



## Full wwPDB EM Validation Report ⓘ

Jul 3, 2026 – 03:17 AM JST

PDB ID : 9V2S / pdb\_00009v2s  
EMDB ID : EMD-64739  
Title : Cryo-EM structure of Runella bGSDM pore  
Authors : Su, Z.; Feng, Y.; Gan, J.H.; Feng, Y.J.  
Deposited on : 2025-05-20  
Resolution : 3.25 Å (reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

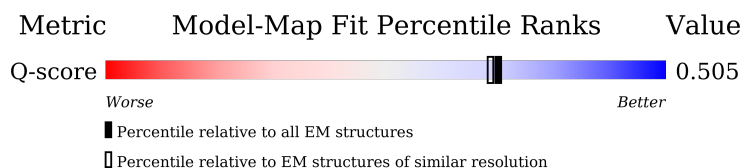
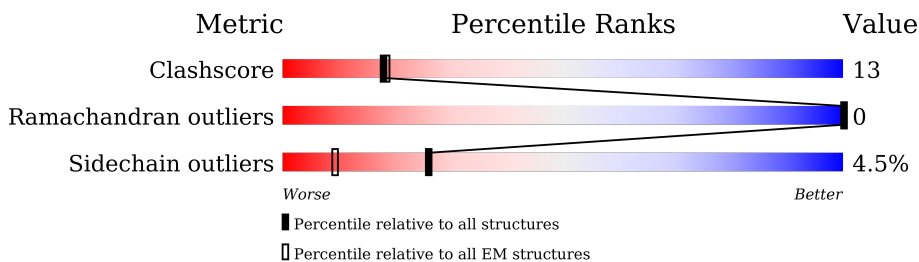
EMDB validation analysis : 0.0.1.dev133  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.50

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.25 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14599 ( 2.75 - 3.75 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	242	<p>61% 29% 10%</p>
1	1	242	<p>67% 23% 10%</p>
1	2	242	<p>60% 30% 10%</p>
1	3	242	<p>68% 22% 10%</p>

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Mol	Chain	Length	Quality of chain		
1	4	242	60%	29%	10%
1	5	242	60%	29%	10%
1	6	242	65%	23%	10%
1	7	242	64%	25%	10%
1	8	242	61%	29%	10%
1	9	242	64%	26%	10%
1	A	242	66%	24%	10%
1	AA	242	62%	27%	10%
1	AB	242	63%	26%	10%
1	AC	242	64%	25%	10%
1	AD	242	67%	21%	10%
1	AE	242	63%	26%	10%
1	AF	242	64%	25%	10%
1	AG	242	62%	28%	10%
1	AH	242	65%	24%	10%
1	AI	242	61%	30%	10%
1	AJ	242	64%	25%	10%
1	AK	242	63%	26%	10%
1	AL	242	67%	23%	10%
1	AM	242	61%	28%	10%
1	AN	242	65%	24%	10%
1	AO	242	63%	26%	10%
1	AP	242	63%	26%	10%
1	AQ	242	60%	31%	10%
1	AR	242	60%	29%	10%

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Mol	Chain	Length	Quality of chain		
1	AS	242	68%	20%	10%
1	AT	242	63%	26%	10%
1	AU	242	64%	26%	10%
1	AV	242	63%	27%	10%
1	AW	242	62%	27%	10%
1	AX	242	62%	26%	10%
1	AY	242	66%	23%	10%
1	AZ	242	61%	28%	10%
1	Aa	242	70%	20%	10%
1	Ab	242	65%	24%	10%
1	Ac	242	63%	26%	10%
1	Ad	242	62%	28%	10%
1	B	242	63%	26%	10%
1	C	242	62%	28%	10%
1	D	242	67%	23%	10%
1	E	242	61%	29%	10%
1	F	242	63%	26%	10%
1	G	242	69%	21%	10%
1	H	242	62%	26%	10%
1	I	242	62%	28%	10%
1	J	242	62%	28%	10%
1	K	242	64%	25%	10%
1	L	242	61%	29%	10%
1	M	242	66%	23%	10%
1	N	242	62%	28%	10%



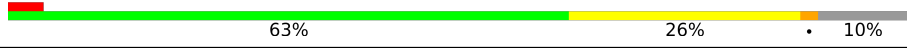




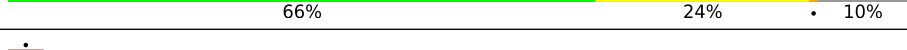
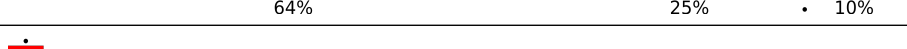
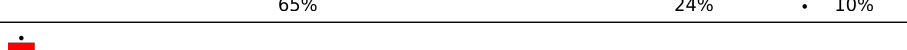

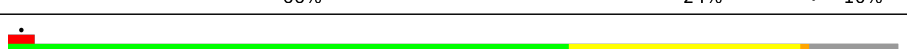
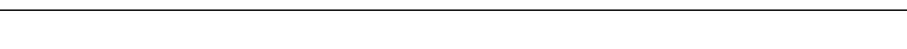
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Mol	Chain	Length	Quality of chain			
1	O	242		61%	29%	10%
1	P	242		61%	29%	10%
1	Q	242		63%	26%	10%
1	R	242		65%	24%	10%
1	S	242		65%	24%	10%
1	T	242		65%	24%	10%
1	U	242		63%	26%	10%
1	V	242		67%	23%	10%
1	W	242		63%	26%	10%
1	X	242		63%	26%	10%
1	Y	242		62%	27%	10%
1	Z	242		63%	26%	10%
1	a	242		64%	26%	10%
1	b	242		60%	30%	10%
1	c	242		65%	24%	10%
1	d	242		69%	19%	10%
1	e	242		62%	26%	10%
1	f	242		62%	28%	10%
1	g	242		62%	27%	10%
1	h	242		66%	23%	10%
1	i	242		60%	29%	10%
1	j	242		64%	24%	10%
1	k	242		61%	28%	10%
1	l	242		62%	27%	10%
1	m	242		61%	29%	10%

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Mol	Chain	Length	Quality of chain
1	n	242	 64% 26% 10%
1	o	242	 65% 24% 10%
1	p	242	 63% 26% 10%
1	q	242	 65% 24% 10%
1	r	242	 63% 26% 10%
1	s	242	 67% 21% 10%
1	t	242	 64% 25% 10%
1	u	242	 66% 24% 10%
1	v	242	 64% 25% 10%
1	w	242	 65% 24% 10%
1	x	242	 65% 24% 10%
1	y	242	 5% 66% 24% 10%
1	z	242	 63% 26% 10%

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 162012 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Gasdermin bGSDM, N-terminus.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	219	1761	1131	299	329	2	0	0
1	B	219	1761	1131	299	329	2	0	0
1	C	219	1761	1131	299	329	2	0	0
1	D	219	1761	1131	299	329	2	0	0
1	E	219	1761	1131	299	329	2	0	0
1	F	219	1761	1131	299	329	2	0	0
1	G	219	1761	1131	299	329	2	0	0
1	H	219	1761	1131	299	329	2	0	0
1	I	219	1761	1131	299	329	2	0	0
1	J	219	1761	1131	299	329	2	0	0
1	K	219	1761	1131	299	329	2	0	0
1	L	219	1761	1131	299	329	2	0	0
1	M	219	1761	1131	299	329	2	0	0
1	N	219	1761	1131	299	329	2	0	0
1	O	219	1761	1131	299	329	2	0	0
1	P	219	1761	1131	299	329	2	0	0
1	Q	219	1761	1131	299	329	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	S	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	T	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	U	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	V	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	W	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	X	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	Y	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	Z	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	a	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	b	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	c	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	d	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	e	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	f	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	g	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	h	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	i	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	j	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	k	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	l	219	Total 1761	C 1131	N 299	O 329	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	n	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	o	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	p	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	q	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	r	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	s	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	t	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	u	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	v	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	w	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	x	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	y	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	z	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	1	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	2	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	3	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	4	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	5	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	6	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	7	219	Total 1761	C 1131	N 299	O 329	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	9	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	0	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AA	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AB	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AC	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AD	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AE	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AF	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AG	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AH	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AI	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AJ	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AK	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AL	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AM	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AN	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AO	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AP	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AQ	219	Total 1761	C 1131	N 299	O 329	S 2	0	0
1	AR	219	Total 1761	C 1131	N 299	O 329	S 2	0	0

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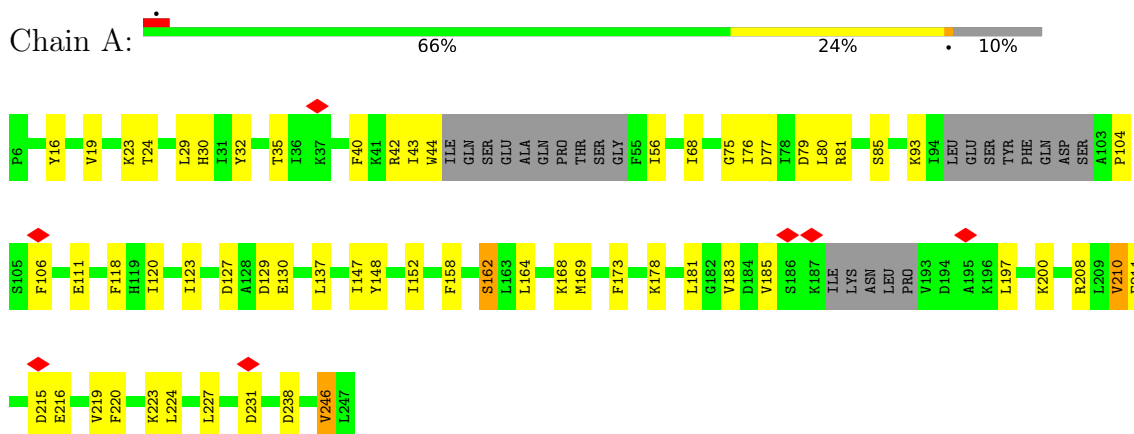
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AS	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	AT	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	AU	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	AV	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	AW	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	AX	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	AY	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	AZ	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	Aa	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	Ab	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	Ac	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		
1	Ad	219	Total	C	N	O	S	0	0
			1761	1131	299	329	2		

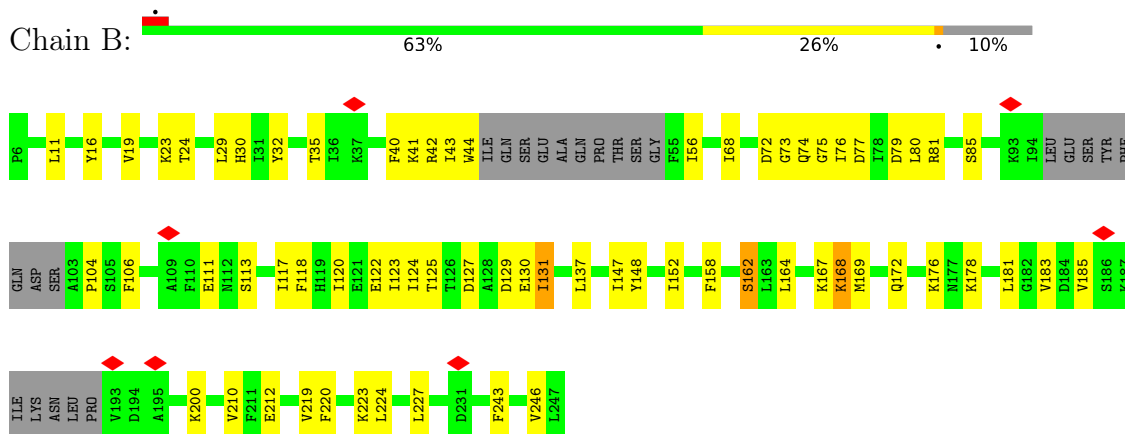
### 3 Residue-property plots [i](#)

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

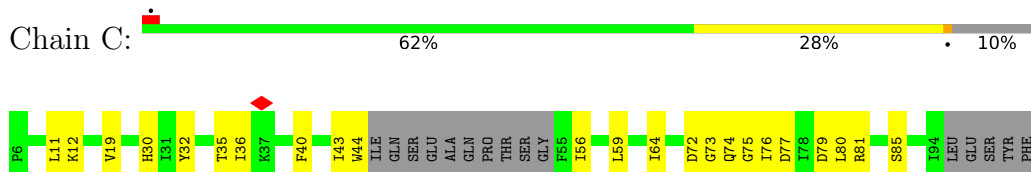
- Molecule 1: Gasdermin bGSDM, N-terminus

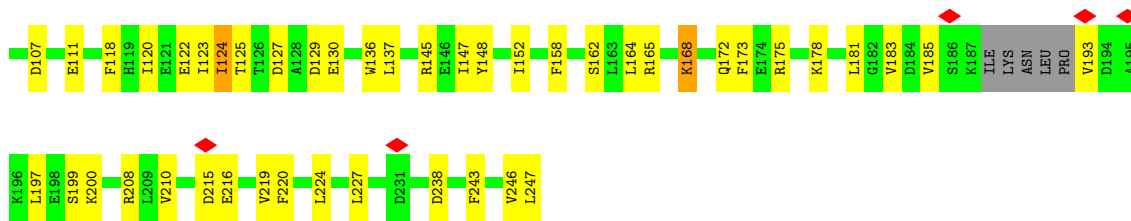


- Molecule 1: Gasdermin bGSDM, N-terminus

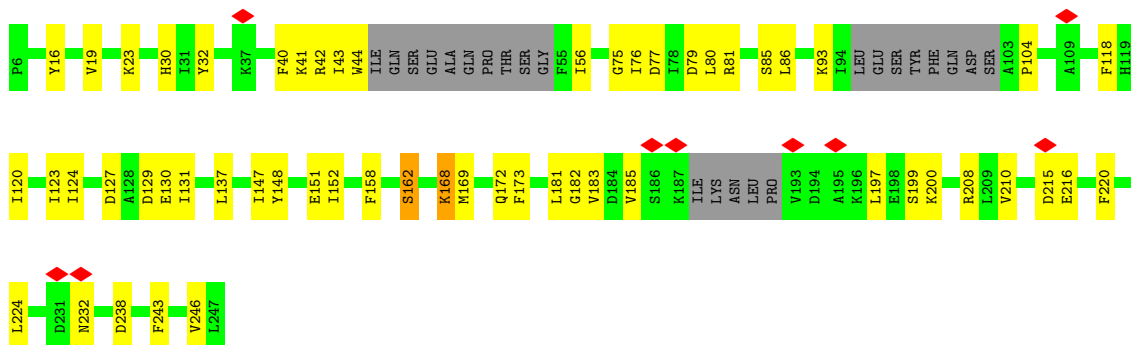


- Molecule 1: Gasdermin bGSDM, N-terminus

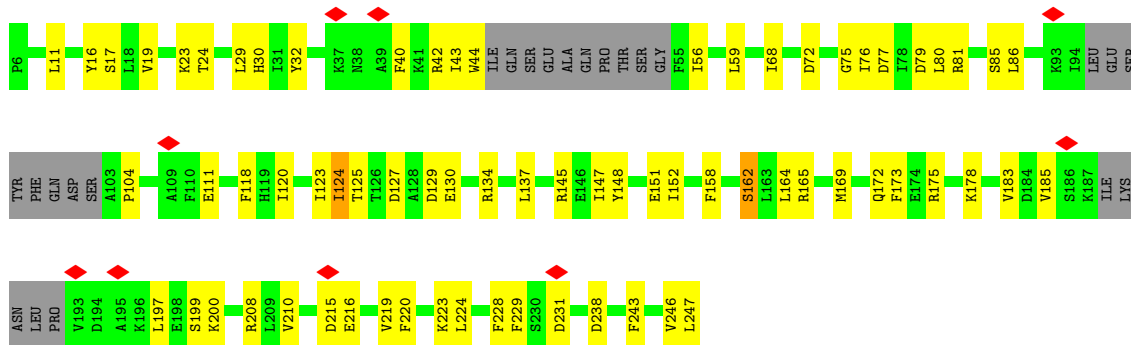




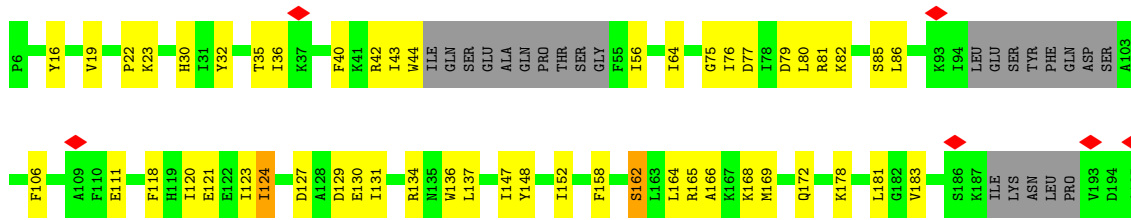
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

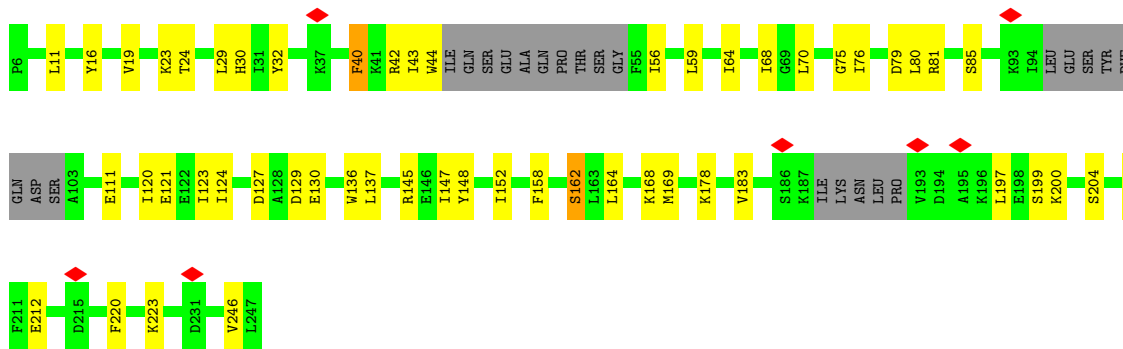


• Molecule 1: Gasdermin bGSDM, N-terminus

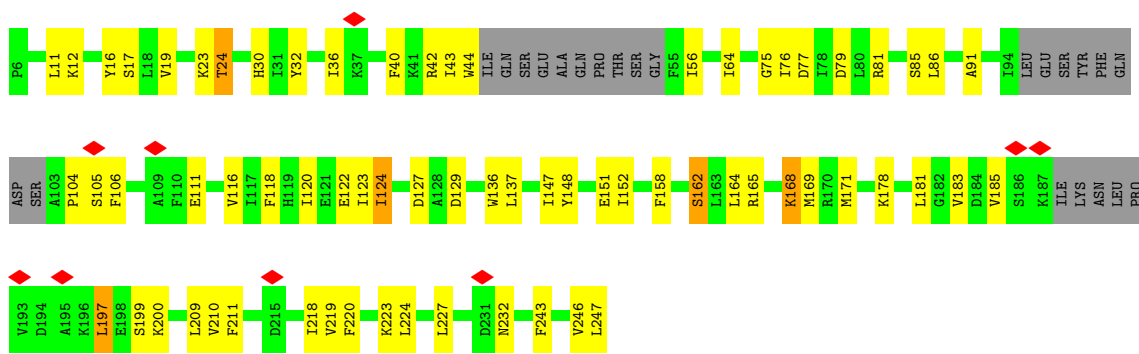




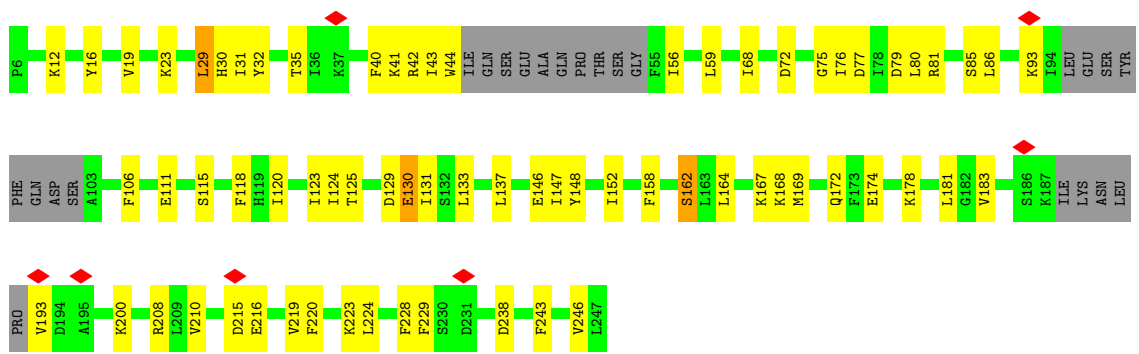
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

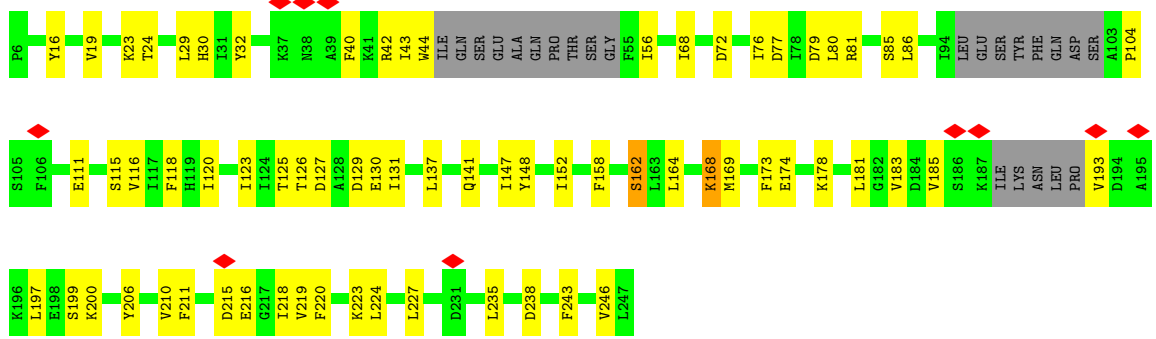


• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

Chain J:



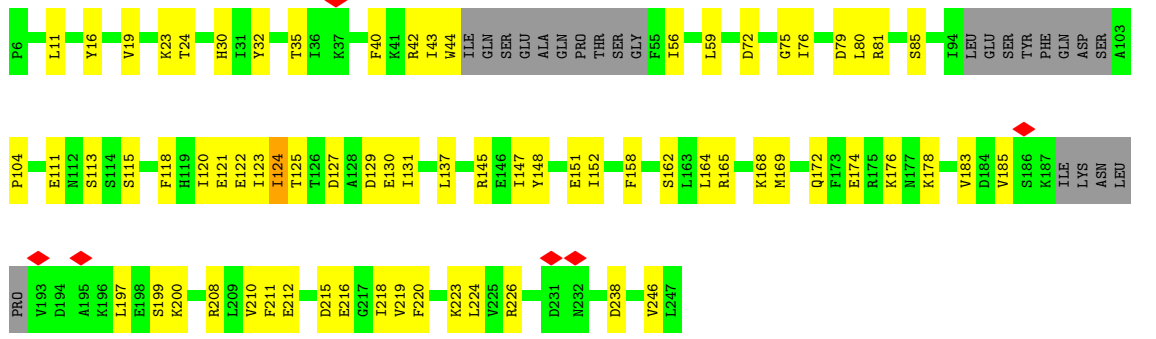
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain K:



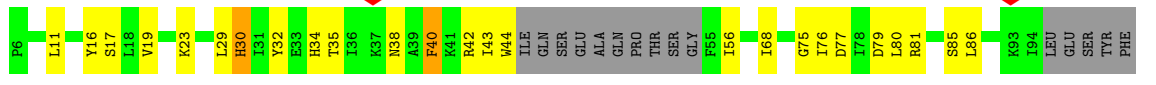
• Molecule 1: Gasdermin bGSDM, N-terminus

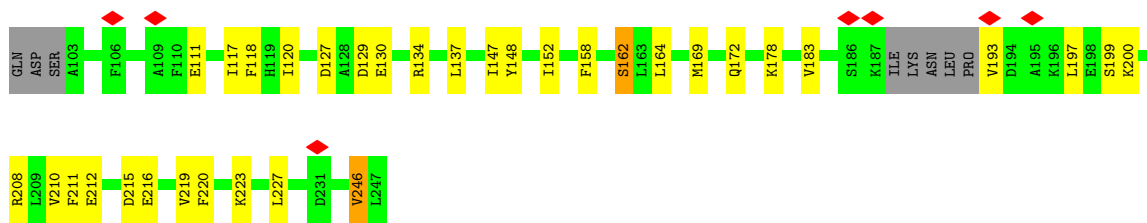
Chain L:



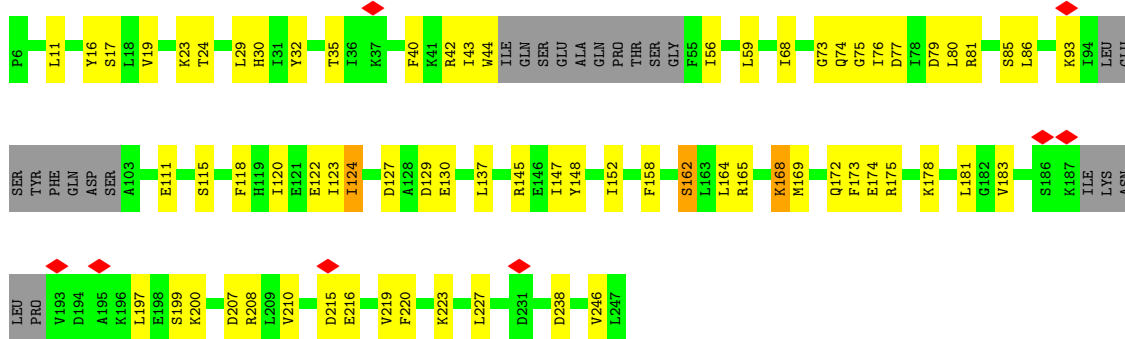
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain M:

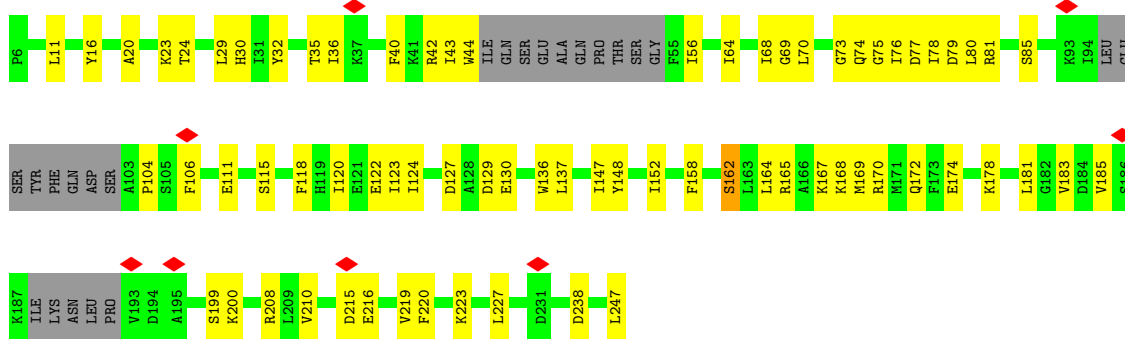




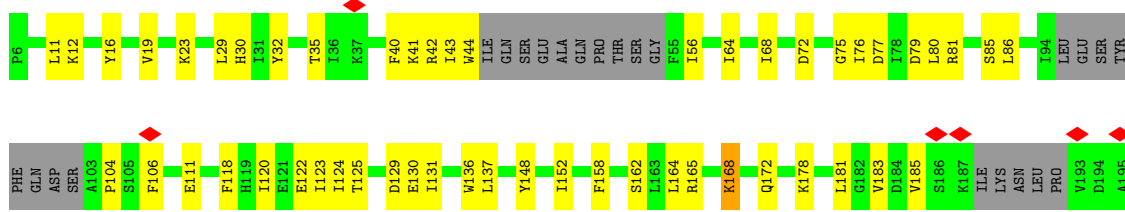
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus



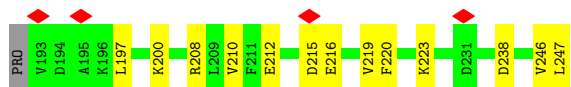
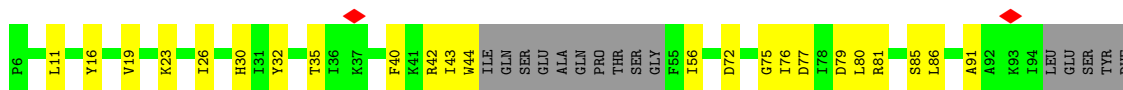
• Molecule 1: Gasdermin bGSDM, N-terminus





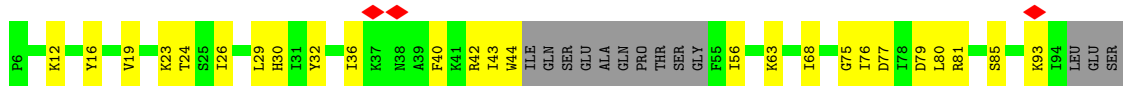
- Molecule 1: Gasdermin bGSDM, N-terminus

Chain Q: 63% 26% 10%



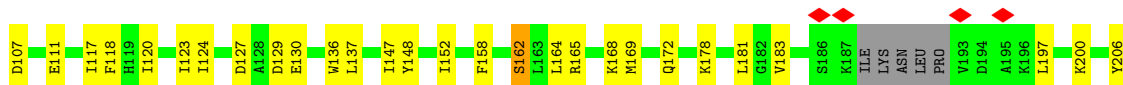
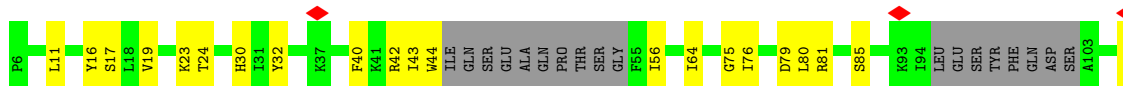
- Molecule 1: Gasdermin bGSDM, N-terminus

Chain R: 65% 24% 10%



- Molecule 1: Gasdermin bGSDM, N-terminus

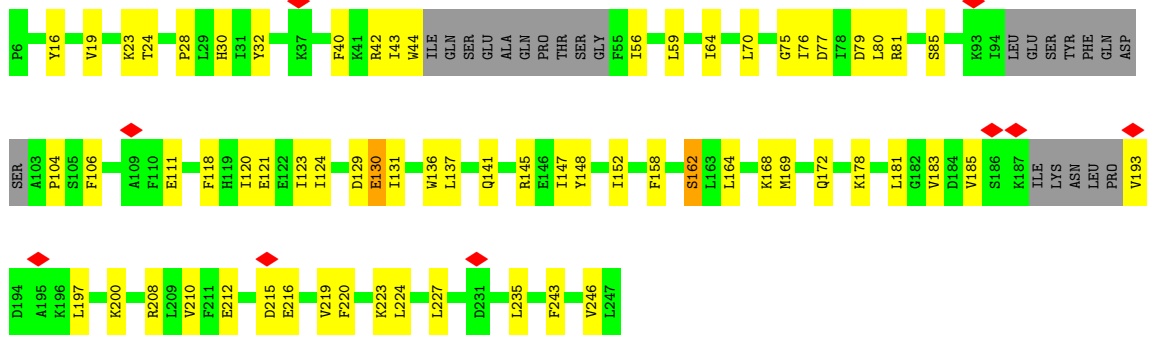
Chain S: 65% 24% 10%



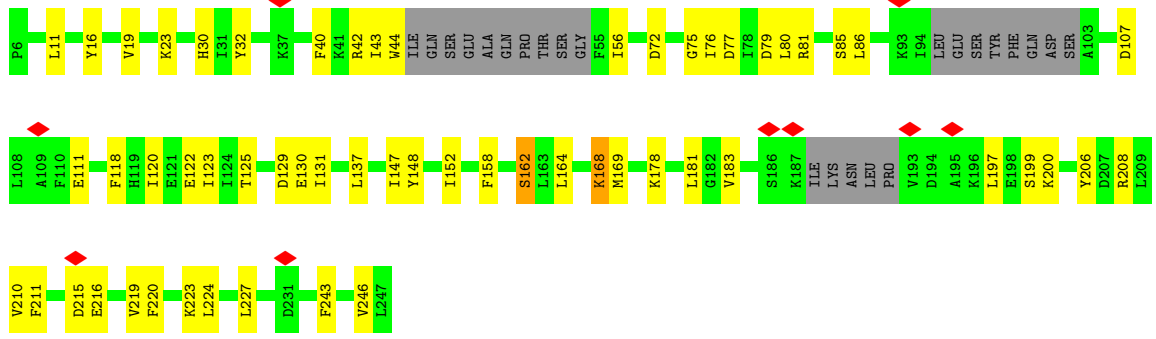
- Molecule 1: Gasdermin bGSDM, N-terminus



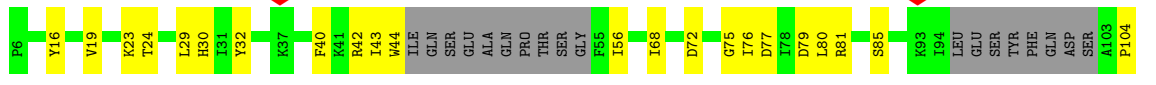
• Molecule 1: Gasdermin bGSDM, N-terminus

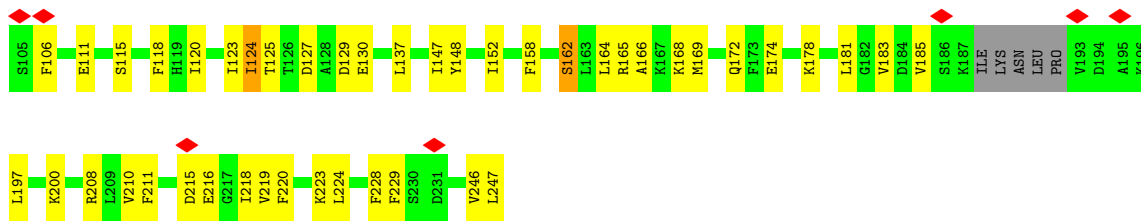


• Molecule 1: Gasdermin bGSDM, N-terminus

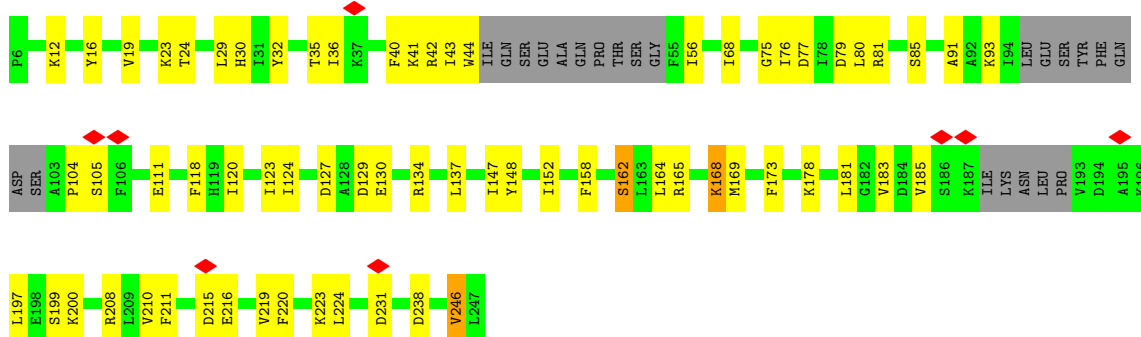


• Molecule 1: Gasdermin bGSDM, N-terminus

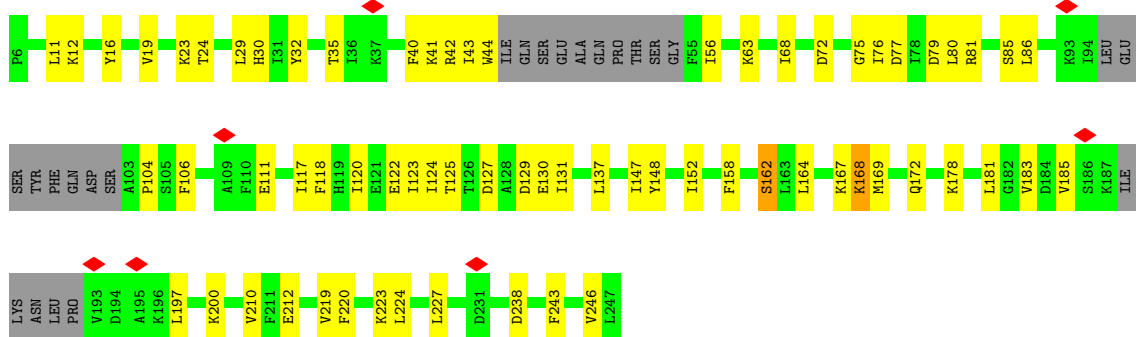




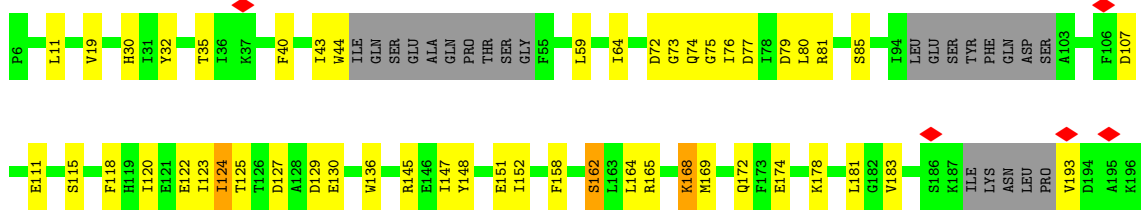
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

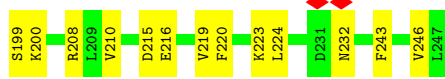
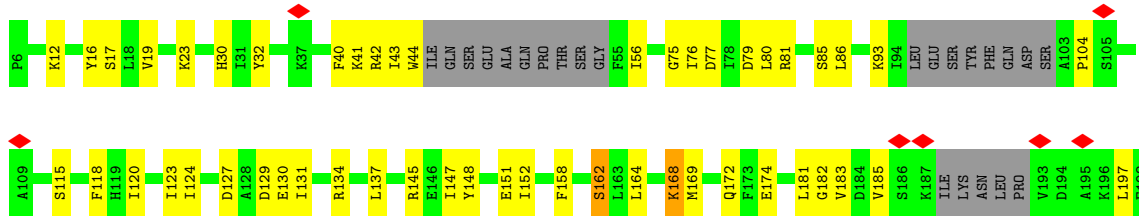


• Molecule 1: Gasdermin bGSDM, N-terminus

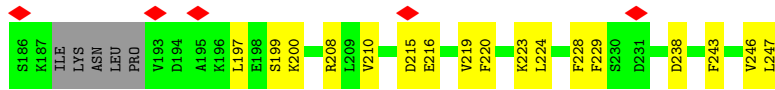
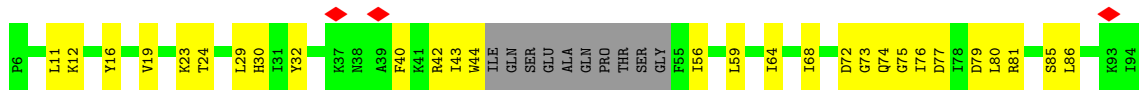




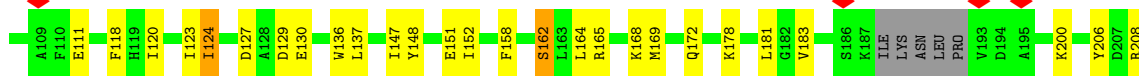
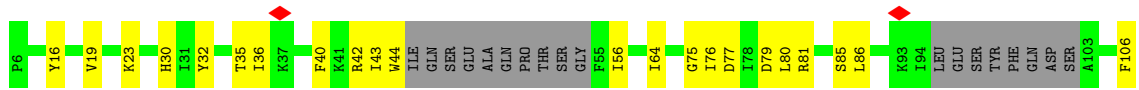
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

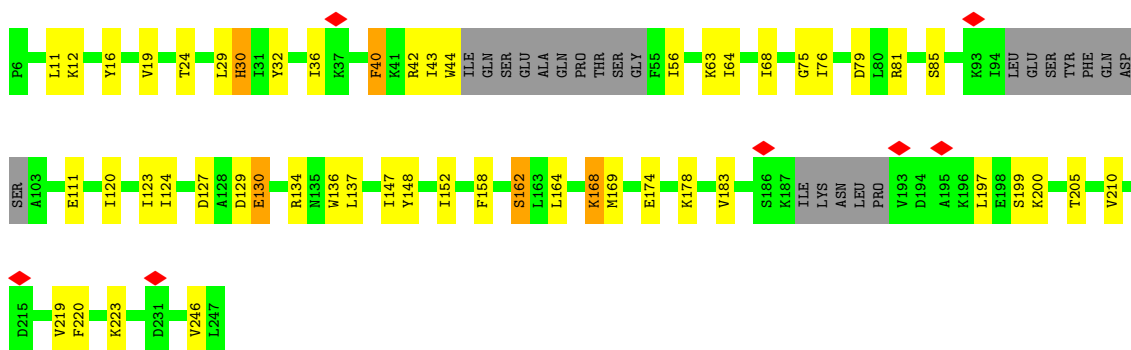


• Molecule 1: Gasdermin bGSDM, N-terminus



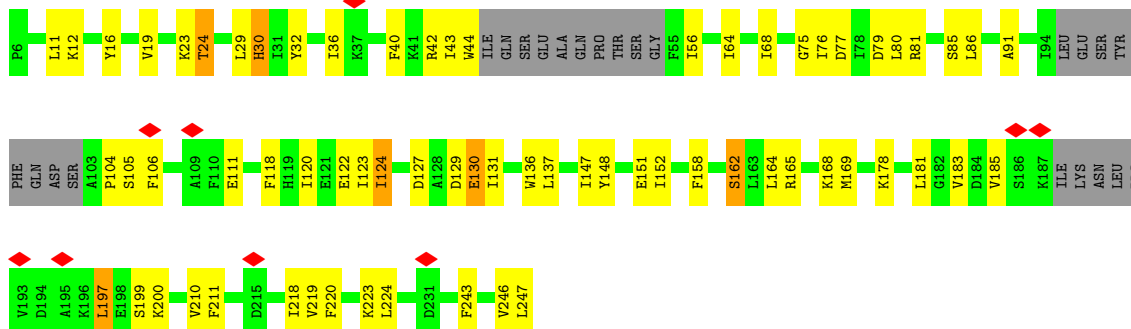
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain d:  69% 19% 10%



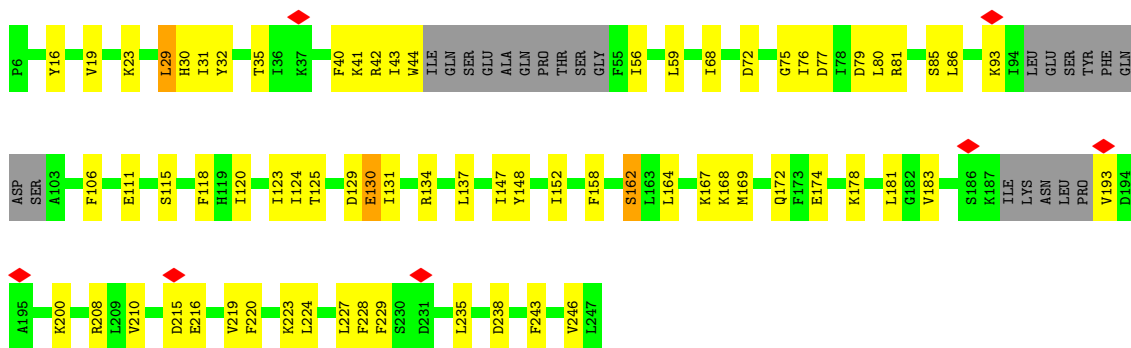
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain e:  62% 26% 10%



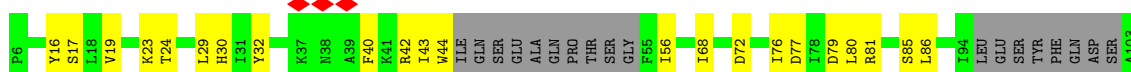
• Molecule 1: Gasdermin bGSDM, N-terminus

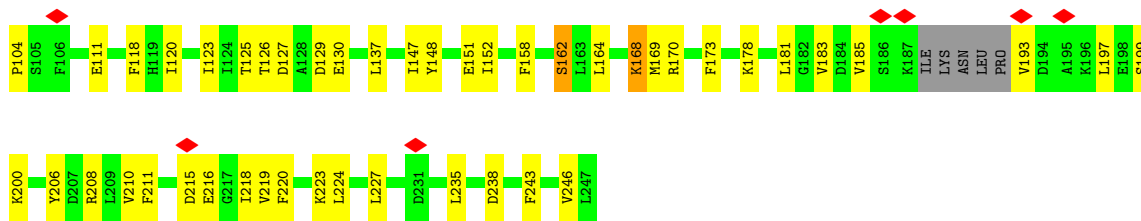
Chain f:  62% 28% 10%



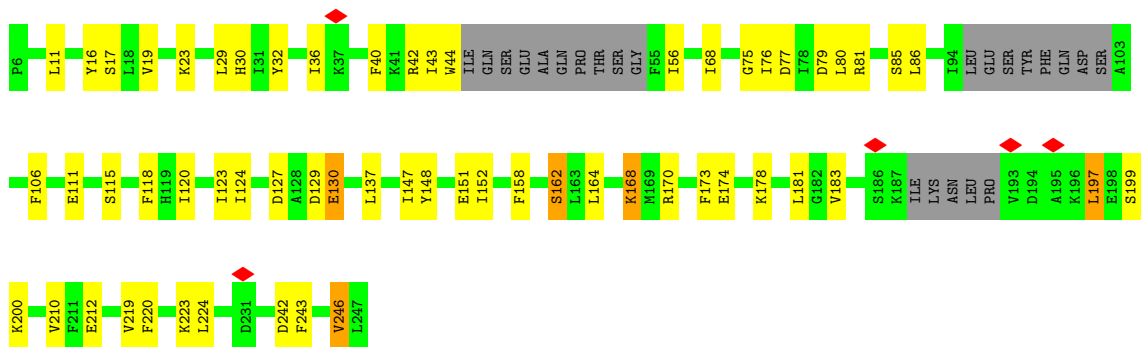
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain g:  62% 27% 10%

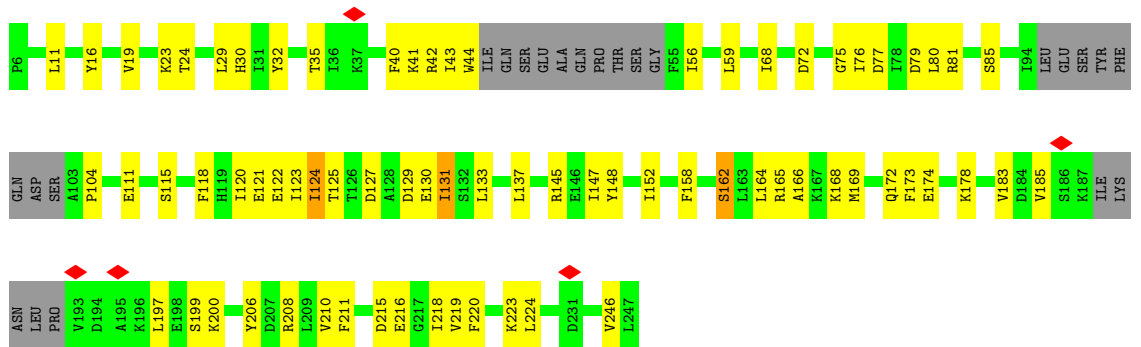




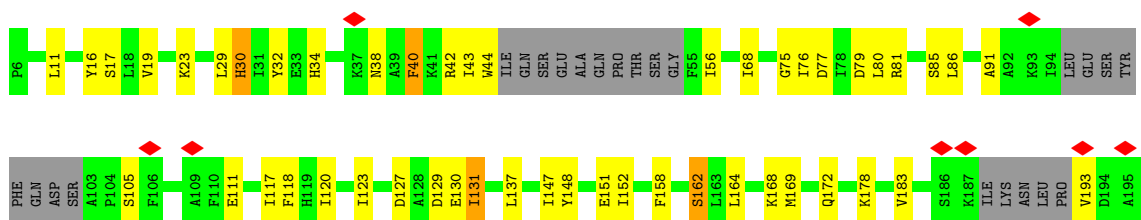
• Molecule 1: Gasdermin bGSDM, N-terminus

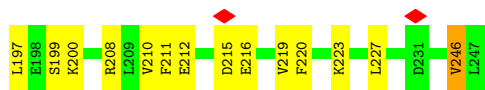


• Molecule 1: Gasdermin bGSDM, N-terminus

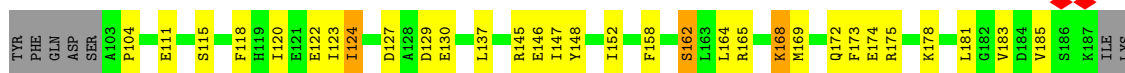
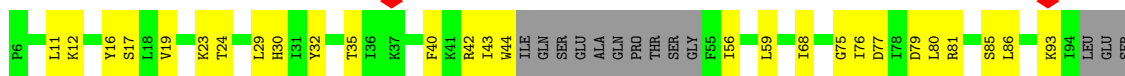


• Molecule 1: Gasdermin bGSDM, N-terminus

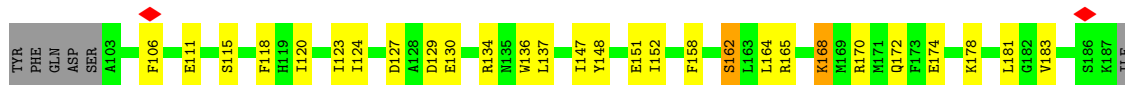
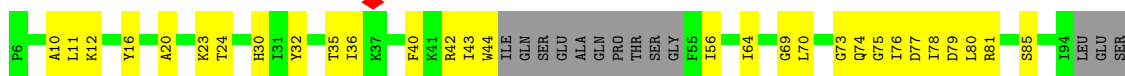




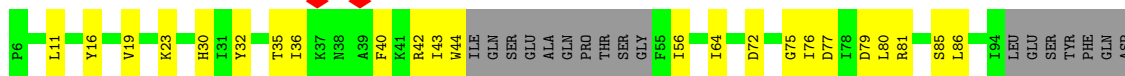
• Molecule 1: Gasdermin bGSDM, N-terminus



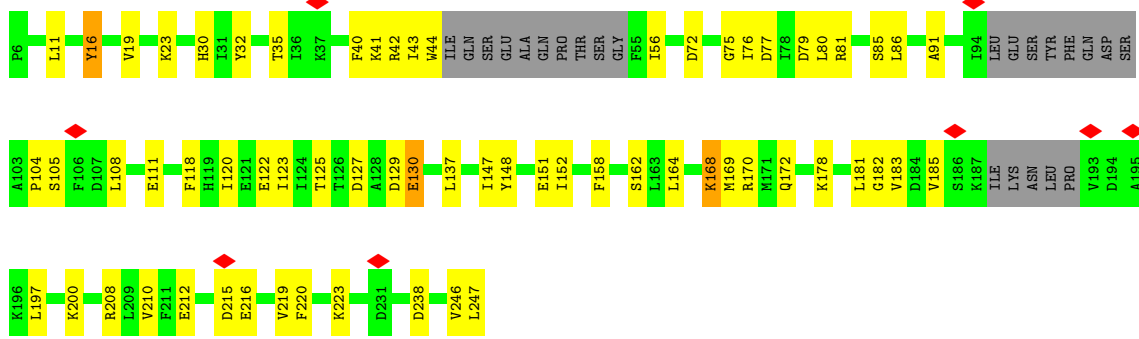
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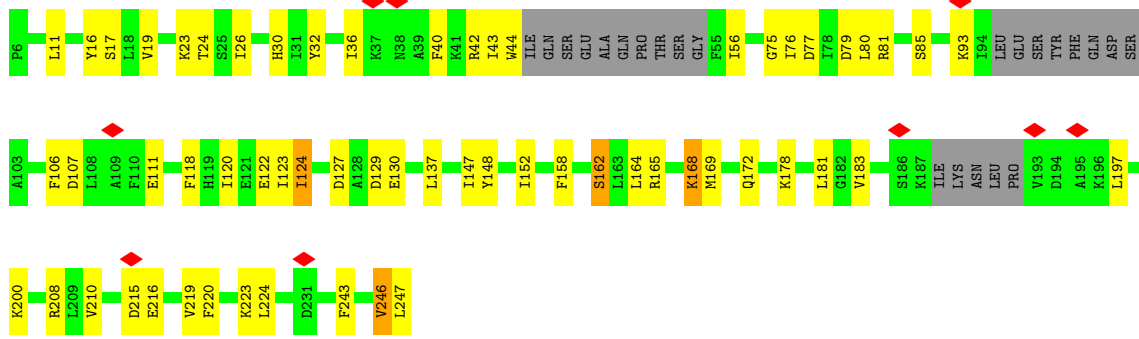
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus



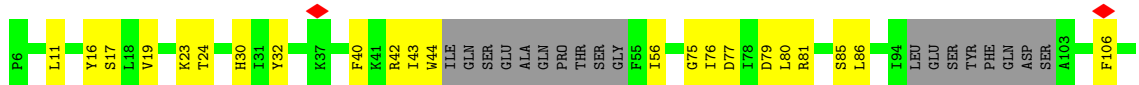
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

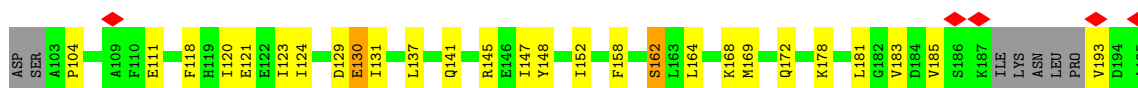
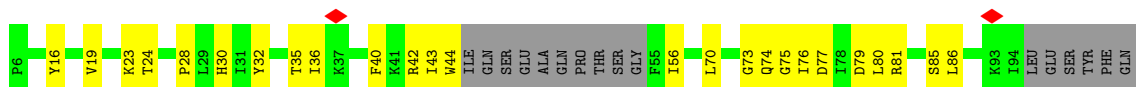


• Molecule 1: Gasdermin bGSDM, N-terminus

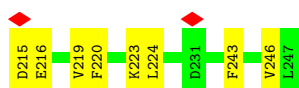
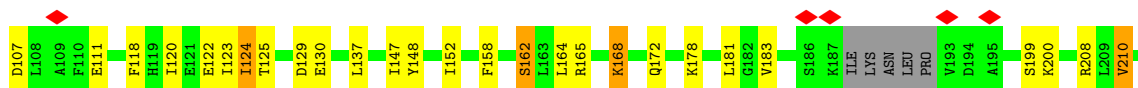
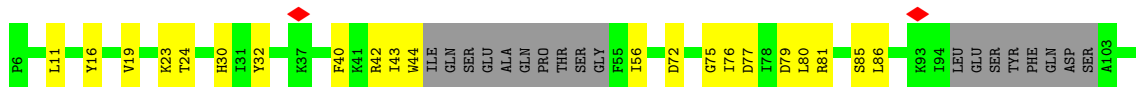




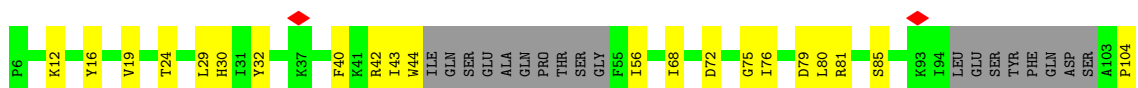
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

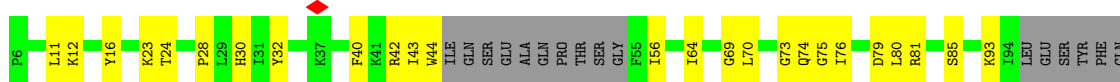


• Molecule 1: Gasdermin bGSDM, N-terminus

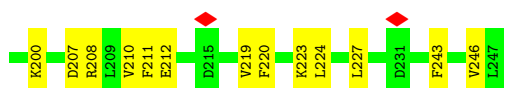
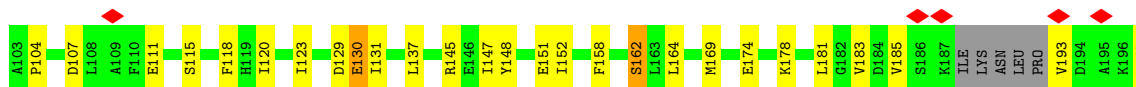
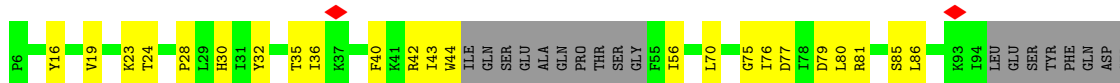




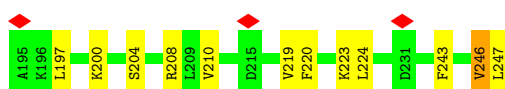
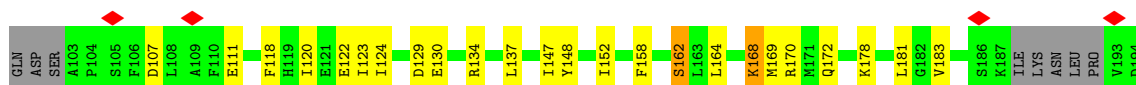
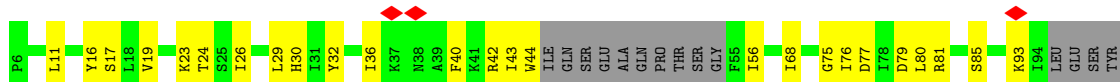
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

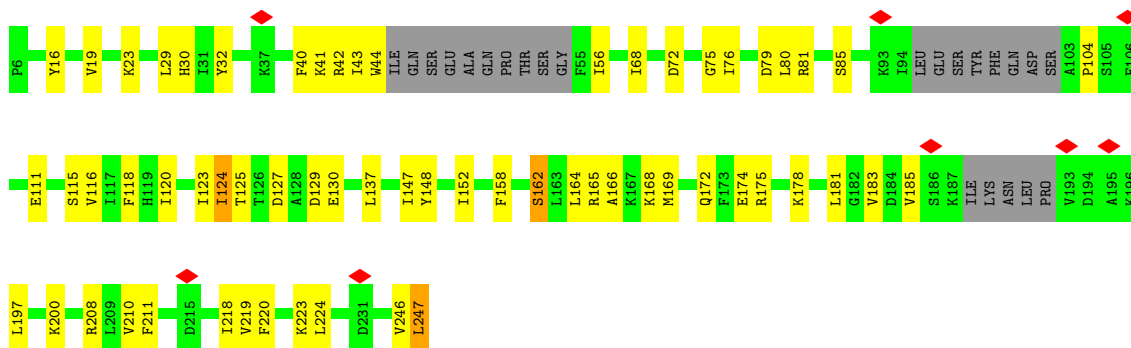


• Molecule 1: Gasdermin bGSDM, N-terminus



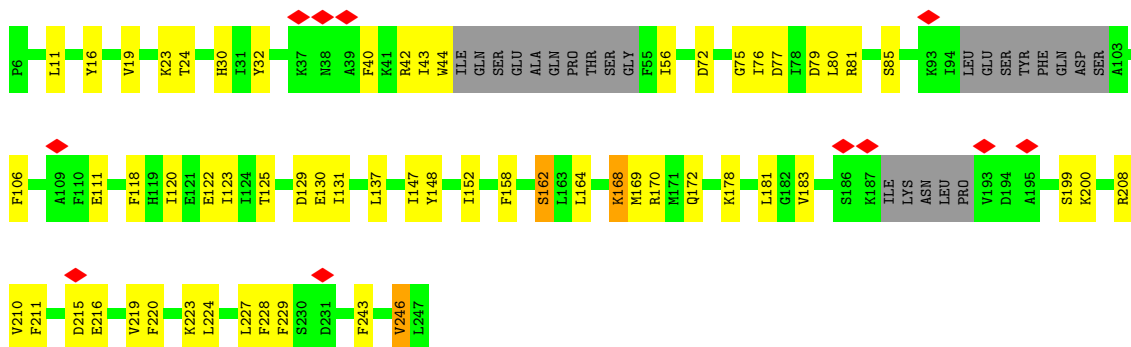
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain x: 



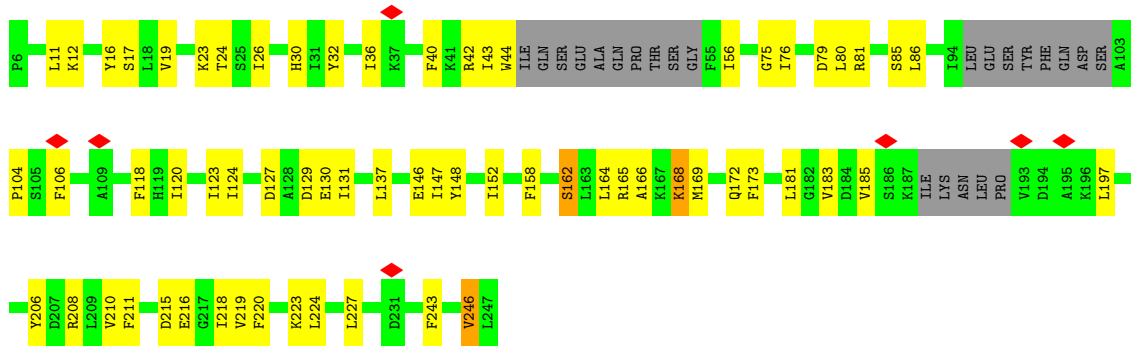
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain y: 



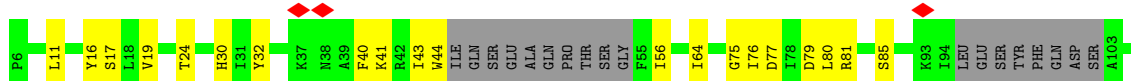
• Molecule 1: Gasdermin bGSDM, N-terminus

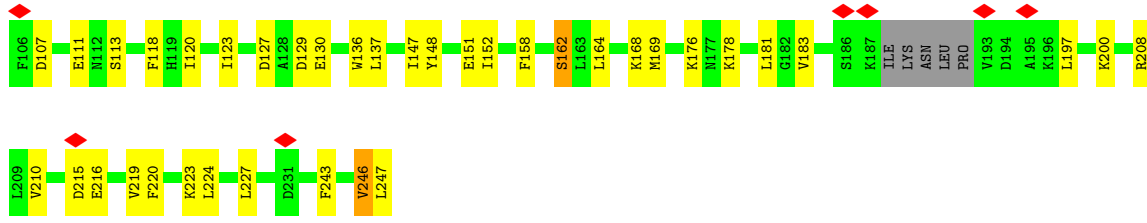
Chain z: 



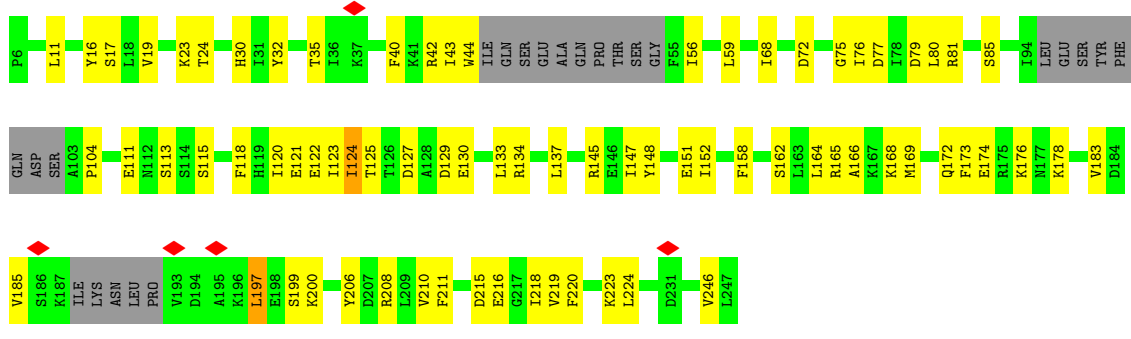
• Molecule 1: Gasdermin bGSDM, N-terminus

Chain 1: 

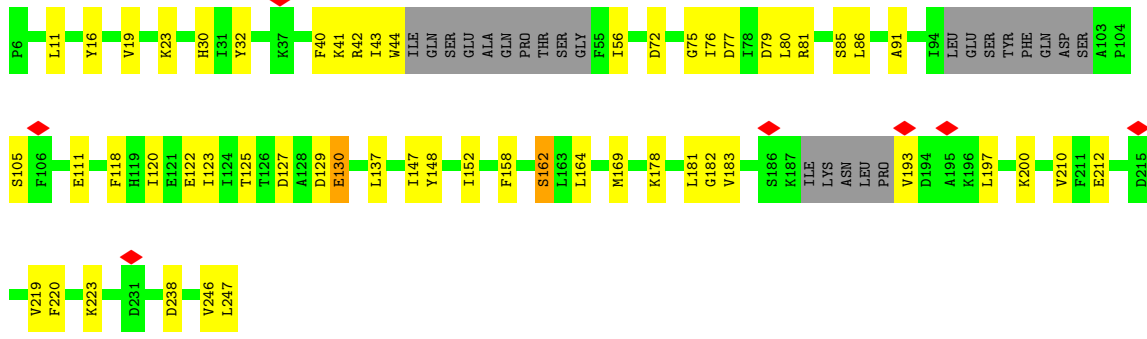




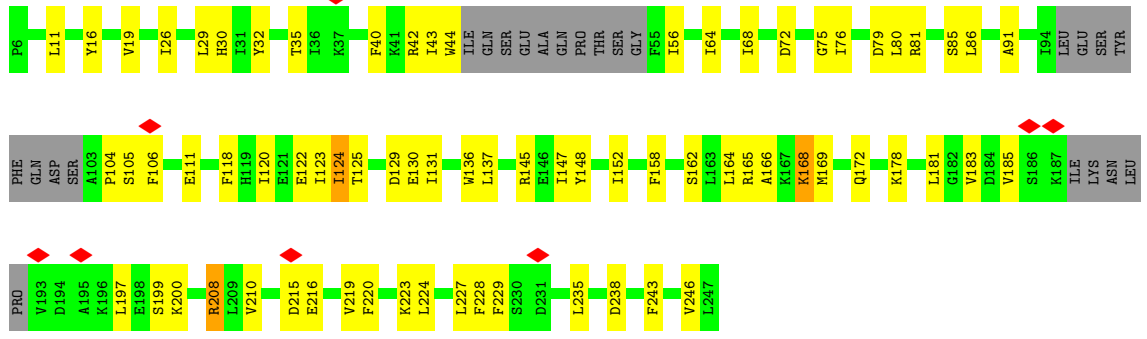
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

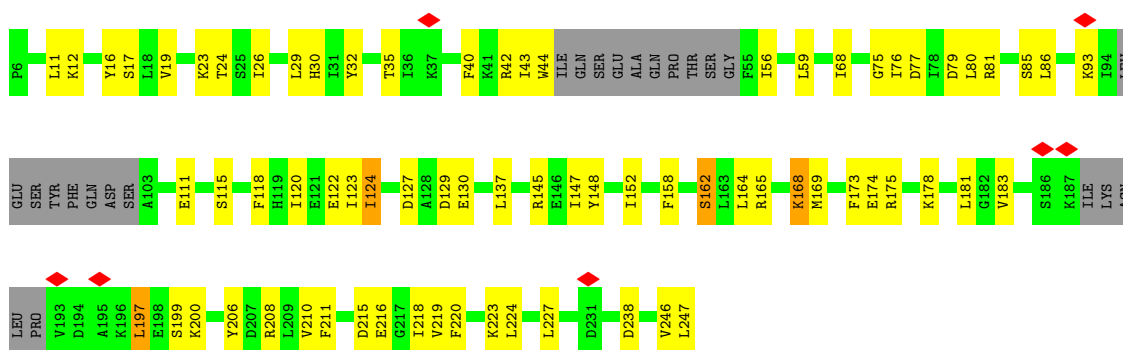


• Molecule 1: Gasdermin bGSDM, N-terminus



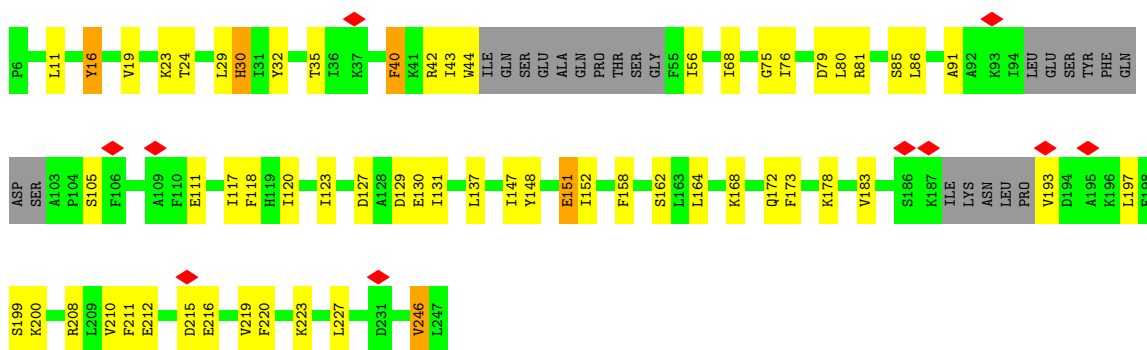
- Molecule 1: Gasdermin bGSDM, N-terminus

