



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2023 – 07:13 PM EDT

PDB ID : 2Q50  
Title : Ensemble refinement of the protein crystal structure of a glyoxylate/hydroxy pyruvate reductase from Homo sapiens  
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)  
Deposited on : 2007-05-31  
Resolution : 2.45 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

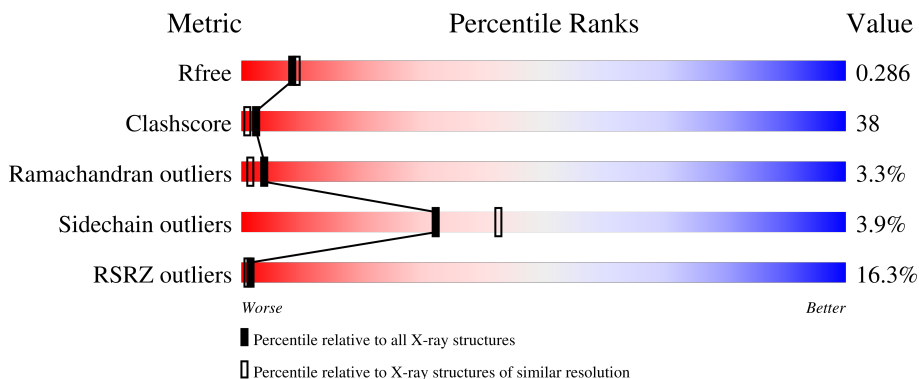
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	1-A	328	
1	1-B	328	
1	1-C	328	
1	1-D	328	
1	2-A	328	

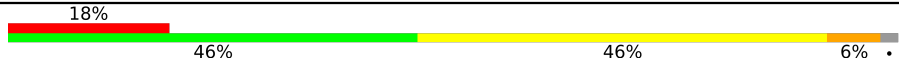

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Mol	Chain	Length	Quality of chain
1	2-B	328	
1	2-C	328	
1	2-D	328	
1	3-A	328	
1	3-B	328	
1	3-C	328	
1	3-D	328	
1	4-A	328	
1	4-B	328	
1	4-C	328	
1	4-D	328	
1	5-A	328	
1	5-B	328	
1	5-C	328	
1	5-D	328	
1	6-A	328	
1	6-B	328	
1	6-C	328	
1	6-D	328	
1	7-A	328	
1	7-B	328	
1	7-C	328	
1	7-D	328	
1	8-A	328	
1	8-B	328	

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Mol	Chain	Length	Quality of chain
1	8-C	328	
1	8-D	328	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 81744 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 Glyoxylate reductase/hydroxypyruvate reductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	1-A	321	2442	1542	431	457	7	5	0	0	0
1	2-A	321	2442	1542	431	457	7	5	0	0	0
1	3-A	321	2442	1542	431	457	7	5	0	0	0
1	4-A	321	2442	1542	431	457	7	5	0	0	0
1	5-A	321	2442	1542	431	457	7	5	0	0	0
1	6-A	321	2442	1542	431	457	7	5	0	0	0
1	7-A	321	2442	1542	431	457	7	5	0	0	0
1	8-A	321	2442	1542	431	457	7	5	0	0	0
1	1-B	321	2442	1542	431	457	7	5	0	0	0
1	2-B	321	2442	1542	431	457	7	5	0	0	0
1	3-B	321	2442	1542	431	457	7	5	0	0	0
1	4-B	321	2442	1542	431	457	7	5	0	0	0
1	5-B	321	2442	1542	431	457	7	5	0	0	0
1	6-B	321	2442	1542	431	457	7	5	0	0	0
1	7-B	321	2442	1542	431	457	7	5	0	0	0
1	8-B	321	2442	1542	431	457	7	5	0	0	0

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	2-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	3-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	4-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	5-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	6-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	7-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	8-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	1-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	2-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	3-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	4-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	5-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	6-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	7-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	8-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q9UBQ7
A	7	MSE	MET	modified residue	UNP Q9UBQ7
A	81	MSE	MET	modified residue	UNP Q9UBQ7
A	234	MSE	MET	modified residue	UNP Q9UBQ7
A	305	MSE	MET	modified residue	UNP Q9UBQ7
A	322	MSE	MET	modified residue	UNP Q9UBQ7
B	1	SER	-	expression tag	UNP Q9UBQ7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	7	MSE	MET	modified residue	UNP Q9UBQ7
B	81	MSE	MET	modified residue	UNP Q9UBQ7
B	234	MSE	MET	modified residue	UNP Q9UBQ7
B	305	MSE	MET	modified residue	UNP Q9UBQ7
B	322	MSE	MET	modified residue	UNP Q9UBQ7
C	1	SER	-	expression tag	UNP Q9UBQ7
C	7	MSE	MET	modified residue	UNP Q9UBQ7
C	81	MSE	MET	modified residue	UNP Q9UBQ7
C	234	MSE	MET	modified residue	UNP Q9UBQ7
C	305	MSE	MET	modified residue	UNP Q9UBQ7
C	322	MSE	MET	modified residue	UNP Q9UBQ7
D	1	SER	-	expression tag	UNP Q9UBQ7
D	7	MSE	MET	modified residue	UNP Q9UBQ7
D	81	MSE	MET	modified residue	UNP Q9UBQ7
D	234	MSE	MET	modified residue	UNP Q9UBQ7
D	305	MSE	MET	modified residue	UNP Q9UBQ7
D	322	MSE	MET	modified residue	UNP Q9UBQ7

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	103	Total O 103 103	0	0
2	2-A	104	Total O 104 104	0	0
2	3-A	104	Total O 104 104	0	0
2	4-A	104	Total O 104 104	0	0
2	5-A	111	Total O 111 111	0	0
2	6-A	107	Total O 107 107	0	0
2	7-A	106	Total O 106 106	0	0
2	8-A	108	Total O 108 108	0	0
2	1-B	130	Total O 130 130	0	0
2	2-B	128	Total O 128 128	0	0
2	3-B	128	Total O 128 128	0	0

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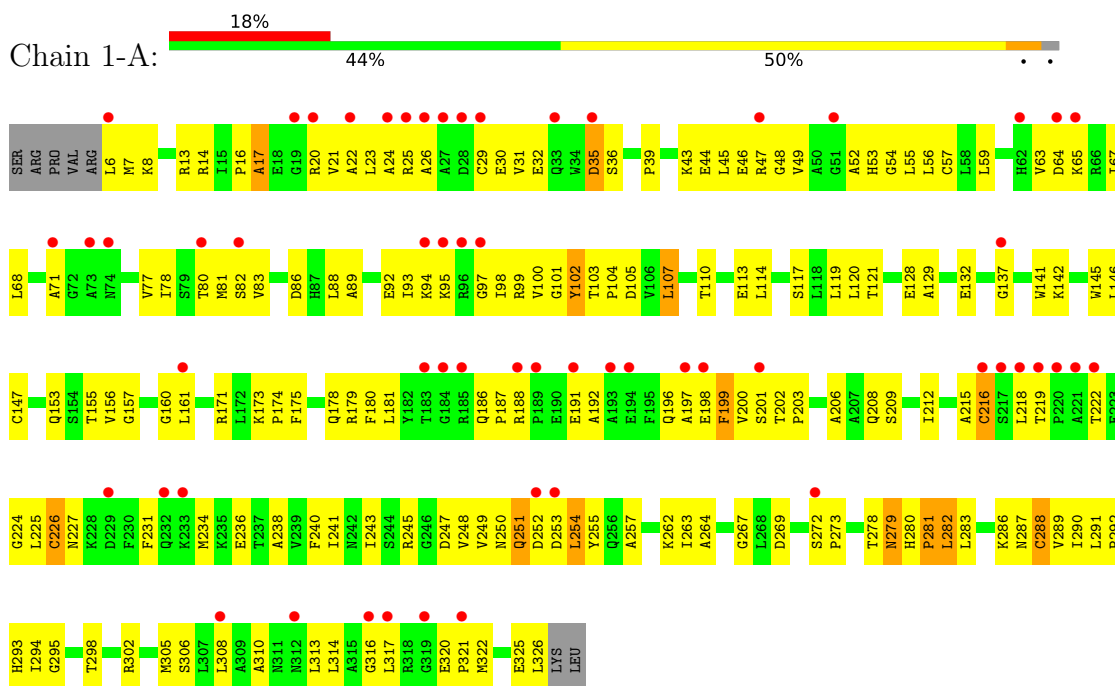
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	4-B	128	Total 128	O 128	0	0
2	5-B	121	Total 121	O 121	0	0
2	6-B	125	Total 125	O 125	0	0
2	7-B	126	Total 126	O 126	0	0
2	8-B	124	Total 124	O 124	0	0
2	1-C	122	Total 122	O 122	0	0
2	2-C	122	Total 122	O 122	0	0
2	3-C	121	Total 121	O 121	0	0
2	4-C	122	Total 122	O 122	0	0
2	5-C	121	Total 121	O 121	0	0
2	6-C	120	Total 120	O 120	0	0
2	7-C	119	Total 119	O 119	0	0
2	8-C	119	Total 119	O 119	0	0
2	1-D	95	Total 95	O 95	0	0
2	2-D	96	Total 96	O 96	0	0
2	3-D	97	Total 97	O 97	0	0
2	4-D	96	Total 96	O 96	0	0
2	5-D	97	Total 97	O 97	0	0
2	6-D	98	Total 98	O 98	0	0
2	7-D	99	Total 99	O 99	0	0
2	8-D	99	Total 99	O 99	0	0



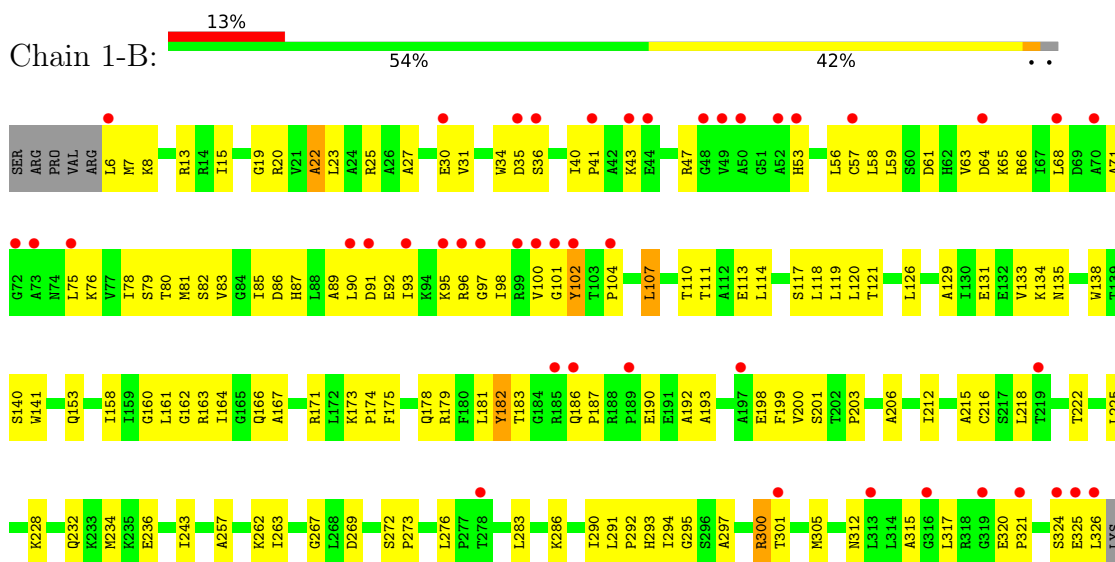
### 3 Residue-property plots [i](#)

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: Glyoxylate reductase/hydroxypyruvate reductase

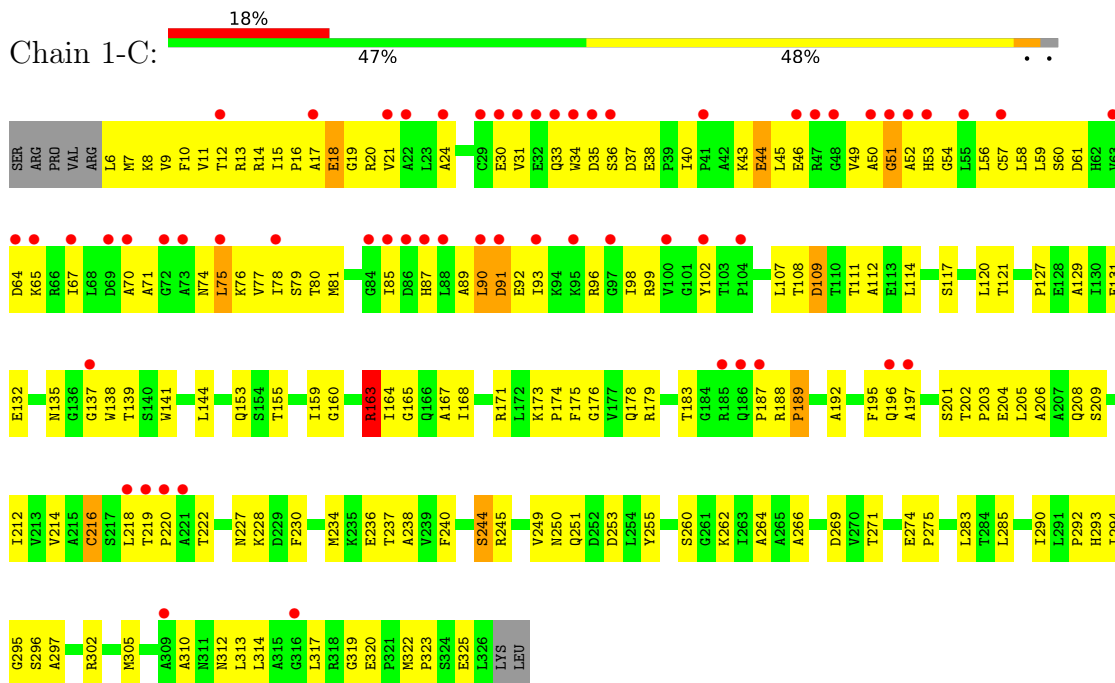


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

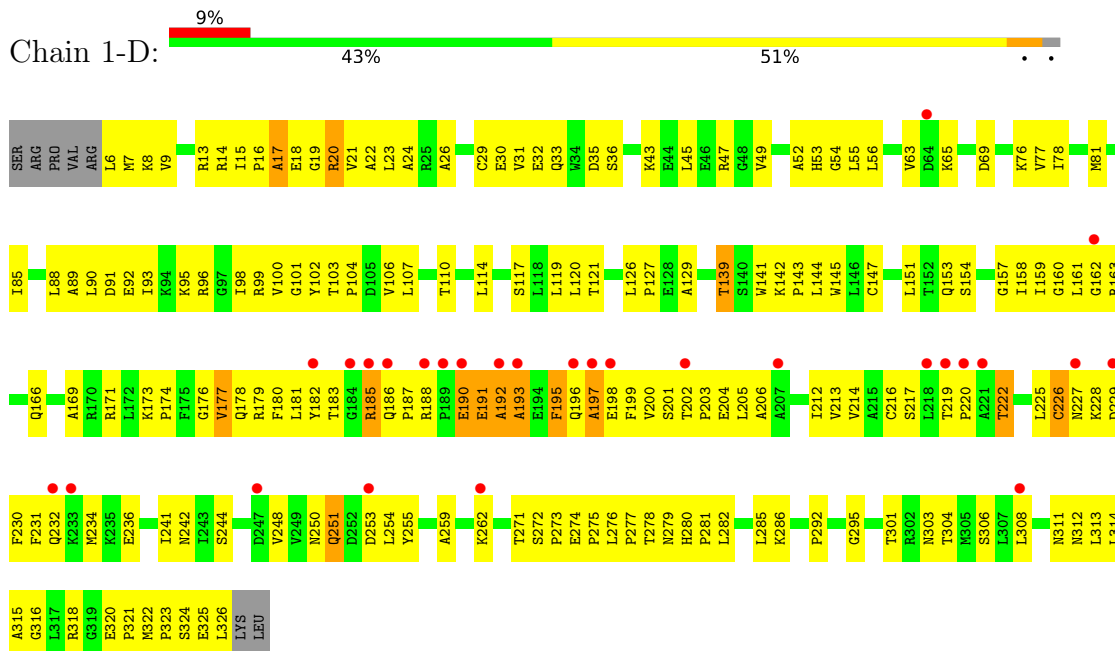


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- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

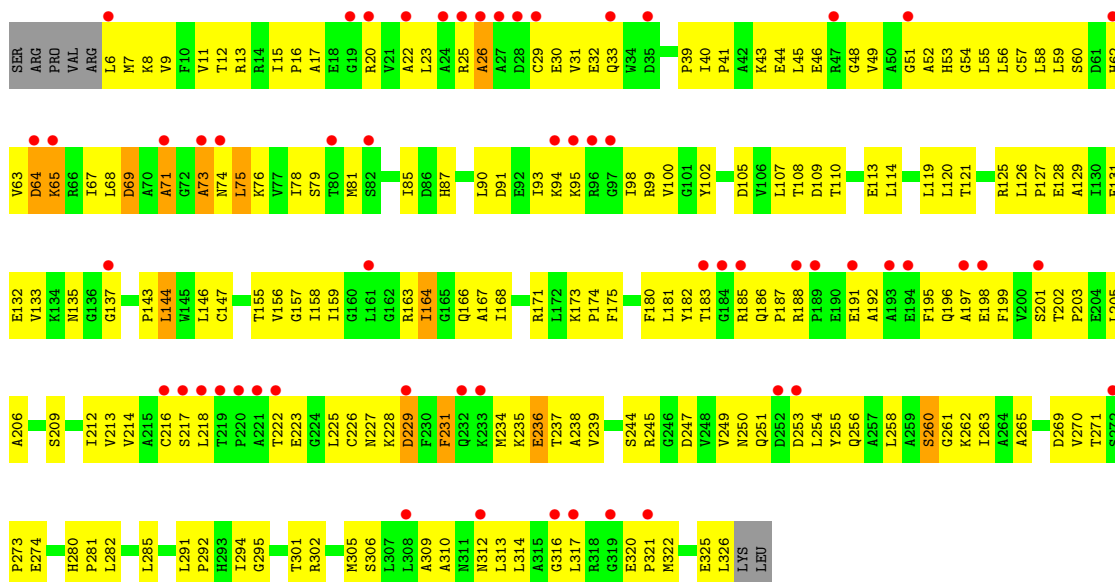


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

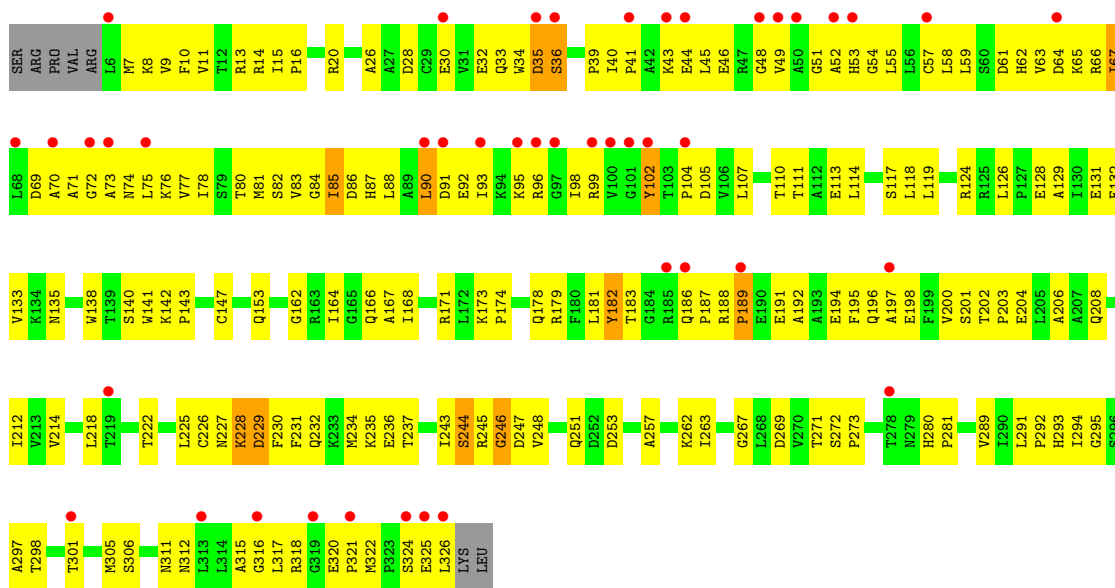
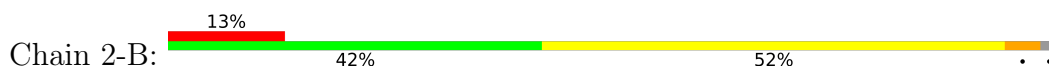


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

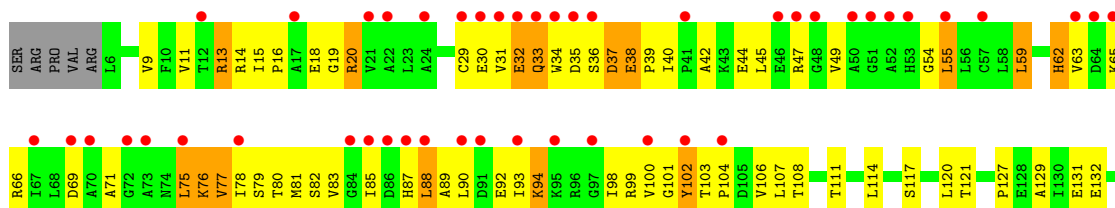


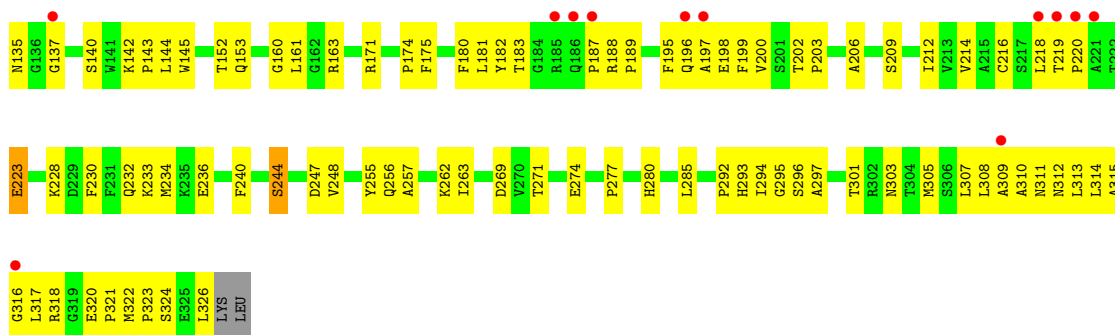


● Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

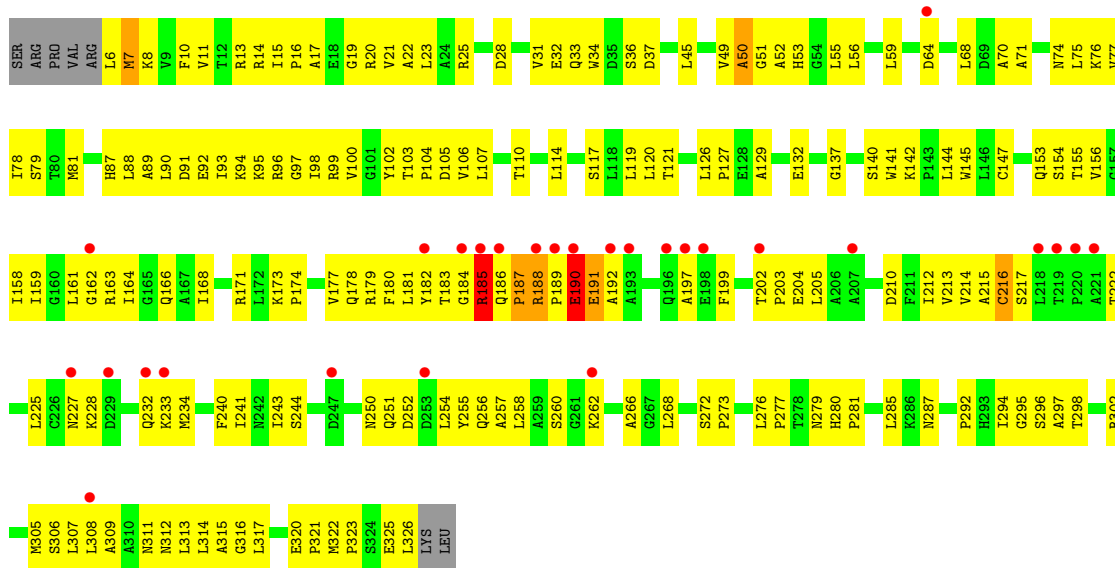


● Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

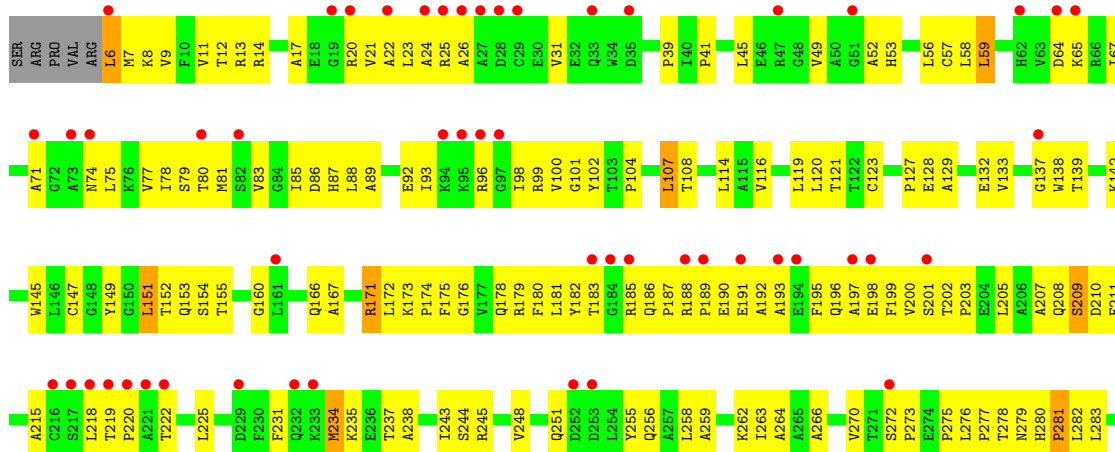
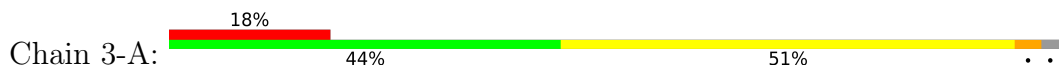




• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

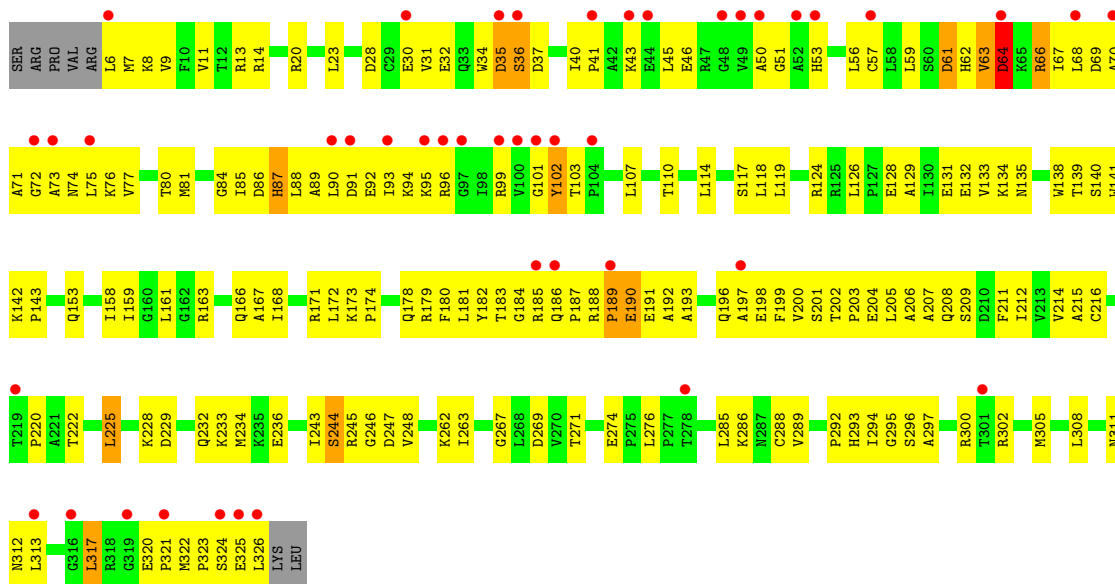


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

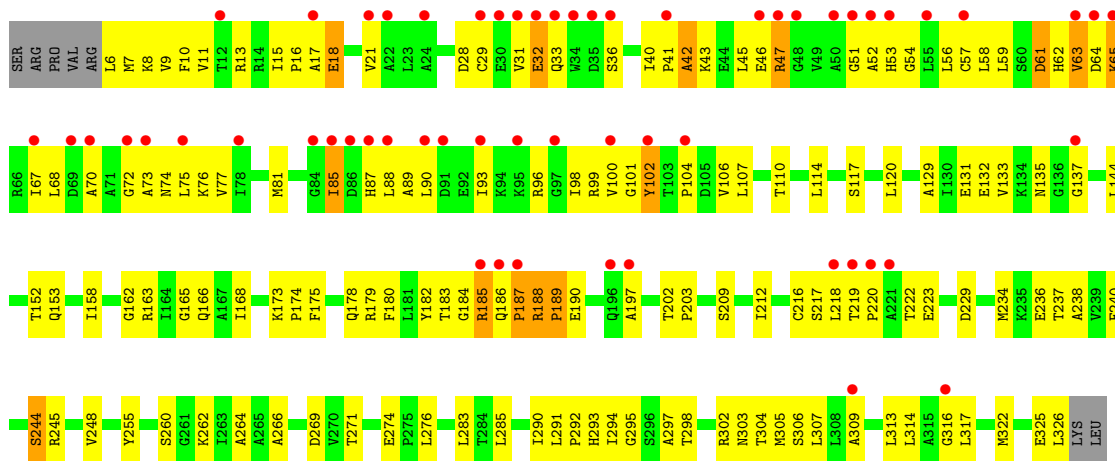




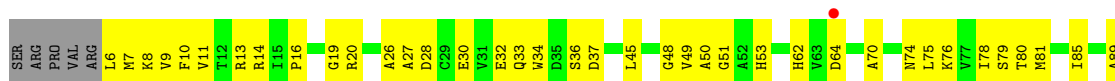
• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

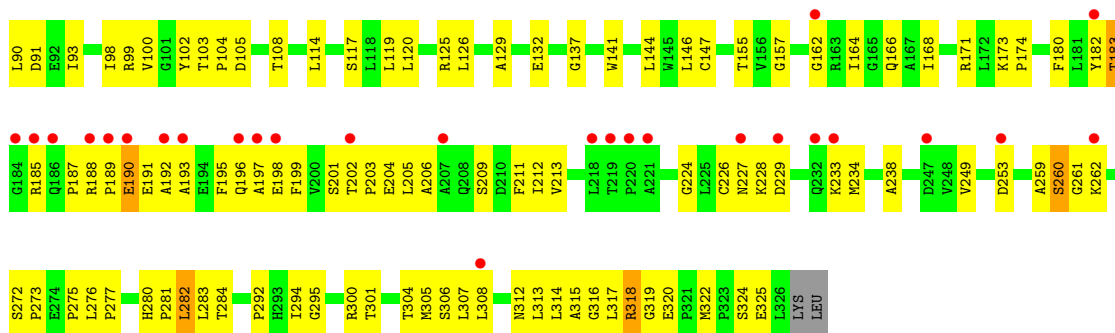


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

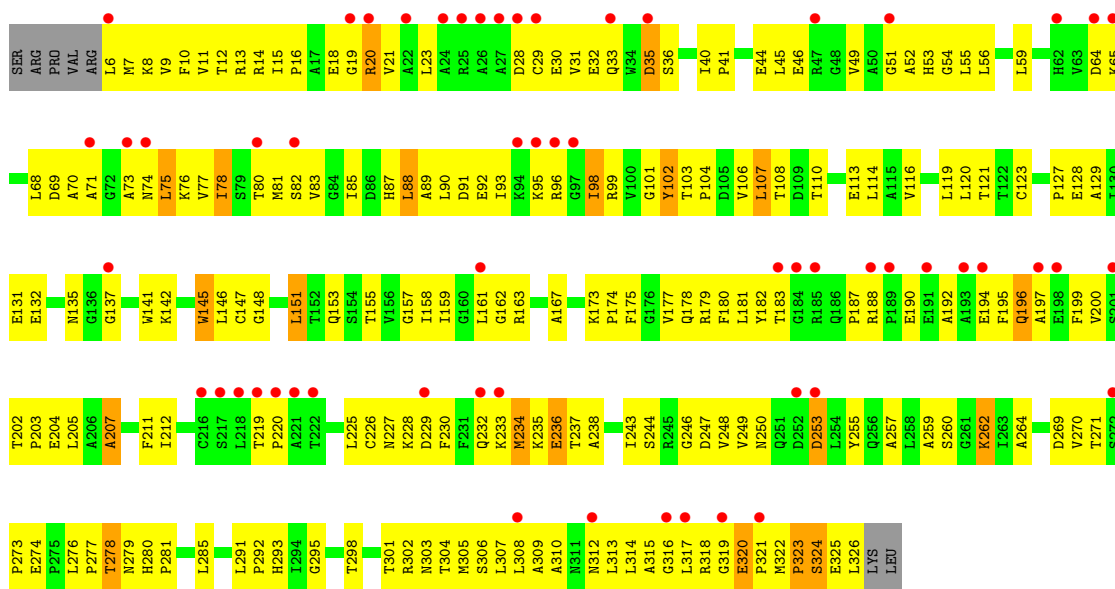


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

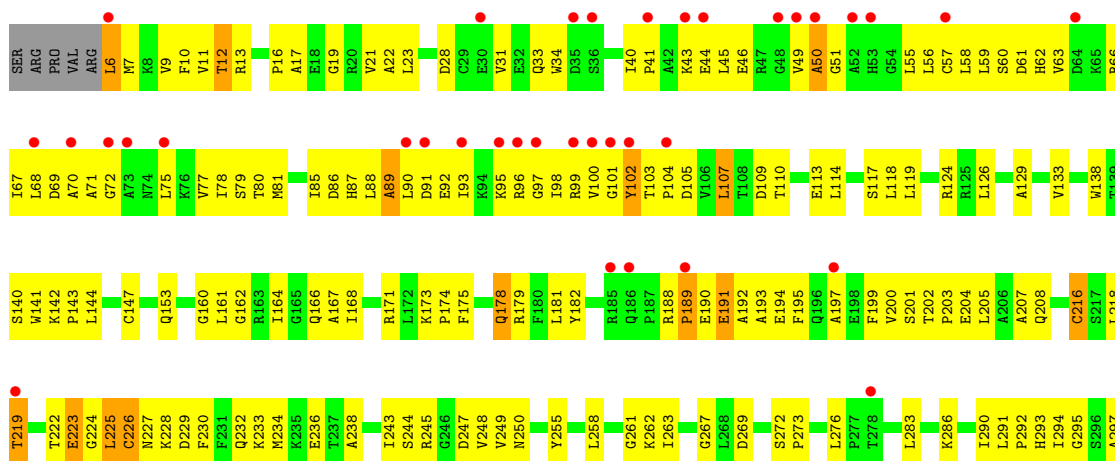


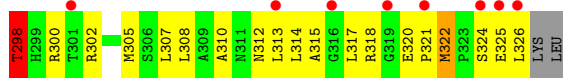


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

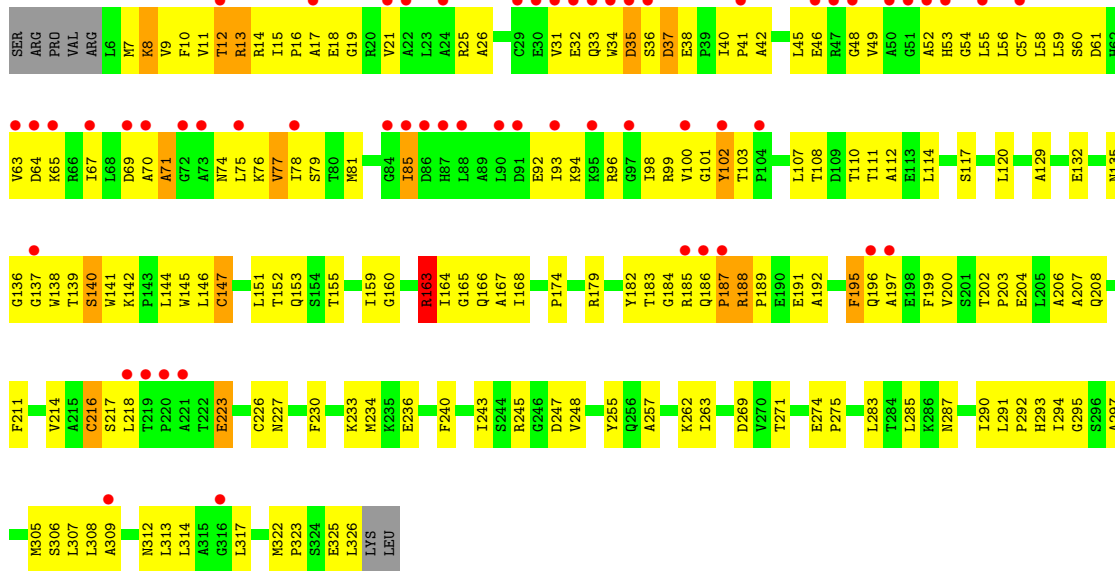


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

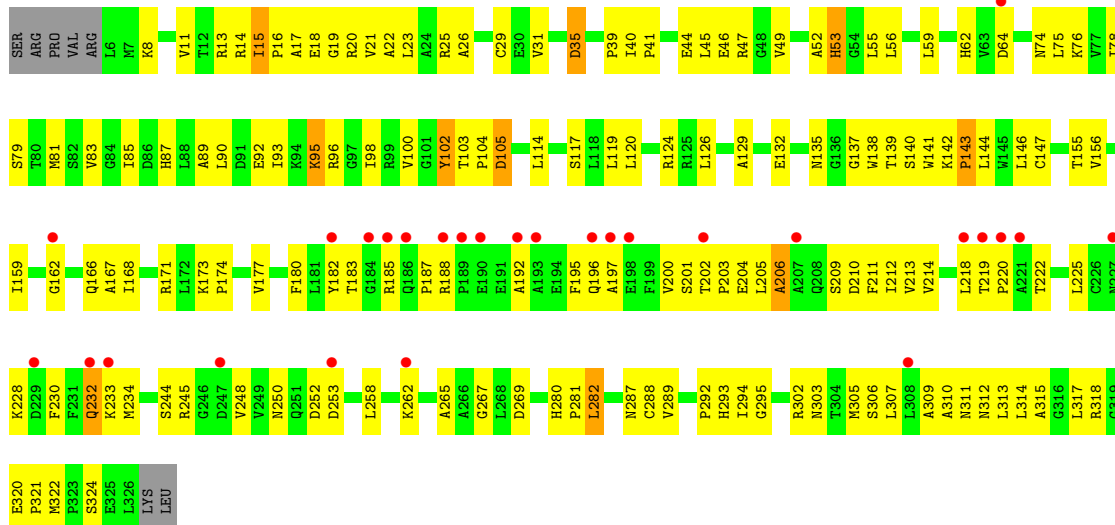




• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

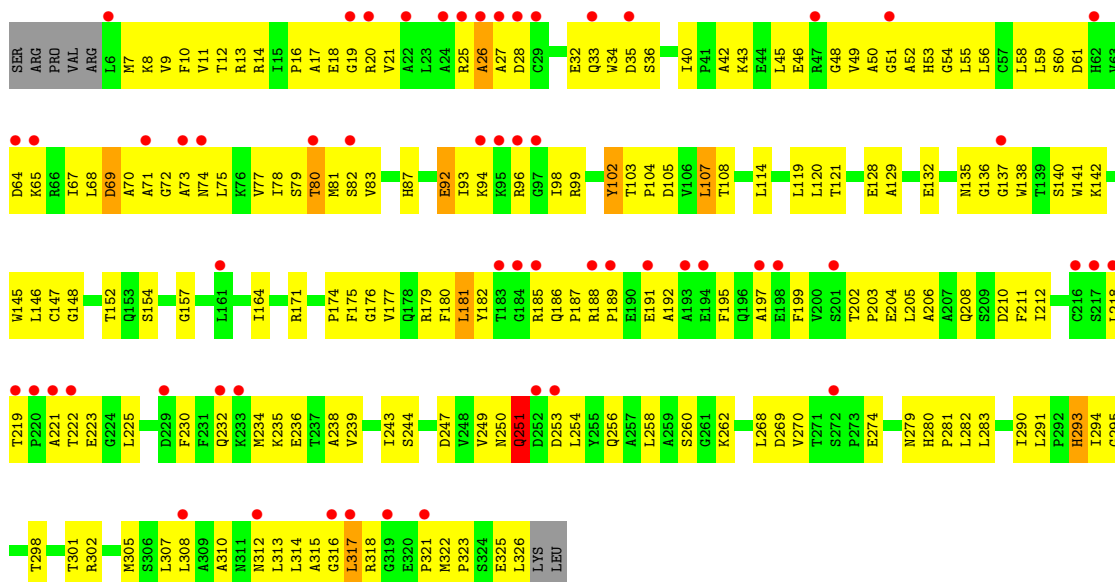


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

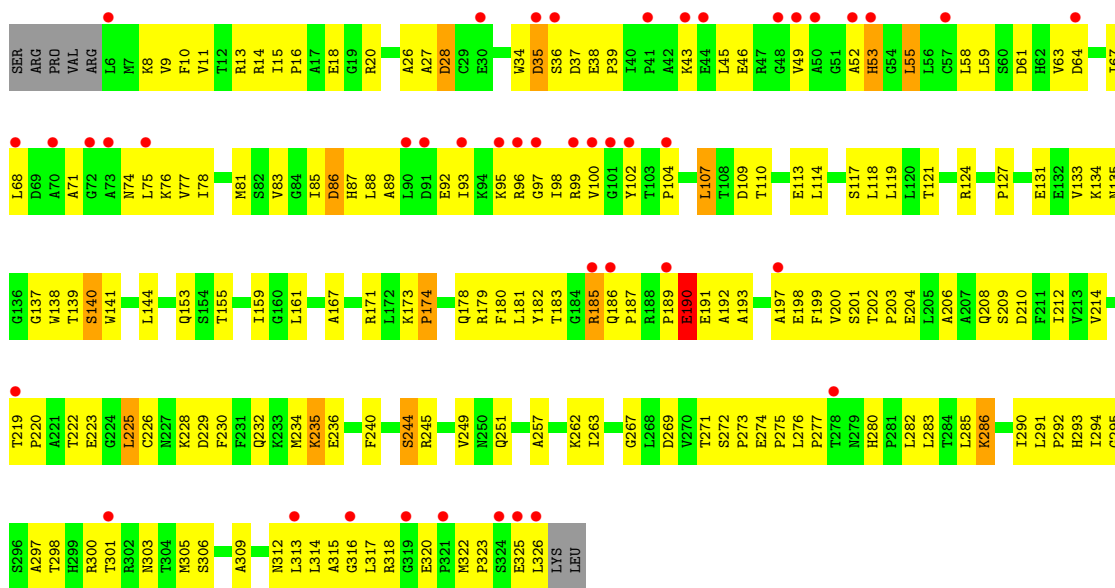


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

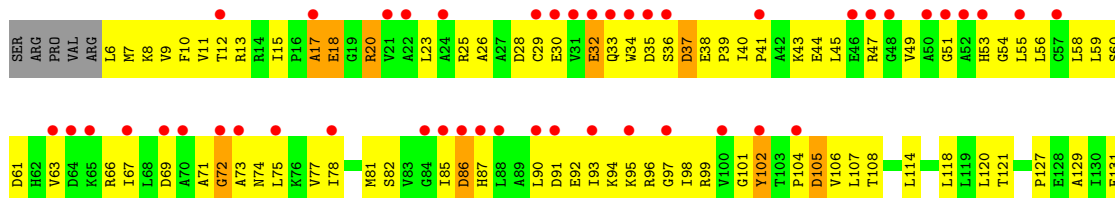




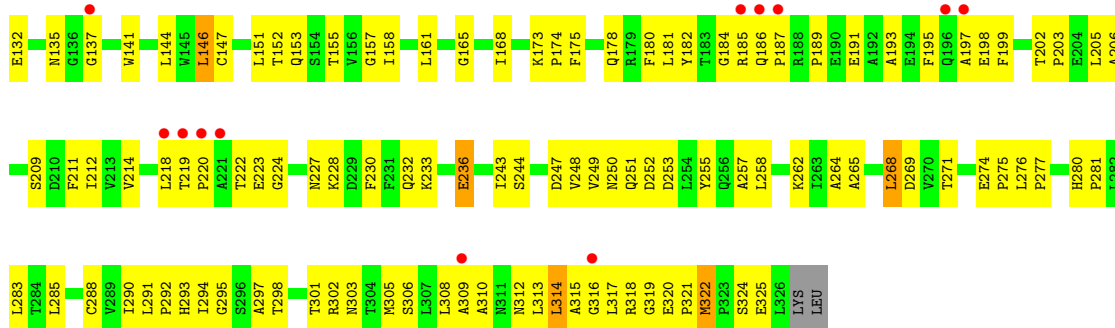
● Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



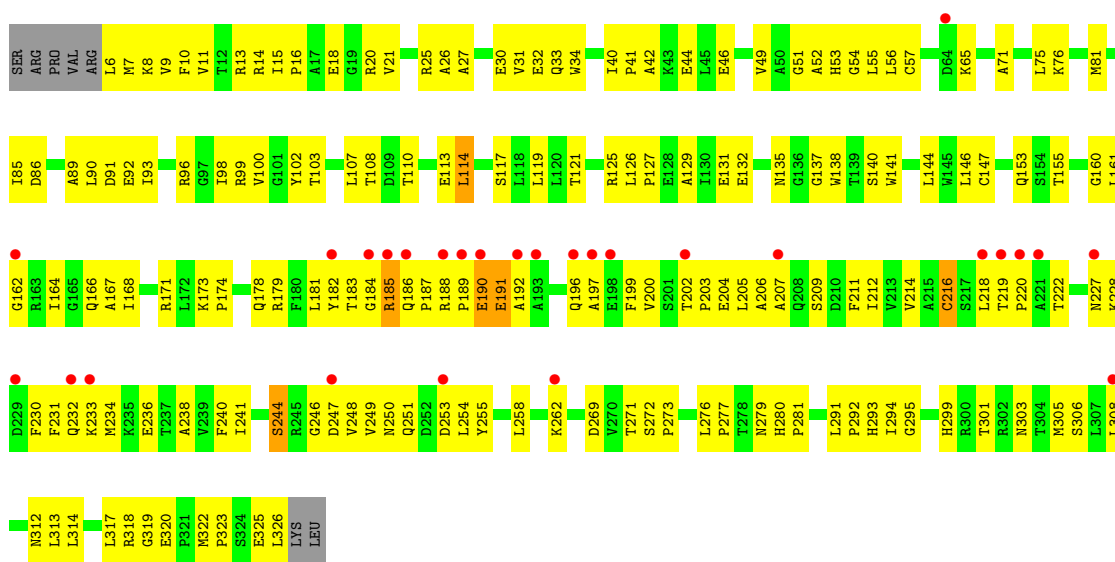
● Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



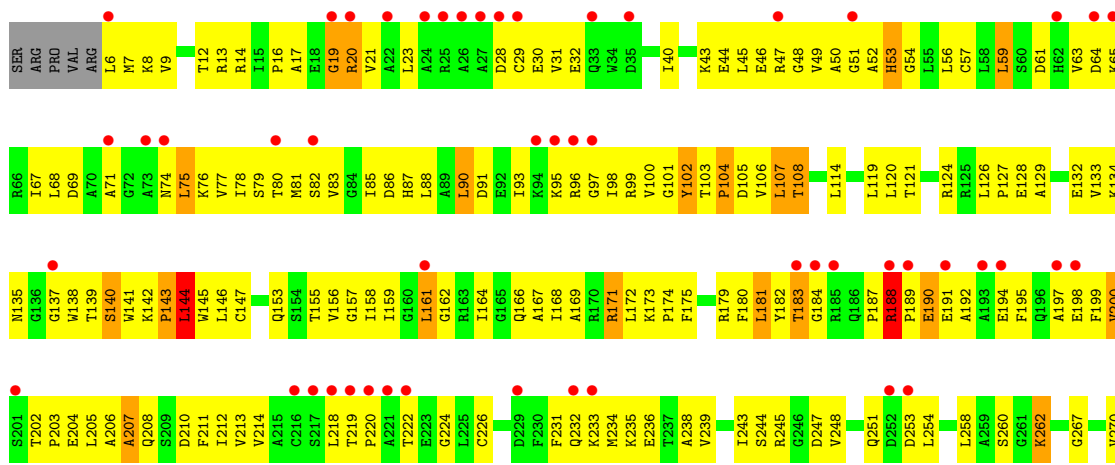


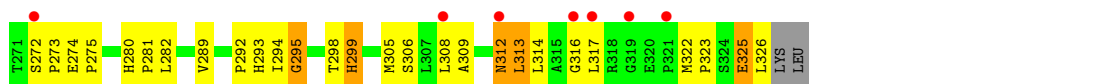


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

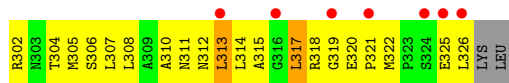
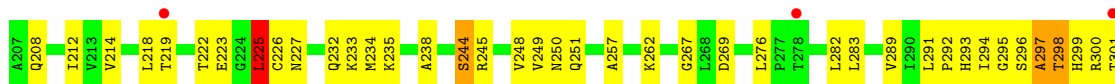
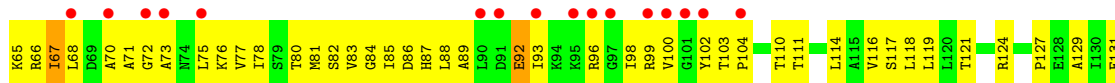


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

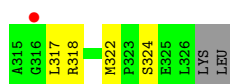
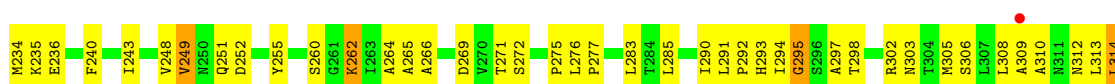
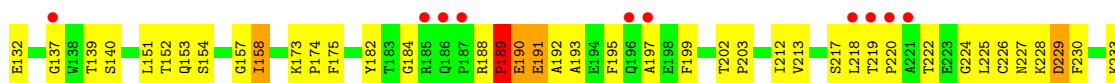
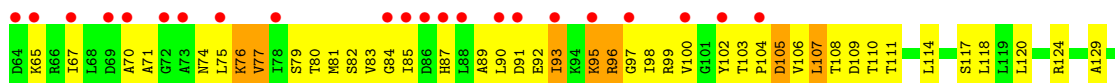
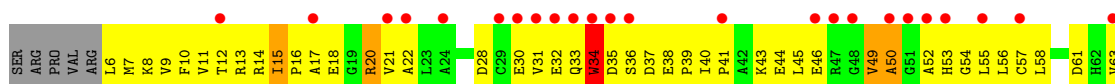




- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

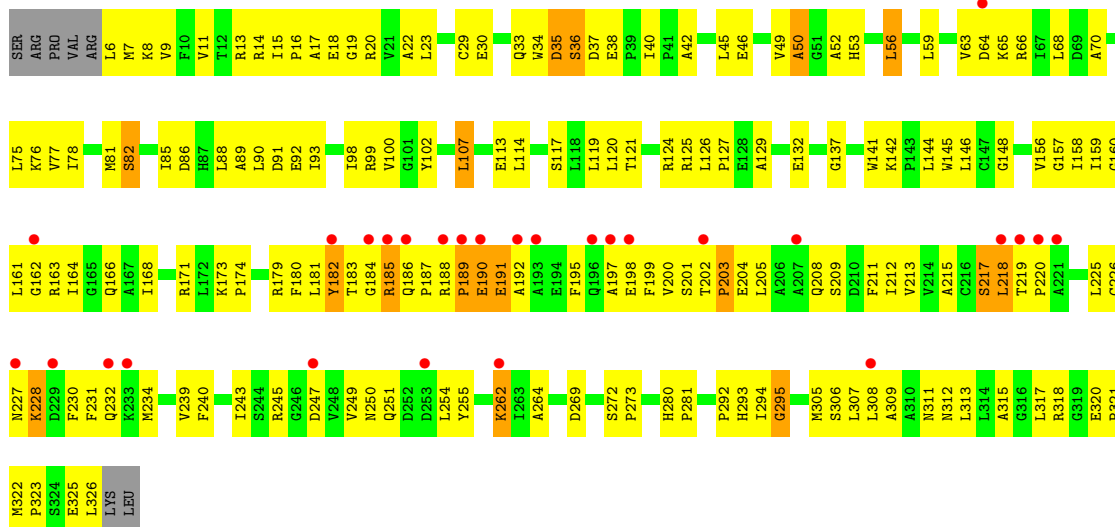


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

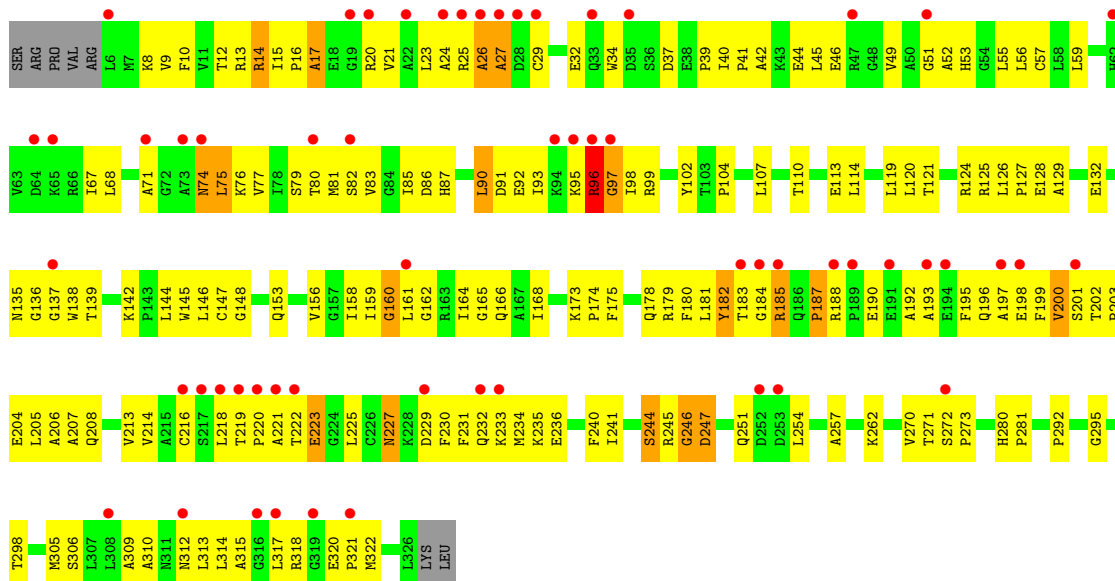


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

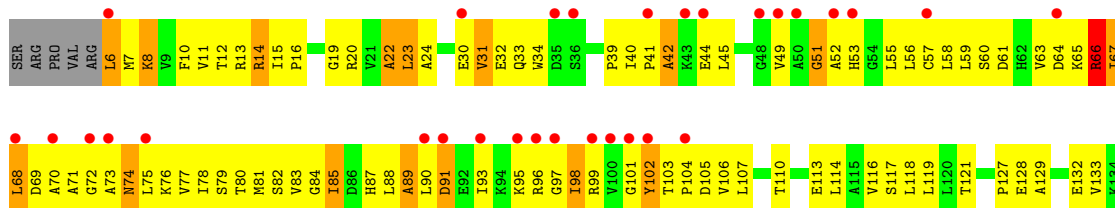
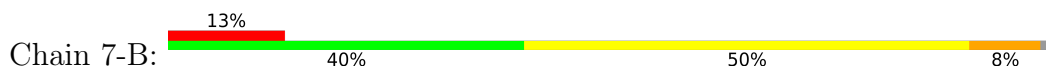


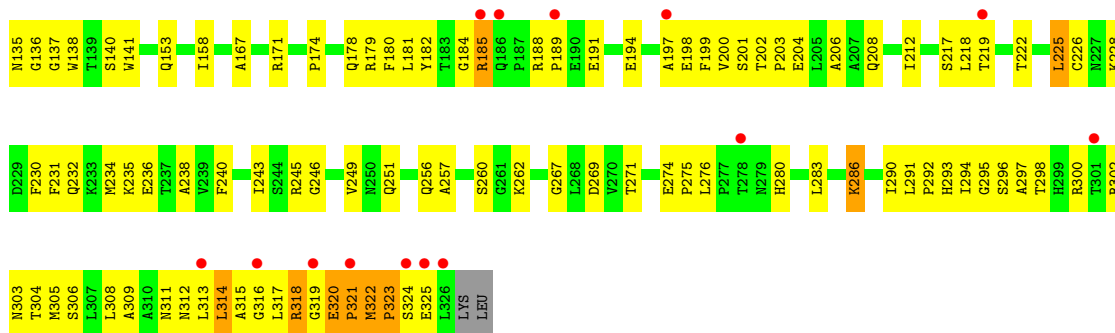


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

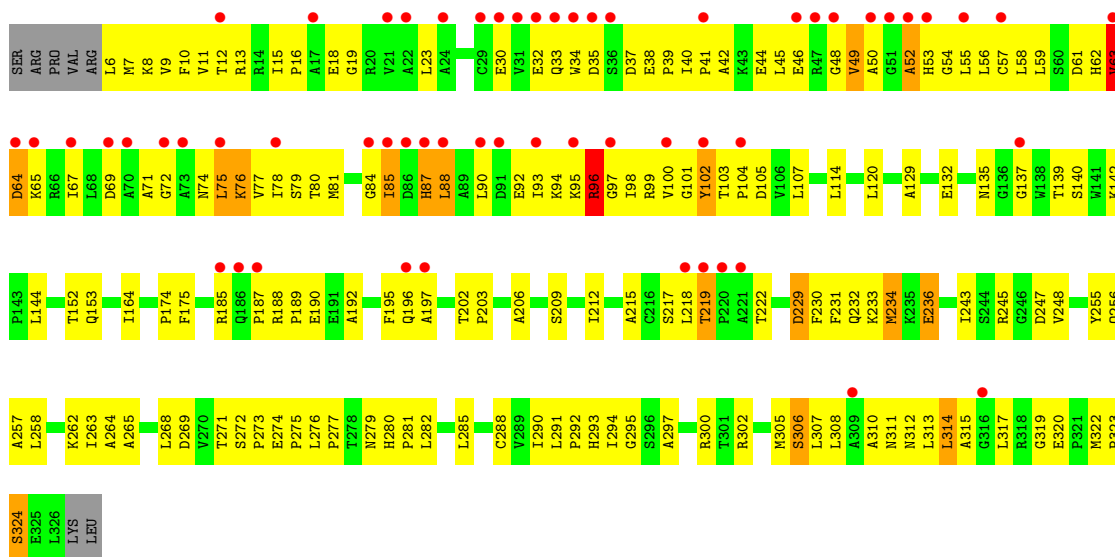


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

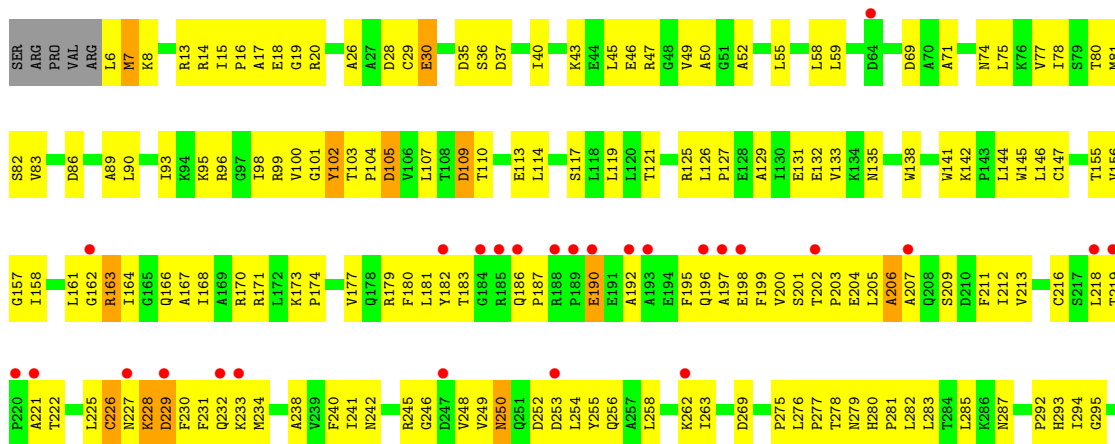




• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

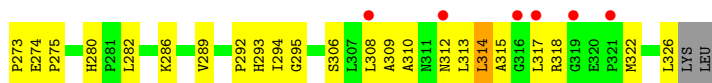
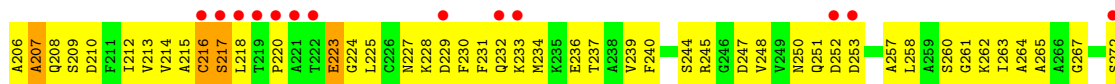
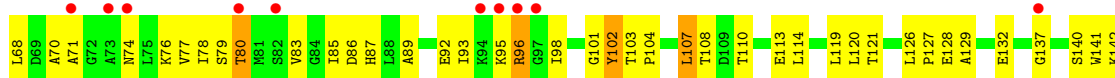
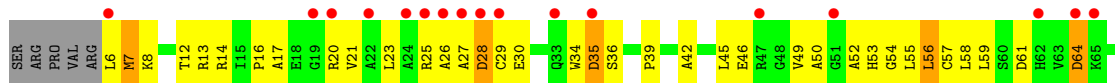


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

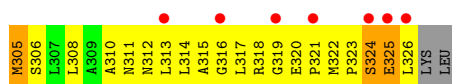
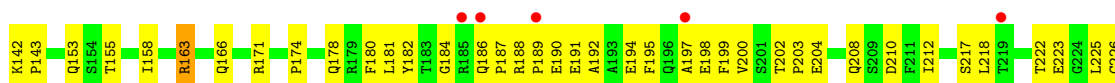
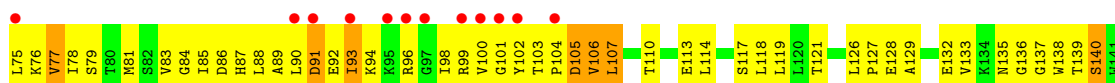
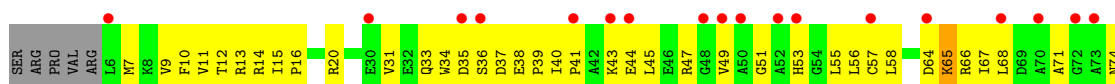
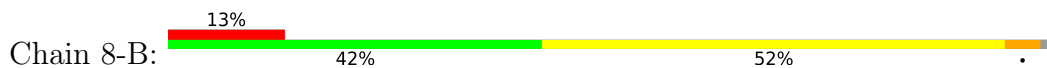




- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

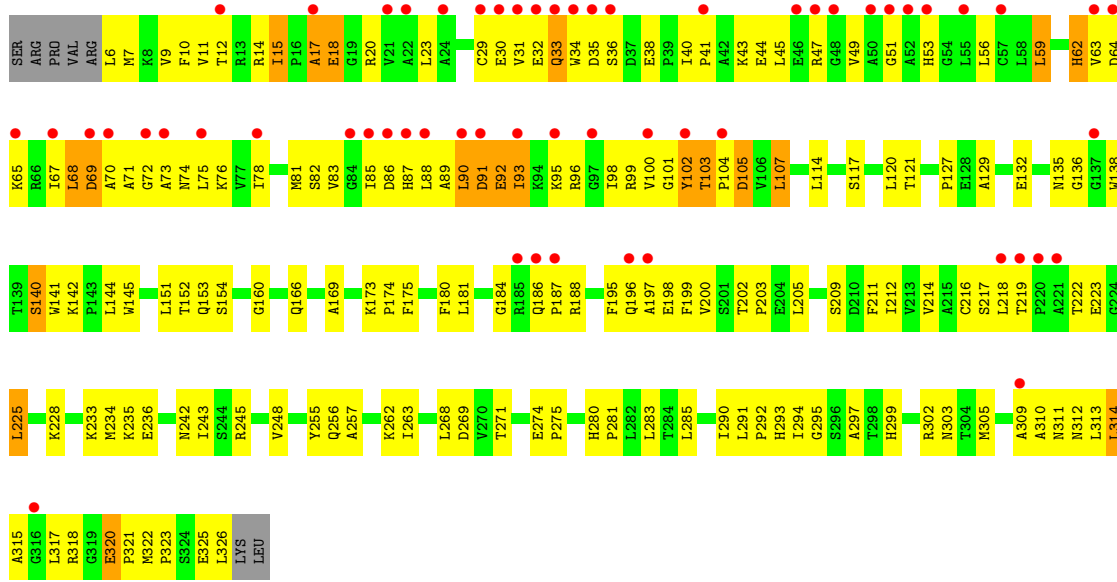


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

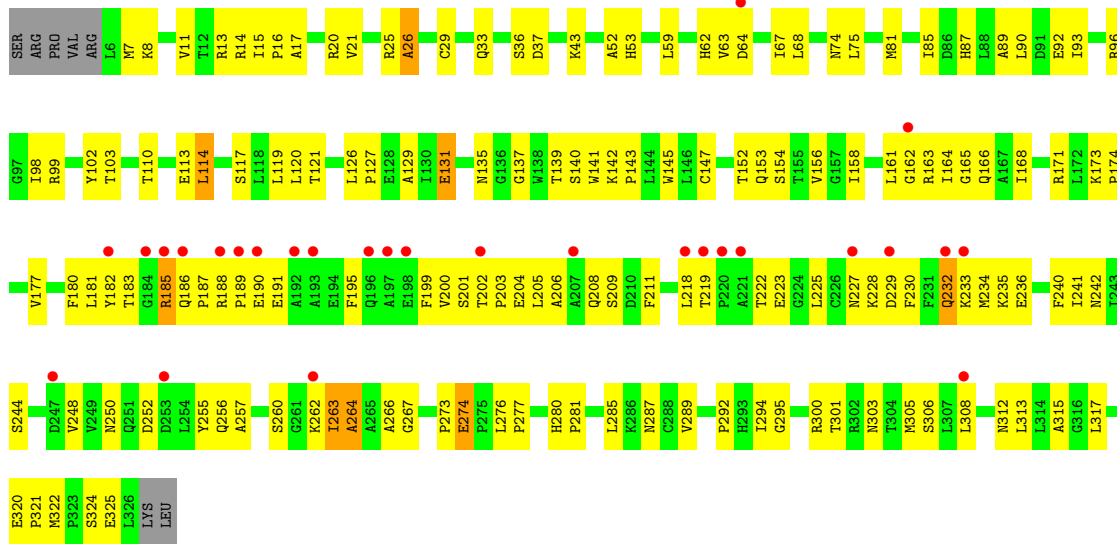


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase





• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.00Å 66.44Å 148.77Å 90.00° 98.59° 90.00°	Depositor
Resolution (Å)	49.33 – 2.45 49.30 – 2.46	Depositor EDS
% Data completeness (in resolution range)	93.0 (49.33-2.45) 93.1 (49.30-2.46)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.19 (at 2.45Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.200 , 0.286 0.204 , 0.286	Depositor DCC
$R_{free}$ test set	2551 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.6	Xtrriage
Anisotropy	0.210	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 74.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	81744	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.90% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	1-A	0.32	0/2481	0.58	0/3363
1	1-B	0.32	0/2481	0.58	0/3363
1	1-C	0.33	0/2481	0.61	0/3363
1	1-D	0.33	0/2481	0.59	0/3363
1	2-A	0.33	0/2481	0.60	0/3363
1	2-B	0.32	0/2481	0.59	0/3363
1	2-C	0.33	0/2481	0.62	0/3363
1	2-D	0.33	0/2481	0.58	0/3363
1	3-A	0.32	0/2481	0.59	0/3363
1	3-B	0.32	0/2481	0.58	0/3363
1	3-C	0.33	0/2481	0.60	0/3363
1	3-D	0.33	0/2481	0.60	0/3363
1	4-A	0.32	0/2481	0.59	0/3363
1	4-B	0.32	0/2481	0.58	0/3363
1	4-C	0.32	0/2481	0.60	0/3363
1	4-D	0.33	0/2481	0.58	0/3363
1	5-A	0.34	0/2481	0.60	0/3363
1	5-B	0.33	0/2481	0.63	0/3363
1	5-C	0.35	0/2481	0.64	0/3363
1	5-D	0.33	0/2481	0.61	0/3363
1	6-A	0.34	0/2481	0.61	0/3363
1	6-B	0.33	0/2481	0.61	0/3363
1	6-C	0.34	0/2481	0.64	0/3363
1	6-D	0.34	0/2481	0.61	0/3363
1	7-A	0.34	0/2481	0.62	0/3363
1	7-B	0.35	0/2481	0.63	0/3363
1	7-C	0.34	0/2481	0.65	0/3363
1	7-D	0.34	0/2481	0.60	0/3363
1	8-A	0.34	0/2481	0.62	0/3363
1	8-B	0.33	0/2481	0.61	0/3363
1	8-C	0.34	0/2481	0.64	0/3363
1	8-D	0.34	0/2481	0.61	0/3363
All	All	0.33	0/79392	0.61	0/107616



There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	2442	0	2491	176	0
1	1-B	2442	0	2491	134	0
1	1-C	2442	0	2491	170	0
1	1-D	2442	0	2491	226	0
1	2-A	2442	0	2491	213	0
1	2-B	2442	0	2491	201	0
1	2-C	2442	0	2491	167	0
1	2-D	2442	0	2491	189	0
1	3-A	2442	0	2491	178	0
1	3-B	2442	0	2491	205	0
1	3-C	2442	0	2491	163	0
1	3-D	2442	0	2491	140	0
1	4-A	2442	0	2491	250	0
1	4-B	2442	0	2491	200	0
1	4-C	2442	0	2491	178	0
1	4-D	2442	0	2491	165	0
1	5-A	2442	0	2491	207	0
1	5-B	2442	0	2491	197	0
1	5-C	2442	0	2491	188	0
1	5-D	2442	0	2491	148	0
1	6-A	2442	0	2491	270	0
1	6-B	2442	0	2491	217	0
1	6-C	2442	0	2491	215	0
1	6-D	2442	0	2491	201	0
1	7-A	2442	0	2491	205	0
1	7-B	2442	0	2491	249	0
1	7-C	2442	0	2491	200	0
1	7-D	2442	0	2491	220	0
1	8-A	2442	0	2491	232	0
1	8-B	2442	0	2491	209	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	8-C	2442	0	2491	191	0
1	8-D	2442	0	2491	147	0
2	1-A	103	0	0	9	0
2	1-B	130	0	0	12	0
2	1-C	122	0	0	11	0
2	1-D	95	0	0	15	0
2	2-A	104	0	0	19	0
2	2-B	128	0	0	18	0
2	2-C	122	0	0	13	0
2	2-D	96	0	0	8	0
2	3-A	104	0	0	11	0
2	3-B	128	0	0	15	0
2	3-C	121	0	0	12	0
2	3-D	97	0	0	9	0
2	4-A	104	0	0	15	0
2	4-B	128	0	0	18	0
2	4-C	122	0	0	7	0
2	4-D	96	0	0	7	0
2	5-A	111	0	0	10	0
2	5-B	121	0	0	12	0
2	5-C	121	0	0	11	0
2	5-D	97	0	0	10	0
2	6-A	107	0	0	24	0
2	6-B	125	0	0	15	0
2	6-C	120	0	0	11	0
2	6-D	98	0	0	10	0
2	7-A	106	0	0	6	0
2	7-B	126	0	0	11	0
2	7-C	119	0	0	8	0
2	7-D	99	0	0	10	0
2	8-A	108	0	0	14	0
2	8-B	124	0	0	19	0
2	8-C	119	0	0	11	0
2	8-D	99	0	0	2	0
All	All	81744	0	79712	5967	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 38.

