



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 01:15 AM UTC

PDB ID : 2HIL / pdb_00002hil
EMDB ID : EMD-1236
Title : Structure of the Neisseria gonorrhoeae Type IV pilus filament from x-ray crystallography and electron cryomicroscopy
Authors : Craig, L.; Volkmann, N.; Egelman, E.H.; Tainer, J.A.
Deposited on : 2006-06-29
Resolution : 12.50 Å(reported)
Based on initial model : 2HI2

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at 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>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
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) : 2.49

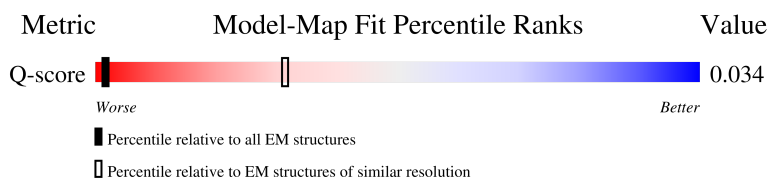
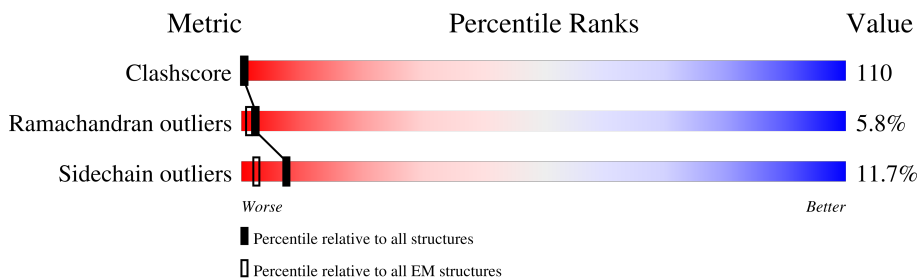
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 12.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	96 (12.00 - 13.00)

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 ≥ 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	A	158	
1	B	158	
1	C	158	
1	D	158	

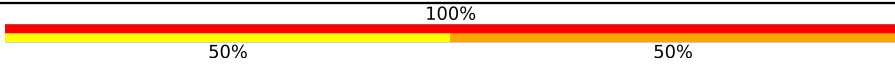
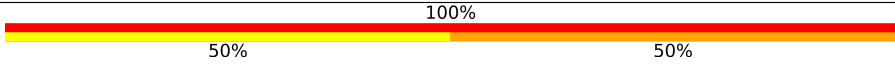
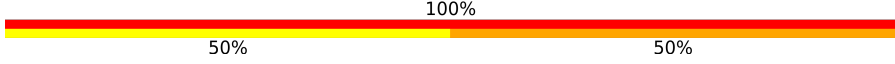
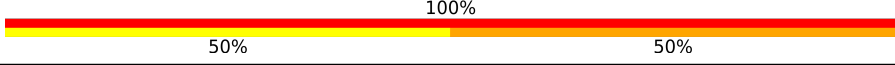
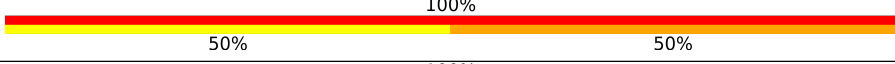
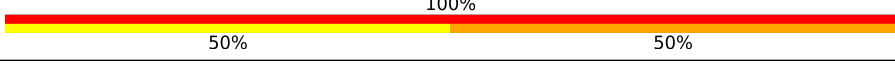
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Mol	Chain	Length	Quality of chain
1	E	158	84% 34% 50% 14%
1	F	158	87% 37% 49% 13%
1	G	158	89% 37% 48% 13%
1	H	158	94% 39% 47% 13%
1	I	158	99% 41% 44% 13%
1	J	158	80% 33% 51% 14%
1	K	158	81% 33% 51% 14%
1	L	158	82% 34% 51% 14%
1	M	158	81% 34% 51% 14%
1	N	158	84% 35% 49% 14%
1	O	158	89% 35% 49% 13%
1	P	158	93% 39% 47% 13%
1	Q	158	98% 37% 48% 13%
1	R	158	100% 37% 48% 13%
2	S	2	100% 50% 50%
2	T	2	100% 50% 50%
2	U	2	100% 50% 50%
2	V	2	100% 50% 50%
2	W	2	100% 50% 50%
2	X	2	100% 50% 50%
2	Y	2	100% 50% 50%
2	Z	2	100% 50% 50%
2	a	2	100% 50% 50%
2	b	2	100% 50% 50%
2	c	2	100% 50% 50%

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Mol	Chain	Length	Quality of chain	
2	d	2		
2	e	2		
2	f	2		
2	g	2		
2	h	2		
2	i	2		
2	j	2		

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	MEA	A	1	-	-	X	-
1	MEA	B	1	-	-	X	-
1	MEA	C	1	-	-	X	-
1	MEA	D	1	-	-	X	-
1	MEA	E	1	-	-	X	-
1	MEA	F	1	-	-	X	-
1	MEA	G	1	-	-	X	-
1	MEA	H	1	-	-	X	-
1	MEA	J	1	-	-	X	-
1	MEA	K	1	-	-	X	-
1	MEA	L	1	-	-	X	-
1	MEA	M	1	-	-	X	-
1	MEA	N	1	-	-	X	-
1	MEA	O	1	-	-	X	-
1	MEA	P	1	-	-	X	-
1	MEA	Q	1	-	-	X	-
1	MEA	R	1	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 22374 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 Fimbrial protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	B	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	C	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	D	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	E	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	F	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	G	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	H	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	I	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	J	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	K	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	L	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	M	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	N	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	O	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	P	158	Total 1207	C 760	N 206	O 237	S 4	0	0
1	Q	158	Total 1207	C 760	N 206	O 237	S 4	0	0

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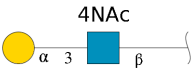
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	158	Total	C	N	O	S	0	0
			1207	760	206	237	4		

There are 36 discrepancies between the modelled and reference sequences:

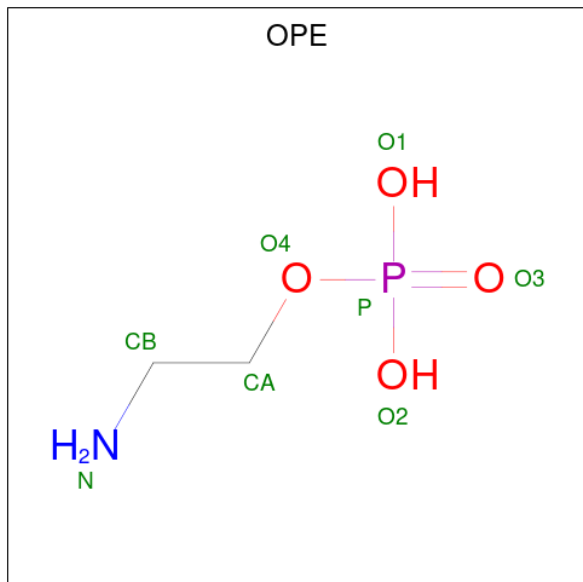
Chain	Residue	Modelled	Actual	Comment	Reference
A	69	SER	PRO	SEE REMARK 999	UNP P02974
A	71	THR	SER	SEE REMARK 999	UNP P02974
B	69	SER	PRO	SEE REMARK 999	UNP P02974
B	71	THR	SER	SEE REMARK 999	UNP P02974
C	69	SER	PRO	SEE REMARK 999	UNP P02974
C	71	THR	SER	SEE REMARK 999	UNP P02974
D	69	SER	PRO	SEE REMARK 999	UNP P02974
D	71	THR	SER	SEE REMARK 999	UNP P02974
E	69	SER	PRO	SEE REMARK 999	UNP P02974
E	71	THR	SER	SEE REMARK 999	UNP P02974
F	69	SER	PRO	SEE REMARK 999	UNP P02974
F	71	THR	SER	SEE REMARK 999	UNP P02974
G	69	SER	PRO	SEE REMARK 999	UNP P02974
G	71	THR	SER	SEE REMARK 999	UNP P02974
H	69	SER	PRO	SEE REMARK 999	UNP P02974
H	71	THR	SER	SEE REMARK 999	UNP P02974
I	69	SER	PRO	SEE REMARK 999	UNP P02974
I	71	THR	SER	SEE REMARK 999	UNP P02974
J	69	SER	PRO	SEE REMARK 999	UNP P02974
J	71	THR	SER	SEE REMARK 999	UNP P02974
K	69	SER	PRO	SEE REMARK 999	UNP P02974
K	71	THR	SER	SEE REMARK 999	UNP P02974
L	69	SER	PRO	SEE REMARK 999	UNP P02974
L	71	THR	SER	SEE REMARK 999	UNP P02974
M	69	SER	PRO	SEE REMARK 999	UNP P02974
M	71	THR	SER	SEE REMARK 999	UNP P02974
N	69	SER	PRO	SEE REMARK 999	UNP P02974
N	71	THR	SER	SEE REMARK 999	UNP P02974
O	69	SER	PRO	SEE REMARK 999	UNP P02974
O	71	THR	SER	SEE REMARK 999	UNP P02974
P	69	SER	PRO	SEE REMARK 999	UNP P02974
P	71	THR	SER	SEE REMARK 999	UNP P02974
Q	69	SER	PRO	SEE REMARK 999	UNP P02974
Q	71	THR	SER	SEE REMARK 999	UNP P02974
R	69	SER	PRO	SEE REMARK 999	UNP P02974
R	71	THR	SER	SEE REMARK 999	UNP P02974

- Molecule 2 is an oligosaccharide called alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
2	S	2	Total	C	N	O	0	0
			28	16	2	10		
2	T	2	Total	C	N	O	0	0
			28	16	2	10		
2	U	2	Total	C	N	O	0	0
			28	16	2	10		
2	V	2	Total	C	N	O	0	0
			28	16	2	10		
2	W	2	Total	C	N	O	0	0
			28	16	2	10		
2	X	2	Total	C	N	O	0	0
			28	16	2	10		
2	Y	2	Total	C	N	O	0	0
			28	16	2	10		
2	Z	2	Total	C	N	O	0	0
			28	16	2	10		
2	a	2	Total	C	N	O	0	0
			28	16	2	10		
2	b	2	Total	C	N	O	0	0
			28	16	2	10		
2	c	2	Total	C	N	O	0	0
			28	16	2	10		
2	d	2	Total	C	N	O	0	0
			28	16	2	10		
2	e	2	Total	C	N	O	0	0
			28	16	2	10		
2	f	2	Total	C	N	O	0	0
			28	16	2	10		
2	g	2	Total	C	N	O	0	0
			28	16	2	10		
2	h	2	Total	C	N	O	0	0
			28	16	2	10		
2	i	2	Total	C	N	O	0	0
			28	16	2	10		
2	j	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is PHOSPHORIC ACID MONO-(2-AMINO-ETHYL) ESTER (CCD ID: OPE) (formula: $C_2H_8NO_4P$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	B	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	C	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	D	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	E	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	F	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	G	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	H	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	I	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	J	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	K	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	L	1	Total	C	N	O	P	0
			8	2	1	4	1	

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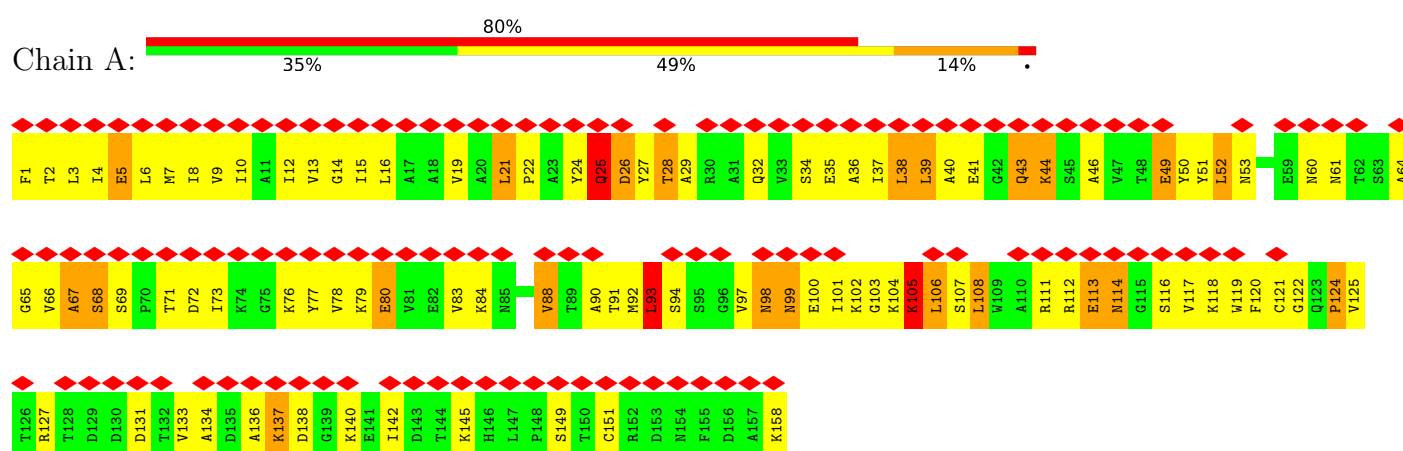
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Mol	Chain	Residues	Atoms					AltConf
3	M	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	N	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	O	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	P	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	Q	1	Total	C	N	O	P	0
			8	2	1	4	1	
3	R	1	Total	C	N	O	P	0
			8	2	1	4	1	

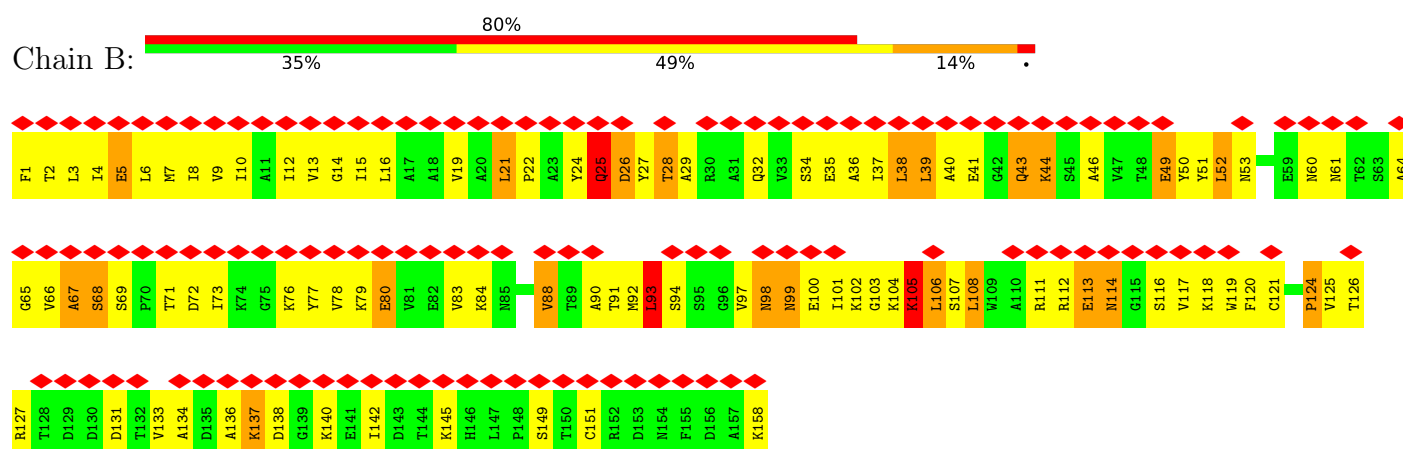
3 Residue-property plots

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.

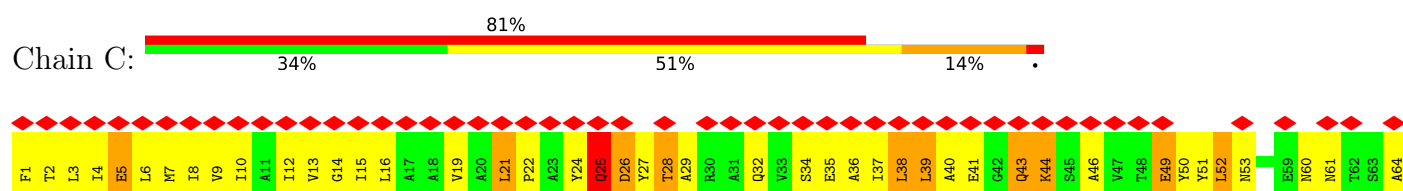
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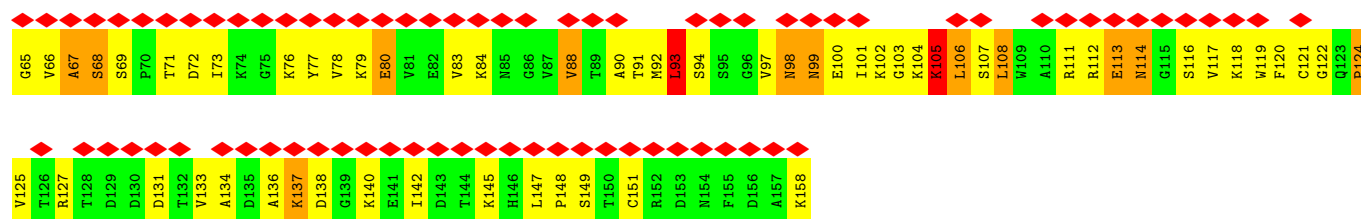


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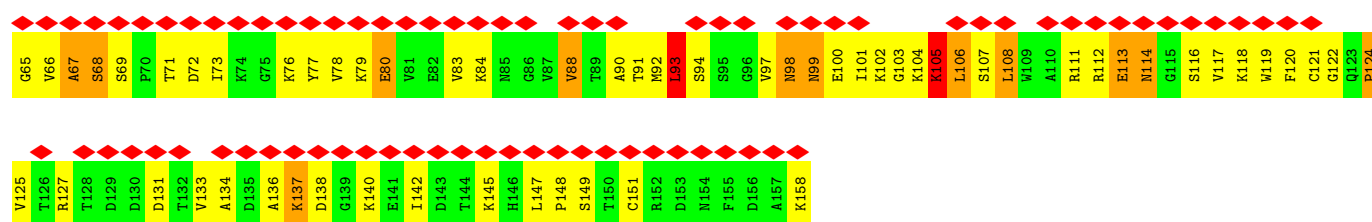
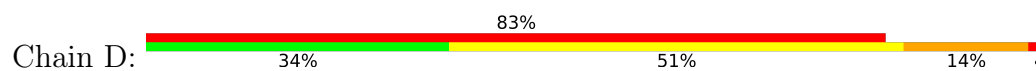


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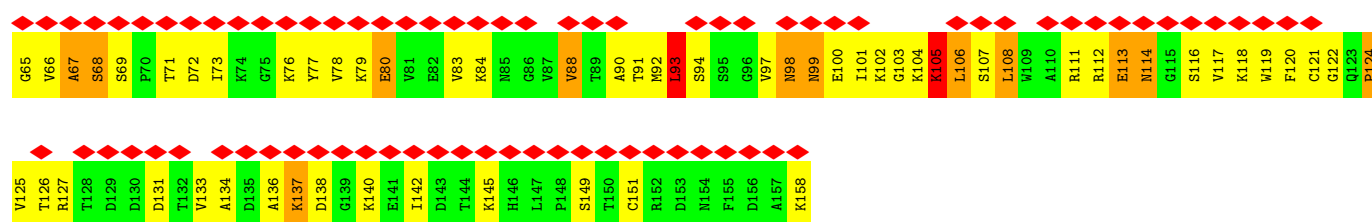
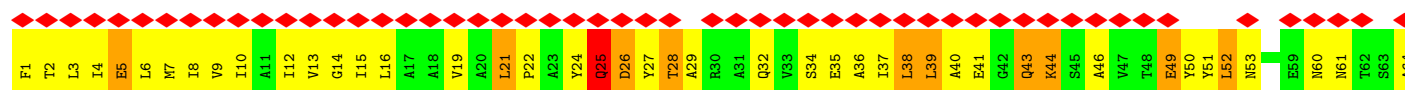
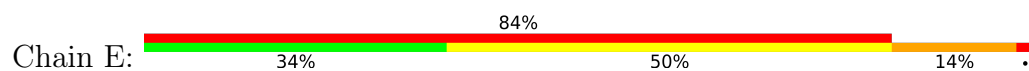




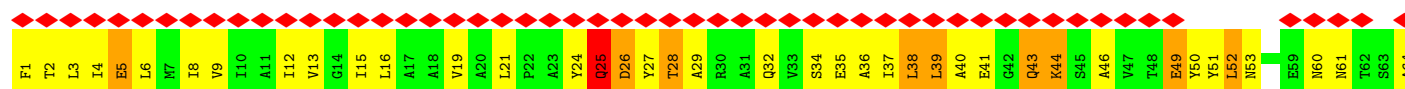
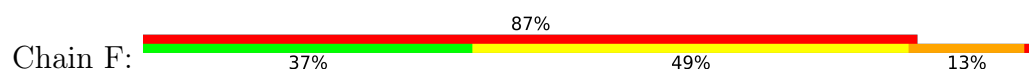
• Molecule 1: Fimbrial protein



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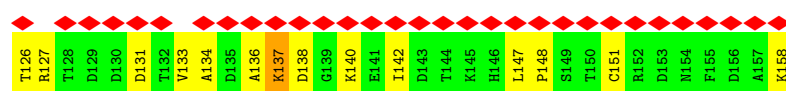
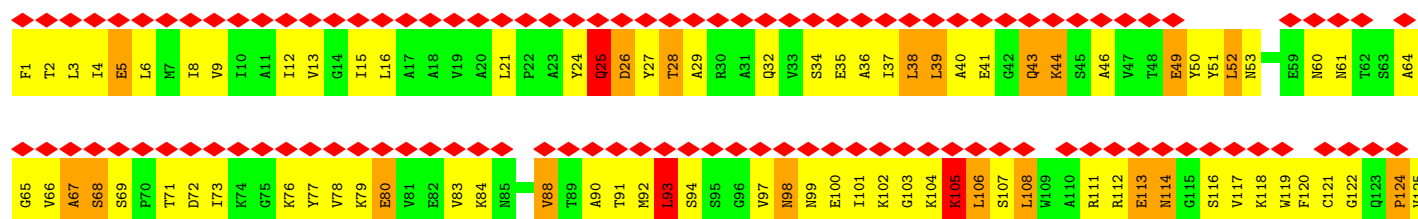
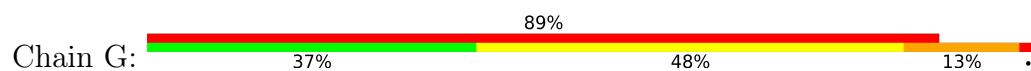


• Molecule 1: Fimbrial protein

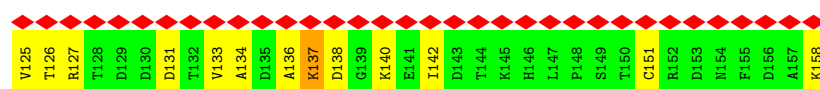
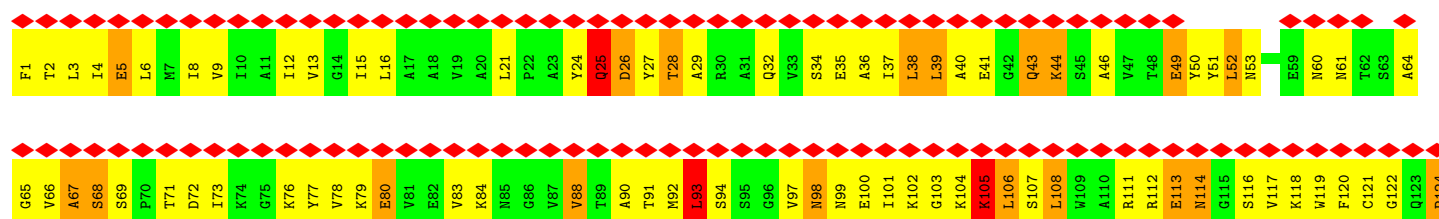




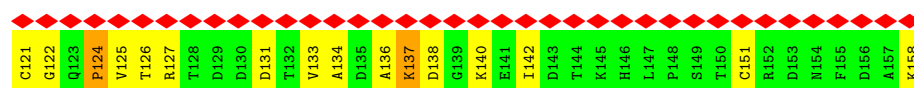
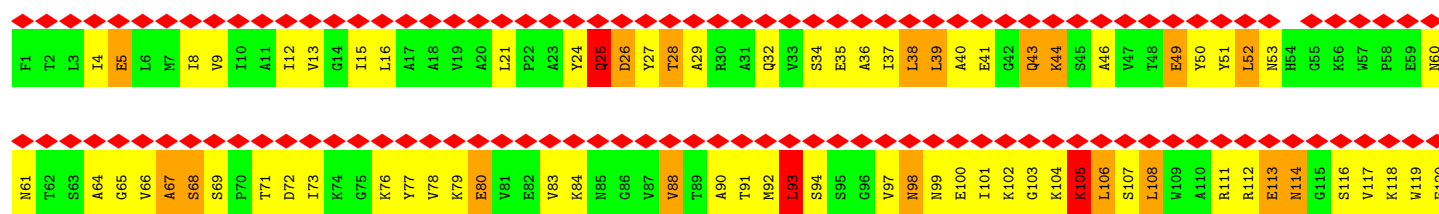
• Molecule 1: Fimbrial protein



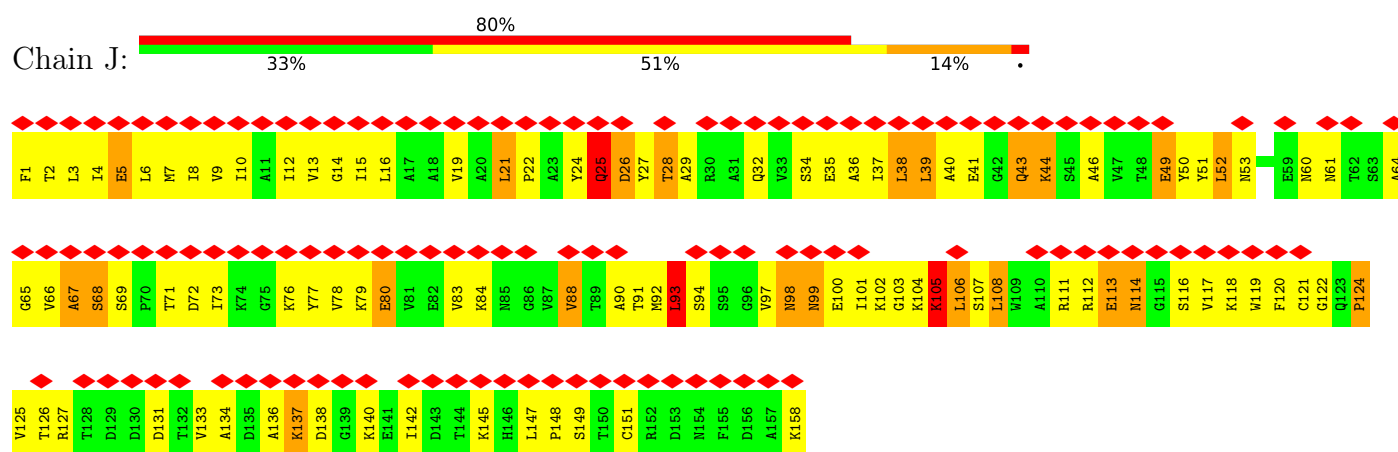
• Molecule 1: Fimbrial protein



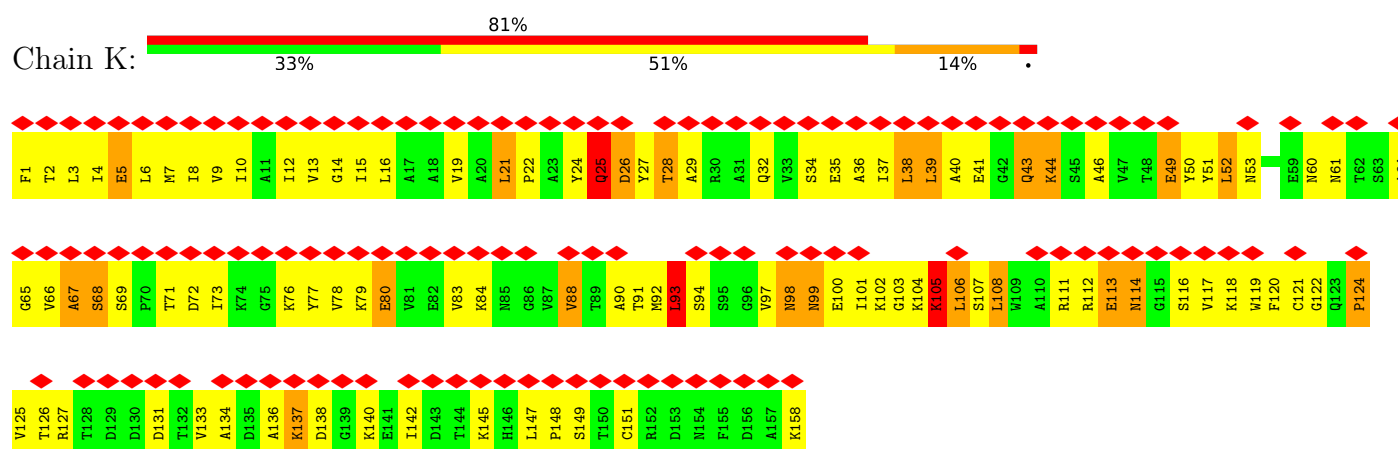
• Molecule 1: Fimbrial protein



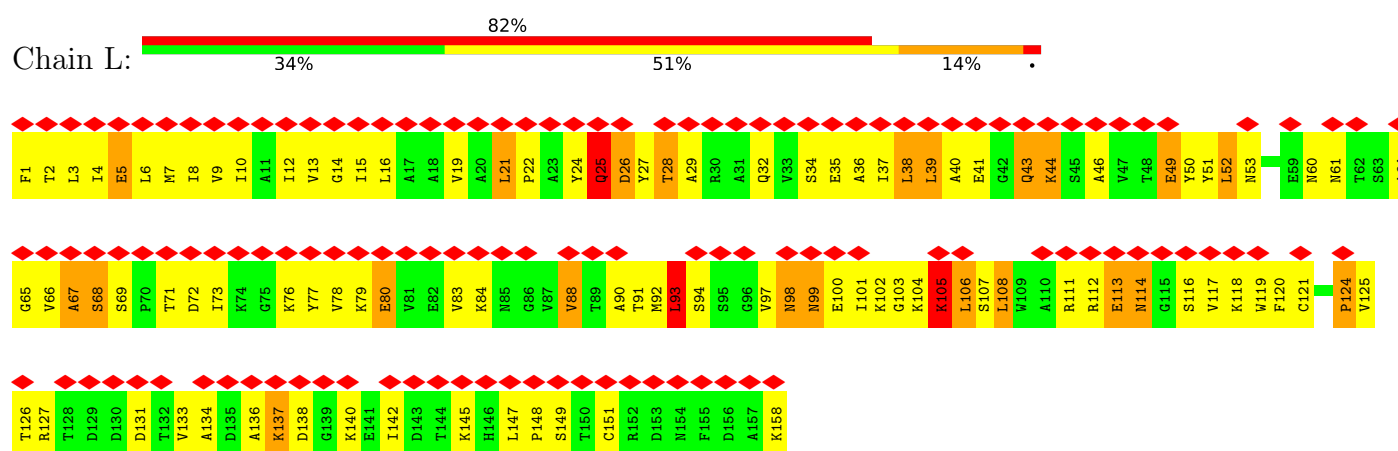
• Molecule 1: Fimbrial protein



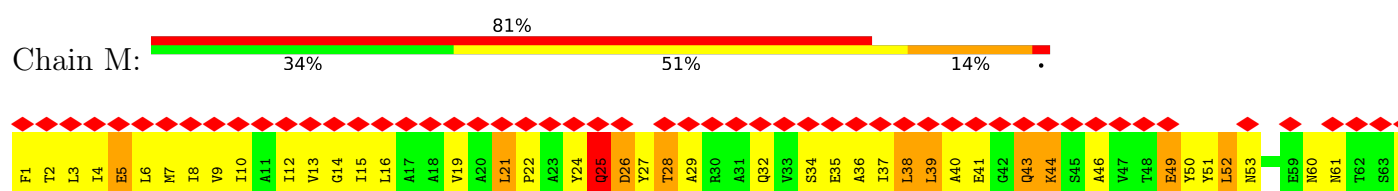
● Molecule 1: Fimbrial protein

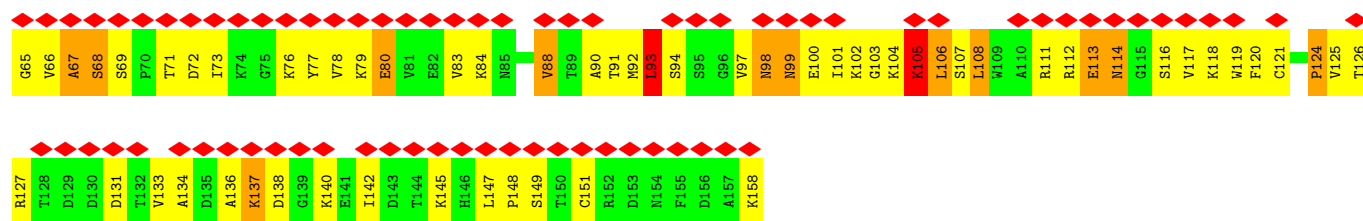


● Molecule 1: Fimbrial protein

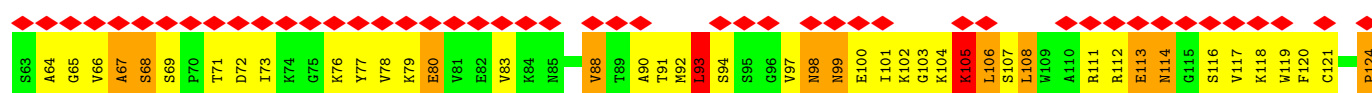
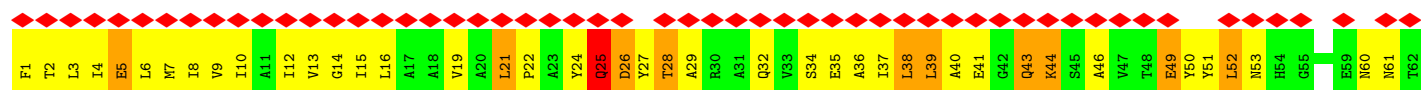
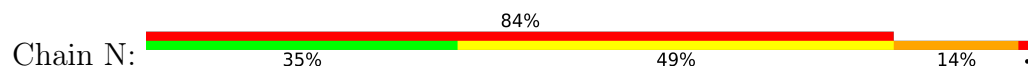


● Molecule 1: Fimbrial protein

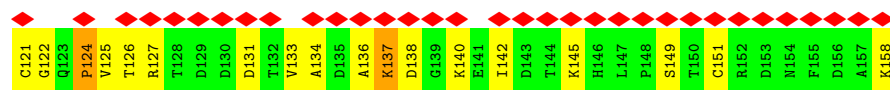
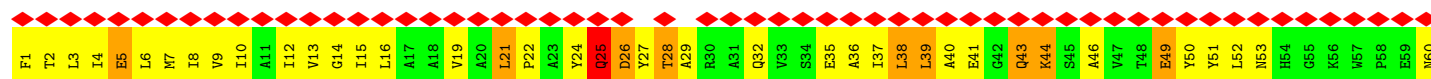
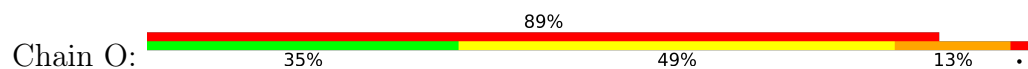




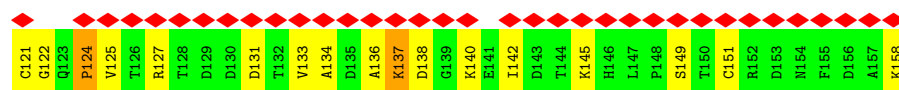
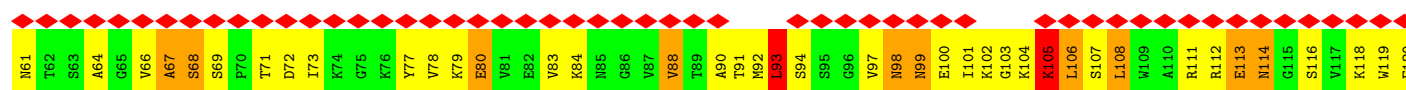
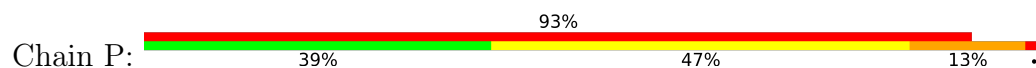
• Molecule 1: Fimbrial protein



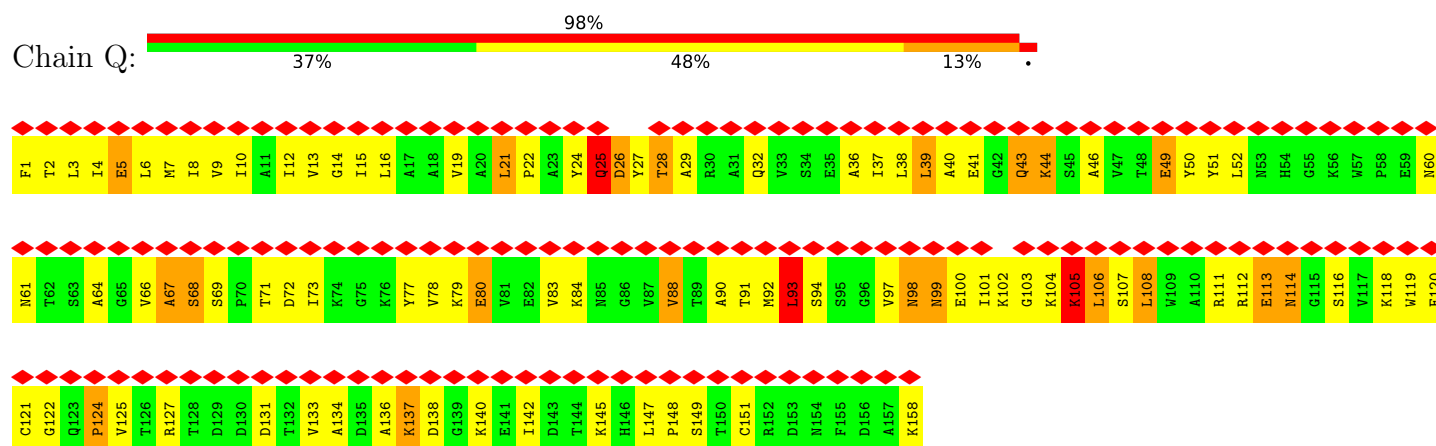
• Molecule 1: Fimbrial protein



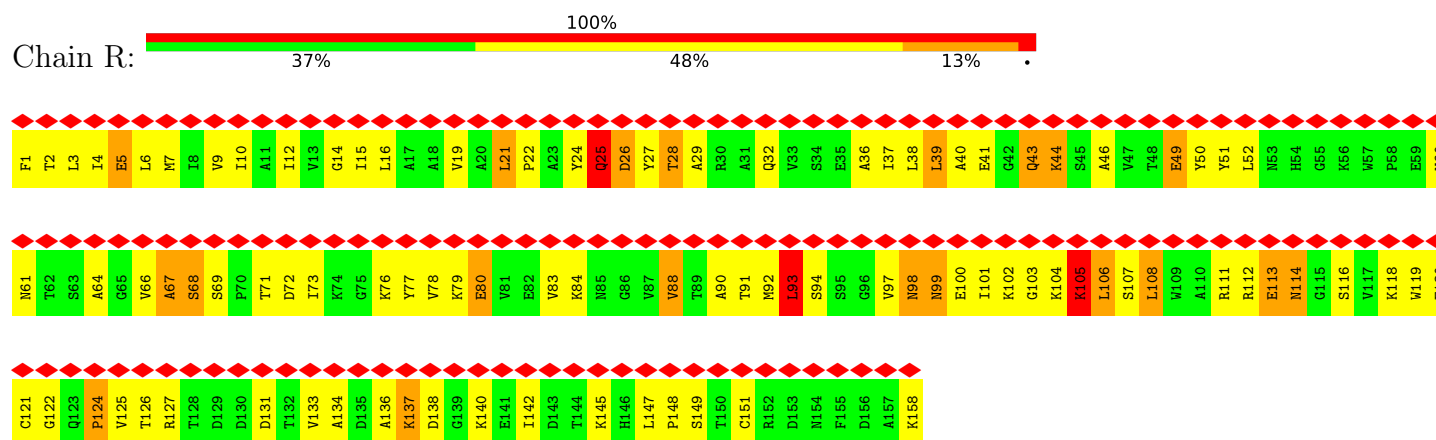
• Molecule 1: Fimbrial protein



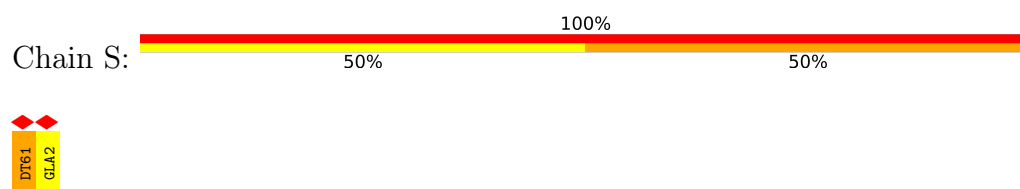
- Molecule 1: Fimbrial protein



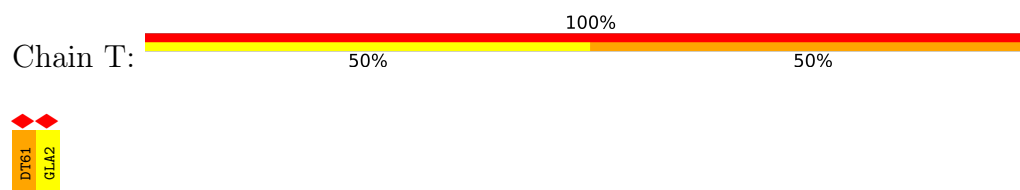
- Molecule 1: Fimbrial protein



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e





- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e





- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e





- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



- Molecule 2: alpha-D-galactopyranose-(1-3)-2,4-bisacetamido-2,4-dideoxy-beta-D-glucopyranos e



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	25000	Depositor
Resolution determination method	Not provided	
CTF correction method	Wiener filter	Depositor
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	3.946	Depositor
Minimum map value	-0.810	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.05	Depositor
Map size (Å)	101.6, 101.6, 152.4	wwPDB
Map dimensions	37, 37, 54	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.54, 2.54, 2.54	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLA, DT6, OPE, MEA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	B	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	C	0.86	1/1215 (0.1%)	1.07	11/1647 (0.7%)
1	D	0.86	1/1215 (0.1%)	1.07	11/1647 (0.7%)
1	E	0.86	1/1215 (0.1%)	1.07	11/1647 (0.7%)
1	F	0.86	1/1215 (0.1%)	1.07	11/1647 (0.7%)
1	G	0.86	1/1215 (0.1%)	1.07	11/1647 (0.7%)
1	H	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	I	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	J	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	K	0.86	1/1215 (0.1%)	1.07	11/1647 (0.7%)
1	L	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	M	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	N	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	O	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	P	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	Q	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
1	R	0.86	1/1215 (0.1%)	1.08	11/1647 (0.7%)
All	All	0.86	18/21870 (0.1%)	1.08	198/29646 (0.7%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	26	ASP	N-CA	23.96	1.76	1.46
1	R	26	ASP	N-CA	23.95	1.76	1.46
1	Q	26	ASP	N-CA	23.95	1.76	1.46
1	D	26	ASP	N-CA	23.94	1.76	1.46
1	F	26	ASP	N-CA	23.93	1.76	1.46
1	B	26	ASP	N-CA	23.92	1.76	1.46
1	P	26	ASP	N-CA	23.92	1.76	1.46
1	C	26	ASP	N-CA	23.92	1.76	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	26	ASP	N-CA	23.91	1.76	1.46
1	G	26	ASP	N-CA	23.91	1.76	1.46
1	L	26	ASP	N-CA	23.90	1.76	1.46
1	H	26	ASP	N-CA	23.90	1.76	1.46
1	K	26	ASP	N-CA	23.90	1.76	1.46
1	O	26	ASP	N-CA	23.90	1.76	1.46
1	J	26	ASP	N-CA	23.89	1.76	1.46
1	A	26	ASP	N-CA	23.88	1.76	1.46
1	M	26	ASP	N-CA	23.88	1.76	1.46
1	N	26	ASP	N-CA	23.88	1.76	1.46

