.46	0.45
1:A4:109:PRO:HG3	1:A4:149:SER:CB	2.46	0.45
1:BC:52:VAL:CG1	1:BC:61:ILE:HD12	2.35	0.45
1:CD:52:VAL:CG1	1:CD:61:ILE:HD12	2.35	0.45
1:CX:18:VAL:HG11	1:CX:30:LEU:HD13	1.98	0.45
1:BS:18:VAL:HG23	1:BS:51:TRP:CE3	2.52	0.45
1:CD:18:VAL:HG11	1:CD:30:LEU:HD13	1.98	0.45
1:AN:18:VAL:HG11	1:AN:30:LEU:HD13	1.98	0.45
1:AI:18:VAL:HG11	1:AI:30:LEU:HD13	1.98	0.45
1:BU:58:ILE:O	1:BU:62:ALA:CB	2.64	0.45
1:CU:58:ILE:H	1:CU:59:PRO:HD2	1.80	0.45
1:BF:58:ILE:O	1:BF:62:ALA:CB	2.64	0.45
1:CA:58:ILE:O	1:CA:62:ALA:CB	2.64	0.45
1:BK:58:ILE:O	1:BK:62:ALA:CB	2.64	0.45
1:CR:108:ILE:O	1:CR:110:VAL:HG23	2.17	0.45
1:BR:108:ILE:O	1:BR:110:VAL:HG23	2.17	0.45
1:BV:4:GLU:CG	1:BW:51:TRP:HD1	2.29	0.45
1:CW:30:LEU:HA	1:CW:77:LEU:HD23	1.97	0.45
1:AN:9:GLY:HA2	1:AN:147:HIS:HE1	1.81	0.45
1:CG:65:MET:HE3	1:CG:71:TYR:CZ	2.51	0.45
1:BQ:65:MET:HE3	1:BQ:71:TYR:CZ	2.50	0.45
1:BB:65:MET:HE3	1:BB:71:TYR:CE2	2.51	0.45
1:CL:70:LYS:O	1:CL:70:LYS:HG2	2.16	0.45
1:CR:104:LEU:HD13	1:CS:102:LEU:HG	1.98	0.45
1:CC:83:GLY:HA3	2:CC:1001:PO4:O4	2.16	0.45
1:CR:9:GLY:HA3	1:CR:12:LEU:HD12	1.98	0.45
1:CY:109:PRO:HG3	1:CY:149:SER:CB	2.46	0.45
1:AQ:100:ALA:CA	1:AR:56:PHE:HZ	2.28	0.45
1:CL:58:ILE:O	1:CL:58:ILE:CG2	2.65	0.45
1:AD:18:VAL:HG11	1:AD:30:LEU:HD13	1.98	0.45
1:BX:18:VAL:HG23	1:BX:51:TRP:CE3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:67:ASN:HD22	1:BH:67:ASN:HA	1.60	0.45
1:AR:30:LEU:HA	1:AR:77:LEU:HD23	1.97	0.45
1:A3:9:GLY:HA2	1:A3:147:HIS:HE1	1.81	0.45
1:CI:9:GLY:HA2	1:CI:147:HIS:HE1	1.81	0.45
1:CB:65:MET:HE3	1:CB:71:TYR:CZ	2.51	0.45
1:BC:104:LEU:HD13	1:BD:102:LEU:HG	1.98	0.45
1:B2:9:GLY:HA3	1:B2:12:LEU:HD12	1.97	0.45
1:CA:28:LYS:NZ	1:CN:28:LYS:NZ	2.65	0.45
1:AR:83:GLY:HA3	2:AR:1001:PO4:O4	2.16	0.45
1:AQ:70:LYS:O	1:AQ:70:LYS:HG2	2.16	0.45
1:BT:109:PRO:HG3	1:BT:149:SER:CB	2.46	0.45
1:CG:55:ALA:CB	1:CG:95:VAL:HG21	2.40	0.45
1:BN:18:VAL:HG23	1:BN:51:TRP:CE3	2.52	0.45
1:AF:58:ILE:O	1:AF:62:ALA:CB	2.64	0.45
1:CN:149:SER:HB3	1:CN:152:TRP:CH2	2.52	0.45
1:BS:149:SER:HB3	1:BS:152:TRP:CH2	2.52	0.45
1:BW:108:ILE:O	1:BW:110:VAL:HG23	2.17	0.45
1:AH:108:ILE:O	1:AH:110:VAL:HG23	2.17	0.45
1:CR:65:MET:HE2	1:CR:65:MET:HB3	1.52	0.45
1:BQ:6:HIS:HB3	1:BQ:147:HIS:CG	2.52	0.45
1:CD:48:ASP:HB2	1:CD:71:TYR:CE1	2.50	0.45
1:C2:75:ILE:HG22	1:C2:77:LEU:HD13	1.97	0.45
1:CD:9:GLY:HA2	1:CD:147:HIS:HE1	1.81	0.45
1:BN:9:GLY:HA2	1:BN:147:HIS:HE1	1.81	0.45
1:CM:104:LEU:HD13	1:CN:102:LEU:HG	1.98	0.45
1:AR:45:ASN:HA	1:AR:45:ASN:HD22	1.63	0.45
1:A3:148:LEU:HD23	1:A3:148:LEU:HA	1.82	0.45
1:B2:83:GLY:HA3	2:B2:1001:PO4:O4	2.16	0.45
1:B1:106:THR:O	1:B1:107:ASP:HB3	2.15	0.45
1:BY:109:PRO:HG3	1:BY:149:SER:CB	2.46	0.45
1:AV:100:ALA:CA	1:AW:56:PHE:HZ	2.28	0.45
1:BG:97:LYS:N	1:BG:100:ALA:HB2	2.31	0.45
1:CI:52:VAL:CG1	1:CI:61:ILE:HD12	2.35	0.45
1:BD:18:VAL:HG23	1:BD:51:TRP:CE3	2.52	0.45
1:AH:67:ASN:HA	1:AH:67:ASN:HD22	1.59	0.45
1:CK:58:ILE:HG21	1:CK:76:THR:OG1	2.17	0.45
1:BA:58:ILE:HG21	1:BA:76:THR:OG1	2.17	0.45
1:BP:58:ILE:HG21	1:BP:76:THR:OG1	2.17	0.45
1:B3:149:SER:HB3	1:B3:152:TRP:CH2	2.52	0.45
1:BI:149:SER:HB3	1:BI:152:TRP:CH2	2.52	0.45
1:B2:108:ILE:O	1:B2:110:VAL:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AR:108:ILE:O	1:AR:110:VAL:HG23	2.17	0.45
1:BB:4:GLU:CG	1:BC:51:TRP:HD1	2.29	0.45
1:CQ:4:GLU:CG	1:CR:51:TRP:HD1	2.29	0.45
1:CL:6:HIS:HB3	1:CL:147:HIS:CG	2.52	0.45
1:BG:6:HIS:HB3	1:BG:147:HIS:CG	2.52	0.45
1:AX:48:ASP:HB2	1:AX:71:TYR:CE1	2.50	0.45
1:CX:117:THR:HG22	1:CY:85:THR:HG21	1.97	0.45
1:AV:9:GLY:HA3	1:AV:12:LEU:HD12	1.99	0.45
1:CL:65:MET:HE3	1:CL:71:TYR:CZ	2.51	0.45
1:BQ:70:LYS:O	1:BQ:70:LYS:HG2	2.17	0.45
1:CA:22:ASN:HA	1:CN:128:GLY:O	2.17	0.45
1:AW:9:GLY:HA3	1:AW:12:LEU:HD12	1.97	0.45
1:BH:9:GLY:HA3	1:BH:12:LEU:HD12	1.98	0.45
1:AJ:109:PRO:HG3	1:AJ:149:SER:CB	2.46	0.45
1:AL:97:LYS:N	1:AL:100:ALA:HB2	2.31	0.45
1:BV:55:ALA:CB	1:BV:95:VAL:HG21	2.40	0.45
1:B3:75:ILE:HG22	1:B3:77:LEU:HD13	1.98	0.45
1:AN:18:VAL:HG23	1:AN:51:TRP:CE3	2.52	0.45
1:AI:18:VAL:HG23	1:AI:51:TRP:CE3	2.52	0.45
1:AU:58:ILE:HG21	1:AU:76:THR:OG1	2.17	0.45
1:BZ:58:ILE:HG21	1:BZ:76:THR:OG1	2.17	0.45
1:AI:149:SER:HB3	1:AI:152:TRP:CH2	2.52	0.45
1:C3:149:SER:HB3	1:C3:152:TRP:CH2	2.52	0.45
1:CD:149:SER:HB3	1:CD:152:TRP:CH2	2.52	0.45
1:BH:108:ILE:O	1:BH:110:VAL:HG23	2.16	0.45
1:BB:6:HIS:HB3	1:BB:147:HIS:CG	2.52	0.45
1:AG:6:HIS:HB3	1:AG:147:HIS:CG	2.52	0.45
1:A3:48:ASP:HB2	1:A3:71:TYR:CE1	2.50	0.45
1:C3:9:GLY:HA2	1:C3:147:HIS:HE1	1.81	0.45
1:CC:104:LEU:HD13	1:CD:102:LEU:HG	1.98	0.45
1:BL:70:LYS:O	1:BL:70:LYS:HG2	2.17	0.45
1:AH:83:GLY:HA3	2:AH:1001:PO4:O4	2.17	0.45
1:CE:29:LEU:HD11	1:CE:134:LYS:HB3	1.97	0.45
1:AZ:65:MET:HE3	1:AZ:71:TYR:CE2	2.51	0.45
1:A2:9:GLY:HA3	1:A2:12:LEU:HD12	1.98	0.45
1:CO:109:PRO:HG3	1:CO:149:SER:CB	2.47	0.45
1:C1:97:LYS:N	1:C1:100:ALA:HB2	2.31	0.45
1:AC:97:LYS:HE3	1:AD:97:LYS:NZ	2.32	0.45
1:CL:97:LYS:N	1:CL:100:ALA:HB2	2.31	0.45
1:AC:52:VAL:CG1	1:AC:61:ILE:HD12	2.35	0.45
1:AX:18:VAL:HG23	1:AX:51:TRP:CE3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:75:ILE:HD13	1:BX:139:ALA:HA	1.99	0.45
1:C3:18:VAL:HG23	1:C3:51:TRP:CE3	2.52	0.45
1:AU:58:ILE:O	1:AU:62:ALA:CB	2.64	0.45
1:AN:149:SER:HB3	1:AN:152:TRP:CH2	2.52	0.45
1:C2:108:ILE:O	1:C2:110:VAL:HG23	2.17	0.45
1:A2:108:ILE:O	1:A2:110:VAL:HG23	2.17	0.45
1:CG:4:GLU:CG	1:CH:51:TRP:HD1	2.29	0.45
1:AL:6:HIS:HB3	1:AL:147:HIS:CG	2.52	0.45
1:AV:6:HIS:HB3	1:AV:147:HIS:CG	2.52	0.45
1:AD:117:THR:HG22	1:AE:85:THR:HG21	1.97	0.45
1:CV:9:GLY:HA3	1:CV:12:LEU:HD12	1.99	0.45
1:BH:83:GLY:HA3	2:BH:1001:PO4:O4	2.16	0.45
1:AN:34:LEU:O	1:AN:38:LYS:HG3	2.17	0.45
1:BC:83:GLY:HA3	2:BC:1001:PO4:O4	2.16	0.45
1:BS:148:LEU:HD23	1:BS:148:LEU:HA	1.82	0.45
1:CW:83:GLY:HA3	2:CW:2201:PO4:O4	2.16	0.45
1:CO:53:PRO:CG	1:CO:57:GLU:CG	2.46	0.45
1:AE:109:PRO:HG3	1:AE:149:SER:CB	2.46	0.45
1:AO:71:TYR:O	1:AO:150:LYS:NZ	2.44	0.45
1:AG:97:LYS:N	1:AG:100:ALA:HB2	2.31	0.45
1:AG:55:ALA:HB1	1:AG:95:VAL:CG2	2.40	0.45
1:BR:52:VAL:CG1	1:BR:61:ILE:HD12	2.35	0.45
1:AD:18:VAL:HG23	1:AD:51:TRP:CE3	2.52	0.45
1:CC:7:LEU:CD2	1:CR:40:HIS:CE1	2.97	0.45
1:BD:75:ILE:HD13	1:BD:139:ALA:HA	1.99	0.45
1:CI:18:VAL:HG11	1:CI:30:LEU:HD13	1.98	0.45
1:CX:18:VAL:HG23	1:CX:51:TRP:CE3	2.52	0.45
1:CC:82:ARG:NH1	1:CC:82:ARG:CG	2.73	0.45
1:AA:58:ILE:HG21	1:AA:76:THR:OG1	2.17	0.45
1:CZ:58:ILE:HG21	1:CZ:76:THR:OG1	2.17	0.45
1:BP:58:ILE:O	1:BP:62:ALA:CB	2.64	0.45
1:AP:58:ILE:O	1:AP:62:ALA:CB	2.64	0.45
1:CX:149:SER:HB3	1:CX:152:TRP:CH2	2.52	0.45
1:CL:4:GLU:CG	1:CM:51:TRP:HD1	2.29	0.45
1:CA:7:LEU:HD12	1:CA:7:LEU:HA	1.84	0.45
1:AS:48:ASP:HB2	1:AS:71:TYR:CE1	2.50	0.45
1:CI:7:LEU:HD23	1:CO:40:HIS:CE1	2.52	0.45
1:B1:65:MET:HE3	1:B1:71:TYR:CZ	2.52	0.45
1:C1:65:MET:HE3	1:C1:71:TYR:CZ	2.51	0.45
1:BL:65:MET:HE3	1:BL:71:TYR:CE2	2.52	0.45
1:CG:70:LYS:O	1:CG:70:LYS:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:22:ASN:HA	1:AR:128:GLY:O	2.17	0.45
1:BD:34:LEU:O	1:BD:38:LYS:HG3	2.17	0.45
1:AX:34:LEU:O	1:AX:38:LYS:HG3	2.17	0.45
1:BW:83:GLY:HA3	2:BW:1001:PO4:O4	2.16	0.45
1:CN:34:LEU:O	1:CN:38:LYS:HG3	2.17	0.45
1:BR:9:GLY:HA3	1:BR:12:LEU:HD12	1.97	0.45
1:AI:34:LEU:O	1:AI:38:LYS:HG3	2.17	0.45
1:AF:65:MET:HE3	1:AF:71:TYR:CE2	2.52	0.45
1:CB:58:ILE:O	1:CB:58:ILE:CG2	2.65	0.45
1:AQ:97:LYS:N	1:AQ:100:ALA:HB2	2.31	0.45
1:CQ:97:LYS:N	1:CQ:100:ALA:HB2	2.31	0.45
1:BG:58:ILE:CG2	1:BG:58:ILE:O	2.65	0.45
1:BH:97:LYS:HE3	1:BI:97:LYS:NZ	2.32	0.45
1:AS:75:ILE:HG22	1:AS:77:LEU:HD13	1.98	0.45
1:CN:18:VAL:HG23	1:CN:51:TRP:CE3	2.52	0.45
1:A3:18:VAL:HG23	1:A3:51:TRP:CE3	2.52	0.45
1:CD:18:VAL:HG23	1:CD:51:TRP:CE3	2.52	0.45
1:CC:34:LEU:HD22	1:CC:38:LYS:CE	2.43	0.45
1:CU:58:ILE:HG21	1:CU:76:THR:OG1	2.17	0.45
1:AK:58:ILE:H	1:AK:59:PRO:HD2	1.80	0.45
1:BU:7:LEU:HA	1:BU:7:LEU:HD12	1.85	0.45
1:AX:149:SER:HB3	1:AX:152:TRP:CH2	2.52	0.45
1:AD:149:SER:HB3	1:AD:152:TRP:CH2	2.52	0.45
1:CW:108:ILE:O	1:CW:110:VAL:HG23	2.17	0.45
1:AA:7:LEU:HD12	1:AA:7:LEU:HA	1.84	0.45
1:CR:67:ASN:HD22	1:CR:67:ASN:HA	1.60	0.45
1:BV:6:HIS:HB3	1:BV:147:HIS:CG	2.52	0.45
1:BL:6:HIS:HB3	1:BL:147:HIS:CG	2.52	0.45
1:C3:48:ASP:HB2	1:C3:71:TYR:CE1	2.50	0.45
1:BL:129:THR:CG2	1:BL:130:LYS:H	2.28	0.45
1:BX:39:ARG:O	1:B4:7:LEU:HB3	2.17	0.45
1:AS:9:GLY:HA2	1:AS:147:HIS:HE1	1.81	0.45
1:AI:9:GLY:HA2	1:AI:147:HIS:HE1	1.81	0.45
1:BM:104:LEU:HD13	1:BN:102:LEU:HG	1.98	0.45
1:BH:104:LEU:HD13	1:BI:102:LEU:HG	1.98	0.45
1:AM:104:LEU:HD13	1:AN:102:LEU:HG	1.97	0.45
1:BG:70:LYS:O	1:BG:70:LYS:HG2	2.17	0.45
1:AM:66:ALA:HB2	1:AM:74:VAL:HG21	1.99	0.45
1:A2:83:GLY:HA3	2:A2:1001:PO4:O4	2.16	0.45
1:CH:83:GLY:HA3	2:CH:2201:PO4:O4	2.16	0.45
1:BW:45:ASN:HA	1:BW:45:ASN:HD22	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CM:66:ALA:HB2	1:CM:74:VAL:HG21	1.99	0.45
1:AT:71:TYR:O	1:AT:150:LYS:NZ	2.44	0.44
1:AW:97:LYS:HE3	1:AX:97:LYS:NZ	2.32	0.44
1:CC:97:LYS:HE3	1:CD:97:LYS:NZ	2.32	0.44
1:AQ:55:ALA:HB1	1:AQ:95:VAL:CG2	2.40	0.44
1:B1:97:LYS:N	1:B1:100:ALA:HB2	2.31	0.44
1:B1:100:ALA:CA	1:B2:56:PHE:HZ	2.28	0.44
1:A2:97:LYS:HE3	1:A3:97:LYS:NZ	2.32	0.44
1:BN:18:VAL:HG11	1:BN:30:LEU:HD13	1.98	0.44
1:AD:75:ILE:HG22	1:AD:77:LEU:HD13	1.98	0.44
1:AS:18:VAL:HG11	1:AS:30:LEU:HD13	1.98	0.44
1:AS:18:VAL:HG23	1:AS:51:TRP:CE3	2.52	0.44
1:CW:38:LYS:HZ2	1:CW:44:GLU:HA	1.81	0.44
1:BS:18:VAL:HG11	1:BS:30:LEU:HD13	1.98	0.44
1:AH:34:LEU:HD22	1:AH:38:LYS:CE	2.43	0.44
1:AR:67:ASN:HD22	1:AR:67:ASN:HA	1.59	0.44
1:BU:58:ILE:HG21	1:BU:76:THR:OG1	2.17	0.44
1:AK:58:ILE:HG21	1:AK:76:THR:OG1	2.17	0.44
1:CF:58:ILE:HG21	1:CF:76:THR:OG1	2.17	0.44
1:AW:108:ILE:O	1:AW:110:VAL:HG23	2.17	0.44
1:CM:108:ILE:O	1:CM:110:VAL:HG23	2.17	0.44
1:CN:121:GLU:O	1:CN:125:GLU:HG3	2.18	0.44
1:AQ:6:HIS:HB3	1:AQ:147:HIS:CG	2.52	0.44
1:CU:144:GLU:O	1:CU:148:LEU:HB2	2.18	0.44
1:BB:9:GLY:HA3	1:BB:12:LEU:HD12	1.99	0.44
1:CL:9:GLY:HA3	1:CL:12:LEU:HD12	1.99	0.44
1:CV:70:LYS:O	1:CV:70:LYS:HG2	2.17	0.44
1:BL:9:GLY:HA3	1:BL:12:LEU:HD12	1.99	0.44
1:BC:9:GLY:HA3	1:BC:12:LEU:HD12	1.98	0.44
1:BM:9:GLY:HA3	1:BM:12:LEU:HD12	1.97	0.44
1:BH:66:ALA:HB2	1:BH:74:VAL:HG21	1.99	0.44
1:AW:66:ALA:HB2	1:AW:74:VAL:HG21	1.99	0.44
1:B3:34:LEU:O	1:B3:38:LYS:HG3	2.17	0.44
1:AU:65:MET:HE3	1:AU:71:TYR:CE2	2.52	0.44
1:C3:34:LEU:O	1:C3:38:LYS:HG3	2.17	0.44
1:BM:83:GLY:HA3	2:BM:1001:PO4:O4	2.16	0.44
1:AC:9:GLY:HA3	1:AC:12:LEU:HD12	1.98	0.44
1:CJ:109:PRO:HG3	1:CJ:149:SER:CB	2.46	0.44
1:B4:109:PRO:HG3	1:B4:149:SER:CB	2.46	0.44
1:BC:97:LYS:HE3	1:BD:97:LYS:HZ3	1.82	0.44
1:AV:58:ILE:O	1:AV:58:ILE:CG2	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:97:LYS:N	1:BL:100:ALA:HB2	2.31	0.44
1:AL:58:ILE:O	1:AL:58:ILE:CG2	2.65	0.44
1:B2:97:LYS:HE3	1:B3:97:LYS:NZ	2.32	0.44
1:BN:75:ILE:HD13	1:BN:139:ALA:HA	1.99	0.44
1:AX:18:VAL:HG11	1:AX:30:LEU:HD13	1.98	0.44
1:BC:82:ARG:HG3	1:BC:118:GLU:OE2	2.18	0.44
1:CW:82:ARG:HG3	1:CW:118:GLU:OE2	2.17	0.44
1:CC:82:ARG:HG3	1:CC:118:GLU:OE2	2.17	0.44
1:AM:82:ARG:HG3	1:AM:118:GLU:OE2	2.17	0.44
1:AU:58:ILE:H	1:AU:59:PRO:HD2	1.80	0.44
1:AU:58:ILE:O	1:AU:62:ALA:HB2	2.17	0.44
1:AZ:58:ILE:O	1:AZ:62:ALA:HB2	2.18	0.44
1:CU:58:ILE:O	1:CU:62:ALA:HB2	2.18	0.44
1:CA:58:ILE:HG21	1:CA:76:THR:OG1	2.17	0.44
1:CF:58:ILE:O	1:CF:62:ALA:HB2	2.18	0.44
1:BK:58:ILE:O	1:BK:62:ALA:HB2	2.18	0.44
1:CH:108:ILE:O	1:CH:110:VAL:HG23	2.17	0.44
1:B1:6:HIS:HB3	1:B1:147:HIS:CG	2.52	0.44
1:BK:144:GLU:O	1:BK:148:LEU:HB2	2.18	0.44
1:AP:144:GLU:O	1:AP:148:LEU:HB2	2.18	0.44
1:CB:6:HIS:HB3	1:CB:147:HIS:CG	2.52	0.44
1:CF:144:GLU:O	1:CF:148:LEU:HB2	2.17	0.44
1:CV:6:HIS:HB3	1:CV:147:HIS:CG	2.52	0.44
1:A1:6:HIS:HB3	1:A1:147:HIS:CG	2.52	0.44
1:AI:28:LYS:NZ	1:AK:28:LYS:HZ2	2.15	0.44
1:BI:9:GLY:HA2	1:BI:147:HIS:HE1	1.81	0.44
1:CH:24:PHE:CD1	1:CU:28:LYS:HD2	2.52	0.44
1:AG:70:LYS:O	1:AG:70:LYS:HG2	2.17	0.44
1:AV:70:LYS:HG2	1:AV:70:LYS:O	2.17	0.44
1:BN:34:LEU:O	1:BN:38:LYS:HG3	2.17	0.44
1:AW:83:GLY:HA3	2:AW:201:PO4:O4	2.16	0.44
1:AM:83:GLY:HA3	2:AM:1001:PO4:O4	2.16	0.44
1:AR:97:LYS:HE3	1:AS:97:LYS:NZ	2.32	0.44
1:AB:55:ALA:CB	1:AB:95:VAL:HG21	2.40	0.44
1:CM:97:LYS:HE3	1:CN:97:LYS:NZ	2.32	0.44
1:AX:75:ILE:HD13	1:AX:139:ALA:HA	1.99	0.44
1:CI:18:VAL:HG23	1:CI:51:TRP:CE3	2.52	0.44
1:AH:82:ARG:HG3	1:AH:118:GLU:OE2	2.17	0.44
1:A3:75:ILE:HD13	1:A3:139:ALA:HA	1.99	0.44
1:CM:82:ARG:HG3	1:CM:118:GLU:OE2	2.18	0.44
1:AS:149:SER:HB3	1:AS:152:TRP:CH2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:4:GLU:CG	1:C2:51:TRP:HD1	2.29	0.44
1:BI:121:GLU:O	1:BI:125:GLU:HG3	2.18	0.44
1:A3:121:GLU:O	1:A3:125:GLU:HG3	2.18	0.44
1:AN:121:GLU:O	1:AN:125:GLU:HG3	2.17	0.44
1:B3:121:GLU:O	1:B3:125:GLU:HG3	2.18	0.44
1:AD:121:GLU:O	1:AD:125:GLU:HG3	2.18	0.44
1:BC:67:ASN:HA	1:BC:67:ASN:HD22	1.59	0.44
1:AZ:144:GLU:O	1:AZ:148:LEU:HB2	2.18	0.44
1:CQ:6:HIS:HB3	1:CQ:147:HIS:CG	2.52	0.44
1:CU:98:GLY:O	1:CU:102:LEU:HB2	2.18	0.44
1:BS:9:GLY:HA2	1:BS:147:HIS:HE1	1.81	0.44
1:BQ:9:GLY:HA3	1:BQ:12:LEU:HD12	1.99	0.44
1:AW:104:LEU:HD13	1:AX:102:LEU:HG	1.98	0.44
1:BR:104:LEU:HD13	1:BS:102:LEU:HG	1.98	0.44
1:BV:65:MET:HE3	1:BV:71:TYR:CZ	2.52	0.44
1:CH:104:LEU:CD2	1:CI:60:LEU:HA	2.48	0.44
1:A1:70:LYS:HG2	1:A1:70:LYS:O	2.17	0.44
1:BR:66:ALA:HB2	1:BR:74:VAL:HG21	1.99	0.44
1:A4:88:TYR:CD2	1:A4:88:TYR:C	2.91	0.44
1:CQ:58:ILE:CG2	1:CQ:58:ILE:O	2.65	0.44
1:CG:7:LEU:HD23	1:CU:40:HIS:CE1	2.52	0.44
1:AD:75:ILE:HD13	1:AD:139:ALA:HA	1.99	0.44
1:BI:18:VAL:HG23	1:BI:51:TRP:CE3	2.52	0.44
1:CD:75:ILE:HD13	1:CD:139:ALA:HA	1.99	0.44
1:AA:58:ILE:O	1:AA:62:ALA:HB2	2.18	0.44
1:B2:82:ARG:HG3	1:B2:118:GLU:OE2	2.18	0.44
1:A2:67:ASN:HA	1:A2:67:ASN:HD22	1.59	0.44
1:BU:58:ILE:O	1:BU:62:ALA:HB2	2.18	0.44
1:BF:58:ILE:O	1:BF:62:ALA:HB2	2.18	0.44
1:BX:149:SER:HB3	1:BX:152:TRP:CH2	2.52	0.44
1:CC:108:ILE:O	1:CC:110:VAL:HG23	2.17	0.44
1:CC:8:VAL:CG2	1:CR:8:VAL:HG13	2.48	0.44
1:C1:6:HIS:HB3	1:C1:147:HIS:CG	2.52	0.44
1:B1:129:THR:HG22	1:B1:130:LYS:N	2.33	0.44
1:AG:9:GLY:HA3	1:AG:12:LEU:HD12	1.99	0.44
1:BH:104:LEU:CD2	1:BI:60:LEU:HA	2.48	0.44
1:BB:70:LYS:HG2	1:BB:70:LYS:O	2.17	0.44
1:CS:34:LEU:O	1:CS:38:LYS:HG3	2.17	0.44
1:AY:88:TYR:CD2	1:AY:88:TYR:C	2.91	0.44
1:BN:148:LEU:HD23	1:BN:148:LEU:HA	1.82	0.44
1:AT:88:TYR:CD2	1:AT:88:TYR:C	2.91	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B2:66:ALA:HB2	1:B2:74:VAL:HG21	1.99	0.44
1:C4:109:PRO:HG3	1:C4:149:SER:CB	2.46	0.44
1:AV:97:LYS:N	1:AV:100:ALA:HB2	2.31	0.44
1:BM:97:LYS:HE3	1:BN:97:LYS:NZ	2.32	0.44
1:C1:55:ALA:CB	1:C1:95:VAL:HG21	2.40	0.44
1:AB:58:ILE:CG2	1:AB:58:ILE:O	2.65	0.44
1:BR:97:LYS:HE3	1:BS:97:LYS:NZ	2.32	0.44
1:B3:75:ILE:HD13	1:B3:139:ALA:HA	1.99	0.44
1:BI:75:ILE:HD13	1:BI:139:ALA:HA	1.99	0.44
1:BW:82:ARG:HG3	1:BW:118:GLU:OE2	2.18	0.44
1:CH:82:ARG:HG3	1:CH:118:GLU:OE2	2.17	0.44
1:BA:58:ILE:H	1:BA:59:PRO:HD2	1.80	0.44
1:BK:58:ILE:HG21	1:BK:76:THR:OG1	2.17	0.44
1:CP:58:ILE:HG21	1:CP:76:THR:OG1	2.17	0.44
1:AF:58:ILE:HG21	1:AF:76:THR:OG1	2.17	0.44
1:A3:149:SER:HB3	1:A3:152:TRP:CH2	2.52	0.44
1:AO:64:LYS:HA	1:AO:64:LYS:HD3	1.85	0.44
1:BS:121:GLU:O	1:BS:125:GLU:HG3	2.18	0.44
1:AK:144:GLU:O	1:AK:148:LEU:HB2	2.17	0.44
1:AB:6:HIS:HB3	1:AB:147:HIS:CG	2.52	0.44
1:BA:144:GLU:O	1:BA:148:LEU:HB2	2.18	0.44
1:AU:98:GLY:O	1:AU:102:LEU:HB2	2.18	0.44
1:CV:129:THR:HG22	1:CV:130:LYS:N	2.33	0.44
1:A1:9:GLY:HA3	1:A1:12:LEU:HD12	1.99	0.44
1:BC:104:LEU:CD2	1:BD:60:LEU:HA	2.48	0.44
1:C2:104:LEU:CD2	1:C3:60:LEU:HA	2.48	0.44
1:BR:83:GLY:HA3	2:BR:1001:PO4:O4	2.16	0.44
1:AJ:88:TYR:C	1:AJ:88:TYR:CD2	2.91	0.44
1:BC:66:ALA:HB2	1:BC:74:VAL:HG21	1.99	0.44
1:BU:90:TYR:O	1:BU:94:GLU:HG2	2.18	0.44
1:BE:109:PRO:HG3	1:BE:149:SER:CB	2.46	0.44
1:AY:109:PRO:HG3	1:AY:149:SER:CB	2.46	0.44
1:B1:58:ILE:O	1:B1:58:ILE:CG2	2.65	0.44
1:CL:96:ALA:O	1:CL:100:ALA:HB2	2.06	0.44
1:CH:97:LYS:HE3	1:CI:97:LYS:NZ	2.32	0.44
1:CS:75:ILE:HD13	1:CS:139:ALA:HA	1.99	0.44
1:CS:18:VAL:HG23	1:CS:51:TRP:CE3	2.52	0.44
1:CR:82:ARG:HG3	1:CR:118:GLU:OE2	2.17	0.44
1:BZ:58:ILE:H	1:BZ:59:PRO:HD2	1.80	0.44
1:CP:58:ILE:O	1:CP:62:ALA:HB2	2.18	0.44
1:AF:58:ILE:O	1:AF:62:ALA:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:45:ASN:C	1:AO:47:ILE:H	2.21	0.44
1:BX:17:VAL:HG13	1:BX:65:MET:CE	2.48	0.44
1:BY:45:ASN:C	1:BY:47:ILE:H	2.21	0.44
1:CY:106:THR:O	1:CY:107:ASP:OD1	2.36	0.44
1:C3:121:GLU:O	1:C3:125:GLU:HG3	2.18	0.44
1:AX:121:GLU:O	1:AX:125:GLU:HG3	2.18	0.44
1:CA:144:GLU:O	1:CA:148:LEU:HB2	2.18	0.44
1:CG:6:HIS:HB3	1:CG:147:HIS:CG	2.52	0.44
1:BZ:98:GLY:O	1:BZ:102:LEU:HB2	2.18	0.44
1:CP:98:GLY:O	1:CP:102:LEU:HB2	2.18	0.44
1:CK:98:GLY:O	1:CK:102:LEU:HB2	2.18	0.44
1:AP:98:GLY:O	1:AP:102:LEU:HB2	2.18	0.44
1:AZ:98:GLY:O	1:AZ:102:LEU:HB2	2.18	0.44
1:BL:129:THR:HG22	1:BL:130:LYS:N	2.33	0.44
1:BG:129:THR:CG2	1:BG:130:LYS:H	2.28	0.44
1:CS:9:GLY:HA2	1:CS:147:HIS:HE1	1.81	0.44
1:BC:28:LYS:NZ	1:BU:28:LYS:CE	2.81	0.44
1:AW:104:LEU:CD2	1:AX:60:LEU:HA	2.48	0.44
1:CG:9:GLY:HA3	1:CG:12:LEU:HD12	1.99	0.44
1:CR:104:LEU:CD2	1:CS:60:LEU:HA	2.48	0.44
1:BF:90:TYR:O	1:BF:94:GLU:HG2	2.18	0.44
1:AO:88:TYR:C	1:AO:88:TYR:CD2	2.91	0.44
1:CD:34:LEU:O	1:CD:38:LYS:HG3	2.17	0.44
1:CD:58:ILE:HB	1:CD:59:PRO:HD3	2.00	0.44
1:BL:104:LEU:HD23	1:BM:60:LEU:HD13	2.00	0.44
1:BG:104:LEU:HD23	1:BH:60:LEU:HD13	2.00	0.44
1:CT:109:PRO:HG3	1:CT:149:SER:CB	2.46	0.44
1:BB:58:ILE:O	1:BB:58:ILE:CG2	2.65	0.44
1:CQ:97:LYS:HE3	1:CR:97:LYS:HZ3	1.83	0.44
1:CW:97:LYS:HE3	1:CX:97:LYS:NZ	2.32	0.44
1:AR:52:VAL:CG1	1:AR:61:ILE:HD12	2.35	0.44
1:CS:18:VAL:HG11	1:CS:30:LEU:HD13	1.98	0.44
1:AN:75:ILE:HD13	1:AN:139:ALA:HA	1.99	0.44
1:CI:149:SER:HB3	1:CI:152:TRP:CH2	2.52	0.44
1:BD:17:VAL:HG13	1:BD:65:MET:CE	2.48	0.44
1:AC:108:ILE:O	1:AC:110:VAL:HG23	2.17	0.44
1:A3:17:VAL:HG13	1:A3:65:MET:CE	2.48	0.44
1:C4:45:ASN:C	1:C4:47:ILE:H	2.21	0.44
1:AY:45:ASN:C	1:AY:47:ILE:H	2.21	0.44
1:CX:121:GLU:O	1:CX:125:GLU:HG3	2.18	0.44
1:C4:106:THR:O	1:C4:107:ASP:OD1	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:121:GLU:O	1:CS:125:GLU:HG3	2.18	0.44
1:BP:98:GLY:O	1:BP:102:LEU:HB2	2.18	0.44
1:AA:98:GLY:O	1:AA:102:LEU:HB2	2.18	0.44
1:BU:98:GLY:O	1:BU:102:LEU:HB2	2.18	0.44
1:BF:98:GLY:O	1:BF:102:LEU:HB2	2.18	0.44
1:CQ:129:THR:HG22	1:CQ:130:LYS:N	2.33	0.44
1:BV:9:GLY:HA3	1:BV:12:LEU:HD12	1.99	0.44
1:AQ:9:GLY:HA3	1:AQ:12:LEU:HD12	1.99	0.44
1:AL:70:LYS:HG2	1:AL:70:LYS:O	2.17	0.44
1:A2:104:LEU:CD2	1:A3:60:LEU:HA	2.48	0.44
1:C1:70:LYS:HG2	1:C1:70:LYS:O	2.17	0.44
1:BV:70:LYS:O	1:BV:70:LYS:HG2	2.17	0.44
1:B1:70:LYS:O	1:B1:70:LYS:HG2	2.17	0.44
1:BZ:65:MET:HE3	1:BZ:71:TYR:CE2	2.53	0.44
1:AA:90:TYR:O	1:AA:94:GLU:HG2	2.18	0.44
1:CJ:88:TYR:C	1:CJ:88:TYR:CD2	2.91	0.44
1:CI:148:LEU:HA	1:CI:148:LEU:HD23	1.82	0.44
1:BY:88:TYR:C	1:BY:88:TYR:CD2	2.91	0.44
1:C4:88:TYR:CD2	1:C4:88:TYR:C	2.91	0.44
1:CW:148:LEU:HD23	1:CW:148:LEU:HA	1.80	0.44
1:CN:150:LYS:HG3	1:CN:150:LYS:H	1.33	0.44
1:AK:90:TYR:O	1:AK:94:GLU:HG2	2.18	0.44
1:C1:104:LEU:HD23	1:C2:60:LEU:HD13	2.00	0.44
1:CT:71:TYR:C	1:CT:150:LYS:HZ3	2.19	0.44
1:CR:97:LYS:HE3	1:CS:97:LYS:NZ	2.32	0.44
1:CV:55:ALA:HB1	1:CV:95:VAL:CG2	2.40	0.44
1:CI:75:ILE:HD13	1:CI:139:ALA:HA	1.99	0.44
1:AR:82:ARG:HG3	1:AR:118:GLU:OE2	2.18	0.44
1:CK:58:ILE:O	1:CK:62:ALA:HB2	2.18	0.44
1:BZ:58:ILE:O	1:BZ:62:ALA:HB2	2.18	0.44
1:AK:58:ILE:O	1:AK:62:ALA:HB2	2.18	0.44
1:AP:58:ILE:HG21	1:AP:76:THR:OG1	2.17	0.44
1:B3:17:VAL:HG13	1:B3:65:MET:CE	2.48	0.44
1:BJ:45:ASN:C	1:BJ:47:ILE:H	2.21	0.44
1:BT:106:THR:O	1:BT:107:ASP:OD1	2.36	0.44
1:CJ:106:THR:O	1:CJ:107:ASP:OD1	2.36	0.44
1:CD:121:GLU:O	1:CD:125:GLU:HG3	2.17	0.44
1:AA:144:GLU:O	1:AA:148:LEU:HB2	2.18	0.44
1:AD:7:LEU:HD23	1:AJ:40:HIS:CE1	2.53	0.44
1:AB:129:THR:HG22	1:AB:130:LYS:N	2.33	0.44
1:AL:9:GLY:HA3	1:AL:12:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:104:LEU:CD2	1:BS:60:LEU:HA	2.48	0.44
1:BL:65:MET:HE3	1:BL:71:TYR:CZ	2.52	0.44
1:AH:66:ALA:HB2	1:AH:74:VAL:HG21	1.99	0.44
1:BS:34:LEU:O	1:BS:38:LYS:HG3	2.17	0.44
1:A3:34:LEU:O	1:A3:38:LYS:HG3	2.17	0.44
1:CM:45:ASN:HD22	1:CM:45:ASN:HA	1.63	0.44
1:CR:45:ASN:HD22	1:CR:45:ASN:HA	1.63	0.44
1:BN:58:ILE:HB	1:BN:59:PRO:HD3	2.00	0.44
1:CC:66:ALA:HB2	1:CC:74:VAL:HG21	1.99	0.44
1:CX:34:LEU:O	1:CX:38:LYS:HG3	2.17	0.44
1:BI:34:LEU:O	1:BI:38:LYS:HG3	2.17	0.44
1:BV:104:LEU:HD23	1:BW:60:LEU:HD13	2.00	0.44
1:BC:97:LYS:HE3	1:BD:97:LYS:NZ	2.32	0.44
1:BQ:58:ILE:O	1:BQ:58:ILE:CG2	2.65	0.44
1:CG:100:ALA:CA	1:CH:56:PHE:HZ	2.28	0.44
1:A1:97:LYS:HA	1:A1:100:ALA:HB3	2.00	0.44
1:A2:52:VAL:CG1	1:A2:61:ILE:HD12	2.35	0.44
1:B3:18:VAL:HG23	1:B3:51:TRP:CE3	2.52	0.44
1:CX:75:ILE:HD13	1:CX:139:ALA:HA	1.99	0.44
1:BS:75:ILE:HD13	1:BS:139:ALA:HA	1.99	0.44
1:A2:82:ARG:HG3	1:A2:118:GLU:OE2	2.18	0.44
1:AW:65:MET:HE2	1:AW:65:MET:HB3	1.79	0.44
1:BA:58:ILE:O	1:BA:62:ALA:HB2	2.18	0.44
1:AP:58:ILE:H	1:AP:59:PRO:HD2	1.80	0.44
1:AP:58:ILE:O	1:AP:62:ALA:HB2	2.18	0.44
1:CS:149:SER:HB3	1:CS:152:TRP:CH2	2.52	0.44
1:AT:45:ASN:C	1:AT:47:ILE:H	2.21	0.44
1:CD:17:VAL:HG13	1:CD:65:MET:CE	2.48	0.44
1:AS:17:VAL:HG13	1:AS:65:MET:CE	2.48	0.44
1:BN:17:VAL:HG13	1:BN:65:MET:CE	2.48	0.44
1:BE:106:THR:O	1:BE:107:ASP:OD1	2.36	0.44
1:AY:106:THR:O	1:AY:107:ASP:OD1	2.36	0.44
1:BP:144:GLU:O	1:BP:148:LEU:HB2	2.18	0.44
1:AG:129:THR:HG22	1:AG:130:LYS:N	2.33	0.44
1:B1:65:MET:HE3	1:B1:71:TYR:CE2	2.53	0.44
1:CV:13:LYS:HG2	1:CV:70:LYS:O	2.18	0.44
1:B2:104:LEU:CD2	1:B3:60:LEU:HA	2.48	0.44
1:CB:13:LYS:HG2	1:CB:70:LYS:O	2.18	0.44
1:CQ:13:LYS:HG2	1:CQ:70:LYS:O	2.18	0.44
1:CI:34:LEU:O	1:CI:38:LYS:HG3	2.17	0.44
1:AP:90:TYR:O	1:AP:94:GLU:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:90:TYR:O	1:BP:94:GLU:HG2	2.18	0.44
1:AD:58:ILE:HB	1:AD:59:PRO:HD3	2.00	0.44
1:A3:58:ILE:HB	1:A3:59:PRO:HD3	2.00	0.44
1:AZ:51:TRP:O	1:A4:148:LEU:HD11	2.18	0.44
1:AS:34:LEU:O	1:AS:38:LYS:HG3	2.17	0.44
1:AF:90:TYR:O	1:AF:94:GLU:HG2	2.18	0.44
1:AQ:13:LYS:HG2	1:AQ:70:LYS:O	2.18	0.43
1:AO:108:ILE:CG1	1:AO:150:LYS:HE3	2.42	0.43
1:CQ:104:LEU:HD23	1:CR:60:LEU:HD13	2.00	0.43
1:AH:97:LYS:HE3	1:AI:97:LYS:NZ	2.32	0.43
1:AM:97:LYS:HE3	1:AN:97:LYS:NZ	2.32	0.43
1:BV:97:LYS:HA	1:BV:100:ALA:HB3	2.00	0.43
1:CN:75:ILE:HD13	1:CN:139:ALA:HA	1.99	0.43
1:BC:82:ARG:NH1	1:BC:82:ARG:CG	2.73	0.43
1:CA:58:ILE:O	1:CA:62:ALA:HB2	2.18	0.43
1:BK:58:ILE:H	1:BK:59:PRO:HD2	1.80	0.43
1:BD:149:SER:HB3	1:BD:152:TRP:CH2	2.52	0.43
1:CI:17:VAL:HG13	1:CI:65:MET:CE	2.48	0.43
1:CE:106:THR:O	1:CE:107:ASP:OD1	2.36	0.43
1:BY:106:THR:O	1:BY:107:ASP:C	2.57	0.43
1:BD:121:GLU:O	1:BD:125:GLU:HG3	2.18	0.43
1:BX:121:GLU:O	1:BX:125:GLU:HG3	2.18	0.43
1:CK:144:GLU:O	1:CK:148:LEU:HB2	2.18	0.43
1:BZ:144:GLU:O	1:BZ:148:LEU:HB2	2.18	0.43
1:AF:144:GLU:O	1:AF:148:LEU:HB2	2.18	0.43
1:CZ:98:GLY:O	1:CZ:102:LEU:HB2	2.18	0.43
1:BK:98:GLY:O	1:BK:102:LEU:HB2	2.18	0.43
1:A1:129:THR:HG22	1:A1:130:LYS:N	2.33	0.43
1:AQ:129:THR:HG22	1:AQ:130:LYS:N	2.33	0.43
1:C1:9:GLY:HA3	1:C1:12:LEU:HD12	1.99	0.43
1:CB:70:LYS:O	1:CB:70:LYS:HG2	2.16	0.43
1:AV:13:LYS:HG2	1:AV:70:LYS:O	2.18	0.43
1:BY:90:TYR:O	1:BY:94:GLU:HG2	2.18	0.43
1:BZ:90:TYR:O	1:BZ:94:GLU:HG2	2.18	0.43
1:BJ:88:TYR:CD2	1:BJ:88:TYR:C	2.91	0.43
1:CP:51:TRP:O	1:CT:148:LEU:HD11	2.18	0.43
1:CX:58:ILE:HB	1:CX:59:PRO:HD3	2.00	0.43
1:CU:90:TYR:O	1:CU:94:GLU:HG2	2.18	0.43
1:A1:104:LEU:HD23	1:A2:60:LEU:HD13	2.00	0.43
1:CG:104:LEU:HD23	1:CH:60:LEU:HD13	2.00	0.43
1:CO:65:MET:HE3	1:CO:71:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:100:ALA:CA	1:BC:56:PHE:HZ	2.28	0.43
1:AG:100:ALA:CA	1:AH:56:PHE:HZ	2.28	0.43
1:CG:55:ALA:HB1	1:CG:95:VAL:CG2	2.40	0.43
1:CG:58:ILE:CG2	1:CG:58:ILE:O	2.65	0.43
1:C2:82:ARG:HG3	1:C2:118:GLU:OE2	2.18	0.43
1:CC:67:ASN:HA	1:CC:67:ASN:HD22	1.59	0.43
1:BM:108:ILE:O	1:BM:110:VAL:HG23	2.17	0.43
1:CY:15:GLY:O	1:CY:74:VAL:HA	2.18	0.43
1:BI:17:VAL:HG13	1:BI:65:MET:CE	2.48	0.43
1:AJ:106:THR:O	1:AJ:107:ASP:OD1	2.36	0.43
1:AI:121:GLU:O	1:AI:125:GLU:HG3	2.18	0.43
1:CZ:144:GLU:O	1:CZ:148:LEU:HB2	2.18	0.43
1:CA:98:GLY:O	1:CA:102:LEU:HB2	2.18	0.43
1:CB:129:THR:CG2	1:CB:130:LYS:H	2.28	0.43
1:BG:129:THR:HG22	1:BG:130:LYS:N	2.33	0.43
1:BF:28:LYS:HD2	1:BR:24:PHE:CE1	2.53	0.43
1:BM:104:LEU:CD2	1:BN:60:LEU:HA	2.48	0.43
1:BW:104:LEU:CD2	1:BX:60:LEU:HA	2.48	0.43
1:AB:70:LYS:HG2	1:AB:70:LYS:O	2.17	0.43
1:CL:13:LYS:HG2	1:CL:70:LYS:O	2.18	0.43
1:B1:13:LYS:HG2	1:B1:70:LYS:O	2.18	0.43
1:BI:58:ILE:HB	1:BI:59:PRO:HD3	2.00	0.43
1:B4:90:TYR:O	1:B4:94:GLU:HG2	2.18	0.43
1:CE:90:TYR:O	1:CE:94:GLU:HG2	2.18	0.43
1:CF:90:TYR:O	1:CF:94:GLU:HG2	2.18	0.43
1:BE:88:TYR:CD2	1:BE:88:TYR:C	2.91	0.43
1:BK:90:TYR:O	1:BK:94:GLU:HG2	2.18	0.43
1:CZ:90:TYR:O	1:CZ:94:GLU:HG2	2.18	0.43
1:C2:66:ALA:HB2	1:C2:74:VAL:HG21	1.99	0.43
1:CU:65:MET:HE3	1:CU:71:TYR:CE2	2.53	0.43
1:AE:90:TYR:O	1:AE:94:GLU:HG2	2.18	0.43
1:AI:58:ILE:HB	1:AI:59:PRO:HD3	2.00	0.43
1:A2:125:GLU:HA	1:A2:129:THR:HB	2.01	0.43
1:CL:104:LEU:HD23	1:CM:60:LEU:HD13	2.00	0.43
1:CG:97:LYS:N	1:CG:100:ALA:HB2	2.31	0.43
1:CV:58:ILE:CG2	1:CV:58:ILE:O	2.65	0.43
1:CV:97:LYS:HA	1:CV:100:ALA:HB3	2.00	0.43
1:A1:58:ILE:O	1:A1:58:ILE:CG2	2.65	0.43
1:A1:55:ALA:CB	1:A1:95:VAL:HG21	2.40	0.43
1:BM:82:ARG:HG3	1:BM:118:GLU:OE2	2.17	0.43
1:BF:58:ILE:HG21	1:BF:76:THR:OG1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BN:149:SER:HB3	1:BN:152:TRP:CH2	2.52	0.43
1:BQ:129:THR:HG22	1:BQ:130:LYS:N	2.33	0.43
1:BF:7:LEU:HA	1:BF:7:LEU:HD12	1.84	0.43
1:AX:17:VAL:HG13	1:AX:65:MET:CE	2.48	0.43
1:C4:15:GLY:O	1:C4:74:VAL:HA	2.19	0.43
1:BJ:106:THR:O	1:BJ:107:ASP:OD1	2.36	0.43
1:BO:106:THR:O	1:BO:107:ASP:OD1	2.36	0.43
1:AU:7:LEU:HA	1:AU:7:LEU:HD12	1.84	0.43
1:BU:144:GLU:O	1:BU:148:LEU:HB2	2.18	0.43
1:CB:9:GLY:HA3	1:CB:12:LEU:HD12	1.99	0.43
1:AC:104:LEU:CD2	1:AD:60:LEU:HA	2.48	0.43
1:CC:104:LEU:CD2	1:CD:60:LEU:HA	2.48	0.43
1:BE:90:TYR:O	1:BE:94:GLU:HG2	2.18	0.43
1:AK:51:TRP:O	1:AO:148:LEU:HD11	2.18	0.43
1:AA:51:TRP:O	1:AE:148:LEU:HD11	2.18	0.43
1:AR:66:ALA:HB2	1:AR:74:VAL:HG21	1.99	0.43
1:AZ:90:TYR:O	1:AZ:94:GLU:HG2	2.18	0.43
1:AA:65:MET:HE3	1:AA:71:TYR:CE2	2.53	0.43
1:CK:51:TRP:O	1:CO:148:LEU:HD11	2.18	0.43
1:AU:90:TYR:O	1:AU:94:GLU:HG2	2.18	0.43
1:BT:90:TYR:O	1:BT:94:GLU:HG2	2.18	0.43
1:CA:65:MET:HE3	1:CA:71:TYR:CE2	2.54	0.43
1:BQ:104:LEU:HD23	1:BR:60:LEU:HD13	2.00	0.43
1:AT:65:MET:HE3	1:AT:71:TYR:CE2	2.54	0.43
1:BB:97:LYS:HA	1:BB:100:ALA:HB3	2.00	0.43
1:AH:97:LYS:HE3	1:AI:97:LYS:HZ1	1.83	0.43
1:BL:58:ILE:O	1:BL:58:ILE:CG2	2.65	0.43
1:C2:97:LYS:HE3	1:C3:97:LYS:NZ	2.32	0.43
1:AQ:58:ILE:O	1:AQ:58:ILE:CG2	2.65	0.43
1:CQ:55:ALA:HB1	1:CQ:95:VAL:CG2	2.40	0.43
1:AS:75:ILE:HD13	1:AS:139:ALA:HA	1.99	0.43
1:BI:75:ILE:HG22	1:BI:77:LEU:CD1	2.48	0.43
1:CI:75:ILE:HG22	1:CI:77:LEU:CD1	2.49	0.43
1:AW:82:ARG:HG3	1:AW:118:GLU:OE2	2.17	0.43
1:AI:75:ILE:HD13	1:AI:139:ALA:HA	1.99	0.43
1:C2:34:LEU:HD22	1:C2:38:LYS:CE	2.43	0.43
1:CZ:58:ILE:O	1:CZ:62:ALA:HB2	2.18	0.43
1:CU:7:LEU:HD12	1:CU:7:LEU:HA	1.84	0.43
1:CN:17:VAL:HG13	1:CN:65:MET:CE	2.48	0.43
1:C3:17:VAL:HG13	1:C3:65:MET:CE	2.48	0.43
1:CS:17:VAL:HG13	1:CS:65:MET:CE	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CX:17:VAL:HG13	1:CX:65:MET:CE	2.48	0.43
1:CT:106:THR:O	1:CT:107:ASP:OD1	2.36	0.43
1:A4:106:THR:O	1:A4:107:ASP:C	2.57	0.43
1:AO:106:THR:O	1:AO:107:ASP:C	2.57	0.43
1:BN:121:GLU:O	1:BN:125:GLU:HG3	2.18	0.43
1:AS:121:GLU:O	1:AS:125:GLU:HG3	2.17	0.43
1:CF:98:GLY:O	1:CF:102:LEU:HB2	2.18	0.43
1:BN:48:ASP:HB2	1:BN:71:TYR:CE1	2.50	0.43
1:BV:129:THR:HG22	1:BV:130:LYS:N	2.33	0.43
1:CG:129:THR:HG22	1:CG:130:LYS:N	2.33	0.43
1:AB:9:GLY:HA3	1:AB:12:LEU:HD12	1.99	0.43
1:BB:65:MET:HE3	1:BB:71:TYR:CZ	2.53	0.43
1:AL:13:LYS:HG2	1:AL:70:LYS:O	2.18	0.43
1:C1:13:LYS:HG2	1:C1:70:LYS:O	2.18	0.43
1:CT:15:GLY:O	1:CT:74:VAL:HA	2.19	0.43
1:B4:88:TYR:CD2	1:B4:88:TYR:C	2.91	0.43
1:BO:88:TYR:CD2	1:BO:88:TYR:C	2.91	0.43
1:CA:90:TYR:O	1:CA:94:GLU:HG2	2.18	0.43
1:A2:66:ALA:HB2	1:A2:74:VAL:HG21	1.99	0.43
1:BT:15:GLY:O	1:BT:74:VAL:HA	2.18	0.43
1:CR:125:GLU:HA	1:CR:129:THR:HB	2.01	0.43
1:BM:125:GLU:HA	1:BM:129:THR:HB	2.01	0.43
1:AG:104:LEU:HD23	1:AH:60:LEU:HD13	2.00	0.43
1:CB:104:LEU:HD23	1:CC:60:LEU:HD13	2.00	0.43
1:CT:71:TYR:O	1:CT:150:LYS:NZ	2.44	0.43
1:AB:97:LYS:N	1:AB:100:ALA:HB2	2.31	0.43
1:BG:97:LYS:HA	1:BG:100:ALA:HB3	2.00	0.43
1:CV:100:ALA:CA	1:CW:56:PHE:HZ	2.28	0.43
1:C3:52:VAL:CG1	1:C3:61:ILE:HD12	2.35	0.43
1:BH:82:ARG:HG3	1:BH:118:GLU:OE2	2.18	0.43
1:AC:82:ARG:HG3	1:AC:118:GLU:OE2	2.17	0.43
1:BP:58:ILE:O	1:BP:62:ALA:HB2	2.18	0.43
1:CT:106:THR:O	1:CT:107:ASP:C	2.57	0.43
1:BY:106:THR:O	1:BY:107:ASP:OD1	2.36	0.43
1:C4:106:THR:O	1:C4:107:ASP:C	2.57	0.43
1:AT:106:THR:O	1:AT:107:ASP:OD1	2.36	0.43
1:AU:144:GLU:O	1:AU:148:LEU:HB2	2.18	0.43
1:CP:144:GLU:O	1:CP:148:LEU:HB2	2.18	0.43
1:BA:98:GLY:O	1:BA:102:LEU:HB2	2.18	0.43
1:AF:98:GLY:O	1:AF:102:LEU:HB2	2.18	0.43
1:AK:98:GLY:O	1:AK:102:LEU:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:129:THR:HG22	1:BB:130:LYS:N	2.33	0.43
1:BY:7:LEU:HD11	1:BY:140:VAL:HG22	2.01	0.43
1:CO:7:LEU:HD11	1:CO:140:VAL:HG22	2.01	0.43
1:AE:7:LEU:HD11	1:AE:140:VAL:HG22	2.01	0.43
1:BQ:13:LYS:HG2	1:BQ:70:LYS:O	2.18	0.43
1:BA:51:TRP:O	1:BE:148:LEU:HD11	2.18	0.43
1:BX:34:LEU:O	1:BX:38:LYS:HG3	2.17	0.43
1:BE:15:GLY:O	1:BE:74:VAL:HA	2.18	0.43
1:BU:51:TRP:O	1:BY:148:LEU:HD11	2.18	0.43
1:BE:21:PHE:O	1:BE:22:ASN:HB2	2.19	0.43
1:CR:66:ALA:HB2	1:CR:74:VAL:HG21	2.00	0.43
1:AF:51:TRP:O	1:AJ:148:LEU:HD11	2.18	0.43
1:CT:88:TYR:CD2	1:CT:88:TYR:C	2.91	0.43
1:CO:88:TYR:C	1:CO:88:TYR:CD2	2.91	0.43
1:BW:66:ALA:HB2	1:BW:74:VAL:HG21	2.00	0.43
1:AM:125:GLU:HA	1:AM:129:THR:HB	2.01	0.43
1:CC:125:GLU:HA	1:CC:129:THR:HB	2.01	0.43
1:AL:104:LEU:HD23	1:AM:60:LEU:HD13	2.00	0.43
1:AB:104:LEU:HD23	1:AC:60:LEU:HD13	2.00	0.43
1:AL:97:LYS:HE3	1:AM:97:LYS:HZ3	1.83	0.43
1:C1:55:ALA:HB1	1:C1:95:VAL:CG2	2.40	0.43
1:CP:39:ARG:NH1	1:CV:7:LEU:HD22	2.33	0.43
1:CX:75:ILE:HG22	1:CX:77:LEU:CD1	2.48	0.43
1:BR:82:ARG:HG3	1:BR:118:GLU:OE2	2.18	0.43
1:AA:58:ILE:H	1:AA:59:PRO:HD2	1.80	0.43
1:BE:45:ASN:C	1:BE:47:ILE:H	2.21	0.43
1:CT:64:LYS:HD3	1:CT:64:LYS:HA	1.85	0.43
1:B4:45:ASN:C	1:B4:47:ILE:H	2.21	0.43
1:BQ:4:GLU:CG	1:BR:51:TRP:HD1	2.29	0.43
1:CB:4:GLU:CG	1:CC:51:TRP:HD1	2.29	0.43
1:AO:106:THR:O	1:AO:107:ASP:OD1	2.36	0.43
1:CO:106:THR:O	1:CO:107:ASP:OD1	2.36	0.43
1:BF:144:GLU:O	1:BF:148:LEU:HB2	2.18	0.43
1:AD:7:LEU:HB3	1:AJ:39:ARG:O	2.19	0.43
1:AV:129:THR:HG22	1:AV:130:LYS:N	2.33	0.43
1:AR:104:LEU:CD2	1:AS:60:LEU:HA	2.48	0.43
1:AH:104:LEU:CD2	1:AI:60:LEU:HA	2.48	0.43
1:CJ:21:PHE:O	1:CJ:22:ASN:HB2	2.19	0.43
1:AU:51:TRP:O	1:AY:148:LEU:HD11	2.19	0.43
1:BJ:90:TYR:O	1:BJ:94:GLU:HG2	2.18	0.43
1:CE:21:PHE:O	1:CE:22:ASN:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:51:TRP:O	1:C4:148:LEU:HD11	2.18	0.43
1:AT:15:GLY:O	1:AT:74:VAL:HA	2.18	0.43
1:AC:66:ALA:HB2	1:AC:74:VAL:HG21	1.99	0.43
1:CQ:24:PHE:CD1	1:CV:28:LYS:HG3	2.53	0.43
1:CY:88:TYR:CD2	1:CY:88:TYR:C	2.91	0.43
1:BM:66:ALA:HB2	1:BM:74:VAL:HG21	1.99	0.43
1:CF:51:TRP:O	1:CJ:148:LEU:HD11	2.19	0.43
1:C2:125:GLU:HA	1:C2:129:THR:HB	2.01	0.43
1:CJ:108:ILE:CG1	1:CJ:150:LYS:HE3	2.42	0.43
1:CJ:65:MET:HE3	1:CJ:71:TYR:CE2	2.54	0.43
1:BV:58:ILE:CG2	1:BV:58:ILE:O	2.65	0.43
1:AM:38:LYS:HZ2	1:AM:44:GLU:HA	1.83	0.43
1:AX:75:ILE:HG22	1:AX:77:LEU:CD1	2.49	0.43
1:CZ:58:ILE:H	1:CZ:59:PRO:HD2	1.80	0.43
1:AZ:58:ILE:HG21	1:AZ:76:THR:OG1	2.17	0.43
1:AD:17:VAL:HG13	1:AD:65:MET:CE	2.48	0.43
1:BT:45:ASN:C	1:BT:47:ILE:H	2.21	0.43
1:AI:17:VAL:HG13	1:AI:65:MET:CE	2.48	0.43
1:BL:4:GLU:CG	1:BM:51:TRP:HD1	2.29	0.43
1:AO:7:LEU:HD11	1:AO:140:VAL:HG22	2.01	0.43
1:B2:18:VAL:HA	1:B2:77:LEU:O	2.19	0.43
1:BG:9:GLY:HA3	1:BG:12:LEU:HD12	1.99	0.43
1:BL:13:LYS:HG2	1:BL:70:LYS:O	2.18	0.43
1:AY:90:TYR:O	1:AY:94:GLU:HG2	2.18	0.43
1:BK:51:TRP:O	1:BO:148:LEU:HD11	2.18	0.43
1:C4:7:LEU:HD11	1:C4:140:VAL:HG22	2.01	0.43
1:BO:15:GLY:O	1:BO:74:VAL:HA	2.19	0.43
1:BT:88:TYR:C	1:BT:88:TYR:CD2	2.91	0.43
1:CS:150:LYS:H	1:CS:150:LYS:HG3	1.33	0.43
1:C2:148:LEU:HD23	1:C2:148:LEU:HA	1.80	0.43
1:AW:45:ASN:HA	1:AW:45:ASN:HD22	1.64	0.43
1:CO:21:PHE:O	1:CO:22:ASN:HB2	2.19	0.43
1:CJ:90:TYR:O	1:CJ:94:GLU:HG2	2.18	0.43
1:BX:58:ILE:HB	1:BX:59:PRO:HD3	2.00	0.43
1:AO:90:TYR:O	1:AO:94:GLU:HG2	2.18	0.43
1:AH:125:GLU:HA	1:AH:129:THR:HB	2.01	0.43
1:AO:65:MET:HE3	1:AO:71:TYR:CE2	2.54	0.43
1:BE:65:MET:HE3	1:BE:71:TYR:CE2	2.53	0.43
1:CL:97:LYS:HA	1:CL:100:ALA:HB3	2.00	0.43
1:CN:75:ILE:HG22	1:CN:77:LEU:CD1	2.49	0.43
1:AN:75:ILE:HG22	1:AN:77:LEU:CD1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C3:75:ILE:HG22	1:C3:77:LEU:CD1	2.49	0.43
1:AI:75:ILE:HG22	1:AI:77:LEU:CD1	2.49	0.43
1:CE:45:ASN:C	1:CE:47:ILE:H	2.21	0.43
1:AE:106:THR:O	1:AE:107:ASP:OD1	2.36	0.43
1:A4:106:THR:O	1:A4:107:ASP:OD1	2.36	0.43
1:BR:18:VAL:HA	1:BR:77:LEU:O	2.19	0.43
1:AC:18:VAL:HA	1:AC:77:LEU:O	2.19	0.43
1:CW:18:VAL:HA	1:CW:77:LEU:O	2.19	0.43
1:CC:18:VAL:HA	1:CC:77:LEU:O	2.19	0.43
1:B4:7:LEU:HD11	1:B4:140:VAL:HG22	2.01	0.43
1:CT:8:VAL:CG2	1:C3:8:VAL:HG13	2.48	0.43
1:AB:13:LYS:HG2	1:AB:70:LYS:O	2.18	0.43
1:CQ:9:GLY:HA3	1:CQ:12:LEU:HD12	1.99	0.43
1:BO:90:TYR:O	1:BO:94:GLU:HG2	2.18	0.43
1:AD:34:LEU:O	1:AD:38:LYS:HG3	2.17	0.43
1:CI:128:GLY:O	1:CK:22:ASN:HA	2.19	0.43
1:AJ:90:TYR:O	1:AJ:94:GLU:HG2	2.18	0.43
1:CE:88:TYR:CD2	1:CE:88:TYR:C	2.91	0.43
1:AT:90:TYR:O	1:AT:94:GLU:HG2	2.18	0.43
1:BP:51:TRP:O	1:BT:148:LEU:HD11	2.18	0.43
1:AJ:21:PHE:O	1:AJ:22:ASN:HB2	2.19	0.43
1:C3:58:ILE:HB	1:C3:59:PRO:HD3	2.00	0.43
1:CK:90:TYR:O	1:CK:94:GLU:HG2	2.18	0.43
1:BB:55:ALA:HB1	1:BB:95:VAL:CG2	2.40	0.43
1:AG:97:LYS:HA	1:AG:100:ALA:HB3	2.00	0.43
1:CL:100:ALA:CA	1:CM:56:PHE:HZ	2.28	0.43
1:CV:97:LYS:N	1:CV:100:ALA:HB2	2.31	0.43
1:AD:75:ILE:HG22	1:AD:77:LEU:CD1	2.49	0.43
1:BX:75:ILE:HG22	1:BX:77:LEU:CD1	2.49	0.43
1:BH:34:LEU:HD22	1:BH:38:LYS:CE	2.43	0.43
1:AU:58:ILE:HG22	1:AU:58:ILE:O	2.11	0.43
1:BG:120:ILE:CD1	1:BQ:125:GLU:HG2	2.49	0.43
1:BO:45:ASN:C	1:BO:47:ILE:H	2.21	0.43
1:AE:45:ASN:C	1:AE:47:ILE:H	2.21	0.43
1:CI:121:GLU:O	1:CI:125:GLU:HG3	2.18	0.43
1:CT:7:LEU:HD11	1:CT:140:VAL:HG22	2.01	0.43
1:CO:106:THR:O	1:CO:107:ASP:C	2.57	0.43
1:A2:18:VAL:HA	1:A2:77:LEU:O	2.19	0.43
1:BE:7:LEU:HD11	1:BE:140:VAL:HG22	2.01	0.43
1:B1:9:GLY:HA3	1:B1:12:LEU:HD12	1.99	0.43
1:BB:13:LYS:HG2	1:BB:70:LYS:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:58:ILE:HB	1:AS:59:PRO:HD3	2.00	0.43
1:BA:90:TYR:O	1:BA:94:GLU:HG2	2.18	0.43
1:BZ:51:TRP:O	1:B4:148:LEU:HD11	2.19	0.43
1:CY:90:TYR:O	1:CY:94:GLU:HG2	2.18	0.43
1:AY:21:PHE:O	1:AY:22:ASN:HB2	2.19	0.43
1:BI:150:LYS:H	1:BI:150:LYS:HG3	1.33	0.43
1:AW:148:LEU:HD23	1:AW:148:LEU:HA	1.80	0.43
1:CW:28:LYS:HZ1	1:C3:28:LYS:NZ	2.16	0.43
1:B2:125:GLU:HA	1:B2:129:THR:HB	2.01	0.43
1:AQ:104:LEU:HD23	1:AR:60:LEU:HD13	2.00	0.43
1:C1:97:LYS:HA	1:C1:100:ALA:HB3	2.00	0.43
1:AQ:97:LYS:HA	1:AQ:100:ALA:HB3	2.00	0.43
1:AQ:55:ALA:CB	1:AQ:95:VAL:HG21	2.40	0.43
1:AB:97:LYS:HA	1:AB:100:ALA:HB3	2.00	0.43
1:CQ:55:ALA:CB	1:CQ:95:VAL:HG21	2.40	0.43
1:A1:97:LYS:HE3	1:A2:97:LYS:HZ1	1.82	0.43
1:BD:75:ILE:HG22	1:BD:77:LEU:CD1	2.49	0.43
1:BS:75:ILE:HG22	1:BS:77:LEU:CD1	2.49	0.43
1:CD:75:ILE:HG22	1:CD:77:LEU:CD1	2.49	0.43
1:C3:75:ILE:HD13	1:C3:139:ALA:HA	1.99	0.43
1:AO:15:GLY:O	1:AO:74:VAL:HA	2.19	0.43
1:CY:45:ASN:C	1:CY:47:ILE:H	2.21	0.43
1:BS:17:VAL:HG13	1:BS:65:MET:CE	2.48	0.43
1:AJ:15:GLY:O	1:AJ:74:VAL:HA	2.18	0.43
1:CY:106:THR:O	1:CY:107:ASP:C	2.57	0.43
1:AJ:106:THR:O	1:AJ:107:ASP:C	2.57	0.43
1:BE:106:THR:O	1:BE:107:ASP:C	2.57	0.43
1:BE:40:HIS:CE1	1:BN:7:LEU:HD23	2.54	0.43
1:AN:48:ASP:HB2	1:AN:71:TYR:CE1	2.50	0.43
1:AW:18:VAL:HA	1:AW:77:LEU:O	2.19	0.43
1:AY:7:LEU:HD11	1:AY:140:VAL:HG22	2.01	0.43
1:CT:21:PHE:O	1:CT:22:ASN:HB2	2.19	0.43
1:AP:51:TRP:O	1:AT:148:LEU:HD11	2.18	0.43
1:AR:91:VAL:O	1:AR:95:VAL:HG23	2.19	0.43
1:BJ:15:GLY:O	1:BJ:74:VAL:HA	2.19	0.43
1:BR:91:VAL:O	1:BR:95:VAL:HG23	2.19	0.43
1:AE:88:TYR:CD2	1:AE:88:TYR:C	2.91	0.43
1:AI:148:LEU:HD23	1:AI:148:LEU:HA	1.82	0.43
1:BW:91:VAL:O	1:BW:95:VAL:HG23	2.19	0.43
1:AT:21:PHE:O	1:AT:22:ASN:HB2	2.19	0.43
1:CJ:145:MET:O	1:CJ:149:SER:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CT:145:MET:O	1:CT:149:SER:HB3	2.19	0.42
1:AG:58:ILE:CG2	1:AG:58:ILE:O	2.65	0.42
1:BL:97:LYS:HA	1:BL:100:ALA:HB3	2.00	0.42
1:BW:97:LYS:HE3	1:BX:97:LYS:NZ	2.32	0.42
1:AH:52:VAL:CG1	1:AH:61:ILE:HD12	2.35	0.42
1:CR:52:VAL:CG1	1:CR:61:ILE:HD12	2.35	0.42
1:A2:34:LEU:HD22	1:A2:38:LYS:CE	2.43	0.42
1:BQ:129:THR:CG2	1:BQ:130:LYS:H	2.28	0.42
1:AT:106:THR:O	1:AT:107:ASP:C	2.57	0.42
1:CJ:106:THR:O	1:CJ:107:ASP:C	2.57	0.42
1:AY:106:THR:O	1:AY:107:ASP:C	2.57	0.42
1:CB:129:THR:HG22	1:CB:130:LYS:N	2.33	0.42
1:BW:18:VAL:HA	1:BW:77:LEU:O	2.19	0.42
1:C2:18:VAL:HA	1:C2:77:LEU:O	2.19	0.42
1:CR:18:VAL:HA	1:CR:77:LEU:O	2.19	0.42
1:CM:104:LEU:CD2	1:CN:60:LEU:HA	2.48	0.42
1:CW:66:ALA:HB2	1:CW:74:VAL:HG21	1.99	0.42
1:AH:91:VAL:O	1:AH:95:VAL:HG23	2.19	0.42
1:CA:51:TRP:O	1:CE:148:LEU:HD11	2.18	0.42