Chain 5: 



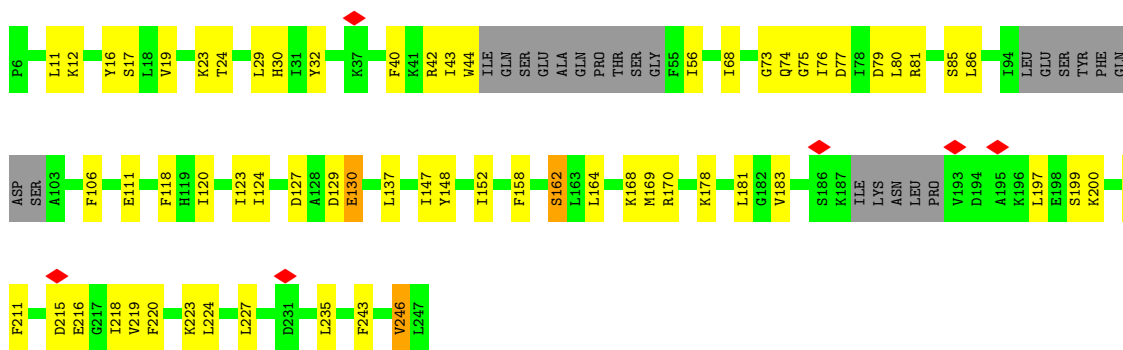
- Molecule 1: Gasdermin bGSDM, N-terminus

Chain 6: 



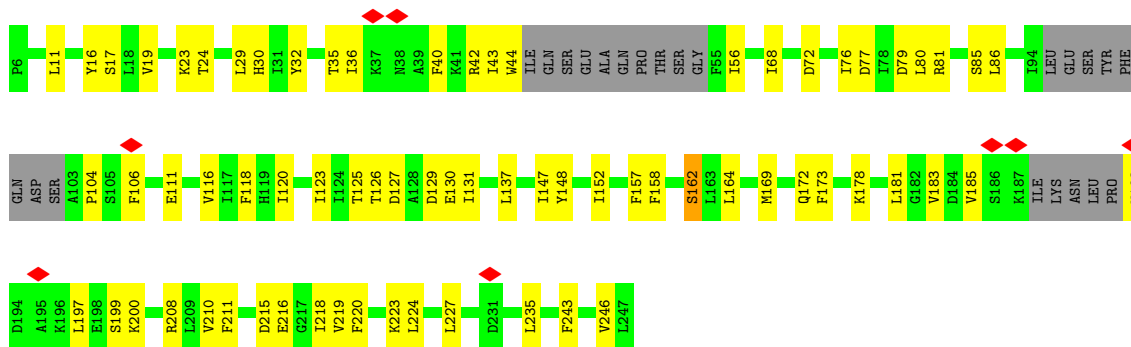
- Molecule 1: Gasdermin bGSDM, N-terminus

Chain 7: 

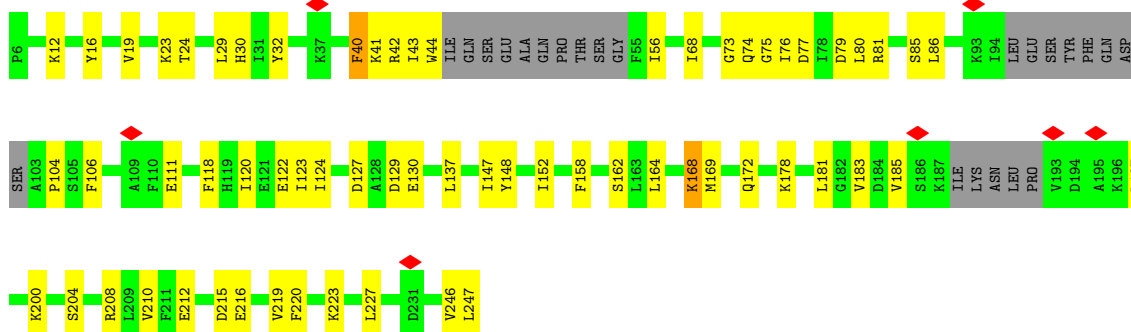


- Molecule 1: Gasdermin bGSDM, N-terminus

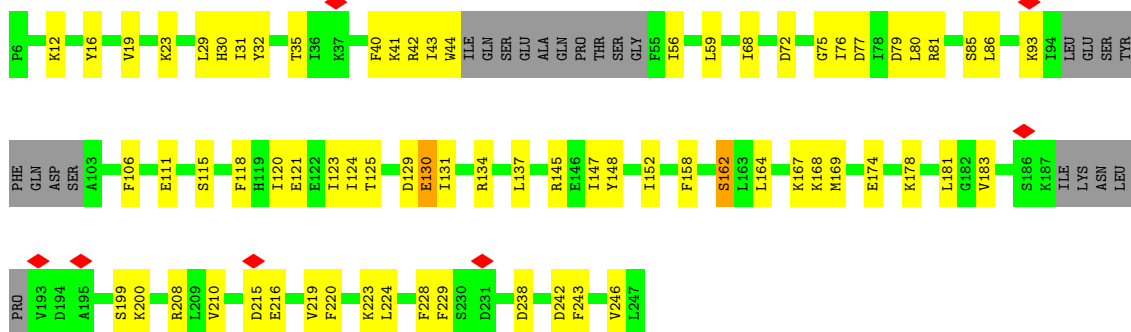
Chain 8: 



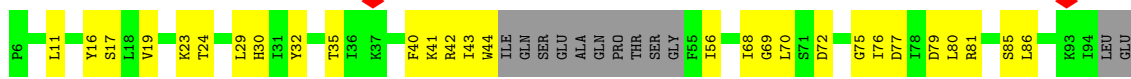
• Molecule 1: Gasdermin bGSDM, N-terminus

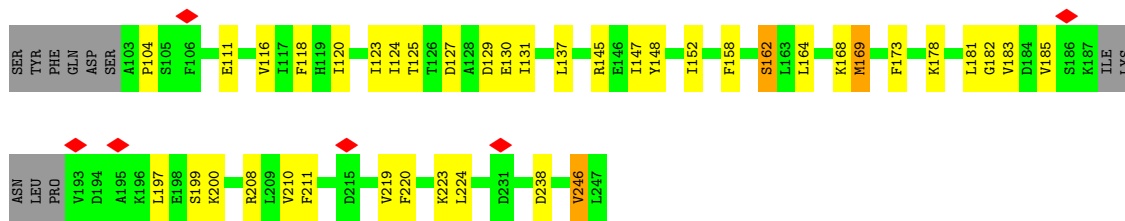


• Molecule 1: Gasdermin bGSDM, N-terminus

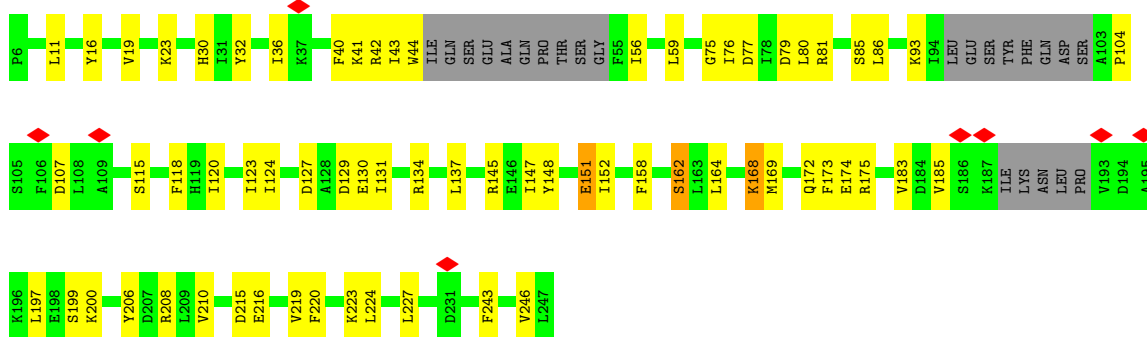


• Molecule 1: Gasdermin bGSDM, N-terminus

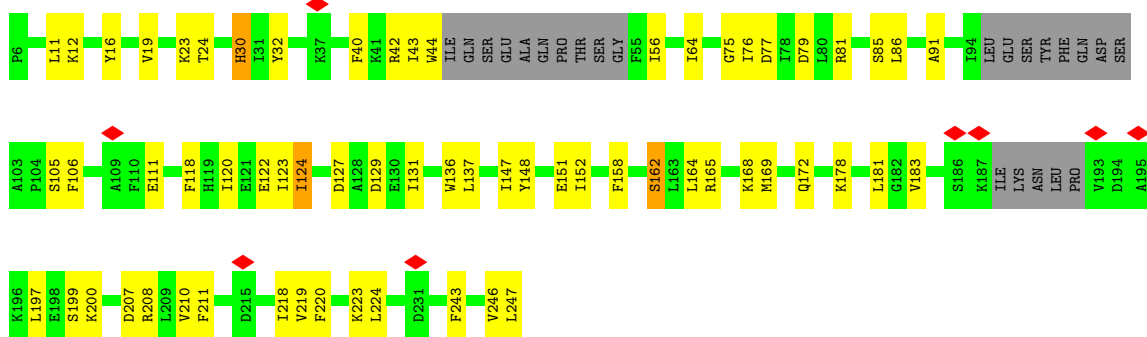




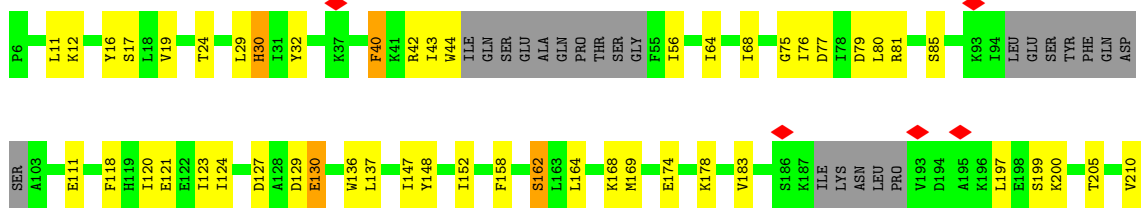
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus



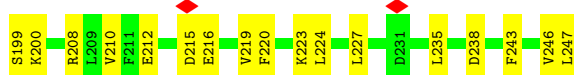
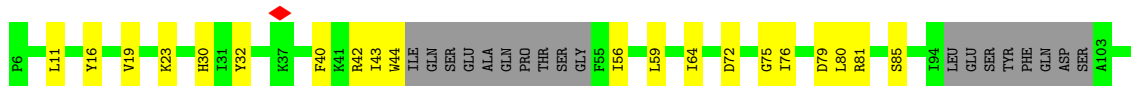
• Molecule 1: Gasdermin bGSDM, N-terminus





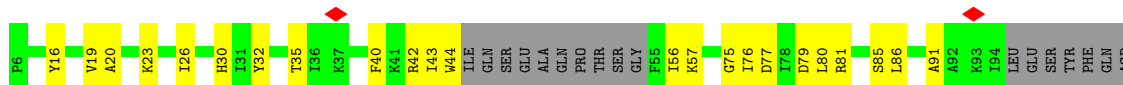
- Molecule 1: Gasdermin bGSDM, N-terminus

Chain AE: 63% 26% 10%



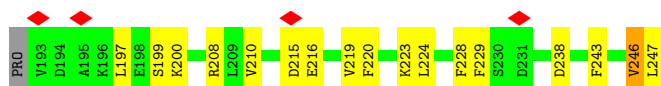
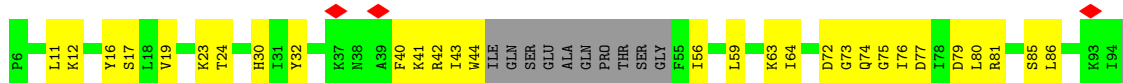
- Molecule 1: Gasdermin bGSDM, N-terminus

Chain AF: 64% 25% 10%

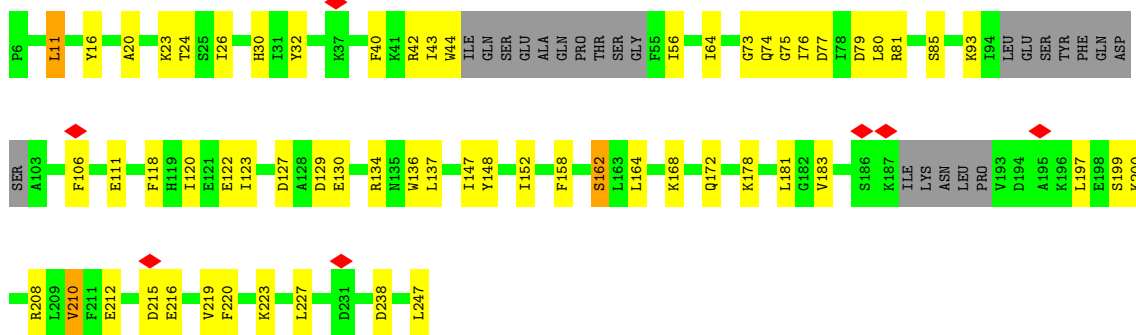


- Molecule 1: Gasdermin bGSDM, N-terminus

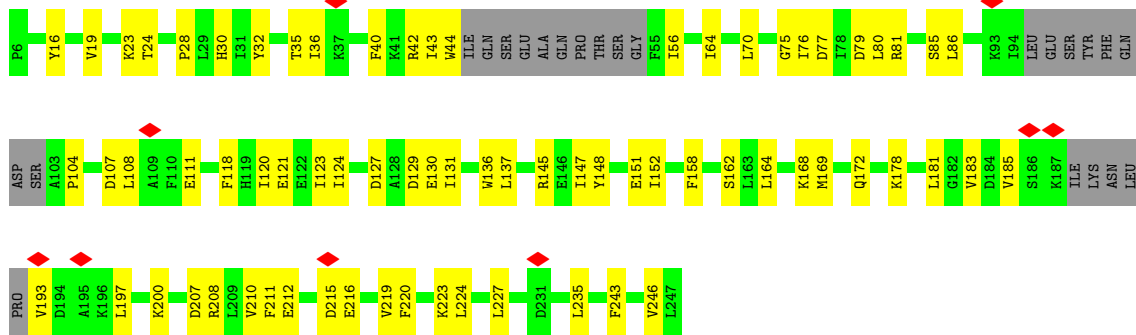
Chain AG: 62% 28% 10%



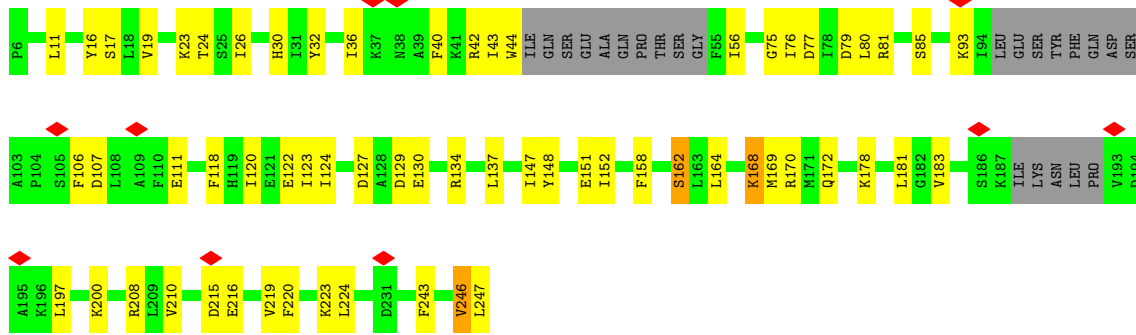
- Molecule 1: Gasdermin bGSDM, N-terminus



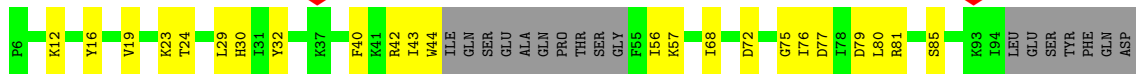
• Molecule 1: Gasdermin bGSDM, N-terminus

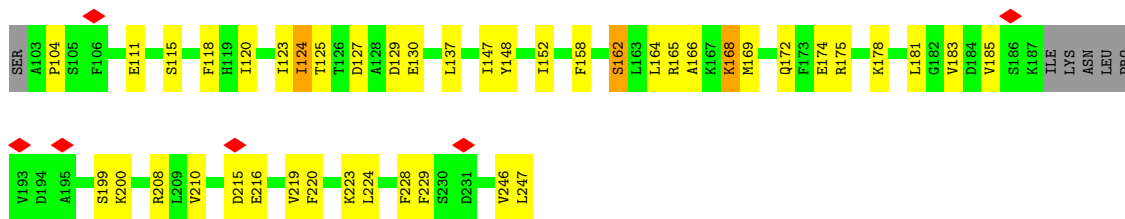


• Molecule 1: Gasdermin bGSDM, N-terminus

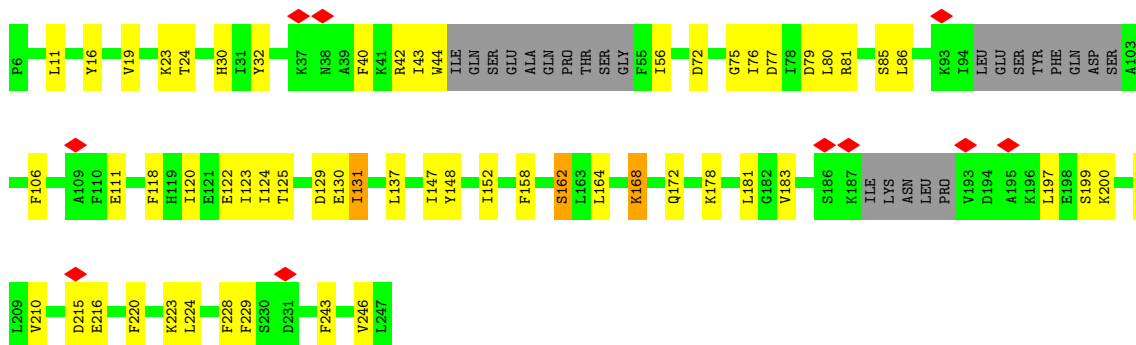


• Molecule 1: Gasdermin bGSDM, N-terminus

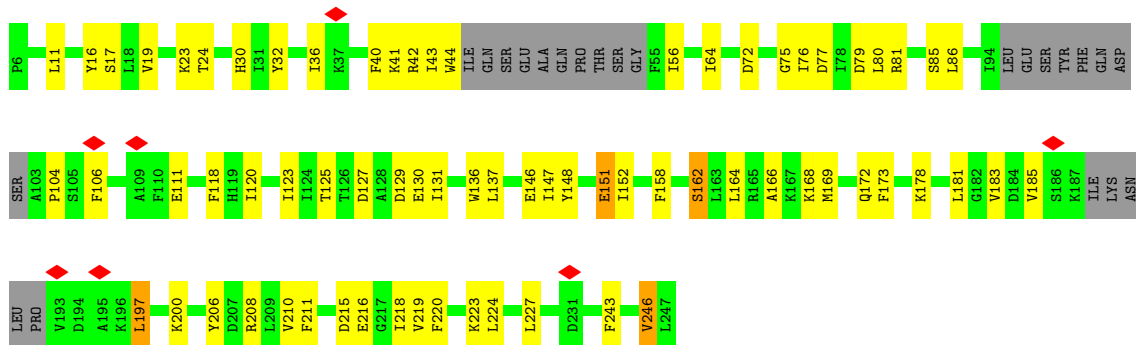




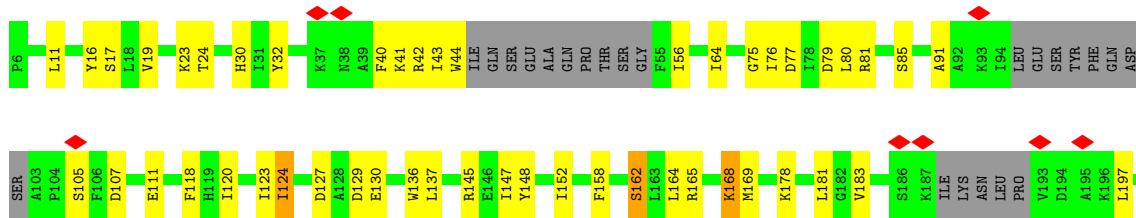
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus

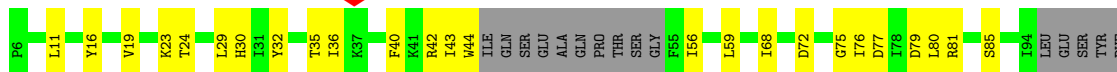


• Molecule 1: Gasdermin bGSDM, N-terminus

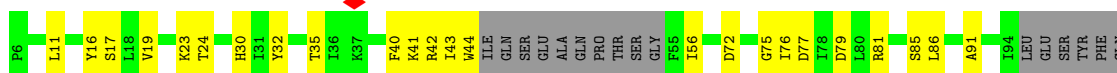




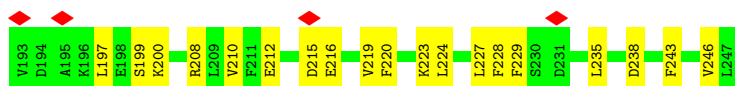
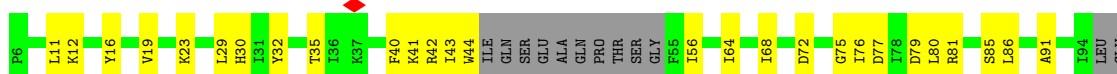
• Molecule 1: Gasdermin bGSDM, N-terminus



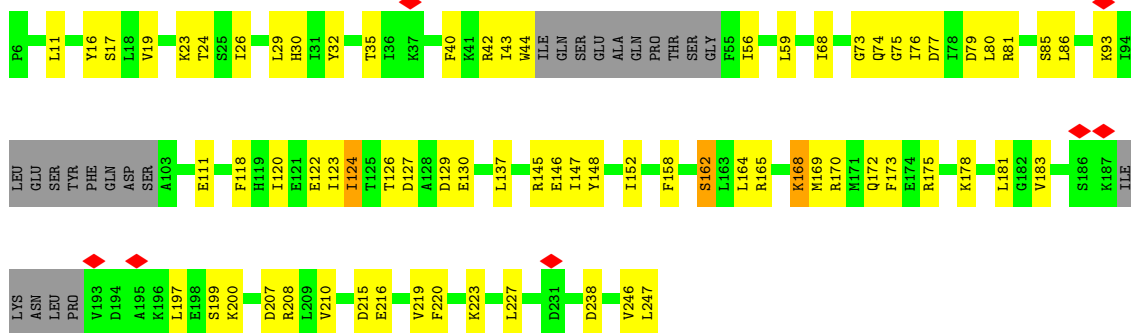
• Molecule 1: Gasdermin bGSDM, N-terminus



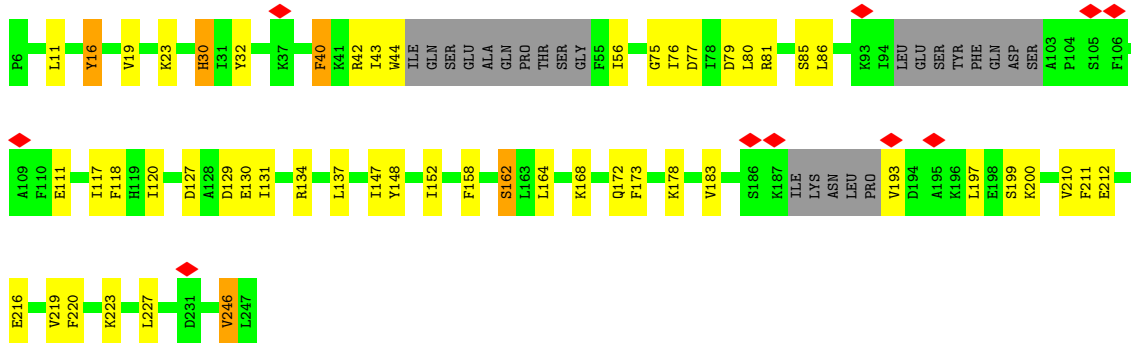
• Molecule 1: Gasdermin bGSDM, N-terminus



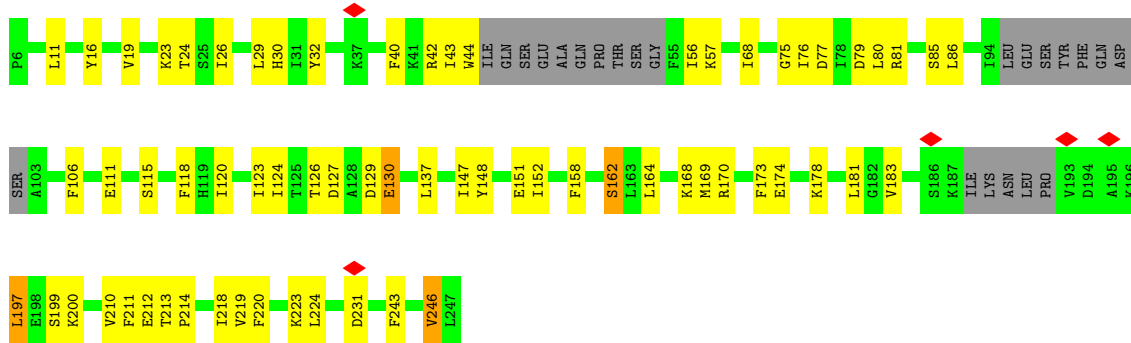
• Molecule 1: Gasdermin bGSDM, N-terminus



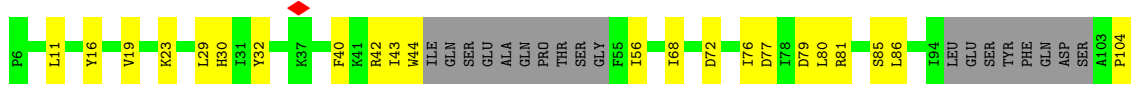
• Molecule 1: Gasdermin bGSDM, N-terminus

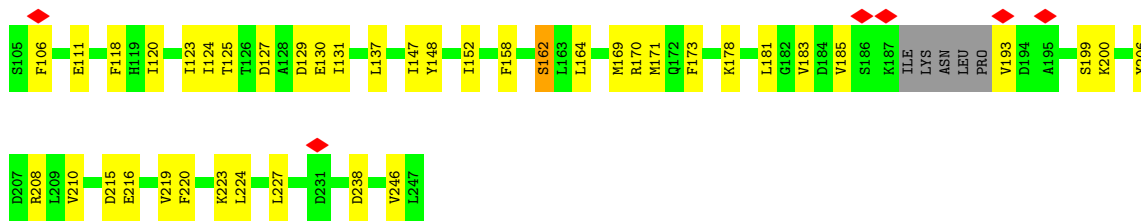


• Molecule 1: Gasdermin bGSDM, N-terminus

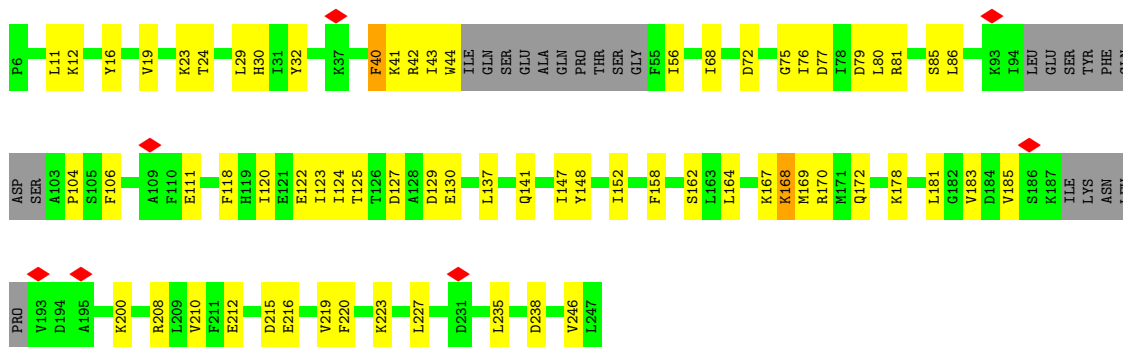


• Molecule 1: Gasdermin bGSDM, N-terminus

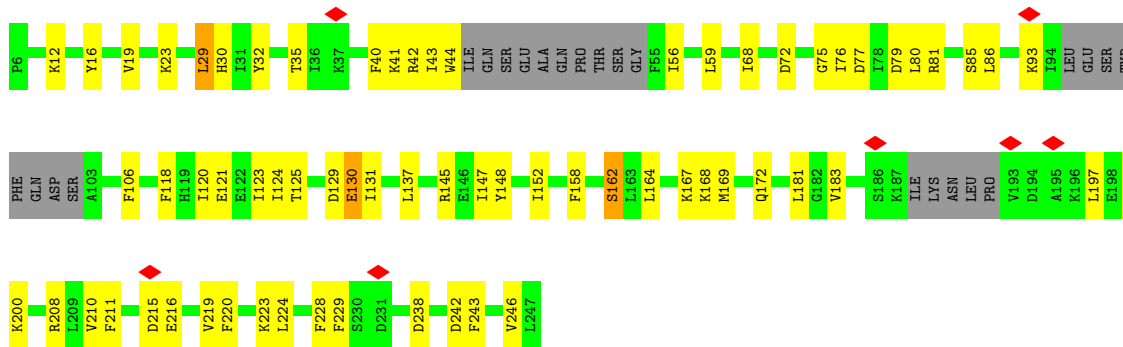




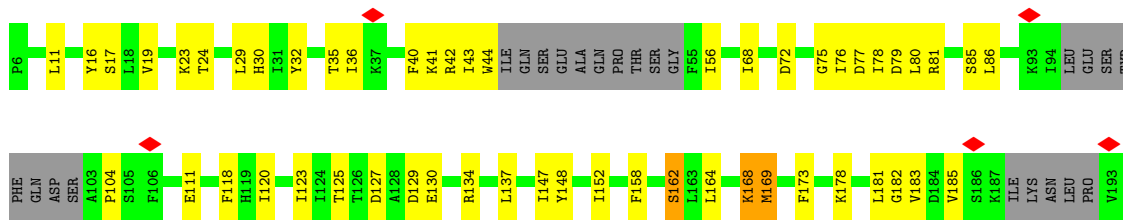
• Molecule 1: Gasdermin bGSDM, N-terminus

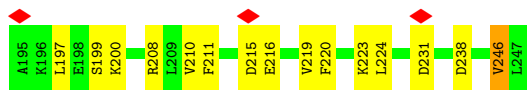


• Molecule 1: Gasdermin bGSDM, N-terminus

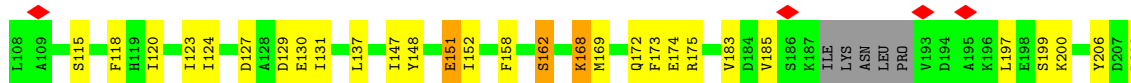
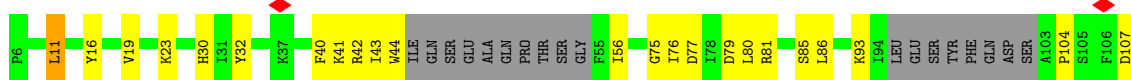


• Molecule 1: Gasdermin bGSDM, N-terminus

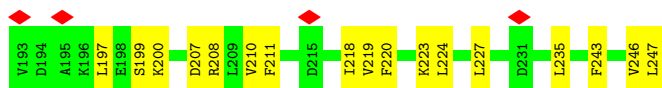
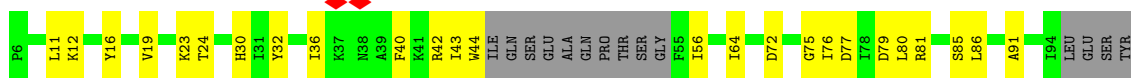




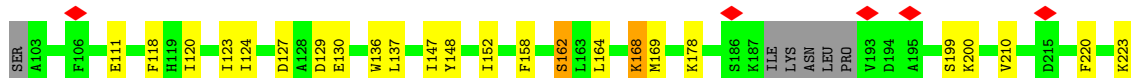
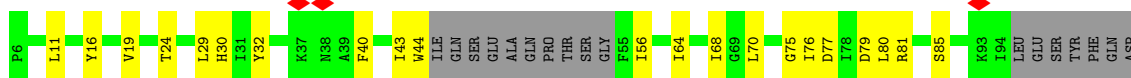
• Molecule 1: Gasdermin bGSDM, N-terminus



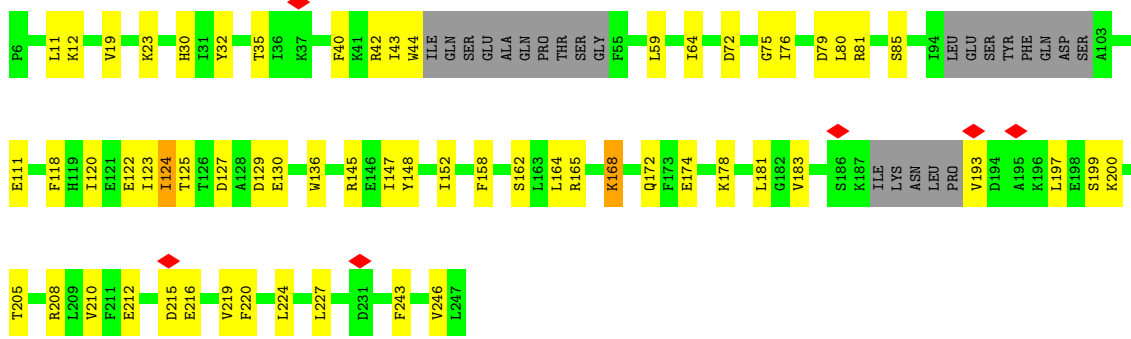
• Molecule 1: Gasdermin bGSDM, N-terminus



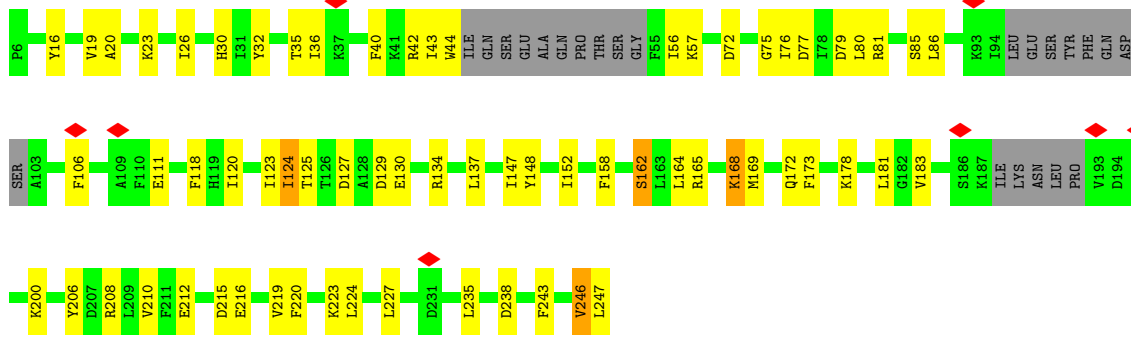
• Molecule 1: Gasdermin bGSDM, N-terminus



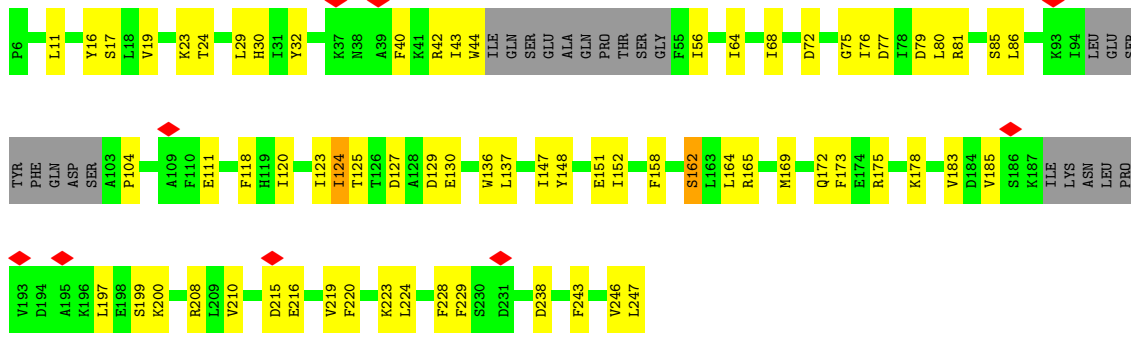
• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus



• Molecule 1: Gasdermin bGSDM, N-terminus



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	528881	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.897	Depositor
Minimum map value	-1.221	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.24	Depositor
Map size ( $\text{\AA}$ )	720.0, 720.0, 720.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.2, 1.2, 1.2	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0	0.26	0/1790	0.43	0/2400
1	1	0.26	0/1790	0.42	0/2400
1	2	0.26	0/1790	0.43	0/2400
1	3	0.26	0/1790	0.43	0/2400
1	4	0.26	0/1790	0.44	0/2400
1	5	0.25	0/1790	0.42	0/2400
1	6	0.25	0/1790	0.42	0/2400
1	7	0.26	0/1790	0.42	0/2400
1	8	0.26	0/1790	0.45	0/2400
1	9	0.26	0/1790	0.45	0/2400
1	A	0.25	0/1790	0.44	0/2400
1	AA	0.26	0/1790	0.44	0/2400
1	AB	0.26	0/1790	0.44	0/2400
1	AC	0.25	0/1790	0.42	0/2400
1	AD	0.25	0/1790	0.41	0/2400
1	AE	0.26	0/1790	0.43	0/2400
1	AF	0.26	0/1790	0.45	0/2400
1	AG	0.25	0/1790	0.43	0/2400
1	AH	0.26	0/1790	0.45	0/2400
1	AI	0.26	0/1790	0.43	0/2400
1	AJ	0.26	0/1790	0.46	0/2400
1	AK	0.26	0/1790	0.42	0/2400
1	AL	0.26	0/1790	0.46	0/2400
1	AM	0.25	0/1790	0.42	0/2400
1	AN	0.26	0/1790	0.44	0/2400
1	AO	0.26	0/1790	0.44	0/2400
1	AP	0.26	0/1790	0.43	0/2400
1	AQ	0.26	0/1790	0.44	0/2400
1	AR	0.25	0/1790	0.42	0/2400
1	AS	0.25	0/1790	0.43	0/2400
1	AT	0.25	0/1790	0.43	0/2400
1	AU	0.26	0/1790	0.44	0/2400
1	AV	0.26	0/1790	0.45	0/2400
1	AW	0.26	0/1790	0.43	0/2400

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	AX	0.26	0/1790	0.44	0/2400
1	AY	0.26	0/1790	0.43	0/2400
1	AZ	0.25	0/1790	0.42	0/2400
1	Aa	0.25	0/1790	0.42	0/2400
1	Ab	0.26	0/1790	0.43	0/2400
1	Ac	0.26	0/1790	0.45	0/2400
1	Ad	0.25	0/1790	0.43	0/2400
1	B	0.26	0/1790	0.44	0/2400
1	C	0.26	0/1790	0.43	0/2400
1	D	0.26	0/1790	0.41	0/2400
1	E	0.26	0/1790	0.44	0/2400
1	F	0.26	0/1790	0.42	0/2400
1	G	0.25	0/1790	0.41	0/2400
1	H	0.25	0/1790	0.40	0/2400
1	I	0.26	0/1790	0.43	0/2400
1	J	0.26	0/1790	0.42	0/2400
1	K	0.26	0/1790	0.43	0/2400
1	L	0.26	0/1790	0.43	0/2400
1	M	0.25	0/1790	0.42	0/2400
1	N	0.25	0/1790	0.42	0/2400
1	O	0.26	0/1790	0.45	0/2400
1	P	0.26	0/1790	0.44	0/2400
1	Q	0.25	0/1790	0.44	0/2400
1	R	0.26	0/1790	0.44	0/2400
1	S	0.26	0/1790	0.43	0/2400
1	T	0.25	0/1790	0.42	0/2400
1	U	0.26	0/1790	0.43	0/2400
1	V	0.26	0/1790	0.46	0/2400
1	W	0.26	0/1790	0.43	0/2400
1	X	0.25	0/1790	0.44	0/2400
1	Y	0.26	0/1790	0.43	0/2400
1	Z	0.26	0/1790	0.43	0/2400
1	a	0.26	0/1790	0.43	0/2400
1	b	0.26	0/1790	0.45	0/2400
1	c	0.26	0/1790	0.42	0/2400
1	d	0.25	0/1790	0.41	0/2400
1	e	0.25	0/1790	0.40	0/2400
1	f	0.26	0/1790	0.43	0/2400
1	g	0.26	0/1790	0.43	0/2400
1	h	0.25	0/1790	0.42	0/2400
1	i	0.26	0/1790	0.45	0/2400
1	j	0.25	0/1790	0.43	0/2400
1	k	0.25	0/1790	0.42	0/2400

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	l	0.27	0/1790	0.45	0/2400
1	m	0.26	0/1790	0.44	0/2400
1	n	0.25	0/1790	0.44	0/2400
1	o	0.26	0/1790	0.44	0/2400
1	p	0.26	0/1790	0.43	0/2400
1	q	0.26	0/1790	0.44	0/2400
1	r	0.26	0/1790	0.43	0/2400
1	s	0.26	0/1790	0.45	0/2400
1	t	0.26	0/1790	0.45	0/2400
1	u	0.26	0/1790	0.45	0/2400
1	v	0.26	0/1790	0.44	0/2400
1	w	0.26	0/1790	0.43	0/2400
1	x	0.26	0/1790	0.45	0/2400
1	y	0.26	0/1790	0.46	0/2400
1	z	0.25	0/1790	0.42	0/2400
All	All	0.26	0/164680	0.43	0/220800

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 [i](#)

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	0	1761	0	1790	56	0
1	1	1761	0	1790	49	0
1	2	1761	0	1790	61	0
1	3	1761	0	1790	47	0
1	4	1761	0	1790	60	0
1	5	1761	0	1790	60	0
1	6	1761	0	1790	51	0
1	7	1761	0	1790	56	0
1	8	1761	0	1790	61	0
1	9	1761	0	1790	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1761	0	1790	51	0
1	AA	1761	0	1790	51	0
1	AB	1761	0	1790	56	0
1	AC	1761	0	1790	49	0
1	AD	1761	0	1790	48	0
1	AE	1761	0	1790	53	0
1	AF	1761	0	1790	56	0
1	AG	1761	0	1790	58	0
1	AH	1761	0	1790	48	0
1	AI	1761	0	1790	58	0
1	AJ	1761	0	1790	56	0
1	AK	1761	0	1790	58	0
1	AL	1761	0	1790	51	0
1	AM	1761	0	1790	63	0
1	AN	1761	0	1790	49	0
1	AO	1761	0	1790	55	0
1	AP	1761	0	1790	51	0
1	AQ	1761	0	1790	56	0
1	AR	1761	0	1790	59	0
1	AS	1761	0	1790	52	0
1	AT	1761	0	1790	53	0
1	AU	1761	0	1790	53	0
1	AV	1761	0	1790	55	0
1	AW	1761	0	1790	52	0
1	AX	1761	0	1790	53	0
1	AY	1761	0	1790	52	0
1	AZ	1761	0	1790	54	0
1	Aa	1761	0	1790	40	0
1	Ab	1761	0	1790	52	0
1	Ac	1761	0	1790	56	0
1	Ad	1761	0	1790	56	0
1	B	1761	0	1790	52	0
1	C	1761	0	1790	51	0
1	D	1761	0	1790	49	0
1	E	1761	0	1790	57	0
1	F	1761	0	1790	55	0
1	G	1761	0	1790	42	0
1	H	1761	0	1790	50	0
1	I	1761	0	1790	54	0
1	J	1761	0	1790	55	0
1	K	1761	0	1790	54	0
1	L	1761	0	1790	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	M	1761	0	1790	53	0
1	N	1761	0	1790	55	0
1	O	1761	0	1790	55	0
1	P	1761	0	1790	57	0
1	Q	1761	0	1790	51	0
1	R	1761	0	1790	56	0
1	S	1761	0	1790	46	0
1	T	1761	0	1790	51	0
1	U	1761	0	1790	55	0
1	V	1761	0	1790	50	0
1	W	1761	0	1790	58	0
1	X	1761	0	1790	58	0
1	Y	1761	0	1790	53	0
1	Z	1761	0	1790	51	0
1	a	1761	0	1790	57	0
1	b	1761	0	1790	62	0
1	c	1761	0	1790	52	0
1	d	1761	0	1790	42	0
1	e	1761	0	1790	55	0
1	f	1761	0	1790	55	0
1	g	1761	0	1790	58	0
1	h	1761	0	1790	49	0
1	i	1761	0	1790	57	0
1	j	1761	0	1790	56	0
1	k	1761	0	1790	56	0
1	l	1761	0	1790	55	0
1	m	1761	0	1790	57	0
1	n	1761	0	1790	52	0
1	o	1761	0	1790	52	0
1	p	1761	0	1790	56	0
1	q	1761	0	1790	53	0
1	r	1761	0	1790	57	0
1	s	1761	0	1790	49	0
1	t	1761	0	1790	53	0
1	u	1761	0	1790	51	0
1	v	1761	0	1790	51	0
1	w	1761	0	1790	54	0
1	x	1761	0	1790	53	0
1	y	1761	0	1790	49	0
1	z	1761	0	1790	58	0
All	All	162012	0	164680	4331	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 13.