All (5967) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ARG:HH21	1:A:316:GLY:HA2	1.07	1.16
1:A:8:LYS:HA	1:A:30:GLU:HB3	1.27	1.15
1:C:46:GLU:HG3	1:C:67:ILE:HD13	1.22	1.14
1:B:167:ALA:HA	1:B:170:ARG:HH12	1.16	1.09
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.33	1.09
1:C:8:LYS:HB3	1:C:52:ALA:HA	1.35	1.09
1:C:18:GLU:HG2	1:C:307:LEU:HD22	1.37	1.07
1:D:185:ARG:HG2	1:D:186:GLN:H	1.15	1.06
1:A:9:VAL:HB	1:A:31:VAL:HG22	1.40	1.04
1:C:81:MSE:HB3	1:C:305:MSE:HE3	1.40	1.04
1:C:69:ASP:HA	1:C:96:ARG:HH22	1.19	1.03
1:C:11:VAL:HB	1:C:33:GLN:HE21	1.19	1.03
1:B:229:ASP:HA	1:B:232:GLN:HE21	1.18	1.03
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.41	1.03
1:D:302:ARG:HA	1:D:305:MSE:SE	2.09	1.03
1:A:81:MSE:HE2	1:A:306:SER:HA	1.41	1.02
1:A:155:THR:HB	1:A:209:SER:HA	1.42	1.02
1:A:59:LEU:H	1:A:59:LEU:HD22	1.17	1.01
1:B:102:TYR:HE1	1:B:326:LEU:HB2	1.22	1.01
1:D:202:THR:HG21	1:D:225:LEU:HD11	1.42	1.01
1:B:66:ARG:HB3	1:B:66:ARG:HH11	1.20	1.01
1:B:170:ARG:HB3	1:B:170:ARG:HH11	1.26	1.01
1:A:53:HIS:HB3	1:A:317:LEU:HD11	1.42	1.01
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.43	1.01
1:D:156:VAL:HG22	1:D:211:PHE:HB2	1.40	1.00
1:D:158:ILE:HG12	1:D:213:VAL:HB	1.38	1.00
1:B:85:ILE:HB	1:B:90:LEU:HD21	1.39	1.00
1:D:192:ALA:HB1	1:D:197:ALA:HB3	1.41	1.00
1:B:226:CYS:HB2	1:B:249:VAL:HA	1.44	1.00
1:A:8:LYS:HB3	1:A:52:ALA:HA	1.41	1.00
1:D:15:ILE:N	1:D:20:ARG:HH21	1.60	0.99
1:C:40:ILE:HD11	1:C:44:GLU:O	1.62	0.99
1:D:15:ILE:N	1:D:20:ARG:HH21	1.60	0.99
1:A:49:VAL:HG21	1:A:67:ILE:HG23	1.42	0.99
1:A:206:ALA:HB1	1:A:234:MSE:HA	1.43	0.99
1:A:143:PRO:HG2	1:A:144:LEU:HD23	1.46	0.98
1:C:218:LEU:HD13	1:C:248:VAL:HG22	1.41	0.98
1:A:125:ARG:NH1	1:A:146:LEU:HA	1.77	0.98
1:C:99:ARG:HH21	1:C:316:GLY:HA2	1.28	0.98
1:D:179:ARG:HE	1:D:181:LEU:HD21	1.29	0.97
1:C:7:MSE:H	1:C:29:CYS:HA	1.28	0.97
1:A:192:ALA:HB1	1:A:197:ALA:HB3	1.45	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:THR:HA	1:B:225:LEU:HD23	1.42	0.97
1:B:83:VAL:HB	1:B:107:LEU:HD11	1.44	0.97
1:C:203:PRO:HB3	1:C:233:LYS:HE2	1.43	0.97
1:D:63:VAL:HG13	1:D:67:ILE:HG21	1.46	0.96
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.46	0.96
1:B:40:ILE:HG21	1:B:45:LEU:HD13	1.46	0.96
1:D:181:LEU:HD13	1:D:200:VAL:HG21	1.46	0.96
1:A:192:ALA:HB1	1:A:197:ALA:HB3	1.47	0.96
1:C:114:LEU:HD11	1:C:294:ILE:HG13	1.47	0.95
1:B:8:LYS:HE3	1:B:52:ALA:HB2	1.49	0.95
1:C:160:GLY:HA3	1:C:216:CYS:HB3	1.47	0.95
1:B:99:ARG:HH22	1:B:319:GLY:HA2	1.28	0.95
1:D:99:ARG:HB3	1:D:322:MSE:HE1	1.49	0.95
1:B:181:LEU:HD22	1:B:198:GLU:HB3	1.49	0.95
1:A:232:GLN:HE22	1:A:262:LYS:NZ	1.63	0.94
1:A:114:LEU:HD11	1:A:294:ILE:HG13	1.48	0.94
1:D:312:ASN:HA	1:D:323:PRO:HD2	1.49	0.94
1:B:7:MSE:HE3	1:B:28:ASP:HB2	1.48	0.94
1:C:114:LEU:HD11	1:C:294:ILE:HG13	1.50	0.94
1:C:8:LYS:HB3	1:C:52:ALA:HA	1.50	0.94
1:A:114:LEU:HD22	1:A:295:GLY:HA2	1.47	0.94
1:A:114:LEU:HD11	1:A:294:ILE:HG13	1.48	0.93
1:A:55:LEU:HD23	1:A:78:ILE:HG12	1.50	0.93
1:B:188:ARG:HD2	2:B:358:HOH:O	1.68	0.93
1:D:15:ILE:H	1:D:20:ARG:HH21	1.00	0.93
1:C:188:ARG:HH11	1:C:188:ARG:HB2	1.31	0.93
1:D:114:LEU:HD11	1:D:294:ILE:HG13	1.49	0.93
1:C:11:VAL:HB	1:C:33:GLN:HB3	1.50	0.92
1:D:225:LEU:HB3	1:D:248:VAL:HG13	1.51	0.92
1:D:93:ILE:HG23	1:D:98:ILE:HB	1.51	0.92
1:D:20:ARG:HD2	1:D:33:GLN:HE22	1.32	0.92
1:D:63:VAL:HA	1:D:67:ILE:HG13	1.50	0.92
1:C:114:LEU:HD11	1:C:294:ILE:HG13	1.52	0.92
1:C:23:LEU:HD21	1:C:313:LEU:HD23	1.52	0.92
1:D:121:THR:HG23	1:D:126:LEU:HB2	1.52	0.91
1:B:66:ARG:HB3	1:B:66:ARG:NH1	1.86	0.91
1:D:14:ARG:HD3	1:D:20:ARG:HH22	1.34	0.91
1:D:85:ILE:HD12	1:D:90:LEU:HD11	1.49	0.91
1:A:114:LEU:HD11	1:A:294:ILE:HG13	1.52	0.91
1:D:167:ALA:HB1	1:D:171:ARG:HH21	1.35	0.91
1:D:192:ALA:HB1	1:D:197:ALA:HB3	1.52	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:ARG:HH22	1:C:319:GLY:HA2	1.33	0.91
1:B:81:MSE:HE2	1:B:306:SER:HA	1.51	0.91
1:B:83:VAL:HG23	1:B:104:PRO:HA	1.52	0.91
1:A:171:ARG:NH1	1:B:175:PHE:HA	1.86	0.91
1:B:102:TYR:CE1	1:B:326:LEU:HB2	2.06	0.91
1:C:202:THR:HG21	1:C:225:LEU:HD11	1.53	0.90
1:D:20:ARG:HD2	1:D:33:GLN:HE22	1.35	0.90
1:C:185:ARG:H	1:C:185:ARG:HE	1.18	0.90
1:B:46:GLU:HG3	1:B:67:ILE:HD13	1.50	0.90
1:B:80:THR:HG22	1:B:82:SER:H	1.36	0.90
1:D:32:GLU:HG2	1:D:33:GLN:H	1.34	0.90
1:D:14:ARG:HG3	1:D:20:ARG:HH22	1.36	0.90
1:C:76:LYS:HE3	1:C:317:LEU:HA	1.54	0.89
1:A:114:LEU:HD22	1:A:295:GLY:HA2	1.54	0.89
1:D:15:ILE:H	1:D:20:ARG:HH21	1.11	0.89
1:C:8:LYS:HG3	1:C:30:GLU:HB3	1.54	0.89
1:B:101:GLY:HA2	1:B:325:GLU:HA	1.53	0.89
1:C:114:LEU:HD11	1:C:294:ILE:HG13	1.55	0.89
1:C:59:LEU:HD12	1:C:59:LEU:H	1.38	0.89
1:B:107:LEU:HD23	1:B:305:MSE:HE3	1.54	0.89
1:A:181:LEU:HB2	1:A:205:LEU:HD13	1.54	0.88
1:B:17:ALA:HA	1:B:20:ARG:HE	1.38	0.88
1:D:302:ARG:HD3	1:D:305:MSE:SE	2.24	0.88
1:D:314:LEU:HA	1:D:317:LEU:HD23	1.55	0.88
1:B:75:LEU:HD21	1:B:78:ILE:HD11	1.53	0.88
1:A:98:ILE:HG22	1:A:99:ARG:H	1.37	0.88
1:B:218:LEU:HD13	1:B:248:VAL:HG22	1.54	0.88
1:D:81:MSE:HE2	1:D:306:SER:HA	1.53	0.88
1:A:26:ALA:HB2	1:A:314:LEU:HD21	1.56	0.88
1:B:81:MSE:HE2	1:B:306:SER:HA	1.55	0.87
1:B:107:LEU:HD23	1:B:305:MSE:HE3	1.54	0.87
1:C:271:THR:HB	1:C:276:LEU:HD13	1.56	0.87
1:D:20:ARG:HG3	2:D:333:HOH:O	1.73	0.87
1:D:185:ARG:H	1:D:185:ARG:HD3	1.35	0.87
1:C:188:ARG:HD2	2:C:359:HOH:O	1.75	0.87
1:B:7:MSE:SE	1:B:76:LYS:HD3	2.24	0.87
1:A:8:LYS:HB3	1:A:51:GLY:O	1.74	0.87
1:C:188:ARG:HB2	1:C:188:ARG:NH1	1.90	0.87
1:D:114:LEU:HD13	1:D:295:GLY:CA	2.05	0.87
1:D:103:THR:HG22	1:D:308:LEU:HG	1.54	0.87
1:A:16:PRO:HD2	1:A:81:MSE:HE1	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:GLN:HE22	1:A:262:LYS:NZ	1.73	0.86
1:D:207:ALA:HB2	1:D:233:LYS:HB3	1.56	0.86
1:D:121:THR:HG23	1:D:126:LEU:HB2	1.57	0.86
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.58	0.86
1:C:15:ILE:HD12	1:C:81:MSE:HE1	1.55	0.86
1:C:79:SER:HB2	2:C:361:HOH:O	1.75	0.86
1:D:18:GLU:HB2	1:D:306:SER:HB3	1.56	0.86
1:C:301:THR:HG22	1:C:305:MSE:SE	2.25	0.86
1:A:58:LEU:HD21	1:A:81:MSE:HE3	1.56	0.86
1:B:114:LEU:HD11	1:B:294:ILE:HG13	1.56	0.86
1:C:68:LEU:HD13	1:C:75:LEU:HD23	1.57	0.86
1:A:93:ILE:HG23	1:A:98:ILE:HB	1.56	0.86
1:A:222:THR:HA	1:A:225:LEU:HD13	1.55	0.86
1:B:71:ALA:HB1	1:B:75:LEU:HD11	1.57	0.86
1:B:80:THR:HG21	1:B:85:ILE:HG23	1.56	0.86
1:C:114:LEU:HD22	1:C:295:GLY:HA2	1.57	0.86
1:D:121:THR:HG23	1:D:126:LEU:HB2	1.57	0.86
1:D:85:ILE:HD13	1:D:90:LEU:HD11	1.57	0.86
1:C:15:ILE:HG12	1:C:20:ARG:NH1	1.89	0.86
1:C:111:THR:HA	1:C:295:GLY:O	1.76	0.86
1:C:99:ARG:HH22	1:C:319:GLY:HA2	1.40	0.86
1:B:325:GLU:HG3	1:B:326:LEU:N	1.90	0.85
1:B:99:ARG:NH2	1:B:316:GLY:HA2	1.91	0.85
1:D:99:ARG:HD2	1:D:325:GLU:OE2	1.76	0.85
1:C:9:VAL:HB	1:C:31:VAL:HG22	1.58	0.85
1:D:7:MSE:SE	1:D:317:LEU:HG	2.26	0.85
1:C:114:LEU:HD22	1:C:295:GLY:HA2	1.58	0.85
1:B:192:ALA:HB1	1:B:197:ALA:HB3	1.56	0.85
1:A:173:LYS:HB3	1:A:174:PRO:HD3	1.58	0.85
1:A:107:LEU:HB3	1:A:305:MSE:SE	2.26	0.85
1:A:205:LEU:HG	1:A:212:ILE:HD11	1.58	0.85
1:B:41:PRO:HB2	1:B:44:GLU:HB2	1.56	0.85
1:D:315:ALA:HB3	1:D:322:MSE:HG3	1.57	0.85
1:A:171:ARG:HH11	1:B:175:PHE:HA	1.40	0.85
1:D:81:MSE:HE2	1:D:306:SER:HA	1.58	0.85
1:D:114:LEU:HD22	1:D:295:GLY:HA2	1.57	0.85
1:C:114:LEU:HD13	1:C:295:GLY:HA2	1.59	0.85
1:B:16:PRO:HD2	1:B:306:SER:HB2	1.56	0.85
1:B:75:LEU:HD23	1:B:98:ILE:HD13	1.58	0.85
1:B:76:LYS:HE2	1:B:317:LEU:HA	1.57	0.85
1:D:81:MSE:HG2	1:D:305:MSE:HE2	1.56	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:LEU:HD23	1:A:263:ILE:HG13	1.58	0.84
1:A:167:ALA:HB1	1:A:171:ARG:HH21	1.41	0.84
1:C:174:PRO:HG3	1:D:174:PRO:HG2	1.56	0.84
1:C:76:LYS:HA	1:C:98:ILE:HG13	1.57	0.84
1:C:219:THR:HB	1:C:220:PRO:HD2	1.58	0.84
1:D:114:LEU:HD22	1:D:295:GLY:HA2	1.59	0.84
1:C:45:LEU:HD21	1:C:63:VAL:HG22	1.58	0.84
1:C:23:LEU:HD21	1:C:313:LEU:HD23	1.60	0.84
1:B:76:LYS:HG3	2:B:444:HOH:O	1.77	0.84
1:C:174:PRO:HG3	1:D:174:PRO:HG2	1.58	0.84
1:D:114:LEU:HD13	1:D:295:GLY:HA2	1.59	0.84
1:A:6:LEU:HD23	1:A:30:GLU:HB2	1.58	0.84
1:C:9:VAL:HB	1:C:31:VAL:HG22	1.58	0.84
1:D:234:MSE:HE2	1:D:238:ALA:HB1	1.58	0.84
1:A:161:LEU:HG	1:A:166:GLN:HE21	1.41	0.84
1:D:121:THR:HG22	1:D:127:PRO:HD3	1.57	0.84
1:C:92:GLU:HA	1:C:95:LYS:HD3	1.59	0.84
1:D:15:ILE:HB	1:D:81:MSE:HE1	1.59	0.84
1:B:167:ALA:HB1	1:B:171:ARG:HH21	1.42	0.83
1:C:206:ALA:O	1:C:234:MSE:HA	1.78	0.83
1:B:229:ASP:HA	1:B:232:GLN:HE21	1.43	0.83
1:C:236:GLU:HG2	2:C:395:HOH:O	1.77	0.83
1:A:77:VAL:HG21	1:A:313:LEU:HA	1.61	0.83
1:B:170:ARG:HB3	1:B:170:ARG:NH1	1.93	0.83
1:C:59:LEU:HD12	1:C:59:LEU:H	1.43	0.83
1:B:114:LEU:HD22	1:B:295:GLY:HA2	1.61	0.83
1:B:167:ALA:HB1	1:B:171:ARG:HH21	1.43	0.83
1:B:200:VAL:HG22	1:B:201:SER:H	1.41	0.83
1:D:53:HIS:HB3	1:D:317:LEU:HD11	1.58	0.83
1:B:99:ARG:HH21	1:B:316:GLY:HA2	1.42	0.83
1:A:309:ALA:HA	2:A:363:HOH:O	1.78	0.83
1:A:86:ASP:OD2	1:A:218:LEU:HD23	1.79	0.83
1:B:107:LEU:HD23	1:B:305:MSE:HE3	1.60	0.83
1:B:99:ARG:HH22	1:B:319:GLY:HA2	1.43	0.83
1:C:114:LEU:HD13	1:C:295:GLY:HA2	1.61	0.83
1:B:234:MSE:HE1	1:B:240:PHE:HB2	1.60	0.83
1:D:181:LEU:HD22	1:D:200:VAL:HG11	1.61	0.82
1:D:85:ILE:HD13	1:D:90:LEU:HD11	1.61	0.82
1:C:45:LEU:HD21	1:C:63:VAL:HG22	1.60	0.82
1:A:151:LEU:HA	1:A:154:SER:HB3	1.62	0.82
1:C:185:ARG:HE	1:C:185:ARG:N	1.77	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:GLU:O	1:A:96:ARG:HD3	1.78	0.82
1:C:203:PRO:HB3	1:C:233:LYS:HE2	1.60	0.82
1:A:93:ILE:HG23	1:A:98:ILE:HB	1.59	0.82
1:B:66:ARG:HB3	1:B:66:ARG:HH11	1.44	0.82
1:C:38:GLU:OE1	1:C:39:PRO:HD2	1.80	0.82
1:B:198:GLU:OE1	1:B:200:VAL:HB	1.80	0.82
1:D:185:ARG:HG2	1:D:186:GLN:N	1.95	0.82
1:B:84:GLY:HA3	1:B:245:ARG:NH2	1.94	0.82
1:C:92:GLU:HG2	1:C:95:LYS:NZ	1.94	0.82
1:B:235:LYS:HB2	1:B:238:ALA:HB2	1.60	0.82
1:B:100:VAL:HG23	1:B:326:LEU:HB3	1.61	0.82
1:D:9:VAL:HB	1:D:31:VAL:HG22	1.60	0.82
1:C:93:ILE:HG23	1:C:98:ILE:HB	1.59	0.82
1:B:92:GLU:O	1:B:96:ARG:HG3	1.79	0.82
1:A:59:LEU:H	1:A:59:LEU:CD2	1.93	0.82
1:D:192:ALA:HB1	1:D:197:ALA:HB3	1.61	0.81
1:A:8:LYS:HD3	1:A:9:VAL:H	1.45	0.81
1:A:223:GLU:OE1	1:A:247:ASP:HB3	1.80	0.81
1:B:79:SER:HA	1:B:101:GLY:O	1.79	0.81
1:A:187:PRO:O	1:A:188:ARG:HD2	1.80	0.81
1:B:315:ALA:HB3	1:B:322:MSE:HG2	1.61	0.81
1:D:16:PRO:HD2	1:D:81:MSE:HE1	1.62	0.81
1:C:75:LEU:H	1:C:75:LEU:HD23	1.45	0.81
1:B:38:GLU:HB3	1:B:39:PRO:HD2	1.62	0.81
1:D:183:THR:HG23	1:D:205:LEU:HD13	1.63	0.81
1:A:318:ARG:HD2	1:A:320:GLU:OE2	1.80	0.81
1:D:50:ALA:HA	1:D:70:ALA:O	1.80	0.81
1:A:8:LYS:HE3	1:A:32:GLU:HG3	1.62	0.81
1:B:58:LEU:HD23	1:B:81:MSE:HE2	1.62	0.81
1:B:107:LEU:HD23	1:B:107:LEU:H	1.43	0.81
1:A:55:LEU:HB2	1:A:75:LEU:HD11	1.61	0.81
1:A:102:TYR:HD1	1:A:102:TYR:H	1.25	0.81
1:C:111:THR:HG21	1:C:164:ILE:HD13	1.63	0.81
1:A:173:LYS:HB3	1:A:174:PRO:HD3	1.62	0.81
1:A:100:VAL:HB	1:A:326:LEU:HB3	1.63	0.81
1:B:8:LYS:HG3	1:B:51:GLY:O	1.81	0.81
1:D:114:LEU:HD22	1:D:295:GLY:HA2	1.61	0.81
1:D:163:ARG:HE	1:D:163:ARG:HA	1.45	0.81
1:A:83:VAL:HG23	1:A:104:PRO:HB3	1.63	0.81
1:A:202:THR:HB	1:A:203:PRO:HD3	1.63	0.80
1:A:22:ALA:HA	1:A:25:ARG:HE	1.46	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:260:SER:OG	1:D:262:LYS:HG2	1.81	0.80
1:A:316:GLY:HA3	1:A:322:MSE:HG2	1.63	0.80
1:A:157:GLY:HA3	1:A:205:LEU:HD11	1.61	0.80
1:A:320:GLU:HB3	1:A:321:PRO:HD2	1.62	0.80
1:A:99:ARG:NH2	1:A:316:GLY:HA2	1.93	0.80
1:D:107:LEU:HD23	1:D:305:MSE:HE2	1.62	0.80
1:B:101:GLY:HA2	1:B:325:GLU:HA	1.64	0.80
1:A:100:VAL:HB	1:A:326:LEU:HB3	1.63	0.80
1:A:77:VAL:HG11	1:A:317:LEU:HG	1.61	0.80
1:A:121:THR:HG22	1:A:127:PRO:HD3	1.61	0.80
1:B:246:GLY:HA3	1:B:271:THR:O	1.80	0.80
1:B:13:ARG:HD2	1:B:58:LEU:HD11	1.63	0.80
1:A:93:ILE:HG23	1:A:98:ILE:HB	1.63	0.80
1:A:121:THR:HG22	1:A:127:PRO:HD3	1.61	0.80
1:D:85:ILE:HD13	1:D:90:LEU:HD11	1.61	0.80
1:B:200:VAL:HG13	1:B:205:LEU:HB2	1.63	0.80
1:B:13:ARG:HD2	1:B:58:LEU:CD1	2.11	0.80
1:D:185:ARG:HH22	1:D:188:ARG:NH2	1.79	0.80
1:A:7:MSE:SE	1:A:7:MSE:H	2.15	0.80
1:C:71:ALA:HB1	1:C:75:LEU:HD11	1.62	0.80
1:B:312:ASN:HA	1:B:323:PRO:HD2	1.62	0.80
1:B:322:MSE:SE	1:B:325:GLU:HB3	2.31	0.80
1:D:99:ARG:HH22	1:D:319:GLY:HA2	1.47	0.80
1:A:212:ILE:HG13	1:A:234:MSE:HE3	1.63	0.80
1:D:185:ARG:HD3	1:D:185:ARG:N	1.97	0.80
1:C:202:THR:HG21	1:C:225:LEU:HD11	1.62	0.80
1:C:8:LYS:HD3	1:C:52:ALA:HB2	1.64	0.79
1:D:181:LEU:HD13	1:D:205:LEU:HA	1.64	0.79
1:C:114:LEU:HD13	1:C:295:GLY:HA2	1.65	0.79
1:B:318:ARG:O	1:B:320:GLU:HG3	1.83	0.79
1:D:231:PHE:HA	1:D:234:MSE:SE	2.32	0.79
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.61	0.79
1:B:228:LYS:O	1:B:232:GLN:HG3	1.81	0.79
1:B:63:VAL:HG11	1:B:78:ILE:HD13	1.64	0.79
1:C:92:GLU:HA	1:C:95:LYS:HD3	1.65	0.79
1:D:125:ARG:NH1	1:D:146:LEU:HA	1.96	0.79
1:C:257:ALA:HA	1:C:262:LYS:HD2	1.63	0.79
1:B:226:CYS:SG	1:B:249:VAL:HG22	2.22	0.79
1:D:99:ARG:NH2	1:D:316:GLY:HA2	1.98	0.79
1:B:245:ARG:HB2	1:B:248:VAL:CG2	2.13	0.79
1:C:77:VAL:HG11	1:C:317:LEU:HD12	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:GLY:HA2	1:A:74:ASN:HD22	1.47	0.79
1:B:163:ARG:HH11	1:B:163:ARG:HA	1.45	0.79
1:C:78:ILE:HB	1:C:100:VAL:HG22	1.65	0.79
1:D:315:ALA:HB1	1:D:322:MSE:HA	1.63	0.79
1:C:6:LEU:HG	1:C:28:ASP:O	1.82	0.79
1:C:51:GLY:HA2	1:C:72:GLY:HA3	1.63	0.79
1:C:34:TRP:NE1	1:C:36:SER:HB3	1.98	0.79
1:A:99:ARG:HD2	1:A:325:GLU:OE2	1.82	0.79
1:A:7:MSE:HE1	1:A:317:LEU:HB3	1.65	0.79
1:D:114:LEU:HD22	1:D:295:GLY:HA2	1.63	0.79
1:B:137:GLY:O	1:B:139:THR:HG23	1.83	0.79
1:C:66:ARG:HG3	2:C:424:HOH:O	1.83	0.78
1:B:66:ARG:HB3	1:B:66:ARG:NH1	1.97	0.78
1:A:68:LEU:HD22	1:A:98:ILE:HD13	1.65	0.78
1:A:23:LEU:HD23	1:A:314:LEU:HD22	1.63	0.78
1:C:45:LEU:O	1:C:49:VAL:HG13	1.84	0.78
1:B:78:ILE:HB	1:B:100:VAL:HG12	1.65	0.78
1:D:103:THR:HB	1:D:308:LEU:HD23	1.65	0.78
1:D:121:THR:HG23	1:D:126:LEU:HB2	1.63	0.78
1:D:6:LEU:HB3	1:D:30:GLU:HB2	1.66	0.78
1:B:80:THR:O	1:B:102:TYR:HA	1.84	0.78
1:A:225:LEU:HB3	1:A:248:VAL:HG13	1.66	0.78
1:A:56:LEU:HD21	1:A:309:ALA:HB1	1.66	0.78
1:A:76:LYS:HD2	1:A:317:LEU:HA	1.63	0.78
1:D:90:LEU:HD23	1:D:93:ILE:HD12	1.65	0.78
1:D:15:ILE:HG12	1:D:20:ARG:HE	1.48	0.78
1:D:202:THR:HG21	1:D:225:LEU:HD11	1.63	0.78
1:A:93:ILE:HG23	1:A:98:ILE:HB	1.66	0.78
1:C:271:THR:O	1:C:274:GLU:HG3	1.84	0.78
1:C:202:THR:HB	1:C:203:PRO:HD3	1.65	0.78
1:B:167:ALA:HB1	1:B:171:ARG:NH2	1.99	0.78
1:A:185:ARG:HH21	1:A:221:ALA:HB2	1.47	0.78
1:B:312:ASN:HD21	1:B:324:SER:HB3	1.48	0.78
1:C:45:LEU:HG	1:C:67:ILE:HD12	1.66	0.78
1:B:63:VAL:HB	1:B:88:LEU:HD23	1.65	0.78
1:A:125:ARG:HH11	1:A:146:LEU:HA	1.45	0.78
1:A:202:THR:HB	1:A:203:PRO:HD3	1.66	0.78
1:B:167:ALA:HB1	1:B:171:ARG:NH2	1.99	0.78
1:B:245:ARG:HB2	1:B:248:VAL:HG23	1.63	0.78
1:A:121:THR:HG22	1:A:127:PRO:HD3	1.63	0.78
1:B:311:ASN:O	1:B:323:PRO:HG2	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:15:ILE:HG12	1:D:20:ARG:HE	1.48	0.78
1:B:206:ALA:HB2	1:B:230:PHE:CE2	2.19	0.77
1:C:312:ASN:HD21	1:C:324:SER:HB3	1.47	0.77
1:B:13:ARG:NH2	1:B:39:PRO:HA	1.99	0.77
1:D:103:THR:HB	1:D:308:LEU:HD23	1.66	0.77
1:B:22:ALA:HB3	1:B:310:ALA:HB1	1.65	0.77
1:B:114:LEU:HD11	1:B:294:ILE:HG13	1.65	0.77
1:C:271:THR:O	1:C:274:GLU:HG3	1.83	0.77
1:C:111:THR:HG21	1:C:164:ILE:HD13	1.67	0.77
1:A:114:LEU:HD13	1:A:295:GLY:HA2	1.67	0.77
1:C:107:LEU:HD23	1:C:305:MSE:HE3	1.65	0.77
1:A:49:VAL:HG12	1:A:55:LEU:HD13	1.66	0.77
1:C:110:THR:HG23	1:D:124:ARG:HH12	1.49	0.77
1:C:15:ILE:HG12	1:C:20:ARG:HH12	1.47	0.77
1:B:106:VAL:HB	1:B:304:THR:HG21	1.64	0.77
1:C:99:ARG:NH2	1:C:316:GLY:HA2	1.98	0.77
1:B:320:GLU:HB3	1:B:321:PRO:HD2	1.65	0.77
1:D:8:LYS:HA	1:D:30:GLU:HB3	1.66	0.77
1:A:65:LYS:HA	1:A:68:LEU:HD12	1.67	0.77
1:D:181:LEU:HD13	1:D:200:VAL:HG21	1.66	0.77
1:D:212:ILE:HD12	1:D:234:MSE:HE3	1.65	0.77
1:B:181:LEU:HD22	1:B:198:GLU:HB3	1.67	0.77
1:C:11:VAL:HB	1:C:33:GLN:HB3	1.66	0.77
1:C:59:LEU:H	1:C:59:LEU:CD1	1.98	0.77
1:B:170:ARG:CZ	2:B:405:HOH:O	2.32	0.77
1:D:59:LEU:HD13	1:D:245:ARG:HH22	1.46	0.77
1:B:49:VAL:HG23	1:B:71:ALA:HB2	1.65	0.77
1:B:55:LEU:HD23	1:B:78:ILE:HG12	1.66	0.77
1:C:271:THR:O	1:C:274:GLU:HG3	1.85	0.77
1:B:181:LEU:CD2	1:B:198:GLU:HB3	2.14	0.77
1:D:121:THR:HG22	1:D:127:PRO:HD3	1.65	0.77
1:A:49:VAL:HG12	1:A:55:LEU:HD13	1.66	0.77
1:D:121:THR:HG22	1:D:127:PRO:HD3	1.67	0.77
1:C:54:GLY:HA3	1:C:317:LEU:HD21	1.67	0.77
1:A:114:LEU:HD22	1:A:295:GLY:HA2	1.66	0.77
1:C:271:THR:O	1:C:274:GLU:HG3	1.85	0.77
1:C:55:LEU:HB3	1:C:78:ILE:HG12	1.67	0.77
1:B:11:VAL:HG11	1:B:33:GLN:HE21	1.50	0.76
1:D:167:ALA:HB1	1:D:171:ARG:NH2	1.99	0.76
1:A:63:VAL:HB	1:A:88:LEU:HD23	1.67	0.76
1:D:202:THR:OG1	1:D:203:PRO:HD3	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:214:VAL:HG11	1:C:248:VAL:HG11	1.67	0.76
1:B:181:LEU:HD23	1:B:198:GLU:HB3	1.67	0.76
1:B:35:ASP:O	1:B:36:SER:HB3	1.83	0.76
1:D:76:LYS:HA	1:D:98:ILE:HG12	1.67	0.76
1:D:162:GLY:O	1:D:166:GLN:HG3	1.85	0.76
1:C:174:PRO:HG3	1:D:174:PRO:HG2	1.65	0.76
1:A:302:ARG:HA	1:A:305:MSE:HE2	1.67	0.76
1:C:218:LEU:HB2	1:C:245:ARG:HG3	1.67	0.76
1:A:90:LEU:HA	1:A:93:ILE:HB	1.67	0.76
1:A:202:THR:OG1	1:A:203:PRO:HD3	1.85	0.76
1:B:99:ARG:NH2	1:B:319:GLY:HA2	1.98	0.76
1:A:202:THR:OG1	1:A:203:PRO:HD3	1.85	0.76
1:A:234:MSE:HE2	1:A:238:ALA:HB1	1.67	0.76
1:C:188:ARG:HD2	2:C:360:HOH:O	1.85	0.76
1:D:184:GLY:HA3	2:D:413:HOH:O	1.85	0.76
1:D:43:LYS:HB3	2:D:406:HOH:O	1.86	0.76
1:B:166:GLN:HG2	1:B:195:PHE:HE2	1.50	0.76
1:A:114:LEU:HD13	1:A:295:GLY:HA2	1.67	0.76
1:C:277:PRO:HD2	1:C:280:HIS:HB2	1.68	0.76
1:D:156:VAL:HG22	1:D:211:PHE:HB2	1.67	0.76
1:A:85:ILE:HG21	1:A:326:LEU:HD22	1.68	0.76
1:A:107:LEU:HD23	1:A:305:MSE:HE3	1.68	0.76
1:A:23:LEU:HD23	1:A:314:LEU:HD22	1.68	0.76
1:A:305:MSE:HE1	1:B:141:TRP:CH2	2.20	0.76
1:C:76:LYS:CA	1:C:98:ILE:HG13	2.16	0.76
1:C:271:THR:O	1:C:274:GLU:HG3	1.86	0.76
1:D:232:GLN:HE22	1:D:262:LYS:HE2	1.50	0.76
1:D:83:VAL:HG23	1:D:104:PRO:HB3	1.67	0.76
1:A:114:LEU:HD21	1:A:294:ILE:HG13	1.68	0.76
1:A:173:LYS:HB3	1:A:174:PRO:HD3	1.68	0.76
1:A:8:LYS:HB3	1:A:52:ALA:HA	1.68	0.76
1:D:81:MSE:HE2	1:D:306:SER:HA	1.68	0.76
1:A:153:GLN:HA	1:A:153:GLN:HE21	1.51	0.76
1:A:8:LYS:HA	1:A:30:GLU:O	1.86	0.75
1:C:271:THR:O	1:C:274:GLU:HG3	1.87	0.75
1:D:50:ALA:HA	1:D:70:ALA:O	1.86	0.75
1:C:92:GLU:HG2	1:C:95:LYS:HZ2	1.50	0.75
1:C:297:ALA:HA	1:C:302:ARG:HD2	1.68	0.75
1:B:107:LEU:HD23	1:B:305:MSE:HE3	1.68	0.75
1:D:114:LEU:HD22	1:D:295:GLY:HA2	1.66	0.75
1:B:202:THR:HB	1:B:203:PRO:HD3	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:231:PHE:HA	1:C:234:MSE:SE	2.36	0.75
1:C:107:LEU:HD23	1:C:305:MSE:HE3	1.68	0.75
1:C:17:ALA:HA	1:C:20:ARG:NH1	2.01	0.75
1:D:121:THR:HG22	1:D:127:PRO:HD3	1.68	0.75
1:B:180:PHE:O	1:B:181:LEU:HD23	1.86	0.75
1:A:20:ARG:HG3	2:A:372:HOH:O	1.85	0.75
1:C:174:PRO:HG3	1:D:174:PRO:HG2	1.67	0.75
1:A:183:THR:HA	1:A:200:VAL:O	1.86	0.75
1:A:95:LYS:HB2	2:A:350:HOH:O	1.86	0.75
1:A:114:LEU:HD22	1:A:295:GLY:HA2	1.68	0.75
1:B:236:GLU:HA	1:B:263:ILE:HA	1.66	0.75
1:A:147:CYS:HA	1:B:297:ALA:O	1.87	0.75
1:A:107:LEU:HD23	1:A:305:MSE:SE	2.37	0.75
1:C:219:THR:HB	1:C:220:PRO:HD2	1.68	0.75
1:B:8:LYS:HA	1:B:30:GLU:HB3	1.67	0.75
1:A:41:PRO:HB2	1:A:44:GLU:HG2	1.68	0.75
1:A:114:LEU:HD13	1:A:295:GLY:CA	2.16	0.75
1:B:312:ASN:OD1	1:B:322:MSE:HB3	1.87	0.75
1:B:10:PHE:CE2	1:B:12:THR:HG22	2.22	0.75
1:A:236:GLU:HA	1:A:263:ILE:HA	1.68	0.75
1:B:14:ARG:HH11	1:B:14:ARG:HB2	1.49	0.74
1:B:107:LEU:HD23	1:B:305:MSE:HE3	1.67	0.74
1:A:202:THR:OG1	1:A:203:PRO:HD3	1.86	0.74
1:B:184:GLY:H	1:B:199:PHE:HE1	1.35	0.74
1:A:95:LYS:HB2	2:A:350:HOH:O	1.86	0.74
1:C:45:LEU:O	1:C:49:VAL:HG22	1.87	0.74
1:C:8:LYS:HB3	1:C:52:ALA:HA	1.68	0.74
1:C:188:ARG:O	1:C:191:GLU:HB2	1.85	0.74
1:C:271:THR:O	1:C:274:GLU:HG3	1.87	0.74
1:A:181:LEU:HD23	1:A:198:GLU:HB2	1.69	0.74
1:B:105:ASP:O	1:B:107:LEU:N	2.20	0.74
1:B:180:PHE:O	1:B:181:LEU:HD23	1.88	0.74
1:C:202:THR:HB	1:C:203:PRO:HD3	1.69	0.74
1:B:85:ILE:HD13	1:B:90:LEU:HD11	1.69	0.74
1:B:228:LYS:O	1:B:232:GLN:HG3	1.86	0.74
1:C:234:MSE:HE1	1:C:240:PHE:HB2	1.67	0.74
1:A:156:VAL:HG12	1:A:158:ILE:HG13	1.69	0.74
1:D:41:PRO:HB2	1:D:44:GLU:HG2	1.68	0.74
1:A:11:VAL:HG13	1:A:56:LEU:HB3	1.70	0.74
1:B:91:ASP:HB2	2:B:428:HOH:O	1.87	0.74
1:A:161:LEU:HD21	1:A:192:ALA:HB2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:THR:O	1:A:305:MSE:HG3	1.88	0.74
1:D:297:ALA:HA	1:D:302:ARG:NH2	2.03	0.74
1:A:114:LEU:HD13	1:A:295:GLY:HA2	1.69	0.74
1:D:202:THR:HB	1:D:203:PRO:HD3	1.70	0.74
1:A:55:LEU:HB3	1:A:78:ILE:HG12	1.68	0.74
1:B:193:ALA:HB3	2:B:416:HOH:O	1.87	0.74
1:B:137:GLY:O	1:B:139:THR:HG23	1.87	0.74
1:B:256:GLN:HE22	1:B:262:LYS:HZ3	1.34	0.74
1:B:206:ALA:O	1:B:234:MSE:HA	1.88	0.74
1:C:45:LEU:O	1:C:49:VAL:HG22	1.87	0.74
1:C:192:ALA:HB1	1:C:197:ALA:HB3	1.70	0.74
1:B:8:LYS:O	1:B:52:ALA:HA	1.88	0.74
1:C:76:LYS:NZ	1:C:76:LYS:HB3	2.02	0.74
1:A:8:LYS:HD2	1:A:52:ALA:HB2	1.70	0.74
1:B:192:ALA:HB1	1:B:197:ALA:HB3	1.70	0.74
1:C:34:TRP:NE1	1:C:36:SER:HB3	2.02	0.74
1:B:92:GLU:HG2	2:B:428:HOH:O	1.87	0.74
1:B:188:ARG:HB3	1:B:191:GLU:OE1	1.87	0.74
1:D:121:THR:HG22	1:D:127:PRO:HD3	1.70	0.74
1:C:11:VAL:HG22	1:C:56:LEU:HB3	1.70	0.74
1:D:212:ILE:HD12	1:D:234:MSE:HE3	1.68	0.74
1:A:206:ALA:HB1	1:A:234:MSE:HG3	1.68	0.74
1:A:16:PRO:O	1:A:20:ARG:HG3	1.88	0.74
1:B:228:LYS:O	1:B:232:GLN:HG3	1.88	0.74
1:C:219:THR:HB	1:C:220:PRO:HD2	1.70	0.73
1:A:143:PRO:HA	1:B:302:ARG:HH11	1.52	0.73
1:A:11:VAL:HB	1:A:33:GLN:HG3	1.70	0.73
1:B:114:LEU:HD13	1:B:295:GLY:HA2	1.70	0.73
1:D:15:ILE:H	1:D:20:ARG:NH2	1.82	0.73
1:A:114:LEU:HD22	1:A:295:GLY:CA	2.17	0.73
1:D:249:VAL:HG12	1:D:250:ASN:H	1.52	0.73
1:A:155:THR:N	1:A:210:ASP:OD2	2.21	0.73
1:A:262:LYS:HG3	2:A:400:HOH:O	1.87	0.73
1:A:147:CYS:HA	1:B:297:ALA:O	1.88	0.73
1:A:314:LEU:HG	1:A:318:ARG:HH11	1.50	0.73
1:C:302:ARG:HA	1:C:305:MSE:SE	2.38	0.73
1:D:11:VAL:HG21	1:D:23:LEU:HD13	1.71	0.73
1:A:51:GLY:CA	1:A:74:ASN:HD22	2.01	0.73
1:B:200:VAL:CG2	1:B:204:GLU:HB3	2.18	0.73
1:C:85:ILE:HD13	1:C:90:LEU:HD11	1.71	0.73
1:D:85:ILE:HD12	1:D:90:LEU:CD1	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ARG:NH2	1:A:322:MSE:HG3	2.04	0.73
1:A:181:LEU:O	1:A:182:TYR:HB3	1.85	0.73
1:B:78:ILE:HG13	1:B:98:ILE:HG21	1.70	0.73
1:B:315:ALA:HA	1:B:320:GLU:OE1	1.88	0.73
1:C:185:ARG:HB2	1:C:186:GLN:OE1	1.88	0.73
1:B:320:GLU:HB3	1:B:321:PRO:HD2	1.70	0.73
1:B:9:VAL:HB	1:B:31:VAL:HG22	1.71	0.73
1:A:8:LYS:HB3	1:A:52:ALA:HA	1.69	0.73
1:A:23:LEU:HD11	1:A:56:LEU:HD12	1.71	0.73
1:D:78:ILE:HB	1:D:100:VAL:HG22	1.70	0.73
1:A:232:GLN:HE22	1:A:262:LYS:HZ2	1.35	0.73
1:A:322:MSE:HB2	1:A:325:GLU:HB2	1.70	0.73
1:D:75:LEU:HD23	1:D:98:ILE:HD13	1.70	0.73
1:D:242:ASN:ND2	1:D:246:GLY:HA2	2.03	0.73
1:C:310:ALA:O	1:C:313:LEU:HB3	1.89	0.73
1:D:16:PRO:HD2	1:D:81:MSE:HE1	1.71	0.73
1:B:222:THR:O	1:B:223:GLU:HB2	1.89	0.73
1:D:8:LYS:HB3	1:D:52:ALA:HA	1.70	0.73
1:C:107:LEU:HD23	1:C:305:MSE:HE3	1.71	0.73
1:C:14:ARG:NH2	1:C:36:SER:HA	2.02	0.73
1:A:99:ARG:HH21	1:A:322:MSE:HG3	1.54	0.73
1:B:222:THR:O	1:B:225:LEU:HB2	1.88	0.73
1:A:298:THR:OG1	1:A:301:THR:HB	1.89	0.73
1:C:57:CYS:HB2	1:C:61:ASP:OD2	1.89	0.73
1:B:45:LEU:O	1:B:49:VAL:HG22	1.89	0.73
1:C:9:VAL:HB	1:C:31:VAL:HG22	1.71	0.72
1:C:99:ARG:NH2	1:C:319:GLY:HA2	2.03	0.72
1:B:193:ALA:HB3	2:B:422:HOH:O	1.88	0.72
1:C:223:GLU:HG2	1:C:247:ASP:HB3	1.70	0.72
1:A:53:HIS:CB	1:A:317:LEU:HD11	2.19	0.72
1:D:13:ARG:HG2	1:D:36:SER:O	1.88	0.72
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.71	0.72
1:A:301:THR:O	1:A:305:MSE:HG3	1.89	0.72
1:B:226:CYS:HB2	1:B:249:VAL:HA	1.70	0.72
1:C:198:GLU:O	1:C:200:VAL:HG13	1.89	0.72
1:C:14:ARG:HH21	1:C:37:ASP:N	1.85	0.72
1:D:81:MSE:HE2	1:D:306:SER:HA	1.72	0.72
1:C:65:LYS:HB3	1:C:92:GLU:HG3	1.70	0.72
1:D:85:ILE:HD13	1:D:90:LEU:HD11	1.71	0.72
1:A:64:ASP:C	1:A:68:LEU:HD12	2.10	0.72
1:C:76:LYS:NZ	1:C:76:LYS:HB3	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ARG:HG2	1:A:96:ARG:HH11	1.55	0.72
1:C:14:ARG:HD3	1:C:35:ASP:OD1	1.89	0.72
1:A:177:VAL:HG21	1:A:180:PHE:CZ	2.24	0.72
1:A:26:ALA:HB2	1:A:314:LEU:HD21	1.69	0.72
1:A:187:PRO:HG3	1:A:199:PHE:CD2	2.24	0.72
1:C:20:ARG:NE	1:C:33:GLN:HE22	1.87	0.72
1:B:322:MSE:HE3	1:B:323:PRO:HD2	1.72	0.72
1:D:249:VAL:HG12	1:D:250:ASN:N	2.04	0.72
1:D:280:HIS:ND1	1:D:281:PRO:HD2	2.05	0.72
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.71	0.72
1:C:18:GLU:OE1	1:C:303:ASN:HB3	1.89	0.72
1:C:166:GLN:HE22	1:C:188:ARG:NH2	1.87	0.72
1:A:29:CYS:HB2	2:A:347:HOH:O	1.89	0.72
1:B:249:VAL:HG12	1:B:250:ASN:N	2.05	0.72
1:A:202:THR:HB	1:A:203:PRO:HD3	1.72	0.72
1:A:17:ALA:O	1:A:21:VAL:HG23	1.89	0.72
1:C:251:GLN:HE22	1:C:272:SER:H	1.35	0.72
1:A:76:LYS:HD2	1:A:317:LEU:HD12	1.71	0.72
1:B:235:LYS:HB2	1:B:238:ALA:HB2	1.71	0.72
1:B:222:THR:O	1:B:225:LEU:HB2	1.89	0.72
1:D:164:ILE:HB	1:D:215:ALA:HB1	1.72	0.72
1:D:8:LYS:H	1:D:53:HIS:CE1	2.07	0.72
1:D:13:ARG:HG2	1:D:14:ARG:H	1.55	0.72
1:A:85:ILE:HD12	1:A:90:LEU:HD11	1.72	0.72
1:B:71:ALA:HB1	1:B:75:LEU:HB3	1.70	0.72
1:B:188:ARG:HA	2:B:343:HOH:O	1.89	0.72
1:C:96:ARG:HB2	1:C:98:ILE:HD13	1.72	0.72
1:D:8:LYS:HA	1:D:30:GLU:O	1.88	0.72
1:A:157:GLY:O	1:A:212:ILE:HA	1.90	0.72
1:A:93:ILE:HG23	1:A:98:ILE:HB	1.71	0.72
1:A:322:MSE:SE	1:A:325:GLU:HB2	2.40	0.71
1:A:223:GLU:OE2	1:A:247:ASP:HB3	1.90	0.71
1:A:11:VAL:HG13	1:A:56:LEU:HD13	1.71	0.71
1:C:202:THR:HB	1:C:203:PRO:HD3	1.72	0.71
1:C:104:PRO:O	1:C:106:VAL:HG13	1.89	0.71
1:A:107:LEU:HD23	1:A:305:MSE:HE3	1.71	0.71
1:C:87:HIS:C	1:C:88:LEU:HD22	2.11	0.71
1:D:8:LYS:NZ	1:D:52:ALA:HB2	2.05	0.71
1:A:114:LEU:HD13	1:A:295:GLY:CA	2.19	0.71
1:D:78:ILE:HB	1:D:100:VAL:HG22	1.71	0.71
1:B:11:VAL:HB	1:B:33:GLN:HG3	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:THR:HG22	1:B:308:LEU:HG	1.70	0.71
1:D:234:MSE:HG2	1:D:235:LYS:N	2.05	0.71
1:D:157:GLY:O	1:D:212:ILE:HA	1.90	0.71
1:D:312:ASN:OD1	1:D:323:PRO:HB2	1.90	0.71
1:A:143:PRO:HA	1:B:302:ARG:NH1	2.04	0.71
1:C:214:VAL:HG12	1:C:244:SER:OG	1.90	0.71
1:A:151:LEU:N	1:A:151:LEU:HD12	2.05	0.71
1:B:63:VAL:HA	1:B:67:ILE:HG13	1.72	0.71
1:A:159:ILE:HG12	1:A:183:THR:HG22	1.72	0.71
1:A:11:VAL:HB	1:A:33:GLN:HE21	1.54	0.71
1:C:152:THR:HG22	1:C:153:GLN:HG3	1.72	0.71
1:C:9:VAL:HG13	1:C:313:LEU:HD21	1.72	0.71
1:B:79:SER:H	1:B:313:LEU:HD13	1.55	0.71
1:B:11:VAL:HG13	1:B:56:LEU:HD22	1.71	0.71
1:B:41:PRO:HB2	1:B:44:GLU:HG2	1.71	0.71
1:C:206:ALA:HB2	1:C:230:PHE:CE1	2.24	0.71
1:C:310:ALA:O	1:C:314:LEU:HD13	1.91	0.71
1:D:315:ALA:HB1	1:D:320:GLU:HB2	1.70	0.71
1:C:163:ARG:HB2	2:C:340:HOH:O	1.91	0.71
1:B:78:ILE:O	1:B:100:VAL:HA	1.91	0.71
1:B:15:ILE:HB	1:B:81:MSE:HE1	1.72	0.71
1:A:49:VAL:HG12	1:A:55:LEU:HD13	1.73	0.71
1:A:114:LEU:HD22	1:A:295:GLY:HA2	1.73	0.71
1:B:79:SER:HB2	1:B:313:LEU:HB2	1.73	0.71
1:A:181:LEU:HD23	1:A:198:GLU:HB2	1.72	0.71
1:A:73:ALA:N	2:A:419:HOH:O	2.22	0.71
1:A:11:VAL:HB	1:A:33:GLN:OE1	1.91	0.71
1:A:45:LEU:O	1:A:49:VAL:HG22	1.91	0.71
1:A:53:HIS:O	1:A:77:VAL:HG12	1.91	0.71
1:C:114:LEU:HD22	1:C:295:GLY:HA2	1.73	0.71
1:C:135:ASN:OD1	1:C:136:GLY:N	2.23	0.71
1:C:152:THR:HG22	1:C:153:GLN:HG3	1.72	0.71
1:A:95:LYS:HB2	2:A:351:HOH:O	1.91	0.71
1:D:49:VAL:HG23	1:D:50:ALA:N	2.06	0.71
1:B:200:VAL:HG22	1:B:204:GLU:HB3	1.72	0.71
1:A:320:GLU:HB3	1:A:321:PRO:HD2	1.73	0.71
1:B:92:GLU:HG2	2:B:434:HOH:O	1.91	0.71
1:B:234:MSE:SE	1:B:263:ILE:HG21	2.40	0.71
1:C:8:LYS:NZ	1:C:52:ALA:HB2	2.06	0.71
1:C:245:ARG:HB2	1:C:248:VAL:HG23	1.71	0.71
1:B:102:TYR:CD1	1:B:326:LEU:HB2	2.26	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:LEU:HD22	1:C:295:GLY:HA2	1.73	0.70
1:D:155:THR:OG1	1:D:179:ARG:HB3	1.91	0.70
1:A:114:LEU:HD13	1:A:295:GLY:CA	2.19	0.70
1:A:161:LEU:HG	1:A:166:GLN:NE2	2.05	0.70
1:C:202:THR:HB	1:C:203:PRO:HD3	1.72	0.70
1:A:257:ALA:HB1	1:A:262:LYS:HB2	1.72	0.70
1:B:111:THR:HG21	1:B:164:ILE:HD13	1.72	0.70
1:C:45:LEU:HD23	1:C:67:ILE:HD12	1.72	0.70
1:B:167:ALA:HA	1:B:170:ARG:NH1	2.00	0.70
1:C:14:ARG:NH2	1:C:36:SER:HA	2.07	0.70
1:D:7:MSE:HE2	1:D:53:HIS:HB3	1.72	0.70
1:B:222:THR:HA	1:B:225:LEU:HD23	1.71	0.70
1:C:63:VAL:HG13	1:C:67:ILE:HB	1.72	0.70
1:D:49:VAL:HG23	1:D:50:ALA:H	1.55	0.70
1:A:86:ASP:HB3	1:A:218:LEU:HD22	1.73	0.70
1:C:85:ILE:HG13	2:C:353:HOH:O	1.92	0.70
1:A:201:SER:OG	1:A:203:PRO:HD2	1.91	0.70
1:A:11:VAL:HA	1:A:56:LEU:HB3	1.72	0.70
1:A:90:LEU:HG	2:A:425:HOH:O	1.90	0.70
1:B:85:ILE:HB	1:B:88:LEU:HD12	1.73	0.70
1:D:43:LYS:HB3	2:D:405:HOH:O	1.92	0.70
1:A:62:HIS:HA	1:A:87:HIS:O	1.92	0.70
1:A:43:LYS:HE3	1:A:47:ARG:HH21	1.54	0.70
1:B:188:ARG:HD3	1:B:191:GLU:OE2	1.90	0.70
1:C:323:PRO:O	1:C:324:SER:HB2	1.92	0.70
1:C:6:LEU:HB2	1:C:30:GLU:HB2	1.73	0.70
1:C:59:LEU:H	1:C:59:LEU:CD1	2.03	0.70
1:B:78:ILE:HD12	1:B:93:ILE:HD13	1.72	0.70
1:B:325:GLU:HG3	1:B:326:LEU:N	2.06	0.70
1:C:202:THR:HB	1:C:203:PRO:HD3	1.72	0.70
1:C:11:VAL:HB	1:C:33:GLN:HE21	1.56	0.70
1:D:159:ILE:HG23	1:D:183:THR:HG21	1.73	0.70
1:A:139:THR:OG1	1:A:142:LYS:HE3	1.92	0.70
1:B:185:ARG:HG3	1:B:185:ARG:HH11	1.56	0.70
1:D:159:ILE:HA	1:D:183:THR:HG23	1.71	0.70
1:D:7:MSE:HG2	1:D:28:ASP:O	1.92	0.70
1:B:163:ARG:HH11	1:B:163:ARG:CA	2.04	0.70
1:A:45:LEU:HG	1:A:67:ILE:HD12	1.72	0.70
1:C:54:GLY:HA2	1:C:77:VAL:HG13	1.73	0.70
1:D:51:GLY:HA2	2:D:414:HOH:O	1.90	0.70
1:B:6:LEU:HD12	1:B:6:LEU:N	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:81:MSE:HE2	1:D:306:SER:HA	1.74	0.70
1:A:83:VAL:HG23	1:A:104:PRO:HB3	1.73	0.70
1:B:55:LEU:HG	1:B:78:ILE:HG23	1.73	0.70
1:C:102:TYR:HE1	2:C:439:HOH:O	1.74	0.70
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.74	0.70
1:C:114:LEU:HD13	1:C:295:GLY:CA	2.22	0.70
1:A:90:LEU:HG	2:A:425:HOH:O	1.91	0.70
1:C:109:ASP:HB2	2:C:338:HOH:O	1.92	0.69
1:B:315:ALA:HB3	1:B:322:MSE:HG2	1.73	0.69
1:D:20:ARG:HD2	1:D:33:GLN:NE2	2.04	0.69
1:C:257:ALA:HA	1:C:262:LYS:HD2	1.73	0.69
1:C:81:MSE:HG2	1:C:305:MSE:HB3	1.74	0.69
1:B:200:VAL:HG22	1:B:201:SER:N	2.07	0.69
1:A:324:SER:HA	2:A:342:HOH:O	1.91	0.69
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.73	0.69
1:B:325:GLU:HG2	1:B:326:LEU:H	1.56	0.69
1:C:63:VAL:HA	1:C:67:ILE:HG13	1.73	0.69
1:C:90:LEU:HD12	2:C:383:HOH:O	1.92	0.69
1:C:217:SER:HA	2:C:349:HOH:O	1.93	0.69
1:D:125:ARG:NH1	1:D:146:LEU:HA	2.08	0.69
1:B:286:LYS:HG3	2:B:362:HOH:O	1.92	0.69
1:B:55:LEU:HB3	1:B:78:ILE:HG12	1.75	0.69
1:C:103:THR:HG22	1:C:308:LEU:HD23	1.73	0.69
1:C:7:MSE:HB2	1:C:29:CYS:SG	2.33	0.69
1:B:226:CYS:SG	1:B:249:VAL:HG22	2.32	0.69
1:B:153:GLN:HG2	2:B:339:HOH:O	1.91	0.69
1:D:191:GLU:HB3	2:D:371:HOH:O	1.91	0.69
1:B:66:ARG:HH11	1:B:66:ARG:CB	2.00	0.69
1:A:232:GLN:HE22	1:A:262:LYS:HZ1	1.38	0.69
1:B:101:GLY:HA2	1:B:325:GLU:HA	1.74	0.69
1:A:206:ALA:O	1:A:234:MSE:HA	1.92	0.69
1:C:163:ARG:HB2	2:C:340:HOH:O	1.93	0.69
1:A:8:LYS:HD3	1:A:30:GLU:O	1.92	0.69
1:C:132:GLU:HA	1:C:135:ASN:ND2	2.07	0.69
1:C:184:GLY:N	1:C:199:PHE:HE1	1.90	0.69
1:B:202:THR:OG1	1:B:203:PRO:HD3	1.92	0.69
1:D:185:ARG:HD3	1:D:185:ARG:N	2.07	0.69
1:A:59:LEU:HD22	1:A:59:LEU:N	2.01	0.69
1:B:184:GLY:N	1:B:199:PHE:HE1	1.90	0.69
1:B:181:LEU:CD2	1:B:198:GLU:HB3	2.21	0.69
1:D:186:GLN:HG3	1:D:187:PRO:HD2	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:161:LEU:HD22	1:D:182:TYR:CE2	2.27	0.69
1:D:181:LEU:HD22	1:D:200:VAL:CG1	2.21	0.69
1:A:312:ASN:O	1:A:316:GLY:HA3	1.92	0.69
1:B:59:LEU:HA	1:B:87:HIS:ND1	2.07	0.69
1:A:182:TYR:CE1	1:A:199:PHE:HB2	2.27	0.69
1:A:192:ALA:HB1	1:A:197:ALA:HB3	1.74	0.69
1:D:159:ILE:O	1:D:216:CYS:HB3	1.93	0.69
1:C:54:GLY:HA3	1:C:313:LEU:HD11	1.74	0.69
1:A:237:THR:HA	1:A:264:ALA:HB2	1.75	0.69
1:D:78:ILE:HB	1:D:100:VAL:HG22	1.73	0.69
1:C:46:GLU:CG	1:C:67:ILE:HD13	2.14	0.69
1:D:20:ARG:HD2	2:D:333:HOH:O	1.93	0.69
1:C:65:LYS:HB2	1:C:92:GLU:HG2	1.75	0.69
1:C:75:LEU:HG	1:C:98:ILE:HD13	1.74	0.69
1:D:15:ILE:H	1:D:20:ARG:NH2	1.88	0.69
1:D:59:LEU:HD13	1:D:245:ARG:NH2	2.07	0.69
1:A:181:LEU:CD2	1:A:198:GLU:HB2	2.23	0.69
1:A:202:THR:OG1	1:A:203:PRO:HD3	1.93	0.69
1:D:187:PRO:HG3	1:D:199:PHE:CD2	2.27	0.69
1:C:85:ILE:HD12	1:C:90:LEU:HD11	1.74	0.69
1:C:202:THR:HB	1:C:203:PRO:HD3	1.75	0.69
1:D:202:THR:OG1	1:D:203:PRO:HD3	1.92	0.69
1:A:236:GLU:HA	1:A:262:LYS:O	1.93	0.69
1:A:9:VAL:HB	1:A:31:VAL:HG22	1.74	0.69
1:A:155:THR:HG23	1:A:179:ARG:HD2	1.75	0.69
1:A:81:MSE:HE2	1:A:306:SER:HA	1.73	0.69
1:A:63:VAL:HG13	1:A:67:ILE:HG21	1.73	0.69
1:A:144:LEU:HD11	1:B:14:ARG:HG2	1.75	0.69
1:B:11:VAL:HG23	1:B:32:GLU:O	1.92	0.69
1:A:34:TRP:CD1	1:A:40:ILE:HB	2.27	0.69
1:A:164:ILE:HG22	1:A:164:ILE:O	1.91	0.68
1:A:151:LEU:N	1:A:151:LEU:HD12	2.08	0.68
1:B:286:LYS:HG2	2:B:364:HOH:O	1.93	0.68
1:B:193:ALA:HB3	2:B:421:HOH:O	1.93	0.68
1:A:98:ILE:HG22	1:A:99:ARG:N	2.08	0.68
1:D:161:LEU:HG	1:D:166:GLN:HG2	1.76	0.68
1:D:220:PRO:HA	2:D:403:HOH:O	1.93	0.68
1:C:277:PRO:HB2	1:C:280:HIS:HB2	1.75	0.68
1:D:163:ARG:HH11	1:D:166:GLN:HE22	1.41	0.68
1:A:85:ILE:HG21	1:A:326:LEU:CD2	2.23	0.68
1:B:75:LEU:HD23	1:B:98:ILE:HD13	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:GLU:OE1	1:C:303:ASN:HB3	1.92	0.68
1:D:102:TYR:CZ	1:D:104:PRO:HG3	2.28	0.68
1:B:114:LEU:HD11	1:B:294:ILE:HG13	1.74	0.68
1:C:38:GLU:OE1	1:D:139:THR:HG21	1.94	0.68
1:B:57:CYS:HB2	1:B:61:ASP:OD2	1.94	0.68
1:B:226:CYS:HA	1:B:230:PHE:CG	2.29	0.68
1:A:179:ARG:NE	1:A:181:LEU:HD21	2.08	0.68
1:C:218:LEU:HD12	1:C:222:THR:OG1	1.92	0.68
1:C:39:PRO:HA	2:C:443:HOH:O	1.93	0.68
1:B:68:LEU:HD13	1:B:96:ARG:HH11	1.58	0.68
1:B:289:VAL:HA	2:B:376:HOH:O	1.93	0.68
1:B:11:VAL:H	1:B:33:GLN:HB3	1.58	0.68
1:D:200:VAL:HB	1:D:204:GLU:HB2	1.75	0.68
1:C:58:LEU:HD23	1:C:81:MSE:HB3	1.76	0.68
1:C:218:LEU:HA	1:C:222:THR:OG1	1.94	0.68
1:D:103:THR:HG22	1:D:308:LEU:CG	2.23	0.68
1:C:38:GLU:OE2	1:D:139:THR:HG21	1.93	0.68
1:C:81:MSE:HB3	1:C:305:MSE:CE	2.22	0.68
1:C:162:GLY:C	1:C:166:GLN:HE21	1.97	0.68
1:B:161:LEU:HD21	1:B:192:ALA:HB2	1.74	0.68
1:D:19:GLY:HA2	1:D:307:LEU:HA	1.74	0.68
1:C:69:ASP:HA	1:C:96:ARG:NH2	2.03	0.68
1:D:55:LEU:HB3	1:D:78:ILE:HG12	1.75	0.68
1:D:142:LYS:HD2	1:D:145:TRP:CD2	2.27	0.68
1:A:80:THR:HG22	1:A:101:GLY:O	1.94	0.68
1:A:277:PRO:HB2	1:A:280:HIS:HB2	1.76	0.68
1:B:223:GLU:HA	1:B:248:VAL:HA	1.75	0.68
1:B:273:PRO:HD2	1:B:277:PRO:HD3	1.75	0.68
1:B:83:VAL:HG23	1:B:104:PRO:HA	1.75	0.68
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.75	0.68
1:D:180:PHE:HB2	1:D:197:ALA:HB2	1.76	0.68
1:C:152:THR:HG22	1:C:153:GLN:HG3	1.76	0.68
1:D:20:ARG:HG3	2:D:333:HOH:O	1.92	0.68
1:D:45:LEU:O	1:D:49:VAL:HG13	1.94	0.68
1:C:11:VAL:O	1:C:33:GLN:HG3	1.94	0.68
1:A:11:VAL:HB	1:A:33:GLN:HE21	1.58	0.68
1:C:26:ALA:HA	1:C:318:ARG:NH2	2.09	0.68
1:C:75:LEU:HD12	1:C:77:VAL:H	1.59	0.68
1:C:85:ILE:HD12	1:C:90:LEU:HD11	1.76	0.68
1:A:181:LEU:HD13	1:A:200:VAL:HG11	1.75	0.68
1:B:40:ILE:HD11	1:B:44:GLU:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:GLY:HA2	2:B:336:HOH:O	1.94	0.68
1:D:20:ARG:HH11	1:D:33:GLN:HE22	1.41	0.68
1:B:153:GLN:HA	1:B:178:GLN:HB2	1.76	0.68
1:A:293:HIS:HB3	1:B:141:TRP:HD1	1.59	0.68
1:B:283:LEU:HD23	1:B:290:ILE:HD12	1.76	0.68
1:B:72:GLY:HA3	2:B:336:HOH:O	1.92	0.68
1:D:234:MSE:HG2	1:D:235:LYS:H	1.59	0.68
1:C:8:LYS:HD3	1:C:52:ALA:N	2.09	0.67
1:D:9:VAL:HG11	1:D:313:LEU:HD21	1.76	0.67
1:A:22:ALA:HA	1:A:25:ARG:NE	2.09	0.67
1:A:58:LEU:CD2	1:A:81:MSE:HB3	2.23	0.67
1:A:81:MSE:HG2	1:A:305:MSE:HE3	1.76	0.67
1:B:98:ILE:HD12	1:B:98:ILE:H	1.59	0.67
1:B:212:ILE:HD12	1:B:234:MSE:SE	2.43	0.67
1:C:312:ASN:HA	1:C:323:PRO:HD2	1.76	0.67
1:C:11:VAL:CB	1:C:33:GLN:HE21	2.03	0.67
1:A:131:GLU:HG3	1:A:135:ASN:ND2	2.08	0.67
1:A:232:GLN:HE22	1:A:262:LYS:HZ3	1.41	0.67
1:C:38:GLU:OE2	1:C:39:PRO:HD2	1.94	0.67
1:A:158:ILE:O	1:A:182:TYR:HA	1.95	0.67
1:B:47:ARG:O	1:B:47:ARG:HD3	1.93	0.67
1:B:153:GLN:HA	1:B:178:GLN:HB2	1.75	0.67
1:C:174:PRO:HG3	1:D:174:PRO:HG2	1.76	0.67
1:C:108:THR:HA	1:C:164:ILE:HG12	1.76	0.67
1:D:234:MSE:HB3	2:D:345:HOH:O	1.92	0.67
1:A:159:ILE:HA	1:A:183:THR:HG23	1.75	0.67
1:A:59:LEU:HD12	1:A:60:SER:N	2.08	0.67
1:B:99:ARG:NH2	1:B:315:ALA:HB1	2.09	0.67
1:B:206:ALA:O	1:B:234:MSE:HA	1.94	0.67
1:D:197:ALA:HA	2:D:349:HOH:O	1.94	0.67
1:D:212:ILE:HD12	1:D:234:MSE:HE3	1.74	0.67
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.76	0.67
1:A:114:LEU:HD22	1:A:295:GLY:CA	2.24	0.67
1:A:312:ASN:HA	1:A:323:PRO:HD2	1.75	0.67
1:B:18:GLU:HB2	1:B:303:ASN:HD22	1.58	0.67
1:D:121:THR:HG23	1:D:126:LEU:HB2	1.75	0.67
1:B:14:ARG:HB2	1:B:14:ARG:NH1	2.09	0.67
1:C:69:ASP:HA	1:C:96:ARG:NH2	2.10	0.67
1:A:17:ALA:O	1:A:20:ARG:HB2	1.95	0.67
1:A:17:ALA:N	1:A:20:ARG:HE	1.92	0.67
1:D:68:LEU:HB3	1:D:96:ARG:CZ	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.76	0.67
1:A:227:ASN:HA	1:A:250:ASN:CB	2.25	0.67
1:C:34:TRP:CD1	1:C:40:ILE:HB	2.30	0.67
1:A:156:VAL:O	1:A:180:PHE:HA	1.94	0.67
1:B:14:ARG:HA	1:B:33:GLN:CD	2.14	0.67
1:B:160:GLY:HA3	1:B:216:CYS:HB3	1.74	0.67
1:C:192:ALA:HB1	1:C:197:ALA:HB3	1.77	0.67
1:A:17:ALA:HA	1:A:20:ARG:HE	1.59	0.67
1:B:212:ILE:HD13	1:B:234:MSE:HE3	1.76	0.67
1:D:305:MSE:O	1:D:308:LEU:HB3	1.95	0.67
1:A:56:LEU:HD11	1:A:310:ALA:HA	1.75	0.67
1:A:155:THR:HG22	1:A:209:SER:HA	1.75	0.67
1:C:14:ARG:NH2	1:C:36:SER:HA	2.10	0.67
1:B:34:TRP:HB2	1:B:40:ILE:HD12	1.77	0.67
1:D:91:ASP:O	1:D:95:LYS:HB2	1.93	0.67
1:D:206:ALA:O	1:D:234:MSE:HA	1.94	0.67
1:D:312:ASN:HD21	1:D:324:SER:HB2	1.58	0.67
1:C:77:VAL:HA	1:C:99:ARG:O	1.93	0.67
1:A:85:ILE:HD12	1:A:86:ASP:N	2.10	0.67
1:B:41:PRO:HD2	1:B:44:GLU:HG3	1.76	0.67
1:B:194:GLU:HB2	2:B:394:HOH:O	1.94	0.67
1:B:85:ILE:HG22	1:B:88:LEU:HB2	1.77	0.67
1:B:312:ASN:O	1:B:322:MSE:HE3	1.93	0.67
1:A:283:LEU:HD21	1:B:134:LYS:HG2	1.76	0.67
1:C:310:ALA:O	1:C:313:LEU:HB3	1.95	0.67
1:A:72:GLY:HA3	2:A:423:HOH:O	1.95	0.67
1:A:206:ALA:O	1:A:234:MSE:HA	1.95	0.67
1:C:20:ARG:NH1	1:C:20:ARG:HB2	2.09	0.67
1:C:53:HIS:HB3	1:C:76:LYS:NZ	2.10	0.67
1:A:283:LEU:HD23	1:A:283:LEU:O	1.95	0.67
1:D:322:MSE:H	1:D:322:MSE:SE	2.28	0.67
1:D:180:PHE:CD2	1:D:195:PHE:HB3	2.29	0.67
1:B:107:LEU:HD23	1:B:305:MSE:CE	2.25	0.67
1:D:53:HIS:HA	1:D:74:ASN:O	1.95	0.67
1:D:192:ALA:HB1	1:D:197:ALA:CB	2.24	0.67
1:A:32:GLU:HG3	2:A:368:HOH:O	1.94	0.67
1:A:244:SER:O	1:A:270:VAL:HG11	1.94	0.67
1:A:93:ILE:HG23	1:A:98:ILE:HB	1.77	0.67
1:A:173:LYS:HB3	1:A:174:PRO:HD3	1.77	0.67
1:B:277:PRO:HB2	1:B:280:HIS:HB2	1.77	0.67
1:D:234:MSE:HE2	1:D:238:ALA:CB	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:MSE:CE	1:A:317:LEU:HB3	2.25	0.67
1:B:114:LEU:HD13	1:B:295:GLY:HA2	1.77	0.67
1:C:12:THR:O	1:C:34:TRP:HB3	1.95	0.66
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.76	0.66
1:D:234:MSE:HA	2:D:344:HOH:O	1.95	0.66
1:C:23:LEU:HD21	1:C:313:LEU:CD2	2.25	0.66
1:B:159:ILE:HB	1:B:214:VAL:HG13	1.76	0.66
1:D:50:ALA:HA	1:D:70:ALA:O	1.94	0.66
1:B:7:MSE:SE	1:B:317:LEU:HG	2.46	0.66
1:D:106:VAL:O	1:D:301:THR:HG23	1.95	0.66
1:B:9:VAL:HG11	1:B:313:LEU:HD11	1.77	0.66
1:A:315:ALA:HB1	1:A:321:PRO:O	1.95	0.66
1:A:114:LEU:HD23	1:A:295:GLY:HA2	1.76	0.66
1:B:212:ILE:HD12	1:B:234:MSE:SE	2.45	0.66
1:D:53:HIS:HA	1:D:74:ASN:O	1.95	0.66
1:A:155:THR:HG23	1:A:179:ARG:HG3	1.77	0.66
1:D:63:VAL:HB	1:D:88:LEU:HD23	1.77	0.66
1:A:81:MSE:O	1:A:305:MSE:HE3	1.95	0.66
1:A:56:LEU:HD21	1:A:309:ALA:HB1	1.77	0.66
1:A:147:CYS:HA	1:B:297:ALA:O	1.96	0.66
1:B:19:GLY:O	1:B:22:ALA:HB3	1.96	0.66
1:C:312:ASN:HA	1:C:323:PRO:HD2	1.78	0.66
1:A:257:ALA:HA	1:A:262:LYS:HD2	1.77	0.66
1:C:174:PRO:HG3	1:D:174:PRO:HG2	1.77	0.66
1:A:204:GLU:HG2	1:D:204:GLU:OE2	1.94	0.66
1:C:302:ARG:HG3	1:D:147:CYS:SG	2.35	0.66
1:B:103:THR:HB	1:B:308:LEU:HD23	1.76	0.66
1:B:153:GLN:HB3	1:B:178:GLN:NE2	2.11	0.66
1:D:93:ILE:HG23	1:D:98:ILE:HB	1.78	0.66
1:D:90:LEU:C	1:D:92:GLU:H	1.99	0.66
1:C:16:PRO:HD2	1:C:81:MSE:HE1	1.78	0.66
1:A:119:LEU:HD13	1:A:172:LEU:HD11	1.78	0.66
1:B:8:LYS:HB3	1:B:52:ALA:HA	1.78	0.66
1:A:230:PHE:O	1:A:234:MSE:HG3	1.95	0.66
1:D:16:PRO:HB2	1:D:18:GLU:HG2	1.77	0.66
1:A:249:VAL:HG12	1:A:250:ASN:N	2.10	0.66
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.76	0.66
1:A:65:LYS:HG3	1:A:92:GLU:HG3	1.78	0.66
1:A:181:LEU:CD2	1:A:198:GLU:HB2	2.25	0.66
1:A:140:SER:HB3	1:B:39:PRO:HD3	1.78	0.66
1:C:14:ARG:HH21	1:C:37:ASP:H	1.42	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:ILE:HD13	1:D:45:LEU:HA	1.78	0.66
1:C:76:LYS:HE2	1:C:317:LEU:HA	1.78	0.66
1:D:32:GLU:HG2	1:D:33:GLN:N	2.10	0.66
1:D:192:ALA:HA	1:D:195:PHE:CE2	2.30	0.66
1:C:114:LEU:HD13	1:C:295:GLY:CA	2.24	0.66
1:D:227:ASN:H	1:D:230:PHE:HB3	1.60	0.66
1:B:14:ARG:HG3	1:B:20:ARG:HD3	1.77	0.66
1:D:222:THR:O	1:D:248:VAL:HA	1.95	0.66
1:B:75:LEU:HD23	1:B:98:ILE:CD1	2.26	0.66
1:B:77:VAL:N	1:B:98:ILE:HG23	2.11	0.66
1:D:34:TRP:HB2	1:D:40:ILE:HD12	1.77	0.66
1:A:257:ALA:HA	1:A:262:LYS:HE3	1.78	0.66
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.77	0.66
1:C:56:LEU:HA	1:C:79:SER:O	1.95	0.66
1:A:214:VAL:HG12	1:A:244:SER:OG	1.96	0.66
1:A:320:GLU:HB3	1:A:321:PRO:HD2	1.77	0.66
1:A:133:VAL:HG23	1:B:292:PRO:HD3	1.76	0.66
1:A:141:TRP:HH2	1:B:305:MSE:SE	2.28	0.66
1:B:58:LEU:HD12	1:B:58:LEU:H	1.60	0.66
1:B:212:ILE:HD12	1:B:234:MSE:SE	2.45	0.66
1:C:17:ALA:O	1:C:21:VAL:HG23	1.95	0.66
1:D:102:TYR:CE1	1:D:326:LEU:HA	2.30	0.66
1:A:188:ARG:HG3	1:A:191:GLU:OE1	1.96	0.65
1:A:143:PRO:HG2	1:A:144:LEU:CD2	2.23	0.65
1:B:188:ARG:HD2	2:B:361:HOH:O	1.95	0.65
1:A:46:GLU:HG2	1:A:70:ALA:HB1	1.77	0.65
1:C:14:ARG:HD3	1:C:35:ASP:CG	2.16	0.65
1:C:65:LYS:CD	1:C:96:ARG:HH22	2.08	0.65
1:C:114:LEU:HD13	1:C:295:GLY:HA2	1.77	0.65
1:B:229:ASP:HA	1:B:232:GLN:NE2	2.02	0.65
1:A:187:PRO:HG3	1:A:199:PHE:CE2	2.31	0.65
1:A:187:PRO:HG3	1:A:199:PHE:CZ	2.31	0.65
1:A:75:LEU:HD21	1:A:78:ILE:HD11	1.78	0.65
1:A:208:GLN:HA	1:A:208:GLN:HE21	1.60	0.65
1:B:53:HIS:O	1:B:75:LEU:HD12	1.96	0.65
1:C:188:ARG:N	1:C:189:PRO:HD3	2.12	0.65
1:C:44:GLU:HA	1:C:44:GLU:OE2	1.96	0.65
1:A:32:GLU:O	1:A:33:GLN:HB2	1.96	0.65
1:A:159:ILE:HG23	1:A:183:THR:OG1	1.97	0.65
1:C:89:ALA:HA	2:C:383:HOH:O	1.96	0.65
1:D:203:PRO:HB3	1:D:233:LYS:HE2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:LEU:CD2	1:B:61:ASP:HB3	2.26	0.65
1:D:158:ILE:HG12	1:D:213:VAL:HB	1.77	0.65
1:D:77:VAL:HG11	1:D:317:LEU:HD22	1.77	0.65
1:D:163:ARG:HH21	1:D:166:GLN:CB	2.09	0.65
1:A:186:GLN:HG3	1:A:187:PRO:HD2	1.79	0.65
1:C:214:VAL:HG12	1:C:244:SER:OG	1.95	0.65
1:C:301:THR:CG2	1:C:305:MSE:SE	2.94	0.65
1:D:99:ARG:HD2	1:D:325:GLU:OE2	1.96	0.65
1:A:11:VAL:HB	1:A:33:GLN:CD	2.17	0.65
1:A:202:THR:HB	1:A:203:PRO:HD3	1.78	0.65
1:D:100:VAL:HB	1:D:326:LEU:HB3	1.78	0.65
1:B:76:LYS:HG3	1:B:77:VAL:HG12	1.78	0.65
1:D:183:THR:HG23	1:D:205:LEU:HD13	1.78	0.65
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.77	0.65
1:A:234:MSE:HG2	2:A:342:HOH:O	1.96	0.65
1:C:252:ASP:HB2	2:C:403:HOH:O	1.97	0.65
1:D:7:MSE:O	1:D:30:GLU:N	2.30	0.65
1:D:59:LEU:HB3	1:D:82:SER:CB	2.26	0.65
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.77	0.65
1:D:205:LEU:HD23	1:D:206:ALA:N	2.10	0.65
1:C:107:LEU:HD23	1:C:305:MSE:HE3	1.79	0.65
1:D:251:GLN:NE2	1:D:280:HIS:NE2	2.44	0.65
1:C:106:VAL:O	1:C:301:THR:HG23	1.97	0.65
1:B:188:ARG:HB3	1:B:191:GLU:OE1	1.97	0.65
1:A:204:GLU:OE2	1:D:204:GLU:HG3	1.97	0.65
1:A:121:THR:CG2	1:A:126:LEU:HB2	2.27	0.65
1:B:317:LEU:HD22	1:B:317:LEU:H	1.62	0.65
1:D:8:LYS:HB3	1:D:53:HIS:ND1	2.11	0.65
1:D:276:LEU:HD11	1:D:280:HIS:HD2	1.62	0.65
1:A:179:ARG:CZ	2:A:411:HOH:O	2.45	0.65
1:B:89:ALA:O	1:B:93:ILE:HD12	1.95	0.65
1:A:85:ILE:HG21	1:A:326:LEU:HD22	1.77	0.65
1:A:49:VAL:HG21	1:A:67:ILE:HG23	1.78	0.65
1:C:75:LEU:H	1:C:75:LEU:HD12	1.62	0.65
1:A:153:GLN:HA	1:A:153:GLN:NE2	2.11	0.65
1:B:9:VAL:HB	1:B:31:VAL:HG22	1.78	0.65
1:B:251:GLN:HE22	1:B:272:SER:H	1.42	0.65
1:C:114:LEU:HD22	1:C:295:GLY:CA	2.25	0.65
1:A:99:ARG:HD2	1:A:325:GLU:OE2	1.95	0.65
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.77	0.65
1:C:142:LYS:HB2	1:C:145:TRP:HB2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:232:GLN:OE1	1:D:262:LYS:HD2	1.96	0.65
1:A:129:ALA:HA	1:A:146:LEU:HD11	1.79	0.65
1:B:76:LYS:HG3	1:B:77:VAL:HG12	1.79	0.65
1:B:234:MSE:HE1	1:B:240:PHE:CD1	2.31	0.65
1:D:8:LYS:HD3	1:D:52:ALA:HA	1.78	0.65
1:A:121:THR:CG2	1:A:126:LEU:HB2	2.27	0.65
1:D:88:LEU:HB3	1:D:93:ILE:HD11	1.78	0.65
1:D:184:GLY:H	1:D:199:PHE:HE1	1.44	0.65
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.78	0.65
1:C:14:ARG:HH21	1:C:37:ASP:N	1.95	0.65
1:D:180:PHE:O	1:D:181:LEU:HD23	1.97	0.65
1:B:19:GLY:O	1:B:22:ALA:HB3	1.97	0.65
1:B:55:LEU:O	1:B:78:ILE:HG23	1.97	0.65
1:B:300:ARG:HG3	2:B:444:HOH:O	1.97	0.65
1:D:225:LEU:HB3	1:D:248:VAL:CG1	2.26	0.65
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.78	0.65
1:D:142:LYS:HB3	2:D:362:HOH:O	1.98	0.64
1:A:100:VAL:CB	1:A:326:LEU:HB3	2.25	0.64
1:A:227:ASN:HD21	1:A:229:ASP:HB2	1.62	0.64
1:B:10:PHE:HA	1:B:32:GLU:O	1.97	0.64
1:C:276:LEU:HG	1:C:277:PRO:HD2	1.79	0.64
1:D:241:ILE:HG22	1:D:242:ASN:N	2.13	0.64
1:A:160:GLY:HA3	1:A:216:CYS:HB3	1.80	0.64
1:D:7:MSE:SE	1:D:317:LEU:HG	2.47	0.64
1:D:20:ARG:HD2	1:D:33:GLN:NE2	2.09	0.64
1:B:162:GLY:O	1:B:166:GLN:HG3	1.98	0.64
1:A:232:GLN:HE22	1:A:262:LYS:HZ2	1.45	0.64
1:C:291:LEU:HD13	1:C:294:ILE:HD11	1.79	0.64
1:A:192:ALA:CB	1:A:197:ALA:HB3	2.25	0.64
1:B:135:ASN:O	1:B:137:GLY:N	2.30	0.64
1:A:167:ALA:HB1	1:A:171:ARG:NH2	2.10	0.64
1:A:93:ILE:CG2	1:A:98:ILE:HB	2.28	0.64
1:D:8:LYS:HB3	1:D:52:ALA:HA	1.79	0.64
1:A:103:THR:HG22	1:A:308:LEU:HD23	1.77	0.64
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.78	0.64
1:A:90:LEU:HD23	1:A:100:VAL:HG21	1.78	0.64
1:C:20:ARG:HB2	1:C:20:ARG:HH11	1.62	0.64
1:A:159:ILE:CG2	1:A:216:CYS:HB3	2.27	0.64
1:D:45:LEU:O	1:D:49:VAL:HG13	1.98	0.64
1:A:94:LYS:O	1:A:94:LYS:HD3	1.98	0.64
1:B:126:LEU:HD12	1:B:126:LEU:N	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:LEU:HD13	1:C:295:GLY:CA	2.27	0.64
1:D:162:GLY:O	1:D:166:GLN:HG3	1.98	0.64
1:B:126:LEU:HD12	1:B:126:LEU:N	2.13	0.64
1:B:271:THR:OG1	1:B:276:LEU:HD13	1.98	0.64
1:D:81:MSE:SE	1:D:306:SER:HA	2.46	0.64
1:A:50:ALA:HA	1:A:70:ALA:O	1.97	0.64
1:B:229:ASP:HA	1:B:232:GLN:NE2	2.12	0.64
1:B:50:ALA:HA	1:B:70:ALA:O	1.97	0.64
1:C:102:TYR:HD1	1:C:102:TYR:H	1.44	0.64
1:B:104:PRO:O	1:B:105:ASP:HB2	1.96	0.64
1:C:6:LEU:HD12	1:C:6:LEU:N	2.12	0.64
1:B:8:LYS:H	1:B:53:HIS:CE1	2.15	0.64
1:B:212:ILE:HD12	1:B:234:MSE:SE	2.47	0.64
1:A:187:PRO:O	1:A:188:ARG:HG3	1.98	0.64
1:D:180:PHE:O	1:D:197:ALA:HA	1.97	0.64
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.78	0.64
1:B:206:ALA:O	1:B:234:MSE:HA	1.98	0.64
1:C:13:ARG:HD2	1:C:37:ASP:C	2.17	0.64
1:C:40:ILE:HD13	1:C:45:LEU:HA	1.78	0.64
1:D:231:PHE:HZ	1:D:249:VAL:HG13	1.62	0.64
1:B:194:GLU:HB2	2:B:419:HOH:O	1.98	0.64
1:B:11:VAL:HB	1:B:33:GLN:HG3	1.79	0.64
1:C:41:PRO:HB2	1:C:44:GLU:HG2	1.80	0.64
1:D:114:LEU:HD22	1:D:295:GLY:HA2	1.80	0.64
1:B:158:ILE:O	1:B:182:TYR:HA	1.96	0.64
1:D:13:ARG:HG2	1:D:14:ARG:N	2.12	0.64
1:C:318:ARG:HB2	1:C:320:GLU:HG3	1.80	0.64
1:A:151:LEU:CA	1:A:154:SER:HB3	2.28	0.64
1:C:132:GLU:OE1	1:C:137:GLY:HA3	1.98	0.64
1:B:66:ARG:HG2	1:B:66:ARG:HH11	1.62	0.64
1:C:202:THR:HB	1:C:203:PRO:HD3	1.79	0.64
1:A:46:GLU:O	1:A:50:ALA:HB2	1.98	0.64
1:D:7:MSE:HA	1:D:53:HIS:CE1	2.32	0.64
1:A:206:ALA:O	1:A:234:MSE:HA	1.97	0.64
1:D:158:ILE:O	1:D:182:TYR:HA	1.97	0.64
1:D:173:LYS:HB3	1:D:174:PRO:HD3	1.78	0.64
1:C:6:LEU:HB3	1:C:30:GLU:HG3	1.78	0.64
1:A:7:MSE:N	1:A:29:CYS:HA	2.13	0.64
1:D:20:ARG:HG3	2:D:333:HOH:O	1.97	0.64
1:A:227:ASN:HA	1:A:250:ASN:HB2	1.79	0.64
1:B:126:LEU:HD12	1:B:126:LEU:N	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:ALA:C	1:B:28:ASP:H	2.00	0.64
1:B:118:LEU:HD13	1:B:291:LEU:HD11	1.80	0.64
1:C:7:MSE:O	1:C:29:CYS:HA	1.98	0.64
1:A:143:PRO:HG2	2:B:437:HOH:O	1.97	0.64
1:B:126:LEU:HD12	1:B:126:LEU:N	2.13	0.64
1:C:114:LEU:HD22	1:C:295:GLY:CA	2.26	0.64
1:A:212:ILE:HG13	1:A:234:MSE:HE3	1.80	0.64
1:B:153:GLN:HG2	2:B:340:HOH:O	1.97	0.64
1:A:68:LEU:HD22	1:A:75:LEU:HD21	1.79	0.64
1:A:161:LEU:CD2	1:A:192:ALA:HB2	2.27	0.64
1:C:75:LEU:HD12	1:C:75:LEU:N	2.12	0.64
1:B:257:ALA:HA	1:B:262:LYS:HG2	1.79	0.64
1:C:268:LEU:HD12	1:C:271:THR:HG22	1.80	0.64
1:D:81:MSE:HE2	1:D:306:SER:HA	1.79	0.64
1:A:159:ILE:HG12	1:A:183:THR:CG2	2.27	0.64
1:C:56:LEU:HA	1:C:79:SER:O	1.98	0.64
1:A:159:ILE:HA	1:A:183:THR:CG2	2.28	0.64
1:A:161:LEU:CD2	1:A:191:GLU:HB2	2.28	0.64
1:A:219:THR:OG1	1:A:222:THR:HG23	1.98	0.63
1:A:250:ASN:O	1:A:252:ASP:N	2.31	0.63
1:B:153:GLN:HG2	2:B:340:HOH:O	1.97	0.63
1:C:8:LYS:HB3	1:C:52:ALA:HA	1.79	0.63
1:A:9:VAL:O	1:A:31:VAL:HG13	1.97	0.63
1:A:312:ASN:OD1	1:A:323:PRO:HG2	1.99	0.63
1:D:320:GLU:HB2	1:D:321:PRO:HD2	1.80	0.63
1:D:18:GLU:OE1	1:D:303:ASN:HB3	1.97	0.63
1:C:75:LEU:HD23	1:C:98:ILE:HG12	1.80	0.63
1:D:79:SER:HB2	1:D:313:LEU:HB2	1.79	0.63
1:D:139:THR:OG1	1:D:142:LYS:HE3	1.99	0.63
1:A:20:ARG:HD2	1:A:20:ARG:C	2.19	0.63
1:C:318:ARG:O	1:C:320:GLU:HG2	1.98	0.63
1:C:162:GLY:O	1:C:166:GLN:HG3	1.99	0.63
1:C:37:ASP:O	1:D:142:LYS:HE2	1.99	0.63
1:C:312:ASN:HA	1:C:322:MSE:CB	2.28	0.63
1:C:95:LYS:HE2	1:C:96:ARG:HH21	1.64	0.63
1:A:121:THR:HG23	1:A:126:LEU:HD22	1.79	0.63
1:A:159:ILE:HG12	1:A:205:LEU:HD21	1.79	0.63
1:B:55:LEU:HB3	1:B:78:ILE:HG12	1.78	0.63
1:A:153:GLN:HA	1:A:178:GLN:HB2	1.79	0.63
1:A:201:SER:OG	1:A:203:PRO:HD2	1.99	0.63
1:B:192:ALA:HB1	1:B:195:PHE:HD2	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:ALA:O	1:A:20:ARG:HG2	1.97	0.63
1:D:10:PHE:CD1	1:D:32:GLU:HG2	2.34	0.63
1:B:92:GLU:N	2:B:428:HOH:O	2.31	0.63
1:C:107:LEU:HB3	1:C:305:MSE:SE	2.49	0.63
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.78	0.63
1:C:47:ARG:NH1	1:C:47:ARG:HB3	2.14	0.63
1:B:85:ILE:HD12	1:B:90:LEU:HD21	1.79	0.63
1:D:18:GLU:HB2	1:D:306:SER:CB	2.28	0.63
1:D:92:GLU:HA	1:D:95:LYS:HE2	1.79	0.63
1:A:310:ALA:O	1:A:314:LEU:HB2	1.98	0.63
1:B:181:LEU:HD23	1:B:198:GLU:HB3	1.81	0.63
1:C:63:VAL:HG13	1:C:67:ILE:HG21	1.81	0.63
1:B:79:SER:H	1:B:313:LEU:CD1	2.11	0.63
1:B:314:LEU:HD13	1:B:318:ARG:NH1	2.13	0.63
1:C:245:ARG:HG2	1:C:245:ARG:HH11	1.62	0.63
1:C:315:ALA:HB3	1:C:322:MSE:HG2	1.81	0.63
1:A:204:GLU:HG2	1:D:204:GLU:OE2	1.99	0.63
1:B:30:GLU:HA	1:B:30:GLU:OE2	1.99	0.63
1:A:158:ILE:O	1:A:182:TYR:HA	1.99	0.63
1:C:202:THR:HB	1:C:203:PRO:HD3	1.79	0.63
1:D:162:GLY:O	1:D:166:GLN:HG3	1.98	0.63
1:A:13:ARG:HG3	1:A:14:ARG:H	1.62	0.63
1:A:190:GLU:HB2	2:A:352:HOH:O	1.99	0.63
1:B:257:ALA:HA	1:B:262:LYS:HG2	1.80	0.63
1:C:6:LEU:HD13	1:C:30:GLU:HB2	1.81	0.63
1:B:12:THR:CG2	1:B:57:CYS:HA	2.27	0.63
1:C:232:GLN:OE1	1:C:262:LYS:HG3	1.99	0.63
1:D:99:ARG:CZ	1:D:322:MSE:HE3	2.29	0.63
1:B:193:ALA:HB3	2:B:423:HOH:O	1.99	0.63
1:D:21:VAL:O	1:D:24:ALA:HB3	1.99	0.63
1:B:45:LEU:HG	1:B:67:ILE:HD12	1.80	0.63
1:B:182:TYR:HE1	1:B:197:ALA:O	1.82	0.63
1:D:7:MSE:CE	1:D:317:LEU:HB3	2.29	0.63
1:B:326:LEU:O	1:B:326:LEU:HG	1.98	0.63
1:C:50:ALA:HA	1:C:70:ALA:O	1.98	0.63
1:B:66:ARG:HH11	1:B:66:ARG:CB	2.12	0.63
1:D:222:THR:O	1:D:248:VAL:HA	1.99	0.63
1:A:159:ILE:HA	1:A:183:THR:HG23	1.80	0.63
1:A:292:PRO:HD2	1:B:129:ALA:HB1	1.80	0.63
1:B:153:GLN:HG2	2:B:340:HOH:O	1.98	0.63
1:A:63:VAL:HG12	1:A:64:ASP:N	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:HIS:H	1:B:87:HIS:CD2	2.17	0.63
1:B:187:PRO:HG3	1:B:199:PHE:CD2	2.34	0.63
1:B:286:LYS:HG3	2:B:362:HOH:O	1.99	0.63
1:D:54:GLY:O	1:D:313:LEU:HD21	1.98	0.63
1:D:192:ALA:CB	1:D:197:ALA:HB3	2.24	0.63
1:A:79:SER:HB2	1:A:313:LEU:HD23	1.81	0.63
1:A:192:ALA:HB1	1:A:197:ALA:HB3	1.79	0.63
1:C:63:VAL:HG12	1:C:63:VAL:O	1.99	0.63
1:C:63:VAL:HG21	1:C:88:LEU:HD23	1.81	0.63
1:C:53:HIS:CE1	1:C:74:ASN:HD22	2.17	0.62
1:D:179:ARG:NE	2:D:396:HOH:O	2.30	0.62
1:A:103:THR:HG22	1:A:308:LEU:HB3	1.81	0.62
1:A:312:ASN:O	1:A:322:MSE:HE3	2.00	0.62
1:D:13:ARG:HG2	1:D:14:ARG:N	2.14	0.62
1:C:13:ARG:HG3	1:C:36:SER:O	1.99	0.62
1:B:65:LYS:NZ	1:B:65:LYS:HB3	2.14	0.62
1:C:83:VAL:HA	1:C:102:TYR:HD2	1.64	0.62
1:C:93:ILE:HG21	1:C:100:VAL:CG2	2.29	0.62
1:C:69:ASP:HA	1:C:96:ARG:HH21	1.64	0.62
1:D:163:ARG:HH21	1:D:166:GLN:HB2	1.64	0.62
1:B:41:PRO:HD2	1:B:44:GLU:HG3	1.80	0.62
1:B:189:PRO:HG2	2:B:344:HOH:O	1.99	0.62
1:C:234:MSE:HE1	1:C:240:PHE:HB2	1.80	0.62
1:B:322:MSE:HE3	1:B:325:GLU:HB2	1.80	0.62
1:A:155:THR:CB	1:A:209:SER:HA	2.25	0.62
1:B:192:ALA:HB1	1:B:197:ALA:HB3	1.81	0.62
1:D:162:GLY:O	1:D:166:GLN:HG3	1.99	0.62
1:C:13:ARG:HG2	1:C:58:LEU:HD11	1.79	0.62
1:D:276:LEU:HG	1:D:277:PRO:HD2	1.82	0.62
1:B:84:GLY:HA3	1:B:245:ARG:HH21	1.65	0.62
1:B:312:ASN:HD21	1:B:324:SER:HB3	1.64	0.62
1:D:114:LEU:HD22	1:D:295:GLY:HA2	1.81	0.62
1:C:7:MSE:O	1:C:30:GLU:N	2.33	0.62
1:B:10:PHE:CG	1:B:49:VAL:HG12	2.34	0.62
1:C:89:ALA:HB1	1:C:91:ASP:OD1	1.99	0.62
1:D:11:VAL:HB	1:D:33:GLN:HG3	1.81	0.62
1:D:68:LEU:CD1	1:D:92:GLU:HB3	2.29	0.62
1:A:121:THR:HG23	1:A:127:PRO:HD3	1.80	0.62
1:A:154:SER:O	1:A:177:VAL:HG13	2.00	0.62
1:B:76:LYS:O	1:B:98:ILE:HA	1.99	0.62
1:D:11:VAL:HG13	1:D:56:LEU:HD22	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ILE:HD13	1:A:90:LEU:HD11	1.81	0.62
1:C:104:PRO:HD3	1:C:324:SER:OG	1.99	0.62
1:A:184:GLY:HA3	1:A:188:ARG:HH12	1.64	0.62
1:A:206:ALA:HB1	1:A:234:MSE:CA	2.24	0.62
1:C:14:ARG:HH21	1:C:37:ASP:H	1.47	0.62
1:D:155:THR:N	1:D:210:ASP:OD2	2.25	0.62
1:B:236:GLU:HA	1:B:263:ILE:HA	1.79	0.62
1:D:79:SER:CB	1:D:313:LEU:HB2	2.29	0.62
1:A:8:LYS:HD3	1:A:52:ALA:HB2	1.80	0.62
1:A:202:THR:HG21	1:A:225:LEU:HD11	1.81	0.62
1:B:49:VAL:HB	1:B:71:ALA:HB2	1.82	0.62
1:D:181:LEU:HD13	1:D:200:VAL:CG2	2.27	0.62
1:B:70:ALA:C	2:B:335:HOH:O	2.38	0.62
1:C:218:LEU:CB	1:C:245:ARG:HG3	2.29	0.62
1:D:10:PHE:HD1	1:D:32:GLU:HG2	1.65	0.62
1:B:218:LEU:HD13	1:B:245:ARG:HG3	1.81	0.62
1:A:93:ILE:HG21	1:A:100:VAL:HG23	1.81	0.62
1:A:121:THR:HG23	1:A:126:LEU:HB2	1.81	0.62
1:C:34:TRP:CD1	1:C:40:ILE:HB	2.35	0.62
1:C:271:THR:CB	1:C:276:LEU:HD13	2.29	0.62
1:C:271:THR:HB	1:C:276:LEU:HD13	1.82	0.62
1:A:74:ASN:HB2	2:A:422:HOH:O	2.00	0.62
1:A:121:THR:HG23	1:A:126:LEU:HB2	1.80	0.62
1:A:188:ARG:NH2	2:A:433:HOH:O	2.33	0.62
1:D:162:GLY:O	1:D:166:GLN:HG3	2.00	0.62
1:C:108:THR:HG23	1:C:164:ILE:N	2.14	0.62
1:D:182:TYR:CD1	1:D:197:ALA:HB1	2.35	0.62
1:B:76:LYS:C	1:B:98:ILE:HG23	2.20	0.62
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.26	0.62
1:A:151:LEU:HG	1:A:211:PHE:CE1	2.35	0.62
1:C:51:GLY:H	1:C:71:ALA:C	2.03	0.62
1:C:132:GLU:HA	1:C:135:ASN:OD1	1.99	0.62
1:B:51:GLY:HA2	1:B:71:ALA:O	1.99	0.62
1:D:56:LEU:HD12	1:D:313:LEU:HD22	1.82	0.62
1:D:205:LEU:HD23	1:D:206:ALA:N	2.14	0.62
1:B:43:LYS:HB2	2:B:456:HOH:O	2.00	0.62
1:C:99:ARG:NE	1:C:322:MSE:HE3	2.14	0.62
1:A:314:LEU:O	1:A:318:ARG:HD3	2.00	0.62
1:D:103:THR:HB	1:D:308:LEU:HD23	1.82	0.62
1:B:201:SER:O	1:B:204:GLU:N	2.33	0.62
1:A:49:VAL:O	1:A:71:ALA:HA	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:104:PRO:HD2	1:C:324:SER:OG	1.99	0.62
1:A:42:ALA:O	1:A:46:GLU:HG3	2.00	0.62
1:C:102:TYR:CD2	1:C:104:PRO:HD3	2.35	0.62
1:A:17:ALA:O	1:A:20:ARG:HG2	2.00	0.62
1:A:269:ASP:OD1	1:A:291:LEU:HB2	1.99	0.62
1:D:201:SER:CB	1:D:203:PRO:HD2	2.30	0.62
1:B:63:VAL:HA	1:B:67:ILE:HG13	1.81	0.62
1:B:200:VAL:HG22	1:B:201:SER:N	2.15	0.62
1:A:100:VAL:HG11	1:A:326:LEU:HD23	1.82	0.62
1:A:68:LEU:HD22	1:A:96:ARG:HD2	1.81	0.62
1:B:18:GLU:H	1:B:303:ASN:ND2	1.98	0.62
1:D:185:ARG:HH21	1:D:188:ARG:HD2	1.65	0.62
1:A:8:LYS:CA	1:A:30:GLU:HB3	2.18	0.62
1:A:167:ALA:HB1	1:A:171:ARG:HH21	1.65	0.62
1:D:225:LEU:O	1:D:230:PHE:HB2	2.00	0.62
1:B:81:MSE:HE2	1:B:309:ALA:HB3	1.81	0.62
1:B:188:ARG:HB2	2:B:432:HOH:O	2.00	0.62
1:A:231:PHE:CE1	1:A:254:LEU:HD12	2.35	0.61
1:C:71:ALA:CB	1:C:75:LEU:HD11	2.31	0.61
1:A:77:VAL:HG21	1:A:313:LEU:O	2.00	0.61
1:A:182:TYR:OH	1:A:187:PRO:HA	2.00	0.61
1:A:260:SER:OG	1:A:262:LYS:HD3	2.00	0.61
1:B:107:LEU:HD23	1:B:107:LEU:N	2.14	0.61
1:A:49:VAL:O	1:A:71:ALA:HA	2.00	0.61
1:A:251:GLN:NE2	2:A:415:HOH:O	2.33	0.61
1:B:245:ARG:HB2	1:B:248:VAL:CG2	2.30	0.61
1:D:216:CYS:SG	1:D:217:SER:N	2.72	0.61
1:B:13:ARG:HG2	1:B:14:ARG:H	1.65	0.61
1:B:23:LEU:HD11	1:B:56:LEU:CD1	2.30	0.61
1:C:251:GLN:HE22	1:C:272:SER:N	1.97	0.61
1:C:292:PRO:HD2	1:D:129:ALA:HB1	1.82	0.61
1:A:83:VAL:HG23	1:A:104:PRO:HB3	1.81	0.61
1:A:49:VAL:HG12	1:A:55:LEU:HD13	1.81	0.61
1:D:161:LEU:HD13	1:D:182:TYR:CD2	2.35	0.61
1:A:65:LYS:O	1:A:69:ASP:HB2	2.00	0.61
1:B:102:TYR:OH	1:B:326:LEU:HD13	1.99	0.61
1:C:297:ALA:O	1:D:147:CYS:HA	2.00	0.61
1:C:314:LEU:O	1:C:318:ARG:HD2	2.00	0.61
1:A:99:ARG:CZ	1:A:322:MSE:HE2	2.31	0.61
1:A:312:ASN:OD1	1:A:323:PRO:HG2	1.99	0.61
1:A:10:PHE:HA	1:A:32:GLU:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:LEU:O	1:A:49:VAL:HG22	2.00	0.61
1:A:102:TYR:CD2	1:A:104:PRO:HD3	2.36	0.61
1:B:299:HIS:HB2	2:B:332:HOH:O	1.99	0.61
1:C:229:ASP:HB3	2:C:352:HOH:O	2.00	0.61
1:D:35:ASP:O	1:D:36:SER:HB2	2.00	0.61
1:C:218:LEU:HD13	1:C:248:VAL:HG22	1.82	0.61
1:B:153:GLN:HB3	1:B:178:GLN:HE21	1.65	0.61
1:A:181:LEU:CD2	1:A:198:GLU:HB2	2.30	0.61
1:A:282:LEU:HD13	1:A:290:ILE:HD11	1.82	0.61
1:C:13:ARG:HG2	1:C:58:LEU:HD11	1.83	0.61
1:D:315:ALA:CB	1:D:322:MSE:HG2	2.30	0.61
1:C:104:PRO:O	1:C:106:VAL:N	2.32	0.61
1:B:114:LEU:HD11	1:B:294:ILE:HG13	1.81	0.61
1:A:179:ARG:NE	2:A:411:HOH:O	2.32	0.61
1:B:170:ARG:NH1	1:B:170:ARG:CB	2.63	0.61
1:B:11:VAL:O	1:B:33:GLN:HB2	2.00	0.61
1:B:274:GLU:HA	1:B:276:LEU:N	2.14	0.61
1:B:75:LEU:HD21	1:B:78:ILE:HD11	1.82	0.61
1:D:183:THR:HG21	1:D:202:THR:HA	1.83	0.61
1:C:7:MSE:SE	1:C:317:LEU:HB3	2.50	0.61
1:B:77:VAL:HB	1:B:316:GLY:O	2.00	0.61
1:B:93:ILE:HG23	1:B:98:ILE:HB	1.82	0.61
1:B:234:MSE:HE1	1:B:240:PHE:HD1	1.65	0.61
1:A:236:GLU:HA	1:A:262:LYS:O	1.99	0.61
1:C:165:GLY:O	1:C:168:ILE:N	2.34	0.61
1:A:166:GLN:HB3	1:A:195:PHE:CZ	2.34	0.61
1:B:23:LEU:HB3	1:B:31:VAL:HG21	1.83	0.61
1:B:236:GLU:HA	1:B:262:LYS:O	2.00	0.61
1:A:42:ALA:O	1:A:46:GLU:HG3	2.01	0.61
1:A:75:LEU:HD21	1:A:78:ILE:HD11	1.83	0.61
1:A:134:LYS:HG2	1:B:283:LEU:HD22	1.83	0.61
1:D:125:ARG:HH12	1:D:146:LEU:HA	1.63	0.61
1:A:231:PHE:O	1:A:234:MSE:N	2.29	0.61
1:D:155:THR:HA	1:D:179:ARG:O	2.00	0.61
1:A:151:LEU:HG	1:A:211:PHE:CE1	2.36	0.61
1:A:231:PHE:HA	1:A:234:MSE:SE	2.51	0.61
1:A:234:MSE:HE2	1:A:238:ALA:HB1	1.82	0.61
1:B:199:PHE:N	2:B:342:HOH:O	2.21	0.61
1:C:8:LYS:HZ2	1:C:52:ALA:HB2	1.65	0.61
1:D:95:LYS:HD2	1:D:96:ARG:HG3	1.81	0.61
1:A:260:SER:OG	1:A:262:LYS:HD3	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:313:LEU:HD23	1:B:314:LEU:N	2.16	0.61
1:C:219:THR:HB	1:C:220:PRO:HD2	1.82	0.61
1:A:183:THR:HG23	1:A:184:GLY:N	2.15	0.61
1:C:81:MSE:HE2	1:C:306:SER:HA	1.82	0.61
1:B:118:LEU:HD13	1:B:291:LEU:HD11	1.81	0.61
1:B:229:ASP:CA	1:B:232:GLN:HE21	2.03	0.61
1:D:185:ARG:NE	2:D:411:HOH:O	2.33	0.61
1:D:318:ARG:HG3	1:D:318:ARG:HH11	1.65	0.61
1:B:68:LEU:HD12	1:B:92:GLU:HB3	1.83	0.61
1:C:108:THR:HG23	1:C:164:ILE:HA	1.83	0.61
1:C:142:LYS:HE2	1:D:37:ASP:O	2.00	0.61
1:D:20:ARG:HD2	2:D:333:HOH:O	2.00	0.61
1:A:159:ILE:HG22	1:A:216:CYS:HB3	1.83	0.61
1:A:68:LEU:HD22	1:A:98:ILE:CD1	2.31	0.61
1:A:239:VAL:HA	1:A:265:ALA:O	2.01	0.61
1:C:99:ARG:NH2	1:C:316:GLY:HA2	2.16	0.61
1:D:75:LEU:HD23	1:D:98:ILE:HD13	1.82	0.61
1:B:214:VAL:HG12	1:B:244:SER:OG	1.99	0.61
1:A:103:THR:HA	1:A:308:LEU:HD23	1.81	0.61
1:D:314:LEU:HD23	1:D:317:LEU:HD22	1.82	0.61
1:A:21:VAL:HG12	1:A:25:ARG:NH2	2.16	0.61
1:A:301:THR:O	1:A:305:MSE:HE2	2.01	0.61
1:B:226:CYS:HB2	1:B:249:VAL:CA	2.27	0.61
1:B:280:HIS:CE1	1:B:282:LEU:HG	2.35	0.61
1:C:312:ASN:HA	1:C:322:MSE:HB3	1.83	0.61
1:D:322:MSE:HE3	1:D:325:GLU:HG3	1.83	0.61
1:B:187:PRO:HG3	1:B:199:PHE:CE2	2.36	0.61
1:A:245:ARG:O	1:A:247:ASP:N	2.33	0.61
1:A:6:LEU:HG	1:A:28:ASP:O	2.01	0.61
1:A:159:ILE:O	1:A:216:CYS:HA	2.01	0.61
1:B:226:CYS:HB2	1:B:249:VAL:HG22	1.83	0.61
1:C:9:VAL:HG12	1:C:10:PHE:N	2.15	0.61
1:D:313:LEU:O	1:D:317:LEU:HB2	2.00	0.61
1:A:114:LEU:CD2	1:A:294:ILE:HG13	2.30	0.61
1:D:100:VAL:HG12	1:D:101:GLY:N	2.16	0.61
1:C:165:GLY:O	1:C:168:ILE:N	2.34	0.61
1:C:184:GLY:H	1:C:199:PHE:HE1	1.47	0.61
1:A:52:ALA:O	1:A:75:LEU:HA	2.00	0.61
1:B:99:ARG:HH22	1:B:319:GLY:CA	2.09	0.61
1:C:40:ILE:CG1	1:C:44:GLU:HB2	2.30	0.61
1:D:242:ASN:HD21	1:D:246:GLY:HA2	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:90:LEU:O	1:D:92:GLU:N	2.34	0.60
1:C:104:PRO:O	1:C:106:VAL:HG22	2.01	0.60
1:D:13:ARG:HG2	1:D:14:ARG:H	1.65	0.60
1:B:110:THR:HG21	1:B:298:THR:OG1	2.00	0.60
1:B:15:ILE:HB	1:B:81:MSE:HE1	1.82	0.60
1:B:49:VAL:O	1:B:71:ALA:HA	2.01	0.60
1:D:314:LEU:HA	1:D:317:LEU:HD23	1.83	0.60
1:C:226:CYS:HB2	1:C:249:VAL:HG23	1.83	0.60
1:A:7:MSE:SE	1:A:7:MSE:N	2.82	0.60
1:A:99:ARG:HD2	1:A:325:GLU:OE2	2.01	0.60
1:A:226:CYS:HB2	1:A:249:VAL:HA	1.83	0.60
1:A:244:SER:O	1:A:270:VAL:HG11	2.01	0.60
1:B:35:ASP:O	1:B:36:SER:HB2	2.00	0.60
1:C:107:LEU:HD12	1:C:108:THR:N	2.15	0.60
1:D:154:SER:O	1:D:178:GLN:N	2.34	0.60
1:A:174:PRO:HB2	1:B:171:ARG:HA	1.82	0.60
1:D:188:ARG:O	1:D:192:ALA:HB3	2.01	0.60
1:B:13:ARG:HG2	1:B:14:ARG:H	1.66	0.60
1:A:51:GLY:H	1:A:71:ALA:HA	1.65	0.60
1:A:235:LYS:N	2:A:342:HOH:O	2.33	0.60
1:B:317:LEU:O	1:B:318:ARG:HG3	2.01	0.60
1:A:257:ALA:HB1	1:A:263:ILE:HG12	1.83	0.60
1:B:63:VAL:HB	1:B:88:LEU:HD23	1.82	0.60
1:D:68:LEU:HD12	1:D:92:GLU:HB3	1.82	0.60
1:C:25:ARG:HG3	1:C:25:ARG:HH11	1.66	0.60
1:C:75:LEU:H	1:C:75:LEU:CD2	2.13	0.60
1:D:236:GLU:HA	1:D:262:LYS:O	1.98	0.60
1:A:137:GLY:O	1:A:139:THR:HG23	2.01	0.60
1:D:157:GLY:HA3	1:D:209:SER:OG	2.01	0.60
1:D:166:GLN:NE2	2:D:371:HOH:O	2.34	0.60
1:A:225:LEU:HB3	1:A:248:VAL:HG13	1.82	0.60
1:D:89:ALA:O	1:D:93:ILE:HG13	2.01	0.60
1:B:9:VAL:HG22	1:B:54:GLY:HA3	1.82	0.60
1:C:49:VAL:HG12	1:C:55:LEU:HD13	1.83	0.60
1:B:92:GLU:HG2	2:B:427:HOH:O	2.00	0.60
1:A:125:ARG:NH1	1:A:146:LEU:HD23	2.17	0.60
1:C:101:GLY:HA2	1:C:325:GLU:HA	1.83	0.60
1:D:85:ILE:HD13	1:D:90:LEU:CD1	2.31	0.60
1:D:162:GLY:O	1:D:166:GLN:HG3	2.02	0.60
1:B:9:VAL:HG13	1:B:54:GLY:HA3	1.84	0.60
1:B:167:ALA:O	1:B:171:ARG:HG3	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:ILE:HB	1:C:45:LEU:CD2	2.32	0.60
1:B:72:GLY:O	1:B:75:LEU:HD13	2.02	0.60
1:B:85:ILE:CD1	1:B:90:LEU:HD21	2.31	0.60
1:D:187:PRO:HG3	1:D:199:PHE:CE2	2.35	0.60
1:D:320:GLU:HB3	1:D:321:PRO:HD2	1.82	0.60
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.82	0.60
1:A:250:ASN:C	1:A:252:ASP:H	2.05	0.60
1:B:128:GLU:O	1:B:132:GLU:HG2	2.01	0.60
1:B:222:THR:O	1:B:225:LEU:HB2	2.01	0.60
1:A:45:LEU:O	1:A:49:VAL:HG22	2.01	0.60
1:A:151:LEU:HA	1:A:154:SER:CB	2.31	0.60
1:A:9:VAL:HA	1:A:54:GLY:HA3	1.83	0.60
1:C:76:LYS:HA	1:C:98:ILE:HG23	1.83	0.60
1:D:59:LEU:HA	1:D:87:HIS:CD2	2.36	0.60
1:C:75:LEU:HD23	1:C:75:LEU:N	2.13	0.60
1:B:47:ARG:O	1:B:47:ARG:HD3	2.01	0.60
1:C:124:ARG:NH2	1:D:114:LEU:HD12	2.15	0.60
1:D:159:ILE:HA	1:D:183:THR:CG2	2.32	0.60
1:A:246:GLY:N	1:A:270:VAL:HB	2.16	0.60
1:B:7:MSE:HG2	1:B:53:HIS:CE1	2.37	0.60
1:C:180:PHE:O	1:C:197:ALA:HA	2.01	0.60
1:D:63:VAL:HG13	1:D:67:ILE:CG2	2.26	0.60
1:C:76:LYS:N	1:C:98:ILE:HD12	2.17	0.60
1:D:13:ARG:HG2	1:D:14:ARG:N	2.17	0.60
1:B:311:ASN:HB3	1:B:323:PRO:HG2	1.84	0.60
1:D:35:ASP:OD1	2:D:384:HOH:O	2.17	0.60
1:C:85:ILE:HD12	1:C:90:LEU:HD11	1.83	0.60
1:A:95:LYS:N	2:A:351:HOH:O	2.34	0.60
1:A:7:MSE:HE1	1:A:28:ASP:HB2	1.83	0.60
1:C:74:ASN:ND2	2:C:434:HOH:O	2.33	0.60
1:D:315:ALA:HB1	1:D:322:MSE:HG2	1.84	0.60
1:A:302:ARG:HD3	1:A:305:MSE:SE	2.52	0.60
1:C:187:PRO:C	1:C:189:PRO:HD3	2.22	0.60
1:D:312:ASN:HD21	1:D:324:SER:HB3	1.66	0.60
1:A:13:ARG:HG3	1:A:14:ARG:N	2.17	0.60
1:D:20:ARG:HG3	2:D:333:HOH:O	2.00	0.60
1:C:104:PRO:O	1:C:106:VAL:N	2.34	0.60
1:C:251:GLN:NE2	1:C:272:SER:H	2.00	0.60
1:D:15:ILE:CG1	1:D:20:ARG:HE	2.14	0.60
1:A:153:GLN:HA	1:A:178:GLN:HB2	1.84	0.60
1:B:53:HIS:HA	1:B:75:LEU:HA	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:GLU:HB2	1:A:261:GLY:O	2.01	0.60
1:B:300:ARG:HG3	2:B:443:HOH:O	2.00	0.60
1:D:99:ARG:HH21	1:D:316:GLY:HA2	1.67	0.60
1:C:260:SER:OG	1:C:262:LYS:HD3	2.01	0.60
1:D:14:ARG:HA	1:D:20:ARG:NH2	2.16	0.60
1:C:174:PRO:HG3	1:D:174:PRO:HG2	1.84	0.60
1:D:262:LYS:HD2	2:D:345:HOH:O	2.00	0.60
1:C:160:GLY:HA3	1:C:216:CYS:HB3	1.82	0.60
1:B:236:GLU:HA	1:B:262:LYS:O	2.02	0.60
1:C:17:ALA:O	1:C:21:VAL:HG23	2.01	0.60
1:A:8:LYS:HE3	1:A:32:GLU:CG	2.32	0.60
1:C:236:GLU:HA	1:C:262:LYS:O	2.02	0.60
1:C:251:GLN:HB2	2:C:357:HOH:O	2.02	0.60
1:B:16:PRO:CD	1:B:306:SER:HB2	2.31	0.60
1:D:23:LEU:HD11	1:D:56:LEU:HD13	1.83	0.60
1:C:93:ILE:HG23	1:C:94:LYS:N	2.17	0.60
1:B:15:ILE:HB	1:B:81:MSE:HE1	1.83	0.60
1:B:65:LYS:HE3	1:B:96:ARG:NH2	2.16	0.60
1:C:49:VAL:O	1:C:71:ALA:HA	2.01	0.59
1:C:16:PRO:O	1:C:20:ARG:HB2	2.01	0.59
1:C:103:THR:HG22	1:C:308:LEU:CD2	2.32	0.59
1:A:179:ARG:CD	1:A:181:LEU:HD21	2.31	0.59
1:A:187:PRO:HG3	1:A:199:PHE:CD2	2.38	0.59
1:C:6:LEU:HD22	1:C:30:GLU:OE1	2.02	0.59
1:B:181:LEU:CD2	1:B:198:GLU:HB3	2.32	0.59
1:D:181:LEU:HB3	1:D:200:VAL:HG22	1.85	0.59
1:D:226:CYS:HA	1:D:230:PHE:CD2	2.37	0.59
1:D:227:ASN:H	1:D:230:PHE:CB	2.15	0.59
1:C:315:ALA:CB	1:C:322:MSE:HA	2.33	0.59
1:C:41:PRO:HD2	1:C:44:GLU:HB2	1.85	0.59
1:A:82:SER:HA	1:A:305:MSE:HE3	1.82	0.59
1:A:207:ALA:HA	1:A:233:LYS:O	2.02	0.59
1:A:221:ALA:O	1:A:225:LEU:HB2	2.00	0.59
1:B:167:ALA:O	1:B:171:ARG:HG2	2.02	0.59
1:C:192:ALA:HB1	1:C:197:ALA:HB3	1.84	0.59
1:D:206:ALA:HB2	1:D:230:PHE:CE1	2.36	0.59
1:B:8:LYS:HD2	1:B:30:GLU:O	2.02	0.59
1:C:132:GLU:OE1	1:C:137:GLY:HA3	2.02	0.59
1:C:43:LYS:HA	1:C:46:GLU:CD	2.23	0.59
1:C:99:ARG:CZ	1:C:322:MSE:HE3	2.32	0.59
1:A:271:THR:OG1	1:A:274:GLU:HG2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:VAL:HG13	1:B:67:ILE:HG21	1.84	0.59
1:C:34:TRP:CH2	1:C:41:PRO:HD3	2.37	0.59
1:C:9:VAL:HG22	1:C:30:GLU:O	2.02	0.59
1:C:184:GLY:N	1:C:199:PHE:HE1	1.99	0.59
1:C:15:ILE:CD1	1:C:81:MSE:HE1	2.27	0.59
1:A:173:LYS:HB3	1:A:174:PRO:HD3	1.85	0.59
1:C:16:PRO:HG2	1:C:302:ARG:O	2.03	0.59
1:C:76:LYS:HB3	1:C:76:LYS:HZ2	1.67	0.59
1:C:88:LEU:HD12	1:C:88:LEU:O	2.01	0.59
1:A:250:ASN:O	1:A:252:ASP:N	2.35	0.59
1:C:315:ALA:HB3	1:C:322:MSE:HG2	1.83	0.59
1:B:100:VAL:HG12	1:B:101:GLY:N	2.17	0.59
1:D:182:TYR:CE1	1:D:197:ALA:HB1	2.37	0.59
1:A:49:VAL:O	1:A:71:ALA:HA	2.02	0.59
1:A:182:TYR:O	1:A:199:PHE:HA	2.02	0.59
1:C:46:GLU:O	1:C:70:ALA:HB1	2.02	0.59
1:A:76:LYS:HA	2:A:415:HOH:O	2.02	0.59
1:A:222:THR:O	1:A:248:VAL:HA	2.02	0.59
1:A:182:TYR:OH	1:A:187:PRO:HA	2.01	0.59
1:A:158:ILE:N	1:A:158:ILE:HD12	2.16	0.59
1:C:13:ARG:CZ	1:C:58:LEU:HD12	2.32	0.59
1:B:13:ARG:HG2	1:B:14:ARG:H	1.68	0.59
1:B:85:ILE:HD13	1:B:326:LEU:HD21	1.84	0.59
1:B:300:ARG:HG3	2:B:446:HOH:O	2.02	0.59
1:B:49:VAL:HG12	1:B:55:LEU:HD13	1.85	0.59
1:D:7:MSE:CE	1:D:317:LEU:HB3	2.33	0.59
1:A:8:LYS:HD3	1:A:9:VAL:N	2.16	0.59
1:B:81:MSE:HG3	1:B:305:MSE:HG2	1.84	0.59
1:C:54:GLY:HA3	1:C:313:LEU:HD11	1.85	0.59
1:C:219:THR:H	1:C:222:THR:HG1	1.50	0.59
1:D:262:LYS:HD2	2:D:346:HOH:O	2.03	0.59
1:D:280:HIS:ND1	1:D:281:PRO:HD2	2.17	0.59
1:D:85:ILE:HD13	1:D:90:LEU:CD1	2.33	0.59
1:B:312:ASN:HA	1:B:323:PRO:CD	2.31	0.59
1:D:214:VAL:HG11	1:D:248:VAL:HG11	1.83	0.59
1:C:184:GLY:N	1:C:199:PHE:HE1	2.00	0.59
1:A:141:TRP:O	1:A:142:LYS:HG3	2.03	0.59
1:B:57:CYS:O	1:B:58:LEU:HD23	2.02	0.59
1:B:64:ASP:OD1	1:B:67:ILE:HG12	2.02	0.59
1:A:250:ASN:C	1:A:252:ASP:H	2.06	0.59
1:B:163:ARG:HD2	2:B:426:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:SER:HA	2:A:380:HOH:O	2.01	0.59
1:B:200:VAL:CG1	1:B:205:LEU:HB2	2.32	0.59
1:B:326:LEU:HG	2:B:386:HOH:O	2.02	0.59
1:D:280:HIS:ND1	1:D:281:PRO:HD2	2.18	0.59
1:D:99:ARG:CB	1:D:322:MSE:HE1	2.26	0.59
1:B:55:LEU:HD23	1:B:78:ILE:HD13	1.84	0.59
1:D:64:ASP:HA	1:D:89:ALA:HB2	1.84	0.59
1:A:8:LYS:HE3	1:A:32:GLU:OE1	2.01	0.59
1:A:280:HIS:ND1	1:A:281:PRO:HD2	2.18	0.59
1:C:78:ILE:HD12	1:C:93:ILE:HD13	1.85	0.59
1:D:24:ALA:O	2:D:354:HOH:O	2.16	0.59
1:C:214:VAL:HG12	1:C:244:SER:HG	1.68	0.59
1:D:103:THR:HG22	1:D:308:LEU:HG	1.84	0.59
1:D:155:THR:HG23	1:D:179:ARG:O	2.02	0.59
1:B:114:LEU:HD13	1:B:295:GLY:HA2	1.85	0.59
1:B:7:MSE:HB2	1:B:28:ASP:O	2.02	0.59
1:D:81:MSE:CE	1:D:306:SER:HA	2.33	0.59
1:A:167:ALA:HB2	2:A:373:HOH:O	2.02	0.59
1:C:34:TRP:HE1	1:C:40:ILE:HA	1.68	0.59
1:A:280:HIS:HE1	1:A:282:LEU:HD12	1.67	0.59
1:D:114:LEU:HD22	1:D:295:GLY:CA	2.32	0.59
1:B:229:ASP:HA	1:B:232:GLN:HE21	1.67	0.59
1:C:17:ALA:HB3	1:C:303:ASN:OD1	2.03	0.59
1:A:16:PRO:HG3	1:B:144:LEU:HG	1.83	0.59
1:A:228:LYS:HA	1:A:253:ASP:OD2	2.02	0.59
1:C:10:PHE:HA	1:C:32:GLU:HB3	1.85	0.59
1:B:152:THR:HG22	1:B:153:GLN:OE1	2.02	0.59
1:A:313:LEU:HD13	1:A:317:LEU:HD13	1.85	0.59
1:C:56:LEU:HA	1:C:79:SER:O	2.03	0.59
1:D:114:LEU:HD22	1:D:295:GLY:CA	2.32	0.59
1:D:282:LEU:HD23	1:D:285:LEU:HD12	1.84	0.59
1:B:202:THR:HB	1:B:203:PRO:HD3	1.83	0.59
1:C:53:HIS:HB3	1:C:76:LYS:HZ3	1.66	0.59
1:A:81:MSE:HG3	1:A:305:MSE:HB3	1.85	0.59
1:C:38:GLU:CD	1:D:139:THR:HG21	2.23	0.59
1:B:64:ASP:OD2	1:B:66:ARG:HG3	2.03	0.59
1:B:68:LEU:CD1	1:B:96:ARG:HH11	2.16	0.59
1:B:322:MSE:HB2	1:B:325:GLU:OE1	2.03	0.59
1:B:206:ALA:HB2	1:B:230:PHE:HE2	1.68	0.59
1:B:228:LYS:O	1:B:228:LYS:HG2	2.03	0.59
1:A:189:PRO:C	1:A:191:GLU:H	2.04	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:309:ALA:O	1:A:312:ASN:HB2	2.03	0.59
1:B:8:LYS:HZ1	1:B:32:GLU:HB3	1.68	0.59
1:B:70:ALA:C	1:B:72:GLY:H	2.05	0.59
1:C:108:THR:HG22	1:C:108:THR:O	2.01	0.59
1:D:89:ALA:O	1:D:93:ILE:HG13	2.03	0.59
1:B:251:GLN:HE22	1:B:276:LEU:HD11	1.67	0.59
1:C:218:LEU:O	1:C:219:THR:HG23	2.02	0.59
1:B:187:PRO:HG3	1:B:199:PHE:CD2	2.38	0.59
1:C:178:GLN:HG3	2:C:387:HOH:O	2.01	0.58
1:D:203:PRO:HB3	1:D:233:LYS:NZ	2.18	0.58
1:D:212:ILE:HD12	1:D:234:MSE:SE	2.53	0.58
1:A:18:GLU:OE1	1:A:307:LEU:HD13	2.03	0.58
1:D:40:ILE:HG12	1:D:44:GLU:HB2	1.85	0.58
1:B:49:VAL:HG11	1:B:67:ILE:HG23	1.85	0.58
1:A:79:SER:OG	1:A:313:LEU:HB3	2.04	0.58
1:A:175:PHE:HA	1:B:171:ARG:NH1	2.18	0.58
1:C:85:ILE:C	1:C:85:ILE:HD12	2.24	0.58
1:A:59:LEU:HD12	1:A:87:HIS:ND1	2.18	0.58
1:B:85:ILE:CB	1:B:90:LEU:HD21	2.24	0.58
1:D:6:LEU:HD22	1:D:28:ASP:C	2.23	0.58
1:A:183:THR:CG2	1:A:205:LEU:HD22	2.33	0.58
1:C:88:LEU:HD13	1:C:100:VAL:HG11	1.85	0.58
1:A:23:LEU:CD2	1:A:314:LEU:HD22	2.33	0.58
1:B:92:GLU:HG2	2:B:432:HOH:O	2.02	0.58
1:C:224:GLY:O	1:C:227:ASN:ND2	2.36	0.58
1:B:283:LEU:HD23	1:B:290:ILE:HD12	1.86	0.58
1:C:53:HIS:HA	1:C:74:ASN:O	2.03	0.58
1:C:310:ALA:O	1:C:314:LEU:HB2	2.04	0.58
1:A:8:LYS:HD2	1:A:32:GLU:HB2	1.86	0.58
1:A:255:TYR:HD1	1:A:282:LEU:HD23	1.69	0.58
1:C:92:GLU:HA	1:C:95:LYS:CD	2.32	0.58
1:A:231:PHE:CZ	1:A:254:LEU:HD13	2.38	0.58
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.39	0.58
1:C:58:LEU:HD22	1:D:141:TRP:HZ3	1.69	0.58
1:C:77:VAL:HG11	1:C:317:LEU:HG	1.84	0.58
1:A:16:PRO:HD2	1:A:306:SER:HB2	1.84	0.58
1:D:312:ASN:HD21	1:D:324:SER:HB3	1.67	0.58
1:A:132:GLU:OE1	1:A:137:GLY:HA3	2.03	0.58
1:B:66:ARG:NH1	2:B:422:HOH:O	2.37	0.58
1:B:320:GLU:HB3	1:B:321:PRO:HD2	1.84	0.58
1:C:102:TYR:CD1	1:C:326:LEU:HD12	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:183:THR:HB	1:B:205:LEU:HD23	1.84	0.58
1:C:53:HIS:HA	1:C:74:ASN:O	2.02	0.58
1:C:81:MSE:SE	1:C:306:SER:HA	2.53	0.58
1:A:129:ALA:HB2	1:A:146:LEU:HD13	1.86	0.58
1:A:157:GLY:O	1:A:212:ILE:HA	2.03	0.58
1:B:153:GLN:HG2	2:B:339:HOH:O	2.02	0.58
1:B:249:VAL:HG12	1:B:250:ASN:H	1.67	0.58
1:A:206:ALA:HB2	1:A:230:PHE:CZ	2.38	0.58
1:B:96:ARG:HB2	1:B:98:ILE:HD12	1.84	0.58
1:C:65:LYS:O	1:C:69:ASP:HB2	2.04	0.58
1:A:64:ASP:HA	1:A:89:ALA:HB2	1.86	0.58
1:C:155:THR:HG23	1:C:179:ARG:HB3	1.85	0.58
1:A:234:MSE:SE	1:A:263:ILE:HG21	2.53	0.58
1:A:258:LEU:HD11	1:A:266:ALA:HB3	1.84	0.58
1:C:99:ARG:HD2	1:C:325:GLU:CD	2.23	0.58
1:D:6:LEU:HD13	2:D:420:HOH:O	2.03	0.58
1:C:78:ILE:HG13	1:C:98:ILE:HG21	1.84	0.58
1:D:163:ARG:HG2	1:D:163:ARG:HH11	1.67	0.58
1:A:156:VAL:CG1	1:A:158:ILE:HG13	2.32	0.58
1:B:314:LEU:HD13	1:B:318:ARG:CZ	2.32	0.58
1:D:107:LEU:HD23	1:D:305:MSE:HE1	1.85	0.58
1:A:56:LEU:HD21	1:A:309:ALA:CB	2.33	0.58
1:A:141:TRP:HE1	1:B:302:ARG:NH2	2.01	0.58
1:B:89:ALA:O	1:B:93:ILE:HG13	2.03	0.58
1:B:256:GLN:HE22	1:B:262:LYS:NZ	1.99	0.58
1:C:68:LEU:CD1	1:C:75:LEU:HD23	2.32	0.58
1:C:209:SER:HB2	1:C:212:ILE:HD11	1.85	0.58
1:C:77:VAL:HA	1:C:98:ILE:HG23	1.84	0.58
1:A:9:VAL:HG13	1:A:54:GLY:C	2.24	0.58
1:D:100:VAL:HB	1:D:326:LEU:HB3	1.86	0.58
1:A:14:ARG:HD3	1:A:35:ASP:OD1	2.03	0.58
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.84	0.58
1:B:312:ASN:OD1	1:B:323:PRO:HB2	2.03	0.58
1:D:187:PRO:HG3	1:D:199:PHE:CD2	2.38	0.58
1:A:59:LEU:HD21	1:A:82:SER:HB3	1.85	0.58
1:A:129:ALA:HA	1:A:146:LEU:HD11	1.85	0.58
1:D:187:PRO:HA	1:D:199:PHE:CE1	2.38	0.58
1:A:157:GLY:HA2	1:A:181:LEU:O	2.02	0.58
1:A:185:ARG:O	1:A:186:GLN:HG3	2.04	0.58
1:A:80:THR:HG22	1:A:101:GLY:O	2.04	0.58
1:B:325:GLU:HG3	1:B:326:LEU:H	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:13:ARG:HG2	1:D:14:ARG:H	1.67	0.58
1:D:185:ARG:CG	1:D:186:GLN:H	2.00	0.58
1:C:41:PRO:O	1:C:42:ALA:HB2	2.03	0.58
1:C:144:LEU:O	1:C:147:CYS:SG	2.62	0.58
1:D:206:ALA:HB2	1:D:230:PHE:CE1	2.39	0.58
1:D:14:ARG:CD	1:D:20:ARG:HH22	2.12	0.58
1:A:142:LYS:O	1:B:302:ARG:NH1	2.35	0.58
1:A:228:LYS:HB2	1:A:253:ASP:OD2	2.02	0.58
1:C:64:ASP:OD1	1:C:67:ILE:HG12	2.03	0.58
1:C:37:ASP:O	1:D:142:LYS:HG2	2.04	0.58
1:A:171:ARG:O	1:A:174:PRO:HD2	2.03	0.58
1:D:188:ARG:CZ	1:D:191:GLU:HG2	2.34	0.58
1:C:9:VAL:HB	1:C:31:VAL:HG22	1.86	0.58
1:D:13:ARG:HG2	1:D:14:ARG:H	1.67	0.58
1:C:187:PRO:C	1:C:189:PRO:HD3	2.24	0.58
1:B:201:SER:OG	1:B:204:GLU:HB2	2.04	0.58
1:C:13:ARG:HD2	1:C:37:ASP:HA	1.86	0.58
1:C:49:VAL:O	1:C:71:ALA:HA	2.04	0.58
1:B:69:ASP:HA	1:B:96:ARG:HH12	1.68	0.58
1:B:217:SER:O	1:B:219:THR:HG23	2.04	0.58
1:C:40:ILE:HG22	1:C:61:ASP:OD1	2.03	0.58
1:D:187:PRO:HA	1:D:199:PHE:CZ	2.39	0.58
1:B:218:LEU:HD12	1:B:222:THR:OG1	2.04	0.58
1:A:83:VAL:HG23	1:A:104:PRO:CB	2.34	0.58
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.84	0.58
1:B:167:ALA:O	1:B:171:ARG:HG3	2.04	0.58
1:D:297:ALA:HA	1:D:302:ARG:HH22	1.68	0.58
1:A:234:MSE:HE1	1:A:263:ILE:HG22	1.85	0.58
1:C:94:LYS:C	1:C:96:ARG:H	2.06	0.58
1:D:182:TYR:OH	1:D:187:PRO:HA	2.03	0.58
1:B:309:ALA:HA	1:B:312:ASN:HD22	1.68	0.58
1:A:121:THR:CG2	1:A:126:LEU:HB2	2.34	0.58
1:C:64:ASP:OD1	1:C:64:ASP:N	2.35	0.58
1:B:13:ARG:HG2	1:B:14:ARG:H	1.68	0.58
1:D:257:ALA:HB1	1:D:263:ILE:CG2	2.34	0.58
1:C:57:CYS:HB2	1:C:61:ASP:HB2	1.84	0.58
1:D:322:MSE:SE	1:D:325:GLU:HB2	2.54	0.58
1:A:141:TRP:NE1	1:B:59:LEU:HD21	2.19	0.58
1:D:162:GLY:O	1:D:166:GLN:HG3	2.04	0.58
1:A:210:ASP:OD1	1:A:235:LYS:HD2	2.04	0.58
1:B:188:ARG:HB3	1:B:191:GLU:OE1	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:LEU:HD13	1:C:294:ILE:O	2.04	0.58
1:A:245:ARG:C	1:A:247:ASP:H	2.07	0.58
1:B:85:ILE:N	1:B:85:ILE:HD12	2.18	0.58
1:D:104:PRO:O	1:D:105:ASP:HB2	2.03	0.58
1:B:118:LEU:HD13	1:B:291:LEU:HD11	1.86	0.58
1:C:217:SER:O	1:C:219:THR:HG23	2.04	0.58
1:A:251:GLN:NE2	2:A:413:HOH:O	2.34	0.57
1:B:85:ILE:HD12	1:B:85:ILE:C	2.24	0.57
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.34	0.57
1:A:120:LEU:HB3	1:B:117:SER:OG	2.04	0.57
1:C:34:TRP:HB2	1:C:40:ILE:HD11	1.86	0.57
1:C:71:ALA:HB1	1:C:75:LEU:HD21	1.84	0.57
1:C:18:GLU:HG2	1:C:307:LEU:HB2	1.85	0.57
1:A:121:THR:HG22	1:B:121:THR:OG1	2.04	0.57
1:A:144:LEU:N	2:A:365:HOH:O	2.37	0.57
1:C:22:ALA:HB3	1:C:310:ALA:CB	2.34	0.57
1:C:13:ARG:HD2	1:C:37:ASP:C	2.24	0.57
1:C:234:MSE:HB3	2:C:343:HOH:O	2.04	0.57
1:C:90:LEU:HA	1:C:93:ILE:HD12	1.85	0.57
1:B:161:LEU:HD23	1:B:161:LEU:O	2.03	0.57
1:D:17:ALA:HB1	1:D:21:VAL:HG23	1.85	0.57
1:A:55:LEU:HD22	1:A:75:LEU:HD21	1.86	0.57
1:B:206:ALA:HA	1:B:212:ILE:HD11	1.86	0.57
1:A:7:MSE:HB3	1:A:53:HIS:CG	2.39	0.57
1:C:298:THR:HA	1:D:148:GLY:O	2.03	0.57
1:D:185:ARG:CZ	1:D:185:ARG:H	2.17	0.57
1:C:40:ILE:HG23	1:C:40:ILE:O	2.04	0.57
1:A:100:VAL:HG11	1:A:326:LEU:HD23	1.87	0.57
1:B:43:LYS:HB2	2:B:458:HOH:O	2.03	0.57
1:A:256:GLN:HE22	1:A:260:SER:HB3	1.69	0.57
1:B:14:ARG:HA	1:B:33:GLN:NE2	2.19	0.57
1:B:57:CYS:O	1:B:58:LEU:HD23	2.04	0.57
1:D:195:PHE:O	1:D:196:GLN:HB2	2.04	0.57
1:A:73:ALA:N	2:A:418:HOH:O	2.38	0.57
1:A:244:SER:O	1:A:270:VAL:HG11	2.03	0.57
1:D:14:ARG:HA	1:D:20:ARG:HH21	1.70	0.57
1:A:96:ARG:HG2	1:A:96:ARG:NH1	2.16	0.57
1:D:75:LEU:O	1:D:98:ILE:HG12	2.05	0.57
1:A:314:LEU:H	1:A:314:LEU:HD22	1.69	0.57
1:D:163:ARG:HD3	1:D:166:GLN:OE1	2.05	0.57
1:D:198:GLU:O	1:D:200:VAL:HG13	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:277:PRO:C	1:D:279:ASN:H	2.07	0.57
1:A:79:SER:OG	2:A:360:HOH:O	2.17	0.57
1:D:81:MSE:HG3	1:D:305:MSE:HB3	1.86	0.57
1:B:188:ARG:HD2	2:B:360:HOH:O	2.04	0.57
1:C:322:MSE:HE1	1:C:325:GLU:HA	1.86	0.57
1:A:51:GLY:HA2	2:A:421:HOH:O	2.02	0.57
1:A:81:MSE:HE2	1:B:141:TRP:HH2	1.68	0.57
1:B:300:ARG:HG3	2:B:444:HOH:O	2.05	0.57
1:A:17:ALA:HA	1:A:20:ARG:NE	2.20	0.57
1:A:79:SER:CB	1:A:313:LEU:HD23	2.34	0.57
1:C:315:ALA:HB1	1:C:321:PRO:O	2.04	0.57
1:B:6:LEU:HD22	1:B:27:ALA:O	2.05	0.57
1:D:213:VAL:HA	1:D:241:ILE:O	2.04	0.57
1:A:238:ALA:O	1:A:264:ALA:HB3	2.04	0.57
1:C:85:ILE:HG12	1:C:326:LEU:HD21	1.87	0.57
1:D:81:MSE:HE2	1:D:306:SER:CA	2.34	0.57
1:D:15:ILE:HB	1:D:81:MSE:HE1	1.86	0.57
1:A:157:GLY:CA	1:A:205:LEU:HD11	2.32	0.57
1:A:206:ALA:HB1	1:A:234:MSE:HG3	1.86	0.57
1:B:314:LEU:HD13	1:B:318:ARG:NH1	2.19	0.57
1:A:251:GLN:HB2	2:A:361:HOH:O	2.04	0.57
1:C:85:ILE:HG21	1:C:326:LEU:HD22	1.87	0.57
1:B:180:PHE:O	1:B:197:ALA:HA	2.04	0.57
1:A:180:PHE:O	1:A:197:ALA:HA	2.04	0.57
1:A:183:THR:HG21	1:A:202:THR:HG22	1.86	0.57
1:C:132:GLU:OE1	1:C:137:GLY:HA3	2.04	0.57
1:D:125:ARG:NH1	1:D:146:LEU:HA	2.20	0.57
1:B:201:SER:OG	1:B:203:PRO:HD2	2.05	0.57
1:D:187:PRO:HG3	1:D:199:PHE:CD2	2.39	0.57
1:B:180:PHE:O	1:B:197:ALA:HA	2.05	0.57
1:A:186:GLN:HB3	1:A:188:ARG:NH1	2.20	0.57
1:A:191:GLU:HG3	2:A:352:HOH:O	2.04	0.57
1:A:244:SER:O	1:A:270:VAL:HG11	2.03	0.57
1:D:59:LEU:HB3	1:D:82:SER:HB3	1.87	0.57
1:D:144:LEU:HB2	2:D:361:HOH:O	2.04	0.57
1:C:152:THR:HG22	1:C:153:GLN:HG3	1.86	0.57
1:D:202:THR:HB	1:D:203:PRO:HD3	1.86	0.57
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.34	0.57
1:A:207:ALA:HB1	1:A:208:GLN:NE2	2.20	0.57
1:A:280:HIS:ND1	1:A:282:LEU:HB2	2.18	0.57
1:A:283:LEU:O	1:A:283:LEU:CD2	2.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:191:GLU:CD	1:D:191:GLU:H	2.08	0.57
1:A:63:VAL:HG12	1:A:64:ASP:H	1.69	0.57
1:D:89:ALA:O	1:D:93:ILE:HG13	2.04	0.57
1:C:42:ALA:O	1:C:45:LEU:HB3	2.04	0.57
1:D:314:LEU:HA	1:D:317:LEU:CD2	2.32	0.57
1:A:200:VAL:HB	1:A:204:GLU:OE1	2.05	0.57
1:B:322:MSE:HB3	1:B:325:GLU:HB3	1.85	0.57
1:D:183:THR:HA	1:D:200:VAL:O	2.04	0.57
1:D:228:LYS:HB2	1:D:253:ASP:OD1	2.05	0.57
1:C:63:VAL:HG13	1:C:67:ILE:CB	2.34	0.57
1:C:132:GLU:OE1	1:C:137:GLY:HA3	2.04	0.57
1:C:206:ALA:HB2	1:C:230:PHE:CE1	2.39	0.57
1:A:129:ALA:HA	1:A:146:LEU:HD11	1.85	0.57
1:B:15:ILE:HG22	1:B:81:MSE:SE	2.54	0.57
1:B:222:THR:O	1:B:248:VAL:HG13	2.05	0.57
1:A:160:GLY:O	1:A:165:GLY:HA3	2.04	0.57
1:C:192:ALA:CB	1:C:197:ALA:HB3	2.35	0.57
1:C:40:ILE:HB	1:C:45:LEU:HD21	1.87	0.57
1:D:212:ILE:HD12	1:D:234:MSE:HE3	1.85	0.57
1:B:13:ARG:HD3	1:B:37:ASP:O	2.04	0.57
1:A:120:LEU:HB3	1:B:117:SER:OG	2.05	0.57
1:A:161:LEU:HD21	1:A:192:ALA:HB2	1.87	0.57
1:C:18:GLU:CG	1:C:307:LEU:HB2	2.35	0.57
1:D:305:MSE:HG2	1:D:306:SER:N	2.19	0.57
1:D:181:LEU:HD22	1:D:200:VAL:CG1	2.35	0.57
1:A:250:ASN:OD1	1:A:252:ASP:HB2	2.05	0.57
1:A:100:VAL:HG12	1:A:101:GLY:N	2.20	0.57
1:A:252:ASP:O	1:A:255:TYR:HB3	2.05	0.57
1:A:163:ARG:NH2	2:A:418:HOH:O	2.37	0.57
1:B:92:GLU:O	1:B:96:ARG:HG3	2.05	0.57
1:D:183:THR:CG2	1:D:205:LEU:HD13	2.34	0.57
1:C:297:ALA:O	1:D:147:CYS:HA	2.05	0.57
1:D:187:PRO:HG3	1:D:199:PHE:CD2	2.39	0.57
1:B:160:GLY:HA3	1:B:216:CYS:CB	2.35	0.57
1:A:325:GLU:HG2	1:A:326:LEU:H	1.69	0.57
1:B:218:LEU:HD11	1:B:223:GLU:HG2	1.87	0.57
1:C:275:PRO:HB3	1:D:138:TRP:CG	2.39	0.57
1:D:186:GLN:HG2	1:D:187:PRO:O	2.05	0.57
1:A:121:THR:HG22	1:B:121:THR:OG1	2.04	0.56
1:D:311:ASN:HB3	1:D:323:PRO:HG2	1.86	0.56
1:A:121:THR:HG23	1:A:127:PRO:HD3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:LEU:H	1:C:75:LEU:CD1	2.18	0.56
1:D:8:LYS:HZ1	1:D:52:ALA:HB2	1.71	0.56
1:D:78:ILE:HG13	1:D:98:ILE:HG21	1.87	0.56
1:A:120:LEU:HB3	1:B:117:SER:OG	2.05	0.56
1:C:163:ARG:N	1:C:166:GLN:HE21	2.03	0.56
1:D:14:ARG:HH21	1:D:37:ASP:CG	2.08	0.56
1:B:167:ALA:O	1:B:171:ARG:HG3	2.05	0.56
1:A:313:LEU:HD23	1:A:314:LEU:N	2.20	0.56
1:B:78:ILE:HG13	1:B:98:ILE:HG21	1.86	0.56
1:B:315:ALA:HB3	1:B:322:MSE:HG2	1.86	0.56
1:A:124:ARG:NH1	1:B:110:THR:HG23	2.20	0.56
1:A:125:ARG:HH12	1:A:146:LEU:HA	1.64	0.56
1:A:161:LEU:HD21	1:A:192:ALA:HA	1.86	0.56
1:B:77:VAL:HA	1:B:99:ARG:O	2.04	0.56
1:D:301:THR:HG22	1:D:305:MSE:SE	2.55	0.56
1:A:29:CYS:HB2	2:A:345:HOH:O	2.03	0.56
1:D:92:GLU:O	1:D:96:ARG:HG3	2.04	0.56
1:C:34:TRP:CD1	1:C:36:SER:HB3	2.40	0.56
1:D:202:THR:HB	1:D:203:PRO:HD3	1.87	0.56
1:D:131:GLU:OE1	1:D:135:ASN:HB3	2.04	0.56
1:A:121:THR:HG23	1:A:126:LEU:HD22	1.87	0.56
1:A:132:GLU:HA	1:A:135:ASN:OD1	2.05	0.56
1:C:12:THR:CG2	1:C:55:LEU:HD11	2.34	0.56
1:B:85:ILE:HD12	1:B:85:ILE:H	1.70	0.56
1:A:8:LYS:HB3	1:A:52:ALA:CA	2.28	0.56
1:B:13:ARG:NH2	1:B:39:PRO:HA	2.20	0.56
1:D:142:LYS:HB2	1:D:145:TRP:HB2	1.86	0.56
1:A:86:ASP:OD1	1:A:245:ARG:NH2	2.39	0.56
1:D:201:SER:OG	1:D:203:PRO:HD2	2.05	0.56
1:A:22:ALA:O	1:A:25:ARG:HB2	2.05	0.56
1:A:173:LYS:HB3	1:A:174:PRO:HD3	1.87	0.56
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.32	0.56
1:D:76:LYS:HD3	1:D:317:LEU:HD12	1.86	0.56
1:A:99:ARG:HD2	1:A:325:GLU:OE2	2.05	0.56
1:A:256:GLN:HA	1:A:259:ALA:HB3	1.87	0.56
1:A:318:ARG:HB2	1:A:320:GLU:HG3	1.87	0.56
1:B:11:VAL:HG13	1:B:56:LEU:HD22	1.86	0.56
1:B:45:LEU:HD21	1:B:61:ASP:HB3	1.86	0.56
1:A:232:GLN:NE2	1:A:262:LYS:NZ	2.45	0.56
1:B:11:VAL:CG1	1:B:33:GLN:HE21	2.17	0.56
1:B:23:LEU:HD11	1:B:56:LEU:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:LEU:O	1:B:78:ILE:HA	2.04	0.56
1:C:93:ILE:HG21	1:C:100:VAL:CG2	2.35	0.56
1:A:10:PHE:O	1:A:55:LEU:HD12	2.06	0.56
1:A:34:TRP:NE1	1:A:36:SER:HB3	2.19	0.56
1:A:251:GLN:HG2	1:A:280:HIS:NE2	2.20	0.56
1:B:89:ALA:HB1	1:B:92:GLU:HB2	1.86	0.56
1:B:93:ILE:HG21	1:B:100:VAL:CG2	2.34	0.56
1:C:26:ALA:HB2	1:C:314:LEU:HD21	1.88	0.56
1:C:184:GLY:H	1:C:199:PHE:HE1	1.53	0.56
1:C:315:ALA:HB3	1:C:322:MSE:HB3	1.87	0.56
1:D:179:ARG:HD2	1:D:181:LEU:HD21	1.87	0.56
1:D:269:ASP:O	1:D:293:HIS:HA	2.05	0.56
1:A:64:ASP:O	1:A:68:LEU:HG	2.06	0.56
1:A:80:THR:HG22	1:A:101:GLY:O	2.05	0.56
1:A:173:LYS:CB	1:A:174:PRO:HD3	2.34	0.56
1:C:81:MSE:HG3	1:C:305:MSE:HG2	1.85	0.56
1:C:95:LYS:C	1:C:97:GLY:H	2.09	0.56
1:D:86:ASP:C	1:D:88:LEU:H	2.08	0.56
1:D:168:ILE:HG21	1:D:213:VAL:HG11	1.88	0.56
1:A:132:GLU:OE1	1:A:137:GLY:HA3	2.04	0.56
1:B:185:ARG:HG3	1:B:185:ARG:NH1	2.18	0.56
1:A:57:CYS:O	1:A:58:LEU:HD23	2.05	0.56
1:B:158:ILE:O	1:B:182:TYR:HA	2.05	0.56
1:C:6:LEU:HD23	1:C:29:CYS:O	2.05	0.56
1:D:11:VAL:HB	1:D:33:GLN:HG3	1.87	0.56
1:B:320:GLU:HB3	1:B:321:PRO:HD2	1.88	0.56
1:C:297:ALA:O	1:D:147:CYS:HA	2.05	0.56
1:B:162:GLY:O	1:B:166:GLN:HG3	2.05	0.56
1:C:236:GLU:HA	1:C:263:ILE:HA	1.87	0.56
1:A:11:VAL:CG1	1:A:56:LEU:HD13	2.33	0.56
1:A:139:THR:OG1	1:A:142:LYS:HE3	2.06	0.56
1:B:85:ILE:HD12	1:B:90:LEU:HD21	1.87	0.56
1:C:85:ILE:HG12	1:C:326:LEU:CD2	2.35	0.56
1:C:185:ARG:N	1:C:185:ARG:NE	2.52	0.56
1:D:168:ILE:HD13	1:D:213:VAL:HG11	1.86	0.56
1:D:183:THR:HG21	1:D:202:THR:HA	1.86	0.56
1:C:34:TRP:CE3	1:C:40:ILE:HG13	2.39	0.56
1:C:39:PRO:CB	1:C:60:SER:HB2	2.36	0.56
1:C:268:LEU:N	1:C:268:LEU:HD23	2.20	0.56
1:D:11:VAL:HB	1:D:33:GLN:HG3	1.86	0.56
1:C:41:PRO:HD2	1:C:44:GLU:HG3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:ILE:CD1	1:D:45:LEU:HA	2.35	0.56
1:B:6:LEU:HD12	1:B:7:MSE:HG3	1.86	0.56
1:B:114:LEU:HD13	1:B:295:GLY:CA	2.36	0.56
1:D:192:ALA:O	1:D:196:GLN:N	2.39	0.56
1:B:55:LEU:HD23	1:B:78:ILE:CD1	2.35	0.56
1:B:110:THR:HG22	1:B:296:SER:HA	1.88	0.56
1:C:89:ALA:C	1:C:91:ASP:H	2.09	0.56
1:A:157:GLY:HA3	1:A:209:SER:OG	2.06	0.56
1:A:269:ASP:O	1:A:293:HIS:HA	2.05	0.56
1:C:36:SER:HB2	2:C:410:HOH:O	2.05	0.56
1:A:255:TYR:O	1:A:259:ALA:N	2.35	0.56
1:A:314:LEU:HG	1:A:318:ARG:NH1	2.19	0.56
1:B:107:LEU:HD23	1:B:305:MSE:CE	2.34	0.56
1:D:81:MSE:HG2	1:D:305:MSE:HG3	1.88	0.56
1:B:13:ARG:HA	1:B:34:TRP:HB3	1.86	0.56
1:C:302:ARG:HH22	1:D:141:TRP:HZ2	1.54	0.56
1:D:78:ILE:O	1:D:100:VAL:HA	2.06	0.56
1:C:11:VAL:O	1:C:33:GLN:HG3	2.05	0.56
1:C:50:ALA:HA	1:C:70:ALA:O	2.05	0.56
1:D:114:LEU:CD2	1:D:295:GLY:HA2	2.32	0.56
1:A:144:LEU:HD23	1:A:144:LEU:N	2.21	0.56
1:B:214:VAL:HG12	1:B:244:SER:OG	2.05	0.56
1:D:213:VAL:HA	1:D:241:ILE:O	2.06	0.56
1:B:186:GLN:HE21	1:B:187:PRO:HD2	1.70	0.56
1:D:32:GLU:OE2	1:D:48:GLY:HA2	2.05	0.56
1:C:65:LYS:HE3	1:C:92:GLU:OE1	2.04	0.56
1:C:182:TYR:O	1:C:199:PHE:HA	2.05	0.56
1:C:72:GLY:O	1:C:74:ASN:N	2.35	0.56
1:A:45:LEU:HG	1:A:67:ILE:HD12	1.88	0.56
1:B:110:THR:O	1:B:113:GLU:HB3	2.06	0.56
1:B:228:LYS:HE2	1:B:232:GLN:HE21	1.70	0.56
1:A:262:LYS:HG3	2:A:398:HOH:O	2.05	0.56
1:C:8:LYS:HB3	1:C:52:ALA:HA	1.88	0.56
1:B:173:LYS:HG3	2:B:437:HOH:O	2.05	0.56
1:D:13:ARG:HG2	1:D:14:ARG:N	2.19	0.56
1:D:276:LEU:HG	1:D:277:PRO:HD2	1.86	0.56
1:A:206:ALA:CB	1:A:234:MSE:HG3	2.36	0.56
1:B:17:ALA:O	1:B:21:VAL:HG23	2.06	0.56
1:B:208:GLN:O	1:B:235:LYS:HE3	2.05	0.56
1:B:308:LEU:O	1:B:312:ASN:HB2	2.05	0.56
1:B:49:VAL:HG11	1:B:67:ILE:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:ALA:CB	1:B:75:LEU:HB3	2.36	0.56
1:C:69:ASP:CA	1:C:96:ARG:HH21	2.18	0.56
1:D:216:CYS:SG	1:D:248:VAL:HG21	2.46	0.56
1:C:40:ILE:CG1	1:C:44:GLU:HB2	2.36	0.56
1:D:216:CYS:SG	1:D:222:THR:HG21	2.46	0.56
1:A:58:LEU:HD22	1:A:81:MSE:HB3	1.87	0.56
1:D:161:LEU:O	1:D:188:ARG:NH1	2.39	0.56
1:A:53:HIS:CD2	1:A:74:ASN:HB3	2.41	0.56
1:A:7:MSE:SE	1:A:317:LEU:HB3	2.56	0.56
1:B:77:VAL:HG13	1:B:313:LEU:HD22	1.88	0.56
1:A:93:ILE:HG23	1:A:98:ILE:HB	1.87	0.56
1:D:144:LEU:HB2	2:D:361:HOH:O	2.05	0.56
1:A:168:ILE:HD13	1:A:213:VAL:HG11	1.86	0.56
1:C:74:ASN:CG	2:C:433:HOH:O	2.44	0.56
1:C:229:ASP:O	1:C:233:LYS:HG3	2.05	0.56
1:A:149:TYR:OH	1:A:237:THR:HG22	2.06	0.56
1:A:161:LEU:HB2	1:A:182:TYR:CD2	2.40	0.56
1:D:279:ASN:HA	2:D:332:HOH:O	2.05	0.56
1:C:56:LEU:HA	1:C:79:SER:O	2.06	0.56
1:D:11:VAL:HG12	1:D:13:ARG:H	1.70	0.56
1:D:144:LEU:N	1:D:144:LEU:HD12	2.21	0.56
1:B:137:GLY:O	1:B:139:THR:HG23	2.05	0.56
1:C:187:PRO:HG3	1:C:199:PHE:CD2	2.41	0.56
1:A:77:VAL:HG23	1:A:99:ARG:O	2.06	0.56
1:B:226:CYS:HB3	1:B:231:PHE:CZ	2.40	0.56
1:D:180:PHE:CD2	1:D:195:PHE:HB3	2.41	0.56
1:B:86:ASP:HA	2:B:415:HOH:O	2.05	0.56
1:D:185:ARG:CZ	2:D:411:HOH:O	2.54	0.56
1:B:45:LEU:O	1:B:49:VAL:HG22	2.05	0.56
1:A:277:PRO:C	1:A:279:ASN:H	2.10	0.56
1:A:315:ALA:HA	1:A:318:ARG:NE	2.21	0.56
1:B:63:VAL:HA	1:B:67:ILE:HG13	1.87	0.56
1:C:219:THR:HB	1:C:220:PRO:CD	2.33	0.56
1:D:16:PRO:CD	1:D:81:MSE:HE1	2.34	0.56
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.86	0.56
1:C:94:LYS:NZ	1:C:94:LYS:HB2	2.21	0.56
1:A:72:GLY:CA	2:A:423:HOH:O	2.52	0.56
1:B:71:ALA:CB	1:B:75:LEU:HD22	2.36	0.56
1:B:139:THR:O	1:B:140:SER:HB3	2.05	0.56
1:D:218:LEU:HD12	1:D:219:THR:N	2.21	0.56
1:B:139:THR:O	1:B:140:SER:HB3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:ALA:HB3	1:B:195:PHE:CE1	2.41	0.56
1:D:249:VAL:CG1	1:D:250:ASN:H	2.19	0.56
1:D:262:LYS:HB3	2:D:345:HOH:O	2.05	0.56
1:D:15:ILE:HB	1:D:81:MSE:HE1	1.87	0.56
1:B:64:ASP:HA	1:B:89:ALA:HB2	1.88	0.55
1:C:163:ARG:CZ	2:C:431:HOH:O	2.54	0.55
1:A:153:GLN:HA	1:A:178:GLN:HB2	1.86	0.55
1:C:43:LYS:HA	1:C:46:GLU:OE2	2.06	0.55
1:D:222:THR:O	1:D:248:VAL:HA	2.05	0.55
1:A:45:LEU:HG	1:A:67:ILE:HD12	1.88	0.55
1:C:264:ALA:O	1:C:265:ALA:HB2	2.06	0.55
1:A:103:THR:HG22	1:A:312:ASN:ND2	2.21	0.55
1:A:310:ALA:O	1:A:314:LEU:HD13	2.05	0.55
1:B:12:THR:HG23	1:B:56:LEU:O	2.07	0.55
1:B:55:LEU:HD23	1:B:78:ILE:HD13	1.88	0.55
1:B:313:LEU:C	1:B:315:ALA:H	2.10	0.55
1:C:13:ARG:HH21	1:C:39:PRO:HA	1.70	0.55
1:C:49:VAL:HG21	1:C:67:ILE:HG22	1.87	0.55
1:C:297:ALA:O	1:D:147:CYS:HA	2.06	0.55
1:B:93:ILE:HG21	1:B:100:VAL:CG2	2.36	0.55
1:B:85:ILE:HD12	1:B:90:LEU:CD2	2.37	0.55
1:B:194:GLU:HB2	2:B:396:HOH:O	2.06	0.55
1:C:18:GLU:O	1:C:307:LEU:HD13	2.06	0.55
1:C:59:LEU:HD12	1:C:59:LEU:N	2.16	0.55
1:D:114:LEU:HD22	1:D:295:GLY:CA	2.31	0.55
1:D:315:ALA:HB3	1:D:322:MSE:HG2	1.87	0.55
1:B:86:ASP:OD2	1:B:245:ARG:HG3	2.06	0.55
1:A:19:GLY:N	1:A:306:SER:HB3	2.21	0.55
1:B:314:LEU:HD23	1:B:317:LEU:HD23	1.87	0.55
1:C:102:TYR:CD1	1:C:102:TYR:N	2.74	0.55
1:C:208:GLN:HG2	2:C:379:HOH:O	2.05	0.55
1:D:314:LEU:HA	1:D:317:LEU:HD22	1.87	0.55
1:A:69:ASP:O	1:A:72:GLY:N	2.38	0.55
1:A:171:ARG:O	1:A:174:PRO:HD2	2.06	0.55
1:C:39:PRO:HB3	1:C:60:SER:HB2	1.87	0.55
1:C:86:ASP:OD1	1:C:86:ASP:N	2.39	0.55
1:C:152:THR:HG22	1:C:153:GLN:HG3	1.88	0.55
1:B:79:SER:CB	1:B:313:LEU:HB2	2.35	0.55
1:B:81:MSE:HA	1:B:103:THR:HG23	1.88	0.55
1:D:226:CYS:N	1:D:248:VAL:O	2.39	0.55
1:A:152:THR:HG22	1:A:153:GLN:OE1	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:92:GLU:OE1	1:C:95:LYS:HB3	2.06	0.55
1:C:65:LYS:HB3	1:C:92:GLU:CG	2.36	0.55
1:D:312:ASN:C	1:D:314:LEU:H	2.10	0.55
1:B:163:ARG:NH2	1:B:166:GLN:HE22	2.05	0.55
1:C:227:ASN:O	1:C:230:PHE:HB3	2.06	0.55
1:D:114:LEU:HD22	1:D:295:GLY:CA	2.36	0.55
1:B:92:GLU:O	1:B:96:ARG:HG3	2.07	0.55
1:B:206:ALA:HB2	1:B:230:PHE:CE2	2.41	0.55
1:B:222:THR:HA	1:B:225:LEU:CD2	2.35	0.55
1:B:222:THR:O	1:B:225:LEU:HD23	2.06	0.55
1:A:236:GLU:HA	1:A:262:LYS:O	2.06	0.55
1:D:181:LEU:HD11	1:D:208:GLN:HB2	1.88	0.55
1:B:23:LEU:HB3	1:B:31:VAL:HG21	1.89	0.55
1:A:228:LYS:HB2	1:A:253:ASP:OD1	2.06	0.55
1:A:283:LEU:HD22	1:B:134:LYS:HG2	1.88	0.55
1:A:10:PHE:HB2	1:A:32:GLU:HB2	1.88	0.55
1:C:18:GLU:HG3	1:C:307:LEU:HD13	1.89	0.55
1:A:108:THR:HG23	1:A:164:ILE:HA	1.88	0.55
1:B:99:ARG:HD2	1:B:325:GLU:OE1	2.06	0.55
1:A:49:VAL:HG21	1:A:67:ILE:HG23	1.87	0.55
1:A:203:PRO:HB3	1:A:233:LYS:HE3	1.88	0.55
1:A:238:ALA:HA	2:A:354:HOH:O	2.06	0.55
1:A:56:LEU:HD11	1:A:309:ALA:HB1	1.89	0.55
1:A:17:ALA:HA	1:A:20:ARG:HE	1.71	0.55
1:A:167:ALA:CB	1:A:171:ARG:HH21	2.16	0.55
1:B:10:PHE:HA	1:B:32:GLU:O	2.05	0.55
1:B:95:LYS:O	1:B:95:LYS:HG2	2.06	0.55
1:A:314:LEU:CG	1:A:318:ARG:HH11	2.20	0.55
1:C:302:ARG:HD3	1:C:305:MSE:SE	2.56	0.55
1:D:182:TYR:HE2	1:D:188:ARG:CB	2.20	0.55
1:A:53:HIS:HB3	1:A:76:LYS:HE2	1.89	0.55
1:D:99:ARG:NH2	1:D:319:GLY:HA2	2.19	0.55
1:D:177:VAL:HG11	1:D:180:PHE:CE1	2.42	0.55
1:C:72:GLY:C	1:C:74:ASN:H	2.10	0.55
1:C:82:SER:O	1:C:102:TYR:HB2	2.06	0.55
1:D:200:VAL:HB	1:D:204:GLU:CB	2.36	0.55
1:B:13:ARG:HH21	1:B:39:PRO:HA	1.71	0.55
1:B:131:GLU:OE2	1:B:135:ASN:HB3	2.07	0.55
1:D:95:LYS:HD2	1:D:96:ARG:N	2.22	0.55
1:D:91:ASP:HB2	2:D:357:HOH:O	2.06	0.55
1:A:49:VAL:O	1:A:71:ALA:HA	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:PRO:HG3	1:B:199:PHE:CD2	2.42	0.55
1:B:192:ALA:HB1	1:B:197:ALA:O	2.07	0.55
1:C:99:ARG:HD2	1:C:325:GLU:OE1	2.07	0.55
1:A:181:LEU:HD22	1:A:200:VAL:CG1	2.37	0.55
1:C:57:CYS:O	1:C:80:THR:HA	2.06	0.55
1:C:98:ILE:HD12	1:C:98:ILE:N	2.22	0.55
1:C:208:GLN:NE2	2:C:444:HOH:O	2.39	0.55
1:C:195:PHE:O	1:C:196:GLN:HB2	2.07	0.55
1:A:16:PRO:HA	1:B:144:LEU:HD11	1.88	0.55
1:A:55:LEU:HB2	1:A:75:LEU:HD11	1.87	0.55
1:D:143:PRO:HB2	1:D:144:LEU:HD12	1.89	0.55
1:A:174:PRO:CG	1:B:174:PRO:HG3	2.23	0.55
1:C:34:TRP:NE1	1:C:36:SER:HB3	2.21	0.55
1:A:180:PHE:CD2	1:A:195:PHE:HB3	2.42	0.55
1:A:251:GLN:HB2	2:A:364:HOH:O	2.06	0.55
1:B:70:ALA:C	1:B:72:GLY:N	2.59	0.55
1:C:45:LEU:HG	1:C:67:ILE:HD12	1.87	0.55
1:D:35:ASP:O	1:D:36:SER:CB	2.54	0.55
1:D:185:ARG:HH22	1:D:188:ARG:HH21	1.53	0.55
1:A:29:CYS:SG	1:A:317:LEU:HD23	2.46	0.55
1:B:179:ARG:HA	2:B:380:HOH:O	2.07	0.55
1:D:192:ALA:HB1	1:D:197:ALA:H	1.72	0.55
1:B:16:PRO:HB2	1:B:306:SER:OG	2.07	0.55
1:C:59:LEU:HD12	1:C:59:LEU:N	2.17	0.55
1:A:175:PHE:CD2	1:B:171:ARG:HD3	2.42	0.55
1:B:257:ALA:HA	1:B:262:LYS:HG2	1.88	0.55
1:C:83:VAL:H	1:C:107:LEU:HD21	1.72	0.55
1:A:11:VAL:CB	1:A:33:GLN:HE21	2.20	0.55
1:A:18:GLU:HB3	1:A:307:LEU:HB2	1.87	0.55
1:A:105:ASP:HA	1:A:108:THR:OG1	2.07	0.55
1:A:312:ASN:O	1:A:322:MSE:HE2	2.06	0.55
1:A:322:MSE:CB	1:A:325:GLU:HB2	2.36	0.55
1:B:325:GLU:O	1:B:326:LEU:HB2	2.06	0.55
1:C:40:ILE:HG22	1:C:61:ASP:OD1	2.07	0.55
1:C:54:GLY:HA3	1:C:313:LEU:HD11	1.88	0.55
1:B:257:ALA:HA	1:B:262:LYS:HG2	1.87	0.55
1:B:99:ARG:NH2	1:B:319:GLY:HA2	2.17	0.55
1:C:315:ALA:CB	1:C:322:MSE:HG2	2.36	0.55
1:C:121:THR:HG23	1:C:127:PRO:HD3	1.89	0.55
1:C:152:THR:HG22	1:C:153:GLN:HG3	1.88	0.55
1:D:62:HIS:NE2	1:D:64:ASP:HB3	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:218:LEU:HB2	1:D:245:ARG:HB2	1.89	0.55
1:B:159:ILE:HD12	1:B:214:VAL:HG22	1.88	0.55
1:A:312:ASN:OD1	1:A:322:MSE:HE2	2.06	0.55
1:D:185:ARG:H	1:D:185:ARG:NE	2.05	0.55
1:A:81:MSE:HG2	1:A:305:MSE:HG2	1.87	0.55
1:C:52:ALA:O	1:C:74:ASN:HB3	2.07	0.55
1:C:90:LEU:C	1:C:93:ILE:HG22	2.27	0.55
1:D:15:ILE:N	1:D:20:ARG:NH2	2.43	0.55
1:B:34:TRP:HB2	1:B:40:ILE:HD12	1.88	0.55
1:C:6:LEU:CB	1:C:30:GLU:HB2	2.37	0.55
1:C:205:LEU:HD23	1:C:212:ILE:HD12	1.89	0.55
1:D:214:VAL:HG12	1:D:244:SER:OG	2.07	0.55
1:A:260:SER:OG	1:A:262:LYS:HG3	2.06	0.55
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.42	0.55
1:B:183:THR:HG21	1:B:202:THR:HG22	1.88	0.55
1:D:42:ALA:O	1:D:46:GLU:HG3	2.07	0.55
1:A:8:LYS:HE3	1:A:30:GLU:HG3	1.88	0.55
1:C:22:ALA:HB3	1:C:310:ALA:HB1	1.87	0.55
1:D:6:LEU:N	1:D:6:LEU:HD12	2.22	0.55
1:A:26:ALA:HB1	1:A:318:ARG:NH2	2.22	0.55
1:A:159:ILE:HG23	1:A:183:THR:CG2	2.37	0.55
1:A:71:ALA:C	2:A:419:HOH:O	2.44	0.54
1:C:71:ALA:CB	1:C:75:LEU:HD21	2.37	0.54
1:D:7:MSE:HB3	1:D:53:HIS:CG	2.42	0.54
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.88	0.54
1:A:229:ASP:HB3	1:A:233:LYS:HZ3	1.71	0.54
1:B:286:LYS:HD2	1:B:286:LYS:C	2.27	0.54
1:C:26:ALA:HA	1:C:318:ARG:HH21	1.70	0.54
1:C:276:LEU:HG	1:C:277:PRO:CD	2.36	0.54
1:D:86:ASP:OD2	1:D:218:LEU:HD23	2.06	0.54
1:C:297:ALA:HA	1:C:302:ARG:CD	2.37	0.54
1:C:12:THR:O	1:C:13:ARG:HB2	2.07	0.54
1:A:191:GLU:HA	2:A:406:HOH:O	2.07	0.54
1:C:297:ALA:O	1:D:147:CYS:HA	2.06	0.54
1:D:53:HIS:CD2	1:D:74:ASN:HB3	2.42	0.54
1:D:191:GLU:CD	1:D:191:GLU:H	2.11	0.54
1:A:54:GLY:HA3	1:A:317:LEU:HD11	1.89	0.54
1:B:47:ARG:O	1:B:47:ARG:HD3	2.07	0.54
1:B:100:VAL:HG12	1:B:101:GLY:H	1.70	0.54
1:B:283:LEU:HD23	1:B:290:ILE:HD12	1.89	0.54
1:A:53:HIS:HA	1:A:75:LEU:HA	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:LEU:HD23	1:C:305:MSE:HE3	1.89	0.54
1:A:119:LEU:C	1:A:119:LEU:HD23	2.28	0.54
1:A:182:TYR:O	1:A:199:PHE:HA	2.07	0.54
1:C:101:GLY:HA2	1:C:324:SER:O	2.07	0.54
1:D:312:ASN:OD1	1:D:323:PRO:HD2	2.06	0.54
1:A:137:GLY:O	1:A:139:THR:N	2.40	0.54
1:B:89:ALA:O	1:B:93:ILE:HG13	2.07	0.54
1:B:11:VAL:HG11	1:B:15:ILE:HD13	1.89	0.54
1:B:88:LEU:O	1:B:90:LEU:HG	2.07	0.54
1:D:110:THR:O	1:D:113:GLU:HB3	2.07	0.54
1:A:140:SER:OG	1:A:141:TRP:N	2.40	0.54
1:D:182:TYR:OH	1:D:187:PRO:HA	2.07	0.54
1:D:192:ALA:HB1	1:D:197:ALA:HB2	1.88	0.54
1:B:51:GLY:HA2	2:B:336:HOH:O	2.06	0.54
1:B:80:THR:HG21	1:B:87:HIS:HE1	1.71	0.54
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.31	0.54
1:C:217:SER:O	1:C:222:THR:HG21	2.08	0.54
1:C:223:GLU:CG	1:C:247:ASP:HB3	2.36	0.54
1:B:179:ARG:HG3	2:B:412:HOH:O	2.06	0.54
1:A:167:ALA:HB1	1:A:171:ARG:NH2	2.22	0.54
1:B:66:ARG:HG2	1:B:66:ARG:NH1	2.20	0.54
1:B:81:MSE:CG	1:B:305:MSE:HG2	2.37	0.54
1:D:8:LYS:H	1:D:53:HIS:CE1	2.26	0.54
1:A:40:ILE:HD11	1:A:44:GLU:HB2	1.90	0.54
1:B:15:ILE:HG13	1:B:20:ARG:HG3	1.90	0.54
1:B:251:GLN:HE21	1:B:280:HIS:CE1	2.25	0.54
1:B:75:LEU:HD23	1:B:98:ILE:HD13	1.88	0.54
1:A:7:MSE:O	1:A:29:CYS:HB2	2.08	0.54
1:A:302:ARG:HG3	1:B:147:CYS:SG	2.47	0.54
1:B:46:GLU:HB3	1:B:70:ALA:HB3	1.89	0.54
1:B:84:GLY:O	1:B:85:ILE:HG23	2.07	0.54
1:A:86:ASP:OD1	1:A:245:ARG:NH2	2.39	0.54
1:D:300:ARG:HB2	2:D:355:HOH:O	2.07	0.54
1:A:195:PHE:O	1:A:196:GLN:HB2	2.08	0.54
1:C:21:VAL:O	1:C:25:ARG:HG2	2.08	0.54
1:A:72:GLY:C	2:A:423:HOH:O	2.45	0.54
1:B:131:GLU:OE2	1:B:135:ASN:HB3	2.07	0.54
1:C:77:VAL:HG13	1:C:313:LEU:HD12	1.88	0.54
1:C:322:MSE:SE	1:C:322:MSE:H	2.40	0.54
1:B:49:VAL:C	1:B:71:ALA:HA	2.28	0.54
1:B:181:LEU:HD23	1:B:198:GLU:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:LYS:O	1:C:95:LYS:HG2	2.08	0.54
1:D:322:MSE:HG3	1:D:325:GLU:HB2	1.88	0.54
1:B:228:LYS:H	1:B:253:ASP:HB3	1.73	0.54
1:C:181:LEU:HD23	1:C:198:GLU:HB3	1.89	0.54
1:A:222:THR:O	1:A:248:VAL:HG13	2.07	0.54
1:C:16:PRO:HD2	1:C:306:SER:HB2	1.89	0.54
1:C:57:CYS:HB2	1:C:61:ASP:OD2	2.08	0.54
1:D:114:LEU:HD22	1:D:295:GLY:CA	2.34	0.54
1:B:251:GLN:OE1	1:B:272:SER:HB2	2.07	0.54
1:C:189:PRO:O	1:C:193:ALA:HB2	2.07	0.54
1:C:297:ALA:O	1:D:147:CYS:HA	2.07	0.54
1:B:114:LEU:CD1	1:B:294:ILE:HG13	2.33	0.54
1:C:65:LYS:HD3	1:C:96:ARG:HH22	1.70	0.54
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.34	0.54
1:B:286:LYS:HD2	1:B:286:LYS:C	2.28	0.54
1:D:155:THR:HG23	1:D:179:ARG:O	2.08	0.54
1:D:14:ARG:HH21	1:D:37:ASP:CG	2.11	0.54
1:D:64:ASP:HA	1:D:89:ALA:CB	2.38	0.54
1:A:17:ALA:HA	1:A:20:ARG:HE	1.72	0.54
1:A:114:LEU:HD11	1:B:126:LEU:HD11	1.89	0.54
1:B:257:ALA:HA	1:B:262:LYS:HG2	1.89	0.54
1:C:260:SER:OG	1:C:262:LYS:HG3	2.08	0.54
1:B:249:VAL:CG1	1:B:250:ASN:N	2.71	0.54
1:C:93:ILE:HG23	1:C:98:ILE:HB	1.90	0.54
1:B:318:ARG:O	1:B:320:GLU:HG3	2.08	0.54
1:A:120:LEU:HB3	1:B:117:SER:OG	2.07	0.54
1:B:49:VAL:O	1:B:71:ALA:HA	2.08	0.54
1:A:120:LEU:HB3	1:B:117:SER:OG	2.07	0.54
1:A:203:PRO:HB3	1:A:233:LYS:HE2	1.88	0.54
1:B:34:TRP:NE1	1:B:36:SER:HB3	2.23	0.54
1:C:132:GLU:OE1	1:C:137:GLY:HA3	2.07	0.54
1:D:95:LYS:HD3	1:D:95:LYS:C	2.28	0.54
1:A:209:SER:HB2	1:A:212:ILE:HD13	1.90	0.54
1:C:78:ILE:O	1:C:100:VAL:HG13	2.07	0.54
1:D:14:ARG:HH21	1:D:37:ASP:CG	2.11	0.54
1:A:172:LEU:HB2	1:A:180:PHE:HZ	1.73	0.54
1:B:246:GLY:HA3	1:B:271:THR:O	2.08	0.54
1:B:178:GLN:OE1	1:B:179:ARG:HB2	2.08	0.54
1:C:161:LEU:HD22	1:C:182:TYR:CD1	2.42	0.54
1:A:204:GLU:HB2	1:D:204:GLU:CD	2.28	0.54
1:D:131:GLU:OE2	1:D:135:ASN:HB3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:277:PRO:HD2	1:D:280:HIS:HD2	1.73	0.54
1:A:17:ALA:CA	1:A:20:ARG:HE	2.21	0.54
1:A:23:LEU:HB3	1:A:31:VAL:HG21	1.90	0.54
1:A:69:ASP:C	1:A:71:ALA:H	2.10	0.54
1:A:83:VAL:HG23	1:A:104:PRO:HB3	1.89	0.54
1:B:87:HIS:H	1:B:87:HIS:HD2	1.55	0.54
1:C:222:THR:O	1:C:248:VAL:HG13	2.07	0.54
1:D:13:ARG:HG3	1:D:36:SER:O	2.08	0.54
1:C:185:ARG:HH12	1:C:217:SER:HB3	1.73	0.54
1:D:81:MSE:HE2	1:D:309:ALA:HB3	1.88	0.54
1:B:95:LYS:C	1:B:97:GLY:H	2.10	0.54
1:A:143:PRO:HB3	1:B:81:MSE:HE3	1.90	0.54
1:B:6:LEU:HD22	1:B:27:ALA:O	2.07	0.54
1:C:14:ARG:HB3	1:C:37:ASP:CG	2.27	0.54
1:C:77:VAL:HG23	1:C:99:ARG:O	2.08	0.54
1:C:271:THR:HG21	1:C:276:LEU:HD22	1.90	0.54
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.29	0.54
1:B:40:ILE:HG23	1:B:45:LEU:HB2	1.90	0.54
1:C:99:ARG:NH2	1:C:319:GLY:HA2	2.17	0.54
1:A:120:LEU:HB3	1:B:117:SER:OG	2.07	0.54
1:A:121:THR:HG23	1:A:126:LEU:HD22	1.90	0.54
1:B:83:VAL:HA	1:B:102:TYR:HB2	1.90	0.54
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.89	0.54
1:D:90:LEU:O	1:D:91:ASP:C	2.45	0.54
1:C:132:GLU:OE1	1:C:137:GLY:HA3	2.08	0.54
1:B:313:LEU:O	1:B:317:LEU:HB2	2.07	0.54
1:B:168:ILE:HG22	1:B:172:LEU:HD12	1.88	0.54
1:C:114:LEU:HD13	1:C:295:GLY:CA	2.38	0.54
1:B:12:THR:HG21	1:B:57:CYS:HA	1.89	0.54
1:B:34:TRP:CD1	1:B:40:ILE:HB	2.42	0.54
1:B:114:LEU:HD13	1:B:295:GLY:CA	2.38	0.54
1:B:251:GLN:HE21	1:B:280:HIS:CE1	2.26	0.54
1:A:119:LEU:C	1:A:119:LEU:HD23	2.29	0.54
1:D:76:LYS:O	1:D:99:ARG:HB2	2.08	0.54
1:D:34:TRP:NE1	1:D:36:SER:HB3	2.23	0.54
1:D:188:ARG:HD2	2:D:412:HOH:O	2.07	0.54
1:B:83:VAL:HG23	1:B:104:PRO:HB3	1.90	0.54
1:B:314:LEU:HD23	1:B:317:LEU:HB2	1.89	0.54
1:C:48:GLY:O	1:C:50:ALA:N	2.40	0.54
1:D:78:ILE:O	1:D:100:VAL:HA	2.07	0.54
1:A:161:LEU:HD22	1:A:188:ARG:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:THR:HG23	1:B:298:THR:HG23	1.90	0.54
1:A:91:ASP:O	1:A:95:LYS:HG3	2.07	0.53
1:D:121:THR:CG2	1:D:127:PRO:HD3	2.38	0.53
1:A:322:MSE:HB2	1:A:325:GLU:HB2	1.89	0.53
1:B:94:LYS:C	1:B:96:ARG:H	2.12	0.53
1:C:138:TRP:HA	2:C:337:HOH:O	2.08	0.53
1:C:236:GLU:HA	1:C:262:LYS:O	2.08	0.53
1:B:114:LEU:HD13	1:B:295:GLY:CA	2.36	0.53
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.43	0.53
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.89	0.53
1:C:218:LEU:HD13	1:C:248:VAL:CG2	2.38	0.53
1:D:229:ASP:O	1:D:233:LYS:HG3	2.08	0.53
1:D:277:PRO:O	1:D:280:HIS:HB2	2.07	0.53
1:C:102:TYR:O	1:C:104:PRO:HD2	2.08	0.53
1:A:132:GLU:OE1	1:A:137:GLY:HA3	2.08	0.53
1:A:257:ALA:CB	1:A:262:LYS:HB2	2.38	0.53
1:C:7:MSE:O	1:C:30:GLU:N	2.39	0.53
1:D:163:ARG:HA	1:D:166:GLN:CD	2.29	0.53
1:C:44:GLU:O	1:C:47:ARG:HB3	2.08	0.53
1:D:163:ARG:CZ	2:D:368:HOH:O	2.56	0.53
1:B:163:ARG:CZ	1:B:166:GLN:HE22	2.19	0.53
1:B:320:GLU:HB3	1:B:321:PRO:HD2	1.90	0.53
1:C:260:SER:OG	1:C:262:LYS:HG3	2.08	0.53
1:D:85:ILE:HD13	1:D:90:LEU:CD1	2.34	0.53
1:B:17:ALA:O	1:B:21:VAL:HG23	2.08	0.53
1:B:225:LEU:O	1:B:227:ASN:N	2.41	0.53
1:C:312:ASN:OD1	1:C:322:MSE:HB3	2.08	0.53
1:C:313:LEU:O	1:C:317:LEU:HG	2.08	0.53
1:D:18:GLU:OE1	1:D:303:ASN:HB3	2.08	0.53
1:D:249:VAL:HG12	1:D:250:ASN:N	2.22	0.53
1:A:63:VAL:HG13	1:A:67:ILE:CG2	2.37	0.53
1:A:88:LEU:HD13	1:A:100:VAL:HG22	1.89	0.53
1:A:224:GLY:N	1:A:247:ASP:O	2.42	0.53
1:B:59:LEU:HD23	1:B:82:SER:HB2	1.91	0.53
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.90	0.53
1:D:14:ARG:HG3	1:D:20:ARG:NH2	2.16	0.53
1:D:231:PHE:HD1	1:D:234:MSE:SE	2.40	0.53
1:A:161:LEU:HD23	1:A:191:GLU:HB2	1.88	0.53
1:D:20:ARG:HD2	1:D:33:GLN:OE1	2.08	0.53
1:A:192:ALA:HB1	1:A:197:ALA:HB3	1.89	0.53
1:B:43:LYS:HB2	2:B:456:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:GLY:HA3	1:B:271:THR:O	2.08	0.53
1:A:155:THR:HG23	1:A:179:ARG:O	2.08	0.53
1:D:81:MSE:HA	1:D:103:THR:HG21	1.90	0.53
1:D:203:PRO:HB3	1:D:233:LYS:HE2	1.91	0.53
1:B:251:GLN:HE22	1:B:271:THR:HB	1.73	0.53
1:B:16:PRO:HB2	1:B:306:SER:OG	2.08	0.53
1:B:95:LYS:O	1:B:95:LYS:HG2	2.08	0.53
1:C:103:THR:HG22	1:C:308:LEU:HD23	1.90	0.53
1:D:43:LYS:O	1:D:47:ARG:HG2	2.08	0.53
1:A:23:LEU:HD23	1:A:314:LEU:HD13	1.89	0.53
1:A:119:LEU:C	1:A:119:LEU:HD23	2.29	0.53
1:A:141:TRP:HA	2:B:354:HOH:O	2.07	0.53
1:A:312:ASN:HA	1:A:322:MSE:HG3	1.90	0.53
1:C:269:ASP:O	1:C:293:HIS:HA	2.09	0.53
1:A:187:PRO:HG3	1:A:199:PHE:CD2	2.44	0.53
1:B:92:GLU:N	2:B:433:HOH:O	2.41	0.53
1:B:103:THR:HA	1:B:308:LEU:HD23	1.88	0.53
1:B:118:LEU:HD13	1:B:291:LEU:HD11	1.91	0.53
1:D:254:LEU:O	1:D:258:LEU:HG	2.08	0.53
1:A:63:VAL:HG12	1:A:68:LEU:HD21	1.90	0.53
1:C:158:ILE:O	1:C:182:TYR:HA	2.08	0.53
1:D:13:ARG:HG2	1:D:36:SER:O	2.09	0.53
1:B:13:ARG:NH2	1:B:39:PRO:HB3	2.24	0.53
1:B:99:ARG:HH21	1:B:315:ALA:HB1	1.74	0.53
1:B:251:GLN:HE22	1:B:276:LEU:CD1	2.22	0.53
1:D:114:LEU:CD2	1:D:295:GLY:HA2	2.36	0.53
1:B:14:ARG:HA	1:B:33:GLN:OE1	2.07	0.53
1:C:68:LEU:HD21	1:C:78:ILE:HD11	1.91	0.53
1:C:187:PRO:HG3	1:C:199:PHE:CD1	2.43	0.53
1:C:322:MSE:SE	1:C:325:GLU:HB3	2.58	0.53
1:D:20:ARG:HH11	1:D:33:GLN:NE2	2.06	0.53
1:B:46:GLU:HG2	1:B:66:ARG:HB3	1.90	0.53
1:D:186:GLN:HG2	1:D:187:PRO:N	2.24	0.53
1:A:175:PHE:CD1	1:B:171:ARG:HG2	2.43	0.53
1:D:202:THR:HB	1:D:203:PRO:HD3	1.89	0.53
1:A:35:ASP:O	1:A:36:SER:HB2	2.09	0.53
1:D:183:THR:HG22	1:D:200:VAL:O	2.07	0.53
1:A:79:SER:HB3	1:A:313:LEU:CB	2.39	0.53
1:B:76:LYS:C	1:B:98:ILE:HG23	2.29	0.53
1:D:77:VAL:HA	1:D:99:ARG:O	2.08	0.53
1:A:183:THR:HG22	1:A:184:GLY:N	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:THR:CA	1:B:225:LEU:HD23	2.38	0.53
1:C:236:GLU:HA	1:C:262:LYS:O	2.09	0.53
1:A:175:PHE:CE2	1:B:171:ARG:HD3	2.44	0.53
1:B:85:ILE:HG13	1:B:90:LEU:HD11	1.90	0.53
1:C:94:LYS:HE3	1:C:94:LYS:HA	1.90	0.53
1:D:183:THR:HG21	1:D:205:LEU:HB2	1.90	0.53
1:B:7:MSE:CE	1:B:28:ASP:HB2	2.32	0.53
1:C:99:ARG:HD2	1:C:325:GLU:OE2	2.09	0.53
1:D:281:PRO:O	1:D:284:THR:N	2.37	0.53
1:C:114:LEU:CD2	1:C:295:GLY:HA2	2.38	0.53
1:A:7:MSE:CE	1:A:28:ASP:HB2	2.39	0.53
1:A:77:VAL:HG22	1:A:313:LEU:HD22	1.89	0.53
1:C:105:ASP:HA	1:C:108:THR:OG1	2.08	0.53
1:D:108:THR:HA	1:D:164:ILE:HG12	1.91	0.53
1:A:9:VAL:HG22	1:A:54:GLY:HA3	1.89	0.53
1:A:56:LEU:C	1:A:56:LEU:HD23	2.29	0.53
1:C:297:ALA:CA	1:C:302:ARG:HD2	2.39	0.53
1:C:78:ILE:HD12	1:C:93:ILE:CD1	2.39	0.53
1:A:229:ASP:O	1:A:233:LYS:HG3	2.09	0.53
1:B:38:GLU:HB3	1:B:39:PRO:CD	2.37	0.53
1:A:257:ALA:HA	1:A:262:LYS:HB2	1.88	0.53
1:C:9:VAL:O	1:C:31:VAL:HA	2.09	0.53
1:A:78:ILE:O	1:A:100:VAL:HA	2.09	0.53
1:C:76:LYS:CE	1:C:317:LEU:HA	2.35	0.53
1:B:89:ALA:O	1:B:93:ILE:HG13	2.08	0.53
1:C:45:LEU:O	1:C:49:VAL:HG22	2.07	0.53
1:C:99:ARG:HB3	1:C:322:MSE:HE2	1.90	0.53
1:C:39:PRO:HA	2:C:442:HOH:O	2.09	0.53
1:A:88:LEU:HD12	1:A:100:VAL:HG13	1.91	0.53
1:A:114:LEU:CD1	1:A:295:GLY:HA2	2.38	0.53
1:D:180:PHE:HB2	1:D:197:ALA:CB	2.39	0.53
1:B:83:VAL:CB	1:B:107:LEU:HD11	2.30	0.53
1:D:17:ALA:O	1:D:21:VAL:HG23	2.09	0.53
1:A:68:LEU:HD13	1:A:92:GLU:HB3	1.91	0.53
1:A:82:SER:O	1:A:102:TYR:HB2	2.09	0.53
1:A:68:LEU:HD21	1:A:78:ILE:HD11	1.90	0.53
1:B:186:GLN:HG3	1:B:187:PRO:CD	2.38	0.53
1:A:322:MSE:HE3	1:A:325:GLU:HB2	1.90	0.53
1:C:195:PHE:O	1:C:196:GLN:HB2	2.09	0.53
1:A:119:LEU:C	1:A:119:LEU:HD23	2.29	0.53
1:A:161:LEU:C	1:A:166:GLN:NE2	2.62	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:TYR:O	1:A:199:PHE:HA	2.09	0.53
1:B:296:SER:O	1:B:298:THR:N	2.42	0.53
1:C:189:PRO:O	1:C:191:GLU:N	2.42	0.53
1:A:174:PRO:HG2	1:B:174:PRO:CG	2.29	0.53
1:A:168:ILE:HD13	1:A:213:VAL:HG11	1.89	0.53
1:B:68:LEU:HD12	1:B:92:GLU:HB3	1.91	0.53
1:B:75:LEU:HD23	1:B:98:ILE:HD13	1.91	0.53
1:B:114:LEU:HD13	1:B:295:GLY:HA2	1.89	0.53
1:B:257:ALA:HA	1:B:262:LYS:HG2	1.91	0.53
1:C:75:LEU:CD2	1:C:98:ILE:HG12	2.39	0.53
1:A:231:PHE:HD1	1:A:234:MSE:SE	2.41	0.53
1:D:81:MSE:HE2	1:D:306:SER:CA	2.35	0.53
1:B:200:VAL:CG2	1:B:201:SER:N	2.71	0.53
1:A:53:HIS:HA	1:A:75:LEU:HA	1.91	0.53
1:A:302:ARG:NH1	1:B:143:PRO:O	2.42	0.53
1:C:291:LEU:HD21	1:D:126:LEU:HG	1.90	0.53
1:D:78:ILE:O	1:D:100:VAL:HA	2.09	0.53
1:B:325:GLU:HG2	1:B:326:LEU:N	2.23	0.53
1:C:41:PRO:HD2	1:C:44:GLU:HG3	1.90	0.53
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.43	0.53
1:D:240:PHE:O	1:D:266:ALA:HA	2.09	0.53
1:D:255:TYR:CD1	1:D:285:LEU:HD11	2.44	0.53
1:D:309:ALA:HA	2:D:357:HOH:O	2.08	0.53
1:A:286:LYS:N	2:A:347:HOH:O	2.42	0.53
1:A:292:PRO:HD2	1:B:129:ALA:HB1	1.90	0.53
1:C:9:VAL:CB	1:C:31:VAL:HG22	2.39	0.53
1:A:302:ARG:HD3	1:A:305:MSE:SE	2.59	0.53
1:D:18:GLU:HG3	1:D:303:ASN:O	2.09	0.53
1:B:89:ALA:O	1:B:93:ILE:HG13	2.09	0.53
1:D:132:GLU:OE1	1:D:137:GLY:HA3	2.09	0.53
1:B:251:GLN:HE22	1:B:276:LEU:HD11	1.74	0.53
1:D:11:VAL:HB	1:D:33:GLN:HB3	1.90	0.53
1:B:11:VAL:H	1:B:33:GLN:CB	2.22	0.53
1:B:200:VAL:HG22	1:B:201:SER:H	1.74	0.53
1:A:64:ASP:HA	1:A:89:ALA:HB2	1.91	0.53
1:B:64:ASP:O	1:B:68:LEU:HD12	2.09	0.52
1:C:38:GLU:OE2	1:D:139:THR:HG21	2.10	0.52
1:A:166:GLN:NE2	1:A:191:GLU:HB3	2.24	0.52
1:C:206:ALA:CB	1:C:233:LYS:HB2	2.38	0.52
1:B:13:ARG:HG2	1:B:14:ARG:N	2.24	0.52
1:B:14:ARG:HG3	1:B:20:ARG:HH11	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:PRO:O	1:B:45:LEU:N	2.41	0.52
1:C:325:GLU:HG2	1:C:326:LEU:N	2.24	0.52
1:A:190:GLU:N	2:A:350:HOH:O	2.32	0.52
1:A:7:MSE:HE3	1:A:28:ASP:HB2	1.90	0.52
1:B:99:ARG:HD2	1:B:325:GLU:CD	2.30	0.52
1:C:218:LEU:HD13	1:C:247:ASP:HB2	1.90	0.52
1:B:81:MSE:HG2	1:B:305:MSE:HE3	1.91	0.52
1:C:13:ARG:HD2	1:C:37:ASP:CA	2.39	0.52
1:D:181:LEU:HD22	1:D:200:VAL:HG13	1.91	0.52
1:A:95:LYS:O	1:A:97:GLY:N	2.43	0.52
1:A:119:LEU:C	1:A:119:LEU:HD23	2.30	0.52
1:D:49:VAL:CG2	1:D:71:ALA:HB2	2.39	0.52
1:B:118:LEU:HD13	1:B:291:LEU:HD11	1.91	0.52
1:C:114:LEU:HD22	1:C:295:GLY:CA	2.36	0.52
1:C:114:LEU:CD2	1:C:295:GLY:HA2	2.39	0.52
1:D:236:GLU:HA	1:D:262:LYS:O	2.10	0.52
1:C:314:LEU:HA	1:C:317:LEU:HD12	1.91	0.52
1:A:133:VAL:HG23	1:B:292:PRO:HD3	1.90	0.52
1:B:183:THR:N	1:B:205:LEU:HD22	2.24	0.52
1:D:108:THR:HA	1:D:164:ILE:HG12	1.91	0.52
1:A:8:LYS:HE3	1:A:32:GLU:HG3	1.90	0.52
1:D:59:LEU:HA	1:D:87:HIS:CG	2.45	0.52
1:A:317:LEU:HD23	1:A:318:ARG:HG3	1.92	0.52
1:C:276:LEU:HG	1:C:277:PRO:HD2	1.91	0.52
1:A:82:SER:O	1:A:102:TYR:HB2	2.09	0.52
1:C:92:GLU:O	1:C:95:LYS:N	2.41	0.52
1:D:164:ILE:HG22	1:D:168:ILE:HD11	1.91	0.52
1:D:14:ARG:HA	1:D:20:ARG:NH2	2.24	0.52
1:D:49:VAL:HG23	1:D:71:ALA:HB2	1.90	0.52
1:A:46:GLU:O	1:A:70:ALA:HB1	2.09	0.52
1:A:156:VAL:HB	1:A:180:PHE:CD1	2.45	0.52
1:A:208:GLN:HB3	2:A:412:HOH:O	2.10	0.52
1:D:165:GLY:HA2	1:D:168:ILE:HD12	1.90	0.52
1:D:280:HIS:ND1	1:D:281:PRO:HD2	2.25	0.52
1:D:285:LEU:HB3	1:D:287:ASN:OD1	2.08	0.52
1:C:101:GLY:HA2	1:C:325:GLU:HA	1.91	0.52
1:D:91:ASP:HB2	2:D:358:HOH:O	2.09	0.52
1:A:13:ARG:O	1:A:15:ILE:N	2.38	0.52
1:A:196:GLN:OE1	1:A:196:GLN:N	2.42	0.52
1:C:269:ASP:O	1:C:293:HIS:HA	2.10	0.52
1:D:81:MSE:HE2	1:D:306:SER:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:LEU:CD1	1:A:295:GLY:HA2	2.38	0.52
1:A:53:HIS:CD2	1:A:74:ASN:HB3	2.45	0.52
1:D:15:ILE:N	1:D:20:ARG:NH2	2.43	0.52
1:A:56:LEU:HG	1:A:79:SER:O	2.10	0.52
1:A:121:THR:HG23	1:A:126:LEU:HB2	1.90	0.52
1:D:163:ARG:NH2	1:D:166:GLN:OE1	2.43	0.52
1:C:83:VAL:HG23	1:C:104:PRO:HB3	1.91	0.52
1:C:218:LEU:HD11	1:C:223:GLU:HA	1.91	0.52
1:C:314:LEU:HD12	1:C:317:LEU:HD12	1.91	0.52
1:A:206:ALA:HB1	1:A:234:MSE:HG3	1.91	0.52
1:D:312:ASN:HA	1:D:315:ALA:HB3	1.91	0.52
1:A:109:ASP:OD2	1:A:171:ARG:NH1	2.43	0.52
1:A:114:LEU:HD22	1:A:294:ILE:O	2.09	0.52
1:A:180:PHE:CD2	1:A:195:PHE:HB3	2.45	0.52
1:C:309:ALA:HA	2:C:361:HOH:O	2.09	0.52
1:D:75:LEU:O	1:D:98:ILE:HG12	2.09	0.52
1:D:49:VAL:HG12	1:D:55:LEU:HD13	1.91	0.52
1:D:206:ALA:HB2	1:D:230:PHE:CD1	2.44	0.52
1:A:280:HIS:HE1	1:A:282:LEU:HG	1.74	0.52
1:B:235:LYS:O	1:B:263:ILE:HG22	2.09	0.52
1:C:92:GLU:HG2	1:C:95:LYS:HZ1	1.74	0.52
1:D:49:VAL:CG2	1:D:50:ALA:H	2.22	0.52
1:C:138:TRP:HA	2:C:338:HOH:O	2.10	0.52
1:D:110:THR:O	1:D:113:GLU:HB3	2.09	0.52
1:A:279:ASN:HD22	1:A:279:ASN:C	2.12	0.52
1:C:8:LYS:CB	1:C:52:ALA:HA	2.32	0.52
1:D:26:ALA:HB3	1:D:29:CYS:SG	2.49	0.52
1:A:11:VAL:CB	1:A:33:GLN:HE21	2.21	0.52
1:A:56:LEU:HD11	1:A:310:ALA:HA	1.91	0.52
1:C:9:VAL:HA	1:C:54:GLY:O	2.10	0.52
1:D:68:LEU:HB3	1:D:96:ARG:CZ	2.40	0.52
1:D:99:ARG:NH1	1:D:325:GLU:OE1	2.42	0.52
1:A:132:GLU:OE1	1:A:137:GLY:HA3	2.09	0.52
1:B:49:VAL:O	1:B:71:ALA:HA	2.10	0.52
1:D:262:LYS:HB3	2:D:345:HOH:O	2.09	0.52
1:C:165:GLY:O	1:C:168:ILE:N	2.43	0.52
1:B:76:LYS:O	1:B:98:ILE:HA	2.10	0.52
1:C:85:ILE:CD1	1:C:90:LEU:HD11	2.39	0.52
1:B:91:ASP:HB2	2:B:430:HOH:O	2.10	0.52
1:C:9:VAL:HG11	1:C:313:LEU:HD21	1.92	0.52
1:D:132:GLU:HA	1:D:135:ASN:OD1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:VAL:HG12	1:A:55:LEU:HD13	1.92	0.52
1:C:8:LYS:HD3	1:C:51:GLY:C	2.30	0.52
1:A:23:LEU:HD11	1:A:56:LEU:CD1	2.40	0.52
1:A:93:ILE:O	1:A:98:ILE:HB	2.10	0.52
1:C:55:LEU:HD23	1:C:55:LEU:N	2.25	0.52
1:A:65:LYS:HG3	1:A:69:ASP:OD2	2.10	0.52
1:A:190:GLU:HB3	2:A:350:HOH:O	2.09	0.52
1:B:269:ASP:O	1:B:293:HIS:HA	2.10	0.52
1:C:114:LEU:HD22	1:C:295:GLY:CA	2.36	0.52
1:A:187:PRO:O	1:A:189:PRO:HD3	2.09	0.52
1:C:13:ARG:O	1:C:15:ILE:HG23	2.10	0.52
1:C:20:ARG:CZ	1:C:33:GLN:HE22	2.21	0.52
1:D:217:SER:O	1:D:219:THR:N	2.42	0.52
1:B:78:ILE:HG13	1:B:98:ILE:CG2	2.37	0.52
1:C:19:GLY:HA3	1:C:306:SER:O	2.10	0.52
1:D:6:LEU:HD13	1:D:30:GLU:HG2	1.92	0.52
1:C:101:GLY:CA	1:C:325:GLU:HA	2.38	0.52
1:A:236:GLU:HA	1:A:262:LYS:O	2.10	0.52
1:C:59:LEU:HD12	1:C:60:SER:N	2.24	0.52
1:D:32:GLU:O	1:D:33:GLN:HB2	2.09	0.52
1:D:93:ILE:HG12	1:D:98:ILE:HD12	1.91	0.52
1:B:83:VAL:HG23	1:B:104:PRO:HB3	1.92	0.52
1:A:100:VAL:CG1	1:A:326:LEU:HB3	2.40	0.52
1:B:40:ILE:HD13	1:B:45:LEU:HA	1.92	0.52
1:C:7:MSE:HE3	1:C:28:ASP:O	2.09	0.52
1:A:269:ASP:HA	1:A:291:LEU:HB2	1.92	0.52
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.37	0.52
1:C:71:ALA:O	1:C:72:GLY:O	2.28	0.52
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.45	0.52
1:D:59:LEU:O	1:D:59:LEU:HD12	2.10	0.52
1:D:280:HIS:ND1	1:D:281:PRO:HD2	2.24	0.52
1:A:9:VAL:CG2	1:A:317:LEU:HD21	2.40	0.52
1:A:59:LEU:HD11	1:A:82:SER:CB	2.39	0.52
1:A:159:ILE:HD12	1:A:214:VAL:HG22	1.90	0.52
1:B:81:MSE:CG	1:B:305:MSE:HB3	2.39	0.52
1:C:9:VAL:CG1	1:C:313:LEU:HD21	2.39	0.52
1:C:139:THR:O	1:D:275:PRO:HD3	2.10	0.52
1:D:282:LEU:CD2	1:D:285:LEU:HD12	2.38	0.52
1:A:17:ALA:HA	1:A:20:ARG:HB2	1.92	0.52
1:A:59:LEU:HA	1:A:87:HIS:CE1	2.45	0.52
1:A:155:THR:HA	1:A:179:ARG:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:VAL:O	1:B:325:GLU:HB2	2.09	0.52
1:C:11:VAL:HG12	1:C:12:THR:N	2.25	0.52
1:B:64:ASP:OD1	1:B:66:ARG:HB2	2.10	0.52
1:B:187:PRO:HG3	1:B:199:PHE:CE2	2.44	0.52
1:D:176:GLY:O	1:D:177:VAL:O	2.27	0.52
1:D:226:CYS:HA	1:D:230:PHE:CG	2.45	0.52
1:A:41:PRO:HD2	1:A:44:GLU:HG3	1.91	0.52
1:A:310:ALA:O	1:A:313:LEU:HB3	2.08	0.52
1:B:52:ALA:O	1:B:74:ASN:HB3	2.09	0.52
1:B:77:VAL:N	1:B:98:ILE:HG23	2.24	0.52
1:B:246:GLY:C	1:B:248:VAL:H	2.13	0.52
1:C:188:ARG:O	1:C:189:PRO:O	2.28	0.52
1:B:38:GLU:HB3	1:B:39:PRO:HD2	1.90	0.52
1:C:302:ARG:NH2	1:D:141:TRP:HZ2	2.08	0.52
1:A:179:ARG:NH2	2:A:412:HOH:O	2.41	0.52
1:B:14:ARG:NH2	2:B:401:HOH:O	2.41	0.52
1:B:283:LEU:HD23	1:B:290:ILE:HD12	1.92	0.52
1:C:187:PRO:HG3	1:C:199:PHE:CE1	2.44	0.52
1:A:35:ASP:O	1:A:36:SER:HB2	2.09	0.52
1:B:315:ALA:HB1	1:B:321:PRO:O	2.09	0.52
1:D:100:VAL:HB	1:D:326:LEU:HB3	1.91	0.52
1:A:144:LEU:HD21	2:B:439:HOH:O	2.08	0.52
1:D:49:VAL:HG12	1:D:55:LEU:HD13	1.92	0.52
1:A:11:VAL:HG13	1:A:56:LEU:HD22	1.92	0.52
1:A:81:MSE:SE	1:B:143:PRO:HB3	2.60	0.52
1:C:46:GLU:OE1	1:C:46:GLU:N	2.43	0.52
1:C:236:GLU:HG3	1:C:237:THR:N	2.24	0.52
1:C:204:GLU:OE2	1:C:208:GLN:NE2	2.42	0.52
1:A:187:PRO:HG3	1:A:199:PHE:CE2	2.44	0.52
1:C:39:PRO:HB3	1:C:60:SER:CB	2.39	0.52
1:A:140:SER:CB	1:B:39:PRO:HD3	2.40	0.52
1:B:17:ALA:HA	1:B:20:ARG:NE	2.16	0.52
1:A:147:CYS:HA	1:B:297:ALA:HB1	1.91	0.52
1:C:40:ILE:HG13	1:C:44:GLU:HB2	1.91	0.52
1:C:209:SER:HB2	1:C:212:ILE:HD11	1.92	0.52
1:C:219:THR:N	1:C:222:THR:OG1	2.43	0.52
1:D:15:ILE:CG1	1:D:20:ARG:HE	2.19	0.52
1:D:102:TYR:CG	1:D:104:PRO:HD3	2.45	0.52
1:B:204:GLU:O	1:B:208:GLN:HG2	2.09	0.52
1:C:11:VAL:HG12	1:C:12:THR:H	1.75	0.52
1:B:236:GLU:HA	1:B:263:ILE:HA	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:269:ASP:O	1:C:293:HIS:HA	2.10	0.52
1:D:19:GLY:O	1:D:22:ALA:HB3	2.09	0.52
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.91	0.52
1:A:68:LEU:HD13	1:A:92:GLU:OE1	2.10	0.52
1:A:79:SER:N	1:A:313:LEU:HD23	2.25	0.52
1:A:293:HIS:HB3	1:B:141:TRP:CD1	2.43	0.52
1:A:102:TYR:O	1:A:103:THR:HG23	2.10	0.52
1:B:315:ALA:CB	1:B:322:MSE:HG2	2.40	0.52
1:C:76:LYS:O	1:C:77:VAL:HB	2.10	0.52
1:C:276:LEU:CD2	1:C:290:ILE:HD13	2.40	0.52
1:A:232:GLN:HA	1:A:262:LYS:HD3	1.92	0.52
1:B:12:THR:HG23	1:B:57:CYS:HA	1.91	0.52
1:B:198:GLU:CD	1:B:200:VAL:HB	2.30	0.52
1:C:114:LEU:CD2	1:C:295:GLY:HA2	2.34	0.52
1:A:191:GLU:HG2	2:A:360:HOH:O	2.10	0.52
1:B:114:LEU:HD13	1:B:294:ILE:O	2.09	0.52
1:D:241:ILE:HG22	1:D:242:ASN:H	1.75	0.52
1:A:215:ALA:O	1:A:216:CYS:HB3	2.09	0.51
1:A:272:SER:HA	2:A:419:HOH:O	2.10	0.51
1:C:313:LEU:C	1:C:313:LEU:HD23	2.30	0.51
1:B:102:TYR:HE1	1:B:326:LEU:CB	2.09	0.51
1:B:325:GLU:HG3	1:B:326:LEU:H	1.75	0.51
1:D:41:PRO:HD2	1:D:44:GLU:HG3	1.91	0.51
1:A:74:ASN:ND2	2:A:406:HOH:O	2.43	0.51
1:A:236:GLU:HA	1:A:262:LYS:O	2.10	0.51
1:A:312:ASN:HA	1:A:322:MSE:HB3	1.91	0.51
1:D:10:PHE:HA	1:D:32:GLU:O	2.09	0.51
1:A:6:LEU:HD22	1:A:30:GLU:OE1	2.10	0.51
1:A:174:PRO:HB2	1:B:171:ARG:HA	1.91	0.51
1:A:182:TYR:CZ	1:A:199:PHE:HB2	2.45	0.51
1:C:49:VAL:O	1:C:71:ALA:HA	2.10	0.51
1:C:120:LEU:HB3	1:D:117:SER:OG	2.10	0.51
1:A:166:GLN:HB3	2:A:419:HOH:O	2.10	0.51
1:B:283:LEU:CD2	1:B:290:ILE:HD12	2.40	0.51
1:C:78:ILE:O	1:C:100:VAL:HG13	2.10	0.51
1:C:214:VAL:HG12	1:C:244:SER:HG	1.76	0.51
1:C:275:PRO:HD3	1:D:139:THR:O	2.10	0.51
1:A:147:CYS:HA	1:B:297:ALA:O	2.10	0.51
1:B:312:ASN:HD21	1:B:324:SER:HB3	1.76	0.51
1:D:13:ARG:HG3	1:D:36:SER:O	2.10	0.51
1:D:114:LEU:CD2	1:D:295:GLY:HA2	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:VAL:HG22	1:B:201:SER:H	1.72	0.51
1:B:202:THR:HB	1:B:203:PRO:HD3	1.93	0.51
1:A:227:ASN:CB	1:A:250:ASN:HD22	2.24	0.51
1:B:212:ILE:HG21	1:B:234:MSE:HE3	1.92	0.51
1:C:75:LEU:HD12	1:C:98:ILE:HD11	1.93	0.51
1:C:141:TRP:O	1:D:13:ARG:NH1	2.36	0.51
1:A:20:ARG:HE	1:A:21:VAL:HG22	1.76	0.51
1:A:162:GLY:O	1:A:166:GLN:NE2	2.43	0.51
1:A:275:PRO:HB3	1:B:138:TRP:CG	2.45	0.51
1:B:81:MSE:HE3	1:B:305:MSE:HE3	1.92	0.51
1:B:225:LEU:O	1:B:227:ASN:N	2.44	0.51
1:C:53:HIS:CE1	1:C:74:ASN:HD22	2.28	0.51
1:A:159:ILE:HG12	1:A:205:LEU:CD2	2.40	0.51
1:B:71:ALA:O	1:B:73:ALA:N	2.43	0.51
1:A:258:LEU:HD22	1:A:265:ALA:HA	1.92	0.51
1:B:10:PHE:CD2	1:B:49:VAL:HG12	2.43	0.51
1:B:114:LEU:CD1	1:B:294:ILE:HG13	2.40	0.51
1:C:114:LEU:CD2	1:C:295:GLY:HA2	2.34	0.51
1:C:121:THR:HG23	1:C:127:PRO:HD3	1.92	0.51
1:A:198:GLU:O	1:A:200:VAL:HG13	2.10	0.51
1:B:53:HIS:O	1:B:76:LYS:HG2	2.09	0.51
1:D:90:LEU:O	1:D:93:ILE:N	2.43	0.51
1:B:183:THR:HB	1:B:205:LEU:CD2	2.40	0.51
1:C:77:VAL:CG1	1:C:317:LEU:HD12	2.39	0.51
1:A:15:ILE:HD12	1:A:19:GLY:HA3	1.91	0.51
1:B:50:ALA:HA	1:B:70:ALA:O	2.11	0.51
1:B:283:LEU:CD2	1:B:290:ILE:HD12	2.40	0.51
1:A:45:LEU:HG	1:A:67:ILE:CD1	2.41	0.51
1:A:95:LYS:CA	2:A:351:HOH:O	2.59	0.51
1:A:322:MSE:SE	1:A:325:GLU:HG3	2.59	0.51
1:C:220:PRO:C	1:C:222:THR:H	2.13	0.51
1:A:25:ARG:O	1:A:27:ALA:N	2.43	0.51
1:B:135:ASN:O	1:B:137:GLY:N	2.43	0.51
1:C:185:ARG:H	1:C:185:ARG:HD2	1.76	0.51
1:A:164:ILE:O	1:A:168:ILE:HG13	2.11	0.51
1:C:212:ILE:HG13	1:C:234:MSE:SE	2.60	0.51
1:B:189:PRO:HG2	2:B:345:HOH:O	2.10	0.51
1:D:21:VAL:HG12	1:D:25:ARG:HD2	1.92	0.51
1:A:8:LYS:HD3	1:A:52:ALA:N	2.25	0.51
1:A:11:VAL:HG22	1:A:56:LEU:HD13	1.91	0.51
1:C:179:ARG:HG3	1:C:179:ARG:HH11	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ALA:O	1:A:75:LEU:HA	2.10	0.51
1:A:77:VAL:HG22	1:A:313:LEU:HA	1.92	0.51
1:B:10:PHE:CD2	1:B:12:THR:HG22	2.44	0.51
1:C:59:LEU:O	1:C:61:ASP:N	2.43	0.51
1:A:56:LEU:C	1:A:56:LEU:HD23	2.31	0.51
1:A:251:GLN:HG2	1:A:280:HIS:HE2	1.75	0.51
1:C:180:PHE:HB2	1:C:197:ALA:HA	1.93	0.51
1:B:57:CYS:O	1:B:81:MSE:N	2.43	0.51
1:B:170:ARG:NH2	2:B:405:HOH:O	2.42	0.51
1:A:74:ASN:O	1:A:75:LEU:C	2.48	0.51
1:C:256:GLN:HE22	1:C:262:LYS:NZ	2.09	0.51
1:D:182:TYR:N	1:D:205:LEU:HD12	2.25	0.51
1:D:200:VAL:CG2	1:D:205:LEU:HB2	2.41	0.51
1:D:276:LEU:HG	1:D:277:PRO:HD2	1.92	0.51
1:C:93:ILE:HD13	1:C:100:VAL:HG21	1.93	0.51
1:C:219:THR:OG1	1:C:222:THR:HG23	2.10	0.51
1:D:312:ASN:HD21	1:D:324:SER:HB2	1.75	0.51
1:B:228:LYS:HE2	1:B:232:GLN:NE2	2.25	0.51
1:D:190:GLU:HB2	1:D:191:GLU:OE2	2.10	0.51
1:B:179:ARG:HA	2:B:381:HOH:O	2.10	0.51
1:D:49:VAL:CG1	1:D:55:LEU:HD13	2.41	0.51
1:A:258:LEU:HB3	1:A:287:ASN:OD1	2.11	0.51
1:B:69:ASP:C	1:B:71:ALA:H	2.14	0.51
1:B:43:LYS:O	1:B:46:GLU:N	2.43	0.51
1:C:165:GLY:O	1:C:168:ILE:HB	2.10	0.51
1:D:54:GLY:C	1:D:313:LEU:HD11	2.31	0.51
1:A:6:LEU:N	1:A:6:LEU:HD12	2.25	0.51
1:C:10:PHE:HA	1:C:32:GLU:O	2.10	0.51
1:C:8:LYS:O	1:C:53:HIS:N	2.41	0.51
1:C:69:ASP:N	1:C:96:ARG:HH21	2.07	0.51
1:D:250:ASN:HB3	1:D:253:ASP:OD2	2.10	0.51
1:A:129:ALA:HB1	1:B:292:PRO:CD	2.41	0.51
1:C:59:LEU:HA	1:C:87:HIS:CE1	2.46	0.51
1:C:77:VAL:CA	1:C:98:ILE:HG23	2.41	0.51
1:A:320:GLU:HB3	1:A:321:PRO:HD2	1.91	0.51
1:B:63:VAL:HG22	1:B:67:ILE:HG21	1.92	0.51
1:C:63:VAL:HB	1:C:88:LEU:HD13	1.93	0.51
1:A:58:LEU:HD23	1:A:81:MSE:HB3	1.93	0.51
1:A:218:LEU:HB2	1:A:245:ARG:HG3	1.93	0.51
1:C:16:PRO:HB2	1:C:306:SER:CB	2.41	0.51
1:C:77:VAL:HG21	1:C:316:GLY:HA3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:LEU:HD21	1:D:126:LEU:HG	1.92	0.51
1:A:188:ARG:HD3	2:A:432:HOH:O	2.09	0.51
1:B:85:ILE:C	1:B:87:HIS:H	2.14	0.51
1:B:186:GLN:HG2	1:B:187:PRO:N	2.25	0.51
1:D:186:GLN:HG2	1:D:187:PRO:N	2.25	0.51
1:C:34:TRP:HA	1:C:34:TRP:CE3	2.45	0.51
1:C:249:VAL:HG12	1:C:249:VAL:O	2.11	0.51
1:D:142:LYS:HB2	1:D:145:TRP:CB	2.40	0.51
1:D:292:PRO:HG2	1:D:294:ILE:HG23	1.93	0.51
1:D:308:LEU:O	1:D:312:ASN:HB2	2.10	0.51
1:B:243:ILE:HD12	1:B:243:ILE:C	2.31	0.51
1:A:274:GLU:CD	1:A:293:HIS:HD1	2.14	0.51
1:B:101:GLY:HA2	1:B:325:GLU:CA	2.38	0.51
1:B:163:ARG:HH11	1:B:163:ARG:N	2.09	0.51
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.46	0.51
1:C:107:LEU:HD12	1:C:108:THR:N	2.26	0.51
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.92	0.51
1:C:269:ASP:O	1:C:293:HIS:HA	2.11	0.51
1:A:52:ALA:O	1:A:75:LEU:HA	2.10	0.51
1:C:230:PHE:C	1:C:232:GLN:H	2.14	0.51
1:A:208:GLN:HA	1:A:208:GLN:NE2	2.26	0.51
1:B:40:ILE:CG2	1:B:45:LEU:HD13	2.31	0.51
1:B:184:GLY:N	1:B:199:PHE:HE1	2.08	0.51
1:B:229:ASP:HA	1:B:232:GLN:NE2	2.25	0.51
1:D:64:ASP:HA	1:D:89:ALA:HB2	1.93	0.51
1:B:99:ARG:HB3	1:B:322:MSE:HE1	1.92	0.51
1:C:10:PHE:CZ	1:C:48:GLY:HA3	2.45	0.51
1:D:18:GLU:HG3	1:D:303:ASN:CA	2.40	0.51
1:D:214:VAL:HG12	1:D:244:SER:OG	2.10	0.51
1:A:218:LEU:HD11	1:A:247:ASP:HB2	1.93	0.51
1:A:270:VAL:HG12	1:A:293:HIS:CE1	2.46	0.51
1:B:167:ALA:O	1:B:171:ARG:HG3	2.10	0.51
1:B:200:VAL:HG13	1:B:204:GLU:HB2	1.92	0.51
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.93	0.51
1:C:152:THR:HG22	1:C:153:GLN:HG3	1.93	0.51
1:D:132:GLU:HA	1:D:135:ASN:OD1	2.11	0.51
1:D:318:ARG:O	1:D:320:GLU:N	2.44	0.51
1:B:59:LEU:HD23	1:B:82:SER:CB	2.41	0.51
1:C:92:GLU:O	1:C:95:LYS:HB2	2.11	0.51
1:A:80:THR:HG23	1:A:80:THR:O	2.10	0.51
1:A:292:PRO:HD2	1:B:129:ALA:HB1	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:121:THR:CG2	1:D:127:PRO:HD3	2.38	0.51
1:A:147:CYS:HA	1:B:297:ALA:HB1	1.93	0.51
1:B:283:LEU:CD2	1:B:290:ILE:HD12	2.40	0.51
1:A:56:LEU:CD2	1:A:309:ALA:HB1	2.38	0.51
1:A:280:HIS:HD1	1:A:282:LEU:HB2	1.75	0.51
1:B:85:ILE:HD13	1:B:326:LEU:CD2	2.40	0.51
1:B:186:GLN:HG3	1:B:187:PRO:HD2	1.92	0.51
1:B:9:VAL:HG21	1:B:317:LEU:HD21	1.92	0.51
1:A:18:GLU:HG3	1:A:303:ASN:O	2.10	0.51
1:B:224:GLY:H	1:B:248:VAL:HA	1.75	0.51
1:B:49:VAL:HG12	1:B:55:LEU:CD1	2.41	0.51
1:C:214:VAL:HG12	1:C:244:SER:OG	2.11	0.51
1:C:228:LYS:HE2	2:C:331:HOH:O	2.09	0.51
1:A:34:TRP:NE1	1:A:40:ILE:HB	2.25	0.51
1:D:163:ARG:CZ	1:D:166:GLN:OE1	2.59	0.51
1:B:257:ALA:HB1	1:B:262:LYS:HB2	1.92	0.51
1:B:317:LEU:HD22	1:B:317:LEU:N	2.24	0.51
1:C:108:THR:HG21	1:C:163:ARG:HD3	1.93	0.51
1:A:110:THR:O	1:A:113:GLU:HB3	2.10	0.51
1:D:7:MSE:HB3	1:D:53:HIS:HB2	1.92	0.51
1:B:72:GLY:C	1:B:74:ASN:H	2.14	0.51
1:D:90:LEU:HD23	1:D:93:ILE:HD12	1.93	0.51
1:D:301:THR:O	1:D:304:THR:N	2.44	0.51
1:A:51:GLY:HA2	1:A:74:ASN:HD22	1.76	0.51
1:A:83:VAL:HB	1:A:107:LEU:HD21	1.93	0.51
1:A:95:LYS:HD2	1:A:95:LYS:O	2.11	0.51
1:A:103:THR:CA	1:A:308:LEU:HD23	2.40	0.51
1:A:276:LEU:HG	1:A:277:PRO:HD2	1.93	0.51
1:B:13:ARG:HG2	1:B:14:ARG:N	2.25	0.51
1:D:8:LYS:HD3	1:D:52:ALA:CA	2.40	0.51
1:D:21:VAL:HG12	1:D:25:ARG:NE	2.25	0.51
1:D:110:THR:O	1:D:113:GLU:HB3	2.11	0.51
1:D:301:THR:HG22	1:D:305:MSE:SE	2.61	0.51
1:A:57:CYS:SG	1:A:87:HIS:NE2	2.83	0.51
1:A:63:VAL:N	1:A:87:HIS:O	2.43	0.51
1:A:175:PHE:CD1	1:B:171:ARG:HG2	2.46	0.51
1:B:9:VAL:O	1:B:31:VAL:HA	2.11	0.51
1:A:246:GLY:HA3	1:A:271:THR:O	2.11	0.51
1:A:114:LEU:HD22	1:A:294:ILE:O	2.10	0.51
1:A:159:ILE:HG23	1:A:183:THR:HG23	1.93	0.51
1:B:188:ARG:HD2	2:B:359:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:9:VAL:HG12	1:C:10:PHE:H	1.75	0.51
1:B:68:LEU:HD22	1:B:92:GLU:HB3	1.91	0.51
1:C:209:SER:HB2	1:C:212:ILE:HD11	1.93	0.51
1:D:250:ASN:HB3	1:D:253:ASP:HB2	1.92	0.51
1:D:276:LEU:O	1:D:277:PRO:C	2.49	0.51
1:A:39:PRO:HD3	1:B:140:SER:HB3	1.93	0.51
1:C:209:SER:HB2	1:C:212:ILE:HD11	1.93	0.51
1:D:20:ARG:HA	1:D:23:LEU:HD12	1.93	0.51
1:B:114:LEU:HD13	1:B:294:ILE:O	2.10	0.51
1:C:269:ASP:O	1:C:293:HIS:HA	2.11	0.51
1:D:64:ASP:HA	1:D:89:ALA:HB2	1.93	0.51
1:A:88:LEU:HB3	1:A:93:ILE:CD1	2.40	0.51
1:A:143:PRO:O	1:A:145:TRP:N	2.43	0.51
1:A:173:LYS:HB3	1:A:174:PRO:CD	2.35	0.51
1:B:19:GLY:HA2	1:B:307:LEU:HA	1.93	0.51
1:D:29:CYS:SG	1:D:317:LEU:HG	2.51	0.51
1:D:325:GLU:HG2	1:D:326:LEU:O	2.09	0.51
1:A:145:TRP:CZ2	1:A:146:LEU:HD12	2.46	0.51
1:B:80:THR:O	1:B:102:TYR:HA	2.11	0.51
1:B:243:ILE:HD12	1:B:243:ILE:C	2.31	0.51
1:C:11:VAL:HG13	1:C:56:LEU:HD22	1.93	0.51
1:C:14:ARG:O	1:C:15:ILE:O	2.29	0.51
1:D:260:SER:C	1:D:262:LYS:H	2.12	0.51
1:A:49:VAL:HG21	1:A:67:ILE:CG2	2.39	0.50
1:B:243:ILE:HD12	1:B:243:ILE:C	2.31	0.50
1:D:144:LEU:HD12	1:D:144:LEU:O	2.11	0.50
1:A:189:PRO:O	1:A:193:ALA:HB2	2.11	0.50
1:B:114:LEU:HD13	1:B:295:GLY:CA	2.41	0.50
1:B:180:PHE:HB2	2:B:382:HOH:O	2.11	0.50
1:B:79:SER:OG	2:B:429:HOH:O	2.20	0.50
1:C:63:VAL:HG13	1:C:67:ILE:HB	1.93	0.50
1:A:28:ASP:CG	1:A:318:ARG:HH21	2.15	0.50
1:C:205:LEU:HG	1:C:212:ILE:HD11	1.92	0.50
1:A:218:LEU:HB2	1:A:245:ARG:HG3	1.92	0.50
1:A:219:THR:HB	1:A:220:PRO:CD	2.40	0.50
1:A:292:PRO:HD2	1:B:129:ALA:HB1	1.92	0.50
1:C:291:LEU:HD21	1:D:126:LEU:HG	1.93	0.50
1:A:81:MSE:HG3	1:A:305:MSE:O	2.11	0.50
1:B:81:MSE:HA	1:B:103:THR:CG2	2.41	0.50
1:B:283:LEU:CD2	1:B:290:ILE:HD12	2.41	0.50
1:B:321:PRO:O	1:B:322:MSE:HB2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:ARG:NE	2:A:391:HOH:O	2.43	0.50
1:A:56:LEU:HG	1:A:79:SER:HB3	1.94	0.50
1:C:175:PHE:HA	1:D:171:ARG:NH1	2.25	0.50
1:C:209:SER:O	1:C:235:LYS:HD3	2.11	0.50
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.40	0.50
1:A:175:PHE:CD2	1:B:171:ARG:HD3	2.46	0.50
1:A:186:GLN:HB3	1:A:188:ARG:NH1	2.27	0.50
1:C:17:ALA:O	1:C:21:VAL:HG23	2.11	0.50
1:A:89:ALA:O	1:A:93:ILE:HG13	2.11	0.50
1:A:160:GLY:HA3	1:A:215:ALA:O	2.11	0.50
1:A:183:THR:HA	1:A:200:VAL:O	2.12	0.50
1:A:313:LEU:O	1:A:317:LEU:HG	2.11	0.50
1:B:8:LYS:HE3	1:B:32:GLU:HB2	1.94	0.50
1:C:9:VAL:HB	1:C:31:VAL:HA	1.93	0.50
1:A:46:GLU:CG	1:A:70:ALA:HB1	2.40	0.50
1:A:76:LYS:NZ	1:A:317:LEU:HA	2.26	0.50
1:A:82:SER:O	1:A:102:TYR:HB2	2.11	0.50
1:A:119:LEU:C	1:A:119:LEU:HD23	2.32	0.50
1:B:45:LEU:O	1:B:49:VAL:HG22	2.12	0.50
1:B:207:ALA:HA	1:B:233:LYS:O	2.11	0.50
1:C:202:THR:HB	1:C:203:PRO:CD	2.38	0.50
1:D:102:TYR:CZ	1:D:104:PRO:HG3	2.46	0.50
1:A:99:ARG:HH12	1:A:321:PRO:HA	1.76	0.50
1:B:189:PRO:O	1:B:190:GLU:C	2.49	0.50
1:C:131:GLU:HG3	1:C:135:ASN:ND2	2.26	0.50
1:D:190:GLU:OE2	1:D:191:GLU:N	2.44	0.50
1:A:103:THR:HG22	1:A:308:LEU:HG	1.92	0.50
1:D:189:PRO:O	1:D:192:ALA:HB3	2.11	0.50
1:B:23:LEU:CB	1:B:31:VAL:HG21	2.41	0.50
1:B:83:VAL:HG23	1:B:104:PRO:HA	1.93	0.50
1:B:188:ARG:N	1:B:189:PRO:CD	2.73	0.50
1:D:15:ILE:CB	1:D:81:MSE:HE1	2.37	0.50
1:D:177:VAL:HG11	1:D:180:PHE:CZ	2.45	0.50
1:B:103:THR:OG1	1:B:305:MSE:SE	2.79	0.50
1:A:129:ALA:HA	1:A:146:LEU:HD11	1.94	0.50
1:B:186:GLN:HG3	1:B:187:PRO:HD2	1.92	0.50
1:B:243:ILE:HD12	1:B:243:ILE:C	2.32	0.50
1:C:206:ALA:O	1:C:234:MSE:HA	2.11	0.50
1:C:227:ASN:O	1:C:230:PHE:HB3	2.10	0.50
1:A:119:LEU:C	1:A:119:LEU:HD23	2.32	0.50
1:A:276:LEU:HD11	1:A:280:HIS:CD2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:219:THR:H	1:C:222:THR:HG1	1.57	0.50
1:A:147:CYS:SG	1:B:298:THR:N	2.85	0.50
1:B:243:ILE:HD12	1:B:243:ILE:C	2.32	0.50
1:B:244:SER:O	1:B:245:ARG:HD3	2.11	0.50
1:B:103:THR:CB	1:B:308:LEU:HD23	2.41	0.50
1:B:310:ALA:C	1:B:312:ASN:H	2.13	0.50
1:A:56:LEU:C	1:A:56:LEU:HD23	2.32	0.50
1:B:106:VAL:HG11	1:B:308:LEU:HD22	1.94	0.50
1:C:18:GLU:CG	1:C:307:LEU:HB2	2.40	0.50
1:C:58:LEU:HD22	1:D:141:TRP:CZ3	2.45	0.50
1:D:83:VAL:HG12	1:D:107:LEU:HD21	1.92	0.50
1:B:302:ARG:NH2	2:B:364:HOH:O	2.43	0.50
1:C:89:ALA:C	1:C:91:ASP:H	2.14	0.50
1:A:114:LEU:HD23	1:A:295:GLY:HA2	1.94	0.50
1:A:181:LEU:HD23	1:A:198:GLU:HB2	1.93	0.50
1:A:292:PRO:HD2	1:B:129:ALA:HB1	1.93	0.50
1:B:289:VAL:HA	2:B:376:HOH:O	2.10	0.50
1:D:23:LEU:HB3	1:D:31:VAL:HG21	1.92	0.50
1:C:120:LEU:HB3	1:D:117:SER:OG	2.12	0.50
1:A:129:ALA:HB1	1:B:292:PRO:CD	2.41	0.50
1:A:188:ARG:HB3	1:A:191:GLU:HB2	1.93	0.50
1:D:56:LEU:HD23	1:D:57:CYS:N	2.26	0.50
1:A:236:GLU:C	1:A:238:ALA:H	2.15	0.50
1:B:103:THR:HA	1:B:308:LEU:CD2	2.41	0.50
1:B:23:LEU:HB3	1:B:31:VAL:HG21	1.94	0.50
1:B:77:VAL:HG11	1:B:313:LEU:O	2.10	0.50
1:B:226:CYS:HG	1:B:240:PHE:HZ	1.57	0.50
1:B:232:GLN:HB3	2:B:426:HOH:O	2.12	0.50
1:D:249:VAL:CG1	1:D:250:ASN:N	2.73	0.50
1:A:132:GLU:OE1	1:A:137:GLY:HA3	2.12	0.50
1:B:223:GLU:HA	1:B:247:ASP:O	2.12	0.50
1:C:17:ALA:O	1:C:20:ARG:N	2.44	0.50
1:D:137:GLY:O	1:D:139:THR:HG23	2.12	0.50
1:D:286:LYS:HD2	2:D:417:HOH:O	2.11	0.50
1:A:313:LEU:O	1:A:317:LEU:HG	2.11	0.50
1:B:85:ILE:HD12	1:B:90:LEU:HD22	1.94	0.50
1:A:119:LEU:C	1:A:119:LEU:HD23	2.32	0.50
1:B:285:LEU:HB2	1:B:288:CYS:HB3	1.93	0.50
1:D:76:LYS:C	1:D:98:ILE:HG23	2.31	0.50
1:A:91:ASP:HB2	2:A:346:HOH:O	2.12	0.50
1:C:53:HIS:CD2	1:C:74:ASN:HB3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:HIS:HE1	1:B:282:LEU:HG	1.76	0.50
1:C:20:ARG:CD	1:C:33:GLN:HE22	2.24	0.50
1:B:78:ILE:HD12	1:B:93:ILE:HD13	1.92	0.50
1:A:81:MSE:HG2	1:A:305:MSE:CE	2.42	0.50
1:B:7:MSE:HB3	1:B:53:HIS:ND1	2.27	0.50
1:C:10:PHE:HA	1:C:32:GLU:O	2.11	0.50
1:D:228:LYS:O	1:D:232:GLN:HB2	2.12	0.50
1:D:8:LYS:HA	1:D:30:GLU:HB3	1.94	0.50
1:B:26:ALA:C	1:B:28:ASP:H	2.15	0.50
1:C:131:GLU:HG3	1:C:135:ASN:ND2	2.26	0.50
1:D:7:MSE:HB3	1:D:53:HIS:CB	2.42	0.50
1:D:256:GLN:O	1:D:260:SER:N	2.44	0.50
1:B:246:GLY:C	1:B:248:VAL:H	2.14	0.50
1:C:72:GLY:C	1:C:74:ASN:H	2.15	0.50
1:C:120:LEU:HB3	1:D:117:SER:OG	2.12	0.50
1:A:153:GLN:NE2	1:A:178:GLN:NE2	2.59	0.50
1:A:232:GLN:NE2	1:A:262:LYS:HZ1	2.05	0.50
1:B:85:ILE:HD11	1:B:90:LEU:HD11	1.92	0.50
1:B:99:ARG:NH2	1:B:322:MSE:SE	2.94	0.50
1:C:14:ARG:HD3	1:C:35:ASP:OD1	2.11	0.50
1:D:206:ALA:O	1:D:234:MSE:HA	2.12	0.50
1:C:82:SER:O	1:C:103:THR:N	2.43	0.50
1:C:158:ILE:HG12	1:C:213:VAL:HB	1.93	0.50
1:D:76:LYS:CA	1:D:98:ILE:HG12	2.38	0.50
1:A:206:ALA:HB2	1:A:230:PHE:CE1	2.47	0.50
1:A:219:THR:O	1:A:221:ALA:N	2.45	0.50
1:A:80:THR:HG1	1:A:87:HIS:HE2	1.60	0.50
1:B:34:TRP:CE2	1:B:36:SER:HB3	2.47	0.50
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.93	0.50
1:A:7:MSE:SE	1:A:317:LEU:HD23	2.61	0.50
1:A:171:ARG:HH11	1:A:171:ARG:HG2	1.77	0.50
1:C:178:GLN:CD	2:C:387:HOH:O	2.49	0.50
1:D:271:THR:HG21	1:D:276:LEU:HD22	1.94	0.50
1:C:81:MSE:HG3	1:C:305:MSE:O	2.11	0.50
1:C:45:LEU:CD2	1:C:67:ILE:HD12	2.40	0.50
1:C:33:GLN:CG	1:C:34:TRP:N	2.75	0.50
1:C:53:HIS:HA	1:C:74:ASN:O	2.12	0.50
1:D:121:THR:CG2	1:D:127:PRO:HD3	2.40	0.50
1:B:183:THR:HA	1:B:199:PHE:CE1	2.47	0.50
1:B:12:THR:OG1	1:B:58:LEU:HG	2.12	0.50
1:C:38:GLU:HB3	1:C:39:PRO:HD2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:299:HIS:CE1	1:D:147:CYS:HB2	2.47	0.50
1:D:318:ARG:HG3	1:D:318:ARG:NH1	2.27	0.50
1:D:255:TYR:HE1	1:D:285:LEU:HD21	1.77	0.50
1:A:219:THR:HB	1:A:220:PRO:CD	2.42	0.50
1:B:40:ILE:HG23	1:B:45:LEU:HB2	1.93	0.50
1:A:121:THR:HG23	1:A:127:PRO:HD3	1.92	0.50
1:A:158:ILE:O	1:A:183:THR:HG22	2.11	0.50