1:C4:90:TYR:O	1:C4:94:GLU:HG2	2.18	0.42
1:A4:21:PHE:O	1:A4:22:ASN:HB2	2.19	0.42
1:CS:58:ILE:HB	1:CS:59:PRO:HD3	2.00	0.42
1:AM:148:LEU:HA	1:AM:148:LEU:HD23	1.80	0.42
1:BX:148:LEU:HD23	1:BX:148:LEU:HA	1.82	0.42
1:AM:45:ASN:HD22	1:AM:45:ASN:HA	1.64	0.42
1:CX:148:LEU:HD23	1:CX:148:LEU:HA	1.82	0.42
1:CT:90:TYR:O	1:CT:94:GLU:HG2	2.18	0.42
1:BM:91:VAL:O	1:BM:95:VAL:HG23	2.19	0.42
1:BW:125:GLU:HA	1:BW:129:THR:HB	2.01	0.42
1:AQ:13:LYS:NZ	1:BU:43:GLU:CB	2.67	0.42
1:CO:145:MET:O	1:CO:149:SER:HB3	2.19	0.42
1:A4:65:MET:HE3	1:A4:71:TYR:CE2	2.54	0.42
1:B4:145:MET:O	1:B4:149:SER:HB3	2.19	0.42
1:AV:97:LYS:HA	1:AV:100:ALA:HB3	2.00	0.42
1:CB:97:LYS:HA	1:CB:100:ALA:HB3	2.00	0.42
1:CL:55:ALA:HB1	1:CL:95:VAL:CG2	2.40	0.42
1:BV:55:ALA:HB1	1:BV:95:VAL:CG2	2.40	0.42
1:B3:75:ILE:HG22	1:B3:77:LEU:CD1	2.49	0.42
1:A3:75:ILE:HG22	1:A3:77:LEU:CD1	2.49	0.42
1:CE:106:THR:O	1:CE:107:ASP:C	2.57	0.42
1:AE:106:THR:O	1:AE:107:ASP:C	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B4:106:THR:O	1:B4:107:ASP:OD1	2.36	0.42
1:BO:106:THR:O	1:BO:107:ASP:C	2.57	0.42
1:CD:20:ARG:NH1	1:CR:39:ARG:NH1	2.67	0.42
1:AR:18:VAL:HA	1:AR:77:LEU:O	2.19	0.42
1:A4:7:LEU:HD11	1:A4:140:VAL:HG22	2.01	0.42
1:AM:104:LEU:CD2	1:AN:60:LEU:HA	2.48	0.42
1:CH:66:ALA:HB2	1:CH:74:VAL:HG21	1.99	0.42
1:BF:51:TRP:O	1:BJ:148:LEU:HD11	2.18	0.42
1:BJ:21:PHE:O	1:BJ:22:ASN:HB2	2.19	0.42
1:AR:125:GLU:HA	1:AR:129:THR:HB	2.01	0.42
1:AD:120:ILE:CG1	1:AR:129:THR:HG21	2.49	0.42
1:AV:104:LEU:HD23	1:AW:60:LEU:HD13	2.00	0.42
1:CH:125:GLU:HA	1:CH:129:THR:HB	2.01	0.42
1:AO:145:MET:O	1:AO:149:SER:HB3	2.20	0.42
1:CO:108:ILE:CG1	1:CO:150:LYS:HE3	2.42	0.42
1:BE:145:MET:O	1:BE:149:SER:HB3	2.20	0.42
1:BT:145:MET:O	1:BT:149:SER:HB3	2.19	0.42
1:C4:108:ILE:CG1	1:C4:150:LYS:HE3	2.42	0.42
1:CR:97:LYS:HE3	1:CS:97:LYS:HZ1	1.84	0.42
1:CA:58:ILE:H	1:CA:59:PRO:HD2	1.80	0.42
1:AN:17:VAL:HG13	1:AN:65:MET:CE	2.48	0.42
1:CT:45:ASN:C	1:CT:47:ILE:H	2.21	0.42
1:BD:7:LEU:CB	1:BJ:39:ARG:O	2.67	0.42
1:BC:18:VAL:HA	1:BC:77:LEU:O	2.19	0.42
1:CP:18:VAL:HG22	1:CP:77:LEU:HB2	2.02	0.42
1:BM:18:VAL:HA	1:BM:77:LEU:O	2.19	0.42
1:CL:129:THR:HG22	1:CL:130:LYS:N	2.33	0.42
1:CW:104:LEU:CD2	1:CX:60:LEU:HA	2.48	0.42
1:CG:13:LYS:HG2	1:CG:70:LYS:O	2.18	0.42
1:CM:83:GLY:HA3	2:CM:2201:PO4:P	2.60	0.42
1:C2:83:GLY:HA3	2:C2:2201:PO4:P	2.60	0.42
1:AE:21:PHE:O	1:AE:22:ASN:HB2	2.19	0.42
1:B3:58:ILE:HB	1:B3:59:PRO:HD3	2.00	0.42
1:CG:31:GLY:O	1:CG:35:ASP:HB2	2.20	0.42
1:B2:91:VAL:O	1:B2:95:VAL:HG23	2.19	0.42
1:CW:125:GLU:HA	1:CW:129:THR:HB	2.01	0.42
1:BR:125:GLU:HA	1:BR:129:THR:HB	2.01	0.42
1:B1:104:LEU:HD23	1:B2:60:LEU:HD13	2.00	0.42
1:BC:125:GLU:HA	1:BC:129:THR:HB	2.01	0.42
1:AE:145:MET:O	1:AE:149:SER:HB3	2.20	0.42
1:BB:104:LEU:HD23	1:BC:60:LEU:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B1:97:LYS:HA	1:B1:100:ALA:HB3	2.00	0.42
1:BG:55:ALA:HB1	1:BG:95:VAL:CG2	2.40	0.42
1:BF:39:ARG:NH2	1:BQ:144:GLU:CD	2.73	0.42
1:AS:75:ILE:HG22	1:AS:77:LEU:CD1	2.49	0.42
1:BH:15:GLY:HA3	1:BH:65:MET:HE1	2.01	0.42
1:BU:58:ILE:H	1:BU:59:PRO:HD2	1.80	0.42
1:AT:95:VAL:HG12	1:AT:112:PHE:HE1	1.85	0.42
1:AE:95:VAL:HG12	1:AE:112:PHE:HE1	1.85	0.42
1:CO:15:GLY:O	1:CO:74:VAL:HA	2.19	0.42
1:BY:15:GLY:O	1:BY:74:VAL:HA	2.18	0.42
1:BO:95:VAL:HG12	1:BO:112:PHE:HE1	1.85	0.42
1:B4:106:THR:O	1:B4:107:ASP:C	2.57	0.42
1:CP:7:LEU:HD12	1:CP:7:LEU:HA	1.84	0.42
1:BZ:18:VAL:HG22	1:BZ:77:LEU:HB2	2.02	0.42
1:CM:18:VAL:HA	1:CM:77:LEU:O	2.19	0.42
1:A1:129:THR:CG2	1:A1:130:LYS:H	2.28	0.42
1:AZ:18:VAL:HG22	1:AZ:77:LEU:HB2	2.02	0.42
1:CP:21:PHE:O	1:CP:22:ASN:HB2	2.20	0.42
1:AD:40:HIS:CE1	1:AJ:7:LEU:HD23	2.54	0.42
1:BG:13:LYS:HG2	1:BG:70:LYS:O	2.18	0.42
1:AG:13:LYS:HG2	1:AG:70:LYS:O	2.18	0.42
1:A1:13:LYS:HG2	1:A1:70:LYS:O	2.18	0.42
1:CC:83:GLY:HA3	2:CC:1001:PO4:O3	2.20	0.42
1:CA:21:PHE:O	1:CA:22:ASN:HB2	2.20	0.42
1:BC:83:GLY:HA3	2:BC:1001:PO4:O3	2.20	0.42
1:BB:31:GLY:O	1:BB:35:ASP:HB2	2.20	0.42
1:AY:6:HIS:HB3	1:AY:147:HIS:CG	2.55	0.42
1:CW:91:VAL:O	1:CW:95:VAL:HG23	2.19	0.42
1:A4:15:GLY:O	1:A4:74:VAL:HA	2.19	0.42
1:CI:58:ILE:HB	1:CI:59:PRO:HD3	2.00	0.42
1:BY:21:PHE:O	1:BY:22:ASN:HB2	2.19	0.42
1:B4:21:PHE:O	1:B4:22:ASN:HB2	2.19	0.42
1:B2:45:ASN:HD22	1:B2:45:ASN:HA	1.63	0.42
1:BZ:21:PHE:O	1:BZ:22:ASN:HB2	2.20	0.42
1:BT:7:LEU:HD11	1:BT:140:VAL:HG22	2.01	0.42
1:AA:21:PHE:O	1:AA:22:ASN:HB2	2.20	0.42
1:AM:91:VAL:O	1:AM:95:VAL:HG23	2.19	0.42
1:AZ:21:PHE:O	1:AZ:22:ASN:HB2	2.20	0.42
1:CN:58:ILE:HB	1:CN:59:PRO:HD3	2.00	0.42
1:AW:91:VAL:O	1:AW:95:VAL:HG23	2.19	0.42
1:BH:125:GLU:HA	1:BH:129:THR:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:145:MET:O	1:AJ:149:SER:HB3	2.19	0.42
1:AY:65:MET:HE3	1:AY:71:TYR:CE2	2.55	0.42
1:BJ:145:MET:O	1:BJ:149:SER:HB3	2.20	0.42
1:AV:55:ALA:HB1	1:AV:95:VAL:CG2	2.40	0.42
1:AL:97:LYS:HA	1:AL:100:ALA:HB3	2.00	0.42
1:BG:100:ALA:CA	1:BH:56:PHE:HZ	2.28	0.42
1:CG:97:LYS:HA	1:CG:100:ALA:HB3	2.00	0.42
1:BX:52:VAL:CG1	1:BX:61:ILE:HD12	2.35	0.42
1:CF:28:LYS:HD2	1:CR:24:PHE:CD1	2.55	0.42
1:CW:39:ARG:CZ	1:C3:20:ARG:CZ	2.97	0.42
1:BO:64:LYS:HD3	1:BO:64:LYS:HA	1.85	0.42
1:CO:45:ASN:C	1:CO:47:ILE:H	2.21	0.42
1:BT:106:THR:O	1:BT:107:ASP:C	2.57	0.42
1:BJ:106:THR:O	1:BJ:107:ASP:C	2.57	0.42
1:CI:48:ASP:HB2	1:CI:71:TYR:CE1	2.50	0.42
1:AP:18:VAL:HG22	1:AP:77:LEU:HB2	2.02	0.42
1:AH:18:VAL:HA	1:AH:77:LEU:O	2.19	0.42
1:BU:18:VAL:HG22	1:BU:77:LEU:HB2	2.02	0.42
1:BI:98:GLY:HA2	1:BI:102:LEU:HD23	2.02	0.42
1:BV:65:MET:HE3	1:BV:71:TYR:CE2	2.55	0.42
1:CC:83:GLY:HA3	2:CC:1001:PO4:P	2.60	0.42
1:AR:83:GLY:HA3	2:AR:1001:PO4:P	2.60	0.42
1:AH:83:GLY:HA3	2:AH:1001:PO4:O3	2.20	0.42
1:BH:83:GLY:HA3	2:BH:1001:PO4:O3	2.20	0.42
1:CH:83:GLY:HA3	2:CH:2201:PO4:P	2.60	0.42
1:A1:31:GLY:O	1:A1:35:ASP:HB2	2.20	0.42
1:BJ:6:HIS:HB3	1:BJ:147:HIS:CG	2.55	0.42
1:BS:58:ILE:HB	1:BS:59:PRO:HD3	2.00	0.42
1:CO:6:HIS:HB3	1:CO:147:HIS:CG	2.55	0.42
1:AS:29:LEU:HD11	1:AS:134:LYS:HB3	2.02	0.42
1:CU:51:TRP:O	1:CY:148:LEU:HD11	2.19	0.42
1:AN:58:ILE:HB	1:AN:59:PRO:HD3	2.00	0.42
1:AG:31:GLY:O	1:AG:35:ASP:HB2	2.20	0.42
1:CY:21:PHE:O	1:CY:22:ASN:HB2	2.19	0.42
1:C2:91:VAL:O	1:C2:95:VAL:HG23	2.19	0.42
1:BA:21:PHE:O	1:BA:22:ASN:HB2	2.20	0.42
1:CC:91:VAL:O	1:CC:95:VAL:HG23	2.19	0.42
1:A4:90:TYR:O	1:A4:94:GLU:HG2	2.18	0.42
1:AQ:104:LEU:HD13	1:AR:102:LEU:CD2	2.46	0.42
1:A4:108:ILE:CG1	1:A4:150:LYS:HE3	2.42	0.42
1:AY:145:MET:O	1:AY:149:SER:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:145:MET:O	1:CY:149:SER:HB3	2.20	0.42
1:BB:97:LYS:N	1:BB:100:ALA:HB2	2.31	0.42
1:C1:55:ALA:HA	1:C1:58:ILE:HG13	2.02	0.42
1:CQ:97:LYS:HE3	1:CR:97:LYS:HZ1	1.84	0.42
1:CK:53:PRO:HD2	1:CK:57:GLU:CB	2.49	0.42
1:AA:18:VAL:HG22	1:AA:77:LEU:HB2	2.02	0.42
1:AJ:7:LEU:HD11	1:AJ:140:VAL:HG22	2.01	0.42
1:AX:6:HIS:HB3	1:AX:147:HIS:CG	2.55	0.42
1:C3:6:HIS:HB3	1:C3:147:HIS:CG	2.55	0.42
1:CX:6:HIS:HB3	1:CX:147:HIS:CG	2.55	0.42
1:BE:7:LEU:HA	1:BE:7:LEU:HD12	1.91	0.42
1:AD:98:GLY:HA2	1:AD:102:LEU:HD23	2.02	0.42
1:CR:83:GLY:HA3	2:CR:2201:PO4:P	2.60	0.42
1:A4:6:HIS:HB3	1:A4:147:HIS:CG	2.55	0.42
1:CO:90:TYR:O	1:CO:94:GLU:HG2	2.18	0.42
1:BP:21:PHE:O	1:BP:22:ASN:HB2	2.20	0.42
1:AJ:6:HIS:HB3	1:AJ:147:HIS:CG	2.55	0.42
1:CN:148:LEU:HA	1:CN:148:LEU:HD23	1.82	0.42
1:AX:58:ILE:HB	1:AX:59:PRO:HD3	2.00	0.42
1:BD:58:ILE:HB	1:BD:59:PRO:HD3	2.00	0.42
1:BQ:31:GLY:O	1:BQ:35:ASP:HB2	2.20	0.42
1:BC:91:VAL:O	1:BC:95:VAL:HG23	2.19	0.42
1:AN:29:LEU:HD11	1:AN:134:LYS:HB3	2.02	0.42
1:BY:145:MET:O	1:BY:149:SER:HB3	2.20	0.42
1:BL:55:ALA:CB	1:BL:95:VAL:HG21	2.40	0.42
1:B1:55:ALA:HA	1:B1:58:ILE:HG13	2.02	0.42
1:CQ:97:LYS:HA	1:CQ:100:ALA:HB3	2.00	0.42
1:CM:67:ASN:HD22	1:CM:67:ASN:HA	1.60	0.42
1:AJ:45:ASN:C	1:AJ:47:ILE:H	2.21	0.42
1:BE:95:VAL:HG12	1:BE:112:PHE:HE1	1.85	0.42
1:CE:95:VAL:HG12	1:CE:112:PHE:HE1	1.85	0.42
1:AL:129:THR:HG22	1:AL:130:LYS:N	2.33	0.42
1:CF:18:VAL:HG22	1:CF:77:LEU:HB2	2.02	0.42
1:AX:98:GLY:HA2	1:AX:102:LEU:HD23	2.02	0.42
1:BS:98:GLY:HA2	1:BS:102:LEU:HD23	2.02	0.42
1:CM:83:GLY:HA3	2:CM:2201:PO4:O3	2.20	0.42
1:CA:24:PHE:CD1	1:CN:28:LYS:HG3	2.54	0.42
1:AH:83:GLY:HA3	2:AH:1001:PO4:P	2.60	0.42
1:BC:83:GLY:HA3	2:BC:1001:PO4:P	2.60	0.42
1:AM:83:GLY:HA3	2:AM:1001:PO4:P	2.60	0.42
1:CK:21:PHE:O	1:CK:22:ASN:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:21:PHE:O	1:BK:22:ASN:HB2	2.20	0.42
1:A3:29:LEU:HD11	1:A3:134:LYS:HB3	2.02	0.42
1:B1:31:GLY:O	1:B1:35:ASP:HB2	2.20	0.42
1:BL:31:GLY:O	1:BL:35:ASP:HB2	2.20	0.42
1:CZ:116:THR:O	1:C1:85:THR:HB	2.20	0.42
1:BY:6:HIS:HB3	1:BY:147:HIS:CG	2.55	0.42
1:BI:29:LEU:HD11	1:BI:134:LYS:HB3	2.02	0.42
1:CP:90:TYR:O	1:CP:94:GLU:HG2	2.18	0.42
1:BU:65:MET:HE3	1:BU:71:TYR:CE2	2.54	0.42
1:AQ:31:GLY:O	1:AQ:35:ASP:HB2	2.20	0.42
1:BE:6:HIS:HB3	1:BE:147:HIS:CG	2.55	0.42
1:BT:6:HIS:HB3	1:BT:147:HIS:CG	2.55	0.42
1:CJ:6:HIS:HB3	1:CJ:147:HIS:CG	2.55	0.42
1:AE:6:HIS:HB3	1:AE:147:HIS:CG	2.55	0.42
1:C4:6:HIS:HB3	1:C4:147:HIS:CG	2.55	0.42
1:B4:15:GLY:O	1:B4:74:VAL:HA	2.18	0.42
1:AU:21:PHE:O	1:AU:22:ASN:HB2	2.20	0.42
1:CV:104:LEU:HD23	1:CW:60:LEU:HD13	2.00	0.42
1:CE:145:MET:O	1:CE:149:SER:HB3	2.20	0.42
1:BT:65:MET:HE3	1:BT:71:TYR:CE2	2.55	0.42
1:AL:55:ALA:HA	1:AL:58:ILE:HG13	2.02	0.42
1:BV:55:ALA:HA	1:BV:58:ILE:HG13	2.02	0.42
1:BQ:55:ALA:HA	1:BQ:58:ILE:HG13	2.02	0.42
1:BH:97:LYS:HE3	1:BI:97:LYS:HZ3	1.84	0.42
1:A4:95:VAL:HG12	1:A4:112:PHE:HE1	1.85	0.42
1:CY:95:VAL:HG12	1:CY:112:PHE:HE1	1.85	0.42
1:C1:129:THR:HG22	1:C1:130:LYS:N	2.33	0.42
1:CN:6:HIS:HB3	1:CN:147:HIS:CG	2.55	0.42
1:CE:7:LEU:HD11	1:CE:140:VAL:HG22	2.01	0.42
1:AK:21:PHE:O	1:AK:22:ASN:HB2	2.20	0.42
1:AW:83:GLY:HA3	2:AW:201:PO4:O3	2.20	0.42
1:AO:6:HIS:HB3	1:AO:147:HIS:CG	2.55	0.42
1:BT:21:PHE:O	1:BT:22:ASN:HB2	2.19	0.42
1:CM:91:VAL:O	1:CM:95:VAL:HG23	2.19	0.42
1:CX:29:LEU:HD11	1:CX:134:LYS:HB3	2.02	0.42
1:AU:116:THR:O	1:AV:85:THR:HB	2.20	0.42
1:A3:150:LYS:HG3	1:A3:150:LYS:H	1.33	0.42
1:AZ:116:THR:O	1:A1:85:THR:HB	2.20	0.42
1:BN:29:LEU:HD11	1:BN:134:LYS:HB3	2.02	0.42
1:CE:15:GLY:O	1:CE:74:VAL:HA	2.18	0.42
1:BC:129:THR:O	1:BC:131:ALA:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:55:ALA:HA	1:BL:58:ILE:HG13	2.02	0.42
1:AQ:55:ALA:HA	1:AQ:58:ILE:HG13	2.02	0.42
1:AB:96:ALA:O	1:AB:100:ALA:HB2	2.06	0.42
1:BV:100:ALA:O	1:BW:56:PHE:CE1	2.73	0.42
1:AP:53:PRO:HD2	1:AP:57:GLU:CB	2.49	0.42
1:CW:34:LEU:HD22	1:CW:38:LYS:CE	2.44	0.42
1:AW:15:GLY:HA3	1:AW:65:MET:HE3	2.01	0.42
1:BR:63:LYS:O	1:BR:65:MET:N	2.53	0.42
1:B4:64:LYS:HD3	1:B4:64:LYS:HA	1.85	0.42
1:AY:95:VAL:HG12	1:AY:112:PHE:HE1	1.85	0.42
1:BJ:95:VAL:HG12	1:BJ:112:PHE:HE1	1.85	0.42
1:CJ:15:GLY:O	1:CJ:74:VAL:HA	2.19	0.42
1:BI:48:ASP:HB2	1:BI:71:TYR:CE1	2.50	0.42
1:AU:18:VAL:HG22	1:AU:77:LEU:HB2	2.02	0.42
1:BI:6:HIS:HB3	1:BI:147:HIS:CG	2.55	0.42
1:BO:7:LEU:HD11	1:BO:140:VAL:HG22	2.01	0.42
1:CD:6:HIS:HB3	1:CD:147:HIS:CG	2.55	0.42
1:CG:65:MET:HE3	1:CG:71:TYR:CE2	2.55	0.42
1:AI:98:GLY:HA2	1:AI:102:LEU:HD23	2.02	0.42
1:BD:98:GLY:HA2	1:BD:102:LEU:HD23	2.02	0.42
1:BV:13:LYS:HG2	1:BV:70:LYS:O	2.18	0.42
1:CX:98:GLY:HA2	1:CX:102:LEU:HD23	2.02	0.42
1:BH:83:GLY:HA3	2:BH:1001:PO4:P	2.60	0.42
1:BW:83:GLY:HA3	2:BW:1001:PO4:P	2.60	0.42
1:A2:83:GLY:HA3	2:A2:1001:PO4:O3	2.20	0.42
1:BM:83:GLY:HA3	2:BM:1001:PO4:P	2.60	0.42
1:BR:83:GLY:HA3	2:BR:1001:PO4:O3	2.20	0.42
1:CS:29:LEU:HD11	1:CS:134:LYS:HB3	2.02	0.42
1:BX:29:LEU:HD11	1:BX:134:LYS:HB3	2.02	0.42
1:AT:7:LEU:HD11	1:AT:140:VAL:HG22	2.01	0.42
1:AO:21:PHE:O	1:AO:22:ASN:HB2	2.19	0.42
1:BO:21:PHE:O	1:BO:22:ASN:HB2	2.19	0.42
1:A2:91:VAL:O	1:A2:95:VAL:HG23	2.19	0.42
1:CJ:7:LEU:HD11	1:CJ:140:VAL:HG22	2.01	0.42
1:AP:116:THR:O	1:AQ:85:THR:HB	2.20	0.42
1:CJ:52:VAL:CB	1:CJ:53:PRO:CD	2.98	0.42
1:CE:52:VAL:CB	1:CE:53:PRO:CD	2.98	0.42
1:AQ:69:GLY:C	1:BU:10:THR:CG2	2.86	0.42
1:AR:129:THR:O	1:AR:131:ALA:N	2.53	0.42
1:A2:129:THR:O	1:A2:131:ALA:N	2.53	0.42
1:BO:145:MET:O	1:BO:149:SER:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:100:ALA:O	1:CC:56:PHE:CE1	2.73	0.42
1:CB:55:ALA:CB	1:CB:95:VAL:HG21	2.40	0.42
1:AB:100:ALA:O	1:AC:56:PHE:CE1	2.73	0.42
1:BQ:97:LYS:HA	1:BQ:100:ALA:HB3	2.00	0.42
1:A3:52:VAL:CG1	1:A3:61:ILE:HD12	2.35	0.42
1:AK:52:VAL:HB	1:AK:53:PRO:CD	2.50	0.42
1:BA:52:VAL:HB	1:BA:53:PRO:CD	2.50	0.42
1:BU:53:PRO:HD2	1:BU:57:GLU:CB	2.49	0.42
1:AZ:52:VAL:HB	1:AZ:53:PRO:CD	2.50	0.42
1:AH:63:LYS:O	1:AH:65:MET:N	2.53	0.42
1:BH:63:LYS:O	1:BH:65:MET:N	2.53	0.42
1:AY:15:GLY:O	1:AY:74:VAL:HA	2.19	0.42
1:BK:7:LEU:HA	1:BK:7:LEU:HD12	1.84	0.42
1:CJ:45:ASN:C	1:CJ:47:ILE:H	2.21	0.42
1:AI:39:ARG:O	1:AO:7:LEU:CB	2.67	0.42
1:BH:18:VAL:HA	1:BH:77:LEU:O	2.19	0.42
1:BX:6:HIS:HB3	1:BX:147:HIS:CG	2.55	0.42
1:CB:65:MET:HE3	1:CB:71:TYR:CE2	2.55	0.42
1:C2:83:GLY:HA3	2:C2:2201:PO4:O3	2.20	0.42
1:B2:83:GLY:HA3	2:B2:1001:PO4:O3	2.20	0.42
1:BR:83:GLY:HA3	2:BR:1001:PO4:P	2.60	0.42
1:C3:29:LEU:HD11	1:C3:134:LYS:HB3	2.02	0.42
1:CP:116:THR:O	1:CQ:85:THR:HB	2.20	0.42
1:BO:6:HIS:HB3	1:BO:147:HIS:CG	2.55	0.42
1:BU:106:THR:C	1:BU:108:ILE:H	2.23	0.42
1:BG:31:GLY:O	1:BG:35:ASP:HB2	2.20	0.42
1:BD:29:LEU:HD11	1:BD:134:LYS:HB3	2.02	0.42
1:AZ:106:THR:C	1:AZ:108:ILE:H	2.23	0.42
1:BP:106:THR:C	1:BP:108:ILE:H	2.23	0.42
1:B3:29:LEU:HD11	1:B3:134:LYS:HB3	2.02	0.42
1:AD:120:ILE:HG12	1:AR:129:THR:HG21	2.02	0.41
1:B2:129:THR:O	1:B2:131:ALA:N	2.53	0.41
1:BM:129:THR:O	1:BM:131:ALA:N	2.53	0.41
1:CC:129:THR:O	1:CC:131:ALA:N	2.53	0.41
1:AW:125:GLU:HA	1:AW:129:THR:HB	2.01	0.41
1:AQ:70:LYS:HE3	1:BU:43:GLU:CD	2.41	0.41
1:A4:145:MET:O	1:A4:149:SER:HB3	2.19	0.41
1:CY:65:MET:HE3	1:CY:71:TYR:CE2	2.55	0.41
1:CB:97:LYS:N	1:CB:100:ALA:HB2	2.31	0.41
1:CV:100:ALA:O	1:CW:56:PHE:CE1	2.73	0.41
1:CV:55:ALA:HA	1:CV:58:ILE:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:52:VAL:HB	1:AU:53:PRO:CD	2.50	0.41
1:AF:53:PRO:HD2	1:AF:57:GLU:CB	2.49	0.41
1:CU:53:PRO:HD2	1:CU:57:GLU:CB	2.49	0.41
1:CS:75:ILE:HG22	1:CS:77:LEU:CD1	2.49	0.41
1:AW:67:ASN:HA	1:AW:67:ASN:HD22	1.59	0.41
1:C4:30:LEU:HA	1:C4:77:LEU:HD23	2.02	0.41
1:CT:95:VAL:HG12	1:CT:112:PHE:HE1	1.85	0.41
1:A4:45:ASN:C	1:A4:47:ILE:H	2.21	0.41
1:BJ:7:LEU:HD11	1:BJ:140:VAL:HG22	2.01	0.41
1:AM:18:VAL:HA	1:AM:77:LEU:O	2.19	0.41
1:AK:18:VAL:HG22	1:AK:77:LEU:HB2	2.02	0.41
1:BS:6:HIS:HB3	1:BS:147:HIS:CG	2.55	0.41
1:BQ:71:TYR:O	1:BQ:108:ILE:HD13	2.21	0.41
1:CR:83:GLY:HA3	2:CR:2201:PO4:O3	2.20	0.41
1:CI:29:LEU:HD11	1:CI:134:LYS:HB3	2.02	0.41
1:CZ:106:THR:C	1:CZ:108:ILE:H	2.24	0.41
1:CT:28:LYS:NZ	1:C4:28:LYS:NZ	2.67	0.41
1:BH:91:VAL:O	1:BH:95:VAL:HG23	2.19	0.41
1:AS:148:LEU:HA	1:AS:148:LEU:HD23	1.82	0.41
1:CF:21:PHE:O	1:CF:22:ASN:HB2	2.20	0.41
1:CR:91:VAL:O	1:CR:95:VAL:HG23	2.19	0.41
1:CH:91:VAL:O	1:CH:95:VAL:HG23	2.19	0.41
1:CQ:31:GLY:O	1:CQ:35:ASP:HB2	2.20	0.41
1:AV:104:LEU:HD13	1:AW:102:LEU:CD2	2.46	0.41
1:AT:145:MET:O	1:AT:149:SER:HB3	2.19	0.41
1:AL:97:LYS:HE3	1:AM:97:LYS:HZ1	1.84	0.41
1:C1:58:ILE:CG2	1:C1:58:ILE:O	2.65	0.41
1:CQ:55:ALA:HA	1:CQ:58:ILE:HG13	2.02	0.41
1:A1:55:ALA:HA	1:A1:58:ILE:HG13	2.02	0.41
1:A1:100:ALA:O	1:A2:56:PHE:CE1	2.73	0.41
1:BK:52:VAL:HB	1:BK:53:PRO:CD	2.51	0.41
1:BF:53:PRO:HD2	1:BF:57:GLU:CB	2.49	0.41
1:AA:53:PRO:HD2	1:AA:57:GLU:CB	2.49	0.41
1:AT:30:LEU:HA	1:AT:77:LEU:HD23	2.02	0.41
1:A2:63:LYS:O	1:A2:65:MET:N	2.53	0.41
1:CH:67:ASN:HD22	1:CH:67:ASN:HA	1.59	0.41
1:C2:63:LYS:O	1:C2:65:MET:N	2.53	0.41
1:CY:64:LYS:HA	1:CY:64:LYS:HD3	1.85	0.41
1:AE:15:GLY:O	1:AE:74:VAL:HA	2.18	0.41
1:B4:95:VAL:HG12	1:B4:112:PHE:HE1	1.85	0.41
1:CA:18:VAL:HG22	1:CA:77:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B3:6:HIS:HB3	1:B3:147:HIS:CG	2.55	0.41
1:BN:6:HIS:HB3	1:BN:147:HIS:CG	2.55	0.41
1:AC:83:GLY:HA3	2:AC:1001:PO4:O3	2.20	0.41
1:AC:83:GLY:HA3	2:AC:1001:PO4:P	2.60	0.41
1:B2:83:GLY:HA3	2:B2:1001:PO4:P	2.60	0.41
1:CW:83:GLY:HA3	2:CW:2201:PO4:O3	2.20	0.41
1:CW:83:GLY:HA3	2:CW:2201:PO4:P	2.60	0.41
1:A2:83:GLY:HA3	2:A2:1001:PO4:P	2.60	0.41
1:BM:83:GLY:HA3	2:BM:1001:PO4:O3	2.20	0.41
1:CY:7:LEU:HD11	1:CY:140:VAL:HG22	2.01	0.41
1:BP:116:THR:O	1:BQ:85:THR:HB	2.20	0.41
1:BR:148:LEU:HA	1:BR:148:LEU:HD23	1.80	0.41
1:BS:29:LEU:HD11	1:BS:134:LYS:HB3	2.02	0.41
1:BH:129:THR:O	1:BH:131:ALA:N	2.53	0.41
1:BW:129:THR:O	1:BW:131:ALA:N	2.53	0.41
1:AV:100:ALA:O	1:AW:56:PHE:CE1	2.73	0.41
1:CB:55:ALA:HA	1:CB:58:ILE:HG13	2.02	0.41
1:AL:55:ALA:HB1	1:AL:95:VAL:CG2	2.40	0.41
1:BQ:100:ALA:O	1:BR:56:PHE:CE1	2.73	0.41
1:BG:55:ALA:HA	1:BG:58:ILE:HG13	2.02	0.41
1:CG:100:ALA:O	1:CH:56:PHE:CE1	2.73	0.41
1:CU:52:VAL:HB	1:CU:53:PRO:CD	2.50	0.41
1:BN:75:ILE:HG22	1:BN:77:LEU:CD1	2.49	0.41
1:CC:39:ARG:CZ	1:CS:20:ARG:CZ	2.98	0.41
1:CJ:30:LEU:HA	1:CJ:77:LEU:HD23	2.02	0.41
1:CT:39:ARG:O	1:C3:7:LEU:CB	2.68	0.41
1:CG:120:ILE:CD1	1:CQ:125:GLU:HG2	2.50	0.41
1:CE:64:LYS:HD3	1:CE:64:LYS:HA	1.85	0.41
1:CO:95:VAL:HG12	1:CO:112:PHE:HE1	1.85	0.41
1:CV:4:GLU:CG	1:CW:51:TRP:HD1	2.29	0.41
1:CZ:18:VAL:HG22	1:CZ:77:LEU:HB2	2.02	0.41
1:BF:18:VAL:HG22	1:BF:77:LEU:HB2	2.02	0.41
1:CH:18:VAL:HA	1:CH:77:LEU:O	2.19	0.41
1:A3:6:HIS:HB3	1:A3:147:HIS:CG	2.55	0.41
1:BC:24:PHE:CE1	1:BU:28:LYS:HD2	2.53	0.41
1:AL:65:MET:HE3	1:AL:71:TYR:CE2	2.54	0.41
1:A1:71:TYR:O	1:A1:108:ILE:HD13	2.21	0.41
1:CG:71:TYR:O	1:CG:108:ILE:HD13	2.21	0.41
1:C1:71:TYR:O	1:C1:108:ILE:HD13	2.21	0.41
1:AM:83:GLY:HA3	2:AM:1001:PO4:O3	2.20	0.41
1:AL:31:GLY:O	1:AL:35:ASP:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:6:HIS:HB3	1:AT:147:HIS:CG	2.55	0.41
1:CU:21:PHE:O	1:CU:22:ASN:HB2	2.20	0.41
1:C1:31:GLY:O	1:C1:35:ASP:HB2	2.20	0.41
1:CL:31:GLY:O	1:CL:35:ASP:HB2	2.20	0.41
1:CD:148:LEU:HA	1:CD:148:LEU:HD23	1.82	0.41
1:AC:91:VAL:O	1:AC:95:VAL:HG23	2.19	0.41
1:AF:106:THR:C	1:AF:108:ILE:H	2.23	0.41
1:AJ:52:VAL:CB	1:AJ:53:PRO:CD	2.98	0.41
1:CM:125:GLU:HA	1:CM:129:THR:HB	2.01	0.41
1:CM:129:THR:O	1:CM:131:ALA:N	2.53	0.41
1:AG:55:ALA:HA	1:AG:58:ILE:HG13	2.02	0.41
1:CP:52:VAL:HB	1:CP:53:PRO:CD	2.50	0.41
1:BY:129:THR:O	1:BY:130:LYS:C	2.59	0.41
1:CO:129:THR:O	1:CO:130:LYS:C	2.59	0.41
1:AJ:30:LEU:HA	1:AJ:77:LEU:HD23	2.03	0.41
1:CC:63:LYS:O	1:CC:65:MET:N	2.53	0.41
1:BM:63:LYS:O	1:BM:65:MET:N	2.53	0.41
1:CM:63:LYS:O	1:CM:65:MET:N	2.53	0.41
1:AM:63:LYS:O	1:AM:65:MET:N	2.53	0.41
1:AE:64:LYS:HA	1:AE:64:LYS:HD3	1.85	0.41
1:AI:48:ASP:HB2	1:AI:71:TYR:CE1	2.50	0.41
1:BK:18:VAL:HG22	1:BK:77:LEU:HB2	2.02	0.41
1:AF:18:VAL:HG22	1:AF:77:LEU:HB2	2.02	0.41
1:AD:6:HIS:HB3	1:AD:147:HIS:CG	2.55	0.41
1:C1:65:MET:HE3	1:C1:71:TYR:CE2	2.54	0.41
1:BG:71:TYR:O	1:BG:108:ILE:HD13	2.21	0.41
1:CS:98:GLY:HA2	1:CS:102:LEU:HD23	2.02	0.41
1:AR:83:GLY:HA3	2:AR:1001:PO4:O3	2.20	0.41
1:CH:83:GLY:HA3	2:CH:2201:PO4:O3	2.20	0.41
1:BM:95:VAL:HG12	1:BM:112:PHE:HE1	1.86	0.41
1:AG:25:ILE:HG23	1:AG:127:ALA:HB2	2.03	0.41
1:BK:116:THR:O	1:BL:85:THR:HB	2.20	0.41
1:AN:150:LYS:HG3	1:AN:150:LYS:H	1.33	0.41
1:AG:24:PHE:CD1	1:AQ:28:LYS:HG3	2.55	0.41
1:AX:29:LEU:HD11	1:AX:134:LYS:HB3	2.02	0.41
1:AC:125:GLU:HA	1:AC:129:THR:HB	2.01	0.41
1:BR:129:THR:O	1:BR:131:ALA:N	2.53	0.41
1:CE:65:MET:HE3	1:CE:71:TYR:CE2	2.55	0.41
1:BJ:65:MET:HE3	1:BJ:71:TYR:CE2	2.55	0.41
1:AV:55:ALA:HA	1:AV:58:ILE:HG13	2.02	0.41
1:CL:100:ALA:O	1:CM:56:PHE:CE1	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BV:97:LYS:N	1:BV:100:ALA:HB2	2.31	0.41
1:AP:52:VAL:HB	1:AP:53:PRO:CD	2.50	0.41
1:BU:52:VAL:HB	1:BU:53:PRO:CD	2.50	0.41
1:CZ:52:VAL:HB	1:CZ:53:PRO:CD	2.50	0.41
1:CY:129:THR:O	1:CY:130:LYS:C	2.59	0.41
1:CJ:129:THR:O	1:CJ:130:LYS:C	2.59	0.41
1:C4:129:THR:O	1:C4:130:LYS:C	2.59	0.41
1:CD:28:LYS:HG3	1:CF:24:PHE:CD1	2.55	0.41
1:AO:30:LEU:HA	1:AO:77:LEU:HD23	2.02	0.41
1:AR:63:LYS:O	1:AR:65:MET:N	2.53	0.41
1:A2:15:GLY:HA3	1:A2:65:MET:HE1	2.03	0.41
1:CW:63:LYS:O	1:CW:65:MET:N	2.53	0.41
1:AT:64:LYS:HA	1:AT:64:LYS:HD3	1.85	0.41
1:BA:18:VAL:HG22	1:BA:77:LEU:HB2	2.02	0.41
1:BF:21:PHE:O	1:BF:22:ASN:HB2	2.20	0.41
1:AE:7:LEU:HD12	1:AE:7:LEU:HA	1.91	0.41
1:AS:39:ARG:O	1:AY:7:LEU:HB3	2.21	0.41
1:CI:6:HIS:HB3	1:CI:147:HIS:CG	2.55	0.41
1:BG:65:MET:HE3	1:BG:71:TYR:CE2	2.56	0.41
1:CJ:7:LEU:HD12	1:CJ:7:LEU:HA	1.91	0.41
1:CY:6:HIS:HB3	1:CY:147:HIS:CG	2.55	0.41
1:AK:106:THR:C	1:AK:108:ILE:H	2.23	0.41
1:CA:106:THR:C	1:CA:108:ILE:H	2.24	0.41
1:BA:116:THR:O	1:BB:85:THR:HB	2.20	0.41
1:AP:21:PHE:O	1:AP:22:ASN:HB2	2.20	0.41
1:AD:148:LEU:HD23	1:AD:148:LEU:HA	1.82	0.41
1:BC:148:LEU:HD23	1:BC:148:LEU:HA	1.80	0.41
1:BF:106:THR:C	1:BF:108:ILE:H	2.24	0.41
1:BU:116:THR:O	1:BV:85:THR:HB	2.20	0.41
1:AB:31:GLY:O	1:AB:35:ASP:HB2	2.20	0.41
1:CU:116:THR:O	1:CV:85:THR:HB	2.20	0.41
1:AW:129:THR:O	1:AW:131:ALA:N	2.53	0.41
1:AH:129:THR:O	1:AH:131:ALA:N	2.53	0.41
1:CB:104:LEU:HD13	1:CC:102:LEU:CD2	2.46	0.41
1:AE:108:ILE:CG1	1:AE:150:LYS:HE3	2.42	0.41
1:AE:65:MET:HE3	1:AE:71:TYR:CE2	2.55	0.41
1:AY:71:TYR:O	1:AY:150:LYS:NZ	2.44	0.41
1:C4:145:MET:O	1:C4:149:SER:HB3	2.20	0.41
1:BB:100:ALA:O	1:BC:56:PHE:CE1	2.73	0.41
1:AQ:100:ALA:O	1:AR:56:PHE:CE1	2.73	0.41
1:AB:55:ALA:HB1	1:AB:95:VAL:CG2	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:55:ALA:HA	1:AB:58:ILE:HG13	2.02	0.41
1:CQ:100:ALA:O	1:CR:56:PHE:CE1	2.73	0.41
1:BG:100:ALA:O	1:BH:56:PHE:CE1	2.73	0.41
1:CN:52:VAL:CG1	1:CN:61:ILE:HD12	2.35	0.41
1:BP:52:VAL:HB	1:BP:53:PRO:CD	2.51	0.41
1:CK:52:VAL:HB	1:CK:53:PRO:CD	2.51	0.41
1:BO:129:THR:O	1:BO:130:LYS:C	2.59	0.41
1:AY:129:THR:O	1:AY:130:LYS:C	2.59	0.41
1:BJ:129:THR:O	1:BJ:130:LYS:C	2.59	0.41
1:CE:129:THR:O	1:CE:130:LYS:C	2.59	0.41
1:B2:34:LEU:HD22	1:B2:38:LYS:CE	2.43	0.41
1:CK:76:THR:CG2	1:CK:112:PHE:HA	2.51	0.41
1:BK:76:THR:CG2	1:BK:112:PHE:HA	2.51	0.41
1:CO:64:LYS:HA	1:CO:64:LYS:HD3	1.85	0.41
1:BT:95:VAL:HG12	1:BT:112:PHE:HE1	1.85	0.41
1:BY:14:VAL:HG21	1:BY:37:LEU:HD22	2.03	0.41
1:BG:4:GLU:CG	1:BH:51:TRP:HD1	2.29	0.41
1:AO:95:VAL:HG12	1:AO:112:PHE:HE1	1.85	0.41
1:BW:63:LYS:O	1:BW:65:MET:N	2.53	0.41
1:AN:6:HIS:HB3	1:AN:147:HIS:CG	2.55	0.41
1:BD:6:HIS:HB3	1:BD:147:HIS:CG	2.55	0.41
1:AI:6:HIS:HB3	1:AI:147:HIS:CG	2.55	0.41
1:B1:71:TYR:O	1:B1:108:ILE:HD13	2.21	0.41
1:AV:71:TYR:O	1:AV:108:ILE:HD13	2.21	0.41
1:CL:65:MET:HE3	1:CL:71:TYR:CE2	2.56	0.41
1:CL:71:TYR:O	1:CL:108:ILE:HD13	2.21	0.41
1:CW:95:VAL:HG12	1:CW:112:PHE:HE1	1.86	0.41
1:CM:95:VAL:HG12	1:CM:112:PHE:HE1	1.86	0.41
1:BZ:116:THR:O	1:B1:85:THR:HB	2.20	0.41
1:BL:25:ILE:HG23	1:BL:127:ALA:HB2	2.03	0.41
1:BQ:25:ILE:HG23	1:BQ:127:ALA:HB2	2.03	0.41
1:CE:6:HIS:HB3	1:CE:147:HIS:CG	2.55	0.41
1:BV:31:GLY:O	1:BV:35:ASP:HB2	2.20	0.41
1:CU:106:THR:C	1:CU:108:ILE:H	2.23	0.41
1:B4:6:HIS:HB3	1:B4:147:HIS:CG	2.55	0.41
1:CZ:21:PHE:O	1:CZ:22:ASN:HB2	2.20	0.41
1:BF:116:THR:O	1:BG:85:THR:HB	2.20	0.41
1:BT:52:VAL:CB	1:BT:53:PRO:CD	2.98	0.41
1:AG:100:ALA:O	1:AH:56:PHE:CE1	2.73	0.41
1:BL:100:ALA:O	1:BM:56:PHE:CE1	2.73	0.41
1:AA:52:VAL:HB	1:AA:53:PRO:CD	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:129:THR:O	1:A4:130:LYS:C	2.59	0.41
1:BT:30:LEU:HA	1:BT:77:LEU:HD23	2.03	0.41
1:BW:34:LEU:HD22	1:BW:38:LYS:CE	2.43	0.41
1:CH:65:MET:HB3	1:CH:65:MET:HE3	1.91	0.41
1:CU:76:THR:CG2	1:CU:112:PHE:HA	2.51	0.41
1:C2:67:ASN:HD22	1:C2:67:ASN:HA	1.59	0.41
1:BF:76:THR:CG2	1:BF:112:PHE:HA	2.51	0.41
1:CF:76:THR:CG2	1:CF:112:PHE:HA	2.51	0.41
1:CT:14:VAL:HG21	1:CT:37:LEU:HD22	2.03	0.41
1:BY:95:VAL:HG12	1:BY:112:PHE:HE1	1.85	0.41
1:C4:95:VAL:HG12	1:C4:112:PHE:HE1	1.85	0.41
1:CR:63:LYS:O	1:CR:65:MET:N	2.53	0.41
1:C4:21:PHE:O	1:C4:22:ASN:HB2	2.19	0.41
1:CU:18:VAL:HG22	1:CU:77:LEU:HB2	2.02	0.41
1:AS:6:HIS:HB3	1:AS:147:HIS:CG	2.55	0.41
1:CS:6:HIS:HB3	1:CS:147:HIS:CG	2.55	0.41
1:AN:98:GLY:HA2	1:AN:102:LEU:HD23	2.02	0.41
1:BX:98:GLY:HA2	1:BX:102:LEU:HD23	2.02	0.41
1:BV:71:TYR:O	1:BV:108:ILE:HD13	2.21	0.41
1:CI:98:GLY:HA2	1:CI:102:LEU:HD23	2.02	0.41
1:AR:95:VAL:HG12	1:AR:112:PHE:HE1	1.86	0.41
1:AH:95:VAL:HG12	1:AH:112:PHE:HE1	1.86	0.41
1:BC:95:VAL:HG12	1:BC:112:PHE:HE1	1.86	0.41
1:CH:95:VAL:HG12	1:CH:112:PHE:HE1	1.86	0.41
1:BU:21:PHE:O	1:BU:22:ASN:HB2	2.20	0.41
1:BA:106:THR:C	1:BA:108:ILE:H	2.24	0.41
1:BV:25:ILE:HG23	1:BV:127:ALA:HB2	2.03	0.41
1:AK:116:THR:O	1:AL:85:THR:HB	2.20	0.41
1:CH:45:ASN:HD22	1:CH:45:ASN:HA	1.64	0.41
1:CG:25:ILE:HG23	1:CG:127:ALA:HB2	2.03	0.41
1:AP:106:THR:C	1:AP:108:ILE:H	2.24	0.41
1:BB:25:ILE:HG23	1:BB:127:ALA:HB2	2.03	0.41
1:AC:129:THR:O	1:AC:131:ALA:N	2.53	0.41
1:AM:129:THR:O	1:AM:131:ALA:N	2.53	0.41
1:CE:71:TYR:O	1:CE:150:LYS:NZ	2.44	0.41
1:BO:65:MET:HE3	1:BO:71:TYR:CE2	2.55	0.41
1:C1:100:ALA:O	1:C2:56:PHE:CE1	2.73	0.41
1:A1:97:LYS:HE3	1:A2:97:LYS:HZ3	1.85	0.41
1:AU:53:PRO:HD2	1:AU:57:GLU:CB	2.49	0.41
1:CX:20:ARG:HD3	1:C2:39:ARG:NH2	2.35	0.41
1:BR:34:LEU:HD22	1:BR:38:LYS:CE	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BO:30:LEU:HA	1:BO:77:LEU:HD23	2.02	0.41
1:CE:30:LEU:HA	1:CE:77:LEU:HD23	2.02	0.41
1:AW:63:LYS:O	1:AW:65:MET:N	2.53	0.41
1:AJ:64:LYS:HA	1:AJ:64:LYS:HD3	1.85	0.41
1:CJ:14:VAL:HG21	1:CJ:37:LEU:HD22	2.03	0.41
1:CV:71:TYR:O	1:CV:108:ILE:HD13	2.21	0.41
1:CB:71:TYR:O	1:CB:108:ILE:HD13	2.21	0.41
1:A3:98:GLY:HA2	1:A3:102:LEU:HD23	2.02	0.41
1:AA:106:THR:C	1:AA:108:ILE:H	2.23	0.41
1:AV:31:GLY:O	1:AV:35:ASP:HB2	2.20	0.41
1:AE:28:LYS:HG3	1:AO:24:PHE:CD1	2.56	0.41
1:AF:21:PHE:O	1:AF:22:ASN:HB2	2.20	0.41
1:CB:83:GLY:HA3	2:CB:1001:PO4:O1	2.21	0.41
1:A1:25:ILE:HG23	1:A1:127:ALA:HB2	2.03	0.41
1:CK:106:THR:C	1:CK:108:ILE:H	2.24	0.41
1:AF:116:THR:O	1:AG:85:THR:HB	2.20	0.41
1:CK:116:THR:O	1:CL:85:THR:HB	2.20	0.41
1:C2:129:THR:O	1:C2:131:ALA:N	2.53	0.41
1:CR:129:THR:O	1:CR:131:ALA:N	2.53	0.41
1:CW:129:THR:O	1:CW:131:ALA:N	2.53	0.41
1:AQ:70:LYS:HG3	1:BU:43:GLU:OE1	2.20	0.41
1:BB:104:LEU:HD13	1:BC:102:LEU:CD2	2.46	0.41
1:AJ:65:MET:HE3	1:AJ:71:TYR:CE2	2.56	0.41
1:AT:108:ILE:CG1	1:AT:150:LYS:HE3	2.42	0.41
1:BB:55:ALA:HA	1:BB:58:ILE:HG13	2.02	0.41
1:AL:100:ALA:O	1:AM:56:PHE:CE1	2.73	0.41
1:AB:58:ILE:O	1:AB:62:ALA:CB	2.69	0.41
1:B1:55:ALA:HB1	1:B1:95:VAL:CG2	2.40	0.41
1:B1:100:ALA:O	1:B2:56:PHE:CE1	2.73	0.41
1:B2:97:LYS:HE3	1:B3:97:LYS:HZ3	1.85	0.41
1:BF:40:HIS:CE1	1:BQ:7:LEU:HD23	2.56	0.41
1:BF:52:VAL:HB	1:BF:53:PRO:CD	2.50	0.41
1:CF:52:VAL:HB	1:CF:53:PRO:CD	2.51	0.41
1:CA:52:VAL:HB	1:CA:53:PRO:CD	2.50	0.41
1:BZ:52:VAL:HB	1:BZ:53:PRO:CD	2.50	0.41
1:BT:129:THR:O	1:BT:130:LYS:C	2.59	0.41
1:AJ:129:THR:O	1:AJ:130:LYS:C	2.59	0.41
1:AE:129:THR:O	1:AE:130:LYS:C	2.59	0.41
1:AM:34:LEU:HD22	1:AM:38:LYS:CE	2.43	0.41
1:AE:30:LEU:HA	1:AE:77:LEU:HD23	2.02	0.41
1:CO:30:LEU:HA	1:CO:77:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:30:LEU:HA	1:BJ:77:LEU:HD23	2.02	0.41
1:BZ:76:THR:CG2	1:BZ:112:PHE:HA	2.51	0.41
1:AM:67:ASN:HD22	1:AM:67:ASN:HA	1.59	0.41
1:AM:15:GLY:HA3	1:AM:65:MET:HE1	2.03	0.41
1:CH:63:LYS:O	1:CH:65:MET:N	2.53	0.41
1:CT:30:LEU:HA	1:CT:77:LEU:HD23	2.02	0.41
1:AC:63:LYS:O	1:AC:65:MET:N	2.53	0.41
1:BU:76:THR:CG2	1:BU:112:PHE:HA	2.51	0.41
1:AK:76:THR:CG2	1:AK:112:PHE:HA	2.51	0.41
1:CA:76:THR:CG2	1:CA:112:PHE:HA	2.51	0.41
1:AF:76:THR:CG2	1:AF:112:PHE:HA	2.51	0.41
1:CP:76:THR:CG2	1:CP:112:PHE:HA	2.51	0.41
1:AY:14:VAL:HG12	1:AY:15:GLY:N	2.36	0.41
1:CJ:95:VAL:HG12	1:CJ:112:PHE:HE1	1.85	0.41
1:BC:63:LYS:O	1:BC:65:MET:N	2.53	0.41
1:CL:129:THR:CG2	1:CL:130:LYS:H	2.28	0.41
1:AE:7:LEU:HD23	1:AN:40:HIS:CE1	2.56	0.41
1:AS:98:GLY:HA2	1:AS:102:LEU:HD23	2.02	0.41
1:AG:71:TYR:O	1:AG:108:ILE:HD13	2.21	0.41
1:BL:71:TYR:O	1:BL:108:ILE:HD13	2.21	0.41
1:C3:98:GLY:HA2	1:C3:102:LEU:HD23	2.02	0.41
1:AM:95:VAL:HG12	1:AM:112:PHE:HE1	1.86	0.41
1:C2:95:VAL:HG12	1:C2:112:PHE:HE1	1.86	0.41
1:AC:95:VAL:HG12	1:AC:112:PHE:HE1	1.86	0.41
1:AQ:25:ILE:HG23	1:AQ:127:ALA:HB2	2.03	0.41
1:CN:29:LEU:HD11	1:CN:134:LYS:HB3	2.02	0.41
1:AA:116:THR:O	1:AB:85:THR:HB	2.20	0.41
1:AU:32:GLY:HA3	1:AU:135:GLY:C	2.42	0.41
1:CA:116:THR:O	1:CB:85:THR:HB	2.20	0.41
1:BC:45:ASN:HD22	1:BC:45:ASN:HA	1.64	0.41
1:AD:29:LEU:HD11	1:AD:134:LYS:HB3	2.02	0.41
1:CT:6:HIS:HB3	1:CT:147:HIS:CG	2.55	0.41
1:CF:106:THR:C	1:CF:108:ILE:H	2.24	0.41
1:CA:26:THR:HA	1:CA:29:LEU:HB3	2.03	0.41
1:AB:83:GLY:HA3	2:AB:1001:PO4:O1	2.21	0.41
1:CL:25:ILE:HG23	1:CL:127:ALA:HB2	2.03	0.41
1:AB:25:ILE:HG23	1:AB:127:ALA:HB2	2.03	0.41
1:AL:111:ILE:N	1:AL:111:ILE:HD12	2.36	0.41
1:CL:83:GLY:HA3	2:CL:1201:PO4:O1	2.21	0.41
1:A1:104:LEU:HD13	1:A2:102:LEU:CD2	2.46	0.41
1:CH:129:THR:O	1:CH:131:ALA:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BL:55:ALA:HB1	1:BL:95:VAL:CG2	2.40	0.41
1:CL:55:ALA:CB	1:CL:95:VAL:HG21	2.40	0.41
1:CG:58:ILE:O	1:CG:62:ALA:CB	2.69	0.41
1:A1:58:ILE:O	1:A1:62:ALA:CB	2.69	0.41
1:AF:52:VAL:HB	1:AF:53:PRO:CD	2.50	0.41
1:CC:39:ARG:NE	1:CS:20:ARG:CZ	2.84	0.41
1:CH:34:LEU:HD22	1:CH:38:LYS:CE	2.43	0.41
1:AA:58:ILE:N	1:AA:59:PRO:CD	2.84	0.41
1:AZ:76:THR:CG2	1:AZ:112:PHE:HA	2.51	0.41
1:BJ:64:LYS:HD3	1:BJ:64:LYS:HA	1.85	0.41
1:AE:14:VAL:HG21	1:AE:37:LEU:HD22	2.03	0.41
1:C4:14:VAL:HG12	1:C4:15:GLY:N	2.36	0.41
1:AY:14:VAL:HG21	1:AY:37:LEU:HD22	2.03	0.41
1:AJ:95:VAL:HG12	1:AJ:112:PHE:HE1	1.85	0.41
1:AJ:14:VAL:HG12	1:AJ:15:GLY:N	2.36	0.41
1:BY:14:VAL:HG12	1:BY:15:GLY:N	2.36	0.41
1:B3:7:LEU:HD12	1:B3:7:LEU:HA	1.96	0.41
1:BP:18:VAL:HG22	1:BP:77:LEU:HB2	2.02	0.41
1:CG:129:THR:CG2	1:CG:130:LYS:H	2.28	0.41
1:C1:129:THR:CG2	1:C1:130:LYS:H	2.28	0.41
1:AQ:71:TYR:O	1:AQ:108:ILE:HD13	2.21	0.41
1:AQ:65:MET:HE3	1:AQ:71:TYR:CE2	2.56	0.41
1:CQ:65:MET:HE3	1:CQ:71:TYR:CE2	2.56	0.41
1:AB:71:TYR:O	1:AB:108:ILE:HD13	2.21	0.41
1:BW:83:GLY:HA3	2:BW:1001:PO4:O3	2.20	0.41
1:AW:83:GLY:HA3	2:AW:201:PO4:P	2.60	0.41
1:BO:14:VAL:HG12	1:BO:15:GLY:N	2.36	0.41
1:B2:95:VAL:HG12	1:B2:112:PHE:HE1	1.86	0.41
1:CP:106:THR:C	1:CP:108:ILE:H	2.23	0.41
1:BG:83:GLY:HA3	2:BG:1001:PO4:O1	2.21	0.41
1:AI:29:LEU:HD11	1:AI:134:LYS:HB3	2.02	0.41
1:BQ:83:GLY:HA3	2:BQ:1001:PO4:O1	2.21	0.41
1:CB:31:GLY:O	1:CB:35:ASP:HB2	2.20	0.41
1:BB:83:GLY:HA3	2:BB:1001:PO4:O1	2.21	0.41
1:AP:26:THR:HA	1:AP:29:LEU:HB3	2.03	0.41
1:CV:31:GLY:O	1:CV:35:ASP:HB2	2.20	0.41
1:BG:111:ILE:HD12	1:BG:111:ILE:N	2.36	0.41
1:CF:26:THR:HA	1:CF:29:LEU:HB3	2.03	0.41
1:C1:83:GLY:HA3	2:C1:1201:PO4:O1	2.21	0.41
1:AS:97:LYS:HG3	1:AT:97:LYS:HZ1	1.86	0.40
1:BQ:58:ILE:O	1:BQ:62:ALA:CB	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:30:LEU:HA	1:AY:77:LEU:HD23	2.02	0.40
1:BR:15:GLY:HA3	1:BR:65:MET:HE1	2.02	0.40
1:AC:15:GLY:HA3	1:AC:65:MET:HE1	2.03	0.40
1:AP:76:THR:CG2	1:AP:112:PHE:HA	2.51	0.40
1:AE:14:VAL:HG12	1:AE:15:GLY:N	2.36	0.40
1:CZ:7:LEU:HA	1:CZ:7:LEU:HD12	1.84	0.40
1:CK:18:VAL:HG22	1:CK:77:LEU:HB2	2.02	0.40
1:CQ:71:TYR:O	1:CQ:108:ILE:HD13	2.21	0.40
1:CD:98:GLY:HA2	1:CD:102:LEU:HD23	2.02	0.40
1:BJ:14:VAL:HG12	1:BJ:15:GLY:N	2.36	0.40
1:AQ:83:GLY:HA3	2:AQ:1001:PO4:O1	2.21	0.40
1:B1:25:ILE:HG23	1:B1:127:ALA:HB2	2.03	0.40
1:CB:25:ILE:HG23	1:CB:127:ALA:HB2	2.03	0.40
1:CD:29:LEU:HD11	1:CD:134:LYS:HB3	2.02	0.40
1:BQ:111:ILE:HD12	1:BQ:111:ILE:N	2.36	0.40
1:CG:111:ILE:N	1:CG:111:ILE:HD12	2.37	0.40
1:AV:25:ILE:HG23	1:AV:127:ALA:HB2	2.03	0.40
1:B1:83:GLY:HA3	2:B1:1001:PO4:O1	2.21	0.40
1:CP:32:GLY:HA3	1:CP:135:GLY:C	2.42	0.40
1:AK:26:THR:HA	1:AK:29:LEU:HB3	2.04	0.40
1:A1:23:GLU:HA	1:A1:26:THR:OG1	2.22	0.40
1:AL:23:GLU:HA	1:AL:26:THR:OG1	2.21	0.40
1:CY:108:ILE:CG1	1:CY:150:LYS:HE3	2.42	0.40
1:BG:58:ILE:O	1:BG:62:ALA:CB	2.69	0.40
1:CG:55:ALA:HA	1:CG:58:ILE:HG13	2.02	0.40
1:A3:97:LYS:HG3	1:A4:97:LYS:HZ1	1.86	0.40
1:BM:20:ARG:HH11	1:BM:20:ARG:HB3	1.87	0.40
1:CZ:76:THR:CG2	1:CZ:112:PHE:HA	2.51	0.40
1:AO:14:VAL:HG21	1:AO:37:LEU:HD22	2.03	0.40
1:CY:14:VAL:HG21	1:CY:37:LEU:HD22	2.03	0.40
1:B2:63:LYS:O	1:B2:65:MET:N	2.53	0.40
1:BW:95:VAL:HG12	1:BW:112:PHE:HE1	1.86	0.40
1:A4:14:VAL:HG12	1:A4:15:GLY:N	2.36	0.40
1:CR:95:VAL:HG12	1:CR:112:PHE:HE1	1.86	0.40
1:BF:32:GLY:HA3	1:BF:135:GLY:C	2.42	0.40
1:CF:116:THR:O	1:CG:85:THR:HB	2.20	0.40
1:CU:32:GLY:HA3	1:CU:135:GLY:C	2.42	0.40
1:CV:25:ILE:HG23	1:CV:127:ALA:HB2	2.03	0.40
1:AQ:111:ILE:N	1:AQ:111:ILE:HD12	2.36	0.40
1:BW:148:LEU:HA	1:BW:148:LEU:HD23	1.80	0.40
1:AG:83:GLY:HA3	2:AG:1001:PO4:O1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:53:PRO:HD2	1:AT:57:GLU:CB	2.52	0.40
1:BW:121:GLU:O	1:BW:125:GLU:HB2	2.22	0.40
1:AG:58:ILE:O	1:AG:62:ALA:CB	2.69	0.40
1:AL:58:ILE:O	1:AL:62:ALA:CB	2.69	0.40
1:B1:58:ILE:O	1:B1:62:ALA:CB	2.69	0.40
1:CL:55:ALA:HA	1:CL:58:ILE:HG13	2.02	0.40
1:AK:53:PRO:HD2	1:AK:57:GLU:CB	2.49	0.40
1:B4:129:THR:O	1:B4:130:LYS:C	2.59	0.40
1:CZ:58:ILE:N	1:CZ:59:PRO:CD	2.84	0.40
1:CW:15:GLY:HA3	1:CW:65:MET:HE1	2.04	0.40
1:CM:106:THR:HG23	1:CM:107:ASP:N	2.37	0.40
1:AO:14:VAL:HG12	1:AO:15:GLY:N	2.36	0.40
1:BH:106:THR:HG23	1:BH:107:ASP:N	2.37	0.40
1:CO:14:VAL:HG12	1:CO:15:GLY:N	2.36	0.40
1:CO:14:VAL:HG21	1:CO:37:LEU:HD22	2.03	0.40
1:AH:106:THR:HG23	1:AH:107:ASP:N	2.37	0.40
1:CJ:14:VAL:HG12	1:CJ:15:GLY:N	2.36	0.40
1:CI:7:LEU:HD12	1:CI:7:LEU:HA	1.96	0.40
1:BF:28:LYS:HE3	1:BR:28:LYS:NZ	2.37	0.40
1:AL:71:TYR:O	1:AL:108:ILE:HD13	2.21	0.40
1:BN:98:GLY:HA2	1:BN:102:LEU:HD23	2.02	0.40
1:BB:71:TYR:O	1:BB:108:ILE:HD13	2.21	0.40
1:BE:14:VAL:HG12	1:BE:15:GLY:N	2.36	0.40
1:BL:23:GLU:HA	1:BL:26:THR:OG1	2.22	0.40
1:BV:23:GLU:HA	1:BV:26:THR:OG1	2.22	0.40
1:BK:106:THR:C	1:BK:108:ILE:H	2.23	0.40
1:CQ:122:GLN:O	1:CQ:126:ARG:HD2	2.22	0.40
1:AP:67:ASN:HA	1:AP:67:ASN:HD22	1.69	0.40
1:AV:83:GLY:HA3	2:AV:1001:PO4:O1	2.21	0.40
1:CG:23:GLU:HA	1:CG:26:THR:OG1	2.22	0.40
1:C1:122:GLN:O	1:C1:126:ARG:HD2	2.22	0.40
1:CK:32:GLY:HA3	1:CK:135:GLY:C	2.42	0.40
1:AE:52:VAL:CB	1:AE:53:PRO:CD	2.98	0.40
1:AJ:53:PRO:HD2	1:AJ:57:GLU:CB	2.52	0.40
1:BY:53:PRO:HD2	1:BY:57:GLU:CB	2.52	0.40
1:C2:121:GLU:O	1:C2:125:GLU:HB2	2.22	0.40
1:BE:71:TYR:O	1:BE:150:LYS:NZ	2.44	0.40
1:B4:65:MET:HE3	1:B4:71:TYR:CE2	2.56	0.40
1:CT:65:MET:HE3	1:CT:71:TYR:CE2	2.57	0.40
1:BB:58:ILE:O	1:BB:62:ALA:CB	2.69	0.40
1:CA:97:LYS:NZ	1:CE:97:LYS:HG3	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:129:THR:O	1:AO:130:LYS:C	2.59	0.40
1:CT:129:THR:O	1:CT:130:LYS:C	2.59	0.40
1:CM:34:LEU:HD22	1:CM:38:LYS:CE	2.43	0.40
1:BY:30:LEU:HA	1:BY:77:LEU:HD23	2.02	0.40
1:AA:76:THR:CG2	1:AA:112:PHE:HA	2.51	0.40
1:AF:58:ILE:N	1:AF:59:PRO:CD	2.84	0.40
1:AW:106:THR:HG23	1:AW:107:ASP:N	2.37	0.40
1:C3:17:VAL:CG2	1:C3:76:THR:HG22	2.52	0.40
1:C4:14:VAL:HG21	1:C4:37:LEU:HD22	2.03	0.40
1:AJ:14:VAL:HG21	1:AJ:37:LEU:HD22	2.03	0.40
1:BN:17:VAL:CG2	1:BN:76:THR:HG22	2.52	0.40
1:CN:98:GLY:HA2	1:CN:102:LEU:HD23	2.02	0.40
1:AW:95:VAL:HG12	1:AW:112:PHE:HE1	1.86	0.40
1:CG:83:GLY:HA3	2:CG:1201:PO4:O1	2.21	0.40
1:BU:26:THR:HA	1:BU:29:LEU:HB3	2.04	0.40
1:CB:23:GLU:HA	1:CB:26:THR:OG1	2.21	0.40
1:CL:23:GLU:HA	1:CL:26:THR:OG1	2.21	0.40
1:BL:83:GLY:HA3	2:BL:1001:PO4:O1	2.21	0.40
1:AB:122:GLN:O	1:AB:126:ARG:HD2	2.22	0.40
1:CQ:25:ILE:HG23	1:CQ:127:ALA:HB2	2.03	0.40
1:AU:151:HIS:O	1:AU:151:HIS:CD2	2.75	0.40
1:BF:151:HIS:CD2	1:BF:151:HIS:O	2.75	0.40
1:CF:151:HIS:CD2	1:CF:151:HIS:O	2.75	0.40
1:AE:53:PRO:HD2	1:AE:57:GLU:CB	2.52	0.40
1:BO:53:PRO:HD2	1:BO:57:GLU:CB	2.52	0.40
1:CE:53:PRO:HD2	1:CE:57:GLU:CB	2.52	0.40
1:AY:53:PRO:HD2	1:AY:57:GLU:CB	2.52	0.40
1:CW:121:GLU:O	1:CW:125:GLU:HB2	2.22	0.40
1:CH:121:GLU:O	1:CH:125:GLU:HB2	2.22	0.40
1:AB:104:LEU:HD23	1:AC:60:LEU:CD1	2.52	0.40
1:BQ:104:LEU:HD23	1:BR:60:LEU:CD1	2.52	0.40
1:BY:65:MET:HE3	1:BY:71:TYR:CE2	2.56	0.40
1:AF:97:LYS:NZ	1:AJ:97:LYS:HG3	2.37	0.40
1:AU:76:THR:CG2	1:AU:112:PHE:HA	2.51	0.40
1:B4:30:LEU:HA	1:B4:77:LEU:HD23	2.02	0.40
1:CU:129:THR:HB	1:CU:130:LYS:H	1.75	0.40
1:CH:15:GLY:HA3	1:CH:65:MET:HE1	2.02	0.40
1:BU:58:ILE:N	1:BU:59:PRO:CD	2.84	0.40
1:BP:76:THR:CG2	1:BP:112:PHE:HA	2.51	0.40
1:C2:106:THR:HG23	1:C2:107:ASP:N	2.37	0.40
1:B2:106:THR:HG23	1:B2:107:ASP:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CN:17:VAL:CG2	1:CN:76:THR:HG22	2.52	0.40
1:BT:64:LYS:HA	1:BT:64:LYS:HD3	1.85	0.40
1:AR:106:THR:HG23	1:AR:107:ASP:N	2.37	0.40
1:AT:14:VAL:HG21	1:AT:37:LEU:HD22	2.03	0.40
1:AC:106:THR:HG23	1:AC:107:ASP:N	2.37	0.40
1:CY:14:VAL:HG12	1:CY:15:GLY:N	2.36	0.40
1:CD:17:VAL:CG2	1:CD:76:THR:HG22	2.52	0.40
1:CX:17:VAL:CG2	1:CX:76:THR:HG22	2.52	0.40
1:BS:40:HIS:CE1	1:BY:7:LEU:HD23	2.57	0.40
1:CT:8:VAL:HG22	1:C3:8:VAL:HG13	2.01	0.40
1:CH:28:LYS:HZ3	1:CU:28:LYS:CE	2.34	0.40
1:BA:15:GLY:HA3	1:BA:65:MET:CE	2.52	0.40
1:BB:23:GLU:HA	1:BB:26:THR:OG1	2.22	0.40
1:BZ:106:THR:C	1:BZ:108:ILE:H	2.23	0.40
1:BK:26:THR:HA	1:BK:29:LEU:HB3	2.04	0.40
1:BU:32:GLY:HA3	1:BU:135:GLY:C	2.42	0.40
1:CF:32:GLY:HA3	1:CF:135:GLY:C	2.42	0.40
1:BH:80:VAL:HG12	1:BH:88:TYR:CD1	2.57	0.40
1:C1:25:ILE:HG23	1:C1:127:ALA:HB2	2.03	0.40
1:BF:26:THR:HA	1:BF:29:LEU:HB3	2.03	0.40
1:AV:111:ILE:N	1:AV:111:ILE:HD12	2.36	0.40
1:CZ:151:HIS:O	1:CZ:151:HIS:CG	2.75	0.40
1:AF:151:HIS:CD2	1:AF:151:HIS:O	2.75	0.40
1:AP:151:HIS:CD2	1:AP:151:HIS:O	2.75	0.40
1:AG:122:GLN:O	1:AG:126:ARG:HD2	2.22	0.40
1:BW:80:VAL:HG12	1:BW:88:TYR:CD1	2.57	0.40
1:CM:80:VAL:HG12	1:CM:88:TYR:CD1	2.57	0.40
1:AU:26:THR:HA	1:AU:29:LEU:HB3	2.03	0.40