All (198) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	25	GLN	CA-C-N	-10.81	102.74	122.09
1	N	25	GLN	C-N-CA	-10.81	102.74	122.09
1	O	25	GLN	CA-C-N	-10.81	102.75	122.09
1	O	25	GLN	C-N-CA	-10.81	102.75	122.09
1	P	25	GLN	CA-C-N	-10.80	102.75	122.09
1	P	25	GLN	C-N-CA	-10.80	102.75	122.09
1	M	25	GLN	CA-C-N	-10.80	102.76	122.09
1	M	25	GLN	C-N-CA	-10.80	102.76	122.09
1	Q	25	GLN	CA-C-N	-10.80	102.76	122.09
1	Q	25	GLN	C-N-CA	-10.80	102.76	122.09
1	R	25	GLN	CA-C-N	-10.79	102.78	122.09
1	R	25	GLN	C-N-CA	-10.79	102.78	122.09
1	K	25	GLN	CA-C-N	-10.78	102.79	122.09
1	K	25	GLN	C-N-CA	-10.78	102.79	122.09
1	L	25	GLN	CA-C-N	-10.78	102.79	122.09
1	L	25	GLN	C-N-CA	-10.78	102.79	122.09
1	J	25	GLN	CA-C-N	-10.78	102.80	122.09
1	J	25	GLN	C-N-CA	-10.78	102.80	122.09
1	A	25	GLN	CA-C-N	-10.77	102.82	122.09
1	A	25	GLN	C-N-CA	-10.77	102.82	122.09
1	B	25	GLN	CA-C-N	-10.76	102.84	122.09
1	B	25	GLN	C-N-CA	-10.76	102.84	122.09
1	C	25	GLN	CA-C-N	-10.76	102.84	122.09
1	C	25	GLN	C-N-CA	-10.76	102.84	122.09
1	D	25	GLN	CA-C-N	-10.75	102.85	122.09
1	D	25	GLN	C-N-CA	-10.75	102.85	122.09
1	G	25	GLN	CA-C-N	-10.75	102.84	122.09
1	G	25	GLN	C-N-CA	-10.75	102.84	122.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	25	GLN	CA-C-N	-10.75	102.85	122.09
1	I	25	GLN	C-N-CA	-10.75	102.85	122.09
1	E	25	GLN	CA-C-N	-10.74	102.86	122.09
1	E	25	GLN	C-N-CA	-10.74	102.86	122.09
1	H	25	GLN	CA-C-N	-10.74	102.86	122.09
1	H	25	GLN	C-N-CA	-10.74	102.86	122.09
1	F	25	GLN	CA-C-N	-10.74	102.87	122.09
1	F	25	GLN	C-N-CA	-10.74	102.87	122.09
1	I	43	GLN	N-CA-C	-6.92	103.24	113.61
1	G	43	GLN	N-CA-C	-6.89	103.27	113.61
1	F	43	GLN	N-CA-C	-6.88	103.29	113.61
1	H	43	GLN	N-CA-C	-6.87	103.30	113.61
1	E	43	GLN	N-CA-C	-6.85	103.33	113.61
1	D	43	GLN	N-CA-C	-6.85	103.34	113.61
1	C	43	GLN	N-CA-C	-6.84	103.34	113.61
1	N	43	GLN	N-CA-C	-6.84	103.35	113.61
1	R	43	GLN	N-CA-C	-6.83	103.36	113.61
1	O	43	GLN	N-CA-C	-6.83	103.37	113.61
1	P	43	GLN	N-CA-C	-6.83	103.37	113.61
1	A	43	GLN	N-CA-C	-6.82	103.38	113.61
1	B	43	GLN	N-CA-C	-6.82	103.38	113.61
1	K	43	GLN	N-CA-C	-6.82	103.39	113.61
1	Q	43	GLN	N-CA-C	-6.81	103.39	113.61
1	M	43	GLN	N-CA-C	-6.81	103.40	113.61
1	J	43	GLN	N-CA-C	-6.80	103.41	113.61
1	L	43	GLN	N-CA-C	-6.80	103.42	113.61
1	Q	27	TYR	N-CA-C	-6.70	103.97	111.28
1	R	27	TYR	N-CA-C	-6.70	103.98	111.28
1	P	27	TYR	N-CA-C	-6.68	104.00	111.28
1	O	27	TYR	N-CA-C	-6.67	104.01	111.28
1	H	27	TYR	N-CA-C	-6.65	104.03	111.28
1	I	27	TYR	N-CA-C	-6.64	104.05	111.28
1	N	27	TYR	N-CA-C	-6.63	104.06	111.28
1	M	27	TYR	N-CA-C	-6.62	104.06	111.28
1	G	27	TYR	N-CA-C	-6.62	104.06	111.28
1	L	27	TYR	N-CA-C	-6.62	104.07	111.28
1	F	27	TYR	N-CA-C	-6.61	104.08	111.28
1	J	27	TYR	N-CA-C	-6.61	104.08	111.28
1	A	27	TYR	N-CA-C	-6.60	104.09	111.28
1	D	27	TYR	N-CA-C	-6.59	104.09	111.28
1	C	27	TYR	N-CA-C	-6.59	104.10	111.28
1	K	27	TYR	N-CA-C	-6.58	104.11	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	27	TYR	N-CA-C	-6.57	104.12	111.28
1	E	27	TYR	N-CA-C	-6.57	104.12	111.28
1	N	36	ALA	N-CA-C	-6.48	104.26	111.71
1	K	105	LYS	N-CA-C	6.47	118.79	109.14
1	O	36	ALA	N-CA-C	-6.46	104.28	111.71
1	R	36	ALA	N-CA-C	-6.46	104.28	111.71
1	L	105	LYS	N-CA-C	6.46	118.77	109.14
1	E	105	LYS	N-CA-C	6.46	118.77	109.14
1	L	36	ALA	N-CA-C	-6.46	104.28	111.71
1	M	36	ALA	N-CA-C	-6.46	104.28	111.71
1	J	105	LYS	N-CA-C	6.45	118.76	109.14
1	C	105	LYS	N-CA-C	6.45	118.75	109.14
1	G	105	LYS	N-CA-C	6.45	118.75	109.14
1	P	36	ALA	N-CA-C	-6.45	104.29	111.71
1	B	105	LYS	N-CA-C	6.45	118.75	109.14
1	Q	36	ALA	N-CA-C	-6.45	104.30	111.71
1	A	105	LYS	N-CA-C	6.45	118.74	109.14
1	K	36	ALA	N-CA-C	-6.44	104.30	111.71
1	M	105	LYS	N-CA-C	6.44	118.74	109.14
1	D	105	LYS	N-CA-C	6.44	118.73	109.14
1	F	105	LYS	N-CA-C	6.44	118.73	109.14
1	P	44	LYS	N-CA-C	-6.44	103.77	111.69
1	J	36	ALA	N-CA-C	-6.43	104.32	111.71
1	N	105	LYS	N-CA-C	6.43	118.72	109.14
1	P	105	LYS	N-CA-C	6.43	118.72	109.14
1	R	44	LYS	N-CA-C	-6.43	103.78	111.69
1	H	105	LYS	N-CA-C	6.43	118.72	109.14
1	Q	105	LYS	N-CA-C	6.43	118.72	109.14
1	Q	44	LYS	N-CA-C	-6.42	103.79	111.69
1	A	36	ALA	N-CA-C	-6.42	104.33	111.71
1	N	44	LYS	N-CA-C	-6.42	103.79	111.69
1	R	105	LYS	N-CA-C	6.42	118.70	109.14
1	I	105	LYS	N-CA-C	6.42	118.70	109.14
1	O	105	LYS	N-CA-C	6.42	118.70	109.14
1	O	44	LYS	N-CA-C	-6.41	103.80	111.69
1	L	44	LYS	N-CA-C	-6.40	103.82	111.69
1	M	44	LYS	N-CA-C	-6.40	103.82	111.69
1	B	36	ALA	N-CA-C	-6.39	104.36	111.71
1	E	36	ALA	N-CA-C	-6.38	104.37	111.71
1	F	36	ALA	N-CA-C	-6.38	104.37	111.71
1	C	36	ALA	N-CA-C	-6.38	104.37	111.71
1	G	36	ALA	N-CA-C	-6.37	104.39	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	44	LYS	N-CA-C	-6.36	103.86	111.69
1	H	36	ALA	N-CA-C	-6.36	104.39	111.71
1	D	36	ALA	N-CA-C	-6.36	104.40	111.71
1	C	44	LYS	N-CA-C	-6.36	103.87	111.69
1	H	44	LYS	N-CA-C	-6.35	103.88	111.69
1	I	36	ALA	N-CA-C	-6.35	104.41	111.71
1	B	44	LYS	N-CA-C	-6.34	103.89	111.69
1	A	44	LYS	N-CA-C	-6.34	103.89	111.69
1	D	44	LYS	N-CA-C	-6.34	103.89	111.69
1	F	44	LYS	N-CA-C	-6.34	103.89	111.69
1	I	44	LYS	N-CA-C	-6.34	103.90	111.69
1	J	44	LYS	N-CA-C	-6.33	103.90	111.69
1	E	44	LYS	N-CA-C	-6.33	103.90	111.69
1	G	44	LYS	N-CA-C	-6.33	103.91	111.69
1	M	113	GLU	N-CA-C	-5.47	106.65	113.38
1	J	113	GLU	N-CA-C	-5.46	106.67	113.38
1	Q	113	GLU	N-CA-C	-5.45	106.67	113.38
1	R	113	GLU	N-CA-C	-5.45	106.67	113.38
1	K	113	GLU	N-CA-C	-5.45	106.68	113.38
1	N	113	GLU	N-CA-C	-5.45	106.68	113.38
1	A	113	GLU	N-CA-C	-5.45	106.68	113.38
1	L	113	GLU	N-CA-C	-5.44	106.69	113.38
1	O	113	GLU	N-CA-C	-5.43	106.69	113.38
1	P	113	GLU	N-CA-C	-5.43	106.70	113.38
1	B	113	GLU	N-CA-C	-5.43	106.70	113.38
1	E	113	GLU	N-CA-C	-5.42	106.71	113.38
1	D	113	GLU	N-CA-C	-5.42	106.71	113.38
1	C	113	GLU	N-CA-C	-5.42	106.72	113.38
1	I	113	GLU	N-CA-C	-5.42	106.71	113.38
1	F	113	GLU	N-CA-C	-5.42	106.72	113.38
1	H	113	GLU	N-CA-C	-5.41	106.72	113.38
1	G	113	GLU	N-CA-C	-5.40	106.73	113.38
1	R	26	ASP	N-CA-C	-5.35	106.89	113.41
1	I	136	ALA	N-CA-C	-5.34	102.42	110.70
1	G	136	ALA	N-CA-C	-5.33	102.43	110.70
1	Q	26	ASP	N-CA-C	-5.33	106.90	113.41
1	H	136	ALA	N-CA-C	-5.33	102.44	110.70
1	P	26	ASP	N-CA-C	-5.32	106.92	113.41
1	F	136	ALA	N-CA-C	-5.32	102.46	110.70
1	D	136	ALA	N-CA-C	-5.32	102.46	110.70
1	C	136	ALA	N-CA-C	-5.31	102.46	110.70
1	E	136	ALA	N-CA-C	-5.31	102.47	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	136	ALA	N-CA-C	-5.31	102.47	110.70
1	B	26	ASP	N-CA-C	-5.31	106.93	113.41
1	E	26	ASP	N-CA-C	-5.31	106.93	113.41
1	O	136	ALA	N-CA-C	-5.31	102.47	110.70
1	R	136	ALA	N-CA-C	-5.31	102.47	110.70
1	Q	136	ALA	N-CA-C	-5.30	102.48	110.70
1	J	26	ASP	N-CA-C	-5.30	106.94	113.41
1	J	136	ALA	N-CA-C	-5.30	102.49	110.70
1	K	136	ALA	N-CA-C	-5.30	102.49	110.70
1	D	26	ASP	N-CA-C	-5.30	106.95	113.41
1	O	26	ASP	N-CA-C	-5.30	106.95	113.41
1	A	26	ASP	N-CA-C	-5.29	106.95	113.41
1	P	136	ALA	N-CA-C	-5.29	102.49	110.70
1	B	136	ALA	N-CA-C	-5.29	102.50	110.70
1	L	136	ALA	N-CA-C	-5.29	102.50	110.70
1	M	136	ALA	N-CA-C	-5.29	102.50	110.70
1	M	26	ASP	N-CA-C	-5.29	106.96	113.41
1	N	26	ASP	N-CA-C	-5.29	106.96	113.41
1	C	26	ASP	N-CA-C	-5.28	106.97	113.41
1	K	26	ASP	N-CA-C	-5.28	106.97	113.41
1	A	136	ALA	N-CA-C	-5.28	102.52	110.70
1	L	26	ASP	N-CA-C	-5.28	106.97	113.41
1	F	26	ASP	N-CA-C	-5.27	106.98	113.41
1	G	26	ASP	N-CA-C	-5.25	107.00	113.41
1	H	26	ASP	N-CA-C	-5.24	107.01	113.41
1	I	26	ASP	N-CA-C	-5.24	107.02	113.41
1	R	103	GLY	N-CA-C	-5.07	108.00	115.30
1	F	103	GLY	N-CA-C	-5.06	108.01	115.30
1	H	103	GLY	N-CA-C	-5.06	108.02	115.30
1	G	103	GLY	N-CA-C	-5.05	108.03	115.30
1	I	103	GLY	N-CA-C	-5.05	108.03	115.30
1	B	103	GLY	N-CA-C	-5.05	108.03	115.30
1	O	103	GLY	N-CA-C	-5.05	108.03	115.30
1	Q	103	GLY	N-CA-C	-5.05	108.03	115.30
1	C	103	GLY	N-CA-C	-5.05	108.03	115.30
1	L	103	GLY	N-CA-C	-5.05	108.03	115.30
1	D	103	GLY	N-CA-C	-5.04	108.03	115.30
1	E	103	GLY	N-CA-C	-5.04	108.04	115.30
1	N	103	GLY	N-CA-C	-5.04	108.04	115.30
1	M	103	GLY	N-CA-C	-5.04	108.04	115.30
1	K	103	GLY	N-CA-C	-5.04	108.05	115.30
1	P	103	GLY	N-CA-C	-5.04	108.05	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	103	GLY	N-CA-C	-5.03	108.06	115.30
1	A	103	GLY	N-CA-C	-5.01	108.08	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1207	0	1199	507	0
1	B	1207	0	1199	504	0
1	C	1207	0	1199	500	0
1	D	1207	0	1199	502	0
1	E	1207	0	1199	507	0
1	F	1207	0	1201	419	0
1	G	1207	0	1201	385	0
1	H	1207	0	1201	386	0
1	I	1207	0	1202	301	0
1	J	1207	0	1199	500	0
1	K	1207	0	1199	507	0
1	L	1207	0	1199	511	0
1	M	1207	0	1199	505	0
1	N	1207	0	1199	506	0
1	O	1207	0	1203	422	0
1	P	1207	0	1203	383	0
1	Q	1207	0	1203	385	0
1	R	1207	0	1203	305	0
2	S	28	0	25	1	0
2	T	28	0	25	1	0
2	U	28	0	25	1	0
2	V	28	0	25	1	0
2	W	28	0	25	1	0
2	X	28	0	25	1	0
2	Y	28	0	25	1	0
2	Z	28	0	25	1	0
2	a	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	b	28	0	25	1	0
2	c	28	0	25	1	0
2	d	28	0	25	1	0
2	e	28	0	25	1	0
2	f	28	0	25	1	0
2	g	28	0	25	1	0
2	h	28	0	25	1	0
2	i	28	0	25	1	0
2	j	28	0	25	1	0
3	A	8	0	6	0	0
3	B	8	0	6	0	0
3	C	8	0	6	0	0
3	D	8	0	6	0	0
3	E	8	0	6	0	0
3	F	8	0	6	0	0
3	G	8	0	6	0	0
3	H	8	0	6	0	0
3	I	8	0	6	0	0
3	J	8	0	6	0	0
3	K	8	0	6	0	0
3	L	8	0	6	0	0
3	M	8	0	6	0	0
3	N	8	0	6	0	0
3	O	8	0	6	0	0
3	P	8	0	6	0	0
3	Q	8	0	6	0	0
3	R	8	0	6	0	0
All	All	22374	0	22165	4895	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 110.

