



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2024 – 05:04 AM EDT

PDB ID : 6GEB  
Title : X-ray structure of the Legionella pneumophila ATPase DotB  
Authors : Prevost, M.S.; Waksman, G.  
Deposited on : 2018-04-26  
Resolution : 3.19 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 2.37.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

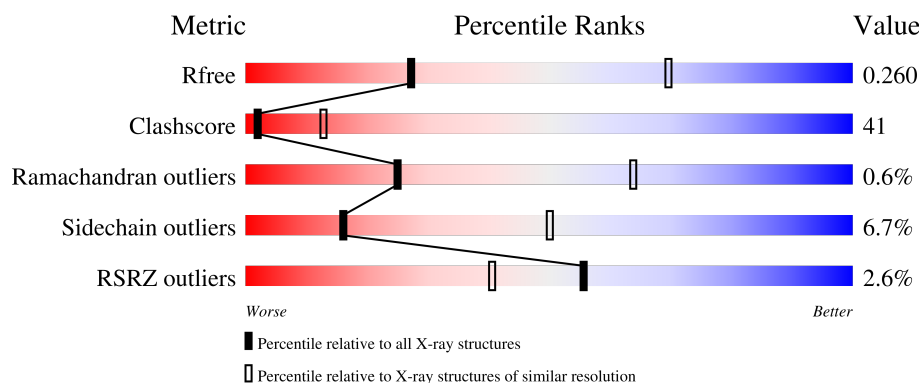
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.19 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	391	<div> <div>4%</div> <div> <div></div> <div>50%</div> <div>42%</div> <div>6%</div> </div> </div>
1	B	391	<div> <div>%</div> <div> <div></div> <div>56%</div> <div>36%</div> <div>5%</div> </div> </div>
1	C	391	<div> <div>%</div> <div> <div></div> <div>50%</div> <div>39%</div> <div>5%</div> <div>6%</div> </div> </div>
1	D	391	<div> <div>2%</div> <div> <div></div> <div>48%</div> <div>44%</div> <div>6%</div> </div> </div>
1	E	391	<div> <div>2%</div> <div> <div></div> <div>49%</div> <div>40%</div> <div>6%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	391	
1	G	391	
1	H	391	
1	I	391	
1	J	391	
1	K	391	
1	L	391	

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	J	401	-	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 34658 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 DotB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	369	Total	C	N	O	S	0	0	0
			2907	1826	512	558	11			
1	B	371	Total	C	N	O	S	0	0	0
			2906	1826	510	559	11			
1	C	369	Total	C	N	O	S	0	0	0
			2886	1814	503	558	11			
1	D	368	Total	C	N	O	S	0	0	0
			2874	1806	503	554	11			
1	E	367	Total	C	N	O	S	0	0	0
			2867	1805	498	553	11			
1	F	366	Total	C	N	O	S	0	0	0
			2859	1800	495	553	11			
1	G	369	Total	C	N	O	S	0	0	0
			2907	1826	512	558	11			
1	H	371	Total	C	N	O	S	0	0	0
			2906	1826	510	559	11			
1	I	369	Total	C	N	O	S	0	0	0
			2886	1814	503	558	11			
1	J	368	Total	C	N	O	S	0	0	0
			2874	1806	503	554	11			
1	K	367	Total	C	N	O	S	0	0	0
			2867	1805	498	553	11			
1	L	366	Total	C	N	O	S	0	0	0
			2859	1800	495	553	11			

There are 180 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP O52185
A	-12	ALA	-	expression tag	UNP O52185
A	-11	SER	-	expression tag	UNP O52185
A	-10	TRP	-	expression tag	UNP O52185
A	-9	SER	-	expression tag	UNP O52185

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	HIS	-	expression tag	UNP O52185
A	-7	PRO	-	expression tag	UNP O52185
A	-6	GLN	-	expression tag	UNP O52185
A	-5	PHE	-	expression tag	UNP O52185
A	-4	GLU	-	expression tag	UNP O52185
A	-3	LYS	-	expression tag	UNP O52185
A	-2	ILE	-	expression tag	UNP O52185
A	-1	GLU	-	expression tag	UNP O52185
A	0	GLY	-	expression tag	UNP O52185
A	1	ARG	-	expression tag	UNP O52185
B	-13	MET	-	initiating methionine	UNP O52185
B	-12	ALA	-	expression tag	UNP O52185
B	-11	SER	-	expression tag	UNP O52185
B	-10	TRP	-	expression tag	UNP O52185
B	-9	SER	-	expression tag	UNP O52185
B	-8	HIS	-	expression tag	UNP O52185
B	-7	PRO	-	expression tag	UNP O52185
B	-6	GLN	-	expression tag	UNP O52185
B	-5	PHE	-	expression tag	UNP O52185
B	-4	GLU	-	expression tag	UNP O52185
B	-3	LYS	-	expression tag	UNP O52185
B	-2	ILE	-	expression tag	UNP O52185
B	-1	GLU	-	expression tag	UNP O52185
B	0	GLY	-	expression tag	UNP O52185
B	1	ARG	-	expression tag	UNP O52185
C	-13	MET	-	initiating methionine	UNP O52185
C	-12	ALA	-	expression tag	UNP O52185
C	-11	SER	-	expression tag	UNP O52185
C	-10	TRP	-	expression tag	UNP O52185
C	-9	SER	-	expression tag	UNP O52185
C	-8	HIS	-	expression tag	UNP O52185
C	-7	PRO	-	expression tag	UNP O52185
C	-6	GLN	-	expression tag	UNP O52185
C	-5	PHE	-	expression tag	UNP O52185
C	-4	GLU	-	expression tag	UNP O52185
C	-3	LYS	-	expression tag	UNP O52185
C	-2	ILE	-	expression tag	UNP O52185
C	-1	GLU	-	expression tag	UNP O52185
C	0	GLY	-	expression tag	UNP O52185
C	1	ARG	-	expression tag	UNP O52185
D	-13	MET	-	initiating methionine	UNP O52185
D	-12	ALA	-	expression tag	UNP O52185

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-11	SER	-	expression tag	UNP O52185
D	-10	TRP	-	expression tag	UNP O52185
D	-9	SER	-	expression tag	UNP O52185
D	-8	HIS	-	expression tag	UNP O52185
D	-7	PRO	-	expression tag	UNP O52185
D	-6	GLN	-	expression tag	UNP O52185
D	-5	PHE	-	expression tag	UNP O52185
D	-4	GLU	-	expression tag	UNP O52185
D	-3	LYS	-	expression tag	UNP O52185
D	-2	ILE	-	expression tag	UNP O52185
D	-1	GLU	-	expression tag	UNP O52185
D	0	GLY	-	expression tag	UNP O52185
D	1	ARG	-	expression tag	UNP O52185
E	-13	MET	-	initiating methionine	UNP O52185
E	-12	ALA	-	expression tag	UNP O52185
E	-11	SER	-	expression tag	UNP O52185
E	-10	TRP	-	expression tag	UNP O52185
E	-9	SER	-	expression tag	UNP O52185
E	-8	HIS	-	expression tag	UNP O52185
E	-7	PRO	-	expression tag	UNP O52185
E	-6	GLN	-	expression tag	UNP O52185
E	-5	PHE	-	expression tag	UNP O52185
E	-4	GLU	-	expression tag	UNP O52185
E	-3	LYS	-	expression tag	UNP O52185
E	-2	ILE	-	expression tag	UNP O52185
E	-1	GLU	-	expression tag	UNP O52185
E	0	GLY	-	expression tag	UNP O52185
E	1	ARG	-	expression tag	UNP O52185
F	-13	MET	-	initiating methionine	UNP O52185
F	-12	ALA	-	expression tag	UNP O52185
F	-11	SER	-	expression tag	UNP O52185
F	-10	TRP	-	expression tag	UNP O52185
F	-9	SER	-	expression tag	UNP O52185
F	-8	HIS	-	expression tag	UNP O52185
F	-7	PRO	-	expression tag	UNP O52185
F	-6	GLN	-	expression tag	UNP O52185
F	-5	PHE	-	expression tag	UNP O52185
F	-4	GLU	-	expression tag	UNP O52185
F	-3	LYS	-	expression tag	UNP O52185
F	-2	ILE	-	expression tag	UNP O52185
F	-1	GLU	-	expression tag	UNP O52185
F	0	GLY	-	expression tag	UNP O52185

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1	ARG	-	expression tag	UNP O52185
G	-13	MET	-	initiating methionine	UNP O52185
G	-12	ALA	-	expression tag	UNP O52185
G	-11	SER	-	expression tag	UNP O52185
G	-10	TRP	-	expression tag	UNP O52185
G	-9	SER	-	expression tag	UNP O52185
G	-8	HIS	-	expression tag	UNP O52185
G	-7	PRO	-	expression tag	UNP O52185
G	-6	GLN	-	expression tag	UNP O52185
G	-5	PHE	-	expression tag	UNP O52185
G	-4	GLU	-	expression tag	UNP O52185
G	-3	LYS	-	expression tag	UNP O52185
G	-2	ILE	-	expression tag	UNP O52185
G	-1	GLU	-	expression tag	UNP O52185
G	0	GLY	-	expression tag	UNP O52185
G	1	ARG	-	expression tag	UNP O52185
H	-13	MET	-	initiating methionine	UNP O52185
H	-12	ALA	-	expression tag	UNP O52185
H	-11	SER	-	expression tag	UNP O52185
H	-10	TRP	-	expression tag	UNP O52185
H	-9	SER	-	expression tag	UNP O52185
H	-8	HIS	-	expression tag	UNP O52185
H	-7	PRO	-	expression tag	UNP O52185
H	-6	GLN	-	expression tag	UNP O52185
H	-5	PHE	-	expression tag	UNP O52185
H	-4	GLU	-	expression tag	UNP O52185
H	-3	LYS	-	expression tag	UNP O52185
H	-2	ILE	-	expression tag	UNP O52185
H	-1	GLU	-	expression tag	UNP O52185
H	0	GLY	-	expression tag	UNP O52185
H	1	ARG	-	expression tag	UNP O52185
I	-13	MET	-	initiating methionine	UNP O52185
I	-12	ALA	-	expression tag	UNP O52185
I	-11	SER	-	expression tag	UNP O52185
I	-10	TRP	-	expression tag	UNP O52185
I	-9	SER	-	expression tag	UNP O52185
I	-8	HIS	-	expression tag	UNP O52185
I	-7	PRO	-	expression tag	UNP O52185
I	-6	GLN	-	expression tag	UNP O52185
I	-5	PHE	-	expression tag	UNP O52185
I	-4	GLU	-	expression tag	UNP O52185
I	-3	LYS	-	expression tag	UNP O52185

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-2	ILE	-	expression tag	UNP O52185
I	-1	GLU	-	expression tag	UNP O52185
I	0	GLY	-	expression tag	UNP O52185
I	1	ARG	-	expression tag	UNP O52185
J	-13	MET	-	initiating methionine	UNP O52185
J	-12	ALA	-	expression tag	UNP O52185
J	-11	SER	-	expression tag	UNP O52185
J	-10	TRP	-	expression tag	UNP O52185
J	-9	SER	-	expression tag	UNP O52185
J	-8	HIS	-	expression tag	UNP O52185
J	-7	PRO	-	expression tag	UNP O52185
J	-6	GLN	-	expression tag	UNP O52185
J	-5	PHE	-	expression tag	UNP O52185
J	-4	GLU	-	expression tag	UNP O52185
J	-3	LYS	-	expression tag	UNP O52185
J	-2	ILE	-	expression tag	UNP O52185
J	-1	GLU	-	expression tag	UNP O52185
J	0	GLY	-	expression tag	UNP O52185
J	1	ARG	-	expression tag	UNP O52185
K	-13	MET	-	initiating methionine	UNP O52185
K	-12	ALA	-	expression tag	UNP O52185
K	-11	SER	-	expression tag	UNP O52185
K	-10	TRP	-	expression tag	UNP O52185
K	-9	SER	-	expression tag	UNP O52185
K	-8	HIS	-	expression tag	UNP O52185
K	-7	PRO	-	expression tag	UNP O52185
K	-6	GLN	-	expression tag	UNP O52185
K	-5	PHE	-	expression tag	UNP O52185
K	-4	GLU	-	expression tag	UNP O52185
K	-3	LYS	-	expression tag	UNP O52185
K	-2	ILE	-	expression tag	UNP O52185
K	-1	GLU	-	expression tag	UNP O52185
K	0	GLY	-	expression tag	UNP O52185
K	1	ARG	-	expression tag	UNP O52185
L	-13	MET	-	initiating methionine	UNP O52185
L	-12	ALA	-	expression tag	UNP O52185
L	-11	SER	-	expression tag	UNP O52185
L	-10	TRP	-	expression tag	UNP O52185
L	-9	SER	-	expression tag	UNP O52185
L	-8	HIS	-	expression tag	UNP O52185
L	-7	PRO	-	expression tag	UNP O52185
L	-6	GLN	-	expression tag	UNP O52185

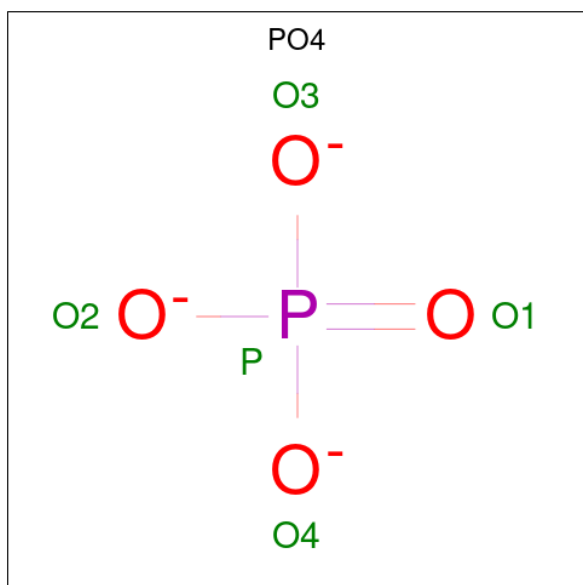
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Chain	Residue	Modelled	Actual	Comment	Reference
L	-5	PHE	-	expression tag	UNP O52185
L	-4	GLU	-	expression tag	UNP O52185
L	-3	LYS	-	expression tag	UNP O52185
L	-2	ILE	-	expression tag	UNP O52185
L	-1	GLU	-	expression tag	UNP O52185
L	0	GLY	-	expression tag	UNP O52185
L	1	ARG	-	expression tag	UNP O52185

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		
2	G	1	Total	O	P	0	0
			5	4	1		
2	H	1	Total	O	P	0	0
			5	4	1		

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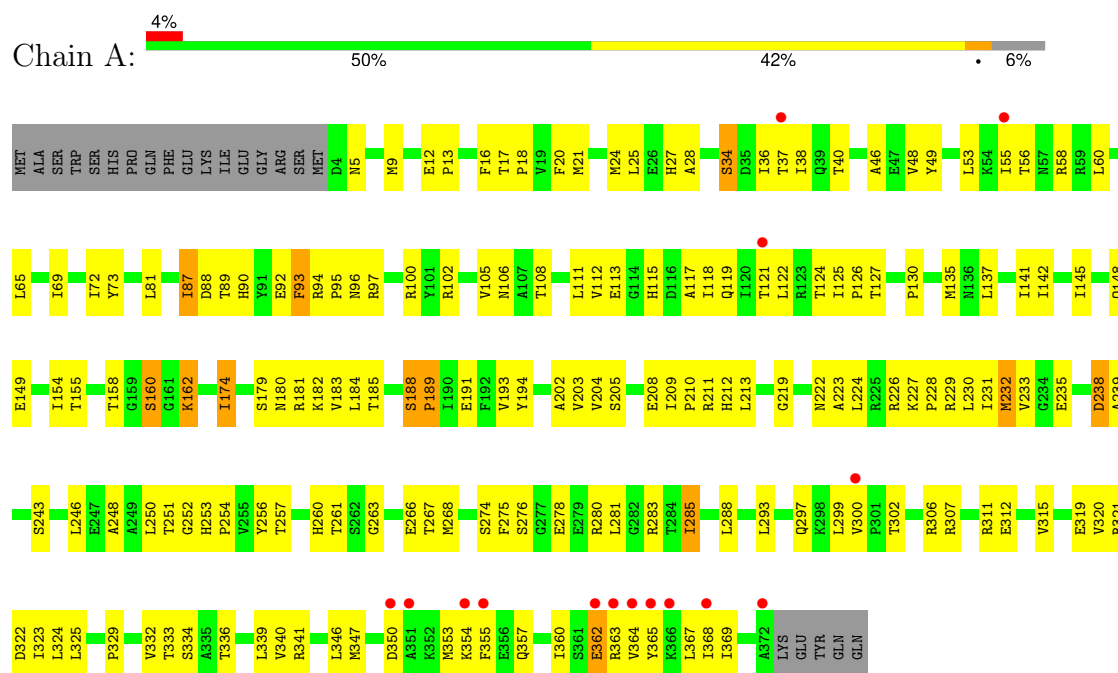
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	I	1	Total	O	P	0	0
			5	4	1		
2	J	1	Total	O	P	0	0
			5	4	1		
2	K	1	Total	O	P	0	0
			5	4	1		
2	L	1	Total	O	P	0	0
			5	4	1		

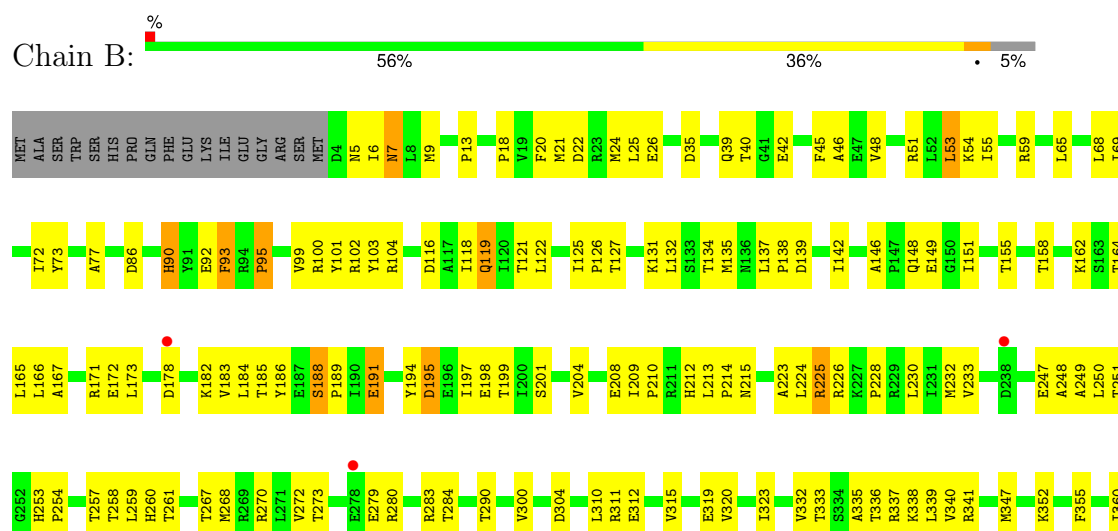
### 3 Residue-property plots [i](#)

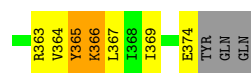
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

#### • Molecule 1: DotB

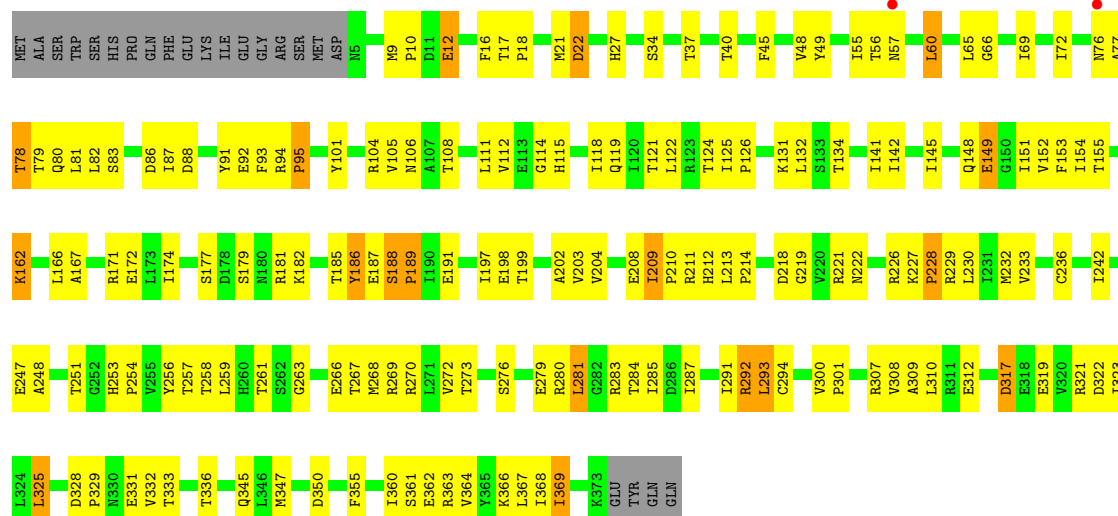


#### • Molecule 1: DotB

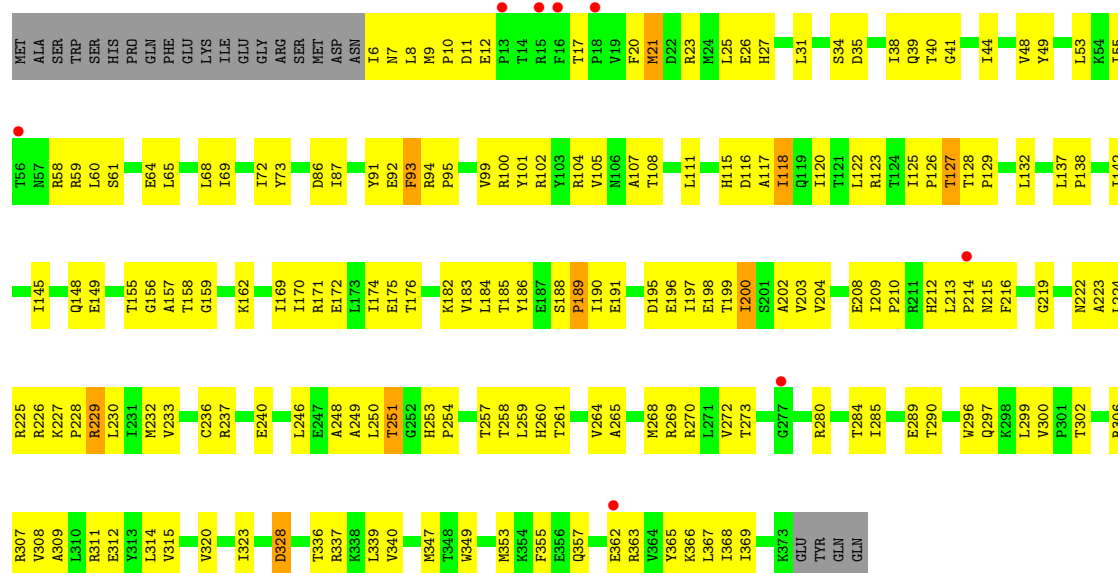




• Molecule 1: DotB

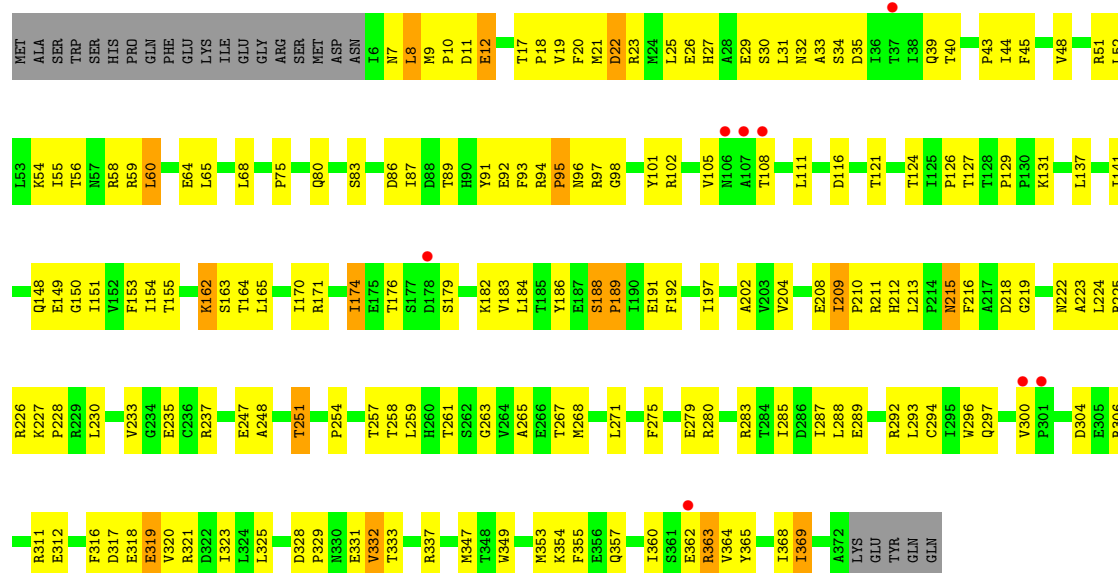


• Molecule 1: DotB

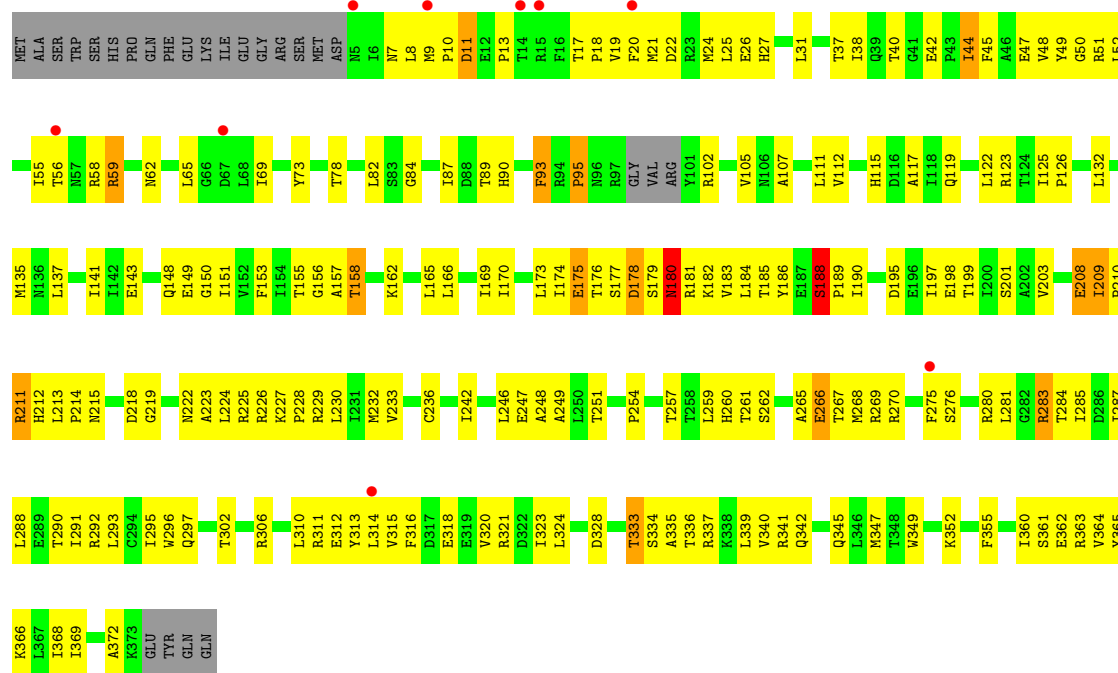


• Molecule 1: DotB



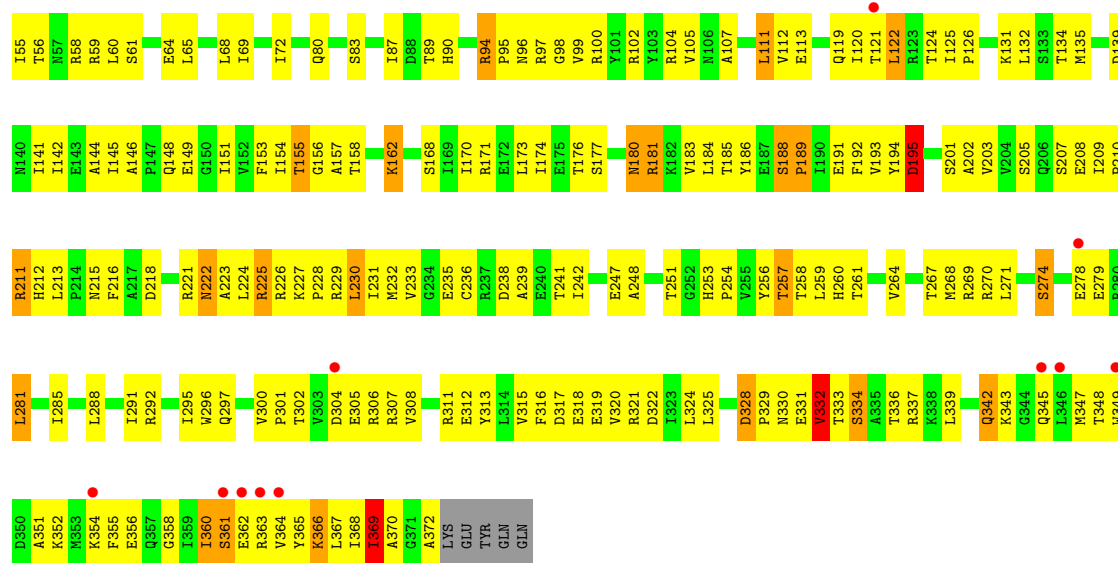


• Molecule 1: DotB

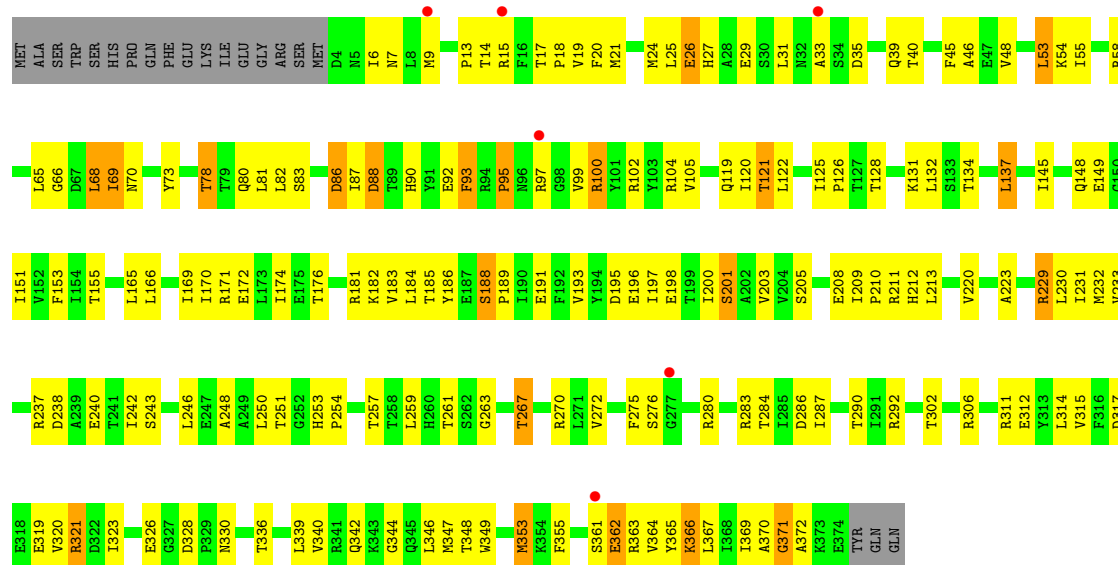


• Molecule 1: DotB

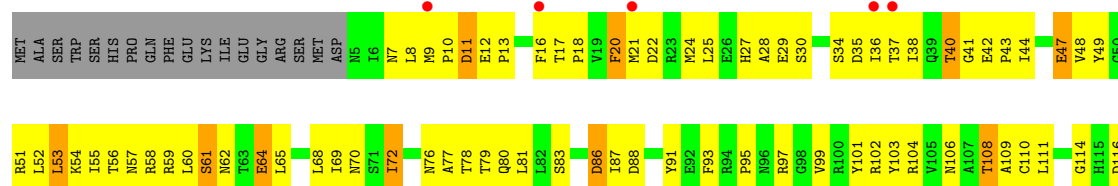


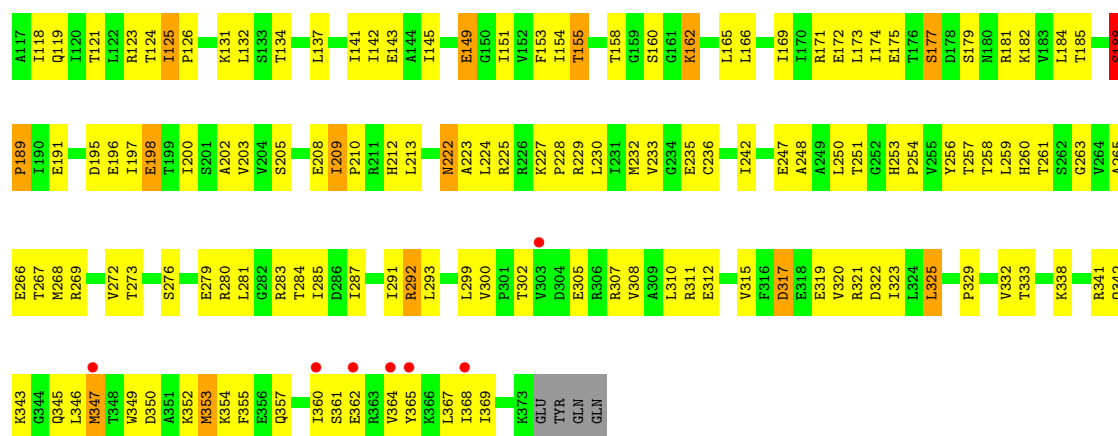


### • Molecule 1: DotB

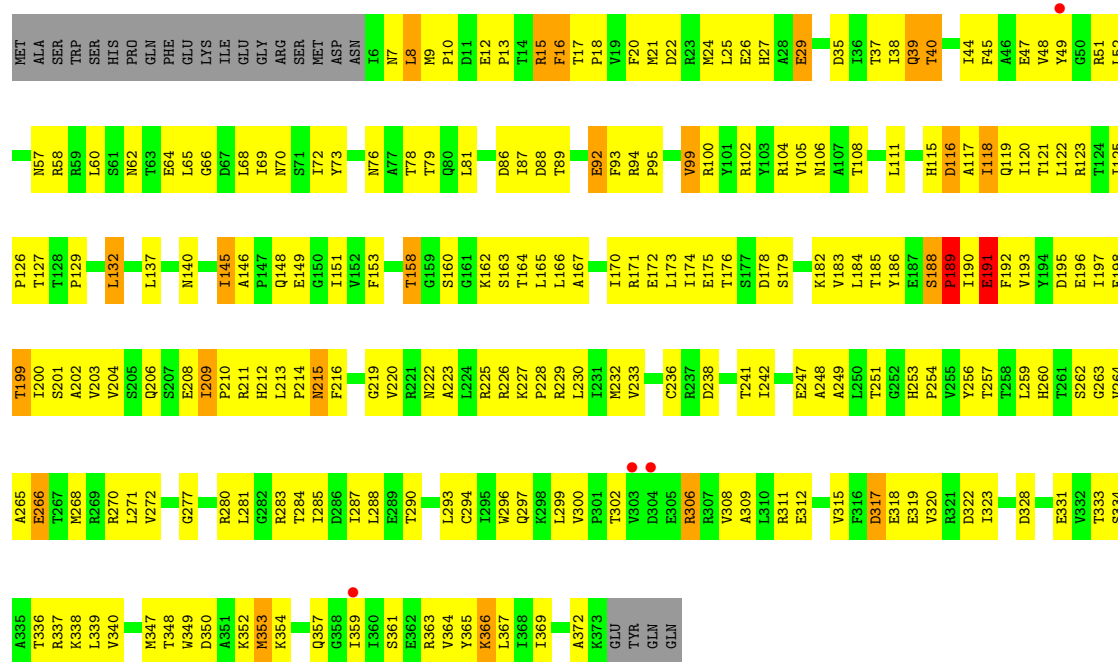


### • Molecule 1: DotB

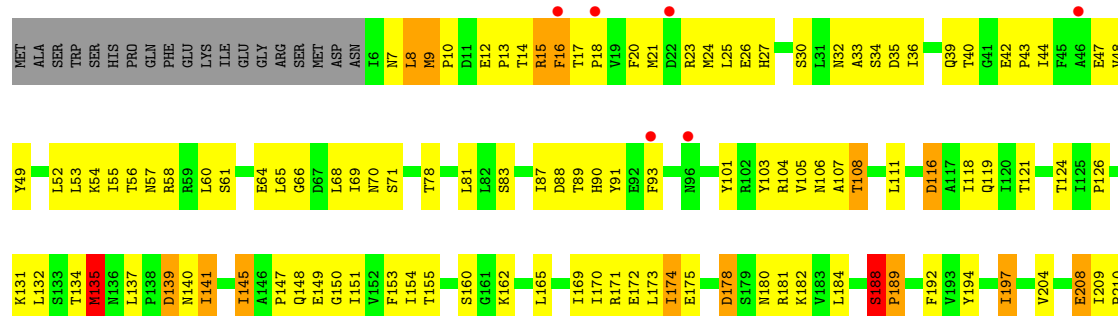


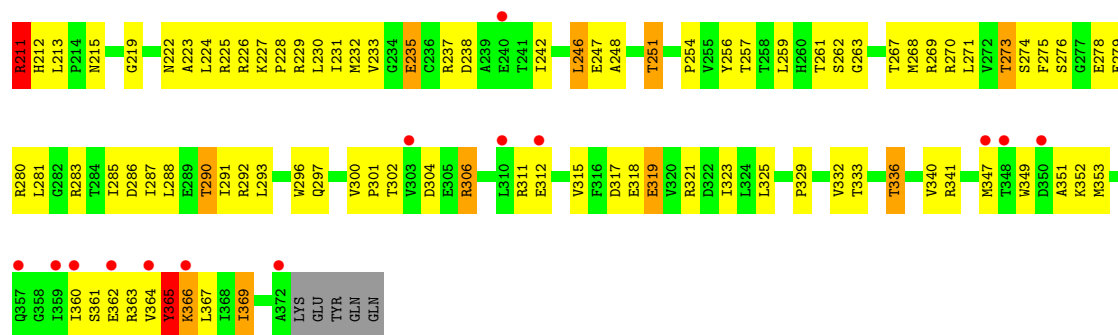


• Molecule 1: DotB

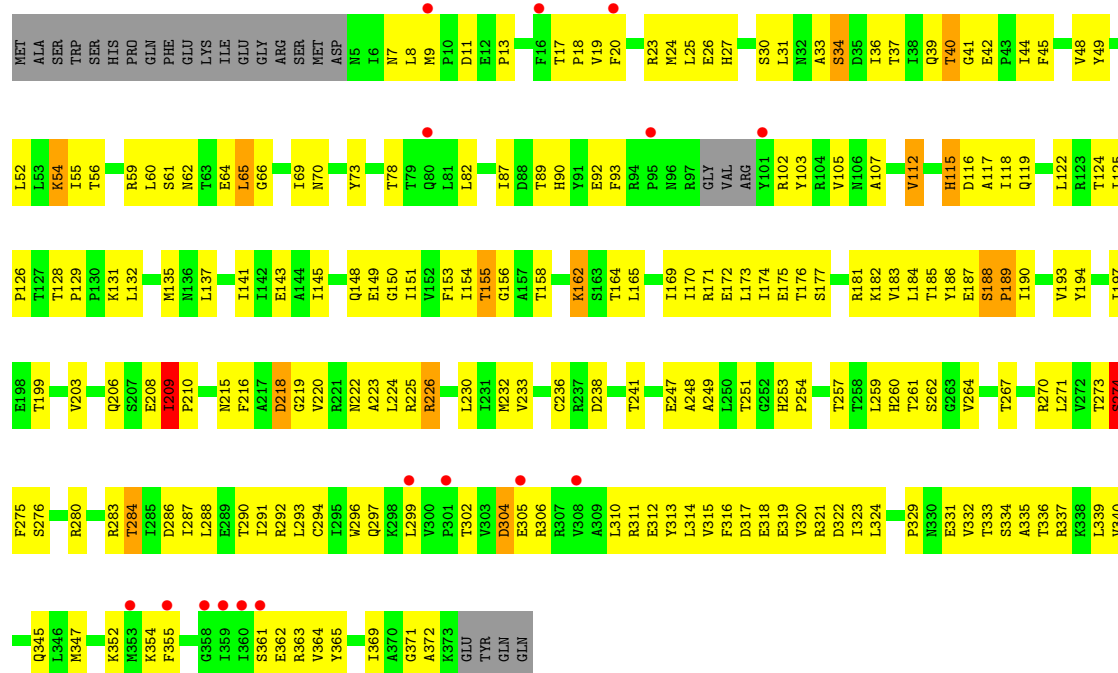


• Molecule 1: DotB





● Molecule 1: DotB





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.20Å 109.30Å 119.80Å 83.70° 86.60° 60.70°	Depositor
Resolution (Å)	36.04 – 3.19 49.10 – 3.19	Depositor EDS
% Data completeness (in resolution range)	98.0 (36.04-3.19) 98.1 (49.10-3.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.233 , 0.261 0.234 , 0.260	Depositor DCC
$R_{free}$ test set	3841 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	103.3	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 64.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.034 for h-k,-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	34658	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