All (13) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:153:ALA:O	1:AH:46:ASP:OD1[2_565]	1.84	0.36
1:AH:69:GLY:O	1:AH:69:GLY:O[2_565]	1.90	0.30
1:BJ:151:HIS:CE1	1:CY:13:LYS:CE[2_665]	1.91	0.29
1:CB:153:ALA:O	1:CC:69:GLY:CA[2_565]	1.94	0.26
1:CH:39:ARG:NH2	1:CM:20:ARG:NH1[2_665]	1.96	0.24
1:BL:11:GLY:O	1:CG:153:ALA:C[1_545]	1.99	0.21
1:BL:72:ASP:OD2	1:CG:153:ALA:O[1_545]	2.03	0.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:153:ALA:O	1:CC:69:GLY:N[2_565]	2.10	0.10
1:CZ:24:PHE:CB	1:C4:128:GLY:O[2_665]	2.12	0.08
1:BL:72:ASP:OD2	1:CG:153:ALA:CB[1_545]	2.13	0.07
1:CH:39:ARG:NH2	1:CM:20:ARG:NH2[2_665]	2.17	0.03
1:AG:153:ALA:CB	1:AH:46:ASP:OD1[2_565]	2.18	0.02
1:CH:39:ARG:NH2	1:CM:20:ARG:CZ[2_665]	2.19	0.01