All (4895) 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:K:8:ILE:HD11	1:L:1:MEA:CE2	1.24	1.68
1:E:1:MEA:CE2	1:F:8:ILE:HD11	1.24	1.66
1:Q:8:ILE:HD11	1:R:1:MEA:CE2	1.24	1.64
1:C:1:MEA:CE2	1:D:8:ILE:HD11	1.24	1.64
1:B:1:MEA:CE2	1:C:8:ILE:HD11	1.24	1.62
1:J:8:ILE:HD11	1:K:1:MEA:CE2	1.24	1.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:8:ILE:HD11	1:N:1:MEA:CE2	1.24	1.61
1:D:1:MEA:CE2	1:E:8:ILE:HD11	1.24	1.61
1:L:8:ILE:HD11	1:M:1:MEA:CE2	1.24	1.61
1:C:1:MEA:CD2	1:D:8:ILE:HD11	1.28	1.60
1:O:8:ILE:HD11	1:P:1:MEA:CE2	1.24	1.60
1:A:1:MEA:CD2	1:B:8:ILE:HD11	1.28	1.60
1:M:8:ILE:HD11	1:N:1:MEA:CD2	1.28	1.60
1:F:1:MEA:CE2	1:G:8:ILE:HD11	1.24	1.59
1:N:8:ILE:HD11	1:O:1:MEA:CE2	1.24	1.59
1:N:8:ILE:HD11	1:O:1:MEA:CD2	1.28	1.59
1:C:38:LEU:CD1	1:K:10:ILE:HD13	1.33	1.59
1:A:10:ILE:HD13	1:E:38:LEU:CD1	1.33	1.58
1:L:8:ILE:HD11	1:M:1:MEA:CD2	1.28	1.58
1:L:38:LEU:CD1	1:P:10:ILE:HD13	1.33	1.58
1:P:8:ILE:HD11	1:Q:1:MEA:CE2	1.24	1.58
1:H:1:MEA:CE2	1:I:8:ILE:HD11	1.24	1.58
1:F:1:MEA:CD2	1:G:8:ILE:HD11	1.28	1.58
1:N:38:LEU:CD1	1:R:10:ILE:HD13	1.33	1.58
1:B:1:MEA:CD2	1:C:8:ILE:HD11	1.28	1.57
1:K:38:LEU:CD1	1:O:10:ILE:HD13	1.33	1.57
1:E:1:MEA:CD2	1:F:8:ILE:HD11	1.28	1.57
1:O:8:ILE:HD11	1:P:1:MEA:CD2	1.28	1.57
1:D:1:MEA:CD2	1:E:8:ILE:HD11	1.28	1.57
1:D:38:LEU:CD1	1:J:10:ILE:HD13	1.33	1.57
1:Q:8:ILE:HD11	1:R:1:MEA:CD2	1.28	1.57
1:A:38:LEU:HD13	1:M:10:ILE:CD1	1.09	1.57
1:M:38:LEU:HD13	1:Q:10:ILE:CD1	1.09	1.57
1:A:1:MEA:CE2	1:B:8:ILE:HD11	1.24	1.56
1:K:8:ILE:HD11	1:L:1:MEA:CD2	1.28	1.56
1:B:10:ILE:HD13	1:F:38:LEU:CD1	1.33	1.56
1:H:1:MEA:CD2	1:I:8:ILE:HD11	1.28	1.56
1:M:38:LEU:CD1	1:Q:10:ILE:HD13	1.33	1.56
1:A:10:ILE:CD1	1:E:38:LEU:HD13	1.09	1.56
1:A:8:ILE:HD11	1:J:1:MEA:CE2	1.24	1.56
1:G:1:MEA:CE2	1:H:8:ILE:HD11	1.24	1.55
1:E:10:ILE:HD13	1:I:38:LEU:CD1	1.33	1.55
1:J:8:ILE:HD11	1:K:1:MEA:CD2	1.28	1.55
1:E:10:ILE:CD1	1:I:38:LEU:HD13	1.09	1.55
1:D:10:ILE:CD1	1:H:38:LEU:HD13	1.09	1.55
1:G:1:MEA:CD2	1:H:8:ILE:HD11	1.28	1.55
1:P:8:ILE:HD11	1:Q:1:MEA:CD2	1.28	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ILE:HD11	1:J:1:MEA:CD2	1.28	1.54
1:E:5:GLU:H	1:F:12:ILE:CD1	1.21	1.54
1:C:10:ILE:HD13	1:G:38:LEU:CD1	1.33	1.53
1:D:38:LEU:HD13	1:J:10:ILE:CD1	1.09	1.53
1:K:12:ILE:CD1	1:L:5:GLU:H	1.21	1.53
1:O:12:ILE:CD1	1:P:5:GLU:H	1.21	1.53
1:B:38:LEU:CD1	1:L:10:ILE:HD13	1.33	1.53
1:J:38:LEU:CD1	1:N:10:ILE:HD13	1.33	1.53
1:A:5:GLU:H	1:B:12:ILE:CD1	1.21	1.53
1:A:38:LEU:CD1	1:M:10:ILE:HD13	1.33	1.53
1:C:10:ILE:CD1	1:G:38:LEU:HD13	1.09	1.53
1:H:5:GLU:H	1:I:12:ILE:CD1	1.21	1.52
1:J:38:LEU:HD13	1:N:10:ILE:CD1	1.09	1.52
1:C:38:LEU:HD13	1:K:10:ILE:CD1	1.09	1.52
1:D:10:ILE:HD13	1:H:38:LEU:CD1	1.33	1.52
1:L:38:LEU:HD13	1:P:10:ILE:CD1	1.09	1.52
1:B:10:ILE:CD1	1:F:38:LEU:HD13	1.09	1.52
1:N:38:LEU:HD13	1:R:10:ILE:CD1	1.09	1.52
1:B:5:GLU:H	1:C:12:ILE:CD1	1.21	1.51
1:B:38:LEU:HD13	1:L:10:ILE:CD1	1.09	1.51
1:L:12:ILE:CD1	1:M:5:GLU:H	1.21	1.51
1:N:12:ILE:CD1	1:O:5:GLU:H	1.21	1.51
1:K:38:LEU:HD13	1:O:10:ILE:CD1	1.09	1.50
1:D:5:GLU:H	1:E:12:ILE:CD1	1.21	1.50
1:F:5:GLU:H	1:G:12:ILE:CD1	1.21	1.49
1:G:26:ASP:N	1:G:26:ASP:CA	1.76	1.49
1:J:26:ASP:N	1:J:26:ASP:CA	1.76	1.49
1:M:12:ILE:CD1	1:N:5:GLU:H	1.21	1.49
1:C:26:ASP:N	1:C:26:ASP:CA	1.76	1.48
1:J:12:ILE:CD1	1:K:5:GLU:H	1.21	1.48
1:C:5:GLU:H	1:D:12:ILE:CD1	1.21	1.48
1:D:26:ASP:N	1:D:26:ASP:CA	1.76	1.48
1:F:26:ASP:N	1:F:26:ASP:CA	1.76	1.48
1:P:12:ILE:CD1	1:Q:5:GLU:H	1.21	1.48
1:Q:12:ILE:CD1	1:R:5:GLU:H	1.21	1.48
1:R:26:ASP:N	1:R:26:ASP:CA	1.76	1.48
1:A:12:ILE:CD1	1:J:5:GLU:H	1.21	1.47
1:G:5:GLU:H	1:H:12:ILE:CD1	1.21	1.47
1:M:26:ASP:N	1:M:26:ASP:CA	1.76	1.47
1:L:26:ASP:N	1:L:26:ASP:CA	1.76	1.47
1:A:15:ILE:CD1	1:J:6:LEU:HD22	1.46	1.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:26:ASP:N	1:Q:26:ASP:CA	1.76	1.47
1:I:26:ASP:N	1:I:26:ASP:CA	1.76	1.46
1:J:15:ILE:CD1	1:K:6:LEU:HD22	1.46	1.46
1:A:1:MEA:CD2	1:B:8:ILE:CD1	1.94	1.46
1:C:6:LEU:HD22	1:D:15:ILE:CD1	1.46	1.46
1:D:6:LEU:HD22	1:E:15:ILE:CD1	1.46	1.46
1:H:1:MEA:CD2	1:I:8:ILE:CD1	1.94	1.46
1:N:26:ASP:N	1:N:26:ASP:CA	1.76	1.46
1:M:15:ILE:CD1	1:N:6:LEU:HD22	1.45	1.46
1:N:15:ILE:CD1	1:O:6:LEU:HD22	1.45	1.46
1:D:1:MEA:CD2	1:E:8:ILE:CD1	1.94	1.46
1:O:26:ASP:N	1:O:26:ASP:CA	1.76	1.46
1:P:8:ILE:CD1	1:Q:1:MEA:CD2	1.93	1.46
1:A:26:ASP:N	1:A:26:ASP:CA	1.76	1.46
1:H:26:ASP:CA	1:H:26:ASP:N	1.76	1.46
1:E:1:MEA:CD2	1:F:8:ILE:CD1	1.94	1.45
1:G:6:LEU:HD22	1:H:15:ILE:CD1	1.46	1.45
1:F:6:LEU:HD22	1:G:15:ILE:CD1	1.46	1.45
1:E:26:ASP:N	1:E:26:ASP:CA	1.76	1.45
1:G:1:MEA:CD2	1:H:8:ILE:CD1	1.93	1.45
1:H:6:LEU:HD22	1:I:15:ILE:CD1	1.46	1.45
1:K:26:ASP:N	1:K:26:ASP:CA	1.76	1.45
1:B:6:LEU:HD22	1:C:15:ILE:CD1	1.45	1.45
1:B:26:ASP:N	1:B:26:ASP:CA	1.76	1.45
1:L:15:ILE:CD1	1:M:6:LEU:HD22	1.46	1.45
1:P:15:ILE:CD1	1:Q:6:LEU:HD22	1.46	1.45
1:Q:15:ILE:CD1	1:R:6:LEU:HD22	1.45	1.45
1:K:8:ILE:CD1	1:L:1:MEA:CD2	1.94	1.44
1:O:8:ILE:CD1	1:P:1:MEA:CD2	1.93	1.44
1:P:26:ASP:N	1:P:26:ASP:CA	1.76	1.44
1:M:8:ILE:CD1	1:N:1:MEA:CD2	1.94	1.44
1:L:8:ILE:CD1	1:M:1:MEA:CD2	1.94	1.44
1:A:6:LEU:HD22	1:B:15:ILE:CD1	1.46	1.43
1:K:15:ILE:CD1	1:L:6:LEU:HD22	1.46	1.43
1:A:8:ILE:CD1	1:J:1:MEA:CD2	1.94	1.43
1:N:8:ILE:CD1	1:O:1:MEA:CD2	1.94	1.43
1:B:1:MEA:CD2	1:C:8:ILE:CD1	1.94	1.43
1:O:15:ILE:CD1	1:P:6:LEU:HD22	1.45	1.43
1:F:1:MEA:CD2	1:G:8:ILE:CD1	1.93	1.43
1:E:6:LEU:HD22	1:F:15:ILE:CD1	1.46	1.42
1:Q:8:ILE:CD1	1:R:1:MEA:CD2	1.94	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MEA:CD2	1:D:8:ILE:CD1	1.94	1.42
1:J:8:ILE:CD1	1:K:1:MEA:CD2	1.94	1.41
1:C:5:GLU:N	1:D:12:ILE:HD12	1.35	1.41
1:M:12:ILE:HD12	1:N:5:GLU:N	1.35	1.41
1:Q:12:ILE:HD12	1:R:5:GLU:N	1.35	1.39
1:A:5:GLU:N	1:B:12:ILE:HD12	1.35	1.38
1:O:12:ILE:HD12	1:P:5:GLU:N	1.35	1.37
1:N:12:ILE:HD12	1:O:5:GLU:N	1.35	1.37
1:B:5:GLU:N	1:C:12:ILE:HD12	1.35	1.37
1:D:5:GLU:N	1:E:12:ILE:HD12	1.35	1.37
1:G:5:GLU:N	1:H:12:ILE:HD12	1.35	1.37
1:H:5:GLU:N	1:I:12:ILE:HD12	1.35	1.36
1:L:12:ILE:HD12	1:M:5:GLU:N	1.35	1.36
1:J:12:ILE:HD12	1:K:5:GLU:N	1.35	1.36
1:P:12:ILE:HD12	1:Q:5:GLU:N	1.35	1.36
1:F:5:GLU:N	1:G:12:ILE:HD12	1.35	1.35
1:A:12:ILE:HD12	1:J:5:GLU:N	1.35	1.34
1:E:5:GLU:N	1:F:12:ILE:HD12	1.35	1.34
1:K:12:ILE:HD12	1:L:5:GLU:N	1.35	1.34
1:C:6:LEU:CD1	1:D:16:LEU:CA	2.09	1.31
1:F:6:LEU:CD1	1:G:16:LEU:CA	2.09	1.30
1:A:8:ILE:CD1	1:J:1:MEA:CE2	2.09	1.30
1:C:1:MEA:CE2	1:D:8:ILE:CD1	2.09	1.30
1:D:1:MEA:CE2	1:E:8:ILE:CD1	2.09	1.30
1:G:6:LEU:CD1	1:H:16:LEU:CA	2.09	1.30
1:J:16:LEU:CA	1:K:6:LEU:CD1	2.09	1.30
1:A:16:LEU:CA	1:J:6:LEU:CD1	2.09	1.30
1:B:6:LEU:CD1	1:C:16:LEU:CA	2.09	1.30
1:H:1:MEA:CE2	1:I:8:ILE:CD1	2.09	1.30
1:M:16:LEU:CA	1:N:6:LEU:CD1	2.09	1.30
1:E:6:LEU:CD1	1:F:16:LEU:CA	2.09	1.29
1:M:8:ILE:CD1	1:N:1:MEA:CE2	2.09	1.29
1:K:16:LEU:HA	1:L:6:LEU:CD1	1.63	1.29
1:M:16:LEU:HA	1:N:6:LEU:CD1	1.63	1.29
1:G:6:LEU:CD1	1:H:16:LEU:HA	1.63	1.29
1:N:16:LEU:CA	1:O:6:LEU:CD1	2.09	1.29
1:A:6:LEU:CD1	1:B:16:LEU:HA	1.63	1.29
1:D:6:LEU:CD1	1:E:16:LEU:HA	1.63	1.29
1:K:16:LEU:CA	1:L:6:LEU:CD1	2.09	1.29
1:N:16:LEU:HA	1:O:6:LEU:CD1	1.63	1.29
1:P:16:LEU:HA	1:Q:6:LEU:CD1	1.63	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:6:LEU:CD1	1:E:16:LEU:CA	2.09	1.29
1:H:6:LEU:CD1	1:I:16:LEU:CA	2.09	1.29
1:J:16:LEU:HA	1:K:6:LEU:CD1	1.63	1.29
1:O:16:LEU:CA	1:P:6:LEU:CD1	2.09	1.29
1:Q:16:LEU:CA	1:R:6:LEU:CD1	2.09	1.29
1:F:6:LEU:CD1	1:G:16:LEU:HA	1.63	1.28
1:J:8:ILE:CD1	1:K:1:MEA:CE2	2.09	1.28
1:A:6:LEU:CD1	1:B:16:LEU:CA	2.09	1.28
1:A:16:LEU:HA	1:J:6:LEU:CD1	1.63	1.28
1:F:1:MEA:CE2	1:G:8:ILE:CD1	2.09	1.28
1:L:8:ILE:CD1	1:M:1:MEA:CE2	2.09	1.28
1:A:1:MEA:CE2	1:B:8:ILE:CD1	2.09	1.27
1:M:41:GLU:OE1	1:Q:10:ILE:CG1	1.82	1.27
1:N:41:GLU:OE1	1:R:10:ILE:CG1	1.82	1.27
1:O:8:ILE:CD1	1:P:1:MEA:CE2	2.09	1.27
1:P:8:ILE:CD1	1:Q:1:MEA:CE2	2.09	1.27
1:P:16:LEU:CA	1:Q:6:LEU:CD1	2.09	1.27
1:B:10:ILE:CG1	1:F:41:GLU:OE1	1.82	1.27
1:E:6:LEU:CD1	1:F:16:LEU:HA	1.63	1.27
1:E:10:ILE:CG1	1:I:41:GLU:OE1	1.82	1.27
1:Q:16:LEU:HA	1:R:6:LEU:CD1	1.63	1.27
1:A:41:GLU:OE1	1:M:10:ILE:CG1	1.82	1.27
1:B:6:LEU:CD1	1:C:16:LEU:HA	1.63	1.27
1:L:16:LEU:CA	1:M:6:LEU:CD1	2.09	1.27
1:Q:8:ILE:CD1	1:R:1:MEA:CE2	2.09	1.27
1:A:10:ILE:CG1	1:E:41:GLU:OE1	1.82	1.27
1:B:41:GLU:OE1	1:L:10:ILE:CG1	1.82	1.27
1:E:1:MEA:CE2	1:F:8:ILE:CD1	2.09	1.27
1:K:16:LEU:CA	1:L:6:LEU:HD12	1.65	1.27
1:L:16:LEU:HA	1:M:6:LEU:CD1	1.63	1.27
1:O:16:LEU:HA	1:P:6:LEU:CD1	1.63	1.27
1:A:6:LEU:HD12	1:B:16:LEU:CA	1.65	1.27
1:C:6:LEU:CD1	1:D:16:LEU:HA	1.63	1.27
1:E:6:LEU:HD12	1:F:16:LEU:CA	1.65	1.27
1:O:16:LEU:CA	1:P:6:LEU:HD12	1.65	1.27
1:H:6:LEU:CD1	1:I:16:LEU:HA	1.63	1.26
1:H:6:LEU:HD12	1:I:16:LEU:CA	1.65	1.26
1:L:16:LEU:CA	1:M:6:LEU:HD12	1.65	1.26
1:L:41:GLU:OE1	1:P:10:ILE:CG1	1.82	1.26
1:C:10:ILE:CG1	1:G:41:GLU:OE1	1.82	1.26
1:J:41:GLU:OE1	1:N:10:ILE:CG1	1.82	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:HD12	1:C:16:LEU:CA	1.65	1.26
1:D:6:LEU:HD12	1:E:16:LEU:CA	1.65	1.26
1:B:1:MEA:CE2	1:C:8:ILE:CD1	2.09	1.26
1:C:99:ASN:ND2	1:G:114:ASN:OD1	1.69	1.26
1:D:41:GLU:OE1	1:J:10:ILE:CG1	1.82	1.26
1:E:10:ILE:CG1	1:I:38:LEU:HA	1.66	1.26
1:A:16:LEU:CA	1:J:6:LEU:HD12	1.65	1.26
1:B:99:ASN:ND2	1:F:114:ASN:OD1	1.69	1.26
1:C:114:ASN:OD1	1:K:99:ASN:ND2	1.69	1.26
1:K:38:LEU:HA	1:O:10:ILE:CG1	1.65	1.26
1:M:114:ASN:OD1	1:Q:99:ASN:ND2	1.69	1.26
1:N:16:LEU:CA	1:O:6:LEU:HD12	1.65	1.26
1:P:16:LEU:CA	1:Q:6:LEU:HD12	1.65	1.26
1:A:114:ASN:OD1	1:M:99:ASN:ND2	1.69	1.25
1:B:38:LEU:HA	1:L:10:ILE:CG1	1.66	1.25
1:C:41:GLU:OE1	1:K:10:ILE:CG1	1.82	1.25
1:D:10:ILE:CG1	1:H:41:GLU:OE1	1.82	1.25
1:B:10:ILE:CG1	1:F:38:LEU:HA	1.65	1.25
1:G:6:LEU:HD12	1:H:16:LEU:CA	1.65	1.25
1:K:41:GLU:OE1	1:O:10:ILE:CG1	1.82	1.25
1:L:38:LEU:HA	1:P:10:ILE:CG1	1.66	1.25
1:E:99:ASN:ND2	1:I:114:ASN:OD1	1.69	1.25
1:F:6:LEU:HD12	1:G:16:LEU:CA	1.65	1.25
1:J:16:LEU:CA	1:K:6:LEU:HD12	1.65	1.25
1:L:114:ASN:OD1	1:P:99:ASN:ND2	1.69	1.25
1:M:16:LEU:CA	1:N:6:LEU:HD12	1.65	1.25
1:C:6:LEU:HD12	1:D:16:LEU:CA	1.65	1.25
1:N:8:ILE:CD1	1:O:1:MEA:CE2	2.09	1.25
1:Q:16:LEU:CA	1:R:6:LEU:HD12	1.65	1.25
1:K:8:ILE:CD1	1:L:1:MEA:CE2	2.09	1.25
1:A:10:ILE:CG1	1:E:38:LEU:HA	1.65	1.24
1:C:38:LEU:HA	1:K:10:ILE:CG1	1.66	1.24
1:C:10:ILE:CG1	1:G:38:LEU:HA	1.66	1.24
1:D:99:ASN:ND2	1:H:114:ASN:OD1	1.69	1.24
1:K:114:ASN:OD1	1:O:99:ASN:ND2	1.69	1.24
1:A:38:LEU:HA	1:M:10:ILE:CG1	1.65	1.24
1:D:10:ILE:CG1	1:H:38:LEU:HA	1.66	1.24
1:D:38:LEU:HA	1:J:10:ILE:CG1	1.66	1.24
1:N:114:ASN:OD1	1:R:99:ASN:ND2	1.69	1.24
1:A:99:ASN:ND2	1:E:114:ASN:OD1	1.69	1.23
1:M:38:LEU:HA	1:Q:10:ILE:CG1	1.66	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:114:ASN:OD1	1:J:99:ASN:ND2	1.69	1.23
1:N:38:LEU:HA	1:R:10:ILE:CG1	1.66	1.23
1:F:6:LEU:CA	1:G:16:LEU:HD13	1.69	1.23
1:Q:16:LEU:HD13	1:R:6:LEU:CA	1.69	1.23
1:C:38:LEU:CD1	1:K:10:ILE:CD1	2.02	1.23
1:J:114:ASN:OD1	1:N:99:ASN:ND2	1.69	1.23
1:J:38:LEU:HA	1:N:10:ILE:CG1	1.65	1.23
1:N:16:LEU:HD13	1:O:6:LEU:CA	1.69	1.23
1:B:6:LEU:CA	1:C:16:LEU:HD13	1.69	1.22
1:B:114:ASN:OD1	1:L:99:ASN:ND2	1.69	1.22
1:C:6:LEU:CA	1:D:16:LEU:HD13	1.69	1.22
1:G:1:MEA:CE2	1:H:8:ILE:CD1	2.09	1.22
1:E:6:LEU:CA	1:F:16:LEU:HD13	1.69	1.22
1:M:16:LEU:HD13	1:N:6:LEU:CA	1.69	1.22
1:M:38:LEU:CD1	1:Q:10:ILE:CD1	2.02	1.22
1:C:117:VAL:O	1:K:21:LEU:HG	1.39	1.22
1:G:6:LEU:CA	1:H:16:LEU:HD13	1.69	1.22
1:J:117:VAL:O	1:N:21:LEU:HG	1.39	1.22
1:O:16:LEU:HD13	1:P:6:LEU:CA	1.69	1.22
1:A:16:LEU:CD1	1:J:6:LEU:HA	1.71	1.21
1:A:16:LEU:HD13	1:J:6:LEU:CA	1.69	1.21
1:K:16:LEU:HD13	1:L:6:LEU:CA	1.69	1.21
1:P:16:LEU:HD13	1:Q:6:LEU:CA	1.69	1.21
1:C:6:LEU:HA	1:D:16:LEU:CD1	1.71	1.21
1:G:6:LEU:HA	1:H:16:LEU:CD1	1.71	1.21
1:H:6:LEU:CA	1:I:16:LEU:HD13	1.69	1.21
1:P:16:LEU:CD1	1:Q:6:LEU:HA	1.71	1.21
1:Q:16:LEU:CD1	1:R:6:LEU:HA	1.70	1.21
1:J:16:LEU:HD13	1:K:6:LEU:CA	1.69	1.21
1:K:117:VAL:O	1:O:21:LEU:HG	1.39	1.21
1:L:16:LEU:HD13	1:M:6:LEU:CA	1.69	1.21
1:D:6:LEU:CA	1:E:16:LEU:HD13	1.69	1.21
1:D:38:LEU:CD1	1:J:10:ILE:CD1	2.02	1.21
1:N:16:LEU:CD1	1:O:6:LEU:HA	1.71	1.20
1:B:38:LEU:CD1	1:L:10:ILE:CD1	2.02	1.20
1:C:21:LEU:HG	1:G:117:VAL:O	1.39	1.20
1:D:117:VAL:O	1:J:21:LEU:HG	1.39	1.20
1:J:16:LEU:CD1	1:K:6:LEU:HA	1.71	1.20
1:L:16:LEU:CD1	1:M:6:LEU:HA	1.71	1.20
1:N:117:VAL:O	1:R:21:LEU:HG	1.39	1.20
1:A:6:LEU:CA	1:B:16:LEU:HD13	1.69	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:16:LEU:CD1	1:N:6:LEU:HA	1.71	1.20
1:B:6:LEU:HA	1:C:16:LEU:CD1	1.71	1.20
1:D:10:ILE:CD1	1:H:38:LEU:CD1	2.02	1.20
1:H:6:LEU:HA	1:I:16:LEU:CD1	1.71	1.20
1:D:6:LEU:HA	1:E:16:LEU:CD1	1.71	1.19
1:E:6:LEU:HA	1:F:16:LEU:CD1	1.71	1.19
1:F:6:LEU:HA	1:G:16:LEU:CD1	1.71	1.19
1:K:16:LEU:CD1	1:L:6:LEU:HA	1.71	1.19
1:B:117:VAL:O	1:L:21:LEU:HG	1.39	1.19
1:E:21:LEU:HG	1:I:117:VAL:O	1.39	1.19
1:O:16:LEU:CD1	1:P:6:LEU:HA	1.71	1.19
1:E:15:ILE:CG2	1:H:76:LYS:HE2	1.73	1.19
1:A:6:LEU:HA	1:B:16:LEU:CD1	1.71	1.19
1:A:16:LEU:N	1:J:6:LEU:HD13	1.58	1.19
1:A:76:LYS:HE2	1:L:15:ILE:CG2	1.73	1.19
1:B:21:LEU:HG	1:F:117:VAL:O	1.39	1.19
1:G:6:LEU:HD13	1:H:16:LEU:N	1.58	1.19
1:P:16:LEU:N	1:Q:6:LEU:HD13	1.58	1.19
1:M:16:LEU:N	1:N:6:LEU:HD13	1.58	1.19
1:M:117:VAL:O	1:Q:21:LEU:HG	1.39	1.19
1:D:6:LEU:HD13	1:E:16:LEU:N	1.58	1.18
1:L:16:LEU:N	1:M:6:LEU:HD13	1.58	1.18
1:L:117:VAL:O	1:P:21:LEU:HG	1.39	1.18
1:M:76:LYS:HE2	1:P:15:ILE:CG2	1.73	1.18
1:N:76:LYS:HE2	1:Q:15:ILE:CG2	1.73	1.18
1:C:6:LEU:HD13	1:D:16:LEU:N	1.58	1.18
1:C:76:LYS:HE2	1:J:15:ILE:CG2	1.73	1.18
1:J:16:LEU:N	1:K:6:LEU:HD13	1.58	1.18
1:K:16:LEU:N	1:L:6:LEU:HD13	1.58	1.18
1:Q:16:LEU:N	1:R:6:LEU:HD13	1.58	1.18
1:A:6:LEU:HD13	1:B:16:LEU:N	1.58	1.18
1:A:15:ILE:CG2	1:D:76:LYS:HE2	1.73	1.18
1:A:21:LEU:HG	1:E:117:VAL:O	1.39	1.18
1:B:6:LEU:HD13	1:C:16:LEU:N	1.58	1.18
1:C:10:ILE:CD1	1:G:38:LEU:CD1	2.02	1.18
1:D:15:ILE:CG2	1:G:76:LYS:HE2	1.73	1.18
1:E:6:LEU:HD13	1:F:16:LEU:N	1.58	1.18
1:F:6:LEU:HD13	1:G:16:LEU:N	1.58	1.18
1:H:6:LEU:HD13	1:I:16:LEU:N	1.58	1.18
1:N:16:LEU:N	1:O:6:LEU:HD13	1.58	1.18
1:O:16:LEU:N	1:P:6:LEU:HD13	1.58	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:10:ILE:CD1	1:I:38:LEU:CD1	2.02	1.17
1:J:76:LYS:HE2	1:M:15:ILE:CG2	1.73	1.17
1:A:10:ILE:CD1	1:E:38:LEU:CD1	2.02	1.17
1:B:76:LYS:HE2	1:K:15:ILE:CG2	1.73	1.17
1:B:10:ILE:CD1	1:F:38:LEU:CD1	2.02	1.17
1:B:15:ILE:CG2	1:E:76:LYS:HE2	1.73	1.17
1:F:15:ILE:CG2	1:I:76:LYS:HE2	1.73	1.17
1:O:76:LYS:HE2	1:R:15:ILE:CG2	1.73	1.17
1:A:117:VAL:O	1:M:21:LEU:HG	1.39	1.17
1:K:38:LEU:CD1	1:O:10:ILE:CD1	2.02	1.17
1:C:15:ILE:CG2	1:F:76:LYS:HE2	1.73	1.16
1:K:76:LYS:HE2	1:N:15:ILE:CG2	1.73	1.16
1:D:21:LEU:HG	1:H:117:VAL:O	1.39	1.16
1:B:38:LEU:HD13	1:L:10:ILE:CG1	1.71	1.16
1:L:76:LYS:HE2	1:O:15:ILE:CG2	1.73	1.16
1:B:15:ILE:HG21	1:E:76:LYS:HE2	1.16	1.15
1:K:76:LYS:HE2	1:N:15:ILE:HG21	1.16	1.15
1:C:15:ILE:HG21	1:F:76:LYS:HE2	1.16	1.14
1:J:38:LEU:CD1	1:N:10:ILE:CD1	2.02	1.14
1:A:38:LEU:HD13	1:M:10:ILE:CG1	1.71	1.14
1:D:25:GLN:OE1	1:H:52:LEU:HG	1.48	1.14
1:L:76:LYS:HE2	1:O:15:ILE:HG21	1.16	1.14
1:A:52:LEU:HG	1:M:25:GLN:OE1	1.48	1.13
1:E:10:ILE:CG1	1:I:38:LEU:HD13	1.71	1.13
1:J:38:LEU:HD13	1:N:10:ILE:CG1	1.71	1.13
1:M:52:LEU:HG	1:Q:25:GLN:OE1	1.48	1.13
1:D:52:LEU:HG	1:J:25:GLN:OE1	1.48	1.13
1:A:25:GLN:OE1	1:E:52:LEU:HG	1.48	1.13
1:K:38:LEU:CA	1:O:10:ILE:HG12	1.79	1.13
1:A:10:ILE:HG12	1:E:38:LEU:CA	1.79	1.13
1:B:10:ILE:HG12	1:F:38:LEU:CA	1.79	1.13
1:D:21:LEU:O	1:H:116:SER:HB3	1.49	1.13
1:E:21:LEU:O	1:I:116:SER:HB3	1.49	1.13
1:J:116:SER:HB3	1:N:21:LEU:O	1.49	1.13
1:L:38:LEU:CA	1:P:10:ILE:HG12	1.79	1.13
1:L:52:LEU:HG	1:P:25:GLN:OE1	1.48	1.13
1:N:38:LEU:CD1	1:R:10:ILE:CD1	2.02	1.13
1:D:38:LEU:CA	1:J:10:ILE:HG12	1.79	1.12
1:E:25:GLN:OE1	1:I:52:LEU:HG	1.48	1.12
1:M:38:LEU:CA	1:Q:10:ILE:HG12	1.79	1.12
1:A:116:SER:HB3	1:M:21:LEU:O	1.49	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:GLN:OE1	1:F:52:LEU:HG	1.48	1.12
1:B:52:LEU:HG	1:L:25:GLN:OE1	1.48	1.12
1:C:21:LEU:O	1:G:116:SER:HB3	1.49	1.12
1:C:25:GLN:OE1	1:G:52:LEU:HG	1.48	1.12
1:J:52:LEU:HG	1:N:25:GLN:OE1	1.48	1.12
1:K:116:SER:HB3	1:O:21:LEU:O	1.49	1.12
1:A:16:LEU:N	1:J:6:LEU:CD1	2.13	1.12
1:K:52:LEU:HG	1:O:25:GLN:OE1	1.48	1.12
1:L:116:SER:HB3	1:P:21:LEU:O	1.49	1.12
1:N:16:LEU:N	1:O:6:LEU:CD1	2.13	1.12
1:B:116:SER:HB3	1:L:21:LEU:O	1.49	1.12
1:C:6:LEU:CD1	1:D:16:LEU:N	2.13	1.12
1:D:10:ILE:HG12	1:H:38:LEU:CA	1.79	1.12
1:E:10:ILE:HG12	1:I:38:LEU:CA	1.79	1.12
1:J:16:LEU:N	1:K:6:LEU:CD1	2.13	1.12
1:L:38:LEU:CD1	1:P:10:ILE:CD1	2.02	1.12
1:M:116:SER:HB3	1:Q:21:LEU:O	1.49	1.12
1:N:52:LEU:HG	1:R:25:GLN:OE1	1.48	1.12
1:Q:16:LEU:N	1:R:6:LEU:CD1	2.13	1.12
1:C:25:GLN:HE22	1:G:52:LEU:CD2	1.63	1.12
1:C:52:LEU:HG	1:K:25:GLN:OE1	1.48	1.12
1:D:10:ILE:CG1	1:H:38:LEU:HD13	1.71	1.12
1:F:6:LEU:CD1	1:G:16:LEU:N	2.13	1.12
1:F:15:ILE:HG21	1:I:76:LYS:CE	1.80	1.12
1:J:38:LEU:CA	1:N:10:ILE:HG12	1.79	1.12
1:A:76:LYS:HE2	1:L:15:ILE:HG21	1.16	1.11
1:B:21:LEU:O	1:F:116:SER:HB3	1.49	1.11
1:B:76:LYS:CE	1:K:15:ILE:HG21	1.80	1.11
1:C:10:ILE:HG12	1:G:38:LEU:CA	1.79	1.11
1:C:38:LEU:CA	1:K:10:ILE:HG12	1.79	1.11
1:D:41:GLU:OE1	1:J:10:ILE:HG13	1.50	1.11
1:D:52:LEU:CD2	1:J:25:GLN:HE22	1.63	1.11
1:J:52:LEU:CD2	1:N:25:GLN:HE22	1.64	1.11
1:A:38:LEU:CA	1:M:10:ILE:HG12	1.79	1.11
1:E:15:ILE:HG21	1:H:76:LYS:CE	1.80	1.11
1:J:76:LYS:CE	1:M:15:ILE:HG21	1.80	1.11
1:M:52:LEU:CD2	1:Q:25:GLN:HE22	1.64	1.11
1:N:52:LEU:CD2	1:R:25:GLN:HE22	1.64	1.11
1:B:6:LEU:CD1	1:C:16:LEU:N	2.13	1.11
1:B:52:LEU:HD21	1:L:25:GLN:HE22	1.13	1.11
1:C:52:LEU:CD2	1:K:25:GLN:HE22	1.64	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:25:GLN:HE22	1:H:52:LEU:CD2	1.63	1.11
1:K:38:LEU:HD13	1:O:10:ILE:CG1	1.71	1.11
1:K:41:GLU:OE1	1:O:10:ILE:HG13	1.50	1.11
1:M:41:GLU:OE1	1:Q:10:ILE:HG13	1.50	1.11
1:O:76:LYS:HE2	1:R:15:ILE:HG21	1.16	1.11
1:A:76:LYS:CE	1:L:15:ILE:HG21	1.80	1.11
1:B:38:LEU:CA	1:L:10:ILE:HG12	1.79	1.11
1:C:10:ILE:CG1	1:G:38:LEU:HD13	1.71	1.11
1:D:15:ILE:HG21	1:G:76:LYS:CE	1.80	1.11
1:K:76:LYS:CE	1:N:15:ILE:HG21	1.80	1.11
1:O:76:LYS:CE	1:R:15:ILE:HG21	1.80	1.11
1:A:21:LEU:O	1:E:116:SER:HB3	1.49	1.11
1:B:25:GLN:HE22	1:F:52:LEU:HD21	1.13	1.11
1:M:12:ILE:CD1	1:N:5:GLU:N	2.02	1.11
1:A:52:LEU:CD2	1:M:25:GLN:HE22	1.64	1.10
1:B:10:ILE:HG13	1:F:41:GLU:OE1	1.50	1.10
1:L:116:SER:HA	1:P:25:GLN:NE2	1.67	1.10
1:N:38:LEU:CA	1:R:10:ILE:HG12	1.79	1.10
1:C:15:ILE:HG21	1:F:76:LYS:CE	1.80	1.10
1:D:116:SER:HB3	1:J:21:LEU:O	1.49	1.10
1:J:12:ILE:CD1	1:K:5:GLU:N	2.02	1.10
1:K:52:LEU:HD21	1:O:25:GLN:HE22	1.13	1.10
1:K:52:LEU:CD2	1:O:25:GLN:HE22	1.64	1.10
1:A:15:ILE:HG21	1:D:76:LYS:CE	1.80	1.10
1:A:116:SER:HA	1:M:25:GLN:NE2	1.67	1.10
1:B:10:ILE:CG1	1:F:38:LEU:HD13	1.71	1.10
1:B:25:GLN:HE22	1:F:52:LEU:CD2	1.63	1.10
1:C:116:SER:HB3	1:K:21:LEU:O	1.49	1.10
1:D:25:GLN:HE22	1:H:52:LEU:HD21	1.13	1.10
1:L:76:LYS:CE	1:O:15:ILE:HG21	1.80	1.10
1:M:76:LYS:CE	1:P:15:ILE:HG21	1.80	1.10
1:B:116:SER:HA	1:L:25:GLN:NE2	1.67	1.10
1:C:76:LYS:CE	1:J:15:ILE:HG21	1.80	1.10
1:K:76:LYS:CE	1:N:15:ILE:CG2	2.30	1.10
1:L:52:LEU:HD21	1:P:25:GLN:HE22	1.13	1.10
1:M:16:LEU:N	1:N:6:LEU:CD1	2.13	1.10
1:E:15:ILE:CG2	1:H:76:LYS:CE	2.30	1.10
1:F:15:ILE:CG2	1:I:76:LYS:CE	2.30	1.10
1:M:116:SER:HA	1:Q:25:GLN:NE2	1.67	1.10
1:A:15:ILE:CG2	1:D:76:LYS:CE	2.30	1.09
1:A:25:GLN:NE2	1:E:116:SER:HA	1.67	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:GLN:HE22	1:E:52:LEU:CD2	1.63	1.09
1:E:25:GLN:NE2	1:I:116:SER:HA	1.67	1.09
1:F:15:ILE:HG21	1:I:76:LYS:HE2	1.16	1.09
1:G:6:LEU:CD1	1:H:16:LEU:N	2.13	1.09
1:M:76:LYS:CE	1:P:15:ILE:CG2	2.30	1.09
1:C:76:LYS:HE2	1:J:15:ILE:HG21	1.16	1.09
1:J:41:GLU:OE1	1:N:10:ILE:HG13	1.50	1.09
1:O:76:LYS:CE	1:R:15:ILE:CG2	2.30	1.09
1:A:25:GLN:HE22	1:E:52:LEU:HD21	1.13	1.09
1:A:76:LYS:CE	1:L:15:ILE:CG2	2.30	1.09
1:B:25:GLN:NE2	1:F:116:SER:HA	1.67	1.09
1:B:76:LYS:HE2	1:K:15:ILE:HG21	1.16	1.09
1:B:76:LYS:CE	1:K:15:ILE:CG2	2.30	1.09
1:D:38:LEU:HD13	1:J:10:ILE:CG1	1.71	1.09
1:E:15:ILE:HG21	1:H:76:LYS:HE2	1.16	1.09
1:J:76:LYS:CE	1:M:15:ILE:CG2	2.30	1.09
1:L:76:LYS:CE	1:O:15:ILE:CG2	2.30	1.09
1:N:38:LEU:HD13	1:R:10:ILE:CG1	1.71	1.09
1:N:116:SER:HB3	1:R:21:LEU:O	1.49	1.09
1:P:16:LEU:N	1:Q:6:LEU:CD1	2.13	1.09
1:C:76:LYS:CE	1:J:15:ILE:CG2	2.30	1.09
1:D:10:ILE:HG13	1:H:41:GLU:OE1	1.50	1.09
1:D:15:ILE:CG2	1:G:76:LYS:CE	2.30	1.09
1:F:15:ILE:HD12	1:I:35:GLU:OE1	1.53	1.09
1:L:35:GLU:OE1	1:O:15:ILE:HD12	1.53	1.09
1:L:52:LEU:CD2	1:P:25:GLN:HE22	1.64	1.09
1:N:76:LYS:CE	1:Q:15:ILE:HG21	1.80	1.09
1:A:15:ILE:HD12	1:D:35:GLU:OE1	1.53	1.09
1:B:15:ILE:HG21	1:E:76:LYS:CE	1.80	1.09
1:B:15:ILE:HD12	1:E:35:GLU:OE1	1.53	1.09
1:B:35:GLU:OE1	1:K:15:ILE:HD12	1.53	1.09
1:K:116:SER:HA	1:O:25:GLN:NE2	1.67	1.09
1:B:52:LEU:CD2	1:L:25:GLN:HE22	1.64	1.08
1:C:15:ILE:CG2	1:F:76:LYS:CE	2.30	1.08
1:H:6:LEU:CD1	1:I:16:LEU:N	2.13	1.08
1:J:35:GLU:OE1	1:M:15:ILE:HD12	1.53	1.08
1:J:76:LYS:HE2	1:M:15:ILE:HG21	1.16	1.08
1:O:35:GLU:OE1	1:R:15:ILE:HD12	1.53	1.08
1:A:52:LEU:HD21	1:M:25:GLN:HE22	1.13	1.08
1:D:6:LEU:CD1	1:E:16:LEU:N	2.13	1.08
1:D:25:GLN:NE2	1:H:116:SER:HA	1.67	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:GLN:HE22	1:I:52:LEU:CD2	1.63	1.08
1:F:6:LEU:HD12	1:G:16:LEU:HA	1.24	1.08
1:A:38:LEU:CD1	1:M:10:ILE:CD1	2.02	1.08
1:C:41:GLU:OE1	1:K:10:ILE:HG13	1.50	1.08
1:E:25:GLN:HE22	1:I:52:LEU:HD21	1.12	1.08
1:K:35:GLU:OE1	1:N:15:ILE:HD12	1.53	1.08
1:A:41:GLU:OE1	1:M:10:ILE:HG13	1.50	1.08
1:B:15:ILE:CG2	1:E:76:LYS:CE	2.30	1.08
1:C:38:LEU:HD13	1:K:10:ILE:CG1	1.71	1.08
1:C:52:LEU:HD21	1:K:25:GLN:HE22	1.13	1.08
1:D:15:ILE:HD12	1:G:35:GLU:OE1	1.53	1.08
1:D:116:SER:HA	1:J:25:GLN:NE2	1.67	1.08
1:K:15:ILE:HD12	1:L:6:LEU:HD22	1.34	1.08
1:L:16:LEU:N	1:M:6:LEU:CD1	2.13	1.08
1:M:35:GLU:OE1	1:P:15:ILE:HD12	1.53	1.08
1:O:16:LEU:N	1:P:6:LEU:CD1	2.13	1.08
1:A:6:LEU:CD2	1:B:15:ILE:CD1	2.32	1.08
1:A:15:ILE:HG21	1:D:76:LYS:HE2	1.16	1.08
1:C:15:ILE:HD12	1:F:35:GLU:OE1	1.53	1.08
1:C:116:SER:HA	1:K:25:GLN:NE2	1.67	1.08
1:G:6:LEU:HD12	1:H:16:LEU:HA	1.25	1.08
1:H:6:LEU:CD2	1:I:15:ILE:CD1	2.32	1.08
1:L:38:LEU:HD13	1:P:10:ILE:CG1	1.71	1.08
1:M:38:LEU:HD13	1:Q:10:ILE:CG1	1.71	1.08
1:N:76:LYS:CE	1:Q:15:ILE:CG2	2.30	1.08
1:N:116:SER:HA	1:R:25:GLN:NE2	1.67	1.08
1:O:15:ILE:CD1	1:P:6:LEU:CD2	2.32	1.08
1:A:6:LEU:CD1	1:B:16:LEU:N	2.13	1.07
1:C:25:GLN:NE2	1:G:116:SER:HA	1.67	1.07
1:D:15:ILE:HG21	1:G:76:LYS:HE2	1.16	1.07
1:K:116:SER:CB	1:O:21:LEU:CD1	2.29	1.07
1:J:52:LEU:HD21	1:N:25:GLN:HE22	1.13	1.07
1:K:16:LEU:N	1:L:6:LEU:CD1	2.13	1.07
1:L:15:ILE:CD1	1:M:6:LEU:CD2	2.32	1.07
1:A:12:ILE:CD1	1:J:5:GLU:N	2.02	1.07
1:C:10:ILE:HG13	1:G:41:GLU:OE1	1.50	1.07
1:D:52:LEU:HD21	1:J:25:GLN:HE22	1.13	1.07
1:E:6:LEU:HD22	1:F:15:ILE:HD12	1.34	1.07
1:E:6:LEU:CD2	1:F:15:ILE:CD1	2.32	1.07
1:K:15:ILE:CD1	1:L:6:LEU:CD2	2.32	1.07
1:M:116:SER:CB	1:Q:21:LEU:CD1	2.29	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:6:LEU:CD2	1:E:15:ILE:CD1	2.32	1.07
1:J:116:SER:HA	1:N:25:GLN:NE2	1.67	1.07
1:M:15:ILE:CD1	1:N:6:LEU:CD2	2.32	1.07
1:A:15:ILE:CD1	1:J:6:LEU:CD2	2.32	1.06
1:B:21:LEU:CD1	1:F:116:SER:CB	2.29	1.06
1:B:41:GLU:OE1	1:L:10:ILE:HG13	1.50	1.06
1:C:6:LEU:CD2	1:D:15:ILE:CD1	2.32	1.06
1:E:6:LEU:CD1	1:F:16:LEU:N	2.13	1.06
1:G:6:LEU:CD2	1:H:15:ILE:CD1	2.32	1.06
1:M:76:LYS:HE2	1:P:15:ILE:HG21	1.16	1.06
1:N:76:LYS:HE2	1:Q:15:ILE:HG21	1.16	1.06
1:A:6:LEU:HD12	1:B:16:LEU:CB	1.86	1.06
1:A:16:LEU:CB	1:J:6:LEU:HD12	1.86	1.06
1:C:25:GLN:HE22	1:G:52:LEU:HD21	1.12	1.06
1:N:35:GLU:OE1	1:Q:15:ILE:HD12	1.53	1.06
1:O:16:LEU:CB	1:P:6:LEU:HD12	1.86	1.06
1:P:15:ILE:CD1	1:Q:6:LEU:CD2	2.32	1.06
1:P:16:LEU:CB	1:Q:6:LEU:HD12	1.86	1.06
1:Q:15:ILE:CD1	1:R:6:LEU:CD2	2.32	1.06
1:A:10:ILE:HG13	1:E:41:GLU:OE1	1.50	1.06
1:B:116:SER:CB	1:L:21:LEU:CD1	2.29	1.06
1:G:6:LEU:HD12	1:H:16:LEU:CB	1.86	1.06
1:N:41:GLU:OE1	1:R:10:ILE:HG13	1.50	1.06
1:C:35:GLU:OE1	1:J:15:ILE:HD12	1.53	1.06
1:E:21:LEU:CD1	1:I:116:SER:CB	2.29	1.06
1:H:6:LEU:HD12	1:I:16:LEU:CB	1.86	1.06
1:J:15:ILE:CD1	1:K:6:LEU:CD2	2.32	1.06
1:J:16:LEU:CB	1:K:6:LEU:HD12	1.86	1.06
1:L:41:GLU:OE1	1:P:10:ILE:HG13	1.50	1.06
1:A:5:GLU:N	1:B:12:ILE:CD1	2.02	1.05
1:B:6:LEU:CD2	1:C:15:ILE:CD1	2.32	1.05
1:F:6:LEU:HD12	1:G:16:LEU:CB	1.86	1.05
1:H:6:LEU:HD12	1:I:16:LEU:HA	1.24	1.05
1:J:16:LEU:HA	1:K:6:LEU:HD12	1.24	1.05
1:N:15:ILE:CD1	1:O:6:LEU:CD2	2.32	1.05
1:O:12:ILE:CD1	1:P:5:GLU:N	2.02	1.05
1:A:10:ILE:CG1	1:E:38:LEU:HD13	1.71	1.05
1:A:35:GLU:OE1	1:L:15:ILE:HD12	1.53	1.05
1:E:6:LEU:HD12	1:F:16:LEU:CB	1.86	1.05
1:E:15:ILE:HD12	1:H:35:GLU:OE1	1.53	1.05
1:F:6:LEU:CD2	1:G:15:ILE:CD1	2.32	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:16:LEU:CB	1:N:6:LEU:HD12	1.86	1.05
1:M:52:LEU:HD21	1:Q:25:GLN:HE22	1.13	1.05
1:N:16:LEU:CB	1:O:6:LEU:HD12	1.86	1.05
1:Q:16:LEU:CB	1:R:6:LEU:HD12	1.86	1.05
1:B:6:LEU:HD12	1:C:16:LEU:CB	1.86	1.05
1:E:10:ILE:HG13	1:I:41:GLU:OE1	1.50	1.05
1:D:6:LEU:HD12	1:E:16:LEU:CB	1.86	1.05
1:F:6:LEU:HD22	1:G:15:ILE:CG1	1.87	1.05
1:H:5:GLU:N	1:I:12:ILE:CD1	2.02	1.05
1:J:15:ILE:CG1	1:K:6:LEU:HD22	1.87	1.05
1:K:16:LEU:HA	1:L:6:LEU:HD12	1.24	1.05
1:L:16:LEU:CB	1:M:6:LEU:HD12	1.86	1.05
1:A:116:SER:CB	1:M:21:LEU:CD1	2.29	1.05
1:E:5:GLU:N	1:F:12:ILE:CD1	2.02	1.05
1:J:116:SER:HB2	1:N:21:LEU:CD1	1.87	1.05
1:A:116:SER:HB2	1:M:21:LEU:CD1	1.87	1.04
1:B:116:SER:HB2	1:L:21:LEU:CD1	1.87	1.04
1:G:6:LEU:HD22	1:H:15:ILE:CG1	1.87	1.04
1:J:41:GLU:OE1	1:N:10:ILE:CG2	2.05	1.04
1:K:16:LEU:CB	1:L:6:LEU:HD12	1.86	1.04
1:M:15:ILE:HD12	1:N:6:LEU:HD22	1.34	1.04
1:N:41:GLU:OE1	1:R:10:ILE:CG2	2.05	1.04
1:N:52:LEU:HD21	1:R:25:GLN:HE22	1.13	1.04
1:Q:15:ILE:CG1	1:R:6:LEU:HD22	1.87	1.04
1:A:15:ILE:HD12	1:J:6:LEU:HD22	1.34	1.04
1:A:15:ILE:CG1	1:J:6:LEU:HD22	1.87	1.04
1:A:21:LEU:CD1	1:E:116:SER:HB2	1.87	1.04
1:A:41:GLU:OE1	1:M:10:ILE:CG2	2.05	1.04
1:B:6:LEU:HD12	1:C:16:LEU:HA	1.24	1.04
1:C:6:LEU:HD12	1:D:16:LEU:CB	1.86	1.04
1:C:10:ILE:CG2	1:G:41:GLU:OE1	2.05	1.04
1:C:41:GLU:OE1	1:K:10:ILE:CG2	2.05	1.04
1:D:10:ILE:CG2	1:H:41:GLU:OE1	2.05	1.04
1:D:41:GLU:OE1	1:J:10:ILE:CG2	2.05	1.04
1:E:10:ILE:CG2	1:I:41:GLU:OE1	2.05	1.04
1:G:6:LEU:HD22	1:H:15:ILE:HD12	1.34	1.04
1:K:41:GLU:OE1	1:O:10:ILE:CG2	2.05	1.04
1:N:15:ILE:CG1	1:O:6:LEU:HD22	1.87	1.04
1:B:10:ILE:CG2	1:F:41:GLU:OE1	2.05	1.04
1:B:41:GLU:OE1	1:L:10:ILE:CG2	2.05	1.04
1:C:21:LEU:CD1	1:G:116:SER:HB2	1.87	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:116:SER:HB2	1:O:21:LEU:CD1	1.87	1.04
1:L:41:GLU:OE1	1:P:10:ILE:CG2	2.05	1.04
1:M:15:ILE:CG1	1:N:6:LEU:HD22	1.87	1.04
1:M:41:GLU:OE1	1:Q:10:ILE:CG2	2.05	1.04
1:N:116:SER:CB	1:R:21:LEU:CD1	2.29	1.04
1:A:15:ILE:HD12	1:J:6:LEU:CD2	1.88	1.04
1:B:21:LEU:CD1	1:F:116:SER:HB2	1.87	1.04
1:C:6:LEU:HD22	1:D:15:ILE:HD12	1.35	1.04
1:D:21:LEU:CD1	1:H:116:SER:HB2	1.87	1.04
1:D:116:SER:CB	1:J:21:LEU:C	2.31	1.04
1:G:6:LEU:CD2	1:H:15:ILE:HD12	1.88	1.04
1:J:116:SER:CB	1:N:21:LEU:CD1	2.29	1.04
1:M:15:ILE:HD12	1:N:6:LEU:CD2	1.88	1.04
1:P:15:ILE:HD12	1:Q:6:LEU:HD22	1.34	1.04
1:A:16:LEU:HA	1:J:6:LEU:HD12	1.24	1.04
1:C:6:LEU:CD2	1:D:15:ILE:HD12	1.88	1.04
1:D:21:LEU:C	1:H:116:SER:CB	2.31	1.04
1:J:116:SER:CB	1:N:21:LEU:C	2.31	1.04
1:L:116:SER:HB2	1:P:21:LEU:CD1	1.87	1.04
1:L:116:SER:CB	1:P:21:LEU:C	2.31	1.04
1:P:15:ILE:CG1	1:Q:6:LEU:HD22	1.87	1.04
1:A:6:LEU:HD12	1:B:16:LEU:HA	1.24	1.03
1:B:6:LEU:HD22	1:C:15:ILE:CG1	1.87	1.03
1:B:21:LEU:C	1:F:116:SER:CB	2.31	1.03
1:C:116:SER:HB2	1:K:21:LEU:CD1	1.87	1.03
1:K:116:SER:CB	1:O:21:LEU:C	2.31	1.03
1:L:16:LEU:HA	1:M:6:LEU:HD12	1.24	1.03
1:O:15:ILE:HD12	1:P:6:LEU:HD22	1.34	1.03
1:P:15:ILE:HD12	1:Q:6:LEU:CD2	1.88	1.03
1:A:6:LEU:HD22	1:B:15:ILE:CG1	1.87	1.03
1:B:116:SER:CB	1:L:21:LEU:C	2.31	1.03
1:C:6:LEU:HD22	1:D:15:ILE:CG1	1.87	1.03
1:D:5:GLU:N	1:E:12:ILE:CD1	2.02	1.03
1:E:6:LEU:HD22	1:F:15:ILE:CG1	1.87	1.03
1:H:6:LEU:HD22	1:I:15:ILE:CG1	1.87	1.03
1:K:12:ILE:CD1	1:L:5:GLU:N	2.02	1.03
1:K:15:ILE:CG1	1:L:6:LEU:HD22	1.87	1.03
1:N:15:ILE:HD12	1:O:6:LEU:CD2	1.88	1.03
1:A:10:ILE:CG2	1:E:41:GLU:OE1	2.05	1.03
1:B:6:LEU:CD2	1:C:15:ILE:HD12	1.88	1.03
1:C:5:GLU:N	1:D:12:ILE:CD1	2.02	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:116:SER:CB	1:K:21:LEU:C	2.31	1.03
1:E:21:LEU:C	1:I:116:SER:CB	2.31	1.03