1:B:10:PHE:HE2	1:B:12:THR:HG22	1.75	0.50
1:B:100:VAL:O	1:B:325:GLU:HB2	2.12	0.50
1:C:16:PRO:CD	1:C:81:MSE:HE1	2.42	0.50
1:B:14:ARG:HG3	1:B:20:ARG:HH11	1.77	0.50
1:B:153:GLN:HG2	2:B:338:HOH:O	2.11	0.50
1:B:301:THR:HG22	1:B:305:MSE:SE	2.62	0.50
1:C:312:ASN:O	1:C:322:MSE:HG2	2.12	0.50
1:A:104:PRO:HB2	2:A:378:HOH:O	2.10	0.50
1:B:121:THR:HG23	1:B:127:PRO:HD3	1.93	0.50
1:B:170:ARG:HH11	1:B:170:ARG:CB	2.11	0.50
1:C:76:LYS:HB3	1:C:76:LYS:HZ2	1.75	0.50
1:D:7:MSE:HE2	1:D:53:HIS:CB	2.41	0.50
1:A:16:PRO:HB2	1:A:306:SER:CB	2.42	0.50
1:B:180:PHE:O	1:B:197:ALA:HA	2.12	0.50
1:B:228:LYS:HE2	1:B:232:GLN:HE21	1.77	0.50
1:A:103:THR:HG22	1:A:308:LEU:HD23	1.94	0.50
1:C:132:GLU:HA	1:C:135:ASN:OD1	2.11	0.50
1:A:56:LEU:C	1:A:56:LEU:HD23	2.32	0.50
1:C:201:SER:OG	1:C:204:GLU:HG2	2.11	0.50
1:D:180:PHE:HB2	1:D:195:PHE:HB2	1.93	0.50
1:A:71:ALA:CB	2:A:419:HOH:O	2.60	0.50
1:D:142:LYS:HD2	1:D:145:TRP:CE3	2.47	0.50
1:B:312:ASN:HA	1:B:322:MSE:HB2	1.94	0.50
1:D:206:ALA:HA	1:D:212:ILE:HD11	1.94	0.50
1:D:318:ARG:HG2	2:D:373:HOH:O	2.11	0.50
1:B:249:VAL:CG1	1:B:250:ASN:H	2.25	0.50
1:A:120:LEU:HB3	1:B:117:SER:OG	2.12	0.50
1:B:251:GLN:NE2	1:B:272:SER:H	2.08	0.50
1:C:49:VAL:HG23	1:C:71:ALA:CB	2.42	0.50
1:A:164:ILE:O	1:A:168:ILE:HG13	2.12	0.50
1:A:190:GLU:C	1:A:191:GLU:HG3	2.32	0.50
1:A:219:THR:HB	1:A:220:PRO:HD2	1.93	0.50
1:C:10:PHE:HD1	1:C:32:GLU:HB3	1.77	0.50
1:C:34:TRP:HA	1:C:34:TRP:HE3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:222:THR:O	1:C:248:VAL:HG13	2.12	0.50
1:A:158:ILE:HG12	1:A:213:VAL:HB	1.94	0.50
1:D:255:TYR:HB3	1:D:256:GLN:OE1	2.12	0.50
1:B:53:HIS:HA	1:B:74:ASN:O	2.12	0.50
1:D:222:THR:O	1:D:248:VAL:HG22	2.12	0.50
1:B:63:VAL:HG11	1:B:78:ILE:HD13	1.93	0.49
1:C:322:MSE:HB3	1:C:325:GLU:HB2	1.94	0.49
1:D:180:PHE:CD2	1:D:195:PHE:HB3	2.46	0.49
1:A:15:ILE:HB	1:A:81:MSE:HE1	1.94	0.49
1:A:249:VAL:CG1	1:A:250:ASN:N	2.74	0.49
1:B:11:VAL:HG12	1:B:13:ARG:O	2.12	0.49
1:C:13:ARG:HD2	1:C:37:ASP:C	2.32	0.49
1:A:245:ARG:HG2	1:A:245:ARG:HH11	1.76	0.49
1:C:223:GLU:HA	1:C:248:VAL:HA	1.93	0.49
1:A:9:VAL:O	1:A:31:VAL:HA	2.12	0.49
1:B:315:ALA:HB3	1:B:322:MSE:HG3	1.93	0.49
1:B:318:ARG:O	1:B:320:GLU:HG3	2.12	0.49
1:A:283:LEU:HD22	1:B:134:LYS:HG2	1.94	0.49
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.47	0.49
1:D:322:MSE:SE	1:D:325:GLU:HB2	2.62	0.49
1:A:147:CYS:HA	1:B:297:ALA:O	2.12	0.49
1:A:183:THR:HG21	1:A:202:THR:OG1	2.12	0.49
1:A:257:ALA:HB1	1:A:262:LYS:HB3	1.94	0.49
1:B:79:SER:HB2	1:B:313:LEU:CA	2.42	0.49
1:C:257:ALA:HA	1:C:262:LYS:HD3	1.93	0.49
1:D:142:LYS:HB2	1:D:145:TRP:CB	2.42	0.49
1:D:227:ASN:O	1:D:230:PHE:HB3	2.12	0.49
1:B:13:ARG:HG2	1:B:14:ARG:N	2.27	0.49
1:B:194:GLU:HB2	2:B:394:HOH:O	2.11	0.49
1:B:269:ASP:O	1:B:293:HIS:HA	2.12	0.49
1:C:71:ALA:CB	1:C:75:LEU:HD22	2.42	0.49
1:D:14:ARG:NH1	1:D:35:ASP:OD2	2.45	0.49
1:D:201:SER:HB2	1:D:203:PRO:HD2	1.93	0.49
1:B:75:LEU:HG	1:B:98:ILE:HD13	1.94	0.49
1:B:126:LEU:N	1:B:126:LEU:CD1	2.74	0.49
1:C:163:ARG:NE	2:C:431:HOH:O	2.44	0.49
1:B:206:ALA:HA	1:B:212:ILE:HD11	1.93	0.49
1:C:58:LEU:HD21	1:C:81:MSE:HE3	1.93	0.49
1:A:103:THR:HA	1:A:308:LEU:CD2	2.42	0.49
1:A:159:ILE:HA	1:A:183:THR:CG2	2.41	0.49
1:D:23:LEU:HB3	1:D:31:VAL:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:VAL:O	1:A:78:ILE:HG13	2.11	0.49
1:D:121:THR:HA	1:D:126:LEU:HD13	1.94	0.49
1:D:214:VAL:HG12	1:D:244:SER:OG	2.11	0.49
1:B:56:LEU:HD23	1:B:56:LEU:C	2.32	0.49
1:B:118:LEU:HD21	1:B:267:GLY:C	2.32	0.49
1:B:301:THR:O	1:B:304:THR:HB	2.11	0.49
1:C:93:ILE:O	1:C:97:GLY:O	2.30	0.49
1:A:221:ALA:O	1:A:225:LEU:HD13	2.12	0.49
1:B:79:SER:HB2	1:B:313:LEU:CB	2.40	0.49
1:B:118:LEU:HD21	1:B:267:GLY:C	2.33	0.49
1:D:182:TYR:OH	1:D:188:ARG:N	2.45	0.49
1:C:131:GLU:HG3	1:C:135:ASN:ND2	2.27	0.49
1:D:90:LEU:C	1:D:92:GLU:N	2.64	0.49
1:A:188:ARG:HB3	1:A:191:GLU:OE2	2.11	0.49
1:A:206:ALA:O	1:A:234:MSE:HA	2.12	0.49
1:A:209:SER:HB2	1:A:212:ILE:CD1	2.43	0.49
1:A:239:VAL:HG22	1:A:265:ALA:HB3	1.94	0.49
1:A:114:LEU:CD1	1:A:295:GLY:HA2	2.41	0.49
1:B:80:THR:HG21	1:B:87:HIS:CE1	2.48	0.49
1:B:126:LEU:N	1:B:126:LEU:CD1	2.74	0.49
1:C:165:GLY:O	1:C:168:ILE:HB	2.11	0.49
1:C:209:SER:HB2	1:C:212:ILE:HD11	1.93	0.49
1:A:196:GLN:HA	2:A:339:HOH:O	2.11	0.49
1:C:61:ASP:O	1:C:63:VAL:HG23	2.11	0.49
1:B:212:ILE:CD1	1:B:234:MSE:HE3	2.43	0.49
1:A:103:THR:HG22	1:A:312:ASN:HD22	1.77	0.49
1:A:162:GLY:CA	1:A:166:GLN:HE22	2.26	0.49
1:A:142:LYS:HD3	2:A:337:HOH:O	2.11	0.49
1:B:110:THR:HG23	1:B:298:THR:HG23	1.95	0.49
1:B:126:LEU:N	1:B:126:LEU:CD1	2.74	0.49
1:C:76:LYS:HA	1:C:98:ILE:HG12	1.95	0.49
1:D:205:LEU:HD23	1:D:205:LEU:C	2.33	0.49
1:C:18:GLU:O	1:C:21:VAL:N	2.45	0.49
1:D:56:LEU:HD12	1:D:313:LEU:CD2	2.42	0.49
1:D:63:VAL:HG11	1:D:78:ILE:HD13	1.94	0.49
1:B:59:LEU:HA	1:B:87:HIS:CD2	2.47	0.49
1:D:153:GLN:C	1:D:178:GLN:HB2	2.32	0.49
1:B:168:ILE:HG22	1:B:172:LEU:HD12	1.94	0.49
1:C:89:ALA:HA	2:C:382:HOH:O	2.13	0.49
1:A:129:ALA:HB1	1:B:292:PRO:CD	2.42	0.49
1:C:85:ILE:HD12	1:C:326:LEU:HD21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:SER:HB2	1:D:39:PRO:HD3	1.95	0.49
1:D:95:LYS:CD	1:D:96:ARG:HG3	2.42	0.49
1:A:174:PRO:HB2	1:B:171:ARG:HA	1.94	0.49
1:B:312:ASN:O	1:B:322:MSE:HE3	2.13	0.49
1:C:228:LYS:HG2	1:C:232:GLN:OE1	2.12	0.49
1:A:81:MSE:HE1	1:B:143:PRO:HB3	1.94	0.49
1:B:56:LEU:HD23	1:B:57:CYS:N	2.27	0.49
1:C:39:PRO:HA	2:C:441:HOH:O	2.12	0.49
1:C:106:VAL:HG23	1:C:107:LEU:HG	1.94	0.49
1:D:160:GLY:HA3	1:D:215:ALA:O	2.12	0.49
1:D:164:ILE:O	1:D:168:ILE:HG13	2.12	0.49
1:A:218:LEU:HA	1:A:222:THR:HG21	1.92	0.49
1:B:121:THR:HG23	1:B:127:PRO:HD3	1.95	0.49
1:B:200:VAL:HG21	1:B:204:GLU:HB3	1.91	0.49
1:C:245:ARG:HG2	1:C:245:ARG:NH1	2.26	0.49
1:D:7:MSE:HG3	1:D:29:CYS:HA	1.95	0.49
1:A:114:LEU:HD23	1:A:295:GLY:HA2	1.94	0.49
1:A:193:ALA:O	1:A:196:GLN:N	2.45	0.49
1:C:100:VAL:O	1:C:326:LEU:HB3	2.12	0.49
1:D:152:THR:O	1:D:154:SER:N	2.45	0.49
1:A:181:LEU:HD22	1:A:200:VAL:HG13	1.93	0.49
1:D:214:VAL:HG11	1:D:248:VAL:HG11	1.94	0.49
1:D:184:GLY:C	1:D:185:ARG:HD3	2.33	0.49
1:D:11:VAL:HB	1:D:33:GLN:HG3	1.93	0.49
1:A:322:MSE:C	1:A:324:SER:H	2.16	0.49
1:B:126:LEU:N	1:B:126:LEU:CD1	2.74	0.49
1:C:129:ALA:HB1	1:D:292:PRO:HD2	1.94	0.49
1:A:132:GLU:OE1	1:A:137:GLY:HA3	2.12	0.49
1:D:218:LEU:HD13	1:D:247:ASP:HB2	1.95	0.49
1:A:81:MSE:HE1	1:B:143:PRO:CB	2.43	0.49
1:D:49:VAL:CG2	1:D:50:ALA:N	2.75	0.49
1:B:57:CYS:O	1:B:58:LEU:HD23	2.12	0.49
1:B:153:GLN:C	1:B:178:GLN:HE22	2.16	0.49
1:C:257:ALA:HB1	1:C:262:LYS:HB2	1.93	0.49
1:D:278:THR:C	1:D:280:HIS:H	2.15	0.49
1:A:156:VAL:HB	1:A:180:PHE:CE1	2.47	0.49
1:A:244:SER:O	1:A:245:ARG:HG2	2.13	0.49
1:A:257:ALA:CB	1:A:262:LYS:HB2	2.41	0.49
1:B:251:GLN:HE22	1:B:276:LEU:HD11	1.76	0.49
1:D:163:ARG:CZ	1:D:188:ARG:HH22	2.25	0.49
1:D:183:THR:HA	1:D:199:PHE:CE1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:218:LEU:HD13	1:C:248:VAL:HG22	1.95	0.49
1:D:183:THR:OG1	1:D:205:LEU:HD22	2.12	0.49
1:D:257:ALA:HA	1:D:260:SER:OG	2.13	0.49
1:A:142:LYS:HB2	1:A:145:TRP:HB3	1.94	0.49
1:A:187:PRO:O	1:A:188:ARG:HD2	2.12	0.49
1:C:63:VAL:HG12	1:C:67:ILE:HG21	1.93	0.49
1:D:34:TRP:NE1	1:D:36:SER:HB3	2.27	0.49
1:D:314:LEU:C	1:D:316:GLY:N	2.64	0.49
1:A:269:ASP:O	1:A:293:HIS:HA	2.13	0.49
1:A:292:PRO:HD2	1:B:129:ALA:HB1	1.93	0.49
1:B:76:LYS:C	1:B:98:ILE:HG23	2.33	0.49
1:B:200:VAL:HG13	1:B:201:SER:N	2.27	0.49
1:C:218:LEU:CD1	1:C:247:ASP:HB2	2.42	0.49
1:D:161:LEU:HD22	1:D:182:TYR:CG	2.47	0.49
1:A:103:THR:HB	1:A:308:LEU:HD23	1.95	0.49
1:B:269:ASP:O	1:B:293:HIS:HA	2.13	0.49
1:A:159:ILE:O	1:A:159:ILE:HG22	2.13	0.49
1:A:200:VAL:HG23	1:A:201:SER:N	2.27	0.49
1:D:13:ARG:NH2	1:D:58:LEU:HD12	2.28	0.49
1:D:192:ALA:O	1:D:195:PHE:N	2.42	0.49
1:A:78:ILE:HD12	1:A:93:ILE:HD13	1.94	0.49
1:A:101:GLY:HA3	1:A:312:ASN:HB3	1.94	0.49
1:B:139:THR:O	1:B:140:SER:HB3	2.12	0.49
1:B:204:GLU:OE1	1:B:204:GLU:HA	2.13	0.49
1:D:292:PRO:HG2	1:D:294:ILE:HG23	1.94	0.49
1:A:156:VAL:HB	1:A:180:PHE:CD1	2.48	0.49
1:D:16:PRO:HD2	1:D:81:MSE:HE1	1.95	0.49
1:D:219:THR:HB	1:D:220:PRO:HD2	1.93	0.49
1:D:251:GLN:HB3	1:D:280:HIS:NE2	2.27	0.49
1:A:228:LYS:O	1:A:228:LYS:HG2	2.12	0.49
1:B:131:GLU:OE2	1:B:135:ASN:HB3	2.12	0.49
1:C:203:PRO:HA	1:C:233:LYS:HD2	1.95	0.49
1:A:138:TRP:CZ3	1:B:276:LEU:HB2	2.48	0.49
1:A:219:THR:HB	1:A:220:PRO:HD2	1.93	0.49
1:B:68:LEU:O	1:B:71:ALA:HB3	2.13	0.49
1:D:132:GLU:OE1	1:D:137:GLY:HA3	2.12	0.49
1:A:141:TRP:CD1	1:B:59:LEU:HD21	2.47	0.49
1:B:234:MSE:HE2	1:B:238:ALA:HB3	1.94	0.49
1:C:8:LYS:HZ3	1:C:52:ALA:HB2	1.77	0.49
1:D:159:ILE:HD12	1:D:214:VAL:HG22	1.93	0.49
1:A:185:ARG:HD3	1:A:221:ALA:CB	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:LEU:HD21	1:B:267:GLY:C	2.32	0.49
1:C:224:GLY:O	1:C:227:ASN:ND2	2.46	0.49
1:B:15:ILE:HD12	1:B:306:SER:OG	2.12	0.49
1:C:190:GLU:O	1:C:193:ALA:HB3	2.13	0.49
1:D:188:ARG:O	1:D:192:ALA:HB2	2.12	0.49
1:A:132:GLU:HA	1:A:135:ASN:OD1	2.12	0.49
1:A:181:LEU:HD22	1:A:200:VAL:CG1	2.42	0.49
1:B:80:THR:HG22	1:B:82:SER:OG	2.13	0.49
1:C:218:LEU:HB2	1:C:245:ARG:CG	2.39	0.49
1:B:303:ASN:O	1:B:306:SER:HB3	2.12	0.49
1:C:68:LEU:O	1:C:71:ALA:HB3	2.13	0.49
1:D:99:ARG:NH1	1:D:322:MSE:HE3	2.27	0.49
1:A:155:THR:O	1:A:209:SER:HA	2.13	0.49
1:B:74:ASN:HB2	2:B:336:HOH:O	2.12	0.49
1:D:75:LEU:O	1:D:98:ILE:HG12	2.12	0.49
1:D:311:ASN:HB3	1:D:323:PRO:HG2	1.95	0.49
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.40	0.49
1:A:151:LEU:HG	1:A:211:PHE:CZ	2.48	0.49
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.47	0.49
1:A:41:PRO:CB	1:A:44:GLU:HG2	2.38	0.49
1:B:63:VAL:HB	1:B:88:LEU:HD23	1.94	0.49
1:B:81:MSE:HG2	1:B:305:MSE:SE	2.63	0.49
1:B:114:LEU:CD1	1:B:294:ILE:HG13	2.37	0.49
1:B:118:LEU:HD21	1:B:267:GLY:C	2.33	0.49
1:B:200:VAL:HG22	1:B:201:SER:N	2.28	0.49
1:B:308:LEU:O	1:B:312:ASN:HB2	2.13	0.49
1:A:161:LEU:HD21	1:A:191:GLU:HB2	1.95	0.49
1:B:323:PRO:O	1:B:324:SER:HB2	2.12	0.49
1:C:99:ARG:HH12	1:C:322:MSE:HG3	1.78	0.49
1:D:229:ASP:OD1	1:D:233:LYS:HE2	2.12	0.49
1:A:57:CYS:SG	1:A:80:THR:HB	2.53	0.49
1:A:103:THR:HG22	1:A:308:LEU:HB3	1.94	0.49
1:A:212:ILE:HG13	1:A:234:MSE:HE3	1.95	0.49
1:D:13:ARG:HG3	1:D:36:SER:O	2.13	0.49
1:D:202:THR:N	1:D:203:PRO:CD	2.75	0.49
1:B:104:PRO:O	1:B:105:ASP:HB2	2.12	0.49
1:B:201:SER:HB2	1:B:203:PRO:HD2	1.95	0.49
1:B:226:CYS:HB3	1:B:231:PHE:CZ	2.48	0.49
1:C:106:VAL:HA	2:C:436:HOH:O	2.12	0.49
1:C:120:LEU:HB3	1:D:117:SER:OG	2.13	0.49
1:D:10:PHE:HA	1:D:32:GLU:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:ALA:HB2	1:B:233:LYS:HB3	1.95	0.49
1:B:302:ARG:HD3	1:B:305:MSE:SE	2.63	0.49
1:A:219:THR:HB	1:A:220:PRO:HD2	1.95	0.49
1:A:302:ARG:HG3	1:B:147:CYS:SG	2.53	0.49
1:C:36:SER:HB2	2:C:410:HOH:O	2.13	0.49
1:A:79:SER:CB	1:A:313:LEU:HB2	2.43	0.49
1:A:114:LEU:HD12	1:B:124:ARG:NH2	2.27	0.49
1:B:300:ARG:HG3	2:B:441:HOH:O	2.11	0.49
1:D:93:ILE:HG23	1:D:98:ILE:HB	1.95	0.49
1:D:206:ALA:HB2	1:D:230:PHE:CE1	2.48	0.49
1:D:246:GLY:HA3	1:D:271:THR:C	2.33	0.49
1:A:14:ARG:CD	2:A:391:HOH:O	2.61	0.49
1:A:93:ILE:CG2	1:A:98:ILE:HB	2.39	0.49
1:C:8:LYS:HD3	1:C:52:ALA:HB2	1.95	0.49
1:D:234:MSE:HE1	1:D:240:PHE:CD1	2.47	0.49
1:C:269:ASP:O	1:C:293:HIS:HA	2.13	0.49
1:D:240:PHE:O	1:D:241:ILE:HD13	2.12	0.49
1:D:280:HIS:CE1	1:D:281:PRO:HD2	2.47	0.49
1:A:17:ALA:HA	1:A:20:ARG:NE	2.27	0.49
1:A:160:GLY:HA3	1:A:215:ALA:O	2.13	0.49
1:C:141:TRP:O	1:D:13:ARG:NH1	2.45	0.49
1:C:251:GLN:HB2	2:C:356:HOH:O	2.13	0.49
1:D:121:THR:CG2	1:D:127:PRO:HD3	2.41	0.49
1:A:235:LYS:C	1:A:237:THR:H	2.16	0.49
1:B:322:MSE:HE3	1:B:325:GLU:CB	2.43	0.49
1:C:99:ARG:HH21	1:C:316:GLY:HA2	1.76	0.49
1:C:100:VAL:HG12	1:C:101:GLY:N	2.27	0.49
1:C:102:TYR:CD1	1:C:102:TYR:N	2.81	0.49
1:A:172:LEU:HB2	1:A:180:PHE:CZ	2.48	0.49
1:C:165:GLY:O	1:C:168:ILE:N	2.46	0.49
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.48	0.49
1:C:325:GLU:HG2	1:C:326:LEU:H	1.78	0.49
1:A:55:LEU:H	1:A:313:LEU:HD21	1.77	0.49
1:A:77:VAL:CG2	1:A:313:LEU:HA	2.43	0.49
1:A:175:PHE:CD2	1:B:171:ARG:HD3	2.48	0.49
1:B:195:PHE:C	1:B:197:ALA:H	2.17	0.49
1:C:139:THR:O	1:C:140:SER:HB2	2.13	0.49
1:C:257:ALA:HB1	1:C:262:LYS:HB2	1.95	0.49
1:C:297:ALA:O	1:D:147:CYS:HA	2.13	0.49
1:D:167:ALA:CB	1:D:171:ARG:HH21	2.18	0.49
1:C:39:PRO:HG3	1:D:140:SER:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.31	0.49
1:A:61:ASP:O	1:A:87:HIS:HB2	2.13	0.49
1:A:188:ARG:N	1:A:189:PRO:CD	2.76	0.49
1:B:111:THR:HG21	1:B:164:ILE:HD13	1.95	0.49
1:C:81:MSE:CG	1:C:305:MSE:HG2	2.42	0.49
1:C:233:LYS:NZ	2:C:352:HOH:O	2.42	0.49
1:C:132:GLU:OE1	1:C:137:GLY:HA3	2.13	0.49
1:C:185:ARG:HD2	1:C:185:ARG:N	2.27	0.49
1:D:95:LYS:HD3	1:D:95:LYS:C	2.33	0.49
1:A:159:ILE:HG13	1:A:214:VAL:HA	1.94	0.49
1:B:40:ILE:HG23	1:B:40:ILE:O	2.12	0.49
1:A:129:ALA:HB1	1:B:292:PRO:CD	2.43	0.48
1:D:277:PRO:O	1:D:279:ASN:N	2.45	0.48
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.48	0.48
1:A:100:VAL:HG12	1:A:101:GLY:N	2.28	0.48
1:C:98:ILE:HD12	1:C:98:ILE:N	2.28	0.48
1:A:65:LYS:HE2	1:A:92:GLU:OE1	2.13	0.48
1:A:246:GLY:HA3	1:A:271:THR:C	2.33	0.48
1:B:51:GLY:HA2	2:B:336:HOH:O	2.13	0.48
1:B:283:LEU:HD23	1:B:290:ILE:HD12	1.95	0.48
1:B:118:LEU:HD13	1:B:291:LEU:CD1	2.43	0.48
1:C:120:LEU:HB3	1:D:117:SER:OG	2.13	0.48
1:A:161:LEU:O	1:A:166:GLN:NE2	2.45	0.48
1:A:308:LEU:O	1:A:312:ASN:N	2.46	0.48
1:B:7:MSE:HB2	1:B:29:CYS:SG	2.53	0.48
1:B:159:ILE:HB	1:B:214:VAL:HG13	1.95	0.48
1:C:157:GLY:O	1:C:212:ILE:HA	2.13	0.48
1:D:13:ARG:HA	1:D:34:TRP:O	2.13	0.48
1:D:46:GLU:HA	1:D:49:VAL:HG22	1.95	0.48
1:A:184:GLY:O	1:A:185:ARG:HB2	2.11	0.48
1:B:7:MSE:HG2	1:B:53:HIS:NE2	2.29	0.48
1:C:323:PRO:O	1:C:324:SER:CB	2.57	0.48
1:B:12:THR:OG1	1:B:57:CYS:HA	2.12	0.48
1:C:85:ILE:HD12	1:C:86:ASP:N	2.28	0.48
1:C:184:GLY:HA2	2:C:365:HOH:O	2.12	0.48
1:D:152:THR:C	1:D:154:SER:H	2.16	0.48
1:D:322:MSE:SE	1:D:325:GLU:HB2	2.64	0.48
1:A:81:MSE:CG	1:A:305:MSE:HB3	2.42	0.48
1:A:120:LEU:HB3	1:B:117:SER:OG	2.12	0.48
1:D:185:ARG:H	1:D:185:ARG:HD3	1.78	0.48
1:A:90:LEU:CA	1:A:93:ILE:HB	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:ALA:O	1:A:314:LEU:HD22	2.13	0.48
1:B:13:ARG:HG2	1:B:14:ARG:N	2.27	0.48
1:B:245:ARG:HB2	1:B:248:VAL:HG21	1.95	0.48
1:C:45:LEU:O	1:C:49:VAL:HG23	2.12	0.48
1:D:159:ILE:HG21	1:D:225:LEU:CD2	2.43	0.48
1:B:313:LEU:O	1:B:317:LEU:HD13	2.12	0.48
1:C:62:HIS:O	1:C:62:HIS:ND1	2.44	0.48
1:D:320:GLU:O	1:D:322:MSE:SE	2.81	0.48
1:A:12:THR:HG23	1:A:56:LEU:O	2.13	0.48
1:D:313:LEU:O	1:D:317:LEU:HD13	2.13	0.48
1:A:10:PHE:CE2	1:A:45:LEU:HD12	2.48	0.48
1:B:53:HIS:HA	1:B:74:ASN:O	2.12	0.48
1:D:121:THR:CG2	1:D:126:LEU:HB2	2.35	0.48
1:A:79:SER:CB	1:A:313:LEU:HB3	2.43	0.48
1:A:83:VAL:CG2	1:A:104:PRO:HB3	2.40	0.48
1:A:245:ARG:NH2	2:A:355:HOH:O	2.43	0.48
1:B:188:ARG:NH1	1:B:191:GLU:OE1	2.46	0.48
1:D:181:LEU:CD1	1:D:205:LEU:HA	2.40	0.48
1:A:159:ILE:HG21	1:A:216:CYS:HB3	1.95	0.48
1:A:196:GLN:O	1:A:198:GLU:OE1	2.31	0.48
1:B:182:TYR:CZ	1:B:192:ALA:HB2	2.48	0.48
1:B:269:ASP:O	1:B:293:HIS:HA	2.14	0.48
1:D:17:ALA:HB1	1:D:21:VAL:CG2	2.42	0.48
1:C:66:ARG:O	1:C:69:ASP:HB2	2.14	0.48
1:D:8:LYS:HZ2	1:D:52:ALA:HB2	1.79	0.48
1:D:56:LEU:HA	1:D:79:SER:O	2.13	0.48
1:D:159:ILE:HB	1:D:214:VAL:HG22	1.93	0.48
1:C:43:LYS:HB2	2:C:390:HOH:O	2.12	0.48
1:C:88:LEU:HB3	1:C:93:ILE:CD1	2.43	0.48
1:D:203:PRO:HB3	1:D:233:LYS:HZ3	1.76	0.48
1:A:49:VAL:HG12	1:A:55:LEU:CD1	2.40	0.48
1:A:93:ILE:HG23	1:A:98:ILE:HD12	1.96	0.48
1:D:318:ARG:NH1	2:D:388:HOH:O	2.46	0.48
1:A:147:CYS:HA	1:B:297:ALA:HB1	1.94	0.48
1:C:315:ALA:HB1	1:C:321:PRO:O	2.13	0.48
1:D:41:PRO:HB2	1:D:44:GLU:HG2	1.95	0.48
1:A:164:ILE:O	1:A:168:ILE:HG13	2.13	0.48
1:A:214:VAL:HG12	1:A:244:SER:OG	2.13	0.48
1:A:246:GLY:O	1:A:272:SER:HB3	2.14	0.48
1:C:48:GLY:C	1:C:50:ALA:H	2.16	0.48
1:D:102:TYR:CZ	1:D:326:LEU:HD12	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:GLU:O	1:D:200:VAL:HG13	2.13	0.48
1:A:17:ALA:HA	1:A:20:ARG:NE	2.28	0.48
1:B:312:ASN:OD1	1:B:324:SER:N	2.45	0.48
1:D:59:LEU:HA	1:D:87:HIS:CD2	2.48	0.48
1:C:59:LEU:HD12	1:C:59:LEU:C	2.34	0.48
1:C:160:GLY:HA3	1:C:216:CYS:HA	1.95	0.48
1:B:35:ASP:O	1:B:36:SER:CB	2.61	0.48
1:C:88:LEU:HD22	1:C:88:LEU:N	2.27	0.48
1:C:175:PHE:HA	1:D:171:ARG:NH1	2.28	0.48
1:A:87:HIS:CE1	1:A:88:LEU:HG	2.48	0.48
1:A:142:LYS:HB2	1:A:145:TRP:HB2	1.95	0.48
1:C:218:LEU:HD22	1:C:245:ARG:HG3	1.94	0.48
1:A:33:GLN:HG2	1:A:34:TRP:N	2.28	0.48
1:A:185:ARG:HD3	1:A:221:ALA:HB1	1.94	0.48
1:B:313:LEU:HD22	1:B:317:LEU:HD21	1.95	0.48
1:C:236:GLU:HA	1:C:262:LYS:O	2.12	0.48
1:C:93:ILE:CG2	1:C:94:LYS:N	2.76	0.48
1:C:315:ALA:HA	1:C:320:GLU:HG2	1.96	0.48
1:A:80:THR:OG1	1:A:87:HIS:NE2	2.44	0.48
1:A:175:PHE:CD2	1:B:171:ARG:HD3	2.48	0.48
1:C:41:PRO:HD2	1:C:44:GLU:HG3	1.95	0.48
1:B:15:ILE:HG13	1:B:20:ARG:HG3	1.95	0.48
1:C:120:LEU:HB3	1:D:117:SER:OG	2.14	0.48
1:D:9:VAL:CG1	1:D:313:LEU:HD21	2.43	0.48
1:D:92:GLU:OE2	1:D:96:ARG:NE	2.46	0.48
1:D:192:ALA:O	1:D:193:ALA:C	2.52	0.48
1:D:182:TYR:HA	1:D:205:LEU:HD12	1.96	0.48
1:A:132:GLU:OE1	1:A:137:GLY:HA3	2.13	0.48
1:B:224:GLY:H	1:B:248:VAL:CA	2.26	0.48
1:B:229:ASP:HA	1:B:232:GLN:HE21	1.78	0.48
1:C:312:ASN:O	1:C:322:MSE:HG2	2.13	0.48
1:A:175:PHE:CD2	1:B:171:ARG:HD3	2.48	0.48
1:B:110:THR:O	1:B:113:GLU:HB3	2.13	0.48
1:A:96:ARG:HB3	1:A:98:ILE:HG13	1.94	0.48
1:A:161:LEU:HD11	1:A:166:GLN:HG3	1.94	0.48
1:B:9:VAL:HB	1:B:30:GLU:O	2.14	0.48
1:C:95:LYS:HE3	1:C:96:ARG:HE	1.78	0.48
1:D:45:LEU:O	1:D:49:VAL:HG13	2.14	0.48
1:D:142:LYS:HB2	1:D:145:TRP:HB3	1.95	0.48
1:D:226:CYS:HB2	1:D:249:VAL:HA	1.95	0.48
1:B:206:ALA:HB2	1:B:230:PHE:CD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:ARG:HG3	1:A:14:ARG:H	1.79	0.48
1:A:153:GLN:HA	1:A:178:GLN:HB2	1.95	0.48
1:C:96:ARG:HG3	1:C:96:ARG:HH11	1.78	0.48
1:C:102:TYR:CE1	1:C:326:LEU:HD13	2.48	0.48
1:C:107:LEU:HD12	1:C:107:LEU:C	2.34	0.48
1:C:120:LEU:HB3	1:D:117:SER:OG	2.14	0.48
1:A:141:TRP:CD1	1:B:59:LEU:HD21	2.48	0.48
1:D:85:ILE:HB	1:D:88:LEU:HD12	1.96	0.48
1:D:228:LYS:HG3	1:D:229:ASP:N	2.28	0.48
1:A:20:ARG:HG3	2:A:369:HOH:O	2.13	0.48
1:A:271:THR:OG1	1:A:274:GLU:HG2	2.13	0.48
1:B:72:GLY:C	2:B:336:HOH:O	2.52	0.48
1:A:173:LYS:HG3	1:A:180:PHE:HE2	1.77	0.48
1:C:36:SER:HB2	2:C:409:HOH:O	2.13	0.48
1:D:99:ARG:NH2	1:D:320:GLU:O	2.44	0.48
1:A:10:PHE:HA	1:A:32:GLU:O	2.13	0.48
1:C:160:GLY:HA3	1:C:216:CYS:HA	1.95	0.48
1:D:218:LEU:HB2	1:D:245:ARG:CB	2.43	0.48
1:C:7:MSE:HE1	1:C:317:LEU:O	2.14	0.48
1:C:10:PHE:O	1:C:55:LEU:HD12	2.13	0.48
1:D:163:ARG:NH2	2:D:367:HOH:O	2.32	0.48
1:B:64:ASP:HA	1:B:93:ILE:HD11	1.95	0.48
1:B:68:LEU:HD22	1:B:75:LEU:HD23	1.96	0.48
1:B:236:GLU:HA	1:B:262:LYS:O	2.13	0.48
1:D:81:MSE:O	1:D:81:MSE:HG2	2.13	0.48
1:D:228:LYS:O	1:D:232:GLN:HG2	2.13	0.48
1:A:8:LYS:HD2	1:A:52:ALA:CB	2.43	0.48
1:A:187:PRO:HG3	1:A:199:PHE:CD2	2.48	0.48
1:B:208:GLN:O	1:B:235:LYS:HE3	2.13	0.48
1:A:142:LYS:HB2	1:A:145:TRP:HB3	1.96	0.48
1:B:218:LEU:HD12	1:B:222:THR:OG1	2.14	0.48
1:D:49:VAL:O	1:D:71:ALA:HA	2.13	0.48
1:D:64:ASP:HA	1:D:89:ALA:HB2	1.95	0.48
1:A:275:PRO:HD3	1:B:139:THR:O	2.12	0.48
1:B:101:GLY:HA3	1:B:322:MSE:SE	2.63	0.48
1:C:309:ALA:HA	2:C:361:HOH:O	2.13	0.48
1:A:192:ALA:HB1	1:A:197:ALA:HB3	1.96	0.48
1:B:297:ALA:HA	1:B:302:ARG:CZ	2.44	0.48
1:C:140:SER:OG	1:C:141:TRP:N	2.45	0.48
1:A:49:VAL:O	1:A:71:ALA:HA	2.13	0.48
1:A:179:ARG:NE	1:A:181:LEU:HD21	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.48	0.48
1:B:315:ALA:CB	1:B:322:MSE:HG2	2.43	0.48
1:C:104:PRO:O	1:C:106:VAL:N	2.40	0.48
1:D:205:LEU:HD21	1:D:212:ILE:HG12	1.96	0.48
1:A:204:GLU:HB2	1:D:204:GLU:OE2	2.13	0.48
1:C:291:LEU:CD2	1:D:126:LEU:HG	2.44	0.48
1:D:167:ALA:HA	1:D:170:ARG:NH1	2.28	0.48
1:A:114:LEU:HD22	1:A:294:ILE:C	2.33	0.48
1:C:181:LEU:CD2	1:C:198:GLU:HB3	2.44	0.48
1:D:65:LYS:HG2	1:D:69:ASP:OD2	2.13	0.48
1:D:227:ASN:OD1	1:D:229:ASP:N	2.47	0.48
1:A:58:LEU:C	1:A:60:SER:H	2.17	0.48
1:B:102:TYR:CE1	1:B:326:LEU:HD22	2.49	0.48
1:C:102:TYR:CD2	1:C:104:PRO:HD3	2.49	0.48
1:D:190:GLU:O	1:D:191:GLU:HB2	2.14	0.48
1:B:244:SER:O	1:B:245:ARG:HD3	2.13	0.48
1:D:250:ASN:OD1	1:D:252:ASP:HB2	2.13	0.48
1:A:83:VAL:HG23	1:A:104:PRO:HA	1.95	0.48
1:B:15:ILE:CB	1:B:81:MSE:HE1	2.43	0.48
1:B:81:MSE:SE	1:B:305:MSE:HE3	2.63	0.48
1:D:81:MSE:HG2	1:D:305:MSE:HG2	1.95	0.48
1:A:236:GLU:HA	1:A:262:LYS:O	2.13	0.48
1:C:70:ALA:C	1:C:72:GLY:N	2.65	0.48
1:A:6:LEU:HD23	1:A:30:GLU:HB2	1.95	0.48
1:B:80:THR:HG21	1:B:87:HIS:CE1	2.49	0.48
1:C:178:GLN:NE2	2:C:387:HOH:O	2.46	0.48
1:A:129:ALA:HB2	1:A:146:LEU:HD13	1.95	0.48
1:B:10:PHE:CE1	1:B:48:GLY:HA3	2.49	0.48
1:B:55:LEU:HD23	1:B:78:ILE:CG1	2.40	0.48
1:B:229:ASP:HB2	2:B:347:HOH:O	2.13	0.48
1:C:14:ARG:HG3	1:C:14:ARG:HH11	1.79	0.48
1:C:234:MSE:HE1	1:C:240:PHE:HB2	1.96	0.48
1:B:56:LEU:HD23	1:B:56:LEU:C	2.34	0.48
1:B:68:LEU:HB3	1:B:96:ARG:NH1	2.29	0.48
1:C:96:ARG:HB2	1:C:98:ILE:CD1	2.43	0.48
1:D:272:SER:HA	1:D:273:PRO:HA	1.70	0.48
1:A:51:GLY:CA	1:A:74:ASN:HD22	2.27	0.48
1:A:56:LEU:HD11	1:A:309:ALA:HB1	1.94	0.48
1:C:63:VAL:HA	1:C:67:ILE:HG13	1.95	0.48
1:C:65:LYS:O	1:C:69:ASP:N	2.47	0.48
1:A:7:MSE:SE	1:A:317:LEU:HD21	2.63	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:GLY:HA2	1:A:307:LEU:HA	1.96	0.48
1:B:322:MSE:SE	1:B:325:GLU:HG3	2.64	0.48
1:C:181:LEU:HD23	1:C:198:GLU:HB3	1.96	0.48
1:A:153:GLN:O	1:A:153:GLN:HG2	2.14	0.48
1:A:192:ALA:HB1	1:A:197:ALA:CB	2.41	0.48
1:C:56:LEU:HD11	1:C:309:ALA:HB1	1.96	0.48
1:D:158:ILE:HG22	1:D:159:ILE:N	2.29	0.48
1:D:179:ARG:HD2	2:D:396:HOH:O	2.13	0.48
1:D:185:ARG:HG2	1:D:186:GLN:H	1.78	0.48
1:B:179:ARG:NH1	1:B:208:GLN:HE22	2.12	0.48
1:C:280:HIS:CG	1:C:281:PRO:HD2	2.49	0.48
1:D:258:LEU:HD22	1:D:287:ASN:ND2	2.29	0.48
1:B:65:LYS:HB2	1:B:92:GLU:HG3	1.96	0.48
1:C:243:ILE:HD12	1:C:243:ILE:C	2.34	0.48
1:D:218:LEU:HD12	1:D:219:THR:H	1.79	0.48
1:D:262:LYS:HB3	2:D:346:HOH:O	2.12	0.48
1:C:296:SER:HB2	1:C:305:MSE:SE	2.63	0.48
1:D:59:LEU:C	1:D:59:LEU:HD12	2.34	0.48
1:D:322:MSE:HB2	1:D:325:GLU:HB2	1.96	0.48
1:A:99:ARG:HB3	1:A:322:MSE:CE	2.44	0.48
1:B:182:TYR:C	1:B:205:LEU:HD22	2.33	0.48
1:D:19:GLY:HA2	1:D:307:LEU:HA	1.96	0.48
1:A:280:HIS:CG	1:A:281:PRO:HD2	2.49	0.48
1:A:274:GLU:HB2	2:A:382:HOH:O	2.13	0.48
1:B:13:ARG:HH21	1:B:39:PRO:HA	1.78	0.48
1:B:26:ALA:O	1:B:28:ASP:N	2.46	0.48
1:C:23:LEU:C	1:C:25:ARG:H	2.16	0.48
1:C:317:LEU:C	1:C:319:GLY:H	2.17	0.48
1:A:23:LEU:O	1:A:31:VAL:HG21	2.14	0.48
1:B:8:LYS:HZ1	1:B:32:GLU:CB	2.25	0.48
1:C:120:LEU:HB3	1:D:117:SER:OG	2.14	0.48
1:B:153:GLN:HG2	2:B:340:HOH:O	2.13	0.48
1:C:40:ILE:HG12	1:C:44:GLU:HB2	1.96	0.48
1:D:131:GLU:CD	1:D:135:ASN:HD22	2.17	0.48
1:B:118:LEU:HD21	1:B:267:GLY:C	2.34	0.47
1:B:218:LEU:HD12	1:B:222:THR:OG1	2.14	0.47
1:D:255:TYR:O	1:D:259:ALA:N	2.47	0.47
1:A:251:GLN:NE2	1:A:280:HIS:NE2	2.61	0.47
1:A:12:THR:OG1	1:A:57:CYS:HA	2.13	0.47
1:C:6:LEU:HD12	1:C:6:LEU:N	2.29	0.47
1:C:62:HIS:O	1:C:64:ASP:OD1	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:PRO:O	1:D:193:ALA:HB2	2.13	0.47
1:B:118:LEU:HD21	1:B:267:GLY:C	2.34	0.47
1:C:53:HIS:NE2	1:C:74:ASN:HB3	2.29	0.47
1:B:86:ASP:HA	2:B:408:HOH:O	2.14	0.47
1:B:178:GLN:NE2	2:B:338:HOH:O	2.47	0.47
1:C:178:GLN:OE1	1:C:178:GLN:HA	2.14	0.47
1:A:14:ARG:HD3	2:A:391:HOH:O	2.13	0.47
1:A:181:LEU:HB2	1:A:205:LEU:CD1	2.35	0.47
1:A:194:GLU:HG2	1:A:195:PHE:CD1	2.49	0.47
1:C:276:LEU:O	1:C:277:PRO:C	2.51	0.47
1:A:240:PHE:O	1:A:241:ILE:HD13	2.13	0.47
1:B:13:ARG:HA	1:B:34:TRP:O	2.14	0.47
1:B:218:LEU:HB2	1:B:245:ARG:HB2	1.96	0.47
1:B:219:THR:OG1	1:B:222:THR:HG23	2.13	0.47
1:A:110:THR:O	1:A:113:GLU:HB3	2.13	0.47
1:A:154:SER:HA	1:A:210:ASP:OD2	2.14	0.47
1:B:103:THR:HG22	1:B:308:LEU:CG	2.43	0.47
1:B:110:THR:O	1:B:113:GLU:HB3	2.14	0.47
1:B:114:LEU:HD13	1:B:294:ILE:C	2.35	0.47
1:C:236:GLU:HA	1:C:263:ILE:HA	1.96	0.47
1:D:7:MSE:C	1:D:30:GLU:HB3	2.35	0.47
1:A:114:LEU:HD22	1:A:294:ILE:C	2.34	0.47
1:B:325:GLU:CG	1:B:326:LEU:N	2.74	0.47
1:C:183:THR:HB	1:C:200:VAL:O	2.14	0.47
1:D:11:VAL:HG21	1:D:23:LEU:CD1	2.42	0.47
1:A:188:ARG:HG2	1:A:191:GLU:OE2	2.13	0.47
1:B:40:ILE:CD1	1:B:45:LEU:HA	2.43	0.47
1:B:102:TYR:HE1	1:B:325:GLU:O	1.97	0.47
1:B:214:VAL:HG12	1:B:244:SER:HG	1.79	0.47
1:A:16:PRO:CA	1:B:144:LEU:HD11	2.44	0.47
1:C:14:ARG:NH2	2:C:373:HOH:O	2.47	0.47
1:C:322:MSE:HE3	1:C:325:GLU:HB2	1.96	0.47
1:D:114:LEU:CD2	1:D:295:GLY:HA2	2.40	0.47
1:C:198:GLU:HG2	1:C:199:PHE:N	2.29	0.47
1:D:212:ILE:HD12	1:D:234:MSE:CE	2.43	0.47
1:C:58:LEU:CD2	1:C:81:MSE:HB3	2.43	0.47
1:A:129:ALA:HB1	1:B:292:PRO:HD2	1.95	0.47
1:B:82:SER:HA	1:B:305:MSE:CE	2.44	0.47
2:C:333:HOH:O	1:D:133:VAL:HB	2.13	0.47
1:D:46:GLU:O	1:D:46:GLU:HG2	2.14	0.47
1:B:40:ILE:CG1	1:B:44:GLU:HB2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:68:LEU:HD21	1:C:78:ILE:CD1	2.44	0.47
1:B:131:GLU:OE2	1:B:135:ASN:HB3	2.14	0.47
1:D:18:GLU:HG3	1:D:303:ASN:HA	1.96	0.47
1:D:196:GLN:O	1:D:198:GLU:N	2.47	0.47
1:A:79:SER:OG	2:A:360:HOH:O	2.19	0.47
1:C:315:ALA:HB1	1:C:322:MSE:HA	1.96	0.47
1:B:312:ASN:HD21	1:B:324:SER:HB3	1.79	0.47
1:A:87:HIS:CG	1:A:88:LEU:H	2.32	0.47
1:D:155:THR:N	1:D:210:ASP:OD2	2.43	0.47
1:D:280:HIS:CG	1:D:281:PRO:HD2	2.49	0.47
1:D:202:THR:HB	1:D:203:PRO:HD3	1.96	0.47
1:A:312:ASN:O	1:A:322:MSE:HG2	2.14	0.47
1:B:11:VAL:HB	1:B:33:GLN:HG3	1.96	0.47
1:B:23:LEU:HD11	1:B:56:LEU:HD13	1.95	0.47
1:B:178:GLN:OE1	1:B:179:ARG:HB2	2.15	0.47
1:C:40:ILE:HG23	1:C:40:ILE:O	2.13	0.47
1:C:276:LEU:HD22	1:C:290:ILE:HG21	1.95	0.47
1:D:19:GLY:O	1:D:22:ALA:HB3	2.13	0.47
1:A:110:THR:O	1:A:113:GLU:HB3	2.13	0.47
1:C:114:LEU:HD11	1:C:294:ILE:HG13	1.96	0.47
1:D:314:LEU:O	1:D:315:ALA:C	2.52	0.47
1:A:76:LYS:HB2	2:A:416:HOH:O	2.14	0.47
1:A:292:PRO:HD2	1:B:129:ALA:HB1	1.95	0.47
1:C:228:LYS:CE	2:C:331:HOH:O	2.62	0.47
1:D:202:THR:HB	1:D:203:PRO:HD3	1.96	0.47
1:D:322:MSE:CG	1:D:325:GLU:HB2	2.44	0.47
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.49	0.47
1:A:322:MSE:SE	1:A:325:GLU:HB2	2.64	0.47
1:B:118:LEU:HD21	1:B:267:GLY:C	2.34	0.47
1:C:218:LEU:HD11	1:C:223:GLU:CB	2.44	0.47
1:B:269:ASP:O	1:B:293:HIS:HA	2.15	0.47
1:A:314:LEU:HD23	2:A:403:HOH:O	2.14	0.47
1:B:181:LEU:O	1:B:182:TYR:HB3	2.14	0.47
1:B:188:ARG:HB3	1:B:191:GLU:OE1	2.14	0.47
1:B:228:LYS:HE3	2:B:431:HOH:O	2.15	0.47
1:D:18:GLU:HG3	1:D:303:ASN:C	2.35	0.47
1:A:65:LYS:HG2	1:A:69:ASP:OD2	2.14	0.47
1:B:11:VAL:HG12	1:B:13:ARG:O	2.15	0.47
1:C:269:ASP:O	1:C:293:HIS:HA	2.14	0.47
1:D:162:GLY:O	1:D:166:GLN:HG3	2.14	0.47
1:A:188:ARG:HG2	1:A:191:GLU:OE2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:28:ASP:OD2	1:C:318:ARG:NH2	2.40	0.47
1:C:57:CYS:SG	1:C:80:THR:HB	2.55	0.47
1:D:164:ILE:HG22	1:D:168:ILE:CD1	2.44	0.47
1:D:218:LEU:HD22	1:D:245:ARG:CB	2.44	0.47
1:A:114:LEU:HD22	1:A:295:GLY:N	2.28	0.47
1:B:128:GLU:O	1:B:132:GLU:HG2	2.14	0.47
1:C:114:LEU:HD22	1:C:295:GLY:N	2.29	0.47
1:D:49:VAL:HG12	1:D:55:LEU:HD13	1.96	0.47
1:D:114:LEU:HG	1:D:114:LEU:O	2.14	0.47
1:D:219:THR:C	1:D:221:ALA:H	2.18	0.47
1:A:198:GLU:O	1:A:200:VAL:HG13	2.14	0.47
1:C:49:VAL:HG11	1:C:67:ILE:HG23	1.96	0.47
1:C:114:LEU:HD22	1:C:295:GLY:N	2.29	0.47
1:C:140:SER:OG	1:C:141:TRP:N	2.46	0.47
1:C:142:LYS:HB2	1:C:145:TRP:CB	2.45	0.47
1:D:257:ALA:HB1	1:D:263:ILE:HG23	1.95	0.47
1:A:114:LEU:HD22	1:A:294:ILE:O	2.14	0.47
1:C:6:LEU:CB	1:C:30:GLU:HG3	2.45	0.47
1:C:45:LEU:HD23	1:C:67:ILE:HD12	1.96	0.47
1:C:121:THR:HG23	1:C:127:PRO:HD3	1.97	0.47
1:C:205:LEU:CD2	1:C:212:ILE:HD12	2.45	0.47
1:A:52:ALA:O	1:A:75:LEU:CA	2.63	0.47
1:A:52:ALA:O	1:A:75:LEU:N	2.48	0.47
1:B:114:LEU:CD2	1:B:295:GLY:HA2	2.44	0.47
1:C:117:SER:OG	1:D:120:LEU:HB3	2.15	0.47
1:A:315:ALA:C	1:A:317:LEU:H	2.16	0.47
1:B:215:ALA:HB2	1:B:243:ILE:HD11	1.97	0.47
1:A:153:GLN:HE21	1:A:153:GLN:CA	2.15	0.47
1:B:229:ASP:HA	1:B:232:GLN:NE2	2.29	0.47
1:C:63:VAL:HG13	1:C:67:ILE:CG2	2.44	0.47
1:C:185:ARG:O	1:C:186:GLN:HG3	2.13	0.47
1:A:53:HIS:O	1:A:77:VAL:HG12	2.13	0.47
1:B:228:LYS:O	1:B:232:GLN:HG3	2.14	0.47
1:D:186:GLN:O	2:D:412:HOH:O	2.20	0.47
1:A:80:THR:CG2	1:A:102:TYR:HA	2.45	0.47
1:A:114:LEU:CD2	1:A:295:GLY:HA2	2.42	0.47
1:A:183:THR:HG21	1:A:202:THR:CG2	2.44	0.47
1:C:283:LEU:CD2	1:C:290:ILE:HD12	2.45	0.47
1:D:187:PRO:HA	1:D:199:PHE:CE1	2.49	0.47
1:C:55:LEU:O	1:C:78:ILE:HA	2.15	0.47
1:D:45:LEU:C	1:D:47:ARG:H	2.16	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:182:TYR:HE1	1:D:197:ALA:HB1	1.78	0.47
1:A:23:LEU:HD11	1:A:56:LEU:CD1	2.44	0.47
1:A:59:LEU:HA	1:A:87:HIS:CD2	2.50	0.47
1:A:114:LEU:HD21	1:A:294:ILE:HG13	1.95	0.47
1:A:149:TYR:HB3	2:A:335:HOH:O	2.15	0.47
1:C:202:THR:HB	1:C:203:PRO:CD	2.41	0.47
1:D:234:MSE:SE	1:D:263:ILE:HB	2.64	0.47
1:B:206:ALA:HA	1:B:212:ILE:HD11	1.95	0.47
1:C:139:THR:O	1:D:275:PRO:HD3	2.14	0.47
1:D:6:LEU:CB	1:D:30:GLU:HB2	2.41	0.47
1:D:13:ARG:CG	1:D:14:ARG:N	2.78	0.47
1:B:61:ASP:O	1:B:87:HIS:HB2	2.14	0.47
1:C:31:VAL:HG12	1:C:32:GLU:N	2.29	0.47
1:C:11:VAL:HG12	1:C:13:ARG:H	1.78	0.47
1:A:19:GLY:HA2	1:A:310:ALA:HB2	1.97	0.47
1:A:229:ASP:HB3	1:A:233:LYS:NZ	2.29	0.47
1:B:93:ILE:HG23	1:B:98:ILE:HB	1.96	0.47
1:C:12:THR:OG1	1:C:57:CYS:HA	2.14	0.47
1:D:81:MSE:HA	1:D:103:THR:CG2	2.44	0.47
1:D:104:PRO:O	1:D:105:ASP:HB2	2.14	0.47
1:D:168:ILE:HD13	1:D:213:VAL:HG11	1.96	0.47
1:B:114:LEU:CD2	1:B:295:GLY:HA2	2.44	0.47
1:C:315:ALA:HB3	1:C:322:MSE:CB	2.44	0.47
1:D:186:GLN:CD	2:D:408:HOH:O	2.52	0.47
1:A:95:LYS:C	1:A:97:GLY:H	2.18	0.47
1:B:195:PHE:CD2	1:B:195:PHE:N	2.82	0.47
1:D:181:LEU:CD1	1:D:205:LEU:HA	2.45	0.47
1:D:231:PHE:CZ	1:D:254:LEU:HD13	2.49	0.47
1:B:222:THR:C	1:B:225:LEU:HD23	2.34	0.47
1:D:7:MSE:HG3	1:D:7:MSE:O	2.15	0.47
1:D:320:GLU:HB3	1:D:321:PRO:HD2	1.97	0.47
1:B:232:GLN:HB3	2:B:430:HOH:O	2.13	0.47
1:C:228:LYS:HB2	1:C:253:ASP:OD1	2.15	0.47
1:D:16:PRO:CB	1:D:18:GLU:HG2	2.44	0.47
1:D:43:LYS:HB3	2:D:403:HOH:O	2.14	0.47
1:D:312:ASN:O	1:D:322:MSE:HE3	2.14	0.47
1:A:9:VAL:HG13	1:A:54:GLY:HA3	1.97	0.47
1:A:166:GLN:HB3	1:A:195:PHE:CE2	2.49	0.47
1:B:269:ASP:O	1:B:293:HIS:HA	2.15	0.47
1:C:19:GLY:HA2	1:C:307:LEU:HA	1.95	0.47
1:D:53:HIS:ND1	1:D:74:ASN:HB3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:140:SER:OG	1:D:141:TRP:N	2.47	0.47
1:D:187:PRO:O	1:D:188:ARG:HB2	2.14	0.47
1:A:21:VAL:O	1:A:25:ARG:HG3	2.15	0.47
1:A:114:LEU:HD12	1:B:124:ARG:NH2	2.29	0.47
1:B:118:LEU:HD21	1:B:267:GLY:C	2.34	0.47
1:B:159:ILE:HD12	1:B:214:VAL:HG22	1.95	0.47
1:B:192:ALA:O	1:B:196:GLN:N	2.48	0.47
1:C:88:LEU:CD1	1:C:100:VAL:HG11	2.44	0.47
1:D:13:ARG:CG	1:D:14:ARG:N	2.77	0.47
1:D:157:GLY:O	1:D:212:ILE:HA	2.15	0.47
1:D:317:LEU:HD22	1:D:317:LEU:H	1.78	0.47
1:A:159:ILE:HG12	1:A:183:THR:HG21	1.97	0.47
1:B:57:CYS:SG	1:B:87:HIS:HE1	2.38	0.47
1:C:140:SER:CB	1:D:39:PRO:HD3	2.44	0.47
1:D:132:GLU:HG3	1:D:146:LEU:HD11	1.97	0.47
1:D:200:VAL:CG2	1:D:205:LEU:HD12	2.45	0.47
1:A:12:THR:HG22	1:A:45:LEU:HD13	1.97	0.47
1:A:77:VAL:HG22	1:A:78:ILE:N	2.30	0.47
1:A:79:SER:H	1:A:313:LEU:HD23	1.80	0.47
1:A:244:SER:O	1:A:270:VAL:HG11	2.14	0.47
1:A:302:ARG:HA	1:A:305:MSE:CE	2.42	0.47
1:B:269:ASP:O	1:B:293:HIS:HA	2.15	0.47
1:C:59:LEU:CD1	1:C:82:SER:HB3	2.45	0.47
1:C:222:THR:O	1:C:248:VAL:HG22	2.14	0.47
1:B:68:LEU:O	1:B:71:ALA:N	2.47	0.47
1:B:131:GLU:OE1	1:B:134:LYS:HB2	2.14	0.47
1:B:235:LYS:HB2	1:B:238:ALA:HB2	1.96	0.47
1:C:15:ILE:HD12	1:C:81:MSE:CE	2.36	0.47
1:C:106:VAL:HG11	1:C:308:LEU:HD22	1.97	0.47
1:C:15:ILE:HB	1:C:81:MSE:HE1	1.97	0.47
1:C:42:ALA:O	1:C:46:GLU:N	2.38	0.47
1:D:183:THR:HG21	1:D:202:THR:OG1	2.14	0.47
1:A:13:ARG:HG3	1:A:14:ARG:N	2.29	0.47
1:A:23:LEU:HD11	1:A:56:LEU:HD12	1.95	0.47
1:A:57:CYS:C	1:A:58:LEU:HD23	2.35	0.47
1:A:142:LYS:HB2	1:A:145:TRP:HB3	1.96	0.47
1:A:154:SER:OG	1:A:177:VAL:HG22	2.15	0.47
1:A:239:VAL:HA	1:A:265:ALA:O	2.15	0.47
1:B:228:LYS:C	1:B:232:GLN:HG3	2.35	0.47
1:B:320:GLU:HB3	1:B:321:PRO:HD2	1.95	0.47
1:C:76:LYS:C	1:C:98:ILE:HG23	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:183:THR:HG22	1:D:200:VAL:O	2.13	0.47
1:D:320:GLU:HB3	1:D:321:PRO:HD2	1.97	0.47
1:B:65:LYS:HG2	1:B:92:GLU:HG3	1.97	0.47
1:A:231:PHE:CZ	1:A:254:LEU:HD13	2.50	0.47
1:A:314:LEU:HD22	1:A:314:LEU:H	1.80	0.47
1:C:232:GLN:OE1	1:C:232:GLN:HA	2.15	0.47
1:A:151:LEU:C	1:A:154:SER:HB3	2.35	0.47
1:A:281:PRO:C	1:A:283:LEU:H	2.18	0.47
1:B:68:LEU:HD23	1:B:75:LEU:HD22	1.97	0.47
1:C:102:TYR:HD1	1:C:102:TYR:H	1.61	0.47
1:C:218:LEU:HD11	1:C:223:GLU:HB2	1.97	0.47
1:D:13:ARG:CG	1:D:14:ARG:H	2.28	0.47
1:A:322:MSE:O	1:A:324:SER:N	2.47	0.47
1:B:190:GLU:C	1:B:192:ALA:H	2.18	0.47
1:B:297:ALA:N	1:B:302:ARG:NH2	2.62	0.47
1:C:11:VAL:HG13	1:C:56:LEU:O	2.14	0.47
1:B:53:HIS:O	1:B:76:LYS:HG2	2.13	0.47
1:B:55:LEU:C	1:B:55:LEU:HD23	2.35	0.47
1:C:243:ILE:HD12	1:C:243:ILE:C	2.35	0.47
1:D:49:VAL:HB	1:D:71:ALA:HB2	1.97	0.47
1:A:74:ASN:O	1:A:76:LYS:N	2.48	0.47
1:A:78:ILE:HG21	1:A:88:LEU:HD22	1.96	0.47
1:A:274:GLU:CD	1:A:293:HIS:HD1	2.18	0.47
1:C:65:LYS:CG	1:C:96:ARG:HH22	2.28	0.47
1:C:76:LYS:HG3	1:C:317:LEU:HA	1.96	0.47
1:C:92:GLU:O	1:C:93:ILE:C	2.53	0.47
1:D:230:PHE:O	1:D:234:MSE:HG3	2.15	0.47
1:B:85:ILE:O	1:B:88:LEU:N	2.41	0.47
1:C:61:ASP:O	1:C:87:HIS:HB2	2.14	0.47
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.44	0.47
1:A:216:CYS:SG	1:A:248:VAL:HG21	2.54	0.47
1:C:257:ALA:CA	1:C:262:LYS:HD2	2.41	0.47
1:B:114:LEU:CD2	1:B:295:GLY:HA2	2.45	0.47
1:B:181:LEU:HD23	1:B:198:GLU:HB3	1.96	0.47
1:C:205:LEU:HD23	1:C:212:ILE:HD12	1.96	0.47
1:D:15:ILE:HB	1:D:81:MSE:HE1	1.97	0.47
1:A:26:ALA:HB2	1:A:314:LEU:CD1	2.44	0.47
1:A:222:THR:CA	1:A:225:LEU:HD13	2.36	0.47
1:C:94:LYS:HE3	1:C:94:LYS:CA	2.45	0.47
1:C:257:ALA:CA	1:C:262:LYS:HD2	2.39	0.47
1:A:180:PHE:O	1:A:197:ALA:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:VAL:CG2	1:B:201:SER:H	2.27	0.47
1:D:155:THR:HG22	1:D:209:SER:HA	1.97	0.47
1:A:87:HIS:CG	1:A:88:LEU:N	2.83	0.47
1:B:99:ARG:NH1	1:B:325:GLU:OE2	2.48	0.47
1:D:59:LEU:C	1:D:59:LEU:HD12	2.35	0.47
1:A:181:LEU:HB2	1:A:205:LEU:HD12	1.97	0.47
1:A:312:ASN:C	1:A:322:MSE:HE3	2.36	0.47
1:A:322:MSE:HB3	1:A:323:PRO:HD2	1.96	0.47
1:C:49:VAL:HG12	1:C:55:LEU:HB2	1.97	0.47
1:C:84:GLY:O	1:C:87:HIS:HE1	1.98	0.47
1:C:109:ASP:CG	2:C:345:HOH:O	2.53	0.47
1:D:23:LEU:HD11	1:D:56:LEU:CD1	2.45	0.47
1:D:182:TYR:HE2	1:D:188:ARG:HB3	1.78	0.47
1:A:42:ALA:HA	1:A:45:LEU:HB3	1.97	0.47
1:D:16:PRO:HB3	1:D:303:ASN:OD1	2.14	0.47
1:A:155:THR:CG2	1:A:209:SER:HA	2.42	0.47
1:A:185:ARG:H	1:A:188:ARG:HH22	1.63	0.47
1:B:49:VAL:HG23	1:B:49:VAL:O	2.14	0.47
1:B:121:THR:HG23	1:B:127:PRO:HD3	1.97	0.47
1:C:233:LYS:NZ	2:C:352:HOH:O	2.43	0.47
1:D:68:LEU:HB3	1:D:96:ARG:NE	2.28	0.47
1:C:13:ARG:NE	2:C:442:HOH:O	2.34	0.47
1:C:21:VAL:HA	1:C:24:ALA:HB3	1.96	0.47
1:C:53:HIS:O	1:C:75:LEU:HA	2.15	0.47
1:C:114:LEU:HD22	1:C:295:GLY:N	2.30	0.47
1:C:187:PRO:C	1:C:189:PRO:HD3	2.35	0.47
1:B:188:ARG:HG2	2:B:433:HOH:O	2.14	0.47
1:D:7:MSE:HE2	1:D:28:ASP:O	2.15	0.47
1:A:302:ARG:HD3	1:A:305:MSE:SE	2.65	0.47
1:B:167:ALA:CB	1:B:171:ARG:HH21	2.22	0.47
1:D:228:LYS:HB2	1:D:253:ASP:CG	2.35	0.47
1:A:110:THR:O	1:A:113:GLU:HB3	2.14	0.47
1:B:322:MSE:CB	1:B:325:GLU:HB3	2.45	0.47
1:D:218:LEU:CB	1:D:245:ARG:HG3	2.45	0.47
1:A:138:TRP:CZ2	1:B:274:GLU:HG2	2.50	0.47
1:B:76:LYS:CG	1:B:77:VAL:HG12	2.45	0.47
1:C:121:THR:HG23	1:C:127:PRO:HD3	1.96	0.47
1:A:68:LEU:O	1:A:96:ARG:NH1	2.48	0.47
1:A:183:THR:H	1:A:205:LEU:HD22	1.80	0.47
1:B:66:ARG:O	1:B:67:ILE:C	2.53	0.47
1:C:235:LYS:HA	2:C:395:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:LEU:O	1:D:114:LEU:HD23	2.15	0.47
1:C:15:ILE:HD12	1:C:81:MSE:HE1	1.96	0.47
1:C:23:LEU:CD2	1:C:313:LEU:HD23	2.36	0.47
1:D:203:PRO:HA	1:D:233:LYS:HZ1	1.80	0.47
1:B:91:ASP:N	1:B:91:ASP:OD1	2.48	0.47
1:C:256:GLN:NE2	2:C:408:HOH:O	2.45	0.47
1:D:186:GLN:CG	1:D:187:PRO:N	2.78	0.47
1:C:34:TRP:CD1	1:C:40:ILE:HB	2.49	0.46
1:D:227:ASN:N	1:D:230:PHE:HB3	2.30	0.46
1:A:175:PHE:CG	1:B:171:ARG:HD3	2.51	0.46
1:B:8:LYS:HB3	1:B:52:ALA:CB	2.45	0.46
1:A:186:GLN:N	1:A:199:PHE:CZ	2.83	0.46
1:C:107:LEU:HD12	1:C:107:LEU:C	2.35	0.46
1:A:78:ILE:HB	1:A:99:ARG:O	2.13	0.46
1:B:190:GLU:O	1:B:192:ALA:N	2.48	0.46
1:A:68:LEU:HD13	1:A:92:GLU:HG3	1.97	0.46
1:B:13:ARG:NH2	1:B:39:PRO:HA	2.30	0.46
1:B:109:ASP:HA	1:B:171:ARG:NH2	2.30	0.46
1:A:17:ALA:C	1:A:19:GLY:H	2.19	0.46
1:A:29:CYS:SG	1:A:314:LEU:HD13	2.55	0.46
1:A:254:LEU:O	1:A:258:LEU:HG	2.14	0.46
1:C:219:THR:N	1:C:222:THR:OG1	2.41	0.46
1:A:99:ARG:HB3	1:A:322:MSE:SE	2.65	0.46
1:A:227:ASN:C	1:A:227:ASN:ND2	2.69	0.46
1:A:320:GLU:HB3	1:A:321:PRO:CD	2.39	0.46
1:C:87:HIS:CE1	1:C:88:LEU:HG	2.50	0.46
1:A:21:VAL:O	1:A:24:ALA:N	2.49	0.46
1:A:43:LYS:HD3	1:A:44:GLU:OE2	2.15	0.46
1:C:16:PRO:HG3	1:D:144:LEU:CD1	2.45	0.46
1:B:202:THR:N	1:B:203:PRO:CD	2.77	0.46
1:C:75:LEU:O	1:C:76:LYS:HB3	2.14	0.46
1:B:92:GLU:OE2	1:B:96:ARG:CZ	2.63	0.46
1:A:204:GLU:HG3	1:D:204:GLU:CD	2.36	0.46
1:D:18:GLU:HB3	1:D:307:LEU:HB2	1.97	0.46
1:A:211:PHE:CD2	1:A:239:VAL:HB	2.50	0.46
1:B:13:ARG:HD3	1:B:38:GLU:O	2.15	0.46
1:B:23:LEU:HD11	1:B:56:LEU:HD12	1.96	0.46
1:B:92:GLU:HB2	2:B:429:HOH:O	2.15	0.46
1:B:103:THR:HA	1:B:308:LEU:HD21	1.96	0.46
1:B:167:ALA:CA	1:B:170:ARG:HH12	2.06	0.46
1:B:289:VAL:HA	2:B:374:HOH:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:PRO:HA	1:D:144:LEU:HD21	1.96	0.46
1:C:103:THR:HB	1:C:106:VAL:HG21	1.96	0.46
1:A:227:ASN:C	1:A:227:ASN:HD22	2.17	0.46
1:B:106:VAL:HB	1:B:304:THR:CG2	2.42	0.46
1:B:313:LEU:O	1:B:315:ALA:N	2.45	0.46
1:C:102:TYR:CD1	1:C:102:TYR:N	2.83	0.46
1:C:291:LEU:HD11	1:D:126:LEU:HG	1.97	0.46
1:B:105:ASP:O	1:B:106:VAL:C	2.54	0.46
1:C:242:ASN:HD21	1:C:248:VAL:HB	1.79	0.46
1:A:103:THR:CB	1:A:308:LEU:HD23	2.46	0.46
1:B:22:ALA:O	1:B:25:ARG:N	2.47	0.46
1:C:144:LEU:CD2	1:D:16:PRO:HG3	2.45	0.46
1:A:164:ILE:O	1:A:164:ILE:CG2	2.62	0.46
1:B:178:GLN:O	1:B:178:GLN:HG2	2.15	0.46
1:C:143:PRO:O	1:D:302:ARG:HG2	2.15	0.46
1:B:103:THR:HA	1:B:308:LEU:CD2	2.44	0.46
1:B:224:GLY:H	1:B:248:VAL:C	2.19	0.46
1:B:85:ILE:C	1:B:87:HIS:H	2.19	0.46
1:C:182:TYR:O	1:C:199:PHE:HA	2.14	0.46
1:D:49:VAL:HG12	1:D:55:LEU:HD13	1.97	0.46
1:D:280:HIS:CE1	1:D:281:PRO:HD2	2.50	0.46
1:B:313:LEU:O	1:B:317:LEU:HD22	2.16	0.46
1:C:269:ASP:O	1:C:293:HIS:HA	2.14	0.46
1:D:65:LYS:HD3	1:D:92:GLU:OE2	2.16	0.46
1:B:236:GLU:HG2	1:B:262:LYS:O	2.15	0.46
1:C:188:ARG:N	1:C:189:PRO:CD	2.79	0.46
1:C:234:MSE:SE	1:C:263:ILE:HG21	2.65	0.46
1:D:142:LYS:HB2	1:D:145:TRP:HB2	1.98	0.46
1:A:49:VAL:HB	1:A:71:ALA:HB2	1.96	0.46
1:C:121:THR:HG1	1:D:121:THR:HG1	1.60	0.46
1:B:236:GLU:HA	1:B:262:LYS:O	2.15	0.46
1:C:56:LEU:HB2	1:C:313:LEU:HD13	1.97	0.46
1:C:121:THR:HG1	1:D:121:THR:HG1	1.61	0.46
1:D:22:ALA:C	1:D:24:ALA:N	2.69	0.46
1:D:161:LEU:CD2	1:D:188:ARG:HB2	2.46	0.46
1:D:274:GLU:HA	1:D:275:PRO:C	2.36	0.46
1:B:74:ASN:N	2:B:336:HOH:O	2.38	0.46
1:B:166:GLN:OE1	1:B:191:GLU:HG2	2.16	0.46
1:B:246:GLY:O	1:B:248:VAL:N	2.48	0.46
1:C:223:GLU:HG2	1:C:247:ASP:HB3	1.96	0.46
1:D:78:ILE:HG13	1:D:98:ILE:CG2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:158:ILE:HG22	1:D:159:ILE:N	2.30	0.46
1:D:312:ASN:O	1:D:314:LEU:N	2.48	0.46
1:B:35:ASP:O	1:B:36:SER:CB	2.57	0.46
1:B:204:GLU:OE1	1:B:204:GLU:HA	2.15	0.46
1:D:78:ILE:O	1:D:100:VAL:HA	2.15	0.46
1:D:125:ARG:NH1	1:D:146:LEU:HA	2.30	0.46
1:A:151:LEU:N	1:A:151:LEU:CD1	2.76	0.46
1:A:314:LEU:O	1:A:318:ARG:NH1	2.49	0.46
1:B:261:GLY:HA2	2:B:375:HOH:O	2.15	0.46
1:C:114:LEU:HD22	1:C:295:GLY:N	2.30	0.46
1:D:16:PRO:C	1:D:18:GLU:H	2.18	0.46
1:A:188:ARG:NH1	2:A:436:HOH:O	2.48	0.46
1:A:214:VAL:HG11	1:A:248:VAL:HG11	1.97	0.46
1:C:175:PHE:HA	1:D:171:ARG:NH1	2.30	0.46
1:D:179:ARG:HA	2:D:348:HOH:O	2.15	0.46
1:D:212:ILE:CD1	1:D:234:MSE:HE3	2.40	0.46
1:B:163:ARG:N	1:B:163:ARG:NH1	2.64	0.46
1:D:187:PRO:HG3	1:D:199:PHE:CG	2.50	0.46
1:B:162:GLY:O	1:B:166:GLN:HG3	2.15	0.46
1:B:65:LYS:HE3	1:B:92:GLU:CD	2.36	0.46
1:B:181:LEU:HB2	1:B:205:LEU:CD1	2.45	0.46
1:A:77:VAL:HG13	1:A:77:VAL:O	2.15	0.46
1:A:155:THR:HG23	1:A:179:ARG:O	2.15	0.46
1:B:95:LYS:C	1:B:97:GLY:H	2.18	0.46
1:B:173:LYS:HB3	1:B:174:PRO:CD	2.46	0.46
1:B:203:PRO:HB3	1:B:233:LYS:HE2	1.98	0.46
1:A:9:VAL:HA	1:A:54:GLY:O	2.16	0.46
1:B:167:ALA:CB	1:B:171:ARG:HH21	2.23	0.46
1:B:201:SER:O	1:B:202:THR:C	2.52	0.46
1:C:219:THR:HB	1:C:220:PRO:CD	2.44	0.46
1:C:251:GLN:NE2	2:C:341:HOH:O	2.48	0.46
1:A:39:PRO:HD3	1:B:140:SER:HB3	1.96	0.46
1:C:280:HIS:HE1	1:C:282:LEU:HG	1.80	0.46
1:D:7:MSE:O	1:D:30:GLU:HB2	2.15	0.46
1:D:203:PRO:HA	1:D:233:LYS:NZ	2.30	0.46
1:D:234:MSE:SE	1:D:263:ILE:HG21	2.66	0.46
1:D:234:MSE:HE2	1:D:238:ALA:CB	2.45	0.46
1:D:280:HIS:CG	1:D:281:PRO:HD2	2.50	0.46
1:B:12:THR:HG23	1:B:56:LEU:O	2.16	0.46
1:B:40:ILE:HG12	1:B:44:GLU:HB2	1.98	0.46
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:257:ALA:HB1	1:D:263:ILE:HG21	1.97	0.46
1:D:315:ALA:HB3	1:D:322:MSE:HB3	1.98	0.46
1:A:280:HIS:ND1	1:A:281:PRO:CD	2.78	0.46
1:B:7:MSE:CB	1:B:317:LEU:HD21	2.46	0.46
1:B:7:MSE:HB2	1:B:317:LEU:HD21	1.96	0.46
1:B:133:VAL:HG22	1:B:138:TRP:CE3	2.50	0.46
1:B:160:GLY:HA3	1:B:216:CYS:HB3	1.98	0.46
1:B:222:THR:O	1:B:225:LEU:HB2	2.16	0.46
1:D:100:VAL:HG12	1:D:101:GLY:H	1.81	0.46
1:A:57:CYS:C	1:A:58:LEU:HD23	2.36	0.46
1:B:73:ALA:N	2:B:336:HOH:O	2.48	0.46
1:C:90:LEU:O	1:C:94:LYS:HB2	2.16	0.46
1:C:107:LEU:HB3	1:C:305:MSE:CE	2.46	0.46
1:D:17:ALA:O	1:D:21:VAL:HG23	2.16	0.46
1:B:173:LYS:N	1:B:174:PRO:HD2	2.30	0.46
1:C:9:VAL:HG21	1:C:31:VAL:HG22	1.96	0.46
1:C:74:ASN:CG	2:C:433:HOH:O	2.54	0.46
1:C:180:PHE:O	1:C:197:ALA:HA	2.16	0.46
1:D:26:ALA:HB1	1:D:28:ASP:OD1	2.15	0.46
1:D:226:CYS:HB2	1:D:249:VAL:HG22	1.97	0.46
1:B:161:LEU:HD21	1:B:192:ALA:CB	2.43	0.46
1:D:15:ILE:HD12	1:D:19:GLY:HA3	1.98	0.46
1:A:43:LYS:O	1:A:46:GLU:HB2	2.15	0.46
1:A:68:LEU:HD13	1:A:92:GLU:CG	2.46	0.46
1:B:201:SER:O	1:B:204:GLU:N	2.47	0.46
1:C:13:ARG:HB3	1:C:58:LEU:HD11	1.97	0.46
1:D:7:MSE:HB3	1:D:53:HIS:CG	2.50	0.46
1:D:100:VAL:HG11	1:D:326:LEU:HD22	1.96	0.46
1:A:8:LYS:HB3	1:A:52:ALA:HA	1.97	0.46
1:B:192:ALA:CB	1:B:197:ALA:HB3	2.39	0.46
1:D:8:LYS:NZ	1:D:52:ALA:HB2	2.31	0.46
1:D:64:ASP:O	1:D:68:LEU:HG	2.16	0.46
1:A:222:THR:O	1:A:223:GLU:C	2.53	0.46
1:C:262:LYS:NZ	2:C:439:HOH:O	2.48	0.46
1:C:312:ASN:ND2	1:C:324:SER:HB3	2.25	0.46
1:A:7:MSE:SE	1:A:29:CYS:HA	2.65	0.46
1:B:217:SER:O	1:B:222:THR:HG21	2.15	0.46
1:C:234:MSE:HG2	2:C:344:HOH:O	2.14	0.46
1:D:186:GLN:HG3	1:D:187:PRO:CD	2.45	0.46
1:D:154:SER:HG	1:D:177:VAL:HG22	1.80	0.46
1:A:249:VAL:HG12	1:A:250:ASN:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:104:PRO:O	1:D:106:VAL:N	2.47	0.46
1:D:255:TYR:HD1	1:D:285:LEU:HD11	1.81	0.46
1:A:6:LEU:N	1:A:6:LEU:HD12	2.31	0.46
1:B:189:PRO:C	1:B:191:GLU:H	2.19	0.46
1:B:274:GLU:HB2	2:B:393:HOH:O	2.16	0.46
1:A:59:LEU:HD12	1:A:59:LEU:C	2.36	0.46
1:A:161:LEU:HD21	1:A:192:ALA:CB	2.45	0.46
1:C:16:PRO:HD2	1:C:81:MSE:CE	2.46	0.46
1:C:94:LYS:C	1:C:96:ARG:N	2.68	0.46
1:C:322:MSE:HB2	1:C:325:GLU:HB3	1.98	0.46
1:D:26:ALA:HB1	1:D:29:CYS:SG	2.56	0.46
1:A:8:LYS:H	1:A:53:HIS:CE1	2.34	0.46
1:A:254:LEU:O	1:A:258:LEU:HG	2.15	0.46
1:B:283:LEU:C	1:B:285:LEU:N	2.68	0.46
1:D:279:ASN:HA	2:D:332:HOH:O	2.15	0.46
1:A:17:ALA:O	1:A:21:VAL:HG23	2.16	0.46
1:A:20:ARG:HG2	1:A:20:ARG:HH11	1.80	0.46
1:C:151:LEU:HA	1:C:154:SER:HB3	1.96	0.46
1:D:9:VAL:CG1	1:D:313:LEU:HD21	2.45	0.46
1:C:100:VAL:HG12	1:C:101:GLY:N	2.31	0.46
1:C:243:ILE:HD12	1:C:243:ILE:C	2.36	0.46
1:B:313:LEU:O	1:B:317:LEU:HD22	2.16	0.46
1:D:227:ASN:HA	1:D:250:ASN:HB3	1.96	0.46
1:A:44:GLU:O	1:A:48:GLY:N	2.49	0.46
1:A:171:ARG:NH1	1:B:175:PHE:CA	2.71	0.46
1:A:280:HIS:CE1	1:A:281:PRO:HD2	2.51	0.46
1:B:56:LEU:HD23	1:B:56:LEU:C	2.35	0.46
1:B:57:CYS:HB2	1:B:61:ASP:HB2	1.96	0.46
1:D:192:ALA:CB	1:D:197:ALA:CB	2.92	0.46
1:B:227:ASN:O	1:B:229:ASP:N	2.49	0.46
1:B:318:ARG:O	1:B:320:GLU:HG2	2.16	0.46
1:C:218:LEU:HD13	1:C:248:VAL:CG2	2.45	0.46
1:B:158:ILE:O	1:B:182:TYR:HA	2.16	0.46
1:B:312:ASN:OD1	1:B:322:MSE:HB2	2.15	0.46
1:C:131:GLU:HG3	1:C:135:ASN:ND2	2.31	0.46
1:C:234:MSE:HE1	1:C:240:PHE:HB2	1.97	0.46
1:D:209:SER:HB3	1:D:211:PHE:O	2.16	0.46
1:B:57:CYS:O	1:B:58:LEU:HD23	2.16	0.46
1:C:63:VAL:HG13	1:C:67:ILE:HG21	1.98	0.46
1:D:53:HIS:O	1:D:76:LYS:HG2	2.15	0.46
1:D:182:TYR:OH	1:D:188:ARG:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:315:ALA:HB3	1:D:322:MSE:HG2	1.97	0.46
1:A:59:LEU:HB3	1:A:82:SER:CB	2.46	0.46
1:B:18:GLU:H	1:B:303:ASN:HD22	1.64	0.46
1:C:72:GLY:C	1:C:74:ASN:H	2.17	0.46
1:A:75:LEU:HB3	1:A:98:ILE:CD1	2.46	0.46
1:A:121:THR:HG22	1:A:126:LEU:HB2	1.97	0.46
1:B:313:LEU:C	1:B:317:LEU:HD22	2.36	0.46
1:A:76:LYS:NZ	1:A:317:LEU:HA	2.31	0.46
1:A:179:ARG:CZ	1:A:181:LEU:HD21	2.46	0.46
1:A:251:GLN:HB2	2:A:363:HOH:O	2.15	0.46
1:B:78:ILE:CG1	1:B:98:ILE:HG21	2.42	0.46
1:D:180:PHE:O	1:D:197:ALA:HB1	2.16	0.46
1:A:244:SER:O	1:A:245:ARG:NH1	2.39	0.46
1:B:212:ILE:HD12	1:B:234:MSE:HE3	1.98	0.46
1:C:320:GLU:HB2	1:C:321:PRO:CD	2.46	0.46
1:A:7:MSE:SE	1:A:317:LEU:HB3	2.65	0.46
1:B:301:THR:HG22	1:B:305:MSE:SE	2.66	0.46
1:C:249:VAL:HG12	1:C:250:ASN:N	2.30	0.46
1:C:40:ILE:HG22	1:C:45:LEU:HG	1.97	0.46
1:C:75:LEU:N	1:C:75:LEU:CD1	2.78	0.46
1:D:76:LYS:C	1:D:98:ILE:HG23	2.36	0.46
1:B:161:LEU:HD22	1:B:182:TYR:CD1	2.50	0.46
1:C:173:LYS:N	1:C:174:PRO:HD2	2.31	0.46
1:A:64:ASP:HA	1:A:89:ALA:CB	2.46	0.46
1:B:56:LEU:HD23	1:B:56:LEU:C	2.36	0.46
1:B:16:PRO:HB3	1:B:303:ASN:OD1	2.16	0.46
1:B:236:GLU:HA	1:B:262:LYS:O	2.16	0.46
1:C:13:ARG:HD2	1:C:37:ASP:C	2.35	0.46
1:C:257:ALA:HA	1:C:262:LYS:CG	2.45	0.46
1:D:103:THR:CB	1:D:308:LEU:HD23	2.45	0.46
1:A:76:LYS:CA	2:A:415:HOH:O	2.63	0.46
1:C:243:ILE:HD12	1:C:243:ILE:C	2.36	0.46
1:A:142:LYS:HB2	1:A:145:TRP:HB3	1.98	0.46
1:B:11:VAL:HG12	1:B:12:THR:N	2.31	0.46
1:C:63:VAL:HB	1:C:88:LEU:HB3	1.98	0.46
1:C:92:GLU:CA	1:C:95:LYS:HD3	2.36	0.46
1:C:81:MSE:HA	1:C:103:THR:CG2	2.46	0.46
1:C:135:ASN:OD1	1:C:136:GLY:N	2.48	0.46
1:D:164:ILE:O	1:D:168:ILE:HG13	2.16	0.46
1:D:81:MSE:HE2	1:D:306:SER:CA	2.43	0.46
1:D:160:GLY:C	1:D:162:GLY:H	2.18	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:251:GLN:HB3	1:D:280:HIS:CE1	2.51	0.46
1:B:202:THR:HB	1:B:203:PRO:HD3	1.98	0.46
1:C:114:LEU:HD13	1:C:294:ILE:O	2.16	0.46
1:C:234:MSE:HA	2:C:343:HOH:O	2.15	0.46
1:D:296:SER:C	1:D:302:ARG:HH21	2.20	0.46
1:A:121:THR:CG2	1:A:127:PRO:HD3	2.46	0.46
1:A:205:LEU:C	1:A:207:ALA:H	2.19	0.46
1:A:236:GLU:OE1	1:A:236:GLU:N	2.41	0.46
1:B:23:LEU:HD23	1:B:314:LEU:HG	1.97	0.46
1:C:102:TYR:HE1	1:C:325:GLU:C	2.20	0.46
1:C:155:THR:HG23	1:C:179:ARG:O	2.15	0.46
1:C:236:GLU:HA	1:C:263:ILE:HA	1.97	0.46
1:D:19:GLY:HA2	1:D:310:ALA:HB2	1.98	0.46
1:D:45:LEU:C	1:D:47:ARG:H	2.19	0.46
1:D:89:ALA:O	1:D:93:ILE:HG13	2.16	0.46
1:A:80:THR:OG1	1:A:87:HIS:NE2	2.43	0.46
1:A:202:THR:HB	1:A:203:PRO:CD	2.44	0.46
1:A:315:ALA:C	1:A:317:LEU:H	2.19	0.46
1:B:159:ILE:CB	1:B:214:VAL:HG13	2.43	0.46
1:B:313:LEU:HD23	1:B:313:LEU:C	2.36	0.46
1:A:157:GLY:O	1:A:212:ILE:HA	2.16	0.46
1:B:13:ARG:NH2	1:B:58:LEU:HD22	2.30	0.46
1:B:58:LEU:HD12	1:B:58:LEU:N	2.30	0.46
1:C:15:ILE:H	1:C:20:ARG:HH12	1.64	0.46
1:A:59:LEU:HD11	1:A:82:SER:HB2	1.98	0.46
1:C:78:ILE:HD12	1:C:93:ILE:HD11	1.98	0.46
1:C:280:HIS:CE1	1:C:282:LEU:H	2.33	0.46
1:D:182:TYR:OH	1:D:192:ALA:HB2	2.16	0.46
1:A:59:LEU:HD12	1:A:59:LEU:C	2.36	0.46
1:A:114:LEU:CD2	1:A:294:ILE:HG13	2.46	0.46
1:C:15:ILE:O	1:C:20:ARG:NH1	2.49	0.46
1:C:169:ALA:HB3	1:C:195:PHE:CE1	2.51	0.46
1:C:228:LYS:HE3	2:C:331:HOH:O	2.15	0.46
1:D:89:ALA:O	1:D:93:ILE:HG13	2.15	0.46
1:D:186:GLN:HG2	1:D:187:PRO:N	2.31	0.46
1:A:243:ILE:HG22	1:A:269:ASP:HB3	1.98	0.45
1:D:227:ASN:O	1:D:230:PHE:HB3	2.16	0.45
1:D:280:HIS:O	1:D:282:LEU:N	2.49	0.45
1:B:114:LEU:HD22	1:B:294:ILE:O	2.17	0.45
1:C:314:LEU:CD1	1:C:314:LEU:N	2.79	0.45
1:C:318:ARG:CB	1:C:320:GLU:HG3	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:SER:HA	1:A:101:GLY:O	2.15	0.45
1:A:92:GLU:O	1:A:96:ARG:HG3	2.16	0.45
1:C:52:ALA:O	1:C:74:ASN:HB3	2.16	0.45
1:A:274:GLU:OE1	1:B:138:TRP:HZ2	1.99	0.45
1:B:204:GLU:O	1:B:208:GLN:HG2	2.15	0.45
1:D:56:LEU:HD21	1:D:81:MSE:HE3	1.98	0.45
1:D:183:THR:HG22	1:D:201:SER:C	2.37	0.45
1:D:307:LEU:HG	1:D:311:ASN:ND2	2.31	0.45
1:A:43:LYS:HA	1:A:46:GLU:OE1	2.17	0.45
1:A:132:GLU:HA	1:A:135:ASN:OD1	2.16	0.45
1:A:222:THR:O	1:A:225:LEU:HB2	2.16	0.45
1:B:107:LEU:HB3	1:B:305:MSE:SE	2.66	0.45
1:A:47:ARG:HG3	1:A:48:GLY:N	2.32	0.45
1:A:183:THR:HG23	1:A:184:GLY:H	1.79	0.45
1:A:194:GLU:HG2	1:A:195:PHE:CE1	2.51	0.45
1:A:204:GLU:OE2	1:D:204:GLU:HG3	2.16	0.45
1:B:9:VAL:N	1:B:30:GLU:O	2.49	0.45
1:B:244:SER:OG	1:B:245:ARG:N	2.47	0.45
1:D:307:LEU:HD11	1:D:311:ASN:HD21	1.81	0.45
1:A:190:GLU:O	1:A:193:ALA:HB3	2.17	0.45
1:B:107:LEU:HD12	1:B:296:SER:HB3	1.98	0.45
1:B:118:LEU:HD13	1:B:291:LEU:CD1	2.45	0.45
1:C:93:ILE:CD1	1:C:100:VAL:HG22	2.46	0.45
1:B:15:ILE:CB	1:B:81:MSE:HE1	2.45	0.45
1:B:34:TRP:CD1	1:B:36:SER:HB3	2.51	0.45
1:B:93:ILE:HG23	1:B:98:ILE:HB	1.98	0.45
1:B:300:ARG:NH2	2:B:424:HOH:O	2.49	0.45
1:D:102:TYR:O	1:D:324:SER:HB3	2.16	0.45
1:A:114:LEU:HD22	1:A:295:GLY:HA2	1.98	0.45
1:B:236:GLU:HA	1:B:262:LYS:O	2.15	0.45
1:C:228:LYS:O	1:C:232:GLN:HB2	2.15	0.45
1:C:303:ASN:HB3	2:C:380:HOH:O	2.15	0.45
1:D:292:PRO:HG2	1:D:294:ILE:HG23	1.98	0.45
1:A:277:PRO:O	1:A:279:ASN:N	2.49	0.45
1:C:88:LEU:HB3	1:C:93:ILE:HD11	1.97	0.45
1:A:56:LEU:C	1:A:56:LEU:HD23	2.36	0.45
1:A:182:TYR:HD1	1:A:197:ALA:O	1.98	0.45
1:B:68:LEU:HD23	1:B:68:LEU:HA	1.82	0.45
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.51	0.45
1:C:92:GLU:HB3	1:C:96:ARG:HE	1.80	0.45
1:D:10:PHE:O	1:D:55:LEU:HD12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:219:THR:HB	1:D:220:PRO:CD	2.47	0.45
1:A:88:LEU:HB3	1:A:93:ILE:HD12	1.98	0.45
1:B:8:LYS:HE3	1:B:51:GLY:HA3	1.98	0.45
1:C:8:LYS:HE2	1:C:30:GLU:OE1	2.15	0.45
1:C:10:PHE:CE1	1:C:48:GLY:HA3	2.51	0.45
1:C:18:GLU:HG2	1:C:307:LEU:HB2	1.99	0.45
1:C:45:LEU:HG	1:C:67:ILE:HD12	1.99	0.45
1:A:54:GLY:HA2	1:A:77:VAL:O	2.17	0.45
1:B:85:ILE:C	1:B:87:HIS:H	2.19	0.45
1:B:99:ARG:HH22	1:B:319:GLY:CA	2.21	0.45
1:A:63:VAL:HB	1:A:88:LEU:HD23	1.99	0.45
1:B:56:LEU:HA	1:B:79:SER:O	2.17	0.45
1:A:16:PRO:HB2	1:A:306:SER:OG	2.15	0.45
1:C:143:PRO:O	1:D:302:ARG:NH1	2.32	0.45
1:D:163:ARG:NH2	2:D:368:HOH:O	2.49	0.45
1:D:272:SER:HA	1:D:273:PRO:HA	1.74	0.45
1:A:202:THR:HG21	1:A:225:LEU:HD11	1.98	0.45
1:B:110:THR:HG22	1:B:296:SER:HA	1.98	0.45
1:D:99:ARG:HD2	1:D:325:GLU:OE2	2.17	0.45
1:D:103:THR:HG22	1:D:308:LEU:HD23	1.98	0.45
1:D:316:GLY:O	1:D:317:LEU:C	2.54	0.45
1:B:102:TYR:CD2	1:B:104:PRO:HD3	2.51	0.45
1:C:11:VAL:HG12	1:C:33:GLN:HE21	1.80	0.45
1:C:206:ALA:HB1	1:C:234:MSE:HG3	1.97	0.45
1:A:141:TRP:CD1	1:B:59:LEU:HD21	2.52	0.45
1:A:181:LEU:HD11	1:A:208:GLN:HB2	1.97	0.45
1:C:77:VAL:HG13	1:C:313:LEU:CD1	2.45	0.45
1:C:322:MSE:SE	1:C:322:MSE:N	2.99	0.45
1:D:7:MSE:HE1	1:D:317:LEU:HB3	1.98	0.45
1:A:47:ARG:HA	2:A:419:HOH:O	2.15	0.45
1:C:182:TYR:CZ	1:C:199:PHE:HB2	2.52	0.45
1:D:81:MSE:CE	1:D:306:SER:HA	2.44	0.45
1:D:69:ASP:OD2	1:D:96:ARG:NH2	2.50	0.45
1:A:202:THR:HG1	1:A:203:PRO:HD3	1.81	0.45
1:C:14:ARG:NH1	1:C:35:ASP:OD1	2.49	0.45
1:C:40:ILE:HG22	2:C:440:HOH:O	2.15	0.45
1:A:22:ALA:O	1:A:25:ARG:HB2	2.17	0.45
1:A:218:LEU:HD22	1:A:247:ASP:OD2	2.16	0.45
1:A:310:ALA:O	1:A:313:LEU:HB3	2.15	0.45
1:B:92:GLU:O	1:B:96:ARG:HG3	2.16	0.45
1:C:188:ARG:N	1:C:189:PRO:HD3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:ILE:N	1:B:99:ARG:O	2.46	0.45
1:B:186:GLN:HA	1:B:187:PRO:HD3	1.80	0.45
1:D:279:ASN:HA	2:D:332:HOH:O	2.16	0.45
1:A:87:HIS:ND1	1:A:87:HIS:N	2.62	0.45
1:B:114:LEU:CD1	1:B:294:ILE:HG13	2.46	0.45
1:C:9:VAL:CG2	1:C:31:VAL:HG22	2.46	0.45
1:C:21:VAL:HG12	1:C:21:VAL:O	2.16	0.45
1:D:114:LEU:CD2	1:D:295:GLY:HA2	2.40	0.45
1:D:281:PRO:O	1:D:283:LEU:N	2.49	0.45
1:A:40:ILE:HG21	1:A:45:LEU:HD13	1.97	0.45
1:A:80:THR:HG23	1:A:80:THR:O	2.15	0.45
1:A:49:VAL:HG21	1:A:67:ILE:CG2	2.30	0.45
1:A:234:MSE:HE2	1:A:238:ALA:CB	2.40	0.45
1:B:71:ALA:HB1	1:B:75:LEU:HB2	1.97	0.45
1:D:7:MSE:HB3	1:D:53:HIS:CB	2.46	0.45
1:A:75:LEU:HB3	1:A:98:ILE:HD13	1.98	0.45
1:B:7:MSE:O	1:B:30:GLU:N	2.36	0.45
1:B:72:GLY:CA	2:B:336:HOH:O	2.59	0.45
1:C:34:TRP:O	1:C:36:SER:N	2.48	0.45
1:C:89:ALA:O	1:C:93:ILE:HG12	2.17	0.45
1:D:16:PRO:HB2	1:D:306:SER:CB	2.46	0.45
1:D:201:SER:HB2	1:D:203:PRO:HD2	1.98	0.45
1:C:74:ASN:ND2	2:C:432:HOH:O	2.49	0.45
1:C:92:GLU:O	1:C:96:ARG:HD2	2.16	0.45
1:A:7:MSE:HE1	1:A:28:ASP:OD2	2.15	0.45
1:A:114:LEU:HD22	1:A:295:GLY:HA2	1.98	0.45
1:A:220:PRO:N	2:A:429:HOH:O	2.48	0.45
1:A:234:MSE:HE1	1:A:240:PHE:HD1	1.82	0.45
1:B:71:ALA:CB	1:B:75:LEU:HD22	2.47	0.45
1:C:34:TRP:CZ3	1:C:44:GLU:HG3	2.52	0.45
1:C:56:LEU:HD12	1:C:313:LEU:HD22	1.97	0.45
1:C:245:ARG:O	1:C:248:VAL:HG23	2.17	0.45
1:C:257:ALA:HB1	1:C:262:LYS:HB2	1.97	0.45
1:D:99:ARG:HD2	1:D:325:GLU:OE2	2.16	0.45
1:A:103:THR:HG22	1:A:308:LEU:HD23	1.98	0.45
1:C:93:ILE:HG23	1:C:98:ILE:HB	1.99	0.45
1:A:76:LYS:HD3	1:A:316:GLY:O	2.17	0.45
1:A:280:HIS:ND1	1:A:282:LEU:HB2	2.32	0.45
1:C:36:SER:OG	1:C:37:ASP:N	2.49	0.45
1:B:128:GLU:O	1:B:132:GLU:HG2	2.17	0.45
1:B:182:TYR:CZ	1:B:199:PHE:HB2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:144:LEU:CD2	1:D:16:PRO:HG3	2.47	0.45
1:A:53:HIS:O	1:A:317:LEU:HD21	2.16	0.45
1:A:227:ASN:HB3	1:A:250:ASN:HD22	1.82	0.45
1:C:42:ALA:O	1:C:45:LEU:HB3	2.17	0.45
1:C:146:LEU:CD1	1:D:294:ILE:HG21	2.46	0.45
1:B:276:LEU:HD22	1:B:290:ILE:HD13	1.98	0.45
1:C:92:GLU:HA	1:C:95:LYS:HZ2	1.81	0.45
1:C:107:LEU:HD12	1:C:107:LEU:C	2.37	0.45
1:A:142:LYS:NZ	1:B:38:GLU:OE2	2.47	0.45
1:C:40:ILE:CD1	1:C:45:LEU:HA	2.44	0.45
1:D:211:PHE:HD1	1:D:239:VAL:HB	1.81	0.45
1:B:158:ILE:O	1:B:182:TYR:HA	2.17	0.45
1:C:54:GLY:HA2	1:C:77:VAL:CG1	2.47	0.45
1:D:78:ILE:HG13	1:D:98:ILE:HG21	1.98	0.45
1:A:158:ILE:N	1:A:158:ILE:CD1	2.78	0.45
1:B:74:ASN:HB2	2:B:336:HOH:O	2.17	0.45
1:C:114:LEU:HD11	1:C:294:ILE:HG13	1.99	0.45
1:D:161:LEU:HB2	1:D:182:TYR:CD2	2.52	0.45
1:A:83:VAL:HG23	1:A:104:PRO:HA	1.99	0.45
1:A:110:THR:O	1:A:113:GLU:HB3	2.16	0.45
1:A:209:SER:HB2	1:A:212:ILE:CD1	2.46	0.45
1:C:188:ARG:HD2	2:C:359:HOH:O	2.16	0.45
1:D:93:ILE:CG2	1:D:98:ILE:HB	2.36	0.45
1:D:185:ARG:CG	1:D:185:ARG:HH11	2.29	0.45
1:A:59:LEU:HA	1:A:87:HIS:CE1	2.51	0.45
1:A:114:LEU:HD21	1:A:294:ILE:HG13	1.98	0.45
1:A:157:GLY:CA	1:A:205:LEU:HD11	2.46	0.45
1:A:157:GLY:HA3	1:A:205:LEU:HD11	1.99	0.45
1:A:181:LEU:CD2	1:A:198:GLU:HB2	2.47	0.45
1:D:258:LEU:HD11	1:D:266:ALA:HB3	1.99	0.45
1:A:142:LYS:HB3	2:A:362:HOH:O	2.16	0.45
1:A:210:ASP:OD1	1:A:235:LYS:HD2	2.17	0.45
1:B:68:LEU:HD13	1:B:96:ARG:NH1	2.30	0.45
1:C:158:ILE:O	1:C:182:TYR:HA	2.17	0.45
1:C:163:ARG:HA	1:C:166:GLN:NE2	2.32	0.45
1:D:51:GLY:HA2	2:D:416:HOH:O	2.15	0.45
1:A:49:VAL:O	1:A:71:ALA:HA	2.17	0.45
1:A:219:THR:HB	1:A:220:PRO:CD	2.47	0.45
1:B:23:LEU:CD2	1:B:314:LEU:HG	2.47	0.45
1:A:10:PHE:CD1	1:A:32:GLU:O	2.70	0.45
1:A:249:VAL:HG12	1:A:250:ASN:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:ARG:HD3	1:A:305:MSE:HE1	1.98	0.45
1:B:159:ILE:CG2	1:B:214:VAL:HG13	2.46	0.45
1:B:173:LYS:N	1:B:174:PRO:HD2	2.31	0.45
1:B:191:GLU:HA	2:B:392:HOH:O	2.16	0.45
1:A:124:ARG:CZ	1:B:298:THR:HG22	2.47	0.45
1:A:155:THR:N	1:A:210:ASP:OD2	2.32	0.45
1:A:158:ILE:CD1	1:A:169:ALA:HB2	2.47	0.45
1:B:100:VAL:O	1:B:325:GLU:HG3	2.17	0.45
1:C:77:VAL:HA	1:C:99:ARG:O	2.17	0.45
1:C:264:ALA:O	1:C:265:ALA:HB2	2.16	0.45
1:B:55:LEU:HG	1:B:78:ILE:HG23	1.99	0.45
1:D:104:PRO:O	1:D:105:ASP:CB	2.65	0.45
1:A:161:LEU:CD2	1:A:188:ARG:HB2	2.46	0.45
1:A:180:PHE:CD2	1:A:195:PHE:HB3	2.52	0.45
1:B:184:GLY:N	1:B:199:PHE:HE1	2.13	0.45
1:B:325:GLU:HG3	1:B:326:LEU:N	2.30	0.45
1:C:117:SER:OG	1:D:120:LEU:HB3	2.17	0.45
1:D:256:GLN:NE2	1:D:260:SER:HB3	2.31	0.45
1:A:143:PRO:HB2	1:B:16:PRO:HD3	1.98	0.45
1:A:182:TYR:CE1	1:A:199:PHE:HA	2.51	0.45
1:B:7:MSE:SE	1:B:317:LEU:HG	2.66	0.45
1:B:110:THR:O	1:B:113:GLU:HB3	2.17	0.45
1:C:161:LEU:HD22	1:C:182:TYR:CD1	2.50	0.45
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.51	0.45
1:D:292:PRO:HG2	1:D:294:ILE:HG23	1.99	0.45
1:A:51:GLY:HA2	1:A:74:ASN:ND2	2.32	0.45
1:C:102:TYR:N	1:C:102:TYR:HD1	2.14	0.45
1:C:159:ILE:HG22	1:C:216:CYS:HB3	1.99	0.45
1:C:192:ALA:HB1	1:C:197:ALA:HB3	1.99	0.45
1:D:183:THR:HG23	1:D:205:LEU:CD1	2.42	0.45
1:D:212:ILE:HD12	1:D:234:MSE:HE3	1.99	0.45
1:C:258:LEU:HD13	1:C:288:CYS:HB2	1.98	0.45
1:D:75:LEU:O	1:D:98:ILE:HG12	2.17	0.45
1:A:98:ILE:CG2	1:A:99:ARG:H	2.17	0.45
1:B:65:LYS:HB3	1:B:65:LYS:HZ3	1.81	0.45
1:B:219:THR:O	1:B:223:GLU:HB2	2.17	0.45
1:C:110:THR:HG23	1:D:124:ARG:NH1	2.32	0.45
1:C:240:PHE:O	1:C:266:ALA:HA	2.16	0.45
1:B:76:LYS:HD3	1:B:316:GLY:O	2.16	0.45
1:B:269:ASP:O	1:B:293:HIS:HA	2.17	0.45
1:A:12:THR:HG22	1:A:45:LEU:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:THR:HG22	1:A:126:LEU:HB2	1.98	0.45
1:A:224:GLY:H	1:A:248:VAL:HA	1.81	0.45
1:C:6:LEU:HD23	1:C:30:GLU:HG3	1.98	0.45
1:D:121:THR:HA	1:D:126:LEU:HD13	1.99	0.45
1:D:142:LYS:HB2	1:D:145:TRP:HB2	1.98	0.45
1:A:125:ARG:NH1	1:A:146:LEU:HA	2.32	0.45
1:B:59:LEU:C	1:B:59:LEU:HD12	2.37	0.45
1:B:191:GLU:OE1	1:B:191:GLU:N	2.41	0.45
1:C:11:VAL:HB	1:C:33:GLN:CB	2.34	0.45
1:D:202:THR:CG2	1:D:225:LEU:HD11	2.30	0.45
1:A:21:VAL:O	1:A:24:ALA:N	2.50	0.45
1:A:152:THR:C	1:A:154:SER:H	2.20	0.45
1:B:99:ARG:HD2	1:B:325:GLU:OE1	2.16	0.45
1:D:10:PHE:HA	1:D:32:GLU:O	2.17	0.45
1:A:157:GLY:HA3	1:A:205:LEU:HD11	1.99	0.45
1:A:174:PRO:HG2	1:B:174:PRO:CG	2.30	0.45
1:B:201:SER:HB2	1:B:203:PRO:HD2	1.98	0.45
1:B:313:LEU:HD13	1:B:317:LEU:HD22	1.98	0.45
1:D:140:SER:OG	1:D:141:TRP:N	2.50	0.45
1:A:51:GLY:N	1:A:71:ALA:O	2.44	0.45
1:A:145:TRP:CZ2	1:A:146:LEU:HD12	2.52	0.45
1:B:26:ALA:C	1:B:28:ASP:N	2.67	0.45
1:C:302:ARG:O	1:C:305:MSE:HG2	2.15	0.45
1:A:325:GLU:HG2	1:A:326:LEU:N	2.32	0.45
1:B:45:LEU:HD23	1:B:67:ILE:HD12	1.98	0.45
1:A:59:LEU:CD2	1:A:59:LEU:N	2.71	0.45
1:A:148:GLY:O	1:B:298:THR:HA	2.16	0.45
1:B:53:HIS:C	1:B:75:LEU:HD12	2.37	0.45
1:C:18:GLU:HG3	1:C:307:LEU:HB2	1.99	0.45
1:C:54:GLY:HA2	1:C:77:VAL:HG12	1.98	0.45
1:A:280:HIS:CE1	1:A:282:LEU:HD12	2.51	0.45
1:B:66:ARG:CZ	2:B:403:HOH:O	2.64	0.45
1:B:77:VAL:HG11	1:B:317:LEU:HD13	1.99	0.45
1:B:83:VAL:HG13	1:B:84:GLY:N	2.32	0.45
1:C:43:LYS:HE3	1:C:47:ARG:NH2	2.32	0.45
1:C:99:ARG:NH2	1:C:320:GLU:O	2.50	0.45
1:C:16:PRO:HD2	1:C:81:MSE:HE1	1.98	0.45
1:C:111:THR:CG2	1:C:164:ILE:HD13	2.44	0.45
1:D:100:VAL:CG1	1:D:101:GLY:N	2.80	0.45
1:D:163:ARG:HD3	1:D:166:GLN:CD	2.37	0.45
1:D:195:PHE:O	1:D:196:GLN:C	2.55	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:THR:O	1:B:305:MSE:HG3	2.17	0.45
1:D:240:PHE:O	1:D:241:ILE:HD13	2.16	0.45
1:A:64:ASP:OD1	1:A:67:ILE:HG12	2.17	0.45
1:D:93:ILE:HG23	1:D:98:ILE:HB	1.99	0.45
1:D:99:ARG:NH1	1:D:325:GLU:OE1	2.48	0.45
1:A:8:LYS:CD	1:A:52:ALA:HB2	2.46	0.45
1:A:128:GLU:HG3	2:A:382:HOH:O	2.17	0.45
1:A:229:ASP:O	1:A:233:LYS:HD2	2.16	0.45
1:A:325:GLU:HG2	1:A:326:LEU:N	2.32	0.45
1:B:283:LEU:CD2	1:B:290:ILE:HD12	2.46	0.45
1:C:49:VAL:O	1:C:71:ALA:HA	2.17	0.45
1:B:244:SER:OG	1:B:245:ARG:N	2.48	0.45
1:C:146:LEU:CD1	1:D:292:PRO:HG3	2.47	0.45
1:A:8:LYS:HE2	1:A:32:GLU:HB2	1.98	0.45
1:A:59:LEU:HD11	1:A:82:SER:OG	2.17	0.45
1:B:76:LYS:CE	1:B:317:LEU:HA	2.38	0.45
1:B:83:VAL:HG13	1:B:84:GLY:N	2.31	0.45
1:C:249:VAL:O	1:C:249:VAL:CG1	2.64	0.45
1:D:161:LEU:O	1:D:161:LEU:HG	2.17	0.45
1:B:316:GLY:C	1:B:318:ARG:H	2.21	0.45
1:A:128:GLU:HG3	2:A:381:HOH:O	2.16	0.45
1:B:76:LYS:C	1:B:98:ILE:HG23	2.37	0.45
1:D:13:ARG:CG	1:D:14:ARG:H	2.30	0.45
1:D:22:ALA:C	1:D:24:ALA:H	2.19	0.45
1:A:76:LYS:HD2	1:A:317:LEU:CA	2.41	0.45
1:A:218:LEU:HD22	1:A:247:ASP:HB2	1.98	0.45
1:B:62:HIS:CE1	2:B:414:HOH:O	2.69	0.45
1:B:62:HIS:O	1:B:64:ASP:N	2.44	0.45
1:C:19:GLY:HA3	1:C:306:SER:O	2.18	0.45
1:C:275:PRO:HA	1:D:138:TRP:CH2	2.52	0.45
1:B:114:LEU:HD22	1:B:295:GLY:HA2	1.99	0.45
1:B:230:PHE:O	1:B:234:MSE:HG3	2.17	0.45
1:C:49:VAL:HG23	1:C:71:ALA:HB2	1.97	0.45
1:C:95:LYS:C	1:C:97:GLY:H	2.21	0.45
1:C:106:VAL:HG11	1:C:308:LEU:HD22	1.99	0.45
1:C:315:ALA:HB3	1:C:322:MSE:CG	2.47	0.45
1:A:208:GLN:O	1:A:235:LYS:HE3	2.17	0.45
1:C:117:SER:OG	1:D:120:LEU:HB3	2.17	0.45
1:C:124:ARG:HD3	1:D:113:GLU:OE1	2.17	0.45
1:C:189:PRO:O	1:C:190:GLU:C	2.56	0.45
1:D:114:LEU:HD13	1:D:295:GLY:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:THR:O	1:A:205:LEU:HB3	2.17	0.45
1:B:82:SER:O	1:B:83:VAL:C	2.56	0.45
1:C:45:LEU:HG	1:C:67:ILE:HG21	1.99	0.45
1:C:53:HIS:CE1	1:C:74:ASN:HD22	2.34	0.45
1:C:139:THR:HA	1:D:275:PRO:HG3	1.99	0.45
1:C:300:ARG:HG2	1:C:300:ARG:HH11	1.82	0.45
1:D:254:LEU:O	1:D:258:LEU:HG	2.16	0.45
1:C:105:ASP:OD2	1:C:105:ASP:N	2.50	0.45
1:B:71:ALA:HB1	1:B:75:LEU:HB2	1.99	0.44
1:A:9:VAL:HG13	1:A:54:GLY:CA	2.46	0.44
1:D:320:GLU:HB3	1:D:321:PRO:HD2	1.99	0.44
1:B:77:VAL:HA	1:B:99:ARG:O	2.16	0.44
1:B:101:GLY:CA	1:B:322:MSE:SE	3.15	0.44
1:B:114:LEU:HD13	1:B:294:ILE:C	2.38	0.44
1:C:244:SER:OG	1:C:245:ARG:N	2.42	0.44
1:D:183:THR:HG21	1:D:202:THR:CA	2.47	0.44
1:D:312:ASN:HB3	2:D:357:HOH:O	2.17	0.44
1:A:138:TRP:CD2	1:B:275:PRO:HB3	2.52	0.44
1:C:90:LEU:HD23	1:C:93:ILE:HD12	1.99	0.44
1:C:310:ALA:O	1:C:314:LEU:HB2	2.16	0.44
1:D:249:VAL:CG1	1:D:250:ASN:N	2.79	0.44
1:D:269:ASP:OD1	1:D:291:LEU:HB2	2.17	0.44
1:D:247:ASP:HA	2:D:406:HOH:O	2.16	0.44
1:B:320:GLU:O	1:B:321:PRO:O	2.35	0.44
1:C:107:LEU:HD12	1:C:107:LEU:C	2.38	0.44
1:C:264:ALA:O	1:C:265:ALA:HB2	2.17	0.44
1:A:250:ASN:C	1:A:252:ASP:N	2.71	0.44
1:B:13:ARG:HH21	1:B:39:PRO:HA	1.80	0.44
1:B:65:LYS:CB	1:B:92:GLU:HG3	2.47	0.44
1:C:7:MSE:O	1:C:30:GLU:HB2	2.16	0.44
1:A:45:LEU:O	1:A:49:VAL:HG13	2.17	0.44
1:B:322:MSE:HB2	1:B:325:GLU:HB2	1.99	0.44
1:D:182:TYR:O	1:D:199:PHE:HA	2.17	0.44
1:A:8:LYS:CB	1:A:52:ALA:HA	2.45	0.44
1:A:208:GLN:HE21	1:A:208:GLN:CA	2.23	0.44
1:B:222:THR:HA	1:B:225:LEU:HD23	1.98	0.44
1:B:245:ARG:HB2	1:B:248:VAL:HG21	1.98	0.44
1:C:243:ILE:HD12	1:C:243:ILE:C	2.38	0.44
1:B:15:ILE:O	1:B:20:ARG:HD3	2.17	0.44
1:B:59:LEU:HD22	1:B:245:ARG:NH2	2.33	0.44
1:B:78:ILE:HD12	1:B:93:ILE:CD1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:ILE:HG21	1:C:100:VAL:HG22	1.98	0.44
1:C:95:LYS:C	1:C:97:GLY:N	2.71	0.44
1:D:86:ASP:C	1:D:88:LEU:N	2.70	0.44
1:A:8:LYS:HB3	1:A:52:ALA:HA	1.98	0.44
1:B:59:LEU:C	1:B:61:ASP:H	2.20	0.44
1:B:140:SER:OG	1:B:141:TRP:N	2.50	0.44
1:D:144:LEU:HB2	2:D:362:HOH:O	2.18	0.44
1:D:164:ILE:O	1:D:168:ILE:HG13	2.18	0.44
1:D:182:TYR:HE1	1:D:197:ALA:CB	2.29	0.44
1:D:292:PRO:HG2	1:D:294:ILE:HG23	1.99	0.44
1:C:107:LEU:HD23	1:C:305:MSE:CE	2.41	0.44
1:C:257:ALA:CB	1:C:262:LYS:HD2	2.48	0.44
1:C:283:LEU:CD2	1:C:290:ILE:HD12	2.46	0.44
1:C:309:ALA:O	1:C:313:LEU:HB2	2.17	0.44
1:D:158:ILE:O	1:D:182:TYR:HB2	2.17	0.44
1:B:200:VAL:HG22	1:B:201:SER:H	1.82	0.44
1:C:109:ASP:CB	2:C:338:HOH:O	2.61	0.44
1:C:312:ASN:O	1:C:322:MSE:HE2	2.17	0.44
1:D:102:TYR:CD2	1:D:104:PRO:HD3	2.53	0.44
1:A:41:PRO:HB2	1:A:44:GLU:HG2	1.99	0.44
1:A:91:ASP:HB2	2:A:346:HOH:O	2.18	0.44
1:B:128:GLU:O	1:B:132:GLU:HG2	2.18	0.44
1:B:192:ALA:CB	1:B:197:ALA:HB3	2.45	0.44
1:B:228:LYS:O	1:B:232:GLN:N	2.51	0.44
1:D:258:LEU:HD22	1:D:287:ASN:ND2	2.32	0.44
1:A:128:GLU:HG3	2:A:381:HOH:O	2.17	0.44
1:B:46:GLU:HG3	1:B:67:ILE:CD1	2.48	0.44
1:C:43:LYS:CB	2:C:390:HOH:O	2.65	0.44
1:D:16:PRO:O	1:D:18:GLU:N	2.48	0.44
1:A:8:LYS:HE3	1:A:32:GLU:CB	2.48	0.44
1:B:173:LYS:HB3	1:B:174:PRO:CD	2.48	0.44
1:C:54:GLY:CA	1:C:313:LEU:HD11	2.47	0.44
1:C:314:LEU:O	1:C:318:ARG:N	2.38	0.44
1:D:9:VAL:HB	1:D:31:VAL:HA	1.98	0.44
1:D:140:SER:OG	1:D:141:TRP:N	2.50	0.44
1:D:240:PHE:O	1:D:241:ILE:HD13	2.17	0.44
1:D:181:LEU:HD12	1:D:205:LEU:HA	1.99	0.44
1:A:95:LYS:C	1:A:97:GLY:N	2.70	0.44
1:A:125:ARG:HH21	1:A:128:GLU:CD	2.21	0.44
1:B:41:PRO:O	1:B:44:GLU:N	2.50	0.44
1:B:317:LEU:C	1:B:318:ARG:HG3	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:74:ASN:O	1:C:75:LEU:C	2.56	0.44
1:A:23:LEU:CD2	1:A:314:LEU:HD13	2.47	0.44
1:A:49:VAL:O	1:A:50:ALA:C	2.55	0.44
1:A:141:TRP:NE1	1:B:302:ARG:NH2	2.65	0.44
1:B:41:PRO:HD2	1:B:44:GLU:CG	2.48	0.44
1:D:7:MSE:HB3	1:D:53:HIS:CG	2.52	0.44
1:D:8:LYS:N	1:D:53:HIS:ND1	2.62	0.44
1:D:241:ILE:CG2	1:D:242:ASN:N	2.79	0.44
1:A:238:ALA:O	1:A:264:ALA:HB3	2.16	0.44
1:B:114:LEU:HD22	1:B:294:ILE:O	2.18	0.44
1:B:276:LEU:HD22	1:B:290:ILE:HD13	2.00	0.44
1:C:18:GLU:O	1:C:20:ARG:N	2.50	0.44
1:C:159:ILE:HG22	1:C:216:CYS:HB3	1.99	0.44
1:D:121:THR:CG2	1:D:126:LEU:HB2	2.40	0.44
1:A:174:PRO:HB2	1:B:171:ARG:HA	1.99	0.44
1:B:34:TRP:CB	1:B:40:ILE:HD12	2.45	0.44
1:C:93:ILE:CG2	1:C:98:ILE:HB	2.39	0.44
1:D:164:ILE:HG21	1:D:243:ILE:HD11	1.98	0.44
1:B:68:LEU:CD2	1:B:75:LEU:HD22	2.48	0.44
1:B:88:LEU:HB2	1:B:90:LEU:HD11	1.99	0.44
1:D:7:MSE:HE3	1:D:317:LEU:HB3	2.00	0.44
1:D:104:PRO:O	1:D:105:ASP:HB2	2.17	0.44
1:A:114:LEU:HD22	1:A:295:GLY:N	2.33	0.44
1:B:202:THR:N	1:B:203:PRO:CD	2.81	0.44
1:C:11:VAL:HG23	1:C:31:VAL:HG13	2.00	0.44
1:B:326:LEU:HD23	1:B:326:LEU:C	2.38	0.44
1:D:8:LYS:HD3	1:D:51:GLY:C	2.38	0.44
1:B:49:VAL:HG12	1:B:55:LEU:HD13	1.99	0.44
1:B:66:ARG:HA	1:B:66:ARG:HD3	1.72	0.44
1:B:173:LYS:O	1:B:175:PHE:N	2.50	0.44
1:D:14:ARG:NH2	1:D:35:ASP:OD2	2.50	0.44
1:D:204:GLU:HB3	1:D:208:GLN:HE21	1.81	0.44
1:C:7:MSE:HE2	1:C:53:HIS:HD2	1.82	0.44
1:C:95:LYS:C	1:C:97:GLY:H	2.20	0.44
1:C:164:ILE:CG2	1:C:215:ALA:HB1	2.48	0.44
1:C:175:PHE:HA	1:D:171:ARG:NH1	2.33	0.44
1:C:219:THR:H	1:C:222:THR:HG1	1.64	0.44
1:A:156:VAL:HG11	1:A:172:LEU:HD12	1.99	0.44
1:D:152:THR:C	1:D:154:SER:N	2.71	0.44
1:D:209:SER:HB3	1:D:211:PHE:O	2.17	0.44
1:A:171:ARG:NH1	1:B:174:PRO:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:ASN:C	1:A:252:ASP:N	2.71	0.44
1:D:192:ALA:HB1	1:D:197:ALA:H	1.82	0.44
1:D:214:VAL:HB	1:D:242:ASN:OD1	2.18	0.44
1:C:106:VAL:HG23	1:C:305:MSE:HG2	2.00	0.44
1:C:307:LEU:HG	1:C:311:ASN:ND2	2.33	0.44
1:D:156:VAL:HB	1:D:180:PHE:CE1	2.53	0.44
1:D:159:ILE:HG21	1:D:225:LEU:HD23	1.98	0.44
1:C:85:ILE:CD1	1:C:90:LEU:HD11	2.44	0.44
1:C:185:ARG:NH2	2:C:359:HOH:O	2.51	0.44
1:A:106:VAL:HB	1:A:304:THR:CG2	2.47	0.44
1:B:59:LEU:HD12	1:B:60:SER:N	2.32	0.44
1:B:297:ALA:O	1:B:298:THR:HG23	2.17	0.44
1:A:103:THR:HG21	1:A:305:MSE:HB3	2.00	0.44
1:B:95:LYS:C	1:B:97:GLY:N	2.70	0.44
1:C:77:VAL:CG1	1:C:317:LEU:HD12	2.48	0.44
1:D:121:THR:CG2	1:D:127:PRO:HD3	2.40	0.44
1:D:209:SER:HB2	1:D:212:ILE:CD1	2.48	0.44
1:A:83:VAL:HG23	1:A:104:PRO:HB3	1.99	0.44
1:A:95:LYS:C	1:A:97:GLY:H	2.20	0.44
1:A:280:HIS:CE1	1:A:281:PRO:HD2	2.53	0.44
1:B:97:GLY:O	1:B:98:ILE:C	2.55	0.44
1:C:195:PHE:O	1:C:196:GLN:HB2	2.18	0.44
1:C:279:ASN:HB3	2:C:355:HOH:O	2.18	0.44
1:C:312:ASN:OD1	1:C:323:PRO:HD2	2.18	0.44
1:A:236:GLU:O	1:A:264:ALA:N	2.50	0.44
1:B:311:ASN:C	1:B:313:LEU:N	2.71	0.44
1:D:62:HIS:NE2	1:D:64:ASP:HB3	2.33	0.44
1:C:219:THR:HB	1:C:220:PRO:CD	2.45	0.44
1:A:114:LEU:CD2	1:A:294:ILE:HG13	2.48	0.44
1:B:245:ARG:HB2	1:B:248:VAL:HG23	1.99	0.44
1:D:8:LYS:O	1:D:52:ALA:HB1	2.18	0.44
1:D:59:LEU:HA	1:D:87:HIS:CD2	2.52	0.44
1:D:99:ARG:HD2	1:D:325:GLU:CD	2.37	0.44
1:B:40:ILE:HA	1:B:41:PRO:HD3	1.88	0.44
1:B:271:THR:HG1	1:B:276:LEU:HD13	1.83	0.44
1:C:183:THR:CG2	1:C:184:GLY:N	2.80	0.44
1:D:203:PRO:HG3	1:D:233:LYS:HZ2	1.83	0.44
1:A:53:HIS:N	1:A:53:HIS:CD2	2.84	0.44
1:A:96:ARG:HG3	1:A:96:ARG:HH11	1.82	0.44
1:C:26:ALA:HB2	1:C:314:LEU:HD11	1.99	0.44
1:D:132:GLU:HB3	1:D:137:GLY:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:LEU:O	1:A:317:LEU:HB3	2.17	0.44
1:C:75:LEU:HD12	1:C:98:ILE:CD1	2.48	0.44
1:D:231:PHE:O	1:D:234:MSE:N	2.51	0.44
1:D:262:LYS:HD2	2:D:345:HOH:O	2.17	0.44
1:A:80:THR:HB	1:A:87:HIS:HE2	1.82	0.44
1:A:99:ARG:NH2	1:A:316:GLY:HA2	2.32	0.44
1:A:106:VAL:HG23	1:A:107:LEU:N	2.33	0.44
1:C:114:LEU:CD1	1:C:294:ILE:O	2.66	0.44
1:C:151:LEU:O	1:C:154:SER:HB3	2.17	0.44
1:D:42:ALA:O	1:D:46:GLU:HG3	2.17	0.44
1:D:181:LEU:HA	1:D:198:GLU:O	2.16	0.44
1:A:121:THR:HG22	1:A:126:LEU:HB2	1.99	0.44
1:A:135:ASN:OD1	1:A:136:GLY:N	2.50	0.44
1:A:161:LEU:O	1:A:161:LEU:HG	2.18	0.44
1:C:13:ARG:HH21	1:C:39:PRO:CA	2.30	0.44
1:C:75:LEU:HG	1:C:98:ILE:HG21	1.99	0.44
1:C:80:THR:HG22	1:C:101:GLY:O	2.18	0.44
1:A:61:ASP:O	1:A:87:HIS:HB2	2.17	0.44
1:B:71:ALA:HB1	1:B:75:LEU:HB2	2.00	0.44
1:D:205:LEU:HD23	1:D:205:LEU:O	2.18	0.44
1:B:140:SER:OG	1:B:141:TRP:N	2.50	0.44
1:C:175:PHE:HA	1:D:171:ARG:NH1	2.33	0.44
1:D:163:ARG:HD3	1:D:166:GLN:NE2	2.33	0.44
1:D:250:ASN:CG	1:D:253:ASP:HB2	2.38	0.44
1:D:320:GLU:HB3	1:D:321:PRO:HD2	2.00	0.44
1:A:188:ARG:HB3	1:A:191:GLU:CD	2.38	0.44
1:B:179:ARG:HD2	1:B:181:LEU:HD21	2.00	0.44
1:A:11:VAL:CG2	1:A:56:LEU:HD13	2.48	0.44
1:C:302:ARG:HG3	1:D:147:CYS:SG	2.58	0.44
1:D:9:VAL:HG22	1:D:317:LEU:HD11	2.00	0.44
1:D:308:LEU:O	1:D:312:ASN:N	2.51	0.44
1:A:182:TYR:OH	1:A:187:PRO:CA	2.65	0.44
1:A:255:TYR:O	1:A:259:ALA:N	2.40	0.44
1:B:195:PHE:C	1:B:197:ALA:N	2.70	0.44
1:C:283:LEU:CD2	1:C:290:ILE:HD12	2.47	0.44
1:A:281:PRO:O	1:A:282:LEU:C	2.56	0.44
1:B:9:VAL:HG13	1:B:313:LEU:HD11	2.00	0.44
1:C:219:THR:O	1:C:223:GLU:HG3	2.17	0.44
1:D:21:VAL:HG12	1:D:25:ARG:CD	2.47	0.44
1:A:325:GLU:O	1:A:326:LEU:HB2	2.17	0.44
1:C:83:VAL:HG23	1:C:103:THR:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:GLY:N	1:C:199:PHE:CE1	2.84	0.44
1:D:8:LYS:N	1:D:53:HIS:ND1	2.64	0.44
1:D:272:SER:HA	1:D:273:PRO:HA	1.70	0.44
1:A:139:THR:HA	1:B:275:PRO:HG3	1.99	0.44
1:A:144:LEU:HD11	1:B:14:ARG:CG	2.48	0.44
1:A:183:THR:CG2	1:A:184:GLY:N	2.80	0.44
1:A:272:SER:HA	1:A:273:PRO:HA	1.87	0.44
1:B:260:SER:OG	1:B:262:LYS:HE2	2.18	0.44
1:C:45:LEU:HG	1:C:67:ILE:CG2	2.48	0.44
1:C:76:LYS:HA	1:C:98:ILE:HG23	2.00	0.44
1:C:87:HIS:NE2	1:C:88:LEU:HG	2.33	0.44
1:C:151:LEU:HA	1:C:154:SER:OG	2.17	0.44
1:A:278:THR:C	1:A:280:HIS:H	2.20	0.44
1:A:286:LYS:HA	2:A:405:HOH:O	2.17	0.44
1:C:107:LEU:HD12	1:C:107:LEU:C	2.39	0.44
1:C:312:ASN:OD1	1:C:322:MSE:HG2	2.17	0.44
1:D:158:ILE:CD1	1:D:169:ALA:HB2	2.47	0.44
1:A:188:ARG:C	2:A:350:HOH:O	2.56	0.44
1:B:8:LYS:HB2	1:B:52:ALA:HA	2.00	0.44
1:B:65:LYS:O	1:B:69:ASP:CB	2.66	0.44
1:C:121:THR:HG1	1:D:121:THR:HG1	1.62	0.44
1:D:227:ASN:HA	1:D:250:ASN:HB3	1.99	0.44
1:B:179:ARG:HH22	1:B:208:GLN:NE2	2.16	0.44
1:B:322:MSE:SE	1:B:324:SER:O	2.86	0.44
1:B:23:LEU:HA	1:B:314:LEU:HD11	2.00	0.44
1:B:144:LEU:HD23	2:B:361:HOH:O	2.17	0.44
1:C:203:PRO:HB3	1:C:233:LYS:CE	2.40	0.44
1:D:303:ASN:O	1:D:306:SER:HB3	2.17	0.44
1:A:211:PHE:CD2	1:A:239:VAL:HB	2.53	0.44
1:B:10:PHE:O	1:B:55:LEU:HG	2.17	0.44
1:D:76:LYS:C	1:D:98:ILE:HG23	2.38	0.44
1:D:255:TYR:CE1	1:D:281:PRO:HB3	2.52	0.44
1:A:78:ILE:HG21	1:A:88:LEU:CD2	2.48	0.44
1:A:102:TYR:CG	1:A:104:PRO:HD3	2.52	0.44
1:B:142:LYS:HA	1:B:143:PRO:HD2	1.81	0.44
1:C:310:ALA:O	1:C:314:LEU:HB2	2.18	0.44
1:D:157:GLY:HA3	1:D:209:SER:OG	2.18	0.44
1:A:175:PHE:CE2	1:B:171:ARG:HD2	2.52	0.44
1:A:180:PHE:O	1:A:197:ALA:HA	2.18	0.44
1:B:49:VAL:HB	1:B:70:ALA:HB3	2.00	0.44
1:C:93:ILE:HD11	1:C:100:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:119:LEU:HD23	1:D:119:LEU:O	2.18	0.44
1:D:258:LEU:HD22	1:D:287:ASN:HD21	1.82	0.44
1:D:262:LYS:HD3	1:D:262:LYS:HA	1.87	0.44
1:A:182:TYR:CD1	1:A:197:ALA:HB1	2.52	0.44
1:B:7:MSE:HE3	1:B:317:LEU:O	2.17	0.44
1:B:139:THR:OG1	1:B:142:LYS:NZ	2.48	0.44
1:A:171:ARG:HD3	1:B:175:PHE:CD2	2.53	0.44
1:A:257:ALA:CA	1:A:262:LYS:HB2	2.48	0.44
1:A:131:GLU:HG3	1:A:135:ASN:ND2	2.32	0.44
1:A:156:VAL:HB	1:A:180:PHE:CD1	2.53	0.44
1:A:271:THR:O	1:A:274:GLU:HG3	2.18	0.44
1:C:175:PHE:HA	1:D:171:ARG:NH1	2.32	0.44
1:D:15:ILE:HD11	1:D:23:LEU:HD11	2.00	0.44
1:D:155:THR:HB	1:D:210:ASP:OD2	2.18	0.44
1:A:154:SER:OG	1:A:210:ASP:HB2	2.18	0.44
1:B:6:LEU:HD12	1:B:30:GLU:OE1	2.17	0.44
1:C:216:CYS:O	1:C:244:SER:HB2	2.18	0.44
1:D:276:LEU:O	1:D:277:PRO:C	2.56	0.44
1:B:49:VAL:HG12	1:B:55:LEU:HD13	1.99	0.44
1:C:142:LYS:HB3	2:C:377:HOH:O	2.17	0.44
1:A:325:GLU:CG	1:A:326:LEU:N	2.81	0.44
1:B:85:ILE:HB	1:B:88:LEU:HD12	1.99	0.44
1:C:315:ALA:HB1	1:C:320:GLU:O	2.18	0.44
1:D:34:TRP:CD2	1:D:40:ILE:HD12	2.53	0.44
1:A:88:LEU:CD1	1:A:100:VAL:HG22	2.48	0.44
1:A:147:CYS:SG	1:B:302:ARG:HG3	2.58	0.44
1:B:185:ARG:HD2	1:B:185:ARG:HA	1.86	0.44
1:A:175:PHE:CD2	1:B:171:ARG:HD2	2.53	0.44
1:C:34:TRP:CH2	1:C:44:GLU:HG3	2.52	0.44
1:D:80:THR:HG22	1:D:101:GLY:O	2.18	0.44
1:D:305:MSE:O	1:D:306:SER:C	2.56	0.44
1:A:184:GLY:N	1:A:199:PHE:HE1	2.15	0.44
1:B:312:ASN:HA	1:B:323:PRO:HD2	1.99	0.44
1:B:58:LEU:N	1:B:61:ASP:OD2	2.46	0.43
1:D:19:GLY:O	1:D:23:LEU:HG	2.18	0.43
1:A:32:GLU:HG3	1:A:33:GLN:H	1.82	0.43
1:A:43:LYS:O	1:A:46:GLU:HB2	2.17	0.43
1:A:227:ASN:C	1:A:229:ASP:H	2.22	0.43
1:A:11:VAL:HG22	1:A:56:LEU:CD1	2.48	0.43
1:A:309:ALA:HA	1:A:312:ASN:HD22	1.81	0.43
1:D:259:ALA:C	1:D:261:GLY:H	2.20	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:LEU:HB2	1:A:205:LEU:HD13	2.00	0.43
1:A:236:GLU:C	1:A:238:ALA:H	2.21	0.43
1:B:297:ALA:N	1:B:302:ARG:HH21	2.16	0.43
1:D:314:LEU:HD23	1:D:317:LEU:CD2	2.46	0.43
1:A:7:MSE:HE3	1:A:28:ASP:O	2.17	0.43
1:A:128:GLU:HG3	2:A:385:HOH:O	2.18	0.43
1:A:182:TYR:CE1	1:A:199:PHE:HB2	2.53	0.43
1:A:182:TYR:OH	1:A:188:ARG:N	2.51	0.43
1:C:155:THR:HG22	1:C:209:SER:HA	2.00	0.43
1:B:180:PHE:HB2	2:B:379:HOH:O	2.18	0.43
1:B:181:LEU:O	1:B:182:TYR:HB3	2.18	0.43
1:C:202:THR:HB	1:C:203:PRO:CD	2.44	0.43
1:C:305:MSE:O	1:C:308:LEU:HB3	2.18	0.43
1:B:188:ARG:O	1:B:188:ARG:HG2	2.17	0.43
1:B:316:GLY:C	1:B:318:ARG:H	2.22	0.43
1:D:7:MSE:HE3	1:D:29:CYS:HB2	1.99	0.43
1:A:76:LYS:CD	1:A:317:LEU:HD12	2.45	0.43
1:A:155:THR:HG23	1:A:179:ARG:CD	2.46	0.43
1:A:258:LEU:CD2	1:A:263:ILE:HG13	2.40	0.43
1:D:7:MSE:HA	1:D:53:HIS:CE1	2.53	0.43
1:D:218:LEU:HD12	1:D:219:THR:N	2.32	0.43
1:A:272:SER:HA	1:A:273:PRO:HA	1.86	0.43
1:B:13:ARG:NH2	1:B:58:LEU:HD12	2.33	0.43
1:D:8:LYS:CG	1:D:52:ALA:HA	2.48	0.43
1:B:65:LYS:HE3	1:B:92:GLU:CG	2.48	0.43
1:C:230:PHE:C	1:C:232:GLN:N	2.71	0.43
1:C:326:LEU:C	1:C:326:LEU:HD23	2.38	0.43
1:D:94:LYS:C	1:D:96:ARG:N	2.70	0.43
1:D:312:ASN:C	1:D:314:LEU:N	2.70	0.43
1:B:72:GLY:HA3	2:B:336:HOH:O	2.17	0.43
1:B:223:GLU:CA	1:B:248:VAL:HA	2.44	0.43
1:C:12:THR:O	1:C:34:TRP:HB3	2.18	0.43
1:A:152:THR:HA	1:A:176:GLY:O	2.19	0.43
1:A:268:LEU:O	1:A:290:ILE:HA	2.18	0.43
1:B:53:HIS:HD2	1:B:76:LYS:CD	2.31	0.43
1:C:81:MSE:O	1:C:81:MSE:HG2	2.18	0.43
1:C:185:ARG:O	1:C:186:GLN:HG2	2.19	0.43
1:D:6:LEU:HD21	1:D:27:ALA:O	2.18	0.43
1:A:59:LEU:HD11	1:A:82:SER:CB	2.48	0.43
1:D:156:VAL:HB	1:D:180:PHE:CE1	2.53	0.43
1:D:161:LEU:HG	1:D:166:GLN:CG	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:251:GLN:OE1	1:D:272:SER:N	2.50	0.43
1:B:64:ASP:CA	1:B:93:ILE:HD11	2.48	0.43
1:C:255:TYR:CD1	1:C:285:LEU:HD11	2.53	0.43
1:D:192:ALA:HB1	1:D:197:ALA:HB3	2.00	0.43
1:D:245:ARG:HD3	1:D:245:ARG:HA	1.80	0.43
1:A:79:SER:HB2	1:A:313:LEU:HB2	1.99	0.43
1:A:155:THR:O	1:A:209:SER:HA	2.18	0.43
1:A:179:ARG:HD2	1:A:179:ARG:O	2.18	0.43
1:B:40:ILE:HG22	2:B:361:HOH:O	2.16	0.43
1:D:185:ARG:CD	1:D:185:ARG:H	2.31	0.43
1:A:83:VAL:HG23	1:A:104:PRO:CA	2.48	0.43
1:C:112:ALA:HB2	1:C:167:ALA:HB3	2.00	0.43
1:C:117:SER:OG	1:D:120:LEU:HB3	2.19	0.43
1:D:231:PHE:CZ	1:D:254:LEU:HD13	2.53	0.43
1:A:11:VAL:HB	1:A:33:GLN:NE2	2.27	0.43
1:B:34:TRP:CD1	1:B:40:ILE:HB	2.53	0.43
1:B:140:SER:OG	1:B:141:TRP:N	2.51	0.43
1:C:256:GLN:NE2	2:C:409:HOH:O	2.47	0.43
1:A:272:SER:HA	1:A:273:PRO:HA	1.66	0.43
1:C:202:THR:HB	1:C:203:PRO:CD	2.45	0.43
1:C:283:LEU:CD2	1:C:290:ILE:HD12	2.48	0.43
1:D:114:LEU:HG	1:D:114:LEU:O	2.18	0.43
1:A:104:PRO:HG2	2:A:398:HOH:O	2.17	0.43
1:D:280:HIS:CE1	1:D:282:LEU:H	2.36	0.43
1:D:315:ALA:CB	1:D:322:MSE:HG2	2.48	0.43
1:B:179:ARG:HH22	1:B:208:GLN:NE2	2.15	0.43
1:C:47:ARG:CZ	2:C:415:HOH:O	2.65	0.43
1:D:206:ALA:HB2	1:D:230:PHE:CD1	2.53	0.43
1:D:209:SER:HB3	1:D:211:PHE:O	2.18	0.43
1:A:126:LEU:HG	1:B:291:LEU:HD21	1.99	0.43
1:A:235:LYS:HB2	1:A:238:ALA:HB2	2.01	0.43
1:C:57:CYS:HB2	1:C:61:ASP:OD2	2.18	0.43
1:C:102:TYR:CG	1:C:103:THR:N	2.86	0.43
1:C:182:TYR:O	1:C:199:PHE:HA	2.18	0.43
1:D:227:ASN:ND2	1:D:228:LYS:N	2.65	0.43
1:B:68:LEU:HD22	1:B:75:LEU:CD2	2.48	0.43
1:B:302:ARG:HA	1:B:302:ARG:HD3	1.80	0.43
1:C:300:ARG:HG2	1:C:300:ARG:NH1	2.33	0.43
1:C:310:ALA:O	1:C:313:LEU:HB3	2.18	0.43
1:C:311:ASN:O	1:C:314:LEU:N	2.51	0.43
1:A:83:VAL:HG23	1:A:104:PRO:CB	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:ARG:O	1:A:166:GLN:N	2.51	0.43
1:B:184:GLY:N	1:B:199:PHE:CE1	2.87	0.43
1:C:76:LYS:O	1:C:98:ILE:HG23	2.18	0.43
1:C:312:ASN:OD1	1:C:323:PRO:HD2	2.19	0.43
1:D:87:HIS:HD1	1:D:87:HIS:H	1.66	0.43
1:D:103:THR:HG22	1:D:308:LEU:HG	2.01	0.43
1:D:252:ASP:O	1:D:255:TYR:HB3	2.18	0.43
1:A:89:ALA:O	1:A:93:ILE:HG13	2.19	0.43
1:B:59:LEU:C	1:B:59:LEU:HD12	2.39	0.43
1:B:234:MSE:HG2	2:B:331:HOH:O	2.18	0.43
1:A:144:LEU:HD23	1:A:144:LEU:H	1.82	0.43
1:A:255:TYR:HE1	1:A:285:LEU:HG	1.83	0.43
1:C:85:ILE:HD12	2:C:352:HOH:O	2.17	0.43
1:D:75:LEU:CD2	1:D:98:ILE:HD13	2.47	0.43
1:A:116:VAL:HG21	1:A:171:ARG:HB3	2.00	0.43
1:C:102:TYR:CZ	1:C:104:PRO:HG3	2.53	0.43
1:D:53:HIS:ND1	1:D:53:HIS:N	2.66	0.43
1:A:21:VAL:C	1:A:23:LEU:H	2.21	0.43
1:A:102:TYR:CD1	1:A:102:TYR:N	2.86	0.43
1:A:322:MSE:C	1:A:324:SER:N	2.71	0.43
1:D:83:VAL:HG23	1:D:104:PRO:HB3	2.00	0.43
1:D:218:LEU:HB3	1:D:245:ARG:HG3	1.99	0.43
1:A:79:SER:OG	2:A:362:HOH:O	2.21	0.43
1:A:94:LYS:HB3	2:A:350:HOH:O	2.18	0.43
1:B:153:GLN:HA	1:B:178:GLN:HB2	2.00	0.43
1:B:183:THR:HA	1:B:199:PHE:CD1	2.54	0.43
1:C:108:THR:O	1:C:108:THR:CG2	2.66	0.43
1:C:227:ASN:H	1:C:230:PHE:HB2	1.82	0.43
1:D:9:VAL:HG11	1:D:313:LEU:HD21	2.00	0.43
1:A:80:THR:HG1	1:A:87:HIS:CE1	2.34	0.43
1:B:40:ILE:CD1	1:B:44:GLU:HB3	2.47	0.43
1:B:179:ARG:HH12	1:B:208:GLN:HE22	1.66	0.43
1:B:212:ILE:HD13	1:B:234:MSE:CE	2.45	0.43
1:C:314:LEU:HD12	1:C:314:LEU:HA	1.90	0.43
1:D:13:ARG:HG2	1:D:36:SER:O	2.18	0.43
1:D:205:LEU:C	1:D:207:ALA:H	2.21	0.43
1:D:305:MSE:O	1:D:309:ALA:N	2.40	0.43
1:A:227:ASN:O	1:A:230:PHE:HB3	2.19	0.43
1:B:11:VAL:HG12	1:B:13:ARG:O	2.18	0.43
1:B:90:LEU:HD23	1:B:93:ILE:HD12	2.00	0.43
1:C:96:ARG:HG3	1:C:96:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:ARG:NH1	1:C:322:MSE:HG3	2.33	0.43
1:C:236:GLU:HA	1:C:262:LYS:O	2.18	0.43
1:D:59:LEU:C	1:D:59:LEU:HD12	2.38	0.43
1:D:163:ARG:HD3	1:D:163:ARG:HA	1.82	0.43
1:D:177:VAL:HG11	1:D:180:PHE:CZ	2.53	0.43
1:A:103:THR:CG2	1:A:308:LEU:HB3	2.49	0.43
1:A:212:ILE:CG1	1:A:234:MSE:HE3	2.49	0.43
1:B:178:GLN:NE2	2:B:340:HOH:O	2.52	0.43
1:C:75:LEU:O	1:C:98:ILE:HD11	2.18	0.43
1:C:283:LEU:CD2	1:C:290:ILE:HD12	2.48	0.43
1:A:133:VAL:HG23	1:B:292:PRO:HD3	2.01	0.43
1:C:206:ALA:HB3	1:C:233:LYS:HB2	2.00	0.43
1:D:164:ILE:CB	1:D:215:ALA:HB1	2.46	0.43
1:B:67:ILE:O	1:B:70:ALA:N	2.51	0.43
1:B:69:ASP:OD1	1:B:96:ARG:NH2	2.50	0.43
1:B:140:SER:OG	1:B:141:TRP:N	2.51	0.43
1:D:183:THR:HG21	1:D:202:THR:N	2.33	0.43
1:A:6:LEU:HD22	1:A:28:ASP:O	2.18	0.43
1:A:53:HIS:HB3	1:A:76:LYS:HG2	2.00	0.43
1:B:62:HIS:CE1	2:B:415:HOH:O	2.71	0.43
1:C:185:ARG:HH22	1:C:217:SER:H	1.65	0.43
1:D:40:ILE:CG1	1:D:44:GLU:HB2	2.48	0.43
1:D:135:ASN:HB3	2:D:342:HOH:O	2.18	0.43
1:A:256:GLN:NE2	1:A:256:GLN:HA	2.34	0.43
1:B:226:CYS:CB	1:B:249:VAL:HG13	2.49	0.43
1:C:102:TYR:HD1	1:C:102:TYR:H	1.66	0.43
1:D:277:PRO:HB2	1:D:280:HIS:HB2	2.01	0.43
1:A:43:LYS:HE3	1:A:47:ARG:NH2	2.26	0.43
1:A:114:LEU:CG	1:A:295:GLY:HA2	2.49	0.43
1:C:43:LYS:O	1:C:46:GLU:HB2	2.19	0.43
1:C:76:LYS:CD	1:C:317:LEU:HA	2.48	0.43
1:C:227:ASN:H	1:C:230:PHE:CB	2.31	0.43
1:D:85:ILE:O	1:D:88:LEU:HB2	2.18	0.43
1:D:179:ARG:O	1:D:180:PHE:CG	2.72	0.43
1:D:181:LEU:HB3	1:D:200:VAL:HG22	2.01	0.43
1:B:45:LEU:HG	1:B:45:LEU:O	2.19	0.43
1:B:53:HIS:CA	1:B:75:LEU:HA	2.47	0.43
1:B:312:ASN:CG	1:B:322:MSE:HE2	2.39	0.43
1:D:186:GLN:HG2	1:D:187:PRO:N	2.33	0.43
1:D:278:THR:O	1:D:280:HIS:N	2.42	0.43
1:A:155:THR:HG22	1:A:155:THR:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:SER:HA	1:A:273:PRO:HA	1.68	0.43
1:C:30:GLU:HG2	2:C:443:HOH:O	2.17	0.43
1:C:10:PHE:CE2	1:C:12:THR:HG22	2.53	0.43
1:C:18:GLU:HA	1:C:18:GLU:OE1	2.18	0.43
1:C:296:SER:O	1:C:302:ARG:NE	2.52	0.43
1:A:168:ILE:HD13	1:A:213:VAL:HG11	2.00	0.43
1:C:236:GLU:HA	1:C:262:LYS:O	2.18	0.43
1:B:119:LEU:HD23	1:B:119:LEU:C	2.39	0.43
1:B:322:MSE:SE	1:B:325:GLU:HA	2.68	0.43
1:C:47:ARG:HB3	1:C:47:ARG:HH11	1.81	0.43
1:C:240:PHE:O	1:C:266:ALA:HA	2.19	0.43
1:D:314:LEU:C	1:D:316:GLY:H	2.20	0.43
1:A:81:MSE:HE2	1:B:141:TRP:HH2	1.84	0.43
1:A:92:GLU:OE1	1:A:96:ARG:NH1	2.46	0.43
1:B:19:GLY:HA2	1:B:307:LEU:HA	2.00	0.43
1:B:140:SER:OG	1:B:141:TRP:N	2.51	0.43
1:B:204:GLU:OE1	1:B:208:GLN:NE2	2.52	0.43
1:B:234:MSE:SE	1:B:263:ILE:CG2	3.13	0.43
1:C:182:TYR:CD1	1:C:197:ALA:HB1	2.53	0.43
1:A:10:PHE:CE1	1:A:48:GLY:HA3	2.53	0.43
1:B:68:LEU:CD2	1:B:75:LEU:HD23	2.49	0.43
1:C:283:LEU:CD2	1:C:290:ILE:HD12	2.49	0.43
1:A:12:THR:O	1:A:13:ARG:HB2	2.18	0.43
1:B:12:THR:O	1:B:13:ARG:HG3	2.19	0.43
1:B:49:VAL:CG1	1:B:55:LEU:HD13	2.48	0.43
1:B:206:ALA:HA	1:B:212:ILE:HD11	2.00	0.43
1:C:18:GLU:O	1:C:21:VAL:HB	2.17	0.43
1:C:49:VAL:HG23	1:C:71:ALA:HA	2.01	0.43
1:C:103:THR:HG22	1:C:308:LEU:HD23	1.99	0.43
1:C:157:GLY:HA3	1:C:212:ILE:HD13	2.01	0.43
1:D:218:LEU:HD22	1:D:245:ARG:HG3	2.01	0.43
1:A:74:ASN:O	1:A:75:LEU:O	2.37	0.43
1:B:114:LEU:HD13	1:B:294:ILE:O	2.19	0.43
1:C:311:ASN:O	1:C:312:ASN:C	2.56	0.43
1:D:74:ASN:HB2	2:D:417:HOH:O	2.18	0.43
1:D:314:LEU:O	1:D:317:LEU:N	2.52	0.43
1:A:228:LYS:HB2	1:A:253:ASP:CG	2.39	0.43
1:A:315:ALA:HB3	1:A:322:MSE:SE	2.68	0.43
1:B:180:PHE:O	1:B:197:ALA:HA	2.18	0.43
1:B:222:THR:O	1:B:248:VAL:HA	2.18	0.43
1:C:144:LEU:CD2	1:D:16:PRO:HG3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:311:ASN:O	1:C:312:ASN:C	2.56	0.43
1:D:276:LEU:HG	1:D:277:PRO:HD2	2.01	0.43
1:D:280:HIS:CE1	1:D:281:PRO:HD2	2.53	0.43
1:A:94:LYS:O	1:A:97:GLY:N	2.49	0.43
1:B:80:THR:HG21	1:B:87:HIS:HE1	1.83	0.43
1:B:95:LYS:C	1:B:97:GLY:H	2.21	0.43
1:C:14:ARG:O	1:C:14:ARG:HG2	2.18	0.43
1:C:75:LEU:HD23	1:C:98:ILE:CG1	2.48	0.43
1:D:8:LYS:N	1:D:30:GLU:HB3	2.34	0.43
1:D:144:LEU:N	1:D:144:LEU:HD12	2.33	0.43
1:D:153:GLN:HE21	1:D:178:GLN:HE22	1.65	0.43
1:A:9:VAL:HG13	1:A:54:GLY:O	2.17	0.43
1:A:63:VAL:CG1	1:A:64:ASP:N	2.81	0.43
1:B:119:LEU:HD23	1:B:119:LEU:C	2.39	0.43
1:B:126:LEU:CD1	1:B:126:LEU:H	2.32	0.43
1:A:20:ARG:HG3	1:A:20:ARG:HH11	1.84	0.43
1:A:23:LEU:HD22	1:A:314:LEU:HD13	1.99	0.43
1:A:40:ILE:HG23	1:A:45:LEU:HB2	1.99	0.43
1:A:123:CYS:O	1:A:148:GLY:HA3	2.18	0.43
1:A:319:GLY:O	1:A:320:GLU:O	2.37	0.43
1:B:49:VAL:CG1	1:B:55:LEU:HD13	2.48	0.43
1:B:58:LEU:O	1:B:61:ASP:HB2	2.19	0.43
1:B:114:LEU:HD11	1:B:294:ILE:HG13	2.01	0.43
1:B:119:LEU:HD23	1:B:119:LEU:C	2.39	0.43
1:C:15:ILE:HB	1:C:81:MSE:HE1	2.01	0.43
1:C:291:LEU:CD2	1:D:126:LEU:HG	2.48	0.43
1:C:312:ASN:OD1	1:C:323:PRO:HD2	2.18	0.43
1:D:202:THR:HG21	1:D:225:LEU:HD11	2.00	0.43
1:A:135:ASN:OD1	1:A:136:GLY:N	2.52	0.43
1:B:8:LYS:HB3	1:B:52:ALA:HA	2.01	0.43
1:B:219:THR:HB	1:B:220:PRO:HD2	2.01	0.43
1:C:175:PHE:HA	1:D:171:ARG:NH1	2.33	0.43
1:C:202:THR:HB	1:C:203:PRO:CD	2.44	0.43
1:A:99:ARG:NH2	1:A:316:GLY:CA	2.82	0.43
1:A:10:PHE:HA	1:A:32:GLU:O	2.19	0.43
1:A:85:ILE:CD1	1:A:90:LEU:HD11	2.46	0.43
1:A:110:THR:HG23	1:A:298:THR:HG23	2.01	0.43
1:B:218:LEU:HB2	1:B:245:ARG:CB	2.48	0.43
1:B:319:GLY:O	1:B:320:GLU:O	2.37	0.43
1:B:99:ARG:HD2	1:B:322:MSE:SE	2.68	0.43
1:B:310:ALA:O	1:B:314:LEU:HG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:89:ALA:O	1:C:91:ASP:N	2.49	0.43
1:C:169:ALA:HB3	1:C:195:PHE:CZ	2.54	0.43
1:D:182:TYR:CE1	1:D:199:PHE:HA	2.54	0.43
1:B:325:GLU:CG	1:B:326:LEU:N	2.72	0.43
1:C:228:LYS:H	1:C:253:ASP:CG	2.22	0.43
1:B:7:MSE:O	1:B:30:GLU:N	2.52	0.43
1:D:64:ASP:HA	1:D:89:ALA:CB	2.49	0.43
1:A:107:LEU:HD12	1:A:108:THR:N	2.34	0.43
1:A:191:GLU:HA	2:A:358:HOH:O	2.19	0.43
1:C:186:GLN:HA	1:C:187:PRO:HD3	1.85	0.43
1:D:280:HIS:CG	1:D:281:PRO:HD2	2.53	0.43
1:A:33:GLN:N	2:A:368:HOH:O	2.47	0.43
1:B:12:THR:C	1:B:34:TRP:HB3	2.39	0.43
1:B:178:GLN:OE1	1:B:178:GLN:O	2.37	0.43
1:B:276:LEU:HD22	1:B:290:ILE:HD13	2.00	0.43
1:C:34:TRP:O	1:C:34:TRP:CD1	2.72	0.43
1:A:49:VAL:HG11	1:A:67:ILE:CG2	2.48	0.43
1:A:65:LYS:NZ	1:A:69:ASP:OD2	2.52	0.43
1:A:280:HIS:HA	1:A:281:PRO:HD3	1.96	0.43
1:C:54:GLY:HA2	1:C:77:VAL:O	2.19	0.43
1:A:121:THR:HG23	1:A:126:LEU:CD2	2.48	0.43
1:A:144:LEU:HD11	1:B:14:ARG:HG2	2.01	0.43
1:A:314:LEU:O	1:A:318:ARG:HD2	2.17	0.43
1:B:10:PHE:CD1	1:B:33:GLN:HA	2.54	0.43
1:B:181:LEU:CD2	1:B:198:GLU:HB3	2.48	0.43
1:A:160:GLY:C	1:A:162:GLY:H	2.20	0.43
1:A:186:GLN:O	1:A:188:ARG:NH1	2.52	0.43
1:B:15:ILE:O	1:B:20:ARG:NH1	2.49	0.43
1:B:65:LYS:HE3	1:B:96:ARG:HH22	1.84	0.43
1:C:62:HIS:O	1:C:67:ILE:HG13	2.19	0.43
1:C:292:PRO:CD	1:D:129:ALA:HB1	2.48	0.43
1:A:107:LEU:HD23	1:A:305:MSE:CE	2.47	0.43
1:A:188:ARG:NE	2:A:431:HOH:O	2.50	0.43
1:A:249:VAL:HB	2:A:399:HOH:O	2.17	0.43
1:D:104:PRO:C	1:D:106:VAL:H	2.22	0.43
1:D:192:ALA:CB	1:D:197:ALA:HB3	2.48	0.43
1:A:59:LEU:O	1:A:59:LEU:HG	2.19	0.43
1:B:126:LEU:CD1	1:B:126:LEU:H	2.32	0.43
1:C:219:THR:HB	1:C:220:PRO:HD2	2.01	0.43
1:C:322:MSE:HG2	1:C:324:SER:H	1.84	0.43
1:A:201:SER:CB	1:A:203:PRO:HD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:ASP:HA	1:B:89:ALA:HB2	2.01	0.43
1:A:13:ARG:O	1:A:15:ILE:HG23	2.19	0.43
1:A:233:LYS:O	1:A:234:MSE:C	2.57	0.43
1:A:235:LYS:HB2	1:A:238:ALA:HB2	2.00	0.43
1:B:58:LEU:N	1:B:61:ASP:OD2	2.51	0.43
1:B:255:TYR:CD1	1:B:255:TYR:C	2.91	0.43
1:C:159:ILE:HB	1:C:214:VAL:HA	2.01	0.43
1:D:155:THR:O	1:D:210:ASP:HB2	2.19	0.43
1:D:262:LYS:HD2	2:D:345:HOH:O	2.18	0.43
1:A:25:ARG:O	1:A:27:ALA:N	2.52	0.43
1:A:148:GLY:O	1:B:298:THR:HA	2.19	0.43
1:C:292:PRO:CD	1:D:129:ALA:HB1	2.48	0.43
1:A:272:SER:HA	1:A:273:PRO:HA	1.65	0.43
1:B:64:ASP:OD2	1:B:67:ILE:HG12	2.18	0.43
1:A:34:TRP:CE2	1:A:40:ILE:HB	2.54	0.43
1:A:161:LEU:O	1:A:166:GLN:HG3	2.18	0.43
1:B:6:LEU:HB3	1:B:7:MSE:H	1.58	0.43
1:B:251:GLN:NE2	1:B:276:LEU:HD11	2.30	0.43
1:B:271:THR:HB	1:B:276:LEU:HD13	2.00	0.43
1:B:271:THR:HG21	1:B:276:LEU:HD22	2.01	0.43
1:C:40:ILE:HG12	1:C:44:GLU:HB2	1.98	0.43
1:A:286:LYS:N	2:A:349:HOH:O	2.46	0.43
1:B:135:ASN:C	1:B:137:GLY:H	2.22	0.43
1:B:302:ARG:HD3	1:B:302:ARG:HA	1.71	0.43
1:D:201:SER:OG	1:D:203:PRO:HD2	2.19	0.43
1:A:147:CYS:HA	1:B:297:ALA:O	2.19	0.43
1:A:180:PHE:O	1:A:197:ALA:HA	2.19	0.43
1:B:119:LEU:HD23	1:B:119:LEU:C	2.39	0.43
1:C:16:PRO:HG3	1:D:144:LEU:HD11	2.01	0.43
1:C:238:ALA:O	1:C:264:ALA:HB3	2.19	0.43
1:C:240:PHE:O	1:C:266:ALA:HA	2.19	0.43
1:A:16:PRO:HD2	1:A:306:SER:HB3	2.01	0.43
1:B:311:ASN:ND2	2:B:404:HOH:O	2.52	0.43
1:D:228:LYS:O	1:D:232:GLN:HG2	2.19	0.43
1:A:277:PRO:C	1:A:279:ASN:N	2.72	0.43
1:C:7:MSE:SE	1:C:53:HIS:ND1	3.02	0.43
1:C:59:LEU:HD12	1:C:59:LEU:C	2.39	0.43
1:C:117:SER:OG	1:D:120:LEU:HB3	2.18	0.43
1:A:16:PRO:HD3	1:B:143:PRO:HB2	2.01	0.43
1:B:88:LEU:O	1:B:90:LEU:N	2.52	0.43
1:B:226:CYS:HA	1:B:230:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:63:VAL:HG13	1:C:67:ILE:CB	2.49	0.43
1:A:322:MSE:CG	1:A:325:GLU:HB2	2.49	0.43
1:B:230:PHE:CD1	1:B:234:MSE:SE	3.22	0.43
1:C:309:ALA:HA	2:C:362:HOH:O	2.17	0.43
1:C:12:THR:HG23	1:C:55:LEU:HD11	2.01	0.43
1:C:249:VAL:O	1:C:251:GLN:N	2.52	0.43
1:D:280:HIS:CE1	1:D:281:PRO:HD2	2.54	0.43
1:A:46:GLU:CG	1:A:67:ILE:HD13	2.49	0.43
1:A:204:GLU:O	1:A:208:GLN:HG2	2.19	0.43
1:B:153:GLN:HA	1:B:178:GLN:NE2	2.34	0.43
1:C:231:PHE:HD1	1:C:234:MSE:SE	2.52	0.43
1:D:156:VAL:HB	1:D:180:PHE:CD1	2.54	0.43
1:C:228:LYS:NZ	2:C:331:HOH:O	2.49	0.43
1:B:110:THR:O	1:B:113:GLU:HB3	2.18	0.42
1:D:18:GLU:HG3	1:D:303:ASN:CA	2.48	0.42
1:D:315:ALA:CB	1:D:322:MSE:HA	2.42	0.42
1:A:163:ARG:HG2	1:A:163:ARG:HH11	1.84	0.42
1:A:167:ALA:O	1:A:171:ARG:HB2	2.19	0.42
1:B:88:LEU:HB2	1:B:90:LEU:CD1	2.49	0.42
1:B:183:THR:N	1:B:205:LEU:CD2	2.82	0.42
1:B:189:PRO:O	1:B:191:GLU:N	2.42	0.42
1:B:285:LEU:HB2	1:B:288:CYS:CB	2.49	0.42
1:C:40:ILE:HG12	1:C:45:LEU:HB2	2.01	0.42
1:C:179:ARG:HG3	1:C:179:ARG:NH1	2.33	0.42
1:D:20:ARG:NH2	2:D:424:HOH:O	2.51	0.42
1:A:14:ARG:NH1	1:A:35:ASP:HB3	2.34	0.42
1:A:250:ASN:OD1	1:A:253:ASP:HB2	2.19	0.42
1:B:326:LEU:HD12	2:B:389:HOH:O	2.18	0.42
1:C:202:THR:CB	1:C:203:PRO:HD3	2.44	0.42
1:D:114:LEU:O	1:D:114:LEU:HG	2.18	0.42
1:B:14:ARG:CG	1:B:20:ARG:HH11	2.31	0.42
1:B:159:ILE:HB	1:B:214:VAL:HA	2.00	0.42
1:C:12:THR:O	1:C:34:TRP:HB3	2.18	0.42
1:C:47:ARG:NH2	2:C:415:HOH:O	2.52	0.42
1:C:51:GLY:CA	1:C:72:GLY:HA3	2.41	0.42
1:D:292:PRO:HG2	1:D:294:ILE:HG23	2.01	0.42
1:A:78:ILE:HG22	1:A:78:ILE:O	2.18	0.42
1:A:175:PHE:CE1	1:B:171:ARG:HG2	2.54	0.42
1:B:16:PRO:O	1:B:20:ARG:HG2	2.19	0.42
1:B:63:VAL:CB	1:B:88:LEU:HD23	2.44	0.42
1:B:67:ILE:O	1:B:70:ALA:HB3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:LYS:NZ	2:C:394:HOH:O	2.45	0.42
1:B:312:ASN:OD1	1:B:322:MSE:HE2	2.18	0.42
1:D:163:ARG:HA	1:D:163:ARG:NE	2.23	0.42
1:D:280:HIS:CB	1:D:283:LEU:HD12	2.49	0.42
1:A:192:ALA:O	1:A:196:GLN:N	2.52	0.42
1:B:79:SER:CB	1:B:313:LEU:HD23	2.49	0.42
1:B:110:THR:CG2	1:B:298:THR:HG23	2.49	0.42
1:D:16:PRO:HB3	1:D:303:ASN:OD1	2.19	0.42
1:A:21:VAL:O	1:A:25:ARG:N	2.51	0.42
1:A:226:CYS:SG	1:A:248:VAL:HG12	2.59	0.42
1:A:227:ASN:HB2	1:A:253:ASP:OD2	2.20	0.42
1:A:280:HIS:ND1	1:A:281:PRO:N	2.66	0.42
1:C:99:ARG:NH1	1:C:320:GLU:O	2.52	0.42
1:D:187:PRO:HG3	1:D:199:PHE:CZ	2.54	0.42
1:A:188:ARG:NH1	2:A:432:HOH:O	2.44	0.42
1:B:186:GLN:HG3	1:B:187:PRO:N	2.34	0.42
1:B:272:SER:HA	1:B:273:PRO:HA	1.80	0.42
1:D:162:GLY:HA2	1:D:188:ARG:HH12	1.84	0.42
1:D:251:GLN:OE1	1:D:272:SER:N	2.50	0.42
1:A:175:PHE:CG	1:B:171:ARG:HG2	2.54	0.42
1:A:235:LYS:C	1:A:237:THR:H	2.22	0.42
1:A:266:ALA:O	1:A:288:CYS:HA	2.19	0.42
1:A:301:THR:O	1:A:305:MSE:HG3	2.19	0.42
1:B:53:HIS:O	1:B:75:LEU:HA	2.19	0.42
1:C:11:VAL:HG11	1:C:15:ILE:CG2	2.48	0.42
1:D:85:ILE:HD12	1:D:85:ILE:C	2.39	0.42
1:A:103:THR:CB	1:A:308:LEU:HD23	2.49	0.42
1:A:153:GLN:NE2	1:A:153:GLN:CA	2.79	0.42
1:A:320:GLU:HB3	1:A:321:PRO:CD	2.48	0.42
1:B:126:LEU:CD1	1:B:126:LEU:H	2.33	0.42
1:C:107:LEU:HD12	1:C:107:LEU:C	2.40	0.42
1:C:203:PRO:HA	1:C:233:LYS:HD3	2.00	0.42
1:D:81:MSE:HA	1:D:103:THR:HG21	2.00	0.42
1:C:312:ASN:OD1	1:C:322:MSE:HB2	2.19	0.42
1:B:320:GLU:HB3	1:B:321:PRO:CD	2.42	0.42
1:C:58:LEU:HD13	1:D:141:TRP:CZ3	2.54	0.42
1:C:192:ALA:CB	1:C:197:ALA:HB3	2.46	0.42
1:C:240:PHE:CE2	1:C:249:VAL:HG21	2.55	0.42
1:B:8:LYS:HE3	1:B:51:GLY:C	2.39	0.42
1:B:116:VAL:HG21	1:B:171:ARG:HB2	2.01	0.42
1:C:76:LYS:HB3	1:C:76:LYS:HZ3	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ASP:O	1:A:68:LEU:HG	2.20	0.42
1:A:182:TYR:CZ	1:A:199:PHE:HB2	2.54	0.42
1:B:118:LEU:HD13	1:B:291:LEU:CD1	2.49	0.42
1:B:255:TYR:CZ	1:B:281:PRO:HB3	2.54	0.42
1:D:273:PRO:C	1:D:274:GLU:HG2	2.39	0.42
1:A:47:ARG:O	1:A:47:ARG:HG2	2.20	0.42
1:A:187:PRO:HG3	1:A:199:PHE:CZ	2.54	0.42
1:C:236:GLU:HG3	1:C:237:THR:N	2.35	0.42
1:D:119:LEU:HD23	1:D:119:LEU:C	2.39	0.42
1:A:188:ARG:CA	2:A:350:HOH:O	2.67	0.42
1:A:188:ARG:HA	2:A:350:HOH:O	2.20	0.42
1:A:256:GLN:NE2	1:A:260:SER:HB3	2.32	0.42
1:C:144:LEU:CD2	1:D:16:PRO:HG3	2.49	0.42
1:C:188:ARG:N	1:C:189:PRO:HD3	2.34	0.42
1:D:164:ILE:O	1:D:168:ILE:HG13	2.19	0.42
1:A:26:ALA:CB	1:A:314:LEU:HD11	2.49	0.42
1:B:246:GLY:O	1:B:248:VAL:N	2.52	0.42
1:C:16:PRO:HA	1:D:144:LEU:HD21	2.02	0.42
1:C:305:MSE:HE1	1:D:141:TRP:CZ2	2.54	0.42
1:B:40:ILE:HA	1:B:41:PRO:HD3	1.91	0.42
1:B:81:MSE:HG2	1:B:305:MSE:HB3	2.02	0.42
1:B:286:LYS:NZ	2:B:395:HOH:O	2.52	0.42
1:C:108:THR:HA	1:C:164:ILE:HG12	2.02	0.42
1:D:22:ALA:HA	1:D:25:ARG:HG3	2.01	0.42
1:A:8:LYS:CE	1:A:32:GLU:HG3	2.42	0.42
1:C:298:THR:HG1	1:C:301:THR:HB	1.84	0.42
1:B:13:ARG:HD3	1:B:38:GLU:C	2.39	0.42
1:C:240:PHE:CZ	1:C:249:VAL:HG21	2.55	0.42
1:D:46:GLU:OE2	1:D:66:ARG:O	2.37	0.42
1:A:204:GLU:HA	1:A:207:ALA:HB3	2.01	0.42
1:C:206:ALA:HB2	1:C:230:PHE:CE1	2.54	0.42
1:C:236:GLU:HA	1:C:263:ILE:HA	2.01	0.42
1:A:102:TYR:CD2	1:A:104:PRO:HD3	2.54	0.42
1:B:110:THR:CG2	1:B:296:SER:HA	2.47	0.42
1:B:314:LEU:C	1:B:316:GLY:N	2.72	0.42
1:C:217:SER:O	1:C:219:THR:N	2.46	0.42
1:A:218:LEU:HD12	1:A:222:THR:OG1	2.19	0.42
1:B:40:ILE:HA	1:B:41:PRO:HD3	1.92	0.42
1:B:102:TYR:CE2	1:B:104:PRO:HB3	2.55	0.42
1:B:286:LYS:NZ	2:B:397:HOH:O	2.52	0.42
1:C:65:LYS:HD3	1:C:92:GLU:OE2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:79:SER:HB3	1:C:313:LEU:HB2	2.00	0.42
1:C:218:LEU:HA	1:C:222:THR:HG1	1.84	0.42
1:D:190:GLU:H	1:D:190:GLU:CD	2.23	0.42
1:D:119:LEU:HD23	1:D:119:LEU:C	2.39	0.42
1:D:177:VAL:HG11	1:D:180:PHE:CE1	2.55	0.42
1:D:276:LEU:HG	1:D:277:PRO:CD	2.48	0.42
1:A:195:PHE:O	1:A:196:GLN:C	2.57	0.42
1:C:238:ALA:O	1:C:264:ALA:HB3	2.19	0.42
1:A:81:MSE:HE1	1:B:143:PRO:HB3	2.00	0.42
1:A:314:LEU:CG	1:A:318:ARG:NH1	2.81	0.42
1:B:200:VAL:HG22	1:B:201:SER:H	1.82	0.42
1:C:9:VAL:HG13	1:C:313:LEU:HD21	2.01	0.42
1:C:203:PRO:CB	1:C:233:LYS:HE2	2.40	0.42
1:C:207:ALA:HA	1:C:233:LYS:O	2.19	0.42
1:D:144:LEU:N	1:D:144:LEU:CD1	2.82	0.42
1:A:96:ARG:HH11	1:A:96:ARG:HG2	1.85	0.42
1:B:34:TRP:C	1:B:36:SER:H	2.22	0.42
1:C:157:GLY:O	1:C:212:ILE:HA	2.19	0.42
1:D:160:GLY:HA3	1:D:216:CYS:HA	2.02	0.42
1:A:108:THR:N	2:A:329:HOH:O	2.52	0.42
1:B:80:THR:HG22	1:B:81:MSE:N	2.34	0.42
1:C:139:THR:O	1:C:140:SER:HB2	2.20	0.42
1:B:212:ILE:HD12	1:B:212:ILE:N	2.34	0.42
1:C:187:PRO:C	1:C:189:PRO:HD3	2.39	0.42
1:D:45:LEU:C	1:D:47:ARG:N	2.71	0.42
1:D:101:GLY:HA3	1:D:312:ASN:HD22	1.84	0.42
1:D:119:LEU:HD21	1:D:211:PHE:CD1	2.55	0.42
1:A:186:GLN:O	1:A:188:ARG:CZ	2.68	0.42
1:A:275:PRO:HB3	1:B:138:TRP:CG	2.54	0.42
1:C:153:GLN:HA	1:C:176:GLY:O	2.18	0.42
1:D:192:ALA:HB1	1:D:197:ALA:HB3	1.99	0.42
1:D:217:SER:O	1:D:219:THR:N	2.52	0.42
1:A:185:ARG:HB3	1:A:186:GLN:NE2	2.35	0.42
1:D:163:ARG:NH1	2:D:368:HOH:O	2.53	0.42
1:A:39:PRO:HD3	1:B:140:SER:HB3	2.01	0.42
1:B:99:ARG:HH12	1:B:321:PRO:HA	1.85	0.42
1:D:229:ASP:HB2	2:D:411:HOH:O	2.19	0.42
1:A:157:GLY:CA	1:A:205:LEU:HD11	2.49	0.42
1:B:205:LEU:C	1:B:205:LEU:HD23	2.39	0.42
1:C:9:VAL:O	1:C:31:VAL:HA	2.18	0.42
1:C:10:PHE:CD1	1:C:32:GLU:O	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:14:ARG:CZ	1:C:36:SER:HA	2.50	0.42
1:C:146:LEU:HD12	1:D:294:ILE:HG21	2.02	0.42
1:A:142:LYS:HB2	1:A:145:TRP:HB3	2.00	0.42
1:B:68:LEU:HD23	1:B:75:LEU:HD23	2.00	0.42
1:B:77:VAL:HA	1:B:98:ILE:HG23	2.01	0.42
1:C:77:VAL:HG23	1:C:99:ARG:O	2.20	0.42
1:C:158:ILE:O	1:C:182:TYR:HA	2.19	0.42
1:D:212:ILE:HD13	1:D:230:PHE:CZ	2.55	0.42
1:A:128:GLU:HG3	2:A:384:HOH:O	2.19	0.42
1:A:210:ASP:O	1:A:238:ALA:HB1	2.19	0.42
1:B:82:SER:HB3	2:B:341:HOH:O	2.18	0.42
1:B:257:ALA:HA	1:B:262:LYS:CG	2.47	0.42
1:C:63:VAL:HG13	1:C:67:ILE:CG2	2.47	0.42
1:C:225:LEU:HD13	1:C:225:LEU:C	2.40	0.42
1:D:49:VAL:O	1:D:50:ALA:C	2.57	0.42
1:D:132:GLU:O	1:D:137:GLY:N	2.52	0.42
1:D:181:LEU:HD22	1:D:200:VAL:HG11	2.01	0.42
1:D:185:ARG:NH1	2:D:413:HOH:O	2.53	0.42
1:A:17:ALA:O	1:A:20:ARG:N	2.53	0.42
1:A:161:LEU:HD11	1:A:195:PHE:CE2	2.55	0.42
1:D:121:THR:HB	1:D:127:PRO:HD3	2.01	0.42
1:D:182:TYR:CE2	1:D:199:PHE:HD1	2.37	0.42
1:D:205:LEU:HD23	1:D:205:LEU:C	2.39	0.42
1:D:322:MSE:CB	1:D:325:GLU:HB2	2.49	0.42
1:A:13:ARG:HE	1:A:39:PRO:HA	1.85	0.42
1:A:56:LEU:HD23	1:A:79:SER:O	2.20	0.42
1:B:74:ASN:ND2	2:B:336:HOH:O	2.53	0.42
1:B:286:LYS:NZ	2:B:393:HOH:O	2.52	0.42
1:A:100:VAL:CG1	1:A:101:GLY:N	2.82	0.42
1:B:236:GLU:HA	1:B:263:ILE:HA	2.00	0.42
1:C:173:LYS:N	1:C:174:PRO:HD2	2.35	0.42
1:A:218:LEU:CD2	1:A:247:ASP:HB2	2.50	0.42
1:A:258:LEU:HB3	1:A:285:LEU:HD13	2.01	0.42
1:C:80:THR:HG23	1:C:82:SER:O	2.20	0.42
1:D:45:LEU:HD12	1:D:45:LEU:O	2.20	0.42
1:D:114:LEU:O	1:D:114:LEU:HG	2.19	0.42
1:D:132:GLU:OE1	1:D:137:GLY:HA3	2.19	0.42
1:D:254:LEU:HD21	1:D:268:LEU:HD11	2.01	0.42
1:A:190:GLU:O	1:A:193:ALA:HB3	2.19	0.42
1:B:102:TYR:CD1	1:B:102:TYR:N	2.88	0.42
1:B:302:ARG:NH2	2:B:366:HOH:O	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:PRO:CG	1:C:306:SER:HB2	2.49	0.42
1:A:85:ILE:HB	1:A:90:LEU:HD11	2.01	0.42
1:B:13:ARG:HD2	1:B:58:LEU:HD12	1.95	0.42
1:C:103:THR:HG22	1:C:308:LEU:HG	2.01	0.42
1:D:218:LEU:HD22	1:D:245:ARG:HB3	2.01	0.42
1:A:314:LEU:HD12	1:A:314:LEU:HA	1.82	0.42
1:D:119:LEU:HD21	1:D:211:PHE:CD1	2.54	0.42
1:D:277:PRO:C	1:D:279:ASN:H	2.21	0.42
1:B:110:THR:HG23	1:B:298:THR:HG21	2.01	0.42
1:B:173:LYS:N	1:B:174:PRO:HD2	2.35	0.42
1:C:313:LEU:O	1:C:317:LEU:HD13	2.19	0.42
1:B:12:THR:O	1:B:13:ARG:HB3	2.20	0.42
1:D:8:LYS:HB3	1:D:52:ALA:HA	2.02	0.42
1:D:102:TYR:CD2	1:D:104:PRO:HD3	2.55	0.42
1:A:257:ALA:O	1:A:260:SER:N	2.52	0.42
1:B:142:LYS:HA	1:B:143:PRO:HD2	1.83	0.42
1:C:186:GLN:HA	1:C:187:PRO:HD3	1.87	0.42
1:A:179:ARG:NH2	1:A:208:GLN:OE1	2.53	0.42
1:A:186:GLN:HB3	1:A:188:ARG:HH12	1.84	0.42
1:B:114:LEU:HD22	1:B:294:ILE:C	2.40	0.42
1:C:153:GLN:HG2	2:C:387:HOH:O	2.18	0.42
1:A:121:THR:CG2	1:A:127:PRO:HD3	2.49	0.42
1:C:14:ARG:HG3	1:C:14:ARG:NH1	2.35	0.42
1:C:142:LYS:HB2	1:C:145:TRP:CB	2.50	0.42
1:C:277:PRO:HD2	1:C:280:HIS:HB2	2.02	0.42
1:A:309:ALA:HB2	2:A:360:HOH:O	2.18	0.42
1:C:133:VAL:CG1	1:D:283:LEU:HD21	2.50	0.42
1:C:183:THR:HG22	1:C:184:GLY:N	2.34	0.42
1:D:280:HIS:CE1	1:D:282:LEU:H	2.37	0.42
1:B:92:GLU:O	1:B:96:ARG:HG3	2.19	0.42
1:C:78:ILE:O	1:C:100:VAL:HA	2.19	0.42
1:C:223:GLU:HA	1:C:248:VAL:HA	2.01	0.42
1:D:18:GLU:HG3	1:D:303:ASN:HB3	2.01	0.42
1:D:19:GLY:O	1:D:23:LEU:HG	2.20	0.42
1:D:269:ASP:O	1:D:293:HIS:HA	2.20	0.42
1:B:119:LEU:HD23	1:B:119:LEU:C	2.40	0.42
1:D:8:LYS:HD3	1:D:52:ALA:N	2.35	0.42
1:D:205:LEU:CD2	1:D:212:ILE:HG12	2.50	0.42
1:D:227:ASN:HA	1:D:250:ASN:HB2	2.00	0.42
1:A:246:GLY:H	1:A:270:VAL:HB	1.82	0.42
1:C:12:THR:C	1:C:34:TRP:HB3	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:72:GLY:C	1:C:74:ASN:N	2.72	0.42
1:D:282:LEU:HD23	1:D:285:LEU:CD1	2.50	0.42
1:A:159:ILE:HB	1:A:215:ALA:H	1.84	0.42
1:A:182:TYR:O	1:A:199:PHE:HA	2.19	0.42
1:B:119:LEU:HD23	1:B:119:LEU:C	2.40	0.42
1:B:273:PRO:HB2	2:B:337:HOH:O	2.20	0.42
1:A:53:HIS:HB2	1:A:317:LEU:HD21	2.01	0.42
1:A:11:VAL:HB	1:A:33:GLN:HG3	2.01	0.42
1:A:57:CYS:O	1:A:58:LEU:HD23	2.20	0.42
1:A:131:GLU:HG3	1:A:135:ASN:HD22	1.85	0.42
1:B:212:ILE:HD13	1:B:230:PHE:HZ	1.85	0.42
1:C:54:GLY:HA2	1:C:77:VAL:CG1	2.47	0.42
1:A:155:THR:O	1:A:210:ASP:N	2.49	0.42
1:B:91:ASP:HB3	2:B:433:HOH:O	2.20	0.42
1:C:65:LYS:HB2	1:C:65:LYS:NZ	2.34	0.42
1:C:68:LEU:C	1:C:70:ALA:H	2.22	0.42
1:C:75:LEU:HD12	1:C:76:LYS:H	1.84	0.42
1:D:275:PRO:O	1:D:277:PRO:HD3	2.20	0.42
1:B:142:LYS:HA	1:B:143:PRO:HD2	1.88	0.42
1:C:100:VAL:HG12	1:C:101:GLY:N	2.35	0.42
1:D:155:THR:HG22	1:D:209:SER:HA	2.02	0.42
1:C:214:VAL:HG11	1:C:248:VAL:HG11	2.01	0.42
1:D:153:GLN:HA	1:D:178:GLN:HB2	2.02	0.42
1:D:216:CYS:SG	1:D:248:VAL:HG21	2.59	0.42
1:B:73:ALA:N	2:B:336:HOH:O	2.52	0.42
1:A:207:ALA:O	1:A:235:LYS:HE2	2.20	0.42
1:A:245:ARG:HA	1:A:270:VAL:HG11	2.02	0.42
1:B:61:ASP:O	1:B:87:HIS:ND1	2.43	0.42
1:C:13:ARG:NH1	1:C:37:ASP:O	2.53	0.42
1:C:32:GLU:HA	1:C:32:GLU:OE1	2.20	0.42
1:A:21:VAL:O	1:A:21:VAL:HG12	2.20	0.42
1:A:102:TYR:CD1	1:A:102:TYR:N	2.87	0.42
1:A:179:ARG:NH2	2:A:407:HOH:O	2.49	0.42
1:D:77:VAL:HA	1:D:99:ARG:O	2.19	0.42
1:D:311:ASN:O	1:D:315:ALA:N	2.52	0.42
1:A:166:GLN:CD	1:A:191:GLU:HB3	2.40	0.42
1:B:257:ALA:HB1	1:B:262:LYS:HB2	2.02	0.42
1:B:315:ALA:C	1:B:317:LEU:H	2.23	0.42
1:C:62:HIS:ND1	1:C:62:HIS:N	2.67	0.42
1:D:204:GLU:HA	1:D:204:GLU:OE2	2.20	0.42
1:A:57:CYS:SG	1:A:80:THR:HB	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:THR:HA	1:A:176:GLY:HA3	2.01	0.42
1:A:192:ALA:HB1	1:A:197:ALA:HB3	2.01	0.42
1:A:245:ARG:HB2	1:A:248:VAL:HG23	2.01	0.42
1:C:18:GLU:HG2	1:C:307:LEU:CD2	2.28	0.42
1:D:80:THR:O	1:D:103:THR:HG23	2.18	0.42
1:A:96:ARG:HG3	1:A:96:ARG:NH1	2.35	0.42
1:A:194:GLU:HG2	1:A:195:PHE:CE1	2.55	0.42
1:C:151:LEU:HD23	1:C:211:PHE:CE1	2.55	0.42
1:C:206:ALA:HB2	1:C:230:PHE:CE1	2.55	0.42
1:C:59:LEU:HD13	1:D:141:TRP:CD2	2.55	0.42
1:C:94:LYS:O	1:C:94:LYS:HD3	2.20	0.42
1:C:233:LYS:NZ	2:C:394:HOH:O	2.52	0.42
1:A:75:LEU:HD23	1:A:98:ILE:HD13	2.02	0.42
1:A:141:TRP:O	1:B:13:ARG:NH1	2.47	0.42
1:B:318:ARG:HB2	1:B:320:GLU:OE1	2.20	0.42
1:A:15:ILE:HB	1:A:81:MSE:HE1	2.01	0.42
1:B:15:ILE:HG13	1:B:20:ARG:CG	2.49	0.42
1:B:99:ARG:NH1	1:B:325:GLU:OE1	2.53	0.42
1:B:119:LEU:HD23	1:B:119:LEU:C	2.40	0.42
1:C:84:GLY:O	1:C:85:ILE:HG23	2.20	0.42
1:C:95:LYS:O	1:C:97:GLY:N	2.53	0.42
1:D:86:ASP:OD2	1:D:218:LEU:HD23	2.19	0.42
1:D:89:ALA:O	1:D:93:ILE:HG13	2.19	0.42
1:D:190:GLU:N	1:D:190:GLU:OE1	2.52	0.42
1:D:140:SER:OG	1:D:141:TRP:N	2.53	0.42
1:C:138:TRP:CH2	1:D:274:GLU:HG2	2.55	0.42
1:C:292:PRO:CD	1:D:129:ALA:HB1	2.47	0.42
1:D:151:LEU:HB3	1:D:177:VAL:CG2	2.50	0.42
1:A:74:ASN:N	2:A:419:HOH:O	2.53	0.42
1:A:218:LEU:HB2	1:A:245:ARG:HB2	2.02	0.42
1:B:53:HIS:HB3	1:B:76:LYS:HG2	2.02	0.42
1:B:202:THR:HG22	1:B:230:PHE:HD2	1.84	0.42
1:B:235:LYS:C	1:B:237:THR:H	2.22	0.42
1:D:250:ASN:OD1	1:D:252:ASP:HB2	2.19	0.42
1:A:56:LEU:C	1:A:56:LEU:HD23	2.40	0.42
1:A:138:TRP:HZ3	1:B:276:LEU:HB2	1.83	0.42
1:A:183:THR:HB	1:A:205:LEU:HB2	2.02	0.42
1:C:58:LEU:HD13	1:D:141:TRP:CZ3	2.55	0.42
1:C:188:ARG:HA	1:C:189:PRO:HD3	1.92	0.42
1:D:180:PHE:O	1:D:197:ALA:HA	2.20	0.42
1:D:234:MSE:HE2	1:D:238:ALA:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:LEU:HD22	1:A:28:ASP:C	2.40	0.42
1:A:45:LEU:O	1:A:45:LEU:HG	2.19	0.42
1:A:162:GLY:O	1:A:163:ARG:C	2.59	0.42
1:B:103:THR:HA	1:B:308:LEU:CD2	2.50	0.42
1:B:105:ASP:O	2:B:380:HOH:O	2.22	0.42
1:B:236:GLU:HG2	2:B:450:HOH:O	2.20	0.42
1:C:64:ASP:O	1:C:67:ILE:N	2.52	0.42
1:C:166:GLN:CD	1:C:191:GLU:HB3	2.40	0.42
1:D:262:LYS:HA	1:D:262:LYS:HD3	1.77	0.42
1:A:114:LEU:HD22	1:A:295:GLY:CA	2.43	0.42
1:A:219:THR:O	1:A:221:ALA:N	2.53	0.42
1:D:299:HIS:O	1:D:303:ASN:HB2	2.20	0.42
1:D:322:MSE:SE	1:D:325:GLU:HA	2.69	0.42
1:A:114:LEU:HD12	1:B:124:ARG:NH2	2.35	0.42
1:A:198:GLU:O	1:A:200:VAL:HG13	2.20	0.42
1:A:231:PHE:HE2	1:A:253:ASP:HB3	1.85	0.42
1:B:119:LEU:HD23	1:B:119:LEU:C	2.40	0.42
1:B:249:VAL:HG12	1:B:250:ASN:N	2.34	0.42
1:D:7:MSE:SE	1:D:317:LEU:HD12	2.69	0.42
1:D:161:LEU:HB2	1:D:182:TYR:HB2	2.02	0.42
1:A:13:ARG:HG3	1:A:14:ARG:N	2.35	0.42
1:A:56:LEU:CD1	1:A:309:ALA:HB1	2.49	0.42
1:A:76:LYS:HG3	1:A:77:VAL:HG12	2.01	0.42
1:A:245:ARG:C	1:A:247:ASP:N	2.71	0.42
1:B:83:VAL:HG13	1:B:84:GLY:N	2.35	0.42
1:C:247:ASP:OD1	1:C:272:SER:HB3	2.20	0.42
1:D:40:ILE:O	1:D:40:ILE:HG23	2.20	0.42
1:D:102:TYR:CE1	1:D:104:PRO:HG3	2.55	0.42
1:A:34:TRP:O	1:A:36:SER:N	2.53	0.42
1:A:95:LYS:HB2	2:A:347:HOH:O	2.19	0.41
1:B:118:LEU:HD13	1:B:291:LEU:CD1	2.50	0.41
1:C:313:LEU:O	1:C:317:LEU:HG	2.19	0.41
1:A:6:LEU:CA	1:A:29:CYS:HA	2.50	0.41
1:B:85:ILE:CD1	1:B:326:LEU:HD21	2.50	0.41
1:B:98:ILE:HG22	1:B:99:ARG:N	2.34	0.41
1:B:188:ARG:N	1:B:189:PRO:CD	2.82	0.41
1:B:228:LYS:H	1:B:253:ASP:CB	2.33	0.41
1:D:307:LEU:HG	1:D:311:ASN:ND2	2.35	0.41
1:B:92:GLU:O	1:B:94:LYS:N	2.53	0.41
1:A:259:ALA:HB2	1:A:285:LEU:HD21	2.03	0.41
1:B:58:LEU:HB3	2:B:341:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:GLU:CD	1:D:139:THR:HG21	2.38	0.41
1:C:117:SER:OG	1:D:120:LEU:HB3	2.20	0.41
1:D:41:PRO:HD2	1:D:44:GLU:CG	2.49	0.41
1:D:219:THR:HB	1:D:220:PRO:CD	2.49	0.41
1:D:232:GLN:OE1	1:D:232:GLN:HA	2.19	0.41
1:B:89:ALA:O	1:B:93:ILE:N	2.52	0.41
1:B:185:ARG:HB2	1:B:185:ARG:NH1	2.35	0.41
1:D:89:ALA:HB1	1:D:92:GLU:HG2	2.01	0.41
1:A:8:LYS:HA	1:A:30:GLU:CB	2.21	0.41
1:A:16:PRO:HD2	1:A:306:SER:HB2	2.01	0.41
1:B:302:ARG:C	1:B:304:THR:N	2.72	0.41
1:C:275:PRO:O	1:C:277:PRO:HD3	2.19	0.41
1:A:280:HIS:ND1	1:A:281:PRO:HD2	2.35	0.41
1:A:315:ALA:HB3	1:A:322:MSE:HG2	2.02	0.41
1:B:114:LEU:HD13	1:B:294:ILE:C	2.40	0.41
1:C:11:VAL:O	1:C:33:GLN:HG3	2.21	0.41
1:C:192:ALA:CB	1:C:197:ALA:HB3	2.50	0.41
1:D:269:ASP:O	1:D:293:HIS:HA	2.20	0.41
1:A:231:PHE:HD2	1:A:253:ASP:HB3	1.85	0.41
1:C:9:VAL:CG1	1:C:10:PHE:N	2.82	0.41
1:D:236:GLU:HG2	1:D:262:LYS:O	2.19	0.41
1:D:267:GLY:HA2	1:D:289:VAL:O	2.20	0.41
1:A:267:GLY:HA2	1:A:289:VAL:HB	2.02	0.41
1:C:16:PRO:CD	1:C:81:MSE:HE1	2.49	0.41
1:C:218:LEU:O	1:C:219:THR:HG23	2.20	0.41
1:C:244:SER:HB2	1:C:245:ARG:H	1.51	0.41
1:D:315:ALA:HB1	1:D:322:MSE:CA	2.42	0.41
1:A:280:HIS:HA	1:A:281:PRO:HD3	1.96	0.41
1:B:194:GLU:N	2:B:420:HOH:O	2.53	0.41
1:B:204:GLU:O	1:B:208:GLN:HG2	2.20	0.41
1:C:13:ARG:O	1:C:15:ILE:HG23	2.19	0.41
1:C:256:GLN:OE1	1:C:262:LYS:NZ	2.53	0.41
1:D:110:THR:HG23	1:D:298:THR:HG23	2.02	0.41
1:A:17:ALA:HA	1:A:20:ARG:HE	1.86	0.41
1:A:10:PHE:HD1	1:A:32:GLU:HB3	1.84	0.41
1:A:312:ASN:O	1:A:322:MSE:HE2	2.19	0.41
1:C:46:GLU:HG3	1:C:67:ILE:HD13	2.02	0.41
1:D:62:HIS:NE2	1:D:64:ASP:HB3	2.35	0.41
1:A:140:SER:OG	1:A:141:TRP:N	2.53	0.41
1:A:250:ASN:O	1:A:253:ASP:HB2	2.21	0.41
1:B:179:ARG:HH22	1:B:208:GLN:CD	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:GLN:OE1	1:B:272:SER:O	2.38	0.41
1:C:250:ASN:ND2	2:C:346:HOH:O	2.52	0.41
1:D:277:PRO:C	1:D:279:ASN:N	2.74	0.41
1:A:140:SER:O	1:A:142:LYS:HG3	2.20	0.41
1:B:297:ALA:HA	1:B:302:ARG:CZ	2.50	0.41
1:C:95:LYS:O	1:C:97:GLY:N	2.53	0.41
1:D:182:TYR:CE1	1:D:199:PHE:HD1	2.38	0.41
1:D:213:VAL:O	1:D:213:VAL:HG12	2.18	0.41
1:A:21:VAL:O	1:A:24:ALA:N	2.53	0.41
1:A:57:CYS:HG	1:A:87:HIS:CD2	2.37	0.41
1:A:129:ALA:HB1	1:B:292:PRO:CD	2.50	0.41
1:B:200:VAL:HG13	1:B:201:SER:O	2.20	0.41
1:A:160:GLY:O	1:A:162:GLY:N	2.46	0.41
1:A:314:LEU:HD12	1:A:314:LEU:HA	1.92	0.41
1:B:314:LEU:O	1:B:318:ARG:HD2	2.20	0.41
1:C:302:ARG:HD2	1:D:143:PRO:O	2.19	0.41
1:D:218:LEU:O	1:D:219:THR:HG23	2.19	0.41
1:D:54:GLY:HA2	1:D:77:VAL:O	2.20	0.41
1:D:179:ARG:NH2	2:D:396:HOH:O	2.53	0.41
1:C:29:CYS:HB3	1:C:30:GLU:H	1.67	0.41
1:D:254:LEU:CD2	1:D:268:LEU:HD11	2.51	0.41
1:A:234:MSE:HE1	1:A:263:ILE:CG2	2.49	0.41
1:B:81:MSE:O	1:B:305:MSE:HE2	2.20	0.41
1:C:51:GLY:HA2	2:C:433:HOH:O	2.20	0.41
1:D:280:HIS:HA	1:D:281:PRO:HD3	1.93	0.41
1:D:132:GLU:O	1:D:137:GLY:N	2.53	0.41
1:A:16:PRO:HG3	1:B:144:LEU:CD2	2.50	0.41
1:A:65:LYS:N	1:A:68:LEU:HD12	2.34	0.41
1:C:118:LEU:HD13	1:C:291:LEU:HD11	2.02	0.41
1:C:173:LYS:N	1:C:174:PRO:HD2	2.35	0.41
1:D:155:THR:HG22	1:D:209:SER:HA	2.02	0.41
1:A:298:THR:HA	1:B:148:GLY:O	2.20	0.41
1:B:203:PRO:HB3	1:B:233:LYS:HE2	2.02	0.41
1:D:312:ASN:OD1	1:D:323:PRO:HD2	2.20	0.41
1:A:138:TRP:CE3	1:B:275:PRO:HA	2.56	0.41
1:A:312:ASN:O	1:A:322:MSE:HE3	2.20	0.41
1:B:107:LEU:N	1:B:107:LEU:CD2	2.82	0.41
1:B:275:PRO:O	1:B:276:LEU:C	2.58	0.41
1:C:218:LEU:HD12	1:C:219:THR:H	1.84	0.41
1:D:49:VAL:CG1	1:D:55:LEU:HD13	2.50	0.41
1:D:77:VAL:CG1	1:D:317:LEU:HD22	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:161:LEU:HD22	1:D:182:TYR:CD1	2.54	0.41
1:A:161:LEU:HB2	1:A:182:TYR:CE2	2.55	0.41
1:B:94:LYS:C	1:B:96:ARG:N	2.74	0.41
1:B:126:LEU:CD1	1:B:126:LEU:H	2.34	0.41
1:C:312:ASN:HB3	1:C:322:MSE:HE2	2.02	0.41
1:A:209:SER:HB2	1:A:212:ILE:HD11	2.03	0.41
1:B:160:GLY:O	1:B:215:ALA:O	2.38	0.41
1:B:272:SER:HA	1:B:273:PRO:HA	1.86	0.41
1:C:11:VAL:HG23	1:C:31:VAL:HG13	2.01	0.41
1:C:12:THR:O	1:C:34:TRP:O	2.37	0.41
1:A:9:VAL:HB	1:A:31:VAL:CG2	2.28	0.41
1:B:124:ARG:HB2	1:B:126:LEU:HD11	2.01	0.41
1:B:142:LYS:HA	1:B:143:PRO:HD2	1.86	0.41
1:B:246:GLY:C	1:B:248:VAL:N	2.74	0.41
1:B:251:GLN:OE1	1:B:272:SER:N	2.53	0.41
1:D:81:MSE:HG2	1:D:305:MSE:HE2	2.02	0.41
1:D:90:LEU:HA	1:D:93:ILE:HD12	2.02	0.41
1:A:166:GLN:HB3	2:A:414:HOH:O	2.19	0.41
1:B:142:LYS:HA	1:B:143:PRO:HD2	1.86	0.41
1:B:325:GLU:HG3	1:B:326:LEU:N	2.35	0.41
1:C:106:VAL:HB	1:C:304:THR:HG22	2.02	0.41
1:C:274:GLU:HA	1:C:275:PRO:C	2.40	0.41
1:D:29:CYS:SG	1:D:317:LEU:HD23	2.60	0.41
1:D:74:ASN:HB2	2:D:415:HOH:O	2.19	0.41
1:D:177:VAL:HG11	1:D:180:PHE:CE1	2.55	0.41
1:D:202:THR:OG1	1:D:225:LEU:HD11	2.21	0.41
1:A:11:VAL:HB	1:A:33:GLN:NE2	2.29	0.41
1:B:43:LYS:O	1:B:46:GLU:HB2	2.20	0.41
1:B:315:ALA:HA	1:B:320:GLU:OE1	2.20	0.41
1:C:186:GLN:OE1	1:C:186:GLN:HA	2.19	0.41
1:C:233:LYS:NZ	2:C:352:HOH:O	2.45	0.41
1:C:301:THR:O	1:C:305:MSE:HG2	2.19	0.41
1:D:186:GLN:HG2	1:D:187:PRO:CD	2.51	0.41
1:A:309:ALA:O	1:A:312:ASN:CB	2.69	0.41
1:C:104:PRO:O	1:C:105:ASP:C	2.59	0.41
1:A:56:LEU:HD11	1:A:309:ALA:CB	2.50	0.41
1:C:62:HIS:O	1:C:64:ASP:N	2.53	0.41
1:D:59:LEU:C	1:D:59:LEU:HD12	2.40	0.41
1:D:245:ARG:HD2	2:D:363:HOH:O	2.20	0.41
1:A:35:ASP:C	1:A:35:ASP:OD2	2.58	0.41
1:C:31:VAL:CG1	1:C:32:GLU:N	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:PRO:HD2	1:C:44:GLU:CG	2.50	0.41
1:C:78:ILE:O	1:C:100:VAL:HA	2.20	0.41
1:C:202:THR:CB	1:C:203:PRO:HD3	2.46	0.41
1:D:199:PHE:O	1:D:200:VAL:HG13	2.20	0.41
1:D:229:ASP:O	1:D:230:PHE:C	2.59	0.41
1:A:39:PRO:HD3	1:B:140:SER:HB3	2.01	0.41
1:C:179:ARG:HG2	1:C:179:ARG:HH11	1.85	0.41
1:D:142:LYS:HE3	1:D:145:TRP:CD2	2.55	0.41
1:D:251:GLN:H	1:D:251:GLN:HG2	1.70	0.41
1:A:126:LEU:HG	1:B:291:LEU:HD21	2.02	0.41
1:A:195:PHE:O	1:A:196:GLN:C	2.59	0.41
1:A:269:ASP:HA	1:A:291:LEU:HB2	2.03	0.41
1:A:100:VAL:HG11	1:A:326:LEU:HB3	2.03	0.41
1:C:13:ARG:NH2	2:C:441:HOH:O	2.46	0.41
1:C:16:PRO:CD	1:C:306:SER:HB2	2.51	0.41
1:D:166:GLN:HE22	1:D:191:GLU:HB3	1.86	0.41
1:A:76:LYS:HZ2	1:A:317:LEU:HA	1.84	0.41
1:A:116:VAL:HG11	1:B:175:PHE:HZ	1.85	0.41
1:A:194:GLU:HG2	1:A:195:PHE:CD1	2.55	0.41
1:B:57:CYS:O	1:B:80:THR:HA	2.19	0.41
1:B:179:ARG:CZ	1:B:181:LEU:HD21	2.50	0.41
1:C:13:ARG:CZ	1:C:58:LEU:HD12	2.51	0.41
1:C:14:ARG:O	1:D:143:PRO:HG3	2.21	0.41
1:C:54:GLY:HA3	1:C:313:LEU:HD11	2.03	0.41
1:C:309:ALA:HA	2:C:361:HOH:O	2.20	0.41
1:A:269:ASP:HA	1:A:291:LEU:HB2	2.02	0.41
1:A:279:ASN:OD1	1:A:279:ASN:C	2.59	0.41
1:B:189:PRO:O	1:B:192:ALA:N	2.53	0.41
1:D:65:LYS:HG3	1:D:96:ARG:NH2	2.34	0.41
1:B:114:LEU:HD23	1:B:114:LEU:C	2.40	0.41
1:D:119:LEU:HD23	1:D:119:LEU:C	2.40	0.41
1:D:322:MSE:HB2	1:D:325:GLU:HB2	2.03	0.41
1:A:57:CYS:SG	1:A:87:HIS:NE2	2.93	0.41
1:B:13:ARG:HH22	1:B:39:PRO:HB3	1.84	0.41
1:B:202:THR:HB	1:B:203:PRO:HD3	2.01	0.41
1:C:7:MSE:HE2	1:C:53:HIS:CD2	2.56	0.41
1:C:95:LYS:C	1:C:97:GLY:N	2.73	0.41
1:D:206:ALA:HB2	1:D:230:PHE:CE1	2.56	0.41
1:B:14:ARG:CZ	1:B:37:ASP:OD1	2.69	0.41
1:D:263:ILE:HG13	1:D:264:ALA:N	2.32	0.41
1:B:179:ARG:HA	2:B:383:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:58:LEU:N	1:C:61:ASP:OD2	2.51	0.41
1:C:75:LEU:HD23	1:C:98:ILE:CD1	2.51	0.41
1:B:110:THR:HG23	1:B:298:THR:HG23	2.03	0.41
1:B:111:THR:HG21	1:B:164:ILE:HD13	2.02	0.41
1:B:124:ARG:HB2	1:B:126:LEU:CD1	2.51	0.41
1:C:16:PRO:CD	1:C:81:MSE:HE1	2.50	0.41
1:C:301:THR:C	1:C:303:ASN:H	2.24	0.41
1:D:262:LYS:HA	1:D:262:LYS:HD3	1.92	0.41
1:D:307:LEU:HG	1:D:311:ASN:HD21	1.84	0.41
1:A:13:ARG:HG3	1:A:14:ARG:N	2.35	0.41
1:A:123:CYS:HB2	1:A:149:TYR:O	2.20	0.41
1:A:185:ARG:O	1:A:186:GLN:HB2	2.21	0.41
1:C:302:ARG:HD3	1:C:302:ARG:HA	1.95	0.41
1:C:317:LEU:HD12	1:C:317:LEU:H	1.85	0.41
1:D:26:ALA:C	1:D:28:ASP:H	2.24	0.41
1:A:74:ASN:N	2:A:418:HOH:O	2.53	0.41
1:A:85:ILE:HD13	1:A:90:LEU:HD11	2.02	0.41
1:A:167:ALA:HB2	2:A:371:HOH:O	2.21	0.41
1:B:40:ILE:HG12	1:B:44:GLU:HB2	2.01	0.41
1:A:114:LEU:CG	1:A:295:GLY:HA2	2.51	0.41
1:A:180:PHE:CD2	1:A:195:PHE:HB3	2.56	0.41
1:B:58:LEU:N	1:B:61:ASP:OD2	2.49	0.41
1:B:283:LEU:C	1:B:285:LEU:H	2.23	0.41
1:C:81:MSE:HE2	1:C:306:SER:HA	2.03	0.41
1:D:205:LEU:HD23	1:D:205:LEU:C	2.40	0.41
1:D:228:LYS:HB2	1:D:253:ASP:OD1	2.21	0.41
1:A:206:ALA:O	1:A:207:ALA:C	2.59	0.41
1:C:7:MSE:SE	1:C:317:LEU:HD23	2.70	0.41
1:C:118:LEU:HD13	1:C:291:LEU:HD11	2.01	0.41
1:C:312:ASN:O	1:C:322:MSE:HE3	2.20	0.41
1:D:157:GLY:O	1:D:212:ILE:HA	2.21	0.41
1:D:164:ILE:HG21	1:D:243:ILE:HD11	2.02	0.41
1:A:79:SER:CB	1:A:313:LEU:HB2	2.50	0.41
1:B:188:ARG:CA	2:B:343:HOH:O	2.58	0.41
1:B:226:CYS:CB	1:B:249:VAL:HG22	2.50	0.41
1:B:256:GLN:NE2	1:B:260:SER:HB3	2.35	0.41
1:C:55:LEU:HD21	1:C:63:VAL:HG11	2.03	0.41
1:C:59:LEU:HD13	1:D:141:TRP:CD2	2.55	0.41
1:D:203:PRO:HB3	1:D:233:LYS:HZ2	1.86	0.41
1:D:209:SER:HB3	1:D:211:PHE:O	2.20	0.41
1:D:234:MSE:HE2	1:D:238:ALA:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:315:ALA:HA	1:D:320:GLU:OE1	2.21	0.41
1:C:17:ALA:O	1:C:18:GLU:C	2.58	0.41
1:C:102:TYR:CD1	1:C:102:TYR:N	2.89	0.41
1:D:181:LEU:CD1	1:D:208:GLN:HB2	2.50	0.41
1:D:219:THR:O	1:D:223:GLU:HB2	2.21	0.41
1:A:240:PHE:O	1:A:241:ILE:HD13	2.21	0.41
1:C:65:LYS:NZ	1:C:92:GLU:OE2	2.42	0.41
1:D:16:PRO:HA	2:D:384:HOH:O	2.19	0.41
1:D:110:THR:HG22	1:D:295:GLY:O	2.20	0.41
1:D:314:LEU:O	1:D:318:ARG:HB2	2.21	0.41
1:A:69:ASP:C	1:A:71:ALA:N	2.72	0.41
1:A:128:GLU:HG3	2:A:382:HOH:O	2.20	0.41
1:B:82:SER:O	1:B:102:TYR:HB2	2.21	0.41
1:B:195:PHE:O	1:B:196:GLN:HB2	2.20	0.41
1:C:111:THR:HA	1:C:295:GLY:O	2.20	0.41
1:D:185:ARG:HA	2:D:398:HOH:O	2.20	0.41
1:A:59:LEU:HA	1:A:59:LEU:HD12	1.81	0.41
1:A:238:ALA:HA	2:A:351:HOH:O	2.20	0.41
1:C:41:PRO:O	1:C:42:ALA:CB	2.68	0.41
1:C:96:ARG:HB2	1:C:98:ILE:HD13	2.03	0.41
1:A:246:GLY:C	1:A:248:VAL:H	2.23	0.41
1:A:249:VAL:CG1	1:A:250:ASN:N	2.83	0.41
1:A:315:ALA:C	1:A:317:LEU:H	2.23	0.41
1:B:219:THR:O	1:B:222:THR:O	2.38	0.41
1:B:272:SER:HA	1:B:273:PRO:HA	1.87	0.41
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.51	0.41
1:D:177:VAL:HG11	1:D:180:PHE:CZ	2.55	0.41
1:D:192:ALA:O	1:D:196:GLN:N	2.54	0.41
1:A:12:THR:HG22	1:A:45:LEU:CD1	2.49	0.41
1:B:161:LEU:HD22	1:B:182:TYR:CG	2.56	0.41
1:C:151:LEU:HD23	1:C:211:PHE:CE1	2.56	0.41
1:C:182:TYR:N	1:C:198:GLU:O	2.53	0.41
1:C:219:THR:H	1:C:222:THR:HG1	1.66	0.41
1:B:103:THR:O	1:B:103:THR:OG1	2.33	0.41
1:C:234:MSE:HB3	2:C:343:HOH:O	2.19	0.41
1:D:17:ALA:O	1:D:18:GLU:C	2.59	0.41
1:D:195:PHE:C	1:D:196:GLN:OE1	2.59	0.41
1:A:186:GLN:N	1:A:199:PHE:CZ	2.88	0.41
1:C:7:MSE:HA	1:C:53:HIS:ND1	2.35	0.41
1:C:154:SER:OG	1:C:211:PHE:HE1	2.04	0.41
1:D:26:ALA:CB	1:D:29:CYS:SG	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:SER:OG	1:B:120:LEU:HB3	2.21	0.41
1:B:89:ALA:O	1:B:93:ILE:HG13	2.21	0.41
1:C:114:LEU:CD1	1:C:294:ILE:HG13	2.51	0.41
1:D:142:LYS:HE3	1:D:145:TRP:CE3	2.55	0.41
1:D:157:GLY:O	1:D:212:ILE:HA	2.21	0.41
1:A:144:LEU:HG	2:A:362:HOH:O	2.19	0.41
1:D:77:VAL:HG12	1:D:317:LEU:HD13	2.02	0.41
1:D:296:SER:C	1:D:302:ARG:NH2	2.74	0.41
1:A:142:LYS:HD3	2:A:336:HOH:O	2.19	0.41
1:A:179:ARG:HH21	1:A:208:GLN:NE2	2.18	0.41
1:A:234:MSE:HE2	1:A:234:MSE:HB2	2.01	0.41
1:B:94:LYS:O	1:B:96:ARG:N	2.54	0.41
1:C:10:PHE:HA	1:C:32:GLU:O	2.21	0.41
1:C:13:ARG:NE	2:C:441:HOH:O	2.47	0.41
1:A:107:LEU:HD12	1:A:108:THR:N	2.35	0.41
1:A:110:THR:HG23	1:A:298:THR:HG23	2.03	0.41
1:A:277:PRO:O	1:A:279:ASN:N	2.54	0.41
1:B:124:ARG:HB2	1:B:126:LEU:CD1	2.51	0.41
1:B:173:LYS:HB3	1:B:174:PRO:HD3	2.02	0.41
1:C:275:PRO:HD3	1:D:139:THR:O	2.19	0.41
1:B:53:HIS:CD2	1:B:76:LYS:HD2	2.56	0.41
1:B:257:ALA:HA	1:B:262:LYS:CG	2.47	0.41
1:C:34:TRP:CD1	1:C:36:SER:HB3	2.56	0.41
1:C:144:LEU:CD2	1:D:16:PRO:HG3	2.51	0.41
1:C:302:ARG:HA	1:C:305:MSE:HG2	2.02	0.41
1:A:53:HIS:HD2	1:A:74:ASN:O	2.04	0.41
1:A:156:VAL:O	1:A:180:PHE:HA	2.21	0.41
1:A:189:PRO:C	1:A:191:GLU:N	2.72	0.41
1:A:206:ALA:C	1:A:234:MSE:HA	2.41	0.41
1:A:267:GLY:HA2	1:A:289:VAL:O	2.21	0.41
1:B:116:VAL:HG22	1:B:172:LEU:HG	2.02	0.41
1:B:302:ARG:HD3	1:B:302:ARG:HA	1.87	0.41
1:C:302:ARG:O	1:C:305:MSE:HB3	2.21	0.41
1:D:13:ARG:HD3	1:D:38:GLU:O	2.21	0.41
1:D:53:HIS:O	1:D:75:LEU:HA	2.21	0.41
1:A:68:LEU:HA	1:A:75:LEU:HD22	2.02	0.41
1:B:22:ALA:O	1:B:24:ALA:N	2.53	0.41
1:C:144:LEU:CD2	1:D:16:PRO:HG3	2.51	0.41
1:C:302:ARG:HG3	1:D:147:CYS:SG	2.61	0.41
1:A:162:GLY:O	1:A:166:GLN:N	2.50	0.41
1:C:31:VAL:HG12	1:C:32:GLU:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:274:GLU:HA	1:C:275:PRO:C	2.41	0.41
1:D:25:ARG:HG2	1:D:25:ARG:HH11	1.84	0.41
1:D:119:LEU:HD23	1:D:119:LEU:C	2.40	0.41
1:D:256:GLN:OE1	1:D:256:GLN:HA	2.21	0.41
1:A:44:GLU:HA	1:A:47:ARG:HB3	2.02	0.41
1:A:46:GLU:HG2	1:A:67:ILE:HD13	2.02	0.41
1:A:78:ILE:O	1:A:101:GLY:N	2.54	0.41
1:A:102:TYR:N	1:A:102:TYR:HD1	2.18	0.41
1:A:286:LYS:C	1:A:288:CYS:H	2.25	0.41
1:B:65:LYS:O	1:B:65:LYS:HD3	2.20	0.41
1:B:86:ASP:OD2	1:B:218:LEU:HD23	2.21	0.41
1:C:76:LYS:HG3	1:C:77:VAL:HG12	2.03	0.41
1:C:195:PHE:O	1:C:196:GLN:HB2	2.21	0.41
1:D:114:LEU:O	1:D:114:LEU:HG	2.21	0.41
1:D:205:LEU:HD23	1:D:205:LEU:C	2.41	0.41
1:A:129:ALA:HA	1:A:146:LEU:HD11	2.03	0.41
1:B:26:ALA:C	1:B:28:ASP:N	2.74	0.41
1:B:49:VAL:HG12	1:B:55:LEU:HD13	2.02	0.41
1:B:63:VAL:HG13	1:B:67:ILE:HB	2.03	0.41
1:B:114:LEU:HD22	1:B:294:ILE:C	2.41	0.41
1:C:13:ARG:HD3	1:C:38:GLU:O	2.20	0.41
1:C:71:ALA:HB1	1:C:75:LEU:CD1	2.42	0.41
1:C:81:MSE:CG	1:C:305:MSE:HB3	2.46	0.41
1:D:94:LYS:O	1:D:97:GLY:N	2.46	0.41
1:D:142:LYS:HB2	1:D:145:TRP:HB3	2.03	0.41
1:A:85:ILE:O	1:A:88:LEU:HG	2.21	0.41
1:B:124:ARG:HB2	1:B:126:LEU:CD1	2.51	0.41
1:B:124:ARG:HB2	1:B:126:LEU:HD11	2.02	0.41
1:B:190:GLU:C	1:B:191:GLU:HG3	2.41	0.41
1:B:203:PRO:HB3	1:B:233:LYS:HE2	2.03	0.41
1:B:245:ARG:O	1:B:248:VAL:HB	2.21	0.41
1:C:133:VAL:HG12	1:D:283:LEU:HD21	2.02	0.41
1:D:195:PHE:O	1:D:196:GLN:CB	2.68	0.41
1:D:226:CYS:O	1:D:249:VAL:HA	2.21	0.41
1:B:43:LYS:O	1:B:44:GLU:C	2.59	0.41
1:B:109:ASP:HB3	1:B:171:ARG:HH22	1.86	0.41
1:B:189:PRO:O	1:B:190:GLU:C	2.59	0.41
1:C:16:PRO:HB2	1:C:306:SER:CB	2.51	0.41
1:C:99:ARG:HB3	1:C:322:MSE:CE	2.51	0.41
1:C:112:ALA:HB2	1:C:167:ALA:HB3	2.02	0.41
1:C:146:LEU:HA	1:C:146:LEU:HD23	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:GLU:HA	1:D:18:GLU:OE2	2.21	0.41
1:D:56:LEU:HA	1:D:79:SER:O	2.20	0.41
1:D:155:THR:HB	1:D:210:ASP:OD2	2.21	0.41
1:A:58:LEU:HB2	1:A:61:ASP:OD2	2.21	0.41
1:A:243:ILE:HD12	1:A:243:ILE:O	2.21	0.41
1:A:280:HIS:CE1	1:A:282:LEU:H	2.39	0.41
1:A:325:GLU:HG2	1:A:326:LEU:N	2.36	0.41
1:C:271:THR:HB	1:C:276:LEU:HD13	2.03	0.41
1:C:275:PRO:HB3	1:D:138:TRP:CG	2.56	0.41
1:A:44:GLU:HA	1:A:47:ARG:HG2	2.03	0.41
1:A:298:THR:O	1:A:299:HIS:C	2.58	0.41
1:C:77:VAL:HG13	1:C:313:LEU:HD12	2.02	0.41
1:D:219:THR:HG22	1:D:220:PRO:HD2	2.03	0.41
1:D:269:ASP:O	1:D:293:HIS:HA	2.20	0.41
1:D:309:ALA:HA	2:D:356:HOH:O	2.20	0.41
1:A:40:ILE:HD11	1:A:44:GLU:CB	2.50	0.41
1:A:68:LEU:HD12	1:A:92:GLU:OE1	2.20	0.41
1:B:41:PRO:O	1:B:42:ALA:C	2.59	0.41
1:B:45:LEU:HD21	1:B:63:VAL:HG12	2.03	0.41
1:B:135:ASN:C	1:B:137:GLY:H	2.24	0.41
1:B:182:TYR:O	1:B:199:PHE:HA	2.21	0.41
1:C:6:LEU:HD12	1:C:6:LEU:N	2.36	0.41
1:C:139:THR:O	1:C:140:SER:HB2	2.21	0.41
1:D:50:ALA:HA	1:D:71:ALA:HA	2.03	0.41
1:D:212:ILE:HD12	1:D:234:MSE:CE	2.44	0.41
1:A:64:ASP:HA	1:A:89:ALA:CB	2.51	0.41
1:B:43:LYS:HB2	2:B:452:HOH:O	2.19	0.41
1:C:268:LEU:HD13	1:C:271:THR:HG22	2.03	0.41
1:D:92:GLU:OE1	1:D:96:ARG:HD2	2.21	0.41
1:D:260:SER:C	1:D:262:LYS:N	2.73	0.41
1:A:104:PRO:O	1:A:105:ASP:HB2	2.21	0.41
1:A:282:LEU:HD23	1:A:282:LEU:HA	1.91	0.41
1:A:302:ARG:HD3	1:A:305:MSE:SE	2.71	0.41
1:B:173:LYS:N	1:B:174:PRO:HD2	2.35	0.41
1:B:200:VAL:HG22	1:B:201:SER:N	2.35	0.41
1:C:17:ALA:HA	1:C:20:ARG:CZ	2.50	0.41
1:D:312:ASN:O	1:D:316:GLY:N	2.39	0.41
1:A:40:ILE:CG1	1:A:44:GLU:HB2	2.51	0.41
1:B:182:TYR:CG	1:B:183:THR:N	2.89	0.41
1:A:77:VAL:HG12	1:A:317:LEU:HD23	2.02	0.41
1:A:243:ILE:HD12	1:A:243:ILE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:110:THR:HG23	1:C:298:THR:HG23	2.02	0.41
1:D:305:MSE:O	1:D:308:LEU:HB3	2.20	0.41
1:A:142:LYS:HB3	2:A:362:HOH:O	2.20	0.41
1:A:228:LYS:O	1:A:229:ASP:C	2.59	0.41
1:A:249:VAL:HG12	1:A:250:ASN:N	2.35	0.41
1:A:302:ARG:HE	1:A:305:MSE:SE	2.54	0.41
1:B:11:VAL:HG12	1:B:13:ARG:O	2.21	0.41
1:B:164:ILE:O	1:B:168:ILE:HG13	2.20	0.41
1:C:292:PRO:CD	1:D:129:ALA:HB1	2.48	0.41
1:A:102:TYR:CE1	1:A:104:PRO:HD3	2.56	0.41
1:A:206:ALA:HB2	1:A:230:PHE:CE1	2.56	0.41
1:A:298:THR:HG1	1:A:301:THR:HB	1.83	0.41
1:A:305:MSE:HE3	1:A:305:MSE:HB2	1.94	0.41
1:A:316:GLY:CA	1:A:322:MSE:HG2	2.43	0.41
1:B:173:LYS:HE3	2:B:437:HOH:O	2.21	0.41
1:C:280:HIS:CG	1:C:281:PRO:HD2	2.56	0.41
1:D:107:LEU:C	1:D:107:LEU:HD12	2.40	0.41
1:D:272:SER:HA	1:D:273:PRO:HA	1.93	0.41
1:A:51:GLY:N	1:A:71:ALA:HA	2.35	0.41
1:A:79:SER:HB3	1:A:313:LEU:HB3	2.03	0.41
1:A:134:LYS:HE3	1:A:134:LYS:HB2	1.80	0.41
1:C:76:LYS:HB3	1:C:76:LYS:HZ3	1.81	0.41
1:D:34:TRP:CD1	1:D:40:ILE:HB	2.56	0.41
1:D:185:ARG:HG2	1:D:186:GLN:N	2.36	0.41
1:A:110:THR:CG2	1:A:298:THR:HG23	2.51	0.41
1:A:216:CYS:SG	1:A:222:THR:HG22	2.61	0.41
1:B:22:ALA:C	1:B:24:ALA:N	2.73	0.41
1:B:81:MSE:HG2	1:B:305:MSE:HB3	2.03	0.41
1:D:226:CYS:H	1:D:248:VAL:HG12	1.86	0.41
1:D:322:MSE:HB2	1:D:325:GLU:HB2	2.02	0.41
1:A:239:VAL:HG22	1:A:265:ALA:HB3	2.03	0.41
1:C:151:LEU:O	1:C:154:SER:HB2	2.21	0.41
1:A:102:TYR:CZ	1:A:326:LEU:HD13	2.56	0.40
1:C:58:LEU:HD13	1:D:141:TRP:HE3	1.86	0.40
1:D:255:TYR:CD1	1:D:285:LEU:HD11	2.56	0.40
1:A:312:ASN:HB3	1:A:322:MSE:SE	2.71	0.40
1:B:86:ASP:OD1	1:B:86:ASP:O	2.39	0.40
1:B:201:SER:CB	1:B:203:PRO:HD2	2.51	0.40
1:C:14:ARG:HB3	1:C:36:SER:O	2.21	0.40
1:C:223:GLU:CG	1:C:247:ASP:HB3	2.51	0.40
1:D:77:VAL:N	1:D:98:ILE:HG23	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:ASP:OD1	1:B:245:ARG:NE	2.54	0.40
1:C:218:LEU:HA	1:C:222:THR:OG1	2.20	0.40
1:D:30:GLU:OE1	1:D:30:GLU:HA	2.21	0.40
1:D:108:THR:HG23	1:D:164:ILE:HA	2.03	0.40
1:D:182:TYR:CD1	1:D:197:ALA:HB1	2.56	0.40
1:D:201:SER:OG	1:D:204:GLU:HG2	2.20	0.40
1:D:224:GLY:O	1:D:227:ASN:ND2	2.54	0.40
1:A:147:CYS:SG	1:B:302:ARG:HG3	2.61	0.40
1:A:187:PRO:C	1:A:188:ARG:HG3	2.41	0.40
1:A:302:ARG:HD3	1:A:302:ARG:HA	1.88	0.40
1:B:110:THR:O	1:B:113:GLU:HB3	2.21	0.40
1:B:124:ARG:HB2	1:B:126:LEU:HD11	2.02	0.40
1:B:313:LEU:CD1	1:B:317:LEU:HD22	2.52	0.40
1:C:183:THR:HB	1:C:200:VAL:O	2.21	0.40
1:D:265:ALA:HB2	1:D:287:ASN:HB2	2.03	0.40
1:D:312:ASN:O	1:D:322:MSE:HE3	2.21	0.40
1:A:11:VAL:HG13	1:A:56:LEU:HD22	2.03	0.40
1:A:40:ILE:O	1:A:40:ILE:HG23	2.21	0.40
1:B:139:THR:O	1:B:140:SER:CB	2.68	0.40
1:B:155:THR:N	1:B:210:ASP:OD2	2.52	0.40
1:C:11:VAL:HG13	1:C:56:LEU:HD22	2.02	0.40
1:C:39:PRO:HB2	1:C:60:SER:HB2	2.03	0.40
1:D:269:ASP:HA	1:D:291:LEU:HB2	2.03	0.40
1:A:20:ARG:HE	1:A:21:VAL:CG2	2.34	0.40
1:A:232:GLN:HE22	1:A:262:LYS:NZ	2.18	0.40
1:A:280:HIS:ND1	1:A:282:LEU:HB2	2.35	0.40
1:B:7:MSE:SE	1:B:76:LYS:NZ	3.05	0.40
1:B:75:LEU:HG	1:B:98:ILE:HG12	2.03	0.40
1:D:180:PHE:CD2	1:D:195:PHE:HB3	2.56	0.40
1:A:20:ARG:O	1:A:23:LEU:HB2	2.21	0.40
1:A:26:ALA:HA	1:A:318:ARG:NH2	2.37	0.40
1:A:142:LYS:HB3	2:A:364:HOH:O	2.20	0.40
1:C:53:HIS:CE1	1:C:74:ASN:ND2	2.89	0.40
1:C:312:ASN:HB3	1:C:322:MSE:HE2	2.03	0.40
1:D:17:ALA:O	1:D:18:GLU:C	2.60	0.40
1:D:90:LEU:HA	1:D:93:ILE:HB	2.02	0.40
1:D:99:ARG:HB3	1:D:322:MSE:CE	2.34	0.40
1:D:102:TYR:CE1	1:D:326:LEU:HD12	2.57	0.40
1:D:256:GLN:OE1	1:D:256:GLN:N	2.53	0.40
1:D:312:ASN:O	1:D:322:MSE:HG3	2.20	0.40
1:A:128:GLU:HG3	2:A:384:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:GLY:HA2	1:A:289:VAL:O	2.21	0.40
1:B:85:ILE:HD12	1:B:90:LEU:HD11	2.03	0.40
1:B:155:THR:N	1:B:210:ASP:OD2	2.53	0.40
1:C:81:MSE:HA	1:C:103:THR:HG21	2.03	0.40
1:C:320:GLU:HB2	1:C:321:PRO:HD2	2.03	0.40
1:D:20:ARG:CZ	1:D:33:GLN:HE22	2.35	0.40
1:B:257:ALA:HB1	1:B:262:LYS:HB2	2.04	0.40
1:D:26:ALA:CB	1:D:29:CYS:SG	3.09	0.40
1:D:179:ARG:CZ	2:D:396:HOH:O	2.68	0.40
1:D:301:THR:O	1:D:304:THR:N	2.54	0.40
1:A:8:LYS:O	1:A:52:ALA:HB2	2.22	0.40
1:A:163:ARG:CZ	2:A:418:HOH:O	2.69	0.40
1:C:182:TYR:O	1:C:199:PHE:HA	2.20	0.40
1:D:177:VAL:HG11	1:D:180:PHE:CZ	2.56	0.40
1:B:216:CYS:SG	1:B:248:VAL:HG11	2.61	0.40
1:B:262:LYS:HE3	2:B:359:HOH:O	2.21	0.40
1:C:271:THR:HB	1:C:276:LEU:HD13	2.03	0.40
1:D:119:LEU:C	1:D:119:LEU:HD23	2.41	0.40
1:A:16:PRO:C	1:A:18:GLU:H	2.23	0.40
1:A:18:GLU:HB3	1:A:306:SER:HB2	2.02	0.40
1:A:21:VAL:C	1:A:23:LEU:N	2.73	0.40
1:A:68:LEU:HD21	1:A:93:ILE:HD11	2.02	0.40
1:A:226:CYS:HA	1:A:230:PHE:CG	2.57	0.40
1:B:85:ILE:O	1:B:87:HIS:N	2.54	0.40
1:B:194:GLU:HG2	1:B:194:GLU:O	2.20	0.40
1:C:40:ILE:HG22	1:C:61:ASP:OD1	2.21	0.40
1:C:135:ASN:CG	1:C:136:GLY:N	2.75	0.40
1:C:152:THR:CG2	1:C:153:GLN:HG3	2.46	0.40
1:D:85:ILE:HD12	1:D:85:ILE:C	2.41	0.40
1:D:119:LEU:C	1:D:119:LEU:HD23	2.41	0.40
1:D:200:VAL:HG23	1:D:205:LEU:HD12	2.03	0.40
1:D:267:GLY:HA2	1:D:289:VAL:O	2.21	0.40
1:D:302:ARG:HA	1:D:302:ARG:HD3	1.89	0.40
1:A:77:VAL:HG11	1:A:317:LEU:HB2	2.03	0.40
1:A:219:THR:O	1:A:223:GLU:N	2.54	0.40
1:B:45:LEU:O	1:B:49:VAL:HG13	2.20	0.40
1:B:64:ASP:OD1	1:B:67:ILE:HG12	2.21	0.40
1:B:68:LEU:HD12	1:B:92:GLU:HB3	2.02	0.40
1:B:114:LEU:HD22	1:B:294:ILE:C	2.42	0.40
1:B:185:ARG:HB2	1:B:185:ARG:HH11	1.86	0.40
1:C:17:ALA:O	1:C:20:ARG:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:188:ARG:HD2	2:D:412:HOH:O	2.20	0.40
1:A:243:ILE:O	1:A:243:ILE:HD12	2.21	0.40
1:B:232:GLN:HB3	2:B:425:HOH:O	2.21	0.40
1:D:90:LEU:O	1:D:91:ASP:C	2.60	0.40
1:A:12:THR:O	1:A:13:ARG:HB2	2.21	0.40
1:A:182:TYR:O	1:A:200:VAL:HG22	2.21	0.40
1:C:34:TRP:HB2	1:C:40:ILE:HD12	2.02	0.40
1:C:103:THR:HG22	1:C:308:LEU:CD2	2.51	0.40
1:C:268:LEU:HB2	1:C:290:ILE:HG12	2.02	0.40
1:A:193:ALA:C	1:A:196:GLN:H	2.24	0.40
1:B:79:SER:HB3	1:B:313:LEU:HD23	2.04	0.40
1:C:40:ILE:HA	1:C:41:PRO:HD3	1.95	0.40
1:C:173:LYS:N	1:C:174:PRO:HD2	2.37	0.40
1:C:280:HIS:CG	1:C:281:PRO:HD2	2.56	0.40
1:D:177:VAL:HG11	1:D:180:PHE:CE1	2.56	0.40
1:A:110:THR:HG23	1:A:298:THR:HG23	2.03	0.40
1:A:155:THR:O	1:A:209:SER:HA	2.21	0.40
1:B:80:THR:C	1:B:82:SER:H	2.25	0.40
1:C:54:GLY:HA3	1:C:77:VAL:HG13	2.04	0.40
1:C:64:ASP:OD1	1:C:64:ASP:N	2.54	0.40
1:D:16:PRO:O	1:D:18:GLU:N	2.54	0.40
1:D:219:THR:HB	1:D:220:PRO:CD	2.51	0.40
1:D:272:SER:HA	1:D:273:PRO:HA	1.80	0.40
1:A:53:HIS:HB3	1:A:76:LYS:HG2	2.03	0.40
1:A:238:ALA:O	1:A:263:ILE:HB	2.22	0.40
1:B:15:ILE:HG21	1:B:81:MSE:HE1	2.03	0.40
1:B:164:ILE:O	1:B:168:ILE:HG13	2.21	0.40
1:C:180:PHE:HB2	1:C:197:ALA:HA	2.03	0.40
1:D:13:ARG:CG	1:D:14:ARG:N	2.83	0.40
1:A:99:ARG:HB3	1:A:322:MSE:HE1	2.03	0.40
1:C:292:PRO:CD	1:D:129:ALA:HB1	2.49	0.40
1:A:65:LYS:HE2	1:A:92:GLU:HG3	2.04	0.40
1:B:201:SER:CB	1:B:203:PRO:HD2	2.51	0.40
1:C:218:LEU:HB2	1:C:245:ARG:HG3	2.02	0.40
1:D:258:LEU:HD13	1:D:288:CYS:HB2	2.03	0.40
1:B:110:THR:HG23	1:B:298:THR:HG23	2.03	0.40
1:C:10:PHE:O	1:C:55:LEU:HD12	2.22	0.40
1:C:86:ASP:HB3	1:C:218:LEU:HD23	2.03	0.40
1:C:249:VAL:HG12	1:C:250:ASN:N	2.36	0.40
1:D:99:ARG:NH1	1:D:325:GLU:OE1	2.51	0.40
1:D:166:GLN:O	1:D:168:ILE:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ILE:HG23	1:A:40:ILE:O	2.20	0.40
1:A:313:LEU:HD23	1:A:313:LEU:C	2.42	0.40
1:B:40:ILE:HA	1:B:41:PRO:HD3	1.92	0.40
1:B:164:ILE:O	1:B:167:ALA:HB3	2.21	0.40
1:B:202:THR:HG21	1:B:225:LEU:HD11	2.02	0.40
1:B:251:GLN:HG2	1:B:282:LEU:HD11	2.03	0.40
1:C:18:GLU:OE1	1:C:303:ASN:CG	2.60	0.40
1:D:315:ALA:HB3	1:D:322:MSE:HG2	2.03	0.40
1:A:40:ILE:HA	1:A:41:PRO:HD3	1.90	0.40
1:A:222:THR:O	1:A:225:LEU:N	2.42	0.40
1:A:305:MSE:HE1	1:B:141:TRP:HH2	1.82	0.40
1:B:59:LEU:HD12	1:B:60:SER:N	2.35	0.40
1:B:188:ARG:N	1:B:189:PRO:HD2	2.37	0.40
1:C:272:SER:HA	1:C:273:PRO:HA	1.84	0.40
1:D:109:ASP:HB2	2:D:329:HOH:O	2.21	0.40
1:C:49:VAL:O	1:C:71:ALA:HA	2.20	0.40
1:B:57:CYS:O	1:B:58:LEU:HD23	2.21	0.40
1:C:43:LYS:O	1:C:46:GLU:HB2	2.22	0.40
1:A:49:VAL:HG11	1:A:67:ILE:HG23	2.04	0.40
1:A:202:THR:N	1:A:203:PRO:CD	2.85	0.40
1:A:231:PHE:CD1	1:A:234:MSE:SE	3.24	0.40
1:A:234:MSE:SE	1:A:263:ILE:CG2	3.20	0.40
1:B:16:PRO:HD2	1:B:306:SER:HB2	2.03	0.40
1:B:114:LEU:HD22	1:B:295:GLY:HA2	2.03	0.40
1:B:273:PRO:HB2	2:B:337:HOH:O	2.20	0.40
1:B:280:HIS:CG	1:B:281:PRO:HD2	2.55	0.40
1:A:81:MSE:SE	1:B:141:TRP:HH2	2.54	0.40
1:B:209:SER:HB3	1:B:211:PHE:O	2.21	0.40
1:B:300:ARG:HG3	2:B:447:HOH:O	2.21	0.40
1:B:302:ARG:HD3	1:B:302:ARG:HA	1.82	0.40
2:C:350:HOH:O	1:D:300:ARG:HD2	2.21	0.40
1:A:77:VAL:CG1	1:A:317:LEU:HG	2.43	0.40
1:A:243:ILE:O	1:A:243:ILE:HD12	2.22	0.40
1:B:16:PRO:HD2	1:B:81:MSE:HE1	2.03	0.40
1:B:66:ARG:O	1:B:69:ASP:HB2	2.21	0.40
1:A:45:LEU:HG	1:A:67:ILE:CD1	2.51	0.40
1:A:65:LYS:HA	1:A:68:LEU:HB2	2.02	0.40
1:A:280:HIS:HA	1:A:281:PRO:HD3	1.98	0.40
1:C:92:GLU:HA	1:C:95:LYS:HB3	2.02	0.40
1:C:218:LEU:HD21	1:C:247:ASP:OD2	2.22	0.40
1:A:90:LEU:HD21	1:A:100:VAL:HG11	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:PRO:O	1:D:204:GLU:C	2.59	0.40
1:D:254:LEU:O	1:D:255:TYR:C	2.58	0.40
1:D:318:ARG:O	1:D:320:GLU:HG3	2.21	0.40
1:A:76:LYS:HZ1	1:A:317:LEU:HA	1.86	0.40
1:A:139:THR:O	1:B:275:PRO:HD3	2.22	0.40
1:C:16:PRO:HA	1:D:144:LEU:HD21	2.03	0.40
1:C:258:LEU:HD13	1:C:288:CYS:HB2	2.03	0.40
1:D:276:LEU:HG	1:D:280:HIS:CD2	2.56	0.40
1:A:182:TYR:CE1	1:A:199:PHE:N	2.89	0.40
1:A:203:PRO:HB3	1:A:233:LYS:HD3	2.03	0.40
1:C:36:SER:C	1:C:38:GLU:H	2.25	0.40
1:C:70:ALA:C	1:C:72:GLY:H	2.25	0.40
1:C:173:LYS:HB3	1:C:174:PRO:CD	2.51	0.40
1:C:291:LEU:HD21	1:D:126:LEU:HG	2.04	0.40
1:A:13:ARG:HG3	1:A:14:ARG:N	2.36	0.40
1:A:77:VAL:HG11	1:A:316:GLY:HA3	2.04	0.40
1:A:202:THR:HB	1:A:203:PRO:CD	2.44	0.40
1:A:322:MSE:HB2	1:A:325:GLU:HB2	2.03	0.40
1:B:8:LYS:CD	1:B:30:GLU:HG3	2.50	0.40
1:C:171:ARG:HG3	1:C:171:ARG:HH11	1.86	0.40
1:A:12:THR:O	1:A:13:ARG:HB2	2.20	0.40
1:A:69:ASP:O	1:A:71:ALA:N	2.48	0.40
1:A:302:ARG:HD3	1:A:302:ARG:HA	1.90	0.40
1:B:34:TRP:CG	1:B:40:ILE:HD12	2.57	0.40
1:B:102:TYR:CD1	1:B:102:TYR:N	2.89	0.40
1:B:173:LYS:HB3	1:B:174:PRO:CD	2.52	0.40
1:C:171:ARG:HG3	1:C:171:ARG:HH11	1.86	0.40
1:D:107:LEU:HD12	1:D:107:LEU:C	2.41	0.40
1:B:34:TRP:CD1	1:B:40:ILE:HB	2.57	0.40
1:B:200:VAL:CG2	1:B:204:GLU:HB2	2.52	0.40
1:C:87:HIS:HD1	1:C:87:HIS:H	1.70	0.40
1:D:280:HIS:ND1	1:D:281:PRO:HD2	2.37	0.40
1:A:40:ILE:HA	1:A:41:PRO:HD3	1.90	0.40
1:A:102:TYR:CZ	1:A:326:LEU:HD13	2.56	0.40
1:A:182:TYR:CD1	1:A:197:ALA:O	2.74	0.40
1:B:88:LEU:HB3	1:B:93:ILE:CD1	2.52	0.40
1:B:258:LEU:HD23	1:B:263:ILE:HG13	2.02	0.40
1:C:186:GLN:HA	1:C:187:PRO:HD3	1.89	0.40
1:D:75:LEU:HG	1:D:98:ILE:HD13	2.04	0.40
1:A:77:VAL:C	1:A:78:ILE:HG13	2.42	0.40
1:A:147:CYS:HA	1:B:297:ALA:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:THR:HG22	1:B:127:PRO:HD3	2.04	0.40
1:C:45:LEU:HB3	1:C:67:ILE:HD12	2.03	0.40
1:C:85:ILE:O	1:C:87:HIS:N	2.55	0.40
1:D:20:ARG:CG	2:D:333:HOH:O	2.65	0.40
1:A:9:VAL:HA	1:A:54:GLY:O	2.21	0.40
1:A:23:LEU:HB3	1:A:31:VAL:HG21	2.03	0.40
1:A:114:LEU:HD13	1:A:295:GLY:N	2.37	0.40
1:C:14:ARG:NE	1:C:37:ASP:OD2	2.54	0.40
1:C:85:ILE:HD12	1:C:90:LEU:CD1	2.48	0.40
1:C:227:ASN:HB2	1:C:228:LYS:H	1.63	0.40
1:D:312:ASN:HA	1:D:323:PRO:HD2	2.03	0.40
1:A:14:ARG:HB3	1:A:37:ASP:OD1	2.22	0.40
1:B:80:THR:HG21	1:B:85:ILE:CG2	2.39	0.40
1:B:319:GLY:O	1:B:320:GLU:C	2.60	0.40
1:D:82:SER:N	1:D:103:THR:HG23	2.37	0.40
1:D:201:SER:HB2	1:D:203:PRO:HD2	2.03	0.40
1:A:107:LEU:HD12	1:A:108:THR:N	2.36	0.40
1:A:159:ILE:HA	1:A:183:THR:HG22	2.02	0.40
1:B:252:ASP:OD1	1:B:255:TYR:HD1	2.04	0.40
1:D:85:ILE:HD12	1:D:85:ILE:C	2.42	0.40
1:D:285:LEU:C	1:D:287:ASN:H	2.24	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [\(i\)](#)