## 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	A1	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	A2	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	A3	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	A4	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	AA	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	AB	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	AC	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	AD	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	AE	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	AF	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	AG	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	AH	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	AI	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	AJ	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	AK	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	AL	150/153 (98%)	132 (88%)	18 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AM	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	AN	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	AO	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	AP	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	AQ	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	AR	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	AS	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	AT	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	AU	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	AV	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	AW	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	AX	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	AY	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	AZ	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	B1	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	B2	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	B3	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	B4	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	BA	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	BB	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	BC	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	BD	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	BE	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	BF	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	BG	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	BH	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	BI	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	BJ	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	BK	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	BL	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	BM	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BN	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	BO	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	BP	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	BQ	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	BR	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	BS	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	BT	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	BU	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	BV	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	BW	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	BX	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	BY	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	BZ	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	C1	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	C2	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	C3	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	C4	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	CA	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	CB	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	CC	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	CD	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	CE	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	CF	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	CG	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	CH	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	CI	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	CJ	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	CK	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	CL	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	CM	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	CN	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CO	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	CP	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	CQ	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	CR	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	CS	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	CT	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	CU	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
1	CV	150/153 (98%)	132 (88%)	18 (12%)	0	100	100
1	CW	150/153 (98%)	126 (84%)	19 (13%)	5 (3%)	5	39
1	CX	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	15	60
1	CY	150/153 (98%)	133 (89%)	17 (11%)	0	100	100
1	CZ	150/153 (98%)	129 (86%)	19 (13%)	2 (1%)	15	60
All	All	13500/13770 (98%)	11826 (88%)	1512 (11%)	162 (1%)	16	61