All (4331) 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)
1:4:79:ASP:HB3	1:4:81:ARG:HH22	1.21	1.05
1:I:79:ASP:HB3	1:I:81:ARG:HH22	1.25	1.01
1:F:120:ILE:HG22	1:F:123:ILE:HD11	1.44	1.00
1:AW:79:ASP:HB3	1:AW:81:ARG:HH22	1.24	0.99
1:AH:79:ASP:HB3	1:AH:81:ARG:HH22	1.25	0.99
1:Ac:120:ILE:HG22	1:Ac:123:ILE:HD11	1.44	0.99
1:f:79:ASP:HB3	1:f:81:ARG:HH22	1.25	0.98
1:AO:120:ILE:HG22	1:AO:123:ILE:HD11	1.47	0.97
1:c:120:ILE:HG22	1:c:123:ILE:HD11	1.44	0.97
1:G:79:ASP:HB3	1:G:81:ARG:HH22	1.29	0.96
1:i:120:ILE:HG22	1:i:123:ILE:HD11	1.48	0.96
1:AF:120:ILE:HG22	1:AF:123:ILE:HD11	1.44	0.96
1:d:79:ASP:HB3	1:d:81:ARG:HH22	1.29	0.96
1:Aa:79:ASP:HB3	1:Aa:81:ARG:HH22	1.29	0.96
1:L:120:ILE:HG22	1:L:123:ILE:HD11	1.48	0.92
1:H:120:ILE:HG22	1:H:123:ILE:HD11	1.50	0.92
1:Ab:120:ILE:HG22	1:Ab:123:ILE:HD11	1.52	0.91
1:J:81:ARG:HB2	1:J:116:VAL:HB	1.53	0.90
1:AE:120:ILE:HG22	1:AE:123:ILE:HD11	1.54	0.90
1:AZ:120:ILE:HG22	1:AZ:123:ILE:HD11	1.52	0.90
1:Z:120:ILE:HG22	1:Z:123:ILE:HD11	1.55	0.89
1:e:120:ILE:HG22	1:e:123:ILE:HD11	1.53	0.89
1:Y:120:ILE:HG22	1:Y:123:ILE:HD11	1.55	0.89
1:B:120:ILE:HG22	1:B:123:ILE:HD11	1.55	0.89
1:9:120:ILE:HG22	1:9:123:ILE:HD11	1.55	0.89
1:AC:120:ILE:HG22	1:AC:123:ILE:HD11	1.53	0.89
1:AV:120:ILE:HG22	1:AV:123:ILE:HD11	1.55	0.89
1:C:120:ILE:HG22	1:C:123:ILE:HD11	1.54	0.88
1:AE:152:ILE:HD12	1:AE:227:LEU:HD22	1.53	0.88
1:AQ:79:ASP:HB3	1:AQ:81:ARG:HH22	1.40	0.87
1:D:79:ASP:HB3	1:D:81:ARG:HH12	1.42	0.85
1:8:79:ASP:HB3	1:8:81:ARG:HH12	1.42	0.85
1:w:79:ASP:HB3	1:w:81:ARG:HH12	1.42	0.84
1:2:120:ILE:HG22	1:2:123:ILE:HD11	1.58	0.84
1:AJ:79:ASP:HB3	1:AJ:81:ARG:HH12	1.42	0.84
1:C:152:ILE:HD12	1:C:227:LEU:HD22	1.59	0.84
1:Ab:152:ILE:HD12	1:Ab:227:LEU:HD22	1.59	0.84
1:Z:152:ILE:HD12	1:Z:227:LEU:HD22	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:120:ILE:HG22	1:AD:123:ILE:HD11	1.60	0.83
1:k:79:ASP:HB3	1:k:81:ARG:HH12	1.44	0.82
1:5:79:ASP:HB3	1:5:81:ARG:HH12	1.44	0.82
1:AY:79:ASP:HB3	1:AY:81:ARG:HH12	1.43	0.82
1:AR:79:ASP:HB3	1:AR:81:ARG:HH12	1.44	0.82
1:L:79:ASP:HB3	1:L:81:ARG:HH12	1.45	0.82
1:i:79:ASP:HB3	1:i:81:ARG:HH12	1.45	0.81
1:AB:79:ASP:HB3	1:AB:81:ARG:HH12	1.45	0.81
1:t:120:ILE:HG22	1:t:123:ILE:HD11	1.61	0.81
1:2:79:ASP:HB3	1:2:81:ARG:HH12	1.45	0.81
1:AO:79:ASP:HB3	1:AO:81:ARG:HH12	1.45	0.81
1:N:79:ASP:HB3	1:N:81:ARG:HH12	1.44	0.81
1:AU:79:ASP:HB3	1:AU:81:ARG:HH12	1.45	0.81
1:p:129:ASP:HA	1:q:44:TRP:HB2	1.63	0.81
1:AM:44:TRP:HB2	1:AN:129:ASP:HA	1.63	0.81
1:X:129:ASP:HA	1:f:44:TRP:HB2	1.63	0.81
1:AK:79:ASP:HB3	1:AK:81:ARG:HH12	1.46	0.81
1:g:79:ASP:HB3	1:g:81:ARG:HH12	1.45	0.81
1:O:120:ILE:HG22	1:O:123:ILE:HD11	1.61	0.81
1:U:129:ASP:HA	1:l:44:TRP:HB2	1.61	0.81
1:AW:44:TRP:HB2	1:AX:129:ASP:HA	1.63	0.81
1:o:79:ASP:HB3	1:o:81:ARG:HH12	1.45	0.80
1:G:120:ILE:HG22	1:G:123:ILE:HD11	1.62	0.80
1:n:79:ASP:HB3	1:n:81:ARG:HH12	1.45	0.80
1:l:120:ILE:HG22	1:l:123:ILE:HD11	1.61	0.80
1:a:79:ASP:HB3	1:a:81:ARG:HH12	1.46	0.80
1:d:120:ILE:HG22	1:d:123:ILE:HD11	1.63	0.80
1:u:120:ILE:HG22	1:u:123:ILE:HD11	1.62	0.80
1:7:23:LYS:HE3	1:7:42:ARG:HH21	1.46	0.80
1:AA:79:ASP:HB3	1:AA:81:ARG:HH12	1.47	0.80
1:Aa:120:ILE:HG22	1:Aa:123:ILE:HD11	1.62	0.80
1:AS:79:ASP:HB3	1:AS:81:ARG:HH12	1.46	0.79
1:v:79:ASP:HB3	1:v:81:ARG:HH12	1.45	0.79
1:AH:120:ILE:HG22	1:AH:123:ILE:HD11	1.62	0.79
1:AW:172:GLN:HG2	1:AW:208:ARG:HG3	1.64	0.79
1:R:79:ASP:HB3	1:R:81:ARG:HH12	1.47	0.79
1:W:79:ASP:HB3	1:W:81:ARG:HH12	1.46	0.79
1:AI:79:ASP:HB3	1:AI:81:ARG:HH12	1.45	0.79
1:AN:79:ASP:HB3	1:AN:81:ARG:HH12	1.48	0.79
1:W:120:ILE:HG22	1:W:123:ILE:HD11	1.63	0.79
1:p:79:ASP:HB3	1:p:81:ARG:HH12	1.48	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:9:152:ILE:HD12	1:9:227:LEU:HD22	1.65	0.79
1:AM:79:ASP:HB3	1:AM:81:ARG:HH12	1.48	0.79
1:3:79:ASP:HB3	1:3:81:ARG:HH12	1.47	0.79
1:c:44:TRP:HB2	1:d:129:ASP:HA	1.64	0.79
1:8:44:TRP:HB2	1:0:129:ASP:HA	1.64	0.79
1:U:79:ASP:HB3	1:U:81:ARG:HH12	1.46	0.78
1:q:79:ASP:HB3	1:q:81:ARG:HH12	1.48	0.78
1:u:79:ASP:HB3	1:u:81:ARG:HH12	1.47	0.78
1:AK:120:ILE:HG22	1:AK:123:ILE:HD11	1.63	0.78
1:7:79:ASP:HB3	1:7:81:ARG:HH12	1.47	0.78
1:B:152:ILE:HD12	1:B:227:LEU:HD22	1.66	0.78
1:K:79:ASP:HB3	1:K:81:ARG:HH12	1.47	0.78
1:r:79:ASP:HB3	1:r:81:ARG:HH12	1.46	0.78
1:5:23:LYS:HE3	1:5:42:ARG:HH21	1.46	0.78
1:Ac:79:ASP:HB3	1:Ac:81:ARG:HH12	1.47	0.78
1:I:129:ASP:HA	1:J:44:TRP:HB2	1.65	0.78
1:Y:152:ILE:HD12	1:Y:227:LEU:HD22	1.65	0.78
1:P:79:ASP:HB3	1:P:81:ARG:HH12	1.46	0.78
1:1:79:ASP:HB3	1:1:81:ARG:HH12	1.47	0.78
1:AT:79:ASP:HB3	1:AT:81:ARG:HH12	1.47	0.78
1:AF:79:ASP:HB3	1:AF:81:ARG:HH12	1.47	0.78
1:AT:23:LYS:HE3	1:AT:42:ARG:HH21	1.47	0.78
1:O:44:TRP:HB2	1:r:129:ASP:HA	1.65	0.78
1:T:79:ASP:HB3	1:T:81:ARG:HH12	1.48	0.78
1:Ab:79:ASP:HB3	1:Ab:81:ARG:HH12	1.47	0.78
1:AP:129:ASP:HA	1:AQ:44:TRP:HB2	1.66	0.77
1:A:129:ASP:HA	1:I:44:TRP:HB2	1.65	0.77
1:F:79:ASP:HB3	1:F:81:ARG:HH12	1.48	0.77
1:K:23:LYS:HE3	1:K:42:ARG:HH21	1.49	0.77
1:S:79:ASP:HB3	1:S:81:ARG:HH12	1.48	0.77
1:h:23:LYS:HE3	1:h:42:ARG:HH21	1.47	0.77
1:6:79:ASP:HB3	1:6:81:ARG:HH12	1.48	0.77
1:z:79:ASP:HB3	1:z:81:ARG:HH12	1.48	0.77
1:AV:152:ILE:HD12	1:AV:227:LEU:HD22	1.67	0.77
1:z:44:TRP:HB2	1:1:129:ASP:HA	1.66	0.77
1:h:79:ASP:HB3	1:h:81:ARG:HH12	1.47	0.77
1:f:129:ASP:HA	1:g:44:TRP:HB2	1.64	0.77
1:m:44:TRP:HB2	1:n:129:ASP:HA	1.66	0.77
1:c:79:ASP:HB3	1:c:81:ARG:HH12	1.48	0.77
1:AS:152:ILE:HD12	1:AS:227:LEU:HD22	1.67	0.77
1:S:129:ASP:HA	1:T:44:TRP:HB2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:79:ASP:HB3	1:M:81:ARG:HH12	1.50	0.77
1:v:44:TRP:HB2	1:w:129:ASP:HA	1.65	0.77
1:AU:120:ILE:HG22	1:AU:123:ILE:HD11	1.67	0.77
1:Ad:79:ASP:HB3	1:Ad:81:ARG:HH12	1.50	0.76
1:k:23:LYS:HE3	1:k:42:ARG:HH21	1.51	0.76
1:u:44:TRP:HB2	1:v:129:ASP:HA	1.66	0.76
1:j:79:ASP:HB3	1:j:81:ARG:HH12	1.49	0.76
1:AI:44:TRP:HB2	1:AJ:129:ASP:HA	1.67	0.76
1:4:129:ASP:HA	1:5:44:TRP:HB2	1.68	0.76
1:Q:81:ARG:HB2	1:Q:116:VAL:HB	1.67	0.76
1:AU:44:TRP:HB2	1:AW:129:ASP:HA	1.65	0.76
1:M:152:ILE:HD12	1:M:227:LEU:HD22	1.68	0.75
1:N:44:TRP:HB2	1:P:129:ASP:HA	1.68	0.75
1:s:40:PHE:HZ	1:s:158:PHE:HB2	1.51	0.75
1:k:44:TRP:HB2	1:m:129:ASP:HA	1.69	0.75
1:3:129:ASP:HA	1:4:44:TRP:HB2	1.66	0.75
1:D:44:TRP:HB2	1:E:129:ASP:HA	1.67	0.75
1:E:79:ASP:HB3	1:E:81:ARG:HH12	1.51	0.75
1:1:44:TRP:HB2	1:2:129:ASP:HA	1.67	0.75
1:N:23:LYS:HE3	1:N:42:ARG:HH21	1.51	0.75
1:h:129:ASP:HA	1:i:44:TRP:HB2	1.69	0.75
1:0:44:TRP:HB2	1:AA:129:ASP:HA	1.69	0.75
1:H:81:ARG:HB3	1:H:116:VAL:HB	1.69	0.75
1:P:44:TRP:HB2	1:Q:129:ASP:HA	1.69	0.75
1:8:172:GLN:HG2	1:8:208:ARG:HG3	1.69	0.75
1:Z:79:ASP:HB3	1:Z:81:ARG:HH12	1.50	0.74
1:AC:79:ASP:HB3	1:AC:81:ARG:HH22	1.52	0.74
1:AY:44:TRP:HB2	1:Ad:129:ASP:HA	1.68	0.74
1:Z:40:PHE:HZ	1:Z:158:PHE:HB2	1.52	0.74
1:AB:44:TRP:HB2	1:AG:129:ASP:HA	1.68	0.74
1:C:172:GLN:HG2	1:C:208:ARG:HG3	1.69	0.74
1:AG:79:ASP:HB3	1:AG:81:ARG:HH12	1.50	0.74
1:C:40:PHE:HZ	1:C:158:PHE:HB2	1.53	0.74
1:a:40:PHE:HZ	1:a:158:PHE:HB2	1.53	0.74
1:2:44:TRP:HB2	1:7:129:ASP:HA	1.69	0.74
1:AX:79:ASP:HB3	1:AX:81:ARG:HH12	1.53	0.74
1:e:79:ASP:HB3	1:e:81:ARG:HH12	1.51	0.74
1:x:44:TRP:HB2	1:y:129:ASP:HA	1.69	0.74
1:AR:23:LYS:HE3	1:AR:42:ARG:HH21	1.51	0.74
1:D:40:PHE:HZ	1:D:158:PHE:HB2	1.53	0.74
1:AD:79:ASP:HB3	1:AD:81:ARG:HH12	1.53	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:44:TRP:HB2	1:AI:129:ASP:HA	1.69	0.74
1:E:44:TRP:HB2	1:F:129:ASP:HA	1.70	0.74
1:K:129:ASP:HA	1:L:44:TRP:HB2	1.69	0.74
1:AZ:79:ASP:HB3	1:AZ:81:ARG:HH22	1.52	0.74
1:b:79:ASP:HB3	1:b:81:ARG:HH12	1.51	0.74
1:l:40:PHE:HZ	1:l:158:PHE:HB2	1.53	0.74
1:Ac:129:ASP:HA	1:Ad:44:TRP:HB2	1.71	0.73
1:AO:44:TRP:HB2	1:AT:129:ASP:HA	1.70	0.73
1:Ab:40:PHE:HZ	1:Ab:158:PHE:HB2	1.54	0.73
1:G:44:TRP:HB2	1:H:129:ASP:HA	1.69	0.73
1:AQ:129:ASP:HA	1:AR:44:TRP:HB2	1.71	0.73
1:V:129:ASP:HA	1:W:44:TRP:HB2	1.69	0.73
1:j:152:ILE:HD12	1:j:227:LEU:HD22	1.71	0.73
1:s:129:ASP:HA	1:t:44:TRP:HB2	1.69	0.73
1:F:44:TRP:HB2	1:G:129:ASP:HA	1.70	0.73
1:e:40:PHE:HZ	1:e:158:PHE:HB2	1.54	0.73
1:AD:129:ASP:HA	1:AF:44:TRP:HB2	1.69	0.73
1:AK:44:TRP:HB2	1:AL:129:ASP:HA	1.70	0.73
1:AS:129:ASP:HA	1:AZ:44:TRP:HB2	1.71	0.73
1:AZ:40:PHE:HZ	1:AZ:158:PHE:HB2	1.53	0.73
1:L:129:ASP:HA	1:S:44:TRP:HB2	1.71	0.73
1:H:40:PHE:HZ	1:H:158:PHE:HB2	1.53	0.73
1:AC:40:PHE:HZ	1:AC:158:PHE:HB2	1.53	0.73
1:AY:40:PHE:HZ	1:AY:158:PHE:HB2	1.54	0.73
1:A:79:ASP:HB3	1:A:81:ARG:HH12	1.54	0.73
1:X:44:TRP:HB2	1:Y:129:ASP:HA	1.70	0.72
1:AM:40:PHE:HZ	1:AM:158:PHE:HB2	1.54	0.72
1:H:44:TRP:HB2	1:M:129:ASP:HA	1.72	0.72
1:a:43:ILE:HB	1:b:130:GLU:HB2	1.71	0.72
1:i:129:ASP:HA	1:p:44:TRP:HB2	1.72	0.72
1:AF:40:PHE:HZ	1:AF:158:PHE:HB2	1.54	0.72
1:AN:44:TRP:HB2	1:AO:129:ASP:HA	1.71	0.72
1:AQ:19:VAL:HA	1:AQ:246:VAL:HG23	1.71	0.72
1:P:40:PHE:HZ	1:P:158:PHE:HB2	1.55	0.72
1:P:19:VAL:HA	1:P:246:VAL:HG23	1.71	0.72
1:V:40:PHE:HZ	1:V:158:PHE:HB2	1.54	0.72
1:m:19:VAL:HA	1:m:246:VAL:HG23	1.72	0.72
1:6:152:ILE:HD12	1:6:227:LEU:HD22	1.72	0.72
1:AQ:40:PHE:HZ	1:AQ:158:PHE:HB2	1.55	0.72
1:4:19:VAL:HA	1:4:246:VAL:HG23	1.71	0.72
1:AE:40:PHE:HZ	1:AE:158:PHE:HB2	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:81:ARG:HB2	1:AP:116:VAL:HB	1.72	0.72
1:o:44:TRP:HB2	1:t:129:ASP:HA	1.70	0.72
1:X:79:ASP:HB3	1:X:81:ARG:HH12	1.54	0.71
1:Z:44:TRP:HB2	1:a:129:ASP:HA	1.72	0.71
1:AJ:44:TRP:HB2	1:AK:129:ASP:HA	1.70	0.71
1:d:44:TRP:HB2	1:e:129:ASP:HA	1.71	0.71
1:i:120:ILE:HD12	1:i:169:MET:HG2	1.71	0.71
1:AB:129:ASP:HA	1:AE:44:TRP:HB2	1.71	0.71
1:a:172:GLN:HG2	1:a:208:ARG:HG3	1.73	0.71
1:w:44:TRP:HB2	1:x:129:ASP:HA	1.70	0.71
1:y:44:TRP:HB2	1:z:129:ASP:HA	1.71	0.71
1:AC:129:ASP:HA	1:AD:44:TRP:HB2	1.71	0.71
1:S:40:PHE:HZ	1:S:158:PHE:HB2	1.56	0.71
1:AC:19:VAL:HA	1:AC:246:VAL:HG23	1.73	0.71
1:AR:19:VAL:HA	1:AR:246:VAL:HG23	1.73	0.71
1:O:40:PHE:HZ	1:O:158:PHE:HB2	1.55	0.71
1:R:129:ASP:HA	1:U:44:TRP:HB2	1.71	0.71
1:g:120:ILE:HG22	1:g:123:ILE:HD11	1.72	0.71
1:z:40:PHE:HZ	1:z:158:PHE:HB2	1.55	0.71
1:Aa:129:ASP:HA	1:Ac:44:TRP:HB2	1.72	0.71
1:e:19:VAL:HA	1:e:246:VAL:HG23	1.73	0.71
1:e:44:TRP:HB2	1:j:129:ASP:HA	1.72	0.71
1:6:129:ASP:HA	1:AC:44:TRP:HB2	1.72	0.71
1:AV:129:ASP:HA	1:AX:44:TRP:HB2	1.71	0.71
1:AE:79:ASP:HB3	1:AE:81:ARG:HH12	1.56	0.71
1:J:120:ILE:HG22	1:J:123:ILE:HD11	1.73	0.71
1:p:40:PHE:HZ	1:p:158:PHE:HB2	1.56	0.71
1:AB:40:PHE:HZ	1:AB:158:PHE:HB2	1.55	0.71
1:AF:129:ASP:HA	1:AG:44:TRP:HB2	1.72	0.71
1:9:129:ASP:HA	1:AA:44:TRP:HB2	1.71	0.70
1:J:40:PHE:HZ	1:J:158:PHE:HB2	1.56	0.70
1:L:120:ILE:HD12	1:L:169:MET:HG2	1.72	0.70
1:AI:19:VAL:HA	1:AI:246:VAL:HG23	1.74	0.70
1:AZ:19:VAL:HA	1:AZ:246:VAL:HG23	1.73	0.70
1:f:40:PHE:HZ	1:f:158:PHE:HB2	1.56	0.70
1:g:40:PHE:HZ	1:g:158:PHE:HB2	1.55	0.70
1:C:79:ASP:HB3	1:C:81:ARG:HH12	1.57	0.70
1:o:129:ASP:HA	1:r:44:TRP:HB2	1.71	0.70
1:8:40:PHE:HZ	1:8:158:PHE:HB2	1.57	0.70
1:x:120:ILE:HG22	1:x:123:ILE:HD11	1.74	0.70
1:AV:172:GLN:HG2	1:AV:208:ARG:HG3	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:m:40:PHE:HZ	1:m:158:PHE:HB2	1.57	0.70
1:4:40:PHE:HZ	1:4:158:PHE:HB2	1.57	0.70
1:H:19:VAL:HA	1:H:246:VAL:HG23	1.73	0.70
1:R:44:TRP:HB2	1:W:129:ASP:HA	1.72	0.70
1:l:129:ASP:HA	1:n:44:TRP:HB2	1.72	0.70
1:AY:129:ASP:HA	1:Ab:44:TRP:HB2	1.74	0.70
1:A:44:TRP:HB2	1:B:129:ASP:HA	1.73	0.70
1:8:120:ILE:HG22	1:8:123:ILE:HD11	1.74	0.70
1:AW:40:PHE:HZ	1:AW:158:PHE:HB2	1.57	0.70
1:9:172:GLN:HG2	1:9:208:ARG:HG3	1.74	0.69
1:I:40:PHE:HZ	1:I:158:PHE:HB2	1.56	0.69
1:b:44:TRP:HB2	1:c:129:ASP:HA	1.73	0.69
1:5:19:VAL:HA	1:5:246:VAL:HG23	1.73	0.69
1:AL:44:TRP:HB2	1:AM:129:ASP:HA	1.72	0.69
1:U:19:VAL:HA	1:U:246:VAL:HG23	1.74	0.69
1:u:40:PHE:HZ	1:u:158:PHE:HB2	1.57	0.69
1:Ac:40:PHE:HZ	1:Ac:158:PHE:HB2	1.58	0.69
1:C:44:TRP:HB2	1:D:129:ASP:HA	1.75	0.69
1:b:19:VAL:HA	1:b:246:VAL:HG23	1.74	0.69
1:0:40:PHE:HZ	1:0:158:PHE:HB2	1.56	0.69
1:N:19:VAL:HA	1:N:246:VAL:HG23	1.75	0.69
1:AG:19:VAL:HA	1:AG:246:VAL:HG23	1.74	0.69
1:f:19:VAL:HA	1:f:246:VAL:HG23	1.75	0.69
1:v:19:VAL:HA	1:v:246:VAL:HG23	1.75	0.69
1:AH:129:ASP:HA	1:AP:44:TRP:HB2	1.73	0.69
1:Aa:130:GLU:HB2	1:Ac:43:ILE:HB	1.75	0.69
1:E:19:VAL:HA	1:E:246:VAL:HG23	1.74	0.69
1:j:44:TRP:HB2	1:k:129:ASP:HA	1.73	0.69
1:q:129:ASP:HA	1:s:44:TRP:HB2	1.73	0.69
1:q:152:ILE:HD12	1:q:227:LEU:HD22	1.75	0.69
1:AW:19:VAL:HA	1:AW:246:VAL:HG23	1.74	0.68
1:x:81:ARG:HB2	1:x:116:VAL:HB	1.75	0.68
1:AM:152:ILE:HD12	1:AM:227:LEU:HD22	1.75	0.68
1:Aa:40:PHE:HZ	1:Aa:158:PHE:HB2	1.58	0.68
1:I:19:VAL:HA	1:I:246:VAL:HG23	1.75	0.68
1:7:120:ILE:HG22	1:7:123:ILE:HD11	1.76	0.68
1:Ad:19:VAL:HA	1:Ad:246:VAL:HG23	1.74	0.68
1:B:19:VAL:HA	1:B:246:VAL:HG23	1.74	0.68
1:r:19:VAL:HA	1:r:246:VAL:HG23	1.74	0.68
1:m:32:TYR:HB3	1:m:40:PHE:CE1	2.28	0.68
1:5:129:ASP:HA	1:6:44:TRP:HB2	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:19:VAL:HA	1:0:246:VAL:HG23	1.74	0.68
1:U:40:PHE:HZ	1:U:158:PHE:HB2	1.59	0.68
1:AP:40:PHE:HZ	1:AP:158:PHE:HB2	1.58	0.68
1:K:120:ILE:HG22	1:K:123:ILE:HD11	1.76	0.68
1:S:19:VAL:HA	1:S:246:VAL:HG23	1.76	0.68
1:k:19:VAL:HA	1:k:246:VAL:HG23	1.75	0.68
1:z:152:ILE:HD12	1:z:227:LEU:HD22	1.75	0.68
1:AN:40:PHE:HZ	1:AN:158:PHE:HB2	1.58	0.68
1:F:40:PHE:HZ	1:F:158:PHE:HB2	1.59	0.68
1:1:40:PHE:HZ	1:1:158:PHE:HB2	1.59	0.68
1:AD:120:ILE:HD12	1:AD:169:MET:HG2	1.76	0.68
1:O:129:ASP:HA	1:Q:44:TRP:HB2	1.74	0.67
1:T:129:ASP:HA	1:V:44:TRP:HB2	1.74	0.67
1:u:129:ASP:HA	1:3:44:TRP:HB2	1.75	0.67
1:Y:19:VAL:HA	1:Y:246:VAL:HG23	1.74	0.67
1:y:19:VAL:HA	1:y:246:VAL:HG23	1.77	0.67
1:AY:19:VAL:HA	1:AY:246:VAL:HG23	1.77	0.67
1:T:79:ASP:HB2	1:T:118:PHE:HB3	1.76	0.67
1:P:32:TYR:HB3	1:P:40:PHE:CE1	2.30	0.67
1:Q:172:GLN:HG2	1:Q:208:ARG:HG3	1.76	0.67
1:p:19:VAL:HA	1:p:246:VAL:HG23	1.76	0.67
1:AQ:32:TYR:HB3	1:AQ:40:PHE:CE1	2.30	0.67
1:h:120:ILE:HG22	1:h:123:ILE:HD11	1.75	0.67
1:AZ:129:ASP:HA	1:Aa:44:TRP:HB2	1.74	0.67
1:D:19:VAL:HA	1:D:246:VAL:HG23	1.77	0.67
1:M:44:TRP:HB2	1:N:129:ASP:HA	1.76	0.67
1:g:129:ASP:HA	1:h:44:TRP:HB2	1.75	0.67
1:o:19:VAL:HA	1:o:246:VAL:HG23	1.77	0.67
1:1:19:VAL:HA	1:1:246:VAL:HG23	1.77	0.67
1:3:40:PHE:HZ	1:3:158:PHE:HB2	1.60	0.67
1:AJ:19:VAL:HA	1:AJ:246:VAL:HG23	1.77	0.67
1:AT:44:TRP:HB2	1:AU:129:ASP:HA	1.75	0.67
1:AT:120:ILE:HG22	1:AT:123:ILE:HD11	1.76	0.67
1:Y:40:PHE:HZ	1:Y:158:PHE:HB2	1.60	0.66
1:AD:19:VAL:HA	1:AD:246:VAL:HG23	1.76	0.66
1:AE:130:GLU:HB2	1:AV:43:ILE:HB	1.76	0.66
1:AN:19:VAL:HA	1:AN:246:VAL:HG23	1.77	0.66
1:r:40:PHE:HZ	1:r:158:PHE:HB2	1.60	0.66
1:H:32:TYR:HB3	1:H:40:PHE:CE1	2.31	0.66
1:e:32:TYR:HB3	1:e:40:PHE:CE1	2.31	0.66
1:u:56:ILE:HD11	1:u:137:LEU:HD21	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:32:TYR:HB3	1:4:40:PHE:CE1	2.30	0.66
1:AY:172:GLN:HG2	1:AY:208:ARG:HG3	1.76	0.66
1:G:19:VAL:HA	1:G:246:VAL:HG23	1.77	0.66
1:R:19:VAL:HA	1:R:246:VAL:HG23	1.77	0.66
1:Y:44:TRP:HB2	1:Z:129:ASP:HA	1.78	0.66
1:v:40:PHE:HZ	1:v:158:PHE:HB2	1.60	0.66
1:AB:19:VAL:HA	1:AB:246:VAL:HG23	1.76	0.66
1:AB:172:GLN:HG2	1:AB:208:ARG:HG3	1.77	0.66
1:AI:40:PHE:HZ	1:AI:158:PHE:HB2	1.60	0.66
1:a:44:TRP:HB2	1:b:129:ASP:HA	1.77	0.66
1:f:32:TYR:HB3	1:f:40:PHE:CE1	2.31	0.66
1:AW:32:TYR:HB3	1:AW:40:PHE:CE1	2.30	0.66
1:AZ:130:GLU:HB2	1:Aa:43:ILE:HB	1.78	0.66
1:c:40:PHE:HZ	1:c:158:PHE:HB2	1.60	0.66
1:AC:32:TYR:HB3	1:AC:40:PHE:CE1	2.31	0.66
1:AR:129:ASP:HA	1:AS:44:TRP:HB2	1.76	0.66
1:D:172:GLN:HG2	1:D:208:ARG:HG3	1.78	0.66
1:n:172:GLN:HG2	1:n:208:ARG:HG3	1.77	0.66
1:r:32:TYR:HB3	1:r:40:PHE:CE1	2.31	0.66
1:0:43:ILE:HB	1:AA:130:GLU:HB2	1.76	0.66
1:AZ:32:TYR:HB3	1:AZ:40:PHE:CE1	2.31	0.66
1:w:19:VAL:HA	1:w:246:VAL:HG23	1.77	0.65
1:AE:129:ASP:HA	1:AV:44:TRP:HB2	1.79	0.65
1:d:19:VAL:HA	1:d:246:VAL:HG23	1.77	0.65
1:U:32:TYR:HB3	1:U:40:PHE:CE1	2.31	0.65
1:AY:120:ILE:HD12	1:AY:169:MET:HG2	1.78	0.65
1:m:79:ASP:HB3	1:m:81:ARG:HH12	1.60	0.65
1:9:19:VAL:HA	1:9:246:VAL:HG23	1.78	0.65
1:AL:19:VAL:HA	1:AL:246:VAL:HG23	1.78	0.65
1:r:172:GLN:HG2	1:r:208:ARG:HG3	1.79	0.65
1:AH:56:ILE:HD11	1:AH:137:LEU:HD21	1.78	0.65
1:l:56:ILE:HD11	1:l:137:LEU:HD21	1.79	0.65
1:O:56:ILE:HD11	1:O:137:LEU:HD21	1.79	0.65
1:U:172:GLN:HG2	1:U:208:ARG:HG3	1.79	0.65
1:a:19:VAL:HA	1:a:246:VAL:HG23	1.77	0.65
1:B:40:PHE:HZ	1:B:158:PHE:HB2	1.61	0.65
1:I:32:TYR:HB3	1:I:40:PHE:CE1	2.30	0.65
1:W:19:VAL:HA	1:W:246:VAL:HG23	1.78	0.65
1:q:19:VAL:HA	1:q:246:VAL:HG23	1.79	0.65
1:0:32:TYR:HB3	1:0:40:PHE:CE1	2.31	0.65
1:AM:79:ASP:HB2	1:AM:118:PHE:HB3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Aa:152:ILE:HD12	1:Aa:227:LEU:HD23	1.77	0.65
1:AM:19:VAL:HA	1:AM:246:VAL:HG23	1.80	0.64
1:O:32:TYR:HB3	1:O:40:PHE:CE1	2.33	0.64
1:7:44:TRP:HB2	1:8:129:ASP:HA	1.77	0.64
1:q:79:ASP:HB2	1:q:118:PHE:HB3	1.80	0.64
1:v:32:TYR:HB3	1:v:40:PHE:CE1	2.32	0.64
1:7:32:TYR:HB3	1:7:40:PHE:CE1	2.33	0.64
1:AI:32:TYR:HB3	1:AI:40:PHE:CE1	2.32	0.64
1:AK:19:VAL:HA	1:AK:246:VAL:HG23	1.79	0.64
1:t:19:VAL:HA	1:t:246:VAL:HG23	1.79	0.64
1:F:19:VAL:HA	1:F:246:VAL:HG23	1.80	0.64
1:R:40:PHE:HZ	1:R:158:PHE:HB2	1.62	0.64
1:7:19:VAL:HA	1:7:246:VAL:HG23	1.79	0.64
1:K:19:VAL:HA	1:K:246:VAL:HG23	1.79	0.64
1:k:40:PHE:HZ	1:k:158:PHE:HB2	1.63	0.64
1:2:40:PHE:HZ	1:2:158:PHE:HB2	1.63	0.64
1:AV:23:LYS:HD2	1:AV:42:ARG:NH2	2.13	0.64
1:K:32:TYR:HB3	1:K:40:PHE:CE1	2.33	0.64
1:h:19:VAL:HA	1:h:246:VAL:HG23	1.79	0.64
1:z:19:VAL:HA	1:z:246:VAL:HG23	1.80	0.64
1:9:23:LYS:HD2	1:9:42:ARG:NH2	2.12	0.64
1:AO:120:ILE:HD12	1:AO:169:MET:HG2	1.79	0.64
1:Ac:32:TYR:HB3	1:Ac:40:PHE:CE1	2.33	0.64
1:V:56:ILE:HD11	1:V:137:LEU:HD21	1.80	0.64
1:l:32:TYR:HB3	1:l:40:PHE:CE2	2.33	0.64
1:x:19:VAL:HA	1:x:246:VAL:HG23	1.79	0.64
1:L:19:VAL:HA	1:L:246:VAL:HG23	1.79	0.64
1:W:172:GLN:HG2	1:W:208:ARG:HG2	1.79	0.64
1:J:129:ASP:HA	1:K:44:TRP:HB2	1.78	0.64
1:K:40:PHE:HZ	1:K:158:PHE:HB2	1.63	0.64
1:V:19:VAL:HA	1:V:246:VAL:HG23	1.79	0.64
1:AV:19:VAL:HA	1:AV:246:VAL:HG23	1.78	0.64
1:Aa:120:ILE:HD12	1:Aa:169:MET:HG2	1.79	0.64
1:F:32:TYR:HB3	1:F:40:PHE:CE1	2.33	0.63
1:W:79:ASP:HB2	1:W:118:PHE:HB3	1.79	0.63
1:9:44:TRP:HB2	1:Ab:129:ASP:HA	1.79	0.63
1:AB:120:ILE:HD12	1:AB:169:MET:HG2	1.78	0.63
1:S:56:ILE:HD11	1:S:137:LEU:HD21	1.80	0.63
1:s:56:ILE:HD11	1:s:137:LEU:HD21	1.80	0.63
1:U:28:PRO:HG2	1:U:70:LEU:HD11	1.81	0.63
1:s:19:VAL:HA	1:s:246:VAL:HG23	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:28:PRO:HG2	1:v:70:LEU:HD11	1.81	0.63
1:AK:32:TYR:HB3	1:AK:40:PHE:CE1	2.34	0.63
1:AT:19:VAL:HA	1:AT:246:VAL:HG23	1.80	0.63
1:c:19:VAL:HA	1:c:246:VAL:HG23	1.80	0.63
1:h:32:TYR:HB3	1:h:40:PHE:CE1	2.33	0.63
1:q:40:PHE:HZ	1:q:158:PHE:HB2	1.64	0.63
1:y:56:ILE:HD11	1:y:137:LEU:HD21	1.80	0.63
1:M:19:VAL:HA	1:M:246:VAL:HG23	1.80	0.63
1:N:40:PHE:HZ	1:N:158:PHE:HB2	1.64	0.63
1:x:32:TYR:HB3	1:x:40:PHE:CE1	2.33	0.63
1:AO:19:VAL:HA	1:AO:246:VAL:HG23	1.79	0.63
1:4:111:GLU:HB2	1:4:178:LYS:HB2	1.80	0.63
1:Ac:19:VAL:HA	1:Ac:246:VAL:HG23	1.81	0.63
1:i:19:VAL:HA	1:i:246:VAL:HG23	1.79	0.63
1:AF:19:VAL:HA	1:AF:246:VAL:HG23	1.80	0.63
1:2:19:VAL:HA	1:2:246:VAL:HG23	1.79	0.63
1:AI:28:PRO:HG2	1:AI:70:LEU:HD11	1.81	0.63
1:AS:19:VAL:HA	1:AS:246:VAL:HG23	1.81	0.62
1:AT:32:TYR:HB3	1:AT:40:PHE:CE1	2.33	0.62
1:c:152:ILE:HD12	1:c:227:LEU:HG	1.81	0.62
1:o:40:PHE:HZ	1:o:158:PHE:HB2	1.63	0.62
1:q:32:TYR:HB3	1:q:40:PHE:CE1	2.33	0.62
1:u:32:TYR:HB3	1:u:40:PHE:CE1	2.34	0.62
1:AO:40:PHE:HZ	1:AO:158:PHE:HB2	1.64	0.62
1:R:43:ILE:HB	1:W:130:GLU:HB2	1.81	0.62
1:w:43:ILE:HB	1:x:130:GLU:HB2	1.81	0.62
1:Z:172:GLN:HG2	1:Z:208:ARG:HG2	1.81	0.62
1:t:32:TYR:HB3	1:t:40:PHE:CE2	2.34	0.62
1:w:172:GLN:HG2	1:w:208:ARG:HB2	1.82	0.62
1:4:148:TYR:O	1:4:152:ILE:HG12	2.00	0.62
1:B:120:ILE:HD12	1:B:169:MET:HG2	1.81	0.62
1:AJ:43:ILE:HB	1:AK:130:GLU:HB2	1.82	0.62
1:D:120:ILE:HD12	1:D:169:MET:HG2	1.81	0.62
1:T:19:VAL:HA	1:T:246:VAL:HG23	1.82	0.62
1:AE:32:TYR:HB3	1:AE:40:PHE:CE1	2.35	0.62
1:AU:19:VAL:HA	1:AU:246:VAL:HG23	1.82	0.62
1:J:19:VAL:HA	1:J:246:VAL:HG23	1.82	0.62
1:O:79:ASP:HB2	1:O:118:PHE:HB3	1.81	0.62
1:AL:56:ILE:HD11	1:AL:137:LEU:HD21	1.80	0.62
1:B:43:ILE:HB	1:C:130:GLU:HB2	1.82	0.62
1:g:19:VAL:HA	1:g:246:VAL:HG23	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:19:VAL:HA	1:6:246:VAL:HG23	1.81	0.62
1:AG:120:ILE:HD12	1:AG:169:MET:HG2	1.82	0.62
1:AH:32:TYR:HB3	1:AH:40:PHE:CE2	2.35	0.62
1:B:32:TYR:HB3	1:B:40:PHE:CE1	2.35	0.62
1:c:32:TYR:HB3	1:c:40:PHE:CE1	2.34	0.62
1:d:120:ILE:HD12	1:d:169:MET:HG2	1.81	0.62
1:j:19:VAL:HA	1:j:246:VAL:HG23	1.80	0.62
1:w:40:PHE:HZ	1:w:158:PHE:HB2	1.65	0.62
1:8:208:ARG:HG2	1:8:210:VAL:HG23	1.82	0.62
1:AF:79:ASP:HB2	1:AF:118:PHE:HB3	1.82	0.62
1:AN:56:ILE:HD11	1:AN:137:LEU:HD21	1.82	0.62
1:Z:32:TYR:HB3	1:Z:40:PHE:CE1	2.35	0.61
1:i:40:PHE:HZ	1:i:158:PHE:HB2	1.64	0.61
1:z:79:ASP:HB2	1:z:118:PHE:HB3	1.80	0.61
1:AD:79:ASP:HB3	1:AD:81:ARG:HH22	1.65	0.61
1:L:40:PHE:HZ	1:L:158:PHE:HB2	1.66	0.61
1:n:79:ASP:HB3	1:n:81:ARG:NH1	2.15	0.61
1:1:56:ILE:HD11	1:1:137:LEU:HD21	1.82	0.61
1:2:120:ILE:HD12	1:2:169:MET:HG2	1.81	0.61
1:AK:172:GLN:HG2	1:AK:208:ARG:HG2	1.82	0.61
1:AR:79:ASP:HB3	1:AR:81:ARG:NH1	2.15	0.61
1:Ac:79:ASP:HB2	1:Ac:118:PHE:HB3	1.81	0.61
1:B:44:TRP:HB2	1:C:129:ASP:HA	1.81	0.61
1:r:28:PRO:HG2	1:r:70:LEU:HD11	1.81	0.61
1:x:172:GLN:HG2	1:x:208:ARG:HG2	1.82	0.61
1:8:19:VAL:HA	1:8:246:VAL:HG23	1.83	0.61
1:z:32:TYR:HB3	1:z:40:PHE:CE2	2.35	0.61
1:m:148:TYR:O	1:m:152:ILE:HG12	2.01	0.61
1:AW:56:ILE:HD11	1:AW:137:LEU:HD21	1.83	0.61
1:AX:19:VAL:HA	1:AX:246:VAL:HG23	1.82	0.61
1:N:79:ASP:HB3	1:N:81:ARG:NH1	2.16	0.61
1:Y:32:TYR:HB3	1:Y:40:PHE:CE1	2.35	0.61
1:AD:56:ILE:HD11	1:AD:137:LEU:HD21	1.83	0.61
1:h:40:PHE:HZ	1:h:158:PHE:HB2	1.64	0.61
1:AF:32:TYR:HB3	1:AF:40:PHE:CE2	2.36	0.61
1:L:172:GLN:HG2	1:L:208:ARG:HB2	1.82	0.61
1:AI:79:ASP:HB3	1:AI:81:ARG:NH1	2.15	0.61
1:AJ:79:ASP:HB3	1:AJ:81:ARG:NH1	2.14	0.61
1:AX:32:TYR:HB3	1:AX:40:PHE:CE2	2.36	0.61
1:I:56:ILE:HD11	1:I:137:LEU:HD21	1.83	0.61
1:Y:43:ILE:HB	1:Z:130:GLU:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:172:GLN:HG2	1:AE:208:ARG:HG2	1.83	0.61
1:AK:79:ASP:HB2	1:AK:118:PHE:HB3	1.82	0.61
1:D:56:ILE:HD11	1:D:137:LEU:HD21	1.84	0.60
1:W:79:ASP:HB3	1:W:81:ARG:NH1	2.16	0.60
1:AB:23:LYS:HD2	1:AB:42:ARG:NH2	2.16	0.60
1:AQ:148:TYR:O	1:AQ:152:ILE:HG12	2.01	0.60
1:AT:40:PHE:HZ	1:AT:158:PHE:HB2	1.66	0.60
1:X:19:VAL:HA	1:X:246:VAL:HG23	1.82	0.60
1:l:79:ASP:HB3	1:l:81:ARG:NH1	2.16	0.60
1:t:172:GLN:HG2	1:t:208:ARG:HG2	1.83	0.60
1:AB:43:ILE:HB	1:AG:130:GLU:HB2	1.83	0.60
1:W:40:PHE:HZ	1:W:158:PHE:HB2	1.67	0.60
1:a:56:ILE:HD11	1:a:137:LEU:HD21	1.84	0.60
1:3:79:ASP:HB3	1:3:81:ARG:NH1	2.16	0.60
1:AA:19:VAL:HA	1:AA:246:VAL:HG23	1.82	0.60
1:AJ:40:PHE:HZ	1:AJ:158:PHE:HB2	1.65	0.60
1:A:19:VAL:HA	1:A:246:VAL:HG23	1.82	0.60
1:Z:79:ASP:HB3	1:Z:81:ARG:HH22	1.65	0.60
1:r:79:ASP:HB3	1:r:81:ARG:NH1	2.16	0.60
1:AJ:172:GLN:HG2	1:AJ:208:ARG:HB2	1.82	0.60
1:Ab:172:GLN:HG2	1:Ab:208:ARG:HG2	1.84	0.60
1:c:79:ASP:HB2	1:c:118:PHE:HB3	1.83	0.60
1:n:79:ASP:HB2	1:n:118:PHE:HB3	1.83	0.60
1:p:56:ILE:HD11	1:p:137:LEU:HD21	1.83	0.60
1:AS:117:ILE:HB	1:AS:172:GLN:HB3	1.83	0.60
1:C:32:TYR:HB3	1:C:40:PHE:CE1	2.37	0.60
1:A:56:ILE:HD11	1:A:137:LEU:HD21	1.83	0.60
1:D:23:LYS:HD2	1:D:42:ARG:NH2	2.16	0.60
1:6:117:ILE:HB	1:6:172:GLN:HB3	1.84	0.60
1:o:43:ILE:HB	1:t:130:GLU:HB2	1.84	0.60
1:AM:32:TYR:HB3	1:AM:40:PHE:CE2	2.36	0.60
1:AU:40:PHE:HZ	1:AU:158:PHE:HB2	1.67	0.60
1:8:32:TYR:HB3	1:8:40:PHE:CE1	2.37	0.60
1:AL:79:ASP:HB3	1:AL:81:ARG:NH1	2.16	0.60
1:AY:79:ASP:HB3	1:AY:81:ARG:NH1	2.14	0.60
1:E:32:TYR:HB3	1:E:40:PHE:CZ	2.37	0.60
1:a:23:LYS:HD2	1:a:42:ARG:NH2	2.16	0.60
1:7:40:PHE:HZ	1:7:158:PHE:HB2	1.67	0.60
1:AA:32:TYR:HB3	1:AA:40:PHE:CE2	2.37	0.60
1:Ac:152:ILE:HD12	1:Ac:227:LEU:HG	1.84	0.60
1:K:79:ASP:HB3	1:K:81:ARG:NH1	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:148:TYR:O	1:P:152:ILE:HG12	2.02	0.59
1:b:120:ILE:HD12	1:b:169:MET:HG2	1.84	0.59
1:o:120:ILE:HD12	1:o:169:MET:HG2	1.83	0.59
1:7:79:ASP:HB3	1:7:81:ARG:NH1	2.17	0.59
1:AX:40:PHE:HZ	1:AX:158:PHE:HB2	1.67	0.59
1:Ad:120:ILE:HD12	1:Ad:169:MET:HG2	1.83	0.59
1:Y:120:ILE:HD12	1:Y:169:MET:HG2	1.84	0.59
1:5:79:ASP:HB3	1:5:81:ARG:NH1	2.16	0.59
1:AL:40:PHE:HZ	1:AL:158:PHE:HB2	1.66	0.59
1:k:79:ASP:HB3	1:k:81:ARG:NH1	2.16	0.59
1:o:79:ASP:HB3	1:o:81:ARG:NH1	2.16	0.59
1:s:79:ASP:HB3	1:s:81:ARG:NH1	2.17	0.59
1:v:56:ILE:HD11	1:v:137:LEU:HD21	1.84	0.59
1:AP:19:VAL:HB	1:AP:247:LEU:HD12	1.85	0.59
1:Ac:79:ASP:HB3	1:Ac:81:ARG:NH1	2.17	0.59
1:D:32:TYR:HB3	1:D:40:PHE:CE2	2.37	0.59
1:f:56:ILE:HD11	1:f:137:LEU:HD21	1.84	0.59
1:g:32:TYR:HB3	1:g:40:PHE:CE1	2.38	0.59
1:w:120:ILE:HD12	1:w:169:MET:HG2	1.85	0.59
1:2:56:ILE:HD11	1:2:137:LEU:HD21	1.84	0.59
1:4:208:ARG:HE	1:4:210:VAL:HG21	1.66	0.59
1:5:120:ILE:HD12	1:5:169:MET:HG2	1.84	0.59
1:Ab:32:TYR:HB3	1:Ab:40:PHE:CE1	2.38	0.59
1:F:79:ASP:HB2	1:F:118:PHE:HB3	1.83	0.59
1:T:120:ILE:HD12	1:T:169:MET:HG2	1.84	0.59
1:e:79:ASP:HB3	1:e:81:ARG:HH22	1.66	0.59
1:AI:56:ILE:HD11	1:AI:137:LEU:HD21	1.85	0.59
1:N:56:ILE:HD11	1:N:137:LEU:HD21	1.84	0.59
1:l:78:ILE:HD12	1:l:208:ARG:HH21	1.68	0.59
1:q:208:ARG:HE	1:q:210:VAL:HG21	1.67	0.59
1:v:79:ASP:HB3	1:v:81:ARG:NH1	2.15	0.59
1:9:120:ILE:HD12	1:9:169:MET:HG2	1.85	0.59
1:AB:56:ILE:HD11	1:AB:137:LEU:HD21	1.85	0.59
1:P:79:ASP:HB3	1:P:81:ARG:NH1	2.17	0.59
1:X:79:ASP:HB3	1:X:81:ARG:HH22	1.68	0.59
1:g:79:ASP:HB2	1:g:118:PHE:HB3	1.85	0.59
1:y:79:ASP:HB3	1:y:81:ARG:NH1	2.17	0.59
1:3:19:VAL:HB	1:3:247:LEU:HD12	1.84	0.59
1:AH:43:ILE:HB	1:AI:130:GLU:HB2	1.84	0.59
1:AO:56:ILE:HD11	1:AO:137:LEU:HD21	1.85	0.59
1:AU:79:ASP:HB2	1:AU:118:PHE:HB3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:56:ILE:HD11	1:AY:137:LEU:HD21	1.85	0.59
1:Ad:32:TYR:HB3	1:Ad:40:PHE:CZ	2.38	0.59
1:B:23:LYS:HD2	1:B:42:ARG:NH2	2.17	0.59
1:E:120:ILE:HD12	1:E:169:MET:HG2	1.84	0.59
1:L:76:ILE:HB	1:S:210:VAL:O	2.03	0.59
1:O:79:ASP:HB3	1:O:81:ARG:NH1	2.17	0.59
1:T:76:ILE:HB	1:V:210:VAL:O	2.03	0.59
1:U:79:ASP:HB3	1:U:81:ARG:NH1	2.16	0.59
1:Y:29:LEU:HD11	1:Y:68:ILE:HD12	1.83	0.59
1:AI:43:ILE:HB	1:AJ:130:GLU:HB2	1.85	0.59
1:V:79:ASP:HB3	1:V:81:ARG:NH1	2.17	0.59
1:Y:79:ASP:HB3	1:Y:81:ARG:NH1	2.18	0.59
1:j:79:ASP:HB3	1:j:81:ARG:HH22	1.68	0.59
1:w:79:ASP:HB3	1:w:81:ARG:NH1	2.15	0.59
1:AK:79:ASP:HB3	1:AK:81:ARG:HH22	1.68	0.59
1:B:29:LEU:HD11	1:B:68:ILE:HD12	1.83	0.59
1:J:32:TYR:HB3	1:J:40:PHE:CE1	2.38	0.59
1:P:43:ILE:HB	1:Q:130:GLU:HB2	1.84	0.59
1:b:32:TYR:HB3	1:b:40:PHE:CZ	2.38	0.59
1:h:79:ASP:HB3	1:h:81:ARG:NH1	2.17	0.59
1:s:76:ILE:HB	1:t:210:VAL:O	2.03	0.59
1:x:210:VAL:O	1:y:76:ILE:HB	2.03	0.59
1:F:79:ASP:HB3	1:F:81:ARG:NH1	2.18	0.58
1:i:56:ILE:HD11	1:i:137:LEU:HD21	1.85	0.58
1:n:56:ILE:HD11	1:n:137:LEU:HD21	1.85	0.58
1:AT:79:ASP:HB3	1:AT:81:ARG:NH1	2.17	0.58
1:a:32:TYR:HB3	1:a:40:PHE:CE2	2.38	0.58
1:g:79:ASP:HB3	1:g:81:ARG:NH1	2.16	0.58
1:y:40:PHE:HZ	1:y:158:PHE:HB2	1.67	0.58
1:AR:32:TYR:HB3	1:AR:40:PHE:CE2	2.38	0.58
1:y:32:TYR:HB3	1:y:40:PHE:CZ	2.38	0.58
1:y:210:VAL:O	1:z:76:ILE:HB	2.03	0.58
1:O:210:VAL:HB	1:AA:76:ILE:HG21	1.85	0.58
1:AH:40:PHE:HZ	1:AH:158:PHE:HB2	1.68	0.58
1:AH:130:GLU:HB2	1:AP:43:ILE:HB	1.86	0.58
1:AJ:120:ILE:HD12	1:AJ:169:MET:HG2	1.84	0.58
1:AK:210:VAL:O	1:AL:76:ILE:HB	2.03	0.58
1:AR:56:ILE:HD11	1:AR:137:LEU:HD21	1.85	0.58
1:AU:79:ASP:HB3	1:AU:81:ARG:NH1	2.16	0.58
1:R:56:ILE:HD11	1:R:137:LEU:HD21	1.85	0.58
1:V:76:ILE:HB	1:W:210:VAL:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:9:43:ILE:HB	1:Ab:130:GLU:HB2	1.86	0.58
1:B:79:ASP:HB3	1:B:81:ARG:NH1	2.18	0.58
1:O:78:ILE:HD12	1:Q:208:ARG:HH21	1.68	0.58
1:AC:172:GLN:HG2	1:AC:208:ARG:HG2	1.84	0.58
1:4:130:GLU:HB2	1:5:43:ILE:HB	1.85	0.58
1:AB:76:ILE:HB	1:AE:210:VAL:O	2.04	0.58
1:Ab:79:ASP:HB3	1:Ab:81:ARG:NH1	2.17	0.58
1:Y:23:LYS:HD2	1:Y:42:ARG:NH2	2.17	0.58
1:i:79:ASP:HB2	1:i:118:PHE:HB3	1.86	0.58
1:0:56:ILE:HD11	1:0:137:LEU:HD21	1.86	0.58
1:AL:43:ILE:HB	1:AM:130:GLU:HB2	1.86	0.58
1:AR:120:ILE:HD12	1:AR:169:MET:HG2	1.86	0.58
1:Aa:19:VAL:HA	1:Aa:246:VAL:HG23	1.86	0.58
1:L:79:ASP:HB2	1:L:118:PHE:HB3	1.85	0.58
1:Z:210:VAL:O	1:a:76:ILE:HB	2.04	0.58
1:r:56:ILE:HD11	1:r:137:LEU:HD21	1.86	0.58
1:t:228:PHE:HD1	1:t:229:PHE:N	2.00	0.58
1:u:79:ASP:HB3	1:u:81:ARG:NH1	2.19	0.58
1:AM:120:ILE:HD12	1:AM:169:MET:HG2	1.85	0.58
1:AV:79:ASP:HB3	1:AV:81:ARG:NH1	2.19	0.58
1:G:56:ILE:HD11	1:G:137:LEU:HD21	1.86	0.58
1:W:32:TYR:HB3	1:W:40:PHE:CE1	2.38	0.58
1:3:79:ASP:HB2	1:3:118:PHE:HB3	1.84	0.58
1:9:79:ASP:HB3	1:9:81:ARG:NH1	2.19	0.58
1:AY:76:ILE:HB	1:Ab:210:VAL:O	2.04	0.58
1:Ad:79:ASP:HB3	1:Ad:81:ARG:NH1	2.19	0.58
1:G:120:ILE:HD12	1:G:169:MET:HG2	1.84	0.58
1:L:56:ILE:HD11	1:L:137:LEU:HD21	1.85	0.58
1:Aa:32:TYR:HB3	1:Aa:40:PHE:CE1	2.39	0.58
1:4:228:PHE:HD2	1:4:229:PHE:H	1.52	0.57
1:6:79:ASP:HB3	1:6:81:ARG:NH1	2.19	0.57
1:AA:79:ASP:HB2	1:AA:118:PHE:HB3	1.86	0.57
1:AZ:172:GLN:HG2	1:AZ:208:ARG:HG2	1.84	0.57
1:M:117:ILE:HB	1:M:172:GLN:HB3	1.86	0.57
1:Q:56:ILE:HD11	1:Q:137:LEU:HD21	1.84	0.57
1:k:56:ILE:HD11	1:k:137:LEU:HD21	1.86	0.57
1:8:79:ASP:HB3	1:8:81:ARG:NH1	2.16	0.57
1:AA:40:PHE:HZ	1:AA:158:PHE:HB2	1.69	0.57
1:AN:210:VAL:O	1:AO:76:ILE:HB	2.03	0.57
1:AO:79:ASP:HB2	1:AO:118:PHE:HB3	1.86	0.57
1:AQ:79:ASP:HB3	1:AQ:81:ARG:NH2	2.16	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:32:TYR:HB3	1:AY:40:PHE:CE2	2.39	0.57
1:AK:228:PHE:HD1	1:AK:229:PHE:H	1.51	0.57
1:AM:79:ASP:HB3	1:AM:81:ARG:NH1	2.17	0.57
1:A:79:ASP:HB3	1:A:81:ARG:HH22	1.68	0.57
1:J:81:ARG:HH11	1:K:205:THR:HG22	1.69	0.57
1:T:130:GLU:HB2	1:V:43:ILE:HB	1.86	0.57
1:U:76:ILE:HB	1:l:210:VAL:O	2.05	0.57
1:q:79:ASP:HB3	1:q:81:ARG:NH1	2.18	0.57
1:w:23:LYS:HD2	1:w:42:ARG:NH2	2.18	0.57
1:l:215:ASP:CG	1:l:216:GLU:H	2.12	0.57
1:4:76:ILE:HB	1:5:210:VAL:O	2.03	0.57
1:AF:79:ASP:HB3	1:AF:81:ARG:NH1	2.18	0.57
1:AV:29:LEU:HD11	1:AV:68:ILE:HD12	1.85	0.57
1:Y:23:LYS:HD2	1:Y:42:ARG:HH21	1.69	0.57
1:5:32:TYR:HB3	1:5:40:PHE:CE2	2.39	0.57
1:9:29:LEU:HD11	1:9:68:ILE:HD12	1.85	0.57
1:AQ:76:ILE:HB	1:AR:210:VAL:O	2.04	0.57
1:c:79:ASP:HB3	1:c:81:ARG:NH1	2.18	0.57
1:g:76:ILE:HB	1:h:210:VAL:O	2.05	0.57
1:j:117:ILE:HB	1:j:172:GLN:HB3	1.87	0.57
1:k:210:VAL:O	1:m:76:ILE:HB	2.04	0.57
1:l:208:ARG:HG2	1:l:210:VAL:HG23	1.87	0.57
1:o:23:LYS:HD2	1:o:42:ARG:NH2	2.19	0.57
1:w:56:ILE:HD11	1:w:137:LEU:HD21	1.87	0.57
1:AA:56:ILE:HD11	1:AA:137:LEU:HD21	1.87	0.57
1:AQ:130:GLU:HB2	1:AR:43:ILE:HB	1.85	0.57
1:AV:120:ILE:HD12	1:AV:169:MET:HG2	1.86	0.57
1:AW:167:LYS:C	1:AW:168:LYS:HD2	2.29	0.57
1:E:79:ASP:HB3	1:E:81:ARG:HH22	1.69	0.57
1:N:210:VAL:O	1:P:76:ILE:HB	2.05	0.57
1:X:56:ILE:HD11	1:X:137:LEU:HD21	1.87	0.57
1:8:24:THR:HG22	1:8:218:ILE:HG13	1.86	0.57
1:AV:130:GLU:HB2	1:AX:43:ILE:HB	1.86	0.57
1:R:79:ASP:HB3	1:R:81:ARG:HH22	1.69	0.57
1:S:76:ILE:HB	1:T:210:VAL:O	2.04	0.57
1:u:79:ASP:HB2	1:u:118:PHE:HB3	1.87	0.57
1:AU:56:ILE:HD11	1:AU:137:LEU:HD21	1.87	0.57
1:P:120:ILE:HG22	1:P:123:ILE:HD11	1.87	0.57
1:R:23:LYS:HD2	1:R:42:ARG:NH2	2.19	0.57
1:h:181:LEU:HD11	1:h:183:VAL:HG23	1.87	0.57
1:l:130:GLU:HB2	1:n:43:ILE:HB	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:z:79:ASP:HB3	1:z:81:ARG:NH1	2.17	0.57
1:7:210:VAL:O	1:8:76:ILE:HB	2.05	0.57
1:AG:79:ASP:HB3	1:AG:81:ARG:NH1	2.19	0.57
1:AK:79:ASP:HB3	1:AK:81:ARG:NH1	2.16	0.57
1:AL:111:GLU:HB2	1:AL:178:LYS:HB2	1.87	0.57
1:AT:79:ASP:HB2	1:AT:118:PHE:HB3	1.87	0.57
1:E:79:ASP:HB3	1:E:81:ARG:NH1	2.20	0.56
1:M:79:ASP:HB3	1:M:81:ARG:HH22	1.69	0.56
1:R:130:GLU:HB2	1:U:43:ILE:HB	1.86	0.56
1:T:79:ASP:HB3	1:T:81:ARG:NH1	2.18	0.56
1:i:79:ASP:HB3	1:i:81:ARG:NH1	2.16	0.56
1:5:56:ILE:HD11	1:5:137:LEU:HD21	1.87	0.56
1:0:79:ASP:HB3	1:0:81:ARG:NH1	2.20	0.56
1:AB:32:TYR:HB3	1:AB:40:PHE:CE1	2.39	0.56
1:AR:130:GLU:HB2	1:AS:43:ILE:HB	1.86	0.56
1:AT:210:VAL:O	1:AU:76:ILE:HB	2.05	0.56
1:AX:79:ASP:HB3	1:AX:81:ARG:NH1	2.20	0.56
1:B:23:LYS:HD2	1:B:42:ARG:HH21	1.70	0.56
1:W:79:ASP:HB3	1:W:81:ARG:HH22	1.70	0.56
1:a:120:ILE:HD12	1:a:169:MET:HG2	1.85	0.56
1:e:19:VAL:HB	1:e:247:LEU:HD12	1.87	0.56
1:e:79:ASP:HB3	1:e:81:ARG:NH1	2.20	0.56
1:j:79:ASP:HB3	1:j:81:ARG:NH1	2.20	0.56
1:7:111:GLU:HB2	1:7:178:LYS:HB2	1.88	0.56
1:AC:76:ILE:HB	1:AD:210:VAL:O	2.05	0.56
1:AX:56:ILE:HD11	1:AX:137:LEU:HD21	1.87	0.56
1:J:76:ILE:HB	1:K:210:VAL:O	2.06	0.56
1:O:210:VAL:O	1:r:76:ILE:HB	2.06	0.56
1:o:130:GLU:HB2	1:r:43:ILE:HB	1.86	0.56
1:p:111:GLU:HB2	1:p:178:LYS:HB2	1.87	0.56
1:AF:56:ILE:HD11	1:AF:137:LEU:HD21	1.87	0.56
1:AJ:23:LYS:HD2	1:AJ:42:ARG:NH2	2.20	0.56
1:AJ:56:ILE:HD11	1:AJ:137:LEU:HD21	1.86	0.56
1:AK:120:ILE:HD12	1:AK:169:MET:HG2	1.87	0.56
1:AT:56:ILE:HD11	1:AT:137:LEU:HD21	1.88	0.56
1:A:40:PHE:HZ	1:A:158:PHE:HB2	1.70	0.56
1:H:19:VAL:HB	1:H:247:LEU:HD12	1.88	0.56
1:b:79:ASP:HB3	1:b:81:ARG:HH22	1.70	0.56
1:c:79:ASP:HB3	1:c:81:ARG:HH22	1.70	0.56
1:s:172:GLN:HG2	1:s:208:ARG:HG3	1.86	0.56
1:2:210:VAL:O	1:7:76:ILE:HB	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:79:ASP:HB2	1:8:118:PHE:HB3	1.86	0.56
1:AG:79:ASP:HB2	1:AG:118:PHE:HB3	1.88	0.56
1:AP:130:GLU:HB2	1:AQ:43:ILE:HB	1.88	0.56
1:R:79:ASP:HB2	1:R:118:PHE:HB3	1.86	0.56
1:V:111:GLU:HB2	1:V:178:LYS:HB2	1.87	0.56
1:b:79:ASP:HB3	1:b:81:ARG:NH1	2.20	0.56
1:o:56:ILE:HD11	1:o:137:LEU:HD21	1.86	0.56
1:3:79:ASP:HB3	1:3:81:ARG:HH22	1.70	0.56
1:AB:79:ASP:HB3	1:AB:81:ARG:NH1	2.17	0.56
1:AC:19:VAL:HB	1:AC:247:LEU:HD12	1.88	0.56
1:AO:79:ASP:HB3	1:AO:81:ARG:NH1	2.16	0.56
1:AQ:120:ILE:HG22	1:AQ:123:ILE:HD11	1.88	0.56
1:AZ:19:VAL:HB	1:AZ:247:LEU:HD12	1.88	0.56
1:AZ:76:ILE:HB	1:Aa:210:VAL:O	2.06	0.56
1:D:79:ASP:HB2	1:D:118:PHE:HB3	1.88	0.56
1:K:56:ILE:HD11	1:K:137:LEU:HD21	1.87	0.56
1:a:79:ASP:HB3	1:a:81:ARG:HH22	1.70	0.56
1:d:56:ILE:HD11	1:d:137:LEU:HD21	1.88	0.56
1:k:120:ILE:HD12	1:k:169:MET:HG2	1.87	0.56
1:6:79:ASP:HB3	1:6:81:ARG:HH22	1.71	0.56
1:0:167:LYS:C	1:0:168:LYS:HD2	2.31	0.56
1:K:181:LEU:HD11	1:K:183:VAL:HG23	1.88	0.56
1:U:56:ILE:HD11	1:U:137:LEU:HD21	1.88	0.56
1:U:79:ASP:HB3	1:U:81:ARG:HH22	1.70	0.56
1:X:120:ILE:HG22	1:X:123:ILE:HD11	1.88	0.56
1:s:77:ASP:HB3	1:s:120:ILE:HB	1.88	0.56
1:s:120:ILE:HG22	1:s:123:ILE:HD11	1.87	0.56
1:AG:32:TYR:HB3	1:AG:40:PHE:CZ	2.40	0.56
1:AW:208:ARG:HH21	1:AX:78:ILE:HD12	1.71	0.56
1:AX:79:ASP:HB2	1:AX:118:PHE:HB3	1.87	0.56
1:I:167:LYS:C	1:I:168:LYS:HD2	2.31	0.56
1:S:79:ASP:HB3	1:S:81:ARG:HH22	1.71	0.56
1:V:120:ILE:HG22	1:V:123:ILE:HD11	1.87	0.56
1:d:210:VAL:O	1:e:76:ILE:HB	2.05	0.56
1:r:43:ILE:HG13	1:r:43:ILE:O	2.05	0.56
1:AL:120:ILE:HG22	1:AL:123:ILE:HD11	1.87	0.56
1:AO:210:VAL:O	1:AT:76:ILE:HB	2.06	0.56
1:K:79:ASP:HB3	1:K:81:ARG:HH22	1.71	0.56
1:K:111:GLU:HB2	1:K:178:LYS:HB2	1.88	0.56
1:R:32:TYR:HB3	1:R:40:PHE:CE1	2.41	0.56
1:U:43:ILE:O	1:U:43:ILE:HG13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:79:ASP:HB3	1:r:81:ARG:HH22	1.70	0.56
1:AW:210:VAL:O	1:AX:76:ILE:HB	2.05	0.56
1:L:79:ASP:HB3	1:L:81:ARG:NH1	2.16	0.56
1:p:79:ASP:HB3	1:p:81:ARG:HH22	1.70	0.56
1:p:79:ASP:HB2	1:p:118:PHE:HB3	1.88	0.56
1:2:79:ASP:HB3	1:2:81:ARG:NH1	2.16	0.56
1:Ad:79:ASP:HB3	1:Ad:81:ARG:HH22	1.71	0.56
1:F:43:ILE:HB	1:G:130:GLU:HB2	1.87	0.55
1:N:79:ASP:HB3	1:N:81:ARG:HH22	1.71	0.55
1:R:79:ASP:HB3	1:R:81:ARG:NH1	2.17	0.55
1:S:79:ASP:HB2	1:S:118:PHE:HB3	1.87	0.55
1:j:23:LYS:HD2	1:j:42:ARG:NH2	2.21	0.55
1:1:79:ASP:HB3	1:1:81:ARG:HH22	1.71	0.55
1:AL:77:ASP:HB3	1:AL:120:ILE:HB	1.88	0.55
1:AT:111:GLU:HB2	1:AT:178:LYS:HB2	1.88	0.55
1:F:56:ILE:HD11	1:F:137:LEU:HD21	1.88	0.55
1:F:79:ASP:HB3	1:F:81:ARG:HH22	1.70	0.55
1:f:167:LYS:C	1:f:168:LYS:HD2	2.31	0.55
1:g:170:ARG:NH2	1:g:208:ARG:HH21	2.03	0.55
1:h:56:ILE:HD11	1:h:137:LEU:HD21	1.89	0.55
1:p:79:ASP:HB3	1:p:81:ARG:NH1	2.18	0.55
1:r:77:ASP:HB3	1:r:120:ILE:HB	1.89	0.55
1:2:79:ASP:HB2	1:2:118:PHE:HB3	1.87	0.55
1:6:23:LYS:HD2	1:6:42:ARG:NH2	2.21	0.55
1:AD:130:GLU:HB2	1:AF:43:ILE:HB	1.87	0.55
1:AQ:152:ILE:HD12	1:AQ:227:LEU:HD23	1.88	0.55
1:L:32:TYR:HB3	1:L:40:PHE:CE1	2.41	0.55
1:i:32:TYR:HB3	1:i:40:PHE:CE1	2.42	0.55
1:z:43:ILE:HB	1:1:130:GLU:HB2	1.88	0.55
1:1:79:ASP:HB2	1:1:118:PHE:HB3	1.87	0.55
1:3:32:TYR:HB3	1:3:40:PHE:CE1	2.41	0.55
1:7:181:LEU:HD11	1:7:183:VAL:HG23	1.89	0.55
1:AI:43:ILE:O	1:AI:43:ILE:HG13	2.06	0.55
1:AK:43:ILE:HB	1:AL:130:GLU:HB2	1.87	0.55
1:AL:32:TYR:HB3	1:AL:40:PHE:CZ	2.40	0.55
1:AN:79:ASP:HB3	1:AN:81:ARG:HH22	1.70	0.55
1:AN:79:ASP:HB2	1:AN:118:PHE:HB3	1.88	0.55
1:AO:32:TYR:HB3	1:AO:40:PHE:CE1	2.42	0.55
1:X:40:PHE:HZ	1:X:158:PHE:HB2	1.71	0.55
1:h:111:GLU:HB2	1:h:178:LYS:HB2	1.88	0.55
1:m:43:ILE:HB	1:n:130:GLU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:76:ILE:HB	1:3:210:VAL:O	2.06	0.55
1:5:40:PHE:HZ	1:5:158:PHE:HB2	1.71	0.55
1:7:79:ASP:HB2	1:7:118:PHE:HB3	1.89	0.55
1:AN:79:ASP:HB3	1:AN:81:ARG:NH1	2.18	0.55
1:AU:32:TYR:HB3	1:AU:40:PHE:CE1	2.42	0.55
1:AU:170:ARG:NH2	1:AU:208:ARG:HH21	2.04	0.55
1:Ad:79:ASP:HB2	1:Ad:118:PHE:HB3	1.88	0.55
1:O:208:ARG:HG2	1:O:210:VAL:HG23	1.87	0.55
1:P:79:ASP:HB3	1:P:81:ARG:HH22	1.70	0.55
1:i:148:TYR:O	1:i:152:ILE:HG12	2.07	0.55
1:3:19:VAL:HA	1:3:246:VAL:HG23	1.89	0.55
1:5:120:ILE:HG22	1:5:123:ILE:HD11	1.88	0.55
1:7:43:ILE:HB	1:8:130:GLU:HB2	1.88	0.55
1:AB:23:LYS:HD2	1:AB:42:ARG:HH21	1.71	0.55
1:AP:32:TYR:HB3	1:AP:40:PHE:CE1	2.41	0.55
1:AT:181:LEU:HD11	1:AT:183:VAL:HG23	1.87	0.55
1:AZ:79:ASP:CB	1:AZ:81:ARG:HH22	2.20	0.55
1:Aa:56:ILE:HD11	1:Aa:137:LEU:HD21	1.86	0.55
1:K:79:ASP:HB2	1:K:118:PHE:HB3	1.89	0.55
1:S:79:ASP:HB3	1:S:81:ARG:NH1	2.18	0.55
1:o:32:TYR:HB3	1:o:40:PHE:CE1	2.42	0.55
1:p:130:GLU:HB2	1:q:43:ILE:HB	1.89	0.55
1:v:79:ASP:HB3	1:v:81:ARG:HH22	1.71	0.55
1:AF:79:ASP:HB3	1:AF:81:ARG:HH22	1.72	0.55
1:AI:79:ASP:HB3	1:AI:81:ARG:HH22	1.71	0.55
1:J:127:ASP:HB3	1:K:44:TRP:CE2	2.42	0.55
1:M:56:ILE:HD11	1:M:137:LEU:HD21	1.89	0.55
1:a:79:ASP:HB3	1:a:81:ARG:NH1	2.17	0.55
1:t:40:PHE:HZ	1:t:158:PHE:HB2	1.71	0.55
1:7:79:ASP:HB3	1:7:81:ARG:HH22	1.71	0.55
1:8:120:ILE:HD12	1:8:169:MET:HG2	1.89	0.55
1:AG:56:ILE:HD11	1:AG:137:LEU:HD21	1.89	0.55
1:J:56:ILE:HD11	1:J:137:LEU:HD21	1.89	0.55
1:V:77:ASP:HB3	1:V:120:ILE:HB	1.88	0.55
1:W:120:ILE:HD12	1:W:169:MET:HG2	1.89	0.55
1:r:215:ASP:CG	1:r:216:GLU:H	2.15	0.55
1:1:79:ASP:HB3	1:1:81:ARG:NH1	2.17	0.55
1:3:56:ILE:HD11	1:3:137:LEU:HD21	1.89	0.55
1:3:181:LEU:HD12	1:3:182:GLY:N	2.22	0.55
1:9:43:ILE:HG13	1:9:43:ILE:O	2.06	0.55
1:AI:77:ASP:HB3	1:AI:120:ILE:HB	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:79:ASP:HB3	1:AS:81:ARG:HH22	1.70	0.55
1:AU:210:VAL:O	1:AW:76:ILE:HB	2.07	0.55
1:M:23:LYS:HD2	1:M:42:ARG:NH2	2.21	0.55
1:V:130:GLU:HB2	1:W:43:ILE:HB	1.88	0.55
1:h:170:ARG:NH1	1:h:170:ARG:HB2	2.22	0.55
1:o:79:ASP:HB3	1:o:81:ARG:HH22	1.72	0.55
1:2:32:TYR:HB3	1:2:40:PHE:CE1	2.42	0.55
1:AG:40:PHE:HZ	1:AG:158:PHE:HB2	1.71	0.55
1:AR:40:PHE:HZ	1:AR:158:PHE:HB2	1.71	0.55
1:AT:79:ASP:HB3	1:AT:81:ARG:HH22	1.71	0.55
1:AT:170:ARG:HB2	1:AT:170:ARG:NH1	2.22	0.55
1:Ab:79:ASP:HB3	1:Ab:81:ARG:HH22	1.71	0.55
1:A:32:TYR:HB3	1:A:40:PHE:CE2	2.42	0.55
1:G:210:VAL:O	1:H:76:ILE:HB	2.07	0.55
1:M:43:ILE:HB	1:N:130:GLU:HB2	1.88	0.55
1:a:79:ASP:HB2	1:a:118:PHE:HB3	1.89	0.55
1:u:130:GLU:HB2	1:3:43:ILE:HB	1.89	0.55
1:AE:79:ASP:HB2	1:AE:118:PHE:HB3	1.87	0.55
1:AJ:210:VAL:O	1:AK:76:ILE:HB	2.07	0.55
1:AP:120:ILE:HD12	1:AP:169:MET:HG2	1.89	0.55
1:C:79:ASP:HB2	1:C:118:PHE:HB3	1.88	0.54
1:P:205:THR:HG22	1:Q:81:ARG:HH11	1.72	0.54
1:U:77:ASP:HB3	1:U:120:ILE:HB	1.89	0.54
1:X:183:VAL:HB	1:X:197:LEU:HG	1.89	0.54
1:h:76:ILE:HB	1:i:210:VAL:O	2.06	0.54
1:h:79:ASP:HB3	1:h:81:ARG:HH22	1.71	0.54
1:w:32:TYR:HB3	1:w:40:PHE:CE1	2.42	0.54
1:3:120:ILE:HD12	1:3:169:MET:HG2	1.89	0.54
1:AG:79:ASP:HB3	1:AG:81:ARG:HH22	1.71	0.54
1:AI:152:ILE:HD12	1:AI:227:LEU:HG	1.88	0.54
1:AK:120:ILE:HG21	1:AK:220:PHE:CZ	2.42	0.54
1:AO:148:TYR:O	1:AO:152:ILE:HG12	2.07	0.54
1:AS:23:LYS:HD2	1:AS:42:ARG:NH2	2.22	0.54
1:R:120:ILE:HD12	1:R:169:MET:HG2	1.88	0.54
1:j:56:ILE:HD11	1:j:137:LEU:HD21	1.89	0.54
1:4:120:ILE:HG22	1:4:123:ILE:HD11	1.90	0.54
1:5:130:GLU:HB2	1:6:43:ILE:HB	1.89	0.54
1:7:44:TRP:CE2	1:8:127:ASP:HB3	2.42	0.54
1:AA:79:ASP:HB3	1:AA:81:ARG:NH1	2.19	0.54
1:AJ:32:TYR:HB3	1:AJ:40:PHE:CE1	2.43	0.54
1:R:210:VAL:O	1:W:76:ILE:HB	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:79:ASP:HB3	1:T:81:ARG:HH22	1.72	0.54
1:V:32:TYR:HB3	1:V:40:PHE:CE1	2.42	0.54
1:g:130:GLU:HB2	1:h:43:ILE:HB	1.89	0.54
1:h:79:ASP:HB2	1:h:118:PHE:HB3	1.89	0.54
1:o:79:ASP:HB2	1:o:118:PHE:HB3	1.90	0.54
1:r:152:ILE:HD12	1:r:227:LEU:HG	1.89	0.54
1:v:152:ILE:HD12	1:v:227:LEU:HG	1.89	0.54
1:AH:76:ILE:HB	1:AP:210:VAL:O	2.07	0.54
1:AM:215:ASP:CG	1:AM:216:GLU:H	2.16	0.54
1:AR:79:ASP:HB3	1:AR:81:ARG:HH22	1.72	0.54
1:AS:79:ASP:HB3	1:AS:81:ARG:NH1	2.18	0.54
1:AT:43:ILE:HB	1:AU:130:GLU:HB2	1.89	0.54
1:D:23:LYS:HD2	1:D:42:ARG:HH21	1.71	0.54
1:N:120:ILE:HD12	1:N:169:MET:HG2	1.89	0.54
1:P:111:GLU:HB2	1:P:178:LYS:HB2	1.89	0.54
1:P:152:ILE:HD12	1:P:227:LEU:HD23	1.89	0.54
1:b:79:ASP:HB2	1:b:118:PHE:HB3	1.90	0.54
1:i:76:ILE:HG21	1:p:210:VAL:HB	1.87	0.54
1:k:43:ILE:HB	1:m:130:GLU:HB2	1.90	0.54
1:w:79:ASP:HB2	1:w:118:PHE:HB3	1.90	0.54
1:x:120:ILE:HD12	1:x:169:MET:HG2	1.89	0.54
1:y:43:ILE:HB	1:z:130:GLU:HB2	1.89	0.54
1:7:169:MET:HB2	1:7:211:PHE:HB3	1.89	0.54
1:AD:121:GLU:HB3	1:AD:168:LYS:HB2	1.90	0.54
1:AM:43:ILE:HB	1:AN:130:GLU:HB2	1.90	0.54
1:AP:181:LEU:HD12	1:AP:182:GLY:N	2.22	0.54
1:AQ:111:GLU:HB2	1:AQ:178:LYS:HB2	1.88	0.54
1:AV:43:ILE:HG13	1:AV:43:ILE:O	2.06	0.54
1:N:43:ILE:HB	1:P:130:GLU:HB2	1.90	0.54
1:U:152:ILE:HD12	1:U:227:LEU:HG	1.89	0.54
1:m:152:ILE:HD12	1:m:227:LEU:HD23	1.89	0.54
1:v:43:ILE:O	1:v:43:ILE:HG13	2.06	0.54
1:v:43:ILE:HB	1:w:130:GLU:HB2	1.88	0.54
1:x:56:ILE:HD11	1:x:137:LEU:HD21	1.90	0.54
1:7:170:ARG:NH1	1:7:170:ARG:HB2	2.22	0.54
1:8:210:VAL:O	1:0:76:ILE:HB	2.07	0.54
1:AP:19:VAL:HA	1:AP:246:VAL:HG23	1.89	0.54
1:Ac:120:ILE:HD12	1:Ac:169:MET:HG2	1.89	0.54
1:C:79:ASP:HB3	1:C:81:ARG:HH22	1.72	0.54
1:O:76:ILE:HB	1:Q:210:VAL:O	2.08	0.54
1:f:76:ILE:HB	1:g:210:VAL:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:y:120:ILE:HG22	1:y:123:ILE:HD11	1.88	0.54
1:4:152:ILE:HD12	1:4:227:LEU:HD23	1.89	0.54
1:AE:79:ASP:HB3	1:AE:81:ARG:HH22	1.73	0.54
1:K:170:ARG:HB2	1:K:170:ARG:NH1	2.23	0.54
1:U:215:ASP:CG	1:U:216:GLU:H	2.15	0.54
1:k:79:ASP:HB3	1:k:81:ARG:HH22	1.71	0.54
1:q:23:LYS:HD2	1:q:42:ARG:NH2	2.22	0.54
1:s:32:TYR:HB3	1:s:40:PHE:CE1	2.42	0.54
1:w:204:SER:C	1:x:81:ARG:HH21	2.15	0.54
1:0:120:ILE:HG22	1:0:123:ILE:HD11	1.90	0.54
1:AM:23:LYS:HD2	1:AM:42:ARG:NH2	2.22	0.54
1:AW:79:ASP:HB3	1:AW:81:ARG:NH2	2.08	0.54
1:R:208:ARG:HE	1:R:210:VAL:HG21	1.73	0.54
1:b:56:ILE:HD11	1:b:137:LEU:HD21	1.90	0.54
1:g:127:ASP:HB3	1:h:44:TRP:CE2	2.42	0.54
1:m:23:LYS:HD2	1:m:42:ARG:NH2	2.23	0.54
1:2:172:GLN:HG2	1:2:208:ARG:HG3	1.89	0.54
1:7:215:ASP:CG	1:7:216:GLU:H	2.16	0.54
1:AV:76:ILE:HB	1:AX:210:VAL:O	2.08	0.54
1:AX:181:LEU:HD12	1:AX:182:GLY:N	2.23	0.54
1:Ac:23:LYS:HD2	1:Ac:42:ARG:NH2	2.23	0.54
1:Q:120:ILE:HD12	1:Q:169:MET:HG2	1.90	0.54
1:Z:79:ASP:HB3	1:Z:81:ARG:NH1	2.19	0.54
1:6:56:ILE:HD11	1:6:137:LEU:HD21	1.90	0.54
1:AE:215:ASP:CG	1:AE:216:GLU:H	2.14	0.54
1:Ab:79:ASP:HB2	1:Ab:118:PHE:HB3	1.89	0.54
1:A:130:GLU:HB2	1:I:43:ILE:HB	1.90	0.54
1:J:81:ARG:NH1	1:K:205:THR:HG22	2.22	0.54
1:K:169:MET:HB2	1:K:211:PHE:HB3	1.90	0.54
1:P:43:ILE:O	1:P:43:ILE:HG13	2.08	0.54
1:k:120:ILE:HG22	1:k:123:ILE:HD11	1.89	0.54
1:v:210:VAL:O	1:w:76:ILE:HB	2.08	0.54
1:AO:170:ARG:HH21	1:AO:208:ARG:NH1	2.06	0.54
1:AW:215:ASP:CG	1:AW:216:GLU:H	2.16	0.54
1:J:130:GLU:HB2	1:K:43:ILE:HB	1.90	0.53
1:P:210:VAL:O	1:Q:76:ILE:HB	2.08	0.53
1:S:130:GLU:HB2	1:T:43:ILE:HB	1.91	0.53
1:n:120:ILE:HG22	1:n:123:ILE:HD11	1.90	0.53
1:q:79:ASP:HB3	1:q:81:ARG:HH22	1.73	0.53
1:u:23:LYS:HD2	1:u:42:ARG:HH22	1.73	0.53
1:w:77:ASP:HB3	1:w:120:ILE:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:29:LEU:HD11	1:5:68:ILE:HD12	1.90	0.53
1:8:56:ILE:HD11	1:8:137:LEU:HD21	1.90	0.53
1:AP:76:ILE:HB	1:AQ:210:VAL:O	2.09	0.53
1:AT:44:TRP:CE2	1:AU:127:ASP:HB3	2.42	0.53
1:H:181:LEU:HD11	1:H:183:VAL:HG23	1.90	0.53
1:J:24:THR:HG22	1:J:218:ILE:HG13	1.89	0.53
1:O:130:GLU:HB2	1:Q:43:ILE:HB	1.89	0.53
1:f:215:ASP:CG	1:f:216:GLU:H	2.16	0.53
1:g:24:THR:HG22	1:g:218:ILE:HG13	1.90	0.53
1:4:120:ILE:HD12	1:4:169:MET:HG2	1.90	0.53
1:6:76:ILE:HB	1:AC:210:VAL:O	2.08	0.53
1:AM:79:ASP:HB3	1:AM:81:ARG:HH22	1.73	0.53
1:AO:111:GLU:HB2	1:AO:178:LYS:HB2	1.90	0.53
1:AP:56:ILE:HD11	1:AP:137:LEU:HD21	1.88	0.53
1:AQ:43:ILE:O	1:AQ:43:ILE:HG13	2.09	0.53
1:AT:24:THR:HG22	1:AT:218:ILE:HG13	1.90	0.53
1:AT:43:ILE:O	1:AT:43:ILE:HG13	2.08	0.53
1:AU:77:ASP:HB3	1:AU:120:ILE:HB	1.89	0.53
1:AX:29:LEU:HD11	1:AX:68:ILE:HD12	1.89	0.53
1:AZ:181:LEU:HD11	1:AZ:183:VAL:HG23	1.90	0.53
1:Ab:215:ASP:CG	1:Ab:216:GLU:H	2.15	0.53
1:E:79:ASP:HB2	1:E:118:PHE:HB3	1.90	0.53
1:m:111:GLU:HB2	1:m:178:LYS:HB2	1.89	0.53
1:u:28:PRO:HG2	1:u:70:LEU:HD21	1.90	0.53
1:x:43:ILE:HB	1:y:130:GLU:HB2	1.89	0.53
1:y:77:ASP:HB3	1:y:120:ILE:HB	1.90	0.53
1:AA:43:ILE:O	1:AA:43:ILE:HG13	2.08	0.53
1:AS:76:ILE:HB	1:AZ:210:VAL:O	2.08	0.53
1:AY:79:ASP:HB3	1:AY:81:ARG:HH22	1.73	0.53
1:E:56:ILE:HD11	1:E:137:LEU:HD21	1.90	0.53
1:G:43:ILE:HG13	1:G:43:ILE:O	2.09	0.53
1:m:32:TYR:CZ	1:m:42:ARG:HD3	2.43	0.53
1:o:210:VAL:O	1:t:76:ILE:HB	2.09	0.53
1:z:23:LYS:HD2	1:z:42:ARG:NH2	2.23	0.53
1:2:148:TYR:O	1:2:152:ILE:HG12	2.08	0.53
1:9:76:ILE:HB	1:AA:210:VAL:O	2.08	0.53
1:AJ:77:ASP:HB3	1:AJ:120:ILE:HB	1.90	0.53
1:AJ:79:ASP:HB2	1:AJ:118:PHE:HB3	1.91	0.53
1:AW:43:ILE:HB	1:AX:130:GLU:HB2	1.91	0.53
1:L:148:TYR:O	1:L:152:ILE:HG12	2.08	0.53
1:N:120:ILE:HG22	1:N:123:ILE:HD11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:215:ASP:CG	1:O:216:GLU:H	2.17	0.53
1:Y:224:LEU:HD12	1:Y:243:PHE:CZ	2.44	0.53
1:h:43:ILE:O	1:h:43:ILE:HG13	2.09	0.53
1:z:215:ASP:CG	1:z:216:GLU:H	2.16	0.53
1:AQ:56:ILE:HD11	1:AQ:137:LEU:HD21	1.89	0.53
1:AR:120:ILE:HG22	1:AR:123:ILE:HD11	1.89	0.53
1:AW:23:LYS:HD2	1:AW:42:ARG:NH2	2.23	0.53
1:AY:43:ILE:HB	1:Ad:130:GLU:HB2	1.90	0.53
1:Ac:215:ASP:OD1	1:Ac:216:GLU:N	2.35	0.53
1:Ac:227:LEU:HD11	1:Ac:235:LEU:HD11	1.90	0.53
1:B:43:ILE:HG13	1:B:43:ILE:O	2.08	0.53
1:E:40:PHE:HZ	1:E:158:PHE:HB2	1.74	0.53
1:l:76:ILE:HB	1:n:210:VAL:O	2.09	0.53
1:l:215:ASP:CG	1:l:216:GLU:H	2.17	0.53
1:p:76:ILE:HB	1:q:210:VAL:O	2.08	0.53
1:z:79:ASP:HB3	1:z:81:ARG:HH22	1.73	0.53
1:5:79:ASP:HB3	1:5:81:ARG:HH22	1.72	0.53
1:AG:215:ASP:CG	1:AG:216:GLU:H	2.16	0.53
1:AN:224:LEU:HD12	1:AN:243:PHE:CZ	2.44	0.53
1:Ad:40:PHE:HZ	1:Ad:158:PHE:HB2	1.74	0.53
1:B:210:VAL:O	1:C:76:ILE:HB	2.09	0.53
1:I:215:ASP:CG	1:I:216:GLU:H	2.16	0.53
1:L:127:ASP:HB3	1:S:44:TRP:CE2	2.44	0.53
1:P:23:LYS:HD2	1:P:42:ARG:NH2	2.24	0.53
1:P:224:LEU:HD11	1:P:246:VAL:HG11	1.91	0.53
1:e:224:LEU:HD12	1:e:243:PHE:CZ	2.44	0.53
1:m:172:GLN:HG2	1:m:208:ARG:HB2	1.91	0.53
1:s:224:LEU:HD11	1:s:246:VAL:HG11	1.91	0.53
1:2:43:ILE:O	1:2:43:ILE:HG13	2.09	0.53
1:AY:210:VAL:HB	1:Ad:76:ILE:HG21	1.91	0.53
1:Aa:29:LEU:HD21	1:Aa:68:ILE:HG21	1.90	0.53
1:Aa:43:ILE:HG13	1:Aa:43:ILE:O	2.09	0.53
1:A:76:ILE:HB	1:I:210:VAL:O	2.09	0.53
1:B:111:GLU:HB2	1:B:178:LYS:HB2	1.90	0.53
1:W:29:LEU:HD21	1:W:68:ILE:HG21	1.91	0.53
1:W:120:ILE:HG21	1:W:220:PHE:CZ	2.44	0.53
1:X:130:GLU:HB2	1:f:43:ILE:HB	1.91	0.53
1:Y:43:ILE:HG13	1:Y:43:ILE:O	2.08	0.53
1:k:32:TYR:HB3	1:k:40:PHE:CE1	2.44	0.53
1:t:56:ILE:HD11	1:t:137:LEU:HD21	1.90	0.53
1:7:43:ILE:HG13	1:7:43:ILE:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:215:ASP:OD1	1:AF:216:GLU:N	2.35	0.53
1:AQ:224:LEU:HD11	1:AQ:246:VAL:HG11	1.90	0.53
1:AW:77:ASP:HB3	1:AW:120:ILE:HB	1.91	0.53
1:g:79:ASP:HB3	1:g:81:ARG:HH22	1.73	0.53
1:i:172:GLN:HG2	1:i:208:ARG:HG3	1.90	0.53
1:m:56:ILE:HD11	1:m:137:LEU:HD21	1.90	0.53
1:n:19:VAL:HA	1:n:246:VAL:HG23	1.91	0.53
1:v:77:ASP:HB3	1:v:120:ILE:HB	1.91	0.53
1:4:56:ILE:HD11	1:4:137:LEU:HD21	1.90	0.53
1:6:79:ASP:HB2	1:6:118:PHE:HB3	1.90	0.53
1:9:127:ASP:HB3	1:AA:44:TRP:CE2	2.43	0.53
1:AO:44:TRP:CE2	1:AT:127:ASP:HB3	2.44	0.53
1:AU:79:ASP:HB3	1:AU:81:ARG:HH22	1.73	0.53
1:B:224:LEU:HD12	1:B:243:PHE:CZ	2.44	0.53
1:H:210:VAL:O	1:M:76:ILE:HB	2.09	0.53
1:I:43:ILE:HG13	1:I:43:ILE:O	2.09	0.53
1:N:32:TYR:HB3	1:N:40:PHE:CE1	2.44	0.53
1:W:56:ILE:HD11	1:W:137:LEU:HD21	1.91	0.53
1:X:32:TYR:HB3	1:X:40:PHE:CE2	2.44	0.53
1:e:210:VAL:O	1:j:76:ILE:HB	2.09	0.53
1:g:120:ILE:HD12	1:g:169:MET:HG2	1.90	0.53
1:j:43:ILE:HB	1:k:130:GLU:HB2	1.91	0.53
1:m:43:ILE:HG13	1:m:43:ILE:O	2.08	0.53
1:m:120:ILE:HG22	1:m:123:ILE:HD11	1.91	0.53
1:q:43:ILE:O	1:q:43:ILE:HG13	2.09	0.53
1:x:120:ILE:HG21	1:x:220:PHE:CZ	2.43	0.53
1:1:183:VAL:HB	1:1:197:LEU:HG	1.91	0.53
1:4:215:ASP:CG	1:4:216:GLU:H	2.17	0.53
1:AS:130:GLU:HB2	1:AZ:43:ILE:HB	1.91	0.53
1:AY:130:GLU:HB2	1:Ab:43:ILE:HB	1.91	0.53
1:Ac:79:ASP:HB3	1:Ac:81:ARG:HH22	1.73	0.53
1:C:210:VAL:O	1:D:76:ILE:HB	2.09	0.52
1:K:43:ILE:O	1:K:43:ILE:HG13	2.09	0.52
1:K:224:LEU:HD12	1:K:243:PHE:CZ	2.44	0.52
1:Z:215:ASP:CG	1:Z:216:GLU:H	2.15	0.52
1:n:79:ASP:HB3	1:n:81:ARG:HH22	1.74	0.52
1:n:181:LEU:HD12	1:n:182:GLY:N	2.24	0.52
1:v:208:ARG:HG2	1:v:210:VAL:HG22	1.90	0.52
1:1:224:LEU:HD12	1:1:243:PHE:CZ	2.44	0.52
1:AG:43:ILE:HG13	1:AG:43:ILE:O	2.09	0.52
1:AT:169:MET:HB2	1:AT:211:PHE:HB3	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:224:LEU:HD12	1:AT:243:PHE:CZ	2.44	0.52
1:C:120:ILE:HG21	1:C:220:PHE:CZ	2.44	0.52
1:D:181:LEU:HD12	1:D:182:GLY:N	2.23	0.52
1:G:121:GLU:HB3	1:G:168:LYS:HB2	1.92	0.52
1:J:152:ILE:HD12	1:J:227:LEU:HD22	1.91	0.52
1:L:43:ILE:HG13	1:L:43:ILE:O	2.10	0.52
1:T:215:ASP:CG	1:T:216:GLU:H	2.17	0.52
1:Z:120:ILE:HG21	1:Z:220:PHE:CZ	2.44	0.52
1:a:210:VAL:O	1:b:76:ILE:HB	2.09	0.52
1:b:43:ILE:HG13	1:b:43:ILE:O	2.09	0.52
1:c:227:LEU:HD11	1:c:235:LEU:HD11	1.90	0.52
1:f:23:LYS:HD2	1:f:42:ARG:NH2	2.24	0.52
1:x:40:PHE:HZ	1:x:158:PHE:HB2	1.74	0.52
1:3:130:GLU:HB2	1:4:43:ILE:HB	1.90	0.52
1:AE:127:ASP:HB3	1:AV:44:TRP:CE2	2.45	0.52
1:AI:215:ASP:CG	1:AI:216:GLU:H	2.17	0.52
1:AQ:210:VAL:HG12	1:AQ:212:GLU:OE1	2.10	0.52
1:P:56:ILE:HD11	1:P:137:LEU:HD21	1.90	0.52
1:X:79:ASP:HB2	1:X:118:PHE:HB3	1.92	0.52
1:q:130:GLU:HB2	1:s:43:ILE:HB	1.90	0.52
1:6:130:GLU:HB2	1:AC:43:ILE:HB	1.92	0.52
1:0:43:ILE:O	1:0:43:ILE:HG13	2.10	0.52
1:AA:181:LEU:HD12	1:AA:182:GLY:N	2.23	0.52
1:AC:181:LEU:HD11	1:AC:183:VAL:HG23	1.90	0.52
1:AC:224:LEU:HD12	1:AC:243:PHE:CZ	2.45	0.52
1:Ad:43:ILE:HG13	1:Ad:43:ILE:O	2.09	0.52
1:C:215:ASP:CG	1:C:216:GLU:H	2.18	0.52
1:H:43:ILE:HB	1:M:130:GLU:HB2	1.92	0.52
1:K:76:ILE:HB	1:L:210:VAL:O	2.09	0.52
1:X:76:ILE:HB	1:f:210:VAL:O	2.09	0.52
1:c:43:ILE:HB	1:d:130:GLU:HB2	1.91	0.52
1:e:43:ILE:HB	1:j:130:GLU:HB2	1.92	0.52
1:f:130:GLU:HB2	1:g:43:ILE:HB	1.91	0.52
1:t:120:ILE:HG21	1:t:220:PHE:CZ	2.44	0.52
1:0:23:LYS:HD2	1:0:42:ARG:NH2	2.24	0.52
1:AS:43:ILE:HG13	1:AS:43:ILE:O	2.09	0.52
1:C:79:ASP:HB3	1:C:81:ARG:NH1	2.23	0.52
1:H:224:LEU:HD12	1:H:243:PHE:CZ	2.45	0.52
1:J:23:LYS:HD2	1:J:42:ARG:NH2	2.23	0.52
1:Q:181:LEU:HD12	1:Q:182:GLY:N	2.24	0.52
1:R:75:GLY:O	1:R:76:ILE:HG12	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:120:ILE:HG22	1:S:123:ILE:HD11	1.91	0.52
1:AF:172:GLN:HG2	1:AF:208:ARG:HB2	1.92	0.52
1:AR:29:LEU:HD11	1:AR:68:ILE:HD12	1.92	0.52
1:D:210:VAL:O	1:E:76:ILE:HB	2.10	0.52
1:E:43:ILE:O	1:E:43:ILE:HG13	2.09	0.52
1:J:120:ILE:HD12	1:J:169:MET:HG2	1.91	0.52
1:S:120:ILE:HD12	1:S:169:MET:HG2	1.92	0.52
1:T:56:ILE:HD11	1:T:137:LEU:HD21	1.90	0.52
1:X:44:TRP:CE2	1:Y:127:ASP:HB3	2.44	0.52
1:e:56:ILE:HD11	1:e:137:LEU:HD21	1.91	0.52
1:g:77:ASP:HB3	1:g:120:ILE:HB	1.90	0.52
1:i:76:ILE:HB	1:p:210:VAL:O	2.10	0.52
1:9:210:VAL:O	1:Ab:76:ILE:HB	2.10	0.52
1:AB:183:VAL:HB	1:AB:197:LEU:HG	1.91	0.52
1:AK:19:VAL:HB	1:AK:247:LEU:HD22	1.91	0.52
1:F:120:ILE:HG21	1:F:220:PHE:CZ	2.45	0.52
1:K:127:ASP:HB3	1:L:44:TRP:CE2	2.44	0.52
1:Q:19:VAL:HA	1:Q:246:VAL:HG23	1.90	0.52
1:Z:79:ASP:HB2	1:Z:118:PHE:HB3	1.92	0.52
1:c:120:ILE:HG21	1:c:220:PHE:CZ	2.45	0.52
1:4:43:ILE:HG13	1:4:43:ILE:O	2.08	0.52
1:8:43:ILE:HD11	1:8:157:PHE:HE1	1.74	0.52
1:8:77:ASP:HB3	1:8:120:ILE:HB	1.91	0.52
1:AB:79:ASP:HB2	1:AB:118:PHE:HB3	1.91	0.52
1:AR:170:ARG:NH1	1:AR:170:ARG:HB2	2.24	0.52
1:AX:43:ILE:HG13	1:AX:43:ILE:O	2.09	0.52
1:AY:183:VAL:HB	1:AY:197:LEU:HG	1.92	0.52
1:AZ:224:LEU:HD12	1:AZ:243:PHE:CZ	2.45	0.52
1:Ac:120:ILE:HG21	1:Ac:220:PHE:CZ	2.45	0.52
1:D:79:ASP:HB3	1:D:81:ARG:NH1	2.19	0.52
1:R:76:ILE:HB	1:U:210:VAL:O	2.10	0.52
1:S:43:ILE:O	1:S:43:ILE:HG13	2.10	0.52
1:T:43:ILE:HG13	1:T:43:ILE:O	2.09	0.52
1:X:32:TYR:CZ	1:X:42:ARG:HD3	2.45	0.52
1:c:215:ASP:CG	1:c:216:GLU:H	2.18	0.52
1:d:111:GLU:HB2	1:d:178:LYS:HB2	1.91	0.52
1:f:79:ASP:HB3	1:f:81:ARG:NH2	2.10	0.52
1:j:183:VAL:HB	1:j:197:LEU:HG	1.91	0.52
1:o:77:ASP:HB3	1:o:120:ILE:HB	1.92	0.52
1:w:210:VAL:HB	1:x:76:ILE:HG21	1.92	0.52
1:AE:120:ILE:HG21	1:AE:220:PHE:CZ	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:120:ILE:HG21	1:AF:220:PHE:CZ	2.45	0.52
1:AH:23:LYS:HD2	1:AH:42:ARG:NH2	2.24	0.52
1:AW:120:ILE:HG22	1:AW:123:ILE:HD11	1.92	0.52
1:Ac:172:GLN:HG2	1:Ac:208:ARG:HB2	1.92	0.52
1:A:79:ASP:HB2	1:A:118:PHE:HB3	1.91	0.52
1:V:16:TYR:CE2	1:V:164:LEU:HG	2.45	0.52
1:c:43:ILE:O	1:c:43:ILE:HG13	2.09	0.52
1:d:43:ILE:HB	1:e:130:GLU:HB2	1.91	0.52
1:i:127:ASP:HB3	1:p:44:TRP:CE2	2.44	0.52
1:j:210:VAL:O	1:k:76:ILE:HB	2.10	0.52
1:t:19:VAL:HB	1:t:247:LEU:HD22	1.92	0.52
1:v:210:VAL:HG12	1:v:212:GLU:OE2	2.08	0.52
1:x:19:VAL:HB	1:x:247:LEU:HD22	1.91	0.52
1:AI:75:GLY:O	1:AI:76:ILE:HG12	2.10	0.52
1:AP:210:VAL:HG12	1:AP:212:GLU:OE1	2.10	0.52
1:AW:16:TYR:CE2	1:AW:164:LEU:HG	2.45	0.52
1:Ac:76:ILE:HB	1:Ad:210:VAL:O	2.10	0.52
1:G:111:GLU:HB2	1:G:178:LYS:HB2	1.91	0.52
1:Y:210:VAL:O	1:Z:76:ILE:HB	2.08	0.52
1:a:181:LEU:HD12	1:a:182:GLY:N	2.25	0.52
1:k:181:LEU:HD11	1:k:183:VAL:HG23	1.92	0.52
1:m:79:ASP:HB2	1:m:118:PHE:HB3	1.92	0.52
1:t:29:LEU:HD21	1:t:68:ILE:HG21	1.91	0.52
1:3:183:VAL:HB	1:3:197:LEU:HG	1.92	0.52
1:4:224:LEU:HD11	1:4:246:VAL:HG11	1.92	0.52
1:5:76:ILE:HB	1:6:210:VAL:O	2.09	0.52
1:7:224:LEU:HD12	1:7:243:PHE:CZ	2.44	0.52
1:9:80:LEU:C	1:9:81:ARG:HD2	2.35	0.52
1:AM:43:ILE:HG13	1:AM:43:ILE:O	2.10	0.52
1:AV:29:LEU:HD13	1:AV:56:ILE:HG22	1.92	0.52
1:M:79:ASP:HB2	1:M:118:PHE:HB3	1.92	0.51
1:O:120:ILE:HG21	1:O:220:PHE:CZ	2.45	0.51
1:e:181:LEU:HD11	1:e:183:VAL:HG23	1.91	0.51
1:f:16:TYR:CE2	1:f:164:LEU:HG	2.45	0.51
1:l:181:LEU:HD11	1:l:183:VAL:HG23	1.92	0.51
1:p:127:ASP:HB3	1:q:44:TRP:CE2	2.45	0.51
1:3:76:ILE:HB	1:4:210:VAL:O	2.10	0.51
1:0:120:ILE:HD12	1:0:169:MET:HG2	1.92	0.51
1:AA:29:LEU:HD11	1:AA:68:ILE:HD12	1.91	0.51
1:AD:76:ILE:HB	1:AF:210:VAL:O	2.10	0.51
1:AE:85:SER:HA	1:AV:200:LYS:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:127:ASP:HB3	1:AX:44:TRP:CE2	2.45	0.51
1:C:43:ILE:O	1:C:43:ILE:HG13	2.10	0.51
1:F:215:ASP:CG	1:F:216:GLU:H	2.18	0.51
1:I:16:TYR:CE2	1:I:164:LEU:HG	2.45	0.51
1:M:43:ILE:O	1:M:43:ILE:HG13	2.10	0.51
1:M:79:ASP:HB3	1:M:81:ARG:NH1	2.20	0.51
1:M:183:VAL:HB	1:M:197:LEU:HG	1.92	0.51
1:N:29:LEU:HD11	1:N:68:ILE:HD12	1.93	0.51
1:R:148:TYR:O	1:R:152:ILE:HG12	2.10	0.51
1:X:210:VAL:O	1:Y:76:ILE:HB	2.11	0.51
1:h:224:LEU:HD12	1:h:243:PHE:CZ	2.45	0.51
1:l:111:GLU:HB2	1:l:178:LYS:HB2	1.91	0.51
1:6:215:ASP:CG	1:6:216:GLU:H	2.18	0.51
1:9:44:TRP:CE2	1:Ab:127:ASP:HB3	2.45	0.51
1:AF:130:GLU:HB2	1:AG:43:ILE:HB	1.92	0.51
1:AL:224:LEU:HD11	1:AL:246:VAL:HG11	1.93	0.51
1:AX:169:MET:HB2	1:AX:211:PHE:HB3	1.92	0.51
1:Ad:120:ILE:HG22	1:Ad:123:ILE:HD11	1.92	0.51
1:Ad:228:PHE:HD1	1:Ad:229:PHE:N	2.09	0.51
1:C:224:LEU:HD12	1:C:243:PHE:CZ	2.46	0.51
1:I:23:LYS:HD2	1:I:42:ARG:NH2	2.24	0.51
1:W:19:VAL:HB	1:W:247:LEU:HD22	1.92	0.51
1:b:43:ILE:HB	1:c:130:GLU:HB2	1.92	0.51
1:b:77:ASP:HB3	1:b:120:ILE:HB	1.93	0.51
1:c:56:ILE:HD11	1:c:137:LEU:HD21	1.92	0.51
1:c:120:ILE:HD12	1:c:169:MET:HG2	1.92	0.51
1:j:43:ILE:HG13	1:j:43:ILE:O	2.09	0.51
1:j:79:ASP:HB2	1:j:118:PHE:HB3	1.92	0.51
1:l:23:LYS:HD2	1:l:42:ARG:NH2	2.24	0.51
1:v:75:GLY:O	1:v:76:ILE:HG12	2.10	0.51
1:y:16:TYR:CE2	1:y:164:LEU:HG	2.46	0.51
1:1:44:TRP:CE2	1:2:127:ASP:HB3	2.45	0.51
1:AC:224:LEU:HD11	1:AC:246:VAL:HG11	1.92	0.51
1:AG:228:PHE:HD1	1:AG:229:PHE:N	2.08	0.51
1:AH:210:VAL:O	1:AI:76:ILE:HB	2.11	0.51
1:AJ:32:TYR:HB3	1:AJ:40:PHE:CZ	2.45	0.51
1:Ac:130:GLU:HB2	1:Ad:43:ILE:HB	1.93	0.51
1:D:43:ILE:HB	1:E:130:GLU:HB2	1.92	0.51
1:E:228:PHE:HD1	1:E:229:PHE:N	2.09	0.51
1:I:130:GLU:HB2	1:J:43:ILE:HB	1.91	0.51
1:R:224:LEU:HD12	1:R:243:PHE:CZ	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:111:GLU:HB2	1:U:178:LYS:HB2	1.93	0.51
1:V:206:TYR:HB2	1:V:208:ARG:HH12	1.75	0.51
1:Y:29:LEU:HD13	1:Y:56:ILE:HG22	1.93	0.51
1:Y:224:LEU:HD11	1:Y:246:VAL:HG11	1.93	0.51
1:f:43:ILE:O	1:f:43:ILE:HG13	2.09	0.51
1:u:43:ILE:HB	1:v:130:GLU:HB2	1.92	0.51
1:w:32:TYR:HB3	1:w:40:PHE:CZ	2.45	0.51
1:w:210:VAL:O	1:x:76:ILE:HB	2.11	0.51
1:2:44:TRP:CE2	1:7:127:ASP:HB3	2.45	0.51
1:2:79:ASP:HB3	1:2:81:ARG:HH22	1.75	0.51
1:6:43:ILE:HG13	1:6:43:ILE:O	2.10	0.51
1:AB:210:VAL:HB	1:AG:76:ILE:HG21	1.92	0.51
1:AD:43:ILE:O	1:AD:43:ILE:HG13	2.09	0.51
1:AD:111:GLU:HB2	1:AD:178:LYS:HB2	1.92	0.51
1:AE:79:ASP:HB3	1:AE:81:ARG:NH1	2.22	0.51
1:AJ:215:ASP:OD1	1:AJ:216:GLU:N	2.37	0.51
1:AK:29:LEU:HD21	1:AK:68:ILE:HG21	1.92	0.51
1:AN:111:GLU:HB2	1:AN:178:LYS:HB3	1.92	0.51
1:AV:40:PHE:CE2	1:AV:158:PHE:HB2	2.46	0.51
1:Ac:56:ILE:HD11	1:Ac:137:LEU:HD21	1.93	0.51
1:K:24:THR:HG22	1:K:218:ILE:HG13	1.92	0.51
1:c:181:LEU:HD11	1:c:183:VAL:HG23	1.93	0.51
1:d:43:ILE:HG13	1:d:43:ILE:O	2.09	0.51
1:e:79:ASP:HB2	1:e:118:PHE:HB3	1.93	0.51
1:e:224:LEU:HD11	1:e:246:VAL:HG11	1.92	0.51
1:k:29:LEU:HD11	1:k:68:ILE:HD12	1.92	0.51
1:n:120:ILE:HD12	1:n:169:MET:HG2	1.93	0.51
1:o:148:TYR:O	1:o:152:ILE:HG12	2.10	0.51
1:p:228:PHE:HD1	1:p:229:PHE:N	2.08	0.51
1:u:120:ILE:HG21	1:u:220:PHE:CZ	2.46	0.51
1:1:43:ILE:HG13	1:1:43:ILE:O	2.11	0.51
1:0:16:TYR:CE2	1:0:164:LEU:HG	2.46	0.51
1:AC:79:ASP:CB	1:AC:81:ARG:HH22	2.20	0.51
1:AF:43:ILE:O	1:AF:43:ILE:HG13	2.11	0.51
1:AO:43:ILE:O	1:AO:43:ILE:HG13	2.10	0.51
1:A:43:ILE:HB	1:B:130:GLU:HB2	1.92	0.51
1:A:44:TRP:CE2	1:B:127:ASP:HB3	2.44	0.51
1:E:43:ILE:HB	1:F:130:GLU:HB2	1.93	0.51
1:G:29:LEU:HD21	1:G:68:ILE:HG21	1.91	0.51
1:N:181:LEU:HD11	1:N:183:VAL:HG23	1.93	0.51
1:S:111:GLU:HB2	1:S:178:LYS:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:43:ILE:HB	1:Y:130:GLU:HB2	1.91	0.51
1:Z:224:LEU:HD12	1:Z:243:PHE:CZ	2.46	0.51
1:b:40:PHE:HZ	1:b:158:PHE:HB2	1.74	0.51
1:b:148:TYR:O	1:b:152:ILE:HG12	2.11	0.51
1:f:120:ILE:HD12	1:f:169:MET:HG2	1.92	0.51
1:f:120:ILE:HG22	1:f:123:ILE:HD11	1.93	0.51
1:i:43:ILE:O	1:i:43:ILE:HG13	2.11	0.51
1:p:43:ILE:O	1:p:43:ILE:HG13	2.10	0.51
1:y:228:PHE:HD2	1:y:229:PHE:H	1.58	0.51
1:AL:210:VAL:O	1:AM:76:ILE:HB	2.10	0.51
1:AV:122:GLU:HB2	1:AV:167:LYS:HB2	1.91	0.51
1:Ad:56:ILE:HD11	1:Ad:137:LEU:HD21	1.92	0.51
1:O:23:LYS:HD2	1:O:42:ARG:NH2	2.26	0.51
1:b:120:ILE:HG22	1:b:123:ILE:HD11	1.92	0.51
1:o:32:TYR:HB3	1:o:40:PHE:CZ	2.46	0.51
1:p:120:ILE:HD12	1:p:169:MET:HG2	1.92	0.51
1:p:224:LEU:HD12	1:p:243:PHE:CZ	2.46	0.51
1:x:79:ASP:HB2	1:x:118:PHE:HB3	1.93	0.51
1:x:175:ARG:NH1	1:x:175:ARG:HB2	2.26	0.51
1:4:224:LEU:HD12	1:4:243:PHE:CZ	2.46	0.51
1:9:40:PHE:CE2	1:9:158:PHE:HB2	2.45	0.51
1:AD:29:LEU:HD21	1:AD:68:ILE:HG21	1.91	0.51
1:AG:77:ASP:HB3	1:AG:120:ILE:HB	1.93	0.51
1:AI:210:VAL:HG12	1:AI:212:GLU:OE2	2.10	0.51
1:AP:120:ILE:HG22	1:AP:123:ILE:HD11	1.92	0.51
1:AP:148:TYR:O	1:AP:152:ILE:HG12	2.11	0.51
1:AR:181:LEU:HD11	1:AR:183:VAL:HG23	1.93	0.51
1:Ab:120:ILE:HG21	1:Ab:220:PHE:CZ	2.45	0.51
1:Ab:224:LEU:HD12	1:Ab:243:PHE:CZ	2.46	0.51
1:Ad:77:ASP:HB3	1:Ad:120:ILE:HB	1.92	0.51
1:B:120:ILE:HG21	1:B:220:PHE:CZ	2.46	0.51
1:E:210:VAL:O	1:F:76:ILE:HB	2.11	0.51
1:I:120:ILE:HG22	1:I:123:ILE:HD11	1.93	0.51
1:I:181:LEU:HD11	1:I:183:VAL:HG23	1.93	0.51
1:O:43:ILE:HB	1:r:130:GLU:HB2	1.93	0.51
1:Q:120:ILE:HG22	1:Q:123:ILE:HD11	1.92	0.51
1:U:23:LYS:HD2	1:U:42:ARG:NH2	2.26	0.51
1:a:43:ILE:O	1:a:43:ILE:HG13	2.09	0.51
1:o:76:ILE:HB	1:r:210:VAL:O	2.10	0.51
1:o:224:LEU:HD12	1:o:243:PHE:CZ	2.46	0.51
1:q:76:ILE:HB	1:s:210:VAL:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:s:111:GLU:HB2	1:s:178:LYS:HB2	1.93	0.51
1:w:148:TYR:O	1:w:152:ILE:HG12	2.11	0.51
1:w:224:LEU:HD12	1:w:243:PHE:CZ	2.46	0.51
1:5:215:ASP:CG	1:5:216:GLU:H	2.18	0.51
1:AF:23:LYS:HD2	1:AF:42:ARG:NH2	2.25	0.51
1:AL:16:TYR:CE2	1:AL:164:LEU:HG	2.45	0.51
1:AU:43:ILE:HB	1:AW:130:GLU:HB2	1.92	0.51
1:E:77:ASP:HB3	1:E:120:ILE:HB	1.93	0.51
1:M:210:VAL:O	1:N:76:ILE:HB	2.10	0.51
1:j:215:ASP:CG	1:j:216:GLU:H	2.18	0.51
1:t:43:ILE:HG13	1:t:43:ILE:O	2.11	0.51
1:t:81:ARG:HB2	1:t:116:VAL:HB	1.91	0.51
1:AH:215:ASP:OD1	1:AH:216:GLU:N	2.37	0.51
1:AI:111:GLU:HB2	1:AI:178:LYS:HB2	1.92	0.51
1:AJ:224:LEU:HD12	1:AJ:243:PHE:CZ	2.46	0.51
1:AP:183:VAL:HB	1:AP:197:LEU:HG	1.92	0.51
1:AR:215:ASP:CG	1:AR:216:GLU:H	2.19	0.51
1:Ab:43:ILE:O	1:Ab:43:ILE:HG13	2.10	0.51
1:Ac:181:LEU:HD11	1:Ac:183:VAL:HG23	1.93	0.51
1:E:183:VAL:HB	1:E:197:LEU:HG	1.92	0.51
1:L:111:GLU:HB2	1:L:178:LYS:HB2	1.92	0.51
1:L:120:ILE:HG21	1:L:220:PHE:CZ	2.46	0.51
1:S:224:LEU:HD12	1:S:243:PHE:CZ	2.46	0.51
1:U:76:ILE:HA	1:U:123:ILE:HD13	1.93	0.51
1:V:224:LEU:HD11	1:V:246:VAL:HG11	1.92	0.51
1:g:152:ILE:HD12	1:g:227:LEU:HD22	1.93	0.51
1:o:75:GLY:O	1:o:76:ILE:HG12	2.11	0.51
1:o:208:ARG:HE	1:o:210:VAL:HG21	1.75	0.51
1:p:215:ASP:CG	1:p:216:GLU:H	2.19	0.51
1:q:210:VAL:HG12	1:q:212:GLU:OE2	2.11	0.51
1:u:181:LEU:HD11	1:u:183:VAL:HG23	1.93	0.51
1:1:210:VAL:O	1:2:76:ILE:HB	2.11	0.51
1:9:40:PHE:HE2	1:9:158:PHE:HB2	1.76	0.51
1:AF:76:ILE:HB	1:AG:210:VAL:O	2.10	0.51
1:AG:120:ILE:HG22	1:AG:123:ILE:HD11	1.92	0.51
1:AJ:148:TYR:O	1:AJ:152:ILE:HG12	2.11	0.51
1:AM:166:ALA:HB3	1:AM:169:MET:HG3	1.93	0.51
1:AM:210:VAL:O	1:AN:76:ILE:HB	2.10	0.51
1:AR:76:ILE:HB	1:AS:210:VAL:O	2.09	0.51
1:AU:40:PHE:CZ	1:AU:158:PHE:HB2	2.46	0.51
1:F:181:LEU:HD11	1:F:183:VAL:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:228:PHE:HD1	1:I:229:PHE:N	2.09	0.50
1:R:77:ASP:HB3	1:R:120:ILE:HB	1.92	0.50
1:b:228:PHE:HD1	1:b:229:PHE:N	2.09	0.50
1:h:127:ASP:HB3	1:i:44:TRP:CE2	2.45	0.50
1:i:23:LYS:HD2	1:i:42:ARG:NH2	2.27	0.50
1:l:120:ILE:HG21	1:l:220:PHE:CZ	2.46	0.50
1:s:130:GLU:HB2	1:t:43:ILE:HB	1.91	0.50
1:0:228:PHE:HD1	1:0:229:PHE:N	2.09	0.50
1:AB:120:ILE:HG22	1:AB:123:ILE:HD11	1.94	0.50
1:AF:120:ILE:HD12	1:AF:169:MET:HG2	1.93	0.50
1:AM:44:TRP:CE2	1:AN:127:ASP:HB3	2.46	0.50
1:AN:43:ILE:HB	1:AO:130:GLU:HB2	1.92	0.50
1:AR:59:LEU:O	1:AR:145:ARG:HG3	2.11	0.50
1:AW:43:ILE:O	1:AW:43:ILE:HG13	2.10	0.50
1:Aa:224:LEU:HD11	1:Aa:246:VAL:HG11	1.93	0.50
1:E:120:ILE:HG22	1:E:123:ILE:HD11	1.92	0.50
1:I:120:ILE:HD12	1:I:169:MET:HG2	1.93	0.50
1:T:148:TYR:O	1:T:152:ILE:HG12	2.11	0.50
1:U:224:LEU:HD12	1:U:243:PHE:CZ	2.46	0.50
1:b:183:VAL:HB	1:b:197:LEU:HG	1.92	0.50
1:f:228:PHE:HD1	1:f:229:PHE:N	2.09	0.50
1:r:111:GLU:HB2	1:r:178:LYS:HB2	1.93	0.50
1:s:16:TYR:CE2	1:s:164:LEU:HG	2.45	0.50
1:u:210:VAL:O	1:v:76:ILE:HB	2.10	0.50
1:5:32:TYR:CZ	1:5:42:ARG:HD3	2.47	0.50
1:AA:169:MET:HB2	1:AA:211:PHE:HB3	1.92	0.50
1:AK:40:PHE:HZ	1:AK:158:PHE:HB2	1.75	0.50
1:AP:79:ASP:HB2	1:AP:118:PHE:HB3	1.93	0.50
1:Aa:111:GLU:HB2	1:Aa:178:LYS:HB2	1.92	0.50
1:B:224:LEU:HD11	1:B:246:VAL:HG11	1.93	0.50
1:H:224:LEU:HD11	1:H:246:VAL:HG11	1.92	0.50
1:M:215:ASP:CG	1:M:216:GLU:H	2.18	0.50
1:N:40:PHE:CZ	1:N:158:PHE:HB2	2.46	0.50
1:S:32:TYR:HB3	1:S:40:PHE:CZ	2.46	0.50
1:U:130:GLU:HB2	1:l:43:ILE:HB	1.92	0.50
1:Z:43:ILE:HG13	1:Z:43:ILE:O	2.10	0.50
1:d:29:LEU:HD21	1:d:68:ILE:HG21	1.92	0.50
1:n:75:GLY:O	1:n:76:ILE:HG12	2.11	0.50
1:o:16:TYR:CE2	1:o:164:LEU:HG	2.47	0.50
1:z:210:VAL:O	1:l:76:ILE:HB	2.10	0.50
1:5:79:ASP:HB2	1:5:118:PHE:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:23:LYS:HD2	1:8:42:ARG:NH2	2.26	0.50
1:0:181:LEU:HD11	1:0:183:VAL:HG23	1.94	0.50
1:AI:32:TYR:CZ	1:AI:42:ARG:HD3	2.46	0.50
1:B:79:ASP:HB2	1:B:118:PHE:HB3	1.93	0.50
1:B:122:GLU:HB2	1:B:167:LYS:HB2	1.93	0.50
1:X:40:PHE:CZ	1:X:158:PHE:HB2	2.46	0.50
1:b:210:VAL:O	1:c:76:ILE:HB	2.10	0.50
1:f:77:ASP:HB3	1:f:120:ILE:HB	1.94	0.50
1:i:120:ILE:HG21	1:i:220:PHE:CZ	2.46	0.50
1:r:76:ILE:HA	1:r:123:ILE:HD13	1.93	0.50
1:r:224:LEU:HD12	1:r:243:PHE:CZ	2.46	0.50
1:s:215:ASP:CG	1:s:216:GLU:H	2.19	0.50
1:t:181:LEU:HD11	1:t:183:VAL:HG23	1.93	0.50
1:v:23:LYS:HD2	1:v:42:ARG:NH2	2.26	0.50
1:x:148:TYR:O	1:x:152:ILE:HG12	2.11	0.50
1:5:181:LEU:HD11	1:5:183:VAL:HG23	1.93	0.50
1:9:200:LYS:O	1:Ab:85:SER:HA	2.11	0.50
1:AE:43:ILE:HG13	1:AE:43:ILE:O	2.11	0.50
1:AH:120:ILE:HG21	1:AH:220:PHE:CZ	2.46	0.50
1:AL:228:PHE:HD1	1:AL:229:PHE:H	1.58	0.50
1:AN:44:TRP:CE2	1:AO:127:ASP:HB3	2.46	0.50
1:AP:75:GLY:O	1:AP:76:ILE:HG12	2.12	0.50
1:AV:23:LYS:HD2	1:AV:42:ARG:HH21	1.76	0.50
1:A:210:VAL:O	1:B:76:ILE:HB	2.11	0.50
1:B:75:GLY:O	1:B:76:ILE:HG12	2.12	0.50
1:r:75:GLY:O	1:r:76:ILE:HG12	2.12	0.50
1:y:215:ASP:CG	1:y:216:GLU:H	2.19	0.50
1:1:181:LEU:HD11	1:1:183:VAL:HG23	1.94	0.50
1:2:215:ASP:CG	1:2:216:GLU:H	2.18	0.50
1:3:148:TYR:O	1:3:152:ILE:HG12	2.12	0.50
1:6:183:VAL:HB	1:6:197:LEU:HG	1.93	0.50
1:9:130:GLU:HB2	1:AA:43:ILE:HB	1.93	0.50
1:AL:148:TYR:O	1:AL:152:ILE:HG12	2.12	0.50
1:AU:148:TYR:O	1:AU:152:ILE:HG12	2.11	0.50
1:AZ:224:LEU:HD11	1:AZ:246:VAL:HG11	1.92	0.50
1:B:29:LEU:HD13	1:B:56:ILE:HG22	1.93	0.50
1:D:43:ILE:HG13	1:D:43:ILE:O	2.12	0.50
1:F:43:ILE:O	1:F:43:ILE:HG13	2.11	0.50
1:N:77:ASP:HB3	1:N:120:ILE:HB	1.94	0.50
1:R:29:LEU:HD21	1:R:68:ILE:HG21	1.94	0.50
1:R:32:TYR:HB3	1:R:40:PHE:CZ	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:120:ILE:HG21	1:Y:220:PHE:CZ	2.46	0.50
1:f:181:LEU:HD11	1:f:183:VAL:HG23	1.92	0.50
1:g:111:GLU:HB2	1:g:178:LYS:HB2	1.93	0.50
1:t:228:PHE:HD1	1:t:229:PHE:H	1.59	0.50
1:v:224:LEU:HD12	1:v:243:PHE:CZ	2.47	0.50
1:3:120:ILE:HG22	1:3:123:ILE:HD11	1.93	0.50
1:7:227:LEU:HD21	1:7:235:LEU:HD11	1.93	0.50
1:9:120:ILE:HG21	1:9:220:PHE:CZ	2.47	0.50
1:AI:224:LEU:HD12	1:AI:243:PHE:CZ	2.47	0.50
1:AJ:16:TYR:CE2	1:AJ:164:LEU:HG	2.47	0.50
1:AK:43:ILE:HG13	1:AK:43:ILE:O	2.10	0.50
1:AN:43:ILE:O	1:AN:43:ILE:HG13	2.11	0.50
1:AR:79:ASP:HB2	1:AR:118:PHE:HB3	1.94	0.50
1:F:210:VAL:O	1:G:76:ILE:HB	2.11	0.50
1:T:40:PHE:CE1	1:T:158:PHE:HB2	2.46	0.50
1:Y:75:GLY:O	1:Y:76:ILE:HG12	2.12	0.50
1:Y:122:GLU:HB2	1:Y:167:LYS:HB2	1.92	0.50
1:c:210:VAL:O	1:d:76:ILE:HB	2.11	0.50
1:o:200:LYS:O	1:t:85:SER:HA	2.12	0.50
1:z:43:ILE:HG13	1:z:43:ILE:O	2.11	0.50
1:3:77:ASP:HB3	1:3:120:ILE:HB	1.92	0.50
1:9:29:LEU:HD13	1:9:56:ILE:HG22	1.93	0.50
1:AD:79:ASP:HB3	1:AD:81:ARG:NH1	2.23	0.50
1:AI:210:VAL:O	1:AJ:76:ILE:HB	2.11	0.50
1:AN:120:ILE:HG22	1:AN:123:ILE:HD11	1.94	0.50
1:AY:210:VAL:O	1:Ad:76:ILE:HB	2.12	0.50
1:S:127:ASP:HB3	1:T:44:TRP:CE2	2.46	0.50
1:V:131:ILE:HG13	1:W:43:ILE:HD12	1.93	0.50
1:W:215:ASP:CG	1:W:216:GLU:H	2.20	0.50
1:Z:75:GLY:O	1:Z:76:ILE:HG12	2.11	0.50
1:g:56:ILE:HD11	1:g:137:LEU:HD21	1.94	0.50
1:i:111:GLU:HB2	1:i:178:LYS:HB2	1.92	0.50
1:2:148:TYR:HA	1:2:151:GLU:HG3	1.93	0.50
1:9:210:VAL:HG12	1:9:212:GLU:OE1	2.11	0.50
1:AA:208:ARG:HG2	1:AA:210:VAL:HG23	1.94	0.50
1:AH:210:VAL:HG12	1:AH:212:GLU:OE1	2.12	0.50
1:AI:23:LYS:HD2	1:AI:42:ARG:NH2	2.27	0.50
1:AJ:75:GLY:O	1:AJ:76:ILE:HG12	2.12	0.50
1:B:200:LYS:O	1:C:85:SER:HA	2.11	0.50
1:S:215:ASP:CG	1:S:216:GLU:H	2.20	0.50
1:X:127:ASP:HB3	1:f:44:TRP:CE2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:111:GLU:HB2	1:Y:178:LYS:HB2	1.92	0.50
1:Y:200:LYS:O	1:Z:85:SER:HA	2.12	0.50
1:5:77:ASP:HB3	1:5:120:ILE:HB	1.93	0.50
1:8:43:ILE:HB	1:0:130:GLU:HB2	1.92	0.50
1:AB:130:GLU:HB2	1:AE:43:ILE:HB	1.94	0.50
1:AO:40:PHE:CZ	1:AO:158:PHE:HB2	2.46	0.50
1:AO:43:ILE:HB	1:AT:130:GLU:HB2	1.93	0.50
1:AZ:152:ILE:HD12	1:AZ:227:LEU:HG	1.94	0.50
1:Aa:120:ILE:HG21	1:Aa:220:PHE:CZ	2.47	0.50
1:Ac:210:VAL:HG12	1:Ac:212:GLU:OE1	2.12	0.50
1:I:75:GLY:O	1:I:76:ILE:HG12	2.12	0.49
1:R:215:ASP:CG	1:R:216:GLU:H	2.20	0.49
1:q:224:LEU:HD11	1:q:246:VAL:HG11	1.94	0.49
1:y:111:GLU:HB2	1:y:178:LYS:HB2	1.94	0.49
1:1:64:ILE:HD12	1:1:136:TRP:HZ2	1.77	0.49
1:7:224:LEU:HD11	1:7:246:VAL:HG11	1.94	0.49
1:AK:148:TYR:O	1:AK:152:ILE:HG12	2.12	0.49
1:AK:215:ASP:CG	1:AK:216:GLU:H	2.20	0.49
1:AL:181:LEU:HD11	1:AL:183:VAL:HG23	1.94	0.49
1:AL:210:VAL:HB	1:AM:76:ILE:HG21	1.94	0.49
1:AQ:224:LEU:HD12	1:AQ:243:PHE:CZ	2.46	0.49
1:AY:120:ILE:HG22	1:AY:123:ILE:HD11	1.93	0.49
1:A:120:ILE:HG22	1:A:123:ILE:HD11	1.93	0.49
1:M:40:PHE:HZ	1:M:158:PHE:CD1	2.30	0.49
1:Q:75:GLY:O	1:Q:76:ILE:HG12	2.13	0.49
1:X:120:ILE:HG21	1:X:220:PHE:CZ	2.47	0.49
1:c:111:GLU:HB2	1:c:178:LYS:HB2	1.94	0.49
1:d:120:ILE:HG21	1:d:220:PHE:CZ	2.47	0.49
1:i:40:PHE:CZ	1:i:158:PHE:HB2	2.46	0.49
1:n:40:PHE:HZ	1:n:158:PHE:CD1	2.30	0.49
1:q:56:ILE:HD11	1:q:137:LEU:HD21	1.95	0.49
1:r:23:LYS:HD2	1:r:42:ARG:NH2	2.26	0.49
1:v:76:ILE:HA	1:v:123:ILE:HD13	1.94	0.49
1:1:32:TYR:HB3	1:1:40:PHE:CE2	2.48	0.49
1:AE:23:LYS:HD2	1:AE:42:ARG:NH2	2.26	0.49
1:AF:127:ASP:HB3	1:AG:44:TRP:CE2	2.47	0.49
1:AO:120:ILE:HG21	1:AO:220:PHE:CZ	2.46	0.49
1:AV:56:ILE:HD11	1:AV:137:LEU:HD21	1.94	0.49
1:AV:210:VAL:HG12	1:AV:212:GLU:OE1	2.11	0.49
1:AW:228:PHE:HD1	1:AW:229:PHE:N	2.10	0.49
1:Ab:183:VAL:HB	1:Ab:197:LEU:HG	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:PHE:CZ	1:A:158:PHE:HB2	2.48	0.49
1:J:77:ASP:HB3	1:J:120:ILE:HB	1.94	0.49
1:c:44:TRP:CE2	1:d:127:ASP:HB3	2.46	0.49
1:h:224:LEU:HD11	1:h:246:VAL:HG11	1.94	0.49
1:k:40:PHE:CZ	1:k:158:PHE:HB2	2.45	0.49
1:k:59:LEU:O	1:k:145:ARG:HG3	2.12	0.49
1:k:79:ASP:HB2	1:k:118:PHE:HB3	1.94	0.49
1:p:64:ILE:HD12	1:p:136:TRP:HZ2	1.78	0.49
1:x:29:LEU:HD21	1:x:68:ILE:HG21	1.94	0.49
1:2:111:GLU:HB2	1:2:178:LYS:HB2	1.95	0.49
1:8:148:TYR:O	1:8:152:ILE:HG12	2.12	0.49
1:9:23:LYS:HD2	1:9:42:ARG:HH21	1.76	0.49
1:9:75:GLY:O	1:9:76:ILE:HG12	2.13	0.49
1:0:75:GLY:O	1:0:76:ILE:HG12	2.12	0.49
1:0:210:VAL:O	1:AA:76:ILE:HB	2.12	0.49
1:AA:32:TYR:CZ	1:AA:42:ARG:HD3	2.47	0.49
1:AE:224:LEU:HD12	1:AE:243:PHE:CZ	2.46	0.49
1:AI:79:ASP:HB2	1:AI:118:PHE:HB3	1.95	0.49
1:AS:183:VAL:HB	1:AS:197:LEU:HG	1.93	0.49
1:AW:29:LEU:HD21	1:AW:68:ILE:HD12	1.94	0.49
1:A:127:ASP:HB3	1:I:44:TRP:CE2	2.47	0.49
1:H:120:ILE:HG21	1:H:220:PHE:CZ	2.48	0.49
1:N:59:LEU:O	1:N:145:ARG:HG3	2.12	0.49
1:P:79:ASP:HB2	1:P:118:PHE:HB3	1.94	0.49
1:R:16:TYR:CE2	1:R:164:LEU:HG	2.48	0.49
1:U:75:GLY:O	1:U:76:ILE:HG12	2.12	0.49
1:W:181:LEU:HD11	1:W:183:VAL:HG23	1.93	0.49
1:e:43:ILE:HG13	1:e:43:ILE:O	2.12	0.49
1:f:168:LYS:HD2	1:f:168:LYS:N	2.28	0.49
1:g:23:LYS:HD2	1:g:42:ARG:NH2	2.27	0.49
1:g:43:ILE:HG13	1:g:43:ILE:O	2.12	0.49
1:k:77:ASP:HB3	1:k:120:ILE:HB	1.94	0.49
1:m:224:LEU:HD12	1:m:243:PHE:CZ	2.48	0.49
1:p:32:TYR:HB3	1:p:40:PHE:CZ	2.47	0.49
1:u:210:VAL:HG12	1:u:212:GLU:OE2	2.12	0.49
1:u:215:ASP:OD1	1:u:216:GLU:N	2.37	0.49
1:z:23:LYS:HD2	1:z:42:ARG:HH21	1.77	0.49
1:z:172:GLN:HG2	1:z:208:ARG:HB2	1.94	0.49
1:AA:81:ARG:HB2	1:AA:116:VAL:HB	1.94	0.49
1:AV:120:ILE:HG21	1:AV:220:PHE:CZ	2.46	0.49
1:AY:215:ASP:CG	1:AY:216:GLU:H	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ILE:HG21	1:A:220:PHE:CZ	2.47	0.49
1:C:75:GLY:O	1:C:76:ILE:HG12	2.12	0.49
1:D:44:TRP:CE2	1:E:127:ASP:HB3	2.47	0.49
1:J:43:ILE:HG13	1:J:43:ILE:O	2.12	0.49
1:L:79:ASP:HB3	1:L:81:ARG:HH22	1.77	0.49
1:j:40:PHE:HZ	1:j:158:PHE:CD1	2.30	0.49
1:o:210:VAL:HB	1:t:76:ILE:HG21	1.93	0.49
1:p:120:ILE:HG22	1:p:123:ILE:HD11	1.94	0.49
1:u:79:ASP:HB3	1:u:81:ARG:HH22	1.78	0.49
1:v:79:ASP:HB2	1:v:118:PHE:HB3	1.94	0.49
1:w:29:LEU:HD21	1:w:68:ILE:HG21	1.95	0.49
1:2:120:ILE:HG21	1:2:220:PHE:CZ	2.47	0.49
1:8:181:LEU:HD11	1:8:183:VAL:HG23	1.94	0.49
1:AF:181:LEU:HD11	1:AF:183:VAL:HG23	1.94	0.49
1:AJ:44:TRP:CE2	1:AK:127:ASP:HB3	2.48	0.49
1:AM:24:THR:HG22	1:AM:218:ILE:HG13	1.94	0.49
1:AV:40:PHE:HE2	1:AV:158:PHE:HB2	1.77	0.49
1:AY:43:ILE:HG13	1:AY:43:ILE:O	2.12	0.49
1:Ac:43:ILE:HG13	1:Ac:43:ILE:O	2.11	0.49
1:F:120:ILE:HD12	1:F:169:MET:HG2	1.94	0.49
1:G:120:ILE:HG21	1:G:220:PHE:CZ	2.47	0.49
1:H:56:ILE:HD11	1:H:137:LEU:HD21	1.95	0.49
1:I:29:LEU:HD21	1:I:68:ILE:HD12	1.94	0.49
1:k:215:ASP:CG	1:k:216:GLU:H	2.20	0.49
1:m:224:LEU:HD11	1:m:246:VAL:HG11	1.95	0.49
1:n:148:TYR:O	1:n:152:ILE:HG12	2.13	0.49
1:q:24:THR:HG22	1:q:218:ILE:HG13	1.94	0.49
1:r:79:ASP:HB2	1:r:118:PHE:HB3	1.95	0.49
1:3:40:PHE:CZ	1:3:158:PHE:HB2	2.45	0.49
1:3:75:GLY:O	1:3:76:ILE:HG12	2.13	0.49
1:AD:120:ILE:HG21	1:AD:220:PHE:CZ	2.47	0.49
1:AO:79:ASP:HB3	1:AO:81:ARG:HH22	1.77	0.49
1:AR:77:ASP:HB3	1:AR:120:ILE:HB	1.95	0.49
1:AY:23:LYS:HD2	1:AY:42:ARG:NH2	2.28	0.49
1:AY:44:TRP:CE2	1:Ad:127:ASP:HB3	2.48	0.49
1:Aa:76:ILE:HB	1:Ac:210:VAL:O	2.11	0.49
1:Ab:23:LYS:HD2	1:Ab:42:ARG:NH2	2.26	0.49
1:I:224:LEU:HD12	1:I:243:PHE:CZ	2.48	0.49
1:J:148:TYR:O	1:J:152:ILE:HG12	2.12	0.49
1:S:64:ILE:HD12	1:S:136:TRP:HZ2	1.77	0.49
1:S:181:LEU:HD11	1:S:183:VAL:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:208:ARG:HE	1:a:210:VAL:CG2	2.26	0.49
1:b:44:TRP:CE2	1:c:127:ASP:HB3	2.48	0.49
1:o:44:TRP:CE2	1:t:127:ASP:HB3	2.48	0.49
1:p:148:TYR:O	1:p:152:ILE:HG12	2.13	0.49
1:p:208:ARG:HE	1:p:210:VAL:CG2	2.26	0.49
1:z:120:ILE:HG22	1:z:123:ILE:HD11	1.93	0.49
1:AB:215:ASP:CG	1:AB:216:GLU:H	2.21	0.49
1:AE:76:ILE:HB	1:AV:210:VAL:O	2.11	0.49
1:AH:181:LEU:HD11	1:AH:183:VAL:HG23	1.94	0.49
1:AI:76:ILE:HA	1:AI:123:ILE:HD13	1.94	0.49
1:AI:224:LEU:HD11	1:AI:246:VAL:HG11	1.94	0.49
1:AJ:200:LYS:O	1:AK:85:SER:HA	2.13	0.49
1:AT:224:LEU:HD11	1:AT:246:VAL:HG11	1.95	0.49
1:AV:75:GLY:O	1:AV:76:ILE:HG12	2.12	0.49
1:A:79:ASP:HB3	1:A:81:ARG:NH1	2.24	0.49
1:C:224:LEU:HD11	1:C:246:VAL:HG11	1.94	0.49
1:Y:79:ASP:HB2	1:Y:118:PHE:HB3	1.93	0.49
1:i:79:ASP:HB3	1:i:81:ARG:HH22	1.77	0.49
1:m:215:ASP:CG	1:m:216:GLU:H	2.20	0.49
1:o:215:ASP:CG	1:o:216:GLU:H	2.19	0.49
1:t:148:TYR:O	1:t:152:ILE:HG12	2.13	0.49
1:x:43:ILE:HD12	1:y:131:ILE:HG13	1.94	0.49
1:5:59:LEU:O	1:5:145:ARG:HG3	2.12	0.49
1:Q:40:PHE:HZ	1:Q:158:PHE:CD1	2.30	0.49
1:Q:148:TYR:O	1:Q:152:ILE:HG12	2.13	0.49
1:W:228:PHE:HD1	1:W:229:PHE:N	2.10	0.49
1:j:77:ASP:HB3	1:j:120:ILE:HB	1.95	0.49
1:m:79:ASP:HB3	1:m:81:ARG:HH22	1.78	0.49
1:s:43:ILE:O	1:s:43:ILE:HG13	2.13	0.49
1:u:106:PHE:HA	1:u:183:VAL:HG22	1.95	0.49
1:0:215:ASP:CG	1:0:216:GLU:H	2.20	0.49
1:AB:145:ARG:HB2	1:AB:148:TYR:HD1	1.78	0.49
1:AK:56:ILE:HD11	1:AK:137:LEU:HD21	1.94	0.49
1:AM:56:ILE:HD11	1:AM:137:LEU:HD21	1.95	0.49
1:AS:111:GLU:HB2	1:AS:178:LYS:HB2	1.93	0.49
1:AW:106:PHE:HA	1:AW:183:VAL:HG22	1.95	0.49
1:AX:77:ASP:HB3	1:AX:120:ILE:HB	1.95	0.49
1:Aa:224:LEU:HD12	1:Aa:243:PHE:CZ	2.48	0.49
1:B:44:TRP:CE2	1:C:127:ASP:HB3	2.48	0.49
1:C:183:VAL:HB	1:C:197:LEU:HG	1.94	0.49
1:O:181:LEU:HD11	1:O:183:VAL:HG23	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:224:LEU:HD12	1:P:243:PHE:CZ	2.46	0.49
1:T:40:PHE:HZ	1:T:158:PHE:CD1	2.31	0.49
1:U:79:ASP:HB2	1:U:118:PHE:HB3	1.95	0.49
1:Y:44:TRP:CE2	1:Z:127:ASP:HB3	2.48	0.49
1:a:120:ILE:HG22	1:a:123:ILE:HD11	1.95	0.49
1:a:215:ASP:CG	1:a:216:GLU:H	2.21	0.49
1:w:16:TYR:CE2	1:w:164:LEU:HG	2.48	0.49
1:z:24:THR:HG22	1:z:218:ILE:HG13	1.94	0.49
1:8:29:LEU:HD21	1:8:68:ILE:HG21	1.95	0.49
1:AB:210:VAL:O	1:AG:76:ILE:HB	2.12	0.49
1:AC:43:ILE:O	1:AC:43:ILE:HG13	2.13	0.49
1:AY:79:ASP:HB2	1:AY:118:PHE:HB3	1.95	0.49
1:Aa:76:ILE:HG21	1:Ac:210:VAL:HB	1.94	0.49
1:Aa:148:TYR:O	1:Aa:152:ILE:HG12	2.12	0.49
1:A:77:ASP:HB3	1:A:120:ILE:HB	1.95	0.48
1:J:29:LEU:HD21	1:J:68:ILE:HG21	1.95	0.48
1:J:215:ASP:CG	1:J:216:GLU:H	2.21	0.48
1:f:106:PHE:HA	1:f:183:VAL:HG22	1.95	0.48
1:s:168:LYS:HB2	1:s:168:LYS:HE3	1.70	0.48
1:w:75:GLY:O	1:w:76:ILE:HG12	2.13	0.48
1:6:40:PHE:HZ	1:6:158:PHE:CD1	2.31	0.48
1:8:81:ARG:HB2	1:8:116:VAL:HB	1.95	0.48
1:9:40:PHE:HZ	1:9:158:PHE:CD1	2.31	0.48
1:AB:43:ILE:HG13	1:AB:43:ILE:O	2.12	0.48
1:AS:40:PHE:HZ	1:AS:158:PHE:CD1	2.31	0.48
1:AU:43:ILE:HG13	1:AU:43:ILE:O	2.13	0.48
1:AX:120:ILE:HG22	1:AX:123:ILE:HD11	1.96	0.48
1:AX:183:VAL:HB	1:AX:197:LEU:HG	1.95	0.48
1:AY:77:ASP:HB3	1:AY:120:ILE:HB	1.95	0.48
1:B:80:LEU:C	1:B:81:ARG:HD2	2.39	0.48
1:D:208:ARG:HE	1:D:210:VAL:CG2	2.26	0.48
1:H:211:PHE:CD1	1:H:218:ILE:HD12	2.48	0.48
1:K:75:GLY:O	1:K:76:ILE:HG12	2.13	0.48
1:K:77:ASP:HB3	1:K:120:ILE:HB	1.95	0.48
1:Q:183:VAL:HB	1:Q:197:LEU:HG	1.95	0.48
1:k:200:LYS:O	1:m:85:SER:HA	2.13	0.48
1:n:43:ILE:O	1:n:43:ILE:HG13	2.13	0.48
1:AV:32:TYR:CZ	1:AV:42:ARG:HD3	2.48	0.48
1:AV:215:ASP:CG	1:AV:216:GLU:H	2.21	0.48
1:AW:75:GLY:O	1:AW:76:ILE:HG12	2.12	0.48
1:AZ:23:LYS:HD2	1:AZ:42:ARG:NH2	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:29:LEU:HD11	1:E:68:ILE:HD12	1.95	0.48
1:J:79:ASP:O	1:J:80:LEU:HD12	2.13	0.48
1:J:120:ILE:HG21	1:J:220:PHE:CZ	2.48	0.48
1:K:224:LEU:HD11	1:K:246:VAL:HG11	1.94	0.48
1:O:127:ASP:HB3	1:Q:44:TRP:CE2	2.48	0.48
1:R:200:LYS:O	1:W:85:SER:HA	2.13	0.48
1:W:124:ILE:HG12	1:W:165:ARG:HB2	1.95	0.48
1:X:148:TYR:O	1:X:152:ILE:HG12	2.13	0.48
1:o:23:LYS:HD2	1:o:42:ARG:HH21	1.79	0.48
1:x:43:ILE:O	1:x:43:ILE:HG13	2.14	0.48
1:2:147:ILE:HG13	1:2:148:TYR:CD1	2.49	0.48
1:7:24:THR:HG22	1:7:218:ILE:HG13	1.95	0.48
1:AD:40:PHE:HZ	1:AD:158:PHE:CD1	2.31	0.48
1:AM:172:GLN:HG2	1:AM:208:ARG:HB2	1.94	0.48
1:AN:64:ILE:HD12	1:AN:136:TRP:HZ2	1.78	0.48
1:AW:168:LYS:HD2	1:AW:168:LYS:N	2.28	0.48
1:A:76:ILE:HG21	1:I:210:VAL:HB	1.96	0.48
1:B:168:LYS:HE3	1:B:168:LYS:HB2	1.70	0.48
1:I:168:LYS:HD2	1:I:168:LYS:N	2.28	0.48
1:R:44:TRP:CE2	1:W:127:ASP:HB3	2.47	0.48
1:d:148:TYR:O	1:d:152:ILE:HG12	2.14	0.48
1:f:29:LEU:HD21	1:f:68:ILE:HD12	1.95	0.48
1:y:43:ILE:O	1:y:43:ILE:HG13	2.14	0.48
1:z:56:ILE:HD11	1:z:137:LEU:HD21	1.95	0.48
1:3:43:ILE:O	1:3:43:ILE:HG13	2.13	0.48
1:6:111:GLU:HB2	1:6:178:LYS:HB2	1.94	0.48
1:AK:181:LEU:HD11	1:AK:183:VAL:HG23	1.95	0.48
1:AN:181:LEU:HD11	1:AN:183:VAL:HG23	1.93	0.48
1:AQ:215:ASP:CG	1:AQ:216:GLU:H	2.20	0.48
1:AU:23:LYS:HD2	1:AU:42:ARG:NH2	2.29	0.48
1:AX:120:ILE:HG21	1:AX:220:PHE:CZ	2.48	0.48
1:AZ:120:ILE:HG21	1:AZ:220:PHE:CZ	2.49	0.48
1:AZ:211:PHE:CD1	1:AZ:218:ILE:HD12	2.49	0.48
1:A:85:SER:HA	1:I:200:LYS:O	2.13	0.48
1:J:181:LEU:HD11	1:J:183:VAL:HG23	1.96	0.48
1:J:224:LEU:HD11	1:J:246:VAL:HG11	1.95	0.48
1:L:147:ILE:HG13	1:L:148:TYR:CD1	2.49	0.48
1:N:111:GLU:HB2	1:N:178:LYS:HB2	1.95	0.48
1:O:80:LEU:C	1:O:81:ARG:HD2	2.38	0.48
1:S:85:SER:HA	1:T:200:LYS:O	2.14	0.48
1:d:40:PHE:HZ	1:d:158:PHE:CD1	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:f:75:GLY:O	1:f:76:ILE:HG12	2.13	0.48
1:k:111:GLU:HB2	1:k:178:LYS:HB2	1.96	0.48
1:l:168:LYS:HB2	1:l:168:LYS:HE3	1.69	0.48
1:p:181:LEU:HD11	1:p:183:VAL:HG23	1.96	0.48
1:t:79:ASP:HB2	1:t:118:PHE:HB3	1.94	0.48
1:w:200:LYS:O	1:x:85:SER:HA	2.13	0.48
1:x:79:ASP:O	1:x:80:LEU:HD12	2.14	0.48
1:z:168:LYS:HE3	1:z:168:LYS:HB2	1.71	0.48
1:2:224:LEU:HD11	1:2:246:VAL:HG11	1.96	0.48
1:AJ:23:LYS:HD2	1:AJ:42:ARG:HH21	1.79	0.48
1:AQ:75:GLY:O	1:AQ:76:ILE:HG12	2.13	0.48
1:AT:106:PHE:HA	1:AT:183:VAL:HG22	1.95	0.48
1:Ac:127:ASP:HB3	1:Ad:44:TRP:CE2	2.47	0.48
1:A:148:TYR:O	1:A:152:ILE:HG12	2.13	0.48
1:G:40:PHE:HZ	1:G:158:PHE:CD1	2.32	0.48
1:H:43:ILE:O	1:H:43:ILE:HG13	2.13	0.48
1:J:85:SER:HA	1:K:200:LYS:O	2.14	0.48
1:P:75:GLY:O	1:P:76:ILE:HG12	2.13	0.48
1:P:200:LYS:O	1:Q:85:SER:HA	2.13	0.48
1:R:120:ILE:HG21	1:R:220:PHE:CZ	2.49	0.48
1:W:43:ILE:HG13	1:W:43:ILE:O	2.14	0.48
1:Z:183:VAL:HB	1:Z:197:LEU:HG	1.95	0.48
1:m:75:GLY:O	1:m:76:ILE:HG12	2.13	0.48
1:m:181:LEU:HD11	1:m:183:VAL:HG23	1.96	0.48
1:m:210:VAL:O	1:n:76:ILE:HB	2.12	0.48
1:x:181:LEU:HD11	1:x:183:VAL:HG23	1.95	0.48
1:3:147:ILE:HG13	1:3:148:TYR:CD1	2.48	0.48
1:7:106:PHE:HA	1:7:183:VAL:HG22	1.96	0.48
1:0:224:LEU:HD12	1:0:243:PHE:CZ	2.49	0.48
1:AA:77:ASP:HB3	1:AA:120:ILE:HB	1.94	0.48
1:AA:183:VAL:HB	1:AA:197:LEU:HG	1.94	0.48
1:AH:106:PHE:HA	1:AH:183:VAL:HG22	1.95	0.48
1:AM:120:ILE:HG21	1:AM:220:PHE:CZ	2.49	0.48
1:AW:181:LEU:HD11	1:AW:183:VAL:HG23	1.94	0.48
1:AX:224:LEU:HD11	1:AX:246:VAL:HG11	1.96	0.48
1:E:44:TRP:CE2	1:F:127:ASP:HB3	2.48	0.48
1:F:16:TYR:CE2	1:F:164:LEU:HG	2.48	0.48
1:L:224:LEU:HD11	1:L:246:VAL:HG11	1.96	0.48
1:M:111:GLU:HB2	1:M:178:LYS:HB2	1.94	0.48
1:N:79:ASP:HB2	1:N:118:PHE:HB3	1.95	0.48
1:N:200:LYS:O	1:P:85:SER:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:77:ASP:HB3	1:X:120:ILE:HB	1.95	0.48
1:c:224:LEU:HD12	1:c:243:PHE:CZ	2.49	0.48
1:e:211:PHE:CD1	1:e:218:ILE:HD12	2.48	0.48
1:f:224:LEU:HD12	1:f:243:PHE:CZ	2.48	0.48
1:g:148:TYR:O	1:g:152:ILE:HG12	2.14	0.48
1:w:120:ILE:HG22	1:w:123:ILE:HD11	1.94	0.48
1:4:75:GLY:O	1:4:76:ILE:HG12	2.13	0.48
1:AG:148:TYR:O	1:AG:152:ILE:HG12	2.14	0.48
1:AQ:85:SER:HA	1:AR:200:LYS:O	2.13	0.48
1:AV:80:LEU:C	1:AV:81:ARG:HD2	2.38	0.48
1:I:224:LEU:HD11	1:I:246:VAL:HG11	1.96	0.48
1:L:215:ASP:CG	1:L:216:GLU:H	2.20	0.48
1:T:120:ILE:HG21	1:T:220:PHE:CZ	2.49	0.48
1:b:29:LEU:HD11	1:b:68:ILE:HD12	1.95	0.48
1:b:59:LEU:O	1:b:145:ARG:HG3	2.14	0.48
1:y:80:LEU:C	1:y:81:ARG:HD2	2.39	0.48
1:z:44:TRP:CE2	1:1:127:ASP:HB3	2.48	0.48
1:z:210:VAL:HB	1:1:76:ILE:HG21	1.96	0.48
1:0:106:PHE:HA	1:0:183:VAL:HG22	1.95	0.48
1:0:168:LYS:HD2	1:0:168:LYS:N	2.28	0.48
1:AA:224:LEU:HD11	1:AA:246:VAL:HG11	1.96	0.48
1:AG:224:LEU:HD11	1:AG:246:VAL:HG11	1.96	0.48
1:AM:224:LEU:HD11	1:AM:246:VAL:HG11	1.96	0.48
1:AN:32:TYR:HB3	1:AN:40:PHE:CE2	2.48	0.48
1:AN:40:PHE:CZ	1:AN:158:PHE:HB2	2.46	0.48
1:AO:124:ILE:HG12	1:AO:165:ARG:HB2	1.96	0.48
1:AX:148:TYR:O	1:AX:152:ILE:HG12	2.14	0.48
1:Aa:127:ASP:HB3	1:Ac:44:TRP:CE2	2.48	0.48
1:Ac:16:TYR:CE2	1:Ac:164:LEU:HG	2.49	0.48
1:A:181:LEU:HD11	1:A:183:VAL:HG23	1.96	0.48
1:A:183:VAL:HB	1:A:197:LEU:HG	1.95	0.48
1:H:171:MET:HE3	1:H:209:LEU:HD12	1.96	0.48
1:I:77:ASP:HB3	1:I:120:ILE:HB	1.94	0.48
1:L:148:TYR:HA	1:L:151:GLU:HG3	1.95	0.48
1:U:121:GLU:HB3	1:U:168:LYS:HB2	1.96	0.48
1:Y:80:LEU:C	1:Y:81:ARG:HD2	2.39	0.48
1:a:183:VAL:HB	1:a:197:LEU:HG	1.96	0.48
1:a:224:LEU:HD11	1:a:246:VAL:HG11	1.96	0.48
1:g:120:ILE:HG21	1:g:220:PHE:CZ	2.49	0.48
1:g:211:PHE:CD1	1:g:218:ILE:HD12	2.49	0.48
1:j:111:GLU:HB2	1:j:178:LYS:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:z:120:ILE:HG21	1:z:220:PHE:CZ	2.49	0.48
1:1:19:VAL:HB	1:1:247:LEU:HD12	1.96	0.48
1:9:111:GLU:HB2	1:9:178:LYS:HB2	1.96	0.48
1:AD:76:ILE:HG21	1:AF:210:VAL:HB	1.96	0.48
1:AF:224:LEU:HD12	1:AF:243:PHE:CZ	2.49	0.48
1:AG:59:LEU:O	1:AG:145:ARG:HG3	2.14	0.48
1:AP:77:ASP:HB3	1:AP:120:ILE:HB	1.96	0.48
1:AU:120:ILE:HG21	1:AU:220:PHE:CZ	2.49	0.48
1:X:85:SER:HA	1:f:200:LYS:O	2.13	0.48
1:c:16:TYR:CE2	1:c:164:LEU:HG	2.49	0.48
1:u:168:LYS:HE3	1:u:168:LYS:HB2	1.70	0.48
1:v:16:TYR:CE2	1:v:164:LEU:HG	2.49	0.48
1:2:43:ILE:HB	1:7:130:GLU:HB2	1.95	0.48
1:2:77:ASP:HB3	1:2:120:ILE:HB	1.96	0.48
1:3:210:VAL:HG12	1:3:212:GLU:OE2	2.13	0.48
1:4:120:ILE:HG21	1:4:220:PHE:CZ	2.49	0.48
1:8:43:ILE:O	1:8:43:ILE:HG13	2.13	0.48
1:AE:19:VAL:HA	1:AE:246:VAL:HG23	1.96	0.48
1:AG:224:LEU:HD12	1:AG:243:PHE:CZ	2.49	0.48
1:AI:23:LYS:HD2	1:AI:42:ARG:HH21	1.78	0.48
1:AL:23:LYS:HD2	1:AL:42:ARG:NH2	2.29	0.48
1:AM:120:ILE:HG22	1:AM:123:ILE:HD11	1.96	0.48
1:AP:85:SER:HA	1:AQ:200:LYS:O	2.14	0.48
1:AU:181:LEU:HD11	1:AU:183:VAL:HG23	1.96	0.48
1:C:43:ILE:HB	1:D:130:GLU:HB2	1.96	0.47
1:S:19:VAL:HB	1:S:247:LEU:HD12	1.96	0.47
1:U:85:SER:HA	1:l:200:LYS:O	2.14	0.47
1:V:181:LEU:HD11	1:V:183:VAL:HG23	1.96	0.47
1:f:224:LEU:HD11	1:f:246:VAL:HG11	1.96	0.47
1:l:79:ASP:O	1:l:80:LEU:HD12	2.14	0.47
1:m:200:LYS:O	1:n:85:SER:HA	2.14	0.47
1:9:79:ASP:HB2	1:9:118:PHE:HB3	1.97	0.47
1:AB:77:ASP:HB3	1:AB:120:ILE:HB	1.95	0.47
1:AB:224:LEU:HD11	1:AB:246:VAL:HG11	1.96	0.47
1:AD:148:TYR:O	1:AD:152:ILE:HG12	2.15	0.47
1:AN:19:VAL:HB	1:AN:247:LEU:HD12	1.96	0.47
1:AO:147:ILE:HG13	1:AO:148:TYR:CD1	2.49	0.47
1:AT:77:ASP:HB3	1:AT:120:ILE:HB	1.96	0.47
1:Ac:111:GLU:HB2	1:Ac:178:LYS:HB2	1.95	0.47
1:C:124:ILE:HG12	1:C:165:ARG:HB2	1.96	0.47
1:O:79:ASP:O	1:O:80:LEU:HD12	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:215:ASP:CG	1:P:216:GLU:H	2.21	0.47
1:i:147:ILE:HG13	1:i:148:TYR:CD1	2.49	0.47
1:s:40:PHE:HE1	1:s:224:LEU:HD13	1.79	0.47
1:6:127:ASP:HB3	1:AC:44:TRP:CE2	2.49	0.47
1:8:199:SER:HA	1:0:86:LEU:O	2.14	0.47
1:9:32:TYR:CZ	1:9:42:ARG:HD3	2.48	0.47
1:9:168:LYS:HE3	1:9:168:LYS:HB2	1.70	0.47
1:AA:120:ILE:HG21	1:AA:220:PHE:CZ	2.48	0.47
1:AB:148:TYR:HA	1:AB:151:GLU:HG3	1.95	0.47
1:AC:211:PHE:CD1	1:AC:218:ILE:HD12	2.49	0.47
1:AD:127:ASP:HB3	1:AF:44:TRP:CE2	2.49	0.47
1:AJ:120:ILE:HG22	1:AJ:123:ILE:HD11	1.96	0.47
1:AM:210:VAL:HB	1:AN:76:ILE:HG21	1.95	0.47
1:AX:208:ARG:HG2	1:AX:210:VAL:HG23	1.95	0.47
1:AY:127:ASP:HB3	1:Ab:44:TRP:CE2	2.49	0.47
1:Ab:124:ILE:HG12	1:Ab:165:ARG:HB2	1.96	0.47
1:C:111:GLU:HB2	1:C:178:LYS:HB2	1.95	0.47
1:J:211:PHE:CD1	1:J:218:ILE:HD12	2.50	0.47
1:S:148:TYR:O	1:S:152:ILE:HG12	2.14	0.47
1:f:86:LEU:O	1:g:199:SER:HA	2.15	0.47
1:i:124:ILE:HG12	1:i:165:ARG:HB2	1.96	0.47
1:w:44:TRP:CE2	1:x:127:ASP:HB3	2.49	0.47
1:1:120:ILE:HG22	1:1:123:ILE:HD11	1.96	0.47
1:1:152:ILE:HD12	1:1:227:LEU:HG	1.96	0.47
1:1:215:ASP:CG	1:1:216:GLU:N	2.73	0.47
1:AL:162:SER:HB2	1:AL:223:LYS:HB2	1.97	0.47
1:Ad:111:GLU:HB2	1:Ad:178:LYS:HB2	1.96	0.47
1:Ad:224:LEU:HD12	1:Ad:243:PHE:CZ	2.49	0.47
1:I:147:ILE:HG13	1:I:148:TYR:CD1	2.49	0.47
1:T:120:ILE:HG22	1:T:123:ILE:HD11	1.95	0.47
1:X:76:ILE:HG21	1:f:210:VAL:HB	1.96	0.47
1:Z:124:ILE:HG12	1:Z:165:ARG:HB2	1.96	0.47
1:q:106:PHE:HA	1:q:183:VAL:HG22	1.96	0.47
1:r:224:LEU:HD11	1:r:246:VAL:HG11	1.97	0.47
1:u:23:LYS:HD2	1:u:42:ARG:NH2	2.30	0.47
1:z:106:PHE:HA	1:z:183:VAL:HG22	1.96	0.47
1:2:23:LYS:HD2	1:2:42:ARG:NH2	2.29	0.47
1:5:111:GLU:HB2	1:5:178:LYS:HB2	1.97	0.47
1:7:77:ASP:HB3	1:7:120:ILE:HB	1.96	0.47
1:8:120:ILE:HG21	1:8:220:PHE:CZ	2.49	0.47
1:0:224:LEU:HD11	1:0:246:VAL:HG11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:123:ILE:N	1:AA:123:ILE:HD12	2.30	0.47
1:AI:121:GLU:HB3	1:AI:168:LYS:HB2	1.96	0.47
1:AK:124:ILE:HG12	1:AK:165:ARG:HB2	1.96	0.47
1:AQ:86:LEU:O	1:AR:199:SER:HA	2.15	0.47
1:AU:16:TYR:CD1	1:AU:223:LYS:HG3	2.48	0.47
1:AV:79:ASP:HB2	1:AV:118:PHE:HB3	1.95	0.47
1:AW:44:TRP:CE2	1:AX:127:ASP:HB3	2.50	0.47
1:AW:224:LEU:HD12	1:AW:243:PHE:CZ	2.48	0.47
1:D:120:ILE:HG22	1:D:123:ILE:HD11	1.95	0.47
1:E:120:ILE:HG21	1:E:220:PHE:CZ	2.50	0.47
1:F:44:TRP:CE2	1:G:127:ASP:HB3	2.49	0.47
1:F:148:TYR:O	1:F:152:ILE:HG12	2.14	0.47
1:H:44:TRP:CE2	1:M:127:ASP:HB3	2.50	0.47
1:I:23:LYS:HD2	1:I:42:ARG:HH22	1.79	0.47
1:O:64:ILE:HD12	1:O:136:TRP:HZ2	1.80	0.47
1:O:75:GLY:O	1:O:76:ILE:HG12	2.15	0.47
1:R:168:LYS:HE3	1:R:168:LYS:HB2	1.68	0.47
1:T:40:PHE:HE1	1:T:158:PHE:HB2	1.79	0.47
1:e:120:ILE:HG21	1:e:220:PHE:CZ	2.49	0.47
1:h:183:VAL:HB	1:h:197:LEU:HG	1.97	0.47
1:n:183:VAL:HB	1:n:197:LEU:HG	1.96	0.47
1:p:19:VAL:HB	1:p:247:LEU:HD12	1.97	0.47
1:u:43:ILE:O	1:u:43:ILE:HG13	2.15	0.47
1:y:224:LEU:HD12	1:y:243:PHE:CZ	2.49	0.47
1:1:32:TYR:HB3	1:1:40:PHE:CZ	2.50	0.47
1:7:56:ILE:HD11	1:7:137:LEU:HD21	1.96	0.47
1:7:200:LYS:O	1:8:85:SER:HA	2.14	0.47
1:AK:175:ARG:NH1	1:AK:175:ARG:HB2	2.29	0.47
1:AM:211:PHE:CD1	1:AM:218:ILE:HD12	2.49	0.47
1:AP:43:ILE:O	1:AP:43:ILE:HG13	2.13	0.47
1:A:29:LEU:HD11	1:A:68:ILE:HD12	1.95	0.47
1:C:19:VAL:HA	1:C:246:VAL:HG23	1.95	0.47
1:C:44:TRP:CE2	1:D:127:ASP:HB3	2.49	0.47
1:E:224:LEU:HD12	1:E:243:PHE:CZ	2.49	0.47
1:J:147:ILE:HG13	1:J:148:TYR:CD1	2.50	0.47
1:S:162:SER:HB2	1:S:223:LYS:HB2	1.97	0.47
1:T:166:ALA:HB3	1:T:169:MET:HG3	1.95	0.47
1:W:148:TYR:O	1:W:152:ILE:HG12	2.14	0.47
1:Y:32:TYR:CZ	1:Y:42:ARG:HD3	2.50	0.47
1:Y:168:LYS:HE3	1:Y:168:LYS:HB2	1.70	0.47
1:b:224:LEU:HD11	1:b:246:VAL:HG11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:44:TRP:CE2	1:j:127:ASP:HB3	2.50	0.47
1:f:76:ILE:HG21	1:g:210:VAL:HB	1.97	0.47
1:g:224:LEU:HD11	1:g:246:VAL:HG11	1.96	0.47
1:m:120:ILE:HG21	1:m:220:PHE:CZ	2.49	0.47
1:q:120:ILE:HG21	1:q:220:PHE:CZ	2.49	0.47
1:t:124:ILE:HG12	1:t:165:ARG:HB2	1.95	0.47
1:y:32:TYR:HB3	1:y:40:PHE:CE2	2.50	0.47
1:4:32:TYR:CZ	1:4:42:ARG:HD3	2.50	0.47
1:0:79:ASP:O	1:0:80:LEU:HD12	2.15	0.47
1:AC:120:ILE:HG21	1:AC:220:PHE:CZ	2.49	0.47
1:AE:183:VAL:HB	1:AE:197:LEU:HG	1.96	0.47
1:AO:23:LYS:HD2	1:AO:42:ARG:HH22	1.79	0.47
1:AS:127:ASP:HB3	1:AZ:44:TRP:CE2	2.50	0.47
1:Ad:120:ILE:HG21	1:Ad:220:PHE:CZ	2.50	0.47
1:G:148:TYR:O	1:G:152:ILE:HG12	2.14	0.47
1:G:199:SER:HA	1:H:86:LEU:O	2.15	0.47
1:H:200:LYS:O	1:M:85:SER:HA	2.14	0.47
1:K:106:PHE:HA	1:K:183:VAL:HG22	1.97	0.47
1:N:120:ILE:HG21	1:N:220:PHE:CZ	2.50	0.47
1:N:199:SER:HA	1:P:86:LEU:O	2.15	0.47
1:Q:210:VAL:HG12	1:Q:212:GLU:OE2	2.15	0.47
1:T:23:LYS:HD2	1:T:42:ARG:NH2	2.29	0.47
1:U:123:ILE:HD12	1:U:123:ILE:N	2.29	0.47
1:U:181:LEU:HD11	1:U:183:VAL:HG23	1.97	0.47
1:b:224:LEU:HD12	1:b:243:PHE:CZ	2.49	0.47
1:d:44:TRP:CE2	1:e:127:ASP:HB3	2.50	0.47
1:l:75:GLY:O	1:l:76:ILE:HG12	2.15	0.47
1:l:106:PHE:HA	1:l:183:VAL:HG22	1.96	0.47
1:l:127:ASP:HB3	1:n:44:TRP:CE2	2.49	0.47
1:q:224:LEU:HD12	1:q:243:PHE:CZ	2.50	0.47
1:s:75:GLY:O	1:s:76:ILE:HG12	2.15	0.47
1:y:79:ASP:C	1:y:80:LEU:HD12	2.40	0.47
1:z:224:LEU:HD11	1:z:246:VAL:HG11	1.96	0.47
1:1:148:TYR:O	1:1:152:ILE:HG12	2.14	0.47
1:4:152:ILE:HD12	1:4:227:LEU:CD2	2.45	0.47
1:6:85:SER:HA	1:AC:200:LYS:O	2.14	0.47
1:0:147:ILE:HG13	1:0:148:TYR:CD1	2.50	0.47
1:AE:124:ILE:HG12	1:AE:165:ARG:HB2	1.96	0.47
1:AG:111:GLU:HB2	1:AG:178:LYS:HB2	1.96	0.47
1:AH:43:ILE:HD12	1:AI:131:ILE:HG13	1.97	0.47
1:AL:215:ASP:CG	1:AL:216:GLU:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:148:TYR:O	1:AN:152:ILE:HG12	2.15	0.47
1:AN:162:SER:HB2	1:AN:223:LYS:HB2	1.97	0.47
1:AP:40:PHE:CZ	1:AP:158:PHE:HB2	2.44	0.47
1:AP:147:ILE:HG13	1:AP:148:TYR:CD1	2.49	0.47
1:AS:215:ASP:CG	1:AS:216:GLU:H	2.23	0.47
1:AU:120:ILE:HD12	1:AU:169:MET:HG2	1.96	0.47
1:AU:199:SER:HA	1:AW:86:LEU:O	2.15	0.47
1:AV:40:PHE:HZ	1:AV:158:PHE:CD1	2.31	0.47
1:AW:79:ASP:HB2	1:AW:118:PHE:HB3	1.96	0.47
1:AW:224:LEU:HD11	1:AW:246:VAL:HG11	1.97	0.47
1:Ad:29:LEU:HD11	1:Ad:68:ILE:HD12	1.97	0.47
1:Ad:147:ILE:HG13	1:Ad:148:TYR:CD1	2.49	0.47
1:D:200:LYS:O	1:E:85:SER:HA	2.15	0.47
1:E:59:LEU:O	1:E:145:ARG:HG3	2.14	0.47
1:E:111:GLU:HB2	1:E:178:LYS:HB2	1.97	0.47
1:I:76:ILE:HB	1:J:210:VAL:O	2.15	0.47
1:S:147:ILE:HG13	1:S:148:TYR:CD1	2.50	0.47
1:b:111:GLU:HB2	1:b:178:LYS:HB2	1.96	0.47
1:e:120:ILE:HD12	1:e:169:MET:HG2	1.97	0.47
1:n:77:ASP:HB3	1:n:120:ILE:HB	1.96	0.47
1:o:43:ILE:O	1:o:43:ILE:HG13	2.14	0.47
1:q:166:ALA:HB3	1:q:169:MET:HG3	1.97	0.47
1:r:121:GLU:HB3	1:r:168:LYS:HB2	1.96	0.47
1:w:43:ILE:HG13	1:w:43:ILE:O	2.14	0.47
1:AS:56:ILE:HD11	1:AS:137:LEU:HD21	1.97	0.47
1:AV:16:TYR:CD1	1:AV:223:LYS:HG3	2.50	0.47
1:AV:111:GLU:HB2	1:AV:178:LYS:HB2	1.97	0.47
1:AY:224:LEU:HD11	1:AY:246:VAL:HG11	1.96	0.47
1:AZ:43:ILE:O	1:AZ:43:ILE:HG13	2.14	0.47
1:Ab:75:GLY:O	1:Ab:76:ILE:HG12	2.15	0.47
1:Ab:224:LEU:HD11	1:Ab:246:VAL:HG11	1.96	0.47
1:O:79:ASP:HB2	1:O:118:PHE:HB3	1.97	0.47
1:S:183:VAL:HB	1:S:197:LEU:HG	1.97	0.47
1:V:79:ASP:C	1:V:80:LEU:HD12	2.40	0.47
1:W:224:LEU:HD11	1:W:246:VAL:HG11	1.96	0.47
1:a:120:ILE:HG21	1:a:220:PHE:CZ	2.50	0.47
1:e:200:LYS:O	1:j:85:SER:HA	2.14	0.47
1:f:147:ILE:HG13	1:f:148:TYR:CD1	2.49	0.47
1:k:120:ILE:HG21	1:k:220:PHE:CZ	2.50	0.47
1:l:79:ASP:HB2	1:l:118:PHE:HB3	1.97	0.47
1:o:120:ILE:HG21	1:o:220:PHE:CZ	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:u:75:GLY:O	1:u:76:ILE:HG12	2.15	0.47
1:3:85:SER:HA	1:4:200:LYS:O	2.15	0.47
1:Ad:183:VAL:HB	1:Ad:197:LEU:HG	1.95	0.47
1:D:224:LEU:HD11	1:D:246:VAL:HG11	1.96	0.47
1:F:23:LYS:HD2	1:F:42:ARG:NH2	2.30	0.47
1:H:79:ASP:HB3	1:H:118:PHE:HB3	1.97	0.47
1:H:162:SER:HB2	1:H:223:LYS:HB2	1.97	0.47
1:I:106:PHE:HA	1:I:183:VAL:HG22	1.97	0.47
1:L:23:LYS:HD2	1:L:42:ARG:NH2	2.30	0.47
1:M:147:ILE:HG13	1:M:148:TYR:CD1	2.50	0.47
1:N:124:ILE:HG12	1:N:165:ARG:HB2	1.96	0.47
1:U:16:TYR:CE2	1:U:164:LEU:HG	2.50	0.47
1:Z:44:TRP:CE2	1:a:127:ASP:HB3	2.50	0.47
1:n:170:ARG:HB3	1:n:170:ARG:NH1	2.30	0.47
1:r:141:GLN:HG3	1:r:235:LEU:HB3	1.97	0.47
1:1:120:ILE:HD12	1:1:169:MET:HG2	1.97	0.47
1:7:120:ILE:HG21	1:7:220:PHE:CZ	2.50	0.47
1:AH:40:PHE:CZ	1:AH:158:PHE:HB2	2.50	0.47
1:AI:148:TYR:O	1:AI:152:ILE:HG12	2.15	0.47
1:AJ:43:ILE:O	1:AJ:43:ILE:HG13	2.14	0.47
1:AL:172:GLN:HG2	1:AL:208:ARG:HB2	1.97	0.47
1:AS:85:SER:HA	1:AZ:200:LYS:O	2.14	0.47
1:AZ:77:ASP:HB3	1:AZ:120:ILE:HB	1.97	0.47
1:B:32:TYR:CZ	1:B:42:ARG:HD3	2.50	0.46
1:M:120:ILE:HG21	1:M:220:PHE:CZ	2.50	0.46
1:Q:77:ASP:HB3	1:Q:120:ILE:HB	1.97	0.46
1:Z:79:ASP:HB3	1:Z:81:ARG:NH2	2.30	0.46
1:u:148:TYR:O	1:u:152:ILE:HG12	2.15	0.46
1:x:115:SER:OG	1:x:174:GLU:HB2	2.15	0.46
1:AH:75:GLY:O	1:AH:76:ILE:HG12	2.15	0.46
1:AL:75:GLY:O	1:AL:76:ILE:HG12	2.15	0.46
1:AM:32:TYR:CZ	1:AM:42:ARG:HD3	2.50	0.46
1:AO:224:LEU:HD11	1:AO:246:VAL:HG11	1.96	0.46
1:D:168:LYS:HE3	1:D:168:LYS:HB2	1.69	0.46
1:G:183:VAL:HB	1:G:197:LEU:HG	1.97	0.46
1:H:77:ASP:HB3	1:H:120:ILE:HB	1.97	0.46
1:H:120:ILE:HD12	1:H:169:MET:HG2	1.97	0.46
1:Q:79:ASP:HB2	1:Q:118:PHE:HB3	1.97	0.46
1:R:43:ILE:HG13	1:R:43:ILE:O	2.14	0.46
1:T:181:LEU:HD11	1:T:183:VAL:HG23	1.98	0.46
1:V:75:GLY:O	1:V:76:ILE:HG12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:215:ASP:CG	1:V:216:GLU:H	2.24	0.46
1:X:29:LEU:HD11	1:X:68:ILE:HD12	1.96	0.46
1:a:44:TRP:CE2	1:b:127:ASP:HB3	2.50	0.46
1:e:148:TYR:O	1:e:152:ILE:HG12	2.16	0.46
1:g:85:SER:HA	1:h:200:LYS:O	2.15	0.46
1:l:64:ILE:HD12	1:l:136:TRP:HZ2	1.80	0.46
1:u:16:TYR:CE2	1:u:164:LEU:HG	2.51	0.46
1:x:147:ILE:HG13	1:x:148:TYR:CD1	2.50	0.46
1:0:44:TRP:CE2	1:AA:127:ASP:HB3	2.50	0.46
1:AB:44:TRP:CE2	1:AG:127:ASP:HB3	2.50	0.46
1:AC:86:LEU:O	1:AD:199:SER:HA	2.15	0.46
1:AF:147:ILE:HG13	1:AF:148:TYR:CD1	2.50	0.46
1:AF:148:TYR:O	1:AF:152:ILE:HG12	2.15	0.46
1:AQ:228:PHE:HD2	1:AQ:229:PHE:H	1.63	0.46
1:AR:120:ILE:HG21	1:AR:220:PHE:CZ	2.50	0.46
1:AW:147:ILE:HG13	1:AW:148:TYR:CD1	2.50	0.46
1:D:183:VAL:HB	1:D:197:LEU:HG	1.96	0.46
1:E:172:GLN:HG2	1:E:208:ARG:HG3	1.97	0.46
1:F:224:LEU:HD11	1:F:246:VAL:HG11	1.97	0.46
1:J:86:LEU:O	1:K:199:SER:HA	2.16	0.46
1:N:215:ASP:CG	1:N:216:GLU:H	2.23	0.46
1:R:19:VAL:HB	1:R:247:LEU:HD12	1.98	0.46
1:d:199:SER:HA	1:e:86:LEU:O	2.15	0.46
1:e:29:LEU:HD11	1:e:68:ILE:HD12	1.98	0.46
1:n:111:GLU:HB2	1:n:178:LYS:HB2	1.98	0.46
1:o:120:ILE:HG22	1:o:123:ILE:HD11	1.97	0.46
1:r:16:TYR:CE2	1:r:164:LEU:HG	2.50	0.46
1:r:123:ILE:HD12	1:r:123:ILE:N	2.29	0.46
1:w:168:LYS:HB2	1:w:168:LYS:HE3	1.69	0.46
1:x:111:GLU:HB2	1:x:178:LYS:HB2	1.97	0.46
1:1:162:SER:HB2	1:1:223:LYS:HB2	1.97	0.46
1:3:16:TYR:CD1	1:3:223:LYS:HG3	2.50	0.46
1:3:23:LYS:HD2	1:3:42:ARG:NH2	2.31	0.46
1:3:32:TYR:CZ	1:3:42:ARG:HD3	2.51	0.46
1:6:30:HIS:CE1	1:6:42:ARG:HH11	2.34	0.46
1:9:16:TYR:CD1	1:9:223:LYS:HG3	2.50	0.46
1:AB:40:PHE:HE1	1:AB:224:LEU:HD13	1.81	0.46
1:AC:127:ASP:HB3	1:AD:44:TRP:CE2	2.51	0.46
1:AG:40:PHE:CZ	1:AG:158:PHE:HB2	2.49	0.46
1:AG:147:ILE:HG13	1:AG:148:TYR:CD1	2.50	0.46
1:AJ:120:ILE:HG21	1:AJ:220:PHE:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:32:TYR:CZ	1:AP:42:ARG:HD3	2.50	0.46
1:AS:79:ASP:HB2	1:AS:118:PHE:HB3	1.97	0.46
1:E:224:LEU:HD11	1:E:246:VAL:HG11	1.97	0.46
1:I:86:LEU:O	1:J:199:SER:HA	2.15	0.46
1:U:224:LEU:HD11	1:U:246:VAL:HG11	1.97	0.46
1:V:43:ILE:O	1:V:43:ILE:HG13	2.15	0.46
1:W:40:PHE:CZ	1:W:158:PHE:HB2	2.48	0.46
1:X:23:LYS:HD2	1:X:42:ARG:NH2	2.30	0.46
1:g:29:LEU:HD21	1:g:68:ILE:HG21	1.97	0.46
1:j:30:HIS:CE1	1:j:42:ARG:HH11	2.34	0.46
1:2:164:LEU:O	1:2:219:VAL:HA	2.15	0.46
1:5:120:ILE:HG21	1:5:220:PHE:CZ	2.50	0.46
1:9:147:ILE:HG13	1:9:148:TYR:CD1	2.50	0.46
1:AC:56:ILE:HD11	1:AC:137:LEU:HD21	1.97	0.46
1:AD:16:TYR:CD1	1:AD:223:LYS:HG3	2.50	0.46
1:AH:43:ILE:HG13	1:AH:43:ILE:O	2.14	0.46
1:AH:64:ILE:HD12	1:AH:136:TRP:HZ2	1.80	0.46
1:AJ:162:SER:HB2	1:AJ:223:LYS:HB2	1.98	0.46
1:AL:79:ASP:HB2	1:AL:118:PHE:HB3	1.98	0.46
1:AM:208:ARG:HE	1:AM:210:VAL:CG2	2.28	0.46
1:AN:32:TYR:HB3	1:AN:40:PHE:CZ	2.50	0.46
1:AP:16:TYR:CD1	1:AP:223:LYS:HG3	2.50	0.46
1:AQ:79:ASP:CB	1:AQ:81:ARG:HH22	2.19	0.46
1:AR:111:GLU:HB2	1:AR:178:LYS:HB2	1.97	0.46
1:AS:120:ILE:HG21	1:AS:220:PHE:CZ	2.51	0.46
1:AZ:75:GLY:O	1:AZ:76:ILE:HG12	2.15	0.46
1:Ad:148:TYR:O	1:Ad:152:ILE:HG12	2.15	0.46
1:F:121:GLU:HB3	1:F:168:LYS:HB2	1.97	0.46
1:G:210:VAL:HG12	1:G:212:GLU:OE1	2.15	0.46
1:L:124:ILE:HG12	1:L:165:ARG:HB2	1.96	0.46
1:Q:43:ILE:O	1:Q:43:ILE:HG13	2.14	0.46
1:R:23:LYS:HD2	1:R:42:ARG:HH21	1.79	0.46
1:U:148:TYR:O	1:U:152:ILE:HG12	2.15	0.46
1:X:123:ILE:HD12	1:X:123:ILE:N	2.31	0.46
1:e:111:GLU:HB2	1:e:178:LYS:HB2	1.97	0.46
1:m:152:ILE:HD12	1:m:227:LEU:CD2	2.46	0.46
1:p:183:VAL:HB	1:p:197:LEU:HG	1.98	0.46
1:v:224:LEU:HD11	1:v:246:VAL:HG11	1.97	0.46
1:y:79:ASP:HB2	1:y:118:PHE:HB3	1.97	0.46
1:z:208:ARG:HE	1:z:210:VAL:CG2	2.28	0.46
1:AD:210:VAL:HG12	1:AD:212:GLU:OE1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:79:ASP:HB2	1:AH:118:PHE:HB3	1.97	0.46
1:AH:148:TYR:O	1:AH:152:ILE:HG12	2.16	0.46
1:AM:75:GLY:O	1:AM:76:ILE:HG12	2.16	0.46
1:AN:120:ILE:HD12	1:AN:169:MET:HG2	1.98	0.46
1:AO:164:LEU:O	1:AO:219:VAL:HA	2.15	0.46
1:AX:215:ASP:OD1	1:AX:216:GLU:N	2.40	0.46
1:AY:168:LYS:HE3	1:AY:168:LYS:HB2	1.69	0.46
1:AY:200:LYS:O	1:Ad:85:SER:HA	2.16	0.46
1:AZ:86:LEU:O	1:Aa:199:SER:HA	2.15	0.46
1:Ac:77:ASP:HB3	1:Ac:120:ILE:HB	1.98	0.46
1:Ac:147:ILE:HG13	1:Ac:148:TYR:CD1	2.50	0.46
1:Ad:224:LEU:HD11	1:Ad:246:VAL:HG11	1.97	0.46
1:F:224:LEU:HD12	1:F:243:PHE:CZ	2.50	0.46
1:G:200:LYS:O	1:H:85:SER:HA	2.16	0.46
1:L:158:PHE:CE1	1:L:226:ARG:HG3	2.50	0.46
1:L:164:LEU:O	1:L:219:VAL:HA	2.16	0.46
1:O:200:LYS:O	1:r:85:SER:HA	2.15	0.46
1:Q:147:ILE:HG13	1:Q:148:TYR:CD1	2.51	0.46
1:R:40:PHE:CZ	1:R:158:PHE:HB2	2.48	0.46
1:S:23:LYS:HD2	1:S:42:ARG:NH2	2.31	0.46
1:X:79:ASP:HB3	1:X:81:ARG:NH1	2.24	0.46
1:k:199:SER:HA	1:m:86:LEU:O	2.15	0.46
1:q:120:ILE:HG22	1:q:123:ILE:HD11	1.98	0.46
1:q:211:PHE:CD1	1:q:218:ILE:HD12	2.51	0.46
1:w:19:VAL:HB	1:w:247:LEU:HD12	1.98	0.46
1:y:75:GLY:O	1:y:76:ILE:HG12	2.15	0.46
1:6:120:ILE:HG21	1:6:220:PHE:CZ	2.50	0.46
1:9:56:ILE:HD11	1:9:137:LEU:HD21	1.97	0.46
1:9:79:ASP:O	1:9:80:LEU:HD12	2.16	0.46
1:AB:127:ASP:HB3	1:AE:44:TRP:CE2	2.50	0.46
1:AC:162:SER:HB2	1:AC:223:LYS:HB2	1.98	0.46
1:AG:23:LYS:HD2	1:AG:42:ARG:NH2	2.30	0.46
1:AL:80:LEU:C	1:AL:81:ARG:HD2	2.40	0.46
1:Ac:164:LEU:O	1:Ac:219:VAL:HA	2.16	0.46
1:F:79:ASP:O	1:F:80:LEU:HD12	2.16	0.46
1:L:23:LYS:HD2	1:L:42:ARG:HH22	1.80	0.46
1:O:111:GLU:HB2	1:O:178:LYS:HB2	1.96	0.46
1:b:23:LYS:HD2	1:b:42:ARG:NH2	2.30	0.46
1:c:200:LYS:O	1:d:85:SER:HA	2.16	0.46
1:e:23:LYS:HD2	1:e:42:ARG:NH2	2.31	0.46
1:k:172:GLN:HG2	1:k:208:ARG:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:170:ARG:HB3	1:l:170:ARG:HH11	1.81	0.46
1:p:162:SER:HB2	1:p:223:LYS:HB2	1.98	0.46
1:q:75:GLY:O	1:q:76:ILE:HG12	2.16	0.46
1:w:120:ILE:HG21	1:w:220:PHE:CZ	2.50	0.46
1:z:224:LEU:HD12	1:z:243:PHE:CZ	2.51	0.46
1:2:40:PHE:CZ	1:2:158:PHE:HB2	2.46	0.46