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	A	0.73	0/2954	0.78	4/4009 (0.1%)
1	B	0.78	0/2953	0.77	6/4009 (0.1%)
1	C	0.73	0/2933	0.77	5/3984 (0.1%)
1	D	0.79	0/2920	0.78	4/3965 (0.1%)
1	E	0.78	1/2914 (0.0%)	0.79	4/3958 (0.1%)
1	F	0.81	2/2904 (0.1%)	0.80	5/3943 (0.1%)
1	G	0.91	1/2954 (0.0%)	0.90	5/4009 (0.1%)
1	H	0.82	0/2953	0.77	4/4009 (0.1%)
1	I	0.84	1/2933 (0.0%)	0.81	4/3984 (0.1%)
1	J	0.82	0/2920	0.84	6/3965 (0.2%)
1	K	0.84	0/2914	0.86	6/3958 (0.2%)
1	L	0.84	0/2904	0.82	2/3943 (0.1%)
All	All	0.81	5/35156 (0.0%)	0.81	55/47736 (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	F	0	1
1	K	0	1
1	L	0	1
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	312	GLU	CD-OE1	5.61	1.31	1.25
1	F	175	GLU	CD-OE2	-5.35	1.19	1.25
1	E	12	GLU	CG-CD	5.23	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	369	ILE	N-CA	-5.10	1.36	1.46
1	I	61	SER	CB-OG	-5.08	1.35	1.42

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	ASP	CB-CG-OD2	10.49	127.74	118.30
1	F	211	ARG	NE-CZ-NH2	9.40	125.00	120.30
1	C	317	ASP	CB-CG-OD2	7.73	125.26	118.30
1	B	304	ASP	CB-CG-OD1	-7.54	111.51	118.30
1	G	195	ASP	CB-CG-OD1	-7.33	111.70	118.30
1	A	238	ASP	CB-CG-OD1	-6.85	112.13	118.30
1	L	286	ASP	CB-CG-OD1	-6.48	112.47	118.30
1	G	59	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	C	186	TYR	CB-CG-CD2	-6.40	117.16	121.00
1	J	116	ASP	CB-CG-OD2	6.36	124.02	118.30
1	K	135	MET	CG-SD-CE	6.23	110.17	100.20
1	E	209	ILE	C-N-CD	6.20	141.42	128.40
1	C	186	TYR	CB-CG-CD1	6.14	124.68	121.00
1	B	304	ASP	CB-CG-OD2	6.08	123.78	118.30
1	H	362	GLU	OE1-CD-OE2	-5.98	116.13	123.30
1	F	123	ARG	NE-CZ-NH1	-5.93	117.34	120.30
1	K	208	GLU	OE1-CD-OE2	-5.92	116.20	123.30
1	C	317	ASP	CB-CG-OD1	-5.91	112.98	118.30
1	B	365	TYR	CB-CG-CD2	-5.90	117.46	121.00
1	K	209	ILE	C-N-CD	5.84	140.67	128.40
1	B	195	ASP	CB-CG-OD2	-5.77	113.11	118.30
1	K	188	SER	C-N-CD	5.73	140.44	128.40
1	H	86	ASP	CB-CG-OD2	5.70	123.43	118.30
1	J	188	SER	C-N-CD	5.67	140.30	128.40
1	E	211	ARG	N-CA-C	5.56	126.02	111.00
1	G	221	ARG	NE-CZ-NH2	5.55	123.07	120.30
1	D	116	ASP	CB-CG-OD2	5.54	123.29	118.30
1	J	191	GLU	OE1-CD-OE2	-5.49	116.71	123.30
1	L	209	ILE	C-N-CD	5.48	139.90	128.40
1	I	317	ASP	CB-CG-OD2	-5.47	113.38	118.30
1	K	365	TYR	CB-CG-CD1	5.47	124.28	121.00
1	E	363	ARG	NE-CZ-NH2	5.40	123.00	120.30
1	D	328	ASP	CB-CG-OD1	-5.35	113.48	118.30
1	A	88	ASP	CB-CG-OD2	5.33	123.10	118.30
1	B	225	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	G	332	VAL	CB-CA-C	-5.32	101.29	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	139	ASP	CB-CG-OD1	5.30	123.07	118.30
1	H	321	ARG	NE-CZ-NH2	5.29	122.94	120.30
1	K	211	ARG	N-CA-C	5.28	125.27	111.00
1	I	20	PHE	CB-CG-CD1	-5.25	117.12	120.80
1	D	229	ARG	NE-CZ-NH1	-5.23	117.68	120.30
1	F	95	PRO	N-CA-CB	5.20	109.55	103.30
1	F	188	SER	C-N-CD	5.19	139.31	128.40
1	I	86	ASP	CB-CG-OD1	5.19	122.97	118.30
1	A	188	SER	C-N-CD	5.19	139.30	128.40
1	H	195	ASP	CB-CG-OD1	5.19	122.97	118.30
1	C	187	GLU	OE1-CD-OE2	-5.18	117.08	123.30
1	B	225	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	E	188	SER	C-N-CD	5.12	139.16	128.40
1	F	318	GLU	OE1-CD-OE2	-5.09	117.19	123.30
1	J	189	PRO	CA-N-CD	-5.08	104.40	111.50
1	I	188	SER	C-N-CD	5.06	139.02	128.40
1	D	250	LEU	CB-CG-CD2	5.03	119.55	111.00
1	J	317	ASP	CB-CG-OD2	-5.01	113.79	118.30
1	J	178	ASP	CB-CG-OD1	-5.01	113.79	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	180	ASN	Mainchain
1	K	246	LEU	Mainchain
1	L	372	ALA	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	A	2907	0	2949	206	0
1	B	2906	0	2929	199	0
1	C	2886	0	2907	195	1
1	D	2874	0	2901	193	0
1	E	2867	0	2891	214	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2859	0	2876	241	1
1	G	2907	0	2949	359	0
1	H	2906	0	2929	230	0
1	I	2886	0	2907	332	0
1	J	2874	0	2901	341	0
1	K	2867	0	2891	273	0
1	L	2859	0	2876	245	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
2	G	5	0	0	0	0
2	H	5	0	0	0	0
2	I	5	0	0	0	0
2	J	5	0	0	2	0
2	K	5	0	0	1	0
2	L	5	0	0	0	0
All	All	34658	0	34906	2849	1

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 41.