All (162) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AC	130	LYS
1	AH	130	LYS
1	AM	130	LYS
1	AR	130	LYS
1	AW	130	LYS
1	A2	130	LYS
1	BC	130	LYS
1	BH	130	LYS
1	BM	130	LYS
1	BR	130	LYS
1	BW	130	LYS
1	B2	130	LYS
1	CC	130	LYS
1	CH	130	LYS
1	CM	130	LYS
1	CR	130	LYS
1	CW	130	LYS
1	C2	130	LYS
1	AA	33	ALA
1	AA	36	GLY
1	AC	64	LYS

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Mol	Chain	Res	Type
1	AF	33	ALA
1	AF	36	GLY
1	AH	64	LYS
1	AK	33	ALA
1	AK	36	GLY
1	AM	64	LYS
1	AP	33	ALA
1	AP	36	GLY
1	AR	64	LYS
1	AU	33	ALA
1	AU	36	GLY
1	AW	64	LYS
1	AZ	33	ALA
1	AZ	36	GLY
1	A2	64	LYS
1	BA	33	ALA
1	BA	36	GLY
1	BC	64	LYS
1	BF	33	ALA
1	BF	36	GLY
1	BH	64	LYS
1	BK	33	ALA
1	BK	36	GLY
1	BM	64	LYS
1	BP	33	ALA
1	BP	36	GLY
1	BR	64	LYS
1	BU	33	ALA
1	BU	36	GLY
1	BW	64	LYS
1	BZ	33	ALA
1	BZ	36	GLY
1	B2	64	LYS
1	CA	33	ALA
1	CA	36	GLY
1	CC	64	LYS
1	CF	33	ALA
1	CF	36	GLY
1	CH	64	LYS
1	CK	33	ALA
1	CK	36	GLY
1	CM	64	LYS