1:F:5:GLU:N	1:G:12:ILE:CD1	2.02	1.03
1:N:116:SER:CB	1:R:21:LEU:C	2.31	1.03
1:O:15:ILE:CG1	1:P:6:LEU:HD22	1.87	1.03
1:Q:15:ILE:HD12	1:R:6:LEU:HD22	1.34	1.03
1:A:6:LEU:CD2	1:B:15:ILE:HD12	1.88	1.03
1:A:21:LEU:C	1:E:116:SER:CB	2.31	1.03
1:A:116:SER:CB	1:M:21:LEU:C	2.31	1.03
1:H:6:LEU:CD2	1:I:15:ILE:HD12	1.88	1.03
1:N:12:ILE:CD1	1:O:5:GLU:N	2.02	1.03
1:Q:12:ILE:CD1	1:R:5:GLU:N	2.02	1.03
1:Q:15:ILE:HD12	1:R:6:LEU:CD2	1.88	1.03
1:J:15:ILE:HD12	1:K:6:LEU:HD22	1.34	1.03
1:L:12:ILE:CD1	1:M:5:GLU:N	2.02	1.03
1:N:116:SER:HB2	1:R:21:LEU:CD1	1.87	1.03
1:O:15:ILE:HD12	1:P:6:LEU:CD2	1.88	1.03
1:C:21:LEU:C	1:G:116:SER:CB	2.31	1.02
1:D:116:SER:HB2	1:J:21:LEU:CD1	1.87	1.02
1:F:6:LEU:CD2	1:G:15:ILE:HD12	1.88	1.02
1:L:15:ILE:CG1	1:M:6:LEU:HD22	1.87	1.02
1:M:116:SER:CB	1:Q:21:LEU:C	2.31	1.02
1:Q:16:LEU:HA	1:R:6:LEU:HD12	1.25	1.02
1:D:6:LEU:HD22	1:E:15:ILE:HD12	1.34	1.02
1:L:15:ILE:HD12	1:M:6:LEU:CD2	1.88	1.02
1:O:16:LEU:HA	1:P:6:LEU:HD12	1.25	1.02
1:D:6:LEU:HD22	1:E:15:ILE:CG1	1.87	1.02
1:E:21:LEU:CD1	1:I:116:SER:HB2	1.87	1.02
1:M:116:SER:HB2	1:Q:21:LEU:CD1	1.87	1.02
1:F:6:LEU:HD22	1:G:15:ILE:HD12	1.34	1.02
1:J:15:ILE:HD12	1:K:6:LEU:CD2	1.88	1.02
1:L:116:SER:HA	1:P:25:GLN:HE21	1.24	1.02
1:A:6:LEU:O	1:E:38:LEU:CD2	2.08	1.01
1:A:38:LEU:CD2	1:M:6:LEU:O	2.08	1.01
1:B:38:LEU:CD2	1:L:6:LEU:O	2.08	1.01
1:C:6:LEU:O	1:G:38:LEU:CD2	2.08	1.01
1:C:38:LEU:CD2	1:K:6:LEU:O	2.08	1.01
1:L:15:ILE:HD12	1:M:6:LEU:HD22	1.34	1.01
1:L:38:LEU:CD2	1:P:6:LEU:O	2.08	1.01
1:D:6:LEU:O	1:H:38:LEU:CD2	2.08	1.01
1:E:5:GLU:H	1:F:12:ILE:HD12	0.88	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:6:LEU:CD2	1:F:15:ILE:HD12	1.88	1.01
1:K:15:ILE:HD12	1:L:6:LEU:CD2	1.88	1.01
1:M:38:LEU:CD2	1:Q:6:LEU:O	2.08	1.01
1:A:6:LEU:HD22	1:B:15:ILE:HD12	1.34	1.01
1:B:6:LEU:O	1:F:38:LEU:CD2	2.08	1.01
1:D:38:LEU:CD2	1:J:6:LEU:O	2.08	1.01
1:K:12:ILE:HD12	1:L:5:GLU:H	0.88	1.01
1:K:38:LEU:CD2	1:O:6:LEU:O	2.08	1.01
1:N:38:LEU:CD2	1:R:6:LEU:O	2.08	1.01
1:A:25:GLN:HE21	1:E:116:SER:HA	1.24	1.01
1:E:6:LEU:O	1:I:38:LEU:CD2	2.08	1.01
1:A:14:GLY:CA	1:E:44:LYS:HZ3	1.74	1.00
1:J:38:LEU:CD2	1:N:6:LEU:O	2.08	1.00
1:M:16:LEU:HA	1:N:6:LEU:HD12	1.24	1.00
1:P:16:LEU:HA	1:Q:6:LEU:HD12	1.25	1.00
1:A:41:GLU:OE1	1:M:10:ILE:HG23	1.62	1.00
1:E:10:ILE:HG23	1:I:41:GLU:OE1	1.62	1.00
1:J:41:GLU:OE1	1:N:10:ILE:HG23	1.62	1.00
1:B:41:GLU:OE1	1:L:10:ILE:HG23	1.62	1.00
1:E:7:MET:SD	1:I:34:SER:OG	2.20	1.00
1:L:41:GLU:OE1	1:P:10:ILE:HG23	1.62	1.00
1:D:10:ILE:HG23	1:H:41:GLU:OE1	1.62	1.00
1:D:116:SER:CB	1:J:21:LEU:CD1	2.29	1.00
1:B:14:GLY:CA	1:F:44:LYS:NZ	2.25	1.00
1:K:44:LYS:NZ	1:O:14:GLY:CA	2.25	1.00
1:N:44:LYS:NZ	1:R:14:GLY:CA	2.25	1.00
1:B:44:LYS:NZ	1:L:14:GLY:CA	2.25	1.00
1:L:34:SER:OG	1:P:7:MET:SD	2.20	1.00
1:P:12:ILE:CD1	1:Q:5:GLU:N	2.02	1.00
1:C:10:ILE:HG23	1:G:41:GLU:OE1	1.62	0.99
1:H:6:LEU:HD22	1:I:15:ILE:HD12	1.35	0.99
1:B:5:GLU:N	1:C:12:ILE:CD1	2.02	0.99
1:B:10:ILE:HG23	1:F:41:GLU:OE1	1.62	0.99
1:A:10:ILE:HG23	1:E:41:GLU:OE1	1.62	0.99
1:C:21:LEU:CD1	1:G:116:SER:CB	2.29	0.99
1:C:14:GLY:CA	1:G:44:LYS:NZ	2.25	0.99
1:K:34:SER:OG	1:O:7:MET:SD	2.20	0.99
1:K:41:GLU:OE1	1:O:10:ILE:HG23	1.62	0.99
1:E:6:LEU:HD12	1:F:16:LEU:HA	1.24	0.99
1:E:14:GLY:CA	1:I:44:LYS:NZ	2.25	0.99
1:B:7:MET:SD	1:F:34:SER:OG	2.20	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:34:SER:OG	1:N:7:MET:SD	2.20	0.99
1:L:44:LYS:NZ	1:P:14:GLY:CA	2.25	0.99
1:A:7:MET:SD	1:E:34:SER:OG	2.20	0.99
1:D:116:SER:HA	1:J:25:GLN:HE21	1.24	0.99
1:B:6:LEU:HD22	1:C:15:ILE:HD11	1.45	0.99
1:E:25:GLN:HE21	1:I:116:SER:HA	1.24	0.99
1:J:44:LYS:NZ	1:N:14:GLY:CA	2.25	0.99
1:M:34:SER:OG	1:Q:7:MET:SD	2.20	0.99
1:N:15:ILE:HD11	1:O:6:LEU:HD22	1.45	0.99
1:E:14:GLY:CA	1:I:44:LYS:HZ3	1.76	0.98
1:N:15:ILE:HD12	1:O:6:LEU:HD22	1.34	0.98
1:C:44:LYS:NZ	1:K:14:GLY:CA	2.25	0.98
1:K:15:ILE:HD11	1:L:6:LEU:HD22	1.45	0.98
1:D:14:GLY:CA	1:H:44:LYS:NZ	2.25	0.98
1:E:6:LEU:HD22	1:F:15:ILE:HD11	1.45	0.98
1:D:44:LYS:NZ	1:J:14:GLY:CA	2.25	0.98
1:F:6:LEU:HD22	1:G:15:ILE:HD11	1.45	0.98
1:A:44:LYS:NZ	1:M:14:GLY:CA	2.25	0.98
1:D:14:GLY:CA	1:H:44:LYS:HZ3	1.76	0.98
1:M:41:GLU:OE1	1:Q:10:ILE:HG23	1.62	0.98
1:B:34:SER:OG	1:L:7:MET:SD	2.20	0.98
1:J:15:ILE:HD11	1:K:6:LEU:HD22	1.45	0.98
1:J:116:SER:HA	1:N:25:GLN:HE21	1.24	0.98
1:J:53:ASN:HB3	1:M:149:SER:OG	1.64	0.98
1:O:15:ILE:HD11	1:P:6:LEU:HD22	1.45	0.98
1:D:7:MET:SD	1:H:34:SER:OG	2.20	0.97
1:D:149:SER:OG	1:G:53:ASN:HB3	1.64	0.97
1:M:44:LYS:NZ	1:Q:14:GLY:CA	2.25	0.97
1:Q:15:ILE:HD11	1:R:6:LEU:HD22	1.45	0.97
1:B:6:LEU:HD22	1:C:15:ILE:HD12	1.34	0.97
1:F:149:SER:OG	1:I:53:ASN:HB3	1.64	0.97
1:P:12:ILE:HD12	1:Q:5:GLU:CA	1.95	0.97
1:Q:12:ILE:HD12	1:R:5:GLU:CA	1.95	0.97
1:A:6:LEU:HD22	1:B:15:ILE:HD11	1.45	0.97
1:C:34:SER:OG	1:K:7:MET:SD	2.20	0.97
1:D:34:SER:OG	1:J:7:MET:SD	2.20	0.97
1:L:12:ILE:HD12	1:M:5:GLU:CA	1.95	0.97
1:N:41:GLU:OE1	1:R:10:ILE:HG23	1.62	0.97
1:M:12:ILE:HD12	1:N:5:GLU:CA	1.95	0.97
1:N:16:LEU:HA	1:O:6:LEU:HD12	1.25	0.97
1:A:5:GLU:CA	1:B:12:ILE:HD12	1.95	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:GLY:CA	1:E:44:LYS:NZ	2.25	0.97
1:B:10:ILE:HG13	1:F:41:GLU:CD	1.90	0.97
1:B:149:SER:OG	1:E:53:ASN:HB3	1.64	0.97
1:C:10:ILE:HG13	1:G:41:GLU:CD	1.90	0.97
1:K:41:GLU:CD	1:O:10:ILE:HG13	1.90	0.97
1:C:6:LEU:HD22	1:D:15:ILE:HD11	1.45	0.97
1:H:6:LEU:HD22	1:I:15:ILE:HD11	1.46	0.97
1:J:41:GLU:CD	1:N:10:ILE:HG13	1.90	0.97
1:A:53:ASN:HB3	1:L:149:SER:OG	1.64	0.97
1:D:10:ILE:HG13	1:H:41:GLU:CD	1.90	0.97
1:E:5:GLU:CA	1:F:12:ILE:HD12	1.95	0.97
1:A:12:ILE:HD12	1:J:5:GLU:CA	1.95	0.97
1:C:7:MET:SD	1:G:34:SER:OG	2.20	0.97
1:C:21:LEU:C	1:G:116:SER:HB3	1.90	0.97
1:C:149:SER:OG	1:F:53:ASN:HB3	1.64	0.97
1:M:15:ILE:HD11	1:N:6:LEU:HD22	1.45	0.97
1:M:116:SER:HA	1:Q:25:GLN:HE21	1.24	0.97
1:B:3:LEU:HD21	1:C:15:ILE:HD11	1.47	0.97
1:F:3:LEU:HD21	1:G:15:ILE:HD11	1.47	0.97
1:J:116:SER:HB3	1:N:21:LEU:C	1.90	0.97
1:N:34:SER:OG	1:R:7:MET:SD	2.20	0.97
1:O:12:ILE:HD12	1:P:5:GLU:CA	1.95	0.97
1:B:53:ASN:HB3	1:K:149:SER:OG	1.64	0.96
1:C:3:LEU:HD21	1:D:15:ILE:HD11	1.47	0.96
1:E:10:ILE:HG13	1:I:41:GLU:CD	1.90	0.96
1:G:3:LEU:HD21	1:H:15:ILE:HD11	1.47	0.96
1:G:5:GLU:N	1:H:12:ILE:CD1	2.02	0.96
1:J:12:ILE:HD12	1:K:5:GLU:CA	1.95	0.96
1:L:15:ILE:HD11	1:M:6:LEU:HD22	1.45	0.96
1:L:41:GLU:CD	1:P:10:ILE:HG13	1.90	0.96
1:F:5:GLU:CA	1:G:12:ILE:HD12	1.94	0.96
1:G:6:LEU:HD22	1:H:15:ILE:HD11	1.45	0.96
1:M:41:GLU:CD	1:Q:10:ILE:HG13	1.90	0.96
1:N:12:ILE:HD12	1:O:5:GLU:CA	1.95	0.96
1:N:116:SER:HB3	1:R:21:LEU:C	1.90	0.96
1:A:15:ILE:HD11	1:J:3:LEU:HD21	1.47	0.96
1:A:41:GLU:CD	1:M:10:ILE:HG13	1.90	0.96
1:C:116:SER:HB3	1:K:21:LEU:C	1.90	0.96
1:D:6:LEU:HD22	1:E:15:ILE:HD11	1.45	0.96
1:L:53:ASN:HB3	1:O:149:SER:OG	1.64	0.96
1:C:5:GLU:CA	1:D:12:ILE:HD12	1.95	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:GLU:OE1	1:K:10:ILE:HG23	1.62	0.96
1:D:41:GLU:OE1	1:J:10:ILE:HG23	1.62	0.96
1:J:15:ILE:HD11	1:K:3:LEU:HD21	1.47	0.96
1:A:10:ILE:HG13	1:E:41:GLU:CD	1.90	0.96
1:A:15:ILE:HD11	1:J:6:LEU:HD22	1.45	0.96
1:D:5:GLU:CA	1:E:12:ILE:HD12	1.95	0.96
1:E:149:SER:OG	1:H:53:ASN:HB3	1.64	0.96
1:P:15:ILE:HD11	1:Q:6:LEU:HD22	1.45	0.96
1:A:34:SER:OG	1:M:7:MET:SD	2.20	0.96
1:G:5:GLU:CA	1:H:12:ILE:HD12	1.95	0.96
1:K:12:ILE:HD12	1:L:5:GLU:CA	1.95	0.96
1:K:53:ASN:HB3	1:N:149:SER:OG	1.64	0.96
1:M:15:ILE:HD11	1:N:3:LEU:HD21	1.47	0.96
1:N:15:ILE:HD11	1:O:3:LEU:HD21	1.47	0.96
1:N:53:ASN:HB3	1:Q:149:SER:OG	1.64	0.96
1:B:5:GLU:CA	1:C:12:ILE:HD12	1.95	0.96
1:B:21:LEU:C	1:F:116:SER:HB3	1.90	0.96
1:B:116:SER:HB3	1:L:21:LEU:C	1.90	0.96
1:E:21:LEU:C	1:I:116:SER:HB3	1.90	0.96
1:K:116:SER:HB3	1:O:21:LEU:C	1.90	0.96
1:P:15:ILE:HD11	1:Q:3:LEU:HD21	1.47	0.96
1:A:149:SER:OG	1:D:53:ASN:HB3	1.64	0.96
1:B:41:GLU:CD	1:L:10:ILE:HG13	1.90	0.96
1:N:41:GLU:CD	1:R:10:ILE:HG13	1.90	0.96
1:Q:15:ILE:HD11	1:R:3:LEU:HD21	1.47	0.96
1:D:5:GLU:HB2	1:E:12:ILE:HD11	1.47	0.96
1:D:41:GLU:CD	1:J:10:ILE:HG13	1.90	0.96
1:K:15:ILE:HD11	1:L:3:LEU:HD21	1.47	0.96
1:L:116:SER:HB3	1:P:21:LEU:C	1.90	0.96
1:M:53:ASN:HB3	1:P:149:SER:OG	1.64	0.96
1:O:35:GLU:OE1	1:R:15:ILE:CD1	2.13	0.96
1:O:53:ASN:HB3	1:R:149:SER:OG	1.64	0.96
1:H:5:GLU:CA	1:I:12:ILE:HD12	1.95	0.96
1:A:5:GLU:HB2	1:B:12:ILE:HD11	1.47	0.95
1:D:3:LEU:HD21	1:E:15:ILE:HD11	1.47	0.95
1:L:15:ILE:HD11	1:M:3:LEU:HD21	1.47	0.95
1:B:116:SER:HA	1:L:25:GLN:HE21	1.24	0.95
1:C:25:GLN:HE21	1:G:116:SER:HA	1.24	0.95
1:A:12:ILE:HD11	1:J:5:GLU:HB2	1.47	0.95
1:M:16:LEU:HA	1:N:6:LEU:HD11	1.49	0.95
1:P:12:ILE:HD11	1:Q:5:GLU:HB2	1.47	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:LEU:HD11	1:B:16:LEU:HA	1.49	0.95
1:G:6:LEU:HD11	1:H:16:LEU:HA	1.49	0.95
1:A:3:LEU:HD21	1:B:15:ILE:HD11	1.47	0.95
1:C:41:GLU:CD	1:K:10:ILE:HG13	1.90	0.95
1:L:12:ILE:HD11	1:M:5:GLU:HB2	1.47	0.95
1:O:16:LEU:HA	1:P:6:LEU:HD11	1.49	0.95
1:H:3:LEU:HD21	1:I:15:ILE:HD11	1.47	0.95
1:A:16:LEU:HA	1:J:6:LEU:HD11	1.49	0.95
1:C:6:LEU:HD12	1:D:16:LEU:HA	1.24	0.95
1:C:6:LEU:HD11	1:D:16:LEU:HA	1.49	0.95
1:E:3:LEU:HD21	1:F:15:ILE:HD11	1.47	0.95
1:G:5:GLU:HB2	1:H:12:ILE:CD1	1.97	0.95
1:C:53:ASN:HB3	1:J:149:SER:OG	1.64	0.95
1:G:5:GLU:HB2	1:H:12:ILE:HD11	1.47	0.95
1:H:5:GLU:HB2	1:I:12:ILE:HD11	1.47	0.95
1:P:12:ILE:CD1	1:Q:5:GLU:HB2	1.97	0.94
1:F:5:GLU:HB2	1:G:12:ILE:HD11	1.47	0.94
1:H:6:LEU:HD11	1:I:16:LEU:HA	1.49	0.94
1:K:116:SER:HA	1:O:25:GLN:HE21	1.24	0.94
1:L:12:ILE:CD1	1:M:5:GLU:HB2	1.97	0.94
1:O:15:ILE:HD11	1:P:3:LEU:HD21	1.47	0.94
1:B:5:GLU:HB2	1:C:12:ILE:CD1	1.97	0.94
1:B:5:GLU:HB2	1:C:12:ILE:HD11	1.47	0.94
1:O:12:ILE:CD1	1:P:5:GLU:HB2	1.97	0.94
1:J:12:ILE:HD11	1:K:5:GLU:HB2	1.47	0.94
1:N:12:ILE:CD1	1:O:5:GLU:HB2	1.97	0.94
1:N:12:ILE:HD11	1:O:5:GLU:HB2	1.47	0.94
1:A:12:ILE:CD1	1:J:5:GLU:HB2	1.97	0.94
1:C:19:VAL:HG11	1:F:38:LEU:O	1.68	0.94
1:H:5:GLU:HB2	1:I:12:ILE:CD1	1.97	0.94
1:A:5:GLU:HB2	1:B:12:ILE:CD1	1.97	0.94
1:B:38:LEU:O	1:K:19:VAL:HG11	1.68	0.94
1:J:38:LEU:O	1:M:19:VAL:HG11	1.68	0.94
1:D:19:VAL:HG11	1:G:38:LEU:O	1.68	0.94
1:K:12:ILE:CD1	1:L:5:GLU:HB2	1.97	0.94
1:K:38:LEU:O	1:N:19:VAL:HG11	1.68	0.94
1:M:12:ILE:CD1	1:N:5:GLU:HB2	1.97	0.94
1:M:38:LEU:O	1:P:19:VAL:HG11	1.68	0.94
1:A:116:SER:HA	1:M:25:GLN:HE21	1.24	0.94
1:D:3:LEU:N	1:E:8:ILE:CG2	2.31	0.94
1:D:6:LEU:CD2	1:E:15:ILE:HD12	1.88	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:5:GLU:HB2	1:F:12:ILE:CD1	1.97	0.94
1:F:5:GLU:HB2	1:G:12:ILE:CD1	1.97	0.94
1:L:38:LEU:O	1:O:19:VAL:HG11	1.68	0.94
1:O:12:ILE:HD11	1:P:5:GLU:HB2	1.47	0.94
1:P:16:LEU:HA	1:Q:6:LEU:HD11	1.49	0.94
1:A:8:ILE:CG2	1:J:3:LEU:N	2.31	0.94
1:C:5:GLU:HB2	1:D:12:ILE:CD1	1.97	0.94
1:M:12:ILE:HD11	1:N:5:GLU:HB2	1.47	0.94
1:N:8:ILE:CG2	1:O:3:LEU:N	2.31	0.94
1:N:16:LEU:HA	1:O:6:LEU:HD11	1.49	0.94
1:D:6:LEU:HD12	1:E:16:LEU:HA	1.24	0.94
1:E:6:LEU:HD11	1:F:16:LEU:HA	1.49	0.94
1:H:3:LEU:N	1:I:8:ILE:CG2	2.31	0.94
1:J:12:ILE:CD1	1:K:5:GLU:HB2	1.97	0.94
1:A:38:LEU:O	1:L:19:VAL:HG11	1.68	0.93
1:B:25:GLN:HE21	1:F:116:SER:HA	1.24	0.93
1:B:38:LEU:HD12	1:L:10:ILE:HD13	1.50	0.93
1:P:8:ILE:CG2	1:Q:3:LEU:N	2.31	0.93
1:B:3:LEU:N	1:C:8:ILE:CG2	2.31	0.93
1:B:6:LEU:HD11	1:C:16:LEU:HA	1.49	0.93
1:E:10:ILE:HD13	1:I:38:LEU:HD12	1.50	0.93
1:M:12:ILE:HD12	1:N:5:GLU:H	0.88	0.93
1:Q:12:ILE:HD11	1:R:5:GLU:HB2	1.47	0.93
1:B:19:VAL:HG11	1:E:38:LEU:O	1.68	0.93
1:C:5:GLU:H	1:D:12:ILE:HD12	0.88	0.93
1:E:5:GLU:HB2	1:F:12:ILE:HD11	1.47	0.93
1:L:8:ILE:CG2	1:M:3:LEU:N	2.31	0.93
1:O:38:LEU:O	1:R:19:VAL:HG11	1.68	0.93
1:Q:12:ILE:CD1	1:R:5:GLU:HB2	1.97	0.93
1:D:5:GLU:HB2	1:E:12:ILE:CD1	1.97	0.93
1:F:3:LEU:N	1:G:8:ILE:CG2	2.31	0.93
1:L:38:LEU:HD12	1:P:10:ILE:HD13	1.50	0.93
1:M:8:ILE:CG2	1:N:3:LEU:N	2.31	0.93
1:A:3:LEU:N	1:B:8:ILE:CG2	2.31	0.93
1:E:3:LEU:N	1:F:8:ILE:CG2	2.31	0.93
1:F:6:LEU:HD11	1:G:16:LEU:HA	1.49	0.93
1:K:12:ILE:HD11	1:L:5:GLU:HB2	1.47	0.93
1:A:10:ILE:HD13	1:E:38:LEU:HD12	1.50	0.93
1:B:10:ILE:HD13	1:F:38:LEU:HD12	1.50	0.93
1:C:116:SER:HA	1:K:25:GLN:HE21	1.24	0.93
1:F:19:VAL:HG11	1:I:38:LEU:O	1.68	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:8:ILE:CG2	1:K:3:LEU:N	2.31	0.93
1:C:5:GLU:HB2	1:D:12:ILE:HD11	1.47	0.93
1:K:38:LEU:HD12	1:O:10:ILE:HD13	1.50	0.93
1:L:16:LEU:HA	1:M:6:LEU:HD11	1.49	0.93
1:N:38:LEU:O	1:Q:19:VAL:HG11	1.68	0.93
1:A:21:LEU:CB	1:E:116:SER:HB2	1.99	0.93
1:A:116:SER:HB2	1:M:21:LEU:C	1.94	0.93
1:D:21:LEU:CB	1:H:116:SER:HB2	1.99	0.93
1:A:38:LEU:HD12	1:M:10:ILE:HD13	1.50	0.92
1:E:19:VAL:HG11	1:H:38:LEU:O	1.68	0.92
1:L:116:SER:HB2	1:P:21:LEU:CB	1.99	0.92
1:A:19:VAL:HG11	1:D:38:LEU:O	1.68	0.92
1:Q:8:ILE:CG2	1:R:3:LEU:N	2.31	0.92
1:C:3:LEU:N	1:D:8:ILE:CG2	2.31	0.92
1:D:6:LEU:HD11	1:E:16:LEU:HA	1.49	0.92
1:D:10:ILE:HD13	1:H:38:LEU:HD12	1.50	0.92
1:D:38:LEU:HD12	1:J:10:ILE:HD13	1.50	0.92
1:D:116:SER:HB2	1:J:21:LEU:CB	1.99	0.92
1:K:16:LEU:HA	1:L:6:LEU:HD11	1.49	0.92
1:C:38:LEU:HD12	1:K:10:ILE:HD13	1.50	0.92
1:D:25:GLN:HE21	1:H:116:SER:HA	1.24	0.92
1:D:116:SER:HB2	1:J:21:LEU:C	1.94	0.92
1:G:3:LEU:N	1:H:8:ILE:CG2	2.31	0.92
1:M:38:LEU:HD12	1:Q:10:ILE:HD13	1.50	0.92
1:D:44:LYS:HZ1	1:J:14:GLY:CA	1.81	0.92
1:J:16:LEU:HA	1:K:6:LEU:HD11	1.49	0.92
1:J:38:LEU:HD12	1:N:10:ILE:HD13	1.50	0.92
1:B:116:SER:HB2	1:L:21:LEU:CB	1.99	0.92
1:J:25:GLN:C	1:J:26:ASP:CA	2.43	0.92
1:L:116:SER:HB2	1:P:21:LEU:C	1.94	0.92
1:N:25:GLN:C	1:N:26:ASP:CA	2.43	0.92
1:C:10:ILE:HD13	1:G:38:LEU:HD12	1.50	0.92
1:D:116:SER:HB3	1:J:21:LEU:C	1.90	0.92
1:M:116:SER:HB3	1:Q:21:LEU:C	1.90	0.92
1:N:38:LEU:HD12	1:R:10:ILE:HD13	1.51	0.92
1:Q:16:LEU:HA	1:R:6:LEU:HD11	1.49	0.92
1:A:116:SER:HB2	1:M:21:LEU:CB	1.99	0.92
1:A:21:LEU:C	1:E:116:SER:HB3	1.90	0.92
1:A:44:LYS:HZ3	1:M:14:GLY:CA	1.81	0.92
1:C:38:LEU:O	1:J:19:VAL:HG11	1.68	0.92
1:D:25:GLN:C	1:D:26:ASP:CA	2.43	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:GLN:C	1:C:26:ASP:CA	2.43	0.91
1:D:21:LEU:C	1:H:116:SER:HB3	1.90	0.91
1:G:25:GLN:C	1:G:26:ASP:CA	2.43	0.91
1:J:116:SER:HB2	1:N:21:LEU:C	1.95	0.91
1:C:116:SER:HB2	1:K:21:LEU:CB	1.99	0.91
1:E:1:MEA:HE2	1:F:8:ILE:HD11	1.53	0.91
1:F:1:MEA:HE2	1:G:8:ILE:HD11	1.52	0.91
1:J:8:ILE:HD11	1:K:1:MEA:HE2	1.53	0.91
1:J:116:SER:HB2	1:N:21:LEU:CB	1.99	0.91
1:M:116:SER:HB2	1:Q:21:LEU:CB	1.99	0.91
1:O:8:ILE:HD11	1:P:1:MEA:HE2	1.52	0.91
1:Q:8:ILE:HD11	1:R:1:MEA:HE2	1.52	0.91
1:E:21:LEU:CB	1:I:116:SER:HB2	1.99	0.91
1:L:25:GLN:C	1:L:26:ASP:CA	2.43	0.91
1:M:116:SER:HB2	1:Q:21:LEU:C	1.95	0.91
1:B:21:LEU:CB	1:F:116:SER:HB2	1.99	0.91
1:K:25:GLN:C	1:K:26:ASP:CA	2.43	0.91
1:R:25:GLN:C	1:R:26:ASP:CA	2.43	0.91
1:A:21:LEU:CD1	1:E:116:SER:CB	2.29	0.91
1:A:116:SER:HB3	1:M:21:LEU:C	1.90	0.91
1:I:25:GLN:C	1:I:26:ASP:CA	2.43	0.91
1:C:21:LEU:CB	1:G:116:SER:HB2	1.99	0.91
1:M:25:GLN:C	1:M:26:ASP:CA	2.43	0.91
1:M:44:LYS:HZ3	1:Q:14:GLY:CA	1.82	0.91
1:O:8:ILE:CG2	1:P:3:LEU:N	2.31	0.91
1:P:8:ILE:HD11	1:Q:1:MEA:HE2	1.52	0.91
1:Q:25:GLN:C	1:Q:26:ASP:CA	2.43	0.91
1:A:1:MEA:HE2	1:B:8:ILE:HD11	1.52	0.91
1:A:4:ILE:O	1:J:2:THR:CG2	2.19	0.91
1:E:21:LEU:C	1:I:116:SER:HB2	1.94	0.91
1:K:8:ILE:CG2	1:L:3:LEU:N	2.31	0.91
1:E:2:THR:CG2	1:F:4:ILE:O	2.19	0.91
1:H:25:GLN:C	1:H:26:ASP:CA	2.43	0.91
1:K:116:SER:HB2	1:O:21:LEU:CB	1.99	0.91
1:D:21:LEU:C	1:H:116:SER:HB2	1.94	0.91
1:N:116:SER:HB2	1:R:21:LEU:CB	1.99	0.91
1:O:4:ILE:O	1:P:2:THR:CG2	2.19	0.91
1:P:25:GLN:C	1:P:26:ASP:CA	2.43	0.91
1:A:8:ILE:HD11	1:J:1:MEA:HE2	1.53	0.90
1:A:14:GLY:HA3	1:E:44:LYS:HZ3	1.35	0.90
1:B:25:GLN:C	1:B:26:ASP:CA	2.43	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:GLN:NE2	1:G:52:LEU:HD21	1.86	0.90
1:D:2:THR:CG2	1:E:4:ILE:O	2.19	0.90
1:H:2:THR:CG2	1:I:4:ILE:O	2.19	0.90
1:P:4:ILE:O	1:Q:2:THR:CG2	2.19	0.90
1:A:2:THR:CG2	1:B:4:ILE:O	2.19	0.90
1:A:25:GLN:C	1:A:26:ASP:CA	2.43	0.90
1:C:21:LEU:C	1:G:116:SER:HB2	1.94	0.90
1:E:25:GLN:C	1:E:26:ASP:CA	2.43	0.90
1:C:2:THR:CG2	1:D:4:ILE:O	2.19	0.90
1:E:14:GLY:HA3	1:I:44:LYS:HZ3	1.36	0.90
1:J:52:LEU:HD21	1:N:25:GLN:NE2	1.86	0.90
1:L:4:ILE:O	1:M:2:THR:CG2	2.19	0.90
1:N:116:SER:HA	1:R:25:GLN:HE21	1.24	0.90
1:O:25:GLN:C	1:O:26:ASP:CA	2.43	0.90
1:A:25:GLN:NE2	1:E:52:LEU:HD21	1.86	0.90
1:G:1:MEA:HE2	1:H:8:ILE:HD11	1.52	0.90
1:H:1:MEA:HE2	1:I:8:ILE:HD11	1.53	0.90
1:K:116:SER:HB2	1:O:21:LEU:C	1.95	0.90
1:Q:4:ILE:O	1:R:2:THR:CG2	2.19	0.90
1:E:25:GLN:NE2	1:I:52:LEU:HD21	1.86	0.90
1:F:25:GLN:C	1:F:26:ASP:CA	2.43	0.90
1:J:4:ILE:O	1:K:2:THR:CG2	2.19	0.90
1:B:2:THR:CG2	1:C:4:ILE:O	2.19	0.90
1:C:116:SER:HB2	1:K:21:LEU:C	1.94	0.90
1:C:116:SER:CB	1:K:21:LEU:CD1	2.29	0.90
1:D:5:GLU:H	1:E:12:ILE:HD12	0.88	0.90
1:A:21:LEU:C	1:E:116:SER:HB2	1.94	0.90
1:L:52:LEU:HD21	1:P:25:GLN:NE2	1.86	0.90
1:M:4:ILE:O	1:N:2:THR:CG2	2.19	0.90
1:N:8:ILE:HD11	1:O:1:MEA:HE2	1.53	0.90
1:B:21:LEU:C	1:F:116:SER:HB2	1.94	0.89
1:F:2:THR:CG2	1:G:4:ILE:O	2.19	0.89
1:G:2:THR:CG2	1:H:4:ILE:O	2.19	0.89
1:F:15:ILE:CD1	1:I:35:GLU:OE1	2.13	0.89
1:N:52:LEU:HD21	1:R:25:GLN:NE2	1.86	0.89
1:B:52:LEU:HD21	1:L:25:GLN:NE2	1.86	0.89
1:D:21:LEU:CD1	1:H:116:SER:CB	2.29	0.89
1:D:52:LEU:HD21	1:J:25:GLN:NE2	1.86	0.89
1:G:4:ILE:N	1:H:12:ILE:HD13	1.88	0.89
1:L:12:ILE:HD13	1:M:4:ILE:N	1.88	0.89
1:P:12:ILE:HD13	1:Q:4:ILE:N	1.88	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LEU:HD21	1:M:25:GLN:NE2	1.86	0.89
1:D:15:ILE:HG22	1:G:76:LYS:CE	2.03	0.89
1:D:25:GLN:NE2	1:H:52:LEU:HD21	1.86	0.89
1:E:4:ILE:N	1:F:12:ILE:HD13	1.88	0.89
1:H:4:ILE:N	1:I:12:ILE:HD13	1.88	0.89
1:K:4:ILE:O	1:L:2:THR:CG2	2.19	0.89
1:C:52:LEU:HD21	1:K:25:GLN:NE2	1.86	0.89
1:B:4:ILE:N	1:C:12:ILE:HD13	1.88	0.89
1:B:116:SER:HB2	1:L:21:LEU:C	1.95	0.89
1:B:15:ILE:HG22	1:E:76:LYS:CE	2.03	0.89
1:D:4:ILE:N	1:E:12:ILE:HD13	1.88	0.89
1:F:4:ILE:N	1:G:12:ILE:HD13	1.88	0.89
1:N:76:LYS:CE	1:Q:15:ILE:HG22	2.03	0.89
1:K:12:ILE:HD13	1:L:4:ILE:N	1.88	0.89
1:N:116:SER:HB2	1:R:21:LEU:C	1.95	0.89
1:Q:12:ILE:HD13	1:R:4:ILE:N	1.88	0.89
1:A:4:ILE:N	1:B:12:ILE:HD13	1.88	0.89
1:B:25:GLN:NE2	1:F:52:LEU:HD21	1.86	0.89
1:C:4:ILE:N	1:D:12:ILE:HD13	1.88	0.89
1:C:15:ILE:HG22	1:F:76:LYS:CE	2.03	0.88
1:C:44:LYS:NZ	1:K:14:GLY:HA2	1.89	0.88
1:L:12:ILE:HD12	1:M:5:GLU:H	0.88	0.88
1:M:12:ILE:HD13	1:N:4:ILE:N	1.88	0.88
1:N:4:ILE:O	1:O:2:THR:CG2	2.19	0.88
1:B:44:LYS:NZ	1:L:14:GLY:HA2	1.88	0.88
1:N:12:ILE:HD13	1:O:4:ILE:N	1.88	0.88
1:B:1:MEA:HE2	1:C:8:ILE:HD11	1.53	0.88
1:B:14:GLY:CA	1:F:44:LYS:HZ3	1.86	0.88
1:B:76:LYS:CE	1:K:15:ILE:HG22	2.03	0.88
1:C:14:GLY:CA	1:G:44:LYS:HZ1	1.83	0.88
1:M:52:LEU:HD21	1:Q:25:GLN:NE2	1.86	0.88
1:O:12:ILE:HD13	1:P:4:ILE:N	1.88	0.88
1:K:52:LEU:HD21	1:O:25:GLN:NE2	1.86	0.88
1:D:14:GLY:HA3	1:H:44:LYS:HZ3	1.36	0.88
1:O:76:LYS:CE	1:R:15:ILE:HG22	2.03	0.88
1:Q:112:ARG:NE	1:Q:114:ASN:HA	1.89	0.88
1:B:14:GLY:HA2	1:F:44:LYS:NZ	1.89	0.88
1:B:44:LYS:HZ3	1:L:14:GLY:CA	1.86	0.88
1:J:112:ARG:NE	1:J:114:ASN:HA	1.89	0.88
1:A:112:ARG:NE	1:A:114:ASN:HA	1.89	0.88
1:C:14:GLY:HA2	1:G:44:LYS:NZ	1.89	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:112:ARG:NE	1:H:114:ASN:HA	1.89	0.88
1:A:12:ILE:HD13	1:J:4:ILE:N	1.88	0.88
1:C:112:ARG:NE	1:C:114:ASN:HA	1.89	0.88
1:P:112:ARG:NE	1:P:114:ASN:HA	1.89	0.88
1:F:15:ILE:HG22	1:I:76:LYS:CE	2.03	0.87
1:J:44:LYS:HZ1	1:N:14:GLY:CA	1.84	0.87
1:N:44:LYS:HZ1	1:R:14:GLY:CA	1.83	0.87
1:E:15:ILE:HG22	1:H:76:LYS:CE	2.03	0.87
1:H:4:ILE:H	1:I:12:ILE:HD13	1.38	0.87
1:L:44:LYS:HZ1	1:P:14:GLY:CA	1.87	0.87
1:A:15:ILE:HG22	1:D:76:LYS:CE	2.03	0.87
1:A:44:LYS:NZ	1:M:14:GLY:HA2	1.89	0.87
1:C:76:LYS:CE	1:J:15:ILE:HG22	2.03	0.87
1:G:112:ARG:NE	1:G:114:ASN:HA	1.89	0.87
1:H:5:GLU:H	1:I:12:ILE:HD12	0.88	0.87
1:J:12:ILE:HD13	1:K:4:ILE:N	1.88	0.87
1:M:8:ILE:HD11	1:N:1:MEA:HE2	1.53	0.87
1:A:4:ILE:H	1:B:12:ILE:HD13	1.39	0.87
1:D:4:ILE:H	1:E:12:ILE:HD13	1.38	0.87
1:D:112:ARG:NE	1:D:114:ASN:HA	1.89	0.87
1:N:44:LYS:NZ	1:R:14:GLY:HA2	1.88	0.87
1:R:112:ARG:NE	1:R:114:ASN:HA	1.89	0.87
1:C:4:ILE:H	1:D:12:ILE:HD13	1.38	0.87
1:K:44:LYS:NZ	1:O:14:GLY:HA2	1.88	0.87
1:L:8:ILE:HD11	1:M:1:MEA:HE2	1.53	0.87
1:M:76:LYS:CE	1:P:15:ILE:HG22	2.03	0.87
1:N:112:ARG:NE	1:N:114:ASN:HA	1.89	0.87
1:J:76:LYS:CE	1:M:15:ILE:HG22	2.03	0.87
1:L:12:ILE:HD13	1:M:4:ILE:H	1.39	0.87
1:L:112:ARG:NE	1:L:114:ASN:HA	1.89	0.87
1:M:12:ILE:HD13	1:N:4:ILE:H	1.38	0.87
1:M:112:ARG:NE	1:M:114:ASN:HA	1.89	0.87
1:Q:12:ILE:HD13	1:R:4:ILE:H	1.39	0.87
1:B:112:ARG:NE	1:B:114:ASN:HA	1.89	0.87
1:F:112:ARG:NE	1:F:114:ASN:HA	1.89	0.87
1:I:112:ARG:NE	1:I:114:ASN:HA	1.89	0.87
1:D:44:LYS:NZ	1:J:14:GLY:HA2	1.89	0.87
1:J:12:ILE:HD13	1:K:4:ILE:H	1.39	0.87
1:K:112:ARG:NE	1:K:114:ASN:HA	1.89	0.87
1:O:12:ILE:HD13	1:P:4:ILE:H	1.38	0.87
1:A:5:GLU:H	1:B:12:ILE:HD12	0.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:LYS:CE	1:L:15:ILE:HG22	2.03	0.86
1:J:44:LYS:NZ	1:N:14:GLY:HA2	1.88	0.86
1:P:12:ILE:HD13	1:Q:4:ILE:H	1.39	0.86
1:C:44:LYS:HZ1	1:K:14:GLY:CA	1.85	0.86
1:D:14:GLY:HA2	1:H:44:LYS:NZ	1.88	0.86
1:F:4:ILE:H	1:G:12:ILE:HD13	1.38	0.86
1:G:5:GLU:H	1:H:12:ILE:HD12	0.88	0.86
1:O:112:ARG:NE	1:O:114:ASN:HA	1.89	0.86
1:A:14:GLY:HA2	1:E:44:LYS:NZ	1.89	0.86
1:D:10:ILE:CB	1:H:41:GLU:OE1	2.23	0.86
1:N:41:GLU:OE1	1:R:10:ILE:HG12	1.75	0.86
1:A:12:ILE:HD12	1:J:5:GLU:H	0.88	0.86
1:A:12:ILE:HD13	1:J:4:ILE:H	1.38	0.86
1:K:76:LYS:CE	1:N:15:ILE:HG22	2.03	0.86
1:L:76:LYS:CE	1:O:15:ILE:HG22	2.03	0.86
1:D:21:LEU:O	1:H:116:SER:CB	2.23	0.86
1:J:41:GLU:OE1	1:N:10:ILE:HG12	1.76	0.86
1:P:12:ILE:HD12	1:Q:5:GLU:H	0.88	0.86
1:R:93:LEU:HD12	1:R:94:SER:H	1.41	0.86
1:G:4:ILE:H	1:H:12:ILE:HD13	1.38	0.86
1:D:41:GLU:OE1	1:J:10:ILE:CB	2.23	0.86
1:N:41:GLU:OE1	1:R:10:ILE:CB	2.23	0.86
1:C:93:LEU:HD12	1:C:94:SER:H	1.41	0.86
1:C:116:SER:CB	1:K:21:LEU:O	2.23	0.86
1:K:93:LEU:HD12	1:K:94:SER:H	1.41	0.86
1:K:116:SER:CB	1:O:21:LEU:O	2.23	0.86
1:L:44:LYS:NZ	1:P:14:GLY:HA2	1.88	0.86
1:O:12:ILE:HD12	1:P:5:GLU:H	0.88	0.86
1:A:41:GLU:OE1	1:M:10:ILE:CB	2.23	0.86
1:E:112:ARG:NE	1:E:114:ASN:HA	1.89	0.86
1:F:93:LEU:HD12	1:F:94:SER:H	1.41	0.86
1:M:41:GLU:OE1	1:Q:10:ILE:CB	2.23	0.86
1:B:2:THR:HG22	1:C:4:ILE:O	1.76	0.85
1:C:1:MEA:HE2	1:D:8:ILE:HD11	1.52	0.85
1:B:10:ILE:CB	1:F:41:GLU:OE1	2.23	0.85
1:D:41:GLU:OE1	1:J:10:ILE:HG12	1.76	0.85
1:E:4:ILE:H	1:F:12:ILE:HD13	1.38	0.85
1:L:41:GLU:OE1	1:P:10:ILE:CB	2.23	0.85
1:N:93:LEU:HD12	1:N:94:SER:H	1.41	0.85
1:Q:12:ILE:HD12	1:R:5:GLU:H	0.88	0.85
1:B:38:LEU:HD13	1:L:10:ILE:HD12	1.56	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:ILE:HG12	1:G:41:GLU:OE1	1.76	0.85
1:E:14:GLY:HA2	1:I:44:LYS:NZ	1.88	0.85
1:N:4:ILE:O	1:O:2:THR:HG22	1.76	0.85
1:N:116:SER:CB	1:R:21:LEU:O	2.23	0.85
1:A:10:ILE:CB	1:E:41:GLU:OE1	2.23	0.85
1:A:41:GLU:HB2	1:M:10:ILE:HG13	1.59	0.85
1:B:4:ILE:H	1:C:12:ILE:HD13	1.38	0.85
1:H:2:THR:HG22	1:I:4:ILE:O	1.76	0.85
1:K:44:LYS:HZ1	1:O:14:GLY:CA	1.86	0.85
1:B:21:LEU:O	1:F:116:SER:CB	2.23	0.85
1:E:93:LEU:HD12	1:E:94:SER:H	1.41	0.85
1:F:2:THR:HG22	1:G:4:ILE:O	1.76	0.85
1:J:41:GLU:OE1	1:N:10:ILE:CB	2.23	0.85
1:K:41:GLU:OE1	1:O:10:ILE:CB	2.23	0.85
1:K:41:GLU:HB2	1:O:10:ILE:HG13	1.59	0.85
1:L:4:ILE:O	1:M:2:THR:HG22	1.76	0.85
1:M:44:LYS:NZ	1:Q:14:GLY:HA2	1.88	0.85
1:C:21:LEU:O	1:G:116:SER:CB	2.23	0.85
1:C:41:GLU:OE1	1:K:10:ILE:CB	2.23	0.85
1:A:2:THR:HG22	1:B:4:ILE:O	1.76	0.85
1:B:14:GLY:HA3	1:F:44:LYS:HZ3	1.42	0.85
1:D:1:MEA:HE2	1:E:8:ILE:HD11	1.53	0.85
1:D:2:THR:HG22	1:E:4:ILE:O	1.76	0.85
1:J:4:ILE:O	1:K:2:THR:HG22	1.76	0.85
1:J:41:GLU:HB2	1:N:10:ILE:HG13	1.59	0.85
1:K:4:ILE:O	1:L:2:THR:HG22	1.76	0.85
1:K:12:ILE:HD13	1:L:4:ILE:H	1.39	0.85
1:L:93:LEU:HD12	1:L:94:SER:H	1.41	0.85
1:N:12:ILE:HD13	1:O:4:ILE:H	1.38	0.85
1:B:10:ILE:HG13	1:F:41:GLU:HB2	1.59	0.85
1:B:41:GLU:OE1	1:L:10:ILE:CB	2.23	0.85
1:L:41:GLU:OE1	1:P:10:ILE:HG12	1.76	0.85
1:O:93:LEU:HD12	1:O:94:SER:H	1.41	0.85
1:P:93:LEU:HD12	1:P:94:SER:H	1.41	0.85
1:Q:4:ILE:O	1:R:2:THR:HG22	1.76	0.85
1:A:10:ILE:HG13	1:E:41:GLU:HB2	1.59	0.85
1:B:1:MEA:CD2	1:C:8:ILE:HD12	2.07	0.85
1:C:2:THR:HG22	1:D:4:ILE:O	1.76	0.85
1:E:10:ILE:CB	1:I:41:GLU:OE1	2.23	0.85
1:G:93:LEU:HD12	1:G:94:SER:H	1.41	0.85
1:K:41:GLU:HB2	1:O:10:ILE:CG1	2.07	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:41:GLU:HB2	1:P:10:ILE:CG1	2.07	0.85
1:L:44:LYS:HZ3	1:P:14:GLY:CA	1.90	0.85
1:A:93:LEU:HD12	1:A:94:SER:H	1.41	0.84
1:B:10:ILE:CG1	1:F:41:GLU:HB2	2.07	0.84
1:B:41:GLU:HB2	1:L:10:ILE:CG1	2.07	0.84
1:B:93:LEU:HD12	1:B:94:SER:H	1.41	0.84
1:C:10:ILE:CG1	1:G:41:GLU:HB2	2.07	0.84
1:D:10:ILE:HG13	1:H:41:GLU:HB2	1.59	0.84
1:M:4:ILE:O	1:N:2:THR:HG22	1.76	0.84
1:B:44:LYS:HZ3	1:L:14:GLY:HA3	1.42	0.84
1:B:116:SER:CB	1:L:21:LEU:O	2.23	0.84
1:C:10:ILE:CB	1:G:41:GLU:OE1	2.23	0.84
1:C:41:GLU:HB2	1:K:10:ILE:HG13	1.59	0.84
1:C:41:GLU:HB2	1:K:10:ILE:CG1	2.07	0.84
1:E:1:MEA:HD2	1:F:8:ILE:HD11	1.57	0.84
1:J:12:ILE:HD12	1:K:5:GLU:H	0.88	0.84
1:C:41:GLU:OE1	1:K:10:ILE:HG12	1.76	0.84
1:E:10:ILE:CG1	1:I:41:GLU:HB2	2.07	0.84
1:I:93:LEU:HD12	1:I:94:SER:H	1.41	0.84
1:J:41:GLU:HB2	1:N:10:ILE:CG1	2.07	0.84
1:L:8:ILE:HD12	1:M:1:MEA:CD2	2.07	0.84
1:A:4:ILE:O	1:J:2:THR:HG22	1.76	0.84
1:C:10:ILE:HG13	1:G:41:GLU:HB2	1.59	0.84
1:H:93:LEU:HD12	1:H:94:SER:H	1.41	0.84
1:N:8:ILE:HD12	1:O:1:MEA:CD2	2.07	0.84
1:N:41:GLU:HB2	1:R:10:ILE:CG1	2.07	0.84
1:O:8:ILE:HD11	1:P:1:MEA:HD2	1.58	0.84
1:A:8:ILE:HD11	1:J:1:MEA:HD2	1.57	0.84
1:B:10:ILE:HG12	1:F:41:GLU:OE1	1.76	0.84
1:D:41:GLU:HB2	1:J:10:ILE:HG13	1.59	0.84
1:E:2:THR:HG22	1:F:4:ILE:O	1.76	0.84
1:A:44:LYS:HZ3	1:M:14:GLY:HA3	1.39	0.84
1:B:41:GLU:OE1	1:L:10:ILE:HG12	1.76	0.84
1:D:41:GLU:HB2	1:J:10:ILE:CG1	2.07	0.84
1:E:10:ILE:HG12	1:I:41:GLU:OE1	1.76	0.84
1:O:4:ILE:O	1:P:2:THR:HG22	1.76	0.84
1:P:4:ILE:O	1:Q:2:THR:HG22	1.76	0.84
1:A:10:ILE:CG1	1:E:41:GLU:HB2	2.07	0.84
1:E:1:MEA:CD2	1:F:8:ILE:HD12	2.07	0.84
1:G:2:THR:HG22	1:H:4:ILE:O	1.76	0.84
1:J:8:ILE:HD12	1:K:1:MEA:CD2	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:93:LEU:HD12	1:J:94:SER:H	1.41	0.84
1:L:41:GLU:HB2	1:P:10:ILE:HG13	1.59	0.84
1:M:44:LYS:HZ3	1:Q:14:GLY:HA3	1.39	0.84
1:D:1:MEA:CD2	1:E:8:ILE:HD12	2.07	0.84
1:M:8:ILE:HD11	1:N:1:MEA:HD2	1.57	0.84
1:C:38:LEU:HA	1:K:10:ILE:HG12	0.85	0.84
1:D:10:ILE:CG1	1:H:41:GLU:HB2	2.07	0.84
1:D:10:ILE:HG12	1:H:41:GLU:OE1	1.75	0.84
1:D:38:LEU:HA	1:J:10:ILE:HG12	0.85	0.84
1:H:1:MEA:HD2	1:I:8:ILE:HD11	1.57	0.84
1:L:38:LEU:HD21	1:P:6:LEU:O	1.78	0.84
1:A:41:GLU:HB2	1:M:10:ILE:CG1	2.07	0.83
1:A:117:VAL:HG22	1:M:21:LEU:HD21	1.60	0.83
1:B:41:GLU:HB2	1:L:10:ILE:HG13	1.59	0.83
1:F:5:GLU:H	1:G:12:ILE:HD12	0.88	0.83
1:F:1:MEA:CD2	1:G:8:ILE:HD12	2.07	0.83
1:K:8:ILE:HD12	1:L:1:MEA:CD2	2.07	0.83
1:N:41:GLU:HB2	1:R:10:ILE:HG13	1.59	0.83
1:Q:93:LEU:HD12	1:Q:94:SER:H	1.41	0.83
1:B:5:GLU:H	1:C:12:ILE:HD12	0.88	0.83
1:C:21:LEU:HD13	1:G:116:SER:CB	1.92	0.83
1:D:1:MEA:HD2	1:E:8:ILE:HD11	1.57	0.83
1:D:93:LEU:HD12	1:D:94:SER:H	1.41	0.83
1:M:93:LEU:HD12	1:M:94:SER:H	1.41	0.83
1:B:1:MEA:HD2	1:C:8:ILE:HD11	1.57	0.83
1:D:21:LEU:HD21	1:H:117:VAL:HG22	1.61	0.83
1:J:117:VAL:HG22	1:N:21:LEU:HD21	1.60	0.83
1:Q:8:ILE:HD12	1:R:1:MEA:CD2	2.07	0.83
1:K:8:ILE:HD11	1:L:1:MEA:HE2	1.53	0.83
1:M:8:ILE:HD12	1:N:1:MEA:CD2	2.07	0.83
1:B:117:VAL:HG22	1:L:21:LEU:HD21	1.60	0.83
1:C:21:LEU:HD21	1:G:117:VAL:HG22	1.61	0.83
1:E:10:ILE:HG13	1:I:41:GLU:HB2	1.58	0.83
1:J:38:LEU:HA	1:N:10:ILE:HG12	0.85	0.83
1:K:38:LEU:HA	1:O:10:ILE:HG12	0.85	0.83
1:L:116:SER:CB	1:P:21:LEU:O	2.23	0.83
1:M:41:GLU:HB2	1:Q:10:ILE:CG1	2.07	0.83
1:A:5:GLU:CB	1:B:12:ILE:CD1	2.57	0.83
1:A:15:ILE:HD12	1:D:35:GLU:CD	2.04	0.83
1:H:5:GLU:CB	1:I:12:ILE:CD1	2.57	0.83
1:M:41:GLU:HB2	1:Q:10:ILE:HG13	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:35:GLU:CD	1:R:15:ILE:HD12	2.04	0.83
1:B:38:LEU:HD21	1:L:6:LEU:O	1.78	0.83
1:D:6:LEU:O	1:H:38:LEU:HD21	1.78	0.83
1:M:12:ILE:CD1	1:N:5:GLU:CB	2.57	0.83
1:B:5:GLU:CB	1:C:12:ILE:CD1	2.57	0.83
1:C:5:GLU:CB	1:D:12:ILE:CD1	2.57	0.83
1:C:35:GLU:CD	1:J:15:ILE:HD12	2.04	0.83
1:D:38:LEU:HD21	1:J:6:LEU:O	1.78	0.83
1:E:21:LEU:O	1:I:116:SER:CB	2.23	0.83
1:E:21:LEU:HD21	1:I:117:VAL:HG22	1.61	0.83
1:G:5:GLU:CB	1:H:12:ILE:CD1	2.57	0.83
1:M:41:GLU:OE1	1:Q:10:ILE:HG12	1.76	0.83
1:N:35:GLU:CD	1:Q:15:ILE:HD12	2.04	0.83
1:O:12:ILE:CD1	1:P:5:GLU:CB	2.57	0.83
1:A:12:ILE:CD1	1:J:5:GLU:CB	2.57	0.83