All (2849) 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:J:9:MET:CE	1:J:24:MET:HA	1.29	1.53
1:J:9:MET:HE3	1:J:24:MET:CA	1.57	1.35
1:G:291:ILE:HD13	1:G:316:PHE:CE2	1.64	1.31
1:G:355:PHE:CZ	1:G:365:TYR:CD2	2.23	1.25
1:D:236:CYS:SG	1:D:259:LEU:HD21	1.79	1.23
1:E:29:GLU:HG2	1:E:101:TYR:CE2	1.74	1.22
1:G:355:PHE:CZ	1:G:365:TYR:HD2	1.55	1.22
1:K:40:THR:HG22	1:K:65:LEU:HD22	1.22	1.21
1:J:280:ARG:O	1:J:284:THR:HG23	1.40	1.20
1:L:215:ASN:OD1	1:L:218:ASP:HB2	1.40	1.20
1:C:280:ARG:O	1:C:284:THR:HG23	1.39	1.19
1:L:112:VAL:HG23	1:L:117:ALA:CB	1.73	1.17
1:I:280:ARG:O	1:I:284:THR:HG23	1.42	1.17
1:J:9:MET:CE	1:J:24:MET:CA	2.13	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:291:ILE:CG2	1:G:316:PHE:HD2	1.57	1.16
1:I:355:PHE:CE2	1:I:362:GLU:HA	1.80	1.15
1:D:8:LEU:HD13	1:D:9:MET:N	1.60	1.15
1:D:261:THR:HG21	1:D:270:ARG:HG3	1.17	1.12
1:K:363:ARG:HA	1:K:366:LYS:CD	1.78	1.12
1:I:261:THR:HG23	1:I:267:THR:HG22	1.21	1.12
1:I:24:MET:CE	1:I:44:ILE:HD13	1.77	1.12
1:B:93:PHE:CZ	1:B:101:TYR:HD2	1.68	1.11
1:F:190:ILE:HG12	1:F:208:GLU:HG3	1.25	1.11
1:J:121:THR:HG21	1:K:182:LYS:HZ3	1.06	1.11
1:D:280:ARG:O	1:D:284:THR:HG23	1.46	1.11
1:G:363:ARG:HA	1:G:366:LYS:HD2	1.17	1.11
1:I:104:ARG:CG	1:I:125:ILE:HD11	1.80	1.11
1:H:48:VAL:HG21	1:H:53:LEU:HD11	1.32	1.11
1:E:162:LYS:HD3	1:E:258:THR:HB	1.32	1.10
1:G:356:GLU:N	1:G:356:GLU:OE2	1.83	1.10
1:L:112:VAL:HG23	1:L:117:ALA:HB2	1.33	1.10
1:B:280:ARG:O	1:B:284:THR:HG23	1.50	1.10
1:G:291:ILE:HG12	1:G:316:PHE:CD2	1.87	1.09
1:I:108:THR:HG21	1:J:222:ASN:HD21	1.08	1.09
1:I:40:THR:HG22	1:I:65:LEU:HD12	1.21	1.09
1:J:15:ARG:HG2	1:J:64:GLU:OE2	1.53	1.09
1:F:48:VAL:HG12	1:F:49:TYR:HD2	1.17	1.09
1:D:102:ARG:HH21	1:D:127:THR:HG22	1.12	1.08
1:D:175:GLU:HA	1:D:199:THR:HG22	1.31	1.08
1:F:174:ILE:HG22	1:F:199:THR:HG21	1.34	1.08
1:C:104:ARG:HG3	1:C:125:ILE:HD11	1.33	1.07
1:J:60:LEU:HD13	1:J:64:GLU:OE1	1.55	1.07
1:I:24:MET:HE2	1:I:44:ILE:CD1	1.83	1.07
1:H:365:TYR:CZ	1:H:369:ILE:HD11	1.90	1.07
1:I:321:ARG:O	1:I:325:LEU:HD12	1.55	1.07
1:J:174:ILE:HG12	1:J:199:THR:HG21	1.37	1.06
1:G:180:ASN:HB3	1:L:52:LEU:HB2	1.38	1.06
1:I:104:ARG:CG	1:I:125:ILE:CD1	2.34	1.06
1:G:291:ILE:CD1	1:G:316:PHE:CE2	2.38	1.05
1:E:40:THR:HG22	1:E:65:LEU:HD22	1.36	1.05
1:I:261:THR:CG2	1:I:267:THR:HG22	1.86	1.04
1:K:288:LEU:HD13	1:K:325:LEU:HD23	1.39	1.04
1:A:355:PHE:HA	1:A:360:ILE:HG22	1.31	1.04
1:E:108:THR:HG21	1:F:226:ARG:NH2	1.72	1.04
1:K:16:PHE:HZ	1:K:24:MET:HE3	1.21	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:119:GLN:HE22	1:H:182:LYS:NZ	1.56	1.04
1:C:321:ARG:O	1:C:325:LEU:HD12	1.57	1.03
1:I:104:ARG:HG2	1:I:125:ILE:HD11	1.32	1.03
1:I:261:THR:HG21	1:I:267:THR:HA	1.39	1.03
1:K:363:ARG:HA	1:K:366:LYS:HD3	1.03	1.03
1:B:155:THR:HG22	1:B:259:LEU:HB2	1.39	1.03
1:K:24:MET:HE1	1:K:44:ILE:HD12	1.38	1.03
1:I:104:ARG:HG2	1:I:125:ILE:CD1	1.89	1.03
1:J:353:MET:O	1:J:357:GLN:HG2	1.59	1.03
1:L:9:MET:SD	1:L:56:THR:HG22	1.97	1.03
1:F:73:TYR:CD1	1:F:89:THR:HG21	1.93	1.03
1:F:9:MET:HG2	1:F:10:PRO:HD2	1.39	1.02
1:G:269:ARG:HG2	1:G:269:ARG:HH11	1.18	1.02
1:F:40:THR:HG23	1:F:65:LEU:HD22	1.40	1.02
1:G:355:PHE:CE2	1:G:365:TYR:CD2	2.48	1.02
1:E:261:THR:OG1	1:E:267:THR:HG22	1.59	1.02
1:F:125:ILE:HD12	1:F:126:PRO:HD2	1.42	1.02
1:F:155:THR:HG22	1:F:259:LEU:HB2	1.39	1.02
1:I:355:PHE:HE2	1:I:362:GLU:CA	1.70	1.02
1:I:355:PHE:HE2	1:I:362:GLU:HA	0.90	1.02
1:C:104:ARG:CG	1:C:125:ILE:HD11	1.89	1.01
1:J:121:THR:HG21	1:K:182:LYS:NZ	1.74	1.01
1:C:79:THR:HA	1:C:82:LEU:HD12	1.04	1.01
1:K:261:THR:OG1	1:K:267:THR:HG22	1.60	1.00
1:D:261:THR:CG2	1:D:270:ARG:HG3	1.91	1.00
1:G:291:ILE:CG2	1:G:316:PHE:CD2	2.44	1.00
1:B:212:HIS:O	1:B:213:LEU:HD12	1.62	1.00
1:A:261:THR:HB	1:A:267:THR:HG22	1.44	0.99
1:J:365:TYR:CE2	1:J:369:ILE:HD11	1.96	0.99
1:F:48:VAL:HG12	1:F:49:TYR:CD2	1.97	0.99
1:C:79:THR:CA	1:C:82:LEU:HD12	1.91	0.99
1:F:24:MET:SD	1:F:44:ILE:HD12	2.03	0.99
1:K:170:ILE:O	1:K:174:ILE:HG22	1.61	0.98
1:L:24:MET:SD	1:L:44:ILE:HD13	2.02	0.98
1:L:183:VAL:HG13	1:L:230:LEU:HD22	1.45	0.98
1:D:40:THR:HG22	1:D:65:LEU:HD22	1.42	0.98
1:J:196:GLU:N	1:J:196:GLU:OE1	1.97	0.98
1:H:188:SER:OG	1:H:189:PRO:HD3	1.62	0.98
1:J:15:ARG:HA	1:J:58:ARG:NH1	1.78	0.98
1:A:285:ILE:H	1:A:285:ILE:HD12	1.25	0.98
1:H:212:HIS:O	1:H:213:LEU:HD12	1.63	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:TYR:CZ	1:B:369:ILE:HD11	2.00	0.97
1:E:40:THR:CG2	1:E:65:LEU:HD22	1.94	0.97
1:E:164:THR:HG22	1:E:192:PHE:HZ	1.26	0.97
1:G:291:ILE:HG23	1:G:316:PHE:HD2	1.30	0.97
1:C:40:THR:HG22	1:C:65:LEU:HD22	1.47	0.97
1:F:13:PRO:HG3	1:F:20:PHE:CD2	2.00	0.97
1:J:272:VAL:HG13	1:J:284:THR:HG22	1.46	0.97
1:K:108:THR:HG21	1:L:222:ASN:HD21	1.27	0.97
1:L:233:VAL:HB	1:L:257:THR:HG22	1.47	0.96
1:G:239:ALA:HA	1:G:242:ILE:HD12	1.47	0.96
1:E:164:THR:HG22	1:E:192:PHE:CZ	2.00	0.96
1:I:13:PRO:HB3	1:I:20:PHE:CE2	1.99	0.96
1:I:272:VAL:HG13	1:I:284:THR:HG22	1.46	0.96
1:D:264:VAL:HG11	1:D:340:VAL:HG11	1.44	0.96
1:J:174:ILE:HG12	1:J:199:THR:CG2	1.94	0.96
1:I:355:PHE:CZ	1:I:362:GLU:HG2	2.00	0.96
1:L:112:VAL:CG2	1:L:117:ALA:CB	2.43	0.96
1:H:14:THR:O	1:H:15:ARG:NE	1.97	0.95
1:J:352:LYS:HG3	1:J:365:TYR:OH	1.65	0.95
1:D:40:THR:CG2	1:D:65:LEU:HD22	1.96	0.95
1:H:125:ILE:HD12	1:H:126:PRO:HD2	1.47	0.95
1:K:40:THR:CG2	1:K:65:LEU:HD22	1.95	0.95
1:K:135:MET:CE	1:K:135:MET:HA	1.96	0.95
1:G:40:THR:HG22	1:G:65:LEU:HD22	1.45	0.95
1:F:233:VAL:HB	1:F:257:THR:HG22	1.49	0.95
1:G:363:ARG:CA	1:G:366:LYS:HD2	1.97	0.95
1:I:24:MET:HE1	1:I:44:ILE:HD13	1.46	0.95
1:L:125:ILE:HD12	1:L:126:PRO:HD2	1.47	0.95
1:H:233:VAL:HB	1:H:257:THR:HG22	1.48	0.94
1:I:233:VAL:HB	1:I:257:THR:HG22	1.49	0.94
1:J:60:LEU:CD1	1:J:64:GLU:OE1	2.14	0.94
1:G:119:GLN:HE22	1:H:182:LYS:HZ1	1.07	0.94
1:G:363:ARG:HA	1:G:366:LYS:CD	1.98	0.94
1:I:154:ILE:CG2	1:I:162:LYS:HB3	1.96	0.94
1:C:154:ILE:CG2	1:C:162:LYS:HB3	1.97	0.94
1:G:216:PHE:HD2	1:G:233:VAL:HG12	1.30	0.94
1:I:25:LEU:HD13	1:I:103:TYR:CE2	2.02	0.94
1:J:121:THR:CG2	1:K:182:LYS:HZ3	1.80	0.94
1:J:233:VAL:HB	1:J:257:THR:HG22	1.46	0.94
1:G:365:TYR:HA	1:G:368:ILE:HD12	1.49	0.94
1:B:233:VAL:HB	1:B:257:THR:HG22	1.47	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:VAL:HB	1:D:257:THR:HG22	1.48	0.94
1:C:233:VAL:HB	1:C:257:THR:HG22	1.50	0.94
1:J:9:MET:HA	1:J:27:HIS:CD2	2.03	0.94
1:F:335:ALA:O	1:F:339:LEU:HD23	1.68	0.93
1:D:8:LEU:HD13	1:D:9:MET:H	1.18	0.93
1:L:24:MET:SD	1:L:44:ILE:CD1	2.57	0.93
1:E:208:GLU:H	1:E:212:HIS:HD2	1.09	0.93
1:K:332:VAL:O	1:K:336:THR:HG22	1.69	0.93
1:L:40:THR:HG22	1:L:65:LEU:HD23	1.49	0.93
1:G:149:GLU:OE1	1:G:149:GLU:N	2.01	0.93
1:J:262:SER:O	1:J:266:GLU:HG3	1.69	0.93
1:K:363:ARG:CA	1:K:366:LYS:HD3	1.98	0.93
1:F:183:VAL:HG13	1:F:230:LEU:HD22	1.49	0.93
1:I:287:ILE:O	1:I:291:ILE:HG13	1.69	0.93
1:K:16:PHE:CZ	1:K:24:MET:CE	2.52	0.92
1:I:61:SER:HB3	1:I:64:GLU:HG3	1.51	0.92
1:I:154:ILE:HG22	1:I:162:LYS:HB3	1.52	0.92
1:I:108:THR:HG21	1:J:222:ASN:ND2	1.84	0.92
1:K:353:MET:HA	1:K:353:MET:HE3	1.52	0.92
1:A:233:VAL:HB	1:A:257:THR:HG22	1.52	0.92
1:B:93:PHE:CZ	1:B:101:TYR:CD2	2.58	0.92
1:E:365:TYR:O	1:E:368:ILE:HG22	1.69	0.92
1:I:104:ARG:HG3	1:I:125:ILE:CD1	1.99	0.92
1:C:261:THR:HB	1:C:267:THR:HG22	1.50	0.92
1:A:12:GLU:OE1	1:A:56:THR:HG23	1.67	0.92
1:G:174:ILE:HD11	1:G:202:ALA:HB1	1.52	0.92
1:I:65:LEU:HA	1:I:68:LEU:HD12	1.51	0.92
1:A:155:THR:HG21	1:A:267:THR:HG21	1.50	0.91
1:A:278:GLU:OE2	1:F:269:ARG:NH2	2.03	0.91
1:D:23:ARG:NH1	1:D:26:GLU:OE2	2.02	0.91
1:E:108:THR:CB	1:F:226:ARG:NH2	2.33	0.91
1:G:291:ILE:CG1	1:G:316:PHE:CD2	2.52	0.91
1:K:16:PHE:CZ	1:K:24:MET:HE3	2.05	0.91
1:D:129:PRO:O	1:D:171:ARG:NH1	2.03	0.91
1:D:175:GLU:HA	1:D:199:THR:CG2	1.99	0.91
1:G:155:THR:HG23	1:G:259:LEU:HB2	1.52	0.91
1:I:24:MET:CE	1:I:44:ILE:CD1	2.47	0.91
1:G:111:LEU:HD12	1:G:112:VAL:N	1.84	0.91
1:C:287:ILE:O	1:C:291:ILE:HG13	1.69	0.91
1:L:48:VAL:HG12	1:L:49:TYR:CD2	2.05	0.91
1:I:40:THR:CG2	1:I:65:LEU:HD12	2.01	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:121:THR:CG2	1:K:182:LYS:NZ	2.32	0.91
1:A:355:PHE:HA	1:A:360:ILE:CG2	2.00	0.90
1:I:261:THR:HG21	1:I:267:THR:CA	2.00	0.90
1:C:293:LEU:HD22	1:C:294:CYS:N	1.86	0.90
1:B:247:GLU:O	1:B:251:THR:HG23	1.72	0.90
1:E:108:THR:CG2	1:F:226:ARG:NH2	2.35	0.90
1:B:119:GLN:NE2	1:C:226:ARG:HH21	1.69	0.90
1:A:94:ARG:HE	1:A:100:ARG:HG2	1.36	0.90
1:G:291:ILE:HD13	1:G:316:PHE:HE2	1.27	0.90
1:L:222:ASN:HA	1:L:225:ARG:HH21	1.37	0.90
1:A:40:THR:HG22	1:A:65:LEU:HD22	1.52	0.90
1:G:216:PHE:HD2	1:G:233:VAL:CG1	1.84	0.89
1:K:135:MET:HA	1:K:135:MET:HE3	1.52	0.89
1:H:272:VAL:HG13	1:H:284:THR:HG22	1.54	0.89
1:I:184:LEU:HD12	1:I:228:PRO:HG3	1.51	0.89
1:J:9:MET:HE1	1:J:24:MET:CA	2.02	0.89
1:H:188:SER:O	1:H:208:GLU:HG3	1.72	0.89
1:B:337:ARG:O	1:B:340:VAL:HG22	1.72	0.89
1:D:353:MET:O	1:D:357:GLN:HG2	1.71	0.89
1:G:291:ILE:HG21	1:G:316:PHE:CD2	2.06	0.89
1:G:17:THR:HG23	1:G:18:PRO:HD2	1.55	0.89
1:H:280:ARG:O	1:H:284:THR:HG23	1.72	0.88
1:G:69:ILE:HD11	1:G:120:ILE:CG1	2.03	0.88
1:L:40:THR:CG2	1:L:65:LEU:HD23	2.02	0.88
1:D:236:CYS:SG	1:D:259:LEU:CD2	2.60	0.88
1:E:35:ASP:OD2	1:F:227:LYS:HD2	1.73	0.88
1:H:48:VAL:HG21	1:H:53:LEU:CD1	2.02	0.88
1:I:266:GLU:OE1	1:I:266:GLU:N	2.06	0.88
1:G:230:LEU:HD13	1:G:231:ILE:N	1.89	0.88
1:J:94:ARG:CB	1:J:100:ARG:HD2	2.04	0.88
1:L:156:GLY:HA2	1:L:296:TRP:CZ3	2.08	0.88
1:E:21:MET:HE2	1:E:68:LEU:HG	1.55	0.88
1:I:175:GLU:O	1:I:200:ILE:HD11	1.74	0.88
1:G:238:ASP:OD1	1:G:239:ALA:N	2.06	0.88
1:J:81:LEU:HD21	1:J:87:ILE:HD12	1.56	0.88
1:H:238:ASP:HB3	1:H:240:GLU:OE1	1.74	0.87
1:A:285:ILE:HG23	1:A:325:LEU:HD11	1.56	0.87
1:H:188:SER:HB3	1:H:189:PRO:CD	2.05	0.87
1:H:188:SER:CB	1:H:189:PRO:CD	2.52	0.87
1:C:208:GLU:H	1:C:212:HIS:HD2	1.23	0.87
1:F:21:MET:O	1:F:25:LEU:HG	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:THR:HG23	1:A:18:PRO:HD2	1.55	0.87
1:B:151:ILE:HG13	1:B:290:THR:HG22	1.56	0.87
1:G:365:TYR:CA	1:G:368:ILE:HD12	2.05	0.87
1:K:288:LEU:CD1	1:K:325:LEU:HD23	2.03	0.87
1:C:40:THR:CG2	1:C:65:LEU:HD22	2.04	0.87
1:F:17:THR:HG23	1:F:18:PRO:HD2	1.57	0.87
1:A:365:TYR:CZ	1:A:369:ILE:HD11	2.10	0.86
1:C:355:PHE:HE1	1:C:362:GLU:HG2	1.40	0.86
1:I:329:PRO:HA	1:I:332:VAL:HG23	1.54	0.86
1:A:94:ARG:HH21	1:A:100:ARG:HG3	1.38	0.86
1:D:102:ARG:NH2	1:D:127:THR:HG22	1.88	0.86
1:E:35:ASP:CG	1:F:227:LYS:HD2	1.96	0.86
1:I:175:GLU:O	1:I:200:ILE:CD1	2.23	0.86
1:K:16:PHE:HZ	1:K:24:MET:CE	1.87	0.86
1:H:171:ARG:HG3	1:H:197:ILE:HD13	1.56	0.86
1:G:230:LEU:HD21	1:G:256:TYR:CE1	2.09	0.86
1:H:73:TYR:OH	1:H:210:PRO:HB2	1.76	0.86
1:D:258:THR:O	1:D:259:LEU:HD23	1.76	0.86
1:G:40:THR:CG2	1:G:65:LEU:HD22	2.05	0.85
1:I:24:MET:HE2	1:I:44:ILE:HD12	1.56	0.85
1:J:125:ILE:CD1	1:J:126:PRO:HD2	2.06	0.85
1:A:355:PHE:CA	1:A:360:ILE:HG22	2.06	0.85
1:C:154:ILE:HG22	1:C:162:LYS:HB3	1.55	0.85
1:I:235:GLU:OE1	1:I:260:HIS:NE2	2.09	0.85
1:K:173:LEU:HD22	1:K:181:ARG:CZ	2.06	0.85
1:E:365:TYR:CE2	1:E:369:ILE:HD11	2.12	0.85
1:D:208:GLU:H	1:D:212:HIS:HD2	1.21	0.85
1:K:137:LEU:HG	1:K:141:ILE:HD11	1.59	0.85
1:E:95:PRO:HG2	1:E:96:ASN:H	1.40	0.85
1:J:183:VAL:HG13	1:J:230:LEU:HD22	1.55	0.85
1:K:90:HIS:NE2	1:K:104:ARG:HG3	1.92	0.85
1:F:9:MET:CG	1:F:10:PRO:HD2	2.05	0.85
1:B:374:GLU:CB	1:C:281:LEU:HD22	2.06	0.85
1:G:216:PHE:CD2	1:G:233:VAL:HG12	2.11	0.84
1:J:102:ARG:NH1	1:J:127:THR:HG22	1.92	0.84
1:A:243:SER:OG	1:A:283:ARG:NH2	2.10	0.84
1:E:29:GLU:HG2	1:E:101:TYR:HE2	1.35	0.84
1:A:208:GLU:H	1:A:212:HIS:HD2	1.22	0.84
1:J:8:LEU:O	1:J:27:HIS:NE2	2.11	0.84
1:A:94:ARG:HH12	1:A:97:ARG:HD2	1.41	0.84
1:F:40:THR:CG2	1:F:65:LEU:HD22	2.06	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:24:MET:SD	1:I:25:LEU:HD23	2.18	0.84
1:J:92:GLU:HG3	1:J:102:ARG:HG2	1.59	0.84
1:J:102:ARG:CZ	1:J:193:VAL:HG21	2.07	0.84
1:G:288:LEU:O	1:G:291:ILE:HG22	1.77	0.83
1:J:81:LEU:HD21	1:J:87:ILE:CD1	2.07	0.83
1:K:108:THR:HG21	1:L:222:ASN:ND2	1.93	0.83
1:F:132:LEU:HD13	1:F:169:ILE:HD13	1.60	0.83
1:G:180:ASN:HA	1:G:201:SER:O	1.79	0.83
1:I:104:ARG:HG3	1:I:125:ILE:HD11	1.60	0.83
1:A:229:ARG:NH1	1:A:252:GLY:O	2.10	0.83
1:G:278:GLU:CD	1:L:337:ARG:NH1	2.31	0.83
1:H:171:ARG:HG3	1:H:197:ILE:CD1	2.08	0.83
1:J:12:GLU:OE2	1:J:57:ASN:N	2.12	0.83
1:L:17:THR:HG23	1:L:18:PRO:HD2	1.58	0.83
1:H:188:SER:HB3	1:H:189:PRO:HD2	1.61	0.83
1:I:38:ILE:HG22	1:I:65:LEU:HD21	1.60	0.83
1:L:9:MET:HE1	1:L:24:MET:HB2	1.61	0.83
1:K:171:ARG:HA	1:K:174:ILE:CG2	2.08	0.83
1:A:40:THR:CG2	1:A:65:LEU:HD22	2.07	0.83
1:D:174:ILE:HG12	1:D:199:THR:HG21	1.58	0.83
1:G:69:ILE:CD1	1:G:120:ILE:HD13	2.08	0.83
1:J:39:GLN:HE21	1:J:119:GLN:HG3	1.44	0.83
1:B:46:ALA:HB2	1:B:55:ILE:HD11	1.61	0.83
1:D:272:VAL:HG13	1:D:284:THR:HG22	1.61	0.83
1:I:25:LEU:CD1	1:I:103:TYR:CE2	2.61	0.83
1:L:190:ILE:HG12	1:L:208:GLU:CG	2.07	0.83
1:L:13:PRO:HB3	1:L:20:PHE:CE2	2.13	0.82
1:C:79:THR:HA	1:C:82:LEU:CD1	2.00	0.82
1:H:208:GLU:H	1:H:212:HIS:HD2	1.26	0.82
1:G:154:ILE:CD1	1:G:295:ILE:HD12	2.09	0.82
1:G:233:VAL:HB	1:G:257:THR:CG2	2.09	0.82
1:I:47:GLU:HA	1:I:52:LEU:HD23	1.59	0.82
1:J:10:PRO:HD3	1:J:27:HIS:HD2	1.44	0.82
1:G:352:LYS:HG3	1:G:365:TYR:CE2	2.14	0.82
1:B:104:ARG:HD3	1:B:191:GLU:OE1	1.80	0.82
1:C:276:SER:O	1:C:280:ARG:HB2	1.80	0.82
1:F:222:ASN:HA	1:F:225:ARG:NH2	1.95	0.82
1:G:365:TYR:HA	1:G:368:ILE:CD1	2.09	0.82
1:J:13:PRO:HB3	1:J:20:PHE:CE1	2.15	0.82
1:L:156:GLY:HA2	1:L:296:TRP:HZ3	1.44	0.82
1:G:318:GLU:HG3	1:L:363:ARG:CZ	2.10	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:317:ASP:HB3	1:J:320:VAL:HG23	1.60	0.81
1:K:194:TYR:O	1:K:197:ILE:HG22	1.80	0.81
1:K:108:THR:CG2	1:L:222:ASN:HD21	1.93	0.81
1:K:276:SER:HA	1:K:280:ARG:HD2	1.60	0.81
1:C:328:ASP:HB3	1:C:331:GLU:HG3	1.60	0.81
1:F:8:LEU:O	1:F:27:HIS:HE1	1.64	0.81
1:F:44:ILE:HG13	1:F:56:THR:HG21	1.60	0.81
1:F:78:THR:O	1:F:82:LEU:HD12	1.81	0.81
1:F:174:ILE:CG2	1:F:199:THR:HG21	2.10	0.81
1:F:293:LEU:HD13	1:F:315:VAL:HG22	1.63	0.81
1:I:49:TYR:O	1:I:307:ARG:HD2	1.80	0.81
1:E:108:THR:HG21	1:F:226:ARG:HH22	1.45	0.81
1:K:230:LEU:HD23	1:K:231:ILE:N	1.95	0.81
1:B:249:ALA:HB1	1:B:290:THR:HG23	1.60	0.81
1:E:170:ILE:O	1:E:174:ILE:HG22	1.79	0.81
1:J:104:ARG:CZ	1:J:123:ARG:HH11	1.93	0.81
1:G:173:LEU:HG	1:G:181:ARG:NH1	1.95	0.81
1:L:132:LEU:HD13	1:L:169:ILE:HD13	1.61	0.81
1:J:352:LYS:HG3	1:J:365:TYR:CZ	2.14	0.81
1:L:89:THR:HG22	1:L:90:HIS:H	1.44	0.81
1:K:361:SER:HB2	1:K:364:VAL:HG23	1.61	0.81
1:G:312:GLU:HB2	1:G:347:MET:HB2	1.63	0.81
1:E:233:VAL:HB	1:E:257:THR:HG22	1.62	0.80
1:G:9:MET:CE	1:G:24:MET:HA	2.11	0.80
1:F:132:LEU:CD1	1:F:169:ILE:HD13	2.11	0.80
1:A:188:SER:O	1:A:208:GLU:HG3	1.80	0.80
1:G:342:GLN:HG2	1:G:343:LYS:HG2	1.63	0.80
1:I:263:GLY:O	1:I:267:THR:HG23	1.81	0.80
1:A:12:GLU:CD	1:A:56:THR:HG23	2.01	0.80
1:H:92:GLU:OE1	1:H:100:ARG:HD2	1.80	0.80
1:L:222:ASN:HA	1:L:225:ARG:NH2	1.95	0.80
1:H:283:ARG:O	1:H:287:ILE:HG13	1.82	0.80
1:J:9:MET:CG	1:J:10:PRO:HD2	2.11	0.80
1:A:119:GLN:HE22	1:B:182:LYS:HE2	1.46	0.80
1:E:208:GLU:H	1:E:212:HIS:CD2	1.99	0.80
1:H:172:GLU:O	1:H:176:THR:HG23	1.80	0.80
1:L:149:GLU:HG2	1:L:150:GLY:N	1.97	0.80
1:K:233:VAL:HB	1:K:257:THR:HG22	1.63	0.80
1:A:365:TYR:CE2	1:A:369:ILE:HD11	2.17	0.80
1:G:69:ILE:HD11	1:G:120:ILE:HG12	1.64	0.80
1:C:361:SER:HB3	1:C:364:VAL:HG23	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:162:LYS:HD3	1:E:258:THR:CB	2.11	0.79
1:F:209:ILE:HG22	1:F:210:PRO:HD3	1.63	0.79
1:L:9:MET:CE	1:L:24:MET:HB2	2.11	0.79
1:L:337:ARG:O	1:L:340:VAL:HG22	1.81	0.79
1:E:355:PHE:HB2	1:E:360:ILE:HD11	1.63	0.79
1:J:45:PHE:HD2	1:J:52:LEU:HG	1.45	0.79
1:E:316:PHE:HA	1:E:320:VAL:HG21	1.62	0.79
1:I:61:SER:HB3	1:I:64:GLU:CG	2.13	0.79
1:K:137:LEU:HD11	1:K:311:ARG:CZ	2.12	0.79
1:E:219:GLY:O	1:E:222:ASN:HB3	1.83	0.79
1:K:286:ASP:O	1:K:290:THR:OG1	2.00	0.79
1:L:25:LEU:HD13	1:L:93:PHE:CE2	2.16	0.79
1:E:164:THR:CG2	1:E:192:PHE:HZ	1.96	0.79
1:G:111:LEU:HD11	1:G:113:GLU:O	1.83	0.79
1:I:279:GLU:HG2	1:I:283:ARG:HG2	1.64	0.79
1:A:238:ASP:OD1	1:A:239:ALA:N	2.15	0.79
1:G:355:PHE:CE2	1:G:365:TYR:CG	2.71	0.79
1:J:199:THR:CG2	1:J:202:ALA:HB3	2.13	0.79
1:K:12:GLU:OE2	1:K:57:ASN:N	2.16	0.79
1:L:365:TYR:CE2	1:L:369:ILE:HD11	2.18	0.79
1:A:89:THR:HG22	1:A:90:HIS:H	1.47	0.79
1:J:52:LEU:N	1:K:180:ASN:OD1	2.15	0.79
1:C:77:ALA:O	1:C:81:LEU:HD13	1.82	0.79
1:G:318:GLU:HG3	1:L:363:ARG:NH2	1.98	0.79
1:J:10:PRO:HD3	1:J:27:HIS:CD2	2.18	0.79
1:F:149:GLU:HG2	1:F:150:GLY:N	1.96	0.78
1:D:183:VAL:HG13	1:D:230:LEU:HD22	1.65	0.78
1:I:166:LEU:HD23	1:I:169:ILE:HD12	1.65	0.78
1:C:174:ILE:HD11	1:C:199:THR:HG21	1.66	0.78
1:D:264:VAL:CG1	1:D:340:VAL:HG11	2.12	0.78
1:F:320:VAL:HA	1:F:323:ILE:HD12	1.65	0.78
1:G:188:SER:OG	1:G:189:PRO:HD3	1.83	0.78
1:G:235:GLU:HA	1:G:258:THR:O	1.83	0.78
1:I:160:SER:HA	1:I:299:LEU:HG	1.64	0.78
1:I:171:ARG:O	1:I:174:ILE:HG22	1.83	0.78
1:G:80:GLN:O	1:G:83:SER:OG	2.02	0.78
1:H:317:ASP:HB2	1:H:320:VAL:HG23	1.66	0.78
1:F:296:TRP:HE1	1:F:347:MET:HE2	1.46	0.78
1:G:69:ILE:HG12	1:G:120:ILE:HD11	1.66	0.78
1:J:99:VAL:O	1:J:100:ARG:HD3	1.82	0.78
1:B:208:GLU:H	1:B:212:HIS:HD2	1.29	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ARG:NH1	1:A:97:ARG:HA	1.99	0.78
1:D:72:ILE:HD11	1:D:105:VAL:HG21	1.63	0.78
1:J:9:MET:HG3	1:J:10:PRO:HD2	1.64	0.78
1:K:219:GLY:O	1:K:222:ASN:HB3	1.83	0.78
1:L:280:ARG:O	1:L:284:THR:OG1	2.01	0.78
1:C:17:THR:HG23	1:C:18:PRO:HD2	1.66	0.78
1:I:35:ASP:OD2	1:I:123:ARG:HG3	1.84	0.78
1:J:337:ARG:O	1:J:340:VAL:HG22	1.83	0.78
1:K:111:LEU:CD2	1:L:90:HIS:NE2	2.47	0.78
1:A:355:PHE:CA	1:A:360:ILE:CG2	2.62	0.78
1:F:9:MET:HG2	1:F:10:PRO:CD	2.14	0.77
1:B:365:TYR:OH	1:B:369:ILE:HD11	1.84	0.77
1:D:104:ARG:CZ	1:D:123:ARG:HH11	1.97	0.77
1:J:89:THR:HA	1:J:208:GLU:OE1	1.84	0.77
1:K:137:LEU:HD11	1:K:311:ARG:NE	2.00	0.77
1:C:80:GLN:O	1:C:83:SER:HB3	1.83	0.77
1:H:186:TYR:OH	1:H:223:ALA:HB2	1.84	0.77
1:E:353:MET:HA	1:E:353:MET:HE3	1.65	0.77
1:J:92:GLU:OE2	1:J:102:ARG:NE	2.16	0.77
1:J:199:THR:HG23	1:J:202:ALA:HB3	1.65	0.77
1:K:208:GLU:H	1:K:212:HIS:HD2	1.31	0.77
1:K:321:ARG:O	1:K:325:LEU:HG	1.84	0.77
1:B:90:HIS:NE2	1:B:92:GLU:HG3	2.00	0.77
1:C:22:ASP:OD2	1:C:93:PHE:CD2	2.37	0.77
1:G:233:VAL:HB	1:G:257:THR:HG22	1.65	0.77
1:D:200:ILE:HD12	1:D:200:ILE:O	1.85	0.77
1:F:190:ILE:CG1	1:F:208:GLU:HG3	2.11	0.77
1:G:345:GLN:HG3	1:G:349:TRP:CE3	2.20	0.77
1:B:186:TYR:OH	1:B:223:ALA:HB2	1.84	0.77
1:J:129:PRO:HG3	1:J:167:ALA:HB1	1.67	0.77
1:L:9:MET:HG3	1:L:55:ILE:O	1.84	0.77
1:J:13:PRO:HG3	1:J:20:PHE:CD1	2.20	0.77
1:F:209:ILE:HD11	1:F:215:ASN:C	2.05	0.77
1:J:209:ILE:HG22	1:J:210:PRO:HD3	1.68	0.76
1:K:8:LEU:N	1:K:8:LEU:HD23	2.00	0.76
1:C:366:LYS:O	1:C:369:ILE:HG22	1.84	0.76
1:H:320:VAL:HG13	1:H:339:LEU:HD13	1.68	0.76
1:I:52:LEU:O	1:I:53:LEU:HD23	1.85	0.76
1:I:258:THR:O	1:I:259:LEU:HD12	1.85	0.76
1:L:194:TYR:HA	1:L:197:ILE:HD13	1.67	0.76
1:I:173:LEU:O	1:I:181:ARG:NH2	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:258:THR:O	1:G:259:LEU:HD23	1.85	0.76
1:G:332:VAL:HG23	1:G:333:THR:H	1.49	0.76
1:F:195:ASP:O	1:F:198:GLU:OE2	2.03	0.76
1:K:269:ARG:HB2	1:K:333:THR:CG2	2.16	0.76
1:E:17:THR:CG2	1:E:18:PRO:HD2	2.15	0.76
1:H:65:LEU:CD1	1:H:120:ILE:HD12	2.15	0.76
1:I:13:PRO:HG3	1:I:20:PHE:CD2	2.21	0.76
1:K:137:LEU:CG	1:K:141:ILE:HD11	2.16	0.76
1:I:17:THR:HG23	1:I:18:PRO:HD2	1.68	0.76
1:C:166:LEU:HD13	1:C:232:MET:HE2	1.67	0.75
1:C:293:LEU:HD22	1:C:294:CYS:H	1.51	0.75
1:G:180:ASN:HB3	1:L:52:LEU:CB	2.15	0.75
1:I:149:GLU:O	1:I:292:ARG:HD2	1.86	0.75
1:A:92:GLU:CG	1:A:102:ARG:HG2	2.16	0.75
1:B:125:ILE:HD12	1:B:126:PRO:HD2	1.69	0.75
1:J:92:GLU:OE2	1:J:102:ARG:CZ	2.34	0.75
1:L:190:ILE:HG12	1:L:208:GLU:HG2	1.66	0.75
1:C:132:LEU:HB2	1:C:172:GLU:HG3	1.68	0.75
1:F:261:THR:HG22	1:F:270:ARG:HE	1.49	0.75
1:F:183:VAL:HG13	1:F:230:LEU:CD2	2.16	0.75
1:J:125:ILE:HD12	1:J:126:PRO:HD2	1.66	0.75
1:F:197:ILE:HD12	1:F:197:ILE:O	1.85	0.75
1:I:209:ILE:O	1:I:213:LEU:O	2.04	0.75
1:F:296:TRP:HE1	1:F:347:MET:CE	2.00	0.75
1:H:18:PRO:O	1:H:21:MET:HB3	1.87	0.75
1:J:219:GLY:O	1:J:222:ASN:HB3	1.87	0.75
1:L:333:THR:O	1:L:336:THR:OG1	2.02	0.75
1:C:88:ASP:OD1	1:C:106:ASN:ND2	2.19	0.75
1:D:38:ILE:HB	1:D:120:ILE:HG23	1.68	0.75
1:F:125:ILE:HD12	1:F:126:PRO:CD	2.17	0.75
1:G:174:ILE:CD1	1:G:202:ALA:HB1	2.15	0.75
1:G:302:THR:OG1	1:G:306:ARG:O	2.05	0.75
1:I:80:GLN:O	1:I:83:SER:HB3	1.87	0.75
1:J:10:PRO:CD	1:J:27:HIS:HD2	1.99	0.75
1:L:293:LEU:HD13	1:L:315:VAL:HG22	1.67	0.75
1:H:209:ILE:O	1:H:213:LEU:O	2.03	0.75
1:L:183:VAL:HG13	1:L:230:LEU:CD2	2.17	0.75
1:L:190:ILE:N	1:L:208:GLU:OE2	2.20	0.75
1:L:296:TRP:NE1	1:L:347:MET:HE2	2.02	0.75
1:F:9:MET:HA	1:F:27:HIS:ND1	2.01	0.75
1:H:68:LEU:HD23	1:H:68:LEU:N	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:40:THR:HG21	1:L:62:ASN:OD1	1.87	0.75
1:B:100:ARG:HE	1:B:102:ARG:HH12	1.33	0.74
1:C:154:ILE:HG21	1:C:162:LYS:HB3	1.69	0.74
1:D:171:ARG:HG3	1:D:197:ILE:HD13	1.69	0.74
1:K:13:PRO:HB2	1:K:15:ARG:O	1.87	0.74
1:E:108:THR:CB	1:F:226:ARG:HH21	1.99	0.74
1:J:175:GLU:HG3	1:J:197:ILE:CG2	2.16	0.74
1:D:61:SER:OG	1:D:64:GLU:OE2	2.04	0.74
1:F:296:TRP:NE1	1:F:347:MET:CE	2.50	0.74
1:J:72:ILE:HD11	1:J:105:VAL:HG21	1.69	0.74
1:K:111:LEU:HD21	1:L:90:HIS:NE2	2.03	0.74
1:L:154:ILE:HG22	1:L:162:LYS:HG2	1.69	0.74
1:L:155:THR:OG1	1:L:261:THR:O	2.05	0.74
1:C:17:THR:CG2	1:C:18:PRO:HD2	2.17	0.74
1:C:155:THR:HG21	1:C:267:THR:HG21	1.70	0.74
1:G:17:THR:CG2	1:G:18:PRO:HD2	2.18	0.74
1:E:183:VAL:HG13	1:E:230:LEU:HD22	1.70	0.74
1:F:297:GLN:HB2	1:F:311:ARG:HG2	1.67	0.74
1:H:119:GLN:OE1	1:I:205:SER:HB2	1.87	0.74
1:G:279:GLU:OE1	1:G:279:GLU:HA	1.86	0.74
1:H:328:ASP:OD1	1:H:330:ASN:N	2.19	0.74
1:G:135:MET:HE2	1:G:135:MET:HA	1.69	0.74
1:I:43:PRO:HD3	1:I:59:ARG:HG2	1.69	0.74
1:I:132:LEU:HB2	1:I:172:GLU:HG3	1.70	0.74
1:J:65:LEU:HD23	1:J:118:ILE:O	1.87	0.74
1:J:102:ARG:NH2	1:J:193:VAL:HG21	2.03	0.74
1:J:145:ILE:CD1	1:J:293:LEU:CD2	2.66	0.74
1:F:174:ILE:HG22	1:F:199:THR:CG2	2.16	0.74
1:K:25:LEU:HD13	1:K:93:PHE:CE2	2.23	0.74
1:B:102:ARG:HE	1:B:127:THR:HG22	1.53	0.73
1:E:108:THR:HG21	1:F:226:ARG:HH21	1.53	0.73
1:G:365:TYR:O	1:G:369:ILE:HG13	1.87	0.73
1:E:89:THR:HG23	1:E:105:VAL:CG1	2.18	0.73
1:F:156:GLY:HA2	1:F:296:TRP:CZ3	2.23	0.73
1:J:99:VAL:C	1:J:100:ARG:HD3	2.09	0.73
1:L:25:LEU:HD13	1:L:93:PHE:HE2	1.51	0.73
1:A:49:TYR:CZ	1:A:306:ARG:HG3	2.22	0.73
1:D:366:LYS:O	1:D:369:ILE:HG23	1.88	0.73
1:E:8:LEU:HD12	1:E:31:LEU:HD11	1.68	0.73
1:E:328:ASP:N	1:E:331:GLU:OE2	2.21	0.73
1:G:102:ARG:NH2	1:G:125:ILE:HG21	2.02	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:9:MET:CE	1:J:24:MET:CB	2.66	0.73
1:H:212:HIS:C	1:H:213:LEU:HD12	2.08	0.73
1:I:110:CYS:O	1:J:212:HIS:HE1	1.72	0.73
1:J:102:ARG:HE	1:J:193:VAL:HG11	1.54	0.73
1:J:352:LYS:HA	1:J:365:TYR:CE1	2.23	0.73
1:K:9:MET:SD	1:K:10:PRO:HD2	2.28	0.73
1:A:203:VAL:HG13	1:F:42:GLU:OE1	1.87	0.73
1:E:21:MET:CE	1:E:68:LEU:HG	2.18	0.73
1:G:235:GLU:CA	1:G:258:THR:OG1	2.36	0.73
1:G:278:GLU:OE1	1:L:337:ARG:NH1	2.22	0.73
1:I:104:ARG:HG3	1:I:125:ILE:HD13	1.68	0.73
1:B:100:ARG:NE	1:B:102:ARG:HH12	1.86	0.73
1:E:17:THR:HG23	1:E:18:PRO:HD2	1.71	0.73
1:G:183:VAL:HG22	1:G:230:LEU:HB3	1.69	0.73
1:K:68:LEU:O	1:K:71:SER:OG	2.05	0.73
1:L:188:SER:HA	1:L:209:ILE:HG22	1.71	0.73
1:C:329:PRO:HA	1:C:332:VAL:HG23	1.70	0.72
1:G:89:THR:HG22	1:G:90:HIS:N	2.04	0.72
1:I:276:SER:O	1:I:280:ARG:HB2	1.88	0.72
1:E:354:LYS:HE2	1:E:354:LYS:HA	1.69	0.72
1:I:365:TYR:O	1:I:368:ILE:HG13	1.89	0.72
1:L:61:SER:OG	1:L:64:GLU:HG3	1.89	0.72
1:D:174:ILE:C	1:D:199:THR:HG21	2.10	0.72
1:G:89:THR:HG22	1:G:90:HIS:H	1.53	0.72
1:G:235:GLU:N	1:G:258:THR:OG1	2.21	0.72
1:I:353:MET:HG2	1:I:357:GLN:HE22	1.54	0.72
1:K:17:THR:HG23	1:K:18:PRO:HD2	1.71	0.72
1:K:171:ARG:HA	1:K:174:ILE:HG21	1.70	0.72
1:K:275:PHE:O	1:K:280:ARG:HD2	1.90	0.72
1:A:34:SER:O	1:A:124:THR:HG23	1.88	0.72
1:G:364:VAL:C	1:G:368:ILE:HD12	2.09	0.72
1:K:362:GLU:O	1:K:366:LYS:HG3	1.90	0.72
1:D:366:LYS:HA	1:D:369:ILE:CG2	2.20	0.72
1:F:188:SER:O	1:F:208:GLU:HG2	1.88	0.72
1:H:92:GLU:HG2	1:H:102:ARG:HG2	1.72	0.72
1:H:363:ARG:NH1	1:I:322:ASP:OD1	2.22	0.72
1:L:143:GLU:OE1	1:L:143:GLU:HA	1.89	0.72
1:G:155:THR:HG23	1:G:259:LEU:CB	2.20	0.72
1:I:197:ILE:HD12	1:I:197:ILE:N	2.04	0.72
1:J:7:ASN:O	1:J:8:LEU:HD12	1.89	0.72
1:L:302:THR:OG1	1:L:306:ARG:O	2.08	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:THR:CG2	1:A:18:PRO:HD2	2.19	0.72
1:C:279:GLU:HG2	1:C:283:ARG:HG2	1.72	0.72
1:G:42:GLU:OE2	1:H:198:GLU:OE2	2.07	0.72
1:H:97:ARG:NH2	1:H:99:VAL:HG21	2.04	0.72
1:K:9:MET:HB2	1:K:55:ILE:O	1.89	0.72
1:F:337:ARG:O	1:F:340:VAL:HG22	1.90	0.72
1:I:37:THR:HG21	1:J:182:LYS:HD2	1.72	0.72
1:E:7:ASN:C	1:E:8:LEU:HG	2.08	0.71
1:F:173:LEU:O	1:F:179:SER:OG	2.07	0.71
1:G:69:ILE:HG12	1:G:120:ILE:CD1	2.19	0.71
1:G:291:ILE:O	1:G:292:ARG:NH1	2.23	0.71
1:G:300:VAL:HG13	1:G:301:PRO:HD2	1.70	0.71
1:K:88:ASP:OD1	1:K:106:ASN:ND2	2.21	0.71
1:K:363:ARG:O	1:K:367:LEU:HG	1.88	0.71
1:A:113:GLU:OE1	1:B:100:ARG:NH2	2.23	0.71
1:H:155:THR:HG22	1:H:259:LEU:HB2	1.72	0.71
1:J:191:GLU:HB3	1:J:192:PHE:CD1	2.24	0.71
1:J:248:ALA:O	1:J:251:THR:OG1	2.08	0.71
1:K:353:MET:HA	1:K:353:MET:CE	2.19	0.71
1:L:248:ALA:O	1:L:251:THR:OG1	2.06	0.71
1:I:230:LEU:HD11	1:I:256:TYR:CD1	2.25	0.71
1:E:45:PHE:CE1	1:E:54:LYS:HG2	2.24	0.71
1:K:296:TRP:CZ3	1:K:347:MET:HE2	2.26	0.71
1:C:149:GLU:O	1:C:292:ARG:HD2	1.90	0.71
1:E:9:MET:HB2	1:E:55:ILE:O	1.90	0.71
1:F:143:GLU:OE1	1:F:143:GLU:HA	1.90	0.71
1:I:17:THR:CG2	1:I:18:PRO:HD2	2.20	0.71
1:G:173:LEU:O	1:G:181:ARG:NH2	2.14	0.71
1:H:35:ASP:OD2	1:I:227:LYS:HD3	1.90	0.71
1:J:182:LYS:NZ	1:J:226:ARG:O	2.24	0.71
1:B:212:HIS:C	1:B:213:LEU:HD12	2.11	0.71
1:G:12:GLU:CD	1:G:56:THR:HG23	2.11	0.71
1:J:183:VAL:HB	1:J:204:VAL:HG22	1.72	0.71
1:K:40:THR:HG22	1:K:65:LEU:CD2	2.14	0.71
1:B:224:LEU:HD21	1:B:248:ALA:HA	1.72	0.71
1:B:249:ALA:CB	1:B:290:THR:CG2	2.68	0.71
1:E:328:ASP:O	1:E:331:GLU:HG2	1.89	0.71
1:E:332:VAL:HG23	1:E:333:THR:H	1.55	0.71
1:J:102:ARG:HH11	1:J:127:THR:HG22	1.53	0.71
1:K:44:ILE:HG22	1:K:55:ILE:HD11	1.73	0.71
1:K:269:ARG:O	1:K:273:THR:OG1	2.09	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:ALA:HB1	1:B:290:THR:CG2	2.20	0.71
1:E:58:ARG:HH12	1:E:64:GLU:CD	1.94	0.71
1:E:43:PRO:HD3	1:E:59:ARG:HD3	1.73	0.70
1:F:9:MET:HE1	1:F:24:MET:HB2	1.72	0.70
1:F:209:ILE:HD11	1:F:215:ASN:O	1.91	0.70
1:H:208:GLU:H	1:H:212:HIS:CD2	2.09	0.70
1:I:34:SER:O	1:I:124:THR:HG23	1.91	0.70
1:I:52:LEU:C	1:I:53:LEU:HD23	2.10	0.70
1:I:54:LYS:C	1:I:55:ILE:HD13	2.12	0.70
1:I:88:ASP:OD1	1:I:106:ASN:ND2	2.24	0.70
1:E:129:PRO:HB2	1:E:171:ARG:HD3	1.73	0.70
1:H:188:SER:CB	1:H:189:PRO:HD3	2.19	0.70
1:I:208:GLU:H	1:I:212:HIS:HD2	1.37	0.70
1:K:111:LEU:HD13	1:L:90:HIS:CE1	2.27	0.70
1:K:288:LEU:HB3	1:K:325:LEU:HD21	1.73	0.70
1:E:108:THR:HB	1:F:226:ARG:NH2	2.07	0.70
1:K:263:GLY:O	1:K:267:THR:HG23	1.91	0.70
1:I:137:LEU:HD23	1:I:311:ARG:NH1	2.06	0.70
1:B:208:GLU:H	1:B:212:HIS:CD2	2.09	0.70
1:F:345:GLN:HG3	1:F:349:TRP:HE3	1.54	0.70
1:G:9:MET:HE1	1:G:24:MET:HB2	1.72	0.70
1:L:125:ILE:HD12	1:L:126:PRO:CD	2.20	0.70
1:I:174:ILE:HG13	1:I:202:ALA:HB1	1.74	0.70
1:J:40:THR:HG23	1:J:62:ASN:HA	1.74	0.70
1:J:58:ARG:NH1	1:J:64:GLU:OE2	2.23	0.70
1:L:112:VAL:HG23	1:L:117:ALA:HB3	1.68	0.70
1:J:15:ARG:CG	1:J:64:GLU:OE2	2.37	0.70
1:J:94:ARG:CB	1:J:100:ARG:CD	2.69	0.70
1:G:69:ILE:HD11	1:G:120:ILE:CD1	2.21	0.70
1:H:9:MET:HE1	1:H:24:MET:HB2	1.74	0.70
1:B:73:TYR:OH	1:B:210:PRO:HB2	1.92	0.70
1:D:155:THR:HG22	1:D:259:LEU:HB2	1.74	0.70
1:E:9:MET:CG	1:E:10:PRO:HD2	2.22	0.70
1:E:263:GLY:O	1:E:267:THR:HG23	1.91	0.70
1:G:235:GLU:HB3	1:G:258:THR:OG1	1.92	0.70
1:G:248:ALA:O	1:G:251:THR:OG1	2.10	0.70
1:I:25:LEU:CD1	1:I:103:TYR:HE2	2.05	0.70
1:I:48:VAL:N	1:I:51:ARG:O	2.20	0.70
1:I:365:TYR:CE2	1:I:369:ILE:HD11	2.27	0.70
1:G:306:ARG:HG2	1:G:307:ARG:N	2.07	0.69
1:G:354:LYS:HB3	1:G:360:ILE:CD1	2.21	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:186:TYR:OH	1:J:223:ALA:HB2	1.91	0.69
1:G:61:SER:OG	1:G:64:GLU:OE1	2.07	0.69
1:K:302:THR:OG1	1:K:304:ASP:OD1	2.07	0.69
1:G:238:ASP:O	1:G:242:ILE:HD12	1.93	0.69
1:H:155:THR:HG21	1:H:267:THR:HG21	1.74	0.69
1:I:22:ASP:OD2	1:I:93:PHE:CE1	2.45	0.69
1:F:73:TYR:CD1	1:F:89:THR:CG2	2.73	0.69
1:G:322:ASP:HA	1:G:325:LEU:HD12	1.72	0.69
1:J:140:ASN:H	1:J:140:ASN:HD22	1.40	0.69
1:K:288:LEU:CB	1:K:325:LEU:HD21	2.23	0.69
1:L:24:MET:SD	1:L:44:ILE:HD12	2.31	0.69
1:D:224:LEU:HD21	1:D:248:ALA:HA	1.72	0.69
1:E:7:ASN:HA	1:E:54:LYS:O	1.92	0.69
1:G:318:GLU:O	1:G:322:ASP:OD2	2.09	0.69
1:D:94:ARG:CB	1:D:100:ARG:HE	2.05	0.69
1:G:119:GLN:NE2	1:H:182:LYS:NZ	2.37	0.69
1:G:208:GLU:H	1:G:212:HIS:HD2	1.39	0.69
1:G:239:ALA:CA	1:G:242:ILE:HD12	2.20	0.69
1:I:95:PRO:HD2	1:I:99:VAL:O	1.92	0.69
1:I:184:LEU:CD1	1:I:228:PRO:HB3	2.23	0.69
1:K:24:MET:SD	1:K:44:ILE:HD13	2.32	0.69
1:B:197:ILE:HG22	1:B:199:THR:HG23	1.75	0.69
1:K:35:ASP:C	1:K:36:ILE:HD12	2.13	0.69
1:A:293:LEU:HD13	1:A:315:VAL:HG22	1.73	0.69
1:F:186:TYR:OH	1:F:223:ALA:HB2	1.92	0.69
1:G:322:ASP:OD1	1:L:363:ARG:NH2	2.24	0.69
1:K:7:ASN:C	1:K:8:LEU:HD23	2.13	0.69
1:L:171:ARG:O	1:L:175:GLU:HG3	1.93	0.69
1:L:296:TRP:NE1	1:L:347:MET:CE	2.55	0.69
1:B:183:VAL:HG13	1:B:230:LEU:HD22	1.74	0.69
1:F:24:MET:SD	1:F:44:ILE:HG21	2.33	0.69
1:L:13:PRO:HB3	1:L:20:PHE:CD2	2.27	0.69
1:L:89:THR:HG22	1:L:90:HIS:N	2.08	0.69
1:C:272:VAL:HG13	1:C:284:THR:HG22	1.73	0.69
1:D:8:LEU:CD1	1:D:9:MET:N	2.49	0.69
1:G:238:ASP:C	1:G:242:ILE:HD12	2.14	0.69
1:H:19:VAL:HG23	1:H:20:PHE:N	2.07	0.69
1:J:9:MET:HE1	1:J:24:MET:CB	2.22	0.69
1:G:132:LEU:O	1:G:132:LEU:HD23	1.92	0.68
1:G:317:ASP:HB3	1:G:320:VAL:HG23	1.75	0.68
1:K:137:LEU:CD1	1:K:311:ARG:CZ	2.71	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:41:GLY:O	1:I:59:ARG:HD2	1.93	0.68
1:I:95:PRO:CD	1:I:99:VAL:O	2.41	0.68
1:J:24:MET:HE3	1:J:25:LEU:N	2.08	0.68
1:J:29:GLU:HA	1:J:29:GLU:OE2	1.93	0.68
1:L:312:GLU:HB2	1:L:347:MET:N	2.08	0.68
1:D:268:MET:HG3	1:D:336:THR:HG21	1.75	0.68
1:G:154:ILE:HD11	1:G:295:ILE:HD12	1.74	0.68
1:G:215:ASN:OD1	1:G:218:ASP:OD2	2.11	0.68
1:G:269:ARG:HH11	1:G:269:ARG:CG	2.03	0.68
1:J:72:ILE:HD13	1:J:105:VAL:HG11	1.75	0.68
1:J:337:ARG:NH1	1:K:278:GLU:OE1	2.26	0.68
1:L:9:MET:SD	1:L:56:THR:CG2	2.80	0.68
1:A:94:ARG:HH21	1:A:100:ARG:CG	2.06	0.68
1:A:285:ILE:HD12	1:A:285:ILE:N	2.06	0.68
1:D:186:TYR:OH	1:D:223:ALA:HB2	1.94	0.68
1:E:353:MET:HA	1:E:353:MET:CE	2.22	0.68
1:J:9:MET:HE1	1:J:24:MET:HB2	1.75	0.68
1:B:352:LYS:HA	1:B:365:TYR:CE1	2.27	0.68
1:C:208:GLU:H	1:C:212:HIS:CD2	2.08	0.68
1:K:16:PHE:CZ	1:K:24:MET:HE1	2.27	0.68
1:K:24:MET:SD	1:K:44:ILE:HG21	2.34	0.68
1:H:272:VAL:HG13	1:H:284:THR:CG2	2.22	0.68
1:I:341:ARG:HG2	1:I:346:LEU:HD11	1.75	0.68
1:J:209:ILE:HG22	1:J:210:PRO:CD	2.23	0.68
1:A:340:VAL:HG12	1:A:346:LEU:HD12	1.75	0.68
1:B:9:MET:HE1	1:B:24:MET:HB2	1.74	0.68
1:F:9:MET:CE	1:F:24:MET:HB2	2.23	0.68
1:H:119:GLN:HE22	1:I:182:LYS:HE3	1.59	0.68
1:I:248:ALA:O	1:I:251:THR:OG1	2.11	0.68
1:K:246:LEU:HD21	1:K:287:ILE:HD13	1.76	0.68
1:L:40:THR:HG22	1:L:65:LEU:CD2	2.24	0.68
1:D:35:ASP:OD2	1:E:227:LYS:HD2	1.93	0.68
1:E:155:THR:HG22	1:E:259:LEU:HB2	1.76	0.68
1:F:17:THR:CG2	1:F:18:PRO:HD2	2.23	0.68
1:I:361:SER:HB3	1:I:364:VAL:HG23	1.75	0.68
1:L:197:ILE:HD12	1:L:197:ILE:N	2.08	0.68
1:K:155:THR:HG22	1:K:259:LEU:HB2	1.74	0.67
1:C:188:SER:O	1:C:208:GLU:HG3	1.94	0.67
1:E:304:ASP:OD2	1:E:306:ARG:HD2	1.94	0.67
1:I:86:ASP:OD2	1:J:225:ARG:NH1	2.24	0.67
1:E:329:PRO:O	1:E:332:VAL:HG13	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:86:ASP:HB2	1:I:213:LEU:HD21	1.76	0.67
1:I:208:GLU:H	1:I:212:HIS:CD2	2.12	0.67
1:I:261:THR:CG2	1:I:267:THR:CG2	2.70	0.67
1:K:288:LEU:CB	1:K:325:LEU:CD2	2.73	0.67
1:L:215:ASN:OD1	1:L:218:ASP:CB	2.31	0.67
1:A:137:LEU:HD23	1:A:141:ILE:HG21	1.75	0.67
1:D:208:GLU:H	1:D:212:HIS:CD2	2.07	0.67
1:D:367:LEU:HD11	1:E:325:LEU:HD13	1.77	0.67
1:G:69:ILE:HD11	1:G:120:ILE:HD13	1.76	0.67
1:G:230:LEU:HD21	1:G:256:TYR:HE1	1.57	0.67
1:K:300:VAL:HG13	1:K:301:PRO:HD2	1.76	0.67
1:G:69:ILE:CD1	1:G:120:ILE:CD1	2.71	0.67
1:J:39:GLN:C	1:J:65:LEU:HD21	2.14	0.67
1:C:287:ILE:HG22	1:C:291:ILE:HD11	1.75	0.67
1:F:296:TRP:NE1	1:F:347:MET:HE1	2.10	0.67
1:I:184:LEU:HD12	1:I:228:PRO:CG	2.25	0.67
1:A:208:GLU:H	1:A:212:HIS:CD2	2.08	0.67
1:B:40:THR:OG1	1:B:65:LEU:HD22	1.95	0.67
1:C:363:ARG:HG3	1:C:364:VAL:N	2.08	0.67
1:E:164:THR:CG2	1:E:192:PHE:CZ	2.74	0.67
1:G:324:LEU:HD21	1:G:339:LEU:HD12	1.77	0.67
1:L:132:LEU:CD1	1:L:169:ILE:HD13	2.24	0.67
1:B:259:LEU:HD12	1:B:267:THR:HG23	1.76	0.67
1:G:230:LEU:HD13	1:G:230:LEU:C	2.15	0.67
1:G:317:ASP:C	1:G:321:ARG:NH1	2.48	0.67
1:G:355:PHE:HZ	1:G:365:TYR:HD2	1.31	0.67
1:J:40:THR:N	1:J:65:LEU:HD21	2.10	0.67
1:J:323:ILE:HD13	1:J:323:ILE:N	2.09	0.67
1:K:292:ARG:HH21	1:K:292:ARG:HG3	1.57	0.67
1:C:166:LEU:CD1	1:C:232:MET:HE2	2.24	0.67
1:D:237:ARG:NH2	1:D:260:HIS:HB2	2.10	0.67
1:E:22:ASP:OD1	1:E:22:ASP:N	2.28	0.67
1:I:65:LEU:HA	1:I:68:LEU:CD1	2.24	0.67
1:J:38:ILE:HB	1:J:120:ILE:HG23	1.77	0.67
1:K:131:LYS:O	1:K:134:THR:OG1	2.10	0.67
1:C:119:GLN:HE22	1:D:182:LYS:HE2	1.58	0.67
1:F:184:LEU:HD13	1:F:226:ARG:HD2	1.75	0.67
1:L:319:GLU:O	1:L:323:ILE:HG13	1.95	0.67
1:A:297:GLN:HE21	1:A:311:ARG:NE	1.93	0.66
1:H:131:LYS:O	1:H:134:THR:OG1	2.14	0.66
1:C:76:ASN:O	1:C:79:THR:OG1	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:18:PRO:O	1:H:21:MET:N	2.28	0.66
1:K:111:LEU:CD1	1:L:90:HIS:NE2	2.59	0.66
1:L:270:ARG:O	1:L:274:SER:OG	2.12	0.66
1:L:313:TYR:CE2	1:L:345:GLN:NE2	2.63	0.66
1:A:92:GLU:HG3	1:A:102:ARG:HG2	1.76	0.66
1:C:300:VAL:HG21	1:C:310:LEU:HD12	1.78	0.66
1:D:198:GLU:HA	1:D:198:GLU:OE2	1.95	0.66
1:G:321:ARG:HH11	1:G:321:ARG:HG3	1.61	0.66
1:L:296:TRP:CD1	1:L:347:MET:HE2	2.30	0.66
1:L:313:TYR:HE2	1:L:345:GLN:NE2	1.93	0.66
1:B:65:LEU:HD23	1:B:118:ILE:O	1.95	0.66
1:F:209:ILE:HG22	1:F:210:PRO:CD	2.25	0.66
1:G:328:ASP:OD1	1:G:330:ASN:N	2.27	0.66
1:A:124:THR:O	1:A:125:ILE:HD13	1.96	0.66
1:F:78:THR:O	1:F:82:LEU:CD1	2.44	0.66
1:G:281:LEU:HD21	1:G:329:PRO:HG2	1.76	0.66
1:G:345:GLN:HG3	1:G:349:TRP:CZ3	2.31	0.66
1:H:46:ALA:HB2	1:H:55:ILE:HD11	1.75	0.66
1:I:49:TYR:C	1:I:307:ARG:HD2	2.16	0.66
1:K:24:MET:CE	1:K:44:ILE:HD12	2.20	0.66
1:K:27:HIS:O	1:K:30:SER:OG	2.10	0.66
1:A:188:SER:OG	1:A:189:PRO:HD3	1.96	0.66
1:G:69:ILE:HD11	1:G:120:ILE:CG2	2.25	0.66
1:G:247:GLU:O	1:G:251:THR:HG23	1.95	0.66
1:G:355:PHE:HZ	1:G:365:TYR:CD2	2.04	0.66
1:G:269:ARG:HG2	1:G:269:ARG:NH1	1.97	0.66
1:I:16:PHE:CE1	1:I:20:PHE:HB3	2.30	0.66
1:B:46:ALA:CB	1:B:55:ILE:HD11	2.25	0.66
1:E:188:SER:HB3	1:E:189:PRO:HD3	1.77	0.66
1:F:125:ILE:CD1	1:F:126:PRO:HD2	2.24	0.66
1:G:212:HIS:O	1:G:213:LEU:HD23	1.96	0.66
1:A:230:LEU:HD13	1:A:231:ILE:N	2.10	0.66
1:C:361:SER:OG	1:C:363:ARG:HG2	1.95	0.66
1:D:272:VAL:HG13	1:D:284:THR:CG2	2.25	0.66
1:I:365:TYR:HA	1:I:368:ILE:HD11	1.78	0.66
1:I:367:LEU:HD23	1:I:367:LEU:C	2.16	0.66
1:K:150:GLY:HA3	1:K:292:ARG:HD2	1.76	0.66
1:G:173:LEU:C	1:G:181:ARG:HH22	1.99	0.65
1:G:239:ALA:HA	1:G:242:ILE:CD1	2.24	0.65
1:G:366:LYS:O	1:G:369:ILE:HB	1.94	0.65
1:B:151:ILE:HG13	1:B:290:THR:CG2	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:33:ALA:HB2	1:E:48:VAL:HG22	1.79	0.65
1:G:317:ASP:OD1	1:G:319:GLU:N	2.25	0.65
1:G:364:VAL:O	1:G:368:ILE:HD12	1.96	0.65
1:G:21:MET:CE	1:G:72:ILE:HD11	2.26	0.65
1:G:354:LYS:CB	1:G:360:ILE:HD11	2.26	0.65
1:I:321:ARG:O	1:I:325:LEU:CD1	2.38	0.65
1:K:171:ARG:CA	1:K:174:ILE:CG2	2.73	0.65
1:A:9:MET:HB3	1:A:55:ILE:HG23	1.78	0.65
1:C:174:ILE:CD1	1:C:199:THR:HG21	2.27	0.65
1:G:355:PHE:CZ	1:G:365:TYR:CG	2.84	0.65
1:I:236:CYS:SG	1:I:242:ILE:HG12	2.37	0.65
1:J:297:GLN:HG3	1:J:311:ARG:HG2	1.77	0.65
1:K:12:GLU:OE2	1:K:58:ARG:N	2.22	0.65
1:K:13:PRO:HG3	1:K:20:PHE:CD2	2.31	0.65
1:A:12:GLU:OE2	1:A:58:ARG:CB	2.44	0.65
1:E:9:MET:HG3	1:E:10:PRO:HD2	1.79	0.65
1:F:313:TYR:CE2	1:F:345:GLN:NE2	2.64	0.65
1:G:291:ILE:HG23	1:G:316:PHE:CD2	2.20	0.65
1:G:355:PHE:O	1:G:358:GLY:N	2.28	0.65
1:I:21:MET:CE	1:I:68:LEU:HD23	2.26	0.65
1:F:13:PRO:HG3	1:F:20:PHE:CE2	2.32	0.65
1:I:177:SER:N	1:I:200:ILE:HD13	2.12	0.65
1:J:17:THR:CG2	1:J:18:PRO:HD2	2.26	0.65
1:J:40:THR:N	1:J:65:LEU:CD2	2.59	0.65
1:F:40:THR:OG1	1:F:117:ALA:HB1	1.96	0.65
1:F:222:ASN:HA	1:F:225:ARG:HH21	1.60	0.65
1:G:216:PHE:CD2	1:G:233:VAL:CG1	2.75	0.65
1:H:243:SER:OG	1:H:283:ARG:NH2	2.30	0.65
1:I:77:ALA:O	1:I:81:LEU:HD13	1.96	0.65
1:J:238:ASP:O	1:J:242:ILE:HG13	1.96	0.65
1:J:333:THR:O	1:J:336:THR:OG1	2.10	0.65
1:B:45:PHE:CE2	1:C:203:VAL:HG22	2.32	0.65
1:E:176:THR:HG23	1:E:179:SER:HB3	1.79	0.65
1:F:281:LEU:O	1:F:285:ILE:HD13	1.96	0.65
1:G:329:PRO:O	1:G:332:VAL:HG13	1.97	0.65
1:H:261:THR:OG1	1:H:267:THR:HG23	1.97	0.65
1:I:174:ILE:HG13	1:I:202:ALA:CB	2.25	0.65
1:K:269:ARG:HB2	1:K:333:THR:HG22	1.78	0.65
1:L:283:ARG:O	1:L:287:ILE:HG13	1.97	0.65
1:A:209:ILE:O	1:A:213:LEU:O	2.15	0.65
1:C:367:LEU:HD23	1:C:367:LEU:C	2.17	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:352:LYS:HB2	1:F:365:TYR:OH	1.97	0.65
1:G:317:ASP:OD1	1:G:318:GLU:N	2.30	0.65
1:J:17:THR:HG22	1:J:18:PRO:HD2	1.79	0.65
1:J:81:LEU:N	1:J:81:LEU:HD23	2.12	0.65
1:J:121:THR:HG22	1:K:182:LYS:HZ1	1.61	0.65
1:C:12:GLU:OE1	1:C:57:ASN:OD1	2.14	0.65
1:D:236:CYS:HG	1:D:259:LEU:HD21	1.57	0.65
1:E:58:ARG:NH1	1:E:64:GLU:OE1	2.29	0.65
1:I:25:LEU:HD12	1:I:103:TYR:HE2	1.62	0.65
1:G:184:LEU:HG	1:G:228:PRO:HB3	1.78	0.64
1:J:92:GLU:HG3	1:J:102:ARG:CG	2.27	0.64
1:K:43:PRO:HG3	1:K:54:LYS:HD3	1.78	0.64
1:L:275:PHE:CE2	1:L:283:ARG:HD3	2.31	0.64
1:I:65:LEU:CA	1:I:68:LEU:HD12	2.25	0.64
1:I:142:ILE:O	1:I:145:ILE:HG13	1.97	0.64
1:F:208:GLU:H	1:F:212:HIS:HD2	1.43	0.64
1:G:105:VAL:HG12	1:G:122:LEU:HG	1.79	0.64
1:I:329:PRO:HA	1:I:332:VAL:CG2	2.26	0.64
1:A:208:GLU:HG2	1:A:210:PRO:HD2	1.80	0.64
1:I:175:GLU:O	1:I:200:ILE:HD12	1.96	0.64
1:I:184:LEU:HG	1:I:228:PRO:HB3	1.77	0.64
1:L:141:ILE:HD11	1:L:313:TYR:CE1	2.32	0.64
1:A:89:THR:HG22	1:A:90:HIS:N	2.13	0.64
1:B:100:ARG:HE	1:B:102:ARG:NH1	1.95	0.64
1:I:21:MET:HE2	1:I:68:LEU:CD2	2.27	0.64
1:I:261:THR:HG23	1:I:267:THR:CG2	2.14	0.64
1:J:15:ARG:HA	1:J:58:ARG:HH11	1.61	0.64
1:K:293:LEU:HD13	1:K:315:VAL:HG22	1.79	0.64
1:C:104:ARG:HG3	1:C:125:ILE:CD1	2.22	0.64
1:D:69:ILE:HA	1:D:72:ILE:HG22	1.79	0.64
1:E:137:LEU:HB3	1:E:141:ILE:HD11	1.78	0.64
1:I:48:VAL:O	1:I:51:ARG:N	2.27	0.64
1:J:9:MET:HE3	1:J:24:MET:HA	0.65	0.64
1:D:261:THR:HG21	1:D:270:ARG:CG	2.11	0.64
1:D:264:VAL:HG11	1:D:340:VAL:CG1	2.25	0.64
1:F:352:LYS:HD2	1:F:365:TYR:OH	1.97	0.64
1:G:9:MET:HE1	1:G:24:MET:CB	2.28	0.64
1:H:200:ILE:HG22	1:H:201:SER:HB3	1.79	0.64
1:J:125:ILE:CG1	1:J:126:PRO:HD2	2.27	0.64
1:L:25:LEU:HD23	1:L:36:ILE:HD13	1.79	0.64
1:D:69:ILE:HD12	1:D:72:ILE:CG2	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:186:TYR:OH	1:E:222:ASN:ND2	2.30	0.64
1:F:246:LEU:HD23	1:F:290:THR:HG21	1.77	0.64
1:G:94:ARG:HB3	1:G:99:VAL:O	1.98	0.64
1:L:131:LYS:HD3	1:L:171:ARG:NH2	2.12	0.64
1:L:197:ILE:HD12	1:L:197:ILE:H	1.63	0.64
1:J:70:ASN:OD1	1:J:78:THR:OG1	2.14	0.64
1:K:208:GLU:H	1:K:212:HIS:CD2	2.14	0.64
1:A:97:ARG:HH11	1:A:97:ARG:HG3	1.62	0.63
1:B:166:LEU:HD11	1:B:258:THR:CG2	2.27	0.63
1:B:171:ARG:HG3	1:B:197:ILE:CD1	2.28	0.63
1:C:22:ASP:OD1	1:C:91:TYR:OH	2.16	0.63
1:G:180:ASN:CB	1:L:52:LEU:HB2	2.23	0.63
1:I:16:PHE:CZ	1:I:21:MET:HA	2.33	0.63
1:L:261:THR:HG21	1:L:267:THR:HA	1.81	0.63
1:E:9:MET:HA	1:E:27:HIS:CE1	2.33	0.63
1:J:121:THR:CG2	1:K:182:LYS:HZ1	2.11	0.63
1:K:7:ASN:HA	1:K:54:LYS:O	1.98	0.63
1:G:112:VAL:HG12	1:G:113:GLU:HG2	1.80	0.63
1:I:22:ASP:OD2	1:I:93:PHE:CD1	2.51	0.63
1:I:61:SER:CB	1:I:64:GLU:HG3	2.26	0.63
1:J:354:LYS:HG3	1:J:359:ILE:HD12	1.80	0.63
1:A:12:GLU:OE2	1:A:58:ARG:HB2	1.97	0.63
1:G:12:GLU:OE1	1:G:56:THR:HG23	1.98	0.63
1:G:122:LEU:N	1:G:122:LEU:HD12	2.14	0.63
1:I:182:LYS:HE2	1:I:184:LEU:HD21	1.81	0.63
1:K:171:ARG:CA	1:K:174:ILE:HG22	2.28	0.63
1:I:61:SER:H	1:I:64:GLU:CD	2.01	0.63
1:J:352:LYS:CA	1:J:365:TYR:CE1	2.80	0.63
1:L:275:PHE:CE2	1:L:283:ARG:HB3	2.32	0.63
1:D:41:GLY:O	1:D:59:ARG:HD3	1.99	0.63
1:G:46:ALA:HB2	1:G:55:ILE:HD12	1.78	0.63
1:I:141:ILE:O	1:I:145:ILE:HG23	1.99	0.63
1:K:137:LEU:HG	1:K:141:ILE:CD1	2.28	0.63
1:G:235:GLU:CB	1:G:258:THR:O	2.47	0.63
1:H:246:LEU:O	1:H:250:LEU:HD12	1.99	0.63
1:J:352:LYS:CA	1:J:365:TYR:HE1	2.12	0.63
1:B:48:VAL:HG23	1:B:48:VAL:O	1.98	0.63
1:B:48:VAL:CG2	1:B:53:LEU:HD11	2.29	0.63
1:B:209:ILE:O	1:B:213:LEU:O	2.15	0.63
1:G:155:THR:CG2	1:G:259:LEU:HB2	2.27	0.63
1:J:69:ILE:HA	1:J:72:ILE:CG2	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:17:THR:CG2	1:K:18:PRO:HD2	2.29	0.63
1:E:154:ILE:HG21	1:E:165:LEU:HD23	1.80	0.62
1:G:111:LEU:HD22	1:H:90:HIS:CE1	2.33	0.62
1:G:224:LEU:HD21	1:G:248:ALA:HA	1.81	0.62
1:J:13:PRO:HG3	1:J:20:PHE:HD1	1.63	0.62
1:E:349:TRP:CZ3	1:E:353:MET:HG3	2.35	0.62
1:F:361:SER:O	1:F:364:VAL:HG12	1.99	0.62
1:K:188:SER:O	1:K:208:GLU:HG3	1.98	0.62
1:C:21:MET:CE	1:C:72:ILE:HD11	2.29	0.62
1:G:367:LEU:O	1:G:367:LEU:HD23	1.99	0.62
1:I:131:LYS:O	1:I:134:THR:OG1	2.15	0.62
1:L:66:GLY:O	1:L:69:ILE:HG22	1.99	0.62
1:C:166:LEU:HD13	1:C:232:MET:CE	2.28	0.62
1:E:48:VAL:O	1:E:51:ARG:HG2	1.99	0.62
1:F:214:PRO:HB2	1:F:218:ASP:OD2	2.00	0.62
1:J:125:ILE:HG13	1:J:126:PRO:HD2	1.82	0.62
1:K:269:ARG:HB2	1:K:333:THR:HG21	1.82	0.62
1:B:332:VAL:O	1:B:336:THR:HG23	1.99	0.62
1:D:209:ILE:O	1:D:213:LEU:O	2.16	0.62
1:E:44:ILE:H	1:E:56:THR:HG22	1.64	0.62
1:H:65:LEU:HD11	1:H:120:ILE:HD12	1.80	0.62
1:A:135:MET:HB3	1:A:137:LEU:CD1	2.29	0.62
1:A:281:LEU:C	1:A:281:LEU:HD13	2.20	0.62
1:F:236:CYS:SG	1:F:242:ILE:HG12	2.39	0.62
1:G:348:THR:O	1:G:351:ALA:HB3	2.00	0.62
1:I:355:PHE:CE2	1:I:362:GLU:HG2	2.33	0.62
1:B:102:ARG:NE	1:B:127:THR:HG22	2.14	0.62
1:B:249:ALA:CB	1:B:290:THR:HG21	2.29	0.62