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Mol	Chain	Res	Type
1	CP	33	ALA
1	CP	36	GLY
1	CR	64	LYS
1	CU	33	ALA
1	CU	36	GLY
1	CW	64	LYS
1	CZ	33	ALA
1	CZ	36	GLY
1	C2	64	LYS
1	AD	53	PRO
1	AI	53	PRO
1	AN	53	PRO
1	AS	53	PRO
1	AX	53	PRO
1	A3	53	PRO
1	BD	53	PRO
1	BI	53	PRO
1	BN	53	PRO
1	BS	53	PRO
1	BX	53	PRO
1	B3	53	PRO
1	CD	53	PRO
1	CI	53	PRO
1	CN	53	PRO
1	CS	53	PRO
1	CX	53	PRO
1	C3	53	PRO
1	AC	36	GLY
1	AC	53	PRO
1	AH	36	GLY
1	AH	53	PRO
1	AM	36	GLY
1	AM	53	PRO
1	AR	36	GLY
1	AR	53	PRO
1	AW	36	GLY
1	AW	53	PRO
1	A2	36	GLY
1	A2	53	PRO
1	BC	36	GLY
1	BC	53	PRO
1	BH	36	GLY

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Mol	Chain	Res	Type
1	BH	53	PRO
1	BM	36	GLY
1	BM	53	PRO
1	BR	36	GLY
1	BR	53	PRO
1	BW	36	GLY
1	BW	53	PRO
1	B2	36	GLY
1	B2	53	PRO
1	CC	36	GLY
1	CC	53	PRO
1	CH	36	GLY
1	CH	53	PRO
1	CM	36	GLY
1	CM	53	PRO
1	CR	36	GLY
1	CR	53	PRO
1	CW	36	GLY
1	CW	53	PRO
1	C2	36	GLY
1	C2	53	PRO
1	AD	130	LYS
1	AI	130	LYS
1	AN	130	LYS
1	AS	130	LYS
1	AX	130	LYS
1	A3	130	LYS
1	BD	130	LYS
1	BI	130	LYS
1	BN	130	LYS
1	BS	130	LYS
1	BX	130	LYS
1	B3	130	LYS
1	CD	130	LYS
1	CI	130	LYS
1	CN	130	LYS
1	CS	130	LYS
1	CX	130	LYS
1	C3	130	LYS
1	AC	69	GLY
1	AH	69	GLY
1	AM	69	GLY

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Mol	Chain	Res	Type
1	AR	69	GLY
1	AW	69	GLY
1	A2	69	GLY
1	BC	69	GLY
1	BH	69	GLY
1	BM	69	GLY
1	BR	69	GLY
1	BW	69	GLY
1	B2	69	GLY
1	CC	69	GLY
1	CH	69	GLY
1	CM	69	GLY
1	CR	69	GLY
1	CW	69	GLY
1	C2	69	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	A1	115/118 (98%)	105 (91%)	10 (9%)	13	48
1	A2	116/118 (98%)	112 (97%)	4 (3%)	44	79
1	A3	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	A4	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AA	115/118 (98%)	110 (96%)	5 (4%)	35	74
1	AB	115/118 (98%)	105 (91%)	10 (9%)	13	48
1	AC	116/118 (98%)	112 (97%)	4 (3%)	44	79
1	AD	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AE	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AF	115/118 (98%)	110 (96%)	5 (4%)	35	74
1	AG	115/118 (98%)	105 (91%)	10 (9%)	13	48
1	AH	116/118 (98%)	112 (97%)	4 (3%)	44	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AI	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AJ	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AK	115/118 (98%)	110 (96%)	5 (4%)	35	74
1	AL	115/118 (98%)	105 (91%)	10 (9%)	13	48
1	AM	116/118 (98%)	112 (97%)	4 (3%)	44	79
1	AN	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AO	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AP	115/118 (98%)	110 (96%)	5 (4%)	35	74
1	AQ	115/118 (98%)	105 (91%)	10 (9%)	13	48
1	AR	116/118 (98%)	112 (97%)	4 (3%)	44	79
1	AS	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AT	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AU	115/118 (98%)	110 (96%)	5 (4%)	35	74
1	AV	115/118 (98%)	105 (91%)	10 (9%)	13	48
1	AW	116/118 (98%)	112 (97%)	4 (3%)	44	79
1	AX	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AY	116/118 (98%)	108 (93%)	8 (7%)	19	59
1	AZ	115/118 (98%)	110 (96%)	5 (4%)	35	74
1	B1	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	B2	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	B3	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	B4	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BA	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	BB	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	BC	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	BD	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BE	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BF	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	BG	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	BH	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	BI	117/118 (99%)	109 (93%)	8 (7%)	20	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BJ	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BK	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	BL	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	BM	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	BN	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BO	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BP	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	BQ	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	BR	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	BS	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BT	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BU	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	BV	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	BW	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	BX	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BY	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	BZ	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	C1	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	C2	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	C3	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	C4	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CA	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	CB	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	CC	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	CD	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CE	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CF	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	CG	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	CH	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	CI	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CJ	117/118 (99%)	109 (93%)	8 (7%)	20	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CK	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	CL	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	CM	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	CN	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CO	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CP	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	CQ	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	CR	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	CS	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CT	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CU	117/118 (99%)	112 (96%)	5 (4%)	35	74
1	CV	117/118 (99%)	107 (92%)	10 (8%)	13	49
1	CW	117/118 (99%)	113 (97%)	4 (3%)	44	79
1	CX	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CY	117/118 (99%)	109 (93%)	8 (7%)	20	60
1	CZ	117/118 (99%)	112 (96%)	5 (4%)	35	74
All	All	10488/10620 (99%)	9858 (94%)	630 (6%)	24	64

All (630) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AA	6	HIS
1	AA	21	PHE
1	AA	116	THR
1	AA	147	HIS
1	AA	150	LYS
1	AB	34	LEU
1	AB	43	GLU
1	AB	77	LEU
1	AB	88	TYR
1	AB	103	SER
1	AB	104	LEU
1	AB	106	THR
1	AB	109	PRO
1	AB	116	THR
1	AB	152	TRP

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Mol	Chain	Res	Type
1	AC	45	ASN
1	AC	67	ASN
1	AC	82	ARG
1	AC	109	PRO
1	AD	67	ASN
1	AD	77	LEU
1	AD	106	THR
1	AD	109	PRO
1	AD	116	THR
1	AD	129	THR
1	AD	130	LYS
1	AD	152	TRP
1	AE	77	LEU
1	AE	88	TYR
1	AE	107	ASP
1	AE	116	THR
1	AE	129	THR
1	AE	149	SER
1	AE	150	LYS
1	AE	152	TRP
1	AF	6	HIS
1	AF	21	PHE
1	AF	116	THR
1	AF	147	HIS
1	AF	150	LYS
1	AG	34	LEU
1	AG	43	GLU
1	AG	77	LEU
1	AG	88	TYR
1	AG	103	SER
1	AG	104	LEU
1	AG	106	THR
1	AG	109	PRO
1	AG	116	THR
1	AG	152	TRP
1	AH	45	ASN
1	AH	67	ASN
1	AH	82	ARG
1	AH	109	PRO
1	AI	67	ASN
1	AI	77	LEU
1	AI	106	THR

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Mol	Chain	Res	Type
1	AI	109	PRO
1	AI	116	THR
1	AI	129	THR
1	AI	130	LYS
1	AI	152	TRP
1	AJ	77	LEU
1	AJ	88	TYR
1	AJ	107	ASP
1	AJ	116	THR
1	AJ	129	THR
1	AJ	149	SER
1	AJ	150	LYS
1	AJ	152	TRP
1	AK	6	HIS
1	AK	21	PHE
1	AK	116	THR
1	AK	147	HIS
1	AK	150	LYS
1	AL	34	LEU
1	AL	43	GLU
1	AL	77	LEU
1	AL	88	TYR
1	AL	103	SER
1	AL	104	LEU
1	AL	106	THR
1	AL	109	PRO
1	AL	116	THR
1	AL	152	TRP
1	AM	45	ASN
1	AM	67	ASN
1	AM	82	ARG
1	AM	109	PRO
1	AN	67	ASN
1	AN	77	LEU
1	AN	106	THR
1	AN	109	PRO
1	AN	116	THR
1	AN	129	THR
1	AN	130	LYS
1	AN	152	TRP
1	AO	77	LEU
1	AO	88	TYR

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Mol	Chain	Res	Type
1	AO	107	ASP
1	AO	116	THR
1	AO	129	THR
1	AO	149	SER
1	AO	150	LYS
1	AO	152	TRP
1	AP	6	HIS
1	AP	21	PHE
1	AP	116	THR
1	AP	147	HIS
1	AP	150	LYS
1	AQ	34	LEU
1	AQ	43	GLU
1	AQ	77	LEU
1	AQ	88	TYR
1	AQ	103	SER
1	AQ	104	LEU
1	AQ	106	THR
1	AQ	109	PRO
1	AQ	116	THR
1	AQ	152	TRP
1	AR	45	ASN
1	AR	67	ASN
1	AR	82	ARG
1	AR	109	PRO
1	AS	67	ASN
1	AS	77	LEU
1	AS	106	THR
1	AS	109	PRO
1	AS	116	THR
1	AS	129	THR
1	AS	130	LYS
1	AS	152	TRP
1	AT	77	LEU
1	AT	88	TYR
1	AT	107	ASP
1	AT	116	THR
1	AT	129	THR
1	AT	149	SER
1	AT	150	LYS
1	AT	152	TRP
1	AU	6	HIS

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Mol	Chain	Res	Type
1	AU	21	PHE
1	AU	116	THR
1	AU	147	HIS
1	AU	150	LYS
1	AV	34	LEU
1	AV	43	GLU
1	AV	77	LEU
1	AV	88	TYR
1	AV	103	SER
1	AV	104	LEU
1	AV	106	THR
1	AV	109	PRO
1	AV	116	THR
1	AV	152	TRP
1	AW	45	ASN
1	AW	67	ASN
1	AW	82	ARG
1	AW	109	PRO
1	AX	67	ASN
1	AX	77	LEU
1	AX	106	THR
1	AX	109	PRO
1	AX	116	THR
1	AX	129	THR
1	AX	130	LYS
1	AX	152	TRP
1	AY	77	LEU
1	AY	88	TYR
1	AY	107	ASP
1	AY	116	THR
1	AY	129	THR
1	AY	149	SER
1	AY	150	LYS
1	AY	152	TRP
1	AZ	6	HIS
1	AZ	21	PHE
1	AZ	116	THR
1	AZ	147	HIS
1	AZ	150	LYS
1	A1	34	LEU
1	A1	43	GLU
1	A1	77	LEU

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Mol	Chain	Res	Type
1	A1	88	TYR
1	A1	103	SER
1	A1	104	LEU
1	A1	106	THR
1	A1	109	PRO
1	A1	116	THR
1	A1	152	TRP
1	A2	45	ASN
1	A2	67	ASN
1	A2	82	ARG
1	A2	109	PRO
1	A3	67	ASN
1	A3	77	LEU
1	A3	106	THR
1	A3	109	PRO
1	A3	116	THR
1	A3	129	THR
1	A3	130	LYS
1	A3	152	TRP
1	A4	77	LEU
1	A4	88	TYR
1	A4	107	ASP
1	A4	116	THR
1	A4	129	THR
1	A4	149	SER
1	A4	150	LYS
1	A4	152	TRP
1	BA	6	HIS
1	BA	21	PHE
1	BA	116	THR
1	BA	147	HIS
1	BA	150	LYS
1	BB	34	LEU
1	BB	43	GLU
1	BB	77	LEU
1	BB	88	TYR
1	BB	103	SER
1	BB	104	LEU
1	BB	106	THR
1	BB	109	PRO
1	BB	116	THR
1	BB	152	TRP

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Mol	Chain	Res	Type
1	BC	45	ASN
1	BC	67	ASN
1	BC	82	ARG
1	BC	109	PRO
1	BD	67	ASN
1	BD	77	LEU
1	BD	106	THR
1	BD	109	PRO
1	BD	116	THR
1	BD	129	THR
1	BD	130	LYS
1	BD	152	TRP
1	BE	77	LEU
1	BE	88	TYR
1	BE	107	ASP
1	BE	116	THR
1	BE	129	THR
1	BE	149	SER
1	BE	150	LYS
1	BE	152	TRP
1	BF	6	HIS
1	BF	21	PHE
1	BF	116	THR
1	BF	147	HIS
1	BF	150	LYS
1	BG	34	LEU
1	BG	43	GLU
1	BG	77	LEU
1	BG	88	TYR
1	BG	103	SER
1	BG	104	LEU
1	BG	106	THR
1	BG	109	PRO
1	BG	116	THR
1	BG	152	TRP
1	BH	45	ASN
1	BH	67	ASN
1	BH	82	ARG
1	BH	109	PRO
1	BI	67	ASN
1	BI	77	LEU
1	BI	106	THR

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Mol	Chain	Res	Type
1	BI	109	PRO
1	BI	116	THR
1	BI	129	THR
1	BI	130	LYS
1	BI	152	TRP
1	BJ	77	LEU
1	BJ	88	TYR
1	BJ	107	ASP
1	BJ	116	THR
1	BJ	129	THR
1	BJ	149	SER
1	BJ	150	LYS
1	BJ	152	TRP
1	BK	6	HIS
1	BK	21	PHE
1	BK	116	THR
1	BK	147	HIS
1	BK	150	LYS
1	BL	34	LEU
1	BL	43	GLU
1	BL	77	LEU
1	BL	88	TYR
1	BL	103	SER
1	BL	104	LEU
1	BL	106	THR
1	BL	109	PRO
1	BL	116	THR
1	BL	152	TRP
1	BM	45	ASN
1	BM	67	ASN
1	BM	82	ARG
1	BM	109	PRO
1	BN	67	ASN
1	BN	77	LEU
1	BN	106	THR
1	BN	109	PRO
1	BN	116	THR
1	BN	129	THR
1	BN	130	LYS
1	BN	152	TRP
1	BO	77	LEU
1	BO	88	TYR

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Mol	Chain	Res	Type
1	BO	107	ASP
1	BO	116	THR
1	BO	129	THR
1	BO	149	SER
1	BO	150	LYS
1	BO	152	TRP
1	BP	6	HIS
1	BP	21	PHE
1	BP	116	THR
1	BP	147	HIS
1	BP	150	LYS
1	BQ	34	LEU
1	BQ	43	GLU
1	BQ	77	LEU
1	BQ	88	TYR
1	BQ	103	SER
1	BQ	104	LEU
1	BQ	106	THR
1	BQ	109	PRO
1	BQ	116	THR
1	BQ	152	TRP
1	BR	45	ASN
1	BR	67	ASN
1	BR	82	ARG
1	BR	109	PRO
1	BS	67	ASN
1	BS	77	LEU
1	BS	106	THR
1	BS	109	PRO
1	BS	116	THR
1	BS	129	THR
1	BS	130	LYS
1	BS	152	TRP
1	BT	77	LEU
1	BT	88	TYR
1	BT	107	ASP
1	BT	116	THR
1	BT	129	THR
1	BT	149	SER
1	BT	150	LYS
1	BT	152	TRP
1	BU	6	HIS

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Mol	Chain	Res	Type
1	BU	21	PHE
1	BU	116	THR
1	BU	147	HIS
1	BU	150	LYS
1	BV	34	LEU
1	BV	43	GLU
1	BV	77	LEU
1	BV	88	TYR
1	BV	103	SER
1	BV	104	LEU
1	BV	106	THR
1	BV	109	PRO
1	BV	116	THR
1	BV	152	TRP
1	BW	45	ASN
1	BW	67	ASN
1	BW	82	ARG
1	BW	109	PRO
1	BX	67	ASN
1	BX	77	LEU
1	BX	106	THR
1	BX	109	PRO
1	BX	116	THR
1	BX	129	THR
1	BX	130	LYS
1	BX	152	TRP
1	BY	77	LEU
1	BY	88	TYR
1	BY	107	ASP
1	BY	116	THR
1	BY	129	THR
1	BY	149	SER
1	BY	150	LYS
1	BY	152	TRP
1	BZ	6	HIS
1	BZ	21	PHE
1	BZ	116	THR
1	BZ	147	HIS
1	BZ	150	LYS
1	B1	34	LEU
1	B1	43	GLU
1	B1	77	LEU

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Mol	Chain	Res	Type
1	B1	88	TYR
1	B1	103	SER
1	B1	104	LEU
1	B1	106	THR
1	B1	109	PRO
1	B1	116	THR
1	B1	152	TRP
1	B2	45	ASN
1	B2	67	ASN
1	B2	82	ARG
1	B2	109	PRO
1	B3	67	ASN
1	B3	77	LEU
1	B3	106	THR
1	B3	109	PRO
1	B3	116	THR
1	B3	129	THR
1	B3	130	LYS
1	B3	152	TRP
1	B4	77	LEU
1	B4	88	TYR
1	B4	107	ASP
1	B4	116	THR
1	B4	129	THR
1	B4	149	SER
1	B4	150	LYS
1	B4	152	TRP
1	CA	6	HIS
1	CA	21	PHE
1	CA	116	THR
1	CA	147	HIS
1	CA	150	LYS
1	CB	34	LEU
1	CB	43	GLU
1	CB	77	LEU
1	CB	88	TYR
1	CB	103	SER
1	CB	104	LEU
1	CB	106	THR
1	CB	109	PRO
1	CB	116	THR
1	CB	152	TRP

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Mol	Chain	Res	Type
1	CC	45	ASN
1	CC	67	ASN
1	CC	82	ARG
1	CC	109	PRO
1	CD	67	ASN
1	CD	77	LEU
1	CD	106	THR
1	CD	109	PRO
1	CD	116	THR
1	CD	129	THR
1	CD	130	LYS
1	CD	152	TRP
1	CE	77	LEU
1	CE	88	TYR
1	CE	107	ASP
1	CE	116	THR
1	CE	129	THR
1	CE	149	SER
1	CE	150	LYS
1	CE	152	TRP
1	CF	6	HIS
1	CF	21	PHE
1	CF	116	THR
1	CF	147	HIS
1	CF	150	LYS
1	CG	34	LEU
1	CG	43	GLU
1	CG	77	LEU
1	CG	88	TYR
1	CG	103	SER
1	CG	104	LEU
1	CG	106	THR
1	CG	109	PRO
1	CG	116	THR
1	CG	152	TRP
1	CH	45	ASN
1	CH	67	ASN
1	CH	82	ARG
1	CH	109	PRO
1	CI	67	ASN
1	CI	77	LEU
1	CI	106	THR

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Mol	Chain	Res	Type
1	CI	109	PRO
1	CI	116	THR
1	CI	129	THR
1	CI	130	LYS
1	CI	152	TRP
1	CJ	77	LEU
1	CJ	88	TYR
1	CJ	107	ASP
1	CJ	116	THR
1	CJ	129	THR
1	CJ	149	SER
1	CJ	150	LYS
1	CJ	152	TRP
1	CK	6	HIS
1	CK	21	PHE
1	CK	116	THR
1	CK	147	HIS
1	CK	150	LYS
1	CL	34	LEU
1	CL	43	GLU
1	CL	77	LEU
1	CL	88	TYR
1	CL	103	SER
1	CL	104	LEU
1	CL	106	THR
1	CL	109	PRO
1	CL	116	THR
1	CL	152	TRP
1	CM	45	ASN
1	CM	67	ASN
1	CM	82	ARG
1	CM	109	PRO
1	CN	67	ASN
1	CN	77	LEU
1	CN	106	THR
1	CN	109	PRO
1	CN	116	THR
1	CN	129	THR
1	CN	130	LYS
1	CN	152	TRP
1	CO	77	LEU
1	CO	88	TYR

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Mol	Chain	Res	Type
1	CO	107	ASP
1	CO	116	THR
1	CO	129	THR
1	CO	149	SER
1	CO	150	LYS
1	CO	152	TRP
1	CP	6	HIS
1	CP	21	PHE
1	CP	116	THR
1	CP	147	HIS
1	CP	150	LYS
1	CQ	34	LEU
1	CQ	43	GLU
1	CQ	77	LEU
1	CQ	88	TYR
1	CQ	103	SER
1	CQ	104	LEU
1	CQ	106	THR
1	CQ	109	PRO
1	CQ	116	THR
1	CQ	152	TRP
1	CR	45	ASN
1	CR	67	ASN
1	CR	82	ARG
1	CR	109	PRO
1	CS	67	ASN
1	CS	77	LEU
1	CS	106	THR
1	CS	109	PRO
1	CS	116	THR
1	CS	129	THR
1	CS	130	LYS
1	CS	152	TRP
1	CT	77	LEU
1	CT	88	TYR
1	CT	107	ASP
1	CT	116	THR
1	CT	129	THR
1	CT	149	SER
1	CT	150	LYS
1	CT	152	TRP
1	CU	6	HIS

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Mol	Chain	Res	Type
1	CU	21	PHE
1	CU	116	THR
1	CU	147	HIS
1	CU	150	LYS
1	CV	34	LEU
1	CV	43	GLU
1	CV	77	LEU
1	CV	88	TYR
1	CV	103	SER
1	CV	104	LEU
1	CV	106	THR
1	CV	109	PRO
1	CV	116	THR
1	CV	152	TRP
1	CW	45	ASN
1	CW	67	ASN
1	CW	82	ARG
1	CW	109	PRO
1	CX	67	ASN
1	CX	77	LEU
1	CX	106	THR
1	CX	109	PRO
1	CX	116	THR
1	CX	129	THR
1	CX	130	LYS
1	CX	152	TRP
1	CY	77	LEU
1	CY	88	TYR
1	CY	107	ASP
1	CY	116	THR
1	CY	129	THR
1	CY	149	SER
1	CY	150	LYS
1	CY	152	TRP
1	CZ	6	HIS
1	CZ	21	PHE
1	CZ	116	THR
1	CZ	147	HIS
1	CZ	150	LYS
1	C1	34	LEU
1	C1	43	GLU
1	C1	77	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C1	88	TYR
1	C1	103	SER
1	C1	104	LEU
1	C1	106	THR
1	C1	109	PRO
1	C1	116	THR
1	C1	152	TRP
1	C2	45	ASN
1	C2	67	ASN
1	C2	82	ARG
1	C2	109	PRO
1	C3	67	ASN
1	C3	77	LEU
1	C3	106	THR
1	C3	109	PRO
1	C3	116	THR
1	C3	129	THR
1	C3	130	LYS
1	C3	152	TRP
1	C4	77	LEU
1	C4	88	TYR
1	C4	107	ASP
1	C4	116	THR
1	C4	129	THR
1	C4	149	SER
1	C4	150	LYS
1	C4	152	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (252) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AA	45	ASN
1	AA	67	ASN
1	AA	151	HIS
1	AB	45	ASN
1	AB	67	ASN
1	AB	93	ASN
1	AC	6	HIS
1	AC	45	ASN
1	AC	67	ASN
1	AC	93	ASN
1	AC	147	HIS