1:5:147:ILE:HG13	1:5:148:TYR:CD1	2.50	0.46
1:AF:164:LEU:O	1:AF:219:VAL:HA	2.15	0.46
1:AM:200:LYS:O	1:AN:85:SER:HA	2.15	0.46
1:AS:147:ILE:HG13	1:AS:148:TYR:CD1	2.51	0.46
1:AT:200:LYS:O	1:AU:85:SER:HA	2.15	0.46
1:AU:208:ARG:HG2	1:AU:210:VAL:HG23	1.98	0.46
1:AV:168:LYS:HE3	1:AV:168:LYS:HB2	1.70	0.46
1:AX:123:ILE:N	1:AX:123:ILE:HD12	2.30	0.46
1:E:148:TYR:O	1:E:152:ILE:HG12	2.15	0.46
1:H:23:LYS:HD2	1:H:42:ARG:NH2	2.31	0.46
1:P:79:ASP:O	1:P:80:LEU:HD12	2.16	0.46
1:V:162:SER:HB2	1:V:223:LYS:HB2	1.98	0.46
1:W:75:GLY:O	1:W:76:ILE:HG12	2.16	0.46
1:a:200:LYS:O	1:b:85:SER:HA	2.15	0.46
1:g:215:ASP:CG	1:g:216:GLU:H	2.23	0.46
1:h:77:ASP:HB3	1:h:120:ILE:HB	1.97	0.46
1:o:181:LEU:HD11	1:o:183:VAL:HG23	1.97	0.46
1:p:85:SER:HA	1:q:200:LYS:O	2.15	0.46
1:s:162:SER:HB2	1:s:223:LYS:HB2	1.98	0.46
1:v:111:GLU:HB2	1:v:178:LYS:HB2	1.97	0.46
1:v:123:ILE:HD12	1:v:123:ILE:N	2.30	0.46
1:z:120:ILE:HD12	1:z:169:MET:HG2	1.96	0.46
1:z:166:ALA:HB3	1:z:169:MET:HG3	1.97	0.46
1:AC:148:TYR:O	1:AC:152:ILE:HG12	2.16	0.46
1:AM:106:PHE:HA	1:AM:183:VAL:HG22	1.97	0.46
1:AN:147:ILE:HG13	1:AN:148:TYR:CD1	2.50	0.46
1:AR:124:ILE:HG12	1:AR:165:ARG:HB2	1.97	0.46
1:AR:127:ASP:HB3	1:AS:44:TRP:CE2	2.51	0.46
1:AS:30:HIS:CE1	1:AS:42:ARG:HH11	2.33	0.46
1:Ac:79:ASP:O	1:Ac:80:LEU:HD12	2.16	0.46
1:D:120:ILE:HG21	1:D:220:PHE:CZ	2.51	0.46
1:E:23:LYS:HD2	1:E:42:ARG:NH2	2.31	0.46
1:E:228:PHE:HD1	1:E:229:PHE:H	1.63	0.46
1:R:85:SER:HA	1:U:200:LYS:O	2.15	0.46
1:V:32:TYR:HB3	1:V:40:PHE:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:120:ILE:HG21	1:b:220:PHE:CZ	2.50	0.46
1:c:224:LEU:HD11	1:c:246:VAL:HG11	1.97	0.46
1:g:162:SER:HB2	1:g:223:LYS:HB2	1.98	0.46
1:h:120:ILE:HG21	1:h:220:PHE:CZ	2.50	0.46
1:n:23:LYS:HD2	1:n:42:ARG:NH2	2.31	0.46
1:o:127:ASP:HB3	1:r:44:TRP:CE2	2.51	0.46
1:y:181:LEU:HD11	1:y:183:VAL:HG23	1.98	0.46
1:z:211:PHE:CD1	1:z:218:ILE:HD12	2.51	0.46
1:2:166:ALA:HB3	1:2:169:MET:HG3	1.98	0.46
1:9:16:TYR:HD1	1:9:223:LYS:HG3	1.80	0.46
1:AA:162:SER:HB2	1:AA:223:LYS:HB2	1.97	0.46
1:AE:227:LEU:HD21	1:AE:235:LEU:HD11	1.98	0.46
1:AG:120:ILE:HG21	1:AG:220:PHE:CZ	2.50	0.46
1:AH:16:TYR:CE2	1:AH:164:LEU:HG	2.51	0.46
1:AJ:181:LEU:HD11	1:AJ:183:VAL:HG23	1.97	0.46
1:AL:224:LEU:HD12	1:AL:243:PHE:CZ	2.50	0.46
1:AM:224:LEU:HD12	1:AM:243:PHE:CZ	2.51	0.46
1:AZ:183:VAL:HB	1:AZ:197:LEU:HG	1.98	0.46
1:Aa:162:SER:HB2	1:Aa:223:LYS:HB2	1.97	0.46
1:Ad:23:LYS:HD2	1:Ad:42:ARG:NH2	2.31	0.46
1:A:123:ILE:N	1:A:123:ILE:HD12	2.31	0.46
1:F:147:ILE:HG13	1:F:148:TYR:CD1	2.50	0.46
1:G:44:TRP:CE2	1:H:127:ASP:HB3	2.51	0.46
1:H:148:TYR:O	1:H:152:ILE:HG12	2.16	0.46
1:K:120:ILE:HG21	1:K:220:PHE:CZ	2.51	0.46
1:L:59:LEU:O	1:L:145:ARG:HG3	2.16	0.46
1:N:75:GLY:O	1:N:76:ILE:HG12	2.16	0.46
1:R:181:LEU:HD11	1:R:183:VAL:HG23	1.97	0.46
1:S:120:ILE:HG21	1:S:220:PHE:CZ	2.51	0.46
1:U:120:ILE:HG21	1:U:220:PHE:CZ	2.51	0.46
1:V:169:MET:HB2	1:V:211:PHE:HB3	1.97	0.46
1:i:59:LEU:O	1:i:145:ARG:HG3	2.16	0.46
1:p:75:GLY:O	1:p:76:ILE:HG12	2.16	0.46
1:r:148:TYR:O	1:r:152:ILE:HG12	2.16	0.46
1:s:79:ASP:C	1:s:80:LEU:HD12	2.41	0.46
1:v:200:LYS:O	1:w:85:SER:HA	2.15	0.46
1:y:147:ILE:HG13	1:y:148:TYR:CD1	2.51	0.46
1:7:147:ILE:HG13	1:7:148:TYR:CD1	2.52	0.46
1:AA:75:GLY:O	1:AA:76:ILE:HG12	2.15	0.46
1:AA:79:ASP:O	1:AA:80:LEU:HD12	2.16	0.46
1:AC:85:SER:HA	1:AD:200:LYS:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:224:LEU:HD11	1:AF:246:VAL:HG11	1.97	0.46
1:AH:111:GLU:HB2	1:AH:178:LYS:HB2	1.97	0.46
1:AI:16:TYR:CE2	1:AI:164:LEU:HG	2.51	0.46
1:AJ:19:VAL:HB	1:AJ:247:LEU:HD12	1.98	0.46
1:AJ:79:ASP:HB3	1:AJ:81:ARG:HH22	1.81	0.46
1:AJ:210:VAL:HB	1:AK:76:ILE:HG21	1.98	0.46
1:AL:32:TYR:HB3	1:AL:40:PHE:CE1	2.51	0.46
1:AP:23:LYS:HD2	1:AP:42:ARG:NH2	2.30	0.46
1:AU:162:SER:HB2	1:AU:223:LYS:HB2	1.98	0.46
1:AY:40:PHE:HE2	1:AY:224:LEU:HD13	1.80	0.46
1:AZ:85:SER:HA	1:Aa:200:LYS:O	2.16	0.46
1:Ac:224:LEU:HD12	1:Ac:243:PHE:CZ	2.50	0.46
1:B:113:SER:OG	1:B:176:LYS:HB2	2.16	0.45
1:C:200:LYS:O	1:D:85:SER:HA	2.16	0.45
1:F:77:ASP:HB3	1:F:120:ILE:HB	1.98	0.45
1:F:200:LYS:O	1:G:85:SER:HA	2.16	0.45
1:F:210:VAL:HB	1:G:76:ILE:HG21	1.97	0.45
1:F:210:VAL:HG12	1:F:212:GLU:OE2	2.16	0.45
1:K:130:GLU:HB2	1:L:43:ILE:HB	1.97	0.45
1:O:162:SER:HB2	1:O:223:LYS:HB2	1.98	0.45
1:c:77:ASP:HB3	1:c:120:ILE:HB	1.99	0.45
1:c:147:ILE:HG13	1:c:148:TYR:CD1	2.51	0.45
1:g:16:TYR:CE2	1:g:164:LEU:HG	2.51	0.45
1:h:130:GLU:HB2	1:i:43:ILE:HB	1.97	0.45
1:i:164:LEU:O	1:i:219:VAL:HA	2.16	0.45
1:l:152:ILE:HD12	1:l:227:LEU:HG	1.98	0.45
1:o:85:SER:HA	1:r:200:LYS:O	2.16	0.45
1:r:181:LEU:HD11	1:r:183:VAL:HG23	1.97	0.45
1:s:181:LEU:HD11	1:s:183:VAL:HG23	1.98	0.45
1:t:16:TYR:CD1	1:t:223:LYS:HG3	2.51	0.45
1:u:147:ILE:HG13	1:u:148:TYR:CD1	2.50	0.45
1:v:148:TYR:O	1:v:152:ILE:HG12	2.16	0.45
1:y:162:SER:HB2	1:y:223:LYS:HB2	1.98	0.45
1:8:162:SER:HB2	1:8:223:LYS:HB2	1.97	0.45
1:AC:77:ASP:HB3	1:AC:120:ILE:HB	1.97	0.45
1:AC:147:ILE:HG13	1:AC:148:TYR:CD1	2.51	0.45
1:AD:77:ASP:HB3	1:AD:120:ILE:HB	1.98	0.45
1:AI:168:LYS:HA	1:AI:168:LYS:HD3	1.86	0.45
1:AK:164:LEU:O	1:AK:219:VAL:HA	2.17	0.45
1:AL:43:ILE:O	1:AL:43:ILE:HG13	2.15	0.45
1:Ad:172:GLN:HG2	1:Ad:208:ARG:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:LYS:HD2	1:A:42:ARG:NH2	2.31	0.45
1:I:120:ILE:HG21	1:I:220:PHE:CZ	2.52	0.45
1:P:181:LEU:HD11	1:P:183:VAL:HG23	1.97	0.45
1:R:127:ASP:HB3	1:U:44:TRP:CE2	2.51	0.45
1:R:170:ARG:NH1	1:R:170:ARG:HB3	2.32	0.45
1:V:147:ILE:HG13	1:V:148:TYR:CD1	2.51	0.45
1:W:115:SER:OG	1:W:174:GLU:HB2	2.17	0.45
1:X:16:TYR:CD1	1:X:223:LYS:HG3	2.52	0.45
1:b:228:PHE:HD1	1:b:229:PHE:H	1.63	0.45
1:c:148:TYR:O	1:c:152:ILE:HG12	2.16	0.45
1:g:16:TYR:CD1	1:g:223:LYS:HG3	2.51	0.45
1:p:23:LYS:HD2	1:p:42:ARG:NH2	2.31	0.45
1:q:32:TYR:CZ	1:q:42:ARG:HD3	2.51	0.45
1:v:120:ILE:HG21	1:v:220:PHE:CZ	2.52	0.45
1:w:170:ARG:HB3	1:w:170:ARG:NH1	2.32	0.45
1:2:211:PHE:CD1	1:2:218:ILE:HD12	2.52	0.45
1:8:211:PHE:CD1	1:8:218:ILE:HD12	2.52	0.45
1:AC:23:LYS:HD2	1:AC:42:ARG:NH2	2.31	0.45
1:AI:123:ILE:HD12	1:AI:123:ILE:N	2.31	0.45
1:AJ:40:PHE:CZ	1:AJ:158:PHE:HB2	2.50	0.45
1:AK:16:TYR:CD1	1:AK:223:LYS:HG3	2.51	0.45
1:AS:40:PHE:CE1	1:AS:158:PHE:HB2	2.51	0.45
1:AV:164:LEU:O	1:AV:219:VAL:HA	2.17	0.45
1:AZ:162:SER:HB2	1:AZ:223:LYS:HB2	1.98	0.45
1:Aa:75:GLY:O	1:Aa:76:ILE:HG12	2.16	0.45
1:A:162:SER:HB2	1:A:223:LYS:HB2	1.97	0.45
1:H:111:GLU:HB2	1:H:178:LYS:HB2	1.97	0.45
1:N:164:LEU:O	1:N:219:VAL:HA	2.17	0.45
1:P:228:PHE:HD2	1:P:229:PHE:H	1.64	0.45
1:c:164:LEU:O	1:c:219:VAL:HA	2.16	0.45
1:o:19:VAL:HB	1:o:247:LEU:HD12	1.98	0.45
1:p:120:ILE:HG21	1:p:220:PHE:CZ	2.51	0.45
1:t:40:PHE:CZ	1:t:158:PHE:HB2	2.51	0.45
1:t:115:SER:OG	1:t:174:GLU:HB2	2.16	0.45
1:w:23:LYS:HD2	1:w:42:ARG:HH21	1.79	0.45
1:z:200:LYS:O	1:1:85:SER:HA	2.16	0.45
1:1:147:ILE:HG13	1:1:148:TYR:CD1	2.52	0.45
1:2:59:LEU:O	1:2:145:ARG:HG3	2.17	0.45
1:2:124:ILE:HG12	1:2:165:ARG:HB2	1.97	0.45
1:4:181:LEU:HD11	1:4:183:VAL:HG23	1.99	0.45
1:8:81:ARG:NH1	1:8:81:ARG:HG3	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:148:TYR:O	1:AA:152:ILE:HG12	2.15	0.45
1:AH:162:SER:HB2	1:AH:223:LYS:HB2	1.99	0.45
1:AL:44:TRP:CE2	1:AM:127:ASP:HB3	2.52	0.45
1:AL:79:ASP:C	1:AL:80:LEU:HD12	2.40	0.45
1:AN:152:ILE:HD12	1:AN:227:LEU:HG	1.98	0.45
1:AW:148:TYR:O	1:AW:152:ILE:HG12	2.17	0.45
1:AX:111:GLU:HB2	1:AX:178:LYS:HB2	1.97	0.45
1:A:111:GLU:HB2	1:A:178:LYS:HB2	1.98	0.45
1:B:79:ASP:O	1:B:80:LEU:HD12	2.17	0.45
1:X:181:LEU:HD11	1:X:183:VAL:HG23	1.98	0.45
1:e:147:ILE:HG13	1:e:148:TYR:CD1	2.52	0.45
1:f:111:GLU:HB2	1:f:178:LYS:HB2	1.97	0.45
1:g:123:ILE:N	1:g:123:ILE:HD12	2.31	0.45
1:h:75:GLY:O	1:h:76:ILE:HG12	2.16	0.45
1:h:164:LEU:O	1:h:219:VAL:HA	2.17	0.45
1:l:79:ASP:HB3	1:l:81:ARG:HH12	1.82	0.45
1:n:164:LEU:O	1:n:219:VAL:HA	2.16	0.45
1:u:152:ILE:HD12	1:u:227:LEU:HG	1.98	0.45
1:1:120:ILE:HG21	1:1:220:PHE:CZ	2.51	0.45
1:3:164:LEU:O	1:3:219:VAL:HA	2.16	0.45
1:5:127:ASP:HB3	1:6:44:TRP:CE2	2.52	0.45
1:AE:148:TYR:O	1:AE:152:ILE:HG12	2.17	0.45
1:AH:147:ILE:HG13	1:AH:148:TYR:CD1	2.51	0.45
1:AO:104:PRO:HB3	1:AO:185:VAL:HG12	1.98	0.45
1:AV:79:ASP:O	1:AV:80:LEU:HD12	2.16	0.45
1:AX:79:ASP:HB3	1:AX:81:ARG:HH22	1.80	0.45
1:AY:162:SER:HB2	1:AY:223:LYS:HB2	1.99	0.45
1:AZ:147:ILE:HG13	1:AZ:148:TYR:CD1	2.51	0.45
1:H:152:ILE:HD12	1:H:227:LEU:HG	1.99	0.45
1:J:16:TYR:CE2	1:J:164:LEU:HG	2.52	0.45
1:J:104:PRO:HB3	1:J:185:VAL:HG12	1.99	0.45
1:L:104:PRO:HB3	1:L:185:VAL:HG12	1.98	0.45
1:N:183:VAL:HB	1:N:197:LEU:HG	1.98	0.45
1:X:43:ILE:O	1:X:43:ILE:HG13	2.16	0.45
1:Y:16:TYR:CD1	1:Y:223:LYS:HG3	2.52	0.45
1:i:224:LEU:HD11	1:i:246:VAL:HG11	1.97	0.45
1:q:127:ASP:HB3	1:s:44:TRP:CE2	2.52	0.45
1:t:111:GLU:HB2	1:t:178:LYS:HB2	1.98	0.45
1:u:64:ILE:HD12	1:u:136:TRP:HZ2	1.82	0.45
1:2:75:GLY:O	1:2:76:ILE:HG12	2.17	0.45
1:2:121:GLU:HB3	1:2:168:LYS:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:147:ILE:HG13	1:8:148:TYR:CD1	2.52	0.45
1:AA:120:ILE:HG22	1:AA:123:ILE:HD11	1.97	0.45
1:AF:162:SER:HB2	1:AF:223:LYS:HB2	1.99	0.45
1:AR:75:GLY:O	1:AR:76:ILE:HG12	2.17	0.45
1:AU:29:LEU:HD21	1:AU:68:ILE:HG21	1.98	0.45
1:A:147:ILE:HG13	1:A:148:TYR:CD1	2.52	0.45
1:D:181:LEU:HD12	1:D:182:GLY:H	1.81	0.45
1:M:40:PHE:CE1	1:M:158:PHE:HB2	2.52	0.45
1:O:16:TYR:CD1	1:O:223:LYS:HG3	2.52	0.45
1:O:148:TYR:O	1:O:152:ILE:HG12	2.17	0.45
1:P:120:ILE:HG21	1:P:220:PHE:CZ	2.51	0.45
1:T:79:ASP:O	1:T:80:LEU:HD12	2.17	0.45
1:V:224:LEU:HD12	1:V:243:PHE:CZ	2.51	0.45
1:W:162:SER:HB2	1:W:223:LYS:HB2	1.98	0.45
1:X:111:GLU:HB2	1:X:178:LYS:HB2	1.98	0.45
1:X:224:LEU:HD11	1:X:246:VAL:HG11	1.98	0.45
1:Z:43:ILE:HB	1:a:130:GLU:HB2	1.98	0.45
1:j:40:PHE:CE1	1:j:158:PHE:HB2	2.51	0.45
1:k:164:LEU:O	1:k:219:VAL:HA	2.17	0.45
1:p:29:LEU:HD11	1:p:68:ILE:HD12	1.99	0.45
1:q:79:ASP:O	1:q:80:LEU:HD12	2.16	0.45
1:v:169:MET:HB2	1:v:211:PHE:HB3	1.98	0.45
1:z:79:ASP:O	1:z:80:LEU:HD12	2.16	0.45
1:4:32:TYR:CE1	1:4:42:ARG:HD3	2.52	0.45
1:5:168:LYS:HE3	1:5:168:LYS:HB2	1.70	0.45
1:7:152:ILE:HD12	1:7:227:LEU:HD22	1.99	0.45
1:8:81:ARG:HG3	1:8:81:ARG:HH11	1.81	0.45
1:8:224:LEU:HD11	1:8:246:VAL:HG11	1.98	0.45
1:AF:77:ASP:HB3	1:AF:120:ILE:HB	1.98	0.45
1:AF:210:VAL:HG12	1:AF:212:GLU:OE2	2.17	0.45
1:AI:44:TRP:CE2	1:AJ:127:ASP:HB3	2.52	0.45
1:AJ:170:ARG:HB3	1:AJ:170:ARG:NH1	2.32	0.45
1:AL:200:LYS:O	1:AM:85:SER:HA	2.17	0.45
1:AM:32:TYR:CE1	1:AM:42:ARG:HD3	2.50	0.45
1:AU:16:TYR:HD1	1:AU:223:LYS:HG3	1.81	0.45
1:AV:16:TYR:HD1	1:AV:223:LYS:HG3	1.81	0.45
1:AY:173:PHE:O	1:AY:206:TYR:HA	2.16	0.45
1:A:16:TYR:CD1	1:A:223:LYS:HG3	2.51	0.45
1:D:162:SER:HB2	1:D:223:LYS:HB2	1.99	0.45
1:E:40:PHE:CZ	1:E:158:PHE:HB2	2.52	0.45
1:E:75:GLY:O	1:E:76:ILE:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:172:GLN:HG2	1:F:208:ARG:HB2	1.98	0.45
1:O:152:ILE:HD12	1:O:227:LEU:HG	1.98	0.45
1:P:77:ASP:HB3	1:P:120:ILE:HB	1.98	0.45
1:W:111:GLU:HB2	1:W:178:LYS:HB2	1.98	0.45
1:b:172:GLN:HG2	1:b:208:ARG:HG3	1.98	0.45
1:i:104:PRO:HB3	1:i:185:VAL:HG12	1.98	0.45
1:k:148:TYR:O	1:k:152:ILE:HG12	2.17	0.45
1:k:168:LYS:HE3	1:k:168:LYS:HB2	1.71	0.45
1:p:168:LYS:HE3	1:p:168:LYS:HB2	1.70	0.45
1:5:164:LEU:O	1:5:219:VAL:HA	2.17	0.45
1:7:199:SER:HA	1:8:86:LEU:O	2.17	0.45
1:8:123:ILE:HD12	1:8:123:ILE:N	2.31	0.45
1:9:85:SER:HA	1:AA:200:LYS:O	2.17	0.45
1:AA:111:GLU:HB2	1:AA:178:LYS:HB2	1.98	0.45
1:AC:183:VAL:HB	1:AC:197:LEU:HG	1.98	0.45
1:AH:152:ILE:HD12	1:AH:227:LEU:HG	1.99	0.45
1:AO:23:LYS:HD2	1:AO:42:ARG:NH2	2.31	0.45
1:AO:183:VAL:HB	1:AO:197:LEU:HG	1.99	0.45
1:AP:164:LEU:O	1:AP:219:VAL:HA	2.16	0.45
1:AR:147:ILE:HG13	1:AR:148:TYR:CD1	2.52	0.45
1:AY:120:ILE:HG21	1:AY:220:PHE:CZ	2.52	0.45
1:AZ:148:TYR:O	1:AZ:152:ILE:HG12	2.17	0.45
1:Ab:19:VAL:HA	1:Ab:246:VAL:HG23	1.98	0.45
1:Ab:147:ILE:HG13	1:Ab:148:TYR:CD1	2.51	0.45
1:Ad:40:PHE:CZ	1:Ad:158:PHE:HB2	2.52	0.45
1:D:215:ASP:CG	1:D:216:GLU:H	2.25	0.45
1:P:16:TYR:CD1	1:P:223:LYS:HG3	2.52	0.45
1:P:44:TRP:CE2	1:Q:127:ASP:HB3	2.52	0.45
1:Y:79:ASP:O	1:Y:80:LEU:HD12	2.17	0.45
1:Y:117:ILE:HB	1:Y:172:GLN:HB3	1.99	0.45
1:Y:164:LEU:O	1:Y:219:VAL:HA	2.17	0.45
1:Z:111:GLU:HB2	1:Z:178:LYS:HB2	1.98	0.45
1:a:148:TYR:O	1:a:152:ILE:HG12	2.17	0.45
1:d:16:TYR:CE2	1:d:164:LEU:HG	2.51	0.45
1:g:104:PRO:HB3	1:g:185:VAL:HG12	1.98	0.45
1:i:16:TYR:CD1	1:i:223:LYS:HG3	2.51	0.45
1:i:215:ASP:OD1	1:i:216:GLU:N	2.40	0.45
1:j:147:ILE:HG13	1:j:148:TYR:CD1	2.51	0.45
1:m:228:PHE:HD2	1:m:229:PHE:H	1.63	0.45
1:s:147:ILE:HG13	1:s:148:TYR:CD1	2.51	0.45
1:t:224:LEU:HD11	1:t:246:VAL:HG11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:145:ARG:HB2	1:v:148:TYR:HD1	1.82	0.45
1:w:162:SER:HB2	1:w:223:LYS:HB2	1.99	0.45
1:2:16:TYR:CD1	1:2:223:LYS:HG3	2.51	0.45
1:3:120:ILE:HG21	1:3:220:PHE:CZ	2.52	0.45
1:4:85:SER:HA	1:5:200:LYS:O	2.16	0.45
1:0:120:ILE:HG21	1:0:220:PHE:CZ	2.52	0.45
1:0:164:LEU:O	1:0:219:VAL:HA	2.17	0.45
1:AA:147:ILE:HG13	1:AA:148:TYR:CD1	2.52	0.45
1:AI:181:LEU:HD11	1:AI:183:VAL:HG23	1.97	0.45
1:AK:79:ASP:HB3	1:AK:81:ARG:NH2	2.31	0.45
1:AL:147:ILE:HG13	1:AL:148:TYR:CD1	2.51	0.45
1:AQ:32:TYR:CZ	1:AQ:42:ARG:HD3	2.52	0.45
1:AQ:77:ASP:HB3	1:AQ:120:ILE:HB	1.98	0.45
1:AT:120:ILE:HG21	1:AT:220:PHE:CZ	2.51	0.45
1:AW:120:ILE:HD12	1:AW:169:MET:HE3	1.99	0.45
1:AX:164:LEU:O	1:AX:219:VAL:HA	2.17	0.45
1:A:43:ILE:HG13	1:A:43:ILE:O	2.16	0.45
1:B:56:ILE:HD11	1:B:137:LEU:HD21	1.99	0.45
1:B:147:ILE:HG13	1:B:148:TYR:CD1	2.52	0.45
1:H:147:ILE:HG13	1:H:148:TYR:CD1	2.51	0.45
1:L:211:PHE:CD1	1:L:218:ILE:HD12	2.52	0.45
1:M:30:HIS:CE1	1:M:42:ARG:HH11	2.33	0.45
1:M:44:TRP:CE2	1:N:127:ASP:HB3	2.52	0.45
1:N:148:TYR:O	1:N:152:ILE:HG12	2.17	0.45
1:O:85:SER:HA	1:Q:200:LYS:O	2.16	0.45
1:O:106:PHE:HA	1:O:183:VAL:HG22	1.97	0.45
1:S:40:PHE:CZ	1:S:158:PHE:HB2	2.43	0.45
1:U:104:PRO:HB3	1:U:185:VAL:HG12	1.99	0.45
1:W:79:ASP:O	1:W:80:LEU:HD12	2.17	0.45
1:Z:200:LYS:O	1:a:85:SER:HA	2.17	0.45
1:c:162:SER:HB2	1:c:223:LYS:HB2	1.99	0.45
1:l:16:TYR:CD1	1:l:223:LYS:HG3	2.52	0.45
1:l:16:TYR:CE2	1:l:164:LEU:HG	2.52	0.45
1:l:124:ILE:HG12	1:l:165:ARG:HB2	1.99	0.45
1:n:147:ILE:HG13	1:n:148:TYR:CD1	2.51	0.45
1:p:124:ILE:HG12	1:p:165:ARG:HB2	1.99	0.45
1:s:79:ASP:HB2	1:s:118:PHE:HB3	1.99	0.45
1:t:75:GLY:O	1:t:76:ILE:HG12	2.16	0.45
1:4:168:LYS:HB2	1:4:168:LYS:HE3	1.69	0.45
1:5:43:ILE:O	1:5:43:ILE:HG13	2.17	0.45
1:6:40:PHE:CE1	1:6:158:PHE:HB2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:148:TYR:O	1:AB:152:ILE:HG12	2.17	0.45
1:AC:111:GLU:HB2	1:AC:178:LYS:HB2	1.99	0.45
1:AE:224:LEU:HD11	1:AE:246:VAL:HG11	1.98	0.45
1:AF:79:ASP:O	1:AF:80:LEU:HD12	2.16	0.45
1:AN:124:ILE:HG12	1:AN:165:ARG:HB2	1.99	0.45
1:AQ:183:VAL:HB	1:AQ:197:LEU:HG	1.98	0.45
1:AX:162:SER:HB2	1:AX:223:LYS:HB2	1.97	0.45
1:AY:85:SER:HA	1:Ab:200:LYS:O	2.16	0.45
1:AY:131:ILE:HG13	1:Ab:43:ILE:HD12	1.98	0.45
1:AZ:127:ASP:HB3	1:Aa:44:TRP:CE2	2.52	0.45
1:L:130:GLU:HB2	1:S:43:ILE:HB	1.98	0.45
1:O:79:ASP:HB3	1:O:81:ARG:HH12	1.82	0.45
1:O:170:ARG:HH11	1:O:170:ARG:HB3	1.81	0.45
1:P:152:ILE:HD12	1:P:227:LEU:CD2	2.46	0.45
1:P:227:LEU:HD21	1:P:235:LEU:HD11	1.98	0.45
1:Q:23:LYS:HD2	1:Q:42:ARG:NH2	2.31	0.45
1:X:162:SER:HB2	1:X:223:LYS:HB2	1.98	0.45
1:b:40:PHE:CD2	1:b:246:VAL:HG12	2.52	0.45
1:c:79:ASP:O	1:c:80:LEU:HD12	2.16	0.45
1:e:77:ASP:HB3	1:e:120:ILE:HB	1.97	0.45
1:g:168:LYS:HB2	1:g:168:LYS:HE3	1.71	0.45
1:k:124:ILE:HG12	1:k:165:ARG:HB2	1.97	0.45
1:l:23:LYS:HD2	1:l:42:ARG:HH22	1.81	0.45
1:l:85:SER:HA	1:n:200:LYS:O	2.17	0.45
1:o:162:SER:HB2	1:o:223:LYS:HB2	1.99	0.45
1:q:120:ILE:HD12	1:q:169:MET:HG2	1.98	0.45
1:u:162:SER:HB2	1:u:223:LYS:HB2	1.98	0.45
1:y:23:LYS:HD2	1:y:42:ARG:NH2	2.32	0.45
1:4:227:LEU:HD21	1:4:235:LEU:HD11	1.99	0.45
1:7:164:LEU:O	1:7:219:VAL:HA	2.16	0.45
1:AE:147:ILE:HG13	1:AE:148:TYR:CD1	2.52	0.45
1:AI:200:LYS:O	1:AJ:85:SER:HA	2.16	0.45
1:AJ:111:GLU:HB2	1:AJ:178:LYS:HB2	1.99	0.45
1:AK:147:ILE:HG13	1:AK:148:TYR:CD1	2.50	0.45
1:AL:120:ILE:HG21	1:AL:220:PHE:CZ	2.52	0.45
1:AM:79:ASP:O	1:AM:80:LEU:HD12	2.17	0.45
1:AM:148:TYR:HA	1:AM:151:GLU:HG3	1.98	0.45
1:AO:16:TYR:CD1	1:AO:223:LYS:HG3	2.52	0.45
1:AO:59:LEU:O	1:AO:145:ARG:HG3	2.17	0.45
1:AR:148:TYR:O	1:AR:152:ILE:HG12	2.17	0.45
1:AR:164:LEU:O	1:AR:219:VAL:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AU:147:ILE:HG13	1:AU:148:TYR:CD1	2.52	0.45
1:AV:147:ILE:HG13	1:AV:148:TYR:CD1	2.52	0.45
1:AY:79:ASP:O	1:AY:80:LEU:HD12	2.17	0.45
1:Ab:40:PHE:CE1	1:Ab:224:LEU:HD13	2.51	0.45
1:F:164:LEU:O	1:F:219:VAL:HA	2.17	0.44
1:J:123:ILE:HD12	1:J:123:ILE:N	2.31	0.44
1:M:34:HIS:CE1	1:M:38:ASN:HA	2.52	0.44
1:M:40:PHE:HE1	1:M:158:PHE:HB2	1.82	0.44
1:M:193:VAL:HG22	1:N:93:LYS:HG2	1.99	0.44
1:Q:16:TYR:CD1	1:Q:223:LYS:HG3	2.52	0.44
1:X:164:LEU:O	1:X:219:VAL:HA	2.18	0.44
1:Z:77:ASP:HB3	1:Z:120:ILE:HB	2.00	0.44
1:b:147:ILE:HG13	1:b:148:TYR:CD1	2.51	0.44
1:f:164:LEU:O	1:f:219:VAL:HA	2.17	0.44
1:h:36:ILE:HD13	1:h:36:ILE:HA	1.90	0.44
1:k:43:ILE:O	1:k:43:ILE:HG13	2.17	0.44
1:k:75:GLY:O	1:k:76:ILE:HG12	2.17	0.44
1:l:162:SER:HB2	1:l:223:LYS:HB2	1.99	0.44
1:t:12:LYS:HA	1:t:12:LYS:HD3	1.82	0.44
1:w:164:LEU:O	1:w:219:VAL:HA	2.17	0.44
1:y:199:SER:HA	1:z:86:LEU:O	2.17	0.44
1:5:124:ILE:HG12	1:5:165:ARG:HB2	1.97	0.44
1:9:164:LEU:O	1:9:219:VAL:HA	2.16	0.44
1:AB:200:LYS:O	1:AG:85:SER:HA	2.16	0.44
1:AE:210:VAL:HG12	1:AE:212:GLU:OE1	2.17	0.44
1:AE:215:ASP:CG	1:AE:216:GLU:N	2.75	0.44
1:AI:120:ILE:HG21	1:AI:220:PHE:CZ	2.51	0.44
1:AK:168:LYS:HB2	1:AK:168:LYS:HE3	1.71	0.44
1:AN:168:LYS:HB2	1:AN:168:LYS:HE3	1.70	0.44
1:AX:16:TYR:CD1	1:AX:223:LYS:HG3	2.52	0.44
1:Ad:75:GLY:O	1:Ad:76:ILE:HG12	2.18	0.44
1:C:147:ILE:HG13	1:C:148:TYR:CD1	2.52	0.44
1:E:147:ILE:HG13	1:E:148:TYR:CD1	2.52	0.44
1:J:16:TYR:CD1	1:J:223:LYS:HG3	2.51	0.44
1:N:147:ILE:HG13	1:N:148:TYR:CD1	2.52	0.44
1:O:43:ILE:HD12	1:r:131:ILE:HG13	2.00	0.44
1:S:75:GLY:O	1:S:76:ILE:HG12	2.18	0.44
1:Y:210:VAL:HG12	1:Y:212:GLU:OE2	2.17	0.44
1:e:162:SER:HB2	1:e:223:LYS:HB2	1.98	0.44
1:o:16:TYR:CD1	1:o:223:LYS:HG3	2.52	0.44
1:o:111:GLU:HB2	1:o:178:LYS:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:r:104:PRO:HB3	1:r:185:VAL:HG12	1.99	0.44
1:s:120:ILE:HG21	1:s:220:PHE:CZ	2.52	0.44
1:t:164:LEU:O	1:t:219:VAL:HA	2.18	0.44
1:z:147:ILE:HG13	1:z:148:TYR:CD1	2.52	0.44
1:3:79:ASP:HB3	1:3:81:ARG:NH2	2.33	0.44
1:4:16:TYR:CD1	1:4:223:LYS:HG3	2.52	0.44
1:7:148:TYR:O	1:7:152:ILE:HG12	2.16	0.44
1:8:215:ASP:OD1	1:8:216:GLU:N	2.39	0.44
1:0:200:LYS:O	1:AA:85:SER:HA	2.17	0.44
1:AA:16:TYR:CD1	1:AA:223:LYS:HG3	2.52	0.44
1:AA:40:PHE:CZ	1:AA:158:PHE:HB2	2.49	0.44
1:AE:168:LYS:HB2	1:AE:168:LYS:HE3	1.70	0.44
1:AF:16:TYR:CE2	1:AF:164:LEU:HG	2.53	0.44
1:AL:168:LYS:HB2	1:AL:168:LYS:HE3	1.70	0.44
1:AN:120:ILE:HG21	1:AN:220:PHE:CZ	2.52	0.44
1:AQ:120:ILE:HG21	1:AQ:220:PHE:CZ	2.51	0.44
1:AS:210:VAL:HG12	1:AS:212:GLU:OE1	2.18	0.44
1:Ac:23:LYS:HD2	1:Ac:42:ARG:HH21	1.81	0.44
1:Ac:148:TYR:O	1:Ac:152:ILE:HG12	2.17	0.44
1:A:224:LEU:HD11	1:A:246:VAL:HG11	1.99	0.44
1:B:181:LEU:HD11	1:B:183:VAL:HG23	1.99	0.44
1:N:152:ILE:HD12	1:N:227:LEU:HG	1.99	0.44
1:P:210:VAL:HG12	1:P:212:GLU:OE1	2.17	0.44
1:Q:79:ASP:O	1:Q:80:LEU:HD12	2.18	0.44
1:Q:164:LEU:O	1:Q:219:VAL:HA	2.17	0.44
1:Z:210:VAL:HG12	1:Z:212:GLU:OE1	2.17	0.44
1:d:16:TYR:CD1	1:d:223:LYS:HG3	2.52	0.44
1:f:120:ILE:HG21	1:f:220:PHE:CZ	2.52	0.44
1:m:16:TYR:CD1	1:m:223:LYS:HG3	2.52	0.44
1:o:36:ILE:HD13	1:o:36:ILE:HA	1.86	0.44
1:w:130:GLU:O	1:w:134:ARG:HG3	2.17	0.44
1:4:79:ASP:HB3	1:4:81:ARG:NH2	2.07	0.44
1:0:148:TYR:O	1:0:152:ILE:HG12	2.17	0.44
1:AB:173:PHE:O	1:AB:206:TYR:HA	2.17	0.44
1:AD:16:TYR:HD1	1:AD:223:LYS:HG3	1.82	0.44
1:AE:145:ARG:HB2	1:AE:148:TYR:HD1	1.81	0.44
1:AG:172:GLN:HG2	1:AG:208:ARG:HG3	1.99	0.44
1:AJ:36:ILE:HD13	1:AJ:36:ILE:HA	1.86	0.44
1:AM:164:LEU:O	1:AM:219:VAL:HA	2.18	0.44
1:AP:16:TYR:HD1	1:AP:223:LYS:HG3	1.83	0.44
1:AR:173:PHE:HE1	1:AR:175:ARG:HE	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ab:59:LEU:O	1:Ab:145:ARG:HG3	2.18	0.44
1:Ab:168:LYS:HB2	1:Ab:168:LYS:HE3	1.69	0.44
1:L:16:TYR:CD1	1:L:223:LYS:HG3	2.52	0.44
1:N:162:SER:HB2	1:N:223:LYS:HB2	1.99	0.44
1:O:16:TYR:CE2	1:O:164:LEU:HG	2.52	0.44
1:R:16:TYR:CD1	1:R:223:LYS:HG3	2.52	0.44
1:R:120:ILE:HG22	1:R:123:ILE:HD11	1.99	0.44
1:R:162:SER:HB2	1:R:223:LYS:HB2	2.00	0.44
1:T:85:SER:HA	1:V:200:LYS:O	2.18	0.44
1:T:127:ASP:HB3	1:V:44:TRP:CE2	2.53	0.44
1:U:79:ASP:HB3	1:U:81:ARG:NH2	2.33	0.44
1:V:148:TYR:O	1:V:152:ILE:HG12	2.17	0.44
1:W:16:TYR:CD1	1:W:223:LYS:HG3	2.51	0.44
1:W:147:ILE:HG13	1:W:148:TYR:CD1	2.52	0.44
1:Z:224:LEU:HD11	1:Z:246:VAL:HG11	1.98	0.44
1:d:168:LYS:HB2	1:d:168:LYS:HE3	1.70	0.44
1:d:200:LYS:O	1:e:85:SER:HA	2.17	0.44
1:g:181:LEU:HD11	1:g:183:VAL:HG23	1.98	0.44
1:g:206:TYR:OH	1:g:208:ARG:HD2	2.18	0.44
1:j:120:ILE:HG21	1:j:220:PHE:CZ	2.52	0.44
1:j:193:VAL:HG22	1:k:93:LYS:HG2	2.00	0.44
1:m:124:ILE:HG12	1:m:165:ARG:HB2	1.99	0.44
1:n:32:TYR:CZ	1:n:42:ARG:HD3	2.52	0.44
1:t:120:ILE:HD12	1:t:169:MET:HG2	1.99	0.44
1:5:75:GLY:O	1:5:76:ILE:HG12	2.17	0.44
1:5:148:TYR:O	1:5:152:ILE:HG12	2.17	0.44
1:7:211:PHE:CD1	1:7:218:ILE:HD12	2.53	0.44
1:AA:80:LEU:O	1:AA:81:ARG:HG3	2.17	0.44
1:AB:120:ILE:HG21	1:AB:220:PHE:CZ	2.52	0.44
1:AF:124:ILE:HG12	1:AF:165:ARG:HB2	2.00	0.44
1:AG:106:PHE:N	1:AG:106:PHE:CD1	2.85	0.44
1:AH:85:SER:HA	1:AP:200:LYS:O	2.18	0.44
1:AK:79:ASP:O	1:AK:80:LEU:HD12	2.17	0.44
1:AN:215:ASP:OD1	1:AN:216:GLU:N	2.42	0.44
1:AQ:16:TYR:CD1	1:AQ:223:LYS:HG3	2.52	0.44
1:AQ:227:LEU:HD21	1:AQ:235:LEU:HD11	1.99	0.44
1:AR:32:TYR:CZ	1:AR:42:ARG:HD3	2.52	0.44
1:AR:40:PHE:CZ	1:AR:158:PHE:HB2	2.52	0.44
1:Ac:224:LEU:HD11	1:Ac:246:VAL:HG11	1.99	0.44
1:F:124:ILE:HG12	1:F:165:ARG:HB2	1.98	0.44
1:G:16:TYR:CD1	1:G:223:LYS:HG3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:199:SER:HA	1:M:86:LEU:O	2.18	0.44
1:J:23:LYS:HD2	1:J:42:ARG:HH22	1.81	0.44
1:O:147:ILE:HG13	1:O:148:TYR:CD1	2.52	0.44
1:R:111:GLU:HB2	1:R:178:LYS:HB2	1.99	0.44
1:W:79:ASP:HB3	1:W:81:ARG:NH2	2.33	0.44
1:Y:12:LYS:HA	1:Y:12:LYS:HD3	1.86	0.44
1:Y:147:ILE:HG13	1:Y:148:TYR:CD1	2.53	0.44
1:Y:148:TYR:O	1:Y:152:ILE:HG12	2.17	0.44
1:Z:193:VAL:HG22	1:a:93:LYS:HG2	1.99	0.44
1:a:16:TYR:CE2	1:a:164:LEU:HG	2.53	0.44
1:e:36:ILE:HD13	1:e:36:ILE:HA	1.89	0.44
1:i:183:VAL:HB	1:i:197:LEU:HG	1.99	0.44
1:j:44:TRP:CE2	1:k:127:ASP:HB3	2.53	0.44
1:k:152:ILE:HD12	1:k:227:LEU:HG	2.00	0.44
1:m:168:LYS:HB2	1:m:168:LYS:HE3	1.69	0.44
1:r:120:ILE:HG21	1:r:220:PHE:CZ	2.52	0.44
1:s:148:TYR:O	1:s:152:ILE:HG12	2.18	0.44
1:w:181:LEU:HD11	1:w:183:VAL:HG23	1.99	0.44
1:y:169:MET:HB2	1:y:211:PHE:HB3	1.99	0.44
1:AB:85:SER:HA	1:AE:200:LYS:O	2.17	0.44
1:AK:12:LYS:HA	1:AK:12:LYS:HD3	1.82	0.44
1:AN:75:GLY:O	1:AN:76:ILE:HG12	2.18	0.44
1:AO:215:ASP:OD1	1:AO:216:GLU:N	2.40	0.44
1:AQ:23:LYS:HD2	1:AQ:42:ARG:NH2	2.32	0.44
1:AW:164:LEU:O	1:AW:219:VAL:HA	2.18	0.44
1:AW:200:LYS:O	1:AX:85:SER:HA	2.18	0.44
1:Aa:77:ASP:HB3	1:Aa:120:ILE:HB	1.99	0.44
1:Ad:19:VAL:HB	1:Ad:247:LEU:HD12	2.00	0.44
1:D:77:ASP:HB3	1:D:120:ILE:HB	1.99	0.44
1:E:130:GLU:O	1:E:134:ARG:HG3	2.18	0.44
1:F:106:PHE:HA	1:F:183:VAL:HG22	2.00	0.44
1:F:130:GLU:O	1:F:134:ARG:HG3	2.17	0.44
1:I:85:SER:HA	1:J:200:LYS:O	2.18	0.44
1:K:115:SER:OG	1:K:174:GLU:HB2	2.18	0.44
1:Q:32:TYR:CZ	1:Q:42:ARG:HD3	2.52	0.44
1:Q:111:GLU:HB2	1:Q:178:LYS:HB2	1.99	0.44
1:S:117:ILE:HB	1:S:172:GLN:HB2	1.99	0.44
1:T:147:ILE:HG13	1:T:148:TYR:CD1	2.52	0.44
1:U:162:SER:HB2	1:U:223:LYS:HB2	2.00	0.44
1:i:41:LYS:HE3	1:i:41:LYS:HB3	1.79	0.44
1:j:34:HIS:CE1	1:j:38:ASN:HA	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:120:ILE:HD12	1:j:169:MET:HE3	1.99	0.44
1:m:227:LEU:HD21	1:m:235:LEU:HD11	2.00	0.44
1:n:19:VAL:HB	1:n:247:LEU:HD12	2.00	0.44
1:n:120:ILE:HG21	1:n:220:PHE:CZ	2.53	0.44
1:n:210:VAL:HG12	1:n:212:GLU:OE1	2.17	0.44
1:s:224:LEU:HD12	1:s:243:PHE:CZ	2.52	0.44
1:x:75:GLY:O	1:x:76:ILE:HG12	2.18	0.44
1:x:162:SER:HB2	1:x:223:LYS:HB2	2.00	0.44
1:y:120:ILE:HG21	1:y:220:PHE:CZ	2.52	0.44
1:3:111:GLU:HB2	1:3:178:LYS:HB2	2.00	0.44
1:5:162:SER:HB2	1:5:223:LYS:HB2	2.00	0.44
1:0:162:SER:HB2	1:0:223:LYS:HB2	2.00	0.44
1:AC:75:GLY:O	1:AC:76:ILE:HG12	2.17	0.44
1:AE:111:GLU:HB2	1:AE:178:LYS:HB2	1.99	0.44
1:AK:115:SER:OG	1:AK:174:GLU:HB2	2.17	0.44
1:AM:147:ILE:HG13	1:AM:148:TYR:CD1	2.52	0.44
1:AM:181:LEU:HD11	1:AM:183:VAL:HG23	1.98	0.44
1:AP:127:ASP:HB3	1:AQ:44:TRP:CE2	2.53	0.44
1:AT:75:GLY:O	1:AT:76:ILE:HG12	2.17	0.44
1:A:75:GLY:O	1:A:76:ILE:HG12	2.18	0.44
1:B:164:LEU:O	1:B:219:VAL:HA	2.17	0.44
1:C:12:LYS:HA	1:C:12:LYS:HD3	1.86	0.44
1:C:43:ILE:HD12	1:D:131:ILE:HG13	1.99	0.44
1:D:79:ASP:O	1:D:80:LEU:HD12	2.18	0.44
1:E:32:TYR:HB3	1:E:40:PHE:CE2	2.53	0.44
1:F:111:GLU:HB2	1:F:178:LYS:HB2	1.99	0.44
1:M:77:ASP:HB3	1:M:120:ILE:HB	1.99	0.44
1:Q:19:VAL:HB	1:Q:247:LEU:HD12	2.00	0.44
1:S:79:ASP:O	1:S:80:LEU:HD12	2.18	0.44
1:V:120:ILE:HG21	1:V:220:PHE:CZ	2.52	0.44
1:a:130:GLU:O	1:a:134:ARG:HG3	2.18	0.44
1:d:40:PHE:HZ	1:d:158:PHE:CG	2.36	0.44
1:i:16:TYR:HD1	1:i:223:LYS:HG3	1.83	0.44
1:l:36:ILE:HD13	1:l:36:ILE:HA	1.90	0.44
1:q:32:TYR:CE1	1:q:42:ARG:HD3	2.51	0.44
1:q:85:SER:HA	1:s:200:LYS:O	2.18	0.44
1:t:168:LYS:HB2	1:t:168:LYS:HE3	1.71	0.44
1:u:40:PHE:CZ	1:u:158:PHE:HB2	2.46	0.44
1:u:85:SER:HA	1:3:200:LYS:O	2.18	0.44
1:w:79:ASP:HB3	1:w:81:ARG:HH22	1.83	0.44
1:x:16:TYR:CD1	1:x:223:LYS:HG3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:124:ILE:HG12	1:x:165:ARG:HB2	2.00	0.44
1:8:104:PRO:HB3	1:8:185:VAL:HG12	2.00	0.44
1:9:106:PHE:N	1:9:106:PHE:CD1	2.86	0.44
1:AE:127:ASP:HB3	1:AV:44:TRP:CZ2	2.53	0.44
1:AK:40:PHE:CZ	1:AK:158:PHE:HB2	2.53	0.44
1:AR:172:GLN:HG2	1:AR:208:ARG:HG2	1.99	0.44
1:AS:16:TYR:CD1	1:AS:223:LYS:HG3	2.52	0.44
1:AT:164:LEU:O	1:AT:219:VAL:HA	2.18	0.44
1:B:210:VAL:HG12	1:B:212:GLU:OE2	2.18	0.44
1:E:40:PHE:CD2	1:E:246:VAL:HG12	2.52	0.44
1:F:36:ILE:HD13	1:F:36:ILE:HA	1.86	0.44
1:F:162:SER:HB2	1:F:223:LYS:HB2	1.99	0.44
1:I:148:TYR:O	1:I:152:ILE:HG12	2.17	0.44
1:J:224:LEU:HD12	1:J:243:PHE:CZ	2.53	0.44
1:K:43:ILE:HD11	1:K:157:PHE:HE1	1.83	0.44
1:L:16:TYR:HD1	1:L:223:LYS:HG3	1.83	0.44
1:L:210:VAL:HG12	1:L:212:GLU:OE1	2.17	0.44
1:P:183:VAL:HB	1:P:197:LEU:HG	1.99	0.44
1:S:152:ILE:HD12	1:S:227:LEU:HG	2.00	0.44
1:T:164:LEU:O	1:T:219:VAL:HA	2.17	0.44
1:V:85:SER:HA	1:W:200:LYS:O	2.17	0.44
1:Z:64:ILE:HD12	1:Z:136:TRP:HZ2	1.82	0.44
1:b:75:GLY:O	1:b:76:ILE:HG12	2.17	0.44
1:e:12:LYS:HA	1:e:12:LYS:HD3	1.87	0.44
1:h:106:PHE:HA	1:h:183:VAL:HG22	1.99	0.44
1:i:85:SER:HA	1:p:200:LYS:O	2.18	0.44
1:l:43:ILE:O	1:l:43:ILE:HG13	2.18	0.44
1:t:147:ILE:HG13	1:t:148:TYR:CD1	2.52	0.44
1:u:16:TYR:CD1	1:u:223:LYS:HG3	2.53	0.44
1:z:32:TYR:CE2	1:z:42:ARG:HB2	2.52	0.44
1:6:147:ILE:HG13	1:6:148:TYR:CD1	2.52	0.44
1:6:164:LEU:O	1:6:219:VAL:HA	2.18	0.44
1:AD:85:SER:HA	1:AF:200:LYS:O	2.17	0.44
1:AE:75:GLY:O	1:AE:76:ILE:HG12	2.17	0.44
1:AF:32:TYR:CZ	1:AF:42:ARG:HD3	2.53	0.44
1:AJ:16:TYR:CD1	1:AJ:223:LYS:HG3	2.53	0.44
1:AK:111:GLU:HB2	1:AK:178:LYS:HB2	2.00	0.44
1:AP:111:GLU:HB2	1:AP:178:LYS:HB2	1.99	0.44
1:AP:215:ASP:CG	1:AP:216:GLU:H	2.25	0.44
1:AS:40:PHE:HE1	1:AS:158:PHE:HB2	1.83	0.44
1:AV:12:LYS:HA	1:AV:12:LYS:HD3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:162:SER:HB2	1:AW:223:LYS:HB2	2.00	0.44
1:AX:23:LYS:HD2	1:AX:42:ARG:NH2	2.32	0.44
1:AY:147:ILE:HG13	1:AY:148:TYR:CD1	2.53	0.44
1:Aa:85:SER:HA	1:Ac:200:LYS:O	2.17	0.44
1:A:80:LEU:O	1:A:81:ARG:HG3	2.18	0.44
1:C:40:PHE:CE1	1:C:224:LEU:HD13	2.53	0.44
1:G:16:TYR:HD1	1:G:223:LYS:HG3	1.83	0.44
1:K:85:SER:HA	1:L:200:LYS:O	2.18	0.44
1:K:106:PHE:N	1:K:106:PHE:CD1	2.86	0.44
1:K:147:ILE:HG13	1:K:148:TYR:CD1	2.53	0.44
1:O:106:PHE:N	1:O:106:PHE:CD1	2.86	0.44
1:P:12:LYS:HA	1:P:12:LYS:HD3	1.86	0.44
1:P:32:TYR:CZ	1:P:42:ARG:HD3	2.53	0.44
1:R:36:ILE:HD13	1:R:36:ILE:HA	1.86	0.44
1:T:86:LEU:O	1:V:199:SER:HA	2.18	0.44
1:V:79:ASP:HB2	1:V:118:PHE:HB3	1.99	0.44
1:X:215:ASP:OD1	1:X:216:GLU:N	2.42	0.44
1:Z:19:VAL:HA	1:Z:246:VAL:HG23	1.99	0.44
1:Z:215:ASP:CG	1:Z:216:GLU:N	2.75	0.44
1:a:168:LYS:HB2	1:a:168:LYS:HE3	1.70	0.44
1:b:40:PHE:CZ	1:b:158:PHE:HB2	2.52	0.44
1:d:130:GLU:O	1:d:134:ARG:HG3	2.17	0.44
1:f:162:SER:HB2	1:f:223:LYS:HB2	2.00	0.44
1:g:147:ILE:HG13	1:g:148:TYR:CD1	2.53	0.44
1:k:145:ARG:HB2	1:k:148:TYR:HD1	1.83	0.44
1:l:148:TYR:O	1:l:152:ILE:HG12	2.17	0.44
1:n:16:TYR:CD1	1:n:223:LYS:HG3	2.52	0.44
1:r:79:ASP:HB3	1:r:81:ARG:NH2	2.33	0.44
1:t:79:ASP:O	1:t:80:LEU:HD12	2.18	0.44
1:v:79:ASP:HB3	1:v:81:ARG:NH2	2.33	0.44
1:1:75:GLY:O	1:1:76:ILE:HG12	2.18	0.44
1:1:79:ASP:O	1:1:80:LEU:HD12	2.18	0.44
1:3:16:TYR:HD1	1:3:223:LYS:HG3	1.82	0.44
1:4:208:ARG:HE	1:4:210:VAL:CG2	2.31	0.44
1:5:29:LEU:HD13	1:5:56:ILE:HG22	2.00	0.44
1:7:106:PHE:N	1:7:106:PHE:CD1	2.86	0.44
1:8:16:TYR:CD1	1:8:223:LYS:HG3	2.52	0.44
1:AC:12:LYS:HA	1:AC:12:LYS:HD3	1.87	0.44
1:AN:200:LYS:O	1:AO:85:SER:HA	2.18	0.44
1:AQ:131:ILE:HG13	1:AR:43:ILE:HD12	1.98	0.44
1:AR:162:SER:HB2	1:AR:223:LYS:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:85:SER:HA	1:AX:200:LYS:O	2.17	0.44
1:AX:75:GLY:O	1:AX:76:ILE:HG12	2.17	0.44
1:Ad:79:ASP:O	1:Ad:80:LEU:HD12	2.17	0.44
1:D:147:ILE:HG13	1:D:148:TYR:CD1	2.53	0.43
1:G:75:GLY:O	1:G:76:ILE:HG12	2.18	0.43
1:H:75:GLY:O	1:H:76:ILE:HG12	2.18	0.43
1:H:106:PHE:HA	1:H:183:VAL:HG22	2.00	0.43
1:H:124:ILE:HG12	1:H:165:ARG:HB2	1.99	0.43
1:I:164:LEU:O	1:I:219:VAL:HA	2.17	0.43
1:L:40:PHE:CZ	1:L:158:PHE:HB2	2.48	0.43
1:M:199:SER:HA	1:N:86:LEU:O	2.18	0.43
1:N:145:ARG:HB2	1:N:148:TYR:HD1	1.82	0.43
1:P:124:ILE:HG12	1:P:165:ARG:HB2	1.99	0.43
1:S:16:TYR:CE2	1:S:164:LEU:HG	2.53	0.43
1:W:106:PHE:CD1	1:W:106:PHE:N	2.86	0.43
1:Z:147:ILE:HG13	1:Z:148:TYR:CD1	2.53	0.43
1:a:145:ARG:HB2	1:a:148:TYR:HD1	1.82	0.43
1:c:106:PHE:N	1:c:106:PHE:CD1	2.86	0.43
1:e:106:PHE:HA	1:e:183:VAL:HG22	1.99	0.43
1:j:148:TYR:O	1:j:152:ILE:HG12	2.18	0.43
1:l:79:ASP:C	1:l:80:LEU:HD12	2.43	0.43
1:r:227:LEU:HD11	1:r:235:LEU:HD11	2.00	0.43
1:s:85:SER:HA	1:t:200:LYS:O	2.17	0.43
1:w:36:ILE:HD13	1:w:36:ILE:HA	1.86	0.43
1:y:43:ILE:HD12	1:z:131:ILE:HG13	2.00	0.43
1:2:16:TYR:HD1	1:2:223:LYS:HG3	1.82	0.43
1:2:24:THR:HG22	1:2:218:ILE:HG13	1.99	0.43
1:5:26:ILE:HA	1:5:42:ARG:NH1	2.33	0.43
1:8:111:GLU:HB2	1:8:178:LYS:HB2	1.99	0.43
1:AB:168:LYS:HB2	1:AB:168:LYS:HE3	1.69	0.43
1:AE:64:ILE:HD12	1:AE:136:TRP:HZ2	1.83	0.43
1:AG:215:ASP:CG	1:AG:216:GLU:N	2.76	0.43
1:AI:145:ARG:HB2	1:AI:148:TYR:HD1	1.82	0.43
1:AJ:147:ILE:HG13	1:AJ:148:TYR:CD1	2.53	0.43
1:AL:32:TYR:CZ	1:AL:42:ARG:HD3	2.53	0.43
1:AR:43:ILE:HG13	1:AR:43:ILE:O	2.17	0.43
1:AU:152:ILE:HD12	1:AU:227:LEU:HG	2.00	0.43
1:Aa:16:TYR:CD1	1:Aa:223:LYS:HG3	2.52	0.43
1:Aa:147:ILE:HG13	1:Aa:148:TYR:CD1	2.53	0.43
1:Ab:12:LYS:HA	1:Ab:12:LYS:HD3	1.86	0.43
1:Ab:210:VAL:HG12	1:Ab:212:GLU:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:PRO:HB3	1:B:185:VAL:HG12	1.99	0.43
1:C:193:VAL:HG22	1:D:93:LYS:HG2	2.01	0.43
1:E:79:ASP:HB3	1:E:81:ARG:NH2	2.33	0.43
1:H:106:PHE:N	1:H:106:PHE:CD1	2.86	0.43
1:I:79:ASP:O	1:I:80:LEU:HD12	2.18	0.43
1:J:111:GLU:HB2	1:J:178:LYS:HB2	2.00	0.43
1:P:80:LEU:O	1:P:81:ARG:HG3	2.19	0.43
1:P:172:GLN:HG2	1:P:208:ARG:HG2	1.99	0.43
1:Q:40:PHE:CE1	1:Q:158:PHE:HB2	2.54	0.43
1:T:183:VAL:HB	1:T:197:LEU:HG	1.99	0.43
1:U:131:ILE:HG13	1:l:43:ILE:HD12	2.00	0.43
1:U:210:VAL:HG12	1:U:212:GLU:OE1	2.18	0.43
1:V:40:PHE:HE1	1:V:224:LEU:HD13	1.83	0.43
1:X:80:LEU:O	1:X:81:ARG:HG3	2.18	0.43
1:b:16:TYR:CD1	1:b:223:LYS:HG3	2.53	0.43
1:c:32:TYR:CZ	1:c:42:ARG:HD3	2.53	0.43
1:d:75:GLY:O	1:d:76:ILE:HG12	2.18	0.43
1:f:16:TYR:CD1	1:f:223:LYS:HG3	2.53	0.43
1:g:79:ASP:O	1:g:80:LEU:HD12	2.18	0.43
1:i:130:GLU:HB2	1:p:43:ILE:HB	1.98	0.43
1:j:79:ASP:HB3	1:j:81:ARG:NH2	2.33	0.43
1:m:210:VAL:HG22	1:m:212:GLU:OE1	2.17	0.43
1:n:40:PHE:CE1	1:n:158:PHE:HB2	2.54	0.43
1:p:79:ASP:HB3	1:p:81:ARG:NH2	2.33	0.43
1:u:127:ASP:HB3	1:3:44:TRP:CE2	2.53	0.43
1:x:118:PHE:CE1	1:x:120:ILE:HD11	2.53	0.43
1:x:164:LEU:O	1:x:219:VAL:HA	2.17	0.43
1:z:183:VAL:HB	1:z:197:LEU:HG	2.00	0.43
1:0:29:LEU:HD12	1:0:56:ILE:HG22	2.00	0.43
1:0:111:GLU:HB2	1:0:178:LYS:HB2	2.00	0.43
1:AB:162:SER:HB2	1:AB:223:LYS:HB2	2.00	0.43
1:AI:80:LEU:O	1:AI:81:ARG:HG3	2.18	0.43
1:AO:16:TYR:HD1	1:AO:223:LYS:HG3	1.83	0.43
1:AT:79:ASP:HB3	1:AT:81:ARG:NH2	2.33	0.43
1:AU:123:ILE:N	1:AU:123:ILE:HD12	2.32	0.43
1:AW:79:ASP:O	1:AW:80:LEU:HD12	2.18	0.43
1:AY:40:PHE:CZ	1:AY:158:PHE:HB2	2.44	0.43
1:AY:75:GLY:O	1:AY:76:ILE:HG12	2.19	0.43
1:B:16:TYR:CD1	1:B:223:LYS:HG3	2.52	0.43
1:D:148:TYR:O	1:D:152:ILE:HG12	2.17	0.43
1:H:183:VAL:HB	1:H:197:LEU:HG	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:172:GLN:HG2	1:I:208:ARG:HG3	1.99	0.43
1:J:79:ASP:HB2	1:J:118:PHE:HB3	2.00	0.43
1:J:162:SER:HB2	1:J:223:LYS:HB2	1.98	0.43
1:K:79:ASP:HB3	1:K:81:ARG:NH2	2.33	0.43
1:S:124:ILE:HG12	1:S:165:ARG:HB2	1.99	0.43
1:W:106:PHE:HA	1:W:183:VAL:HG22	2.01	0.43
1:Y:16:TYR:HD1	1:Y:223:LYS:HG3	1.83	0.43
1:Y:181:LEU:HD11	1:Y:183:VAL:HG23	1.98	0.43
1:a:162:SER:HB2	1:a:223:LYS:HB2	2.00	0.43
1:f:79:ASP:HB2	1:f:118:PHE:HB3	1.99	0.43
1:k:16:TYR:CD1	1:k:223:LYS:HG3	2.53	0.43
1:l:130:GLU:O	1:l:134:ARG:HG3	2.18	0.43
1:m:77:ASP:HB3	1:m:120:ILE:HB	2.00	0.43
1:o:79:ASP:O	1:o:80:LEU:HD12	2.18	0.43
1:t:162:SER:HB2	1:t:223:LYS:HB2	1.99	0.43
1:x:166:ALA:HB3	1:x:169:MET:HG3	2.00	0.43
1:y:148:TYR:O	1:y:152:ILE:HG12	2.18	0.43
1:1:43:ILE:HB	1:2:130:GLU:HB2	2.00	0.43
1:2:145:ARG:HB2	1:2:148:TYR:HD1	1.82	0.43
1:AD:147:ILE:HG13	1:AD:148:TYR:CD1	2.53	0.43
1:AH:127:ASP:HB3	1:AP:44:TRP:CE2	2.54	0.43
1:AO:168:LYS:HB2	1:AO:168:LYS:HE3	1.70	0.43
1:AR:16:TYR:CE2	1:AR:164:LEU:HG	2.53	0.43
1:AR:79:ASP:O	1:AR:80:LEU:HD12	2.18	0.43
1:AY:148:TYR:O	1:AY:152:ILE:HG12	2.17	0.43
1:Ac:168:LYS:HE3	1:Ac:168:LYS:HB2	1.71	0.43
1:A:164:LEU:O	1:A:219:VAL:HA	2.17	0.43
1:B:106:PHE:N	1:B:106:PHE:CD2	2.87	0.43
1:K:16:TYR:CD1	1:K:223:LYS:HG3	2.54	0.43
1:L:121:GLU:HB3	1:L:168:LYS:HB2	2.00	0.43
1:R:79:ASP:O	1:R:80:LEU:HD12	2.18	0.43
1:R:106:PHE:N	1:R:106:PHE:CD1	2.86	0.43
1:S:164:LEU:O	1:S:219:VAL:HA	2.18	0.43
1:X:147:ILE:HG13	1:X:148:TYR:CD1	2.53	0.43
1:Z:43:ILE:HD12	1:a:131:ILE:HG13	1.99	0.43
1:Z:148:TYR:O	1:Z:152:ILE:HG12	2.19	0.43
1:f:85:SER:HA	1:g:200:LYS:O	2.18	0.43
1:k:147:ILE:HG13	1:k:148:TYR:CD1	2.52	0.43
1:p:16:TYR:CE2	1:p:164:LEU:HG	2.54	0.43
1:p:106:PHE:N	1:p:106:PHE:CD1	2.86	0.43
1:q:147:ILE:HG13	1:q:148:TYR:CD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:173:PHE:O	1:q:206:TYR:HA	2.19	0.43
1:t:16:TYR:HD1	1:t:223:LYS:HG3	1.83	0.43
1:t:106:PHE:N	1:t:106:PHE:CD1	2.86	0.43
1:u:43:ILE:HD12	1:v:131:ILE:HG13	2.00	0.43
1:w:16:TYR:CD1	1:w:223:LYS:HG3	2.53	0.43
1:y:200:LYS:O	1:z:85:SER:HA	2.18	0.43
1:5:40:PHE:CZ	1:5:158:PHE:HB2	2.52	0.43
1:6:16:TYR:CD1	1:6:223:LYS:HG3	2.54	0.43
1:7:16:TYR:CE2	1:7:164:LEU:HG	2.53	0.43
1:8:106:PHE:N	1:8:106:PHE:CD2	2.87	0.43
1:AG:32:TYR:HB3	1:AG:40:PHE:CE2	2.53	0.43
1:AH:200:LYS:O	1:AI:85:SER:HA	2.18	0.43
1:AK:16:TYR:HD1	1:AK:223:LYS:HG3	1.83	0.43
1:AK:23:LYS:HD2	1:AK:42:ARG:NH2	2.33	0.43
1:AN:79:ASP:HB3	1:AN:81:ARG:NH2	2.33	0.43
1:AQ:170:ARG:HB3	1:AQ:170:ARG:HH11	1.83	0.43
1:AS:148:TYR:O	1:AS:152:ILE:HG12	2.18	0.43
1:C:59:LEU:O	1:C:145:ARG:HG3	2.19	0.43
1:G:40:PHE:HZ	1:G:158:PHE:CG	2.36	0.43
1:J:168:LYS:HE3	1:J:168:LYS:HB2	1.71	0.43
1:K:12:LYS:HA	1:K:12:LYS:HD3	1.87	0.43
1:N:172:GLN:HG2	1:N:208:ARG:HG2	2.00	0.43
1:T:106:PHE:HA	1:T:183:VAL:HG22	2.00	0.43
1:W:164:LEU:O	1:W:219:VAL:HA	2.17	0.43
1:Z:168:LYS:HB2	1:Z:168:LYS:HE3	1.70	0.43
1:a:40:PHE:HE2	1:a:224:LEU:HD13	1.83	0.43
1:a:79:ASP:HB3	1:a:81:ARG:NH2	2.34	0.43
1:a:164:LEU:O	1:a:219:VAL:HA	2.19	0.43
1:c:79:ASP:HB3	1:c:81:ARG:NH2	2.34	0.43
1:e:199:SER:HA	1:j:86:LEU:O	2.18	0.43
1:i:211:PHE:CD1	1:i:218:ILE:HD12	2.54	0.43
1:j:40:PHE:HE1	1:j:158:PHE:HB2	1.82	0.43
1:p:147:ILE:HG13	1:p:148:TYR:CD1	2.53	0.43
1:p:164:LEU:O	1:p:219:VAL:HA	2.19	0.43
1:r:16:TYR:CD1	1:r:223:LYS:HG3	2.54	0.43
1:v:181:LEU:HD11	1:v:183:VAL:HG23	2.01	0.43
1:w:40:PHE:CZ	1:w:158:PHE:HB2	2.50	0.43
1:w:147:ILE:HG13	1:w:148:TYR:CD1	2.53	0.43
1:z:26:ILE:HA	1:z:42:ARG:NH1	2.34	0.43
1:z:208:ARG:HE	1:z:210:VAL:HG21	1.83	0.43
1:1:164:LEU:O	1:1:219:VAL:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:211:PHE:CE2	1:8:218:ILE:HB	2.53	0.43
1:0:16:TYR:CD1	1:0:223:LYS:HG3	2.53	0.43
1:AB:131:ILE:HG13	1:AE:43:ILE:HD12	2.00	0.43
1:AE:79:ASP:O	1:AE:80:LEU:HD12	2.18	0.43
1:AF:106:PHE:N	1:AF:106:PHE:CD1	2.86	0.43
1:AF:111:GLU:HB2	1:AF:178:LYS:HB2	1.99	0.43
1:AF:121:GLU:HB3	1:AF:168:LYS:HB2	1.99	0.43
1:AI:79:ASP:HB3	1:AI:81:ARG:NH2	2.33	0.43
1:AI:210:VAL:HB	1:AJ:76:ILE:HG21	2.01	0.43
1:AP:120:ILE:HG21	1:AP:220:PHE:CZ	2.53	0.43
1:AR:86:LEU:O	1:AS:199:SER:HA	2.19	0.43
1:AR:183:VAL:HB	1:AR:197:LEU:HG	1.99	0.43
1:AU:164:LEU:O	1:AU:219:VAL:HA	2.19	0.43
1:AW:23:LYS:HD2	1:AW:42:ARG:HH22	1.83	0.43
1:AW:120:ILE:HG21	1:AW:220:PHE:CZ	2.53	0.43
1:AZ:111:GLU:HB2	1:AZ:178:LYS:HB2	1.99	0.43
1:Ab:215:ASP:CG	1:Ab:216:GLU:N	2.76	0.43
1:Ad:16:TYR:CD1	1:Ad:223:LYS:HG3	2.53	0.43
1:Ad:32:TYR:HB3	1:Ad:40:PHE:CE2	2.54	0.43
1:I:162:SER:HB2	1:I:223:LYS:HB2	2.00	0.43
1:N:79:ASP:O	1:N:80:LEU:HD12	2.18	0.43
1:Q:120:ILE:HG21	1:Q:220:PHE:CZ	2.52	0.43
1:T:29:LEU:HD11	1:T:68:ILE:HD12	2.00	0.43
1:U:147:ILE:HG13	1:U:148:TYR:CD1	2.53	0.43
1:Y:79:ASP:C	1:Y:80:LEU:HD12	2.44	0.43
1:a:16:TYR:CD1	1:a:223:LYS:HG3	2.54	0.43
1:a:79:ASP:O	1:a:80:LEU:HD12	2.18	0.43
1:d:30:HIS:CE1	1:d:42:ARG:HH11	2.37	0.43
1:f:23:LYS:HD2	1:f:42:ARG:HH22	1.83	0.43
1:f:79:ASP:O	1:f:80:LEU:HD12	2.19	0.43
1:f:148:TYR:O	1:f:152:ILE:HG12	2.19	0.43
1:h:16:TYR:CD1	1:h:223:LYS:HG3	2.54	0.43
1:k:162:SER:HB2	1:k:223:LYS:HB2	2.00	0.43
1:o:164:LEU:O	1:o:219:VAL:HA	2.19	0.43
1:v:80:LEU:O	1:v:81:ARG:HG3	2.18	0.43
1:7:75:GLY:O	1:7:76:ILE:HG12	2.17	0.43
1:8:224:LEU:HD12	1:8:243:PHE:CZ	2.54	0.43
1:9:79:ASP:C	1:9:80:LEU:HD12	2.43	0.43
1:0:29:LEU:HD11	1:0:68:ILE:HD12	2.00	0.43
1:AB:79:ASP:HB3	1:AB:81:ARG:HH22	1.83	0.43
1:AD:75:GLY:O	1:AD:76:ILE:HG12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:16:TYR:CD1	1:AH:223:LYS:HG3	2.53	0.43
1:AI:172:GLN:HG2	1:AI:208:ARG:HB2	2.00	0.43
1:AJ:164:LEU:O	1:AJ:219:VAL:HA	2.19	0.43
1:AL:16:TYR:CD1	1:AL:223:LYS:HG3	2.54	0.43
1:AM:36:ILE:HD13	1:AM:36:ILE:HA	1.91	0.43
1:AQ:12:LYS:HA	1:AQ:12:LYS:HD3	1.86	0.43
1:AQ:64:ILE:HD12	1:AQ:136:TRP:HZ2	1.84	0.43
1:AT:162:SER:HB2	1:AT:223:LYS:HB2	2.01	0.43
1:AU:104:PRO:HB3	1:AU:185:VAL:HG12	1.99	0.43
1:AU:200:LYS:O	1:AW:85:SER:HA	2.18	0.43
1:AU:215:ASP:OD2	1:AU:216:GLU:N	2.42	0.43
1:AX:40:PHE:CZ	1:AX:158:PHE:HB2	2.49	0.43
1:AZ:79:ASP:HB2	1:AZ:118:PHE:HB3	2.01	0.43
1:Ac:124:ILE:HG12	1:Ac:165:ARG:HB2	1.99	0.43
1:Ad:40:PHE:CD2	1:Ad:246:VAL:HG12	2.53	0.43
1:A:32:TYR:CZ	1:A:42:ARG:HD3	2.53	0.43
1:I:12:LYS:HA	1:I:12:LYS:HD3	1.82	0.43
1:I:93:LYS:HG2	1:J:193:VAL:HG22	2.01	0.43
1:J:16:TYR:HD1	1:J:223:LYS:HG3	1.83	0.43
1:L:75:GLY:O	1:L:76:ILE:HG12	2.19	0.43
1:M:210:VAL:HB	1:N:76:ILE:HG21	2.00	0.43
1:P:64:ILE:HD12	1:P:136:TRP:HZ2	1.83	0.43
1:P:164:LEU:O	1:P:219:VAL:HA	2.19	0.43
1:Q:215:ASP:CG	1:Q:216:GLU:H	2.26	0.43
1:R:79:ASP:HB3	1:R:81:ARG:NH2	2.33	0.43
1:T:75:GLY:O	1:T:76:ILE:HG12	2.18	0.43
1:U:141:GLN:HG3	1:U:235:LEU:HB3	2.00	0.43
1:V:168:LYS:HE3	1:V:168:LYS:HB2	1.70	0.43
1:c:23:LYS:HD2	1:c:42:ARG:NH2	2.34	0.43
1:f:172:GLN:HG2	1:f:208:ARG:HG3	2.00	0.43
1:g:86:LEU:O	1:h:199:SER:HA	2.18	0.43
1:i:121:GLU:HB3	1:i:168:LYS:HB2	2.00	0.43
1:j:16:TYR:CD1	1:j:223:LYS:HG3	2.54	0.43
1:j:164:LEU:O	1:j:219:VAL:HA	2.19	0.43
1:j:210:VAL:HB	1:k:76:ILE:HG21	2.00	0.43
1:l:69:GLY:O	1:l:70:LEU:HD12	2.19	0.43
1:l:147:ILE:HG13	1:l:148:TYR:CD1	2.53	0.43
1:p:152:ILE:HD12	1:p:227:LEU:HG	2.00	0.43
1:q:181:LEU:HD11	1:q:183:VAL:HG23	1.99	0.43
1:s:16:TYR:CD1	1:s:223:LYS:HG3	2.54	0.43
1:v:164:LEU:O	1:v:219:VAL:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:w:111:GLU:HB2	1:w:178:LYS:HB2	2.00	0.43
1:x:123:ILE:HD12	1:x:123:ILE:N	2.34	0.43
1:3:127:ASP:HB3	1:4:44:TRP:CE2	2.53	0.43
1:6:210:VAL:HG12	1:6:212:GLU:OE1	2.19	0.43
1:8:200:LYS:O	1:0:85:SER:HA	2.19	0.43
1:AB:147:ILE:HG13	1:AB:148:TYR:CD1	2.53	0.43
1:AG:16:TYR:CD1	1:AG:223:LYS:HG3	2.54	0.43
1:AH:106:PHE:N	1:AH:106:PHE:CD1	2.86	0.43
1:AH:130:GLU:O	1:AH:134:ARG:HG3	2.18	0.43
1:AP:181:LEU:HD12	1:AP:182:GLY:H	1.84	0.43
1:AQ:152:ILE:HD12	1:AQ:227:LEU:CD2	2.47	0.43
1:AQ:164:LEU:O	1:AQ:219:VAL:HA	2.19	0.43
1:AU:79:ASP:O	1:AU:80:LEU:HD12	2.18	0.43
1:AV:104:PRO:HB3	1:AV:185:VAL:HG12	2.00	0.43
1:Ab:148:TYR:O	1:Ab:152:ILE:HG12	2.18	0.43
1:M:79:ASP:HB3	1:M:81:ARG:NH2	2.33	0.43
1:O:172:GLN:HG2	1:O:208:ARG:HG3	2.00	0.43
1:R:26:ILE:HA	1:R:42:ARG:NH1	2.34	0.43
1:R:210:VAL:HB	1:W:76:ILE:HG21	1.99	0.43
1:Z:164:LEU:O	1:Z:219:VAL:HA	2.19	0.43
1:b:32:TYR:HB3	1:b:40:PHE:CE2	2.54	0.43
1:d:16:TYR:HD1	1:d:223:LYS:HG3	1.83	0.43
1:d:147:ILE:HG13	1:d:148:TYR:CD1	2.54	0.43
1:e:75:GLY:O	1:e:76:ILE:HG12	2.18	0.43
1:h:16:TYR:CE2	1:h:164:LEU:HG	2.54	0.43
1:h:79:ASP:HB3	1:h:81:ARG:NH2	2.34	0.43
1:k:23:LYS:H	1:k:23:LYS:HG2	1.65	0.43
1:m:80:LEU:O	1:m:81:ARG:HG3	2.18	0.43
1:o:147:ILE:HG13	1:o:148:TYR:CD1	2.53	0.43
1:p:16:TYR:CD1	1:p:223:LYS:HG3	2.53	0.43
1:p:79:ASP:O	1:p:80:LEU:HD12	2.18	0.43
1:p:148:TYR:HA	1:p:151:GLU:HG3	2.00	0.43
1:q:86:LEU:O	1:s:199:SER:HA	2.18	0.43
1:q:164:LEU:O	1:q:219:VAL:HA	2.19	0.43
1:w:208:ARG:HE	1:w:210:VAL:HG21	1.84	0.43
1:x:41:LYS:HB3	1:x:41:LYS:HE3	1.86	0.43
1:2:104:PRO:HB3	1:2:185:VAL:HG12	2.01	0.43
1:2:208:ARG:HG2	1:2:210:VAL:HG23	2.00	0.43
1:9:44:TRP:CZ2	1:Ab:127:ASP:HB3	2.54	0.43
1:0:12:LYS:HA	1:0:12:LYS:HD3	1.82	0.43
1:0:76:ILE:HA	1:0:123:ILE:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:169:MET:HE2	1:AC:169:MET:HB3	1.95	0.43
1:AI:104:PRO:HB3	1:AI:185:VAL:HG12	2.00	0.43
1:AK:118:PHE:CE1	1:AK:120:ILE:HD11	2.53	0.43
1:AK:162:SER:HB2	1:AK:223:LYS:HB2	2.00	0.43
1:AL:199:SER:HA	1:AM:86:LEU:O	2.18	0.43
1:AR:29:LEU:HD13	1:AR:56:ILE:HG22	2.01	0.43
1:AR:145:ARG:HB2	1:AR:148:TYR:HD1	1.83	0.43
1:AR:152:ILE:HD12	1:AR:227:LEU:HG	2.01	0.43
1:AV:77:ASP:HB3	1:AV:120:ILE:HB	2.00	0.43
1:AV:79:ASP:C	1:AV:80:LEU:HD12	2.44	0.43
1:AW:121:GLU:HB3	1:AW:168:LYS:HB2	2.00	0.43
1:AX:147:ILE:HG13	1:AX:148:TYR:CD1	2.54	0.43
1:AZ:24:THR:HG22	1:AZ:218:ILE:HG13	2.00	0.43
1:Ac:36:ILE:HD13	1:Ac:36:ILE:HA	1.86	0.43
1:Ac:162:SER:HB2	1:Ac:223:LYS:HB2	2.00	0.43
1:A:104:PRO:HB3	1:A:185:VAL:HG12	2.00	0.43
1:B:117:ILE:HB	1:B:172:GLN:HB3	2.01	0.43
1:E:19:VAL:HB	1:E:247:LEU:HD12	2.01	0.43
1:G:23:LYS:HD2	1:G:42:ARG:NH2	2.34	0.43
1:I:111:GLU:HB2	1:I:178:LYS:HB2	1.99	0.43
1:K:164:LEU:O	1:K:219:VAL:HA	2.18	0.43
1:P:168:LYS:HE3	1:P:168:LYS:HB2	1.69	0.43
1:W:16:TYR:HD1	1:W:223:LYS:HG3	1.83	0.43
1:e:183:VAL:HB	1:e:197:LEU:HG	2.00	0.43
1:h:40:PHE:CZ	1:h:158:PHE:HB2	2.50	0.43
1:h:162:SER:HB2	1:h:223:LYS:HB2	2.01	0.43
1:l:106:PHE:N	1:l:106:PHE:CD1	2.86	0.43
1:m:79:ASP:HB3	1:m:81:ARG:NH1	2.32	0.43
1:r:80:LEU:O	1:r:81:ARG:HG3	2.19	0.43
1:y:118:PHE:CE1	1:y:120:ILE:HD11	2.54	0.43
1:2:113:SER:OG	1:2:176:LYS:HB2	2.19	0.43
1:2:130:GLU:O	1:2:134:ARG:HG3	2.19	0.43
1:4:26:ILE:HG12	1:4:42:ARG:NH2	2.34	0.43
1:4:106:PHE:CD1	1:4:106:PHE:N	2.86	0.43
1:4:131:ILE:HG13	1:5:43:ILE:HD12	2.00	0.43
1:7:12:LYS:HA	1:7:12:LYS:HD3	1.87	0.43
1:AG:40:PHE:CD2	1:AG:246:VAL:HG12	2.54	0.43
1:AG:75:GLY:O	1:AG:76:ILE:HG12	2.18	0.43
1:AG:79:ASP:O	1:AG:80:LEU:HD12	2.18	0.43
1:AL:79:ASP:HB3	1:AL:81:ARG:HH12	1.83	0.43
1:AN:79:ASP:O	1:AN:80:LEU:HD12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:16:TYR:CE2	1:AT:164:LEU:HG	2.54	0.43
1:AY:148:TYR:HA	1:AY:151:GLU:HG3	2.01	0.43
1:Ab:80:LEU:O	1:Ab:81:ARG:HG3	2.19	0.43
1:Ab:111:GLU:HB2	1:Ab:178:LYS:HB2	1.99	0.43
1:A:93:LYS:HG2	1:I:193:VAL:HG22	2.01	0.43
1:C:79:ASP:O	1:C:80:LEU:HD12	2.19	0.43
1:C:168:LYS:HB2	1:C:168:LYS:HE3	1.70	0.43
1:G:147:ILE:HG13	1:G:148:TYR:CD1	2.54	0.43
1:I:16:TYR:CD1	1:I:223:LYS:HG3	2.54	0.43
1:K:16:TYR:CE2	1:K:164:LEU:HG	2.53	0.43
1:K:183:VAL:HB	1:K:197:LEU:HG	2.00	0.43
1:M:23:LYS:HD2	1:M:42:ARG:HH22	1.84	0.43
1:P:104:PRO:HB3	1:P:185:VAL:HG12	2.00	0.43
1:R:93:LYS:HG2	1:U:193:VAL:HG22	2.01	0.43
1:R:124:ILE:HG12	1:R:165:ARG:HB2	2.00	0.43
1:R:147:ILE:HG13	1:R:148:TYR:CD1	2.53	0.43
1:X:104:PRO:HB3	1:X:185:VAL:HG12	2.00	0.43
1:Y:56:ILE:HD11	1:Y:137:LEU:HD21	2.00	0.43
1:Y:104:PRO:HB3	1:Y:185:VAL:HG12	2.00	0.43
1:a:77:ASP:HB3	1:a:120:ILE:HB	2.01	0.43
1:b:79:ASP:HB3	1:b:81:ARG:NH2	2.33	0.43
1:i:173:PHE:O	1:i:206:TYR:HA	2.19	0.43
1:n:168:LYS:HE3	1:n:168:LYS:HB2	1.69	0.43
1:t:72:ASP:HA	1:t:125:THR:O	2.19	0.43
1:t:106:PHE:HA	1:t:183:VAL:HG22	2.00	0.43
1:u:200:LYS:O	1:v:85:SER:HA	2.19	0.43
1:v:104:PRO:HB3	1:v:185:VAL:HG12	2.01	0.43
1:v:162:SER:HB2	1:v:223:LYS:HB2	2.01	0.43
1:w:183:VAL:HB	1:w:197:LEU:HG	2.00	0.43
1:2:23:LYS:HD2	1:2:42:ARG:HH22	1.83	0.43
1:4:124:ILE:HG12	1:4:165:ARG:HB2	2.01	0.43
1:6:40:PHE:HE1	1:6:158:PHE:HB2	1.83	0.43
1:6:148:TYR:O	1:6:152:ILE:HG12	2.19	0.43
1:7:16:TYR:CD1	1:7:223:LYS:HG3	2.54	0.43
1:8:193:VAL:HG22	1:0:93:LYS:HG2	2.01	0.43
1:8:227:LEU:HD21	1:8:235:LEU:HD11	2.01	0.43
1:AA:164:LEU:O	1:AA:219:VAL:HA	2.17	0.43
1:AB:199:SER:HA	1:AG:86:LEU:O	2.19	0.43
1:AC:79:ASP:HB2	1:AC:118:PHE:HB3	2.01	0.43
1:AD:16:TYR:CE2	1:AD:164:LEU:HG	2.53	0.43
1:AE:164:LEU:O	1:AE:219:VAL:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AJ:79:ASP:O	1:AJ:80:LEU:HD12	2.19	0.43
1:AO:75:GLY:O	1:AO:76:ILE:HG12	2.18	0.43
1:AT:199:SER:HA	1:AU:86:LEU:O	2.19	0.43
1:Ac:206:TYR:OH	1:Ac:208:ARG:HD3	2.19	0.43
1:A:118:PHE:CE1	1:A:120:ILE:HD11	2.53	0.42
1:C:72:ASP:HA	1:C:125:THR:O	2.19	0.42
1:F:79:ASP:HB3	1:F:81:ARG:NH2	2.34	0.42
1:I:106:PHE:N	1:I:106:PHE:CD1	2.86	0.42
1:M:148:TYR:O	1:M:152:ILE:HG12	2.19	0.42
1:O:36:ILE:HD13	1:O:36:ILE:HA	1.90	0.42
1:O:79:ASP:C	1:O:80:LEU:HD12	2.43	0.42
1:S:32:TYR:HB3	1:S:40:PHE:CE1	2.54	0.42
1:T:111:GLU:HB2	1:T:178:LYS:HB2	2.00	0.42
1:T:131:ILE:HG13	1:V:43:ILE:HD12	2.01	0.42
1:h:115:SER:OG	1:h:174:GLU:HB2	2.18	0.42
1:i:24:THR:HG22	1:i:218:ILE:HG13	2.02	0.42
1:n:76:ILE:HA	1:n:123:ILE:HD13	2.01	0.42
1:o:172:GLN:HG2	1:o:208:ARG:HB2	2.01	0.42
1:r:210:VAL:HG12	1:r:212:GLU:OE1	2.18	0.42
1:v:147:ILE:HG13	1:v:148:TYR:CD1	2.54	0.42
1:8:79:ASP:O	1:8:80:LEU:HD12	2.19	0.42
1:8:183:VAL:HB	1:8:197:LEU:HG	2.01	0.42
1:AC:106:PHE:N	1:AC:106:PHE:CD1	2.86	0.42
1:AF:20:ALA:HB3	1:AF:247:LEU:HB3	2.01	0.42
1:AI:16:TYR:CD1	1:AI:223:LYS:HG3	2.54	0.42
1:AO:200:LYS:O	1:AT:85:SER:HA	2.18	0.42
1:AQ:120:ILE:HD12	1:AQ:169:MET:HE3	2.01	0.42
1:AU:215:ASP:CG	1:AU:216:GLU:H	2.24	0.42
1:AV:106:PHE:N	1:AV:106:PHE:CD1	2.86	0.42
1:Ad:79:ASP:HB3	1:Ad:81:ARG:NH2	2.34	0.42
1:E:79:ASP:O	1:E:80:LEU:HD12	2.19	0.42
1:L:85:SER:HA	1:S:200:LYS:O	2.19	0.42
1:P:72:ASP:HA	1:P:125:THR:O	2.19	0.42
1:T:146:GLU:CD	1:T:146:GLU:H	2.27	0.42
1:U:80:LEU:O	1:U:81:ARG:HG3	2.19	0.42
1:V:79:ASP:O	1:V:80:LEU:HD12	2.19	0.42
1:W:72:ASP:HA	1:W:125:THR:O	2.19	0.42
1:X:36:ILE:HD13	1:X:36:ILE:HA	1.90	0.42
1:X:130:GLU:O	1:X:134:ARG:HG3	2.19	0.42
1:a:224:LEU:HD12	1:a:243:PHE:CZ	2.54	0.42
1:b:12:LYS:HA	1:b:12:LYS:HD3	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:172:GLN:HG2	1:c:208:ARG:HB2	2.00	0.42
1:g:16:TYR:HD1	1:g:223:LYS:HG3	1.83	0.42
1:j:168:LYS:HA	1:j:211:PHE:O	2.19	0.42
1:j:208:ARG:HE	1:j:210:VAL:HG21	1.85	0.42
1:m:72:ASP:HA	1:m:125:THR:O	2.19	0.42
1:q:168:LYS:HB2	1:q:168:LYS:HE3	1.71	0.42
1:z:173:PHE:O	1:z:206:TYR:HA	2.19	0.42
1:1:16:TYR:CE2	1:1:164:LEU:HG	2.54	0.42
1:4:215:ASP:CG	1:4:216:GLU:N	2.77	0.42
1:5:23:LYS:H	1:5:23:LYS:HG2	1.65	0.42
1:5:42:ARG:CZ	1:5:44:TRP:NE1	2.82	0.42
1:5:152:ILE:HD12	1:5:227:LEU:HG	2.01	0.42
1:5:215:ASP:CG	1:5:216:GLU:N	2.77	0.42
1:7:29:LEU:HD21	1:7:68:ILE:HG21	2.01	0.42
1:AB:93:LYS:HG2	1:AE:193:VAL:HG22	2.01	0.42
1:AH:199:SER:HA	1:AI:86:LEU:O	2.19	0.42
1:AI:183:VAL:HB	1:AI:197:LEU:HG	2.01	0.42
1:AJ:130:GLU:O	1:AJ:134:ARG:HG3	2.19	0.42
1:AM:208:ARG:HE	1:AM:210:VAL:HG21	1.83	0.42
1:AN:23:LYS:HD2	1:AN:42:ARG:NH2	2.35	0.42
1:AO:145:ARG:HB2	1:AO:148:TYR:HD1	1.84	0.42
1:AO:166:ALA:HB3	1:AO:169:MET:HG3	2.00	0.42
1:AR:168:LYS:HE3	1:AR:168:LYS:HB2	1.70	0.42
1:AS:23:LYS:HD2	1:AS:42:ARG:HH22	1.84	0.42
1:AX:104:PRO:HB3	1:AX:185:VAL:HG12	2.01	0.42
1:AY:40:PHE:HD2	1:AY:246:VAL:HG12	1.84	0.42
1:AY:173:PHE:HE2	1:AY:175:ARG:HE	1.66	0.42
1:Ab:79:ASP:HB3	1:Ab:81:ARG:NH2	2.34	0.42
1:Ad:72:ASP:HA	1:Ad:125:THR:O	2.19	0.42
1:B:79:ASP:C	1:B:80:LEU:HD12	2.44	0.42
1:F:82:LYS:HZ3	1:F:82:LYS:HG3	1.76	0.42
1:G:59:LEU:O	1:G:145:ARG:HG3	2.19	0.42
1:K:162:SER:HB2	1:K:223:LYS:HB2	2.01	0.42
1:Q:16:TYR:HD1	1:Q:223:LYS:HG3	1.84	0.42
1:T:16:TYR:CD1	1:T:223:LYS:HG3	2.54	0.42
1:W:118:PHE:CE1	1:W:120:ILE:HD11	2.54	0.42
1:b:173:PHE:HE1	1:b:175:ARG:HE	1.67	0.42
1:h:40:PHE:HD1	1:h:246:VAL:HG12	1.85	0.42
1:h:85:SER:HA	1:i:200:LYS:O	2.18	0.42
1:i:75:GLY:O	1:i:76:ILE:HG12	2.19	0.42
1:j:23:LYS:HD2	1:j:42:ARG:HH22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:j:120:ILE:CD1	1:j:169:MET:HE3	2.49	0.42
1:k:12:LYS:HA	1:k:12:LYS:HD3	1.85	0.42
1:k:29:LEU:HD13	1:k:56:ILE:HG22	2.02	0.42
1:l:10:ALA:HB2	1:l:81:ARG:HH22	1.84	0.42
1:m:106:PHE:CD2	1:m:106:PHE:N	2.86	0.42
1:p:32:TYR:HB3	1:p:40:PHE:CE1	2.54	0.42
1:q:131:ILE:HG13	1:s:43:ILE:HD12	2.00	0.42
1:r:162:SER:HB2	1:r:223:LYS:HB2	2.00	0.42
1:t:215:ASP:OD1	1:t:216:GLU:N	2.41	0.42
1:x:200:LYS:O	1:y:85:SER:HA	2.19	0.42
1:y:44:TRP:CE2	1:z:127:ASP:HB3	2.55	0.42
1:4:164:LEU:O	1:4:219:VAL:HA	2.19	0.42
1:4:228:PHE:CD2	1:4:229:PHE:N	2.87	0.42
1:7:40:PHE:CZ	1:7:158:PHE:HB2	2.52	0.42
1:AB:173:PHE:HE2	1:AB:175:ARG:HE	1.66	0.42
1:AD:40:PHE:HZ	1:AD:158:PHE:CG	2.37	0.42
1:AD:64:ILE:HD12	1:AD:136:TRP:HZ2	1.85	0.42
1:AD:168:LYS:HA	1:AD:168:LYS:HD3	1.82	0.42
1:AF:79:ASP:HB3	1:AF:81:ARG:NH2	2.35	0.42
1:AH:164:LEU:O	1:AH:219:VAL:HA	2.19	0.42
1:AK:200:LYS:O	1:AL:85:SER:HA	2.18	0.42
1:AT:16:TYR:CD1	1:AT:223:LYS:HG3	2.54	0.42
1:AW:16:TYR:CD1	1:AW:223:LYS:HG3	2.55	0.42
1:AY:199:SER:HA	1:Ad:86:LEU:O	2.19	0.42
1:AZ:56:ILE:HD11	1:AZ:137:LEU:HD21	2.02	0.42
1:Ad:104:PRO:HB3	1:Ad:185:VAL:HG12	2.01	0.42
1:A:208:ARG:HG2	1:A:210:VAL:HG22	2.01	0.42
1:C:148:TYR:O	1:C:152:ILE:HG12	2.19	0.42
1:E:72:ASP:HA	1:E:125:THR:O	2.19	0.42
1:L:183:VAL:HB	1:L:197:LEU:HG	1.99	0.42
1:Q:104:PRO:HB3	1:Q:185:VAL:HG12	2.01	0.42
1:T:30:HIS:CE1	1:T:42:ARG:HH11	2.37	0.42
1:T:172:GLN:HG2	1:T:208:ARG:HG2	2.01	0.42
1:U:168:LYS:HA	1:U:168:LYS:HD3	1.89	0.42
1:Y:106:PHE:N	1:Y:106:PHE:CD2	2.87	0.42
1:Z:40:PHE:CE1	1:Z:224:LEU:HD13	2.54	0.42
1:Z:59:LEU:O	1:Z:145:ARG:HG3	2.19	0.42
1:b:72:ASP:HA	1:b:125:THR:O	2.19	0.42
1:e:106:PHE:N	1:e:106:PHE:CD1	2.86	0.42
1:g:164:LEU:O	1:g:219:VAL:HA	2.20	0.42
1:k:79:ASP:O	1:k:80:LEU:HD12	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:m:104:PRO:HB3	1:m:185:VAL:HG12	2.00	0.42
1:m:164:LEU:O	1:m:219:VAL:HA	2.19	0.42
1:q:77:ASP:HB3	1:q:120:ILE:HB	2.02	0.42
1:r:147:ILE:HG13	1:r:148:TYR:CD1	2.53	0.42
1:s:72:ASP:HA	1:s:125:THR:O	2.20	0.42
1:u:106:PHE:N	1:u:106:PHE:CD1	2.86	0.42
1:v:36:ILE:HD13	1:v:36:ILE:HA	1.86	0.42
1:x:16:TYR:HD1	1:x:223:LYS:HG3	1.83	0.42
1:y:106:PHE:HA	1:y:183:VAL:HG22	2.01	0.42
1:z:164:LEU:O	1:z:219:VAL:HA	2.18	0.42
1:2:183:VAL:HB	1:2:197:LEU:HG	2.00	0.42
1:7:183:VAL:HB	1:7:197:LEU:HG	2.00	0.42
1:AB:79:ASP:O	1:AB:80:LEU:HD12	2.18	0.42
1:AF:26:ILE:HA	1:AF:42:ARG:NH1	2.34	0.42
1:AI:79:ASP:O	1:AI:80:LEU:HD12	2.19	0.42
1:AJ:80:LEU:O	1:AJ:81:ARG:HG3	2.18	0.42
1:AJ:208:ARG:HE	1:AJ:210:VAL:HG21	1.85	0.42
1:AK:75:GLY:O	1:AK:76:ILE:HG12	2.19	0.42
1:AK:228:PHE:CD1	1:AK:229:PHE:N	2.87	0.42
1:AM:111:GLU:HB2	1:AM:178:LYS:HB2	2.00	0.42
1:AQ:172:GLN:HG2	1:AQ:208:ARG:HG2	2.01	0.42
1:AR:215:ASP:CG	1:AR:216:GLU:N	2.77	0.42
1:AU:193:VAL:HG22	1:AW:93:LYS:HG2	2.01	0.42
1:Ac:16:TYR:CD1	1:Ac:223:LYS:HG3	2.54	0.42
1:C:56:ILE:HD11	1:C:137:LEU:HD21	2.01	0.42
1:C:164:LEU:O	1:C:219:VAL:HA	2.19	0.42
1:D:40:PHE:HE2	1:D:224:LEU:HD13	1.83	0.42
1:E:16:TYR:CD1	1:E:223:LYS:HG3	2.54	0.42
1:H:12:LYS:HA	1:H:12:LYS:HD3	1.87	0.42
1:N:16:TYR:CD1	1:N:223:LYS:HG3	2.53	0.42
1:R:16:TYR:HD1	1:R:223:LYS:HG3	1.84	0.42
1:T:79:ASP:HB3	1:T:81:ARG:NH2	2.35	0.42
1:V:16:TYR:CD1	1:V:223:LYS:HG3	2.54	0.42
1:V:72:ASP:HA	1:V:125:THR:O	2.19	0.42
1:d:43:ILE:HD12	1:e:131:ILE:HG13	2.02	0.42
1:d:64:ILE:HD12	1:d:136:TRP:HZ2	1.84	0.42
1:g:224:LEU:HD12	1:g:243:PHE:CZ	2.54	0.42
1:j:29:LEU:HD11	1:j:68:ILE:HD12	2.02	0.42
1:j:199:SER:HA	1:k:86:LEU:O	2.19	0.42
1:l:16:TYR:HD1	1:l:223:LYS:HG3	1.84	0.42
1:m:183:VAL:HB	1:m:197:LEU:HG	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:n:215:ASP:OD2	1:n:216:GLU:N	2.42	0.42
1:t:118:PHE:CE1	1:t:120:ILE:HD11	2.54	0.42
1:y:168:LYS:HB2	1:y:168:LYS:HE3	1.70	0.42
1:1:210:VAL:HB	1:2:76:ILE:HG21	2.01	0.42
1:2:200:LYS:O	1:7:85:SER:HA	2.19	0.42
1:3:181:LEU:HD12	1:3:182:GLY:H	1.84	0.42
1:5:79:ASP:O	1:5:80:LEU:HD12	2.18	0.42
1:6:131:ILE:HG13	1:AC:43:ILE:HD12	2.02	0.42
1:7:79:ASP:O	1:7:80:LEU:HD12	2.20	0.42
1:0:121:GLU:HB3	1:0:168:LYS:HB2	2.01	0.42
1:AC:91:ALA:O	1:AC:105:SER:HA	2.19	0.42
1:AF:16:TYR:CD1	1:AF:223:LYS:HG3	2.54	0.42
1:AG:164:LEU:O	1:AG:219:VAL:HA	2.19	0.42
1:AK:80:LEU:O	1:AK:81:ARG:HG3	2.20	0.42
1:AN:164:LEU:O	1:AN:219:VAL:HA	2.19	0.42
1:AO:36:ILE:HD13	1:AO:36:ILE:HA	1.87	0.42
1:AR:93:LYS:HG2	1:AS:193:VAL:HG22	2.01	0.42
1:AT:40:PHE:CZ	1:AT:158:PHE:HB2	2.50	0.42
1:AT:106:PHE:N	1:AT:106:PHE:CD1	2.86	0.42
1:AT:115:SER:OG	1:AT:174:GLU:HB2	2.18	0.42
1:AU:106:PHE:N	1:AU:106:PHE:CD2	2.86	0.42
1:AZ:36:ILE:HD13	1:AZ:36:ILE:HA	1.85	0.42
1:Ab:79:ASP:O	1:Ab:80:LEU:HD12	2.19	0.42
1:Ac:32:TYR:CZ	1:Ac:42:ARG:HD3	2.54	0.42
1:Ad:215:ASP:CG	1:Ad:216:GLU:H	2.24	0.42
1:B:16:TYR:HD1	1:B:223:LYS:HG3	1.83	0.42
1:D:210:VAL:HB	1:E:76:ILE:HG21	2.01	0.42
1:E:104:PRO:HB3	1:E:185:VAL:HG12	2.01	0.42
1:F:206:TYR:OH	1:F:208:ARG:HD3	2.20	0.42
1:G:145:ARG:HB2	1:G:148:TYR:HD1	1.84	0.42
1:H:168:LYS:HE3	1:H:168:LYS:HB2	1.71	0.42
1:M:208:ARG:HE	1:M:210:VAL:HG21	1.84	0.42
1:N:16:TYR:HD1	1:N:223:LYS:HG3	1.85	0.42
1:O:115:SER:OG	1:O:174:GLU:HB2	2.20	0.42
1:U:227:LEU:HD11	1:U:235:LEU:HD11	2.01	0.42
1:V:80:LEU:C	1:V:81:ARG:HD2	2.45	0.42
1:X:16:TYR:HD1	1:X:223:LYS:HG3	1.85	0.42
1:Z:72:ASP:HA	1:Z:125:THR:O	2.19	0.42
1:c:40:PHE:CZ	1:c:158:PHE:HB2	2.48	0.42
1:c:124:ILE:HG12	1:c:165:ARG:HB2	2.01	0.42
1:c:206:TYR:OH	1:c:208:ARG:HD3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:29:LEU:HD21	1:h:68:ILE:HG21	2.02	0.42
1:l:80:LEU:C	1:l:81:ARG:HD2	2.44	0.42
1:n:104:PRO:HB3	1:n:185:VAL:HG12	2.01	0.42
1:s:32:TYR:HB3	1:s:40:PHE:CZ	2.54	0.42
1:x:40:PHE:CZ	1:x:158:PHE:HB2	2.52	0.42
1:1:200:LYS:O	1:2:85:SER:HA	2.20	0.42
1:2:199:SER:HA	1:7:86:LEU:O	2.20	0.42
1:5:86:LEU:O	1:6:199:SER:HA	2.19	0.42
1:6:168:LYS:HA	1:6:211:PHE:O	2.19	0.42
1:0:199:SER:HA	1:AA:86:LEU:O	2.19	0.42
1:AB:130:GLU:O	1:AB:134:ARG:HG3	2.19	0.42
1:AE:59:LEU:O	1:AE:145:ARG:HG3	2.18	0.42
1:AI:164:LEU:O	1:AI:219:VAL:HA	2.20	0.42
1:AN:77:ASP:HB3	1:AN:120:ILE:HB	2.01	0.42
1:AU:72:ASP:HA	1:AU:125:THR:O	2.20	0.42
1:Ab:72:ASP:HA	1:Ab:125:THR:O	2.20	0.42
1:Ac:85:SER:HA	1:Ad:200:LYS:O	2.19	0.42
1:A:79:ASP:C	1:A:80:LEU:HD12	2.45	0.42
1:A:79:ASP:O	1:A:80:LEU:HD12	2.20	0.42
1:C:181:LEU:HD11	1:C:183:VAL:HG23	2.02	0.42
1:K:79:ASP:O	1:K:80:LEU:HD12	2.20	0.42
1:M:169:MET:HB2	1:M:211:PHE:HB3	2.01	0.42
1:N:16:TYR:CE2	1:N:164:LEU:HG	2.54	0.42
1:O:43:ILE:HG13	1:O:43:ILE:O	2.18	0.42
1:R:164:LEU:O	1:R:219:VAL:HA	2.19	0.42
1:S:172:GLN:HG2	1:S:208:ARG:HG2	2.01	0.42
1:a:75:GLY:O	1:a:76:ILE:HG12	2.19	0.42
1:c:80:LEU:O	1:c:81:ARG:HG3	2.19	0.42
1:e:164:LEU:O	1:e:219:VAL:HA	2.20	0.42
1:l:12:LYS:HA	1:l:12:LYS:HD3	1.87	0.42
1:n:41:LYS:HB3	1:n:41:LYS:HE3	1.79	0.42
1:p:77:ASP:HB3	1:p:120:ILE:HB	2.02	0.42
1:t:42:ARG:CZ	1:t:44:TRP:NE1	2.83	0.42
1:u:164:LEU:O	1:u:219:VAL:HA	2.18	0.42
1:u:199:SER:HA	1:v:86:LEU:O	2.20	0.42
1:v:183:VAL:HB	1:v:197:LEU:HG	2.01	0.42
1:w:26:ILE:HA	1:w:42:ARG:NH1	2.35	0.42
1:y:40:PHE:CZ	1:y:158:PHE:HB2	2.52	0.42
1:z:79:ASP:HB3	1:z:81:ARG:NH2	2.35	0.42
1:2:215:ASP:CG	1:2:216:GLU:N	2.78	0.42
1:8:43:ILE:HD12	1:0:131:ILE:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:23:LYS:HD2	1:0:42:ARG:HH22	1.84	0.42
1:AB:75:GLY:O	1:AB:76:ILE:HG12	2.19	0.42
1:AD:30:HIS:CE1	1:AD:42:ARG:HH11	2.38	0.42
1:AG:12:LYS:HA	1:AG:12:LYS:HD3	1.87	0.42
1:AH:26:ILE:HA	1:AH:42:ARG:NH1	2.35	0.42
1:AK:72:ASP:HA	1:AK:125:THR:O	2.19	0.42
1:AK:104:PRO:HB3	1:AK:185:VAL:HG12	2.02	0.42
1:AM:77:ASP:HB3	1:AM:120:ILE:HB	2.02	0.42
1:AP:72:ASP:HA	1:AP:125:THR:O	2.20	0.42
1:AQ:124:ILE:HG12	1:AQ:165:ARG:HB2	2.01	0.42
1:AS:77:ASP:HB3	1:AS:120:ILE:HB	2.01	0.42
1:AS:86:LEU:O	1:AZ:199:SER:HA	2.20	0.42
1:AS:118:PHE:CE1	1:AS:120:ILE:HD11	2.55	0.42
1:AT:148:TYR:O	1:AT:152:ILE:HG12	2.20	0.42
1:AX:79:ASP:O	1:AX:80:LEU:HD12	2.19	0.42
1:Aa:16:TYR:CE2	1:Aa:164:LEU:HG	2.54	0.42
1:Ac:20:ALA:HB3	1:Ac:247:LEU:HB3	2.01	0.42
1:Ac:80:LEU:O	1:Ac:81:ARG:HG3	2.20	0.42
1:Ac:106:PHE:N	1:Ac:106:PHE:CD1	2.86	0.42
1:A:169:MET:HB2	1:A:211:PHE:HB3	2.02	0.42
1:B:162:SER:HB2	1:B:223:LYS:HB2	2.02	0.42
1:E:200:LYS:O	1:F:85:SER:HA	2.19	0.42
1:F:80:LEU:O	1:F:81:ARG:HG3	2.20	0.42
1:G:16:TYR:CE2	1:G:164:LEU:HG	2.54	0.42
1:J:173:PHE:O	1:J:206:TYR:HA	2.20	0.42
1:L:24:THR:HG22	1:L:218:ILE:HG13	2.01	0.42
1:N:29:LEU:HD13	1:N:56:ILE:HG22	2.02	0.42
1:N:43:ILE:O	1:N:43:ILE:HG13	2.18	0.42
1:O:164:LEU:O	1:O:219:VAL:HA	2.20	0.42
1:a:147:ILE:HG13	1:a:148:TYR:CD1	2.54	0.42
1:b:19:VAL:HB	1:b:247:LEU:HD12	2.00	0.42
1:b:79:ASP:O	1:b:80:LEU:HD12	2.19	0.42
1:b:215:ASP:OD1	1:b:216:GLU:N	2.45	0.42
1:e:79:ASP:HB3	1:e:81:ARG:NH2	2.31	0.42
1:i:40:PHE:HZ	1:i:158:PHE:CG	2.38	0.42
1:i:68:ILE:HD13	1:i:133:LEU:HD13	2.01	0.42
1:y:72:ASP:HA	1:y:125:THR:O	2.20	0.42
1:y:172:GLN:HG2	1:y:208:ARG:HG2	2.02	0.42
1:1:111:GLU:HB2	1:1:178:LYS:HB2	2.01	0.42
1:5:93:LYS:HG2	1:6:193:VAL:HG22	2.02	0.42
1:7:162:SER:HB2	1:7:223:LYS:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:16:TYR:HD1	1:8:223:LYS:HG3	1.84	0.42
1:0:59:LEU:O	1:0:145:ARG:HG3	2.20	0.42
1:AB:115:SER:OG	1:AB:174:GLU:HB2	2.20	0.42
1:AE:79:ASP:HB3	1:AE:81:ARG:NH2	2.35	0.42
1:AH:20:ALA:HB3	1:AH:247:LEU:HB3	2.01	0.42
1:AK:77:ASP:HB3	1:AK:120:ILE:HB	2.01	0.42
1:AL:43:ILE:HD12	1:AM:131:ILE:HG13	2.01	0.42
1:AQ:104:PRO:HB3	1:AQ:185:VAL:HG12	2.01	0.42
1:AS:130:GLU:O	1:AS:134:ARG:HG3	2.20	0.42
1:AX:72:ASP:HA	1:AX:125:THR:O	2.20	0.42
1:AX:130:GLU:O	1:AX:134:ARG:HG3	2.19	0.42
1:AY:93:LYS:HG2	1:Ab:193:VAL:HG22	2.02	0.42
1:AZ:16:TYR:HE1	1:AZ:162:SER:HB2	1.85	0.42
1:A:16:TYR:HD1	1:A:223:LYS:HG3	1.85	0.42
1:A:200:LYS:O	1:B:85:SER:HA	2.20	0.42
1:C:77:ASP:HB3	1:C:120:ILE:HB	2.00	0.42
1:E:162:SER:HB2	1:E:223:LYS:HB2	2.01	0.42
1:F:106:PHE:N	1:F:106:PHE:CD1	2.86	0.42
1:G:40:PHE:CZ	1:G:158:PHE:CG	3.08	0.42
1:J:152:ILE:HD12	1:J:227:LEU:CD2	2.50	0.42
1:N:43:ILE:HD12	1:P:131:ILE:HG13	2.01	0.42
1:O:69:GLY:O	1:O:70:LEU:HD12	2.19	0.42
1:S:106:PHE:N	1:S:106:PHE:CD1	2.86	0.42
1:T:32:TYR:HB3	1:T:40:PHE:CD1	2.55	0.42
1:U:16:TYR:CD1	1:U:223:LYS:HG3	2.54	0.42
1:W:77:ASP:HB3	1:W:120:ILE:HB	2.00	0.42
1:a:199:SER:HA	1:b:86:LEU:O	2.20	0.42
1:b:130:GLU:O	1:b:134:ARG:HG3	2.19	0.42
1:c:75:GLY:O	1:c:76:ILE:HG12	2.19	0.42
1:d:40:PHE:CZ	1:d:158:PHE:CG	3.08	0.42
1:e:43:ILE:HD12	1:j:131:ILE:HG13	2.02	0.42
1:f:131:ILE:HG13	1:g:43:ILE:HD12	2.02	0.42
1:h:86:LEU:O	1:i:199:SER:HA	2.20	0.42
1:h:147:ILE:HG13	1:h:148:TYR:CD1	2.54	0.42
1:h:148:TYR:O	1:h:152:ILE:HG12	2.20	0.42
1:m:23:LYS:HD2	1:m:42:ARG:HH21	1.85	0.42
1:m:64:ILE:HD12	1:m:136:TRP:HZ2	1.84	0.42
1:q:215:ASP:CG	1:q:216:GLU:H	2.26	0.42
1:r:164:LEU:O	1:r:219:VAL:HA	2.20	0.42
1:s:23:LYS:HD2	1:s:42:ARG:NH2	2.35	0.42
1:u:172:GLN:HG2	1:u:208:ARG:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:v:16:TYR:CD1	1:v:223:LYS:HG3	2.53	0.42
1:z:36:ILE:HD13	1:z:36:ILE:HA	1.91	0.42
1:z:106:PHE:N	1:z:106:PHE:CD1	2.88	0.42
1:z:181:LEU:HD11	1:z:183:VAL:HG23	2.02	0.42
1:1:16:TYR:CD1	1:1:223:LYS:HG3	2.54	0.42
1:4:104:PRO:HB3	1:4:185:VAL:HG12	2.01	0.42
1:5:79:ASP:HB3	1:5:81:ARG:NH2	2.35	0.42
1:5:173:PHE:HE1	1:5:175:ARG:HE	1.68	0.42
1:6:79:ASP:O	1:6:80:LEU:HD12	2.19	0.42
1:7:123:ILE:HD12	1:7:123:ILE:N	2.34	0.42
1:0:77:ASP:HB3	1:0:120:ILE:HB	2.01	0.42
1:AF:75:GLY:O	1:AF:76:ILE:HG12	2.19	0.42
1:AI:147:ILE:HG13	1:AI:148:TYR:CD1	2.53	0.42
1:AJ:26:ILE:HA	1:AJ:42:ARG:NH1	2.35	0.42
1:AL:40:PHE:CZ	1:AL:158:PHE:HB2	2.50	0.42
1:AN:16:TYR:CD1	1:AN:223:LYS:HG3	2.54	0.42
1:AQ:29:LEU:HD11	1:AQ:68:ILE:HD12	2.02	0.42
1:AS:79:ASP:O	1:AS:80:LEU:HD12	2.20	0.42
1:AX:36:ILE:HD13	1:AX:36:ILE:HA	1.90	0.42
1:AZ:12:LYS:HA	1:AZ:12:LYS:HD3	1.87	0.42
1:AZ:227:LEU:HD11	1:AZ:235:LEU:HD11	2.02	0.42
1:Aa:168:LYS:HE3	1:Aa:168:LYS:HB2	1.70	0.42
1:Ab:164:LEU:O	1:Ab:219:VAL:HA	2.19	0.42
1:Ac:75:GLY:O	1:Ac:76:ILE:HG12	2.20	0.42
1:I:146:GLU:H	1:I:146:GLU:CD	2.27	0.42
1:K:123:ILE:HD12	1:K:123:ILE:N	2.34	0.42
1:L:80:LEU:O	1:L:81:ARG:HG3	2.20	0.42
1:M:79:ASP:O	1:M:80:LEU:HD12	2.20	0.42
1:P:29:LEU:HD11	1:P:68:ILE:HD12	2.02	0.42
1:P:79:ASP:HB3	1:P:81:ARG:NH2	2.34	0.42
1:P:199:SER:HA	1:Q:86:LEU:O	2.19	0.42
1:Q:168:LYS:HE3	1:Q:168:LYS:HB2	1.70	0.42
1:U:64:ILE:HD12	1:U:136:TRP:HZ2	1.85	0.42
1:X:79:ASP:C	1:X:80:LEU:HD12	2.45	0.42
1:X:169:MET:HB2	1:X:211:PHE:HB3	2.02	0.42
1:Y:40:PHE:CZ	1:Y:158:PHE:HB2	2.49	0.42
1:Y:77:ASP:HB3	1:Y:120:ILE:HB	2.01	0.42
1:Y:162:SER:HB2	1:Y:223:LYS:HB2	2.02	0.42
1:Z:145:ARG:HB2	1:Z:148:TYR:HD1	1.85	0.42
1:a:208:ARG:HE	1:a:210:VAL:HG21	1.85	0.42
1:b:162:SER:HB2	1:b:223:LYS:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:b:200:LYS:O	1:c:85:SER:HA	2.19	0.42
1:e:91:ALA:O	1:e:105:SER:HA	2.19	0.42
1:k:43:ILE:HD12	1:m:131:ILE:HG13	2.01	0.42
1:l:172:GLN:HG2	1:l:208:ARG:HG3	2.01	0.42
1:o:26:ILE:HA	1:o:42:ARG:NH1	2.35	0.42
1:r:79:ASP:O	1:r:80:LEU:HD12	2.20	0.42
1:u:12:LYS:HA	1:u:12:LYS:HD3	1.87	0.42
1:v:79:ASP:O	1:v:80:LEU:HD12	2.19	0.42
1:y:170:ARG:HB3	1:y:170:ARG:NH1	2.35	0.42
1:z:146:GLU:CD	1:z:146:GLU:H	2.28	0.42
1:z:162:SER:HB2	1:z:223:LYS:HB2	2.02	0.42
1:1:208:ARG:HE	1:1:210:VAL:CG2	2.33	0.42
1:3:91:ALA:O	1:3:105:SER:HA	2.20	0.42
1:4:166:ALA:HB3	1:4:169:MET:HG3	2.02	0.42
1:AG:79:ASP:HB3	1:AG:81:ARG:NH2	2.34	0.42
1:AH:79:ASP:C	1:AH:80:LEU:HD12	2.44	0.42
1:AJ:23:LYS:HE2	1:AJ:23:LYS:HB3	1.94	0.42
1:AO:72:ASP:HA	1:AO:125:THR:O	2.20	0.42
1:AQ:168:LYS:HB2	1:AQ:168:LYS:HE3	1.68	0.42
1:AS:79:ASP:HB3	1:AS:81:ARG:NH2	2.34	0.42
1:AS:215:ASP:OD2	1:AS:216:GLU:N	2.46	0.42
1:AT:147:ILE:HG13	1:AT:148:TYR:CD1	2.54	0.42
1:AT:211:PHE:CD1	1:AT:218:ILE:HD12	2.55	0.42
1:Ad:228:PHE:HD1	1:Ad:229:PHE:H	1.67	0.42
1:C:19:VAL:HB	1:C:247:LEU:HD12	2.02	0.41
1:I:131:ILE:HG13	1:J:43:ILE:HD12	2.01	0.41
1:K:86:LEU:O	1:L:199:SER:HA	2.20	0.41
1:M:164:LEU:O	1:M:219:VAL:HA	2.19	0.41
1:O:124:ILE:HG12	1:O:165:ARG:HB2	2.01	0.41
1:U:79:ASP:O	1:U:80:LEU:HD12	2.19	0.41
1:W:42:ARG:CZ	1:W:44:TRP:NE1	2.83	0.41
1:b:73:GLY:C	1:b:74:GLN:HG2	2.45	0.41
1:g:72:ASP:HA	1:g:125:THR:O	2.20	0.41
1:i:72:ASP:HA	1:i:125:THR:O	2.20	0.41
1:k:173:PHE:HE1	1:k:175:ARG:HE	1.68	0.41
1:n:91:ALA:O	1:n:105:SER:HA	2.20	0.41
1:r:16:TYR:HD1	1:r:223:LYS:HG3	1.85	0.41
1:s:124:ILE:HG12	1:s:165:ARG:HB2	2.02	0.41
1:v:193:VAL:HG22	1:w:93:LYS:HG2	2.02	0.41
1:x:42:ARG:CZ	1:x:44:TRP:NE1	2.83	0.41
1:z:75:GLY:O	1:z:76:ILE:HG12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:72:ASP:HA	1:3:125:THR:O	2.20	0.41
1:4:72:ASP:HA	1:4:125:THR:O	2.20	0.41
1:5:12:LYS:HA	1:5:12:LYS:HD3	1.86	0.41
1:6:23:LYS:HD2	1:6:42:ARG:HH22	1.85	0.41
1:0:31:ILE:HG13	1:0:59:LEU:HD21	2.01	0.41
1:AA:16:TYR:HD1	1:AA:223:LYS:HG3	1.85	0.41
1:AA:104:PRO:HB3	1:AA:185:VAL:HG12	2.01	0.41
1:AJ:151:GLU:H	1:AJ:151:GLU:HG3	1.71	0.41
1:AS:164:LEU:O	1:AS:219:VAL:HA	2.19	0.41
1:AW:199:SER:HA	1:AX:86:LEU:O	2.20	0.41
1:AY:115:SER:OG	1:AY:174:GLU:HB2	2.20	0.41
1:Ac:130:GLU:O	1:Ac:134:ARG:HG3	2.20	0.41
1:A:106:PHE:N	1:A:106:PHE:CD1	2.88	0.41
1:C:79:ASP:HB3	1:C:81:ARG:NH2	2.34	0.41
1:H:91:ALA:O	1:H:105:SER:HA	2.19	0.41
1:J:72:ASP:HA	1:J:125:THR:O	2.20	0.41
1:K:40:PHE:HD1	1:K:246:VAL:HG12	1.84	0.41
1:M:200:LYS:O	1:N:85:SER:HA	2.20	0.41
1:S:16:TYR:CD1	1:S:223:LYS:HG3	2.54	0.41
1:T:32:TYR:CE1	1:T:42:ARG:HD3	2.55	0.41
1:U:120:ILE:HD12	1:U:169:MET:HE3	2.01	0.41
1:V:40:PHE:HD1	1:V:246:VAL:HG12	1.84	0.41
1:X:118:PHE:CE1	1:X:120:ILE:HD11	2.54	0.41
1:a:181:LEU:HD12	1:a:182:GLY:H	1.85	0.41
1:b:104:PRO:HB3	1:b:185:VAL:HG12	2.00	0.41
1:b:124:ILE:HG12	1:b:165:ARG:HB2	2.02	0.41
1:e:24:THR:HG22	1:e:218:ILE:HG13	2.01	0.41
1:g:208:ARG:HG2	1:g:210:VAL:HG23	2.01	0.41
1:h:123:ILE:HD12	1:h:123:ILE:N	2.34	0.41
1:i:131:ILE:HG13	1:p:43:ILE:HD12	2.01	0.41
1:i:162:SER:HB2	1:i:223:LYS:HB2	2.02	0.41
1:m:81:ARG:HB2	1:m:116:VAL:HB	2.02	0.41
1:n:79:ASP:HB3	1:n:81:ARG:NH2	2.36	0.41
1:o:16:TYR:HD1	1:o:223:LYS:HG3	1.85	0.41
1:w:79:ASP:O	1:w:80:LEU:HD12	2.19	0.41
1:y:79:ASP:O	1:y:80:LEU:HD12	2.20	0.41
1:1:40:PHE:CZ	1:1:158:PHE:HB2	2.46	0.41
1:4:64:ILE:HD12	1:4:136:TRP:HZ2	1.84	0.41
1:4:228:PHE:HD2	1:4:229:PHE:N	2.18	0.41
1:6:32:TYR:HB3	1:6:40:PHE:CE1	2.56	0.41
1:9:16:TYR:CE2	1:9:164:LEU:HG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:9:215:ASP:CG	1:9:216:GLU:H	2.25	0.41
1:AB:16:TYR:CD1	1:AB:223:LYS:HG3	2.55	0.41
1:AE:72:ASP:HA	1:AE:125:THR:O	2.20	0.41
1:AE:169:MET:HE2	1:AE:169:MET:HB3	1.93	0.41
1:AF:80:LEU:O	1:AF:81:ARG:HG3	2.20	0.41
1:AH:44:TRP:CE2	1:AI:127:ASP:HB3	2.55	0.41
1:AL:40:PHE:CD1	1:AL:246:VAL:HG12	2.55	0.41
1:AP:168:LYS:HE3	1:AP:168:LYS:HB2	1.69	0.41
1:AS:75:GLY:O	1:AS:76:ILE:HG12	2.20	0.41
1:AT:123:ILE:HD12	1:AT:123:ILE:N	2.34	0.41
1:AV:127:ASP:HB3	1:AX:44:TRP:CZ2	2.55	0.41
1:AW:59:LEU:O	1:AW:145:ARG:HG3	2.19	0.41
1:Aa:16:TYR:HD1	1:Aa:223:LYS:HG3	1.84	0.41
1:Ad:80:LEU:O	1:Ad:81:ARG:HG3	2.20	0.41
1:Ad:124:ILE:HG12	1:Ad:165:ARG:HB2	2.01	0.41
1:A:215:ASP:CG	1:A:216:GLU:H	2.26	0.41
1:F:75:GLY:O	1:F:76:ILE:HG12	2.20	0.41
1:J:131:ILE:HG13	1:K:43:ILE:HD12	2.01	0.41
1:K:73:GLY:C	1:K:74:GLN:HG2	2.45	0.41
1:O:77:ASP:HB3	1:O:120:ILE:HB	2.03	0.41
1:Q:72:ASP:HA	1:Q:125:THR:O	2.21	0.41
1:Q:91:ALA:O	1:Q:105:SER:HA	2.20	0.41
1:T:77:ASP:HB3	1:T:120:ILE:HB	2.01	0.41
1:U:145:ARG:HB2	1:U:148:TYR:HD1	1.85	0.41
1:V:183:VAL:HB	1:V:197:LEU:HG	2.02	0.41
1:X:12:LYS:HA	1:X:12:LYS:HD3	1.81	0.41
1:X:215:ASP:CG	1:X:216:GLU:H	2.25	0.41
1:a:43:ILE:HD12	1:b:131:ILE:HG13	2.03	0.41
1:a:115:SER:OG	1:a:174:GLU:HB2	2.20	0.41
1:c:64:ILE:HD12	1:c:136:TRP:HZ2	1.85	0.41
1:d:32:TYR:HB3	1:d:40:PHE:CE1	2.55	0.41
1:e:79:ASP:O	1:e:80:LEU:HD12	2.19	0.41
1:e:124:ILE:HG12	1:e:165:ARG:HB2	2.01	0.41
1:f:106:PHE:N	1:f:106:PHE:CD1	2.88	0.41
1:j:200:LYS:O	1:k:85:SER:HA	2.20	0.41
1:k:16:TYR:HD1	1:k:223:LYS:HG3	1.84	0.41
1:p:130:GLU:O	1:p:134:ARG:HG3	2.20	0.41
1:q:146:GLU:H	1:q:146:GLU:CD	2.28	0.41
1:r:215:ASP:CG	1:r:216:GLU:N	2.78	0.41
1:s:80:LEU:C	1:s:81:ARG:HD2	2.46	0.41
1:w:44:TRP:CZ2	1:x:127:ASP:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:y:152:ILE:HD12	1:y:227:LEU:HG	2.01	0.41
1:y:224:LEU:HD11	1:y:246:VAL:HG11	2.01	0.41
1:1:79:ASP:HB3	1:1:81:ARG:NH2	2.34	0.41
1:2:173:PHE:O	1:2:206:TYR:HA	2.19	0.41
1:3:16:TYR:CE2	1:3:164:LEU:HG	2.55	0.41
1:6:75:GLY:O	1:6:76:ILE:HG12	2.20	0.41
1:6:79:ASP:HB3	1:6:81:ARG:NH2	2.35	0.41
1:9:40:PHE:CZ	1:9:158:PHE:CG	3.09	0.41
1:9:104:PRO:HB3	1:9:185:VAL:HG12	2.01	0.41
1:AB:36:ILE:HD13	1:AB:36:ILE:HA	1.92	0.41
1:AB:152:ILE:HD12	1:AB:227:LEU:HG	2.02	0.41
1:AC:16:TYR:HE1	1:AC:162:SER:HB2	1.85	0.41
1:AD:32:TYR:HB3	1:AD:40:PHE:CE1	2.55	0.41
1:AF:85:SER:HA	1:AG:200:LYS:O	2.20	0.41
1:AH:172:GLN:HG2	1:AH:208:ARG:HG2	2.02	0.41
1:AI:169:MET:HB2	1:AI:211:PHE:HB3	2.02	0.41
1:AM:146:GLU:H	1:AM:146:GLU:CD	2.28	0.41
1:AN:16:TYR:CE2	1:AN:164:LEU:HG	2.56	0.41
1:AO:40:PHE:HZ	1:AO:158:PHE:CG	2.39	0.41
1:AP:86:LEU:O	1:AQ:199:SER:HA	2.20	0.41
1:AQ:106:PHE:N	1:AQ:106:PHE:CD2	2.86	0.41
1:AR:85:SER:HA	1:AS:200:LYS:O	2.20	0.41
1:AS:16:TYR:HD1	1:AS:223:LYS:HG3	1.85	0.41
1:AS:168:LYS:HA	1:AS:211:PHE:O	2.19	0.41
1:AT:29:LEU:HD21	1:AT:68:ILE:HG21	2.03	0.41
1:AX:79:ASP:C	1:AX:80:LEU:HD12	2.45	0.41
1:Ac:26:ILE:HA	1:Ac:42:ARG:NH1	2.35	0.41
1:Ad:162:SER:HB2	1:Ad:223:LYS:HB2	2.02	0.41
1:Ad:164:LEU:O	1:Ad:219:VAL:HA	2.20	0.41
1:B:148:TYR:O	1:B:152:ILE:HG12	2.20	0.41
1:F:22:PRO:O	1:F:218:ILE:HD11	2.20	0.41
1:G:79:ASP:O	1:G:80:LEU:HD12	2.21	0.41
1:J:164:LEU:O	1:J:219:VAL:HA	2.20	0.41
1:M:118:PHE:CE1	1:M:120:ILE:HD11	2.56	0.41
1:N:79:ASP:HB3	1:N:81:ARG:NH2	2.35	0.41
1:S:79:ASP:HB3	1:S:81:ARG:NH2	2.34	0.41
1:V:23:LYS:HD2	1:V:42:ARG:NH2	2.35	0.41
1:X:93:LYS:HG2	1:f:193:VAL:HG22	2.02	0.41
1:a:210:VAL:HB	1:b:76:ILE:HG21	2.01	0.41
1:f:227:LEU:HD11	1:f:235:LEU:HD11	2.03	0.41
1:i:77:ASP:HB3	1:i:120:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:k:16:TYR:CE2	1:k:164:LEU:HG	2.55	0.41
1:n:16:TYR:HD1	1:n:223:LYS:HG3	1.84	0.41
1:o:93:LYS:HG2	1:r:193:VAL:HG22	2.01	0.41
1:r:120:ILE:HD12	1:r:169:MET:HE3	2.02	0.41
1:t:32:TYR:CZ	1:t:42:ARG:HD3	2.55	0.41
1:5:85:SER:HA	1:6:200:LYS:O	2.20	0.41
1:8:32:TYR:CZ	1:8:42:ARG:HD3	2.55	0.41
1:8:208:ARG:CZ	1:8:210:VAL:HG21	2.50	0.41
1:0:115:SER:OG	1:0:174:GLU:HB2	2.20	0.41
1:AA:72:ASP:HA	1:AA:125:THR:O	2.20	0.41
1:AD:40:PHE:CE1	1:AD:158:PHE:HB2	2.55	0.41
1:AD:40:PHE:CZ	1:AD:158:PHE:CG	3.09	0.41
1:AD:183:VAL:HB	1:AD:197:LEU:HG	2.03	0.41
1:AF:86:LEU:O	1:AG:199:SER:HA	2.20	0.41
1:AF:206:TYR:OH	1:AF:208:ARG:HD3	2.20	0.41
1:AG:72:ASP:HA	1:AG:125:THR:O	2.20	0.41
1:AH:40:PHE:HZ	1:AH:158:PHE:CG	2.38	0.41
1:AM:79:ASP:HB3	1:AM:81:ARG:NH2	2.35	0.41
1:AO:199:SER:HA	1:AT:86:LEU:O	2.20	0.41
1:AV:86:LEU:O	1:AX:199:SER:HA	2.20	0.41
1:AX:168:LYS:HB2	1:AX:168:LYS:HE3	1.70	0.41
1:AZ:164:LEU:O	1:AZ:219:VAL:HA	2.21	0.41
1:Ad:215:ASP:OD2	1:Ad:216:GLU:N	2.46	0.41
1:C:64:ILE:HD12	1:C:136:TRP:HZ2	1.86	0.41
1:D:199:SER:HA	1:E:86:LEU:O	2.20	0.41
1:E:124:ILE:HG12	1:E:165:ARG:HB2	2.01	0.41
1:G:40:PHE:CE1	1:G:158:PHE:HB2	2.56	0.41
1:I:79:ASP:HB2	1:I:118:PHE:HB3	2.03	0.41
1:M:16:TYR:CD1	1:M:223:LYS:HG3	2.54	0.41
1:O:118:PHE:CE1	1:O:120:ILE:HD11	2.56	0.41
1:O:120:ILE:HD12	1:O:169:MET:HG2	2.02	0.41
1:T:40:PHE:CZ	1:T:158:PHE:CG	3.09	0.41
1:T:210:VAL:HG12	1:T:212:GLU:OE2	2.21	0.41
1:W:16:TYR:CE2	1:W:164:LEU:HG	2.56	0.41
1:W:23:LYS:HD2	1:W:42:ARG:NH2	2.36	0.41
1:X:200:LYS:O	1:Y:85:SER:HA	2.20	0.41
1:b:64:ILE:HD12	1:b:136:TRP:HZ2	1.86	0.41
1:g:227:LEU:HD21	1:g:235:LEU:HD11	2.03	0.41
1:i:79:ASP:C	1:i:80:LEU:HD12	2.46	0.41
1:l:115:SER:OG	1:l:174:GLU:HB2	2.20	0.41
1:o:183:VAL:HB	1:o:197:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:q:148:TYR:O	1:q:152:ILE:HG12	2.21	0.41
1:r:168:LYS:HA	1:r:168:LYS:HD3	1.89	0.41
1:s:79:ASP:O	1:s:80:LEU:HD12	2.21	0.41
1:u:69:GLY:O	1:u:70:LEU:HD12	2.20	0.41
1:x:72:ASP:HA	1:x:125:THR:O	2.20	0.41
1:z:16:TYR:CD1	1:z:223:LYS:HG3	2.55	0.41
1:2:72:ASP:HA	1:2:125:THR:O	2.20	0.41
1:2:79:ASP:O	1:2:80:LEU:HD12	2.21	0.41
1:4:29:LEU:HD11	1:4:68:ILE:HD12	2.01	0.41
1:5:206:TYR:HB2	1:5:208:ARG:HH12	1.86	0.41
1:8:72:ASP:HA	1:8:125:THR:O	2.20	0.41
1:AC:106:PHE:HA	1:AC:183:VAL:HG22	2.01	0.41
1:AD:162:SER:HB2	1:AD:223:LYS:HB2	2.02	0.41
1:AG:19:VAL:HB	1:AG:247:LEU:HD12	2.01	0.41
1:AI:36:ILE:HD13	1:AI:36:ILE:HA	1.86	0.41
1:AJ:106:PHE:CD1	1:AJ:106:PHE:N	2.88	0.41
1:AM:173:PHE:O	1:AM:206:TYR:HA	2.20	0.41
1:AO:40:PHE:HD1	1:AO:246:VAL:HG12	1.86	0.41
1:AP:16:TYR:CE2	1:AP:164:LEU:HG	2.55	0.41
1:AP:41:LYS:HE3	1:AP:41:LYS:HB3	1.76	0.41
1:AQ:145:ARG:HB2	1:AQ:148:TYR:HD1	1.85	0.41
1:AR:16:TYR:CD1	1:AR:223:LYS:HG3	2.56	0.41
1:AS:131:ILE:HG13	1:AZ:43:ILE:HD12	2.02	0.41
1:AT:40:PHE:HD1	1:AT:246:VAL:HG12	1.86	0.41
1:AT:210:VAL:HG12	1:AT:212:GLU:OE2	2.21	0.41
1:AU:43:ILE:HD12	1:AW:131:ILE:HG13	2.03	0.41
1:B:40:PHE:CZ	1:B:158:PHE:HB2	2.49	0.41
1:C:173:PHE:HE1	1:C:175:ARG:HE	1.67	0.41
1:E:80:LEU:O	1:E:81:ARG:HG3	2.20	0.41
1:H:24:THR:HG22	1:H:218:ILE:HG13	2.01	0.41
1:H:36:ILE:HD13	1:H:36:ILE:HA	1.89	0.41
1:H:164:LEU:O	1:H:219:VAL:HA	2.21	0.41
1:L:72:ASP:HA	1:L:125:THR:O	2.20	0.41
1:M:80:LEU:O	1:M:81:ARG:HG3	2.21	0.41
1:M:130:GLU:O	1:M:134:ARG:HG3	2.20	0.41
1:N:115:SER:OG	1:N:174:GLU:HB2	2.20	0.41
1:N:168:LYS:HB2	1:N:168:LYS:HE3	1.71	0.41
1:O:29:LEU:HD11	1:O:68:ILE:HD12	2.03	0.41
1:Q:40:PHE:HZ	1:Q:158:PHE:CG	2.39	0.41
1:Q:215:ASP:OD2	1:Q:216:GLU:N	2.42	0.41
1:R:224:LEU:HD11	1:R:246:VAL:HG11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:43:ILE:HD12	1:Y:131:ILE:HG13	2.03	0.41
1:X:79:ASP:O	1:X:80:LEU:HD12	2.20	0.41
1:Z:162:SER:HB2	1:Z:223:LYS:HB2	2.02	0.41
1:Z:169:MET:HE2	1:Z:169:MET:HB3	1.95	0.41
1:a:12:LYS:HA	1:a:12:LYS:HD3	1.83	0.41
1:c:210:VAL:HG12	1:c:212:GLU:OE2	2.20	0.41
1:f:72:ASP:HA	1:f:125:THR:O	2.21	0.41
1:f:208:ARG:HG2	1:f:210:VAL:CG2	2.51	0.41
1:j:215:ASP:CG	1:j:216:GLU:N	2.79	0.41
1:k:115:SER:OG	1:k:174:GLU:HB2	2.20	0.41
1:l:164:LEU:O	1:l:219:VAL:HA	2.19	0.41
1:m:44:TRP:CE2	1:n:127:ASP:HB3	2.56	0.41
1:m:208:ARG:HE	1:m:210:VAL:HB	1.86	0.41
1:o:106:PHE:N	1:o:106:PHE:CD1	2.88	0.41
1:q:79:ASP:HB3	1:q:81:ARG:NH2	2.35	0.41
1:q:162:SER:HB2	1:q:223:LYS:HB2	2.02	0.41
1:r:36:ILE:HD13	1:r:36:ILE:HA	1.86	0.41
1:s:208:ARG:HG2	1:s:210:VAL:HG22	2.01	0.41
1:t:123:ILE:N	1:t:123:ILE:HD12	2.35	0.41
1:w:16:TYR:HD1	1:w:223:LYS:HG3	1.86	0.41
1:1:113:SER:OG	1:1:176:LYS:HB2	2.20	0.41
1:2:40:PHE:HZ	1:2:158:PHE:CB	2.32	0.41
1:4:145:ARG:HB2	1:4:148:TYR:HD1	1.85	0.41
1:5:16:TYR:CD1	1:5:223:LYS:HG3	2.55	0.41
1:5:115:SER:OG	1:5:174:GLU:HB2	2.20	0.41
1:7:79:ASP:HB3	1:7:81:ARG:NH2	2.34	0.41
1:7:152:ILE:HD12	1:7:227:LEU:CD2	2.51	0.41
1:AB:40:PHE:HD1	1:AB:246:VAL:HG12	1.85	0.41
1:AC:24:THR:HG22	1:AC:218:ILE:HG13	2.01	0.41
1:AG:162:SER:HB2	1:AG:223:LYS:HB2	2.02	0.41
1:AK:224:LEU:HD11	1:AK:246:VAL:HG11	2.03	0.41
1:AO:162:SER:HB2	1:AO:223:LYS:HB2	2.03	0.41
1:AP:91:ALA:O	1:AP:105:SER:HA	2.20	0.41
1:AR:146:GLU:CD	1:AR:146:GLU:H	2.28	0.41
1:AS:80:LEU:O	1:AS:81:ARG:HG3	2.21	0.41
1:AV:44:TRP:H	1:AV:44:TRP:HE3	1.67	0.41
1:AY:86:LEU:O	1:Ab:199:SER:HA	2.20	0.41
1:Ac:79:ASP:HB3	1:Ac:81:ARG:NH2	2.35	0.41
1:Ac:86:LEU:O	1:Ad:199:SER:HA	2.21	0.41
1:B:73:GLY:C	1:B:74:GLN:HG2	2.46	0.41
1:D:118:PHE:CE1	1:D:120:ILE:HD11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:166:ALA:O	1:F:218:ILE:HG22	2.20	0.41
1:G:32:TYR:HB3	1:G:40:PHE:CE1	2.56	0.41
1:G:168:LYS:HA	1:G:168:LYS:HD3	1.82	0.41
1:I:72:ASP:HA	1:I:125:THR:O	2.21	0.41
1:R:44:TRP:CZ2	1:W:127:ASP:HB3	2.56	0.41
1:U:215:ASP:CG	1:U:216:GLU:N	2.78	0.41
1:V:118:PHE:CE1	1:V:120:ILE:HD11	2.55	0.41
1:W:40:PHE:HE1	1:W:224:LEU:HD13	1.85	0.41
1:W:123:ILE:HD12	1:W:123:ILE:N	2.35	0.41
1:X:75:GLY:O	1:X:76:ILE:HG12	2.19	0.41
1:X:124:ILE:HG12	1:X:165:ARG:HB2	2.03	0.41
1:X:168:LYS:HB2	1:X:168:LYS:HE3	1.70	0.41
1:b:146:GLU:OE1	1:b:146:GLU:N	2.52	0.41
1:l:77:ASP:HB3	1:l:120:ILE:HB	2.02	0.41
1:o:80:LEU:O	1:o:81:ARG:HG3	2.20	0.41
1:o:124:ILE:HG12	1:o:165:ARG:HB2	2.02	0.41
1:r:183:VAL:HB	1:r:197:LEU:HG	2.03	0.41
1:u:16:TYR:HD1	1:u:223:LYS:HG3	1.86	0.41
1:u:73:GLY:C	1:u:74:GLN:HG2	2.45	0.41
1:v:115:SER:OG	1:v:174:GLU:HB2	2.21	0.41
1:y:16:TYR:CD1	1:y:223:LYS:HG3	2.55	0.41
1:1:77:ASP:HB3	1:1:120:ILE:HB	2.02	0.41
1:3:86:LEU:O	1:4:199:SER:HA	2.21	0.41
1:4:172:GLN:HG2	1:4:208:ARG:HB2	2.03	0.41
1:4:183:VAL:HB	1:4:197:LEU:HG	2.02	0.41
1:7:73:GLY:C	1:7:74:GLN:HG2	2.46	0.41
1:9:181:LEU:HD11	1:9:183:VAL:HG23	2.01	0.41
1:AB:164:LEU:O	1:AB:219:VAL:HA	2.21	0.41
1:AC:16:TYR:CD1	1:AC:223:LYS:HG3	2.56	0.41
1:AC:164:LEU:O	1:AC:219:VAL:HA	2.21	0.41
1:AF:23:LYS:HD2	1:AF:42:ARG:HH21	1.85	0.41
1:AG:16:TYR:HD1	1:AG:223:LYS:HG3	1.85	0.41
1:AG:73:GLY:C	1:AG:74:GLN:HG2	2.46	0.41
1:AI:16:TYR:HD1	1:AI:223:LYS:HG3	1.86	0.41
1:AM:162:SER:HB2	1:AM:223:LYS:HB2	2.02	0.41
1:AO:79:ASP:C	1:AO:80:LEU:HD12	2.46	0.41
1:AQ:79:ASP:O	1:AQ:80:LEU:HD12	2.21	0.41
1:AS:32:TYR:HB3	1:AS:40:PHE:CE1	2.56	0.41
1:AU:111:GLU:HB2	1:AU:178:LYS:HB2	2.03	0.41
1:AW:169:MET:HB2	1:AW:211:PHE:HB3	2.02	0.41
1:AX:181:LEU:HD11	1:AX:183:VAL:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:ASP:HB3	1:B:120:ILE:HB	2.02	0.41
1:D:16:TYR:CD1	1:D:223:LYS:HG3	2.55	0.41
1:J:141:GLN:HB2	1:J:235:LEU:HB3	2.03	0.41
1:J:183:VAL:HB	1:J:197:LEU:HG	2.02	0.41
1:K:40:PHE:CZ	1:K:158:PHE:HB2	2.50	0.41
1:M:29:LEU:HD11	1:M:68:ILE:HD12	2.02	0.41
1:Y:72:ASP:HA	1:Y:125:THR:O	2.21	0.41
1:d:36:ILE:HD13	1:d:36:ILE:HA	1.94	0.41
1:d:174:GLU:HA	1:d:205:THR:O	2.21	0.41
1:f:130:GLU:O	1:f:134:ARG:HG3	2.21	0.41
1:h:79:ASP:O	1:h:80:LEU:HD12	2.19	0.41
1:k:146:GLU:H	1:k:146:GLU:CD	2.28	0.41
1:l:118:PHE:CE1	1:l:120:ILE:HD11	2.56	0.41
1:m:36:ILE:HD13	1:m:36:ILE:HA	1.91	0.41
1:n:72:ASP:HA	1:n:125:THR:O	2.21	0.41
1:q:40:PHE:CZ	1:q:158:PHE:HB2	2.50	0.41
1:s:118:PHE:CE1	1:s:120:ILE:HD11	2.56	0.41
1:t:104:PRO:HB3	1:t:185:VAL:HG12	2.03	0.41
1:u:79:ASP:C	1:u:80:LEU:HD12	2.46	0.41
1:x:32:TYR:CZ	1:x:42:ARG:HD3	2.56	0.41
1:1:208:ARG:HE	1:1:210:VAL:HG22	1.86	0.41
1:2:80:LEU:O	1:2:81:ARG:HG3	2.21	0.41
1:4:118:PHE:CE1	1:4:120:ILE:HD11	2.55	0.41
1:6:29:LEU:HD11	1:6:68:ILE:HD12	2.02	0.41
1:6:148:TYR:HA	1:6:151:GLU:HG3	2.02	0.41
1:9:86:LEU:O	1:AA:199:SER:HA	2.20	0.41
1:0:130:GLU:O	1:0:134:ARG:HG3	2.21	0.41
1:AF:106:PHE:HA	1:AF:183:VAL:HG22	2.02	0.41
1:AH:11:LEU:HD23	1:AH:11:LEU:HA	1.86	0.41
1:AH:77:ASP:HB3	1:AH:120:ILE:HB	2.03	0.41
1:AJ:16:TYR:HD1	1:AJ:223:LYS:HG3	1.86	0.41
1:AK:166:ALA:HB3	1:AK:169:MET:HG3	2.02	0.41
1:AL:72:ASP:HA	1:AL:125:THR:O	2.21	0.41
1:AN:145:ARG:HB2	1:AN:148:TYR:HD1	1.85	0.41
1:AW:72:ASP:HA	1:AW:125:THR:O	2.21	0.41
1:AW:118:PHE:CE1	1:AW:120:ILE:HD11	2.55	0.41
1:AZ:64:ILE:HD12	1:AZ:136:TRP:HZ2	1.86	0.41
1:AZ:124:ILE:HG12	1:AZ:165:ARG:HB2	2.01	0.41
1:C:36:ILE:HD13	1:C:36:ILE:HA	1.89	0.41
1:D:75:GLY:O	1:D:76:ILE:HG12	2.21	0.41
1:D:104:PRO:HB3	1:D:185:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:208:ARG:HE	1:D:210:VAL:HG21	1.86	0.41
1:E:199:SER:HA	1:F:86:LEU:O	2.21	0.41
1:E:215:ASP:CG	1:E:216:GLU:H	2.26	0.41
1:H:169:MET:HB2	1:H:211:PHE:HB3	2.03	0.41
1:I:115:SER:OG	1:I:174:GLU:HB2	2.21	0.41
1:K:130:GLU:O	1:K:134:ARG:HG3	2.20	0.41
1:L:79:ASP:C	1:L:80:LEU:HD12	2.46	0.41
1:M:210:VAL:HG12	1:M:212:GLU:OE1	2.21	0.41
1:N:73:GLY:C	1:N:74:GLN:HG2	2.46	0.41
1:O:16:TYR:HD1	1:O:223:LYS:HG3	1.84	0.41
1:O:122:GLU:HB2	1:O:167:LYS:HB2	2.03	0.41
1:O:199:SER:HA	1:r:86:LEU:O	2.21	0.41
1:P:16:TYR:HD1	1:P:223:LYS:HG3	1.85	0.41
1:P:106:PHE:N	1:P:106:PHE:CD2	2.86	0.41
1:Q:118:PHE:CE1	1:Q:120:ILE:HD11	2.56	0.41
1:T:104:PRO:HB3	1:T:185:VAL:HG12	2.03	0.41
1:U:164:LEU:O	1:U:219:VAL:HA	2.21	0.41
1:W:104:PRO:HB3	1:W:185:VAL:HG12	2.03	0.41
1:X:44:TRP:CZ2	1:Y:127:ASP:HB3	2.56	0.41
1:Z:73:GLY:C	1:Z:74:GLN:HG2	2.46	0.41
1:b:16:TYR:HD1	1:b:223:LYS:HG3	1.85	0.41
1:b:199:SER:HA	1:c:86:LEU:O	2.20	0.41
1:c:106:PHE:HA	1:c:183:VAL:HG22	2.02	0.41
1:d:162:SER:HB2	1:d:223:LYS:HB2	2.03	0.41
1:d:164:LEU:O	1:d:219:VAL:HA	2.21	0.41
1:d:183:VAL:HB	1:d:197:LEU:HG	2.03	0.41
1:i:29:LEU:HD11	1:i:68:ILE:HD12	2.03	0.41
1:i:80:LEU:O	1:i:81:ARG:HG3	2.20	0.41
1:i:115:SER:OG	1:i:174:GLU:HB2	2.21	0.41
1:k:44:TRP:CE2	1:m:127:ASP:HB3	2.56	0.41
1:l:20:ALA:HB3	1:l:247:LEU:HB3	2.02	0.41
1:m:16:TYR:HD1	1:m:223:LYS:HG3	1.86	0.41
1:o:79:ASP:HB3	1:o:81:ARG:NH2	2.35	0.41
1:s:16:TYR:HD1	1:s:223:LYS:HG3	1.86	0.41
1:t:40:PHE:HZ	1:t:158:PHE:CG	2.39	0.41
1:u:93:LYS:HG2	1:3:193:VAL:HG22	2.03	0.41
1:v:16:TYR:HD1	1:v:223:LYS:HG3	1.85	0.41
1:x:104:PRO:HB3	1:x:185:VAL:HG12	2.02	0.41
1:x:211:PHE:CE2	1:x:218:ILE:HB	2.56	0.41
1:2:79:ASP:C	1:2:80:LEU:HD12	2.46	0.41
1:2:115:SER:OG	1:2:174:GLU:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:80:LEU:O	1:3:81:ARG:HG3	2.21	0.41
1:4:79:ASP:HB2	1:4:118:PHE:HB3	2.02	0.41
1:4:79:ASP:O	1:4:80:LEU:HD12	2.21	0.41
1:4:86:LEU:O	1:5:199:SER:HA	2.20	0.41
1:5:211:PHE:CE2	1:5:218:ILE:HB	2.56	0.41
1:6:80:LEU:O	1:6:81:ARG:HG3	2.21	0.41
1:6:86:LEU:O	1:AC:199:SER:HA	2.20	0.41
1:7:43:ILE:HD12	1:8:131:ILE:HG13	2.02	0.41
1:8:36:ILE:HD13	1:8:36:ILE:HA	1.91	0.41
1:9:44:TRP:HE3	1:9:44:TRP:H	1.68	0.41
1:AA:23:LYS:HD2	1:AA:42:ARG:NH2	2.36	0.41
1:AA:40:PHE:HZ	1:AA:158:PHE:CG	2.39	0.41
1:AA:69:GLY:O	1:AA:70:LEU:HD12	2.20	0.41
1:AC:64:ILE:HD12	1:AC:136:TRP:HZ2	1.86	0.41
1:AD:80:LEU:O	1:AD:81:ARG:HG3	2.20	0.41
1:AE:16:TYR:CD1	1:AE:223:LYS:HG3	2.56	0.41
1:AE:181:LEU:HD11	1:AE:183:VAL:HG23	2.02	0.41
1:AH:73:GLY:C	1:AH:74:GLN:HG2	2.45	0.41
1:AI:64:ILE:HD12	1:AI:136:TRP:HZ2	1.86	0.41
1:AI:193:VAL:HG22	1:AJ:93:LYS:HG2	2.02	0.41
1:AJ:168:LYS:HE3	1:AJ:168:LYS:HB2	1.69	0.41
1:AK:43:ILE:HD12	1:AL:131:ILE:HG13	2.02	0.41
1:AK:199:SER:HA	1:AL:86:LEU:O	2.21	0.41
1:AL:16:TYR:HD1	1:AL:223:LYS:HG3	1.86	0.41
1:AM:16:TYR:CD1	1:AM:223:LYS:HG3	2.56	0.41
1:AM:64:ILE:HD12	1:AM:136:TRP:HZ2	1.85	0.41
1:AM:72:ASP:HA	1:AM:125:THR:O	2.20	0.41
1:AM:183:VAL:HB	1:AM:197:LEU:HG	2.03	0.41
1:AN:43:ILE:HD12	1:AO:131:ILE:HG13	2.01	0.41
1:AN:183:VAL:HB	1:AN:197:LEU:HG	2.02	0.41
1:AO:80:LEU:O	1:AO:81:ARG:HG3	2.20	0.41
1:AO:115:SER:OG	1:AO:174:GLU:HB2	2.21	0.41
1:AP:104:PRO:HB3	1:AP:185:VAL:HG12	2.03	0.41
1:AQ:215:ASP:CG	1:AQ:216:GLU:N	2.78	0.41
1:AR:73:GLY:C	1:AR:74:GLN:HG2	2.46	0.41
1:AT:183:VAL:HB	1:AT:197:LEU:HG	2.03	0.41
1:AT:213:THR:HA	1:AT:214:PRO:HD3	1.96	0.41
1:AU:173:PHE:O	1:AU:206:TYR:HA	2.21	0.41
1:AU:224:LEU:HD11	1:AU:246:VAL:HG11	2.02	0.41
1:AV:40:PHE:CZ	1:AV:158:PHE:CG	3.08	0.41
1:AV:170:ARG:HB3	1:AV:170:ARG:HH11	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:181:LEU:HD11	1:AV:183:VAL:HG23	2.02	0.41
1:AX:16:TYR:HD1	1:AX:223:LYS:HG3	1.86	0.41
1:AZ:79:ASP:O	1:AZ:80:LEU:HD12	2.21	0.41
1:AZ:106:PHE:HA	1:AZ:183:VAL:HG22	2.03	0.41
1:Ab:181:LEU:HD11	1:Ab:183:VAL:HG23	2.03	0.41
1:B:72:ASP:HA	1:B:125:THR:O	2.21	0.41
1:C:199:SER:HA	1:D:86:LEU:O	2.21	0.41
1:D:40:PHE:HD2	1:D:246:VAL:HG12	1.86	0.41
1:M:162:SER:HB2	1:M:223:LYS:HB2	2.03	0.41
1:O:73:GLY:C	1:O:74:GLN:HG2	2.45	0.41
1:Q:16:TYR:CE2	1:Q:164:LEU:HG	2.56	0.41
1:T:12:LYS:HA	1:T:12:LYS:HD3	1.87	0.41
1:U:106:PHE:HA	1:U:183:VAL:HG22	2.01	0.41
1:W:32:TYR:CZ	1:W:42:ARG:HD3	2.56	0.41
1:Z:181:LEU:HD11	1:Z:183:VAL:HG23	2.02	0.41
1:a:16:TYR:HD1	1:a:223:LYS:HG3	1.84	0.41
1:e:104:PRO:HB3	1:e:185:VAL:HG12	2.03	0.41
1:f:93:LYS:HG2	1:g:193:VAL:HG22	2.02	0.41
1:i:40:PHE:HZ	1:i:158:PHE:CB	2.33	0.41
1:j:32:TYR:HB3	1:j:40:PHE:CE1	2.57	0.41
1:j:75:GLY:O	1:j:76:ILE:HG12	2.21	0.41
1:j:118:PHE:CE1	1:j:120:ILE:HD11	2.56	0.41
1:j:210:VAL:HG12	1:j:212:GLU:OE1	2.21	0.41
1:n:16:TYR:CE2	1:n:164:LEU:HG	2.56	0.41
1:p:166:ALA:HB3	1:p:169:MET:HG3	2.03	0.41
1:s:32:TYR:CZ	1:s:42:ARG:HD3	2.56	0.41
1:w:80:LEU:O	1:w:81:ARG:HG3	2.20	0.41
1:x:16:TYR:CE2	1:x:164:LEU:HG	2.56	0.41
1:2:40:PHE:HD1	1:2:246:VAL:HG12	1.86	0.41
1:3:162:SER:HB2	1:3:223:LYS:HB2	2.03	0.41
1:5:183:VAL:HB	1:5:197:LEU:HG	2.02	0.41
1:6:215:ASP:CG	1:6:216:GLU:N	2.79	0.41
1:9:32:TYR:HE2	1:9:247:LEU:HD12	1.86	0.41
1:9:32:TYR:HB3	1:9:40:PHE:CD2	2.56	0.41
1:9:77:ASP:HB3	1:9:120:ILE:HB	2.02	0.41
1:AB:59:LEU:O	1:AB:145:ARG:HG3	2.21	0.41
1:AE:19:VAL:HB	1:AE:247:LEU:HD12	2.02	0.41
1:AF:131:ILE:HG13	1:AG:43:ILE:HD12	2.03	0.41
1:AG:85:SER:C	1:AG:86:LEU:HD23	2.46	0.41
1:AG:181:LEU:HD11	1:AG:183:VAL:HG23	2.03	0.41
1:AO:40:PHE:HZ	1:AO:158:PHE:CB	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AQ:72:ASP:HA	1:AQ:125:THR:O	2.20	0.41
1:AR:19:VAL:HB	1:AR:247:LEU:HD12	2.03	0.41
1:AR:79:ASP:HB3	1:AR:81:ARG:NH2	2.35	0.41
1:AV:141:GLN:HB2	1:AV:235:LEU:HB3	2.02	0.41
1:AY:16:TYR:CD1	1:AY:223:LYS:HG3	2.56	0.41
1:AZ:91:ALA:O	1:AZ:105:SER:HA	2.21	0.41
1:Ab:145:ARG:HB2	1:Ab:148:TYR:HD1	1.86	0.41
1:Ac:72:ASP:HA	1:Ac:125:THR:O	2.20	0.41
1:Ad:64:ILE:HD12	1:Ad:136:TRP:HZ2	1.85	0.41
1:Ad:173:PHE:HE1	1:Ad:175:ARG:HE	1.67	0.41
1:D:224:LEU:HD12	1:D:243:PHE:CZ	2.55	0.40
1:E:164:LEU:O	1:E:219:VAL:HA	2.21	0.40
1:F:208:ARG:HE	1:F:210:VAL:CG2	2.34	0.40
1:G:204:SER:N	1:H:81:ARG:HH21	2.19	0.40
1:L:113:SER:OG	1:L:176:LYS:HB2	2.21	0.40
1:N:173:PHE:HE1	1:N:175:ARG:HE	1.68	0.40
1:P:118:PHE:CE1	1:P:120:ILE:HD11	2.57	0.40
1:R:12:LYS:HA	1:R:12:LYS:HD3	1.84	0.40
1:V:152:ILE:HD12	1:V:227:LEU:HG	2.03	0.40
1:X:208:ARG:HG2	1:X:210:VAL:HG22	2.01	0.40
1:a:104:PRO:HB3	1:a:185:VAL:HG12	2.02	0.40
1:d:12:LYS:HA	1:d:12:LYS:HD3	1.86	0.40
1:e:30:HIS:CE1	1:e:42:ARG:HH11	2.39	0.40
1:e:169:MET:HB2	1:e:211:PHE:HB3	2.03	0.40
1:f:115:SER:OG	1:f:174:GLU:HB2	2.21	0.40
1:j:80:LEU:O	1:j:81:ARG:HG3	2.21	0.40
1:l:73:GLY:C	1:l:74:GLN:HG2	2.45	0.40
1:n:40:PHE:CZ	1:n:158:PHE:CG	3.09	0.40
1:p:145:ARG:HB2	1:p:148:TYR:HD1	1.86	0.40
1:z:104:PRO:HB3	1:z:185:VAL:HG12	2.04	0.40
1:6:120:ILE:HG22	1:6:123:ILE:HD11	2.02	0.40
1:6:208:ARG:HE	1:6:210:VAL:HG21	1.86	0.40
1:8:164:LEU:O	1:8:219:VAL:HA	2.20	0.40
1:9:73:GLY:C	1:9:74:GLN:HG2	2.46	0.40
1:9:85:SER:O	1:9:86:LEU:HD23	2.21	0.40
1:9:118:PHE:CE1	1:9:120:ILE:HD11	2.56	0.40
1:AB:118:PHE:CE1	1:AB:120:ILE:HD11	2.57	0.40
1:AB:224:LEU:HD12	1:AB:243:PHE:CZ	2.56	0.40
1:AC:124:ILE:HG12	1:AC:165:ARG:HB2	2.02	0.40
1:AD:79:ASP:HB2	1:AD:118:PHE:HB3	2.03	0.40
1:AE:162:SER:HB2	1:AE:223:LYS:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:16:TYR:HD1	1:AF:223:LYS:HG3	1.86	0.40
1:AF:40:PHE:HD2	1:AF:246:VAL:HG12	1.86	0.40
1:AF:91:ALA:O	1:AF:105:SER:HA	2.20	0.40
1:AK:16:TYR:CE2	1:AK:164:LEU:HG	2.56	0.40
1:AK:32:TYR:CZ	1:AK:42:ARG:HD3	2.56	0.40
1:AL:79:ASP:O	1:AL:80:LEU:HD12	2.21	0.40
1:AM:148:TYR:O	1:AM:152:ILE:HG12	2.21	0.40
1:AO:77:ASP:HB3	1:AO:120:ILE:HB	2.03	0.40
1:AQ:118:PHE:CE1	1:AQ:120:ILE:HD11	2.56	0.40
1:AR:42:ARG:CZ	1:AR:44:TRP:NE1	2.84	0.40
1:AS:162:SER:HB2	1:AS:223:LYS:HB2	2.03	0.40
1:AV:32:TYR:HB3	1:AV:40:PHE:CD2	2.56	0.40
1:AV:72:ASP:HA	1:AV:125:THR:O	2.21	0.40
1:AY:79:ASP:HB3	1:AY:81:ARG:NH2	2.35	0.40
1:AY:104:PRO:HB3	1:AY:185:VAL:HG12	2.02	0.40
1:AY:208:ARG:HE	1:AY:210:VAL:CG2	2.35	0.40
1:AZ:16:TYR:CD1	1:AZ:223:LYS:HG3	2.56	0.40
1:AZ:131:ILE:HG13	1:Aa:43:ILE:HD12	2.03	0.40
1:Aa:64:ILE:HD12	1:Aa:136:TRP:HZ2	1.86	0.40
1:Aa:118:PHE:CE1	1:Aa:120:ILE:HD11	2.56	0.40
1:A:43:ILE:HD12	1:B:131:ILE:HG13	2.02	0.40
1:A:152:ILE:HD12	1:A:227:LEU:HG	2.04	0.40
1:C:104:PRO:HB3	1:C:185:VAL:HG12	2.02	0.40
1:E:173:PHE:HE1	1:E:175:ARG:HE	1.67	0.40
1:G:64:ILE:HD12	1:G:136:TRP:HZ2	1.85	0.40
1:G:162:SER:HB2	1:G:223:LYS:HB2	2.02	0.40
1:J:115:SER:OG	1:J:174:GLU:HB2	2.21	0.40
1:L:40:PHE:HD1	1:L:246:VAL:HG12	1.86	0.40
1:L:115:SER:OG	1:L:174:GLU:HB2	2.20	0.40
1:M:75:GLY:O	1:M:76:ILE:HG12	2.21	0.40
1:M:215:ASP:CG	1:M:216:GLU:N	2.79	0.40
1:Q:40:PHE:CZ	1:Q:158:PHE:CG	3.09	0.40
1:Q:117:ILE:HB	1:Q:172:GLN:HB2	2.03	0.40
1:U:59:LEU:O	1:U:145:ARG:HG3	2.21	0.40
1:d:40:PHE:CE1	1:d:158:PHE:HB2	2.56	0.40
1:i:166:ALA:HB3	1:i:169:MET:HG3	2.03	0.40
1:j:162:SER:HB2	1:j:223:LYS:HB2	2.02	0.40
1:p:40:PHE:CZ	1:p:158:PHE:HB2	2.44	0.40
1:s:86:LEU:O	1:t:199:SER:HA	2.22	0.40
1:u:80:LEU:O	1:u:81:ARG:HG3	2.21	0.40
1:x:183:VAL:HB	1:x:197:LEU:HG	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:224:LEU:HD11	1:x:246:VAL:HG11	2.03	0.40
1:4:91:ALA:O	1:4:105:SER:HA	2.21	0.40
1:5:19:VAL:HB	1:5:247:LEU:HD12	2.04	0.40
1:8:152:ILE:HD12	1:8:227:LEU:HD22	2.04	0.40
1:9:12:LYS:HA	1:9:12:LYS:HD3	1.82	0.40
1:0:72:ASP:HA	1:0:125:THR:O	2.21	0.40
1:AD:79:ASP:O	1:AD:80:LEU:HD12	2.20	0.40
1:AE:56:ILE:HD11	1:AE:137:LEU:HD21	2.03	0.40
1:AG:228:PHE:HD1	1:AG:229:PHE:H	1.68	0.40
1:AK:123:ILE:N	1:AK:123:ILE:HD12	2.35	0.40
1:AM:80:LEU:O	1:AM:81:ARG:HG3	2.21	0.40
1:AP:211:PHE:CE1	1:AP:218:ILE:HD12	2.56	0.40
1:AT:79:ASP:O	1:AT:80:LEU:HD12	2.20	0.40
1:AU:206:TYR:OH	1:AU:208:ARG:HD2	2.21	0.40
1:AX:118:PHE:CE1	1:AX:120:ILE:HD11	2.56	0.40
1:AZ:168:LYS:HE3	1:AZ:168:LYS:HB2	1.70	0.40
1:Ad:85:SER:C	1:Ad:86:LEU:HD23	2.46	0.40
1:C:73:GLY:C	1:C:74:GLN:HG2	2.46	0.40
1:E:43:ILE:HD12	1:F:131:ILE:HG13	2.03	0.40
1:I:31:ILE:HG13	1:I:59:LEU:HD21	2.03	0.40
1:M:79:ASP:C	1:M:80:LEU:HD12	2.47	0.40
1:P:43:ILE:HD12	1:Q:131:ILE:HG13	2.03	0.40
1:T:168:LYS:HB2	1:T:168:LYS:HE3	1.69	0.40
1:V:164:LEU:O	1:V:219:VAL:HA	2.21	0.40
1:Z:79:ASP:C	1:Z:80:LEU:HD12	2.46	0.40
1:b:215:ASP:CG	1:b:216:GLU:H	2.26	0.40
1:g:32:TYR:CZ	1:g:42:ARG:HD3	2.57	0.40
1:g:79:ASP:HB3	1:g:81:ARG:NH2	2.36	0.40
1:g:80:LEU:O	1:g:81:ARG:HG3	2.21	0.40
1:j:91:ALA:O	1:j:105:SER:HA	2.21	0.40
1:j:120:ILE:HG22	1:j:123:ILE:HD11	2.03	0.40
1:m:215:ASP:CG	1:m:216:GLU:N	2.79	0.40
1:n:80:LEU:O	1:n:81:ARG:HG3	2.21	0.40
1:n:215:ASP:CG	1:n:216:GLU:H	2.26	0.40
1:o:168:LYS:HE3	1:o:168:LYS:HB2	1.69	0.40
1:p:16:TYR:HD1	1:p:223:LYS:HG3	1.85	0.40
1:q:16:TYR:CD1	1:q:223:LYS:HG3	2.56	0.40
1:q:215:ASP:OD1	1:q:216:GLU:N	2.44	0.40
1:r:73:GLY:C	1:r:74:GLN:HG2	2.45	0.40
1:t:16:TYR:CE2	1:t:164:LEU:HG	2.57	0.40
1:u:111:GLU:HB2	1:u:178:LYS:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:x:23:LYS:HD2	1:x:42:ARG:NH2	2.37	0.40
1:z:206:TYR:OH	1:z:208:ARG:HD3	2.21	0.40
1:2:68:ILE:HD13	1:2:133:LEU:HD13	2.04	0.40
1:3:41:LYS:HB3	1:3:41:LYS:HE3	1.77	0.40
1:4:16:TYR:HD1	1:4:223:LYS:HG3	1.86	0.40
1:5:16:TYR:CE2	1:5:164:LEU:HG	2.55	0.40
1:0:43:ILE:HD12	1:AA:131:ILE:HG13	2.03	0.40
1:AB:86:LEU:O	1:AE:199:SER:HA	2.21	0.40
1:AB:104:PRO:HB3	1:AB:185:VAL:HG12	2.02	0.40
1:AC:131:ILE:HG13	1:AD:43:ILE:HD12	2.04	0.40
1:AG:80:LEU:O	1:AG:81:ARG:HG3	2.20	0.40
1:AM:104:PRO:HB3	1:AM:185:VAL:HG12	2.02	0.40
1:AM:215:ASP:CG	1:AM:216:GLU:N	2.80	0.40
1:AO:29:LEU:HD11	1:AO:68:ILE:HD12	2.03	0.40
1:AP:24:THR:HG22	1:AP:218:ILE:HG13	2.01	0.40
1:AP:118:PHE:CE1	1:AP:120:ILE:HD11	2.57	0.40
1:AP:162:SER:HB2	1:AP:223:LYS:HB2	2.02	0.40
1:AQ:91:ALA:O	1:AQ:105:SER:HA	2.21	0.40
1:AR:40:PHE:HZ	1:AR:158:PHE:CG	2.39	0.40
1:AU:80:LEU:O	1:AU:81:ARG:HG3	2.21	0.40
1:AY:224:LEU:HD12	1:AY:243:PHE:CZ	2.56	0.40
1:Ab:64:ILE:HD12	1:Ab:136:TRP:HZ2	1.86	0.40
1:H:104:PRO:HB3	1:H:185:VAL:HG12	2.02	0.40
1:L:40:PHE:HZ	1:L:158:PHE:CG	2.38	0.40
1:L:79:ASP:O	1:L:80:LEU:HD12	2.22	0.40
1:O:20:ALA:HB3	1:O:247:LEU:HB3	2.03	0.40
1:X:199:SER:HA	1:Y:86:LEU:O	2.21	0.40
1:Z:115:SER:OG	1:Z:174:GLU:HB2	2.21	0.40
1:Z:199:SER:HA	1:a:86:LEU:O	2.21	0.40
1:a:40:PHE:HD2	1:a:246:VAL:HG12	1.86	0.40
1:b:80:LEU:O	1:b:81:ARG:HG3	2.20	0.40
1:c:36:ILE:HD13	1:c:36:ILE:HA	1.86	0.40
1:g:173:PHE:O	1:g:206:TYR:HA	2.22	0.40
1:j:79:ASP:O	1:j:80:LEU:HD12	2.20	0.40
1:m:121:GLU:HG2	1:m:122:GLU:OE1	2.20	0.40
1:q:16:TYR:HE1	1:q:162:SER:HB2	1.86	0.40
1:u:79:ASP:O	1:u:80:LEU:HD12	2.21	0.40
1:u:118:PHE:CE1	1:u:120:ILE:HD11	2.57	0.40
1:v:40:PHE:HD1	1:v:246:VAL:HG12	1.87	0.40
1:y:164:LEU:O	1:y:219:VAL:HA	2.21	0.40
1:z:12:LYS:HA	1:z:12:LYS:HD3	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:z:124:ILE:HG12	1:z:165:ARG:HB2	2.04	0.40
1:5:40:PHE:HZ	1:5:158:PHE:CG	2.39	0.40
1:5:224:LEU:HD11	1:5:246:VAL:HG11	2.03	0.40
1:8:118:PHE:CE1	1:8:120:ILE:HD11	2.56	0.40
1:8:152:ILE:HD12	1:8:227:LEU:CD2	2.52	0.40
1:0:208:ARG:HE	1:0:210:VAL:CG2	2.34	0.40
1:AC:30:HIS:CE1	1:AC:42:ARG:HH11	2.39	0.40
1:AD:164:LEU:O	1:AD:219:VAL:HA	2.22	0.40
1:AD:174:GLU:HA	1:AD:205:THR:O	2.22	0.40
1:AG:64:ILE:HD12	1:AG:136:TRP:HZ2	1.85	0.40
1:AI:227:LEU:HD11	1:AI:235:LEU:HD11	2.04	0.40
1:AL:106:PHE:HA	1:AL:183:VAL:HG22	2.02	0.40
1:AM:16:TYR:HE1	1:AM:162:SER:HB2	1.87	0.40
1:AM:206:TYR:OH	1:AM:208:ARG:HD3	2.21	0.40
1:AN:91:ALA:O	1:AN:105:SER:HA	2.21	0.40
1:AP:131:ILE:HG13	1:AQ:43:ILE:HD12	2.04	0.40
1:AP:215:ASP:OD2	1:AP:216:GLU:N	2.42	0.40
1:AS:40:PHE:CZ	1:AS:158:PHE:CG	3.09	0.40
1:AU:79:ASP:HB3	1:AU:81:ARG:NH2	2.36	0.40
1:AW:12:LYS:HD3	1:AW:12:LYS:HA	1.81	0.40
1:AY:11:LEU:HD11	1:AY:220:PHE:CD1	2.57	0.40
1:AZ:72:ASP:HA	1:AZ:125:THR:O	2.21	0.40
1:AZ:169:MET:HE2	1:AZ:169:MET:HB3	1.95	0.40
1:Aa:79:ASP:O	1:Aa:80:LEU:HD12	2.22	0.40
1:Ab:174:GLU:HA	1:Ab:205:THR:O	2.22	0.40
1:E:85:SER:C	1:E:86:LEU:HD23	2.47	0.40
1:F:64:ILE:HD12	1:F:136:TRP:HZ2	1.85	0.40
1:H:16:TYR:CD1	1:H:223:LYS:HG3	2.56	0.40
1:H:64:ILE:HD12	1:H:136:TRP:HZ2	1.87	0.40
1:I:68:ILE:HD13	1:I:133:LEU:HD13	2.04	0.40
1:I:208:ARG:HG2	1:I:210:VAL:CG2	2.51	0.40
1:M:32:TYR:HB3	1:M:40:PHE:CE1	2.57	0.40
1:N:80:LEU:O	1:N:81:ARG:HG3	2.22	0.40
1:O:104:PRO:HB3	1:O:185:VAL:HG12	2.02	0.40
1:R:80:LEU:O	1:R:81:ARG:HG3	2.20	0.40
1:V:16:TYR:HD1	1:V:223:LYS:HG3	1.86	0.40
1:V:85:SER:O	1:V:86:LEU:HD23	2.21	0.40
1:W:166:ALA:HB3	1:W:169:MET:HG3	2.02	0.40
1:W:211:PHE:CE2	1:W:218:ILE:HB	2.57	0.40
1:X:91:ALA:O	1:X:105:SER:HA	2.20	0.40
1:b:164:LEU:O	1:b:219:VAL:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:208:ARG:HE	1:c:210:VAL:CG2	2.34	0.40
1:e:16:TYR:CD1	1:e:223:LYS:HG3	2.57	0.40
1:e:64:ILE:HD12	1:e:136:TRP:HZ2	1.87	0.40
1:f:31:ILE:HG13	1:f:59:LEU:HD21	2.03	0.40
1:g:183:VAL:HB	1:g:197:LEU:HG	2.04	0.40
1:h:168:LYS:HE3	1:h:168:LYS:HB2	1.69	0.40
1:h:210:VAL:HG12	1:h:212:GLU:OE2	2.22	0.40
1:k:104:PRO:HB3	1:k:185:VAL:HG12	2.04	0.40
1:m:199:SER:HA	1:n:86:LEU:O	2.22	0.40
1:r:145:ARG:HB2	1:r:148:TYR:HD1	1.85	0.40
1:s:85:SER:O	1:s:86:LEU:HD23	2.21	0.40
1:s:164:LEU:O	1:s:219:VAL:HA	2.21	0.40
1:w:79:ASP:C	1:w:80:LEU:HD12	2.47	0.40
1:1:40:PHE:CD2	1:1:246:VAL:HG12	2.57	0.40
1:4:147:ILE:HG13	1:4:148:TYR:CD1	2.56	0.40
1:6:91:ALA:O	1:6:105:SER:HA	2.21	0.40
1:6:118:PHE:CE1	1:6:120:ILE:HD11	2.55	0.40
1:7:80:LEU:O	1:7:81:ARG:HG3	2.22	0.40
1:9:204:SER:O	1:Ab:81:ARG:HA	2.22	0.40
1:AA:145:ARG:HB2	1:AA:148:TYR:HD1	1.87	0.40
1:AD:12:LYS:HA	1:AD:12:LYS:HD3	1.86	0.40
1:AH:93:LYS:HG2	1:AP:193:VAL:HG22	2.03	0.40
1:AH:118:PHE:CE1	1:AH:120:ILE:HD11	2.56	0.40
1:AJ:79:ASP:C	1:AJ:80:LEU:HD12	2.47	0.40
1:AL:118:PHE:CE1	1:AL:120:ILE:HD11	2.56	0.40
1:AR:26:ILE:HA	1:AR:42:ARG:NH1	2.36	0.40
1:AS:79:ASP:C	1:AS:80:LEU:HD12	2.47	0.40
1:AT:43:ILE:HD12	1:AU:131:ILE:HG13	2.04	0.40
1:Aa:79:ASP:C	1:Aa:80:LEU:HD12	2.46	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	1	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	2	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	3	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	4	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	5	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	6	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	7	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	8	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	9	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	A	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AA	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	AB	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	AC	211/242 (87%)	192 (91%)	19 (9%)	0	100	100
1	AD	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AE	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AF	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	AG	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AH	211/242 (87%)	191 (90%)	20 (10%)	0	100	100
1	AI	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	AJ	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	AK	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	AL	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AM	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	AN	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AO	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AP	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AQ	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	AR	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	AS	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	AT	211/242 (87%)	192 (91%)	19 (9%)	0	100	100
1	AU	211/242 (87%)	195 (92%)	16 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AV	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	AW	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	AX	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	AY	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	AZ	211/242 (87%)	192 (91%)	19 (9%)	0	100	100
1	Aa	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	Ab	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	Ac	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	Ad	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	B	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	C	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	D	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	E	211/242 (87%)	197 (93%)	14 (7%)	0	100	100
1	F	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	G	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	H	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	I	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	J	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	K	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	L	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	M	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	N	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	O	211/242 (87%)	191 (90%)	20 (10%)	0	100	100
1	P	211/242 (87%)	192 (91%)	19 (9%)	0	100	100
1	Q	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	R	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	S	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	T	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	U	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	V	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	W	211/242 (87%)	194 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	X	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	Y	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	Z	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	a	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	b	211/242 (87%)	197 (93%)	14 (7%)	0	100	100
1	c	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	d	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	e	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	f	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	g	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	h	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	i	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	j	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	k	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	l	211/242 (87%)	191 (90%)	20 (10%)	0	100	100
1	m	211/242 (87%)	191 (90%)	20 (10%)	0	100	100
1	n	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	o	211/242 (87%)	196 (93%)	15 (7%)	0	100	100
1	p	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	q	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	r	211/242 (87%)	193 (92%)	18 (8%)	0	100	100
1	s	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	t	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	u	211/242 (87%)	192 (91%)	19 (9%)	0	100	100
1	v	211/242 (87%)	192 (91%)	19 (9%)	0	100	100
1	w	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	x	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
1	y	211/242 (87%)	194 (92%)	17 (8%)	0	100	100
1	z	211/242 (87%)	195 (92%)	16 (8%)	0	100	100
All	All	19412/22264 (87%)	17888 (92%)	1524 (8%)	0	100	100