1:C:81:LEU:HD11	1:C:87:ILE:CD1	2.30	0.62
1:E:7:ASN:O	1:E:8:LEU:HD23	2.00	0.62
1:G:230:LEU:CD2	1:G:256:TYR:HE1	2.13	0.62
1:G:352:LYS:O	1:G:355:PHE:HB2	1.98	0.62
1:K:171:ARG:O	1:K:174:ILE:CG2	2.48	0.62
1:G:268:MET:HG3	1:G:336:THR:HG21	1.80	0.62
1:J:172:GLU:O	1:J:176:THR:HG23	1.99	0.62
1:A:141:ILE:O	1:A:145:ILE:HG23	1.99	0.62
1:B:184:LEU:HD22	1:B:226:ARG:HH21	1.65	0.62
1:B:188:SER:HB3	1:B:189:PRO:HD2	1.82	0.62
1:D:69:ILE:HA	1:D:72:ILE:CG2	2.30	0.62
1:G:302:THR:OG1	1:G:304:ASP:OD1	2.07	0.62
1:H:81:LEU:HD21	1:H:87:ILE:HG13	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:230:LEU:CD1	1:I:256:TYR:CE1	2.82	0.62
1:I:354:LYS:O	1:I:357:GLN:N	2.33	0.62
1:L:264:VAL:HG22	1:L:294:CYS:SG	2.39	0.62
1:B:352:LYS:HA	1:B:365:TYR:HE1	1.64	0.61
1:C:236:CYS:SG	1:C:242:ILE:HG12	2.40	0.61
1:D:174:ILE:O	1:D:199:THR:HG21	2.00	0.61
1:D:307:ARG:NH2	1:E:251:THR:O	2.32	0.61
1:D:320:VAL:HG13	1:D:339:LEU:HD13	1.80	0.61
1:E:162:LYS:CD	1:E:258:THR:HB	2.21	0.61
1:E:317:ASP:OD1	1:E:318:GLU:N	2.31	0.61
1:I:109:ALA:C	1:J:212:HIS:ND1	2.54	0.61
1:F:22:ASP:O	1:F:26:GLU:HG3	2.00	0.61
1:G:144:ALA:HB2	1:G:315:VAL:CG1	2.30	0.61
1:I:197:ILE:HD12	1:I:197:ILE:H	1.65	0.61
1:I:355:PHE:CZ	1:I:362:GLU:CG	2.81	0.61
1:A:49:TYR:CE1	1:A:306:ARG:HG3	2.35	0.61
1:C:81:LEU:HD11	1:C:87:ILE:HD12	1.82	0.61
1:F:132:LEU:HD11	1:F:169:ILE:CD1	2.30	0.61
1:G:365:TYR:N	1:G:368:ILE:HD12	2.14	0.61
1:H:248:ALA:O	1:H:251:THR:HB	2.00	0.61
1:C:209:ILE:O	1:C:213:LEU:O	2.18	0.61
1:G:235:GLU:CA	1:G:258:THR:O	2.47	0.61
1:I:76:ASN:O	1:I:79:THR:OG1	2.15	0.61
1:L:27:HIS:O	1:L:30:SER:OG	2.17	0.61
1:D:249:ALA:HB1	1:D:290:THR:OG1	2.00	0.61
1:F:328:ASP:O	1:F:328:ASP:OD1	2.17	0.61
1:G:69:ILE:CG1	1:G:120:ILE:CD1	2.78	0.61
1:G:333:THR:O	1:G:336:THR:OG1	2.13	0.61
1:I:287:ILE:HG22	1:I:291:ILE:HD11	1.81	0.61
1:J:24:MET:CE	1:J:25:LEU:HD23	2.30	0.61
1:J:88:ASP:OD1	1:J:106:ASN:ND2	2.33	0.61
1:J:171:ARG:O	1:J:175:GLU:HB2	2.00	0.61
1:K:14:THR:OG1	1:K:15:ARG:N	2.32	0.61
1:L:310:LEU:HD22	1:L:354:LYS:HG3	1.81	0.61
1:A:94:ARG:HH11	1:A:97:ARG:HA	1.66	0.61
1:C:132:LEU:HB2	1:C:172:GLU:CG	2.31	0.61
1:G:188:SER:O	1:G:208:GLU:HG3	2.00	0.61
1:J:37:THR:OG1	1:K:182:LYS:HE3	2.00	0.61
1:A:46:ALA:HB2	1:A:55:ILE:HD12	1.83	0.61
1:H:125:ILE:HD12	1:H:126:PRO:CD	2.25	0.61
1:J:174:ILE:HG23	1:J:175:GLU:N	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:171:ARG:C	1:K:174:ILE:HG22	2.21	0.61
1:K:296:TRP:CE3	1:K:347:MET:HE2	2.35	0.61
1:A:224:LEU:HD21	1:A:248:ALA:HA	1.82	0.61
1:B:363:ARG:NH1	1:C:322:ASP:OD1	2.33	0.61
1:G:317:ASP:O	1:G:321:ARG:N	2.19	0.61
1:J:175:GLU:HG3	1:J:197:ILE:HG23	1.81	0.61
1:L:186:TYR:HB3	1:L:209:ILE:HD13	1.83	0.61
1:B:319:GLU:O	1:B:323:ILE:HG13	2.00	0.61
1:C:197:ILE:HD12	1:C:197:ILE:N	2.16	0.61
1:E:27:HIS:O	1:E:30:SER:OG	2.03	0.61
1:H:21:MET:HE3	1:H:68:LEU:HB3	1.83	0.61
1:H:251:THR:HG22	1:H:253:HIS:CD2	2.35	0.61
1:J:213:LEU:HD22	1:J:214:PRO:HD3	1.83	0.61
1:K:70:ASN:OD1	1:K:78:THR:HG23	2.00	0.61
1:A:261:THR:HG21	1:A:267:THR:N	2.16	0.61
1:G:318:GLU:O	1:G:322:ASP:CG	2.38	0.61
1:J:272:VAL:HG13	1:J:284:THR:CG2	2.26	0.61
1:K:208:GLU:HG2	1:K:210:PRO:HD2	1.83	0.61
1:K:262:SER:HB2	1:K:296:TRP:CZ2	2.35	0.61
1:L:355:PHE:CZ	1:L:362:GLU:HG3	2.36	0.61
1:A:365:TYR:CE1	1:A:369:ILE:HD11	2.35	0.60
1:C:188:SER:OG	1:C:189:PRO:HD3	2.01	0.60
1:C:188:SER:CB	1:C:189:PRO:HD3	2.30	0.60
1:D:99:VAL:HG12	1:D:100:ARG:N	2.16	0.60
1:E:188:SER:O	1:E:208:GLU:HG3	2.01	0.60
1:H:48:VAL:CG2	1:H:53:LEU:CD1	2.76	0.60
1:J:60:LEU:HD12	1:J:64:GLU:OE1	2.01	0.60
1:K:47:GLU:HG3	1:K:52:LEU:HD12	1.83	0.60
1:K:175:GLU:OE2	1:K:197:ILE:HD11	2.01	0.60
1:I:7:ASN:O	1:I:55:ILE:HA	2.01	0.60
1:I:34:SER:OG	1:I:35:ASP:OD1	2.12	0.60
1:I:110:CYS:C	1:J:212:HIS:CE1	2.75	0.60
1:I:116:ASP:OD1	1:J:211:ARG:NH2	2.34	0.60
1:A:119:GLN:HE22	1:B:182:LYS:CE	2.14	0.60
1:F:281:LEU:O	1:F:285:ILE:CD1	2.50	0.60
1:I:132:LEU:CB	1:I:172:GLU:HG3	2.31	0.60
1:K:317:ASP:OD1	1:K:318:GLU:N	2.34	0.60
1:B:367:LEU:CD2	1:C:325:LEU:HD22	2.31	0.60
1:G:352:LYS:HG3	1:G:365:TYR:CZ	2.35	0.60
1:K:24:MET:HE1	1:K:44:ILE:CD1	2.22	0.60
1:L:149:GLU:HG2	1:L:150:GLY:H	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:189:PRO:HA	1:L:208:GLU:OE2	2.01	0.60
1:E:188:SER:HA	1:E:210:PRO:HD3	1.83	0.60
1:F:212:HIS:O	1:F:213:LEU:HG	2.02	0.60
1:G:291:ILE:CG1	1:G:316:PHE:CE2	2.81	0.60
1:I:47:GLU:CA	1:I:52:LEU:HD23	2.31	0.60
1:I:174:ILE:CG1	1:I:202:ALA:CB	2.79	0.60
1:K:288:LEU:HB3	1:K:325:LEU:CD2	2.30	0.60
1:L:219:GLY:O	1:L:222:ASN:HB3	2.02	0.60
1:L:333:THR:HG23	1:L:334:SER:N	2.17	0.60
1:A:275:PHE:O	1:A:280:ARG:NE	2.31	0.60
1:B:116:ASP:OD2	1:C:211:ARG:NH1	2.34	0.60
1:B:209:ILE:N	1:B:210:PRO:HD2	2.17	0.60
1:K:304:ASP:CG	1:K:306:ARG:HG3	2.21	0.60
1:I:132:LEU:HB2	1:I:172:GLU:CG	2.31	0.60
1:I:300:VAL:HG21	1:I:310:LEU:HD12	1.82	0.60
1:K:170:ILE:O	1:K:174:ILE:CG2	2.45	0.60
1:A:233:VAL:HB	1:A:257:THR:CG2	2.29	0.60
1:A:251:THR:OG1	1:A:253:HIS:HD2	1.84	0.60
1:A:268:MET:HG3	1:A:336:THR:HG21	1.84	0.60
1:E:275:PHE:O	1:E:280:ARG:HB2	2.02	0.60
1:F:236:CYS:SG	1:F:242:ILE:CG1	2.90	0.60
1:G:9:MET:HE1	1:G:24:MET:CA	2.30	0.60
1:G:355:PHE:CZ	1:G:365:TYR:CB	2.84	0.60
1:G:355:PHE:CE2	1:G:365:TYR:HB2	2.36	0.60
1:J:191:GLU:HB3	1:J:192:PHE:CE1	2.36	0.60
1:J:264:VAL:CG1	1:J:340:VAL:HG11	2.32	0.60
1:D:296:TRP:CE3	1:D:347:MET:HE2	2.37	0.60
1:F:111:LEU:HD12	1:F:115:HIS:O	2.02	0.60
1:F:208:GLU:N	1:F:212:HIS:HD2	2.00	0.60
1:H:230:LEU:HD23	1:H:231:ILE:N	2.17	0.60
1:I:21:MET:HE2	1:I:68:LEU:HD23	1.82	0.60
1:I:188:SER:O	1:I:208:GLU:HG3	2.02	0.60
1:G:111:LEU:HD12	1:G:111:LEU:C	2.22	0.60
1:I:236:CYS:SG	1:I:242:ILE:CG1	2.90	0.60
1:A:341:ARG:HG2	1:A:346:LEU:HD21	1.84	0.59
1:B:21:MET:CE	1:B:72:ILE:HD11	2.31	0.59
1:C:300:VAL:HG11	1:C:368:ILE:HD11	1.84	0.59
1:D:170:ILE:O	1:D:174:ILE:HG22	2.02	0.59
1:D:214:PRO:C	1:D:215:ASN:HD22	2.05	0.59
1:D:355:PHE:HE1	1:D:362:GLU:HG3	1.67	0.59
1:E:40:THR:HG23	1:E:65:LEU:HD22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:154:ILE:HG21	1:I:162:LYS:HB3	1.84	0.59
1:K:171:ARG:O	1:K:174:ILE:HG23	2.02	0.59
1:C:236:CYS:SG	1:C:242:ILE:CG1	2.90	0.59
1:E:108:THR:CG2	1:F:226:ARG:HH21	2.05	0.59
1:G:235:GLU:HB2	1:G:258:THR:O	2.02	0.59
1:G:355:PHE:CE2	1:G:365:TYR:CB	2.85	0.59
1:J:146:ALA:HB2	1:J:173:LEU:HD21	1.85	0.59
1:K:352:LYS:HB2	1:K:365:TYR:OH	2.01	0.59
1:B:125:ILE:CD1	1:B:126:PRO:HD2	2.31	0.59
1:F:291:ILE:HD13	1:F:316:PHE:CZ	2.36	0.59
1:J:69:ILE:HA	1:J:72:ILE:HG22	1.85	0.59
1:K:61:SER:HB3	1:K:64:GLU:OE1	2.02	0.59
1:C:78:THR:O	1:C:82:LEU:HG	2.02	0.59
1:F:259:LEU:HD13	1:F:267:THR:HG23	1.83	0.59
1:G:211:ARG:NH2	1:L:116:ASP:OD1	2.36	0.59
1:G:278:GLU:CD	1:L:337:ARG:HH12	2.02	0.59
1:H:48:VAL:CG2	1:H:53:LEU:HD11	2.21	0.59
1:H:104:ARG:HH21	1:H:191:GLU:CD	2.05	0.59
1:I:353:MET:CG	1:I:357:GLN:HE22	2.15	0.59
1:L:24:MET:SD	1:L:44:ILE:HG21	2.43	0.59
1:L:125:ILE:CD1	1:L:126:PRO:HD2	2.28	0.59
1:L:324:LEU:HD22	1:L:332:VAL:HG13	1.84	0.59
1:J:317:ASP:OD1	1:J:318:GLU:N	2.35	0.59
1:D:65:LEU:HB3	1:D:118:ILE:CG1	2.33	0.59
1:F:209:ILE:HD13	1:F:209:ILE:O	2.02	0.59
1:H:188:SER:OG	1:H:189:PRO:CD	2.42	0.59
1:C:171:ARG:O	1:C:174:ILE:HG22	2.03	0.59
1:I:155:THR:HG21	1:I:267:THR:HG21	1.84	0.59
1:I:365:TYR:O	1:I:368:ILE:CG1	2.51	0.59
1:J:216:PHE:O	1:J:220:VAL:HG23	2.02	0.59
1:L:73:TYR:CE1	1:L:87:ILE:HG23	2.38	0.59
1:B:272:VAL:HG13	1:B:284:THR:HG22	1.85	0.59
1:D:171:ARG:HG3	1:D:197:ILE:CD1	2.33	0.59
1:I:319:GLU:OE2	1:I:343:LYS:NZ	2.35	0.59
1:B:365:TYR:CE2	1:B:369:ILE:HD11	2.38	0.59
1:E:44:ILE:H	1:E:56:THR:CG2	2.16	0.59
1:F:178:ASP:O	1:F:180:ASN:ND2	2.36	0.59
1:G:345:GLN:HB2	1:G:349:TRP:HZ3	1.68	0.59
1:H:27:HIS:HD2	1:H:55:ILE:CG2	2.16	0.59
1:F:156:GLY:HA2	1:F:296:TRP:HZ3	1.66	0.58
1:I:81:LEU:HD11	1:I:87:ILE:CD1	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:119:GLN:HE21	1:K:121:THR:HG23	1.67	0.58
1:A:9:MET:HA	1:A:27:HIS:CE1	2.38	0.58
1:B:46:ALA:HB2	1:B:55:ILE:CD1	2.31	0.58
1:D:296:TRP:CH2	1:D:347:MET:HE3	2.38	0.58
1:E:21:MET:O	1:E:25:LEU:N	2.28	0.58
1:F:209:ILE:CG2	1:F:210:PRO:HD3	2.32	0.58
1:G:296:TRP:CH2	1:G:347:MET:HE1	2.38	0.58
1:H:92:GLU:CG	1:H:102:ARG:HG2	2.33	0.58
1:F:180:ASN:HA	1:F:201:SER:O	2.03	0.58
1:J:40:THR:HG23	1:J:62:ASN:CA	2.33	0.58
1:J:145:ILE:HD12	1:J:293:LEU:CD2	2.33	0.58
1:F:111:LEU:HD12	1:F:115:HIS:C	2.23	0.58
1:G:9:MET:HE1	1:G:24:MET:HA	1.85	0.58
1:J:174:ILE:O	1:J:199:THR:HG21	2.03	0.58
1:C:111:LEU:C	1:C:111:LEU:HD13	2.23	0.58
1:J:9:MET:HG2	1:J:10:PRO:HD2	1.84	0.58
1:D:92:GLU:OE2	1:D:102:ARG:NH1	2.37	0.58
1:I:302:THR:HG21	1:I:308:VAL:HB	1.85	0.58
1:K:137:LEU:CD2	1:K:141:ILE:HD11	2.34	0.58
1:L:275:PHE:CE2	1:L:283:ARG:CD	2.87	0.58
1:B:365:TYR:CE2	1:B:369:ILE:CD1	2.87	0.58
1:C:12:GLU:CD	1:C:56:THR:OG1	2.42	0.58
1:F:73:TYR:CE1	1:F:89:THR:CG2	2.87	0.58
1:G:264:VAL:HG23	1:G:312:GLU:OE2	2.03	0.58
1:I:108:THR:CG2	1:J:222:ASN:HD21	2.00	0.58
1:J:26:GLU:OE1	1:J:95:PRO:HB2	2.02	0.58
1:K:44:ILE:CG2	1:K:55:ILE:HD11	2.33	0.58
1:K:222:ASN:O	1:K:225:ARG:N	2.35	0.58
1:B:102:ARG:HH21	1:B:127:THR:HB	1.68	0.58
1:D:10:PRO:HD3	1:D:27:HIS:ND1	2.18	0.58
1:E:209:ILE:HG13	1:E:216:PHE:CD1	2.38	0.58
1:G:170:ILE:HD12	1:G:194:TYR:OH	2.04	0.58
1:H:21:MET:CE	1:H:68:LEU:HB3	2.34	0.58
1:I:317:ASP:H	1:I:320:VAL:CG2	2.17	0.58
1:J:68:LEU:O	1:J:72:ILE:HG22	2.04	0.58
1:K:180:ASN:N	1:K:180:ASN:HD22	2.00	0.58
1:K:283:ARG:O	1:K:287:ILE:HG12	2.04	0.58
1:L:112:VAL:CG2	1:L:117:ALA:HB3	2.30	0.58
1:L:190:ILE:CG1	1:L:208:GLU:HG2	2.34	0.58
1:A:94:ARG:NE	1:A:100:ARG:HE	2.00	0.58
1:B:21:MET:HE1	1:B:72:ILE:HD11	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:230:LEU:C	1:G:230:LEU:CD1	2.72	0.58
1:H:290:THR:O	1:H:292:ARG:NH2	2.37	0.58
1:I:104:ARG:CG	1:I:125:ILE:HD13	2.24	0.58
1:J:352:LYS:CG	1:J:365:TYR:OH	2.48	0.58
1:K:223:ALA:O	1:K:228:PRO:HD3	2.04	0.58
1:C:152:VAL:HG13	1:C:293:LEU:HD12	1.85	0.58
1:E:184:LEU:HG	1:E:228:PRO:HB3	1.86	0.58
1:K:184:LEU:HG	1:K:228:PRO:HB3	1.85	0.58
1:A:230:LEU:HD21	1:A:256:TYR:CE1	2.39	0.57
1:J:182:LYS:HZ1	1:J:226:ARG:HB3	1.69	0.57
1:L:173:LEU:HD22	1:L:181:ARG:NH2	2.19	0.57
1:E:355:PHE:HE2	1:E:362:GLU:HA	1.68	0.57
1:F:149:GLU:HG2	1:F:150:GLY:H	1.64	0.57
1:H:65:LEU:HD12	1:H:120:ILE:HD12	1.86	0.57
1:J:145:ILE:CD1	1:J:293:LEU:HD21	2.34	0.57
1:L:275:PHE:CD2	1:L:283:ARG:HB3	2.39	0.57
1:B:188:SER:O	1:B:208:GLU:HG3	2.04	0.57
1:E:80:GLN:O	1:E:83:SER:HB3	2.04	0.57
1:G:354:LYS:HB3	1:G:360:ILE:HD11	1.86	0.57
1:I:62:ASN:OD1	1:I:118:ILE:HD12	2.05	0.57
1:I:177:SER:CA	1:I:200:ILE:HD13	2.34	0.57
1:C:214:PRO:HG2	1:C:218:ASP:OD2	2.04	0.57
1:H:230:LEU:HD23	1:H:230:LEU:C	2.24	0.57
1:J:9:MET:HE3	1:J:24:MET:CB	2.29	0.57
1:J:22:ASP:O	1:J:25:LEU:HB2	2.05	0.57
1:E:321:ARG:O	1:E:325:LEU:HG	2.05	0.57
1:F:219:GLY:O	1:F:222:ASN:HB3	2.04	0.57
1:K:194:TYR:CD2	1:K:204:VAL:HG11	2.40	0.57
1:A:46:ALA:HB2	1:A:55:ILE:CD1	2.35	0.57
1:C:209:ILE:N	1:C:210:PRO:HD2	2.19	0.57
1:E:93:PHE:HE2	1:E:95:PRO:HA	1.69	0.57
1:E:275:PHE:O	1:E:280:ARG:CB	2.52	0.57
1:H:21:MET:HE3	1:H:68:LEU:HD13	1.86	0.57
1:J:24:MET:HE3	1:J:25:LEU:HG	1.85	0.57
1:J:238:ASP:OD1	1:J:241:THR:HG23	2.04	0.57
1:L:27:HIS:CD2	1:L:31:LEU:HD13	2.39	0.57
1:L:40:THR:HG23	1:L:118:ILE:O	2.04	0.57
1:A:92:GLU:OE2	1:A:100:ARG:NH1	2.36	0.57
1:B:48:VAL:HG22	1:B:53:LEU:HD11	1.86	0.57
1:B:90:HIS:C	1:B:90:HIS:CD2	2.78	0.57
1:F:188:SER:HA	1:F:209:ILE:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:222:ASN:O	1:G:225:ARG:HG3	2.05	0.57
1:H:251:THR:CG2	1:H:253:HIS:CD2	2.87	0.57
1:I:110:CYS:O	1:J:212:HIS:CE1	2.55	0.57
1:K:171:ARG:O	1:K:175:GLU:HB2	2.04	0.57
1:A:119:GLN:NE2	1:B:182:LYS:HE2	2.16	0.57
1:A:184:LEU:HG	1:A:228:PRO:HB3	1.86	0.57
1:H:365:TYR:OH	1:H:369:ILE:HD11	2.04	0.57
1:I:81:LEU:HD11	1:I:87:ILE:HD12	1.85	0.57
1:I:111:LEU:HD12	1:J:190:ILE:HD12	1.85	0.57
1:K:25:LEU:CD1	1:K:93:PHE:CE2	2.88	0.57
1:K:111:LEU:HD11	1:L:90:HIS:NE2	2.19	0.57
1:A:154:ILE:HG22	1:A:162:LYS:HB3	1.87	0.57
1:A:320:VAL:HG13	1:A:339:LEU:HD13	1.87	0.57
1:F:313:TYR:HE2	1:F:345:GLN:NE2	2.02	0.57
1:G:122:LEU:N	1:G:122:LEU:CD1	2.68	0.57
1:G:135:MET:HA	1:G:135:MET:CE	2.34	0.57
1:G:144:ALA:CB	1:G:315:VAL:HG13	2.35	0.57
1:G:235:GLU:CB	1:G:258:THR:OG1	2.52	0.57
1:I:13:PRO:CG	1:I:20:PHE:CD2	2.88	0.57
1:I:197:ILE:H	1:I:197:ILE:CD1	2.17	0.57
1:K:281:LEU:HD12	1:K:281:LEU:O	2.05	0.57
1:L:317:ASP:OD1	1:L:318:GLU:N	2.38	0.57
1:B:171:ARG:HG3	1:B:197:ILE:HD13	1.86	0.57
1:C:34:SER:O	1:C:124:THR:HG23	2.05	0.57
1:C:48:VAL:HG12	1:C:49:TYR:HD2	1.70	0.57
1:C:333:THR:O	1:C:336:THR:OG1	2.14	0.57
1:E:43:PRO:HG2	1:E:54:LYS:HD3	1.85	0.57
1:G:126:PRO:HB2	1:G:192:PHE:CE1	2.39	0.57
1:G:260:HIS:CD2	1:G:261:THR:CG2	2.88	0.57
1:I:179:SER:HB2	1:I:181:ARG:NH2	2.20	0.57
1:J:92:GLU:OE2	1:J:102:ARG:NH2	2.38	0.57
1:K:25:LEU:HD13	1:K:93:PHE:HE2	1.69	0.57
1:L:320:VAL:HG13	1:L:339:LEU:HD12	1.87	0.57
1:E:150:GLY:HA3	1:E:292:ARG:HD2	1.86	0.56
1:F:49:TYR:CD1	1:F:50:GLY:N	2.71	0.56
1:I:197:ILE:N	1:I:197:ILE:CD1	2.68	0.56
1:C:131:LYS:O	1:C:134:THR:OG1	2.22	0.56
1:D:111:LEU:HD22	1:D:115:HIS:O	2.05	0.56
1:H:185:THR:HG22	1:H:232:MET:HB3	1.86	0.56
1:H:229:ARG:HG2	1:H:229:ARG:HH21	1.68	0.56
1:H:276:SER:O	1:H:280:ARG:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:93:PHE:CE2	1:K:103:TYR:CE1	2.93	0.56
1:L:40:THR:HG23	1:L:65:LEU:HD23	1.86	0.56
1:A:297:GLN:HG3	1:A:311:ARG:HG2	1.86	0.56
1:B:21:MET:SD	1:B:68:LEU:HD22	2.45	0.56
1:C:104:ARG:CD	1:C:125:ILE:HD11	2.34	0.56
1:D:184:LEU:HG	1:D:228:PRO:HB3	1.87	0.56
1:D:246:LEU:HD23	1:D:290:THR:HG21	1.87	0.56
1:D:355:PHE:CE1	1:D:362:GLU:HG3	2.40	0.56
1:E:9:MET:HG2	1:E:10:PRO:HD2	1.86	0.56
1:E:17:THR:HG22	1:E:18:PRO:HD2	1.87	0.56
1:E:223:ALA:O	1:E:228:PRO:HD3	2.04	0.56
1:E:288:LEU:HB3	1:E:325:LEU:HD21	1.86	0.56
1:F:44:ILE:HB	1:F:56:THR:HG23	1.87	0.56
1:G:208:GLU:H	1:G:212:HIS:CD2	2.21	0.56
1:I:22:ASP:HB3	1:I:93:PHE:CE2	2.40	0.56
1:I:367:LEU:HD23	1:I:368:ILE:N	2.19	0.56
1:K:89:THR:HG23	1:K:105:VAL:CG1	2.34	0.56
1:A:211:ARG:O	1:F:84:GLY:HA2	2.06	0.56
1:C:355:PHE:CE1	1:C:362:GLU:HG2	2.31	0.56
1:G:46:ALA:HB2	1:G:55:ILE:CD1	2.34	0.56
1:I:22:ASP:OD2	1:I:93:PHE:CZ	2.58	0.56
1:L:61:SER:O	1:L:64:GLU:N	2.38	0.56
1:L:365:TYR:CZ	1:L:369:ILE:HD11	2.40	0.56
1:A:25:LEU:HD23	1:A:36:ILE:CD1	2.36	0.56
1:A:306:ARG:HG2	1:A:307:ARG:H	1.71	0.56
1:B:279:GLU:O	1:B:283:ARG:HG2	2.05	0.56
1:C:166:LEU:HD12	1:C:167:ALA:N	2.20	0.56
1:D:86:ASP:OD1	1:D:87:ILE:N	2.39	0.56
1:I:174:ILE:HG12	1:I:202:ALA:HB3	1.87	0.56
1:J:102:ARG:NE	1:J:193:VAL:HG21	2.20	0.56
1:L:297:GLN:OE1	1:L:311:ARG:NH2	2.37	0.56
1:A:182:LYS:HD2	1:F:37:THR:HG21	1.88	0.56
1:A:340:VAL:HG12	1:A:346:LEU:CD1	2.36	0.56
1:C:361:SER:HB3	1:C:364:VAL:CG2	2.34	0.56
1:F:135:MET:HB3	1:F:137:LEU:HD13	1.88	0.56
1:G:291:ILE:HG21	1:G:316:PHE:CE2	2.41	0.56
1:H:209:ILE:N	1:H:210:PRO:HD2	2.21	0.56
1:I:86:ASP:CG	1:J:225:ARG:HH12	2.09	0.56
1:L:333:THR:HG23	1:L:334:SER:H	1.70	0.56
1:L:337:ARG:O	1:L:340:VAL:CG2	2.53	0.56
1:B:132:LEU:HB2	1:B:172:GLU:HG3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:367:LEU:HD23	1:C:325:LEU:HD22	1.88	0.56
1:E:8:LEU:CD1	1:E:31:LEU:HD11	2.36	0.56
1:E:23:ARG:NH1	1:E:26:GLU:OE1	2.39	0.56
1:F:283:ARG:O	1:F:287:ILE:HG13	2.06	0.56
1:G:89:THR:CG2	1:G:90:HIS:H	2.18	0.56
1:G:320:VAL:CG1	1:G:339:LEU:HD13	2.35	0.56
1:A:94:ARG:HD3	1:A:96:ASN:O	2.06	0.56
1:A:126:PRO:O	1:A:191:GLU:O	2.23	0.56
1:A:288:LEU:O	1:A:321:ARG:HD2	2.06	0.56
1:H:58:ARG:NH2	1:H:58:ARG:HB3	2.21	0.56
1:H:68:LEU:HD23	1:H:68:LEU:H	1.69	0.56
1:H:276:SER:O	1:H:280:ARG:N	2.37	0.56
1:A:142:ILE:HA	1:A:145:ILE:HG12	1.87	0.56
1:B:9:MET:CE	1:B:24:MET:HB2	2.34	0.56
1:E:17:THR:CG2	1:E:18:PRO:CD	2.84	0.56
1:E:208:GLU:N	1:E:212:HIS:HD2	1.92	0.56
1:G:121:THR:C	1:G:122:LEU:HD12	2.26	0.56
1:B:55:ILE:O	1:B:55:ILE:HG22	2.06	0.56
1:D:365:TYR:O	1:D:369:ILE:HG22	2.05	0.56
1:E:108:THR:CG2	1:F:226:ARG:HH22	2.11	0.56
1:I:68:LEU:O	1:I:72:ILE:HG13	2.06	0.56
1:J:185:THR:HG22	1:J:232:MET:HB3	1.88	0.56
1:K:329:PRO:O	1:K:332:VAL:HG13	2.06	0.56
1:A:37:THR:HG21	1:B:182:LYS:HD2	1.86	0.55
1:D:174:ILE:HG12	1:D:199:THR:CG2	2.31	0.55
1:D:188:SER:HB3	1:D:189:PRO:HD3	1.88	0.55
1:D:296:TRP:CZ3	1:D:347:MET:HE3	2.41	0.55
1:E:102:ARG:NH1	1:E:127:THR:HG21	2.21	0.55
1:E:275:PHE:O	1:E:280:ARG:HG3	2.06	0.55
1:H:355:PHE:CZ	1:H:362:GLU:HG3	2.41	0.55
1:J:299:LEU:HA	1:J:308:VAL:O	2.06	0.55
1:K:270:ARG:O	1:K:274:SER:OG	2.20	0.55
1:B:102:ARG:HE	1:B:127:THR:HA	1.70	0.55
1:E:10:PRO:HG2	1:E:11:ASP:OD1	2.05	0.55
1:H:81:LEU:CD2	1:H:87:ILE:HG13	2.36	0.55
1:K:93:PHE:CE2	1:K:103:TYR:HE1	2.23	0.55
1:K:169:ILE:O	1:K:172:GLU:HB3	2.06	0.55
1:C:149:GLU:O	1:C:292:ARG:CD	2.53	0.55
1:D:155:THR:HB	1:D:261:THR:O	2.06	0.55
1:G:144:ALA:HB2	1:G:315:VAL:HG11	1.89	0.55
1:G:355:PHE:HE2	1:G:365:TYR:CG	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:121:THR:HG21	1:I:182:LYS:NZ	2.20	0.55
1:J:209:ILE:HD11	1:J:215:ASN:O	2.05	0.55
1:K:173:LEU:HD22	1:K:181:ARG:NE	2.21	0.55
1:B:249:ALA:HB3	1:B:290:THR:HG21	1.88	0.55
1:F:93:PHE:O	1:F:93:PHE:CD1	2.60	0.55
1:F:132:LEU:CD1	1:F:169:ILE:CD1	2.83	0.55
1:G:34:SER:O	1:G:124:THR:HG23	2.07	0.55
1:G:288:LEU:CD1	1:G:325:LEU:HD23	2.36	0.55
1:B:259:LEU:HD12	1:B:267:THR:CG2	2.37	0.55
1:D:65:LEU:HD23	1:D:118:ILE:O	2.06	0.55
1:G:25:LEU:HD23	1:G:36:ILE:CD1	2.37	0.55
1:J:10:PRO:CD	1:J:27:HIS:CD2	2.84	0.55
1:G:145:ILE:C	1:G:145:ILE:HD12	2.27	0.55
1:G:361:SER:HB3	1:G:364:VAL:HG23	1.88	0.55
1:H:312:GLU:HB2	1:H:347:MET:N	2.22	0.55
1:I:171:ARG:HA	1:I:174:ILE:HG22	1.88	0.55
1:A:251:THR:OG1	1:A:253:HIS:CD2	2.60	0.55
1:G:365:TYR:CZ	1:G:369:ILE:HD11	2.41	0.55
1:I:230:LEU:CD1	1:I:256:TYR:CD1	2.90	0.55
1:J:45:PHE:CD2	1:J:52:LEU:HG	2.35	0.55
1:B:102:ARG:HB2	1:B:125:ILE:CG2	2.37	0.55
1:F:166:LEU:HD13	1:F:232:MET:SD	2.47	0.55
1:I:247:GLU:O	1:I:251:THR:HG23	2.07	0.55
1:I:272:VAL:HG13	1:I:284:THR:CG2	2.31	0.55
1:J:140:ASN:H	1:J:140:ASN:ND2	2.05	0.55
1:L:73:TYR:CD1	1:L:87:ILE:HG23	2.42	0.55
1:A:203:VAL:CG1	1:F:42:GLU:OE1	2.55	0.55
1:E:43:PRO:CG	1:E:54:LYS:HD3	2.37	0.55
1:F:314:LEU:HD23	1:F:315:VAL:C	2.27	0.55
1:G:320:VAL:HG13	1:G:339:LEU:HD13	1.88	0.55
1:H:261:THR:CG2	1:H:270:ARG:HD2	2.36	0.55
1:B:92:GLU:HA	1:B:101:TYR:O	2.07	0.55
1:C:186:TYR:CE2	1:C:219:GLY:CA	2.90	0.55
1:F:291:ILE:CD1	1:F:316:PHE:CE1	2.90	0.55
1:I:352:LYS:HD2	1:I:365:TYR:OH	2.06	0.55
1:K:36:ILE:HD12	1:K:36:ILE:N	2.22	0.55
1:K:149:GLU:OE1	1:K:149:GLU:N	2.40	0.55
1:L:273:THR:O	1:L:275:PHE:N	2.40	0.55
1:B:280:ARG:O	1:B:284:THR:CG2	2.42	0.54
1:E:89:THR:HG23	1:E:105:VAL:HG13	1.87	0.54
1:G:94:ARG:CB	1:G:99:VAL:O	2.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:340:VAL:HG23	1:H:346:LEU:CD2	2.38	0.54
1:A:105:VAL:HG12	1:A:122:LEU:HG	1.88	0.54
1:D:104:ARG:NE	1:D:123:ARG:HH11	2.05	0.54
1:D:172:GLU:O	1:D:176:THR:HG23	2.07	0.54
1:H:181:ARG:HG2	1:H:229:ARG:CG	2.37	0.54
1:I:209:ILE:N	1:I:210:PRO:HD2	2.22	0.54
1:J:69:ILE:HD12	1:J:72:ILE:CG2	2.37	0.54
1:J:170:ILE:O	1:J:174:ILE:HG22	2.08	0.54
1:A:135:MET:CB	1:A:137:LEU:CD1	2.85	0.54
1:H:70:ASN:OD1	1:H:78:THR:OG1	2.22	0.54
1:K:238:ASP:O	1:K:242:ILE:HG13	2.07	0.54
1:G:174:ILE:CD1	1:G:202:ALA:CB	2.85	0.54
1:G:230:LEU:CD2	1:G:256:TYR:CE1	2.86	0.54
1:G:288:LEU:HD13	1:G:325:LEU:HD23	1.90	0.54
1:L:17:THR:HG23	1:L:18:PRO:CD	2.34	0.54
1:L:132:LEU:HD23	1:L:172:GLU:OE1	2.07	0.54
1:D:296:TRP:CE3	1:D:347:MET:CE	2.91	0.54
1:E:116:ASP:OD1	1:F:211:ARG:NH1	2.37	0.54
1:E:319:GLU:O	1:E:323:ILE:HG13	2.07	0.54
1:F:8:LEU:O	1:F:27:HIS:CE1	2.54	0.54
1:G:184:LEU:HD22	1:G:226:ARG:HH21	1.73	0.54
1:H:13:PRO:HB2	1:H:15:ARG:O	2.08	0.54
1:B:9:MET:SD	1:B:24:MET:HB2	2.48	0.54
1:D:156:GLY:O	1:D:162:LYS:NZ	2.40	0.54
1:F:180:ASN:ND2	1:F:180:ASN:H	2.06	0.54
1:G:132:LEU:HD23	1:G:132:LEU:C	2.27	0.54
1:G:229:ARG:NE	1:G:229:ARG:HA	2.22	0.54
1:I:55:ILE:HD13	1:I:55:ILE:N	2.19	0.54
1:I:174:ILE:CG1	1:I:202:ALA:HB3	2.38	0.54
1:J:25:LEU:CD1	1:J:93:PHE:CE2	2.90	0.54
1:K:12:GLU:CD	1:K:57:ASN:H	2.11	0.54
1:K:171:ARG:NE	1:K:197:ILE:HD11	2.23	0.54
1:B:95:PRO:HD2	1:B:99:VAL:O	2.08	0.54
1:E:174:ILE:HG13	1:E:202:ALA:CB	2.37	0.54
1:G:6:ILE:C	1:G:6:ILE:HD12	2.28	0.54
1:J:95:PRO:HD2	1:J:99:VAL:O	2.07	0.54
1:C:251:THR:OG1	1:C:253:HIS:HD2	1.91	0.54
1:C:261:THR:HG21	1:C:267:THR:N	2.23	0.54
1:G:296:TRP:CZ3	1:G:347:MET:SD	3.01	0.54
1:G:355:PHE:HE2	1:G:365:TYR:HB2	1.73	0.54
1:J:102:ARG:NH1	1:J:127:THR:CG2	2.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:116:ASP:OD1	1:K:211:ARG:NH2	2.40	0.54
1:L:141:ILE:HG22	1:L:145:ILE:HD13	1.89	0.54
1:L:291:ILE:CD1	1:L:316:PHE:CE1	2.90	0.54
1:L:314:LEU:HD23	1:L:315:VAL:C	2.28	0.54
1:A:155:THR:HG21	1:A:267:THR:CG2	2.31	0.54
1:B:26:GLU:OE1	1:B:95:PRO:HB3	2.08	0.54
1:E:320:VAL:HG23	1:E:321:ARG:N	2.23	0.54
1:G:345:GLN:CG	1:G:349:TRP:CZ3	2.90	0.54
1:H:17:THR:OG1	1:H:20:PHE:HD2	1.90	0.54
1:H:121:THR:HG21	1:I:182:LYS:HZ1	1.73	0.54
1:J:296:TRP:CH2	1:J:347:MET:HE3	2.42	0.54
1:L:304:ASP:OD1	1:L:304:ASP:N	2.41	0.54
1:C:9:MET:HA	1:C:27:HIS:CE1	2.43	0.54
1:D:17:THR:OG1	1:D:20:PHE:HD2	1.91	0.54
1:D:65:LEU:HB3	1:D:118:ILE:HG12	1.89	0.54
1:H:119:GLN:OE1	1:I:205:SER:CB	2.55	0.54
1:J:191:GLU:OE2	1:J:192:PHE:HE1	1.91	0.54
1:J:365:TYR:CE2	1:J:369:ILE:CD1	2.84	0.54
1:B:5:ASN:CB	1:B:51:ARG:NH2	2.71	0.53
1:C:108:THR:HG21	1:D:222:ASN:HD21	1.73	0.53
1:F:361:SER:O	1:F:364:VAL:CG1	2.56	0.53
1:G:260:HIS:CD2	1:G:261:THR:HG23	2.43	0.53
1:I:293:LEU:HD13	1:I:315:VAL:HG22	1.90	0.53
1:J:104:ARG:NE	1:J:123:ARG:HH11	2.07	0.53
1:L:105:VAL:HG22	1:L:122:LEU:HG	1.90	0.53
1:L:352:LYS:HA	1:L:365:TYR:CE1	2.43	0.53
1:D:171:ARG:O	1:D:174:ILE:HG22	2.08	0.53
1:H:86:ASP:OD2	1:I:225:ARG:NH1	2.38	0.53
1:H:348:THR:CG2	1:H:372:ALA:HB3	2.39	0.53
1:I:10:PRO:HG2	1:I:11:ASP:OD1	2.08	0.53
1:K:349:TRP:O	1:K:353:MET:HG2	2.09	0.53
1:K:361:SER:HB2	1:K:364:VAL:CG2	2.37	0.53
1:D:125:ILE:CD1	1:D:126:PRO:HD2	2.38	0.53
1:F:38:ILE:HG12	1:F:44:ILE:HD13	1.90	0.53
1:G:296:TRP:CH2	1:G:347:MET:CE	2.90	0.53
1:J:86:ASP:OD1	1:J:87:ILE:N	2.41	0.53
1:H:198:GLU:OE1	1:H:198:GLU:HA	2.07	0.53
1:I:184:LEU:CG	1:I:228:PRO:HB3	2.39	0.53
1:J:171:ARG:O	1:J:174:ILE:HG22	2.09	0.53
1:K:349:TRP:CZ3	1:K:353:MET:HG3	2.43	0.53
1:A:94:ARG:NH1	1:A:97:ARG:HD2	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:THR:HG22	1:B:232:MET:HB3	1.91	0.53
1:B:352:LYS:CA	1:B:365:TYR:HE1	2.22	0.53
1:D:302:THR:OG1	1:D:306:ARG:O	2.19	0.53
1:D:312:GLU:HB2	1:D:347:MET:N	2.23	0.53
1:E:149:GLU:OE1	1:E:149:GLU:N	2.41	0.53
1:J:132:LEU:CD2	1:J:137:LEU:HD12	2.39	0.53
1:K:40:THR:CG2	1:K:65:LEU:CD2	2.80	0.53
1:L:188:SER:HB2	1:L:189:PRO:HD3	1.91	0.53
1:A:179:SER:HB2	1:A:181:ARG:NH2	2.24	0.53
1:A:355:PHE:HB2	1:A:360:ILE:HG21	1.90	0.53
1:G:203:VAL:HG12	1:L:39:GLN:HE22	1.74	0.53
1:H:125:ILE:CD1	1:H:126:PRO:HD2	2.29	0.53
1:H:370:ALA:O	1:H:371:GLY:C	2.47	0.53
1:I:355:PHE:CE2	1:I:362:GLU:CA	2.61	0.53
1:J:25:LEU:HD13	1:J:93:PHE:HE2	1.74	0.53
1:D:72:ILE:HD13	1:D:105:VAL:HG11	1.90	0.53
1:D:222:ASN:OD1	1:D:226:ARG:NH1	2.42	0.53
1:F:276:SER:O	1:F:280:ARG:HB2	2.09	0.53
1:F:291:ILE:HD11	1:F:316:PHE:CE1	2.42	0.53
1:H:102:ARG:CZ	1:H:193:VAL:CG2	2.87	0.53
1:H:229:ARG:O	1:H:229:ARG:HD3	2.09	0.53
1:I:7:ASN:C	1:I:8:LEU:HD12	2.29	0.53
1:A:21:MET:CE	1:A:72:ILE:HD11	2.39	0.53
1:D:184:LEU:HD22	1:D:226:ARG:HH21	1.73	0.53
1:F:285:ILE:HD12	1:F:285:ILE:N	2.24	0.53
1:G:94:ARG:HB3	1:G:100:ARG:HG2	1.89	0.53
1:G:144:ALA:CB	1:G:315:VAL:CG1	2.86	0.53
1:G:271:LEU:O	1:G:274:SER:OG	2.20	0.53
1:K:288:LEU:HB2	1:K:325:LEU:CD2	2.38	0.53
1:A:97:ARG:HG3	1:A:97:ARG:NH1	2.24	0.53
1:B:132:LEU:HB2	1:B:172:GLU:CG	2.39	0.53
1:C:197:ILE:N	1:C:197:ILE:CD1	2.71	0.53
1:C:300:VAL:CG1	1:C:301:PRO:HD2	2.39	0.53
1:D:100:ARG:HH21	1:D:100:ARG:HG3	1.74	0.53
1:D:145:ILE:HG12	1:D:169:ILE:HD12	1.91	0.53
1:D:248:ALA:O	1:D:253:HIS:HD2	1.92	0.53
1:J:209:ILE:O	1:J:213:LEU:N	2.35	0.53
1:K:34:SER:OG	1:K:35:ASP:OD1	2.13	0.53
1:A:94:ARG:NE	1:A:100:ARG:HG2	2.17	0.53
1:B:319:GLU:HG2	1:B:320:VAL:N	2.23	0.53
1:C:88:ASP:OD2	1:D:225:ARG:HD2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:TYR:CD2	1:C:219:GLY:HA3	2.43	0.53
1:G:28:ALA:CB	1:G:36:ILE:HD11	2.39	0.53
1:L:90:HIS:CD2	1:L:102:ARG:NH2	2.77	0.53
1:L:276:SER:O	1:L:280:ARG:HB2	2.09	0.53
1:A:28:ALA:CB	1:A:36:ILE:HD11	2.39	0.52
1:C:270:ARG:NH1	1:D:289:GLU:OE2	2.42	0.52
1:D:35:ASP:OD2	1:E:227:LYS:CD	2.56	0.52
1:H:261:THR:CG2	1:H:270:ARG:CD	2.87	0.52
1:I:184:LEU:CD1	1:I:228:PRO:HG3	2.33	0.52
1:J:40:THR:OG1	1:J:117:ALA:HB1	2.09	0.52
1:J:264:VAL:HG23	1:J:294:CYS:SG	2.48	0.52
1:K:21:MET:HE2	1:K:68:LEU:HG	1.91	0.52
1:K:111:LEU:CD1	1:L:90:HIS:CE1	2.92	0.52
1:K:121:THR:HG21	1:L:182:LYS:HZ1	1.74	0.52
1:K:155:THR:O	1:K:296:TRP:HA	2.08	0.52
1:K:319:GLU:O	1:K:323:ILE:HG13	2.08	0.52
1:C:171:ARG:HA	1:C:174:ILE:HG22	1.92	0.52
1:C:185:THR:HG22	1:C:232:MET:HB3	1.90	0.52
1:D:40:THR:HG23	1:D:65:LEU:HD22	1.84	0.52
1:D:248:ALA:O	1:D:251:THR:OG1	2.28	0.52
1:E:93:PHE:CD2	1:E:94:ARG:N	2.78	0.52
1:F:11:ASP:O	1:F:13:PRO:HD3	2.09	0.52
1:H:119:GLN:NE2	1:I:182:LYS:HE3	2.23	0.52
1:I:16:PHE:CZ	1:I:21:MET:N	2.77	0.52
1:I:230:LEU:HD11	1:I:256:TYR:CE1	2.42	0.52
1:J:16:PHE:CD2	1:J:60:LEU:HD11	2.44	0.52
1:L:132:LEU:CD2	1:L:172:GLU:OE1	2.58	0.52
1:L:141:ILE:HD11	1:L:313:TYR:CD1	2.45	0.52
1:A:25:LEU:HD23	1:A:36:ILE:HD13	1.91	0.52
1:G:260:HIS:CD2	1:G:261:THR:N	2.77	0.52
1:G:352:LYS:HA	1:G:355:PHE:CD2	2.45	0.52
1:I:355:PHE:HZ	1:I:362:GLU:HG2	1.63	0.52
1:J:212:HIS:O	1:J:213:LEU:HD23	2.09	0.52
1:K:116:ASP:N	1:K:116:ASP:OD1	2.43	0.52
1:K:188:SER:OG	1:K:189:PRO:HD3	2.08	0.52
1:B:24:MET:SD	1:B:25:LEU:HD23	2.49	0.52
1:C:21:MET:HE1	1:C:72:ILE:HD11	1.90	0.52
1:D:69:ILE:HD12	1:D:72:ILE:HG23	1.92	0.52
1:F:290:THR:O	1:F:292:ARG:NH2	2.43	0.52
1:H:19:VAL:HG23	1:H:20:PHE:H	1.73	0.52
1:H:68:LEU:N	1:H:68:LEU:CD2	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:183:VAL:HG13	1:H:230:LEU:HD22	1.91	0.52
1:I:302:THR:CG2	1:I:308:VAL:HB	2.39	0.52
1:J:263:GLY:HA3	1:J:266:GLU:HG2	1.92	0.52
1:A:185:THR:HG22	1:A:232:MET:HB3	1.92	0.52
1:A:208:GLU:CG	1:A:210:PRO:HD2	2.39	0.52
1:B:279:GLU:HG2	1:B:283:ARG:HG2	1.91	0.52
1:B:312:GLU:HB2	1:B:347:MET:N	2.25	0.52
1:C:17:THR:CG2	1:C:18:PRO:CD	2.87	0.52
1:G:180:ASN:HD22	1:G:180:ASN:H	1.57	0.52
1:H:99:VAL:HG12	1:H:100:ARG:N	2.24	0.52
1:H:137:LEU:HD11	1:H:311:ARG:CZ	2.39	0.52
1:K:23:ARG:NH1	1:K:26:GLU:OE2	2.42	0.52
1:L:186:TYR:HB3	1:L:209:ILE:CD1	2.40	0.52
1:G:131:LYS:CG	1:G:171:ARG:NH1	2.73	0.52
1:H:181:ARG:HG2	1:H:229:ARG:HG3	1.91	0.52
1:I:61:SER:N	1:I:64:GLU:OE1	2.41	0.52
1:K:292:ARG:HG3	1:K:292:ARG:NH2	2.20	0.52
1:L:291:ILE:HD13	1:L:316:PHE:CZ	2.44	0.52
1:B:337:ARG:CZ	1:B:341:ARG:NH1	2.73	0.52
1:F:9:MET:HA	1:F:27:HIS:CE1	2.45	0.52
1:A:17:THR:CG2	1:A:18:PRO:CD	2.88	0.52
1:A:263:GLY:O	1:A:267:THR:HG23	2.09	0.52
1:A:300:VAL:HG21	1:A:368:ILE:HD11	1.89	0.52
1:D:12:GLU:OE2	1:D:58:ARG:HB2	2.09	0.52
1:D:21:MET:O	1:D:25:LEU:HG	2.09	0.52
1:D:159:GLY:O	1:D:299:LEU:HD12	2.10	0.52
1:J:312:GLU:HB2	1:J:347:MET:N	2.25	0.52
1:K:90:HIS:CD2	1:K:104:ARG:HG3	2.45	0.52
1:D:40:THR:HG21	1:D:117:ALA:HB1	1.91	0.52
1:G:365:TYR:CE1	1:G:369:ILE:HD11	2.45	0.52
1:H:275:PHE:CD1	1:H:283:ARG:HG3	2.45	0.52
1:I:44:ILE:H	1:I:56:THR:CG2	2.23	0.52
1:I:119:GLN:HE22	1:J:182:LYS:HE2	1.74	0.52
1:J:263:GLY:HA3	1:J:266:GLU:CG	2.40	0.52
1:L:187:GLU:O	1:L:209:ILE:N	2.36	0.52
1:H:27:HIS:CD2	1:H:55:ILE:HG23	2.45	0.52
1:J:25:LEU:HD13	1:J:93:PHE:CE2	2.44	0.52
1:K:208:GLU:CG	1:K:210:PRO:HD2	2.39	0.52
1:K:333:THR:O	1:K:336:THR:HG23	2.10	0.52
1:A:205:SER:HB2	1:F:119:GLN:OE1	2.10	0.51
1:E:21:MET:HE1	1:E:68:LEU:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:21:MET:CE	1:G:68:LEU:HD22	2.40	0.51
1:H:27:HIS:CD2	1:H:55:ILE:CG2	2.93	0.51
1:I:184:LEU:CD1	1:I:228:PRO:CG	2.88	0.51
1:J:21:MET:O	1:J:25:LEU:HG	2.10	0.51
1:A:223:ALA:O	1:A:228:PRO:CD	2.59	0.51
1:C:319:GLU:O	1:C:323:ILE:HG13	2.10	0.51
1:D:44:ILE:HG22	1:D:55:ILE:HD11	1.91	0.51
1:E:154:ILE:CG2	1:E:165:LEU:HD23	2.39	0.51
1:E:297:GLN:NE2	1:E:311:ARG:NE	2.58	0.51
1:F:209:ILE:CG2	1:F:210:PRO:CD	2.87	0.51
1:G:25:LEU:HD23	1:G:36:ILE:HD13	1.91	0.51
1:G:270:ARG:NH2	1:H:286:ASP:OD1	2.38	0.51
1:H:119:GLN:HE22	1:I:182:LYS:CE	2.21	0.51
1:I:251:THR:OG1	1:I:253:HIS:HD2	1.92	0.51
1:K:365:TYR:HE1	1:K:369:ILE:HD11	1.76	0.51
1:L:70:ASN:OD1	1:L:78:THR:OG1	2.27	0.51
1:A:160:SER:O	1:A:299:LEU:HG	2.10	0.51
1:B:35:ASP:OD2	1:C:227:LYS:HD3	2.10	0.51
1:F:265:ALA:HB3	1:F:337:ARG:NH2	2.26	0.51
1:G:5:ASN:C	1:G:6:ILE:HG23	2.31	0.51
1:H:319:GLU:O	1:H:323:ILE:HG13	2.11	0.51
1:I:29:GLU:HG2	1:I:101:TYR:CZ	2.45	0.51
1:I:265:ALA:O	1:I:268:MET:HB2	2.11	0.51
1:I:345:GLN:HE21	1:I:350:ASP:HB2	1.76	0.51
1:L:40:THR:N	1:L:65:LEU:HD23	2.25	0.51
1:B:7:ASN:N	1:B:7:ASN:HD22	2.09	0.51
1:D:104:ARG:HD2	1:D:125:ILE:HD13	1.92	0.51
1:D:249:ALA:CB	1:D:290:THR:OG1	2.58	0.51
1:E:75:PRO:HD3	1:J:323:ILE:HD12	1.92	0.51
1:F:208:GLU:H	1:F:212:HIS:CD2	2.25	0.51
1:F:259:LEU:CD1	1:F:267:THR:HG23	2.40	0.51
1:F:314:LEU:HD11	1:F:339:LEU:HB3	1.92	0.51
1:F:336:THR:O	1:F:340:VAL:HG13	2.11	0.51
1:A:227:LYS:HE3	1:F:47:GLU:OE1	2.09	0.51
1:C:132:LEU:CB	1:C:172:GLU:HG3	2.39	0.51
1:D:125:ILE:HG13	1:D:126:PRO:HD2	1.93	0.51
1:F:360:ILE:HB	1:F:364:VAL:HG11	1.92	0.51
1:G:236:CYS:HB2	1:G:241:THR:OG1	2.10	0.51
1:A:38:ILE:CG2	1:A:60:LEU:HD22	2.41	0.51
1:B:99:VAL:HG12	1:B:100:ARG:H	1.75	0.51
1:B:194:TYR:CD2	1:B:204:VAL:HG11	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:273:THR:HG22	1:C:280:ARG:HH11	1.76	0.51
1:E:349:TRP:CH2	1:E:353:MET:HG3	2.45	0.51
1:G:174:ILE:CG1	1:G:202:ALA:HB1	2.40	0.51
1:G:352:LYS:HD2	1:G:365:TYR:OH	2.10	0.51
1:I:281:LEU:HD23	1:I:285:ILE:HD13	1.91	0.51
1:J:171:ARG:C	1:J:174:ILE:HG22	2.31	0.51
1:J:174:ILE:C	1:J:199:THR:HG21	2.31	0.51
1:J:200:ILE:HG23	1:J:201:SER:N	2.25	0.51
1:J:233:VAL:HB	1:J:257:THR:CG2	2.32	0.51
1:K:55:ILE:HG13	1:K:56:THR:HG23	1.92	0.51
1:A:92:GLU:HG2	1:A:102:ARG:HG2	1.90	0.51
1:B:360:ILE:HD12	1:B:365:TYR:HB2	1.92	0.51
1:C:263:GLY:O	1:C:267:THR:HG23	2.11	0.51
1:G:351:ALA:O	1:G:354:LYS:HB2	2.10	0.51
1:J:21:MET:O	1:J:24:MET:HB3	2.11	0.51
1:J:24:MET:HE3	1:J:25:LEU:CG	2.41	0.51
1:J:145:ILE:HD12	1:J:293:LEU:HD23	1.92	0.51
1:J:208:GLU:HB3	1:J:211:ARG:HB3	1.93	0.51
1:B:18:PRO:O	1:B:21:MET:HB3	2.11	0.51
1:C:230:LEU:HD11	1:C:256:TYR:CD1	2.45	0.51
1:C:248:ALA:O	1:C:251:THR:OG1	2.25	0.51
1:I:102:ARG:O	1:I:103:TYR:CD1	2.64	0.51
1:J:238:ASP:OD1	1:J:241:THR:OG1	2.15	0.51
1:J:352:LYS:N	1:J:365:TYR:HE1	2.09	0.51
1:L:296:TRP:CD1	1:L:347:MET:CE	2.94	0.51
1:A:142:ILE:O	1:A:145:ILE:HG13	2.11	0.51
1:B:6:ILE:HG23	1:B:54:LYS:HG3	1.91	0.51
1:B:272:VAL:HG13	1:B:284:THR:CG2	2.41	0.51
1:D:209:ILE:N	1:D:210:PRO:HD2	2.25	0.51
1:H:19:VAL:CG2	1:H:20:PHE:N	2.72	0.51
1:I:261:THR:HG21	1:I:267:THR:CB	2.41	0.51
1:J:132:LEU:HD21	1:J:137:LEU:HD12	1.92	0.51
1:K:288:LEU:HB2	1:K:325:LEU:HD21	1.92	0.51
1:L:87:ILE:HB	1:L:107:ALA:HB3	1.93	0.51
1:C:81:LEU:HD12	1:C:81:LEU:N	2.25	0.51
1:C:111:LEU:HD11	1:C:114:GLY:H	1.75	0.51
1:C:229:ARG:HG3	1:C:229:ARG:O	2.10	0.51
1:E:174:ILE:HD12	1:E:204:VAL:CG2	2.40	0.51
1:F:355:PHE:CZ	1:F:362:GLU:HG3	2.46	0.51
1:G:21:MET:HE1	1:G:72:ILE:HD11	1.91	0.51
1:I:9:MET:CE	1:I:12:GLU:HG3	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:115:HIS:N	1:L:115:HIS:CD2	2.79	0.51
1:A:223:ALA:O	1:A:228:PRO:HD3	2.11	0.50
1:D:6:ILE:HA	1:D:53:LEU:HD13	1.93	0.50
1:D:125:ILE:HD12	1:D:126:PRO:HD2	1.93	0.50
1:H:9:MET:CE	1:H:24:MET:HB2	2.42	0.50
1:H:188:SER:HG	1:H:189:PRO:HD3	1.70	0.50
1:H:240:GLU:H	1:H:240:GLU:CD	2.12	0.50
1:I:302:THR:CG2	1:I:308:VAL:CG1	2.89	0.50
1:I:353:MET:CG	1:I:357:GLN:NE2	2.74	0.50
1:A:363:ARG:HG3	1:A:364:VAL:N	2.26	0.50
1:D:248:ALA:HA	1:D:251:THR:OG1	2.11	0.50
1:G:355:PHE:HZ	1:G:365:TYR:HB3	1.76	0.50
1:G:367:LEU:HD23	1:G:367:LEU:C	2.32	0.50
1:H:229:ARG:CZ	1:H:229:ARG:HB2	2.41	0.50
1:J:123:ARG:NH2	1:K:225:ARG:O	2.44	0.50
1:J:264:VAL:HG23	1:J:294:CYS:CB	2.41	0.50
1:A:12:GLU:OE2	1:A:58:ARG:HB3	2.11	0.50
1:B:336:THR:O	1:B:340:VAL:HG13	2.12	0.50
1:D:105:VAL:HG22	1:D:122:LEU:HG	1.92	0.50
1:I:27:HIS:O	1:I:30:SER:HB3	2.12	0.50
1:L:73:TYR:CD1	1:L:87:ILE:CG2	2.94	0.50
1:L:291:ILE:HD11	1:L:316:PHE:CE1	2.47	0.50
1:A:158:THR:CG2	1:A:260:HIS:CE1	2.94	0.50
1:E:7:ASN:C	1:E:8:LEU:CG	2.79	0.50
1:E:9:MET:HG2	1:E:10:PRO:CD	2.41	0.50
1:E:332:VAL:HG23	1:E:333:THR:N	2.26	0.50
1:H:104:ARG:HD3	1:H:191:GLU:CD	2.31	0.50
1:I:24:MET:SD	1:I:25:LEU:CD2	2.96	0.50
1:J:24:MET:CE	1:J:25:LEU:CD2	2.89	0.50
1:J:264:VAL:HG11	1:J:340:VAL:HG11	1.94	0.50
1:J:348:THR:CG2	1:J:372:ALA:CB	2.90	0.50
1:K:137:LEU:HD23	1:K:141:ILE:HD11	1.94	0.50
1:K:171:ARG:NE	1:K:197:ILE:CD1	2.74	0.50
1:A:261:THR:HG21	1:A:267:THR:HA	1.93	0.50
1:A:261:THR:HG21	1:A:267:THR:CA	2.41	0.50
1:B:93:PHE:CD1	1:B:93:PHE:C	2.85	0.50
1:C:363:ARG:HG3	1:C:364:VAL:H	1.75	0.50
1:E:288:LEU:HB3	1:E:325:LEU:CD2	2.41	0.50
1:F:364:VAL:HG13	1:F:365:TYR:H	1.76	0.50
1:G:17:THR:CG2	1:G:18:PRO:CD	2.88	0.50
1:G:345:GLN:CB	1:G:349:TRP:HZ3	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:9:MET:HE3	1:H:24:MET:HA	1.93	0.50
1:H:251:THR:CG2	1:H:253:HIS:NE2	2.74	0.50
1:I:149:GLU:O	1:I:292:ARG:CD	2.57	0.50
1:J:24:MET:HE1	1:J:25:LEU:HD23	1.93	0.50
1:K:180:ASN:N	1:K:180:ASN:ND2	2.60	0.50
1:B:125:ILE:HG12	1:B:191:GLU:O	2.11	0.50
1:D:174:ILE:HG23	1:D:175:GLU:N	2.26	0.50
1:D:367:LEU:CD1	1:E:325:LEU:HD13	2.41	0.50
1:E:224:LEU:HD21	1:E:248:ALA:HA	1.94	0.50
1:G:291:ILE:CB	1:G:316:PHE:HD2	2.22	0.50
1:J:264:VAL:HG23	1:J:294:CYS:HB3	1.94	0.50
1:K:65:LEU:HD23	1:K:118:ILE:O	2.12	0.50
1:A:124:THR:C	1:A:125:ILE:HD13	2.32	0.50
1:B:188:SER:CB	1:B:189:PRO:CD	2.90	0.50
1:F:87:ILE:HB	1:F:107:ALA:HB3	1.92	0.50
1:F:102:ARG:C	1:F:125:ILE:HG22	2.32	0.50
1:G:369:ILE:O	1:G:372:ALA:N	2.43	0.50
1:H:17:THR:OG1	1:H:20:PHE:CD2	2.65	0.50
1:H:365:TYR:CE1	1:H:369:ILE:HD11	2.45	0.50
1:I:25:LEU:HD12	1:I:103:TYR:CE2	2.40	0.50
1:J:184:LEU:HD22	1:J:226:ARG:HH21	1.76	0.50
1:K:363:ARG:HA	1:K:366:LYS:HD2	1.85	0.50
1:B:360:ILE:CD1	1:B:365:TYR:HB2	2.41	0.50
1:C:230:LEU:CD1	1:C:256:TYR:CE1	2.95	0.50
1:E:155:THR:HG21	1:E:267:THR:HG21	1.94	0.50
1:G:135:MET:CE	1:G:135:MET:CA	2.89	0.50
1:H:137:LEU:CD1	1:H:311:ARG:CZ	2.90	0.50
1:I:17:THR:CG2	1:I:18:PRO:CD	2.88	0.50
1:I:300:VAL:O	1:I:308:VAL:HG12	2.11	0.50
1:J:16:PHE:CZ	1:J:44:ILE:CD1	2.95	0.50
1:L:275:PHE:CD2	1:L:283:ARG:CB	2.95	0.50
1:A:312:GLU:HB2	1:A:347:MET:N	2.26	0.50
1:B:99:VAL:HG12	1:B:100:ARG:N	2.27	0.50
1:B:135:MET:HB3	1:B:137:LEU:HD13	1.92	0.50
1:C:40:THR:HG23	1:C:65:LEU:HD22	1.91	0.50
1:I:154:ILE:HD13	1:I:166:LEU:HD21	1.94	0.50
1:K:276:SER:HA	1:K:280:ARG:CD	2.35	0.50
1:L:310:LEU:CD2	1:L:354:LYS:HG3	2.41	0.50
1:A:21:MET:HE1	1:A:72:ILE:HD11	1.93	0.49
1:A:324:LEU:HD21	1:A:336:THR:HG23	1.94	0.49
1:B:146:ALA:HB2	1:B:173:LEU:HD21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:29:GLU:CG	1:E:101:TYR:HE2	2.16	0.49
1:F:17:THR:HG22	1:F:19:VAL:H	1.76	0.49
1:H:184:LEU:HD22	1:H:205:SER:OG	2.12	0.49
1:H:320:VAL:CG1	1:H:339:LEU:HD13	2.41	0.49
1:I:25:LEU:HD22	1:I:36:ILE:HD13	1.93	0.49
1:I:28:ALA:CB	1:I:36:ILE:HD11	2.42	0.49
1:I:81:LEU:HD23	1:I:118:ILE:HG12	1.94	0.49
1:J:17:THR:CG2	1:J:18:PRO:CD	2.90	0.49
1:J:17:THR:HG22	1:J:18:PRO:CD	2.41	0.49
1:J:264:VAL:HG11	1:J:340:VAL:CG1	2.42	0.49
1:L:296:TRP:HE1	1:L:347:MET:HE2	1.73	0.49
1:A:17:THR:HG23	1:A:18:PRO:CD	2.35	0.49
1:A:184:LEU:HD22	1:A:226:ARG:HH21	1.77	0.49
1:A:319:GLU:O	1:A:323:ILE:HG13	2.12	0.49
1:C:258:THR:O	1:C:259:LEU:HD12	2.12	0.49
1:D:104:ARG:NE	1:D:123:ARG:NH1	2.60	0.49
1:E:288:LEU:HD23	1:E:325:LEU:HD23	1.94	0.49
1:E:354:LYS:HE2	1:E:357:GLN:HG3	1.93	0.49
1:G:56:THR:HG22	1:G:58:ARG:H	1.76	0.49
1:G:145:ILE:HD12	1:G:146:ALA:N	2.27	0.49
1:G:180:ASN:H	1:G:180:ASN:ND2	2.09	0.49
1:J:86:ASP:HB2	1:K:213:LEU:HD21	1.93	0.49
1:J:236:CYS:SG	1:J:259:LEU:HD11	2.53	0.49
1:K:269:ARG:HG3	1:K:333:THR:HG21	1.94	0.49
1:A:230:LEU:HD13	1:A:230:LEU:C	2.31	0.49
1:A:246:LEU:O	1:A:250:LEU:HG	2.12	0.49
1:C:188:SER:HB3	1:C:189:PRO:HD3	1.94	0.49
1:E:275:PHE:O	1:E:280:ARG:CG	2.60	0.49
1:G:42:GLU:OE1	1:H:203:VAL:HG13	2.11	0.49
1:G:89:THR:CG2	1:G:90:HIS:N	2.71	0.49
1:G:174:ILE:HG13	1:G:202:ALA:CB	2.43	0.49
1:G:269:ARG:CG	1:G:269:ARG:NH1	2.68	0.49
1:H:340:VAL:O	1:H:344:GLY:N	2.44	0.49
1:K:171:ARG:HE	1:K:197:ILE:HD11	1.78	0.49
1:K:173:LEU:CD2	1:K:181:ARG:NH1	2.75	0.49
1:A:12:GLU:OE1	1:A:56:THR:CG2	2.52	0.49
1:B:155:THR:CG2	1:B:259:LEU:HB2	2.26	0.49
1:C:152:VAL:HG13	1:C:293:LEU:CD1	2.41	0.49
1:D:92:GLU:OE2	1:D:102:ARG:NE	2.45	0.49
1:D:320:VAL:CG1	1:D:339:LEU:HD13	2.42	0.49
1:F:13:PRO:HG3	1:F:20:PHE:CG	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:248:ALA:O	1:F:251:THR:OG1	2.28	0.49
1:J:24:MET:HE1	1:J:25:LEU:CD2	2.41	0.49
1:K:312:GLU:HB2	1:K:347:MET:N	2.28	0.49
1:A:306:ARG:HG2	1:A:307:ARG:N	2.27	0.49
1:E:154:ILE:HG22	1:E:162:LYS:HB2	1.94	0.49
1:F:49:TYR:HD1	1:F:50:GLY:H	1.56	0.49
1:G:185:THR:HG22	1:G:232:MET:HB3	1.94	0.49
1:H:340:VAL:HG23	1:H:346:LEU:HD21	1.93	0.49
1:I:16:PHE:CE2	1:I:21:MET:HA	2.47	0.49
1:L:209:ILE:HG21	1:L:216:PHE:CE1	2.47	0.49
1:C:312:GLU:HB2	1:C:347:MET:N	2.27	0.49
1:D:314:LEU:HB2	1:D:340:VAL:HG12	1.93	0.49
1:G:102:ARG:HH21	1:G:125:ILE:HG21	1.75	0.49
1:H:233:VAL:HB	1:H:257:THR:CG2	2.32	0.49
1:J:15:ARG:HB3	1:J:15:ARG:HH21	1.78	0.49
1:D:148:GLN:O	1:D:254:PRO:HD3	2.13	0.49
1:D:171:ARG:HA	1:D:174:ILE:HG22	1.94	0.49
1:G:38:ILE:CG2	1:G:60:LEU:HD22	2.42	0.49
1:G:291:ILE:CB	1:G:316:PHE:CD2	2.95	0.49
1:H:66:GLY:O	1:H:69:ILE:HG22	2.12	0.49
1:H:86:ASP:OD1	1:I:222:ASN:ND2	2.45	0.49
1:I:269:ARG:HG3	1:I:333:THR:HG21	1.93	0.49
1:J:105:VAL:HG22	1:J:122:LEU:HG	1.95	0.49
1:J:296:TRP:CZ3	1:J:347:MET:HE3	2.48	0.49
1:J:361:SER:HB3	1:J:364:VAL:HG23	1.94	0.49
1:L:90:HIS:CD2	1:L:102:ARG:HH22	2.31	0.49
1:L:197:ILE:HG22	1:L:197:ILE:O	2.12	0.49
1:A:97:ARG:HD2	1:A:97:ARG:O	2.12	0.49
1:B:366:LYS:HD3	1:B:366:LYS:C	2.33	0.49
1:E:137:LEU:HD23	1:E:141:ILE:HD11	1.95	0.49
1:E:317:ASP:O	1:E:320:VAL:HG22	2.13	0.49
1:K:42:GLU:OE1	1:K:43:PRO:HD2	2.13	0.49
1:L:156:GLY:O	1:L:260:HIS:HA	2.12	0.49
1:L:170:ILE:HG22	1:L:174:ILE:CD1	2.43	0.49
1:A:55:ILE:CG2	1:A:55:ILE:O	2.60	0.49
1:B:73:TYR:O	1:B:77:ALA:HB2	2.12	0.49
1:F:335:ALA:O	1:F:339:LEU:CD2	2.54	0.49
1:G:47:GLU:HG3	1:G:52:LEU:CD2	2.42	0.49
1:G:354:LYS:HB3	1:G:360:ILE:HD12	1.93	0.49
1:H:95:PRO:HG2	1:H:97:ARG:HH11	1.76	0.49
1:J:76:ASN:O	1:J:79:THR:OG1	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:224:LEU:HD21	1:K:248:ALA:HA	1.94	0.49
1:L:305:GLU:CG	1:L:305:GLU:O	2.61	0.49
1:A:154:ILE:CG2	1:A:162:LYS:HB3	2.42	0.49
1:B:259:LEU:CD1	1:B:267:THR:HG23	2.43	0.49
1:C:81:LEU:N	1:C:81:LEU:CD1	2.75	0.49
1:F:17:THR:OG1	1:H:362:GLU:OE2	2.31	0.49
1:I:281:LEU:HD23	1:I:285:ILE:CD1	2.43	0.49
1:J:51:ARG:HA	1:K:180:ASN:OD1	2.12	0.49
1:J:148:GLN:O	1:J:254:PRO:HD3	2.13	0.49
1:K:155:THR:HG21	1:K:267:THR:HG21	1.94	0.49
1:L:335:ALA:O	1:L:339:LEU:HD23	2.12	0.49
1:A:108:THR:HG23	1:B:213:LEU:HD11	1.95	0.48
1:E:91:TYR:OH	1:J:338:LYS:NZ	2.46	0.48
1:E:162:LYS:HG2	1:E:163:SER:N	2.28	0.48
1:F:137:LEU:HD11	1:F:311:ARG:NH2	2.28	0.48
1:F:233:VAL:HB	1:F:257:THR:CG2	2.34	0.48
1:G:69:ILE:CD1	1:G:120:ILE:HG12	2.38	0.48
1:H:17:THR:HG1	1:H:20:PHE:HD2	1.58	0.48
1:J:166:LEU:CD2	1:J:256:TYR:HB3	2.42	0.48
1:K:91:TYR:CE1	1:K:93:PHE:CD2	3.01	0.48
1:K:126:PRO:HB2	1:K:192:PHE:CE1	2.48	0.48
1:B:119:GLN:HE22	1:C:226:ARG:HD2	1.77	0.48
1:B:164:THR:OG1	1:B:165:LEU:N	2.46	0.48
1:B:337:ARG:NE	1:B:341:ARG:HH11	2.11	0.48
1:F:27:HIS:HE2	1:F:31:LEU:HD11	1.77	0.48
1:F:73:TYR:HD1	1:F:89:THR:HG21	1.65	0.48
1:H:229:ARG:HH21	1:H:229:ARG:CG	2.25	0.48
1:I:109:ALA:CB	1:J:212:HIS:ND1	2.76	0.48
1:J:199:THR:CG2	1:J:202:ALA:CB	2.87	0.48
1:K:172:GLU:OE1	1:K:172:GLU:HA	2.13	0.48
1:L:170:ILE:HG22	1:L:174:ILE:HD12	1.94	0.48
1:A:111:LEU:HD12	1:A:115:HIS:O	2.13	0.48
1:A:297:GLN:HE21	1:A:311:ARG:CZ	2.25	0.48
1:C:119:GLN:HE22	1:D:182:LYS:CE	2.25	0.48
1:C:300:VAL:HG12	1:C:301:PRO:HD2	1.95	0.48
1:C:360:ILE:HG23	1:C:364:VAL:HB	1.95	0.48
1:E:64:GLU:O	1:E:68:LEU:HD13	2.12	0.48
1:F:345:GLN:HG3	1:F:349:TRP:CE3	2.43	0.48
1:G:203:VAL:CG1	1:L:39:GLN:NE2	2.76	0.48
1:H:33:ALA:HA	1:H:48:VAL:HA	1.96	0.48
1:H:45:PHE:CE2	1:I:203:VAL:HG22	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:188:SER:HB3	1:I:189:PRO:HD3	1.95	0.48
1:L:17:THR:HG22	1:L:19:VAL:H	1.77	0.48
1:D:171:ARG:CA	1:D:174:ILE:HG22	2.44	0.48
1:E:300:VAL:HG13	1:E:364:VAL:HG11	1.95	0.48
1:H:128:THR:CG2	1:H:196:GLU:HG3	2.42	0.48
1:J:125:ILE:HD12	1:J:126:PRO:CD	2.42	0.48
1:K:39:GLN:C	1:K:65:LEU:HD21	2.33	0.48
1:K:262:SER:HB2	1:K:296:TRP:CE2	2.48	0.48
1:L:132:LEU:CD1	1:L:169:ILE:CD1	2.89	0.48
1:A:92:GLU:OE1	1:A:102:ARG:NH2	2.44	0.48
1:A:108:THR:HG21	1:B:226:ARG:HH12	1.78	0.48
1:D:44:ILE:CG2	1:D:55:ILE:HD11	2.43	0.48
1:F:284:THR:O	1:F:288:LEU:HD23	2.13	0.48
1:G:131:LYS:O	1:G:134:THR:HB	2.12	0.48
1:G:142:ILE:O	1:G:145:ILE:HG13	2.14	0.48
1:G:360:ILE:HG22	1:G:361:SER:N	2.28	0.48
1:H:6:ILE:O	1:H:7:ASN:ND2	2.46	0.48
1:I:355:PHE:HZ	1:I:362:GLU:CG	2.24	0.48
1:J:209:ILE:HG22	1:J:210:PRO:N	2.29	0.48
1:L:48:VAL:CG1	1:L:49:TYR:CD2	2.90	0.48
1:C:111:LEU:HD22	1:C:115:HIS:O	2.13	0.48
1:C:268:MET:SD	1:C:291:ILE:CD1	3.01	0.48
1:D:297:GLN:OE1	1:D:311:ARG:NE	2.46	0.48
1:E:312:GLU:HB2	1:E:347:MET:N	2.27	0.48
1:G:174:ILE:HD11	1:G:202:ALA:CB	2.32	0.48
1:J:40:THR:HG23	1:J:62:ASN:N	2.29	0.48
1:J:69:ILE:HD12	1:J:72:ILE:HG23	1.96	0.48
1:J:72:ILE:CD1	1:J:105:VAL:HG21	2.40	0.48
1:J:353:MET:HE2	1:J:353:MET:N	2.29	0.48
1:L:149:GLU:CG	1:L:150:GLY:N	2.73	0.48
1:F:158:THR:HB	1:F:260:HIS:HE1	1.78	0.48
1:F:365:TYR:CE2	1:F:369:ILE:HD11	2.49	0.48
1:G:157:ALA:O	1:G:162:LYS:NZ	2.46	0.48
1:H:21:MET:O	1:H:25:LEU:HG	2.14	0.48
1:H:251:THR:HG22	1:H:253:HIS:NE2	2.27	0.48