### 5.3.1 Protein backbone [\(i\)](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	1-A	319/328 (97%)	263 (82%)	48 (15%)	8 (2%)	<b>5</b> <b>3</b>
1	1-B	319/328 (97%)	276 (86%)	42 (13%)	1 (0%)	41 49
1	1-C	319/328 (97%)	269 (84%)	41 (13%)	9 (3%)	<b>5</b> <b>2</b>
1	1-D	319/328 (97%)	258 (81%)	44 (14%)	17 (5%)	<b>2</b> <b>0</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2-A	319/328 (97%)	253 (79%)	53 (17%)	13 (4%)	3	1
1	2-B	319/328 (97%)	269 (84%)	40 (12%)	10 (3%)	4	1
1	2-C	319/328 (97%)	272 (85%)	41 (13%)	6 (2%)	8	6
1	2-D	319/328 (97%)	276 (86%)	33 (10%)	10 (3%)	4	1
1	3-A	319/328 (97%)	263 (82%)	48 (15%)	8 (2%)	5	3
1	3-B	319/328 (97%)	275 (86%)	31 (10%)	13 (4%)	3	1
1	3-C	319/328 (97%)	276 (86%)	35 (11%)	8 (2%)	5	3
1	3-D	319/328 (97%)	266 (83%)	47 (15%)	6 (2%)	8	6
1	4-A	319/328 (97%)	253 (79%)	55 (17%)	11 (3%)	3	1
1	4-B	319/328 (97%)	267 (84%)	44 (14%)	8 (2%)	5	3
1	4-C	319/328 (97%)	266 (83%)	39 (12%)	14 (4%)	2	1
1	4-D	319/328 (97%)	275 (86%)	35 (11%)	9 (3%)	5	2
1	5-A	319/328 (97%)	276 (86%)	39 (12%)	4 (1%)	12	11
1	5-B	319/328 (97%)	272 (85%)	38 (12%)	9 (3%)	5	2
1	5-C	319/328 (97%)	274 (86%)	37 (12%)	8 (2%)	5	3
1	5-D	319/328 (97%)	278 (87%)	34 (11%)	7 (2%)	6	4
1	6-A	319/328 (97%)	247 (77%)	51 (16%)	21 (7%)	1	0
1	6-B	319/328 (97%)	268 (84%)	37 (12%)	14 (4%)	2	1
1	6-C	319/328 (97%)	263 (82%)	42 (13%)	14 (4%)	2	1
1	6-D	319/328 (97%)	268 (84%)	40 (12%)	11 (3%)	3	1
1	7-A	319/328 (97%)	255 (80%)	45 (14%)	19 (6%)	1	0
1	7-B	319/328 (97%)	239 (75%)	59 (18%)	21 (7%)	1	0
1	7-C	319/328 (97%)	273 (86%)	35 (11%)	11 (3%)	3	1
1	7-D	319/328 (97%)	270 (85%)	41 (13%)	8 (2%)	5	3
1	8-A	319/328 (97%)	264 (83%)	45 (14%)	10 (3%)	4	1
1	8-B	319/328 (97%)	275 (86%)	35 (11%)	9 (3%)	5	2
1	8-C	319/328 (97%)	271 (85%)	39 (12%)	9 (3%)	5	2
1	8-D	319/328 (97%)	277 (87%)	36 (11%)	6 (2%)	8	6
All	All	10208/10496 (97%)	8547 (84%)	1329 (13%)	332 (3%)	4	1