1:C:6:LEU:O	1:G:38:LEU:HD21	1.78	0.83
1:D:5:GLU:CB	1:E:12:ILE:CD1	2.57	0.83
1:K:41:GLU:OE1	1:O:10:ILE:HG12	1.76	0.83
1:L:12:ILE:CD1	1:M:5:GLU:CB	2.57	0.83
1:M:35:GLU:CD	1:P:15:ILE:HD12	2.04	0.83
1:N:12:ILE:CD1	1:O:5:GLU:CB	2.57	0.83
1:N:12:ILE:HD12	1:O:5:GLU:H	0.88	0.82
1:N:15:ILE:HG13	1:O:6:LEU:HD22	1.61	0.82
1:P:12:ILE:CD1	1:Q:5:GLU:CB	2.57	0.82
1:B:10:ILE:HD12	1:F:38:LEU:HD13	1.56	0.82
1:B:35:GLU:CD	1:K:15:ILE:HD12	2.04	0.82
1:C:6:LEU:HD22	1:D:15:ILE:HG13	1.61	0.82
1:J:9:VAL:HA	1:J:12:ILE:HG12	1.62	0.82
1:L:8:ILE:HD11	1:M:1:MEA:HD2	1.57	0.82
1:N:117:VAL:HG22	1:R:21:LEU:HD21	1.60	0.82
1:O:9:VAL:HA	1:O:12:ILE:HG12	1.62	0.82
1:O:35:GLU:CD	1:R:15:ILE:CD1	2.53	0.82
1:Q:9:VAL:HA	1:Q:12:ILE:HG12	1.62	0.82
1:A:10:ILE:HD12	1:E:38:LEU:HD13	1.56	0.82
1:B:15:ILE:HD12	1:E:35:GLU:CD	2.04	0.82
1:C:15:ILE:HD12	1:F:35:GLU:CD	2.04	0.82
1:K:44:LYS:HZ3	1:O:14:GLY:CA	1.91	0.82
1:M:38:LEU:HD21	1:Q:6:LEU:O	1.78	0.82
1:N:35:GLU:CD	1:Q:15:ILE:CD1	2.53	0.82
1:A:10:ILE:HG12	1:E:38:LEU:HA	0.85	0.82
1:C:44:LYS:HZ3	1:K:14:GLY:CA	1.93	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:8:ILE:HD11	1:K:1:MEA:HD2	1.57	0.82
1:M:116:SER:CB	1:Q:21:LEU:O	2.23	0.82
1:M:117:VAL:HG22	1:Q:21:LEU:HD21	1.60	0.82
1:Q:8:ILE:HD11	1:R:1:MEA:HD2	1.58	0.82
1:A:35:GLU:CD	1:L:15:ILE:HD12	2.04	0.82
1:A:38:LEU:HD21	1:M:6:LEU:O	1.78	0.82
1:B:9:VAL:HA	1:B:12:ILE:HG12	1.62	0.82
1:F:5:GLU:CB	1:G:12:ILE:CD1	2.57	0.82
1:J:35:GLU:CD	1:M:15:ILE:CD1	2.53	0.82
1:B:6:LEU:HD22	1:C:15:ILE:HG13	1.61	0.82
1:G:9:VAL:HA	1:G:12:ILE:HG12	1.62	0.82
1:M:15:ILE:HG13	1:N:6:LEU:HD22	1.61	0.82
1:N:38:LEU:HA	1:R:10:ILE:HG12	0.85	0.82
1:A:6:LEU:O	1:E:38:LEU:HD21	1.78	0.82
1:A:41:GLU:OE1	1:M:10:ILE:HG12	1.76	0.82
1:C:15:ILE:CD1	1:F:35:GLU:CD	2.53	0.82
1:D:15:ILE:CD1	1:G:35:GLU:CD	2.53	0.82
1:G:1:MEA:HD2	1:H:8:ILE:HD11	1.57	0.82
1:K:35:GLU:CD	1:N:15:ILE:CD1	2.53	0.82
1:Q:12:ILE:CD1	1:R:5:GLU:CB	2.57	0.82
1:E:5:GLU:CB	1:F:12:ILE:CD1	2.57	0.82
1:E:9:VAL:HB	1:F:16:LEU:HD21	1.62	0.82
1:F:9:VAL:HA	1:F:12:ILE:HG12	1.62	0.82
1:K:35:GLU:CD	1:N:15:ILE:HD12	2.04	0.82
1:L:35:GLU:CD	1:O:15:ILE:HD12	2.04	0.82
1:P:9:VAL:HA	1:P:12:ILE:HG12	1.62	0.82
1:A:9:VAL:HA	1:A:12:ILE:HG12	1.62	0.82
1:C:38:LEU:HD13	1:K:10:ILE:HD12	1.56	0.82
1:L:38:LEU:HA	1:P:10:ILE:HG12	0.85	0.82
1:B:21:LEU:HD21	1:F:117:VAL:HG22	1.61	0.82
1:D:44:LYS:NZ	1:J:14:GLY:HA3	1.95	0.82
1:F:6:LEU:HD22	1:G:15:ILE:HG13	1.61	0.82
1:F:15:ILE:HD12	1:I:35:GLU:CD	2.04	0.82
1:I:9:VAL:HA	1:I:12:ILE:HG12	1.62	0.82
1:J:12:ILE:CD1	1:K:5:GLU:CB	2.57	0.82
1:J:35:GLU:CD	1:M:15:ILE:HD12	2.04	0.82
1:J:116:SER:CB	1:N:21:LEU:O	2.23	0.82
1:K:12:ILE:CD1	1:L:5:GLU:CB	2.57	0.82
1:K:38:LEU:HD21	1:O:6:LEU:O	1.78	0.82
1:M:38:LEU:HA	1:Q:10:ILE:HG12	0.85	0.82
1:Q:8:ILE:HG21	1:R:3:LEU:N	1.89	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MEA:CD2	1:B:8:ILE:HD12	2.07	0.81
1:A:21:LEU:HD21	1:E:117:VAL:HG22	1.61	0.81
1:A:38:LEU:HA	1:M:10:ILE:HG12	0.85	0.81
1:B:9:VAL:HB	1:C:16:LEU:HD21	1.62	0.81
1:C:1:MEA:CD2	1:D:8:ILE:HD12	2.07	0.81
1:D:9:VAL:HA	1:D:12:ILE:HG12	1.62	0.81
1:D:15:ILE:HD12	1:G:35:GLU:CD	2.04	0.81
1:K:16:LEU:HD21	1:L:9:VAL:HB	1.62	0.81
1:L:117:VAL:HG22	1:P:21:LEU:HD21	1.60	0.81
1:A:9:VAL:HB	1:B:16:LEU:HD21	1.62	0.81
1:A:21:LEU:O	1:E:116:SER:CB	2.23	0.81
1:B:44:LYS:HZ1	1:L:14:GLY:CA	1.91	0.81
1:G:9:VAL:HB	1:H:16:LEU:HD21	1.62	0.81
1:M:35:GLU:CD	1:P:15:ILE:CD1	2.53	0.81
1:O:16:LEU:HD21	1:P:9:VAL:HB	1.62	0.81
1:P:16:LEU:HD21	1:Q:9:VAL:HB	1.62	0.81
1:A:10:ILE:HG12	1:E:41:GLU:OE1	1.76	0.81
1:B:15:ILE:CD1	1:E:35:GLU:CD	2.53	0.81
1:C:117:VAL:HG22	1:K:21:LEU:HD21	1.61	0.81
1:E:15:ILE:HD12	1:H:35:GLU:CD	2.04	0.81
1:H:1:MEA:CD2	1:I:8:ILE:HD12	2.07	0.81
1:J:38:LEU:HD21	1:N:6:LEU:O	1.78	0.81
1:K:9:VAL:HA	1:K:12:ILE:HG12	1.62	0.81
1:L:16:LEU:HD21	1:M:9:VAL:HB	1.63	0.81
1:N:38:LEU:HD21	1:R:6:LEU:O	1.78	0.81
1:B:10:ILE:HG12	1:F:38:LEU:HA	0.85	0.81
1:B:116:SER:CB	1:L:21:LEU:HD13	1.92	0.81
1:D:9:VAL:HB	1:E:16:LEU:HD21	1.62	0.81
1:H:9:VAL:HA	1:H:12:ILE:HG12	1.62	0.81
1:N:9:VAL:HA	1:N:12:ILE:HG12	1.62	0.81
1:E:6:LEU:O	1:I:38:LEU:HD21	1.78	0.81
1:F:9:VAL:HB	1:G:16:LEU:HD21	1.62	0.81
1:H:9:VAL:HB	1:I:16:LEU:HD21	1.62	0.81
1:K:117:VAL:HG22	1:O:21:LEU:HD21	1.60	0.81
1:Q:15:ILE:HG13	1:R:6:LEU:HD22	1.61	0.81
1:C:35:GLU:CD	1:J:15:ILE:CD1	2.53	0.81
1:D:3:LEU:N	1:E:8:ILE:HG21	1.90	0.81
1:E:9:VAL:HA	1:E:12:ILE:HG12	1.62	0.81
1:F:15:ILE:CD1	1:I:35:GLU:CD	2.53	0.81
1:J:44:LYS:NZ	1:N:14:GLY:HA3	1.95	0.81
1:K:44:LYS:HZ3	1:O:14:GLY:HA3	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:LEU:HD21	1:J:9:VAL:HB	1.62	0.81
1:C:9:VAL:HB	1:D:16:LEU:HD21	1.62	0.81
1:D:117:VAL:HG22	1:J:21:LEU:HD21	1.61	0.81
1:L:15:ILE:HG13	1:M:6:LEU:HD22	1.61	0.81
1:A:116:SER:CB	1:M:21:LEU:O	2.23	0.81
1:C:25:GLN:CD	1:G:52:LEU:HG	2.06	0.81
1:E:15:ILE:CD1	1:H:35:GLU:CD	2.53	0.81
1:O:8:ILE:HD12	1:P:1:MEA:CD2	2.07	0.81
1:P:8:ILE:HD12	1:Q:1:MEA:CD2	2.07	0.81
1:K:44:LYS:NZ	1:O:14:GLY:HA3	1.95	0.81
1:L:8:ILE:HG21	1:M:3:LEU:N	1.90	0.81
1:L:35:GLU:CD	1:O:15:ILE:CD1	2.53	0.81
1:M:52:LEU:HG	1:Q:25:GLN:CD	2.06	0.81
1:N:16:LEU:HD21	1:O:9:VAL:HB	1.63	0.81
1:A:35:GLU:CD	1:L:15:ILE:CD1	2.53	0.81
1:B:6:LEU:O	1:F:38:LEU:HD21	1.78	0.81
1:C:9:VAL:HA	1:C:12:ILE:HG12	1.62	0.81
1:D:6:LEU:HD22	1:E:15:ILE:HG13	1.61	0.81
1:E:6:LEU:HD22	1:F:15:ILE:HG13	1.61	0.81
1:L:44:LYS:HZ3	1:P:14:GLY:HA3	1.44	0.81
1:L:52:LEU:HG	1:P:25:GLN:CD	2.06	0.81
1:M:9:VAL:HA	1:M:12:ILE:HG12	1.62	0.81
1:R:9:VAL:HA	1:R:12:ILE:HG12	1.62	0.81
1:A:15:ILE:CD1	1:D:35:GLU:CD	2.53	0.80
1:A:43:GLN:HE22	1:A:73:ILE:HD13	1.46	0.80
1:C:1:MEA:HD2	1:D:8:ILE:HD11	1.57	0.80
1:D:21:LEU:HD13	1:H:116:SER:CB	1.92	0.80
1:D:52:LEU:HG	1:J:25:GLN:CD	2.06	0.80
1:G:43:GLN:HE22	1:G:73:ILE:HD13	1.47	0.80
1:J:43:GLN:HE22	1:J:73:ILE:HD13	1.46	0.80
1:L:116:SER:CB	1:P:21:LEU:CD1	2.29	0.80
1:M:16:LEU:HD21	1:N:9:VAL:HB	1.63	0.80
1:N:52:LEU:HG	1:R:25:GLN:CD	2.06	0.80
1:O:97:VAL:HG21	1:O:102:LYS:HB3	1.64	0.80
1:A:25:GLN:CD	1:E:52:LEU:HG	2.06	0.80
1:J:15:ILE:HG13	1:K:6:LEU:HD22	1.61	0.80
1:J:16:LEU:HD21	1:K:9:VAL:HB	1.62	0.80
1:P:43:GLN:HE22	1:P:73:ILE:HD13	1.46	0.80
1:B:97:VAL:HG21	1:B:102:LYS:HB3	1.64	0.80
1:C:38:LEU:HD21	1:K:6:LEU:O	1.78	0.80
1:G:97:VAL:HG21	1:G:102:LYS:HB3	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:VAL:HG21	1:F:102:LYS:HB3	1.64	0.80
1:J:52:LEU:HG	1:N:25:GLN:CD	2.06	0.80
1:J:97:VAL:HG21	1:J:102:LYS:HB3	1.64	0.80
1:O:15:ILE:HG13	1:P:6:LEU:HD22	1.61	0.80
1:Q:16:LEU:HD21	1:R:9:VAL:HB	1.62	0.80
1:D:14:GLY:HA3	1:H:44:LYS:NZ	1.95	0.80
1:E:10:ILE:HG12	1:I:38:LEU:HA	0.85	0.80
1:H:43:GLN:HE22	1:H:73:ILE:HD13	1.47	0.80
1:M:44:LYS:NZ	1:Q:14:GLY:HA3	1.95	0.80
1:M:116:SER:CB	1:Q:21:LEU:HD13	1.92	0.80
1:B:25:GLN:CD	1:F:52:LEU:HG	2.06	0.80
1:B:35:GLU:CD	1:K:15:ILE:CD1	2.53	0.80
1:C:52:LEU:HG	1:K:25:GLN:CD	2.06	0.80
1:H:6:LEU:HD22	1:I:15:ILE:HG13	1.61	0.80
1:I:97:VAL:HG21	1:I:102:LYS:HB3	1.64	0.80
1:K:15:ILE:HG13	1:L:6:LEU:HD22	1.61	0.80
1:L:9:VAL:HA	1:L:12:ILE:HG12	1.62	0.80
1:M:44:LYS:HZ1	1:Q:14:GLY:CA	1.95	0.80
1:Q:43:GLN:HE22	1:Q:73:ILE:HD13	1.46	0.80
1:G:6:LEU:HD22	1:H:15:ILE:HG13	1.61	0.80
1:O:43:GLN:HE22	1:O:73:ILE:HD13	1.46	0.80
1:A:12:ILE:HD11	1:J:5:GLU:H	1.45	0.80
1:A:44:LYS:NZ	1:M:14:GLY:HA3	1.95	0.80
1:G:5:GLU:H	1:H:12:ILE:HD11	1.45	0.80
1:H:3:LEU:N	1:I:8:ILE:HG21	1.90	0.80
1:J:44:LYS:HZ3	1:N:14:GLY:CA	1.93	0.80
1:K:97:VAL:HG21	1:K:102:LYS:HB3	1.64	0.80
1:M:12:ILE:HD11	1:N:5:GLU:H	1.45	0.80
1:N:97:VAL:HG21	1:N:102:LYS:HB3	1.64	0.80
1:P:15:ILE:HG13	1:Q:6:LEU:HD22	1.61	0.80
1:B:44:LYS:NZ	1:L:14:GLY:HA3	1.95	0.80
1:D:25:GLN:CD	1:H:52:LEU:HG	2.06	0.80
1:K:52:LEU:HG	1:O:25:GLN:CD	2.06	0.80
1:N:44:LYS:NZ	1:R:14:GLY:HA3	1.95	0.80
1:N:116:SER:CB	1:R:21:LEU:HD13	1.92	0.80
1:P:12:ILE:HD11	1:Q:5:GLU:H	1.45	0.80
1:E:25:GLN:CD	1:I:52:LEU:HG	2.06	0.79
1:Q:97:VAL:HG21	1:Q:102:LYS:HB3	1.64	0.79
1:A:97:VAL:HG21	1:A:102:LYS:HB3	1.64	0.79
1:B:43:GLN:HE22	1:B:73:ILE:HD13	1.46	0.79
1:B:52:LEU:HG	1:L:25:GLN:CD	2.06	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:SER:CB	1:J:21:LEU:O	2.23	0.79
1:N:43:GLN:HE22	1:N:73:ILE:HD13	1.46	0.79
1:P:97:VAL:HG21	1:P:102:LYS:HB3	1.64	0.79
1:A:6:LEU:HD22	1:B:15:ILE:HG13	1.61	0.79
1:A:8:ILE:HD12	1:J:1:MEA:CD2	2.07	0.79
1:B:14:GLY:CA	1:F:44:LYS:HZ1	1.91	0.79
1:C:14:GLY:CA	1:G:44:LYS:HZ3	1.94	0.79
1:J:8:ILE:HG21	1:K:3:LEU:N	1.90	0.79
1:J:38:LEU:HD13	1:N:10:ILE:HD12	1.56	0.79
1:A:3:LEU:N	1:B:8:ILE:HG21	1.90	0.79
1:A:21:LEU:HD13	1:E:116:SER:CB	1.92	0.79
1:C:14:GLY:HA3	1:G:44:LYS:NZ	1.95	0.79
1:C:43:GLN:HE22	1:C:73:ILE:HD13	1.46	0.79
1:D:10:ILE:HG12	1:H:38:LEU:HA	0.85	0.79
1:D:10:ILE:HD12	1:H:38:LEU:HD13	1.56	0.79
1:E:10:ILE:HD12	1:I:38:LEU:HD13	1.56	0.79
1:F:43:GLN:HE22	1:F:73:ILE:HD13	1.47	0.79
1:H:97:VAL:HG21	1:H:102:LYS:HB3	1.64	0.79
1:A:15:ILE:HG13	1:J:6:LEU:HD22	1.61	0.79
1:C:97:VAL:HG21	1:C:102:LYS:HB3	1.64	0.79
1:R:43:GLN:HE22	1:R:73:ILE:HD13	1.46	0.79
1:C:3:LEU:N	1:D:8:ILE:HG21	1.90	0.79
1:K:43:GLN:HE22	1:K:73:ILE:HD13	1.46	0.79
1:L:53:ASN:HB3	1:O:149:SER:CB	2.13	0.79
1:A:14:GLY:HA2	1:E:44:LYS:HZ3	1.45	0.79
1:A:116:SER:CB	1:M:21:LEU:HD13	1.92	0.79
1:B:14:GLY:HA3	1:F:44:LYS:NZ	1.95	0.79
1:C:44:LYS:HZ3	1:K:14:GLY:HA3	1.46	0.79
1:G:1:MEA:CD2	1:H:8:ILE:HD12	2.07	0.79
1:L:43:GLN:HE22	1:L:73:ILE:HD13	1.46	0.79
1:B:149:SER:CB	1:E:53:ASN:HB3	2.13	0.79
1:E:43:GLN:HE22	1:E:73:ILE:HD13	1.47	0.79
1:L:44:LYS:NZ	1:P:14:GLY:HA3	1.95	0.79
1:R:97:VAL:HG21	1:R:102:LYS:HB3	1.64	0.79
1:F:149:SER:CB	1:I:53:ASN:HB3	2.13	0.79
1:O:8:ILE:HG21	1:P:3:LEU:N	1.90	0.79
1:P:15:ILE:HG13	1:Q:6:LEU:HD13	1.64	0.79
1:C:44:LYS:NZ	1:K:14:GLY:HA3	1.95	0.79
1:C:97:VAL:CG2	1:C:102:LYS:HB3	2.13	0.79
1:E:6:LEU:HD13	1:F:15:ILE:HG13	1.64	0.79
1:I:43:GLN:HE22	1:I:73:ILE:HD13	1.47	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LEU:HG	1:M:25:GLN:CD	2.06	0.78
1:A:149:SER:CB	1:D:53:ASN:HB3	2.13	0.78
1:B:6:LEU:HD13	1:C:15:ILE:HG13	1.64	0.78
1:B:9:VAL:CB	1:C:16:LEU:HD21	2.14	0.78
1:B:38:LEU:HA	1:L:10:ILE:HG12	0.85	0.78
1:D:5:GLU:H	1:E:12:ILE:HD11	1.45	0.78
1:P:8:ILE:HD11	1:Q:1:MEA:HD2	1.58	0.78
1:B:53:ASN:HB3	1:K:149:SER:CB	2.13	0.78
1:E:97:VAL:HG21	1:E:102:LYS:HB3	1.64	0.78
1:G:6:LEU:HD13	1:H:15:ILE:HG13	1.65	0.78
1:K:15:ILE:HG13	1:L:6:LEU:HD13	1.64	0.78
1:M:38:LEU:HD13	1:Q:10:ILE:HD12	1.56	0.78
1:M:43:GLN:HE22	1:M:73:ILE:HD13	1.46	0.78
1:M:53:ASN:HB3	1:P:149:SER:CB	2.13	0.78
1:N:97:VAL:CG2	1:N:102:LYS:HB3	2.14	0.78
1:O:97:VAL:CG2	1:O:102:LYS:HB3	2.14	0.78
1:Q:97:VAL:CG2	1:Q:102:LYS:HB3	2.14	0.78
1:A:116:SER:CA	1:M:25:GLN:HE21	1.97	0.78
1:M:15:ILE:HG13	1:N:6:LEU:HD13	1.64	0.78
1:N:44:LYS:HZ3	1:R:14:GLY:CA	1.94	0.78
1:B:97:VAL:CG2	1:B:102:LYS:HB3	2.13	0.78
1:D:6:LEU:HD13	1:E:15:ILE:HG13	1.64	0.78
1:D:43:GLN:HE22	1:D:73:ILE:HD13	1.47	0.78
1:E:97:VAL:CG2	1:E:102:LYS:HB3	2.14	0.78
1:F:97:VAL:CG2	1:F:102:LYS:HB3	2.14	0.78
1:G:9:VAL:CB	1:H:16:LEU:HD21	2.14	0.78
1:N:53:ASN:HB3	1:Q:149:SER:CB	2.13	0.78
1:D:97:VAL:CG2	1:D:102:LYS:HB3	2.14	0.78
1:K:53:ASN:HB3	1:N:149:SER:CB	2.13	0.78
1:L:12:ILE:HD11	1:M:5:GLU:H	1.45	0.78
1:B:19:VAL:CG1	1:E:38:LEU:O	2.32	0.78
1:B:21:LEU:HD13	1:F:116:SER:CB	1.92	0.78
1:C:9:VAL:CB	1:D:16:LEU:HD21	2.14	0.78
1:D:25:GLN:HE21	1:H:116:SER:CA	1.96	0.78
1:J:97:VAL:CG2	1:J:102:LYS:HB3	2.14	0.78
1:L:97:VAL:HG21	1:L:102:LYS:HB3	1.64	0.78
1:M:16:LEU:HD21	1:N:9:VAL:CB	2.14	0.78
1:O:53:ASN:HB3	1:R:149:SER:CB	2.13	0.78
1:B:116:SER:CA	1:L:25:GLN:HE21	1.96	0.78
1:E:25:GLN:HE21	1:I:116:SER:CA	1.96	0.78
1:L:97:VAL:CG2	1:L:102:LYS:HB3	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:15:ILE:HG13	1:P:6:LEU:HD13	1.64	0.78
1:A:38:LEU:O	1:L:19:VAL:CG1	2.32	0.78
1:F:9:VAL:CB	1:G:16:LEU:HD21	2.14	0.78
1:A:53:ASN:HB3	1:L:149:SER:CB	2.13	0.78
1:J:53:ASN:HB3	1:M:149:SER:CB	2.13	0.78
1:M:97:VAL:CG2	1:M:102:LYS:HB3	2.14	0.78
1:M:97:VAL:HG21	1:M:102:LYS:HB3	1.64	0.78
1:N:15:ILE:HG13	1:O:6:LEU:HD13	1.64	0.78
1:Q:16:LEU:HD21	1:R:9:VAL:CB	2.14	0.78
1:A:6:LEU:HD13	1:B:15:ILE:HG13	1.64	0.78
1:A:15:ILE:HG13	1:J:6:LEU:HD13	1.64	0.78
1:C:53:ASN:HB3	1:J:149:SER:CB	2.13	0.78
1:F:6:LEU:HD13	1:G:15:ILE:HG13	1.64	0.78
1:F:19:VAL:CG1	1:I:38:LEU:O	2.32	0.78
1:G:97:VAL:CG2	1:G:102:LYS:HB3	2.14	0.78
1:N:8:ILE:HD11	1:O:1:MEA:HD2	1.57	0.78
1:O:16:LEU:HD21	1:P:9:VAL:CB	2.14	0.78
1:P:97:VAL:CG2	1:P:102:LYS:HB3	2.14	0.78
1:A:9:VAL:CB	1:B:16:LEU:HD21	2.14	0.77
1:A:16:LEU:HD21	1:J:9:VAL:CB	2.14	0.77
1:C:6:LEU:HD13	1:D:15:ILE:HG13	1.64	0.77
1:K:97:VAL:CG2	1:K:102:LYS:HB3	2.14	0.77
1:C:149:SER:CB	1:F:53:ASN:HB3	2.13	0.77
1:D:97:VAL:HG21	1:D:102:LYS:HB3	1.64	0.77
1:M:38:LEU:O	1:P:19:VAL:CG1	2.32	0.77
1:N:44:LYS:HZ3	1:R:14:GLY:HA3	1.47	0.77
1:A:14:GLY:HA3	1:E:44:LYS:NZ	1.95	0.77
1:E:3:LEU:N	1:F:8:ILE:HG21	1.90	0.77
1:E:149:SER:CB	1:H:53:ASN:HB3	2.13	0.77
1:H:6:LEU:HD13	1:I:15:ILE:HG13	1.64	0.77
1:I:97:VAL:CG2	1:I:102:LYS:HB3	2.14	0.77
1:N:16:LEU:HD21	1:O:9:VAL:CB	2.14	0.77
1:A:97:VAL:CG2	1:A:102:LYS:HB3	2.14	0.77
1:C:25:GLN:NE2	1:G:116:SER:CA	2.48	0.77
1:E:14:GLY:HA3	1:I:44:LYS:NZ	1.95	0.77
1:H:9:VAL:CB	1:I:16:LEU:HD21	2.14	0.77
1:R:97:VAL:CG2	1:R:102:LYS:HB3	2.14	0.77
1:C:38:LEU:O	1:J:19:VAL:CG1	2.32	0.77
1:A:1:MEA:HD2	1:B:8:ILE:HD11	1.57	0.77
1:D:19:VAL:CG1	1:G:38:LEU:O	2.32	0.77
1:D:116:SER:CA	1:J:25:GLN:NE2	2.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:149:SER:CB	1:G:53:ASN:HB3	2.13	0.77
1:E:9:VAL:CB	1:F:16:LEU:HD21	2.13	0.77
1:K:116:SER:CA	1:O:25:GLN:NE2	2.48	0.77
1:L:38:LEU:HD13	1:P:10:ILE:HD12	1.56	0.77
1:L:38:LEU:O	1:O:19:VAL:CG1	2.32	0.77
1:M:38:LEU:HD23	1:Q:6:LEU:O	1.84	0.77
1:O:38:LEU:O	1:R:19:VAL:CG1	2.32	0.77
1:A:38:LEU:HD23	1:M:6:LEU:O	1.84	0.77
1:D:44:LYS:HZ3	1:J:14:GLY:HA3	1.48	0.77
1:J:44:LYS:HZ3	1:N:14:GLY:HA3	1.46	0.77
1:J:116:SER:CA	1:N:25:GLN:HE21	1.97	0.77
1:K:8:ILE:HD11	1:L:1:MEA:HD2	1.57	0.77
1:Q:15:ILE:HG13	1:R:6:LEU:HD13	1.64	0.77
1:E:19:VAL:CG1	1:H:38:LEU:O	2.32	0.77
1:G:3:LEU:N	1:H:8:ILE:HG21	1.90	0.77
1:J:15:ILE:HG13	1:K:6:LEU:HD13	1.64	0.77
1:K:38:LEU:HD13	1:O:10:ILE:HD12	1.56	0.77
1:J:12:ILE:HD11	1:K:5:GLU:H	1.45	0.77
1:K:38:LEU:HD23	1:O:6:LEU:O	1.84	0.77
1:N:38:LEU:HD13	1:R:10:ILE:HD12	1.56	0.77
1:D:9:VAL:CB	1:E:16:LEU:HD21	2.14	0.77
1:J:116:SER:CA	1:N:25:GLN:NE2	2.48	0.77
1:K:38:LEU:O	1:N:19:VAL:CG1	2.32	0.77
1:D:6:LEU:O	1:H:38:LEU:HD23	1.85	0.76
1:J:16:LEU:HD21	1:K:9:VAL:CB	2.14	0.76
1:K:8:ILE:HG21	1:L:3:LEU:N	1.90	0.76
1:K:116:SER:CA	1:O:25:GLN:HE21	1.97	0.76
1:L:15:ILE:HG13	1:M:6:LEU:HD13	1.64	0.76
1:L:116:SER:CA	1:P:25:GLN:HE21	1.97	0.76
1:M:116:SER:CA	1:Q:25:GLN:NE2	2.48	0.76
1:N:38:LEU:O	1:Q:19:VAL:CG1	2.32	0.76
1:B:25:GLN:HE21	1:F:116:SER:CA	1.96	0.76
1:H:97:VAL:CG2	1:H:102:LYS:HB3	2.14	0.76
1:A:44:LYS:HZ1	1:M:14:GLY:CA	1.96	0.76
1:C:38:LEU:HD23	1:K:6:LEU:O	1.84	0.76
1:C:116:SER:CA	1:K:25:GLN:HE21	1.96	0.76
1:P:16:LEU:HD21	1:Q:9:VAL:CB	2.14	0.76
1:B:25:GLN:NE2	1:F:116:SER:CA	2.48	0.76
1:B:38:LEU:O	1:K:19:VAL:CG1	2.32	0.76
1:D:38:LEU:HD23	1:J:6:LEU:O	1.84	0.76
1:H:5:GLU:H	1:I:12:ILE:HD11	1.45	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:116:SER:CB	1:N:21:LEU:HD13	1.92	0.76
1:L:16:LEU:HD21	1:M:9:VAL:CB	2.14	0.76
1:M:116:SER:CA	1:Q:25:GLN:HE21	1.97	0.76
1:C:25:GLN:HE21	1:G:116:SER:CA	1.97	0.76
1:N:38:LEU:HD23	1:R:6:LEU:O	1.84	0.76
1:A:6:LEU:O	1:E:38:LEU:HD23	1.84	0.76
1:A:116:SER:CA	1:M:25:GLN:NE2	2.48	0.76
1:B:116:SER:CA	1:L:25:GLN:NE2	2.48	0.76
1:C:10:ILE:HG12	1:G:38:LEU:HA	0.85	0.76
1:A:19:VAL:CG1	1:D:38:LEU:O	2.32	0.76
1:B:3:LEU:N	1:C:8:ILE:HG21	1.90	0.76
1:C:14:GLY:HA3	1:G:44:LYS:HZ3	1.47	0.76
1:D:25:GLN:NE2	1:H:116:SER:CA	2.48	0.76
1:N:116:SER:CA	1:R:25:GLN:HE21	1.97	0.76
1:J:38:LEU:O	1:M:19:VAL:CG1	2.32	0.76
1:K:16:LEU:HD21	1:L:9:VAL:CB	2.14	0.76
1:P:8:ILE:HG22	1:Q:3:LEU:N	2.01	0.76
1:A:5:GLU:H	1:B:12:ILE:HD11	1.45	0.76
1:B:3:LEU:N	1:C:8:ILE:HG22	2.01	0.76
1:C:116:SER:CA	1:K:25:GLN:NE2	2.48	0.76
1:D:116:SER:CA	1:J:25:GLN:HE21	1.96	0.76
1:F:3:LEU:N	1:G:8:ILE:HG21	1.90	0.76
1:M:12:ILE:HD13	1:N:5:GLU:H	1.48	0.76
1:A:8:ILE:HG21	1:J:3:LEU:N	1.90	0.75
1:A:25:GLN:HE21	1:E:116:SER:CA	1.96	0.75
1:E:3:LEU:N	1:F:8:ILE:HG22	2.01	0.75
1:G:3:LEU:N	1:H:8:ILE:HG22	2.01	0.75
1:L:116:SER:CA	1:P:25:GLN:NE2	2.48	0.75
1:C:19:VAL:CG1	1:F:38:LEU:O	2.32	0.75
1:D:3:LEU:N	1:E:8:ILE:HG22	2.01	0.75
1:G:5:GLU:H	1:H:12:ILE:HD13	1.48	0.75
1:M:8:ILE:HG22	1:N:3:LEU:N	2.01	0.75
1:N:79:LYS:HA	1:N:93:LEU:HD22	1.69	0.75
1:R:79:LYS:HA	1:R:93:LEU:HD22	1.69	0.75
1:A:25:GLN:NE2	1:E:116:SER:CA	2.48	0.75
1:O:8:ILE:HG22	1:P:3:LEU:N	2.01	0.75
1:C:10:ILE:HD12	1:G:38:LEU:HD13	1.56	0.75
1:E:25:GLN:NE2	1:I:116:SER:CA	2.48	0.75
1:A:3:LEU:N	1:B:8:ILE:HG22	2.01	0.75
1:B:116:SER:CB	1:L:21:LEU:HD12	1.95	0.75
1:E:6:LEU:O	1:I:38:LEU:HD23	1.85	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:8:ILE:HG22	1:K:3:LEU:N	2.01	0.75
1:K:79:LYS:HA	1:K:93:LEU:HD22	1.69	0.75
1:O:79:LYS:HA	1:O:93:LEU:HD22	1.69	0.75
1:Q:12:ILE:HD11	1:R:5:GLU:H	1.45	0.75
1:Q:79:LYS:HA	1:Q:93:LEU:HD22	1.69	0.75
1:D:44:LYS:HZ3	1:J:14:GLY:CA	1.97	0.75
1:P:12:ILE:HD13	1:Q:5:GLU:H	1.48	0.75
1:H:3:LEU:N	1:I:8:ILE:HG22	2.01	0.75
1:J:38:LEU:HD23	1:N:6:LEU:O	1.84	0.75
1:L:8:ILE:HG22	1:M:3:LEU:N	2.01	0.75
1:H:1:MEA:CG	1:I:8:ILE:CD1	2.65	0.74
1:J:12:ILE:HD13	1:K:5:GLU:H	1.48	0.74
1:K:8:ILE:HG22	1:L:3:LEU:N	2.01	0.74
1:O:12:ILE:HD11	1:P:5:GLU:H	1.45	0.74
1:B:6:LEU:O	1:F:38:LEU:HD23	1.84	0.74
1:D:1:MEA:CG	1:E:8:ILE:CD1	2.65	0.74
1:F:1:MEA:HD2	1:G:8:ILE:HD11	1.57	0.74
1:A:8:ILE:HG22	1:J:3:LEU:N	2.01	0.74
1:O:8:ILE:CD1	1:P:1:MEA:CG	2.65	0.74
1:E:21:LEU:HD12	1:I:116:SER:CB	1.95	0.74
1:A:8:ILE:CD1	1:J:1:MEA:CG	2.65	0.74
1:D:5:GLU:H	1:E:12:ILE:HD13	1.48	0.74
1:J:79:LYS:HA	1:J:93:LEU:HD22	1.69	0.74
1:L:38:LEU:HD23	1:P:6:LEU:O	1.84	0.74
1:P:8:ILE:HG21	1:Q:3:LEU:N	1.90	0.74
1:C:6:LEU:O	1:G:38:LEU:HD23	1.85	0.74
1:B:38:LEU:HD23	1:L:6:LEU:O	1.84	0.74
1:B:79:LYS:HA	1:B:93:LEU:HD22	1.69	0.74
1:C:79:LYS:HA	1:C:93:LEU:HD22	1.69	0.74
1:D:21:LEU:HB3	1:H:116:SER:HB2	1.70	0.74
1:N:8:ILE:HG21	1:O:3:LEU:N	1.90	0.74
1:E:1:MEA:CG	1:F:8:ILE:CD1	2.65	0.74
1:C:21:LEU:HB3	1:G:116:SER:HB2	1.70	0.74
1:L:79:LYS:HA	1:L:93:LEU:HD22	1.69	0.74
1:A:5:GLU:H	1:B:12:ILE:HD13	1.48	0.73
1:M:116:SER:HB2	1:Q:21:LEU:HB3	1.70	0.73
1:N:8:ILE:HG22	1:O:3:LEU:N	2.01	0.73
1:A:1:MEA:CG	1:B:8:ILE:CD1	2.65	0.73
1:D:5:GLU:CB	1:E:12:ILE:HD12	2.18	0.73
1:E:79:LYS:HA	1:E:93:LEU:HD22	1.69	0.73
1:H:79:LYS:HA	1:H:93:LEU:HD22	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:116:SER:HB2	1:R:21:LEU:HB3	1.70	0.73
1:A:21:LEU:HB3	1:E:116:SER:HB2	1.70	0.73
1:A:38:LEU:HD13	1:M:10:ILE:HD12	1.56	0.73
1:L:8:ILE:CD1	1:M:1:MEA:CG	2.65	0.73
1:D:14:GLY:CA	1:H:44:LYS:HZ1	2.02	0.73
1:D:32:GLN:NE2	1:D:97:VAL:HA	2.04	0.73
1:A:35:GLU:HG3	1:L:15:ILE:CD1	2.19	0.73
1:E:14:GLY:CA	1:I:44:LYS:HZ1	2.02	0.73
1:K:38:LEU:O	1:O:10:ILE:CD1	2.37	0.73
1:L:12:ILE:HD12	1:M:5:GLU:CB	2.18	0.73
1:P:12:ILE:HD12	1:Q:5:GLU:CB	2.18	0.73
1:B:15:ILE:CD1	1:E:35:GLU:HG3	2.19	0.73
1:C:3:LEU:N	1:D:8:ILE:HG22	2.01	0.73
1:D:10:ILE:CD1	1:H:38:LEU:O	2.37	0.73
1:D:38:LEU:O	1:J:10:ILE:CD1	2.37	0.73
1:G:79:LYS:HA	1:G:93:LEU:HD22	1.69	0.73
1:J:38:LEU:O	1:N:10:ILE:CD1	2.37	0.73
1:L:38:LEU:O	1:P:10:ILE:CD1	2.37	0.73
1:D:116:SER:HB2	1:J:21:LEU:HB3	1.70	0.73
1:E:10:ILE:CD1	1:I:38:LEU:O	2.37	0.73
1:F:1:MEA:CG	1:G:8:ILE:CD1	2.65	0.73
1:P:79:LYS:HA	1:P:93:LEU:HD22	1.69	0.73
1:Q:8:ILE:CD1	1:R:1:MEA:CG	2.65	0.73
1:A:12:ILE:HD12	1:J:5:GLU:CB	2.18	0.73
1:F:3:LEU:N	1:G:8:ILE:HG22	2.01	0.73
1:M:32:GLN:NE2	1:M:97:VAL:HA	2.04	0.73
1:N:38:LEU:O	1:R:10:ILE:CD1	2.37	0.73
1:P:8:ILE:CD1	1:Q:1:MEA:CG	2.65	0.73
1:Q:8:ILE:HG22	1:R:3:LEU:N	2.01	0.73
1:B:1:MEA:CG	1:C:8:ILE:CD1	2.65	0.73
1:C:10:ILE:CD1	1:G:38:LEU:O	2.37	0.73
1:D:38:LEU:HD13	1:J:10:ILE:HD12	1.56	0.73
1:C:32:GLN:NE2	1:C:97:VAL:HA	2.04	0.72
1:C:35:GLU:HG3	1:J:15:ILE:CD1	2.19	0.72
1:C:38:LEU:O	1:K:10:ILE:CD1	2.37	0.72
1:E:32:GLN:NE2	1:E:97:VAL:HA	2.04	0.72
1:F:79:LYS:HA	1:F:93:LEU:HD22	1.69	0.72
1:H:32:GLN:NE2	1:H:97:VAL:HA	2.04	0.72
1:J:32:GLN:NE2	1:J:97:VAL:HA	2.04	0.72
1:M:35:GLU:HG3	1:P:15:ILE:CD1	2.19	0.72
1:N:32:GLN:NE2	1:N:97:VAL:HA	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:32:GLN:NE2	1:P:97:VAL:HA	2.04	0.72
1:Q:32:GLN:NE2	1:Q:97:VAL:HA	2.04	0.72
1:E:5:GLU:H	1:F:12:ILE:HD11	1.45	0.72
1:H:1:MEA:HD2	1:I:8:ILE:CD1	2.16	0.72
1:H:5:GLU:CB	1:I:12:ILE:HD12	2.18	0.72
1:I:107:SER:OG	1:I:124:PRO:HA	1.90	0.72
1:N:15:ILE:C	1:O:6:LEU:HD13	2.15	0.72
1:A:10:ILE:CD1	1:E:38:LEU:O	2.37	0.72
1:A:15:ILE:C	1:J:6:LEU:HD13	2.15	0.72
1:A:79:LYS:HA	1:A:93:LEU:HD22	1.69	0.72
1:B:35:GLU:HG3	1:K:15:ILE:CD1	2.19	0.72
1:B:107:SER:OG	1:B:124:PRO:HA	1.90	0.72
1:D:15:ILE:HG21	1:G:76:LYS:NZ	2.05	0.72
1:E:14:GLY:HA2	1:I:44:LYS:HZ3	1.48	0.72
1:J:76:LYS:NZ	1:M:15:ILE:HG21	2.05	0.72
1:K:116:SER:HB2	1:O:21:LEU:HB3	1.70	0.72
1:L:107:SER:OG	1:L:124:PRO:HA	1.89	0.72
1:L:116:SER:HB2	1:P:21:LEU:HB3	1.70	0.72
1:M:79:LYS:HA	1:M:93:LEU:HD22	1.69	0.72
1:A:32:GLN:NE2	1:A:97:VAL:HA	2.04	0.72
1:B:15:ILE:HG21	1:E:76:LYS:NZ	2.05	0.72
1:F:32:GLN:NE2	1:F:97:VAL:HA	2.04	0.72
1:G:5:GLU:CB	1:H:12:ILE:HD12	2.18	0.72
1:J:116:SER:HB2	1:N:21:LEU:HB3	1.70	0.72
1:L:35:GLU:OE1	1:O:15:ILE:CD1	2.13	0.72
1:M:8:ILE:CD1	1:N:1:MEA:CG	2.65	0.72
1:O:32:GLN:NE2	1:O:97:VAL:HA	2.04	0.72
1:P:15:ILE:C	1:Q:6:LEU:HD13	2.15	0.72
1:B:116:SER:HB2	1:L:21:LEU:HB3	1.70	0.72
1:D:79:LYS:HA	1:D:93:LEU:HD22	1.69	0.72
1:F:6:LEU:HD13	1:G:15:ILE:C	2.15	0.72
1:G:6:LEU:HD13	1:H:15:ILE:C	2.15	0.72
1:J:35:GLU:HG3	1:M:15:ILE:CD1	2.19	0.72
1:K:35:GLU:HG3	1:N:15:ILE:CD1	2.19	0.72
1:N:107:SER:OG	1:N:124:PRO:HA	1.89	0.72
1:O:15:ILE:C	1:P:6:LEU:HD13	2.15	0.72
1:A:6:LEU:HD13	1:B:15:ILE:C	2.15	0.72
1:A:38:LEU:O	1:M:10:ILE:CD1	2.37	0.72
1:A:76:LYS:NZ	1:L:15:ILE:HG21	2.05	0.72
1:B:6:LEU:HD13	1:C:15:ILE:C	2.15	0.72
1:B:38:LEU:O	1:L:10:ILE:CD1	2.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MEA:CG	1:D:8:ILE:CD1	2.65	0.72
1:D:15:ILE:CD1	1:G:35:GLU:HG3	2.19	0.72
1:E:21:LEU:HB3	1:I:116:SER:HB2	1.70	0.72
1:E:107:SER:OG	1:E:124:PRO:HA	1.90	0.72
1:F:15:ILE:CD1	1:I:35:GLU:HG3	2.19	0.72
1:H:6:LEU:CD1	1:I:15:ILE:C	2.63	0.72
1:K:15:ILE:C	1:L:6:LEU:CD1	2.63	0.72
1:K:116:SER:CB	1:O:21:LEU:HD12	1.95	0.72
1:L:116:SER:CB	1:P:21:LEU:HD12	1.95	0.72
1:N:8:ILE:CD1	1:O:1:MEA:CG	2.65	0.72
1:O:15:ILE:C	1:P:6:LEU:CD1	2.63	0.72
1:O:107:SER:OG	1:O:124:PRO:HA	1.90	0.72
1:C:15:ILE:HG21	1:F:76:LYS:NZ	2.05	0.72
1:C:107:SER:OG	1:C:124:PRO:HA	1.90	0.72
1:D:149:SER:HB2	1:G:53:ASN:CG	2.15	0.72
1:I:32:GLN:NE2	1:I:97:VAL:HA	2.04	0.72
1:J:15:ILE:C	1:K:6:LEU:HD13	2.15	0.72
1:J:53:ASN:CG	1:M:149:SER:HB2	2.15	0.72
1:K:8:ILE:CD1	1:L:1:MEA:CG	2.65	0.72
1:O:35:GLU:HG3	1:R:15:ILE:CD1	2.19	0.72
1:A:107:SER:OG	1:A:124:PRO:HA	1.89	0.72
1:A:116:SER:HB2	1:M:21:LEU:HB3	1.70	0.72
1:A:149:SER:HB2	1:D:53:ASN:CG	2.15	0.72
1:B:53:ASN:CG	1:K:149:SER:HB2	2.15	0.72
1:C:53:ASN:CG	1:J:149:SER:HB2	2.15	0.72
1:H:6:LEU:HD13	1:I:15:ILE:C	2.15	0.72
1:J:8:ILE:CD1	1:K:1:MEA:CG	2.65	0.72
1:K:76:LYS:NZ	1:N:15:ILE:HG21	2.05	0.72
1:L:76:LYS:NZ	1:O:15:ILE:HG21	2.05	0.72
1:M:8:ILE:HG21	1:N:3:LEU:N	1.90	0.72
1:M:38:LEU:O	1:Q:10:ILE:CD1	2.37	0.72
1:N:53:ASN:CG	1:Q:149:SER:HB2	2.15	0.72
1:P:107:SER:OG	1:P:124:PRO:HA	1.90	0.72
1:B:10:ILE:CD1	1:F:38:LEU:O	2.37	0.72
1:C:149:SER:HB2	1:F:53:ASN:CG	2.15	0.72
1:G:32:GLN:NE2	1:G:97:VAL:HA	2.04	0.72
1:G:107:SER:OG	1:G:124:PRO:HA	1.90	0.72
1:K:12:ILE:HD11	1:L:5:GLU:H	1.45	0.72
1:L:32:GLN:NE2	1:L:97:VAL:HA	2.04	0.72
1:M:53:ASN:CG	1:P:149:SER:HB2	2.15	0.72
1:N:35:GLU:HG3	1:Q:15:ILE:CD1	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:107:SER:OG	1:R:124:PRO:HA	1.89	0.72
1:A:5:GLU:CB	1:B:12:ILE:HD12	2.18	0.72
1:A:15:ILE:CD1	1:D:35:GLU:HG3	2.19	0.72
1:B:21:LEU:HD12	1:F:116:SER:CB	1.95	0.72
1:B:32:GLN:NE2	1:B:97:VAL:HA	2.04	0.72
1:D:6:LEU:CD1	1:E:15:ILE:C	2.63	0.72
1:H:107:SER:OG	1:H:124:PRO:HA	1.90	0.72
1:I:79:LYS:HA	1:I:93:LEU:HD22	1.69	0.72
1:L:53:ASN:CG	1:O:149:SER:HB2	2.15	0.72
1:O:76:LYS:NZ	1:R:15:ILE:HG21	2.05	0.72
1:A:41:GLU:HB2	1:M:10:ILE:CD1	2.20	0.71
1:B:6:LEU:CD1	1:C:15:ILE:C	2.63	0.71
1:C:5:GLU:CB	1:D:12:ILE:HD12	2.18	0.71
1:C:15:ILE:CD1	1:F:35:GLU:HG3	2.19	0.71
1:D:6:LEU:HD13	1:E:15:ILE:C	2.15	0.71
1:E:5:GLU:CB	1:F:12:ILE:HD12	2.18	0.71
1:E:6:LEU:HD13	1:F:15:ILE:C	2.15	0.71
1:E:15:ILE:HG21	1:H:76:LYS:NZ	2.05	0.71
1:L:41:GLU:HB2	1:P:10:ILE:CD1	2.20	0.71
1:M:15:ILE:C	1:N:6:LEU:HD13	2.15	0.71
1:N:76:LYS:NZ	1:Q:15:ILE:HG21	2.05	0.71
1:R:32:GLN:NE2	1:R:97:VAL:HA	2.04	0.71
1:B:5:GLU:H	1:C:12:ILE:HD13	1.48	0.71
1:E:15:ILE:CD1	1:H:35:GLU:HG3	2.19	0.71
1:E:149:SER:HB2	1:H:53:ASN:CG	2.15	0.71
1:F:1:MEA:HD2	1:G:8:ILE:CD1	2.16	0.71
1:M:15:ILE:C	1:N:6:LEU:CD1	2.63	0.71
1:M:107:SER:OG	1:M:124:PRO:HA	1.90	0.71
1:O:53:ASN:CG	1:R:149:SER:HB2	2.15	0.71
1:A:53:ASN:CG	1:L:149:SER:HB2	2.15	0.71
1:C:116:SER:CB	1:K:21:LEU:HD12	1.95	0.71
1:G:1:MEA:CG	1:H:8:ILE:CD1	2.65	0.71
1:J:107:SER:OG	1:J:124:PRO:HA	1.89	0.71
1:K:12:ILE:HD12	1:L:5:GLU:CB	2.18	0.71
1:K:53:ASN:CG	1:N:149:SER:HB2	2.15	0.71
1:Q:15:ILE:C	1:R:6:LEU:HD13	2.15	0.71
1:A:15:ILE:HG21	1:D:76:LYS:NZ	2.05	0.71
1:B:76:LYS:NZ	1:K:15:ILE:HG21	2.05	0.71
1:C:116:SER:HB2	1:K:21:LEU:HB3	1.70	0.71
1:E:5:GLU:HG2	1:F:13:VAL:HG22	1.73	0.71
1:G:112:ARG:CZ	1:G:114:ASN:HA	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:112:ARG:CZ	1:J:114:ASN:HA	2.21	0.71
1:K:15:ILE:C	1:L:6:LEU:HD13	2.15	0.71
1:O:13:VAL:HG22	1:P:5:GLU:HG2	1.72	0.71
1:P:112:ARG:CZ	1:P:114:ASN:HA	2.21	0.71
1:Q:12:ILE:HD12	1:R:5:GLU:CB	2.18	0.71
1:Q:15:ILE:C	1:R:6:LEU:CD1	2.63	0.71
1:Q:112:ARG:CZ	1:Q:114:ASN:HA	2.21	0.71
1:D:10:ILE:CD1	1:H:41:GLU:HB2	2.21	0.71
1:D:41:GLU:HB2	1:J:10:ILE:CD1	2.20	0.71
1:K:107:SER:OG	1:K:124:PRO:HA	1.89	0.71
1:L:35:GLU:HG3	1:O:15:ILE:CD1	2.19	0.71
1:M:12:ILE:HD12	1:N:5:GLU:CB	2.18	0.71
1:Q:107:SER:OG	1:Q:124:PRO:HA	1.90	0.71
1:C:6:LEU:HD13	1:D:15:ILE:C	2.15	0.71
1:D:107:SER:OG	1:D:124:PRO:HA	1.90	0.71
1:E:6:LEU:CD1	1:F:15:ILE:C	2.63	0.71
1:K:13:VAL:HG22	1:L:5:GLU:HG2	1.73	0.71
1:A:1:MEA:HD2	1:B:8:ILE:CD1	2.16	0.71
1:B:112:ARG:CZ	1:B:114:ASN:HA	2.21	0.71
1:D:41:GLU:CB	1:J:10:ILE:HG13	2.21	0.71
1:D:98:ASN:HD22	1:D:100:GLU:H	1.39	0.71
1:E:112:ARG:CZ	1:E:114:ASN:HA	2.21	0.71
1:J:12:ILE:HD12	1:K:5:GLU:CB	2.18	0.71
1:L:15:ILE:C	1:M:6:LEU:CD1	2.63	0.71
1:L:15:ILE:C	1:M:6:LEU:HD13	2.15	0.71
1:M:98:ASN:HD22	1:M:100:GLU:H	1.39	0.71
1:M:137:LYS:HD3	1:M:137:LYS:N	2.06	0.71
1:O:12:ILE:HD12	1:P:5:GLU:CB	2.18	0.71
1:A:15:ILE:C	1:J:6:LEU:CD1	2.63	0.71
1:A:41:GLU:CB	1:M:10:ILE:HG13	2.21	0.71
1:A:112:ARG:CZ	1:A:114:ASN:HA	2.21	0.71
1:B:149:SER:HB2	1:E:53:ASN:CG	2.15	0.71
1:C:76:LYS:NZ	1:J:15:ILE:HG21	2.05	0.71
1:F:6:LEU:CD1	1:G:15:ILE:C	2.63	0.71
1:H:98:ASN:HD22	1:H:100:GLU:H	1.39	0.71
1:R:112:ARG:CZ	1:R:114:ASN:HA	2.21	0.71
1:A:6:LEU:CD1	1:B:15:ILE:C	2.63	0.71
1:A:98:ASN:HD22	1:A:100:GLU:H	1.39	0.71
1:A:137:LYS:N	1:A:137:LYS:HD3	2.06	0.71
1:B:21:LEU:HB3	1:F:116:SER:HB2	1.70	0.71
1:B:41:GLU:HB2	1:L:10:ILE:CD1	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:112:ARG:CZ	1:D:114:ASN:HA	2.21	0.71
1:E:137:LYS:HD3	1:E:137:LYS:N	2.06	0.71
1:K:32:GLN:NE2	1:K:97:VAL:HA	2.04	0.71
1:N:116:SER:CB	1:R:21:LEU:HD12	1.95	0.71
1:Q:98:ASN:HD22	1:Q:100:GLU:H	1.39	0.71
1:C:116:SER:CB	1:K:21:LEU:HD13	1.92	0.71
1:D:52:LEU:CD2	1:J:25:GLN:NE2	2.48	0.71
1:F:5:GLU:CB	1:G:12:ILE:HD12	2.18	0.71
1:F:15:ILE:HG21	1:I:76:LYS:NZ	2.05	0.71
1:F:107:SER:OG	1:F:124:PRO:HA	1.90	0.71
1:F:149:SER:HB2	1:I:53:ASN:CG	2.15	0.71
1:H:112:ARG:CZ	1:H:114:ASN:HA	2.21	0.71
1:L:112:ARG:CZ	1:L:114:ASN:HA	2.21	0.71
1:P:137:LYS:HD3	1:P:137:LYS:N	2.06	0.71
1:A:10:ILE:CD1	1:E:41:GLU:HB2	2.20	0.70
1:A:10:ILE:HG13	1:E:41:GLU:CB	2.21	0.70
1:C:6:LEU:CD1	1:D:15:ILE:C	2.63	0.70
1:J:98:ASN:HD22	1:J:100:GLU:H	1.39	0.70
1:M:41:GLU:HB2	1:Q:10:ILE:CD1	2.20	0.70
1:M:41:GLU:CB	1:Q:10:ILE:HG13	2.21	0.70
1:P:15:ILE:C	1:Q:6:LEU:CD1	2.63	0.70
1:P:98:ASN:HD22	1:P:100:GLU:H	1.39	0.70
1:Q:137:LYS:N	1:Q:137:LYS:HD3	2.06	0.70
1:A:5:GLU:HG2	1:B:13:VAL:HG22	1.73	0.70