1:J:35:ASP:OD2	1:K:227:LYS:HD2	2.13	0.48
1:K:259:LEU:HD11	1:K:271:LEU:HD21	1.96	0.48
1:A:194:TYR:CD2	1:A:204:VAL:HG11	2.48	0.48
1:A:297:GLN:HG3	1:A:311:ARG:CG	2.44	0.48
1:D:366:LYS:HA	1:D:369:ILE:HG22	1.93	0.48
1:E:182:LYS:NZ	1:E:226:ARG:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:247:GLU:O	1:E:251:THR:OG1	2.31	0.48
1:G:55:ILE:CG2	1:G:55:ILE:O	2.62	0.48
1:G:193:VAL:HG21	1:G:195:ASP:OD2	2.13	0.48
1:H:170:ILE:O	1:H:174:ILE:HG12	2.14	0.48
1:I:16:PHE:HZ	1:I:21:MET:HA	1.79	0.48
1:K:60:LEU:HB3	1:K:65:LEU:CD1	2.44	0.48
1:K:91:TYR:HE1	1:K:93:PHE:CD2	2.31	0.48
1:L:112:VAL:CG2	1:L:117:ALA:HB2	2.19	0.48
1:A:94:ARG:HE	1:A:100:ARG:CG	2.19	0.48
1:B:223:ALA:O	1:B:228:PRO:HD3	2.13	0.48
1:C:188:SER:CB	1:C:189:PRO:CD	2.92	0.48
1:E:126:PRO:O	1:E:191:GLU:O	2.31	0.48
1:F:135:MET:CB	1:F:137:LEU:HD13	2.43	0.48
1:G:21:MET:SD	1:G:68:LEU:HD22	2.54	0.48
1:J:40:THR:CG2	1:J:62:ASN:CA	2.92	0.48
1:J:209:ILE:HD13	1:J:209:ILE:HA	1.71	0.48
1:K:189:PRO:HD2	1:K:189:PRO:O	2.14	0.48
1:K:336:THR:O	1:K:340:VAL:HG23	2.14	0.48
1:L:93:PHE:CE2	1:L:103:TYR:HE2	2.32	0.48
1:A:353:MET:HG3	1:A:357:GLN:HE21	1.78	0.48
1:B:55:ILE:O	1:B:55:ILE:CG2	2.62	0.48
1:D:366:LYS:O	1:D:369:ILE:CG2	2.59	0.48
1:F:48:VAL:O	1:F:49:TYR:CD2	2.66	0.48
1:F:182:LYS:HG3	1:F:203:VAL:HG13	1.96	0.48
1:F:291:ILE:HD13	1:F:316:PHE:CE2	2.49	0.48
1:G:193:VAL:HG22	1:G:195:ASP:H	1.79	0.48
1:K:300:VAL:CG1	1:K:301:PRO:HD2	2.42	0.48
1:A:329:PRO:O	1:A:332:VAL:HG13	2.14	0.47
1:B:268:MET:HG3	1:B:336:THR:HG21	1.96	0.47
1:C:166:LEU:HD22	1:C:232:MET:HE1	1.96	0.47
1:D:349:TRP:CZ3	1:D:353:MET:HE2	2.49	0.47
1:E:148:GLN:O	1:E:254:PRO:HD3	2.14	0.47
1:E:215:ASN:HD22	1:E:218:ASP:HB2	1.78	0.47
1:G:296:TRP:CZ3	1:G:347:MET:CE	2.96	0.47
1:G:313:TYR:CE2	1:G:345:GLN:CD	2.87	0.47
1:I:174:ILE:HG23	1:I:175:GLU:N	2.28	0.47
1:I:365:TYR:CZ	1:I:369:ILE:HD11	2.49	0.47
1:J:158:THR:HA	1:J:162:LYS:HZ1	1.79	0.47
1:B:42:GLU:OE1	1:C:203:VAL:HG13	2.14	0.47
1:C:92:GLU:HG2	1:C:93:PHE:N	2.29	0.47
1:D:94:ARG:CB	1:D:100:ARG:NE	2.74	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:329:PRO:O	1:G:332:VAL:HG22	2.14	0.47
1:G:365:TYR:HA	1:G:368:ILE:HD13	1.96	0.47
1:H:88:ASP:OD2	1:I:225:ARG:NE	2.47	0.47
1:J:190:ILE:HG22	1:J:190:ILE:O	2.13	0.47
1:K:171:ARG:C	1:K:174:ILE:CG2	2.82	0.47
1:L:7:ASN:O	1:L:54:LYS:O	2.31	0.47
1:A:302:THR:OG1	1:A:306:ARG:O	2.29	0.47
1:B:100:ARG:NE	1:B:102:ARG:NH1	2.56	0.47
1:B:365:TYR:CD2	1:B:365:TYR:C	2.87	0.47
1:C:209:ILE:H	1:C:210:PRO:HD2	1.80	0.47
1:G:69:ILE:HD12	1:G:107:ALA:HB2	1.96	0.47
1:G:155:THR:HG23	1:G:259:LEU:C	2.35	0.47
1:G:362:GLU:HG2	1:G:366:LYS:HE2	1.96	0.47
1:H:27:HIS:HD2	1:H:55:ILE:HG21	1.79	0.47
1:I:11:ASP:OD1	1:I:11:ASP:N	2.48	0.47
1:J:40:THR:CG2	1:J:62:ASN:HA	2.43	0.47
1:J:184:LEU:HG	1:J:228:PRO:HB3	1.95	0.47
1:J:348:THR:CG2	1:J:372:ALA:HB2	2.45	0.47
1:A:278:GLU:OE2	1:F:266:GLU:HG3	2.14	0.47
1:A:365:TYR:CD2	1:A:369:ILE:HD11	2.49	0.47
1:E:288:LEU:CD2	1:E:325:LEU:HD23	2.45	0.47
1:F:44:ILE:HB	1:F:56:THR:CG2	2.45	0.47
1:K:160:SER:N	2:K:401:PO4:O1	2.36	0.47
1:K:230:LEU:HD23	1:K:230:LEU:C	2.35	0.47
1:K:285:ILE:HD12	1:K:285:ILE:N	2.28	0.47
1:A:81:LEU:HD12	1:A:118:ILE:HG12	1.95	0.47
1:C:281:LEU:HD23	1:C:285:ILE:CD1	2.44	0.47
1:H:211:ARG:HD2	1:H:212:HIS:CE1	2.48	0.47
1:H:314:LEU:HD13	1:H:340:VAL:HA	1.97	0.47
1:I:114:GLY:N	1:J:92:GLU:OE1	2.47	0.47
1:I:184:LEU:HD11	1:I:228:PRO:HB3	1.96	0.47
1:I:265:ALA:HB3	1:I:266:GLU:OE1	2.14	0.47
1:I:319:GLU:O	1:I:323:ILE:HG13	2.15	0.47
1:K:34:SER:O	1:K:124:THR:HG23	2.15	0.47
1:L:8:LEU:O	1:L:27:HIS:CE1	2.68	0.47
1:L:190:ILE:CG1	1:L:208:GLU:CG	2.86	0.47
1:A:332:VAL:HG23	1:A:333:THR:H	1.79	0.47
1:C:197:ILE:CD1	1:C:197:ILE:H	2.26	0.47
1:G:235:GLU:HG3	1:G:235:GLU:O	2.14	0.47
1:G:297:GLN:HE22	1:G:311:ARG:HH21	1.62	0.47
1:J:195:ASP:O	1:J:198:GLU:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:24:MET:SD	1:K:44:ILE:CD1	3.01	0.47
1:K:119:GLN:HE21	1:K:121:THR:CG2	2.26	0.47
1:A:40:THR:HG23	1:A:65:LEU:HD22	1.93	0.47
1:C:236:CYS:SG	1:C:242:ILE:HG13	2.55	0.47
1:F:24:MET:SD	1:F:44:ILE:CD1	2.90	0.47
1:F:102:ARG:HB3	1:F:125:ILE:CG2	2.45	0.47
1:F:105:VAL:HG22	1:F:122:LEU:HG	1.96	0.47
1:F:334:SER:HA	1:F:337:ARG:HG3	1.97	0.47
1:G:131:LYS:HG2	1:G:171:ARG:NH1	2.29	0.47
1:G:369:ILE:HG22	1:G:370:ALA:N	2.30	0.47
1:H:6:ILE:HD13	1:H:54:LYS:HD2	1.97	0.47
1:I:13:PRO:CB	1:I:20:PHE:CE2	2.86	0.47
1:I:24:MET:HE1	1:I:44:ILE:HG21	1.96	0.47
1:I:224:LEU:HD21	1:I:248:ALA:HA	1.96	0.47
1:I:229:ARG:HG3	1:I:229:ARG:O	2.15	0.47
1:I:235:GLU:OE1	1:I:260:HIS:CE1	2.67	0.47
1:K:17:THR:CG2	1:K:18:PRO:CD	2.93	0.47
1:K:25:LEU:HD13	1:K:93:PHE:CZ	2.49	0.47
1:L:41:GLY:C	1:L:42:GLU:HG2	2.34	0.47
1:L:175:GLU:HA	1:L:199:THR:HG21	1.96	0.47
1:L:183:VAL:CG1	1:L:230:LEU:HD22	2.31	0.47
1:A:48:VAL:HG12	1:A:49:TYR:HD2	1.80	0.47
1:A:56:THR:HG22	1:A:58:ARG:H	1.80	0.47
1:A:112:VAL:HG23	1:A:117:ALA:HB3	1.96	0.47
1:A:261:THR:HG21	1:A:266:GLU:C	2.35	0.47
1:B:9:MET:HE1	1:B:24:MET:CB	2.44	0.47
1:B:374:GLU:CB	1:C:281:LEU:CD2	2.88	0.47
1:C:9:MET:HB2	1:C:10:PRO:HD2	1.97	0.47
1:D:240:GLU:HA	1:D:240:GLU:OE2	2.15	0.47
1:F:310:LEU:CD1	1:F:368:ILE:CD1	2.92	0.47
1:G:362:GLU:OE1	1:G:366:LYS:HE3	2.15	0.47
1:H:166:LEU:HD13	1:H:232:MET:SD	2.54	0.47
1:I:21:MET:HE2	1:I:68:LEU:HD22	1.95	0.47
1:K:333:THR:O	1:K:336:THR:CG2	2.62	0.47
1:K:363:ARG:CA	1:K:366:LYS:CD	2.71	0.47
1:L:135:MET:HB2	1:L:137:LEU:HD13	1.97	0.47
1:B:337:ARG:HG2	1:B:341:ARG:NH1	2.30	0.47
1:C:141:ILE:O	1:C:145:ILE:HG23	2.15	0.47
1:C:329:PRO:O	1:C:332:VAL:HG23	2.15	0.47
1:H:14:THR:C	1:H:15:ARG:HE	2.03	0.47
1:H:302:THR:OG1	1:H:306:ARG:O	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:364:VAL:HA	1:H:367:LEU:HD12	1.97	0.47
1:I:329:PRO:CA	1:I:332:VAL:HG23	2.36	0.47
1:J:283:ARG:O	1:J:287:ILE:HG13	2.15	0.47
1:A:213:LEU:HD13	1:A:219:GLY:HA2	1.96	0.47
1:A:281:LEU:HD13	1:A:285:ILE:HD11	1.97	0.47
1:C:93:PHE:CE1	1:C:101:TYR:HB2	2.50	0.47
1:D:92:GLU:HA	1:D:101:TYR:O	2.15	0.47
1:G:238:ASP:O	1:G:242:ILE:CD1	2.63	0.47
1:J:40:THR:N	1:J:65:LEU:HD22	2.30	0.47
1:K:148:GLN:HB3	1:K:149:GLU:OE1	2.15	0.47
1:B:119:GLN:HE22	1:C:226:ARG:CD	2.28	0.46
1:B:272:VAL:HG21	1:B:332:VAL:HG11	1.97	0.46
1:C:268:MET:HG3	1:C:336:THR:HG21	1.97	0.46
1:D:40:THR:O	1:D:60:LEU:O	2.31	0.46
1:F:17:THR:CG2	1:F:18:PRO:CD	2.92	0.46
1:H:220:VAL:O	1:H:223:ALA:N	2.49	0.46
1:J:104:ARG:NE	1:J:123:ARG:NH1	2.62	0.46
1:J:174:ILE:CG2	1:J:175:GLU:N	2.78	0.46
1:K:40:THR:N	1:K:65:LEU:CD2	2.78	0.46
1:K:223:ALA:O	1:K:228:PRO:CD	2.62	0.46
1:B:39:GLN:C	1:B:65:LEU:HD21	2.36	0.46
1:E:261:THR:OG1	1:E:267:THR:CG2	2.49	0.46
1:F:102:ARG:HB3	1:F:125:ILE:HG23	1.96	0.46
1:F:236:CYS:SG	1:F:242:ILE:HG13	2.54	0.46
1:G:94:ARG:HD3	1:G:97:ARG:HA	1.98	0.46
1:G:111:LEU:CD2	1:H:90:HIS:CE1	2.97	0.46
1:G:193:VAL:HG22	1:G:194:TYR:N	2.31	0.46
1:G:318:GLU:CG	1:L:363:ARG:NH2	2.74	0.46
1:H:270:ARG:HH11	1:H:270:ARG:HG3	1.79	0.46
1:I:64:GLU:O	1:I:68:LEU:HD12	2.15	0.46
1:I:137:LEU:CD2	1:I:311:ARG:NH1	2.76	0.46
1:I:273:THR:HG22	1:I:280:ARG:HH11	1.80	0.46
1:K:261:THR:OG1	1:K:267:THR:CG2	2.49	0.46
1:L:148:GLN:O	1:L:254:PRO:HD3	2.15	0.46
1:L:184:LEU:HD11	1:L:226:ARG:HB2	1.97	0.46
1:L:190:ILE:CD1	1:L:208:GLU:HG2	2.45	0.46
1:L:291:ILE:HD13	1:L:316:PHE:CE1	2.49	0.46
1:A:137:LEU:HD23	1:A:141:ILE:CG2	2.45	0.46
1:C:86:ASP:OD1	1:C:87:ILE:N	2.48	0.46
1:F:291:ILE:CD1	1:F:316:PHE:CZ	2.99	0.46
1:J:108:THR:HB	1:K:226:ARG:NH1	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:173:LEU:HD22	1:K:181:ARG:NH1	2.29	0.46
1:L:90:HIS:H	1:L:90:HIS:HD1	1.62	0.46
1:B:48:VAL:O	1:B:48:VAL:CG2	2.63	0.46
1:C:182:LYS:HE2	1:C:226:ARG:O	2.16	0.46
1:D:264:VAL:HG13	1:D:265:ALA:N	2.31	0.46
1:F:182:LYS:HZ3	1:F:184:LEU:HD21	1.81	0.46
1:G:297:GLN:NE2	1:G:311:ARG:HE	2.13	0.46
1:H:19:VAL:CG2	1:H:20:PHE:H	2.29	0.46
1:H:39:GLN:HA	1:H:65:LEU:HD21	1.98	0.46
1:I:109:ALA:HB1	1:J:212:HIS:ND1	2.30	0.46
1:L:27:HIS:CD2	1:L:31:LEU:CD1	2.98	0.46
1:B:260:HIS:HE1	1:C:221:ARG:NH2	2.14	0.46
1:G:260:HIS:CD2	1:G:261:THR:HG22	2.49	0.46
1:H:40:THR:N	1:H:65:LEU:CD2	2.78	0.46
1:J:48:VAL:HG12	1:J:49:TYR:CD2	2.49	0.46
1:B:158:THR:HG22	1:C:247:GLU:CD	2.36	0.46
1:C:60:LEU:HB3	1:C:65:LEU:CD1	2.46	0.46
1:D:269:ARG:O	1:D:273:THR:HG23	2.16	0.46
1:D:337:ARG:O	1:D:340:VAL:HG22	2.15	0.46
1:E:316:PHE:HA	1:E:320:VAL:CG2	2.40	0.46
1:H:229:ARG:CG	1:H:229:ARG:NH2	2.79	0.46
1:H:366:LYS:HE3	1:H:366:LYS:HB3	1.72	0.46
1:I:43:PRO:CB	1:I:56:THR:HG23	2.45	0.46
1:I:47:GLU:HB2	1:I:52:LEU:CD2	2.46	0.46
1:J:16:PHE:CZ	1:J:44:ILE:HD12	2.50	0.46
1:J:39:GLN:NE2	1:J:119:GLN:HG3	2.20	0.46
1:J:72:ILE:CD1	1:J:105:VAL:HG11	2.43	0.46
1:K:173:LEU:CD2	1:K:181:ARG:CZ	2.87	0.46
1:B:335:ALA:HA	1:B:338:LYS:HD3	1.98	0.46
1:E:39:GLN:C	1:E:65:LEU:HD21	2.35	0.46
1:F:141:ILE:HD11	1:F:313:TYR:CE2	2.51	0.46
1:G:131:LYS:HG3	1:G:171:ARG:NH1	2.31	0.46
1:I:7:ASN:OD1	1:I:27:HIS:CE1	2.68	0.46
1:I:13:PRO:HD3	1:I:20:PHE:CD1	2.51	0.46
1:I:355:PHE:HE2	1:I:362:GLU:CB	2.27	0.46
1:J:13:PRO:CG	1:J:20:PHE:CD1	2.97	0.46
1:A:235:GLU:OE1	1:A:260:HIS:NE2	2.48	0.46
1:B:135:MET:CB	1:B:137:LEU:HD13	2.46	0.46
1:C:119:GLN:NE2	1:D:182:LYS:HE2	2.28	0.46
1:G:297:GLN:NE2	1:G:311:ARG:NE	2.64	0.46
1:J:175:GLU:HG3	1:J:197:ILE:HG21	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:320:VAL:CG1	1:J:339:LEU:HD13	2.46	0.46
1:J:348:THR:HG22	1:J:372:ALA:HB2	1.97	0.46
1:L:251:THR:OG1	1:L:253:HIS:CD2	2.69	0.46
1:A:130:PRO:HB2	1:A:135:MET:CE	2.46	0.46
1:B:273:THR:O	1:B:273:THR:HG22	2.14	0.46
1:D:7:ASN:CB	1:D:31:LEU:HD21	2.45	0.46
1:E:137:LEU:CG	1:E:141:ILE:HD11	2.46	0.46
1:G:135:MET:N	1:G:135:MET:HE3	2.30	0.46
1:G:155:THR:HG23	1:G:259:LEU:CA	2.46	0.46
1:G:321:ARG:NH1	1:G:321:ARG:HG3	2.29	0.46
1:I:42:GLU:OE1	1:J:203:VAL:HG13	2.16	0.46
1:I:69:ILE:HG23	1:I:70:ASN:N	2.31	0.46
1:I:251:THR:OG1	1:I:253:HIS:CD2	2.69	0.46
1:A:341:ARG:HA	1:A:346:LEU:HD11	1.98	0.46
1:B:102:ARG:HB2	1:B:125:ILE:HG22	1.98	0.46
1:C:142:ILE:O	1:C:145:ILE:HG13	2.16	0.46
1:D:99:VAL:CG1	1:D:100:ARG:N	2.78	0.46
1:E:293:LEU:HD12	1:E:294:CYS:N	2.31	0.46
1:F:262:SER:HA	1:F:296:TRP:CE3	2.51	0.46
1:F:302:THR:OG1	1:F:306:ARG:O	2.32	0.46
1:G:13:PRO:HG3	1:G:20:PHE:CG	2.51	0.46
1:G:180:ASN:ND2	1:G:180:ASN:N	2.64	0.46
1:G:251:THR:OG1	1:G:253:HIS:CD2	2.69	0.46
1:G:352:LYS:HB2	1:G:365:TYR:CZ	2.51	0.46
1:I:355:PHE:CE2	1:I:362:GLU:CB	2.99	0.46
1:J:118:ILE:O	1:J:118:ILE:HG13	2.12	0.46
1:J:127:THR:O	1:J:193:VAL:HG22	2.15	0.46
1:J:192:PHE:CD1	1:J:192:PHE:N	2.84	0.46
1:K:64:GLU:O	1:K:68:LEU:HD13	2.16	0.46
1:E:18:PRO:O	1:E:21:MET:HB2	2.16	0.45
1:E:21:MET:CE	1:E:68:LEU:CG	2.91	0.45
1:E:96:ASN:O	1:E:98:GLY:N	2.41	0.45
1:E:223:ALA:O	1:E:228:PRO:CD	2.64	0.45
1:F:364:VAL:HG13	1:F:365:TYR:N	2.31	0.45
1:I:185:THR:HG22	1:I:232:MET:HB3	1.99	0.45
1:K:148:GLN:O	1:K:254:PRO:HD3	2.16	0.45
1:K:247:GLU:O	1:K:251:THR:OG1	2.33	0.45
1:L:40:THR:H	1:L:65:LEU:HD23	1.81	0.45
1:B:333:THR:O	1:B:336:THR:OG1	2.30	0.45
1:G:40:THR:HG23	1:G:65:LEU:HD22	1.94	0.45
1:G:69:ILE:HD11	1:G:120:ILE:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:174:ILE:HD12	1:G:174:ILE:HA	1.69	0.45
1:G:236:CYS:SG	1:G:259:LEU:HD21	2.55	0.45
1:H:148:GLN:O	1:H:254:PRO:HD3	2.16	0.45
1:J:145:ILE:HD13	1:J:293:LEU:HD21	1.97	0.45
1:K:285:ILE:N	1:K:285:ILE:CD1	2.79	0.45
1:C:132:LEU:HD22	1:C:172:GLU:HG3	1.98	0.45
1:D:68:LEU:O	1:D:72:ILE:HG22	2.16	0.45
1:D:195:ASP:OD1	1:D:196:GLU:N	2.49	0.45
1:D:367:LEU:HD21	1:E:289:GLU:CD	2.37	0.45
1:E:148:GLN:HB3	1:E:149:GLU:OE1	2.16	0.45
1:E:197:ILE:O	1:E:197:ILE:HG23	2.15	0.45
1:F:268:MET:HG2	1:F:336:THR:HG21	1.96	0.45
1:G:132:LEU:HA	1:G:168:SER:OG	2.17	0.45
1:H:104:ARG:HD3	1:H:191:GLU:HG2	1.98	0.45
1:J:48:VAL:HG12	1:J:49:TYR:HD2	1.81	0.45
1:A:49:TYR:OH	1:A:306:ARG:HG3	2.15	0.45
1:A:95:PRO:HG2	1:A:96:ASN:ND2	2.31	0.45
1:B:40:THR:N	1:B:65:LEU:CD2	2.79	0.45
1:B:138:PRO:O	1:B:142:ILE:HG12	2.16	0.45
1:H:132:LEU:CB	1:H:172:GLU:HG3	2.46	0.45
1:H:340:VAL:CG2	1:H:346:LEU:HD21	2.46	0.45
1:I:40:THR:N	1:I:65:LEU:HD11	2.31	0.45
1:I:185:THR:HA	1:I:232:MET:HB3	1.99	0.45
1:J:199:THR:HG21	1:J:202:ALA:CB	2.47	0.45
1:J:229:ARG:O	1:J:229:ARG:HG3	2.17	0.45
1:K:174:ILE:HG23	1:K:175:GLU:N	2.32	0.45
1:L:25:LEU:CD1	1:L:93:PHE:CE2	2.93	0.45
1:B:148:GLN:O	1:B:254:PRO:HD3	2.16	0.45
1:B:261:THR:CG2	1:B:270:ARG:HD2	2.46	0.45
1:F:292:ARG:HD3	1:F:321:ARG:NH1	2.32	0.45
1:I:17:THR:HG23	1:I:18:PRO:CD	2.44	0.45
1:I:353:MET:HG2	1:I:357:GLN:NE2	2.28	0.45
1:J:17:THR:HG23	1:J:18:PRO:HD2	1.97	0.45
1:K:111:LEU:HD22	1:L:90:HIS:NE2	2.30	0.45
1:L:34:SER:O	1:L:124:THR:HG23	2.17	0.45
1:L:89:THR:CG2	1:L:90:HIS:H	2.20	0.45
1:L:92:GLU:HB2	1:L:102:ARG:HG3	1.98	0.45
1:L:233:VAL:HB	1:L:257:THR:CG2	2.33	0.45
1:L:249:ALA:CB	1:L:290:THR:OG1	2.64	0.45
1:A:281:LEU:HD13	1:A:281:LEU:O	2.16	0.45
1:B:208:GLU:HG3	1:B:210:PRO:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:ILE:HB	1:B:364:VAL:CG1	2.47	0.45
1:C:185:THR:HA	1:C:232:MET:HB3	1.99	0.45
1:E:162:LYS:CD	1:E:258:THR:CB	2.90	0.45
1:E:176:THR:HG23	1:E:179:SER:CB	2.46	0.45
1:F:27:HIS:C	1:F:27:HIS:CD2	2.90	0.45
1:G:188:SER:HA	1:G:210:PRO:HD3	1.97	0.45
1:G:239:ALA:N	1:G:242:ILE:HD12	2.31	0.45
1:G:355:PHE:HZ	1:G:365:TYR:CB	2.27	0.45
1:H:7:ASN:HB3	1:H:31:LEU:HD21	1.98	0.45
1:I:38:ILE:CG2	1:I:65:LEU:HD21	2.40	0.45
1:I:48:VAL:HG12	1:I:49:TYR:CD2	2.51	0.45
1:I:229:ARG:O	1:I:254:PRO:HD2	2.17	0.45
1:K:365:TYR:CE1	1:K:369:ILE:HD11	2.52	0.45
1:L:216:PHE:O	1:L:220:VAL:HG23	2.17	0.45
1:A:261:THR:CB	1:A:267:THR:HG22	2.30	0.45
1:A:278:GLU:HB3	1:F:269:ARG:HH22	1.82	0.45
1:B:21:MET:O	1:B:25:LEU:HG	2.15	0.45
1:C:81:LEU:HD23	1:C:118:ILE:HG12	1.99	0.45
1:D:93:PHE:CD1	1:D:93:PHE:C	2.89	0.45
1:D:157:ALA:O	1:D:162:LYS:NZ	2.50	0.45
1:F:27:HIS:HD2	1:F:27:HIS:O	1.99	0.45
1:H:78:THR:O	1:H:82:LEU:HD23	2.16	0.45
1:H:99:VAL:CG1	1:H:100:ARG:N	2.79	0.45
1:I:177:SER:OG	1:I:200:ILE:HG21	2.17	0.45
1:J:160:SER:N	2:J:401:PO4:O1	2.49	0.45
1:A:174:ILE:HG13	1:A:202:ALA:CB	2.46	0.45
1:B:6:ILE:C	1:B:7:ASN:HD22	2.20	0.45
1:B:54:LYS:HG3	1:B:54:LYS:O	2.16	0.45
1:B:261:THR:HG21	1:B:270:ARG:HD2	1.98	0.45
1:D:39:GLN:C	1:D:65:LEU:HD21	2.37	0.45
1:D:125:ILE:CG1	1:D:126:PRO:HD2	2.46	0.45
1:D:190:ILE:O	1:D:190:ILE:HG22	2.17	0.45
1:D:269:ARG:NH1	1:D:270:ARG:HH12	2.15	0.45
1:E:22:ASP:OD2	1:E:93:PHE:CD1	2.70	0.45
1:H:18:PRO:O	1:H:21:MET:CB	2.61	0.45
1:I:137:LEU:HD11	1:I:165:LEU:HD11	1.99	0.45
1:J:39:GLN:CA	1:J:65:LEU:HD21	2.46	0.45
1:J:73:TYR:CD2	1:J:73:TYR:O	2.70	0.45
1:J:81:LEU:HD23	1:J:81:LEU:H	1.80	0.45
1:J:238:ASP:OD1	1:J:241:THR:CG2	2.65	0.45
1:A:180:ASN:HB3	1:F:52:LEU:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:ASP:HB2	1:C:213:LEU:HD21	1.99	0.45
1:C:111:LEU:HD21	1:C:114:GLY:C	2.37	0.45
1:C:179:SER:HB2	1:C:181:ARG:NH2	2.31	0.45
1:C:345:GLN:NE2	1:C:350:ASP:OD1	2.49	0.45
1:E:215:ASN:HD21	1:E:218:ASP:CG	2.19	0.45
1:F:249:ALA:HB1	1:F:290:THR:OG1	2.17	0.45
1:G:17:THR:HG23	1:G:18:PRO:CD	2.36	0.45
1:G:233:VAL:O	1:G:257:THR:HG22	2.17	0.45
1:I:223:ALA:O	1:I:228:PRO:CD	2.65	0.45
1:J:125:ILE:HG13	1:J:126:PRO:CD	2.45	0.45
1:J:247:GLU:O	1:J:251:THR:HG23	2.17	0.45
1:J:281:LEU:O	1:J:285:ILE:HD13	2.17	0.45
1:J:323:ILE:HD13	1:J:323:ILE:H	1.78	0.45
1:A:148:GLN:O	1:A:254:PRO:HD3	2.17	0.45
1:A:230:LEU:HD22	1:A:254:PRO:HB2	1.98	0.45
1:C:17:THR:HG22	1:C:18:PRO:HD2	1.96	0.45
1:D:118:ILE:O	1:D:118:ILE:HG13	2.16	0.45
1:D:138:PRO:O	1:D:142:ILE:HG12	2.17	0.45
1:E:27:HIS:C	1:E:27:HIS:CD2	2.90	0.45
1:H:155:THR:HG21	1:H:267:THR:CG2	2.44	0.45
1:I:47:GLU:HB2	1:I:52:LEU:HD21	1.98	0.45
1:I:104:ARG:N	1:I:125:ILE:HD11	2.32	0.45
1:J:102:ARG:NE	1:J:193:VAL:HG11	2.25	0.45
1:J:198:GLU:OE2	1:J:198:GLU:HA	2.16	0.45
1:J:300:VAL:O	1:J:308:VAL:HG12	2.17	0.45
1:K:188:SER:OG	1:K:189:PRO:CD	2.65	0.45
1:L:33:ALA:HA	1:L:48:VAL:HA	1.98	0.45
1:L:40:THR:N	1:L:65:LEU:CD2	2.80	0.45
1:A:227:LYS:CE	1:F:47:GLU:OE1	2.64	0.44
1:C:12:GLU:CD	1:C:56:THR:HG1	2.21	0.44
1:D:38:ILE:HB	1:D:120:ILE:CG2	2.42	0.44
1:D:73:TYR:CG	1:D:73:TYR:O	2.69	0.44
1:E:34:SER:O	1:E:124:THR:HG23	2.17	0.44
1:E:60:LEU:HB3	1:E:65:LEU:CD1	2.47	0.44
1:E:349:TRP:CZ3	1:E:353:MET:CG	2.99	0.44
1:G:322:ASP:O	1:G:325:LEU:HB2	2.17	0.44
1:G:355:PHE:HE2	1:G:365:TYR:CB	2.29	0.44
1:H:209:ILE:H	1:H:210:PRO:HD2	1.81	0.44
1:I:65:LEU:HD23	1:I:68:LEU:HD13	1.98	0.44
1:J:65:LEU:HB3	1:J:118:ILE:HG12	1.98	0.44
1:L:78:THR:O	1:L:82:LEU:HD13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:185:THR:HG22	1:L:232:MET:HB3	1.99	0.44
1:L:209:ILE:HD12	1:L:209:ILE:HA	1.73	0.44
1:C:142:ILE:HA	1:C:145:ILE:HG12	1.98	0.44
1:D:69:ILE:CA	1:D:72:ILE:HG22	2.47	0.44
1:H:6:ILE:HG23	1:H:54:LYS:HG3	1.99	0.44
1:H:261:THR:HG23	1:H:270:ARG:HD3	1.98	0.44
1:I:293:LEU:CD1	1:I:315:VAL:HG22	2.47	0.44
1:J:176:THR:O	1:J:179:SER:HB3	2.18	0.44
1:J:214:PRO:O	1:J:215:ASN:ND2	2.50	0.44
1:B:102:ARG:HH21	1:B:127:THR:CG2	2.30	0.44
1:D:175:GLU:CA	1:D:199:THR:CG2	2.86	0.44
1:E:285:ILE:N	1:E:285:ILE:CD1	2.80	0.44
1:G:9:MET:CE	1:G:24:MET:CA	2.85	0.44
1:G:306:ARG:CG	1:G:307:ARG:N	2.78	0.44
1:I:16:PHE:CZ	1:I:21:MET:CA	3.00	0.44
1:I:17:THR:HG22	1:I:18:PRO:HD2	1.99	0.44
1:I:61:SER:HB2	1:I:64:GLU:OE1	2.17	0.44
1:I:209:ILE:H	1:I:210:PRO:HD2	1.81	0.44
1:A:28:ALA:HB3	1:A:36:ILE:HD11	2.00	0.44
1:B:102:ARG:HH21	1:B:127:THR:CB	2.31	0.44
1:B:337:ARG:NE	1:B:341:ARG:NH1	2.65	0.44
1:B:365:TYR:CZ	1:B:369:ILE:CD1	2.86	0.44
1:C:126:PRO:O	1:C:191:GLU:O	2.35	0.44
1:D:156:GLY:C	1:D:162:LYS:HZ1	2.20	0.44
1:H:9:MET:HE3	1:H:24:MET:CA	2.47	0.44
1:H:364:VAL:HG13	1:H:365:TYR:N	2.33	0.44
1:I:97:ARG:CB	1:I:99:VAL:HG23	2.48	0.44
1:K:304:ASP:OD2	1:K:306:ARG:HG3	2.18	0.44
1:A:350:ASP:OD1	1:A:354:LYS:HD3	2.17	0.44
1:C:55:ILE:HG22	1:C:55:ILE:O	2.17	0.44
1:C:148:GLN:O	1:C:254:PRO:HD3	2.18	0.44
1:E:285:ILE:N	1:E:285:ILE:HD12	2.31	0.44
1:H:88:ASP:OD2	1:I:225:ARG:CD	2.65	0.44
1:H:151:ILE:HG21	1:H:153:PHE:CZ	2.53	0.44
1:I:184:LEU:CD1	1:I:228:PRO:CB	2.92	0.44
1:I:195:ASP:OD1	1:I:196:GLU:N	2.50	0.44
1:J:264:VAL:HG13	1:J:265:ALA:N	2.33	0.44
1:K:132:LEU:HD23	1:K:132:LEU:C	2.38	0.44
1:K:135:MET:CE	1:K:135:MET:CA	2.77	0.44
1:L:40:THR:HG22	1:L:65:LEU:CB	2.48	0.44
1:L:288:LEU:CD1	1:L:324:LEU:HD13	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ASN:HD22	1:B:225:ARG:HB3	1.82	0.44
1:B:249:ALA:CB	1:B:290:THR:HG23	2.32	0.44
1:B:251:THR:OG1	1:B:253:HIS:CD2	2.71	0.44
1:D:108:THR:HB	1:E:226:ARG:NH1	2.33	0.44
1:D:171:ARG:HA	1:D:174:ILE:CG2	2.47	0.44
1:E:89:THR:CG2	1:E:105:VAL:HG13	2.47	0.44
1:E:259:LEU:HD11	1:E:271:LEU:HD21	2.00	0.44
1:F:285:ILE:HD12	1:F:285:ILE:H	1.82	0.44
1:G:111:LEU:HD22	1:H:90:HIS:NE2	2.33	0.44
1:H:9:MET:CE	1:H:24:MET:CA	2.95	0.44
1:H:92:GLU:OE2	1:H:102:ARG:NH1	2.49	0.44
1:J:13:PRO:HB3	1:J:20:PHE:CD1	2.52	0.44
1:J:111:LEU:HD22	1:J:115:HIS:O	2.18	0.44
1:J:166:LEU:HD13	1:J:232:MET:SD	2.57	0.44
1:L:129:PRO:O	1:L:171:ARG:NH1	2.48	0.44
1:L:365:TYR:O	1:L:369:ILE:HG13	2.18	0.44
1:B:214:PRO:C	1:B:215:ASN:HD22	2.21	0.44
1:E:162:LYS:CD	1:E:258:THR:CG2	2.96	0.44
1:G:334:SER:O	1:G:337:ARG:HB3	2.18	0.44
1:H:165:LEU:O	1:H:169:ILE:HG13	2.18	0.44
1:H:183:VAL:O	1:H:184:LEU:HD23	2.17	0.44
1:H:261:THR:HG23	1:H:270:ARG:CD	2.48	0.44
1:J:308:VAL:HG22	1:J:309:ALA:N	2.33	0.44
1:L:89:THR:CG2	1:L:90:HIS:N	2.78	0.44
1:A:174:ILE:CD1	1:A:183:VAL:HG21	2.48	0.44
1:B:209:ILE:H	1:B:210:PRO:HD2	1.83	0.44
1:C:108:THR:HG21	1:D:222:ASN:ND2	2.32	0.44
1:C:108:THR:HG21	1:D:226:ARG:HH11	1.82	0.44
1:E:34:SER:OG	1:E:35:ASP:OD1	2.12	0.44
1:E:131:LYS:HB2	1:E:171:ARG:HH21	1.82	0.44
1:F:156:GLY:N	1:F:162:LYS:HD3	2.33	0.44
1:F:288:LEU:CD1	1:F:324:LEU:HD13	2.47	0.44
1:G:201:SER:C	1:L:52:LEU:HD23	2.38	0.44
1:H:6:ILE:C	1:H:7:ASN:HD22	2.21	0.44
1:H:229:ARG:HB2	1:H:229:ARG:NH2	2.33	0.44
1:I:166:LEU:HD13	1:I:232:MET:SD	2.58	0.44
1:I:365:TYR:HA	1:I:368:ILE:CD1	2.46	0.44
1:K:81:LEU:HD12	1:K:118:ILE:HG12	1.99	0.44
1:C:94:ARG:O	1:C:95:PRO:O	2.36	0.44
1:C:301:PRO:HA	1:C:307:ARG:HD3	2.00	0.44
1:D:128:THR:HG23	1:D:196:GLU:OE1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:229:ARG:HG3	1:D:229:ARG:O	2.18	0.44
1:D:363:ARG:O	1:D:366:LYS:HG2	2.17	0.44
1:E:354:LYS:HE2	1:E:354:LYS:CA	2.42	0.44
1:G:186:TYR:HB3	1:G:209:ILE:HD11	2.00	0.44
1:H:137:LEU:HD11	1:H:311:ARG:NE	2.33	0.44
1:J:78:THR:H	1:J:78:THR:HG1	1.55	0.44
1:K:145:ILE:O	1:K:147:PRO:HD2	2.17	0.44
1:K:366:LYS:HG3	1:K:366:LYS:H	1.57	0.44
1:A:332:VAL:HG23	1:A:333:THR:N	2.33	0.43
1:B:209:ILE:N	1:B:210:PRO:CD	2.80	0.43
1:C:209:ILE:HD13	1:C:209:ILE:HA	1.73	0.43
1:D:233:VAL:HB	1:D:257:THR:CG2	2.33	0.43
1:E:17:THR:HG23	1:E:18:PRO:CD	2.44	0.43
1:E:21:MET:HE1	1:E:68:LEU:CB	2.48	0.43
1:E:111:LEU:CD2	1:F:90:HIS:NE2	2.80	0.43
1:F:291:ILE:HD13	1:F:316:PHE:CE1	2.52	0.43
1:H:317:ASP:O	1:H:321:ARG:HG3	2.18	0.43
1:I:22:ASP:OD2	1:I:93:PHE:CG	2.71	0.43
1:I:126:PRO:O	1:I:191:GLU:O	2.35	0.43
1:I:349:TRP:C	1:I:349:TRP:CD1	2.91	0.43
1:J:145:ILE:HD13	1:J:293:LEU:CD2	2.47	0.43
1:K:111:LEU:HD21	1:L:90:HIS:CD2	2.52	0.43
1:K:302:THR:OG1	1:K:306:ARG:O	2.36	0.43
1:K:333:THR:HA	1:K:336:THR:CG2	2.49	0.43
1:L:331:GLU:HG3	1:L:334:SER:HB2	2.00	0.43
1:D:300:VAL:HG11	1:D:368:ILE:HD11	1.99	0.43
1:E:353:MET:O	1:E:357:GLN:HG2	2.17	0.43
1:F:40:THR:CG2	1:F:62:ASN:HA	2.48	0.43
1:G:145:ILE:C	1:G:145:ILE:CD1	2.86	0.43
1:H:105:VAL:HG22	1:H:122:LEU:HG	2.00	0.43
1:I:47:GLU:CB	1:I:52:LEU:CD2	2.96	0.43
1:I:165:LEU:O	1:I:169:ILE:HG13	2.18	0.43
1:I:236:CYS:SG	1:I:242:ILE:HG13	2.58	0.43
1:I:283:ARG:HD3	1:I:283:ARG:HA	1.70	0.43
1:J:158:THR:HB	1:J:260:HIS:HE1	1.82	0.43
1:K:40:THR:N	1:K:65:LEU:HD21	2.33	0.43
1:L:222:ASN:CA	1:L:225:ARG:NH2	2.75	0.43
1:L:290:THR:O	1:L:292:ARG:NH2	2.52	0.43
1:A:222:ASN:OD1	1:A:226:ARG:NH1	2.52	0.43
1:A:355:PHE:CB	1:A:360:ILE:CG2	2.96	0.43
1:C:230:LEU:HD11	1:C:256:TYR:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:222:ASN:O	1:E:225:ARG:N	2.49	0.43
1:F:148:GLN:O	1:F:254:PRO:HD3	2.17	0.43
1:F:249:ALA:CB	1:F:290:THR:OG1	2.65	0.43
1:F:369:ILE:O	1:F:372:ALA:CB	2.66	0.43
1:H:93:PHE:CD1	1:H:93:PHE:C	2.91	0.43
1:H:183:VAL:C	1:H:184:LEU:HD23	2.38	0.43
1:H:361:SER:O	1:H:364:VAL:HG12	2.19	0.43
1:I:70:ASN:ND2	1:I:78:THR:OG1	2.52	0.43
1:J:151:ILE:HG21	1:J:153:PHE:CZ	2.53	0.43
1:A:355:PHE:N	1:A:360:ILE:HG22	2.33	0.43
1:B:40:THR:N	1:B:65:LEU:HD21	2.33	0.43
1:B:48:VAL:HG21	1:B:53:LEU:HD11	2.00	0.43
1:B:139:ASP:OD1	1:B:139:ASP:N	2.49	0.43
1:C:105:VAL:HG22	1:C:122:LEU:HG	2.01	0.43
1:C:269:ARG:HG3	1:C:333:THR:HG21	2.00	0.43
1:E:23:ARG:HD3	1:E:23:ARG:HA	1.75	0.43
1:F:333:THR:O	1:F:336:THR:OG1	2.28	0.43
1:H:55:ILE:HG22	1:H:55:ILE:O	2.18	0.43
1:I:60:LEU:HD23	1:I:60:LEU:N	2.33	0.43
1:K:178:ASP:OD1	1:K:178:ASP:N	2.50	0.43
1:B:102:ARG:HE	1:B:127:THR:CG2	2.27	0.43
1:C:363:ARG:CG	1:C:364:VAL:N	2.77	0.43
1:F:37:THR:OG1	1:F:45:PHE:HB2	2.18	0.43
1:F:135:MET:HB3	1:F:137:LEU:CD1	2.48	0.43
1:F:179:SER:OG	1:F:179:SER:O	2.37	0.43
1:G:28:ALA:HB3	1:G:36:ILE:HD11	1.99	0.43
1:G:223:ALA:O	1:G:228:PRO:HD3	2.19	0.43
1:J:24:MET:HE3	1:J:25:LEU:HD23	2.00	0.43
1:J:183:VAL:HG13	1:J:230:LEU:CD2	2.37	0.43
1:J:268:MET:HE1	1:J:288:LEU:CD1	2.48	0.43
1:A:9:MET:HE1	1:A:24:MET:HB2	2.01	0.43
1:A:13:PRO:HG3	1:A:20:PHE:CG	2.53	0.43
1:A:355:PHE:HB2	1:A:360:ILE:CG2	2.48	0.43
1:G:96:ASN:CG	1:G:98:GLY:H	2.20	0.43
1:G:151:ILE:HG21	1:G:153:PHE:CZ	2.53	0.43
1:G:235:GLU:HA	1:G:258:THR:OG1	2.17	0.43
1:I:13:PRO:HG3	1:I:20:PHE:CG	2.53	0.43
1:I:360:ILE:HG23	1:I:364:VAL:HB	2.01	0.43
1:J:25:LEU:HD12	1:J:93:PHE:CE2	2.53	0.43
1:J:223:ALA:O	1:J:228:PRO:HD3	2.17	0.43
1:L:162:LYS:HE2	1:L:162:LYS:HB2	1.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:361:SER:HB2	1:L:364:VAL:HG23	2.00	0.43
1:B:21:MET:HE1	1:B:122:LEU:HD21	2.01	0.43
1:C:16:PHE:HE1	1:C:21:MET:HA	1.83	0.43
1:D:69:ILE:HA	1:D:69:ILE:HD12	1.87	0.43
1:E:86:ASP:OD2	1:F:222:ASN:ND2	2.50	0.43
1:F:157:ALA:O	1:F:162:LYS:NZ	2.50	0.43
1:G:134:THR:HB	1:G:135:MET:HE3	1.99	0.43
1:H:88:ASP:OD2	1:I:225:ARG:HD2	2.19	0.43
1:I:12:GLU:OE1	1:I:58:ARG:NE	2.52	0.43
1:I:48:VAL:HG12	1:I:49:TYR:HD2	1.84	0.43
1:I:230:LEU:HD13	1:I:256:TYR:CE1	2.53	0.43
1:J:174:ILE:O	1:J:199:THR:CG2	2.67	0.43
1:L:220:VAL:O	1:L:223:ALA:HB3	2.18	0.43
1:L:236:CYS:O	1:L:259:LEU:HD21	2.18	0.43
1:L:238:ASP:O	1:L:241:THR:HG22	2.18	0.43
1:B:73:TYR:O	1:B:73:TYR:CD2	2.72	0.43
1:B:315:VAL:O	1:B:315:VAL:HG13	2.18	0.43
1:C:45:PHE:CE2	1:D:203:VAL:HG22	2.54	0.43
1:C:174:ILE:CD1	1:C:199:THR:CG2	2.96	0.43
1:C:174:ILE:HG13	1:C:202:ALA:HB1	2.01	0.43
1:C:268:MET:SD	1:C:291:ILE:HD13	2.59	0.43
1:D:73:TYR:O	1:D:73:TYR:CD2	2.72	0.43
1:H:65:LEU:HD12	1:H:120:ILE:CD1	2.49	0.43
1:K:48:VAL:HG12	1:K:49:TYR:CD2	2.54	0.43
1:K:93:PHE:HE2	1:K:103:TYR:CE1	2.36	0.43
1:K:235:GLU:OE2	1:K:237:ARG:NE	2.51	0.43
1:K:317:ASP:O	1:K:321:ARG:HG3	2.18	0.43
1:L:60:LEU:N	1:L:60:LEU:HD12	2.33	0.43
1:A:37:THR:CG2	1:B:182:LYS:HE3	2.49	0.43
1:D:185:THR:HG22	1:D:232:MET:HB3	2.00	0.43
1:E:137:LEU:CB	1:E:141:ILE:HD11	2.46	0.43
1:E:155:THR:O	1:E:296:TRP:HA	2.18	0.43
1:F:362:GLU:O	1:F:366:LYS:HG3	2.19	0.43
1:G:313:TYR:HE2	1:G:345:GLN:CD	2.22	0.43
1:H:188:SER:C	1:H:208:GLU:HG3	2.37	0.43
1:H:261:THR:CG2	1:H:270:ARG:HD3	2.49	0.43
1:I:222:ASN:C	1:I:222:ASN:OD1	2.57	0.43
1:J:73:TYR:O	1:J:73:TYR:CG	2.71	0.43
1:J:160:SER:O	1:J:297:GLN:NE2	2.52	0.43
1:J:249:ALA:HB1	1:J:290:THR:OG1	2.19	0.43
1:K:8:LEU:O	1:K:27:HIS:CE1	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:21:MET:CE	1:K:68:LEU:HG	2.48	0.43
1:B:188:SER:CB	1:B:189:PRO:HD2	2.48	0.43
1:E:209:ILE:HG13	1:E:216:PHE:CE1	2.54	0.43
1:F:59:ARG:H	1:F:59:ARG:HG3	1.66	0.43
1:G:223:ALA:O	1:G:228:PRO:CD	2.66	0.43
1:H:9:MET:CE	1:H:24:MET:N	2.82	0.43
1:H:369:ILE:O	1:H:370:ALA:C	2.58	0.43
1:I:81:LEU:N	1:I:81:LEU:CD1	2.82	0.43
1:J:13:PRO:HB3	1:J:20:PHE:HE1	1.73	0.43
1:J:283:ARG:HA	1:J:283:ARG:HE	1.84	0.43
1:K:9:MET:SD	1:K:10:PRO:CD	3.03	0.43
1:K:171:ARG:O	1:K:174:ILE:HG22	2.14	0.43
1:L:305:GLU:O	1:L:306:ARG:HD3	2.19	0.43
1:B:195:ASP:O	1:B:198:GLU:HB2	2.19	0.42
1:C:37:THR:OG1	1:C:45:PHE:HB2	2.18	0.42
1:E:9:MET:CG	1:E:10:PRO:CD	2.96	0.42
1:E:17:THR:HB	1:E:20:PHE:HD2	1.84	0.42
1:E:151:ILE:HG21	1:E:153:PHE:CZ	2.54	0.42
1:E:162:LYS:HD3	1:E:258:THR:CG2	2.47	0.42
1:F:17:THR:HB	1:F:20:PHE:HD1	1.84	0.42
1:G:155:THR:CG2	1:G:259:LEU:O	2.67	0.42
1:G:354:LYS:CB	1:G:360:ILE:CD1	2.88	0.42
1:H:339:LEU:HD23	1:H:339:LEU:HA	1.81	0.42
1:I:312:GLU:HB2	1:I:347:MET:N	2.33	0.42
1:K:181:ARG:HA	1:K:229:ARG:HB3	2.01	0.42
1:L:17:THR:HB	1:L:20:PHE:CD1	2.54	0.42
1:L:112:VAL:CG2	1:L:117:ALA:HB1	2.41	0.42
1:L:238:ASP:C	1:L:238:ASP:OD1	2.57	0.42
1:A:102:ARG:HH11	1:A:127:THR:HG21	1.85	0.42
1:A:306:ARG:CG	1:A:307:ARG:H	2.32	0.42
1:D:123:ARG:NH2	1:E:225:ARG:O	2.52	0.42
1:E:8:LEU:O	1:E:27:HIS:CE1	2.73	0.42
1:E:174:ILE:HG13	1:E:202:ALA:HB1	2.00	0.42
1:E:265:ALA:CB	1:E:337:ARG:HG3	2.49	0.42
1:F:175:GLU:HA	1:F:199:THR:HG22	2.00	0.42
1:G:355:PHE:HB2	1:G:356:GLU:OE2	2.18	0.42
1:J:171:ARG:HA	1:J:174:ILE:CG2	2.49	0.42
1:J:173:LEU:O	1:J:179:SER:HB2	2.18	0.42
1:J:209:ILE:CD1	1:J:215:ASN:C	2.88	0.42
1:J:251:THR:OG1	1:J:253:HIS:CD2	2.72	0.42
1:K:269:ARG:NH2	1:L:322:ASP:OD1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ARG:HH12	1:A:97:ARG:CD	2.22	0.42
1:A:333:THR:OG1	1:A:334:SER:N	2.52	0.42
1:A:355:PHE:CE1	1:A:362:GLU:HA	2.54	0.42
1:C:111:LEU:HD13	1:C:112:VAL:N	2.33	0.42
1:D:349:TRP:CH2	1:D:353:MET:HE2	2.53	0.42
1:E:22:ASP:OD2	1:E:93:PHE:CE1	2.72	0.42
1:F:112:VAL:O	1:F:112:VAL:HG23	2.17	0.42
1:G:181:ARG:HD3	1:G:229:ARG:HG3	2.00	0.42
1:G:296:TRP:CE3	1:G:347:MET:SD	3.12	0.42
1:I:13:PRO:HB3	1:I:20:PHE:CD2	2.51	0.42
1:I:54:LYS:O	1:I:55:ILE:HD13	2.18	0.42
1:L:194:TYR:HA	1:L:197:ILE:CD1	2.43	0.42
1:L:292:ARG:HD3	1:L:321:ARG:NH1	2.34	0.42
1:A:179:SER:HB2	1:A:181:ARG:HH21	1.83	0.42
1:A:281:LEU:O	1:A:285:ILE:CD1	2.67	0.42
1:E:174:ILE:HG13	1:E:202:ALA:HB3	2.01	0.42
1:E:271:LEU:HB3	1:E:287:ILE:HD12	2.01	0.42
1:F:151:ILE:HG21	1:F:153:PHE:CZ	2.54	0.42
1:G:95:PRO:HD2	1:G:99:VAL:HG23	2.01	0.42
1:G:96:ASN:OD1	1:G:97:ARG:N	2.52	0.42
1:H:40:THR:OG1	1:H:65:LEU:HD23	2.19	0.42
1:H:80:GLN:O	1:H:83:SER:HB2	2.18	0.42
1:H:263:GLY:O	1:H:267:THR:OG1	2.34	0.42
1:I:57:ASN:OD1	1:I:57:ASN:N	2.51	0.42
1:I:72:ILE:CG2	1:I:91:TYR:HB2	2.49	0.42
1:I:364:VAL:O	1:I:368:ILE:HG12	2.20	0.42
1:K:90:HIS:CD2	1:K:104:ARG:HA	2.54	0.42
1:K:91:TYR:CE1	1:K:93:PHE:HD2	2.37	0.42
1:L:299:LEU:HD23	1:L:299:LEU:HA	1.93	0.42
1:E:95:PRO:CG	1:E:96:ASN:H	2.11	0.42
1:E:368:ILE:HD12	1:E:368:ILE:HA	1.91	0.42
1:F:184:LEU:CD1	1:F:228:PRO:HB3	2.49	0.42
1:G:203:VAL:CG1	1:L:39:GLN:HE22	2.32	0.42
1:H:119:GLN:NE2	1:I:182:LYS:CE	2.82	0.42
1:I:338:LYS:HE3	1:I:342:GLN:OE1	2.20	0.42
1:K:66:GLY:O	1:K:69:ILE:HG22	2.20	0.42
1:L:165:LEU:O	1:L:169:ILE:HG12	2.20	0.42
1:L:329:PRO:HA	1:L:332:VAL:HG23	2.01	0.42
1:A:188:SER:OG	1:A:189:PRO:CD	2.67	0.42
1:B:132:LEU:CB	1:B:172:GLU:HG3	2.49	0.42
1:B:250:LEU:HD23	1:B:250:LEU:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:296:TRP:CZ3	1:D:347:MET:CE	3.02	0.42
1:E:149:GLU:O	1:E:292:ARG:HD3	2.20	0.42
1:E:213:LEU:HD23	1:E:213:LEU:HA	1.82	0.42
1:E:215:ASN:N	1:E:215:ASN:ND2	2.66	0.42
1:F:170:ILE:HG22	1:F:174:ILE:HD12	2.00	0.42
1:G:317:ASP:CA	1:G:321:ARG:HH12	2.32	0.42
1:I:12:GLU:OE2	1:I:58:ARG:HG3	2.20	0.42
1:I:61:SER:CB	1:I:64:GLU:OE1	2.67	0.42
1:J:263:GLY:CA	1:J:266:GLU:HG2	2.50	0.42
1:J:268:MET:HG3	1:J:336:THR:HG21	2.00	0.42
1:K:151:ILE:HG21	1:K:153:PHE:CZ	2.54	0.42
1:L:149:GLU:CG	1:L:150:GLY:H	2.32	0.42
1:A:365:TYR:O	1:A:369:ILE:HD12	2.19	0.42
1:B:137:LEU:HD11	1:B:311:ARG:NH2	2.35	0.42
1:C:69:ILE:HD12	1:C:69:ILE:HA	1.90	0.42
1:C:155:THR:HG22	1:C:259:LEU:HB2	2.02	0.42
1:G:48:VAL:HG12	1:G:49:TYR:CD2	2.55	0.42
1:H:73:TYR:CG	1:H:73:TYR:O	2.73	0.42
1:H:340:VAL:CG2	1:H:346:LEU:CD2	2.97	0.42
1:J:40:THR:HG21	1:J:62:ASN:HB2	2.01	0.42
1:K:25:LEU:CD1	1:K:93:PHE:CZ	3.03	0.42
1:K:293:LEU:CD1	1:K:315:VAL:HG22	2.46	0.42
1:A:230:LEU:C	1:A:230:LEU:CD1	2.88	0.42
1:B:102:ARG:C	1:B:125:ILE:HG22	2.40	0.42
1:C:48:VAL:HG12	1:C:49:TYR:CD2	2.51	0.42
1:F:132:LEU:HD11	1:F:169:ILE:HD11	2.02	0.42
1:G:104:ARG:HB2	1:G:125:ILE:HD11	2.01	0.42
1:H:26:GLU:OE1	1:H:95:PRO:HB3	2.19	0.42
1:H:145:ILE:HD12	1:H:145:ILE:HA	1.92	0.42
1:H:240:GLU:CD	1:H:240:GLU:N	2.72	0.42
1:I:24:MET:CE	1:I:44:ILE:HG21	2.49	0.42
1:I:349:TRP:O	1:I:349:TRP:HD1	2.03	0.42
1:B:131:LYS:HB2	1:B:134:THR:HG23	2.01	0.42
1:D:65:LEU:HD23	1:D:118:ILE:HG13	2.01	0.42
1:D:186:TYR:CZ	1:D:219:GLY:O	2.72	0.42
1:F:73:TYR:CE1	1:F:89:THR:HG22	2.54	0.42
1:F:185:THR:HG22	1:F:232:MET:HB3	2.00	0.42
1:F:209:ILE:C	1:F:209:ILE:CD1	2.88	0.42
1:G:235:GLU:N	1:G:258:THR:HG1	2.18	0.42
1:G:306:ARG:HG2	1:G:307:ARG:H	1.83	0.42
1:G:362:GLU:O	1:G:366:LYS:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:70:ASN:OD1	1:I:78:THR:OG1	2.34	0.42
1:J:163:SER:CB	1:J:191:GLU:OE2	2.68	0.42
1:K:91:TYR:CD1	1:K:93:PHE:HD2	2.37	0.42
1:K:268:MET:HE1	1:K:291:ILE:HG21	2.02	0.42
1:K:288:LEU:CB	1:K:325:LEU:HD23	2.47	0.42
1:A:37:THR:HG21	1:B:182:LYS:HE3	2.02	0.42
1:E:19:VAL:HG21	1:J:331:GLU:HG3	2.01	0.42
1:G:205:SER:HB2	1:L:119:GLN:OE1	2.19	0.42
1:H:54:LYS:HG3	1:H:54:LYS:O	2.19	0.42
1:H:348:THR:HG22	1:H:372:ALA:HB3	2.02	0.42
1:H:349:TRP:CZ3	1:H:353:MET:CE	3.03	0.42
1:J:9:MET:CE	1:J:24:MET:N	2.78	0.42
1:J:81:LEU:CD2	1:J:87:ILE:CD1	2.89	0.42
1:J:319:GLU:O	1:J:323:ILE:HG12	2.19	0.42
1:J:363:ARG:HG3	1:J:366:LYS:HE3	2.02	0.42
1:K:154:ILE:HG21	1:K:165:LEU:HD23	2.02	0.42
1:B:164:THR:O	1:B:167:ALA:N	2.53	0.41
1:C:174:ILE:HD12	1:C:204:VAL:CG2	2.50	0.41
1:D:87:ILE:HB	1:D:107:ALA:HB3	2.02	0.41
1:D:308:VAL:HG22	1:D:309:ALA:N	2.35	0.41
1:G:148:GLN:O	1:G:254:PRO:HD3	2.20	0.41
1:G:279:GLU:OE1	1:G:279:GLU:CA	2.61	0.41
1:H:172:GLU:O	1:H:176:THR:CG2	2.62	0.41
1:I:198:GLU:H	1:I:198:GLU:HG2	1.55	0.41
1:J:69:ILE:CA	1:J:72:ILE:HG22	2.50	0.41
1:J:249:ALA:CB	1:J:290:THR:OG1	2.68	0.41
1:K:242:ILE:HD13	1:K:271:LEU:CD2	2.49	0.41
1:K:297:GLN:HE21	1:K:311:ARG:NE	2.17	0.41
1:K:352:LYS:HA	1:K:365:TYR:CE2	2.56	0.41
1:L:9:MET:HE3	1:L:24:MET:HB2	1.98	0.41
1:L:193:VAL:HA	1:L:206:GLN:HE22	1.84	0.41
1:A:278:GLU:OE2	1:F:337:ARG:NH1	2.52	0.41
1:A:320:VAL:CG1	1:A:339:LEU:HD13	2.50	0.41
1:B:119:GLN:NE2	1:C:226:ARG:NH2	2.53	0.41
1:B:125:ILE:HD12	1:B:125:ILE:HA	1.93	0.41
1:C:162:LYS:O	1:C:166:LEU:HG	2.20	0.41
1:C:251:THR:OG1	1:C:253:HIS:CD2	2.71	0.41
1:D:171:ARG:C	1:D:174:ILE:HG22	2.40	0.41
1:D:174:ILE:HD12	1:D:204:VAL:HG21	2.01	0.41
1:E:108:THR:OG1	1:F:226:ARG:NH2	2.47	0.41
1:E:237:ARG:CZ	1:F:247:GLU:OE1	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:183:VAL:CG1	1:F:230:LEU:HD22	2.36	0.41
1:F:340:VAL:HG23	1:F:341:ARG:N	2.35	0.41
1:G:126:PRO:O	1:G:191:GLU:O	2.38	0.41
1:G:300:VAL:O	1:G:308:VAL:HG12	2.20	0.41
1:G:318:GLU:CG	1:L:363:ARG:CZ	2.91	0.41
1:I:44:ILE:H	1:I:56:THR:HG22	1.84	0.41
1:J:7:ASN:C	1:J:8:LEU:HD12	2.40	0.41
1:J:315:VAL:O	1:J:315:VAL:HG13	2.19	0.41
1:K:351:ALA:O	1:K:360:ILE:HD11	2.20	0.41
1:L:182:LYS:HG3	1:L:203:VAL:HG13	2.01	0.41
1:A:73:TYR:CD2	1:A:87:ILE:HG12	2.54	0.41
1:A:209:ILE:N	1:A:210:PRO:CD	2.84	0.41
1:B:13:PRO:HG3	1:B:20:PHE:CG	2.55	0.41
1:C:209:ILE:N	1:C:210:PRO:CD	2.83	0.41
1:D:48:VAL:HG12	1:D:49:TYR:HD2	1.86	0.41
1:F:111:LEU:CD1	1:F:115:HIS:C	2.87	0.41
1:F:222:ASN:OD1	1:F:226:ARG:NE	2.53	0.41
1:G:158:THR:HA	1:G:162:LYS:NZ	2.34	0.41
1:G:173:LEU:C	1:G:181:ARG:NH2	2.67	0.41
1:G:352:LYS:CG	1:G:365:TYR:CZ	3.02	0.41
1:H:246:LEU:O	1:H:250:LEU:CD1	2.67	0.41
1:H:336:THR:O	1:H:340:VAL:HG13	2.20	0.41
1:H:367:LEU:HD23	1:I:325:LEU:HD22	2.02	0.41
1:I:171:ARG:C	1:I:174:ILE:HG22	2.40	0.41
1:J:302:THR:N	1:J:306:ARG:O	2.53	0.41
1:J:349:TRP:CE2	1:J:353:MET:HE1	2.54	0.41
1:J:350:ASP:OD1	1:J:354:LYS:HD3	2.20	0.41
1:K:7:ASN:C	1:K:8:LEU:CD2	2.87	0.41
1:K:139:ASP:O	1:K:140:ASN:C	2.59	0.41
1:A:297:GLN:HE21	1:A:311:ARG:HE	1.65	0.41
1:B:69:ILE:HD12	1:B:69:ILE:HA	1.92	0.41
1:B:135:MET:HB3	1:B:137:LEU:CD1	2.49	0.41
1:I:119:GLN:HE22	1:J:182:LYS:CE	2.32	0.41
1:J:100:ARG:HD3	1:J:100:ARG:N	2.30	0.41
1:J:166:LEU:HD21	1:J:256:TYR:HB3	2.02	0.41
1:J:212:HIS:O	1:J:213:LEU:HG	2.20	0.41
1:L:37:THR:OG1	1:L:45:PHE:HB2	2.21	0.41
1:L:314:LEU:HD11	1:L:339:LEU:HB3	2.03	0.41
1:A:60:LEU:HB3	1:A:65:LEU:CD1	2.50	0.41
1:A:89:THR:C	1:A:105:VAL:HG22	2.41	0.41
1:C:166:LEU:CD2	1:C:232:MET:HE1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:95:PRO:HD2	1:D:99:VAL:O	2.21	0.41
1:D:315:VAL:HG13	1:D:315:VAL:O	2.20	0.41
1:F:141:ILE:HG23	1:F:295:ILE:HD11	2.01	0.41
1:F:275:PHE:CE1	1:F:283:ARG:HD3	2.56	0.41
1:H:58:ARG:HB3	1:H:58:ARG:CZ	2.51	0.41
1:J:162:LYS:HE3	2:J:401:PO4:O1	2.20	0.41
1:K:87:ILE:HB	1:K:107:ALA:HB3	2.02	0.41
1:A:37:THR:HG22	1:A:121:THR:HG23	2.02	0.41
1:A:183:VAL:HG13	1:A:230:LEU:HD12	2.02	0.41
1:A:322:ASP:OD1	1:F:363:ARG:NH2	2.54	0.41
1:B:9:MET:HE1	1:B:24:MET:N	2.35	0.41
1:D:72:ILE:HG13	1:D:91:TYR:CD1	2.55	0.41
1:D:280:ARG:O	1:D:284:THR:CG2	2.40	0.41
1:E:121:THR:CG2	1:F:182:LYS:HE3	2.51	0.41
1:E:288:LEU:CB	1:E:325:LEU:HD21	2.50	0.41
1:F:8:LEU:C	1:F:27:HIS:HE1	2.22	0.41
1:G:69:ILE:HD11	1:G:120:ILE:HG23	2.02	0.41
1:G:176:THR:CG2	1:G:177:SER:N	2.84	0.41
1:H:29:GLU:OE1	1:H:29:GLU:HA	2.19	0.41
1:H:208:GLU:HG2	1:H:210:PRO:HD2	2.03	0.41
1:I:110:CYS:HB2	1:J:206:GLN:O	2.20	0.41
1:I:171:ARG:CA	1:I:174:ILE:HG22	2.50	0.41
1:I:174:ILE:HG12	1:I:202:ALA:CB	2.50	0.41
1:J:165:LEU:HD12	1:J:165:LEU:O	2.20	0.41
1:K:111:LEU:HD13	1:L:90:HIS:HE1	1.78	0.41
1:K:279:GLU:H	1:K:279:GLU:HG2	1.61	0.41
1:L:17:THR:CG2	1:L:18:PRO:HD2	2.41	0.41
1:L:188:SER:HA	1:L:209:ILE:CG2	2.45	0.41
1:C:261:THR:HG21	1:C:266:GLU:C	2.40	0.41
1:C:281:LEU:HD23	1:C:285:ILE:HD13	2.02	0.41
1:C:308:VAL:HG22	1:C:309:ALA:N	2.36	0.41
1:D:158:THR:HG22	1:E:247:GLU:OE1	2.21	0.41
1:D:223:ALA:O	1:D:228:PRO:HD3	2.20	0.41
1:E:215:ASN:ND2	1:E:218:ASP:HB2	2.35	0.41
1:G:141:ILE:O	1:G:144:ALA:N	2.45	0.41
1:G:208:GLU:CG	1:G:210:PRO:HD2	2.51	0.41
1:H:132:LEU:HB2	1:H:172:GLU:CG	2.51	0.41
1:H:349:TRP:CZ3	1:H:353:MET:HE2	2.56	0.41
1:J:47:GLU:HA	1:J:51:ARG:O	2.21	0.41
1:K:283:ARG:HD2	1:K:283:ARG:N	2.35	0.41
1:L:332:VAL:O	1:L:336:THR:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:PHE:CD1	1:A:93:PHE:C	2.94	0.41
1:C:17:THR:HG23	1:C:18:PRO:CD	2.44	0.41
1:C:66:GLY:O	1:C:69:ILE:HG22	2.21	0.41
1:C:182:LYS:HB3	1:C:228:PRO:HA	2.02	0.41
1:E:86:ASP:OD1	1:E:87:ILE:N	2.53	0.41
1:E:268:MET:HE3	1:E:288:LEU:HD12	2.03	0.41
1:F:69:ILE:HD12	1:F:69:ILE:HA	1.88	0.41
1:I:151:ILE:CG2	1:I:153:PHE:CE1	3.04	0.41
1:J:60:LEU:HB3	1:J:65:LEU:CD1	2.50	0.41
1:K:33:ALA:HB2	1:K:48:VAL:HG22	2.03	0.41
1:L:93:PHE:HE2	1:L:103:TYR:HE2	1.67	0.41
1:L:247:GLU:O	1:L:251:THR:HG23	2.20	0.41
1:L:271:LEU:HD23	1:L:271:LEU:HA	1.92	0.41
1:L:287:ILE:O	1:L:290:THR:HG22	2.20	0.41
1:A:89:THR:CG2	1:A:90:HIS:H	2.25	0.41
1:B:90:HIS:NE2	1:B:92:GLU:CG	2.79	0.41
1:B:223:ALA:O	1:B:228:PRO:CD	2.69	0.41
1:B:300:VAL:HG21	1:B:310:LEU:HD11	2.02	0.41
1:C:81:LEU:CD1	1:C:87:ILE:CD1	2.99	0.41
1:E:268:MET:CE	1:E:288:LEU:HD12	2.51	0.41
1:F:93:PHE:CD1	1:F:93:PHE:C	2.94	0.41
1:F:149:GLU:CG	1:F:150:GLY:N	2.73	0.41
1:F:269:ARG:HG3	1:F:333:THR:HB	2.03	0.41
1:F:288:LEU:HD11	1:F:324:LEU:HD13	2.03	0.41
1:G:47:GLU:HG3	1:G:52:LEU:HD23	2.03	0.41
1:G:119:GLN:NE2	1:H:182:LYS:HZ1	1.92	0.41
1:G:183:VAL:HG13	1:G:230:LEU:HD12	2.02	0.41
1:H:242:ILE:O	1:H:246:LEU:HG	2.21	0.41
1:I:47:GLU:CB	1:I:52:LEU:HD23	2.50	0.41
1:J:24:MET:HB3	1:J:24:MET:HE2	1.83	0.41
1:J:188:SER:HB3	1:J:189:PRO:HD3	2.03	0.41
1:K:188:SER:HA	1:K:210:PRO:HD3	2.03	0.41
1:C:151:ILE:HG21	1:C:153:PHE:CZ	2.57	0.41
1:F:44:ILE:HG22	1:F:55:ILE:HD11	2.03	0.41
1:G:229:ARG:NE	1:G:229:ARG:CA	2.84	0.41
1:G:264:VAL:O	1:G:267:THR:HB	2.21	0.41
1:G:345:GLN:CB	1:G:349:TRP:CZ3	3.03	0.41
1:H:209:ILE:N	1:H:210:PRO:CD	2.83	0.41
1:I:353:MET:HG3	1:I:357:GLN:NE2	2.36	0.41
1:J:9:MET:CG	1:J:10:PRO:CD	2.93	0.41
1:J:24:MET:HE3	1:J:25:LEU:CD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:183:VAL:O	1:J:204:VAL:HA	2.20	0.41
1:K:230:LEU:HD21	1:K:256:TYR:CD1	2.56	0.41
1:L:7:ASN:O	1:L:55:ILE:HA	2.21	0.41
1:L:262:SER:HA	1:L:296:TRP:CZ3	2.56	0.41
1:L:352:LYS:CA	1:L:365:TYR:CE1	3.04	0.41
1:B:7:ASN:N	1:B:7:ASN:ND2	2.68	0.40
1:B:93:PHE:CE1	1:B:101:TYR:CD2	3.06	0.40
1:B:260:HIS:CE1	1:C:221:ARG:NH2	2.89	0.40
1:B:320:VAL:HG13	1:B:339:LEU:HD13	2.04	0.40
1:D:199:THR:OG1	1:D:202:ALA:HB3	2.20	0.40
1:E:279:GLU:O	1:E:283:ARG:HG2	2.21	0.40
1:F:165:LEU:O	1:F:169:ILE:HG12	2.21	0.40
1:G:9:MET:HA	1:G:27:HIS:CE1	2.56	0.40
1:G:156:GLY:O	1:G:162:LYS:NZ	2.53	0.40
1:G:186:TYR:HA	1:G:207:SER:O	2.21	0.40
1:G:313:TYR:CE2	1:G:345:GLN:OE1	2.74	0.40
1:H:65:LEU:HA	1:H:68:LEU:HG	2.03	0.40
1:I:209:ILE:N	1:I:210:PRO:CD	2.84	0.40
1:I:317:ASP:H	1:I:320:VAL:HG23	1.86	0.40
1:J:35:ASP:OD2	1:K:227:LYS:CD	2.69	0.40
1:J:119:GLN:NE2	1:K:182:LYS:HE2	2.36	0.40
1:J:277:GLY:HA2	1:J:280:ARG:HB3	2.03	0.40
1:J:354:LYS:HG3	1:J:359:ILE:CD1	2.48	0.40
1:L:44:ILE:CG2	1:L:55:ILE:HD11	2.51	0.40
1:B:188:SER:OG	1:B:189:PRO:CD	2.69	0.40
1:B:366:LYS:C	1:B:366:LYS:CD	2.89	0.40
1:D:367:LEU:HD12	1:D:367:LEU:HA	1.88	0.40
1:F:182:LYS:HG3	1:F:203:VAL:CG1	2.51	0.40
1:G:222:ASN:O	1:G:225:ARG:CG	2.69	0.40
1:H:186:TYR:HB3	1:H:209:ILE:HD11	2.02	0.40
1:H:211:ARG:CD	1:H:212:HIS:CE1	3.04	0.40
1:K:23:ARG:O	1:K:26:GLU:HB2	2.21	0.40
1:K:24:MET:CE	1:K:44:ILE:CD1	2.91	0.40
1:K:288:LEU:CD1	1:K:325:LEU:CD2	2.88	0.40
1:A:40:THR:HG23	1:A:118:ILE:O	2.22	0.40
1:B:92:GLU:OE1	1:B:100:ARG:HD2	2.21	0.40
1:D:208:GLU:HG2	1:D:210:PRO:HD2	2.03	0.40
1:D:209:ILE:HD13	1:D:209:ILE:HA	1.82	0.40
1:E:137:LEU:HD23	1:E:141:ILE:CD1	2.51	0.40
1:E:208:GLU:HB3	1:E:212:HIS:CD2	2.56	0.40
1:F:49:TYR:CG	1:F:50:GLY:N	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:229:ARG:O	1:F:229:ARG:HG3	2.21	0.40
1:F:296:TRP:NE1	1:F:347:MET:HE2	2.18	0.40
1:F:342:GLN:NE2	1:F:342:GLN:HA	2.36	0.40
1:G:131:LYS:O	1:G:134:THR:CB	2.69	0.40
1:G:285:ILE:HD13	1:L:371:GLY:HA2	2.04	0.40
1:I:17:THR:O	1:I:20:PHE:N	2.55	0.40
1:I:69:ILE:CG2	1:I:70:ASN:N	2.84	0.40
1:I:80:GLN:HE21	1:I:80:GLN:HB2	1.79	0.40
1:I:110:CYS:CA	1:J:212:HIS:CE1	3.04	0.40
1:I:352:LYS:HA	1:I:365:TYR:CE1	2.57	0.40
1:J:27:HIS:ND1	1:J:27:HIS:C	2.75	0.40
1:J:65:LEU:CD2	1:J:118:ILE:O	2.62	0.40
1:J:271:LEU:HB3	1:J:287:ILE:HD13	2.03	0.40
1:K:101:TYR:N	1:K:101:TYR:CD1	2.90	0.40
1:L:128:THR:HG22	1:L:197:ILE:HD11	2.03	0.40
1:A:158:THR:HG23	1:A:260:HIS:CE1	2.57	0.40
1:B:355:PHE:CD1	1:B:355:PHE:O	2.75	0.40
1:C:37:THR:HG21	1:D:182:LYS:HD2	2.02	0.40
1:D:125:ILE:HG12	1:D:191:GLU:O	2.22	0.40
1:E:52:LEU:H	1:F:180:ASN:HB3	1.86	0.40
1:F:51:ARG:HG3	1:F:52:LEU:N	2.36	0.40
1:I:151:ILE:HG21	1:I:153:PHE:CZ	2.57	0.40
1:I:166:LEU:HD23	1:I:166:LEU:HA	1.92	0.40
1:I:177:SER:HA	1:I:200:ILE:HD13	2.03	0.40
1:J:183:VAL:CG1	1:J:230:LEU:HD22	2.40	0.40
1:J:302:THR:HG23	1:J:306:ARG:O	2.21	0.40
1:K:17:THR:HG23	1:K:18:PRO:CD	2.44	0.40
1:K:145:ILE:HA	1:K:145:ILE:HD12	1.90	0.40
1:A:250:LEU:HD23	1:A:250:LEU:HA	1.77	0.40
1:B:6:ILE:C	1:B:7:ASN:ND2	2.75	0.40
1:B:184:LEU:HG	1:B:228:PRO:HB3	2.03	0.40
1:C:319:GLU:H	1:C:319:GLU:HG3	1.67	0.40
1:D:209:ILE:HG13	1:D:216:PHE:CD1	2.57	0.40
1:D:223:ALA:O	1:D:228:PRO:CD	2.69	0.40
1:E:288:LEU:CB	1:E:325:LEU:CD2	2.99	0.40
1:E:368:ILE:HG23	1:E:369:ILE:N	2.36	0.40
1:F:13:PRO:CG	1:F:20:PHE:CG	3.04	0.40
1:F:112:VAL:HG13	1:F:117:ALA:HB3	2.02	0.40
1:F:288:LEU:HD12	1:F:324:LEU:CB	2.51	0.40
1:G:9:MET:CE	1:G:24:MET:CB	2.99	0.40
1:G:288:LEU:HD12	1:G:325:LEU:HD23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:315:VAL:HG13	1:H:315:VAL:O	2.21	0.40
1:I:111:LEU:CD2	1:J:212:HIS:HE2	2.35	0.40
1:J:66:GLY:O	1:J:69:ILE:HG22	2.22	0.40
1:K:135:MET:HA	1:K:135:MET:HE2	1.92	0.40
1:L:23:ARG:O	1:L:26:GLU:HB2	2.21	0.40
1:L:151:ILE:HG21	1:L:153:PHE:CZ	2.56	0.40