There are no Ramachandran outliers to report.

### 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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	1	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	2	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	3	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	4	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	5	194/215 (90%)	183 (94%)	11 (6%)	18	46
1	6	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	7	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	8	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	9	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	A	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	AA	194/215 (90%)	181 (93%)	13 (7%)	15	41
1	AB	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	AC	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	AD	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AE	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AF	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AG	194/215 (90%)	182 (94%)	12 (6%)	16	43
1	AH	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AI	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AJ	194/215 (90%)	183 (94%)	11 (6%)	18	46
1	AK	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	AL	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AM	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AN	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	AO	194/215 (90%)	185 (95%)	9 (5%)	24	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AP	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	AQ	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	AR	194/215 (90%)	182 (94%)	12 (6%)	16	43
1	AS	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	AT	194/215 (90%)	180 (93%)	14 (7%)	13	39
1	AU	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	AV	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	AW	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	AX	194/215 (90%)	181 (93%)	13 (7%)	15	41
1	AY	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	AZ	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	Aa	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	Ab	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	Ac	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	Ad	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	B	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	C	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	D	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	E	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	F	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	G	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	H	194/215 (90%)	183 (94%)	11 (6%)	18	46
1	I	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	J	194/215 (90%)	189 (97%)	5 (3%)	40	62
1	K	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	L	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	M	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	N	194/215 (90%)	183 (94%)	11 (6%)	18	46
1	O	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	P	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	Q	194/215 (90%)	184 (95%)	10 (5%)	21	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	S	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	T	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	U	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	V	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	W	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	X	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	Y	194/215 (90%)	183 (94%)	11 (6%)	18	46
1	Z	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	a	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	b	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	c	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	d	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	e	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	f	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	g	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	h	194/215 (90%)	182 (94%)	12 (6%)	16	43
1	i	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	j	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	k	194/215 (90%)	183 (94%)	11 (6%)	18	46
1	l	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	m	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	n	194/215 (90%)	183 (94%)	11 (6%)	18	46
1	o	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	p	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	q	194/215 (90%)	186 (96%)	8 (4%)	27	53
1	r	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	s	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	t	194/215 (90%)	188 (97%)	6 (3%)	35	59
1	u	194/215 (90%)	185 (95%)	9 (5%)	24	51
1	v	194/215 (90%)	186 (96%)	8 (4%)	27	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	w	194/215 (90%)	184 (95%)	10 (5%)	21	48
1	x	194/215 (90%)	189 (97%)	5 (3%)	40	62
1	y	194/215 (90%)	187 (96%)	7 (4%)	31	56
1	z	194/215 (90%)	188 (97%)	6 (3%)	35	59
All	All	17848/19780 (90%)	17053 (96%)	795 (4%)	26	52