1:G:6:LEU:CD1	1:H:15:ILE:C	2.63	0.70
1:G:98:ASN:HD22	1:G:100:GLU:H	1.39	0.70
1:L:137:LYS:HD3	1:L:137:LYS:N	2.06	0.70
1:M:76:LYS:NZ	1:P:15:ILE:HG21	2.05	0.70
1:N:15:ILE:C	1:O:6:LEU:CD1	2.63	0.70
1:N:112:ARG:CZ	1:N:114:ASN:HA	2.21	0.70
1:A:21:LEU:HD12	1:E:116:SER:CB	1.95	0.70
1:B:25:GLN:HE22	1:F:52:LEU:CG	2.04	0.70
1:D:5:GLU:HG2	1:E:13:VAL:HG22	1.73	0.70
1:E:15:ILE:CD1	1:H:35:GLU:OE1	2.13	0.70
1:I:137:LYS:N	1:I:137:LYS:HD3	2.06	0.70
1:L:13:VAL:HG22	1:M:5:GLU:HG2	1.73	0.70
1:N:116:SER:CA	1:R:25:GLN:NE2	2.48	0.70
1:D:10:ILE:HG13	1:H:41:GLU:CB	2.21	0.70
1:D:14:GLY:HA2	1:H:44:LYS:HZ3	1.48	0.70
1:J:41:GLU:CB	1:N:10:ILE:HG13	2.21	0.70
1:K:52:LEU:CG	1:O:25:GLN:HE22	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:ILE:HG13	1:F:41:GLU:CB	2.21	0.70
1:B:52:LEU:CG	1:L:25:GLN:HE22	2.05	0.70
1:E:25:GLN:HE22	1:I:52:LEU:CG	2.04	0.70
1:E:98:ASN:HD22	1:E:100:GLU:H	1.39	0.70
1:F:112:ARG:CZ	1:F:114:ASN:HA	2.21	0.70
1:K:112:ARG:CZ	1:K:114:ASN:HA	2.21	0.70
1:M:112:ARG:CZ	1:M:114:ASN:HA	2.21	0.70
1:N:13:VAL:HG22	1:O:5:GLU:HG2	1.73	0.70
1:P:13:VAL:HG22	1:Q:5:GLU:HG2	1.73	0.70
1:E:10:ILE:CD1	1:I:41:GLU:HB2	2.21	0.70
1:F:5:GLU:HG2	1:G:13:VAL:HG22	1.73	0.70
1:G:137:LYS:HD3	1:G:137:LYS:N	2.06	0.70
1:L:41:GLU:CB	1:P:10:ILE:HG13	2.21	0.70
1:B:5:GLU:CB	1:C:12:ILE:HD12	2.18	0.70
1:C:52:LEU:CD2	1:K:25:GLN:NE2	2.48	0.70
1:J:13:VAL:HG22	1:K:5:GLU:HG2	1.73	0.70
1:J:15:ILE:C	1:K:6:LEU:CD1	2.63	0.70
1:A:25:GLN:OE1	1:E:52:LEU:CG	2.36	0.70
1:B:38:LEU:C	1:K:19:VAL:HG11	2.17	0.70
1:O:38:LEU:C	1:R:19:VAL:HG11	2.17	0.70
1:O:112:ARG:CZ	1:O:114:ASN:HA	2.21	0.70
1:A:38:LEU:C	1:L:19:VAL:HG11	2.17	0.70
1:E:19:VAL:HG11	1:H:38:LEU:C	2.17	0.70
1:F:19:VAL:HG11	1:I:38:LEU:C	2.17	0.70
1:J:38:LEU:C	1:M:19:VAL:HG11	2.17	0.70
1:J:41:GLU:HB2	1:N:10:ILE:CD1	2.20	0.70
1:K:41:GLU:HB2	1:O:10:ILE:CD1	2.20	0.70
1:L:52:LEU:CG	1:P:25:GLN:HE22	2.04	0.70
1:A:13:VAL:HG22	1:J:5:GLU:HG2	1.73	0.70
1:A:14:GLY:CA	1:E:44:LYS:HZ1	2.04	0.70
1:B:10:ILE:CD1	1:F:41:GLU:HB2	2.21	0.70
1:C:10:ILE:CD1	1:G:41:GLU:HB2	2.21	0.70
1:C:52:LEU:CG	1:K:25:GLN:HE22	2.05	0.70
1:D:19:VAL:HG11	1:G:38:LEU:C	2.17	0.70
1:L:98:ASN:HD22	1:L:100:GLU:H	1.39	0.70
1:N:98:ASN:HD22	1:N:100:GLU:H	1.39	0.70
1:B:5:GLU:H	1:C:12:ILE:HD11	1.45	0.69
1:B:5:GLU:HG2	1:C:13:VAL:HG22	1.73	0.69
1:B:137:LYS:HD3	1:B:137:LYS:N	2.06	0.69
1:C:10:ILE:HG13	1:G:41:GLU:CB	2.21	0.69
1:C:41:GLU:HB2	1:K:10:ILE:CD1	2.20	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:GLU:CB	1:K:10:ILE:HG13	2.21	0.69
1:C:112:ARG:CZ	1:C:114:ASN:HA	2.21	0.69
1:C:137:LYS:HD3	1:C:137:LYS:N	2.06	0.69
1:K:106:LEU:HD12	1:K:142:ILE:HD12	1.74	0.69
1:A:25:GLN:HE22	1:E:52:LEU:CG	2.04	0.69
1:B:41:GLU:CB	1:L:10:ILE:HG13	2.21	0.69
1:C:98:ASN:HD22	1:C:100:GLU:H	1.39	0.69
1:E:10:ILE:HG13	1:I:41:GLU:CB	2.21	0.69
1:J:8:ILE:CD1	1:K:1:MEA:HD2	2.16	0.69
1:K:41:GLU:CB	1:O:10:ILE:HG13	2.21	0.69
1:N:41:GLU:HB2	1:R:10:ILE:CD1	2.20	0.69
1:N:41:GLU:CB	1:R:10:ILE:HG13	2.21	0.69
1:N:52:LEU:CG	1:R:25:GLN:HE22	2.05	0.69
1:Q:13:VAL:HG22	1:R:5:GLU:HG2	1.73	0.69
1:R:106:LEU:HD12	1:R:142:ILE:HD12	1.74	0.69
1:R:137:LYS:HD3	1:R:137:LYS:N	2.06	0.69
1:C:25:GLN:OE1	1:G:52:LEU:CG	2.36	0.69
1:E:1:MEA:HD2	1:F:8:ILE:CD1	2.16	0.69
1:L:52:LEU:CG	1:P:25:GLN:OE1	2.36	0.69
1:N:38:LEU:C	1:Q:19:VAL:HG11	2.17	0.69
1:C:21:LEU:HD12	1:G:116:SER:CB	1.95	0.69
1:C:106:LEU:HD12	1:C:142:ILE:HD12	1.74	0.69
1:D:137:LYS:HD3	1:D:137:LYS:N	2.06	0.69
1:H:5:GLU:HG2	1:I:13:VAL:HG22	1.73	0.69
1:H:137:LYS:HD3	1:H:137:LYS:N	2.06	0.69
1:I:112:ARG:CZ	1:I:114:ASN:HA	2.21	0.69
1:O:106:LEU:HD12	1:O:142:ILE:HD12	1.74	0.69
1:B:35:GLU:OE1	1:K:15:ILE:CD1	2.13	0.69
1:C:5:GLU:H	1:D:12:ILE:HD11	1.45	0.69
1:C:19:VAL:HG11	1:F:38:LEU:C	2.17	0.69
1:F:106:LEU:HD12	1:F:142:ILE:HD12	1.74	0.69
1:I:98:ASN:HD22	1:I:100:GLU:H	1.39	0.69
1:N:12:ILE:HD12	1:O:5:GLU:CB	2.18	0.69
1:N:106:LEU:HD12	1:N:142:ILE:HD12	1.74	0.69
1:C:25:GLN:HE22	1:G:52:LEU:CG	2.04	0.69
1:C:38:LEU:C	1:J:19:VAL:HG11	2.17	0.69
1:K:137:LYS:HD3	1:K:137:LYS:N	2.06	0.69
1:M:38:LEU:C	1:P:19:VAL:HG11	2.17	0.69
1:O:8:ILE:CD1	1:P:1:MEA:HD2	2.16	0.69
1:O:137:LYS:HD3	1:O:137:LYS:N	2.06	0.69
1:C:5:GLU:HG2	1:D:13:VAL:HG22	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:16:LEU:HB2	1:K:6:LEU:HD12	1.74	0.69
1:O:76:LYS:HE3	1:R:15:ILE:HG22	1.74	0.69
1:B:98:ASN:HD22	1:B:100:GLU:H	1.39	0.69
1:B:106:LEU:HD12	1:B:142:ILE:HD12	1.74	0.69
1:F:137:LYS:HD3	1:F:137:LYS:N	2.06	0.69
1:G:5:GLU:HG2	1:H:13:VAL:HG22	1.73	0.69
1:K:16:LEU:HB2	1:L:6:LEU:HD12	1.75	0.69
1:L:38:LEU:C	1:O:19:VAL:HG11	2.17	0.69
1:M:13:VAL:HG22	1:N:5:GLU:HG2	1.72	0.69
1:B:76:LYS:HE3	1:K:15:ILE:HG22	1.74	0.69
1:C:92:MET:HG2	1:C:104:LYS:O	1.93	0.69
1:F:6:LEU:HD12	1:G:16:LEU:HB2	1.75	0.69
1:H:106:LEU:HD12	1:H:142:ILE:HD12	1.74	0.69
1:K:38:LEU:C	1:N:19:VAL:HG11	2.17	0.69
1:N:12:ILE:HD11	1:O:5:GLU:H	1.45	0.69
1:N:137:LYS:HD3	1:N:137:LYS:N	2.06	0.69
1:Q:16:LEU:HB2	1:R:6:LEU:HD12	1.74	0.69
1:R:98:ASN:HD22	1:R:100:GLU:H	1.39	0.69
1:B:116:SER:HB2	1:L:21:LEU:HD13	1.63	0.69
1:E:6:LEU:HD12	1:F:16:LEU:HB2	1.75	0.69
1:F:92:MET:HG2	1:F:104:LYS:O	1.93	0.69
1:F:98:ASN:HD22	1:F:100:GLU:H	1.39	0.69
1:J:52:LEU:CG	1:N:25:GLN:HE22	2.05	0.69
1:J:116:SER:CB	1:N:21:LEU:HD12	1.95	0.69
1:J:137:LYS:HD3	1:J:137:LYS:N	2.06	0.69
1:K:98:ASN:HD22	1:K:100:GLU:H	1.39	0.69
1:A:19:VAL:HG11	1:D:38:LEU:C	2.17	0.68
1:A:116:SER:CB	1:M:21:LEU:HD12	1.95	0.68
1:B:19:VAL:HG11	1:E:38:LEU:C	2.17	0.68
1:E:25:GLN:OE1	1:I:52:LEU:CG	2.36	0.68
1:G:106:LEU:HD12	1:G:142:ILE:HD12	1.74	0.68
1:I:106:LEU:HD12	1:I:142:ILE:HD12	1.74	0.68
1:K:52:LEU:CG	1:O:25:GLN:OE1	2.36	0.68
1:K:92:MET:HG2	1:K:104:LYS:O	1.93	0.68
1:M:106:LEU:HD12	1:M:142:ILE:HD12	1.74	0.68
1:O:98:ASN:HD22	1:O:100:GLU:H	1.39	0.68
1:P:106:LEU:HD12	1:P:142:ILE:HD12	1.74	0.68
1:F:15:ILE:HG22	1:I:76:LYS:HE3	1.74	0.68
1:J:38:LEU:O	1:N:10:ILE:HD11	1.94	0.68
1:J:106:LEU:HD12	1:J:142:ILE:HD12	1.74	0.68
1:O:92:MET:HG2	1:O:104:LYS:O	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LEU:CG	1:M:25:GLN:HE22	2.04	0.68
1:G:92:MET:HG2	1:G:104:LYS:O	1.93	0.68
1:C:5:GLU:H	1:D:12:ILE:HD13	1.48	0.68
1:C:10:ILE:HD11	1:G:38:LEU:O	1.94	0.68
1:C:15:ILE:HG22	1:F:76:LYS:HE3	1.74	0.68
1:C:76:LYS:HE3	1:J:15:ILE:HG22	1.74	0.68
1:E:5:GLU:H	1:F:12:ILE:HD13	1.48	0.68
1:I:92:MET:HG2	1:I:104:LYS:O	1.93	0.68
1:J:52:LEU:CG	1:N:25:GLN:OE1	2.36	0.68
1:B:52:LEU:CD2	1:L:25:GLN:NE2	2.48	0.68
1:D:52:LEU:CG	1:J:25:GLN:HE22	2.04	0.68
1:E:15:ILE:HG22	1:H:76:LYS:HE3	1.74	0.68
1:M:52:LEU:CG	1:Q:25:GLN:HE22	2.04	0.68
1:N:92:MET:HG2	1:N:104:LYS:O	1.94	0.68
1:R:92:MET:HG2	1:R:104:LYS:O	1.94	0.68
1:A:76:LYS:HE3	1:L:15:ILE:HG22	1.74	0.68
1:B:10:ILE:HD13	1:F:38:LEU:HD13	0.68	0.68
1:B:52:LEU:CG	1:L:25:GLN:OE1	2.36	0.68
1:D:116:SER:CB	1:J:21:LEU:HD13	1.92	0.68
1:E:106:LEU:HD12	1:E:142:ILE:HD12	1.74	0.68
1:J:76:LYS:HE3	1:M:15:ILE:HG22	1.75	0.68
1:A:15:ILE:HG22	1:D:76:LYS:HE3	1.74	0.68
1:B:10:ILE:HD11	1:F:38:LEU:O	1.94	0.68
1:B:38:LEU:HD13	1:L:10:ILE:HD13	0.68	0.68
1:B:38:LEU:O	1:L:10:ILE:HD11	1.94	0.68
1:C:38:LEU:HD13	1:K:10:ILE:HD13	0.68	0.68
1:D:25:GLN:HE22	1:H:52:LEU:CG	2.04	0.68
1:E:10:ILE:HD11	1:I:38:LEU:O	1.94	0.68
1:J:92:MET:HG2	1:J:104:LYS:O	1.93	0.68
1:K:38:LEU:HD13	1:O:10:ILE:HD13	0.68	0.68
1:N:76:LYS:HE3	1:Q:15:ILE:HG22	1.74	0.68
1:B:1:MEA:HD2	1:C:8:ILE:CD1	2.16	0.68
1:D:15:ILE:HG22	1:G:76:LYS:HE3	1.74	0.68
1:D:38:LEU:O	1:J:10:ILE:HD11	1.94	0.68
1:E:10:ILE:HD13	1:I:38:LEU:HD13	0.68	0.68
1:L:106:LEU:HD12	1:L:142:ILE:HD12	1.74	0.68
1:A:35:GLU:CG	1:L:15:ILE:HD12	2.24	0.68
1:A:116:SER:HB2	1:M:21:LEU:HD13	1.63	0.68
1:K:35:GLU:CG	1:N:15:ILE:HD12	2.24	0.68
1:K:38:LEU:O	1:O:10:ILE:HD11	1.94	0.68
1:Q:12:ILE:HD13	1:R:5:GLU:H	1.48	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:106:LEU:HD12	1:Q:142:ILE:HD12	1.74	0.68
1:A:10:ILE:HD13	1:E:38:LEU:HD13	0.68	0.68
1:A:10:ILE:HD11	1:E:38:LEU:O	1.94	0.68
1:B:25:GLN:OE1	1:F:52:LEU:CG	2.36	0.68
1:C:10:ILE:HD13	1:G:38:LEU:HD13	0.68	0.68
1:C:15:ILE:HD12	1:F:35:GLU:CG	2.24	0.68
1:D:21:LEU:HD12	1:H:116:SER:CB	1.95	0.68
1:E:92:MET:HG2	1:E:104:LYS:O	1.93	0.68
1:F:5:GLU:H	1:G:12:ILE:HD11	1.45	0.68
1:A:15:ILE:HD12	1:D:35:GLU:CG	2.24	0.67
1:A:38:LEU:HD13	1:M:10:ILE:HD13	0.68	0.67
1:B:6:LEU:HD12	1:C:16:LEU:HB2	1.75	0.67
1:B:15:ILE:HG22	1:E:76:LYS:HE3	1.74	0.67
1:D:92:MET:HG2	1:D:104:LYS:O	1.93	0.67
1:L:38:LEU:O	1:P:10:ILE:HD11	1.94	0.67
1:N:13:VAL:CG2	1:O:5:GLU:HG2	2.25	0.67
1:N:16:LEU:HB2	1:O:6:LEU:HD12	1.75	0.67
1:N:38:LEU:HD13	1:R:10:ILE:HD13	0.68	0.67
1:O:13:VAL:CG2	1:P:5:GLU:HG2	2.24	0.67
1:Q:8:ILE:CD1	1:R:1:MEA:HD2	2.16	0.67
1:A:12:ILE:HD13	1:J:5:GLU:H	1.48	0.67
1:A:38:LEU:O	1:M:10:ILE:HD11	1.94	0.67
1:D:10:ILE:HD13	1:H:38:LEU:HD13	0.68	0.67
1:D:25:GLN:OE1	1:H:52:LEU:CG	2.36	0.67
1:D:38:LEU:HD13	1:J:10:ILE:HD13	0.68	0.67
1:D:52:LEU:CG	1:J:25:GLN:OE1	2.36	0.67
1:J:35:GLU:CG	1:M:15:ILE:HD12	2.24	0.67
1:J:38:LEU:HD13	1:N:10:ILE:HD13	0.68	0.67
1:K:8:ILE:CD1	1:L:1:MEA:HD2	2.16	0.67
1:L:38:LEU:HD13	1:P:10:ILE:HD13	0.68	0.67
1:M:52:LEU:CG	1:Q:25:GLN:OE1	2.36	0.67
1:B:5:GLU:HG2	1:C:13:VAL:CG2	2.25	0.67
1:D:5:GLU:HG2	1:E:13:VAL:CG2	2.25	0.67
1:H:5:GLU:HG2	1:I:13:VAL:CG2	2.25	0.67
1:K:13:VAL:CG2	1:L:5:GLU:HG2	2.25	0.67
1:L:92:MET:HG2	1:L:104:LYS:O	1.93	0.67
1:A:52:LEU:CG	1:M:25:GLN:OE1	2.36	0.67
1:B:15:ILE:HD12	1:E:35:GLU:CG	2.24	0.67
1:C:25:GLN:NE2	1:G:52:LEU:CD2	2.48	0.67
1:D:106:LEU:HD12	1:D:142:ILE:HD12	1.74	0.67
1:H:92:MET:HG2	1:H:104:LYS:O	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:13:VAL:CG2	1:M:5:GLU:HG2	2.24	0.67
1:M:35:GLU:CG	1:P:15:ILE:HD12	2.25	0.67
1:B:92:MET:HG2	1:B:104:LYS:O	1.93	0.67
1:E:5:GLU:HG2	1:F:13:VAL:CG2	2.25	0.67
1:M:13:VAL:CG2	1:N:5:GLU:HG2	2.24	0.67
1:M:38:LEU:HD13	1:Q:10:ILE:HD13	0.68	0.67
1:O:16:LEU:HB2	1:P:6:LEU:HD12	1.74	0.67
1:O:35:GLU:CG	1:R:15:ILE:HD12	2.25	0.67
1:P:13:VAL:CG2	1:Q:5:GLU:HG2	2.25	0.67
1:Q:92:MET:HG2	1:Q:104:LYS:O	1.94	0.67
1:C:6:LEU:HD12	1:D:16:LEU:HB2	1.75	0.67
1:C:35:GLU:HG3	1:J:15:ILE:HD12	1.76	0.67
1:C:117:VAL:C	1:K:21:LEU:HG	2.19	0.67
1:D:10:ILE:HD11	1:H:38:LEU:O	1.94	0.67
1:D:15:ILE:HD12	1:G:35:GLU:CG	2.24	0.67
1:F:137:LYS:HD3	1:F:137:LYS:H	1.59	0.67
1:K:76:LYS:HE3	1:N:15:ILE:HG22	1.74	0.67
1:L:35:GLU:CG	1:O:15:ILE:HD12	2.24	0.67
1:L:41:GLU:HB2	1:P:10:ILE:HD11	1.77	0.67
1:M:38:LEU:O	1:Q:10:ILE:HD11	1.94	0.67
1:A:5:GLU:HG2	1:B:13:VAL:CG2	2.25	0.67
1:A:10:ILE:HD11	1:E:41:GLU:HB2	1.77	0.67
1:C:5:GLU:HG2	1:D:13:VAL:CG2	2.25	0.67
1:C:35:GLU:CG	1:J:15:ILE:HD12	2.24	0.67
1:C:38:LEU:O	1:K:10:ILE:HD11	1.94	0.67
1:J:116:SER:HB2	1:N:21:LEU:HD13	1.63	0.67
1:K:35:GLU:HG3	1:N:15:ILE:HD12	1.76	0.67
1:K:137:LYS:HD3	1:K:137:LYS:H	1.59	0.67
1:M:92:MET:HG2	1:M:104:LYS:O	1.94	0.67
1:N:38:LEU:O	1:R:10:ILE:HD11	1.94	0.67
1:O:137:LYS:HD3	1:O:137:LYS:H	1.59	0.67
1:A:41:GLU:HB2	1:M:10:ILE:HD11	1.77	0.67
1:C:15:ILE:HD12	1:F:35:GLU:HG3	1.76	0.67
1:E:15:ILE:HD12	1:H:35:GLU:HG3	1.76	0.67
1:E:21:LEU:HD13	1:I:116:SER:CB	1.92	0.67
1:L:76:LYS:HE3	1:O:15:ILE:HG22	1.74	0.67
1:O:12:ILE:HD13	1:P:5:GLU:H	1.48	0.67
1:A:35:GLU:CD	1:L:15:ILE:HD11	2.20	0.67
1:A:106:LEU:HD12	1:A:142:ILE:HD12	1.74	0.67
1:B:35:GLU:CG	1:K:15:ILE:HD12	2.24	0.67
1:E:15:ILE:HD12	1:H:35:GLU:CG	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:35:GLU:HG3	1:P:15:ILE:HD12	1.76	0.67
1:A:15:ILE:HD12	1:D:35:GLU:HG3	1.76	0.67
1:A:35:GLU:HG3	1:L:15:ILE:HD12	1.76	0.67
1:B:41:GLU:HB2	1:L:10:ILE:HD11	1.77	0.67
1:F:5:GLU:HG2	1:G:13:VAL:CG2	2.25	0.67
1:P:92:MET:HG2	1:P:104:LYS:O	1.94	0.67
1:R:137:LYS:HD3	1:R:137:LYS:H	1.59	0.67
1:F:5:GLU:H	1:G:12:ILE:HD13	1.48	0.66
1:N:35:GLU:HG3	1:Q:15:ILE:HD12	1.76	0.66
1:N:117:VAL:O	1:R:21:LEU:CG	2.33	0.66
1:A:13:VAL:CG2	1:J:5:GLU:HG2	2.25	0.66
1:A:25:GLN:NE2	1:E:52:LEU:CD2	2.48	0.66
1:A:92:MET:HG2	1:A:104:LYS:O	1.93	0.66
1:M:41:GLU:HB2	1:Q:10:ILE:HD11	1.77	0.66
1:P:16:LEU:HB2	1:Q:6:LEU:HD12	1.74	0.66
1:E:10:ILE:HD11	1:I:41:GLU:HB2	1.77	0.66
1:H:5:GLU:H	1:I:12:ILE:HD13	1.48	0.66
1:Q:13:VAL:CG2	1:R:5:GLU:HG2	2.25	0.66
1:C:137:LYS:HD3	1:C:137:LYS:H	1.59	0.66
1:D:6:LEU:HD12	1:E:16:LEU:HB2	1.75	0.66
1:D:32:GLN:HE22	1:D:97:VAL:HA	1.61	0.66
1:F:15:ILE:HD12	1:I:35:GLU:CG	2.24	0.66
1:H:32:GLN:HE22	1:H:97:VAL:HA	1.61	0.66
1:J:91:THR:HA	1:J:105:LYS:HB3	1.78	0.66
1:L:12:ILE:HD13	1:M:5:GLU:H	1.48	0.66
1:L:16:LEU:HB2	1:M:6:LEU:HD12	1.74	0.66
1:M:116:SER:CB	1:Q:21:LEU:HD12	1.95	0.66
1:N:12:ILE:HD13	1:O:5:GLU:H	1.48	0.66
1:N:35:GLU:CG	1:Q:15:ILE:HD12	2.25	0.66
1:O:35:GLU:HG3	1:R:15:ILE:HD12	1.76	0.66
1:R:91:THR:HA	1:R:105:LYS:HB3	1.78	0.66
1:A:16:LEU:HB2	1:J:6:LEU:HD12	1.75	0.66
1:A:32:GLN:HE22	1:A:97:VAL:HA	1.61	0.66
1:D:15:ILE:HD12	1:G:35:GLU:HG3	1.76	0.66
1:J:116:SER:HB2	1:N:21:LEU:CA	2.26	0.66
1:K:79:LYS:HB2	1:K:93:LEU:HA	1.78	0.66
1:M:76:LYS:HE3	1:P:15:ILE:HG22	1.74	0.66
1:A:21:LEU:CA	1:E:116:SER:HB2	2.26	0.66
1:A:44:LYS:HZ3	1:M:14:GLY:HA2	1.54	0.66
1:B:21:LEU:CA	1:F:116:SER:HB2	2.26	0.66
1:B:35:GLU:HG3	1:K:15:ILE:HD12	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:21:LEU:CA	1:G:116:SER:HB2	2.26	0.66
1:D:10:ILE:HD11	1:H:41:GLU:HB2	1.77	0.66
1:D:91:THR:HA	1:D:105:LYS:HB3	1.78	0.66
1:H:137:LYS:HD3	1:H:137:LYS:H	1.60	0.66
1:K:116:SER:HB2	1:O:21:LEU:CA	2.26	0.66
1:L:116:SER:HB2	1:P:21:LEU:CA	2.26	0.66
1:N:91:THR:HA	1:N:105:LYS:HB3	1.78	0.66
1:N:137:LYS:HD3	1:N:137:LYS:H	1.59	0.66
1:O:79:LYS:HB2	1:O:93:LEU:HA	1.78	0.66
1:Q:91:THR:HA	1:Q:105:LYS:HB3	1.78	0.66
1:B:79:LYS:HB2	1:B:93:LEU:HA	1.78	0.66
1:D:25:GLN:NE2	1:H:52:LEU:CD2	2.48	0.66
1:J:13:VAL:CG2	1:K:5:GLU:HG2	2.25	0.66
1:K:91:THR:HA	1:K:105:LYS:HB3	1.78	0.66
1:K:116:SER:CB	1:O:21:LEU:HD13	1.92	0.66
1:L:79:LYS:HB2	1:L:93:LEU:HA	1.78	0.66
1:M:16:LEU:HB2	1:N:6:LEU:HD12	1.75	0.66
1:M:32:GLN:HE22	1:M:97:VAL:HA	1.61	0.66
1:M:91:THR:HA	1:M:105:LYS:HB3	1.78	0.66
1:M:137:LYS:HD3	1:M:137:LYS:H	1.59	0.66
1:N:35:GLU:CD	1:Q:15:ILE:HD11	2.20	0.66
1:P:16:LEU:HD21	1:Q:9:VAL:CG1	2.26	0.66
1:B:91:THR:HA	1:B:105:LYS:HB3	1.78	0.66
1:D:41:GLU:HB2	1:J:10:ILE:HD11	1.77	0.66
1:F:91:THR:HA	1:F:105:LYS:HB3	1.78	0.66
1:G:5:GLU:HG2	1:H:13:VAL:CG2	2.25	0.66
1:G:137:LYS:HD3	1:G:137:LYS:H	1.59	0.66
1:I:91:THR:HA	1:I:105:LYS:HB3	1.78	0.66
1:N:79:LYS:HB2	1:N:93:LEU:HA	1.78	0.66
1:O:16:LEU:HD13	1:P:6:LEU:HA	0.78	0.66
1:O:91:THR:HA	1:O:105:LYS:HB3	1.78	0.66
1:Q:16:LEU:HD21	1:R:9:VAL:CG1	2.26	0.66
1:Q:32:GLN:HE22	1:Q:97:VAL:HA	1.61	0.66
1:A:6:LEU:HD12	1:B:16:LEU:HB2	1.75	0.66
1:A:137:LYS:HD3	1:A:137:LYS:H	1.59	0.66
1:C:91:THR:HA	1:C:105:LYS:HB3	1.78	0.66
1:E:9:VAL:CG1	1:F:16:LEU:HD21	2.26	0.66
1:E:21:LEU:CG	1:I:117:VAL:O	2.33	0.66
1:F:15:ILE:HD12	1:I:35:GLU:HG3	1.76	0.66
1:J:32:GLN:HE22	1:J:97:VAL:HA	1.61	0.66
1:J:35:GLU:HG3	1:M:15:ILE:HD12	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:16:LEU:HD21	1:M:9:VAL:CG1	2.26	0.66
1:N:8:ILE:CD1	1:O:1:MEA:HD2	2.16	0.66
1:N:41:GLU:HB2	1:R:10:ILE:HD11	1.77	0.66
1:P:32:GLN:HE22	1:P:97:VAL:HA	1.61	0.66
1:A:91:THR:HA	1:A:105:LYS:HB3	1.78	0.66
1:B:10:ILE:HD11	1:F:41:GLU:HB2	1.77	0.66
1:C:41:GLU:HB2	1:K:10:ILE:HD11	1.77	0.66
1:D:116:SER:HB2	1:J:21:LEU:CA	2.26	0.66
1:E:15:ILE:HD11	1:H:35:GLU:CD	2.20	0.66
1:E:32:GLN:HE22	1:E:97:VAL:HA	1.61	0.66
1:F:9:VAL:CG1	1:G:16:LEU:HD21	2.26	0.66
1:G:6:LEU:HD12	1:H:16:LEU:HB2	1.75	0.66
1:G:32:GLN:HE22	1:G:97:VAL:HA	1.61	0.66
1:G:91:THR:HA	1:G:105:LYS:HB3	1.78	0.66
1:H:91:THR:HA	1:H:105:LYS:HB3	1.78	0.66
1:I:61:ASN:HB3	1:I:66:VAL:HG23	1.78	0.66
1:N:61:ASN:HB3	1:N:66:VAL:HG23	1.78	0.66
1:P:137:LYS:HD3	1:P:137:LYS:H	1.59	0.66
1:R:61:ASN:HB3	1:R:66:VAL:HG23	1.79	0.66
1:R:79:LYS:HB2	1:R:93:LEU:HA	1.78	0.66
1:A:9:VAL:CG1	1:B:16:LEU:HD21	2.26	0.65
1:B:137:LYS:HD3	1:B:137:LYS:H	1.59	0.65
1:D:69:SER:HB3	1:D:72:ASP:OD1	1.97	0.65
1:D:116:SER:CB	1:J:21:LEU:HD12	1.95	0.65
1:E:21:LEU:HD13	1:I:116:SER:HB2	1.63	0.65
1:E:69:SER:HB3	1:E:72:ASP:OD1	1.97	0.65
1:E:91:THR:HA	1:E:105:LYS:HB3	1.78	0.65
1:G:9:VAL:CG1	1:H:16:LEU:HD21	2.26	0.65
1:J:16:LEU:HD21	1:K:9:VAL:CG1	2.26	0.65
1:M:16:LEU:HD21	1:N:9:VAL:CG1	2.26	0.65
1:M:69:SER:HB3	1:M:72:ASP:OD1	1.97	0.65
1:O:61:ASN:HB3	1:O:66:VAL:HG23	1.78	0.65
1:C:79:LYS:HB2	1:C:93:LEU:HA	1.78	0.65
1:E:61:ASN:HB3	1:E:66:VAL:HG23	1.78	0.65
1:F:61:ASN:HB3	1:F:66:VAL:HG23	1.78	0.65
1:K:61:ASN:HB3	1:K:66:VAL:HG23	1.78	0.65
1:N:16:LEU:HD21	1:O:9:VAL:CG1	2.26	0.65
1:A:116:SER:HB2	1:M:21:LEU:CA	2.26	0.65
1:B:25:GLN:NE2	1:F:52:LEU:CD2	2.48	0.65
1:E:21:LEU:CA	1:I:116:SER:HB2	2.26	0.65
1:E:79:LYS:HB2	1:E:93:LEU:HA	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:69:SER:HB3	1:F:72:ASP:OD1	1.96	0.65
1:F:79:LYS:HB2	1:F:93:LEU:HA	1.78	0.65
1:J:137:LYS:HD3	1:J:137:LYS:H	1.59	0.65
1:L:35:GLU:HG3	1:O:15:ILE:HD12	1.76	0.65
1:L:61:ASN:HB3	1:L:66:VAL:HG23	1.78	0.65
1:L:69:SER:HB3	1:L:72:ASP:OD1	1.97	0.65
1:C:15:ILE:HD11	1:F:35:GLU:CD	2.20	0.65
1:C:61:ASN:HB3	1:C:66:VAL:HG23	1.79	0.65
1:H:6:LEU:HD12	1:I:16:LEU:HB2	1.75	0.65
1:L:91:THR:HA	1:L:105:LYS:HB3	1.78	0.65
1:O:35:GLU:CD	1:R:15:ILE:HD11	2.20	0.65
1:P:91:THR:HA	1:P:105:LYS:HB3	1.78	0.65
1:A:16:LEU:HD21	1:J:9:VAL:CG1	2.26	0.65
1:B:61:ASN:HB3	1:B:66:VAL:HG23	1.78	0.65
1:C:9:VAL:CG1	1:D:16:LEU:HD21	2.26	0.65
1:C:69:SER:HB3	1:C:72:ASP:OD1	1.97	0.65
1:C:116:SER:HB2	1:K:21:LEU:CA	2.26	0.65
1:D:137:LYS:HD3	1:D:137:LYS:H	1.59	0.65
1:J:61:ASN:HB3	1:J:66:VAL:HG23	1.78	0.65
1:K:41:GLU:HB2	1:O:10:ILE:HD11	1.77	0.65
1:K:69:SER:HB3	1:K:72:ASP:OD1	1.97	0.65
1:L:32:GLN:HE22	1:L:97:VAL:HA	1.61	0.65
1:N:32:GLN:HE22	1:N:97:VAL:HA	1.61	0.65
1:N:69:SER:HB3	1:N:72:ASP:OD1	1.97	0.65
1:A:21:LEU:HG	1:E:117:VAL:C	2.19	0.65
1:B:9:VAL:CG1	1:C:16:LEU:HD21	2.26	0.65
1:B:15:ILE:HD12	1:E:35:GLU:HG3	1.76	0.65
1:B:117:VAL:C	1:L:21:LEU:HG	2.19	0.65
1:C:32:GLN:HE22	1:C:97:VAL:HA	1.61	0.65
1:L:137:LYS:HD3	1:L:137:LYS:H	1.59	0.65
1:M:116:SER:HB2	1:Q:21:LEU:CA	2.26	0.65
1:Q:69:SER:HB3	1:Q:72:ASP:OD1	1.97	0.65
1:R:69:SER:HB3	1:R:72:ASP:OD1	1.97	0.65
1:D:21:LEU:CA	1:H:116:SER:HB2	2.26	0.65
1:E:6:LEU:HA	1:F:16:LEU:HD13	0.78	0.65
1:E:137:LYS:HD3	1:E:137:LYS:H	1.59	0.65
1:G:61:ASN:HB3	1:G:66:VAL:HG23	1.79	0.65
1:H:79:LYS:HB2	1:H:93:LEU:HA	1.78	0.65
1:J:35:GLU:CD	1:M:15:ILE:HD11	2.20	0.65
1:O:16:LEU:HD21	1:P:9:VAL:CG1	2.26	0.65
1:O:69:SER:HB3	1:O:72:ASP:OD1	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:79:LYS:HB2	1:Q:93:LEU:HA	1.78	0.65
1:Q:137:LYS:HD3	1:Q:137:LYS:H	1.59	0.65
1:A:79:LYS:HB2	1:A:93:LEU:HA	1.78	0.65
1:B:116:SER:HB3	1:L:25:GLN:HB2	1.79	0.65
1:C:35:GLU:CD	1:J:15:ILE:HD11	2.20	0.65
1:E:1:MEA:O	1:F:5:GLU:OE2	2.15	0.65
1:G:69:SER:HB3	1:G:72:ASP:OD1	1.96	0.65
1:K:16:LEU:HD21	1:L:9:VAL:CG1	2.26	0.65
1:N:5:GLU:OE2	1:O:1:MEA:O	2.15	0.65
1:N:116:SER:HB2	1:R:21:LEU:CA	2.26	0.65
1:P:69:SER:HB3	1:P:72:ASP:OD1	1.97	0.65
1:Q:61:ASN:HB3	1:Q:66:VAL:HG23	1.78	0.65
1:A:61:ASN:HB3	1:A:66:VAL:HG23	1.78	0.65
1:A:117:VAL:C	1:M:21:LEU:HG	2.19	0.65
1:B:25:GLN:HB2	1:F:116:SER:HB3	1.79	0.65
1:B:116:SER:HB2	1:L:21:LEU:CA	2.26	0.65
1:C:10:ILE:HD11	1:G:41:GLU:HB2	1.77	0.65
1:D:21:LEU:HD13	1:H:116:SER:HB2	1.63	0.65
1:H:61:ASN:HB3	1:H:66:VAL:HG23	1.78	0.65
1:I:32:GLN:HE22	1:I:97:VAL:HA	1.61	0.65
1:N:52:LEU:CG	1:R:25:GLN:OE1	2.36	0.65
1:A:1:MEA:O	1:B:5:GLU:OE2	2.15	0.65
1:B:3:LEU:HD21	1:C:15:ILE:CD1	2.26	0.65
1:D:9:VAL:CG1	1:E:16:LEU:HD21	2.26	0.65
1:D:21:LEU:HG	1:H:117:VAL:C	2.19	0.65
1:D:61:ASN:HB3	1:D:66:VAL:HG23	1.78	0.65
1:E:25:GLN:HB2	1:I:116:SER:HB3	1.79	0.65
1:H:1:MEA:O	1:I:5:GLU:OE2	2.15	0.65
1:H:9:VAL:CG1	1:I:16:LEU:HD21	2.26	0.65
1:J:41:GLU:HB2	1:N:10:ILE:HD11	1.77	0.65
1:K:116:SER:HB3	1:O:25:GLN:HB2	1.79	0.65
1:M:52:LEU:CD2	1:Q:25:GLN:NE2	2.48	0.65
1:M:61:ASN:HB3	1:M:66:VAL:HG23	1.78	0.65
1:P:61:ASN:HB3	1:P:66:VAL:HG23	1.78	0.65
1:A:69:SER:HB3	1:A:72:ASP:OD1	1.97	0.64
1:D:15:ILE:HD11	1:G:35:GLU:CD	2.20	0.64
1:H:69:SER:HB3	1:H:72:ASP:OD1	1.96	0.64
1:J:5:GLU:OE2	1:K:1:MEA:O	2.15	0.64
1:B:1:MEA:O	1:C:5:GLU:OE2	2.15	0.64
1:B:32:GLN:HE22	1:B:97:VAL:HA	1.61	0.64
1:F:1:MEA:O	1:G:5:GLU:OE2	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:137:LYS:HD3	1:I:137:LYS:H	1.59	0.64
1:J:69:SER:HB3	1:J:72:ASP:OD1	1.97	0.64
1:K:5:GLU:OE2	1:L:1:MEA:O	2.15	0.64
1:O:5:GLU:OE2	1:P:1:MEA:O	2.15	0.64
1:A:35:GLU:CG	1:L:15:ILE:CD1	2.76	0.64
1:I:79:LYS:HB2	1:I:93:LEU:HA	1.78	0.64
1:I:112:ARG:HE	1:I:114:ASN:HA	1.62	0.64
1:K:35:GLU:CD	1:N:15:ILE:HD11	2.20	0.64
1:L:35:GLU:CG	1:O:15:ILE:CD1	2.76	0.64
1:N:52:LEU:CD2	1:R:25:GLN:NE2	2.48	0.64
1:Q:5:GLU:OE2	1:R:1:MEA:O	2.15	0.64
1:A:15:ILE:CD1	1:D:35:GLU:CG	2.76	0.64
1:B:15:ILE:CD1	1:E:35:GLU:CG	2.76	0.64
1:B:69:SER:HB3	1:B:72:ASP:OD1	1.97	0.64
1:F:32:GLN:HE22	1:F:97:VAL:HA	1.61	0.64
1:I:69:SER:HB3	1:I:72:ASP:OD1	1.96	0.64
1:K:32:GLN:HE22	1:K:97:VAL:HA	1.61	0.64
1:M:35:GLU:CG	1:P:15:ILE:CD1	2.76	0.64
1:R:32:GLN:HE22	1:R:97:VAL:HA	1.61	0.64
1:B:35:GLU:CG	1:K:15:ILE:CD1	2.76	0.64
1:E:15:ILE:CD1	1:H:35:GLU:CG	2.76	0.64
1:J:79:LYS:HB2	1:J:93:LEU:HA	1.78	0.64
1:L:5:GLU:OE2	1:M:1:MEA:O	2.15	0.64
1:L:116:SER:HB3	1:P:25:GLN:HB2	1.79	0.64
1:A:3:LEU:H	1:B:8:ILE:HG21	1.63	0.64
1:C:1:MEA:O	1:D:5:GLU:OE2	2.15	0.64
1:L:8:ILE:HG21	1:M:3:LEU:H	1.63	0.64
1:M:117:VAL:C	1:Q:21:LEU:HG	2.19	0.64
1:B:112:ARG:HE	1:B:114:ASN:HA	1.62	0.64
1:F:15:ILE:CD1	1:I:35:GLU:CG	2.76	0.64
1:J:35:GLU:CG	1:M:15:ILE:CD1	2.76	0.64
1:N:16:LEU:HD13	1:O:6:LEU:HA	0.78	0.64
1:O:8:ILE:HG21	1:P:3:LEU:H	1.63	0.64
1:O:32:GLN:HE22	1:O:97:VAL:HA	1.61	0.64
1:A:25:GLN:HB2	1:E:116:SER:HB3	1.79	0.64
1:D:1:MEA:O	1:E:5:GLU:OE2	2.15	0.64
1:D:3:LEU:H	1:E:8:ILE:HG21	1.63	0.64
1:D:25:GLN:HB2	1:H:116:SER:HB3	1.79	0.64
1:H:3:LEU:H	1:I:8:ILE:HG21	1.63	0.64
1:J:116:SER:HB3	1:N:25:GLN:HB2	1.79	0.64
1:O:35:GLU:CG	1:R:15:ILE:CD1	2.76	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:8:ILE:HG21	1:Q:3:LEU:H	1.63	0.64
1:D:117:VAL:C	1:J:21:LEU:HG	2.19	0.64
1:P:79:LYS:HB2	1:P:93:LEU:HA	1.78	0.64
1:A:6:LEU:HA	1:B:16:LEU:HD13	0.78	0.64
1:C:25:GLN:HB2	1:G:116:SER:HB3	1.79	0.64
1:C:52:LEU:CG	1:K:25:GLN:OE1	2.36	0.64
1:C:116:SER:HB3	1:K:25:GLN:HB2	1.79	0.64
1:D:79:LYS:HB2	1:D:93:LEU:HA	1.78	0.64
1:L:112:ARG:HE	1:L:114:ASN:HA	1.62	0.64
1:P:5:GLU:OE2	1:Q:1:MEA:O	2.15	0.64
1:A:8:ILE:HG21	1:J:3:LEU:H	1.63	0.63
1:A:112:ARG:HE	1:A:114:ASN:HA	1.62	0.63
1:C:21:LEU:HD13	1:G:116:SER:HB2	1.63	0.63
1:D:6:LEU:HA	1:E:16:LEU:HD13	0.78	0.63
1:G:1:MEA:O	1:H:5:GLU:OE2	2.15	0.63
1:M:5:GLU:OE2	1:N:1:MEA:O	2.15	0.63
1:M:116:SER:HB3	1:Q:25:GLN:HB2	1.79	0.63
1:A:16:LEU:HD13	1:J:6:LEU:HA	0.78	0.63
1:A:116:SER:HB3	1:M:25:GLN:HB2	1.79	0.63
1:B:35:GLU:CD	1:K:15:ILE:HD11	2.20	0.63
1:C:1:MEA:HD2	1:D:8:ILE:CD1	2.16	0.63
1:C:15:ILE:CG2	1:F:76:LYS:NZ	2.61	0.63
1:D:15:ILE:CD1	1:G:35:GLU:CG	2.76	0.63
1:E:3:LEU:H	1:F:8:ILE:HG21	1.63	0.63
1:K:76:LYS:NZ	1:N:15:ILE:CG2	2.61	0.63
1:K:116:SER:HB2	1:O:21:LEU:HD13	1.63	0.63
1:M:79:LYS:HB2	1:M:93:LEU:HA	1.78	0.63
1:P:112:ARG:HE	1:P:114:ASN:HA	1.62	0.63
1:C:15:ILE:CD1	1:F:35:GLU:CG	2.76	0.63
1:K:112:ARG:HE	1:K:114:ASN:HA	1.62	0.63
1:N:116:SER:HB3	1:R:25:GLN:HB2	1.79	0.63
1:A:5:GLU:OE2	1:J:1:MEA:O	2.15	0.63
1:F:15:ILE:HD11	1:I:35:GLU:CD	2.20	0.63
1:H:93:LEU:CD1	1:H:94:SER:H	2.12	0.63
1:K:8:ILE:HG21	1:L:3:LEU:H	1.63	0.63
1:K:35:GLU:CG	1:N:15:ILE:CD1	2.76	0.63
1:N:35:GLU:CG	1:Q:15:ILE:CD1	2.76	0.63
1:O:76:LYS:NZ	1:R:15:ILE:CG2	2.61	0.63
1:P:8:ILE:CD1	1:Q:1:MEA:HD2	2.16	0.63
1:C:35:GLU:CG	1:J:15:ILE:CD1	2.76	0.63
1:G:1:MEA:HD2	1:H:8:ILE:CD1	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:79:LYS:HB2	1:G:93:LEU:HA	1.78	0.63
1:I:93:LEU:CD1	1:I:94:SER:H	2.12	0.63
1:J:112:ARG:HE	1:J:114:ASN:HA	1.62	0.63
1:N:24:TYR:O	1:N:28:THR:HB	1.99	0.63
1:P:24:TYR:O	1:P:28:THR:HB	1.99	0.63
1:A:15:ILE:HD11	1:D:35:GLU:CD	2.20	0.63
1:C:76:LYS:NZ	1:J:15:ILE:CG2	2.61	0.63
1:D:24:TYR:O	1:D:28:THR:HB	1.99	0.63
1:G:3:LEU:H	1:H:8:ILE:HG21	1.63	0.63
1:H:112:ARG:HE	1:H:114:ASN:HA	1.62	0.63
1:Q:24:TYR:O	1:Q:28:THR:HB	1.99	0.63
1:C:24:TYR:O	1:C:28:THR:HB	1.99	0.63
1:D:116:SER:HB3	1:J:25:GLN:HB2	1.79	0.63
1:E:24:TYR:O	1:E:28:THR:HB	1.99	0.63
1:I:24:TYR:O	1:I:28:THR:HB	1.99	0.63
1:L:116:SER:CB	1:P:21:LEU:HD13	1.92	0.63
1:M:24:TYR:O	1:M:28:THR:HB	1.99	0.63
1:R:24:TYR:O	1:R:28:THR:HB	1.99	0.63
1:D:93:LEU:CD1	1:D:94:SER:H	2.12	0.63
1:E:93:LEU:CD1	1:E:94:SER:H	2.12	0.63
1:O:24:TYR:O	1:O:28:THR:HB	1.99	0.63
1:R:112:ARG:HE	1:R:114:ASN:HA	1.63	0.63
1:A:21:LEU:CG	1:E:117:VAL:O	2.33	0.63
1:L:24:TYR:O	1:L:28:THR:HB	1.99	0.63
1:A:24:TYR:O	1:A:28:THR:HB	1.99	0.62
1:B:24:TYR:O	1:B:28:THR:HB	1.99	0.62
1:B:76:LYS:NZ	1:K:15:ILE:CG2	2.61	0.62
1:F:6:LEU:HA	1:G:16:LEU:HD13	0.78	0.62
1:L:35:GLU:CD	1:O:15:ILE:HD11	2.20	0.62
1:Q:112:ARG:HE	1:Q:114:ASN:HA	1.62	0.62
1:B:3:LEU:H	1:C:8:ILE:HG21	1.63	0.62
1:B:15:ILE:HD11	1:E:35:GLU:CD	2.20	0.62
1:F:112:ARG:HE	1:F:114:ASN:HA	1.62	0.62
1:G:112:ARG:HE	1:G:114:ASN:HA	1.62	0.62
1:M:8:ILE:HG21	1:N:3:LEU:H	1.63	0.62
1:O:93:LEU:CD1	1:O:94:SER:H	2.12	0.62
1:R:93:LEU:CD1	1:R:94:SER:H	2.12	0.62
1:A:38:LEU:CA	1:M:10:ILE:CG1	2.58	0.62
1:J:93:LEU:CD1	1:J:94:SER:H	2.12	0.62
1:K:24:TYR:O	1:K:28:THR:HB	1.99	0.62
1:N:8:ILE:HG21	1:O:3:LEU:H	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:16:LEU:HD13	1:Q:6:LEU:HA	0.78	0.62
1:G:93:LEU:CD1	1:G:94:SER:H	2.12	0.62
1:J:24:TYR:O	1:J:28:THR:HB	1.99	0.62
1:L:38:LEU:CA	1:P:10:ILE:CG1	2.58	0.62
1:N:93:LEU:CD1	1:N:94:SER:H	2.12	0.62
1:A:93:LEU:CD1	1:A:94:SER:H	2.12	0.62
1:C:3:LEU:H	1:D:8:ILE:HG21	1.63	0.62
1:K:93:LEU:CD1	1:K:94:SER:H	2.12	0.62
1:M:117:VAL:O	1:Q:21:LEU:CG	2.33	0.62
1:N:76:LYS:NZ	1:Q:15:ILE:CG2	2.61	0.62
1:P:15:ILE:CD1	1:Q:3:LEU:HD21	2.26	0.62
1:C:93:LEU:CD1	1:C:94:SER:H	2.12	0.62
1:F:24:TYR:O	1:F:28:THR:HB	1.99	0.62
1:K:15:ILE:CD1	1:L:3:LEU:HD21	2.26	0.62
1:Q:8:ILE:HG21	1:R:3:LEU:H	1.63	0.62
1:C:3:LEU:HD21	1:D:15:ILE:CD1	2.26	0.62
1:C:112:ARG:HG2	1:C:112:ARG:HH11	1.65	0.62
1:E:112:ARG:HG2	1:E:112:ARG:HH11	1.65	0.62
1:F:112:ARG:HG2	1:F:112:ARG:HH11	1.65	0.62
1:Q:16:LEU:HD13	1:R:6:LEU:HA	0.78	0.62
1:B:6:LEU:HG	1:F:38:LEU:HG	1.82	0.62
1:B:93:LEU:CD1	1:B:94:SER:H	2.12	0.62
1:B:112:ARG:HG2	1:B:112:ARG:HH11	1.65	0.62
1:D:15:ILE:CG2	1:G:76:LYS:NZ	2.61	0.62
1:D:21:LEU:CG	1:H:117:VAL:O	2.33	0.62
1:D:38:LEU:HG	1:J:6:LEU:HG	1.82	0.62
1:E:112:ARG:HE	1:E:114:ASN:HA	1.62	0.62
1:F:15:ILE:CG2	1:I:76:LYS:NZ	2.61	0.62
1:Q:15:ILE:CD1	1:R:3:LEU:HD21	2.26	0.62
1:A:6:LEU:HG	1:E:38:LEU:HG	1.82	0.62
1:F:3:LEU:H	1:G:8:ILE:HG21	1.63	0.62
1:G:40:ALA:HB1	1:G:108:LEU:HD22	1.82	0.62
1:H:24:TYR:O	1:H:28:THR:HB	1.99	0.62
1:J:15:ILE:CD1	1:K:3:LEU:HD21	2.26	0.62
1:J:40:ALA:HB1	1:J:108:LEU:HD22	1.82	0.62
1:L:16:LEU:HD13	1:M:6:LEU:HA	0.78	0.62
1:M:15:ILE:CD1	1:N:3:LEU:HD21	2.26	0.62
1:B:6:LEU:HA	1:C:16:LEU:HD13	0.78	0.62
1:C:6:LEU:HA	1:D:16:LEU:HD13	0.78	0.62
1:F:93:LEU:CD1	1:F:94:SER:H	2.12	0.62
1:I:112:ARG:HH11	1:I:112:ARG:HG2	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:8:ILE:HG21	1:K:3:LEU:H	1.63	0.62
1:J:38:LEU:CA	1:N:10:ILE:CG1	2.58	0.62
1:J:112:ARG:HG2	1:J:112:ARG:HH11	1.65	0.62
1:M:35:GLU:CD	1:P:15:ILE:HD11	2.20	0.62
1:Q:40:ALA:HB1	1:Q:108:LEU:HD22	1.82	0.62
1:B:38:LEU:HG	1:L:6:LEU:HG	1.82	0.61
1:D:6:LEU:HG	1:H:38:LEU:HG	1.82	0.61
1:D:40:ALA:HB1	1:D:108:LEU:HD22	1.82	0.61
1:G:24:TYR:O	1:G:28:THR:HB	1.99	0.61
1:H:112:ARG:HG2	1:H:112:ARG:HH11	1.65	0.61
1:M:93:LEU:CD1	1:M:94:SER:H	2.12	0.61
1:N:40:ALA:HB1	1:N:108:LEU:HD22	1.82	0.61
1:C:38:LEU:HG	1:K:6:LEU:HG	1.82	0.61
1:C:40:ALA:HB1	1:C:108:LEU:HD22	1.82	0.61
1:J:76:LYS:NZ	1:M:15:ILE:CG2	2.61	0.61
1:K:112:ARG:HG2	1:K:112:ARG:HH11	1.65	0.61
1:M:8:ILE:CD1	1:N:1:MEA:HD2	2.16	0.61
1:M:40:ALA:HB1	1:M:108:LEU:HD22	1.82	0.61
1:N:112:ARG:HG2	1:N:112:ARG:HH11	1.65	0.61
1:Q:112:ARG:HG2	1:Q:112:ARG:HH11	1.65	0.61
1:C:6:LEU:HG	1:G:38:LEU:HG	1.82	0.61
1:C:28:THR:O	1:C:32:GLN:HG3	2.01	0.61
1:F:3:LEU:HD21	1:G:15:ILE:CD1	2.26	0.61
1:H:6:LEU:HA	1:I:16:LEU:HD13	0.78	0.61
1:L:93:LEU:CD1	1:L:94:SER:H	2.12	0.61
1:M:38:LEU:CA	1:Q:10:ILE:CG1	2.58	0.61
1:B:21:LEU:CG	1:F:117:VAL:O	2.33	0.61
1:D:44:LYS:HZ1	1:J:14:GLY:C	2.08	0.61
1:J:52:LEU:CG	1:N:25:GLN:NE2	2.64	0.61
1:L:112:ARG:HG2	1:L:112:ARG:HH11	1.65	0.61