All (1) 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:C:198:GLU:OE1	1:F:7:ASN:ND2[1_565]	2.18	0.02

## 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	A	367/391 (94%)	352 (96%)	14 (4%)	1 (0%)	41 74
1	B	369/391 (94%)	351 (95%)	16 (4%)	2 (0%)	29 67
1	C	367/391 (94%)	349 (95%)	15 (4%)	3 (1%)	19 58
1	D	366/391 (94%)	352 (96%)	13 (4%)	1 (0%)	41 74
1	E	365/391 (93%)	346 (95%)	15 (4%)	4 (1%)	14 51
1	F	362/391 (93%)	344 (95%)	16 (4%)	2 (1%)	25 64
1	G	367/391 (94%)	351 (96%)	13 (4%)	3 (1%)	19 58
1	H	369/391 (94%)	346 (94%)	19 (5%)	4 (1%)	14 51
1	I	367/391 (94%)	347 (95%)	19 (5%)	1 (0%)	41 74
1	J	366/391 (94%)	347 (95%)	18 (5%)	1 (0%)	41 74
1	K	365/391 (93%)	346 (95%)	18 (5%)	1 (0%)	41 74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	362/391 (93%)	345 (95%)	14 (4%)	3 (1%)	19	58
All	All	4392/4692 (94%)	4176 (95%)	190 (4%)	26 (1%)	25	64