All (795) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	THR
1	A	30	HIS
1	A	35	THR
1	A	162	SER
1	A	168	LYS
1	A	173	PHE
1	A	210	VAL
1	A	231	ASP
1	A	238	ASP
1	A	246	VAL
1	B	11	LEU
1	B	24	THR
1	B	30	HIS
1	B	35	THR
1	B	41	LYS
1	B	124	ILE
1	B	131	ILE
1	B	162	SER
1	B	168	LYS
1	C	11	LEU
1	C	30	HIS
1	C	35	THR
1	C	107	ASP
1	C	122	GLU
1	C	124	ILE
1	C	162	SER
1	C	168	LYS
1	C	238	ASP
1	D	30	HIS
1	D	41	LYS
1	D	124	ILE
1	D	151	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	D	162	SER
1	D	168	LYS
1	D	173	PHE
1	D	232	ASN
1	D	238	ASP
1	E	11	LEU
1	E	17	SER
1	E	24	THR
1	E	30	HIS
1	E	124	ILE
1	E	151	GLU
1	E	162	SER
1	E	231	ASP
1	E	238	ASP
1	F	30	HIS
1	F	35	THR
1	F	124	ILE
1	F	162	SER
1	F	231	ASP
1	F	238	ASP
1	F	246	VAL
1	G	11	LEU
1	G	24	THR
1	G	30	HIS
1	G	40	PHE
1	G	70	LEU
1	G	124	ILE
1	G	162	SER
1	H	11	LEU
1	H	17	SER
1	H	24	THR
1	H	30	HIS
1	H	122	GLU
1	H	124	ILE
1	H	151	GLU
1	H	162	SER
1	H	168	LYS
1	H	197	LEU
1	H	232	ASN
1	I	29	LEU
1	I	30	HIS
1	I	35	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	I	41	LYS
1	I	124	ILE
1	I	130	GLU
1	I	162	SER
1	I	238	ASP
1	J	30	HIS
1	J	126	THR
1	J	162	SER
1	J	168	LYS
1	J	238	ASP
1	K	11	LEU
1	K	17	SER
1	K	30	HIS
1	K	124	ILE
1	K	126	THR
1	K	130	GLU
1	K	162	SER
1	K	168	LYS
1	K	231	ASP
1	K	246	VAL
1	L	11	LEU
1	L	30	HIS
1	L	35	THR
1	L	122	GLU
1	L	124	ILE
1	L	131	ILE
1	L	162	SER
1	L	238	ASP
1	M	11	LEU
1	M	17	SER
1	M	30	HIS
1	M	35	THR
1	M	40	PHE
1	M	162	SER
1	M	246	VAL
1	N	11	LEU
1	N	17	SER
1	N	24	THR
1	N	30	HIS
1	N	35	THR
1	N	122	GLU
1	N	124	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	N	162	SER
1	N	168	LYS
1	N	207	ASP
1	N	238	ASP
1	O	11	LEU
1	O	24	THR
1	O	30	HIS
1	O	35	THR
1	O	162	SER
1	O	168	LYS
1	O	238	ASP
1	P	11	LEU
1	P	30	HIS
1	P	35	THR
1	P	41	LYS
1	P	122	GLU
1	P	162	SER
1	P	168	LYS
1	Q	11	LEU
1	Q	26	ILE
1	Q	30	HIS
1	Q	35	THR
1	Q	108	LEU
1	Q	122	GLU
1	Q	130	GLU
1	Q	162	SER
1	Q	168	LYS
1	Q	238	ASP
1	R	24	THR
1	R	30	HIS
1	R	63	LYS
1	R	107	ASP
1	R	122	GLU
1	R	124	ILE
1	R	162	SER
1	R	168	LYS
1	R	246	VAL
1	S	11	LEU
1	S	17	SER
1	S	24	THR
1	S	30	HIS
1	S	107	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	S	162	SER
1	S	168	LYS
1	S	206	TYR
1	S	246	VAL
1	T	11	LEU
1	T	30	HIS
1	T	41	LYS
1	T	124	ILE
1	T	162	SER
1	T	168	LYS
1	T	238	ASP
1	T	246	VAL
1	U	24	THR
1	U	30	HIS
1	U	124	ILE
1	U	130	GLU
1	U	162	SER
1	U	197	LEU
1	V	11	LEU
1	V	30	HIS
1	V	107	ASP
1	V	122	GLU
1	V	162	SER
1	V	168	LYS
1	W	24	THR
1	W	30	HIS
1	W	124	ILE
1	W	162	SER
1	W	168	LYS
1	W	197	LEU
1	X	24	THR
1	X	30	HIS
1	X	35	THR
1	X	41	LYS
1	X	162	SER
1	X	168	LYS
1	X	173	PHE
1	X	231	ASP
1	X	238	ASP
1	X	246	VAL
1	Y	11	LEU
1	Y	24	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	Y	30	HIS
1	Y	35	THR
1	Y	41	LYS
1	Y	63	LYS
1	Y	124	ILE
1	Y	162	SER
1	Y	168	LYS
1	Y	197	LEU
1	Y	238	ASP
1	Z	11	LEU
1	Z	30	HIS
1	Z	35	THR
1	Z	107	ASP
1	Z	122	GLU
1	Z	124	ILE
1	Z	151	GLU
1	Z	162	SER
1	Z	168	LYS
1	Z	238	ASP
1	a	17	SER
1	a	30	HIS
1	a	41	LYS
1	a	124	ILE
1	a	151	GLU
1	a	162	SER
1	a	168	LYS
1	a	232	ASN
1	b	11	LEU
1	b	24	THR
1	b	30	HIS
1	b	124	ILE
1	b	162	SER
1	b	238	ASP
1	c	30	HIS
1	c	35	THR
1	c	124	ILE
1	c	151	GLU
1	c	162	SER
1	c	168	LYS
1	c	238	ASP
1	c	246	VAL
1	d	11	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	d	24	THR
1	d	30	HIS
1	d	40	PHE
1	d	63	LYS
1	d	124	ILE
1	d	130	GLU
1	d	162	SER
1	d	168	LYS
1	e	11	LEU
1	e	24	THR
1	e	30	HIS
1	e	122	GLU
1	e	124	ILE
1	e	130	GLU
1	e	151	GLU
1	e	162	SER
1	e	168	LYS
1	e	197	LEU
1	f	29	LEU
1	f	30	HIS
1	f	35	THR
1	f	41	LYS
1	f	124	ILE
1	f	130	GLU
1	f	162	SER
1	f	238	ASP
1	g	17	SER
1	g	30	HIS
1	g	126	THR
1	g	151	GLU
1	g	162	SER
1	g	168	LYS
1	g	238	ASP
1	h	11	LEU
1	h	17	SER
1	h	30	HIS
1	h	124	ILE
1	h	130	GLU
1	h	151	GLU
1	h	162	SER
1	h	168	LYS
1	h	173	PHE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	h	197	LEU
1	h	242	ASP
1	h	246	VAL
1	i	11	LEU
1	i	30	HIS
1	i	35	THR
1	i	122	GLU
1	i	124	ILE
1	i	131	ILE
1	i	162	SER
1	j	11	LEU
1	j	17	SER
1	j	30	HIS
1	j	40	PHE
1	j	131	ILE
1	j	151	GLU
1	j	162	SER
1	j	246	VAL
1	k	11	LEU
1	k	17	SER
1	k	24	THR
1	k	30	HIS
1	k	35	THR
1	k	122	GLU
1	k	124	ILE
1	k	162	SER
1	k	168	LYS
1	k	197	LEU
1	k	238	ASP
1	l	11	LEU
1	l	24	THR
1	l	30	HIS
1	l	35	THR
1	l	151	GLU
1	l	162	SER
1	l	168	LYS
1	l	238	ASP
1	m	11	LEU
1	m	30	HIS
1	m	35	THR
1	m	162	SER
1	m	168	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	m	238	ASP
1	n	11	LEU
1	n	16	TYR
1	n	30	HIS
1	n	35	THR
1	n	108	LEU
1	n	122	GLU
1	n	130	GLU
1	n	151	GLU
1	n	162	SER
1	n	168	LYS
1	n	238	ASP
1	o	11	LEU
1	o	17	SER
1	o	24	THR
1	o	30	HIS
1	o	107	ASP
1	o	122	GLU
1	o	124	ILE
1	o	162	SER
1	o	168	LYS
1	o	246	VAL
1	p	11	LEU
1	p	24	THR
1	p	30	HIS
1	p	107	ASP
1	p	124	ILE
1	p	162	SER
1	p	168	LYS
1	p	238	ASP
1	p	246	VAL
1	q	11	LEU
1	q	17	SER
1	q	30	HIS
1	q	151	GLU
1	q	162	SER
1	q	168	LYS
1	q	197	LEU
1	q	246	VAL
1	r	24	THR
1	r	30	HIS
1	r	35	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	r	124	ILE
1	r	130	GLU
1	r	162	SER
1	r	197	LEU
1	s	11	LEU
1	s	24	THR
1	s	30	HIS
1	s	107	ASP
1	s	122	GLU
1	s	124	ILE
1	s	162	SER
1	s	168	LYS
1	s	210	VAL
1	t	24	THR
1	t	30	HIS
1	t	124	ILE
1	t	162	SER
1	t	197	LEU
1	t	247	LEU
1	u	11	LEU
1	u	24	THR
1	u	30	HIS
1	u	122	GLU
1	u	162	SER
1	u	168	LYS
1	u	197	LEU
1	u	210	VAL
1	u	238	ASP
1	v	24	THR
1	v	30	HIS
1	v	35	THR
1	v	107	ASP
1	v	130	GLU
1	v	151	GLU
1	v	162	SER
1	v	207	ASP
1	w	11	LEU
1	w	17	SER
1	w	24	THR
1	w	30	HIS
1	w	107	ASP
1	w	122	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	w	124	ILE
1	w	162	SER
1	w	168	LYS
1	w	246	VAL
1	x	30	HIS
1	x	124	ILE
1	x	162	SER
1	x	168	LYS
1	x	247	LEU
1	y	11	LEU
1	y	24	THR
1	y	30	HIS
1	y	122	GLU
1	y	162	SER
1	y	168	LYS
1	y	246	VAL
1	z	11	LEU
1	z	17	SER
1	z	30	HIS
1	z	162	SER
1	z	168	LYS
1	z	246	VAL
1	1	11	LEU
1	1	17	SER
1	1	24	THR
1	1	30	HIS
1	1	41	LYS
1	1	107	ASP
1	1	151	GLU
1	1	162	SER
1	1	168	LYS
1	1	246	VAL
1	2	11	LEU
1	2	17	SER
1	2	30	HIS
1	2	35	THR
1	2	122	GLU
1	2	124	ILE
1	2	162	SER
1	2	197	LEU
1	3	11	LEU
1	3	30	HIS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	3	122	GLU
1	3	130	GLU
1	3	162	SER
1	3	238	ASP
1	4	11	LEU
1	4	30	HIS
1	4	35	THR
1	4	122	GLU
1	4	124	ILE
1	4	162	SER
1	4	168	LYS
1	4	208	ARG
1	4	238	ASP
1	5	11	LEU
1	5	17	SER
1	5	24	THR
1	5	30	HIS
1	5	35	THR
1	5	122	GLU
1	5	124	ILE
1	5	162	SER
1	5	168	LYS
1	5	197	LEU
1	5	238	ASP
1	6	11	LEU
1	6	16	TYR
1	6	24	THR
1	6	30	HIS
1	6	35	THR
1	6	40	PHE
1	6	151	GLU
1	6	162	SER
1	6	173	PHE
1	6	246	VAL
1	7	11	LEU
1	7	17	SER
1	7	30	HIS
1	7	124	ILE
1	7	130	GLU
1	7	162	SER
1	7	168	LYS
1	7	246	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	8	11	LEU
1	8	17	SER
1	8	30	HIS
1	8	35	THR
1	8	126	THR
1	8	162	SER
1	8	173	PHE
1	9	24	THR
1	9	30	HIS
1	9	40	PHE
1	9	41	LYS
1	9	122	GLU
1	9	124	ILE
1	9	162	SER
1	9	168	LYS
1	9	197	LEU
1	0	30	HIS
1	0	35	THR
1	0	41	LYS
1	0	124	ILE
1	0	130	GLU
1	0	162	SER
1	0	238	ASP
1	0	242	ASP
1	AA	11	LEU
1	AA	17	SER
1	AA	24	THR
1	AA	30	HIS
1	AA	35	THR
1	AA	41	LYS
1	AA	124	ILE
1	AA	162	SER
1	AA	168	LYS
1	AA	169	MET
1	AA	173	PHE
1	AA	238	ASP
1	AA	246	VAL
1	AB	11	LEU
1	AB	30	HIS
1	AB	41	LYS
1	AB	107	ASP
1	AB	124	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AB	151	GLU
1	AB	162	SER
1	AB	168	LYS
1	AC	11	LEU
1	AC	30	HIS
1	AC	122	GLU
1	AC	124	ILE
1	AC	151	GLU
1	AC	162	SER
1	AC	168	LYS
1	AC	207	ASP
1	AD	11	LEU
1	AD	17	SER
1	AD	24	THR
1	AD	30	HIS
1	AD	40	PHE
1	AD	124	ILE
1	AD	130	GLU
1	AD	162	SER
1	AD	231	ASP
1	AE	11	LEU
1	AE	30	HIS
1	AE	122	GLU
1	AE	124	ILE
1	AE	130	GLU
1	AE	151	GLU
1	AE	162	SER
1	AE	168	LYS
1	AE	238	ASP
1	AF	30	HIS
1	AF	35	THR
1	AF	57	LYS
1	AF	124	ILE
1	AF	162	SER
1	AF	173	PHE
1	AF	238	ASP
1	AF	246	VAL
1	AF	247	LEU
1	AG	11	LEU
1	AG	17	SER
1	AG	24	THR
1	AG	30	HIS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AG	41	LYS
1	AG	63	LYS
1	AG	124	ILE
1	AG	130	GLU
1	AG	162	SER
1	AG	197	LEU
1	AG	238	ASP
1	AG	246	VAL
1	AH	11	LEU
1	AH	24	THR
1	AH	30	HIS
1	AH	122	GLU
1	AH	162	SER
1	AH	168	LYS
1	AH	197	LEU
1	AH	210	VAL
1	AH	238	ASP
1	AI	24	THR
1	AI	30	HIS
1	AI	35	THR
1	AI	107	ASP
1	AI	108	LEU
1	AI	124	ILE
1	AI	151	GLU
1	AI	162	SER
1	AI	207	ASP
1	AJ	11	LEU
1	AJ	17	SER
1	AJ	24	THR
1	AJ	30	HIS
1	AJ	107	ASP
1	AJ	122	GLU
1	AJ	124	ILE
1	AJ	162	SER
1	AJ	168	LYS
1	AJ	197	LEU
1	AJ	246	VAL
1	AK	24	THR
1	AK	30	HIS
1	AK	57	LYS
1	AK	124	ILE
1	AK	162	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AK	168	LYS
1	AL	11	LEU
1	AL	24	THR
1	AL	30	HIS
1	AL	122	GLU
1	AL	124	ILE
1	AL	131	ILE
1	AL	162	SER
1	AL	168	LYS
1	AL	197	LEU
1	AM	11	LEU
1	AM	17	SER
1	AM	30	HIS
1	AM	41	LYS
1	AM	151	GLU
1	AM	162	SER
1	AM	168	LYS
1	AM	197	LEU
1	AM	246	VAL
1	AN	11	LEU
1	AN	17	SER
1	AN	24	THR
1	AN	30	HIS
1	AN	41	LYS
1	AN	107	ASP
1	AN	124	ILE
1	AN	162	SER
1	AN	168	LYS
1	AN	246	VAL
1	AO	11	LEU
1	AO	24	THR
1	AO	30	HIS
1	AO	35	THR
1	AO	122	GLU
1	AO	124	ILE
1	AO	131	ILE
1	AO	162	SER
1	AO	168	LYS
1	AP	11	LEU
1	AP	17	SER
1	AP	30	HIS
1	AP	35	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AP	122	GLU
1	AP	130	GLU
1	AP	151	GLU
1	AP	162	SER
1	AP	168	LYS
1	AP	238	ASP
1	AQ	11	LEU
1	AQ	30	HIS
1	AQ	35	THR
1	AQ	41	LYS
1	AQ	122	GLU
1	AQ	162	SER
1	AQ	168	LYS
1	AQ	238	ASP
1	AR	11	LEU
1	AR	17	SER
1	AR	24	THR
1	AR	30	HIS
1	AR	35	THR
1	AR	122	GLU
1	AR	124	ILE
1	AR	126	THR
1	AR	162	SER
1	AR	168	LYS
1	AR	207	ASP
1	AR	238	ASP
1	AS	11	LEU
1	AS	16	TYR
1	AS	30	HIS
1	AS	40	PHE
1	AS	162	SER
1	AS	173	PHE
1	AS	246	VAL
1	AT	11	LEU
1	AT	26	ILE
1	AT	30	HIS
1	AT	57	LYS
1	AT	124	ILE
1	AT	126	THR
1	AT	130	GLU
1	AT	151	GLU
1	AT	162	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AT	168	LYS
1	AT	173	PHE
1	AT	197	LEU
1	AT	231	ASP
1	AT	246	VAL
1	AU	11	LEU
1	AU	30	HIS
1	AU	124	ILE
1	AU	162	SER
1	AU	171	MET
1	AU	238	ASP
1	AV	11	LEU
1	AV	24	THR
1	AV	30	HIS
1	AV	40	PHE
1	AV	41	LYS
1	AV	124	ILE
1	AV	162	SER
1	AV	168	LYS
1	AV	238	ASP
1	AW	29	LEU
1	AW	30	HIS
1	AW	35	THR
1	AW	41	LYS
1	AW	124	ILE
1	AW	130	GLU
1	AW	162	SER
1	AW	197	LEU
1	AW	238	ASP
1	AW	242	ASP
1	AX	11	LEU
1	AX	17	SER
1	AX	24	THR
1	AX	30	HIS
1	AX	35	THR
1	AX	41	LYS
1	AX	162	SER
1	AX	168	LYS
1	AX	169	MET
1	AX	173	PHE
1	AX	231	ASP
1	AX	238	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	AX	246	VAL
1	AY	11	LEU
1	AY	30	HIS
1	AY	41	LYS
1	AY	107	ASP
1	AY	124	ILE
1	AY	151	GLU
1	AY	162	SER
1	AY	168	LYS
1	AZ	11	LEU
1	AZ	30	HIS
1	AZ	122	GLU
1	AZ	124	ILE
1	AZ	151	GLU
1	AZ	162	SER
1	AZ	168	LYS
1	AZ	207	ASP
1	Aa	11	LEU
1	Aa	24	THR
1	Aa	30	HIS
1	Aa	70	LEU
1	Aa	124	ILE
1	Aa	162	SER
1	Aa	168	LYS
1	Aa	231	ASP
1	Ab	11	LEU
1	Ab	30	HIS
1	Ab	35	THR
1	Ab	122	GLU
1	Ab	124	ILE
1	Ab	162	SER
1	Ab	168	LYS
1	Ac	30	HIS
1	Ac	35	THR
1	Ac	57	LYS
1	Ac	124	ILE
1	Ac	162	SER
1	Ac	168	LYS
1	Ac	173	PHE
1	Ac	238	ASP
1	Ac	246	VAL
1	Ad	11	LEU