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Mol	Chain	Res	Type
1	AD	67	ASN
1	AD	93	ASN
1	AD	147	HIS
1	AE	67	ASN
1	AF	45	ASN
1	AF	67	ASN
1	AG	45	ASN
1	AG	67	ASN
1	AG	93	ASN
1	AH	6	HIS
1	AH	45	ASN
1	AH	67	ASN
1	AH	93	ASN
1	AH	147	HIS
1	AI	67	ASN
1	AI	93	ASN
1	AI	147	HIS
1	AJ	67	ASN
1	AK	45	ASN
1	AK	67	ASN
1	AK	151	HIS
1	AL	45	ASN
1	AL	67	ASN
1	AL	93	ASN
1	AM	45	ASN
1	AM	67	ASN
1	AM	93	ASN
1	AM	147	HIS
1	AN	67	ASN
1	AN	93	ASN
1	AN	147	HIS
1	AO	67	ASN
1	AP	45	ASN
1	AP	67	ASN
1	AP	151	HIS
1	AQ	45	ASN
1	AQ	67	ASN
1	AQ	93	ASN
1	AR	6	HIS
1	AR	45	ASN
1	AR	67	ASN
1	AR	93	ASN

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Mol	Chain	Res	Type
1	AR	147	HIS
1	AS	67	ASN
1	AS	93	ASN
1	AS	147	HIS
1	AT	67	ASN
1	AU	45	ASN
1	AU	67	ASN
1	AU	151	HIS
1	AV	45	ASN
1	AV	67	ASN
1	AV	93	ASN
1	AW	45	ASN
1	AW	67	ASN
1	AW	93	ASN
1	AW	147	HIS
1	AX	67	ASN
1	AX	93	ASN
1	AX	147	HIS
1	AY	67	ASN
1	AZ	45	ASN
1	AZ	67	ASN
1	AZ	151	HIS
1	A1	45	ASN
1	A1	67	ASN
1	A1	93	ASN
1	A2	6	HIS
1	A2	45	ASN
1	A2	67	ASN
1	A2	93	ASN
1	A2	147	HIS
1	A3	67	ASN
1	A3	93	ASN
1	A3	147	HIS
1	A4	67	ASN
1	BA	45	ASN
1	BA	67	ASN
1	BB	45	ASN
1	BB	67	ASN
1	BB	93	ASN
1	BC	45	ASN
1	BC	67	ASN
1	BC	93	ASN

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Mol	Chain	Res	Type
1	BC	147	HIS
1	BD	67	ASN
1	BD	147	HIS
1	BE	67	ASN
1	BF	45	ASN
1	BF	67	ASN
1	BF	151	HIS
1	BG	45	ASN
1	BG	67	ASN
1	BG	93	ASN
1	BH	45	ASN
1	BH	67	ASN
1	BH	93	ASN
1	BH	147	HIS
1	BI	67	ASN
1	BI	147	HIS
1	BJ	67	ASN
1	BK	45	ASN
1	BK	67	ASN
1	BK	151	HIS
1	BL	45	ASN
1	BL	67	ASN
1	BL	93	ASN
1	BM	45	ASN
1	BM	67	ASN
1	BM	93	ASN
1	BM	147	HIS
1	BN	67	ASN
1	BN	93	ASN
1	BN	147	HIS
1	BO	67	ASN
1	BP	45	ASN
1	BP	67	ASN
1	BP	151	HIS
1	BQ	45	ASN
1	BQ	67	ASN
1	BQ	93	ASN
1	BR	6	HIS
1	BR	45	ASN
1	BR	67	ASN
1	BR	93	ASN
1	BR	147	HIS

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Mol	Chain	Res	Type
1	BS	67	ASN
1	BS	93	ASN
1	BS	147	HIS
1	BT	67	ASN
1	BU	45	ASN
1	BU	67	ASN
1	BU	151	HIS
1	BV	45	ASN
1	BV	67	ASN
1	BV	93	ASN
1	BW	6	HIS
1	BW	45	ASN
1	BW	67	ASN
1	BW	93	ASN
1	BW	147	HIS
1	BX	67	ASN
1	BX	147	HIS
1	BY	67	ASN
1	BZ	45	ASN
1	BZ	67	ASN
1	BZ	151	HIS
1	B1	45	ASN
1	B1	67	ASN
1	B1	93	ASN
1	B2	45	ASN
1	B2	67	ASN
1	B2	93	ASN
1	B2	147	HIS
1	B3	67	ASN
1	B3	147	HIS
1	B4	67	ASN
1	CA	45	ASN
1	CA	67	ASN
1	CA	151	HIS
1	CB	45	ASN
1	CB	67	ASN
1	CB	93	ASN
1	CC	45	ASN
1	CC	67	ASN
1	CC	93	ASN
1	CC	147	HIS
1	CD	67	ASN

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Mol	Chain	Res	Type
1	CD	147	HIS
1	CE	67	ASN
1	CF	45	ASN
1	CF	67	ASN
1	CF	151	HIS
1	CG	45	ASN
1	CG	67	ASN
1	CG	93	ASN
1	CH	6	HIS
1	CH	45	ASN
1	CH	67	ASN
1	CH	93	ASN
1	CH	147	HIS
1	CI	67	ASN
1	CI	93	ASN
1	CI	147	HIS
1	CJ	67	ASN
1	CK	45	ASN
1	CK	67	ASN
1	CK	151	HIS
1	CL	45	ASN
1	CL	67	ASN
1	CL	93	ASN
1	CM	45	ASN
1	CM	67	ASN
1	CM	93	ASN
1	CM	147	HIS
1	CN	67	ASN
1	CN	147	HIS
1	CO	67	ASN
1	CP	45	ASN
1	CP	67	ASN
1	CP	151	HIS
1	CQ	45	ASN
1	CQ	67	ASN
1	CQ	93	ASN
1	CR	45	ASN
1	CR	67	ASN
1	CR	93	ASN
1	CR	147	HIS
1	CS	67	ASN
1	CS	93	ASN

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Mol	Chain	Res	Type
1	CS	147	HIS
1	CT	67	ASN
1	CU	45	ASN
1	CU	67	ASN
1	CU	151	HIS
1	CV	45	ASN
1	CV	67	ASN
1	CV	93	ASN
1	CW	6	HIS
1	CW	45	ASN
1	CW	67	ASN
1	CW	93	ASN
1	CW	147	HIS
1	CX	67	ASN
1	CX	93	ASN
1	CX	147	HIS
1	CY	67	ASN
1	CZ	45	ASN
1	CZ	67	ASN
1	CZ	151	HIS
1	C1	45	ASN
1	C1	67	ASN
1	C1	93	ASN
1	C2	45	ASN
1	C2	67	ASN
1	C2	93	ASN
1	C2	147	HIS
1	C3	67	ASN
1	C3	93	ASN
1	C3	147	HIS
1	C4	67	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

90 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	PO4	A1	1001	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	A2	1001	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	A3	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	A4	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	AA	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	AB	1001	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	AC	1001	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	AD	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	AE	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	AF	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	AG	1001	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	AH	1001	-	4,4,4	0.55	0	6,6,6	0.27	0
2	PO4	AI	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	AJ	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	AK	1001	-	4,4,4	0.45	0	6,6,6	0.28	0
2	PO4	AL	1001	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	AM	1001	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	AN	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	AO	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	AP	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	AQ	1001	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	AR	1001	-	4,4,4	0.55	0	6,6,6	0.27	0
2	PO4	AS	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	AT	1001	-	4,4,4	0.55	0	6,6,6	0.28	0
2	PO4	AU	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	AV	1001	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	AW	201	-	4,4,4	0.55	0	6,6,6	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PO4	AX	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	AY	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	AZ	1001	-	4,4,4	0.45	0	6,6,6	0.28	0
2	PO4	B1	1001	-	4,4,4	0.46	0	6,6,6	0.27	0
2	PO4	B2	1001	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	B3	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	B4	1001	-	4,4,4	0.53	0	6,6,6	0.28	0
2	PO4	BA	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	BB	1001	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	BC	1001	-	4,4,4	0.55	0	6,6,6	0.27	0
2	PO4	BD	1001	-	4,4,4	0.51	0	6,6,6	0.27	0
2	PO4	BE	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	BF	1001	-	4,4,4	0.45	0	6,6,6	0.28	0
2	PO4	BG	1001	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	BH	1001	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	BI	1001	-	4,4,4	0.53	0	6,6,6	0.27	0
2	PO4	BJ	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	BK	1001	-	4,4,4	0.45	0	6,6,6	0.28	0
2	PO4	BL	1001	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	BM	1001	-	4,4,4	0.55	0	6,6,6	0.27	0
2	PO4	BN	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	BO	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	BP	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	BQ	1001	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	BR	1001	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	BS	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	BT	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	BU	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	BV	1001	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	BW	1001	-	4,4,4	0.55	0	6,6,6	0.27	0
2	PO4	BX	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	BY	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	BZ	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	C1	1201	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	C2	2201	-	4,4,4	0.55	0	6,6,6	0.27	0
2	PO4	C3	3201	-	4,4,4	0.53	0	6,6,6	0.27	0
2	PO4	C4	4201	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	CA	1001	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	CB	1001	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	CC	1001	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	CD	1001	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	CE	1001	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	CF	201	-	4,4,4	0.43	0	6,6,6	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PO4	CG	1201	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	CH	2201	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	CI	3201	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	CJ	4201	-	4,4,4	0.54	0	6,6,6	0.28	0
2	PO4	CK	201	-	4,4,4	0.45	0	6,6,6	0.28	0
2	PO4	CL	1201	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	CM	2201	-	4,4,4	0.55	0	6,6,6	0.27	0
2	PO4	CN	3201	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	CO	4201	-	4,4,4	0.53	0	6,6,6	0.28	0
2	PO4	CP	201	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	CQ	1201	-	4,4,4	0.44	0	6,6,6	0.27	0
2	PO4	CR	2201	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	CS	3201	-	4,4,4	0.52	0	6,6,6	0.27	0
2	PO4	CT	4201	-	4,4,4	0.55	0	6,6,6	0.28	0
2	PO4	CU	201	-	4,4,4	0.44	0	6,6,6	0.28	0
2	PO4	CV	1201	-	4,4,4	0.45	0	6,6,6	0.27	0
2	PO4	CW	2201	-	4,4,4	0.56	0	6,6,6	0.27	0
2	PO4	CX	3201	-	4,4,4	0.51	0	6,6,6	0.27	0
2	PO4	CY	4201	-	4,4,4	0.53	0	6,6,6	0.28	0
2	PO4	CZ	201	-	4,4,4	0.44	0	6,6,6	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PO4	A1	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	A2	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	A3	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	A4	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AA	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AB	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AC	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AD	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AE	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AF	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AG	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AH	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AI	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AJ	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AK	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AL	1001	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PO4	AM	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AN	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AO	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AP	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AQ	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AR	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AS	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AT	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AU	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AV	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AW	201	-	-	0/0/0/0	0/0/0/0
2	PO4	AX	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AY	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	AZ	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	B1	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	B2	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	B3	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	B4	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BA	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BB	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BC	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BD	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BE	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BF	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BG	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BH	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BI	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BJ	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BK	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BL	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BM	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BN	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BO	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BP	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BQ	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BR	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BS	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BT	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BU	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BV	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BW	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BX	1001	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PO4	BY	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	BZ	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	C1	1201	-	-	0/0/0/0	0/0/0/0
2	PO4	C2	2201	-	-	0/0/0/0	0/0/0/0
2	PO4	C3	3201	-	-	0/0/0/0	0/0/0/0
2	PO4	C4	4201	-	-	0/0/0/0	0/0/0/0
2	PO4	CA	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	CB	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	CC	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	CD	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	CE	1001	-	-	0/0/0/0	0/0/0/0
2	PO4	CF	201	-	-	0/0/0/0	0/0/0/0
2	PO4	CG	1201	-	-	0/0/0/0	0/0/0/0
2	PO4	CH	2201	-	-	0/0/0/0	0/0/0/0
2	PO4	CI	3201	-	-	0/0/0/0	0/0/0/0
2	PO4	CJ	4201	-	-	0/0/0/0	0/0/0/0
2	PO4	CK	201	-	-	0/0/0/0	0/0/0/0
2	PO4	CL	1201	-	-	0/0/0/0	0/0/0/0
2	PO4	CM	2201	-	-	0/0/0/0	0/0/0/0
2	PO4	CN	3201	-	-	0/0/0/0	0/0/0/0
2	PO4	CO	4201	-	-	0/0/0/0	0/0/0/0
2	PO4	CP	201	-	-	0/0/0/0	0/0/0/0
2	PO4	CQ	1201	-	-	0/0/0/0	0/0/0/0
2	PO4	CR	2201	-	-	0/0/0/0	0/0/0/0
2	PO4	CS	3201	-	-	0/0/0/0	0/0/0/0
2	PO4	CT	4201	-	-	0/0/0/0	0/0/0/0
2	PO4	CU	201	-	-	0/0/0/0	0/0/0/0
2	PO4	CV	1201	-	-	0/0/0/0	0/0/0/0
2	PO4	CW	2201	-	-	0/0/0/0	0/0/0/0
2	PO4	CX	3201	-	-	0/0/0/0	0/0/0/0
2	PO4	CY	4201	-	-	0/0/0/0	0/0/0/0
2	PO4	CZ	201	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

67 monomers are involved in 121 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A2	1001	PO4	3	0
2	A4	1001	PO4	2	0
2	AA	1001	PO4	1	0
2	AB	1001	PO4	1	0
2	AC	1001	PO4	3	0
2	AE	1001	PO4	2	0
2	AF	1001	PO4	1	0
2	AG	1001	PO4	1	0
2	AH	1001	PO4	3	0
2	AJ	1001	PO4	2	0
2	AK	1001	PO4	1	0
2	AM	1001	PO4	3	0
2	AO	1001	PO4	2	0
2	AP	1001	PO4	1	0
2	AQ	1001	PO4	1	0
2	AR	1001	PO4	3	0
2	AT	1001	PO4	2	0
2	AU	1001	PO4	1	0
2	AV	1001	PO4	1	0
2	AW	201	PO4	3	0
2	AY	1001	PO4	2	0
2	AZ	1001	PO4	1	0
2	B1	1001	PO4	1	0
2	B2	1001	PO4	3	0
2	B4	1001	PO4	2	0
2	BA	1001	PO4	1	0
2	BB	1001	PO4	1	0
2	BC	1001	PO4	3	0
2	BE	1001	PO4	2	0
2	BF	1001	PO4	1	0
2	BG	1001	PO4	1	0
2	BH	1001	PO4	3	0
2	BJ	1001	PO4	2	0
2	BK	1001	PO4	1	0
2	BL	1001	PO4	1	0
2	BM	1001	PO4	3	0
2	BO	1001	PO4	2	0
2	BP	1001	PO4	1	0
2	BQ	1001	PO4	1	0
2	BR	1001	PO4	3	0
2	BT	1001	PO4	2	0
2	BU	1001	PO4	1	0
2	BW	1001	PO4	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BY	1001	PO4	2	0
2	BZ	1001	PO4	1	0
2	C1	1201	PO4	1	0
2	C2	2201	PO4	3	0
2	C4	4201	PO4	2	0
2	CA	1001	PO4	1	0
2	CB	1001	PO4	1	0
2	CC	1001	PO4	3	0
2	CE	1001	PO4	2	0
2	CF	201	PO4	1	0
2	CG	1201	PO4	1	0
2	CH	2201	PO4	3	0
2	CJ	4201	PO4	2	0
2	CK	201	PO4	1	0
2	CL	1201	PO4	1	0
2	CM	2201	PO4	3	0
2	CO	4201	PO4	2	0
2	CP	201	PO4	1	0
2	CR	2201	PO4	3	0
2	CT	4201	PO4	2	0
2	CU	201	PO4	1	0
2	CW	2201	PO4	3	0
2	CY	4201	PO4	2	0
2	CZ	201	PO4	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	A1	152/153 (99%)	0.05	4 (2%) 59 49	65, 95, 151, 347	0
1	A2	152/153 (99%)	0.01	3 (1%) 68 59	56, 97, 184, 226	0
1	A3	152/153 (99%)	0.01	5 (3%) 50 41	57, 96, 147, 259	0
1	A4	152/153 (99%)	-0.01	4 (2%) 59 49	56, 94, 153, 393	0
1	AA	152/153 (99%)	-0.10	1 (0%) 89 82	55, 97, 150, 271	0
1	AB	152/153 (99%)	-0.01	4 (2%) 59 49	65, 95, 151, 347	0
1	AC	152/153 (99%)	-0.01	3 (1%) 68 59	56, 97, 184, 226	0
1	AD	152/153 (99%)	-0.04	2 (1%) 79 70	57, 96, 147, 259	0
1	AE	152/153 (99%)	-0.08	2 (1%) 79 70	56, 94, 153, 393	0
1	AF	152/153 (99%)	0.02	1 (0%) 89 82	55, 97, 150, 271	0
1	AG	152/153 (99%)	0.19	3 (1%) 68 59	65, 95, 151, 347	0
1	AH	152/153 (99%)	0.18	3 (1%) 68 59	56, 97, 184, 226	0
1	AI	152/153 (99%)	0.06	2 (1%) 79 70	57, 96, 147, 259	0
1	AJ	152/153 (99%)	0.15	3 (1%) 68 59	56, 94, 153, 393	0
1	AK	152/153 (99%)	0.01	2 (1%) 79 70	55, 97, 150, 271	0
1	AL	152/153 (99%)	0.11	3 (1%) 68 59	65, 95, 151, 347	0
1	AM	152/153 (99%)	0.07	2 (1%) 79 70	56, 97, 184, 226	0
1	AN	152/153 (99%)	0.10	2 (1%) 79 70	57, 96, 147, 259	0
1	AO	152/153 (99%)	0.08	3 (1%) 68 59	56, 94, 153, 393	0
1	AP	152/153 (99%)	-0.07	1 (0%) 89 82	55, 97, 150, 271	0
1	AQ	152/153 (99%)	0.01	2 (1%) 79 70	65, 95, 151, 347	0
1	AR	152/153 (99%)	0.04	3 (1%) 68 59	56, 97, 184, 226	0
1	AS	152/153 (99%)	0.04	2 (1%) 79 70	57, 96, 147, 259	0
1	AT	152/153 (99%)	-0.09	3 (1%) 68 59	56, 94, 153, 393	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	AU	152/153 (99%)	0.04	2 (1%) 79 70	55, 97, 150, 271	0
1	AV	152/153 (99%)	0.12	4 (2%) 59 49	65, 95, 151, 347	0
1	AW	152/153 (99%)	0.26	2 (1%) 79 70	56, 97, 184, 226	0
1	AX	152/153 (99%)	0.09	2 (1%) 79 70	57, 96, 147, 259	0
1	AY	152/153 (99%)	-0.01	3 (1%) 68 59	56, 94, 153, 393	0
1	AZ	152/153 (99%)	-0.02	1 (0%) 89 82	55, 97, 150, 271	0
1	B1	152/153 (99%)	0.14	4 (2%) 59 49	60, 95, 151, 347	0
1	B2	152/153 (99%)	0.18	5 (3%) 50 41	56, 97, 184, 226	0
1	B3	152/153 (99%)	0.13	4 (2%) 59 49	57, 96, 147, 259	0
1	B4	152/153 (99%)	0.10	5 (3%) 50 41	55, 93, 153, 393	0
1	BA	152/153 (99%)	0.08	6 (3%) 43 35	55, 97, 147, 271	0
1	BB	152/153 (99%)	0.28	5 (3%) 50 41	60, 95, 151, 347	0
1	BC	152/153 (99%)	0.16	5 (3%) 50 41	56, 97, 184, 226	0
1	BD	152/153 (99%)	0.02	1 (0%) 89 82	57, 96, 147, 259	0
1	BE	152/153 (99%)	0.30	7 (4%) 36 28	55, 93, 153, 393	0
1	BF	152/153 (99%)	0.18	5 (3%) 50 41	55, 97, 147, 271	0
1	BG	152/153 (99%)	0.09	4 (2%) 59 49	60, 95, 151, 347	0
1	BH	152/153 (99%)	0.06	2 (1%) 79 70	56, 97, 184, 226	0
1	BI	152/153 (99%)	0.16	3 (1%) 68 59	57, 96, 147, 259	0
1	BJ	152/153 (99%)	0.05	3 (1%) 68 59	55, 93, 153, 393	0
1	BK	152/153 (99%)	-0.07	3 (1%) 68 59	55, 97, 147, 271	0
1	BL	152/153 (99%)	0.12	5 (3%) 50 41	60, 95, 151, 347	0
1	BM	152/153 (99%)	0.21	4 (2%) 59 49	56, 97, 184, 226	0
1	BN	152/153 (99%)	-0.04	3 (1%) 68 59	57, 96, 147, 259	0
1	BO	152/153 (99%)	0.04	5 (3%) 50 41	55, 93, 153, 393	0
1	BP	152/153 (99%)	0.07	3 (1%) 68 59	55, 97, 147, 271	0
1	BQ	152/153 (99%)	0.10	4 (2%) 59 49	60, 95, 151, 347	0
1	BR	152/153 (99%)	0.10	5 (3%) 50 41	56, 97, 184, 226	0
1	BS	152/153 (99%)	0.17	5 (3%) 50 41	57, 96, 147, 259	0
1	BT	152/153 (99%)	0.12	5 (3%) 50 41	55, 93, 153, 393	0
1	BU	152/153 (99%)	0.15	2 (1%) 79 70	55, 97, 147, 271	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	BV	152/153 (99%)	0.25	9 (5%) 26 20	60, 95, 151, 347	0
1	BW	152/153 (99%)	0.13	3 (1%) 68 59	56, 97, 184, 226	0
1	BX	152/153 (99%)	0.07	3 (1%) 68 59	57, 96, 147, 259	0
1	BY	152/153 (99%)	0.15	5 (3%) 50 41	55, 93, 153, 393	0
1	BZ	152/153 (99%)	0.07	2 (1%) 79 70	55, 97, 147, 271	0
1	C1	152/153 (99%)	1.11	29 (19%) 2 2	60, 95, 151, 347	0
1	C2	152/153 (99%)	0.83	18 (11%) 6 6	56, 97, 184, 226	0
1	C3	152/153 (99%)	1.05	19 (12%) 5 6	57, 96, 147, 259	0
1	C4	152/153 (99%)	1.23	29 (19%) 2 2	55, 93, 153, 393	0
1	CA	152/153 (99%)	0.39	8 (5%) 30 23	55, 97, 147, 271	0
1	CB	152/153 (99%)	0.70	15 (9%) 9 9	60, 95, 151, 347	0
1	CC	152/153 (99%)	0.77	14 (9%) 11 10	56, 97, 184, 226	0
1	CD	152/153 (99%)	0.77	12 (7%) 15 13	57, 96, 147, 259	0
1	CE	152/153 (99%)	0.31	6 (3%) 43 35	55, 93, 153, 393	0
1	CF	152/153 (99%)	0.86	20 (13%) 4 5	55, 97, 147, 271	0
1	CG	152/153 (99%)	0.44	6 (3%) 43 35	60, 95, 151, 347	0
1	CH	152/153 (99%)	0.02	2 (1%) 79 70	56, 97, 184, 226	0
1	CI	152/153 (99%)	0.08	7 (4%) 36 28	57, 96, 147, 259	0
1	CJ	152/153 (99%)	0.57	14 (9%) 11 10	55, 93, 153, 393	0
1	CK	152/153 (99%)	-0.09	2 (1%) 79 70	55, 97, 147, 271	0
1	CL	152/153 (99%)	0.08	2 (1%) 79 70	60, 95, 151, 347	0
1	CM	152/153 (99%)	0.01	3 (1%) 68 59	56, 97, 184, 226	0
1	CN	152/153 (99%)	0.18	3 (1%) 68 59	57, 96, 147, 259	0
1	CO	152/153 (99%)	0.09	5 (3%) 50 41	55, 93, 153, 393	0
1	CP	152/153 (99%)	0.88	19 (12%) 5 6	55, 97, 147, 271	0
1	CQ	152/153 (99%)	1.18	25 (16%) 2 3	60, 95, 151, 347	0
1	CR	152/153 (99%)	1.36	33 (21%) 1 1	56, 97, 184, 226	0
1	CS	152/153 (99%)	1.47	42 (27%) 1 1	57, 96, 147, 259	0
1	CT	152/153 (99%)	1.37	33 (21%) 1 1	55, 93, 153, 393	0
1	CU	152/153 (99%)	0.32	5 (3%) 50 41	55, 97, 147, 271	0
1	CV	152/153 (99%)	0.66	13 (8%) 13 12	60, 95, 151, 347	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	CW	152/153 (99%)	0.71	14 (9%) 11 10	56, 97, 184, 226	0
1	CX	152/153 (99%)	0.37	7 (4%) 36 28	57, 96, 147, 259	0
1	CY	152/153 (99%)	0.14	4 (2%) 59 49	55, 93, 153, 393	0
1	CZ	152/153 (99%)	1.33	32 (21%) 1 1	55, 97, 147, 271	0
All	All	13680/13770 (99%)	0.27	643 (4%) 35 28	55, 96, 157, 393	0

All (643) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BE	151	HIS	14.1
1	AN	153	ALA	13.7
1	BM	153	ALA	13.4
1	AM	153	ALA	11.9
1	CD	153	ALA	11.6
1	B3	153	ALA	10.8
1	CR	153	ALA	10.7
1	CW	153	ALA	10.3
1	BI	153	ALA	9.7
1	AO	151	HIS	9.6
1	AS	153	ALA	9.2
1	BJ	151	HIS	9.2
1	AJ	151	HIS	9.0
1	CQ	153	ALA	8.9
1	BP	153	ALA	8.6
1	AW	153	ALA	8.4
1	AG	152	TRP	8.3
1	B4	151	HIS	8.2
1	CM	153	ALA	8.1
1	CQ	152	TRP	8.1
1	CC	153	ALA	8.0
1	AE	151	HIS	8.0
1	CT	151	HIS	7.9
1	BA	153	ALA	7.8
1	A1	152	TRP	7.7
1	AC	153	ALA	7.6
1	CS	73	ALA	7.5
1	BB	152	TRP	7.5
1	CN	153	ALA	7.5
1	BW	153	ALA	7.5
1	AD	153	ALA	7.3
1	AL	152	TRP	7.2

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Mol	Chain	Res	Type	RSRZ
1	A2	152	TRP	7.1
1	CY	149	SER	7.1
1	CQ	9	GLY	7.0
1	AW	152	TRP	7.0
1	AV	153	ALA	6.9
1	CD	152	TRP	6.8
1	BE	150	LYS	6.7
1	AI	153	ALA	6.7
1	AU	153	ALA	6.6
1	BH	153	ALA	6.6
1	AX	153	ALA	6.6
1	AO	149	SER	6.5
1	B1	152	TRP	6.5
1	AV	152	TRP	6.5
1	AJ	150	LYS	6.5
1	AQ	152	TRP	6.5
1	CJ	149	SER	6.4
1	BM	152	TRP	6.4
1	C3	152	TRP	6.4
1	AM	152	TRP	6.3
1	AR	153	ALA	6.1
1	CO	151	HIS	6.1
1	BY	149	SER	6.1
1	CZ	73	ALA	6.0
1	A4	151	HIS	6.0
1	CX	153	ALA	6.0
1	AH	153	ALA	6.0
1	CI	153	ALA	5.9
1	A4	149	SER	5.8
1	AB	152	TRP	5.6
1	CR	142	ALA	5.6
1	C1	153	ALA	5.6
1	C1	152	TRP	5.6
1	CZ	72	ASP	5.6
1	CF	73	ALA	5.5
1	BB	153	ALA	5.5
1	A2	153	ALA	5.4
1	C2	152	TRP	5.4
1	A3	153	ALA	5.4
1	BV	152	TRP	5.4
1	B2	152	TRP	5.4
1	AO	150	LYS	5.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	CG	152	TRP	5.3
1	C4	149	SER	5.3
1	A4	150	LYS	5.3
1	AJ	149	SER	5.2
1	AH	152	TRP	5.2
1	C3	9	GLY	5.2
1	BD	153	ALA	5.2
1	B1	153	ALA	5.1
1	BL	153	ALA	5.1
1	B2	153	ALA	5.1
1	C4	105	GLN	5.0
1	C3	153	ALA	5.0
1	CS	72	ASP	5.0
1	CL	152	TRP	5.0
1	A1	153	ALA	4.9
1	C4	145	MET	4.9
1	AL	153	ALA	4.9
1	BT	151	HIS	4.8
1	CH	153	ALA	4.8
1	CT	45	ASN	4.8
1	CV	153	ALA	4.8
1	BO	149	SER	4.7
1	BJ	149	SER	4.7
1	CT	15	GLY	4.6
1	AB	153	ALA	4.6
1	CJ	72	ASP	4.6
1	CB	72	ASP	4.5
1	C2	153	ALA	4.5
1	CZ	78	GLY	4.5
1	AY	151	HIS	4.5
1	BI	152	TRP	4.5
1	CO	149	SER	4.5
1	BR	152	TRP	4.5
1	BT	150	LYS	4.4
1	CS	74	VAL	4.4
1	BL	151	HIS	4.4
1	CZ	113	GLY	4.4
1	BW	152	TRP	4.4
1	B1	151	HIS	4.4
1	C4	92	CYS	4.4
1	AY	149	SER	4.3
1	CM	152	TRP	4.3