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	188	SER
1	E	332	VAL
1	G	332	VAL
1	H	188	SER
1	C	95	PRO
1	E	97	ARG
1	G	189	PRO
1	I	189	PRO
1	L	274	SER
1	A	189	PRO
1	C	188	SER
1	C	189	PRO
1	E	189	PRO
1	F	189	PRO
1	G	369	ILE
1	H	95	PRO
1	H	201	SER
1	H	371	GLY
1	L	189	PRO
1	L	210	PRO
1	E	95	PRO
1	F	95	PRO
1	B	95	PRO
1	D	189	PRO
1	J	189	PRO
1	K	189	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	A	322/343 (94%)	304 (94%)	18 (6%)	21	57
1	B	319/343 (93%)	304 (95%)	15 (5%)	26	62
1	C	318/343 (93%)	301 (95%)	17 (5%)	22	58
1	D	316/343 (92%)	301 (95%)	15 (5%)	26	62
1	E	315/343 (92%)	301 (96%)	14 (4%)	28	64
1	F	314/343 (92%)	296 (94%)	18 (6%)	20	56
1	G	322/343 (94%)	289 (90%)	33 (10%)	7	29
1	H	319/343 (93%)	301 (94%)	18 (6%)	21	57
1	I	318/343 (93%)	293 (92%)	25 (8%)	12	43
1	J	316/343 (92%)	288 (91%)	28 (9%)	9	35
1	K	315/343 (92%)	283 (90%)	32 (10%)	7	29
1	L	314/343 (92%)	292 (93%)	22 (7%)	15	48
All	All	3808/4116 (92%)	3553 (93%)	255 (7%)	16	50