All (332) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	251	GLN
1	1-B	22	ALA
1	1-C	18	GLU
1	1-C	163	ARG
1	1-C	244	SER
1	1-D	91	ASP
1	1-D	177	VAL
1	1-D	197	ALA
1	1-D	225	LEU
1	2-A	260	SER
1	2-B	228	LYS
1	2-C	76	LYS
1	2-D	187	PRO
1	2-D	188	ARG
1	2-D	191	GLU
1	3-A	209	SER
1	3-A	315	ALA
1	3-B	64	ASP
1	3-B	244	SER
1	3-C	42	ALA
1	3-C	189	PRO
1	3-C	244	SER
1	4-A	98	ILE
1	4-A	262	LYS
1	4-A	320	GLU
1	4-B	89	ALA
1	4-B	223	GLU
1	4-B	298	THR
1	4-C	12	THR
1	4-C	60	SER
1	4-C	140	SER
1	4-C	163	ARG
1	5-B	140	SER
1	5-B	209	SER
1	5-B	244	SER
1	5-C	17	ALA
1	5-C	73	ALA
1	6-A	75	LEU
1	6-A	108	THR
1	6-A	138	TRP
1	6-A	161	LEU
1	6-A	183	THR
1	6-B	226	CYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	6-B	244	SER
1	6-B	297	ALA
1	6-C	35	ASP
1	6-C	95	LYS
1	6-C	105	ASP
1	6-C	189	PRO
1	6-D	36	SER
1	6-D	218	LEU
1	7-A	26	ALA
1	7-A	27	ALA
1	7-A	75	LEU
1	7-A	185	ARG
1	7-B	22	ALA
1	7-B	74	ASN
1	7-B	321	PRO
1	7-C	49	VAL
1	7-C	105	ASP
1	7-C	324	SER
1	8-A	216	CYS
1	8-A	251	GLN
1	8-B	106	VAL
1	8-B	136	GLY
1	8-B	324	SER
1	8-B	325	GLU
1	8-C	15	ILE
1	1-A	26	ALA
1	1-C	216	CYS
1	1-D	191	GLU
1	1-D	192	ALA
1	1-D	226	CYS
1	1-D	278	THR
1	2-A	17	ALA
1	2-A	26	ALA
1	2-A	231	PHE
1	2-B	36	SER
1	2-B	85	ILE
1	2-B	90	LEU
1	2-B	247	ASP
1	2-C	244	SER
1	2-D	185	ARG
1	2-D	313	LEU
1	3-A	278	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	3-A	282	LEU
1	3-B	63	VAL
1	3-B	95	LYS
1	3-B	190	GLU
1	3-B	247	ASP
1	3-C	63	VAL
1	3-C	190	GLU
1	3-D	282	LEU
1	4-A	35	ASP
1	4-A	207	ALA
1	4-A	234	MSE
1	4-B	86	ASP
1	4-B	189	PRO
1	4-B	191	GLU
1	4-B	226	CYS
1	4-C	71	ALA
1	4-C	216	CYS
1	4-D	282	LEU
1	5-A	26	ALA
1	5-A	73	ALA
1	5-B	27	ALA
1	5-B	35	ASP
1	5-C	72	GLY
1	5-C	86	ASP
1	5-C	105	ASP
1	5-C	146	LEU
1	5-D	216	CYS
1	5-D	319	GLY
1	6-A	90	LEU
1	6-A	105	ASP
1	6-A	207	ALA
1	6-B	140	SER
1	6-B	185	ARG
1	6-B	225	LEU
1	6-C	77	VAL
1	6-C	190	GLU
1	6-C	191	GLU
1	6-D	50	ALA
1	7-A	96	ARG
1	7-A	182	TYR
1	7-A	223	GLU
1	7-A	244	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	7-B	31	VAL
1	7-B	51	GLY
1	7-B	66	ARG
1	7-B	72	GLY
1	7-B	98	ILE
1	7-B	105	ASP
1	7-B	136	GLY
1	7-B	314	LEU
1	7-C	35	ASP
1	7-C	63	VAL
1	7-C	87	HIS
1	7-D	105	ASP
1	7-D	279	ASN
1	8-A	28	ASP
1	8-A	35	ASP
1	8-A	207	ALA
1	8-A	217	SER
1	8-B	105	ASP
1	8-B	140	SER
1	8-C	17	ALA
1	8-D	153	GLN
1	1-A	199	PHE
1	1-A	226	CYS
1	1-C	19	GLY
1	1-D	17	ALA
1	1-D	139	THR
1	1-D	190	GLU
1	1-D	193	ALA
1	2-A	71	ALA
1	2-A	73	ALA
1	2-A	216	CYS
1	2-B	244	SER
1	2-C	42	ALA
1	2-D	105	ASP
1	2-D	216	CYS
1	3-A	207	ALA
1	3-B	50	ALA
1	3-B	73	ALA
1	3-B	185	ARG
1	3-D	27	ALA
1	3-D	190	GLU
1	4-A	278	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	4-C	226	CYS
1	4-D	17	ALA
1	4-D	35	ASP
1	4-D	206	ALA
1	5-B	235	LYS
1	5-D	26	ALA
1	5-D	244	SER
1	6-A	104	PRO
1	6-A	143	PRO
1	6-A	144	LEU
1	6-A	226	CYS
1	6-B	86	ASP
1	6-C	96	ARG
1	6-D	190	GLU
1	6-D	203	PRO
1	6-D	264	ALA
1	7-A	97	GLY
1	7-A	160	GLY
1	7-A	220	PRO
1	7-B	89	ALA
1	7-B	323	PRO
1	7-C	52	ALA
1	7-C	75	LEU
1	7-C	190	GLU
1	7-D	226	CYS
1	7-D	306	SER
1	8-C	73	ALA
1	8-C	90	LEU
1	8-C	140	SER
1	8-D	190	GLU
1	8-D	244	SER
1	1-A	287	ASN
1	1-D	222	THR
1	1-D	244	SER
1	2-A	236	GLU
1	2-A	261	GLY
1	2-B	51	GLY
1	2-C	75	LEU
1	2-C	140	SER
1	2-D	190	GLU
1	3-A	41	PRO
1	3-B	36	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	3-B	189	PRO
1	3-C	73	ALA
1	3-D	183	THR
1	4-A	324	SER
1	4-C	8	LYS
1	4-D	143	PRO
1	5-A	251	GLN
1	5-B	190	GLU
1	5-C	18	GLU
1	5-D	167	ALA
1	5-D	189	PRO
1	6-A	140	SER
1	6-A	299	HIS
1	6-B	87	HIS
1	6-B	174	PRO
1	6-B	311	ASN
1	6-D	189	PRO
1	6-D	191	GLU
1	6-D	262	LYS
1	6-D	295	GLY
1	7-A	90	LEU
1	7-A	187	PRO
1	7-B	23	LEU
1	7-B	30	GLU
1	7-B	42	ALA
1	7-B	320	GLU
1	7-C	85	ILE
1	7-C	96	ARG
1	7-D	229	ASP
1	8-A	25	ARG
1	8-A	232	GLN
1	8-B	86	ASP
1	8-D	26	ALA
1	8-D	264	ALA
1	1-A	17	ALA
1	1-A	216	CYS
1	1-C	15	ILE
1	1-C	90	LEU
1	1-C	189	PRO
1	1-D	204	GLU
1	1-D	281	PRO
1	2-A	48	GLY