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Mol	Chain	Res	Type	RSRZ
1	BS	153	ALA	4.3
1	CI	152	TRP	4.3
1	CY	150	LYS	4.3
1	BV	153	ALA	4.3
1	CE	149	SER	4.3
1	CS	67	ASN	4.2
1	CS	109	PRO	4.2
1	BC	152	TRP	4.2
1	BL	152	TRP	4.2
1	CS	76	THR	4.2
1	CB	151	HIS	4.2
1	CD	8	VAL	4.2
1	CJ	73	ALA	4.1
1	CT	72	ASP	4.1
1	AG	151	HIS	4.1
1	CT	16	VAL	4.1
1	CQ	41	GLY	4.1
1	CD	45	ASN	4.1
1	C1	40	HIS	4.0
1	CS	79	THR	4.0
1	CU	153	ALA	4.0
1	C1	48	ASP	4.0
1	AN	152	TRP	4.0
1	AE	149	SER	4.0
1	CG	151	HIS	4.0
1	C1	151	HIS	4.0
1	AD	152	TRP	4.0
1	CP	153	ALA	4.0
1	CS	68	SER	4.0
1	CW	15	GLY	3.9
1	CT	49	VAL	3.9
1	AT	151	HIS	3.9
1	CA	153	ALA	3.9
1	CV	152	TRP	3.9
1	C3	50	ALA	3.9
1	BG	152	TRP	3.9
1	C4	107	ASP	3.9
1	AA	153	ALA	3.9
1	C4	72	ASP	3.9
1	CT	19	GLY	3.9
1	CS	108	ILE	3.8
1	A2	151	HIS	3.8

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Mol	Chain	Res	Type	RSRZ
1	CQ	40	HIS	3.8
1	CU	45	ASN	3.8
1	B4	149	SER	3.8
1	CQ	151	HIS	3.8
1	C1	7	LEU	3.8
1	CZ	153	ALA	3.8
1	BY	151	HIS	3.8
1	B4	150	LYS	3.8
1	CV	44	GLU	3.8
1	CR	11	GLY	3.8
1	CB	73	ALA	3.8
1	C1	132	GLY	3.8
1	CZ	93	ASN	3.8
1	CY	151	HIS	3.8
1	CW	67	ASN	3.7
1	CJ	151	HIS	3.7
1	CR	45	ASN	3.7
1	CC	68	SER	3.7
1	CE	150	LYS	3.7
1	CB	152	TRP	3.7
1	C2	151	HIS	3.7
1	CZ	8	VAL	3.7
1	CW	72	ASP	3.7
1	BO	73	ALA	3.7
1	CT	50	ALA	3.7
1	CR	68	SER	3.6
1	CA	14	VAL	3.6
1	BV	151	HIS	3.6
1	CQ	43	GLU	3.6
1	C1	43	GLU	3.6
1	C2	145	MET	3.6
1	BY	150	LYS	3.6
1	CS	153	ALA	3.6
1	CA	45	ASN	3.6
1	CT	36	GLY	3.6
1	CF	5	GLY	3.5
1	CO	150	LYS	3.5
1	CQ	73	ALA	3.5
1	CU	146	ALA	3.5
1	CS	15	GLY	3.5
1	CQ	74	VAL	3.5
1	BN	153	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	CW	14	VAL	3.5
1	C1	19	GLY	3.5
1	CZ	65	MET	3.5
1	CR	62	ALA	3.4
1	B3	70	LYS	3.4
1	C4	37	LEU	3.4
1	BF	153	ALA	3.4
1	CP	45	ASN	3.4
1	CS	5	GLY	3.4
1	CP	108	ILE	3.4
1	BA	152	TRP	3.4
1	C4	10	THR	3.4
1	C4	153	ALA	3.4
1	CK	153	ALA	3.3
1	BO	151	HIS	3.3
1	CC	72	ASP	3.3
1	BC	153	ALA	3.3
1	CS	141	ALA	3.3
1	CZ	145	MET	3.3
1	C4	11	GLY	3.3
1	CL	151	HIS	3.3
1	C4	69	GLY	3.3
1	CB	8	VAL	3.3
1	CV	6	HIS	3.3
1	CZ	14	VAL	3.3
1	CQ	42	VAL	3.3
1	B2	35	ASP	3.3
1	CP	10	THR	3.3
1	CQ	8	VAL	3.3
1	CR	72	ASP	3.2
1	CP	152	TRP	3.2
1	CT	68	SER	3.2
1	CT	10	THR	3.2
1	CZ	76	THR	3.2
1	CZ	67	ASN	3.2
1	CT	9	GLY	3.2
1	CC	152	TRP	3.2
1	CZ	116	THR	3.2
1	CS	62	ALA	3.2
1	CF	10	THR	3.2
1	CW	143	ILE	3.2
1	CX	5	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	CA	73	ALA	3.2
1	CW	86	THR	3.2
1	CR	35	ASP	3.2
1	CX	6	HIS	3.2
1	CW	152	TRP	3.2
1	CR	63	LYS	3.2
1	AR	152	TRP	3.2
1	AX	152	TRP	3.2
1	BB	151	HIS	3.1
1	C4	46	ASP	3.1
1	BT	149	SER	3.1
1	C4	63	LYS	3.1
1	C2	40	HIS	3.1
1	CJ	109	PRO	3.1
1	BQ	151	HIS	3.1
1	CD	151	HIS	3.1
1	CZ	139	ALA	3.1
1	CW	73	ALA	3.1
1	CS	48	ASP	3.1
1	C3	72	ASP	3.1
1	CZ	74	VAL	3.1
1	BQ	153	ALA	3.1
1	B3	72	ASP	3.1
1	BU	153	ALA	3.1
1	CE	107	ASP	3.1
1	CD	130	LYS	3.1
1	CJ	10	THR	3.1
1	CE	14	VAL	3.1
1	BQ	152	TRP	3.0
1	CF	106	THR	3.0
1	CR	107	ASP	3.0
1	BP	152	TRP	3.0
1	CS	78	GLY	3.0
1	C4	101	SER	3.0
1	AF	153	ALA	3.0
1	BH	152	TRP	3.0
1	CF	7	LEU	3.0
1	CZ	143	ILE	3.0
1	BK	153	ALA	3.0
1	CV	101	SER	3.0
1	CZ	50	ALA	3.0
1	BV	6	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
1	C4	146	ALA	2.9
1	CS	51	TRP	2.9
1	BF	45	ASN	2.9
1	CR	67	ASN	2.9
1	CF	45	ASN	2.9
1	CP	49	VAL	2.9
1	CT	46	ASP	2.9
1	AT	149	SER	2.9
1	CP	48	ASP	2.9
1	CE	151	HIS	2.9
1	CT	40	HIS	2.9
1	CS	66	ALA	2.9
1	C1	106	THR	2.9
1	CN	152	TRP	2.9
1	CF	69	GLY	2.9
1	CQ	132	GLY	2.9
1	C3	19	GLY	2.9
1	CA	66	ALA	2.9
1	CV	142	ALA	2.9
1	AG	153	ALA	2.9
1	BQ	72	ASP	2.9
1	C1	15	GLY	2.9
1	CB	50	ALA	2.9
1	AK	153	ALA	2.8
1	CR	90	TYR	2.8
1	CR	78	GLY	2.8
1	CT	14	VAL	2.8
1	C4	151	HIS	2.8
1	AL	101	SER	2.8
1	C3	3	PHE	2.8
1	AY	150	LYS	2.8
1	CS	50	ALA	2.8
1	CS	145	MET	2.8
1	CQ	45	ASN	2.8
1	CU	152	TRP	2.8
1	BT	40	HIS	2.8
1	CF	50	ALA	2.8
1	C4	108	ILE	2.8
1	CT	142	ALA	2.8
1	CB	83	GLY	2.8
1	CG	10	THR	2.8
1	BA	43	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	CQ	10	THR	2.7
1	CS	59	PRO	2.7
1	CT	73	ALA	2.7
1	AR	35	ASP	2.7
1	C2	74	VAL	2.7
1	CT	78	GLY	2.7
1	BA	3	PHE	2.7
1	CS	35	ASP	2.7
1	C3	4	GLU	2.7
1	CW	35	ASP	2.7
1	BC	6	HIS	2.7
1	BG	153	ALA	2.7
1	CS	6	HIS	2.7
1	B4	45	ASN	2.7
1	C2	142	ALA	2.7
1	BJ	150	LYS	2.7
1	C4	66	ALA	2.7
1	CS	75	ILE	2.7
1	A3	45	ASN	2.7
1	CT	4	GLU	2.7
1	BI	70	LYS	2.7
1	C4	109	PRO	2.7
1	AC	152	TRP	2.7
1	CA	72	ASP	2.7
1	CV	72	ASP	2.7
1	CR	92	CYS	2.6
1	C4	142	ALA	2.6
1	BV	5	GLY	2.6
1	CQ	148	LEU	2.6
1	CP	65	MET	2.6
1	C3	73	ALA	2.6
1	CZ	48	ASP	2.6
1	CR	141	ALA	2.6
1	CE	90	TYR	2.6
1	CF	72	ASP	2.6
1	CZ	152	TRP	2.6
1	CI	10	THR	2.6
1	BX	153	ALA	2.6
1	CV	151	HIS	2.6
1	CB	9	GLY	2.6
1	C3	101	SER	2.6
1	CC	107	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	C4	67	ASN	2.6
1	CX	73	ALA	2.6
1	CV	4	GLU	2.6
1	CQ	133	ASN	2.6
1	CI	151	HIS	2.6
1	CR	69	GLY	2.6
1	C1	44	GLU	2.6
1	CF	35	ASP	2.6
1	CB	15	GLY	2.6
1	CJ	45	ASN	2.6
1	CR	14	VAL	2.5
1	CR	73	ALA	2.6
1	BZ	8	VAL	2.5
1	CF	15	GLY	2.5
1	CS	33	ALA	2.5
1	A1	101	SER	2.5
1	BC	5	GLY	2.5
1	CC	49	VAL	2.5
1	CW	5	GLY	2.5
1	C1	14	VAL	2.5
1	CP	106	THR	2.5
1	CP	50	ALA	2.5
1	CR	108	ILE	2.5
1	CZ	46	ASP	2.5
1	CZ	149	SER	2.5
1	CU	44	GLU	2.5
1	CQ	44	GLU	2.5
1	CB	153	ALA	2.5
1	CR	46	ASP	2.5
1	CR	79	THR	2.5
1	CP	37	LEU	2.5
1	CR	152	TRP	2.5
1	C2	79	THR	2.5
1	AV	101	SER	2.5
1	CF	143	ILE	2.5
1	BN	107	ASP	2.5
1	C3	142	ALA	2.5
1	CC	12	LEU	2.4
1	CD	7	LEU	2.4
1	CS	65	MET	2.4
1	BF	43	GLU	2.4
1	CV	11	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	BR	153	ALA	2.4
1	CF	14	VAL	2.4
1	CH	152	TRP	2.4
1	AQ	153	ALA	2.4
1	CR	151	HIS	2.4
1	BS	45	ASN	2.4
1	CV	143	ILE	2.4
1	CV	7	LEU	2.4
1	CT	47	ILE	2.4
1	BG	68	SER	2.4
1	CS	85	THR	2.4
1	C4	17	VAL	2.4
1	CT	3	PHE	2.4
1	CQ	72	ASP	2.4
1	BK	10	THR	2.4
1	CI	147	HIS	2.4
1	A1	44	GLU	2.4
1	C3	14	VAL	2.4
1	CZ	45	ASN	2.4
1	BV	44	GLU	2.4
1	BX	71	TYR	2.4
1	CD	76	THR	2.4
1	CP	70	LYS	2.4
1	CT	146	ALA	2.4
1	BU	10	THR	2.4
1	AZ	153	ALA	2.4
1	C4	35	ASP	2.4
1	AV	45	ASN	2.4
1	CS	54	GLY	2.4
1	CV	5	GLY	2.4
1	CW	22	ASN	2.4
1	C3	15	GLY	2.4
1	CX	19	GLY	2.4
1	CF	49	VAL	2.4
1	CR	145	MET	2.4
1	AK	152	TRP	2.4
1	AP	153	ALA	2.4
1	CT	2	VAL	2.4
1	CB	34	LEU	2.4
1	C2	92	CYS	2.4
1	C1	41	GLY	2.3
1	CJ	145	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	CD	42	VAL	2.3
1	C2	51	TRP	2.3
1	CQ	5	GLY	2.3
1	C3	17	VAL	2.3
1	CC	9	GLY	2.3
1	CF	46	ASP	2.3
1	C2	65	MET	2.3
1	CG	67	ASN	2.3
1	BA	6	HIS	2.3
1	BR	10	THR	2.3
1	CJ	148	LEU	2.3
1	CZ	68	SER	2.3
1	CZ	57	GLU	2.3
1	CZ	148	LEU	2.3
1	AB	151	HIS	2.3
1	CP	6	HIS	2.3
1	CB	10	THR	2.3
1	CF	44	GLU	2.3
1	CQ	146	ALA	2.3
1	CM	11	GLY	2.3
1	CZ	15	GLY	2.3
1	BE	73	ALA	2.3
1	CW	7	LEU	2.3
1	CS	10	THR	2.3
1	BV	67	ASN	2.3
1	CC	146	ALA	2.3
1	AS	13	LYS	2.3
1	CR	15	GLY	2.3
1	C2	14	VAL	2.3
1	CT	43	GLU	2.3
1	CT	101	SER	2.3
1	CC	69	GLY	2.3
1	CZ	61	ILE	2.3
1	CS	40	HIS	2.3
1	BE	68	SER	2.3
1	CX	45	ASN	2.3
1	BA	107	ASP	2.3
1	BC	72	ASP	2.3
1	C2	143	ILE	2.3
1	C3	44	GLU	2.2
1	CC	11	GLY	2.2
1	CJ	150	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	CD	71	TYR	2.2
1	CT	100	ALA	2.2
1	BN	48	ASP	2.2
1	BS	152	TRP	2.2
1	CP	68	SER	2.2
1	CR	149	SER	2.2
1	C1	146	ALA	2.2
1	BE	48	ASP	2.2
1	CF	48	ASP	2.2
1	CF	129	THR	2.2
1	CP	46	ASP	2.2
1	CY	13	LYS	2.2
1	C1	109	PRO	2.2
1	C1	42	VAL	2.2
1	CR	146	ALA	2.2
1	CO	12	LEU	2.2
1	CQ	92	CYS	2.2
1	CR	12	LEU	2.2
1	BG	72	ASP	2.2
1	CZ	59	PRO	2.2
1	C1	89	ASP	2.2
1	CR	138	SER	2.2
1	C1	142	ALA	2.2
1	C4	53	PRO	2.2
1	CJ	9	GLY	2.2
1	CS	55	ALA	2.2
1	C1	82	ARG	2.2
1	BY	4	GLU	2.2
1	C4	94	GLU	2.2
1	AU	152	TRP	2.2
1	BF	151	HIS	2.2
1	CG	92	CYS	2.2
1	BK	73	ALA	2.2
1	C1	6	HIS	2.2
1	BL	101	SER	2.2
1	CZ	52	VAL	2.2
1	AT	150	LYS	2.2
1	CA	47	ILE	2.2
1	CC	13	LYS	2.2
1	CZ	13	LYS	2.2
1	CP	72	ASP	2.2
1	CB	49	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	BR	73	ALA	2.2
1	CI	3	PHE	2.2
1	CJ	6	HIS	2.2
1	C1	83	GLY	2.2
1	BF	66	ALA	2.2
1	BX	152	TRP	2.2
1	BE	72	ASP	2.2
1	BB	101	SER	2.2
1	CT	113	GLY	2.2
1	BT	38	LYS	2.2
1	B2	44	GLU	2.2
1	CB	4	GLU	2.2
1	C1	18	VAL	2.2
1	CQ	59	PRO	2.2
1	C2	84	ALA	2.2
1	CW	119	THR	2.2
1	CD	92	CYS	2.2
1	CS	63	LYS	2.2
1	CP	151	HIS	2.1
1	CR	66	ALA	2.1
1	C3	42	VAL	2.1
1	CR	143	ILE	2.1
1	BM	70	LYS	2.1
1	CS	14	VAL	2.1
1	C4	68	SER	2.1
1	CJ	147	HIS	2.1
1	CT	87	HIS	2.1
1	BV	101	SER	2.1
1	CT	145	MET	2.1
1	C1	38	LYS	2.1
1	AC	35	ASP	2.1
1	C2	85	THR	2.1
1	A3	73	ALA	2.1
1	CG	153	ALA	2.1
1	CZ	40	HIS	2.1
1	CJ	143	ILE	2.1
1	CT	150	LYS	2.1
1	C3	18	VAL	2.1
1	BR	5	GLY	2.1
1	BS	72	ASP	2.1
1	B1	72	ASP	2.1
1	CS	131	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	C3	40	HIS	2.1
1	CC	8	VAL	2.1
1	C2	76	THR	2.1
1	CQ	67	ASN	2.1
1	B2	47	ILE	2.1
1	CS	143	ILE	2.1
1	CT	84	ALA	2.1
1	CC	10	THR	2.1
1	AH	151	HIS	2.1
1	C4	6	HIS	2.1
1	CQ	7	LEU	2.1
1	CS	116	THR	2.1
1	CT	79	THR	2.1
1	CB	6	HIS	2.1
1	BZ	48	ASP	2.1
1	CR	109	PRO	2.1
1	C2	129	THR	2.1
1	CS	126	ARG	2.1
1	CQ	62	ALA	2.1
1	A3	15	GLY	2.1
1	CF	27	SER	2.1
1	CP	12	LEU	2.1
1	BV	13	LYS	2.1
1	CI	43	GLU	2.1
1	BO	69	GLY	2.1
1	CD	9	GLY	2.1
1	CF	6	HIS	2.1
1	CR	41	GLY	2.1
1	CS	90	TYR	2.1
1	CK	45	ASN	2.1
1	BY	109	PRO	2.1
1	B4	109	PRO	2.1
1	CS	64	LYS	2.1
1	CZ	3	PHE	2.1
1	BL	10	THR	2.0
1	C3	11	GLY	2.0
1	BO	72	ASP	2.0
1	BP	66	ALA	2.0
1	BW	73	ALA	2.0
1	C1	62	ALA	2.0
1	CN	72	ASP	2.0
1	CS	46	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	C4	59	PRO	2.0
1	B3	151	HIS	2.0
1	A4	153	ALA	2.0
1	CO	73	ALA	2.0
1	CX	66	ALA	2.0
1	C1	68	SER	2.0
1	BE	45	ASN	2.0
1	BM	69	GLY	2.0
1	C1	133	ASN	2.0
1	C2	75	ILE	2.0
1	A3	66	ALA	2.0
1	CP	133	ASN	2.0
1	CS	2	VAL	2.0
1	AB	6	HIS	2.0
1	AI	107	ASP	2.0
1	C1	88	TYR	2.0
1	CA	151	HIS	2.0
1	BB	14	VAL	2.0
1	CT	83	GLY	2.0
1	C1	51	TRP	2.0
1	BS	48	ASP	2.0
1	CS	45	ASN	2.0
1	C4	93	ASN	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	AX	1001	5/5	0.88	0.32	1.97	58,65,106,138	0
2	PO4	CD	1001	5/5	0.72	0.36	1.85	58,65,106,138	0
2	PO4	CQ	1201	5/5	0.71	0.40	1.39	74,78,104,213	0
2	PO4	AI	1001	5/5	0.86	0.30	1.30	58,65,106,138	0
2	PO4	BG	1001	5/5	0.80	0.27	0.79	74,78,104,213	0
2	PO4	BL	1001	5/5	0.73	0.31	0.27	74,78,104,213	0
2	PO4	CJ	4201	5/5	0.86	0.30	0.15	23,28,53,142	0
2	PO4	AG	1001	5/5	0.88	0.23	0.14	74,78,104,213	0
2	PO4	BA	1001	5/5	0.90	0.24	0.10	80,81,83,167	0
2	PO4	AW	201	5/5	0.89	0.24	0.09	34,46,111,116	0
2	PO4	BD	1001	5/5	0.85	0.26	0.04	58,65,106,138	0
2	PO4	AL	1001	5/5	0.91	0.23	0.02	74,78,104,213	0
2	PO4	AJ	1001	5/5	0.92	0.22	-0.11	23,28,53,142	0
2	PO4	CZ	201	5/5	0.77	0.30	-0.18	80,81,83,167	0
2	PO4	BR	1001	5/5	0.86	0.23	-0.21	34,46,111,116	0
2	PO4	CK	201	5/5	0.89	0.21	-0.23	80,81,83,167	0
2	PO4	CB	1001	5/5	0.84	0.34	-0.23	74,78,104,213	0
2	PO4	BV	1001	5/5	0.86	0.23	-0.34	74,78,104,213	0
2	PO4	CG	1201	5/5	0.82	0.26	-0.35	74,78,104,213	0
2	PO4	BF	1001	5/5	0.88	0.24	-0.35	80,81,83,167	0
2	PO4	AK	1001	5/5	0.94	0.22	-0.37	80,81,83,167	0
2	PO4	AY	1001	5/5	0.86	0.23	-0.43	23,28,53,142	0
2	PO4	BE	1001	5/5	0.84	0.24	-0.49	23,28,53,142	0
2	PO4	CY	4201	5/5	0.83	0.31	-0.53	23,28,53,142	0
2	PO4	CN	3201	5/5	0.89	0.19	-0.61	58,65,106,138	0
2	PO4	AM	1001	5/5	0.89	0.19	-0.63	34,46,111,116	0
2	PO4	AB	1001	5/5	0.90	0.20	-0.63	74,78,104,213	0
2	PO4	CH	2201	5/5	0.81	0.25	-0.63	34,46,111,116	0
2	PO4	BB	1001	5/5	0.86	0.22	-0.64	74,78,104,213	0
2	PO4	AH	1001	5/5	0.90	0.19	-0.66	34,46,111,116	0
2	PO4	CS	3201	5/5	0.91	0.35	-0.66	58,65,106,138	0
2	PO4	BZ	1001	5/5	0.95	0.19	-0.68	80,81,83,167	0
2	PO4	C2	2201	5/5	0.83	0.30	-0.71	34,46,111,116	0
2	PO4	AP	1001	5/5	0.90	0.19	-0.73	80,81,83,167	0
2	PO4	BM	1001	5/5	0.93	0.17	-0.74	34,46,111,116	0
2	PO4	CW	2201	5/5	0.84	0.27	-0.74	34,46,111,116	0
2	PO4	BW	1001	5/5	0.88	0.20	-0.74	34,46,111,116	0
2	PO4	CL	1201	5/5	0.80	0.20	-0.75	74,78,104,213	0
2	PO4	A4	1001	5/5	0.89	0.18	-0.75	23,28,53,142	0
2	PO4	AC	1001	5/5	0.92	0.17	-0.76	34,46,111,116	0
2	PO4	CT	4201	5/5	0.69	0.38	-0.79	23,28,53,142	0
2	PO4	AV	1001	5/5	0.87	0.19	-0.80	74,78,104,213	0
2	PO4	B1	1001	5/5	0.91	0.20	-0.81	74,78,104,213	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	CX	3201	5/5	0.85	0.25	-0.82	58,65,106,138	0
2	PO4	BQ	1001	5/5	0.86	0.17	-0.91	74,78,104,213	0
2	PO4	BP	1001	5/5	0.94	0.16	-0.91	80,81,83,167	0
2	PO4	BK	1001	5/5	0.92	0.20	-0.93	80,81,83,167	0
2	PO4	B2	1001	5/5	0.89	0.21	-0.95	34,46,111,116	0
2	PO4	BX	1001	5/5	0.92	0.18	-0.99	58,65,106,138	0
2	PO4	CF	201	5/5	0.91	0.19	-0.99	80,81,83,167	0
2	PO4	AZ	1001	5/5	0.93	0.19	-1.01	80,81,83,167	0
2	PO4	AT	1001	5/5	0.90	0.18	-1.02	23,28,53,142	0
2	PO4	CC	1001	5/5	0.67	0.28	-1.03	34,46,111,116	0
2	PO4	BH	1001	5/5	0.91	0.18	-1.07	34,46,111,116	0
2	PO4	B3	1001	5/5	0.87	0.19	-1.07	58,65,106,138	0
2	PO4	CA	1001	5/5	0.91	0.20	-1.10	80,81,83,167	0
2	PO4	AA	1001	5/5	0.97	0.15	-1.16	80,81,83,167	0
2	PO4	AS	1001	5/5	0.93	0.18	-1.22	58,65,106,138	0
2	PO4	B4	1001	5/5	0.91	0.18	-1.26	23,28,53,142	0
2	PO4	CI	3201	5/5	0.90	0.16	-1.30	58,65,106,138	0
2	PO4	A1	1001	5/5	0.94	0.16	-1.31	74,78,104,213	0
2	PO4	BS	1001	5/5	0.84	0.20	-1.31	58,65,106,138	0
2	PO4	CR	2201	5/5	0.89	0.30	-1.32	34,46,111,116	0
2	PO4	A3	1001	5/5	0.92	0.17	-1.34	58,65,106,138	0
2	PO4	AU	1001	5/5	0.93	0.18	-1.35	80,81,83,167	0
2	PO4	A2	1001	5/5	0.92	0.16	-1.38	34,46,111,116	0
2	PO4	C3	3201	5/5	0.84	0.23	-1.40	58,65,106,138	0
2	PO4	BT	1001	5/5	0.95	0.12	-1.40	23,28,53,142	0
2	PO4	CE	1001	5/5	0.86	0.29	-1.50	23,28,53,142	0
2	PO4	BO	1001	5/5	0.95	0.14	-1.51	23,28,53,142	0
2	PO4	CP	201	5/5	0.85	0.25	-1.53	80,81,83,167	0
2	PO4	CU	201	5/5	0.95	0.14	-1.58	80,81,83,167	0
2	PO4	CM	2201	5/5	0.91	0.16	-1.63	34,46,111,116	0
2	PO4	BJ	1001	5/5	0.93	0.13	-1.69	23,28,53,142	0
2	PO4	AN	1001	5/5	0.89	0.17	-1.70	58,65,106,138	0
2	PO4	AO	1001	5/5	0.89	0.18	-1.73	23,28,53,142	0
2	PO4	BC	1001	5/5	0.92	0.14	-1.80	34,46,111,116	0
2	PO4	CV	1201	5/5	0.87	0.18	-2.01	74,78,104,213	0
2	PO4	AD	1001	5/5	0.92	0.16	-2.02	58,65,106,138	0
2	PO4	BY	1001	5/5	0.95	0.14	-2.02	23,28,53,142	0
2	PO4	CO	4201	5/5	0.94	0.17	-2.17	23,28,53,142	0
2	PO4	BU	1001	5/5	0.94	0.14	-2.24	80,81,83,167	0
2	PO4	AF	1001	5/5	0.95	0.14	-2.27	80,81,83,167	0
2	PO4	AQ	1001	5/5	0.93	0.15	-2.28	74,78,104,213	0
2	PO4	C1	1201	5/5	0.83	0.22	-2.36	74,78,104,213	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	AR	1001	5/5	0.93	0.13	-2.64	34,46,111,116	0
2	PO4	C4	4201	5/5	0.90	0.27	-2.88	23,28,53,142	0
2	PO4	BN	1001	5/5	0.93	0.16	-3.34	58,65,106,138	0
2	PO4	BI	1001	5/5	0.94	0.12	-3.44	58,65,106,138	0
2	PO4	AE	1001	5/5	0.95	0.12	-3.47	23,28,53,142	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.