All (255) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	16	PHE
1	A	34	SER
1	A	53	LEU
1	A	69	ILE
1	A	87	ILE
1	A	93	PHE
1	A	149	GLU
1	A	160	SER
1	A	162	LYS
1	A	174	ILE
1	A	193	VAL
1	A	232	MET
1	A	274	SER
1	A	276	SER
1	A	285	ILE
1	A	362	GLU
1	A	367	LEU
1	B	7	ASN
1	B	22	ASP
1	B	53	LEU
1	B	59	ARG

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Mol	Chain	Res	Type
1	B	90	HIS
1	B	93	PHE
1	B	103	TYR
1	B	119	GLN
1	B	121	THR
1	B	149	GLU
1	B	162	LYS
1	B	178	ASP
1	B	191	GLU
1	B	201	SER
1	B	366	LYS
1	C	12	GLU
1	C	22	ASP
1	C	60	LEU
1	C	78	THR
1	C	121	THR
1	C	149	GLU
1	C	162	LYS
1	C	177	SER
1	C	209	ILE
1	C	222	ASN
1	C	228	PRO
1	C	281	LEU
1	C	292	ARG
1	C	293	LEU
1	C	317	ASP
1	C	325	LEU
1	C	369	ILE
1	D	11	ASP
1	D	21	MET
1	D	34	SER
1	D	93	PHE
1	D	118	ILE
1	D	127	THR
1	D	132	LEU
1	D	137	LEU
1	D	149	GLU
1	D	200	ILE
1	D	227	LYS
1	D	251	THR
1	D	285	ILE
1	D	323	ILE

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Mol	Chain	Res	Type
1	D	328	ASP
1	E	8	LEU
1	E	12	GLU
1	E	22	ASP
1	E	32	ASN
1	E	60	LEU
1	E	92	GLU
1	E	162	LYS
1	E	174	ILE
1	E	215	ASN
1	E	235	GLU
1	E	251	THR
1	E	319	GLU
1	E	363	ARG
1	E	369	ILE
1	F	11	ASP
1	F	44	ILE
1	F	58	ARG
1	F	59	ARG
1	F	93	PHE
1	F	158	THR
1	F	176	THR
1	F	177	SER
1	F	178	ASP
1	F	180	ASN
1	F	181	ARG
1	F	188	SER
1	F	208	GLU
1	F	209	ILE
1	F	224	LEU
1	F	266	GLU
1	F	283	ARG
1	F	333	THR
1	G	9	MET
1	G	16	PHE
1	G	32	ASN
1	G	34	SER
1	G	51	ARG
1	G	53	LEU
1	G	87	ILE
1	G	94	ARG
1	G	111	LEU

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Mol	Chain	Res	Type
1	G	122	LEU
1	G	155	THR
1	G	162	LYS
1	G	180	ASN
1	G	181	ARG
1	G	188	SER
1	G	195	ASP
1	G	211	ARG
1	G	222	ASN
1	G	225	ARG
1	G	227	LYS
1	G	230	LEU
1	G	257	THR
1	G	274	SER
1	G	281	LEU
1	G	305	GLU
1	G	328	ASP
1	G	331	GLU
1	G	332	VAL
1	G	334	SER
1	G	342	GLN
1	G	360	ILE
1	G	361	SER
1	G	366	LYS
1	H	26	GLU
1	H	53	LEU
1	H	68	LEU
1	H	69	ILE
1	H	78	THR
1	H	88	ASP
1	H	93	PHE
1	H	100	ARG
1	H	121	THR
1	H	137	LEU
1	H	149	GLU
1	H	229	ARG
1	H	237	ARG
1	H	267	THR
1	H	326	GLU
1	H	342	GLN
1	H	353	MET
1	H	366	LYS

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Mol	Chain	Res	Type
1	I	11	ASP
1	I	40	THR
1	I	47	GLU
1	I	53	LEU
1	I	64	GLU
1	I	72	ILE
1	I	108	THR
1	I	121	THR
1	I	125	ILE
1	I	143	GLU
1	I	149	GLU
1	I	155	THR
1	I	158	THR
1	I	162	LYS
1	I	177	SER
1	I	188	SER
1	I	198	GLU
1	I	209	ILE
1	I	222	ASN
1	I	250	LEU
1	I	292	ARG
1	I	305	GLU
1	I	325	LEU
1	I	347	MET
1	I	353	MET
1	J	8	LEU
1	J	15	ARG
1	J	16	PHE
1	J	29	GLU
1	J	39	GLN
1	J	40	THR
1	J	92	GLU
1	J	99	VAL
1	J	118	ILE
1	J	132	LEU
1	J	145	ILE
1	J	149	GLU
1	J	158	THR
1	J	164	THR
1	J	191	GLU
1	J	199	THR
1	J	209	ILE

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Mol	Chain	Res	Type
1	J	215	ASN
1	J	227	LYS
1	J	266	GLU
1	J	270	ARG
1	J	306	ARG
1	J	322	ASP
1	J	328	ASP
1	J	334	SER
1	J	353	MET
1	J	366	LYS
1	J	367	LEU
1	K	8	LEU
1	K	9	MET
1	K	15	ARG
1	K	16	PHE
1	K	32	ASN
1	K	53	LEU
1	K	83	SER
1	K	108	THR
1	K	116	ASP
1	K	135	MET
1	K	139	ASP
1	K	141	ILE
1	K	145	ILE
1	K	162	LYS
1	K	174	ILE
1	K	178	ASP
1	K	188	SER
1	K	197	ILE
1	K	211	ARG
1	K	215	ASN
1	K	232	MET
1	K	235	GLU
1	K	251	THR
1	K	273	THR
1	K	290	THR
1	K	306	ARG
1	K	319	GLU
1	K	336	THR
1	K	341	ARG
1	K	365	TYR
1	K	366	LYS

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Mol	Chain	Res	Type
1	K	369	ILE
1	L	11	ASP
1	L	34	SER
1	L	40	THR
1	L	54	LYS
1	L	59	ARG
1	L	65	LEU
1	L	112	VAL
1	L	115	HIS
1	L	155	THR
1	L	158	THR
1	L	162	LYS
1	L	164	THR
1	L	176	THR
1	L	177	SER
1	L	188	SER
1	L	209	ILE
1	L	218	ASP
1	L	224	LEU
1	L	226	ARG
1	L	274	SER
1	L	284	THR
1	L	304	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	119	GLN
1	A	212	HIS
1	A	253	HIS
1	A	297	GLN
1	A	357	GLN
1	B	7	ASN
1	B	119	GLN
1	B	212	HIS
1	B	215	ASN
1	B	253	HIS
1	B	260	HIS
1	C	80	GLN
1	C	119	GLN
1	C	212	HIS

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Mol	Chain	Res	Type
1	C	215	ASN
1	C	253	HIS
1	C	297	GLN
1	C	345	GLN
1	D	39	GLN
1	D	80	GLN
1	D	136	ASN
1	D	212	HIS
1	D	215	ASN
1	D	253	HIS
1	D	260	HIS
1	E	119	GLN
1	E	212	HIS
1	E	215	ASN
1	E	222	ASN
1	E	297	GLN
1	F	27	HIS
1	F	39	GLN
1	F	80	GLN
1	F	180	ASN
1	F	212	HIS
1	F	253	HIS
1	F	260	HIS
1	F	342	GLN
1	G	80	GLN
1	G	119	GLN
1	G	180	ASN
1	G	212	HIS
1	G	253	HIS
1	G	260	HIS
1	G	297	GLN
1	H	7	ASN
1	H	27	HIS
1	H	212	HIS
1	H	215	ASN
1	H	260	HIS
1	H	330	ASN
1	H	357	GLN
1	I	27	HIS
1	I	80	GLN
1	I	180	ASN
1	I	212	HIS

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Mol	Chain	Res	Type
1	I	253	HIS
1	I	345	GLN
1	I	357	GLN
1	J	39	GLN
1	J	140	ASN
1	J	215	ASN
1	J	253	HIS
1	J	260	HIS
1	K	27	HIS
1	K	62	ASN
1	K	119	GLN
1	K	212	HIS
1	K	222	ASN
1	K	297	GLN
1	L	39	GLN
1	L	115	HIS
1	L	180	ASN
1	L	206	GLN
1	L	222	ASN
1	L	253	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

12 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	C	401	-	4,4,4	0.82	0	6,6,6	0.81	0
2	PO4	I	401	-	4,4,4	0.82	0	6,6,6	1.40	0
2	PO4	L	401	-	4,4,4	0.87	0	6,6,6	0.67	0
2	PO4	H	401	-	4,4,4	0.85	0	6,6,6	1.37	1 (16%)
2	PO4	E	401	-	4,4,4	1.08	0	6,6,6	0.95	0
2	PO4	K	401	-	4,4,4	0.90	0	6,6,6	1.18	0
2	PO4	A	401	-	4,4,4	0.66	0	6,6,6	0.93	0
2	PO4	B	401	-	4,4,4	0.88	0	6,6,6	1.32	1 (16%)
2	PO4	F	401	-	4,4,4	0.94	0	6,6,6	1.41	0
2	PO4	G	401	-	4,4,4	0.85	0	6,6,6	1.29	1 (16%)
2	PO4	J	401	-	4,4,4	0.71	0	6,6,6	1.37	0
2	PO4	D	401	-	4,4,4	0.94	0	6,6,6	1.41	2 (33%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	PO4	O4-P-O3	2.65	116.15	107.91
2	H	401	PO4	O4-P-O1	-2.54	101.98	110.95
2	G	401	PO4	O3-P-O1	-2.51	102.08	110.95
2	D	401	PO4	O4-P-O1	-2.14	103.37	110.95
2	B	401	PO4	O2-P-O1	-2.08	103.58	110.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	401	PO4	1	0
2	J	401	PO4	2	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



## 6 Fit of model and data

### 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	A	369/391 (94%)	0.12	15 (4%) 37 24	60, 96, 130, 172	0
1	B	371/391 (94%)	-0.07	3 (0%) 86 78	62, 86, 119, 162	0
1	C	369/391 (94%)	-0.06	2 (0%) 91 86	57, 85, 115, 161	0
1	D	368/391 (94%)	-0.01	8 (2%) 62 48	57, 90, 121, 160	0
1	E	367/391 (93%)	0.08	8 (2%) 62 48	66, 96, 139, 164	0
1	F	366/391 (93%)	0.04	9 (2%) 57 43	64, 93, 122, 140	0
1	G	369/391 (94%)	0.08	12 (3%) 46 30	69, 101, 142, 165	0
1	H	371/391 (94%)	-0.02	6 (1%) 72 59	58, 89, 118, 169	0
1	I	369/391 (94%)	0.20	12 (3%) 46 30	71, 111, 151, 170	0
1	J	368/391 (94%)	0.08	4 (1%) 80 69	75, 102, 125, 141	0
1	K	367/391 (93%)	0.20	20 (5%) 25 14	74, 112, 150, 168	0
1	L	366/391 (93%)	0.31	16 (4%) 34 21	79, 110, 138, 162	0
All	All	4420/4692 (94%)	0.08	115 (2%) 56 40	57, 98, 136, 172	0

All (115) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	178	ASP	5.3
1	J	49	TYR	5.3
1	F	56	THR	4.4
1	J	304	ASP	4.3
1	G	362	GLU	4.2
1	L	9	MET	4.2
1	K	18	PRO	4.1
1	L	95	PRO	4.0
1	J	303	VAL	3.9
1	L	16	PHE	3.8
1	L	359	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	I	16	PHE	3.7
1	L	305	GLU	3.6
1	E	300	VAL	3.6
1	D	15	ARG	3.5
1	K	350	ASP	3.5
1	K	347	MET	3.5
1	K	310	LEU	3.5
1	F	14	THR	3.4
1	K	364	VAL	3.4
1	A	300	VAL	3.4
1	K	312	GLU	3.3
1	A	351	ALA	3.3
1	A	362	GLU	3.3
1	G	346	LEU	3.2
1	B	178	ASP	3.2
1	K	372	ALA	3.2
1	K	359	ILE	3.2
1	H	97	ARG	3.1
1	I	347	MET	3.1
1	K	362	GLU	3.0
1	G	363	ARG	3.0
1	B	278	GLU	3.0
1	G	121	THR	3.0
1	L	20	PHE	3.0
1	L	308	VAL	2.9
1	L	301	PRO	2.9
1	F	9	MET	2.9
1	D	13	PRO	2.8
1	D	16	PHE	2.8
1	L	360	ILE	2.8
1	K	46	ALA	2.8
1	J	359	ILE	2.8
1	F	15	ARG	2.8
1	I	21	MET	2.7
1	I	37	THR	2.7
1	G	361	SER	2.7
1	L	299	LEU	2.6
1	K	22	ASP	2.6
1	A	368	ILE	2.6
1	L	358	GLY	2.6
1	H	361	SER	2.6
1	I	364	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	55	ILE	2.6
1	D	56	THR	2.6
1	A	350	ASP	2.6
1	G	278	GLU	2.6
1	A	365	TYR	2.6
1	D	214	PRO	2.6
1	I	368	ILE	2.5
1	F	67	ASP	2.5
1	D	277	GLY	2.5
1	K	93	PHE	2.5
1	G	364	VAL	2.5
1	K	357	GLN	2.5
1	K	360	ILE	2.4
1	L	80	GLN	2.4
1	I	362	GLU	2.4
1	I	303	VAL	2.4
1	E	106	ASN	2.4
1	L	353	MET	2.4
1	C	76	ASN	2.4
1	A	37	THR	2.4
1	G	349	TRP	2.3
1	K	366	LYS	2.3
1	L	101	TYR	2.3
1	I	365	TYR	2.3
1	C	57	ASN	2.3
1	G	354	LYS	2.3
1	L	361	SER	2.3
1	F	314	LEU	2.3
1	G	4	ASP	2.3
1	A	364	VAL	2.3
1	G	345	GLN	2.3
1	E	108	THR	2.3
1	K	96	ASN	2.3
1	K	16	PHE	2.2
1	E	362	GLU	2.2
1	B	238	ASP	2.2
1	F	5	ASN	2.2
1	H	15	ARG	2.2
1	E	37	THR	2.2
1	D	362	GLU	2.2
1	A	121	THR	2.2
1	K	348	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	277	GLY	2.2
1	E	301	PRO	2.2
1	D	18	PRO	2.1
1	K	303	VAL	2.1
1	F	275	PHE	2.1
1	A	366	LYS	2.1
1	I	9	MET	2.1
1	E	107	ALA	2.1
1	A	372	ALA	2.1
1	I	360	ILE	2.1
1	K	240	GLU	2.1
1	A	354	LYS	2.0
1	L	355	PHE	2.0
1	G	304	ASP	2.0
1	H	33	ALA	2.0
1	A	355	PHE	2.0
1	A	363	ARG	2.0
1	I	36	ILE	2.0
1	F	20	PHE	2.0
1	H	9	MET	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 monosaccharides 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	PO4	E	401	5/5	0.89	0.21	82,82,85,88	0
2	PO4	A	401	5/5	0.90	0.24	65,68,71,73	0
2	PO4	H	401	5/5	0.90	0.34	72,73,74,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	L	401	5/5	0.91	0.22	100,104,115,124	0
2	PO4	F	401	5/5	0.93	0.29	73,74,78,84	0
2	PO4	J	401	5/5	0.94	0.23	86,89,99,104	0
2	PO4	G	401	5/5	0.95	0.29	65,71,78,82	0
2	PO4	K	401	5/5	0.95	0.27	93,97,98,101	0
2	PO4	I	401	5/5	0.95	0.26	88,91,104,105	0
2	PO4	B	401	5/5	0.96	0.27	66,67,72,74	0
2	PO4	D	401	5/5	0.96	0.18	75,77,83,88	0
2	PO4	C	401	5/5	0.98	0.27	69,71,73,77	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.