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	2-A	65	LYS
1	2-A	108	THR
1	2-D	50	ALA
1	2-D	189	PRO
1	3-D	319	GLY
1	4-A	88	LEU
1	4-A	247	ASP
1	4-B	50	ALA
1	4-C	189	PRO
1	4-D	105	ASP
1	5-A	69	ASP
1	5-B	86	ASP
1	5-B	174	PRO
1	5-C	35	ASP
1	5-D	251	GLN
1	6-A	188	ARG
1	6-A	190	GLU
1	6-A	325	GLU
1	7-A	74	ASN
1	7-A	200	VAL
1	7-B	68	LEU
1	7-B	91	ASP
1	7-B	318	ARG
1	7-D	26	ALA
1	7-D	228	LYS
1	8-A	27	ALA
1	2-B	189	PRO
1	3-C	85	ILE
1	3-C	187	PRO
1	3-D	260	SER
1	4-C	17	ALA
1	4-C	187	PRO
1	4-C	287	ASN
1	4-D	46	GLU
1	6-A	200	VAL
1	6-C	34	TRP
1	6-C	50	ALA
1	6-C	98	ILE
1	6-D	228	LYS
1	7-A	17	ALA
1	7-A	246	GLY
1	7-D	206	ALA

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Mol	Chain	Res	Type
1	8-B	93	ILE
1	8-C	18	GLU
1	1-A	281	PRO
1	1-D	143	PRO
1	6-A	19	GLY
1	6-A	295	GLY
1	6-B	202	THR
1	6-C	93	ILE
1	7-A	162	GLY
1	2-A	164	ILE
1	2-B	67	ILE
1	2-B	246	GLY
1	3-A	281	PRO
1	4-A	323	PRO
1	4-C	77	VAL
1	4-C	85	ILE
1	4-D	21	VAL
1	6-B	67	ILE
1	8-C	51	GLY
1	8-C	103	THR
1	1-C	51	GLY
1	2-C	321	PRO
1	3-A	321	PRO
1	6-B	85	ILE
1	6-C	295	GLY
1	8-A	224	GLY
1	8-B	77	VAL
1	8-C	93	ILE
1	6-A	187	PRO
1	6-B	184	GLY
1	6-C	49	VAL
1	7-B	322	MSE
1	3-B	93	ILE
1	3-B	220	PRO
1	4-D	15	ILE
1	7-A	188	ARG
1	8-D	189	PRO