1:M:38:LEU:HG	1:Q:6:LEU:HG	1.82	0.61
1:N:28:THR:O	1:N:32:GLN:HG3	2.01	0.61
1:A:28:THR:O	1:A:32:GLN:HG3	2.01	0.61
1:A:38:LEU:HG	1:M:6:LEU:HG	1.82	0.61
1:C:25:GLN:NE2	1:G:52:LEU:CG	2.64	0.61
1:D:15:ILE:HG21	1:G:76:LYS:HZ3	1.65	0.61
1:D:52:LEU:CG	1:J:25:GLN:NE2	2.64	0.61
1:E:3:LEU:HD21	1:F:15:ILE:CD1	2.26	0.61
1:E:6:LEU:HG	1:I:38:LEU:HG	1.82	0.61
1:I:40:ALA:HB1	1:I:108:LEU:HD22	1.82	0.61
1:J:28:THR:O	1:J:32:GLN:HG3	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:28:THR:O	1:K:32:GLN:HG3	2.01	0.61
1:K:38:LEU:HG	1:O:6:LEU:HG	1.82	0.61
1:R:28:THR:O	1:R:32:GLN:HG3	2.01	0.61
1:A:21:LEU:CG	1:E:116:SER:HB2	2.30	0.61
1:B:40:ALA:HB1	1:B:108:LEU:HD22	1.82	0.61
1:D:28:THR:O	1:D:32:GLN:HG3	2.01	0.61
1:E:25:GLN:NE2	1:I:52:LEU:CD2	2.48	0.61
1:F:28:THR:O	1:F:32:GLN:HG3	2.01	0.61
1:G:3:LEU:HD21	1:H:15:ILE:CD1	2.26	0.61
1:G:6:LEU:HA	1:H:16:LEU:HD13	0.78	0.61
1:G:28:THR:O	1:G:32:GLN:HG3	2.01	0.61
1:H:40:ALA:HB1	1:H:108:LEU:HD22	1.82	0.61
1:J:38:LEU:HG	1:N:6:LEU:HG	1.82	0.61
1:K:16:LEU:HD13	1:L:6:LEU:HA	0.78	0.61
1:L:76:LYS:NZ	1:O:15:ILE:CG2	2.61	0.61
1:M:28:THR:O	1:M:32:GLN:HG3	2.01	0.61
1:N:38:LEU:HG	1:R:6:LEU:HG	1.82	0.61
1:Q:28:THR:O	1:Q:32:GLN:HG3	2.01	0.61
1:Q:93:LEU:CD1	1:Q:94:SER:H	2.12	0.61
1:A:76:LYS:HZ3	1:L:15:ILE:HG21	1.65	0.61
1:E:28:THR:O	1:E:32:GLN:HG3	2.01	0.61
1:H:28:THR:O	1:H:32:GLN:HG3	2.01	0.61
1:L:116:SER:HB2	1:P:21:LEU:CG	2.30	0.61
1:M:112:ARG:HG2	1:M:112:ARG:HH11	1.65	0.61
1:P:28:THR:O	1:P:32:GLN:HG3	2.01	0.61
1:A:15:ILE:CD1	1:J:3:LEU:HD21	2.26	0.61
1:A:15:ILE:HG21	1:D:76:LYS:HZ3	1.65	0.61
1:A:40:ALA:HB1	1:A:108:LEU:HD22	1.82	0.61
1:B:15:ILE:CG2	1:E:76:LYS:NZ	2.61	0.61
1:B:21:LEU:CG	1:F:116:SER:HB2	2.30	0.61
1:B:28:THR:O	1:B:32:GLN:HG3	2.01	0.61
1:B:125:VAL:HG22	1:B:133:VAL:HB	1.83	0.61
1:G:112:ARG:HG2	1:G:112:ARG:HH11	1.65	0.61
1:L:28:THR:O	1:L:32:GLN:HG3	2.01	0.61
1:N:52:LEU:CG	1:R:25:GLN:NE2	2.64	0.61
1:O:28:THR:O	1:O:32:GLN:HG3	2.01	0.61
1:R:40:ALA:HB1	1:R:108:LEU:HD22	1.82	0.61
1:B:117:VAL:O	1:L:21:LEU:CG	2.33	0.61
1:Q:25:GLN:O	1:Q:26:ASP:CA	2.49	0.61
1:A:8:ILE:CD1	1:J:1:MEA:HD2	2.16	0.61
1:B:25:GLN:NE2	1:F:52:LEU:CG	2.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:LEU:CG	1:L:25:GLN:NE2	2.64	0.61
1:D:6:LEU:CD2	1:E:15:ILE:HG13	2.31	0.61
1:D:25:GLN:NE2	1:H:52:LEU:CG	2.64	0.61
1:D:114:ASN:CG	1:J:99:ASN:HD22	2.08	0.61
1:I:28:THR:O	1:I:32:GLN:HG3	2.01	0.61
1:J:114:ASN:CG	1:N:99:ASN:HD22	2.08	0.61
1:K:38:LEU:CA	1:O:10:ILE:CG1	2.58	0.61
1:K:40:ALA:HB1	1:K:108:LEU:HD22	1.82	0.61
1:O:40:ALA:HB1	1:O:108:LEU:HD22	1.82	0.61
1:O:112:ARG:HG2	1:O:112:ARG:HH11	1.65	0.61
1:B:116:SER:HB2	1:L:21:LEU:CG	2.30	0.60
1:C:25:GLN:O	1:C:26:ASP:CA	2.49	0.60
1:M:25:GLN:O	1:M:26:ASP:CA	2.49	0.60
1:M:53:ASN:OD1	1:P:149:SER:HB2	2.01	0.60
1:A:112:ARG:HH11	1:A:112:ARG:HG2	1.65	0.60
1:C:21:LEU:CG	1:G:116:SER:HB2	2.30	0.60
1:D:10:ILE:O	1:H:41:GLU:OE2	2.19	0.60
1:H:25:GLN:O	1:H:26:ASP:CA	2.49	0.60
1:L:40:ALA:HB1	1:L:108:LEU:HD22	1.82	0.60
1:M:112:ARG:HE	1:M:114:ASN:HA	1.62	0.60
1:N:15:ILE:CD1	1:O:3:LEU:HD21	2.26	0.60
1:Q:26:ASP:N	1:Q:26:ASP:CB	2.63	0.60
1:A:15:ILE:CG2	1:D:76:LYS:NZ	2.61	0.60
1:A:149:SER:HB2	1:D:53:ASN:OD1	2.02	0.60
1:B:97:VAL:CG2	1:B:102:LYS:HE2	2.32	0.60
1:C:97:VAL:CG2	1:C:102:LYS:HE2	2.32	0.60
1:E:101:ILE:HA	1:E:104:LYS:HD2	1.84	0.60
1:F:40:ALA:HB1	1:F:108:LEU:HD22	1.82	0.60
1:J:26:ASP:N	1:J:26:ASP:CB	2.63	0.60
1:J:52:LEU:CD2	1:N:25:GLN:NE2	2.48	0.60
1:K:116:SER:HB2	1:O:21:LEU:CG	2.30	0.60
1:L:101:ILE:HA	1:L:104:LYS:HD2	1.84	0.60
1:P:112:ARG:HG2	1:P:112:ARG:HH11	1.65	0.60
1:R:97:VAL:CG2	1:R:102:LYS:HE2	2.31	0.60
1:B:10:ILE:O	1:F:41:GLU:OE2	2.19	0.60
1:D:10:ILE:CG1	1:H:38:LEU:CA	2.58	0.60
1:D:25:GLN:O	1:D:26:ASP:CA	2.49	0.60
1:F:125:VAL:HG22	1:F:133:VAL:HB	1.83	0.60
1:F:149:SER:HB2	1:I:53:ASN:OD1	2.01	0.60
1:G:25:GLN:O	1:G:26:ASP:CA	2.49	0.60
1:K:76:LYS:HZ3	1:N:15:ILE:HG21	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:97:VAL:CG2	1:L:102:LYS:HE2	2.32	0.60
1:P:40:ALA:HB1	1:P:108:LEU:HD22	1.82	0.60
1:P:93:LEU:CD1	1:P:94:SER:H	2.12	0.60
1:R:125:VAL:HG22	1:R:133:VAL:HB	1.83	0.60
1:A:10:ILE:O	1:E:41:GLU:OE2	2.19	0.60
1:C:26:ASP:N	1:C:26:ASP:CB	2.63	0.60
1:C:41:GLU:OE2	1:K:10:ILE:O	2.19	0.60
1:C:99:ASN:HD22	1:G:114:ASN:CG	2.08	0.60
1:E:97:VAL:CG2	1:E:102:LYS:HE2	2.32	0.60
1:E:125:VAL:HG22	1:E:133:VAL:HB	1.83	0.60
1:I:97:VAL:CG2	1:I:102:LYS:HE2	2.32	0.60
1:K:25:GLN:O	1:K:26:ASP:CA	2.49	0.60
1:K:41:GLU:OE2	1:O:10:ILE:O	2.19	0.60
1:L:15:ILE:HG13	1:M:6:LEU:CD2	2.31	0.60
1:L:16:LEU:CB	1:M:6:LEU:CD1	2.67	0.60
1:L:38:LEU:HG	1:P:6:LEU:HG	1.82	0.60
1:L:125:VAL:HG22	1:L:133:VAL:HB	1.83	0.60
1:M:41:GLU:OE2	1:Q:10:ILE:O	2.19	0.60
1:M:76:LYS:NZ	1:P:15:ILE:CG2	2.61	0.60
1:M:116:SER:HB2	1:Q:21:LEU:CG	2.30	0.60
1:Q:101:ILE:HA	1:Q:104:LYS:HD2	1.83	0.60
1:R:25:GLN:O	1:R:26:ASP:CA	2.49	0.60
1:A:25:GLN:NE2	1:E:52:LEU:CG	2.64	0.60
1:A:41:GLU:OE2	1:M:10:ILE:O	2.19	0.60
1:A:76:LYS:NZ	1:L:15:ILE:CG2	2.61	0.60
1:D:99:ASN:HD22	1:H:114:ASN:CG	2.08	0.60
1:E:25:GLN:NE2	1:I:52:LEU:CG	2.64	0.60
1:E:149:SER:HB2	1:H:53:ASN:OD1	2.02	0.60
1:K:97:VAL:CG2	1:K:102:LYS:HE2	2.32	0.60
1:K:125:VAL:HG22	1:K:133:VAL:HB	1.83	0.60
1:L:52:LEU:CG	1:P:25:GLN:NE2	2.64	0.60
1:N:41:GLU:OE2	1:R:10:ILE:O	2.19	0.60
1:N:114:ASN:CG	1:R:99:ASN:HD22	2.08	0.60
1:N:116:SER:HB2	1:R:21:LEU:CG	2.30	0.60
1:P:101:ILE:HA	1:P:104:LYS:HD2	1.83	0.60
1:R:112:ARG:HG2	1:R:112:ARG:HH11	1.65	0.60
1:D:101:ILE:HA	1:D:104:LYS:HD2	1.84	0.60
1:E:15:ILE:CG2	1:H:76:LYS:NZ	2.61	0.60
1:E:21:LEU:CG	1:I:116:SER:HB2	2.30	0.60
1:M:16:LEU:HD13	1:N:6:LEU:HA	0.78	0.60
1:O:76:LYS:HZ3	1:R:15:ILE:HG21	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:97:VAL:CG2	1:O:102:LYS:HE2	2.32	0.60
1:P:16:LEU:CB	1:Q:6:LEU:CD1	2.67	0.60
1:P:25:GLN:O	1:P:26:ASP:CA	2.49	0.60
1:A:125:VAL:HG22	1:A:133:VAL:HB	1.83	0.60
1:C:53:ASN:OD1	1:J:149:SER:HB2	2.02	0.60
1:C:149:SER:HB2	1:F:53:ASN:OD1	2.02	0.60
1:D:41:GLU:OE2	1:J:10:ILE:O	2.19	0.60
1:F:15:ILE:HG21	1:I:76:LYS:HZ3	1.65	0.60
1:F:97:VAL:CG2	1:F:102:LYS:HE2	2.32	0.60
1:K:52:LEU:CG	1:O:25:GLN:NE2	2.64	0.60
1:M:52:LEU:CG	1:Q:25:GLN:NE2	2.64	0.60
1:N:53:ASN:OD1	1:Q:149:SER:HB2	2.02	0.60
1:P:97:VAL:CG2	1:P:102:LYS:HE2	2.32	0.60
1:A:52:LEU:CG	1:M:25:GLN:NE2	2.64	0.60
1:A:97:VAL:CG2	1:A:102:LYS:HE2	2.32	0.60
1:C:14:GLY:C	1:G:44:LYS:HZ1	2.09	0.60
1:C:15:ILE:HG21	1:F:76:LYS:HZ3	1.64	0.60
1:C:125:VAL:HG22	1:C:133:VAL:HB	1.83	0.60
1:E:6:LEU:HB2	1:F:12:ILE:O	2.02	0.60
1:E:40:ALA:HB1	1:E:108:LEU:HD22	1.82	0.60
1:I:101:ILE:HA	1:I:104:LYS:HD2	1.83	0.60
1:I:125:VAL:HG23	1:I:134:ALA:C	2.27	0.60
1:J:76:LYS:HZ3	1:M:15:ILE:HG21	1.67	0.60
1:J:116:SER:HB2	1:N:21:LEU:CG	2.30	0.60
1:K:52:LEU:CD2	1:O:25:GLN:NE2	2.48	0.60
1:M:44:LYS:HZ3	1:Q:14:GLY:HA2	1.55	0.60
1:N:112:ARG:HE	1:N:114:ASN:HA	1.62	0.60
1:O:53:ASN:OD1	1:R:149:SER:HB2	2.02	0.60
1:A:6:LEU:HB2	1:B:12:ILE:O	2.02	0.60
1:A:25:GLN:O	1:A:26:ASP:CA	2.49	0.60
1:A:53:ASN:OD1	1:L:149:SER:HB2	2.02	0.60
1:A:116:SER:HB2	1:M:21:LEU:CG	2.30	0.60
1:B:21:LEU:HD13	1:F:116:SER:HB2	1.63	0.60
1:B:41:GLU:OE2	1:L:10:ILE:O	2.19	0.60
1:C:52:LEU:CG	1:K:25:GLN:NE2	2.64	0.60
1:D:116:SER:HB2	1:J:21:LEU:CG	2.30	0.60
1:G:6:LEU:HB2	1:H:12:ILE:O	2.02	0.60
1:I:125:VAL:HG22	1:I:133:VAL:HB	1.83	0.60
1:J:25:GLN:O	1:J:26:ASP:CA	2.49	0.60
1:J:125:VAL:HG23	1:J:134:ALA:C	2.27	0.60
1:K:12:ILE:O	1:L:6:LEU:HB2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:101:ILE:HA	1:M:104:LYS:HD2	1.84	0.60
1:M:114:ASN:CG	1:Q:99:ASN:HD22	2.08	0.60
1:N:125:VAL:HG23	1:N:134:ALA:C	2.27	0.60
1:A:12:ILE:O	1:J:6:LEU:HB2	2.02	0.59
1:C:10:ILE:O	1:G:41:GLU:OE2	2.19	0.59
1:C:125:VAL:HG23	1:C:134:ALA:C	2.27	0.59
1:G:26:ASP:N	1:G:26:ASP:CB	2.63	0.59
1:H:6:LEU:HB2	1:I:12:ILE:O	2.02	0.59
1:H:97:VAL:CG2	1:H:102:LYS:HE2	2.32	0.59
1:J:66:VAL:O	1:J:67:ALA:C	2.45	0.59
1:J:101:ILE:HA	1:J:104:LYS:HD2	1.84	0.59
1:L:12:ILE:O	1:M:6:LEU:HB2	2.02	0.59
1:L:25:GLN:O	1:L:26:ASP:CA	2.49	0.59
1:N:25:GLN:O	1:N:26:ASP:CA	2.49	0.59
1:N:26:ASP:N	1:N:26:ASP:CB	2.63	0.59
1:O:112:ARG:HE	1:O:114:ASN:HA	1.62	0.59
1:O:125:VAL:HG23	1:O:134:ALA:C	2.27	0.59
1:O:125:VAL:HG22	1:O:133:VAL:HB	1.83	0.59
1:Q:66:VAL:O	1:Q:67:ALA:C	2.45	0.59
1:R:26:ASP:N	1:R:26:ASP:CB	2.63	0.59
1:B:149:SER:HB2	1:E:53:ASN:OD1	2.02	0.59
1:C:114:ASN:CG	1:K:99:ASN:HD22	2.08	0.59
1:D:21:LEU:CG	1:H:116:SER:HB2	2.30	0.59
1:E:125:VAL:HG23	1:E:134:ALA:C	2.27	0.59
1:J:16:LEU:HD13	1:K:6:LEU:HA	0.78	0.59
1:L:41:GLU:OE2	1:P:10:ILE:O	2.19	0.59
1:N:44:LYS:HZ1	1:R:14:GLY:C	2.09	0.59
1:P:125:VAL:HG22	1:P:133:VAL:HB	1.83	0.59
1:A:101:ILE:HA	1:A:104:LYS:HD2	1.84	0.59
1:A:114:ASN:CG	1:M:99:ASN:HD22	2.08	0.59
1:C:66:VAL:O	1:C:67:ALA:C	2.45	0.59
1:C:116:SER:HB2	1:K:21:LEU:CG	2.31	0.59
1:C:117:VAL:O	1:K:21:LEU:CG	2.33	0.59
1:D:125:VAL:HG22	1:D:133:VAL:HB	1.83	0.59
1:D:149:SER:HB2	1:G:53:ASN:OD1	2.02	0.59
1:F:125:VAL:HG23	1:F:134:ALA:C	2.27	0.59
1:J:41:GLU:OE2	1:N:10:ILE:O	2.19	0.59
1:J:125:VAL:HG22	1:J:133:VAL:HB	1.83	0.59
1:K:12:ILE:HD13	1:L:5:GLU:H	1.48	0.59
1:L:8:ILE:CD1	1:M:1:MEA:HD2	2.16	0.59
1:L:116:SER:HB2	1:P:21:LEU:HD13	1.63	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:66:VAL:O	1:M:67:ALA:C	2.45	0.59
1:O:15:ILE:CD1	1:P:3:LEU:HD21	2.26	0.59
1:D:112:ARG:HG2	1:D:112:ARG:HH11	1.65	0.59
1:L:117:VAL:O	1:P:21:LEU:CG	2.33	0.59
1:N:66:VAL:O	1:N:67:ALA:C	2.45	0.59
1:N:97:VAL:CG2	1:N:102:LYS:HE2	2.32	0.59
1:O:12:ILE:O	1:P:6:LEU:HB2	2.02	0.59
1:A:117:VAL:O	1:M:21:LEU:CG	2.33	0.59
1:B:53:ASN:OD1	1:K:149:SER:HB2	2.01	0.59
1:B:125:VAL:HG23	1:B:134:ALA:C	2.27	0.59
1:C:6:LEU:HB2	1:D:12:ILE:O	2.02	0.59
1:D:97:VAL:CG2	1:D:102:LYS:HE2	2.32	0.59
1:D:112:ARG:HE	1:D:114:ASN:HA	1.62	0.59
1:D:125:VAL:HG23	1:D:134:ALA:C	2.27	0.59
1:F:6:LEU:CD2	1:G:15:ILE:HG13	2.31	0.59
1:G:97:VAL:CG2	1:G:102:LYS:HE2	2.32	0.59
1:J:44:LYS:HZ1	1:N:14:GLY:C	2.10	0.59
1:J:97:VAL:CG2	1:J:102:LYS:HE2	2.32	0.59
1:K:53:ASN:OD1	1:N:149:SER:HB2	2.02	0.59
1:M:16:LEU:CB	1:N:6:LEU:CD1	2.67	0.59
1:M:97:VAL:CG2	1:M:102:LYS:HE2	2.32	0.59
1:N:15:ILE:HG13	1:O:6:LEU:CD2	2.31	0.59
1:P:12:ILE:O	1:Q:6:LEU:HB2	2.02	0.59
1:B:25:GLN:O	1:B:26:ASP:CA	2.49	0.59
1:K:125:VAL:HG23	1:K:134:ALA:C	2.27	0.59
1:P:125:VAL:HG23	1:P:134:ALA:C	2.27	0.59
1:Q:97:VAL:CG2	1:Q:102:LYS:HE2	2.32	0.59
1:D:3:LEU:HD21	1:E:15:ILE:CD1	2.26	0.59
1:E:10:ILE:O	1:I:41:GLU:OE2	2.19	0.59
1:G:66:VAL:O	1:G:67:ALA:C	2.45	0.59
1:G:101:ILE:HA	1:G:104:LYS:HD2	1.84	0.59
1:G:125:VAL:HG22	1:G:133:VAL:HB	1.83	0.59
1:I:25:GLN:O	1:I:26:ASP:CA	2.50	0.59
1:J:12:ILE:O	1:K:6:LEU:HB2	2.02	0.59
1:J:16:LEU:HD21	1:K:9:VAL:HG11	1.85	0.59
1:K:101:ILE:HA	1:K:104:LYS:HD2	1.84	0.59
1:R:101:ILE:HA	1:R:104:LYS:HD2	1.83	0.59
1:A:6:LEU:CD1	1:B:16:LEU:CB	2.67	0.59
1:B:101:ILE:HA	1:B:104:LYS:HD2	1.84	0.59
1:D:6:LEU:HB2	1:E:12:ILE:O	2.02	0.59
1:F:1:MEA:CE2	1:G:8:ILE:HD13	2.27	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:25:GLN:O	1:F:26:ASP:CA	2.49	0.59
1:F:101:ILE:HA	1:F:104:LYS:HD2	1.83	0.59
1:G:125:VAL:HG23	1:G:134:ALA:C	2.27	0.59
1:H:101:ILE:HA	1:H:104:LYS:HD2	1.83	0.59
1:L:114:ASN:CG	1:P:99:ASN:HD22	2.08	0.59
1:N:125:VAL:HG22	1:N:133:VAL:HB	1.83	0.59
1:F:6:LEU:HB2	1:G:12:ILE:O	2.02	0.59
1:H:125:VAL:HG22	1:H:133:VAL:HB	1.83	0.59
1:J:8:ILE:HD13	1:K:1:MEA:CE2	2.27	0.59
1:J:53:ASN:OD1	1:M:149:SER:HB2	2.01	0.59
1:J:117:VAL:O	1:N:21:LEU:CG	2.33	0.59
1:K:114:ASN:CG	1:O:99:ASN:HD22	2.08	0.59
1:L:16:LEU:HD21	1:M:9:VAL:HG11	1.85	0.59
1:L:125:VAL:HG23	1:L:134:ALA:C	2.27	0.59
1:M:12:ILE:O	1:N:6:LEU:HB2	2.02	0.59
1:M:16:LEU:HD21	1:N:9:VAL:HG11	1.85	0.59
1:M:125:VAL:HG22	1:M:133:VAL:HB	1.83	0.59
1:N:12:ILE:O	1:O:6:LEU:HB2	2.02	0.59
1:O:25:GLN:O	1:O:26:ASP:CA	2.49	0.59
1:B:6:LEU:CD2	1:C:15:ILE:HG13	2.31	0.59
1:B:114:ASN:CG	1:L:99:ASN:HD22	2.08	0.59
1:C:6:LEU:CD2	1:D:15:ILE:HG13	2.31	0.59
1:C:44:LYS:HZ1	1:K:14:GLY:C	2.10	0.59
1:D:66:VAL:O	1:D:67:ALA:C	2.45	0.59
1:J:15:ILE:HG13	1:K:6:LEU:CD2	2.31	0.59
1:K:66:VAL:O	1:K:67:ALA:C	2.45	0.59
1:P:66:VAL:O	1:P:67:ALA:C	2.45	0.59
1:Q:8:ILE:HD13	1:R:1:MEA:CE2	2.27	0.59
1:A:3:LEU:HD21	1:B:15:ILE:CD1	2.26	0.58
1:A:16:LEU:HD21	1:J:9:VAL:HG11	1.85	0.58
1:A:125:VAL:HG23	1:A:134:ALA:C	2.27	0.58
1:B:10:ILE:CG1	1:F:38:LEU:CA	2.58	0.58
1:K:16:LEU:HD21	1:L:9:VAL:HG11	1.85	0.58
1:L:66:VAL:O	1:L:67:ALA:C	2.45	0.58
1:M:15:ILE:HG13	1:N:6:LEU:CD2	2.31	0.58
1:M:116:SER:HB2	1:Q:21:LEU:HD13	1.63	0.58
1:Q:12:ILE:O	1:R:6:LEU:HB2	2.02	0.58
1:R:125:VAL:HG23	1:R:134:ALA:C	2.27	0.58
1:A:9:VAL:HG11	1:B:16:LEU:HD21	1.85	0.58
1:A:34:SER:HB3	1:M:7:MET:HB2	1.86	0.58
1:E:25:GLN:O	1:E:26:ASP:CA	2.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:9:VAL:HG11	1:H:16:LEU:HD21	1.85	0.58
1:L:15:ILE:CD1	1:M:3:LEU:HD21	2.26	0.58
1:L:53:ASN:OD1	1:O:149:SER:HB2	2.01	0.58
1:Q:125:VAL:HG23	1:Q:134:ALA:C	2.27	0.58
1:A:10:ILE:CG1	1:E:38:LEU:CA	2.58	0.58
1:C:1:MEA:CE2	1:D:8:ILE:HD13	2.27	0.58
1:C:10:ILE:CG1	1:G:38:LEU:CA	2.58	0.58
1:D:9:VAL:HG11	1:E:16:LEU:HD21	1.85	0.58
1:E:66:VAL:O	1:E:67:ALA:C	2.45	0.58
1:M:125:VAL:HG23	1:M:134:ALA:C	2.27	0.58
1:N:16:LEU:HD21	1:O:9:VAL:HG11	1.85	0.58
1:P:16:LEU:HD21	1:Q:9:VAL:HG11	1.85	0.58
1:Q:125:VAL:HG22	1:Q:133:VAL:HB	1.83	0.58
1:A:99:ASN:HD22	1:E:114:ASN:CG	2.08	0.58
1:B:1:MEA:CE2	1:C:8:ILE:HD13	2.27	0.58
1:B:113:GLU:O	1:B:114:ASN:HB2	2.04	0.58
1:D:1:MEA:HD2	1:E:8:ILE:CD1	2.16	0.58
1:D:7:MET:HB2	1:H:34:SER:HB3	1.86	0.58
1:G:113:GLU:O	1:G:114:ASN:HB2	2.04	0.58
1:H:6:LEU:CD2	1:I:15:ILE:HG13	2.31	0.58
1:H:9:VAL:HG11	1:I:16:LEU:HD21	1.85	0.58
1:H:125:VAL:HG23	1:H:134:ALA:C	2.27	0.58
1:I:66:VAL:O	1:I:67:ALA:C	2.45	0.58
1:I:113:GLU:O	1:I:114:ASN:HB2	2.04	0.58
1:A:66:VAL:O	1:A:67:ALA:C	2.45	0.58
1:C:101:ILE:HA	1:C:104:LYS:HD2	1.84	0.58
1:F:66:VAL:O	1:F:67:ALA:C	2.45	0.58
1:F:113:GLU:O	1:F:114:ASN:HB2	2.04	0.58
1:J:34:SER:HB3	1:N:7:MET:HB2	1.86	0.58
1:C:7:MET:HB2	1:G:34:SER:HB3	1.86	0.58
1:C:113:GLU:O	1:C:114:ASN:HB2	2.04	0.58
1:D:113:GLU:O	1:D:114:ASN:HB2	2.04	0.58
1:F:9:VAL:HG11	1:G:16:LEU:HD21	1.85	0.58
1:F:149:SER:HG	1:I:53:ASN:HB3	1.67	0.58
1:M:8:ILE:HD13	1:N:1:MEA:CE2	2.27	0.58
1:Q:16:LEU:HD21	1:R:9:VAL:HG11	1.85	0.58
1:B:6:LEU:HB2	1:C:12:ILE:O	2.02	0.58
1:C:9:VAL:HG11	1:D:16:LEU:HD21	1.85	0.58
1:G:6:LEU:CD2	1:H:15:ILE:HG13	2.31	0.58
1:J:113:GLU:O	1:J:114:ASN:HB2	2.04	0.58
1:N:101:ILE:HA	1:N:104:LYS:HD2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:113:GLU:O	1:P:114:ASN:HB2	2.04	0.58
1:B:9:VAL:HG11	1:C:16:LEU:HD21	1.85	0.58
1:B:66:VAL:O	1:B:67:ALA:C	2.45	0.58
1:K:113:GLU:O	1:K:114:ASN:HB2	2.04	0.58
1:O:66:VAL:O	1:O:67:ALA:C	2.45	0.58
1:O:101:ILE:HA	1:O:104:LYS:HD2	1.84	0.58
1:Q:15:ILE:HG13	1:R:6:LEU:CD2	2.31	0.58
1:C:6:LEU:CD1	1:D:15:ILE:HG13	2.34	0.58
1:E:7:MET:SD	1:I:34:SER:CB	2.92	0.58
1:K:52:LEU:HG	1:O:25:GLN:NE2	2.19	0.58
1:O:16:LEU:HD21	1:P:9:VAL:HG11	1.85	0.58
1:A:15:ILE:HG13	1:J:6:LEU:CD2	2.31	0.58
1:A:15:ILE:HG13	1:J:6:LEU:CD1	2.34	0.58
1:B:25:GLN:NE2	1:F:52:LEU:HG	2.19	0.58
1:G:1:MEA:CE2	1:H:8:ILE:HD13	2.27	0.58
1:K:15:ILE:HG13	1:L:6:LEU:CD1	2.34	0.58
1:L:52:LEU:CD2	1:P:25:GLN:NE2	2.48	0.58
1:M:34:SER:HB3	1:Q:7:MET:HB2	1.86	0.58
1:O:15:ILE:HG13	1:P:6:LEU:CD1	2.34	0.58
1:C:7:MET:SD	1:G:34:SER:CB	2.92	0.57
1:C:21:LEU:CG	1:G:117:VAL:O	2.33	0.57
1:C:52:LEU:HG	1:K:25:GLN:NE2	2.19	0.57
1:C:112:ARG:HE	1:C:114:ASN:HA	1.62	0.57
1:E:99:ASN:HD22	1:I:114:ASN:CG	2.08	0.57
1:H:3:LEU:HD21	1:I:15:ILE:CD1	2.26	0.57
1:M:113:GLU:O	1:M:114:ASN:HB2	2.04	0.57
1:Q:15:ILE:HG13	1:R:6:LEU:CD1	2.34	0.57
1:B:34:SER:CB	1:L:7:MET:SD	2.92	0.57
1:B:52:LEU:HG	1:L:25:GLN:NE2	2.19	0.57
1:B:99:ASN:HD22	1:F:114:ASN:CG	2.08	0.57
1:J:34:SER:CB	1:N:7:MET:SD	2.92	0.57
1:K:44:LYS:HZ1	1:O:14:GLY:C	2.10	0.57
1:R:66:VAL:O	1:R:67:ALA:C	2.45	0.57
1:D:34:SER:CB	1:J:7:MET:SD	2.92	0.57
1:E:25:GLN:NE2	1:I:52:LEU:HG	2.19	0.57
1:L:44:LYS:HZ1	1:P:14:GLY:C	2.11	0.57
1:L:52:LEU:HG	1:P:25:GLN:NE2	2.19	0.57
1:L:79:LYS:CA	1:L:93:LEU:HD22	2.35	0.57
1:N:34:SER:HB3	1:R:7:MET:HB2	1.86	0.57
1:N:52:LEU:HG	1:R:25:GLN:NE2	2.19	0.57
1:B:7:MET:SD	1:F:34:SER:CB	2.92	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:LYS:CA	1:B:93:LEU:HD22	2.35	0.57
1:E:6:LEU:HD12	1:F:16:LEU:CD1	2.35	0.57
1:E:113:GLU:O	1:E:114:ASN:HB2	2.04	0.57
1:H:6:LEU:CD1	1:I:15:ILE:HG13	2.34	0.57
1:H:6:LEU:HD12	1:I:16:LEU:CD1	2.35	0.57
1:M:34:SER:CB	1:Q:7:MET:SD	2.92	0.57
1:P:79:LYS:CA	1:P:93:LEU:HD22	2.35	0.57
1:A:113:GLU:O	1:A:114:ASN:HB2	2.04	0.57
1:F:6:LEU:CD1	1:G:15:ILE:HG13	2.34	0.57
1:F:79:LYS:CA	1:F:93:LEU:HD22	2.35	0.57
1:K:34:SER:CB	1:O:7:MET:SD	2.92	0.57
1:L:34:SER:CB	1:P:7:MET:SD	2.92	0.57
1:O:16:LEU:CD1	1:P:6:LEU:HD12	2.35	0.57
1:A:6:LEU:CD2	1:B:15:ILE:HG13	2.31	0.57
1:A:25:GLN:NE2	1:E:52:LEU:HG	2.19	0.57
1:B:6:LEU:CD1	1:C:15:ILE:HG13	2.34	0.57
1:B:127:ARG:HA	1:B:133:VAL:HG12	1.87	0.57
1:C:25:GLN:NE2	1:G:52:LEU:HG	2.19	0.57
1:F:127:ARG:HA	1:F:133:VAL:HG12	1.87	0.57
1:I:79:LYS:CA	1:I:93:LEU:HD22	2.35	0.57
1:M:52:LEU:HG	1:Q:25:GLN:NE2	2.19	0.57
1:N:38:LEU:CA	1:R:10:ILE:CG1	2.58	0.57
1:O:8:ILE:HD13	1:P:1:MEA:CE2	2.27	0.57
1:O:113:GLU:O	1:O:114:ASN:HB2	2.04	0.57
1:R:113:GLU:O	1:R:114:ASN:HB2	2.04	0.57
1:A:8:ILE:HD13	1:J:1:MEA:CE2	2.27	0.57
1:A:34:SER:CB	1:M:7:MET:SD	2.92	0.57
1:A:52:LEU:HG	1:M:25:GLN:NE2	2.19	0.57
1:B:34:SER:HB3	1:L:7:MET:HB2	1.86	0.57
1:D:26:ASP:N	1:D:26:ASP:CB	2.63	0.57
1:D:79:LYS:CA	1:D:93:LEU:HD22	2.35	0.57
1:G:79:LYS:CA	1:G:93:LEU:HD22	2.35	0.57
1:J:52:LEU:HG	1:N:25:GLN:NE2	2.19	0.57
1:K:117:VAL:O	1:O:21:LEU:CG	2.33	0.57
1:L:127:ARG:HA	1:L:133:VAL:HG12	1.87	0.57
1:A:6:LEU:HD12	1:B:16:LEU:CD1	2.35	0.57
1:B:38:LEU:CA	1:L:10:ILE:CG1	2.58	0.57
1:C:34:SER:CB	1:K:7:MET:SD	2.92	0.57
1:C:76:LYS:HZ3	1:J:15:ILE:HG21	1.68	0.57
1:C:127:ARG:HA	1:C:133:VAL:HG12	1.87	0.57
1:D:25:GLN:NE2	1:H:52:LEU:HG	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:6:LEU:CD1	1:F:16:LEU:CB	2.67	0.57
1:E:7:MET:HB2	1:I:34:SER:HB3	1.86	0.57
1:E:79:LYS:CA	1:E:93:LEU:HD22	2.35	0.57
1:H:66:VAL:O	1:H:67:ALA:C	2.45	0.57
1:H:79:LYS:CA	1:H:93:LEU:HD22	2.35	0.57
1:N:15:ILE:HG13	1:O:6:LEU:CD1	2.34	0.57
1:N:113:GLU:O	1:N:114:ASN:HB2	2.04	0.57
1:A:7:MET:SD	1:E:34:SER:CB	2.92	0.57
1:C:6:LEU:HD12	1:D:16:LEU:CD1	2.35	0.57
1:D:6:LEU:CD1	1:E:15:ILE:HG13	2.34	0.57
1:D:34:SER:HB3	1:J:7:MET:HB2	1.86	0.57
1:D:52:LEU:HG	1:J:25:GLN:NE2	2.19	0.57
1:E:127:ARG:HA	1:E:133:VAL:HG12	1.87	0.57
1:G:127:ARG:HA	1:G:133:VAL:HG12	1.87	0.57
1:I:127:ARG:HA	1:I:133:VAL:HG12	1.87	0.57
1:K:127:ARG:HA	1:K:133:VAL:HG12	1.87	0.57
1:L:16:LEU:CD1	1:M:6:LEU:HD12	2.35	0.57
1:N:16:LEU:CD1	1:O:6:LEU:HD12	2.35	0.57
1:P:127:ARG:HA	1:P:133:VAL:HG12	1.87	0.57
1:B:6:LEU:HD12	1:C:16:LEU:CD1	2.35	0.57
1:E:9:VAL:HG11	1:F:16:LEU:HD21	1.85	0.57
1:F:6:LEU:HD12	1:G:16:LEU:CD1	2.35	0.57
1:G:6:LEU:HD12	1:H:16:LEU:CD1	2.35	0.57
1:L:15:ILE:HG13	1:M:6:LEU:CD1	2.34	0.57
1:N:116:SER:HB2	1:R:21:LEU:HD13	1.63	0.57
1:O:127:ARG:HA	1:O:133:VAL:HG12	1.87	0.57
1:A:7:MET:HB2	1:E:34:SER:HB3	1.86	0.56
1:A:79:LYS:CA	1:A:93:LEU:HD22	2.35	0.56
1:C:34:SER:HB3	1:K:7:MET:HB2	1.86	0.56
1:C:79:LYS:CA	1:C:93:LEU:HD22	2.35	0.56
1:D:117:VAL:O	1:J:21:LEU:CG	2.33	0.56
1:E:6:LEU:CD2	1:F:15:ILE:HG13	2.31	0.56
1:M:16:LEU:CD1	1:N:6:LEU:HD12	2.35	0.56
1:N:127:ARG:HA	1:N:133:VAL:HG12	1.87	0.56
1:R:127:ARG:HA	1:R:133:VAL:HG12	1.87	0.56
1:A:16:LEU:CD1	1:J:6:LEU:HD12	2.35	0.56
1:E:15:ILE:HG21	1:H:76:LYS:HZ3	1.68	0.56
1:E:26:ASP:N	1:E:26:ASP:CB	2.63	0.56
1:K:16:LEU:CD1	1:L:6:LEU:HD12	2.35	0.56
1:M:79:LYS:CA	1:M:93:LEU:HD22	2.35	0.56
1:O:15:ILE:HG13	1:P:6:LEU:CD2	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:113:GLU:O	1:Q:114:ASN:HB2	2.04	0.56
1:A:127:ARG:HA	1:A:133:VAL:HG12	1.87	0.56
1:B:7:MET:HB2	1:F:34:SER:HB3	1.86	0.56
1:F:6:LEU:CD1	1:G:16:LEU:CB	2.67	0.56
1:J:79:LYS:CA	1:J:93:LEU:HD22	2.35	0.56
1:J:127:ARG:HA	1:J:133:VAL:HG12	1.87	0.56
1:K:15:ILE:HG13	1:L:6:LEU:CD2	2.31	0.56
1:K:79:LYS:CA	1:K:93:LEU:HD22	2.35	0.56
1:L:34:SER:HB3	1:P:7:MET:HB2	1.86	0.56
1:L:113:GLU:O	1:L:114:ASN:HB2	2.04	0.56
1:N:34:SER:CB	1:R:7:MET:SD	2.92	0.56
1:P:8:ILE:HD13	1:Q:1:MEA:CE2	2.27	0.56
1:P:15:ILE:HG13	1:Q:6:LEU:CD2	2.31	0.56
1:Q:16:LEU:CD1	1:R:6:LEU:HD12	2.35	0.56
1:Q:79:LYS:CA	1:Q:93:LEU:HD22	2.35	0.56
1:Q:127:ARG:HA	1:Q:133:VAL:HG12	1.87	0.56
1:R:79:LYS:CA	1:R:93:LEU:HD22	2.35	0.56
1:A:6:LEU:CD1	1:B:15:ILE:HG13	2.34	0.56
1:H:127:ARG:HA	1:H:133:VAL:HG12	1.87	0.56
1:J:16:LEU:CD1	1:K:6:LEU:HD12	2.35	0.56
1:K:34:SER:HB3	1:O:7:MET:HB2	1.86	0.56
1:L:26:ASP:N	1:L:26:ASP:CB	2.63	0.56
1:M:127:ARG:HA	1:M:133:VAL:HG12	1.87	0.56
1:O:79:LYS:CA	1:O:93:LEU:HD22	2.35	0.56
1:P:16:LEU:CD1	1:Q:6:LEU:HD12	2.35	0.56
1:P:26:ASP:N	1:P:26:ASP:CB	2.63	0.56
1:D:7:MET:SD	1:H:34:SER:CB	2.92	0.56
1:A:21:LEU:HD13	1:E:116:SER:HB2	1.63	0.56
1:D:6:LEU:HD12	1:E:16:LEU:CD1	2.35	0.56
1:I:26:ASP:N	1:I:26:ASP:CB	2.63	0.56
1:D:127:ARG:HA	1:D:133:VAL:HG12	1.87	0.56
1:J:16:LEU:CB	1:K:6:LEU:CD1	2.67	0.56
1:M:38:LEU:CD1	1:Q:10:ILE:HD12	2.26	0.56
1:E:6:LEU:CD1	1:F:15:ILE:HG13	2.34	0.56
1:H:113:GLU:O	1:H:114:ASN:HB2	2.04	0.56
1:C:149:SER:HG	1:F:53:ASN:HB3	1.68	0.56
1:D:38:LEU:CA	1:J:10:ILE:CG1	2.58	0.56
1:M:76:LYS:HZ3	1:P:15:ILE:HG21	1.68	0.56
1:N:79:LYS:CA	1:N:93:LEU:HD22	2.35	0.56
1:G:6:LEU:CD1	1:H:15:ILE:HG13	2.34	0.55
1:J:15:ILE:HG13	1:K:6:LEU:CD1	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:15:ILE:HD11	1:P:6:LEU:CD2	2.23	0.55
1:K:8:ILE:HD13	1:L:1:MEA:CE2	2.27	0.55
1:O:16:LEU:CB	1:P:6:LEU:CD1	2.67	0.55
1:A:26:ASP:N	1:A:26:ASP:CB	2.63	0.55
1:H:26:ASP:N	1:H:26:ASP:CB	2.63	0.55
1:O:90:ALA:O	1:O:105:LYS:CB	2.55	0.55
1:R:90:ALA:O	1:R:105:LYS:CB	2.55	0.55
1:R:125:VAL:HG23	1:R:134:ALA:O	2.07	0.55
1:C:116:SER:HB2	1:K:21:LEU:HD13	1.63	0.55
1:J:90:ALA:O	1:J:105:LYS:CB	2.55	0.55
1:M:15:ILE:HG13	1:N:6:LEU:CD1	2.34	0.55
1:P:15:ILE:HG13	1:Q:6:LEU:CD1	2.34	0.55
1:B:44:LYS:HZ1	1:L:14:GLY:C	2.13	0.55
1:C:90:ALA:O	1:C:105:LYS:CB	2.55	0.55
1:D:10:ILE:HD12	1:H:38:LEU:CD1	2.26	0.55
1:G:90:ALA:O	1:G:105:LYS:CB	2.55	0.55
1:K:15:ILE:HD11	1:L:6:LEU:CD2	2.23	0.55
1:K:90:ALA:O	1:K:105:LYS:CB	2.55	0.55
1:N:90:ALA:O	1:N:105:LYS:CB	2.55	0.55
1:N:125:VAL:HG23	1:N:134:ALA:O	2.07	0.55
1:B:90:ALA:O	1:B:105:LYS:CB	2.55	0.55
1:D:90:ALA:O	1:D:105:LYS:CB	2.55	0.55
1:D:116:SER:HB2	1:J:21:LEU:HD13	1.63	0.55
1:F:90:ALA:O	1:F:105:LYS:CB	2.55	0.55
1:K:125:VAL:HG23	1:K:134:ALA:O	2.07	0.55
1:L:90:ALA:O	1:L:105:LYS:CB	2.55	0.55
1:L:125:VAL:HG23	1:L:134:ALA:O	2.07	0.55
1:A:53:ASN:HB3	1:L:149:SER:HG	1.71	0.55
1:G:125:VAL:HG23	1:G:134:ALA:O	2.07	0.55
1:H:90:ALA:O	1:H:105:LYS:CB	2.55	0.55
1:J:125:VAL:HG23	1:J:134:ALA:O	2.07	0.55
1:O:26:ASP:N	1:O:26:ASP:CB	2.63	0.55
1:P:125:VAL:HG23	1:P:134:ALA:O	2.07	0.55
1:Q:16:LEU:CB	1:R:6:LEU:CD1	2.67	0.55
1:B:125:VAL:HG23	1:B:134:ALA:O	2.07	0.55
1:E:6:LEU:HD11	1:F:15:ILE:C	2.32	0.55
1:I:125:VAL:HG23	1:I:134:ALA:O	2.07	0.55
1:P:90:ALA:O	1:P:105:LYS:CB	2.55	0.55
1:B:14:GLY:C	1:F:44:LYS:HZ1	2.13	0.54
1:E:125:VAL:HG23	1:E:134:ALA:O	2.07	0.54
1:F:125:VAL:HG23	1:F:134:ALA:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:LEU:HD11	1:B:15:ILE:C	2.32	0.54
1:B:26:ASP:N	1:B:26:ASP:CB	2.63	0.54
1:H:125:VAL:HG23	1:H:134:ALA:O	2.07	0.54
1:M:90:ALA:O	1:M:105:LYS:CB	2.55	0.54
1:O:15:ILE:C	1:P:6:LEU:HD11	2.32	0.54
1:B:15:ILE:HG21	1:E:76:LYS:HZ3	1.71	0.54
1:D:6:LEU:HD11	1:E:15:ILE:C	2.32	0.54
1:E:1:MEA:CE2	1:F:8:ILE:HD13	2.27	0.54
1:M:125:VAL:HG23	1:M:134:ALA:O	2.07	0.54
1:Q:125:VAL:HG23	1:Q:134:ALA:O	2.07	0.54
1:B:6:LEU:CD1	1:C:16:LEU:CB	2.67	0.54
1:I:90:ALA:O	1:I:105:LYS:CB	2.55	0.54
1:A:125:VAL:HG23	1:A:134:ALA:O	2.07	0.54
1:E:10:ILE:HD12	1:I:38:LEU:CD1	2.26	0.54
1:F:6:LEU:CD2	1:G:15:ILE:CG1	2.76	0.54
1:Q:90:ALA:O	1:Q:105:LYS:CB	2.55	0.54
1:C:125:VAL:HG23	1:C:134:ALA:O	2.07	0.54
1:H:6:LEU:HD11	1:I:15:ILE:C	2.32	0.54
1:I:39:LEU:HD22	1:I:73:ILE:HG22	1.90	0.54
1:K:16:LEU:CB	1:L:6:LEU:CD1	2.67	0.54
1:M:44:LYS:HZ1	1:Q:14:GLY:C	2.15	0.54
1:B:39:LEU:HD22	1:B:73:ILE:HG22	1.90	0.54
1:D:1:MEA:CE2	1:E:8:ILE:HD13	2.27	0.54
1:D:6:LEU:HD12	1:E:16:LEU:HD12	1.90	0.54
1:E:90:ALA:O	1:E:105:LYS:CB	2.55	0.54
1:K:53:ASN:HB3	1:N:149:SER:HG	1.71	0.54
1:A:15:ILE:C	1:J:6:LEU:HD11	2.32	0.54
1:B:24:TYR:O	1:B:28:THR:CB	2.56	0.54
1:D:125:VAL:HG23	1:D:134:ALA:O	2.07	0.54
1:F:39:LEU:HD22	1:F:73:ILE:HG22	1.90	0.54
1:I:24:TYR:O	1:I:28:THR:CB	2.56	0.54
1:A:15:ILE:HD11	1:J:6:LEU:CD2	2.23	0.54
1:A:90:ALA:O	1:A:105:LYS:CB	2.55	0.54
1:B:6:LEU:HD12	1:C:16:LEU:HD12	1.90	0.54
1:H:6:LEU:HD12	1:I:16:LEU:HD12	1.90	0.54
1:L:24:TYR:O	1:L:28:THR:CB	2.56	0.54
1:N:15:ILE:HD11	1:O:6:LEU:CD2	2.23	0.54
1:E:39:LEU:HD22	1:E:73:ILE:HG22	1.90	0.54
1:K:39:LEU:HD22	1:K:73:ILE:HG22	1.90	0.54
1:L:39:LEU:HD22	1:L:73:ILE:HG22	1.90	0.54
1:O:39:LEU:HD22	1:O:73:ILE:HG22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:125:VAL:HG23	1:O:134:ALA:O	2.07	0.54
1:A:16:LEU:HD12	1:J:6:LEU:HD12	1.90	0.53
1:E:6:LEU:HD12	1:F:16:LEU:HD12	1.90	0.53
1:E:24:TYR:O	1:E:28:THR:CB	2.56	0.53
1:G:6:LEU:HD12	1:H:16:LEU:HD12	1.90	0.53
1:G:24:TYR:O	1:G:28:THR:CB	2.56	0.53
1:N:16:LEU:HD12	1:O:6:LEU:HD12	1.90	0.53
1:A:6:LEU:HD12	1:B:16:LEU:HD12	1.90	0.53
1:C:6:LEU:HD11	1:D:15:ILE:C	2.32	0.53
1:L:16:LEU:HD12	1:M:6:LEU:HD12	1.90	0.53
1:N:24:TYR:O	1:N:28:THR:CB	2.56	0.53
1:O:24:TYR:O	1:O:28:THR:CB	2.56	0.53
1:P:16:LEU:HD12	1:Q:6:LEU:HD12	1.90	0.53
1:R:98:ASN:HB3	1:R:101:ILE:HG12	1.90	0.53
1:B:149:SER:HB2	1:E:53:ASN:HB3	1.91	0.53
1:F:6:LEU:HD12	1:G:16:LEU:HD12	1.90	0.53
1:G:60:ASN:HA	1:G:83:VAL:O	2.09	0.53
1:K:16:LEU:HD12	1:L:6:LEU:HD12	1.90	0.53
1:L:15:ILE:C	1:M:6:LEU:HD11	2.32	0.53
1:M:26:ASP:N	1:M:26:ASP:CB	2.63	0.53
1:N:15:ILE:C	1:O:6:LEU:HD11	2.32	0.53
1:P:15:ILE:C	1:Q:6:LEU:HD11	2.32	0.53
1:Q:15:ILE:C	1:R:6:LEU:HD11	2.33	0.53
1:B:76:LYS:HZ3	1:K:15:ILE:HG21	1.70	0.53
1:D:41:GLU:CD	1:J:10:ILE:O	2.52	0.53
1:J:24:TYR:O	1:J:28:THR:CB	2.56	0.53
1:K:15:ILE:C	1:L:6:LEU:HD11	2.32	0.53
1:M:24:TYR:O	1:M:28:THR:CB	2.56	0.53
1:M:41:GLU:CD	1:Q:10:ILE:O	2.52	0.53
1:N:38:LEU:CD1	1:R:10:ILE:HD12	2.26	0.53
1:O:98:ASN:HB3	1:O:101:ILE:HG12	1.90	0.53
1:R:39:LEU:HD22	1:R:73:ILE:HG22	1.90	0.53
1:A:41:GLU:CD	1:M:10:ILE:O	2.52	0.53
1:A:44:LYS:HZ1	1:M:14:GLY:C	2.16	0.53
1:C:26:ASP:N	1:C:26:ASP:C	2.63	0.53
1:C:39:LEU:HD22	1:C:73:ILE:HG22	1.90	0.53
1:C:60:ASN:HA	1:C:83:VAL:O	2.09	0.53
1:K:38:LEU:CD1	1:O:10:ILE:HD12	2.26	0.53
1:O:16:LEU:HD12	1:P:6:LEU:HD12	1.90	0.53
1:A:98:ASN:HB3	1:A:101:ILE:HG12	1.90	0.53
1:C:6:LEU:HD12	1:D:16:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:TYR:O	1:C:28:THR:CB	2.56	0.53
1:D:24:TYR:O	1:D:28:THR:CB	2.56	0.53
1:F:26:ASP:N	1:F:26:ASP:CB	2.63	0.53
1:H:24:TYR:O	1:H:28:THR:CB	2.56	0.53
1:Q:15:ILE:CG1	1:R:6:LEU:CD2	2.76	0.53
1:Q:60:ASN:HA	1:Q:83:VAL:O	2.09	0.53
1:A:39:LEU:HD22	1:A:73:ILE:HG22	1.90	0.53
1:F:6:LEU:HD11	1:G:15:ILE:C	2.32	0.53
1:G:6:LEU:HD11	1:H:15:ILE:C	2.32	0.53
1:H:101:ILE:O	1:H:104:LYS:HB2	2.09	0.53
1:J:16:LEU:HD12	1:K:6:LEU:HD12	1.90	0.53
1:J:41:GLU:CD	1:N:10:ILE:O	2.52	0.53
1:K:41:GLU:CD	1:O:10:ILE:O	2.52	0.53
1:L:101:ILE:O	1:L:104:LYS:HB2	2.09	0.53
1:M:16:LEU:HD12	1:N:6:LEU:HD12	1.90	0.53
1:M:60:ASN:HA	1:M:83:VAL:O	2.09	0.53
1:P:24:TYR:O	1:P:28:THR:CB	2.56	0.53
1:A:52:LEU:CG	1:M:25:GLN:CD	2.81	0.53
1:B:6:LEU:CD2	1:C:15:ILE:HD11	2.23	0.53
1:B:60:ASN:HA	1:B:83:VAL:O	2.09	0.53
1:D:10:ILE:O	1:H:41:GLU:CD	2.52	0.53
1:D:98:ASN:HB3	1:D:101:ILE:HG12	1.90	0.53
1:H:39:LEU:HD22	1:H:73:ILE:HG22	1.90	0.53
1:P:39:LEU:HD22	1:P:73:ILE:HG22	1.90	0.53
1:A:24:TYR:O	1:A:28:THR:CB	2.56	0.53
1:A:149:SER:HB2	1:D:53:ASN:CB	2.39	0.53
1:E:6:LEU:CD2	1:F:15:ILE:HD11	2.23	0.53
1:E:101:ILE:O	1:E:104:LYS:HB2	2.09	0.53
1:J:34:SER:HB3	1:N:7:MET:CG	2.39	0.53
1:K:24:TYR:O	1:K:28:THR:CB	2.56	0.53
1:K:34:SER:HB3	1:O:7:MET:CG	2.39	0.53
1:L:76:LYS:HZ3	1:O:15:ILE:HG21	1.73	0.53
1:M:53:ASN:CB	1:P:149:SER:HB2	2.39	0.53
1:Q:16:LEU:HD12	1:R:6:LEU:HD12	1.90	0.53
1:Q:24:TYR:O	1:Q:28:THR:CB	2.56	0.53
1:A:34:SER:HB3	1:M:7:MET:CG	2.39	0.53
1:A:101:ILE:O	1:A:104:LYS:HB2	2.09	0.53
1:B:10:ILE:O	1:F:41:GLU:CD	2.52	0.53
1:B:41:GLU:CD	1:L:10:ILE:O	2.52	0.53