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Mol	Chain	Res	Type
1	Ad	17	SER
1	Ad	24	THR
1	Ad	30	HIS
1	Ad	124	ILE
1	Ad	151	GLU
1	Ad	162	SER
1	Ad	238	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	138	ASN
1	C	138	ASN
1	E	141	GLN
1	E	172	GLN
1	H	232	ASN
1	K	138	ASN
1	K	142	ASN
1	M	138	ASN
1	N	241	GLN
1	P	138	ASN
1	Q	65	HIS
1	Q	138	ASN
1	S	142	ASN
1	S	241	GLN
1	T	138	ASN
1	U	138	ASN
1	Y	138	ASN
1	Z	65	HIS
1	b	138	ASN
1	b	141	GLN
1	c	241	GLN
1	e	241	GLN
1	f	65	HIS
1	g	138	ASN
1	g	241	GLN
1	h	138	ASN
1	h	241	GLN
1	i	138	ASN
1	i	241	GLN
1	j	138	ASN
1	k	142	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	k	241	GLN
1	m	138	ASN
1	n	65	HIS
1	n	138	ASN
1	o	138	ASN
1	o	241	GLN
1	p	241	GLN
1	q	241	GLN
1	s	138	ASN
1	u	138	ASN
1	u	142	ASN
1	v	138	ASN
1	w	65	HIS
1	w	135	ASN
1	w	138	ASN
1	1	142	ASN
1	1	241	GLN
1	2	135	ASN
1	2	138	ASN
1	3	135	ASN
1	3	138	ASN
1	3	241	GLN
1	4	135	ASN
1	4	138	ASN
1	4	142	ASN
1	4	241	GLN
1	5	138	ASN
1	5	142	ASN
1	5	241	GLN
1	6	135	ASN
1	6	138	ASN
1	7	135	ASN
1	7	138	ASN
1	8	138	ASN
1	8	232	ASN
1	8	241	GLN
1	9	142	ASN
1	0	135	ASN
1	0	142	ASN
1	AD	135	ASN
1	AD	142	ASN
1	AE	138	ASN