### 5.3.2 Protein sidechains [i](#)

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	1-A	262/264 (99%)	253 (97%)	9 (3%)	37	48
1	1-B	262/264 (99%)	254 (97%)	8 (3%)	40	52
1	1-C	262/264 (99%)	255 (97%)	7 (3%)	44	57
1	1-D	262/264 (99%)	255 (97%)	7 (3%)	44	57
1	2-A	262/264 (99%)	253 (97%)	9 (3%)	37	48
1	2-B	262/264 (99%)	257 (98%)	5 (2%)	57	69
1	2-C	262/264 (99%)	247 (94%)	15 (6%)	20	26
1	2-D	262/264 (99%)	257 (98%)	5 (2%)	57	69
1	3-A	262/264 (99%)	254 (97%)	8 (3%)	40	52
1	3-B	262/264 (99%)	254 (97%)	8 (3%)	40	52
1	3-C	262/264 (99%)	252 (96%)	10 (4%)	33	43
1	3-D	262/264 (99%)	257 (98%)	5 (2%)	57	69
1	4-A	262/264 (99%)	249 (95%)	13 (5%)	24	32
1	4-B	262/264 (99%)	250 (95%)	12 (5%)	27	35
1	4-C	262/264 (99%)	251 (96%)	11 (4%)	30	39
1	4-D	262/264 (99%)	257 (98%)	5 (2%)	57	69
1	5-A	262/264 (99%)	253 (97%)	9 (3%)	37	48
1	5-B	262/264 (99%)	249 (95%)	13 (5%)	24	32
1	5-C	262/264 (99%)	246 (94%)	16 (6%)	18	24
1	5-D	262/264 (99%)	253 (97%)	9 (3%)	37	48
1	6-A	262/264 (99%)	248 (95%)	14 (5%)	22	29
1	6-B	262/264 (99%)	248 (95%)	14 (5%)	22	29
1	6-C	262/264 (99%)	247 (94%)	15 (6%)	20	26
1	6-D	262/264 (99%)	251 (96%)	11 (4%)	30	39
1	7-A	262/264 (99%)	253 (97%)	9 (3%)	37	48
1	7-B	262/264 (99%)	248 (95%)	14 (5%)	22	29
1	7-C	262/264 (99%)	250 (95%)	12 (5%)	27	35
1	7-D	262/264 (99%)	251 (96%)	11 (4%)	30	39
1	8-A	262/264 (99%)	249 (95%)	13 (5%)	24	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	8-B	262/264 (99%)	252 (96%)	10 (4%)	33	43
1	8-C	262/264 (99%)	248 (95%)	14 (5%)	22	29
1	8-D	262/264 (99%)	254 (97%)	8 (3%)	40	52
All	All	8384/8448 (99%)	8055 (96%)	329 (4%)	32	42