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Mol	Chain	Res	Type
1	AE	241	GLN
1	AG	34	HIS
1	AG	135	ASN
1	AG	138	ASN
1	AH	138	ASN
1	AH	142	ASN
1	AJ	138	ASN
1	AK	138	ASN
1	AL	138	ASN
1	AN	138	ASN
1	AO	241	GLN
1	AP	135	ASN
1	AP	138	ASN
1	AQ	138	ASN
1	AR	142	ASN
1	AS	135	ASN
1	AS	138	ASN
1	AT	135	ASN
1	AT	138	ASN
1	AU	138	ASN
1	AV	135	ASN
1	AV	142	ASN
1	AV	241	GLN
1	AW	135	ASN
1	AW	142	ASN
1	AX	135	ASN
1	AX	138	ASN
1	AZ	65	HIS
1	Ab	138	ASN
1	Ac	135	ASN
1	Ad	135	ASN
1	Ad	138	ASN
1	Ad	172	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 oligosaccharides 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.

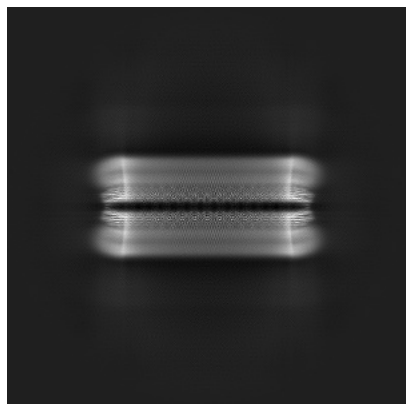
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64739. These allow visual inspection of the internal detail of the map and identification of artifacts.

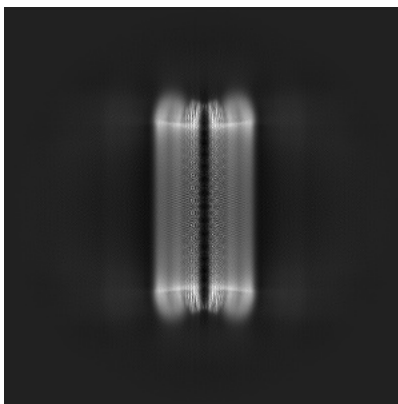
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

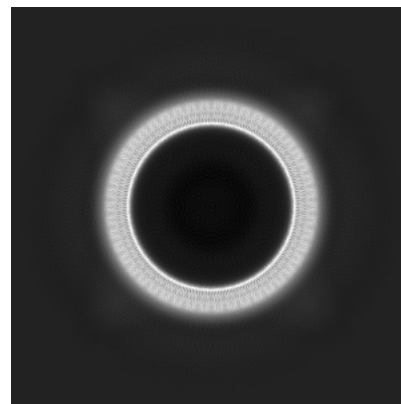
#### 6.1.1 Primary map



X

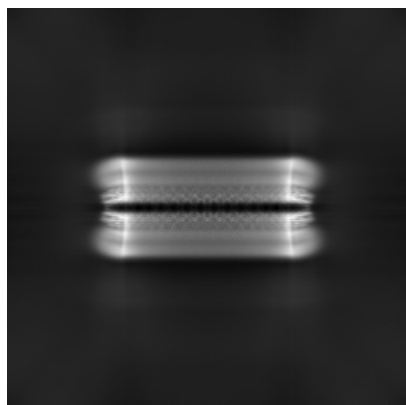


Y

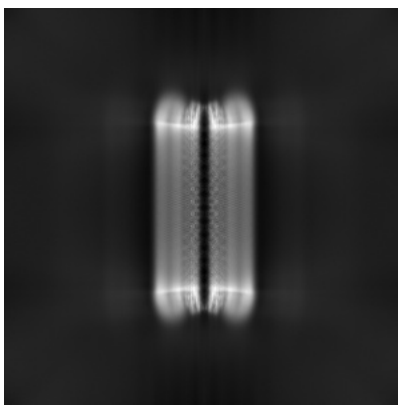


Z

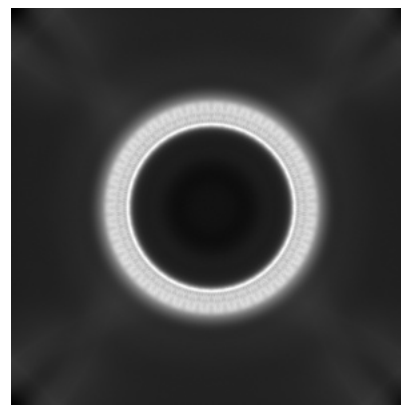
#### 6.1.2 Raw map



X



Y

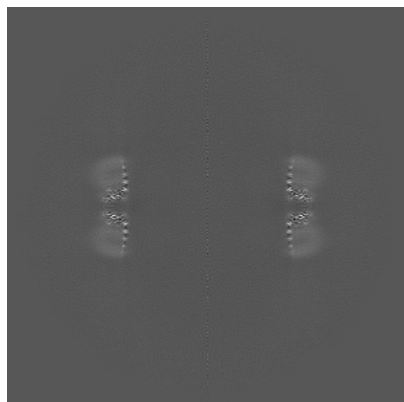


Z

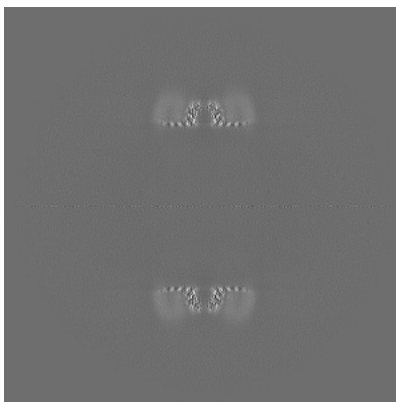
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

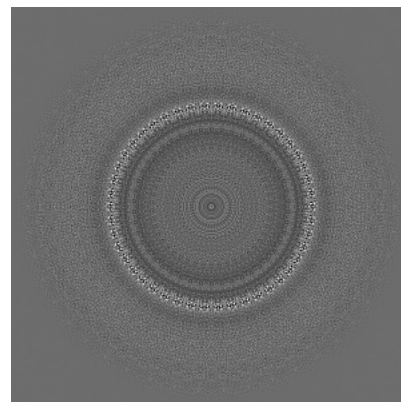
### 6.2.1 Primary map



X Index: 300

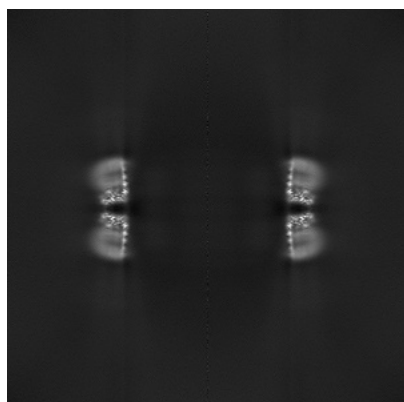


Y Index: 300

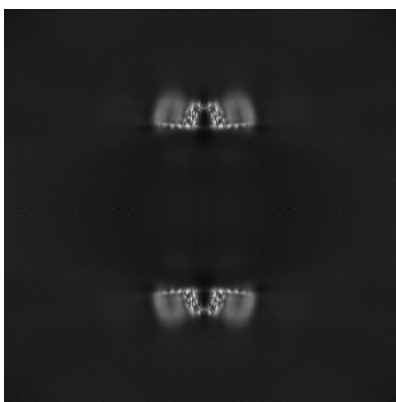


Z Index: 300

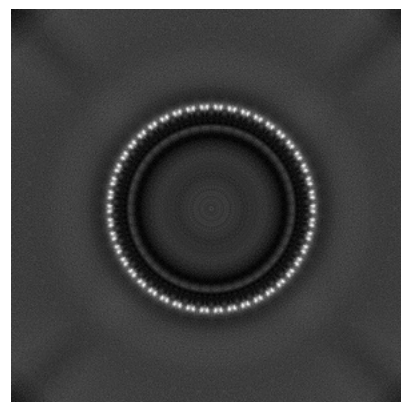
### 6.2.2 Raw map



X Index: 300



Y Index: 300

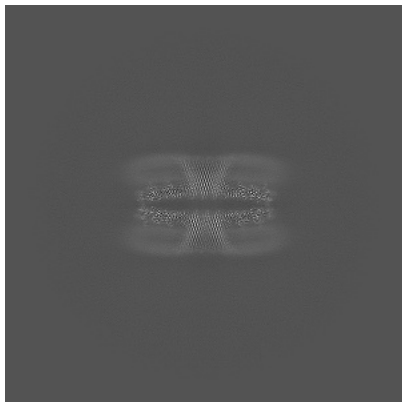


Z Index: 300

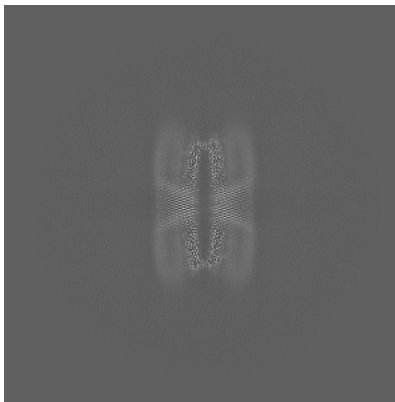
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

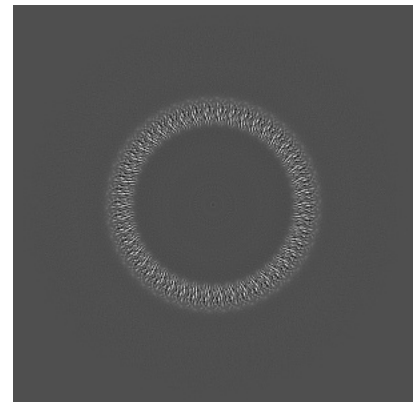
### 6.3.1 Primary map



X Index: 177

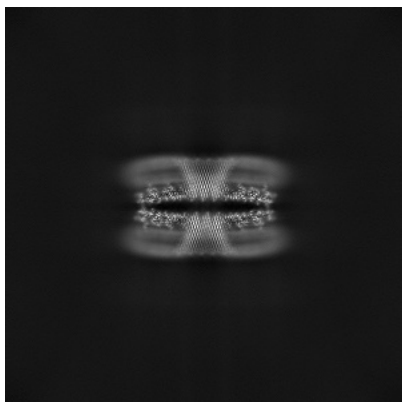


Y Index: 177

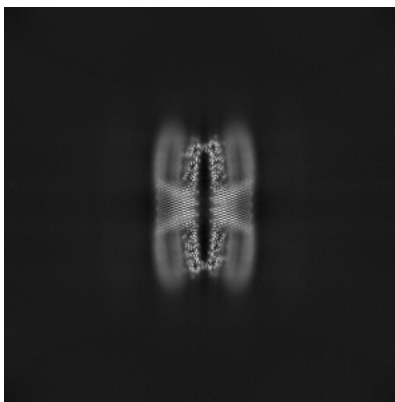


Z Index: 284

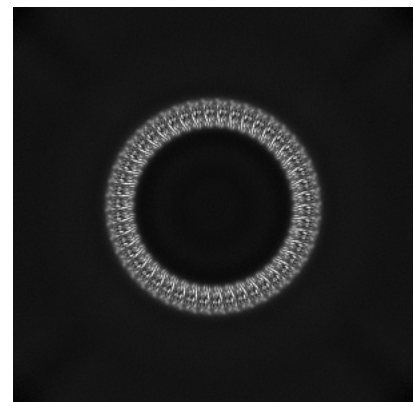
### 6.3.2 Raw map



X Index: 177



Y Index: 177

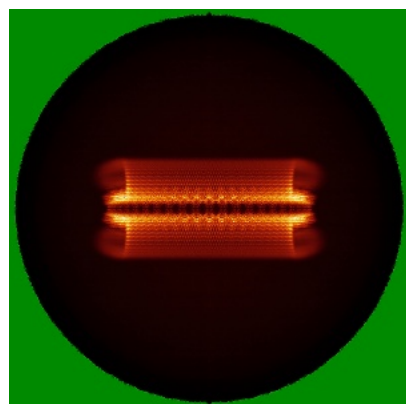


Z Index: 284

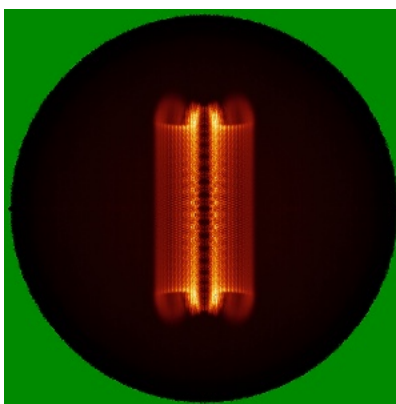
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

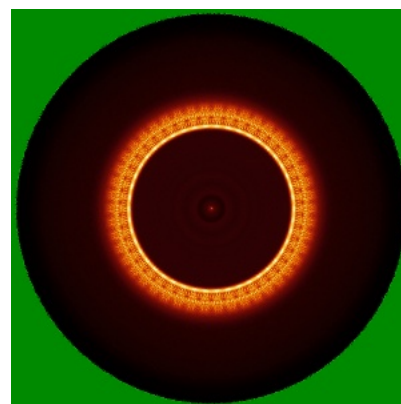
### 6.4.1 Primary map



X

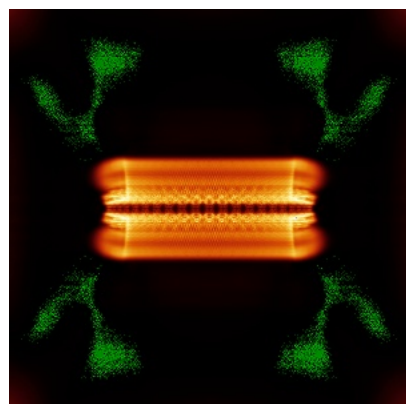


Y

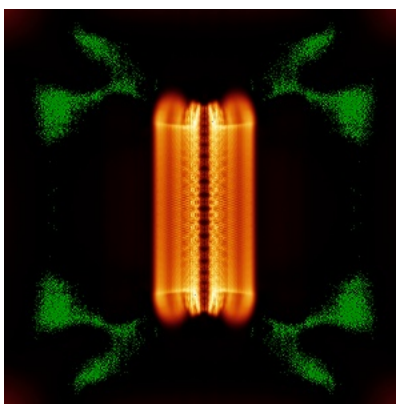


Z

### 6.4.2 Raw map



X



Y

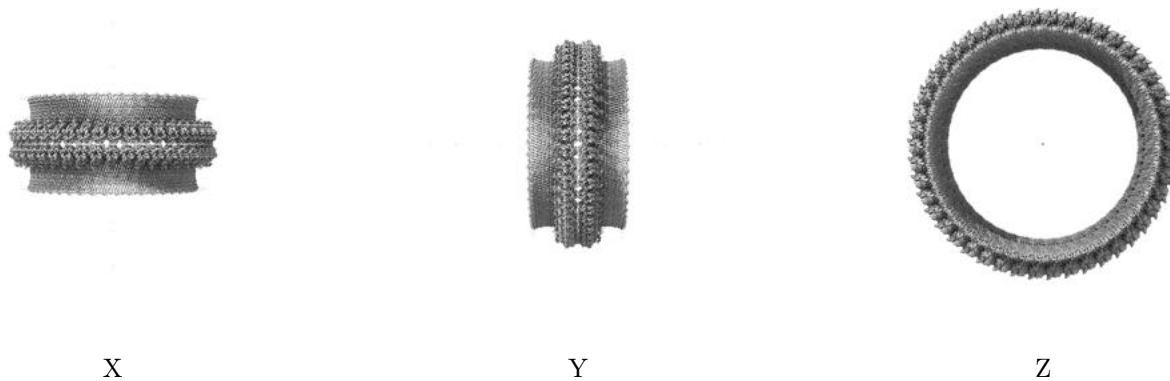


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.24. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

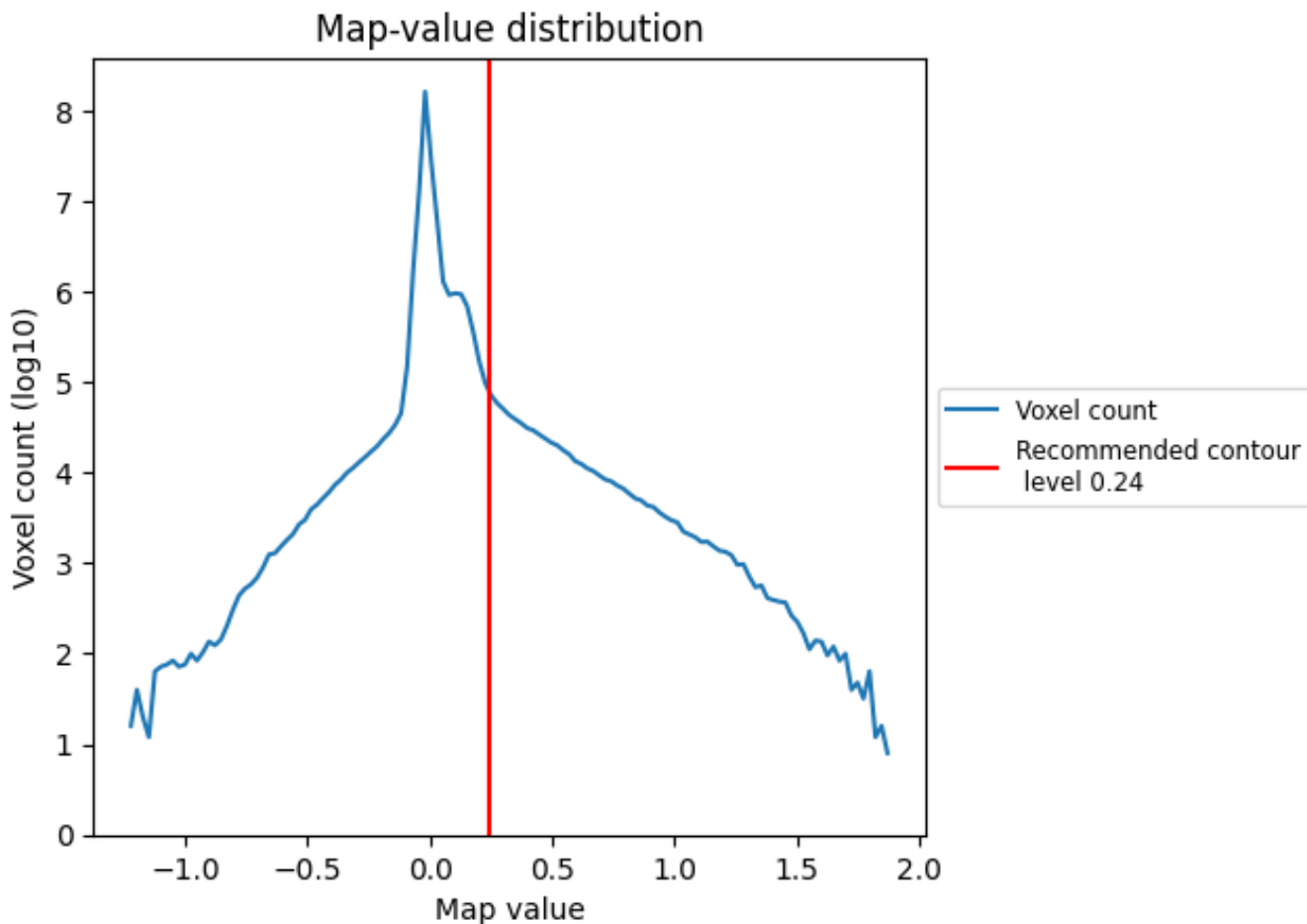
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

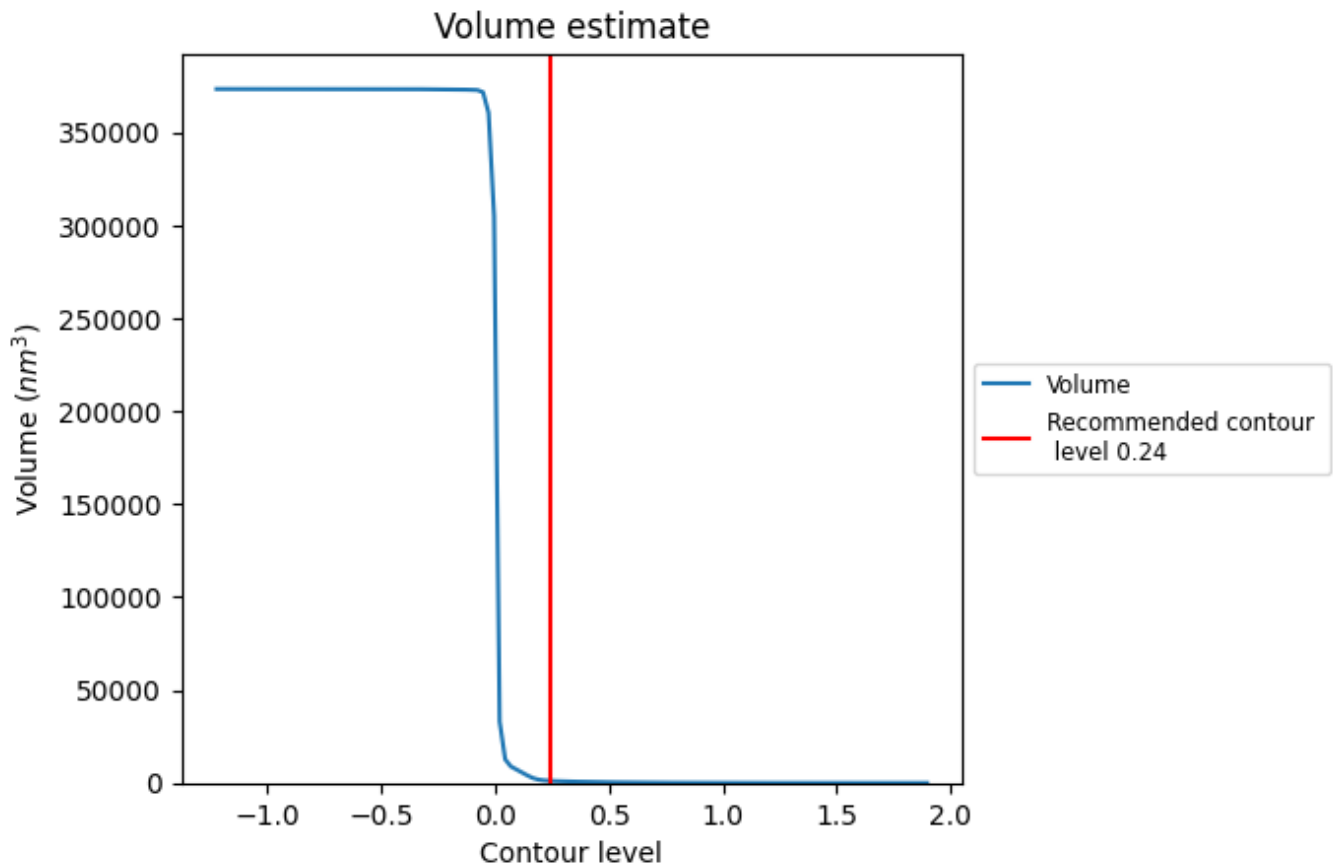
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

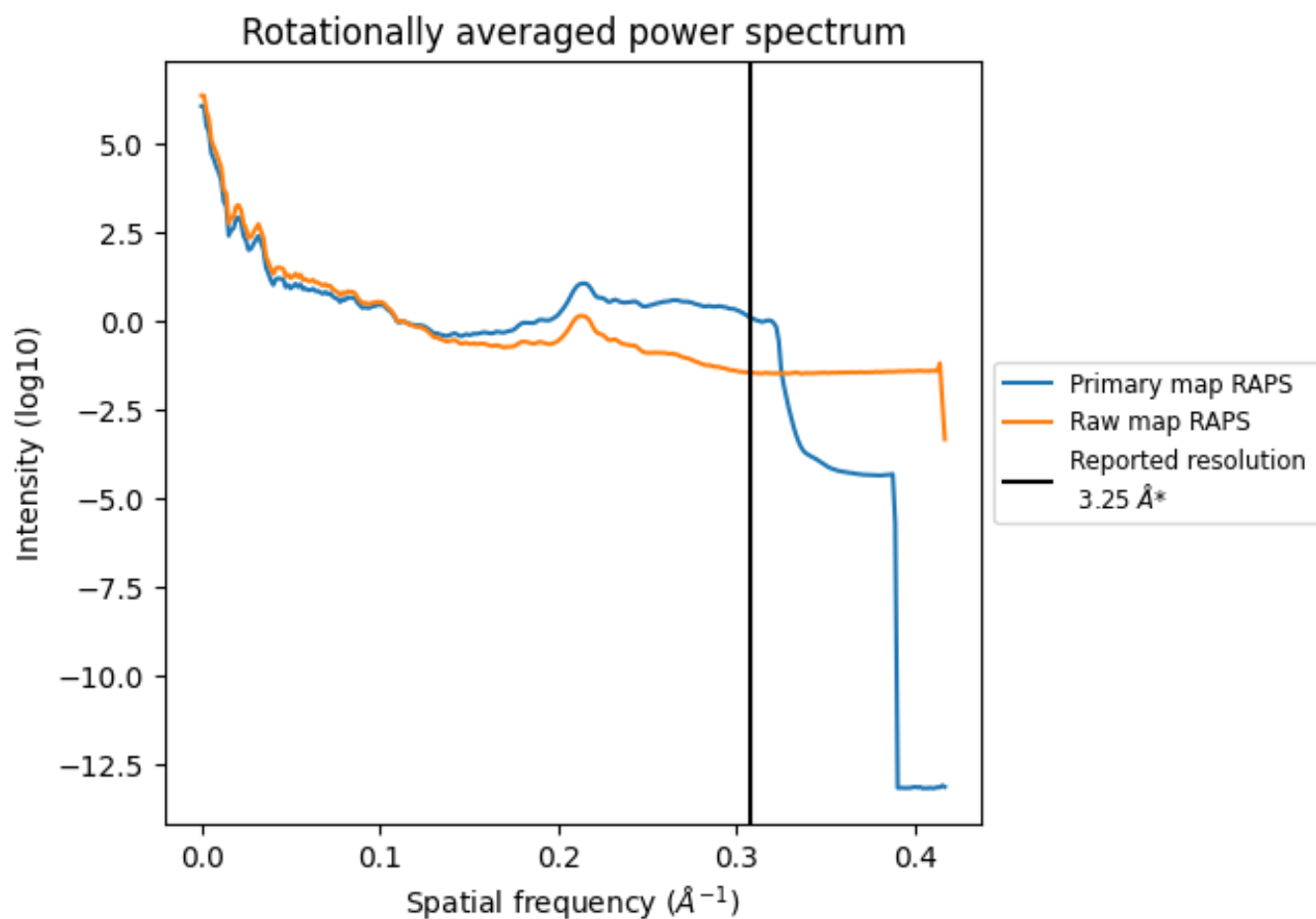
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1162 nm<sup>3</sup>; this corresponds to an approximate mass of 1049 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

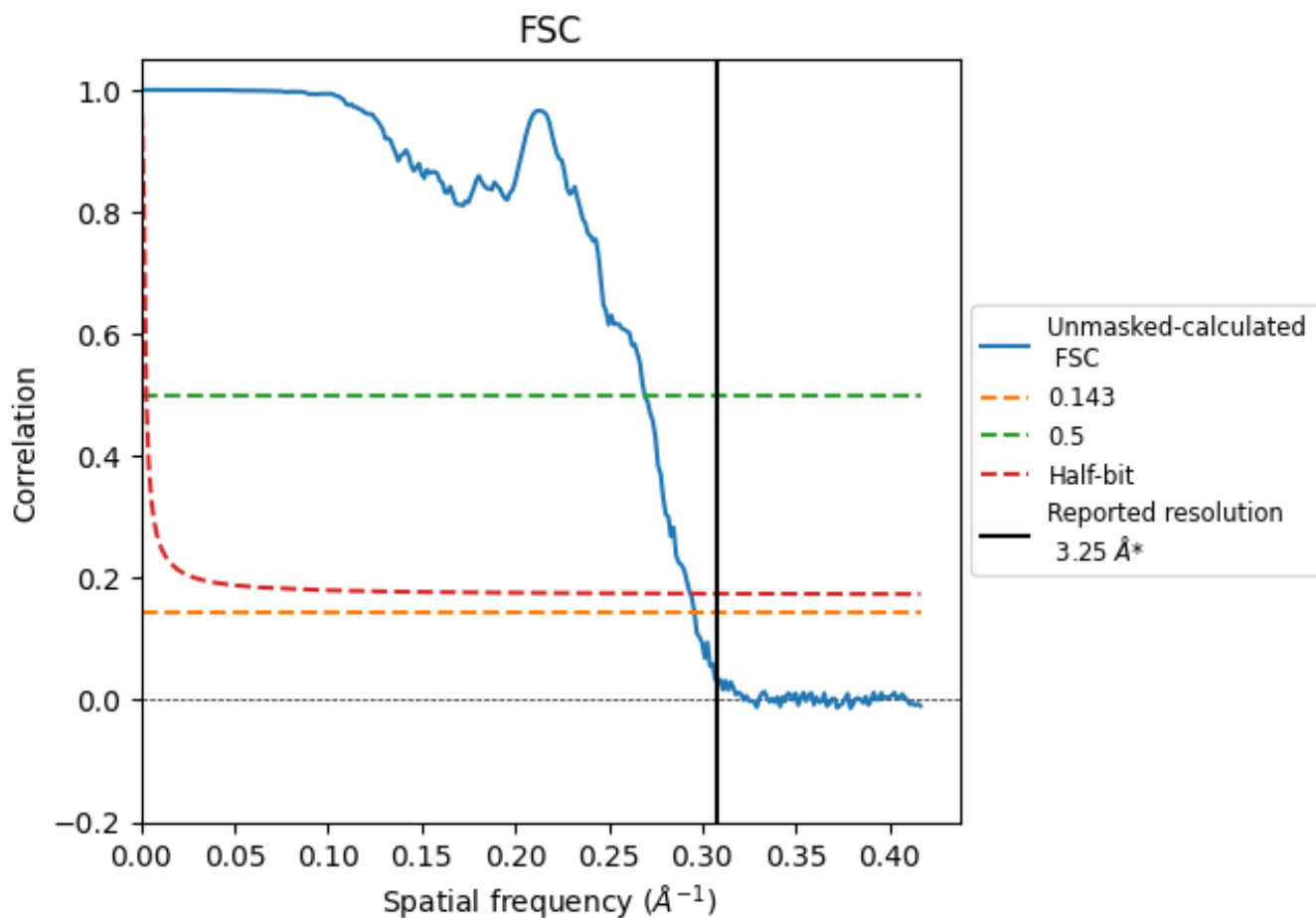


\*Reported resolution corresponds to spatial frequency of 0.308 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.308 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.38	3.71	3.40

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

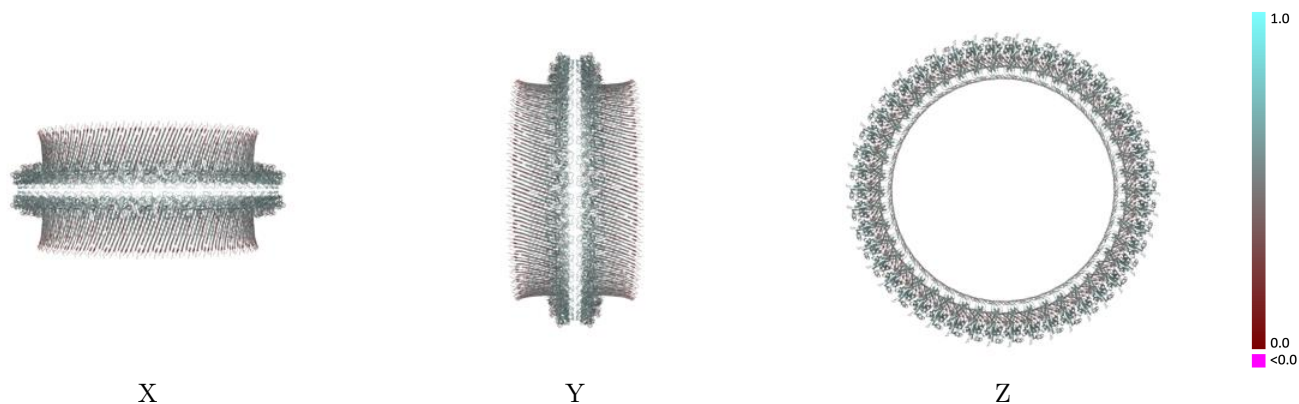
This section contains information regarding the fit between EMDB map EMD-64739 and PDB model 9V2S. Per-residue inclusion information can be found in section 3 on page 12.

### 9.1 Map-model overlay [i](#)



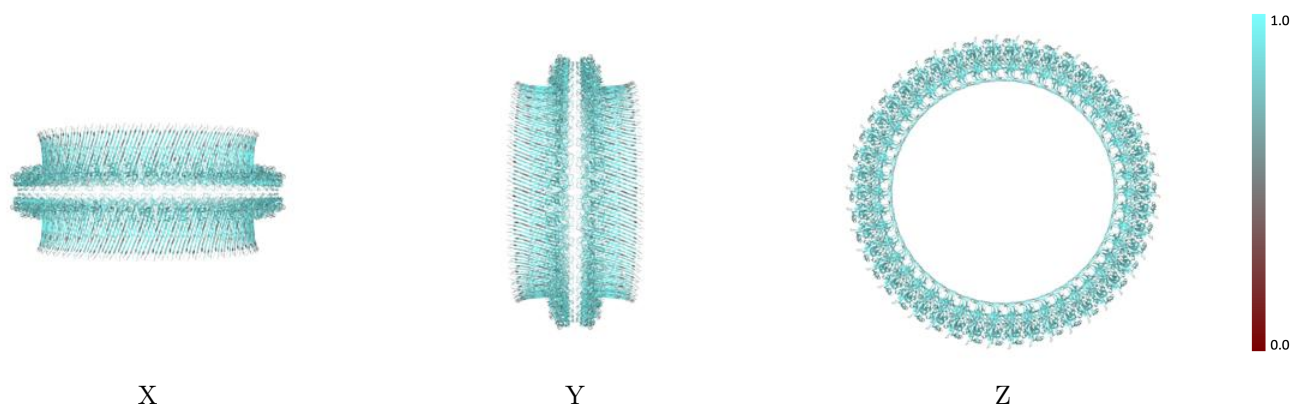
The images above show the 3D surface view of the map at the recommended contour level 0.24 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



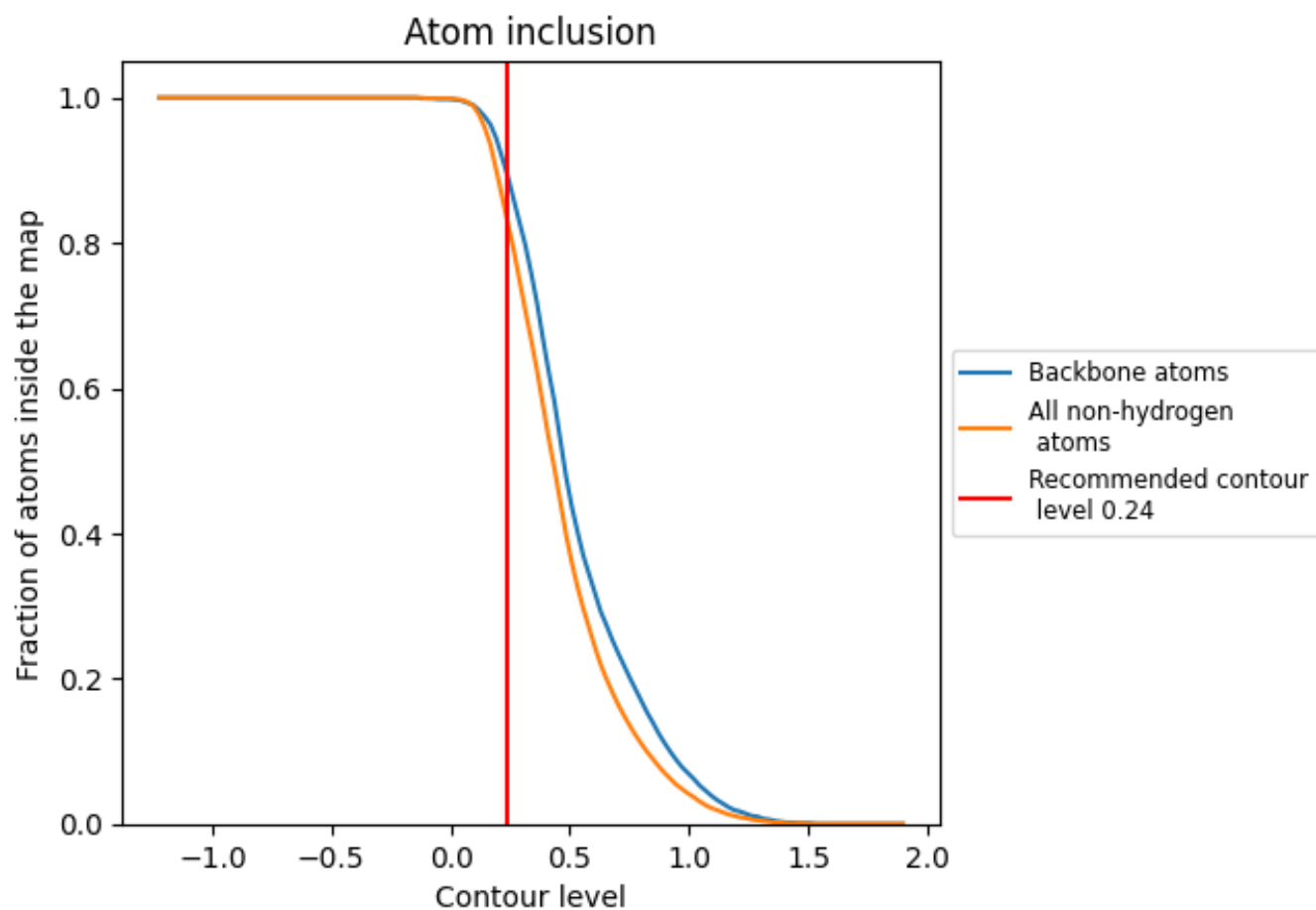
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.24).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.24) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8270	 0.5050
0	 0.8310	 0.5040
1	 0.8260	 0.5070
2	 0.8300	 0.5090
3	 0.8290	 0.5100
4	 0.8280	 0.5090
5	 0.8270	 0.5050
6	 0.8280	 0.5060
7	 0.8240	 0.5030
8	 0.8290	 0.5020
9	 0.8300	 0.5060
A	 0.8320	 0.5070
AA	 0.8320	 0.5070
AB	 0.8290	 0.5060
AC	 0.8250	 0.5050
AD	 0.8230	 0.5030
AE	 0.8270	 0.5030
AF	 0.8300	 0.5060
AG	 0.8300	 0.5060
AH	 0.8230	 0.5030
AI	 0.8250	 0.5040
AJ	 0.8290	 0.5040
AK	 0.8290	 0.5030
AL	 0.8270	 0.5040
AM	 0.8320	 0.5040
AN	 0.8220	 0.4990
AO	 0.8290	 0.5070
AP	 0.8270	 0.5070
AQ	 0.8260	 0.5020
AR	 0.8250	 0.5000
AS	 0.8270	 0.5030
AT	 0.8250	 0.5020
AU	 0.8260	 0.5050
AV	 0.8280	 0.5070
AW	 0.8270	 0.5050



































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Chain	Atom inclusion	Q-score
AX	 0.8330	 0.5070
AY	 0.8300	 0.5060
AZ	 0.8250	 0.5040
Aa	 0.8200	 0.5020
Ab	 0.8290	 0.5030
Ac	 0.8290	 0.5060
Ad	 0.8300	 0.5060
B	 0.8290	 0.5060
C	 0.8310	 0.5090
D	 0.8310	 0.5100
E	 0.8330	 0.5080
F	 0.8310	 0.5080
G	 0.8220	 0.5040
H	 0.8250	 0.5070
I	 0.8300	 0.5040
J	 0.8260	 0.5030
K	 0.8240	 0.5010
L	 0.8290	 0.5070
M	 0.8270	 0.5070
N	 0.8260	 0.5070
O	 0.8290	 0.5060
P	 0.8280	 0.5070
Q	 0.8260	 0.5080
R	 0.8300	 0.5040
S	 0.8230	 0.5040
T	 0.8230	 0.5050
U	 0.8270	 0.5030
V	 0.8230	 0.5040
W	 0.8290	 0.5030
X	 0.8270	 0.5030
Y	 0.8290	 0.5010
Z	 0.8300	 0.5030
a	 0.8320	 0.5070
b	 0.8320	 0.5060
c	 0.8280	 0.5050
d	 0.8220	 0.5010
e	 0.8250	 0.5030
f	 0.8260	 0.5050
g	 0.8260	 0.5060
h	 0.8240	 0.5050
i	 0.8270	 0.5080
j	 0.8270	 0.5020

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Chain	Atom inclusion	Q-score
k	 0.8270	 0.5010
l	 0.8260	 0.5020
m	 0.8270	 0.5040
n	 0.8290	 0.5040
o	 0.8300	 0.5070
p	 0.8230	 0.5050
q	 0.8310	 0.5090
r	 0.8260	 0.5060
s	 0.8290	 0.5090
t	 0.8290	 0.5070
u	 0.8230	 0.5100
v	 0.8270	 0.5080
w	 0.8290	 0.5070
x	 0.8280	 0.5060
y	 0.8260	 0.5080
z	 0.8340	 0.5090