All (329) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-A	35	ASP
1	1-A	59	LEU
1	1-A	102	TYR
1	1-A	107	LEU
1	1-A	196	GLN
1	1-A	254	LEU
1	1-A	279	ASN
1	1-A	282	LEU
1	1-A	288	CYS
1	1-B	35	ASP
1	1-B	91	ASP
1	1-B	102	TYR
1	1-B	107	LEU
1	1-B	182	TYR
1	1-B	183	THR
1	1-B	190	GLU
1	1-B	300	ARG
1	1-C	44	GLU
1	1-C	75	LEU
1	1-C	91	ASP
1	1-C	102	TYR
1	1-C	109	ASP
1	1-C	163	ARG
1	1-C	183	THR
1	1-D	20	ARG
1	1-D	47	ARG
1	1-D	107	LEU
1	1-D	185	ARG
1	1-D	195	PHE
1	1-D	232	GLN
1	1-D	251	GLN
1	2-A	64	ASP
1	2-A	69	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	2-A	75	LEU
1	2-A	102	TYR
1	2-A	105	ASP
1	2-A	107	LEU
1	2-A	144	LEU
1	2-A	229	ASP
1	2-A	273	PRO
1	2-B	35	ASP
1	2-B	91	ASP
1	2-B	102	TYR
1	2-B	182	TYR
1	2-B	229	ASP
1	2-C	13	ARG
1	2-C	20	ARG
1	2-C	32	GLU
1	2-C	33	GLN
1	2-C	35	ASP
1	2-C	37	ASP
1	2-C	38	GLU
1	2-C	55	LEU
1	2-C	59	LEU
1	2-C	62	HIS
1	2-C	77	VAL
1	2-C	88	LEU
1	2-C	94	LYS
1	2-C	102	TYR
1	2-C	223	GLU
1	2-D	7	MSE
1	2-D	102	TYR
1	2-D	185	ARG
1	2-D	190	GLU
1	2-D	222	THR
1	3-A	6	LEU
1	3-A	59	LEU
1	3-A	102	TYR
1	3-A	107	LEU
1	3-A	151	LEU
1	3-A	171	ARG
1	3-A	234	MSE
1	3-A	313	LEU
1	3-B	35	ASP
1	3-B	61	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	3-B	64	ASP
1	3-B	66	ARG
1	3-B	87	HIS
1	3-B	102	TYR
1	3-B	225	LEU
1	3-B	317	LEU
1	3-C	18	GLU
1	3-C	32	GLU
1	3-C	47	ARG
1	3-C	61	ASP
1	3-C	65	LYS
1	3-C	102	TYR
1	3-C	185	ARG
1	3-C	188	ARG
1	3-C	229	ASP
1	3-C	314	LEU
1	3-D	102	TYR
1	3-D	185	ARG
1	3-D	190	GLU
1	3-D	198	GLU
1	3-D	318	ARG
1	4-A	20	ARG
1	4-A	30	GLU
1	4-A	75	LEU
1	4-A	78	ILE
1	4-A	102	TYR
1	4-A	107	LEU
1	4-A	145	TRP
1	4-A	151	LEU
1	4-A	196	GLN
1	4-A	236	GLU
1	4-A	253	ASP
1	4-A	273	PRO
1	4-A	278	THR
1	4-B	6	LEU
1	4-B	12	THR
1	4-B	91	ASP
1	4-B	102	TYR
1	4-B	107	LEU
1	4-B	178	GLN
1	4-B	216	CYS
1	4-B	219	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	4-B	225	LEU
1	4-B	247	ASP
1	4-B	298	THR
1	4-B	322	MSE
1	4-C	7	MSE
1	4-C	13	ARG
1	4-C	35	ASP
1	4-C	37	ASP
1	4-C	75	LEU
1	4-C	102	TYR
1	4-C	147	CYS
1	4-C	163	ARG
1	4-C	188	ARG
1	4-C	195	PHE
1	4-C	223	GLU
1	4-D	53	HIS
1	4-D	95	LYS
1	4-D	102	TYR
1	4-D	185	ARG
1	4-D	232	GLN
1	5-A	80	THR
1	5-A	81	MSE
1	5-A	92	GLU
1	5-A	102	TYR
1	5-A	107	LEU
1	5-A	181	LEU
1	5-A	251	GLN
1	5-A	293	HIS
1	5-A	317	LEU
1	5-B	28	ASP
1	5-B	35	ASP
1	5-B	37	ASP
1	5-B	53	HIS
1	5-B	55	LEU
1	5-B	102	TYR
1	5-B	107	LEU
1	5-B	185	ARG
1	5-B	190	GLU
1	5-B	223	GLU
1	5-B	225	LEU
1	5-B	286	LYS
1	5-B	317	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5-C	20	ARG
1	5-C	32	GLU
1	5-C	37	ASP
1	5-C	43	LYS
1	5-C	69	ASP
1	5-C	91	ASP
1	5-C	102	TYR
1	5-C	147	CYS
1	5-C	191	GLU
1	5-C	195	PHE
1	5-C	236	GLU
1	5-C	252	ASP
1	5-C	253	ASP
1	5-C	268	LEU
1	5-C	314	LEU
1	5-C	322	MSE
1	5-D	30	GLU
1	5-D	102	TYR
1	5-D	114	LEU
1	5-D	185	ARG
1	5-D	190	GLU
1	5-D	191	GLU
1	5-D	196	GLN
1	5-D	227	ASN
1	5-D	232	GLN
1	6-A	20	ARG
1	6-A	28	ASP
1	6-A	53	HIS
1	6-A	59	LEU
1	6-A	91	ASP
1	6-A	102	TYR
1	6-A	107	LEU
1	6-A	144	LEU
1	6-A	171	ARG
1	6-A	181	LEU
1	6-A	188	ARG
1	6-A	262	LYS
1	6-A	312	ASN
1	6-A	313	LEU
1	6-B	11	VAL
1	6-B	28	ASP
1	6-B	35	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	6-B	58	LEU
1	6-B	92	GLU
1	6-B	102	TYR
1	6-B	178	GLN
1	6-B	195	PHE
1	6-B	200	VAL
1	6-B	204	GLU
1	6-B	225	LEU
1	6-B	298	THR
1	6-B	313	LEU
1	6-B	317	LEU
1	6-C	15	ILE
1	6-C	20	ARG
1	6-C	34	TRP
1	6-C	76	LYS
1	6-C	91	ASP
1	6-C	107	LEU
1	6-C	158	ILE
1	6-C	173	LYS
1	6-C	189	PRO
1	6-C	195	PHE
1	6-C	217	SER
1	6-C	229	ASP
1	6-C	249	VAL
1	6-C	262	LYS
1	6-C	314	LEU
1	6-D	35	ASP
1	6-D	37	ASP
1	6-D	56	LEU
1	6-D	82	SER
1	6-D	102	TYR
1	6-D	107	LEU
1	6-D	182	TYR
1	6-D	185	ARG
1	6-D	190	GLU
1	6-D	191	GLU
1	6-D	217	SER
1	7-A	14	ARG
1	7-A	91	ASP
1	7-A	96	ARG
1	7-A	102	TYR
1	7-A	107	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	7-A	196	GLN
1	7-A	198	GLU
1	7-A	227	ASN
1	7-A	247	ASP
1	7-B	6	LEU
1	7-B	8	LYS
1	7-B	14	ARG
1	7-B	65	LYS
1	7-B	66	ARG
1	7-B	67	ILE
1	7-B	74	ASN
1	7-B	85	ILE
1	7-B	102	TYR
1	7-B	185	ARG
1	7-B	225	LEU
1	7-B	286	LYS
1	7-B	303	ASN
1	7-B	324	SER
1	7-C	63	VAL
1	7-C	64	ASP
1	7-C	76	LYS
1	7-C	88	LEU
1	7-C	96	ARG
1	7-C	102	TYR
1	7-C	219	THR
1	7-C	229	ASP
1	7-C	234	MSE
1	7-C	236	GLU
1	7-C	306	SER
1	7-C	314	LEU
1	7-D	7	MSE
1	7-D	30	GLU
1	7-D	35	ASP
1	7-D	102	TYR
1	7-D	109	ASP
1	7-D	163	ARG
1	7-D	190	GLU
1	7-D	204	GLU
1	7-D	250	ASN
1	7-D	252	ASP
1	7-D	305	MSE
1	8-A	7	MSE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	8-A	56	LEU
1	8-A	64	ASP
1	8-A	80	THR
1	8-A	96	ARG
1	8-A	102	TYR
1	8-A	107	LEU
1	8-A	159	ILE
1	8-A	179	ARG
1	8-A	183	THR
1	8-A	217	SER
1	8-A	223	GLU
1	8-A	314	LEU
1	8-B	35	ASP
1	8-B	65	LYS
1	8-B	91	ASP
1	8-B	107	LEU
1	8-B	163	ARG
1	8-B	186	GLN
1	8-B	190	GLU
1	8-B	200	VAL
1	8-B	256	GLN
1	8-B	305	MSE
1	8-C	33	GLN
1	8-C	59	LEU
1	8-C	62	HIS
1	8-C	68	LEU
1	8-C	69	ASP
1	8-C	91	ASP
1	8-C	92	GLU
1	8-C	102	TYR
1	8-C	105	ASP
1	8-C	107	LEU
1	8-C	196	GLN
1	8-C	225	LEU
1	8-C	314	LEU
1	8-C	320	GLU
1	8-D	102	TYR
1	8-D	114	LEU
1	8-D	131	GLU
1	8-D	185	ARG
1	8-D	232	GLN
1	8-D	263	ILE

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Mol	Chain	Res	Type
1	8-D	274	GLU
1	8-D	300	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (142) such sidechains are listed below:

Mol	Chain	Res	Type
1	1-A	251	GLN
1	1-A	279	ASN
1	1-B	33	GLN
1	1-B	87	HIS
1	1-B	166	GLN
1	1-B	178	GLN
1	1-B	232	GLN
1	1-B	303	ASN
1	1-C	33	GLN
1	1-C	53	HIS
1	1-C	178	GLN
1	1-D	33	GLN
1	1-D	166	GLN
1	1-D	178	GLN
1	1-D	251	GLN
1	1-D	311	ASN
1	2-A	53	HIS
1	2-A	62	HIS
1	2-A	74	ASN
1	2-A	135	ASN
1	2-A	186	GLN
1	2-A	251	GLN
1	2-A	256	GLN
1	2-B	33	GLN
1	2-B	62	HIS
1	2-B	74	ASN
1	2-B	87	HIS
1	2-B	178	GLN
1	2-B	232	GLN
1	2-B	303	ASN
1	2-C	178	GLN
1	2-C	311	ASN
1	2-D	33	GLN
1	2-D	153	GLN
1	2-D	208	GLN
1	2-D	303	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	2-D	311	ASN
1	3-A	208	GLN
1	3-B	33	GLN
1	3-B	87	HIS
1	3-B	166	GLN
1	3-B	186	GLN
1	3-B	208	GLN
1	3-B	232	GLN
1	3-B	256	GLN
1	3-B	299	HIS
1	3-B	303	ASN
1	3-B	311	ASN
1	3-C	33	GLN
1	3-C	74	ASN
1	3-C	166	GLN
1	3-C	178	GLN
1	3-D	33	GLN
1	3-D	166	GLN
1	3-D	312	ASN
1	4-A	53	HIS
1	4-A	74	ASN
1	4-A	153	GLN
1	4-A	178	GLN
1	4-A	232	GLN
1	4-A	250	ASN
1	4-B	33	GLN
1	4-B	87	HIS
1	4-B	166	GLN
1	4-B	232	GLN
1	4-B	256	GLN
1	4-B	299	HIS
1	4-B	303	ASN
1	4-C	33	GLN
1	4-C	87	HIS
1	4-C	178	GLN
1	4-D	311	ASN
1	5-A	33	GLN
1	5-A	232	GLN
1	5-A	251	GLN
1	5-A	256	GLN
1	5-A	293	HIS
1	5-A	299	HIS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	5-B	53	HIS
1	5-B	74	ASN
1	5-B	166	GLN
1	5-B	178	GLN
1	5-B	186	GLN
1	5-B	208	GLN
1	5-B	232	GLN
1	5-B	251	GLN
1	5-B	303	ASN
1	5-C	33	GLN
1	5-C	74	ASN
1	5-C	299	HIS
1	5-D	33	GLN
1	5-D	279	ASN
1	6-A	53	HIS
1	6-A	166	GLN
1	6-A	232	GLN
1	6-B	166	GLN
1	6-B	186	GLN
1	6-B	251	GLN
1	6-B	303	ASN
1	6-C	53	HIS
1	6-C	178	GLN
1	6-C	186	GLN
1	6-C	251	GLN
1	6-C	299	HIS
1	6-D	166	GLN
1	6-D	208	GLN
1	6-D	227	ASN
1	6-D	232	GLN
1	6-D	311	ASN
1	7-A	53	HIS
1	7-A	74	ASN
1	7-A	186	GLN
1	7-A	227	ASN
1	7-A	256	GLN
1	7-B	166	GLN
1	7-B	208	GLN
1	7-B	232	GLN
1	7-B	251	GLN
1	7-B	256	GLN
1	7-B	303	ASN

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Mol	Chain	Res	Type
1	7-B	311	ASN
1	7-C	33	GLN
1	7-C	74	ASN
1	7-C	299	HIS
1	7-D	153	GLN
1	7-D	232	GLN
1	7-D	242	ASN
1	7-D	250	ASN
1	7-D	280	HIS
1	8-A	53	HIS
1	8-A	74	ASN
1	8-A	208	GLN
1	8-B	178	GLN
1	8-B	232	GLN
1	8-B	256	GLN
1	8-B	311	ASN
1	8-C	33	GLN
1	8-C	178	GLN
1	8-C	299	HIS
1	8-D	33	GLN
1	8-D	166	GLN
1	8-D	178	GLN

### 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](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	1-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	1-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	1-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	1-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)
1	2-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	2-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	2-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	2-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)
1	3-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	3-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	3-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	3-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)
1	4-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	4-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	4-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	4-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)
1	5-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	5-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	5-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	5-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)
1	6-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	6-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	6-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	6-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	7-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	7-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	7-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	7-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)
1	8-A	316/328 (96%)	1.03	58 (18%) 1 0	18, 24, 31, 38	316 (100%)
1	8-B	316/328 (96%)	0.86	44 (13%) 2 1	18, 24, 31, 39	316 (100%)
1	8-C	316/328 (96%)	0.96	58 (18%) 1 0	17, 23, 31, 39	316 (100%)
1	8-D	316/328 (96%)	0.58	28 (8%) 9 6	18, 24, 30, 39	316 (100%)
All	All	10112/10496 (96%)	0.86	1504 (14%) 1 1	17, 24, 31, 39	10112 (100%)

All (1504) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-C	219	THR	11.4
1	2-C	219	THR	11.4
1	3-C	219	THR	11.4
1	4-C	219	THR	11.4
1	5-C	219	THR	11.4
1	6-C	219	THR	11.4
1	7-C	219	THR	11.4
1	8-C	219	THR	11.4
1	1-C	64	ASP	8.9
1	2-C	64	ASP	8.9
1	3-C	64	ASP	8.9
1	4-C	64	ASP	8.9
1	5-C	64	ASP	8.9
1	6-C	64	ASP	8.9
1	7-C	64	ASP	8.9
1	8-C	64	ASP	8.9
1	1-B	72	GLY	6.9
1	2-B	72	GLY	6.9
1	3-B	72	GLY	6.9
1	4-B	72	GLY	6.9
1	5-B	72	GLY	6.9
1	6-B	72	GLY	6.9
1	7-B	72	GLY	6.9
1	8-B	72	GLY	6.9
1	1-B	325	GLU	6.2
1	2-B	325	GLU	6.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-B	325	GLU	6.2
1	4-B	325	GLU	6.2
1	5-B	325	GLU	6.2
1	6-B	325	GLU	6.2
1	7-B	325	GLU	6.2
1	8-B	325	GLU	6.2
1	1-A	193	ALA	6.1
1	2-A	193	ALA	6.1
1	3-A	193	ALA	6.1
1	4-A	193	ALA	6.1
1	5-A	193	ALA	6.1
1	6-A	193	ALA	6.1
1	7-A	193	ALA	6.1
1	8-A	193	ALA	6.1
1	1-A	221	ALA	6.0
1	2-A	221	ALA	6.0
1	3-A	221	ALA	6.0
1	4-A	221	ALA	6.0
1	5-A	221	ALA	6.0
1	6-A	221	ALA	6.0
1	7-A	221	ALA	6.0
1	8-A	221	ALA	6.0
1	1-C	63	VAL	5.9
1	2-C	63	VAL	5.9
1	3-C	63	VAL	5.9
1	4-C	63	VAL	5.9
1	5-C	63	VAL	5.9
1	6-C	63	VAL	5.9
1	7-C	63	VAL	5.9
1	8-C	63	VAL	5.9
1	1-C	220	PRO	5.9
1	2-C	220	PRO	5.9
1	3-C	220	PRO	5.9
1	4-C	220	PRO	5.9
1	5-C	220	PRO	5.9
1	6-C	220	PRO	5.9
1	7-C	220	PRO	5.9
1	8-C	220	PRO	5.9
1	1-A	73	ALA	5.8
1	2-A	73	ALA	5.8
1	3-A	73	ALA	5.8
1	4-A	73	ALA	5.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	5-A	73	ALA	5.8
1	6-A	73	ALA	5.8
1	7-A	73	ALA	5.8
1	8-A	73	ALA	5.8
1	1-B	185	ARG	5.7
1	2-B	185	ARG	5.7
1	3-B	185	ARG	5.7
1	4-B	185	ARG	5.7
1	5-B	185	ARG	5.7
1	6-B	185	ARG	5.7
1	7-B	185	ARG	5.7
1	8-B	185	ARG	5.7
1	1-B	91	ASP	5.7
1	2-B	91	ASP	5.7
1	3-B	91	ASP	5.7
1	4-B	91	ASP	5.7
1	5-B	91	ASP	5.7
1	6-B	91	ASP	5.7
1	7-B	91	ASP	5.7
1	8-B	91	ASP	5.7
1	1-B	319	GLY	5.6
1	2-B	319	GLY	5.6
1	3-B	319	GLY	5.6
1	4-B	319	GLY	5.6
1	5-B	319	GLY	5.6
1	6-B	319	GLY	5.6
1	7-B	319	GLY	5.6
1	8-B	319	GLY	5.6
1	1-A	219	THR	5.6
1	2-A	219	THR	5.6
1	3-A	219	THR	5.6
1	4-A	219	THR	5.6
1	5-A	219	THR	5.6
1	6-A	219	THR	5.6
1	7-A	219	THR	5.6
1	8-A	219	THR	5.6
1	1-C	31	VAL	5.6
1	2-C	31	VAL	5.6
1	3-C	31	VAL	5.6
1	4-C	31	VAL	5.6
1	5-C	31	VAL	5.6
1	6-C	31	VAL	5.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-C	31	VAL	5.6
1	8-C	31	VAL	5.6
1	1-C	50	ALA	5.5
1	2-C	50	ALA	5.5
1	3-C	50	ALA	5.5
1	4-C	50	ALA	5.5
1	5-C	50	ALA	5.5
1	6-C	50	ALA	5.5
1	7-C	50	ALA	5.5
1	8-C	50	ALA	5.5
1	1-D	233	LYS	5.5
1	2-D	233	LYS	5.5
1	3-D	233	LYS	5.5
1	4-D	233	LYS	5.5
1	5-D	233	LYS	5.5
1	6-D	233	LYS	5.5
1	7-D	233	LYS	5.5
1	8-D	233	LYS	5.5
1	1-A	229	ASP	5.4
1	2-A	229	ASP	5.4
1	3-A	229	ASP	5.4
1	4-A	229	ASP	5.4
1	5-A	229	ASP	5.4
1	6-A	229	ASP	5.4
1	7-A	229	ASP	5.4
1	8-A	229	ASP	5.4
1	1-A	321	PRO	5.1
1	1-B	104	PRO	5.1
1	2-A	321	PRO	5.1
1	2-B	104	PRO	5.1
1	3-A	321	PRO	5.1
1	3-B	104	PRO	5.1
1	4-A	321	PRO	5.1
1	4-B	104	PRO	5.1
1	5-A	321	PRO	5.1
1	5-B	104	PRO	5.1
1	6-A	321	PRO	5.1
1	6-B	104	PRO	5.1
1	7-A	321	PRO	5.1
1	7-B	104	PRO	5.1
1	8-A	321	PRO	5.1
1	8-B	104	PRO	5.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-C	46	GLU	5.0
1	2-C	46	GLU	5.0
1	3-C	46	GLU	5.0
1	4-C	46	GLU	5.0
1	5-C	46	GLU	5.0
1	6-C	46	GLU	5.0
1	7-C	46	GLU	5.0
1	8-C	46	GLU	5.0
1	1-D	189	PRO	5.0
1	2-D	189	PRO	5.0
1	3-D	189	PRO	5.0
1	4-D	189	PRO	5.0
1	5-D	189	PRO	5.0
1	6-D	189	PRO	5.0
1	7-D	189	PRO	5.0
1	8-D	189	PRO	5.0
1	1-C	70	ALA	4.9
1	2-C	70	ALA	4.9
1	3-C	70	ALA	4.9
1	4-C	70	ALA	4.9
1	5-C	70	ALA	4.9
1	6-C	70	ALA	4.9
1	7-C	70	ALA	4.9
1	8-C	70	ALA	4.9
1	1-D	229	ASP	4.8
1	2-D	229	ASP	4.8
1	3-D	229	ASP	4.8
1	4-D	229	ASP	4.8
1	5-D	229	ASP	4.8
1	6-D	229	ASP	4.8
1	7-D	229	ASP	4.8
1	8-D	229	ASP	4.8
1	1-C	36	SER	4.8
1	2-C	36	SER	4.8
1	3-C	36	SER	4.8
1	4-C	36	SER	4.8
1	5-C	36	SER	4.8
1	6-C	36	SER	4.8
1	7-C	36	SER	4.8
1	8-C	36	SER	4.8
1	1-C	35	ASP	4.7
1	2-C	35	ASP	4.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-C	35	ASP	4.7
1	4-C	35	ASP	4.7
1	5-C	35	ASP	4.7
1	6-C	35	ASP	4.7
1	7-C	35	ASP	4.7
1	8-C	35	ASP	4.7
1	1-C	78	ILE	4.7
1	2-C	78	ILE	4.7
1	3-C	78	ILE	4.7
1	4-C	78	ILE	4.7
1	5-C	78	ILE	4.7
1	6-C	78	ILE	4.7
1	7-C	78	ILE	4.7
1	8-C	78	ILE	4.7
1	1-D	185	ARG	4.7
1	2-D	185	ARG	4.7
1	3-D	185	ARG	4.7
1	4-D	185	ARG	4.7
1	5-D	185	ARG	4.7
1	6-D	185	ARG	4.7
1	7-D	185	ARG	4.7
1	8-D	185	ARG	4.7
1	1-B	326	LEU	4.6
1	2-B	326	LEU	4.6
1	3-B	326	LEU	4.6
1	4-B	326	LEU	4.6
1	5-B	326	LEU	4.6
1	6-B	326	LEU	4.6
1	7-B	326	LEU	4.6
1	8-B	326	LEU	4.6
1	1-D	220	PRO	4.5
1	2-D	220	PRO	4.5
1	3-D	220	PRO	4.5
1	4-D	220	PRO	4.5
1	5-D	220	PRO	4.5
1	6-D	220	PRO	4.5
1	7-D	220	PRO	4.5
1	8-D	220	PRO	4.5
1	1-D	219	THR	4.5
1	2-D	219	THR	4.5
1	3-D	219	THR	4.5
1	4-D	219	THR	4.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	5-D	219	THR	4.5
1	6-D	219	THR	4.5
1	7-D	219	THR	4.5
1	8-D	219	THR	4.5
1	1-B	64	ASP	4.4
1	2-B	64	ASP	4.4
1	3-B	64	ASP	4.4
1	4-B	64	ASP	4.4
1	5-B	64	ASP	4.4
1	6-B	64	ASP	4.4
1	7-B	64	ASP	4.4
1	8-B	64	ASP	4.4
1	1-A	188	ARG	4.4
1	1-C	88	LEU	4.4
1	2-A	188	ARG	4.4
1	2-C	88	LEU	4.4
1	3-A	188	ARG	4.4
1	3-C	88	LEU	4.4
1	4-A	188	ARG	4.4
1	4-C	88	LEU	4.4
1	5-A	188	ARG	4.4
1	5-C	88	LEU	4.4
1	6-A	188	ARG	4.4
1	6-C	88	LEU	4.4
1	7-A	188	ARG	4.4
1	7-C	88	LEU	4.4
1	8-A	188	ARG	4.4
1	8-C	88	LEU	4.4
1	1-C	75	LEU	4.3
1	2-C	75	LEU	4.3
1	3-C	75	LEU	4.3
1	4-C	75	LEU	4.3
1	5-C	75	LEU	4.3
1	6-C	75	LEU	4.3
1	7-C	75	LEU	4.3
1	8-C	75	LEU	4.3
1	1-D	184	GLY	4.3
1	2-D	184	GLY	4.3
1	3-D	184	GLY	4.3
1	4-D	184	GLY	4.3
1	5-D	184	GLY	4.3
1	6-D	184	GLY	4.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-D	184	GLY	4.3
1	8-D	184	GLY	4.3
1	1-B	219	THR	4.3
1	2-B	219	THR	4.3
1	3-B	219	THR	4.3
1	4-B	219	THR	4.3
1	5-B	219	THR	4.3
1	6-B	219	THR	4.3
1	7-B	219	THR	4.3
1	8-B	219	THR	4.3
1	1-A	33	GLN	4.1
1	2-A	33	GLN	4.1
1	3-A	33	GLN	4.1
1	4-A	33	GLN	4.1
1	5-A	33	GLN	4.1
1	6-A	33	GLN	4.1
1	7-A	33	GLN	4.1
1	8-A	33	GLN	4.1
1	1-A	222	THR	4.1
1	2-A	222	THR	4.1
1	3-A	222	THR	4.1
1	4-A	222	THR	4.1
1	5-A	222	THR	4.1
1	6-A	222	THR	4.1
1	7-A	222	THR	4.1
1	8-A	222	THR	4.1
1	1-A	232	GLN	4.1
1	2-A	232	GLN	4.1
1	3-A	232	GLN	4.1
1	4-A	232	GLN	4.1
1	5-A	232	GLN	4.1
1	6-A	232	GLN	4.1
1	7-A	232	GLN	4.1
1	8-A	232	GLN	4.1
1	1-C	85	ILE	4.0
1	2-C	85	ILE	4.0
1	3-C	85	ILE	4.0
1	4-C	85	ILE	4.0
1	5-C	85	ILE	4.0
1	6-C	85	ILE	4.0
1	7-C	85	ILE	4.0
1	8-C	85	ILE	4.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-D	221	ALA	4.0
1	2-D	221	ALA	4.0
1	3-D	221	ALA	4.0
1	4-D	221	ALA	4.0
1	5-D	221	ALA	4.0
1	6-D	221	ALA	4.0
1	7-D	221	ALA	4.0
1	8-D	221	ALA	4.0
1	1-C	186	GLN	3.9
1	2-C	186	GLN	3.9
1	3-C	186	GLN	3.9
1	4-C	186	GLN	3.9
1	5-C	186	GLN	3.9
1	6-C	186	GLN	3.9
1	7-C	186	GLN	3.9
1	8-C	186	GLN	3.9
1	1-A	96	ARG	3.9
1	2-A	96	ARG	3.9
1	3-A	96	ARG	3.9
1	4-A	96	ARG	3.9
1	5-A	96	ARG	3.9
1	6-A	96	ARG	3.9
1	7-A	96	ARG	3.9
1	8-A	96	ARG	3.9
1	1-A	51	GLY	3.8
1	2-A	51	GLY	3.8
1	3-A	51	GLY	3.8
1	4-A	51	GLY	3.8
1	5-A	51	GLY	3.8
1	6-A	51	GLY	3.8
1	7-A	51	GLY	3.8
1	8-A	51	GLY	3.8
1	1-C	21	VAL	3.8
1	2-C	21	VAL	3.8
1	3-C	21	VAL	3.8
1	4-C	21	VAL	3.8
1	5-C	21	VAL	3.8
1	6-C	21	VAL	3.8
1	7-C	21	VAL	3.8
1	8-C	21	VAL	3.8
1	1-A	233	LYS	3.8
1	2-A	233	LYS	3.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-A	233	LYS	3.8
1	4-A	233	LYS	3.8
1	5-A	233	LYS	3.8
1	6-A	233	LYS	3.8
1	7-A	233	LYS	3.8
1	8-A	233	LYS	3.8
1	1-B	189	PRO	3.7
1	2-B	189	PRO	3.7
1	3-B	189	PRO	3.7
1	4-B	189	PRO	3.7
1	5-B	189	PRO	3.7
1	6-B	189	PRO	3.7
1	7-B	189	PRO	3.7
1	8-B	189	PRO	3.7
1	1-C	87	HIS	3.7
1	2-C	87	HIS	3.7
1	3-C	87	HIS	3.7
1	4-C	87	HIS	3.7
1	5-C	87	HIS	3.7
1	6-C	87	HIS	3.7
1	7-C	87	HIS	3.7
1	8-C	87	HIS	3.7
1	1-A	253	ASP	3.7
1	2-A	253	ASP	3.7
1	3-A	253	ASP	3.7
1	4-A	253	ASP	3.7
1	5-A	253	ASP	3.7
1	6-A	253	ASP	3.7
1	7-A	253	ASP	3.7
1	8-A	253	ASP	3.7
1	1-C	221	ALA	3.7
1	2-C	221	ALA	3.7
1	3-C	221	ALA	3.7
1	4-C	221	ALA	3.7
1	5-C	221	ALA	3.7
1	6-C	221	ALA	3.7
1	7-C	221	ALA	3.7
1	8-C	221	ALA	3.7
1	1-A	20	ARG	3.7
1	2-A	20	ARG	3.7
1	3-A	20	ARG	3.7
1	4-A	20	ARG	3.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	5-A	20	ARG	3.7
1	6-A	20	ARG	3.7
1	7-A	20	ARG	3.7
1	8-A	20	ARG	3.7
1	1-A	28	ASP	3.7
1	2-A	28	ASP	3.7
1	3-A	28	ASP	3.7
1	4-A	28	ASP	3.7
1	5-A	28	ASP	3.7
1	6-A	28	ASP	3.7
1	7-A	28	ASP	3.7
1	8-A	28	ASP	3.7
1	1-B	49	VAL	3.6
1	2-B	49	VAL	3.6
1	3-B	49	VAL	3.6
1	4-B	49	VAL	3.6
1	5-B	49	VAL	3.6
1	6-B	49	VAL	3.6
1	7-B	49	VAL	3.6
1	8-B	49	VAL	3.6
1	1-C	51	GLY	3.6
1	2-C	51	GLY	3.6
1	3-C	51	GLY	3.6
1	4-C	51	GLY	3.6
1	5-C	51	GLY	3.6
1	6-C	51	GLY	3.6
1	7-C	51	GLY	3.6
1	8-C	51	GLY	3.6
1	1-D	232	GLN	3.6
1	2-D	232	GLN	3.6
1	3-D	232	GLN	3.6
1	4-D	232	GLN	3.6
1	5-D	232	GLN	3.6
1	6-D	232	GLN	3.6
1	7-D	232	GLN	3.6
1	8-D	232	GLN	3.6
1	1-D	190	GLU	3.6
1	2-D	190	GLU	3.6
1	3-D	190	GLU	3.6
1	4-D	190	GLU	3.6
1	5-D	190	GLU	3.6
1	6-D	190	GLU	3.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-D	190	GLU	3.6
1	8-D	190	GLU	3.6
1	1-A	184	GLY	3.5
1	2-A	184	GLY	3.5
1	3-A	184	GLY	3.5
1	4-A	184	GLY	3.5
1	5-A	184	GLY	3.5
1	6-A	184	GLY	3.5
1	7-A	184	GLY	3.5
1	8-A	184	GLY	3.5
1	1-A	217	SER	3.5
1	2-A	217	SER	3.5
1	3-A	217	SER	3.5
1	4-A	217	SER	3.5
1	5-A	217	SER	3.5
1	6-A	217	SER	3.5
1	7-A	217	SER	3.5
1	8-A	217	SER	3.5
1	1-B	53	HIS	3.5
1	2-B	53	HIS	3.5
1	3-B	53	HIS	3.5
1	4-B	53	HIS	3.5
1	5-B	53	HIS	3.5
1	6-B	53	HIS	3.5
1	7-B	53	HIS	3.5
1	8-B	53	HIS	3.5
1	1-A	74	ASN	3.5
1	2-A	74	ASN	3.5
1	3-A	74	ASN	3.5
1	4-A	74	ASN	3.5
1	5-A	74	ASN	3.5
1	6-A	74	ASN	3.5
1	7-A	74	ASN	3.5
1	8-A	74	ASN	3.5
1	1-A	137	GLY	3.5
1	2-A	137	GLY	3.5
1	3-A	137	GLY	3.5
1	4-A	137	GLY	3.5
1	5-A	137	GLY	3.5
1	6-A	137	GLY	3.5
1	7-A	137	GLY	3.5
1	8-A	137	GLY	3.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-B	75	LEU	3.4
1	2-B	75	LEU	3.4
1	3-B	75	LEU	3.4
1	4-B	75	LEU	3.4
1	5-B	75	LEU	3.4
1	6-B	75	LEU	3.4
1	7-B	75	LEU	3.4
1	8-B	75	LEU	3.4
1	1-B	90	LEU	3.4
1	2-B	90	LEU	3.4
1	3-B	90	LEU	3.4
1	4-B	90	LEU	3.4
1	5-B	90	LEU	3.4
1	6-B	90	LEU	3.4
1	7-B	90	LEU	3.4
1	8-B	90	LEU	3.4
1	1-A	19	GLY	3.4
1	2-A	19	GLY	3.4
1	3-A	19	GLY	3.4
1	4-A	19	GLY	3.4
1	5-A	19	GLY	3.4
1	6-A	19	GLY	3.4
1	7-A	19	GLY	3.4
1	8-A	19	GLY	3.4
1	1-B	73	ALA	3.4
1	2-B	73	ALA	3.4
1	3-B	73	ALA	3.4
1	4-B	73	ALA	3.4
1	5-B	73	ALA	3.4
1	6-B	73	ALA	3.4
1	7-B	73	ALA	3.4
1	8-B	73	ALA	3.4
1	1-A	218	LEU	3.3
1	2-A	218	LEU	3.3
1	3-A	218	LEU	3.3
1	4-A	218	LEU	3.3
1	5-A	218	LEU	3.3
1	6-A	218	LEU	3.3
1	7-A	218	LEU	3.3
1	8-A	218	LEU	3.3
1	1-B	70	ALA	3.3
1	2-B	70	ALA	3.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-B	70	ALA	3.3
1	4-B	70	ALA	3.3
1	5-B	70	ALA	3.3
1	6-B	70	ALA	3.3
1	7-B	70	ALA	3.3
1	8-B	70	ALA	3.3
1	1-B	36	SER	3.3
1	2-B	36	SER	3.3
1	3-B	36	SER	3.3
1	4-B	36	SER	3.3
1	5-B	36	SER	3.3
1	6-B	36	SER	3.3
1	7-B	36	SER	3.3
1	8-B	36	SER	3.3
1	1-C	57	CYS	3.2
1	2-C	57	CYS	3.2
1	3-C	57	CYS	3.2
1	4-C	57	CYS	3.2
1	5-C	57	CYS	3.2
1	6-C	57	CYS	3.2
1	7-C	57	CYS	3.2
1	8-C	57	CYS	3.2
1	1-C	22	ALA	3.2
1	2-C	22	ALA	3.2
1	3-C	22	ALA	3.2
1	4-C	22	ALA	3.2
1	5-C	22	ALA	3.2
1	6-C	22	ALA	3.2
1	7-C	22	ALA	3.2
1	8-C	22	ALA	3.2
1	1-C	100	VAL	3.2
1	2-C	100	VAL	3.2
1	3-C	100	VAL	3.2
1	4-C	100	VAL	3.2
1	5-C	100	VAL	3.2
1	6-C	100	VAL	3.2
1	7-C	100	VAL	3.2
1	8-C	100	VAL	3.2
1	1-B	30	GLU	3.2
1	1-B	41	PRO	3.2
1	1-B	48	GLY	3.2
1	2-B	30	GLU	3.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	2-B	41	PRO	3.2
1	2-B	48	GLY	3.2
1	3-B	30	GLU	3.2
1	3-B	41	PRO	3.2
1	3-B	48	GLY	3.2
1	4-B	30	GLU	3.2
1	4-B	41	PRO	3.2
1	4-B	48	GLY	3.2
1	5-B	30	GLU	3.2
1	5-B	41	PRO	3.2
1	5-B	48	GLY	3.2
1	6-B	30	GLU	3.2
1	6-B	41	PRO	3.2
1	6-B	48	GLY	3.2
1	7-B	30	GLU	3.2
1	7-B	41	PRO	3.2
1	7-B	48	GLY	3.2
1	8-B	30	GLU	3.2
1	8-B	41	PRO	3.2
1	8-B	48	GLY	3.2
1	1-C	52	ALA	3.1
1	2-C	52	ALA	3.1
1	3-C	52	ALA	3.1
1	4-C	52	ALA	3.1
1	5-C	52	ALA	3.1
1	6-C	52	ALA	3.1
1	7-C	52	ALA	3.1
1	8-C	52	ALA	3.1
1	1-C	218	LEU	3.1
1	2-C	218	LEU	3.1
1	3-C	218	LEU	3.1
1	4-C	218	LEU	3.1
1	5-C	218	LEU	3.1
1	6-C	218	LEU	3.1
1	7-C	218	LEU	3.1
1	8-C	218	LEU	3.1
1	1-D	193	ALA	3.1
1	2-D	193	ALA	3.1
1	3-D	193	ALA	3.1
1	4-D	193	ALA	3.1
1	5-D	193	ALA	3.1
1	6-D	193	ALA	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-D	193	ALA	3.1
1	8-D	193	ALA	3.1
1	1-D	196	GLN	3.1
1	2-D	196	GLN	3.1
1	3-D	196	GLN	3.1
1	4-D	196	GLN	3.1
1	5-D	196	GLN	3.1
1	6-D	196	GLN	3.1
1	7-D	196	GLN	3.1
1	8-D	196	GLN	3.1
1	1-C	32	GLU	3.1
1	2-C	32	GLU	3.1
1	3-C	32	GLU	3.1
1	4-C	32	GLU	3.1
1	5-C	32	GLU	3.1
1	6-C	32	GLU	3.1
1	7-C	32	GLU	3.1
1	8-C	32	GLU	3.1
1	1-B	186	GLN	3.0
1	2-B	186	GLN	3.0
1	3-B	186	GLN	3.0
1	4-B	186	GLN	3.0
1	5-B	186	GLN	3.0
1	6-B	186	GLN	3.0
1	7-B	186	GLN	3.0
1	8-B	186	GLN	3.0
1	1-A	185	ARG	3.0
1	2-A	185	ARG	3.0
1	3-A	185	ARG	3.0
1	4-A	185	ARG	3.0
1	5-A	185	ARG	3.0
1	6-A	185	ARG	3.0
1	7-A	185	ARG	3.0
1	8-A	185	ARG	3.0
1	1-D	197	ALA	3.0
1	2-D	197	ALA	3.0
1	3-D	197	ALA	3.0
1	4-D	197	ALA	3.0
1	5-D	197	ALA	3.0
1	6-D	197	ALA	3.0
1	7-D	197	ALA	3.0
1	8-D	197	ALA	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-B	321	PRO	3.0
1	2-B	321	PRO	3.0
1	3-B	321	PRO	3.0
1	4-B	321	PRO	3.0
1	5-B	321	PRO	3.0
1	6-B	321	PRO	3.0
1	7-B	321	PRO	3.0
1	8-B	321	PRO	3.0
1	1-C	93	ILE	3.0
1	2-C	93	ILE	3.0
1	3-C	93	ILE	3.0
1	4-C	93	ILE	3.0
1	5-C	93	ILE	3.0
1	6-C	93	ILE	3.0
1	7-C	93	ILE	3.0
1	8-C	93	ILE	3.0
1	1-B	313	LEU	3.0
1	2-B	313	LEU	3.0
1	3-B	313	LEU	3.0
1	4-B	313	LEU	3.0
1	5-B	313	LEU	3.0
1	6-B	313	LEU	3.0
1	7-B	313	LEU	3.0
1	8-B	313	LEU	3.0
1	1-A	47	ARG	2.9
1	2-A	47	ARG	2.9
1	3-A	47	ARG	2.9
1	4-A	47	ARG	2.9
1	5-A	47	ARG	2.9
1	6-A	47	ARG	2.9
1	7-A	47	ARG	2.9
1	8-A	47	ARG	2.9
1	1-A	197	ALA	2.9
1	2-A	197	ALA	2.9
1	3-A	197	ALA	2.9
1	4-A	197	ALA	2.9
1	5-A	197	ALA	2.9
1	6-A	197	ALA	2.9
1	7-A	197	ALA	2.9
1	8-A	197	ALA	2.9
1	1-C	41	PRO	2.9
1	2-C	41	PRO	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-C	41	PRO	2.9
1	4-C	41	PRO	2.9
1	5-C	41	PRO	2.9
1	6-C	41	PRO	2.9
1	7-C	41	PRO	2.9
1	8-C	41	PRO	2.9
1	1-A	308	LEU	2.9
1	2-A	308	LEU	2.9
1	3-A	308	LEU	2.9
1	4-A	308	LEU	2.9
1	5-A	308	LEU	2.9
1	6-A	308	LEU	2.9
1	7-A	308	LEU	2.9
1	8-A	308	LEU	2.9
1	1-C	67	ILE	2.9
1	2-C	67	ILE	2.9
1	3-C	67	ILE	2.9
1	4-C	67	ILE	2.9
1	5-C	67	ILE	2.9
1	6-C	67	ILE	2.9
1	7-C	67	ILE	2.9
1	8-C	67	ILE	2.9
1	1-A	27	ALA	2.9
1	2-A	27	ALA	2.9
1	3-A	27	ALA	2.9
1	4-A	27	ALA	2.9
1	5-A	27	ALA	2.9
1	6-A	27	ALA	2.9
1	7-A	27	ALA	2.9
1	8-A	27	ALA	2.9
1	1-C	55	LEU	2.8
1	2-C	55	LEU	2.8
1	3-C	55	LEU	2.8
1	4-C	55	LEU	2.8
1	5-C	55	LEU	2.8
1	6-C	55	LEU	2.8
1	7-C	55	LEU	2.8
1	8-C	55	LEU	2.8
1	1-B	324	SER	2.8
1	1-C	47	ARG	2.8
1	2-B	324	SER	2.8
1	2-C	47	ARG	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-B	324	SER	2.8
1	3-C	47	ARG	2.8
1	4-B	324	SER	2.8
1	4-C	47	ARG	2.8
1	5-B	324	SER	2.8
1	5-C	47	ARG	2.8
1	6-B	324	SER	2.8
1	6-C	47	ARG	2.8
1	7-B	324	SER	2.8
1	7-C	47	ARG	2.8
1	8-B	324	SER	2.8
1	8-C	47	ARG	2.8
1	1-D	188	ARG	2.8
1	2-D	188	ARG	2.8
1	3-D	188	ARG	2.8
1	4-D	188	ARG	2.8
1	5-D	188	ARG	2.8
1	6-D	188	ARG	2.8
1	7-D	188	ARG	2.8
1	8-D	188	ARG	2.8
1	1-C	33	GLN	2.8
1	2-C	33	GLN	2.8
1	3-C	33	GLN	2.8
1	4-C	33	GLN	2.8
1	5-C	33	GLN	2.8
1	6-C	33	GLN	2.8
1	7-C	33	GLN	2.8
1	8-C	33	GLN	2.8
1	1-C	53	HIS	2.8
1	2-C	53	HIS	2.8
1	3-C	53	HIS	2.8
1	4-C	53	HIS	2.8
1	5-C	53	HIS	2.8
1	6-C	53	HIS	2.8
1	7-C	53	HIS	2.8
1	8-C	53	HIS	2.8
1	1-C	73	ALA	2.8
1	2-C	73	ALA	2.8
1	3-C	73	ALA	2.8
1	4-C	73	ALA	2.8
1	5-C	73	ALA	2.8
1	6-C	73	ALA	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-C	73	ALA	2.8
1	8-C	73	ALA	2.8
1	1-B	197	ALA	2.8
1	2-B	197	ALA	2.8
1	3-B	197	ALA	2.8
1	4-B	197	ALA	2.8
1	5-B	197	ALA	2.8
1	6-B	197	ALA	2.8
1	7-B	197	ALA	2.8
1	8-B	197	ALA	2.8
1	1-A	82	SER	2.8
1	2-A	82	SER	2.8
1	3-A	82	SER	2.8
1	4-A	82	SER	2.8
1	5-A	82	SER	2.8
1	6-A	82	SER	2.8
1	7-A	82	SER	2.8
1	8-A	82	SER	2.8
1	1-A	216	CYS	2.8
1	2-A	216	CYS	2.8
1	3-A	216	CYS	2.8
1	4-A	216	CYS	2.8
1	5-A	216	CYS	2.8
1	6-A	216	CYS	2.8
1	7-A	216	CYS	2.8
1	8-A	216	CYS	2.8
1	1-B	301	THR	2.8
1	2-B	301	THR	2.8
1	3-B	301	THR	2.8
1	4-B	301	THR	2.8
1	5-B	301	THR	2.8
1	6-B	301	THR	2.8
1	7-B	301	THR	2.8
1	8-B	301	THR	2.8
1	1-C	137	GLY	2.7
1	2-C	137	GLY	2.7
1	3-C	137	GLY	2.7
1	4-C	137	GLY	2.7
1	5-C	137	GLY	2.7
1	6-C	137	GLY	2.7
1	7-C	137	GLY	2.7
1	8-C	137	GLY	2.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-A	319	GLY	2.7
1	1-C	72	GLY	2.7
1	2-A	319	GLY	2.7
1	2-C	72	GLY	2.7
1	3-A	319	GLY	2.7
1	3-C	72	GLY	2.7
1	4-A	319	GLY	2.7
1	4-C	72	GLY	2.7
1	5-A	319	GLY	2.7
1	5-C	72	GLY	2.7
1	6-A	319	GLY	2.7
1	6-C	72	GLY	2.7
1	7-A	319	GLY	2.7
1	7-C	72	GLY	2.7
1	8-A	319	GLY	2.7
1	8-C	72	GLY	2.7
1	1-A	71	ALA	2.7
1	2-A	71	ALA	2.7
1	3-A	71	ALA	2.7
1	4-A	71	ALA	2.7
1	5-A	71	ALA	2.7
1	6-A	71	ALA	2.7
1	7-A	71	ALA	2.7
1	8-A	71	ALA	2.7
1	1-A	312	ASN	2.7
1	2-A	312	ASN	2.7
1	3-A	312	ASN	2.7
1	4-A	312	ASN	2.7
1	5-A	312	ASN	2.7
1	6-A	312	ASN	2.7
1	7-A	312	ASN	2.7
1	8-A	312	ASN	2.7
1	1-B	35	ASP	2.7
1	2-B	35	ASP	2.7
1	3-B	35	ASP	2.7
1	4-B	35	ASP	2.7
1	5-B	35	ASP	2.7
1	6-B	35	ASP	2.7
1	7-B	35	ASP	2.7
1	8-B	35	ASP	2.7
1	1-D	218	LEU	2.7
1	2-D	218	LEU	2.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-D	218	LEU	2.7
1	4-D	218	LEU	2.7
1	5-D	218	LEU	2.7
1	6-D	218	LEU	2.7
1	7-D	218	LEU	2.7
1	8-D	218	LEU	2.7
1	1-A	189	PRO	2.7
1	2-A	189	PRO	2.7
1	3-A	189	PRO	2.7
1	4-A	189	PRO	2.7
1	5-A	189	PRO	2.7
1	6-A	189	PRO	2.7
1	7-A	189	PRO	2.7
1	8-A	189	PRO	2.7
1	1-B	100	VAL	2.7
1	2-B	100	VAL	2.7
1	3-B	100	VAL	2.7
1	4-B	100	VAL	2.7
1	5-B	100	VAL	2.7
1	6-B	100	VAL	2.7
1	7-B	100	VAL	2.7
1	8-B	100	VAL	2.7
1	1-A	35	ASP	2.6
1	2-A	35	ASP	2.6
1	3-A	35	ASP	2.6
1	4-A	35	ASP	2.6
1	5-A	35	ASP	2.6
1	6-A	35	ASP	2.6
1	7-A	35	ASP	2.6
1	8-A	35	ASP	2.6
1	1-B	96	ARG	2.5
1	2-B	96	ARG	2.5
1	3-B	96	ARG	2.5
1	4-B	96	ARG	2.5
1	5-B	96	ARG	2.5
1	6-B	96	ARG	2.5
1	7-B	96	ARG	2.5
1	8-B	96	ARG	2.5
1	1-A	97	GLY	2.5
1	2-A	97	GLY	2.5
1	3-A	97	GLY	2.5
1	4-A	97	GLY	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	5-A	97	GLY	2.5
1	6-A	97	GLY	2.5
1	7-A	97	GLY	2.5
1	8-A	97	GLY	2.5
1	1-A	316	GLY	2.5
1	1-C	48	GLY	2.5
1	2-A	316	GLY	2.5
1	2-C	48	GLY	2.5
1	3-A	316	GLY	2.5
1	3-C	48	GLY	2.5
1	4-A	316	GLY	2.5
1	4-C	48	GLY	2.5
1	5-A	316	GLY	2.5
1	5-C	48	GLY	2.5
1	6-A	316	GLY	2.5
1	6-C	48	GLY	2.5
1	7-A	316	GLY	2.5
1	7-C	48	GLY	2.5
1	8-A	316	GLY	2.5
1	8-C	48	GLY	2.5
1	1-B	102	TYR	2.5
1	2-B	102	TYR	2.5
1	3-B	102	TYR	2.5
1	4-B	102	TYR	2.5
1	5-B	102	TYR	2.5
1	6-B	102	TYR	2.5
1	7-B	102	TYR	2.5
1	8-B	102	TYR	2.5
1	1-A	220	PRO	2.5
1	2-A	220	PRO	2.5
1	3-A	220	PRO	2.5
1	4-A	220	PRO	2.5
1	5-A	220	PRO	2.5
1	6-A	220	PRO	2.5
1	7-A	220	PRO	2.5
1	8-A	220	PRO	2.5
1	1-B	57	CYS	2.5
1	1-B	95	LYS	2.5
1	2-B	57	CYS	2.5
1	2-B	95	LYS	2.5
1	3-B	57	CYS	2.5
1	3-B	95	LYS	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	4-B	57	CYS	2.5
1	4-B	95	LYS	2.5
1	5-B	57	CYS	2.5
1	5-B	95	LYS	2.5
1	6-B	57	CYS	2.5
1	6-B	95	LYS	2.5
1	7-B	57	CYS	2.5
1	7-B	95	LYS	2.5
1	8-B	57	CYS	2.5
1	8-B	95	LYS	2.5
1	1-C	29	CYS	2.5
1	2-C	29	CYS	2.5
1	3-C	29	CYS	2.5
1	4-C	29	CYS	2.5
1	5-C	29	CYS	2.5
1	6-C	29	CYS	2.5
1	7-C	29	CYS	2.5
1	8-C	29	CYS	2.5
1	1-D	192	ALA	2.5
1	2-D	192	ALA	2.5
1	3-D	192	ALA	2.5
1	4-D	192	ALA	2.5
1	5-D	192	ALA	2.5
1	6-D	192	ALA	2.5
1	7-D	192	ALA	2.5
1	8-D	192	ALA	2.5
1	1-C	24	ALA	2.5
1	2-C	24	ALA	2.5
1	3-C	24	ALA	2.5
1	4-C	24	ALA	2.5
1	5-C	24	ALA	2.5
1	6-C	24	ALA	2.5
1	7-C	24	ALA	2.5
1	8-C	24	ALA	2.5
1	1-C	12	THR	2.5
1	1-D	202	THR	2.5
1	2-C	12	THR	2.5
1	2-D	202	THR	2.5
1	3-C	12	THR	2.5
1	3-D	202	THR	2.5
1	4-C	12	THR	2.5
1	4-D	202	THR	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	5-C	12	THR	2.5
1	5-D	202	THR	2.5
1	6-C	12	THR	2.5
1	6-D	202	THR	2.5
1	7-C	12	THR	2.5
1	7-D	202	THR	2.5
1	8-C	12	THR	2.5
1	8-D	202	THR	2.5
1	1-A	64	ASP	2.4
1	1-C	69	ASP	2.4
1	2-A	64	ASP	2.4
1	2-C	69	ASP	2.4
1	3-A	64	ASP	2.4
1	3-C	69	ASP	2.4
1	4-A	64	ASP	2.4
1	4-C	69	ASP	2.4
1	5-A	64	ASP	2.4
1	5-C	69	ASP	2.4
1	6-A	64	ASP	2.4
1	6-C	69	ASP	2.4
1	7-A	64	ASP	2.4
1	7-C	69	ASP	2.4
1	8-A	64	ASP	2.4
1	8-C	69	ASP	2.4
1	1-D	247	ASP	2.4
1	2-D	247	ASP	2.4
1	3-D	247	ASP	2.4
1	4-D	247	ASP	2.4
1	5-D	247	ASP	2.4
1	6-D	247	ASP	2.4
1	7-D	247	ASP	2.4
1	8-D	247	ASP	2.4
1	1-A	24	ALA	2.4
1	2-A	24	ALA	2.4
1	3-A	24	ALA	2.4
1	4-A	24	ALA	2.4
1	5-A	24	ALA	2.4
1	6-A	24	ALA	2.4
1	7-A	24	ALA	2.4
1	8-A	24	ALA	2.4
1	1-C	197	ALA	2.4
1	2-C	197	ALA	2.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-C	197	ALA	2.4
1	4-C	197	ALA	2.4
1	5-C	197	ALA	2.4
1	6-C	197	ALA	2.4
1	7-C	197	ALA	2.4
1	8-C	197	ALA	2.4
1	1-A	252	ASP	2.4
1	2-A	252	ASP	2.4
1	3-A	252	ASP	2.4
1	4-A	252	ASP	2.4
1	5-A	252	ASP	2.4
1	6-A	252	ASP	2.4
1	7-A	252	ASP	2.4
1	8-A	252	ASP	2.4
1	1-B	99	ARG	2.4
1	2-B	99	ARG	2.4
1	3-B	99	ARG	2.4
1	4-B	99	ARG	2.4
1	5-B	99	ARG	2.4
1	6-B	99	ARG	2.4
1	7-B	99	ARG	2.4
1	8-B	99	ARG	2.4
1	1-A	6	LEU	2.4
1	2-A	6	LEU	2.4
1	3-A	6	LEU	2.4
1	4-A	6	LEU	2.4
1	5-A	6	LEU	2.4
1	6-A	6	LEU	2.4
1	7-A	6	LEU	2.4
1	8-A	6	LEU	2.4
1	1-C	86	ASP	2.3
1	2-C	86	ASP	2.3
1	3-C	86	ASP	2.3
1	4-C	86	ASP	2.3
1	5-C	86	ASP	2.3
1	6-C	86	ASP	2.3
1	7-C	86	ASP	2.3
1	8-C	86	ASP	2.3
1	1-B	50	ALA	2.3
1	1-C	17	ALA	2.3
1	2-B	50	ALA	2.3
1	2-C	17	ALA	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-B	50	ALA	2.3
1	3-C	17	ALA	2.3
1	4-B	50	ALA	2.3
1	4-C	17	ALA	2.3
1	5-B	50	ALA	2.3
1	5-C	17	ALA	2.3
1	6-B	50	ALA	2.3
1	6-C	17	ALA	2.3
1	7-B	50	ALA	2.3
1	7-C	17	ALA	2.3
1	8-B	50	ALA	2.3
1	8-C	17	ALA	2.3
1	1-B	93	ILE	2.3
1	2-B	93	ILE	2.3
1	3-B	93	ILE	2.3
1	4-B	93	ILE	2.3
1	5-B	93	ILE	2.3
1	6-B	93	ILE	2.3
1	7-B	93	ILE	2.3
1	8-B	93	ILE	2.3
1	1-C	84	GLY	2.3
1	2-C	84	GLY	2.3
1	3-C	84	GLY	2.3
1	4-C	84	GLY	2.3
1	5-C	84	GLY	2.3
1	6-C	84	GLY	2.3
1	7-C	84	GLY	2.3
1	8-C	84	GLY	2.3
1	1-A	161	LEU	2.3
1	2-A	161	LEU	2.3
1	3-A	161	LEU	2.3
1	4-A	161	LEU	2.3
1	5-A	161	LEU	2.3
1	6-A	161	LEU	2.3
1	7-A	161	LEU	2.3
1	8-A	161	LEU	2.3
1	1-B	97	GLY	2.3
1	2-B	97	GLY	2.3
1	3-B	97	GLY	2.3
1	4-B	97	GLY	2.3
1	5-B	97	GLY	2.3
1	6-B	97	GLY	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-B	97	GLY	2.3
1	8-B	97	GLY	2.3
1	1-D	308	LEU	2.3
1	2-D	308	LEU	2.3
1	3-D	308	LEU	2.3
1	4-D	308	LEU	2.3
1	5-D	308	LEU	2.3
1	6-D	308	LEU	2.3
1	7-D	308	LEU	2.3
1	8-D	308	LEU	2.3
1	1-D	262	LYS	2.3
1	2-D	262	LYS	2.3
1	3-D	262	LYS	2.3
1	4-D	262	LYS	2.3
1	5-D	262	LYS	2.3
1	6-D	262	LYS	2.3
1	7-D	262	LYS	2.3
1	8-D	262	LYS	2.3
1	1-D	227	ASN	2.3
1	2-D	227	ASN	2.3
1	3-D	227	ASN	2.3
1	4-D	227	ASN	2.3
1	5-D	227	ASN	2.3
1	6-D	227	ASN	2.3
1	7-D	227	ASN	2.3
1	8-D	227	ASN	2.3
1	1-C	65	LYS	2.3
1	2-C	65	LYS	2.3
1	3-C	65	LYS	2.3
1	4-C	65	LYS	2.3
1	5-C	65	LYS	2.3
1	6-C	65	LYS	2.3
1	7-C	65	LYS	2.3
1	8-C	65	LYS	2.3
1	1-C	34	TRP	2.3
1	2-C	34	TRP	2.3
1	3-C	34	TRP	2.3
1	4-C	34	TRP	2.3
1	5-C	34	TRP	2.3
1	6-C	34	TRP	2.3
1	7-C	34	TRP	2.3
1	8-C	34	TRP	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-A	29	CYS	2.3
1	2-A	29	CYS	2.3
1	3-A	29	CYS	2.3
1	4-A	29	CYS	2.3
1	5-A	29	CYS	2.3
1	6-A	29	CYS	2.3
1	7-A	29	CYS	2.3
1	8-A	29	CYS	2.3
1	1-D	162	GLY	2.3
1	2-D	162	GLY	2.3
1	3-D	162	GLY	2.3
1	4-D	162	GLY	2.3
1	5-D	162	GLY	2.3
1	6-D	162	GLY	2.3
1	7-D	162	GLY	2.3
1	8-D	162	GLY	2.3
1	1-C	91	ASP	2.2
1	2-C	91	ASP	2.2
1	3-C	91	ASP	2.2
1	4-C	91	ASP	2.2
1	5-C	91	ASP	2.2
1	6-C	91	ASP	2.2
1	7-C	91	ASP	2.2
1	8-C	91	ASP	2.2
1	1-A	22	ALA	2.2
1	2-A	22	ALA	2.2
1	3-A	22	ALA	2.2
1	4-A	22	ALA	2.2
1	5-A	22	ALA	2.2
1	6-A	22	ALA	2.2
1	7-A	22	ALA	2.2
1	8-A	22	ALA	2.2
1	1-A	183	THR	2.2
1	2-A	183	THR	2.2
1	3-A	183	THR	2.2
1	4-A	183	THR	2.2
1	5-A	183	THR	2.2
1	6-A	183	THR	2.2
1	7-A	183	THR	2.2
1	8-A	183	THR	2.2
1	1-B	68	LEU	2.2
1	2-B	68	LEU	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-B	68	LEU	2.2
1	4-B	68	LEU	2.2
1	5-B	68	LEU	2.2
1	6-B	68	LEU	2.2
1	7-B	68	LEU	2.2
1	8-B	68	LEU	2.2
1	1-B	43	LYS	2.2
1	2-B	43	LYS	2.2
1	3-B	43	LYS	2.2
1	4-B	43	LYS	2.2
1	5-B	43	LYS	2.2
1	6-B	43	LYS	2.2
1	7-B	43	LYS	2.2
1	8-B	43	LYS	2.2
1	1-A	317	LEU	2.2
1	2-A	317	LEU	2.2
1	3-A	317	LEU	2.2
1	4-A	317	LEU	2.2
1	5-A	317	LEU	2.2
1	6-A	317	LEU	2.2
1	7-A	317	LEU	2.2
1	8-A	317	LEU	2.2
1	1-C	30	GLU	2.2
1	2-C	30	GLU	2.2
1	3-C	30	GLU	2.2
1	4-C	30	GLU	2.2
1	5-C	30	GLU	2.2
1	6-C	30	GLU	2.2
1	7-C	30	GLU	2.2
1	8-C	30	GLU	2.2
1	1-A	95	LYS	2.2
1	2-A	95	LYS	2.2
1	3-A	95	LYS	2.2
1	4-A	95	LYS	2.2
1	5-A	95	LYS	2.2
1	6-A	95	LYS	2.2
1	7-A	95	LYS	2.2
1	8-A	95	LYS	2.2
1	1-C	187	PRO	2.2
1	1-C	316	GLY	2.2
1	2-C	187	PRO	2.2
1	2-C	316	GLY	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-C	187	PRO	2.2
1	3-C	316	GLY	2.2
1	4-C	187	PRO	2.2
1	4-C	316	GLY	2.2
1	5-C	187	PRO	2.2
1	5-C	316	GLY	2.2
1	6-C	187	PRO	2.2
1	6-C	316	GLY	2.2
1	7-C	187	PRO	2.2
1	7-C	316	GLY	2.2
1	8-C	187	PRO	2.2
1	8-C	316	GLY	2.2
1	1-A	201	SER	2.2
1	1-A	272	SER	2.2
1	2-A	201	SER	2.2
1	2-A	272	SER	2.2
1	3-A	201	SER	2.2
1	3-A	272	SER	2.2
1	4-A	201	SER	2.2
1	4-A	272	SER	2.2
1	5-A	201	SER	2.2
1	5-A	272	SER	2.2
1	6-A	201	SER	2.2
1	6-A	272	SER	2.2
1	7-A	201	SER	2.2
1	7-A	272	SER	2.2
1	8-A	201	SER	2.2
1	8-A	272	SER	2.2
1	1-B	101	GLY	2.2
1	2-B	101	GLY	2.2
1	3-B	101	GLY	2.2
1	4-B	101	GLY	2.2
1	5-B	101	GLY	2.2
1	6-B	101	GLY	2.2
1	7-B	101	GLY	2.2
1	8-B	101	GLY	2.2
1	1-B	6	LEU	2.1
1	2-B	6	LEU	2.1
1	3-B	6	LEU	2.1
1	4-B	6	LEU	2.1
1	5-B	6	LEU	2.1
1	6-B	6	LEU	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-B	6	LEU	2.1
1	8-B	6	LEU	2.1
1	1-B	44	GLU	2.1
1	1-B	52	ALA	2.1
1	1-D	198	GLU	2.1
1	2-B	44	GLU	2.1
1	2-B	52	ALA	2.1
1	2-D	198	GLU	2.1
1	3-B	44	GLU	2.1
1	3-B	52	ALA	2.1
1	3-D	198	GLU	2.1
1	4-B	44	GLU	2.1
1	4-B	52	ALA	2.1
1	4-D	198	GLU	2.1
1	5-B	44	GLU	2.1
1	5-B	52	ALA	2.1
1	5-D	198	GLU	2.1
1	6-B	44	GLU	2.1
1	6-B	52	ALA	2.1
1	6-D	198	GLU	2.1
1	7-B	44	GLU	2.1
1	7-B	52	ALA	2.1
1	7-D	198	GLU	2.1
1	8-B	44	GLU	2.1
1	8-B	52	ALA	2.1
1	8-D	198	GLU	2.1
1	1-A	25	ARG	2.1
1	2-A	25	ARG	2.1
1	3-A	25	ARG	2.1
1	4-A	25	ARG	2.1
1	5-A	25	ARG	2.1
1	6-A	25	ARG	2.1
1	7-A	25	ARG	2.1
1	8-A	25	ARG	2.1
1	1-C	309	ALA	2.1
1	2-C	309	ALA	2.1
1	3-C	309	ALA	2.1
1	4-C	309	ALA	2.1
1	5-C	309	ALA	2.1
1	6-C	309	ALA	2.1
1	7-C	309	ALA	2.1
1	8-C	309	ALA	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	1-B	278	THR	2.1
1	2-B	278	THR	2.1
1	3-B	278	THR	2.1
1	4-B	278	THR	2.1
1	5-B	278	THR	2.1
1	6-B	278	THR	2.1
1	7-B	278	THR	2.1
1	8-B	278	THR	2.1
1	1-C	104	PRO	2.1
1	1-C	196	GLN	2.1
1	2-C	104	PRO	2.1
1	2-C	196	GLN	2.1
1	3-C	104	PRO	2.1
1	3-C	196	GLN	2.1
1	4-C	104	PRO	2.1
1	4-C	196	GLN	2.1
1	5-C	104	PRO	2.1
1	5-C	196	GLN	2.1
1	6-C	104	PRO	2.1
1	6-C	196	GLN	2.1
1	7-C	104	PRO	2.1
1	7-C	196	GLN	2.1
1	8-C	104	PRO	2.1
1	8-C	196	GLN	2.1
1	1-C	90	LEU	2.1
1	2-C	90	LEU	2.1
1	3-C	90	LEU	2.1
1	4-C	90	LEU	2.1
1	5-C	90	LEU	2.1
1	6-C	90	LEU	2.1
1	7-C	90	LEU	2.1
1	8-C	90	LEU	2.1
1	1-D	186	GLN	2.1
1	2-D	186	GLN	2.1
1	3-D	186	GLN	2.1
1	4-D	186	GLN	2.1
1	5-D	186	GLN	2.1
1	6-D	186	GLN	2.1
1	7-D	186	GLN	2.1
1	8-D	186	GLN	2.1
1	1-D	207	ALA	2.1
1	2-D	207	ALA	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-D	207	ALA	2.1
1	4-D	207	ALA	2.1
1	5-D	207	ALA	2.1
1	6-D	207	ALA	2.1
1	7-D	207	ALA	2.1
1	8-D	207	ALA	2.1
1	1-A	62	HIS	2.1
1	2-A	62	HIS	2.1
1	3-A	62	HIS	2.1
1	4-A	62	HIS	2.1
1	5-A	62	HIS	2.1
1	6-A	62	HIS	2.1
1	7-A	62	HIS	2.1
1	8-A	62	HIS	2.1
1	1-C	97	GLY	2.1
1	2-C	97	GLY	2.1
1	3-C	97	GLY	2.1
1	4-C	97	GLY	2.1
1	5-C	97	GLY	2.1
1	6-C	97	GLY	2.1
1	7-C	97	GLY	2.1
1	8-C	97	GLY	2.1
1	1-A	194	GLU	2.1
1	2-A	194	GLU	2.1
1	3-A	194	GLU	2.1
1	4-A	194	GLU	2.1
1	5-A	194	GLU	2.1
1	6-A	194	GLU	2.1
1	7-A	194	GLU	2.1
1	8-A	194	GLU	2.1
1	1-A	80	THR	2.1
1	2-A	80	THR	2.1
1	3-A	80	THR	2.1
1	4-A	80	THR	2.1
1	5-A	80	THR	2.1
1	6-A	80	THR	2.1
1	7-A	80	THR	2.1
1	8-A	80	THR	2.1
1	1-A	191	GLU	2.1
1	1-B	316	GLY	2.1
1	2-A	191	GLU	2.1
1	2-B	316	GLY	2.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	3-A	191	GLU	2.1
1	3-B	316	GLY	2.1
1	4-A	191	GLU	2.1
1	4-B	316	GLY	2.1
1	5-A	191	GLU	2.1
1	5-B	316	GLY	2.1
1	6-A	191	GLU	2.1
1	6-B	316	GLY	2.1
1	7-A	191	GLU	2.1
1	7-B	316	GLY	2.1
1	8-A	191	GLU	2.1
1	8-B	316	GLY	2.1
1	1-A	26	ALA	2.0
1	2-A	26	ALA	2.0
1	3-A	26	ALA	2.0
1	4-A	26	ALA	2.0
1	5-A	26	ALA	2.0
1	6-A	26	ALA	2.0
1	7-A	26	ALA	2.0
1	8-A	26	ALA	2.0
1	1-C	102	TYR	2.0
1	1-D	182	TYR	2.0
1	2-C	102	TYR	2.0
1	2-D	182	TYR	2.0
1	3-C	102	TYR	2.0
1	3-D	182	TYR	2.0
1	4-C	102	TYR	2.0
1	4-D	182	TYR	2.0
1	5-C	102	TYR	2.0
1	5-D	182	TYR	2.0
1	6-C	102	TYR	2.0
1	6-D	182	TYR	2.0
1	7-C	102	TYR	2.0
1	7-D	182	TYR	2.0
1	8-C	102	TYR	2.0
1	8-D	182	TYR	2.0
1	1-D	253	ASP	2.0
1	2-D	253	ASP	2.0
1	3-D	253	ASP	2.0
1	4-D	253	ASP	2.0
1	5-D	253	ASP	2.0
1	6-D	253	ASP	2.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	7-D	253	ASP	2.0
1	8-D	253	ASP	2.0
1	1-A	198	GLU	2.0
1	2-A	198	GLU	2.0
1	3-A	198	GLU	2.0
1	4-A	198	GLU	2.0
1	5-A	198	GLU	2.0
1	6-A	198	GLU	2.0
1	7-A	198	GLU	2.0
1	8-A	198	GLU	2.0
1	1-C	185	ARG	2.0
1	2-C	185	ARG	2.0
1	3-C	185	ARG	2.0
1	4-C	185	ARG	2.0
1	5-C	185	ARG	2.0
1	6-C	185	ARG	2.0
1	7-C	185	ARG	2.0
1	8-C	185	ARG	2.0
1	1-A	65	LYS	2.0
1	1-C	95	LYS	2.0
1	2-A	65	LYS	2.0
1	2-C	95	LYS	2.0
1	3-A	65	LYS	2.0
1	3-C	95	LYS	2.0
1	4-A	65	LYS	2.0
1	4-C	95	LYS	2.0
1	5-A	65	LYS	2.0
1	5-C	95	LYS	2.0
1	6-A	65	LYS	2.0
1	6-C	95	LYS	2.0
1	7-A	65	LYS	2.0
1	7-C	95	LYS	2.0
1	8-A	65	LYS	2.0
1	8-C	95	LYS	2.0
1	1-D	64	ASP	2.0
1	2-D	64	ASP	2.0
1	3-D	64	ASP	2.0
1	4-D	64	ASP	2.0
1	5-D	64	ASP	2.0
1	6-D	64	ASP	2.0
1	7-D	64	ASP	2.0
1	8-D	64	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	1-A	94	LYS	2.0
1	2-A	94	LYS	2.0
1	3-A	94	LYS	2.0
1	4-A	94	LYS	2.0
1	5-A	94	LYS	2.0
1	6-A	94	LYS	2.0
1	7-A	94	LYS	2.0
1	8-A	94	LYS	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.