1:E:149:SER:HB2	1:H:53:ASN:CB	2.39	0.53
1:G:6:LEU:CD1	1:H:16:LEU:CB	2.67	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:98:ASN:HB3	1:K:101:ILE:HG12	1.90	0.53
1:L:60:ASN:HA	1:L:83:VAL:O	2.09	0.53
1:M:34:SER:HB3	1:Q:7:MET:CG	2.39	0.53
1:N:34:SER:HB3	1:R:7:MET:CG	2.39	0.53
1:N:39:LEU:HD22	1:N:73:ILE:HG22	1.90	0.53
1:N:41:GLU:CD	1:R:10:ILE:O	2.52	0.53
1:O:101:ILE:O	1:O:104:LYS:HB2	2.09	0.53
1:A:53:ASN:CB	1:L:149:SER:HB2	2.39	0.52
1:B:149:SER:HB2	1:E:53:ASN:CB	2.39	0.52
1:C:34:SER:HB3	1:K:7:MET:CG	2.40	0.52
1:C:149:SER:HB2	1:F:53:ASN:CB	2.39	0.52
1:D:25:GLN:CD	1:H:52:LEU:CG	2.81	0.52
1:D:149:SER:HB2	1:G:53:ASN:CB	2.39	0.52
1:F:60:ASN:HA	1:F:83:VAL:O	2.09	0.52
1:J:15:ILE:C	1:K:6:LEU:HD11	2.32	0.52
1:J:98:ASN:HB3	1:J:101:ILE:HG12	1.90	0.52
1:A:10:ILE:O	1:E:41:GLU:CD	2.52	0.52
1:B:25:GLN:CD	1:F:52:LEU:CG	2.81	0.52
1:B:101:ILE:O	1:B:104:LYS:HB2	2.09	0.52
1:C:53:ASN:CB	1:J:149:SER:HB2	2.39	0.52
1:D:34:SER:HB3	1:J:7:MET:CG	2.40	0.52
1:D:39:LEU:HD22	1:D:73:ILE:HG22	1.90	0.52
1:E:60:ASN:HA	1:E:83:VAL:O	2.09	0.52
1:F:149:SER:HB2	1:I:53:ASN:CB	2.39	0.52
1:G:39:LEU:HD22	1:G:73:ILE:HG22	1.90	0.52
1:I:60:ASN:HA	1:I:83:VAL:O	2.09	0.52
1:J:53:ASN:CB	1:M:149:SER:HB2	2.39	0.52
1:L:34:SER:HB3	1:P:7:MET:CG	2.39	0.52
1:L:53:ASN:CB	1:O:149:SER:HB2	2.39	0.52
1:M:98:ASN:HB3	1:M:101:ILE:HG12	1.90	0.52
1:N:53:ASN:CB	1:Q:149:SER:HB2	2.39	0.52
1:O:53:ASN:CB	1:R:149:SER:HB2	2.39	0.52
1:P:60:ASN:HA	1:P:83:VAL:O	2.09	0.52
1:Q:15:ILE:HD11	1:R:6:LEU:CD2	2.23	0.52
1:R:24:TYR:O	1:R:28:THR:CB	2.56	0.52
1:B:7:MET:CG	1:F:34:SER:HB3	2.40	0.52
1:B:34:SER:HB3	1:L:7:MET:CG	2.39	0.52
1:B:53:ASN:CB	1:K:149:SER:HB2	2.39	0.52
1:C:7:MET:CG	1:G:34:SER:HB3	2.40	0.52
1:D:7:MET:CG	1:H:34:SER:HB3	2.40	0.52
1:E:10:ILE:CG1	1:I:38:LEU:CA	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:6:LEU:HD11	1:G:16:LEU:CA	2.17	0.52
1:K:53:ASN:CB	1:N:149:SER:HB2	2.39	0.52
1:K:60:ASN:HA	1:K:83:VAL:O	2.09	0.52
1:M:15:ILE:HD11	1:N:6:LEU:CD2	2.23	0.52
1:A:6:LEU:CD2	1:B:15:ILE:HD11	2.23	0.52
1:A:7:MET:CG	1:E:34:SER:HB3	2.40	0.52
1:C:10:ILE:O	1:G:41:GLU:CD	2.52	0.52
1:E:10:ILE:O	1:I:41:GLU:CD	2.52	0.52
1:F:26:ASP:N	1:F:26:ASP:C	2.63	0.52
1:J:101:ILE:O	1:J:104:LYS:HB2	2.09	0.52
1:K:25:GLN:O	1:K:26:ASP:HA	2.10	0.52
1:L:8:ILE:HD13	1:M:1:MEA:CE2	2.27	0.52
1:M:39:LEU:HD22	1:M:73:ILE:HG22	1.90	0.52
1:N:16:LEU:CB	1:O:6:LEU:CD1	2.67	0.52
1:N:98:ASN:HB3	1:N:101:ILE:HG12	1.90	0.52
1:O:60:ASN:HA	1:O:83:VAL:O	2.09	0.52
1:A:60:ASN:HA	1:A:83:VAL:O	2.09	0.52
1:C:15:ILE:CG2	1:F:76:LYS:HZ3	2.22	0.52
1:C:41:GLU:CD	1:K:10:ILE:O	2.52	0.52
1:D:101:ILE:O	1:D:104:LYS:HB2	2.09	0.52
1:E:16:LEU:HD12	1:H:38:LEU:HG	1.92	0.52
1:F:24:TYR:O	1:F:28:THR:CB	2.56	0.52
1:H:60:ASN:HA	1:H:83:VAL:O	2.09	0.52
1:J:39:LEU:HD22	1:J:73:ILE:HG22	1.90	0.52
1:K:26:ASP:N	1:K:26:ASP:CB	2.63	0.52
1:L:117:VAL:C	1:P:21:LEU:HG	2.19	0.52
1:M:25:GLN:O	1:M:26:ASP:HA	2.10	0.52
1:N:25:GLN:O	1:N:26:ASP:HA	2.10	0.52
1:P:98:ASN:HB3	1:P:101:ILE:HG12	1.90	0.52
1:Q:101:ILE:O	1:Q:104:LYS:HB2	2.09	0.52
1:A:16:LEU:HD12	1:D:38:LEU:HG	1.92	0.52
1:D:60:ASN:HA	1:D:83:VAL:O	2.09	0.52
1:E:7:MET:CG	1:I:34:SER:HB3	2.40	0.52
1:E:98:ASN:HB3	1:E:101:ILE:HG12	1.90	0.52
1:F:98:ASN:HB3	1:F:101:ILE:HG12	1.90	0.52
1:L:98:ASN:HB3	1:L:101:ILE:HG12	1.90	0.52
1:M:38:LEU:HG	1:P:16:LEU:HD12	1.92	0.52
1:Q:25:GLN:O	1:Q:26:ASP:HA	2.10	0.52
1:Q:98:ASN:HB3	1:Q:101:ILE:HG12	1.90	0.52
1:A:1:MEA:HD2	1:B:4:ILE:HG12	1.92	0.52
1:A:38:LEU:HG	1:L:16:LEU:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:HD11	1:C:15:ILE:C	2.32	0.52
1:B:26:ASP:N	1:B:26:ASP:C	2.63	0.52
1:G:101:ILE:O	1:G:104:LYS:HB2	2.09	0.52
1:I:98:ASN:HB3	1:I:101:ILE:HG12	1.90	0.52
1:J:60:ASN:HA	1:J:83:VAL:O	2.09	0.52
1:L:4:ILE:HG12	1:M:1:MEA:HD2	1.92	0.52
1:N:52:LEU:CG	1:R:25:GLN:CD	2.81	0.52
1:N:76:LYS:HZ3	1:Q:15:ILE:HG21	1.71	0.52
1:O:4:ILE:HG12	1:P:1:MEA:HD2	1.92	0.52
1:P:25:GLN:O	1:P:26:ASP:HA	2.10	0.52
1:C:38:LEU:CA	1:K:10:ILE:CG1	2.58	0.52
1:E:21:LEU:HG	1:I:117:VAL:C	2.19	0.52
1:F:1:MEA:CD2	1:G:8:ILE:HD13	2.26	0.52
1:L:41:GLU:CD	1:P:10:ILE:O	2.52	0.52
1:M:101:ILE:O	1:M:104:LYS:HB2	2.09	0.52
1:P:4:ILE:HG12	1:Q:1:MEA:HD2	1.92	0.52
1:R:25:GLN:O	1:R:26:ASP:HA	2.10	0.52
1:R:101:ILE:O	1:R:104:LYS:HB2	2.09	0.52
1:B:16:LEU:HD12	1:E:38:LEU:HG	1.92	0.52
1:B:149:SER:CB	1:E:53:ASN:CB	2.88	0.52
1:E:25:GLN:CD	1:I:52:LEU:CG	2.81	0.52
1:J:26:ASP:N	1:J:26:ASP:C	2.63	0.52
1:K:101:ILE:O	1:K:104:LYS:HB2	2.09	0.52
1:L:52:LEU:CG	1:P:25:GLN:CD	2.81	0.52
1:N:101:ILE:O	1:N:104:LYS:HB2	2.09	0.52
1:R:60:ASN:HA	1:R:83:VAL:O	2.09	0.52
1:B:25:GLN:O	1:B:26:ASP:HA	2.10	0.52
1:B:98:ASN:HB3	1:B:101:ILE:HG12	1.90	0.52
1:C:101:ILE:O	1:C:104:LYS:HB2	2.09	0.52
1:D:1:MEA:HD2	1:E:4:ILE:HG12	1.92	0.52
1:E:1:MEA:HD2	1:F:4:ILE:HG12	1.92	0.52
1:F:25:GLN:O	1:F:26:ASP:HA	2.10	0.52
1:G:1:MEA:HD2	1:H:4:ILE:HG12	1.92	0.52
1:G:98:ASN:HB3	1:G:101:ILE:HG12	1.90	0.52
1:H:1:MEA:HD2	1:I:4:ILE:HG12	1.92	0.52
1:H:98:ASN:HB3	1:H:101:ILE:HG12	1.90	0.52
1:J:25:GLN:O	1:J:26:ASP:HA	2.10	0.52
1:K:4:ILE:HG12	1:L:1:MEA:HD2	1.92	0.52
1:K:52:LEU:CG	1:O:25:GLN:CD	2.81	0.52
1:M:39:LEU:HD13	1:M:78:VAL:HG11	1.92	0.52
1:N:60:ASN:HA	1:N:83:VAL:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:101:ILE:O	1:P:104:LYS:HB2	2.09	0.52
1:Q:39:LEU:HD22	1:Q:73:ILE:HG22	1.90	0.52
1:A:39:LEU:HD13	1:A:78:VAL:HG11	1.93	0.51
1:A:53:ASN:HB3	1:L:149:SER:HB2	1.91	0.51
1:C:10:ILE:HD12	1:G:38:LEU:CD1	2.26	0.51
1:C:25:GLN:O	1:C:26:ASP:HA	2.10	0.51
1:I:25:GLN:O	1:I:26:ASP:HA	2.10	0.51
1:J:38:LEU:HG	1:M:16:LEU:HD12	1.92	0.51
1:L:26:ASP:N	1:L:26:ASP:C	2.63	0.51
1:P:26:ASP:N	1:P:26:ASP:C	2.63	0.51
1:P:39:LEU:HD13	1:P:78:VAL:HG11	1.92	0.51
1:C:10:ILE:HG13	1:G:41:GLU:CG	2.41	0.51
1:H:39:LEU:HD13	1:H:78:VAL:HG11	1.93	0.51
1:L:38:LEU:CD1	1:P:10:ILE:HD12	2.26	0.51
1:O:25:GLN:O	1:O:26:ASP:HA	2.10	0.51
1:A:4:ILE:HG12	1:J:1:MEA:HD2	1.92	0.51
1:B:10:ILE:HG13	1:F:41:GLU:CG	2.41	0.51
1:F:101:ILE:O	1:F:104:LYS:HB2	2.09	0.51
1:J:41:GLU:CG	1:N:10:ILE:HG13	2.41	0.51
1:M:15:ILE:C	1:N:6:LEU:HD11	2.32	0.51
1:N:41:GLU:CG	1:R:10:ILE:HG13	2.41	0.51
1:Q:16:LEU:CD2	1:R:9:VAL:HB	2.39	0.51
1:A:16:LEU:CD2	1:J:9:VAL:HB	2.39	0.51
1:A:41:GLU:CG	1:M:10:ILE:HG13	2.40	0.51
1:B:41:GLU:CG	1:L:10:ILE:HG13	2.41	0.51
1:D:39:LEU:HD13	1:D:78:VAL:HG11	1.93	0.51
1:H:25:GLN:O	1:H:26:ASP:HA	2.10	0.51
1:I:101:ILE:O	1:I:104:LYS:HB2	2.09	0.51
1:J:15:ILE:HD11	1:K:6:LEU:CD2	2.23	0.51
1:L:38:LEU:HG	1:O:16:LEU:HD12	1.92	0.51
1:A:149:SER:CB	1:D:53:ASN:CB	2.88	0.51
1:B:1:MEA:HD2	1:C:4:ILE:HG12	1.92	0.51
1:C:149:SER:CB	1:F:53:ASN:CB	2.88	0.51
1:E:25:GLN:O	1:E:26:ASP:HA	2.10	0.51
1:M:15:ILE:CG1	1:N:6:LEU:CD2	2.76	0.51
1:O:12:ILE:CD1	1:P:5:GLU:CA	2.73	0.51
1:O:39:LEU:HD13	1:O:78:VAL:HG11	1.92	0.51
1:A:25:GLN:CD	1:E:52:LEU:CG	2.81	0.51
1:B:39:LEU:HD13	1:B:78:VAL:HG11	1.92	0.51
1:D:10:ILE:HG13	1:H:41:GLU:CG	2.41	0.51
1:D:16:LEU:HD12	1:G:38:LEU:HG	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:16:LEU:HD12	1:I:38:LEU:HG	1.92	0.51
1:K:41:GLU:CG	1:O:10:ILE:HG13	2.41	0.51
1:A:65:GLY:O	1:L:145:LYS:HE3	2.11	0.51
1:C:41:GLU:CG	1:K:10:ILE:HG13	2.41	0.51
1:C:98:ASN:HB3	1:C:101:ILE:HG12	1.90	0.51
1:L:53:ASN:CB	1:O:149:SER:CB	2.88	0.51
1:M:53:ASN:CB	1:P:149:SER:CB	2.88	0.51
1:N:39:LEU:HD13	1:N:78:VAL:HG11	1.92	0.51
1:A:25:GLN:O	1:A:26:ASP:HA	2.10	0.51
1:A:52:LEU:CD2	1:M:25:GLN:NE2	2.48	0.51
1:C:1:MEA:HD2	1:D:4:ILE:HG12	1.92	0.51
1:C:53:ASN:HB3	1:J:149:SER:HB2	1.91	0.51
1:D:25:GLN:O	1:D:26:ASP:HA	2.10	0.51
1:E:10:ILE:HG13	1:I:41:GLU:CG	2.41	0.51
1:G:26:ASP:N	1:G:26:ASP:C	2.63	0.51
1:L:65:GLY:O	1:O:145:LYS:HE3	2.11	0.51
1:M:4:ILE:HG12	1:N:1:MEA:HD2	1.92	0.51
1:R:90:ALA:O	1:R:105:LYS:HB2	2.11	0.51
1:B:52:LEU:CG	1:L:25:GLN:CD	2.81	0.51
1:E:5:GLU:CA	1:F:12:ILE:CD1	2.73	0.51
1:E:37:ILE:O	1:E:41:GLU:HG3	2.11	0.51
1:F:90:ALA:O	1:F:105:LYS:HB2	2.11	0.51
1:J:15:ILE:CG1	1:K:6:LEU:CD2	2.76	0.51
1:K:38:LEU:HG	1:N:16:LEU:HD12	1.92	0.51
1:K:90:ALA:O	1:K:105:LYS:HB2	2.11	0.51
1:N:16:LEU:CA	1:O:6:LEU:HD11	2.17	0.51
1:N:38:LEU:HG	1:Q:16:LEU:HD12	1.92	0.51
1:N:53:ASN:HB3	1:Q:149:SER:HB2	1.91	0.51
1:A:10:ILE:HG13	1:E:41:GLU:CG	2.41	0.51
1:A:37:ILE:O	1:A:41:GLU:HG3	2.11	0.51
1:B:53:ASN:HB3	1:K:149:SER:HB2	1.91	0.51
1:C:37:ILE:O	1:C:41:GLU:HG3	2.11	0.51
1:F:1:MEA:HD2	1:G:4:ILE:HG12	1.92	0.51
1:I:37:ILE:O	1:I:41:GLU:HG3	2.11	0.51
1:I:39:LEU:HD13	1:I:78:VAL:HG11	1.93	0.51
1:J:37:ILE:O	1:J:41:GLU:HG3	2.11	0.51
1:J:90:ALA:O	1:J:105:LYS:HB2	2.11	0.51
1:M:37:ILE:O	1:M:41:GLU:HG3	2.11	0.51
1:M:41:GLU:CG	1:Q:10:ILE:HG13	2.41	0.51
1:O:65:GLY:O	1:R:145:LYS:HE3	2.11	0.51
1:A:1:MEA:CE2	1:B:8:ILE:HD13	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:GLY:O	1:K:145:LYS:HE3	2.11	0.50
1:B:90:ALA:O	1:B:105:LYS:HB2	2.11	0.50
1:C:38:LEU:HG	1:J:16:LEU:HD12	1.92	0.50
1:E:149:SER:HB2	1:H:53:ASN:HB3	1.91	0.50
1:G:37:ILE:O	1:G:41:GLU:HG3	2.11	0.50
1:G:90:ALA:O	1:G:105:LYS:HB2	2.11	0.50
1:N:4:ILE:HG12	1:O:1:MEA:HD2	1.92	0.50
1:O:38:LEU:HG	1:R:16:LEU:HD12	1.92	0.50
1:P:16:LEU:CD2	1:Q:9:VAL:HB	2.39	0.50
1:Q:4:ILE:HG12	1:R:1:MEA:HD2	1.92	0.50
1:B:145:LYS:HE3	1:E:65:GLY:O	2.11	0.50
1:C:16:LEU:HD12	1:F:38:LEU:HG	1.92	0.50
1:D:37:ILE:O	1:D:41:GLU:HG3	2.11	0.50
1:E:98:ASN:ND2	1:E:100:GLU:HG2	2.27	0.50
1:G:6:LEU:CD2	1:H:15:ILE:HD11	2.23	0.50
1:G:25:GLN:O	1:G:26:ASP:HA	2.10	0.50
1:J:53:ASN:CB	1:M:149:SER:CB	2.88	0.50
1:L:25:GLN:O	1:L:26:ASP:HA	2.10	0.50
1:L:98:ASN:ND2	1:L:100:GLU:HG2	2.27	0.50
1:M:26:ASP:N	1:M:26:ASP:C	2.63	0.50
1:N:90:ALA:O	1:N:105:LYS:HB2	2.11	0.50
1:O:90:ALA:O	1:O:105:LYS:HB2	2.11	0.50
1:A:145:LYS:HE3	1:D:65:GLY:O	2.11	0.50
1:B:38:LEU:HG	1:K:16:LEU:HD12	1.92	0.50
1:B:98:ASN:ND2	1:B:100:GLU:HG2	2.27	0.50
1:C:39:LEU:HD13	1:C:78:VAL:HG11	1.93	0.50
1:D:14:GLY:C	1:H:44:LYS:HZ1	2.19	0.50
1:E:39:LEU:HD13	1:E:78:VAL:HG11	1.93	0.50
1:F:37:ILE:O	1:F:41:GLU:HG3	2.11	0.50
1:H:98:ASN:ND2	1:H:100:GLU:HG2	2.27	0.50
1:J:4:ILE:HG12	1:K:1:MEA:HD2	1.92	0.50
1:K:53:ASN:CB	1:N:149:SER:CB	2.88	0.50
1:L:41:GLU:CG	1:P:10:ILE:HG13	2.41	0.50
1:M:65:GLY:O	1:P:145:LYS:HE3	2.11	0.50
1:O:37:ILE:O	1:O:41:GLU:HG3	2.11	0.50
1:P:98:ASN:ND2	1:P:100:GLU:HG2	2.27	0.50
1:Q:90:ALA:O	1:Q:105:LYS:HB2	2.11	0.50
1:R:37:ILE:O	1:R:41:GLU:HG3	2.11	0.50
1:D:41:GLU:CG	1:J:10:ILE:HG13	2.41	0.50
1:F:145:LYS:HE3	1:I:65:GLY:O	2.11	0.50
1:I:90:ALA:O	1:I:105:LYS:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:12:ILE:CD1	1:L:5:GLU:CA	2.73	0.50
1:K:37:ILE:O	1:K:41:GLU:HG3	2.11	0.50
1:L:15:ILE:HD11	1:M:6:LEU:CD2	2.23	0.50
1:M:98:ASN:ND2	1:M:100:GLU:HG2	2.27	0.50
1:P:37:ILE:O	1:P:41:GLU:HG3	2.11	0.50
1:Q:39:LEU:HD13	1:Q:78:VAL:HG11	1.92	0.50
1:B:44:LYS:HE3	1:B:119:TRP:CG	2.47	0.50
1:C:9:VAL:HB	1:D:16:LEU:CD2	2.39	0.50
1:C:53:ASN:CB	1:J:149:SER:CB	2.88	0.50
1:D:44:LYS:HE3	1:D:119:TRP:CG	2.47	0.50
1:E:44:LYS:HE3	1:E:119:TRP:CG	2.47	0.50
1:G:39:LEU:HD13	1:G:78:VAL:HG11	1.93	0.50
1:I:41:GLU:C	1:I:43:GLN:H	2.20	0.50
1:N:15:ILE:CG1	1:O:6:LEU:CD2	2.76	0.50
1:F:41:GLU:C	1:F:43:GLN:H	2.20	0.50
1:G:98:ASN:ND2	1:G:100:GLU:HG2	2.27	0.50
1:K:41:GLU:C	1:K:43:GLN:H	2.20	0.50
1:K:88:VAL:HG13	1:K:108:LEU:HB2	1.94	0.50
1:K:111:ARG:HG3	1:K:131:ASP:OD1	2.12	0.50
1:Q:37:ILE:O	1:Q:41:GLU:HG3	2.11	0.50
1:Q:44:LYS:HE3	1:Q:119:TRP:CG	2.47	0.50
1:A:49:GLU:HA	1:A:49:GLU:OE2	2.12	0.50
1:B:21:LEU:HG	1:F:117:VAL:C	2.19	0.50
1:C:6:LEU:CD2	1:D:15:ILE:HD11	2.23	0.50
1:D:61:ASN:O	1:D:66:VAL:HG22	2.12	0.50
1:D:90:ALA:O	1:D:105:LYS:HB2	2.11	0.50
1:D:113:GLU:O	1:D:114:ASN:CB	2.60	0.50
1:E:40:ALA:CB	1:E:108:LEU:HD22	2.42	0.50
1:F:6:LEU:CD2	1:G:15:ILE:HD11	2.23	0.50
1:F:111:ARG:HG3	1:F:131:ASP:OD1	2.12	0.50
1:I:98:ASN:ND2	1:I:100:GLU:HG2	2.27	0.50
1:J:39:LEU:HD13	1:J:78:VAL:HG11	1.92	0.50
1:K:65:GLY:O	1:N:145:LYS:HE3	2.11	0.50
1:L:37:ILE:O	1:L:41:GLU:HG3	2.11	0.50
1:L:39:LEU:HD13	1:L:78:VAL:HG11	1.92	0.50
1:L:40:ALA:CB	1:L:108:LEU:HD22	2.42	0.50
1:L:88:VAL:HG13	1:L:108:LEU:HB2	1.94	0.50
1:L:111:ARG:HG3	1:L:131:ASP:OD1	2.12	0.50
1:M:49:GLU:HA	1:M:49:GLU:OE2	2.12	0.50
1:O:88:VAL:HG13	1:O:108:LEU:HB2	1.94	0.50
1:P:44:LYS:HE3	1:P:119:TRP:CG	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ALA:CB	1:A:108:LEU:HD22	2.41	0.50
1:A:98:ASN:ND2	1:A:100:GLU:HG2	2.27	0.50
1:B:149:SER:HG	1:E:53:ASN:HB3	1.72	0.50
1:C:90:ALA:O	1:C:105:LYS:HB2	2.11	0.50
1:E:61:ASN:O	1:E:66:VAL:HG22	2.12	0.50
1:E:145:LYS:HE3	1:H:65:GLY:O	2.11	0.50
1:F:61:ASN:O	1:F:66:VAL:HG22	2.12	0.50
1:F:98:ASN:ND2	1:F:100:GLU:HG2	2.27	0.50
1:H:44:LYS:HE3	1:H:119:TRP:CG	2.47	0.50
1:H:113:GLU:O	1:H:114:ASN:CB	2.60	0.50
1:I:88:VAL:HG13	1:I:108:LEU:HB2	1.94	0.50
1:I:111:ARG:HG3	1:I:131:ASP:OD1	2.12	0.50
1:J:65:GLY:O	1:M:145:LYS:HE3	2.11	0.50
1:J:98:ASN:ND2	1:J:100:GLU:HG2	2.27	0.50
1:J:113:GLU:O	1:J:114:ASN:CB	2.60	0.50
1:M:113:GLU:O	1:M:114:ASN:CB	2.60	0.50
1:N:37:ILE:O	1:N:41:GLU:HG3	2.11	0.50
1:N:41:GLU:C	1:N:43:GLN:H	2.20	0.50
1:P:40:ALA:CB	1:P:108:LEU:HD22	2.42	0.50
1:R:111:ARG:HG3	1:R:131:ASP:OD1	2.12	0.50
1:A:113:GLU:O	1:A:114:ASN:CB	2.60	0.50
1:B:15:ILE:HG22	1:E:76:LYS:HE2	1.72	0.50
1:B:37:ILE:O	1:B:41:GLU:HG3	2.11	0.50
1:B:41:GLU:C	1:B:43:GLN:H	2.20	0.50
1:B:88:VAL:HG13	1:B:108:LEU:HB2	1.94	0.50
1:B:111:ARG:HG3	1:B:131:ASP:OD1	2.12	0.50
1:C:41:GLU:C	1:C:43:GLN:H	2.20	0.50
1:E:88:VAL:HG13	1:E:108:LEU:HB2	1.94	0.50
1:F:39:LEU:HD13	1:F:78:VAL:HG11	1.93	0.50
1:F:88:VAL:HG13	1:F:108:LEU:HB2	1.94	0.50
1:K:61:ASN:O	1:K:66:VAL:HG22	2.12	0.50
1:L:90:ALA:O	1:L:105:LYS:HB2	2.11	0.50
1:M:44:LYS:HE3	1:M:119:TRP:CG	2.47	0.50
1:O:111:ARG:HG3	1:O:131:ASP:OD1	2.12	0.50
1:P:88:VAL:HG13	1:P:108:LEU:HB2	1.94	0.50
1:Q:113:GLU:O	1:Q:114:ASN:CB	2.60	0.50
1:B:61:ASN:O	1:B:66:VAL:HG22	2.12	0.49
1:C:61:ASN:O	1:C:66:VAL:HG22	2.12	0.49
1:C:145:LYS:HE3	1:F:65:GLY:O	2.11	0.49
1:D:98:ASN:ND2	1:D:100:GLU:HG2	2.27	0.49
1:E:9:VAL:HB	1:F:16:LEU:CD2	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:111:ARG:HG3	1:E:131:ASP:OD1	2.12	0.49
1:E:149:SER:CB	1:H:53:ASN:CB	2.88	0.49
1:F:5:GLU:CA	1:G:12:ILE:CD1	2.73	0.49
1:F:149:SER:HB2	1:I:53:ASN:HB3	1.91	0.49
1:G:44:LYS:HE3	1:G:119:TRP:CG	2.47	0.49
1:G:111:ARG:HG3	1:G:131:ASP:OD1	2.12	0.49
1:I:40:ALA:CB	1:I:108:LEU:HD22	2.42	0.49
1:J:44:LYS:HE3	1:J:119:TRP:CG	2.47	0.49
1:J:111:ARG:HG3	1:J:131:ASP:OD1	2.12	0.49
1:K:98:ASN:ND2	1:K:100:GLU:HG2	2.27	0.49
1:O:61:ASN:O	1:O:66:VAL:HG22	2.12	0.49
1:P:137:LYS:O	1:P:137:LYS:HG2	2.12	0.49
1:Q:98:ASN:ND2	1:Q:100:GLU:HG2	2.27	0.49
1:D:40:ALA:CB	1:D:108:LEU:HD22	2.42	0.49
1:D:49:GLU:HA	1:D:49:GLU:OE2	2.12	0.49
1:D:145:LYS:HE3	1:G:65:GLY:O	2.11	0.49
1:E:14:GLY:C	1:I:44:LYS:HZ1	2.19	0.49
1:E:41:GLU:C	1:E:43:GLN:H	2.20	0.49
1:E:149:SER:HG	1:H:53:ASN:HB3	1.71	0.49
1:H:90:ALA:O	1:H:105:LYS:HB2	2.11	0.49
1:J:49:GLU:HA	1:J:49:GLU:OE2	2.12	0.49
1:K:117:VAL:C	1:O:21:LEU:HG	2.19	0.49
1:M:61:ASN:O	1:M:66:VAL:HG22	2.12	0.49
1:P:61:ASN:O	1:P:66:VAL:HG22	2.12	0.49
1:P:71:THR:HG22	1:P:71:THR:O	2.13	0.49
1:Q:40:ALA:CB	1:Q:108:LEU:HD22	2.42	0.49
1:Q:49:GLU:OE2	1:Q:49:GLU:HA	2.12	0.49
1:R:39:LEU:HD13	1:R:78:VAL:HG11	1.92	0.49
1:A:44:LYS:HE3	1:A:119:TRP:CG	2.47	0.49
1:B:38:LEU:CD1	1:L:10:ILE:HD12	2.26	0.49
1:B:40:ALA:CB	1:B:108:LEU:HD22	2.42	0.49
1:C:6:LEU:CD2	1:D:15:ILE:CG1	2.76	0.49
1:C:88:VAL:HG13	1:C:108:LEU:HB2	1.94	0.49
1:H:37:ILE:O	1:H:41:GLU:HG3	2.11	0.49
1:H:40:ALA:CB	1:H:108:LEU:HD22	2.42	0.49
1:I:44:LYS:HE3	1:I:119:TRP:CG	2.47	0.49
1:L:137:LYS:HG2	1:L:137:LYS:O	2.12	0.49
1:M:71:THR:HG22	1:M:71:THR:O	2.13	0.49
1:M:90:ALA:O	1:M:105:LYS:HB2	2.11	0.49
1:N:61:ASN:O	1:N:66:VAL:HG22	2.12	0.49
1:N:111:ARG:HG3	1:N:131:ASP:OD1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:8:ILE:HD13	1:R:1:MEA:CD2	2.26	0.49
1:Q:71:THR:O	1:Q:71:THR:HG22	2.13	0.49
1:Q:111:ARG:HG3	1:Q:131:ASP:OD1	2.12	0.49
1:A:9:VAL:HB	1:B:16:LEU:CD2	2.39	0.49
1:A:88:VAL:HG13	1:A:108:LEU:HB2	1.94	0.49
1:B:113:GLU:O	1:B:114:ASN:CB	2.60	0.49
1:H:9:VAL:HB	1:I:16:LEU:CD2	2.39	0.49
1:I:61:ASN:O	1:I:66:VAL:HG22	2.12	0.49
1:I:137:LYS:HG2	1:I:137:LYS:O	2.12	0.49
1:K:16:LEU:CD2	1:L:9:VAL:HB	2.39	0.49
1:K:113:GLU:O	1:K:114:ASN:CB	2.60	0.49
1:L:61:ASN:O	1:L:66:VAL:HG22	2.12	0.49
1:M:40:ALA:CB	1:M:108:LEU:HD22	2.41	0.49
1:N:71:THR:O	1:N:71:THR:HG22	2.13	0.49
1:N:98:ASN:ND2	1:N:100:GLU:HG2	2.27	0.49
1:N:113:GLU:O	1:N:114:ASN:CB	2.60	0.49
1:O:40:ALA:CB	1:O:108:LEU:HD22	2.42	0.49
1:O:44:LYS:HE3	1:O:119:TRP:CG	2.47	0.49
1:Q:61:ASN:O	1:Q:66:VAL:HG22	2.12	0.49
1:R:61:ASN:O	1:R:66:VAL:HG22	2.13	0.49
1:R:88:VAL:HG13	1:R:108:LEU:HB2	1.94	0.49
1:R:98:ASN:ND2	1:R:100:GLU:HG2	2.27	0.49
2:T:1:DT6:H8B	2:T:2:GLA:H61	1.95	0.49
2:X:1:DT6:H8B	2:X:2:GLA:H61	1.95	0.49
1:A:61:ASN:O	1:A:66:VAL:HG22	2.12	0.49
1:C:40:ALA:CB	1:C:108:LEU:HD22	2.42	0.49
1:E:49:GLU:HA	1:E:49:GLU:OE2	2.12	0.49
1:E:113:GLU:O	1:E:114:ASN:CB	2.60	0.49
1:J:40:ALA:CB	1:J:108:LEU:HD22	2.42	0.49
1:J:71:THR:HG22	1:J:71:THR:O	2.13	0.49
1:J:125:VAL:HG21	1:J:133:VAL:CG2	2.43	0.49
1:K:44:LYS:HE3	1:K:119:TRP:CG	2.47	0.49
1:L:44:LYS:HE3	1:L:119:TRP:CG	2.47	0.49
1:N:44:LYS:HE3	1:N:119:TRP:CG	2.47	0.49
1:O:16:LEU:CD2	1:P:9:VAL:HB	2.39	0.49
1:P:111:ARG:HG3	1:P:131:ASP:OD1	2.12	0.49
1:R:40:ALA:CB	1:R:108:LEU:HD22	2.42	0.49
1:R:41:GLU:C	1:R:43:GLN:H	2.20	0.49
1:A:26:ASP:N	1:A:26:ASP:C	2.63	0.49
1:B:137:LYS:O	1:B:137:LYS:HG2	2.12	0.49
1:C:44:LYS:HE3	1:C:119:TRP:CG	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:65:GLY:O	1:J:145:LYS:HE3	2.11	0.49
1:C:111:ARG:HG3	1:C:131:ASP:OD1	2.12	0.49
1:C:149:SER:HB2	1:F:53:ASN:HB3	1.91	0.49
1:K:38:LEU:O	1:O:10:ILE:HD13	2.13	0.49
1:N:53:ASN:CB	1:Q:149:SER:CB	2.88	0.49
1:O:98:ASN:ND2	1:O:100:GLU:HG2	2.27	0.49
1:P:49:GLU:HA	1:P:49:GLU:OE2	2.12	0.49
1:B:145:LYS:HB3	1:E:65:GLY:HA2	1.95	0.49
1:C:71:THR:O	1:C:71:THR:HG22	2.13	0.49
1:C:125:VAL:HG21	1:C:133:VAL:CG2	2.43	0.49
1:D:9:VAL:HB	1:E:16:LEU:CD2	2.39	0.49
1:D:26:ASP:N	1:D:26:ASP:C	2.63	0.49
1:D:149:SER:HB2	1:G:53:ASN:HB3	1.91	0.49
1:E:137:LYS:O	1:E:137:LYS:HG2	2.13	0.49
1:F:44:LYS:HE3	1:F:119:TRP:CG	2.47	0.49
1:H:88:VAL:HG13	1:H:108:LEU:HB2	1.94	0.49
1:J:41:GLU:C	1:J:43:GLN:H	2.20	0.49
1:J:61:ASN:O	1:J:66:VAL:HG22	2.12	0.49
1:M:125:VAL:HG21	1:M:133:VAL:CG2	2.43	0.49
1:N:40:ALA:CB	1:N:108:LEU:HD22	2.42	0.49
1:O:53:ASN:HB3	1:R:149:SER:HB2	1.91	0.49
1:C:98:ASN:ND2	1:C:100:GLU:HG2	2.27	0.49
1:E:10:ILE:HD13	1:I:38:LEU:O	2.13	0.49
1:E:145:LYS:HB3	1:H:65:GLY:HA2	1.95	0.49
1:F:145:LYS:HB3	1:I:65:GLY:HA2	1.95	0.49
1:G:88:VAL:HG13	1:G:108:LEU:HB2	1.94	0.49
1:G:125:VAL:HG21	1:G:133:VAL:CG2	2.43	0.49
1:H:1:MEA:CE2	1:I:8:ILE:HD13	2.27	0.49
1:K:39:LEU:HD13	1:K:78:VAL:HG11	1.93	0.49
1:K:40:ALA:CB	1:K:108:LEU:HD22	2.42	0.49
1:L:49:GLU:HA	1:L:49:GLU:OE2	2.12	0.49
1:M:88:VAL:HG13	1:M:108:LEU:HB2	1.94	0.49
1:P:73:ILE:HG22	1:P:73:ILE:O	2.13	0.49
1:P:90:ALA:O	1:P:105:LYS:HB2	2.11	0.49
1:Q:73:ILE:HG22	1:Q:73:ILE:O	2.13	0.49
1:R:44:LYS:HE3	1:R:119:TRP:CG	2.47	0.49
2:U:1:DT6:H8B	2:U:2:GLA:H61	1.95	0.49
2:W:1:DT6:H8B	2:W:2:GLA:H61	1.95	0.49
2:c:1:DT6:H8B	2:c:2:GLA:H61	1.95	0.49
1:A:65:GLY:HA2	1:L:145:LYS:HB3	1.95	0.49
1:A:90:ALA:O	1:A:105:LYS:HB2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ARG:HG3	1:A:131:ASP:OD1	2.12	0.49
1:D:125:VAL:HG21	1:D:133:VAL:CG2	2.43	0.49
1:F:40:ALA:CB	1:F:108:LEU:HD22	2.42	0.49
1:G:113:GLU:O	1:G:114:ASN:CB	2.60	0.49
1:H:49:GLU:HA	1:H:49:GLU:OE2	2.12	0.49
1:M:73:ILE:HG22	1:M:73:ILE:O	2.13	0.49
1:N:44:LYS:HZ1	1:R:14:GLY:HA2	1.59	0.49
1:N:88:VAL:HG13	1:N:108:LEU:HB2	1.94	0.49
1:N:125:VAL:HG21	1:N:133:VAL:CG2	2.43	0.49
1:Q:125:VAL:HG21	1:Q:133:VAL:CG2	2.43	0.49
1:R:12:ILE:HA	1:R:15:ILE:HG12	1.95	0.49
1:R:26:ASP:N	1:R:26:ASP:C	2.63	0.49
2:a:1:DT6:H8B	2:a:2:GLA:H61	1.95	0.49
1:B:65:GLY:HA2	1:K:145:LYS:HB3	1.95	0.49
1:C:12:ILE:HA	1:C:15:ILE:HG12	1.95	0.49
1:D:111:ARG:HG3	1:D:131:ASP:OD1	2.12	0.49
1:G:40:ALA:CB	1:G:108:LEU:HD22	2.42	0.49
1:H:41:GLU:C	1:H:43:GLN:H	2.20	0.49
1:H:137:LYS:O	1:H:137:LYS:HG2	2.12	0.49
1:K:49:GLU:HA	1:K:49:GLU:OE2	2.12	0.49
1:L:65:GLY:HA2	1:O:145:LYS:HB3	1.95	0.49
1:N:49:GLU:OE2	1:N:49:GLU:HA	2.12	0.49
1:O:113:GLU:HB2	1:O:116:SER:O	2.13	0.49
1:Q:88:VAL:HG13	1:Q:108:LEU:HB2	1.94	0.49
1:R:125:VAL:CG2	1:R:133:VAL:HB	2.43	0.49
1:A:71:THR:O	1:A:71:THR:HG22	2.13	0.48
1:A:137:LYS:HG2	1:A:137:LYS:O	2.12	0.48
1:C:38:LEU:O	1:K:10:ILE:HD13	2.13	0.48
1:C:113:GLU:O	1:C:114:ASN:CB	2.60	0.48
1:E:90:ALA:O	1:E:105:LYS:HB2	2.11	0.48
1:F:71:THR:O	1:F:71:THR:HG22	2.13	0.48
1:F:149:SER:CB	1:I:53:ASN:CB	2.88	0.48
1:H:111:ARG:HG3	1:H:131:ASP:OD1	2.12	0.48
1:I:26:ASP:N	1:I:26:ASP:C	2.63	0.48
1:I:71:THR:O	1:I:71:THR:HG22	2.13	0.48
1:I:73:ILE:HG22	1:I:73:ILE:O	2.13	0.48
1:K:12:ILE:HA	1:K:15:ILE:HG12	1.95	0.48
1:K:125:VAL:CG2	1:K:133:VAL:HB	2.43	0.48
1:L:113:GLU:HB2	1:L:116:SER:O	2.13	0.48
1:M:16:LEU:CD2	1:N:9:VAL:HB	2.39	0.48
1:N:12:ILE:HA	1:N:15:ILE:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:73:ILE:HG22	1:N:73:ILE:O	2.13	0.48
1:N:125:VAL:CG2	1:N:133:VAL:HB	2.43	0.48
1:N:137:LYS:HG2	1:N:137:LYS:O	2.12	0.48
1:O:41:GLU:C	1:O:43:GLN:H	2.20	0.48
1:O:65:GLY:HA2	1:R:145:LYS:HB3	1.95	0.48
1:O:125:VAL:CG2	1:O:133:VAL:HB	2.43	0.48
1:P:113:GLU:O	1:P:114:ASN:CB	2.60	0.48
1:P:113:GLU:HB2	1:P:116:SER:O	2.13	0.48
1:A:53:ASN:CB	1:L:149:SER:CB	2.88	0.48
1:C:125:VAL:CG2	1:C:133:VAL:HB	2.44	0.48
1:E:26:ASP:N	1:E:26:ASP:C	2.63	0.48
1:F:12:ILE:HA	1:F:15:ILE:HG12	1.95	0.48
1:F:125:VAL:CG2	1:F:133:VAL:HB	2.44	0.48
1:G:41:GLU:C	1:G:43:GLN:H	2.20	0.48
1:K:44:LYS:HZ1	1:O:14:GLY:HA2	1.62	0.48
1:L:113:GLU:O	1:L:114:ASN:CB	2.60	0.48
1:N:65:GLY:O	1:Q:145:LYS:HE3	2.11	0.48
1:O:137:LYS:HG2	1:O:137:LYS:O	2.12	0.48
2:d:1:DT6:H8B	2:d:2:GLA:H61	1.95	0.48
1:A:113:GLU:HB2	1:A:116:SER:O	2.13	0.48
1:A:145:LYS:HB3	1:D:65:GLY:HA2	1.95	0.48
1:B:9:VAL:HB	1:C:16:LEU:CD2	2.39	0.48
1:B:73:ILE:HG22	1:B:73:ILE:O	2.13	0.48
1:B:125:VAL:CG2	1:B:133:VAL:HB	2.43	0.48
1:D:71:THR:O	1:D:71:THR:HG22	2.13	0.48
1:D:88:VAL:HG13	1:D:108:LEU:HB2	1.94	0.48
1:G:61:ASN:O	1:G:66:VAL:HG22	2.12	0.48
1:H:61:ASN:O	1:H:66:VAL:HG22	2.12	0.48
1:I:113:GLU:O	1:I:114:ASN:CB	2.60	0.48
1:J:117:VAL:C	1:N:21:LEU:HG	2.19	0.48
1:K:53:ASN:HB3	1:N:149:SER:HB2	1.91	0.48
1:K:71:THR:HG22	1:K:71:THR:O	2.13	0.48
1:L:73:ILE:HG22	1:L:73:ILE:O	2.13	0.48
1:M:111:ARG:HG3	1:M:131:ASP:OD1	2.12	0.48
1:R:113:GLU:HB2	1:R:116:SER:O	2.13	0.48
2:f:1:DT6:H8B	2:f:2:GLA:H61	1.95	0.48
2:g:1:DT6:H8B	2:g:2:GLA:H61	1.95	0.48
1:A:14:GLY:C	1:E:44:LYS:HZ1	2.21	0.48
1:A:73:ILE:HG22	1:A:73:ILE:O	2.13	0.48
1:A:149:SER:HB2	1:D:53:ASN:HB3	1.91	0.48
1:B:49:GLU:HA	1:B:49:GLU:OE2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:145:LYS:HB3	1:F:65:GLY:HA2	1.95	0.48
1:D:38:LEU:CD1	1:J:10:ILE:HD12	2.26	0.48
1:G:12:ILE:HA	1:G:15:ILE:HG12	1.95	0.48
1:G:71:THR:O	1:G:71:THR:HG22	2.13	0.48
1:J:73:ILE:HG22	1:J:73:ILE:O	2.13	0.48
1:J:88:VAL:HG13	1:J:108:LEU:HB2	1.94	0.48
1:O:12:ILE:HA	1:O:15:ILE:HG12	1.95	0.48
1:P:125:VAL:HG21	1:P:133:VAL:CG2	2.43	0.48
1:R:73:ILE:HG22	1:R:73:ILE:O	2.13	0.48
1:R:113:GLU:O	1:R:114:ASN:CB	2.60	0.48
1:A:10:ILE:HD13	1:E:38:LEU:O	2.13	0.48
1:A:41:GLU:C	1:A:43:GLN:H	2.20	0.48
1:A:125:VAL:HG21	1:A:133:VAL:CG2	2.43	0.48
1:C:21:LEU:HG	1:G:117:VAL:C	2.19	0.48
1:D:41:GLU:C	1:D:43:GLN:H	2.20	0.48
1:F:49:GLU:OE2	1:F:49:GLU:HA	2.12	0.48
1:G:125:VAL:CG2	1:G:133:VAL:HB	2.44	0.48
1:G:137:LYS:HG2	1:G:137:LYS:O	2.12	0.48
1:H:71:THR:HG22	1:H:71:THR:O	2.13	0.48
1:H:125:VAL:HG21	1:H:133:VAL:CG2	2.43	0.48
1:I:49:GLU:OE2	1:I:49:GLU:HA	2.12	0.48
1:I:125:VAL:CG2	1:I:133:VAL:HB	2.44	0.48
1:J:125:VAL:CG2	1:J:133:VAL:HB	2.43	0.48
1:M:65:GLY:HA2	1:P:145:LYS:HB3	1.95	0.48
1:N:117:VAL:C	1:R:21:LEU:HG	2.19	0.48
1:Q:125:VAL:CG2	1:Q:133:VAL:HB	2.43	0.48
1:Q:137:LYS:HG2	1:Q:137:LYS:O	2.12	0.48
1:R:137:LYS:O	1:R:137:LYS:HG2	2.12	0.48
1:J:12:ILE:HA	1:J:15:ILE:HG12	1.95	0.48
1:K:113:GLU:HB2	1:K:116:SER:O	2.13	0.48
1:L:41:GLU:C	1:L:43:GLN:H	2.20	0.48
1:L:71:THR:O	1:L:71:THR:HG22	2.13	0.48
1:L:125:VAL:CG2	1:L:133:VAL:HB	2.43	0.48
1:O:49:GLU:HA	1:O:49:GLU:OE2	2.12	0.48
1:O:73:ILE:HG22	1:O:73:ILE:O	2.13	0.48
1:P:15:ILE:HD11	1:Q:6:LEU:CD2	2.23	0.48
1:R:79:LYS:O	1:R:80:GLU:HB3	2.14	0.48
1:A:38:LEU:CD1	1:M:10:ILE:HD12	2.26	0.48
1:B:12:ILE:HA	1:B:15:ILE:HG12	1.95	0.48
1:C:79:LYS:O	1:C:80:GLU:HB3	2.14	0.48
1:D:137:LYS:HG2	1:D:137:LYS:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:71:THR:HG22	1:E:71:THR:O	2.13	0.48
1:F:73:ILE:HG22	1:F:73:ILE:O	2.13	0.48
1:F:113:GLU:O	1:F:114:ASN:CB	2.60	0.48
1:J:137:LYS:O	1:J:137:LYS:HG2	2.12	0.48
1:K:65:GLY:HA2	1:N:145:LYS:HB3	1.95	0.48
1:K:125:VAL:HG21	1:K:133:VAL:CG2	2.43	0.48
1:R:49:GLU:HA	1:R:49:GLU:OE2	2.12	0.48
2:b:1:DT6:H8B	2:b:2:GLA:H61	1.95	0.48
1:A:16:LEU:CB	1:J:6:LEU:CD1	2.67	0.48
1:B:113:GLU:HB2	1:B:116:SER:O	2.13	0.48
1:C:137:LYS:O	1:C:137:LYS:HG2	2.13	0.48
1:E:125:VAL:CG2	1:E:133:VAL:HB	2.44	0.48
1:F:79:LYS:O	1:F:80:GLU:HB3	2.14	0.48
1:F:125:VAL:HG21	1:F:133:VAL:CG2	2.43	0.48
1:H:6:LEU:CD2	1:I:15:ILE:HD11	2.23	0.48
1:I:12:ILE:HA	1:I:15:ILE:HG12	1.95	0.48
1:J:79:LYS:O	1:J:80:GLU:HB3	2.14	0.48
1:K:16:LEU:CA	1:L:6:LEU:HD11	2.17	0.48
1:K:73:ILE:HG22	1:K:73:ILE:O	2.13	0.48
1:M:125:VAL:CG2	1:M:133:VAL:HB	2.43	0.48
1:N:8:ILE:HD13	1:O:1:MEA:CD2	2.26	0.48
1:O:113:GLU:O	1:O:114:ASN:CB	2.60	0.48
1:O:125:VAL:HG21	1:O:133:VAL:CG2	2.43	0.48
1:P:15:ILE:CG1	1:Q:6:LEU:CD2	2.76	0.48
1:P:125:VAL:CG2	1:P:133:VAL:HB	2.43	0.48
1:R:71:THR:O	1:R:71:THR:HG22	2.13	0.48
2:Z:1:DT6:H8B	2:Z:2:GLA:H61	1.95	0.48
2:i:1:DT6:H8B	2:i:2:GLA:H61	1.95	0.48
1:A:125:VAL:CG2	1:A:133:VAL:HB	2.43	0.48
1:B:71:THR:HG22	1:B:71:THR:O	2.13	0.48
1:B:125:VAL:HG21	1:B:133:VAL:CG2	2.43	0.48
1:D:125:VAL:CG2	1:D:133:VAL:HB	2.44	0.48
1:E:73:ILE:HG22	1:E:73:ILE:O	2.13	0.48
1:F:137:LYS:HG2	1:F:137:LYS:O	2.13	0.48
1:G:49:GLU:HA	1:G:49:GLU:OE2	2.12	0.48
1:M:113:GLU:HB2	1:M:116:SER:O	2.13	0.48
1:M:137:LYS:O	1:M:137:LYS:HG2	2.12	0.48
1:O:77:TYR:O	1:O:93:LEU:N	2.36	0.48
1:O:79:LYS:O	1:O:80:GLU:HB3	2.14	0.48
1:B:10:ILE:HD12	1:F:38:LEU:CD1	2.26	0.48
1:C:44:LYS:HZ1	1:K:14:GLY:HA2	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:113:GLU:HB2	1:D:116:SER:O	2.13	0.48
1:H:125:VAL:CG2	1:H:133:VAL:HB	2.44	0.48
1:I:113:GLU:HB2	1:I:116:SER:O	2.13	0.48
1:J:12:ILE:CD1	1:K:5:GLU:CA	2.73	0.48
1:J:65:GLY:HA2	1:M:145:LYS:HB3	1.95	0.48
1:L:16:LEU:CD2	1:M:9:VAL:HB	2.39	0.48
1:L:125:VAL:HG21	1:L:133:VAL:CG2	2.43	0.48
1:P:41:GLU:C	1:P:43:GLN:H	2.20	0.48
1:P:79:LYS:O	1:P:80:GLU:HB3	2.14	0.48
1:Q:12:ILE:HA	1:Q:15:ILE:HG12	1.95	0.48
1:Q:41:GLU:C	1:Q:43:GLN:H	2.20	0.48
1:C:10:ILE:HD13	1:G:38:LEU:O	2.13	0.47
1:C:49:GLU:HA	1:C:49:GLU:OE2	2.12	0.47
1:C:73:ILE:HG22	1:C:73:ILE:O	2.13	0.47
1:D:73:ILE:HG22	1:D:73:ILE:O	2.13	0.47
1:E:113:GLU:HB2	1:E:116:SER:O	2.13	0.47
1:E:125:VAL:HG21	1:E:133:VAL:CG2	2.43	0.47
1:F:97:VAL:HG23	1:F:102:LYS:HE2	1.96	0.47
1:I:125:VAL:HG21	1:I:133:VAL:CG2	2.43	0.47
1:M:41:GLU:C	1:M:43:GLN:H	2.20	0.47
1:R:125:VAL:HG21	1:R:133:VAL:CG2	2.43	0.47
1:B:38:LEU:O	1:L:10:ILE:HD13	2.13	0.47
1:C:65:GLY:HA2	1:J:145:LYS:HB3	1.95	0.47
1:D:91:THR:OG1	1:D:105:LYS:HD2	2.15	0.47
1:D:145:LYS:HB3	1:G:65:GLY:HA2	1.95	0.47
1:G:73:ILE:HG22	1:G:73:ILE:O	2.13	0.47
1:G:113:GLU:HB2	1:G:116:SER:O	2.13	0.47
1:J:53:ASN:HB3	1:M:149:SER:HB2	1.91	0.47
2:j:1:DT6:H8B	2:j:2:GLA:H61	1.95	0.47
1:B:91:THR:OG1	1:B:105:LYS:HD2	2.14	0.47
1:C:25:GLN:CD	1:G:52:LEU:CG	2.81	0.47
1:E:84:LYS:HB2	1:E:84:LYS:HE3	1.69	0.47
1:G:84:LYS:HE3	1:G:84:LYS:HB2	1.69	0.47
1:H:12:ILE:HA	1:H:15:ILE:HG12	1.95	0.47
1:H:113:GLU:HB2	1:H:116:SER:O	2.13	0.47
1:K:91:THR:OG1	1:K:105:LYS:HD2	2.15	0.47
1:K:97:VAL:HG23	1:K:102:LYS:HE2	1.96	0.47
1:L:12:ILE:HA	1:L:15:ILE:HG12	1.95	0.47
1:L:38:LEU:O	1:P:10:ILE:HD13	2.13	0.47
1:L:79:LYS:O	1:L:80:GLU:HB3	2.14	0.47
1:M:53:ASN:HB3	1:P:149:SER:HB2	1.91	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:79:LYS:O	1:M:80:GLU:HB3	2.14	0.47
1:N:38:LEU:O	1:R:10:ILE:HD13	2.13	0.47
1:Q:113:GLU:HB2	1:Q:116:SER:O	2.13	0.47
1:R:91:THR:OG1	1:R:105:LYS:HD2	2.15	0.47
2:S:1:DT6:H8B	2:S:2:GLA:H61	1.95	0.47
1:A:15:ILE:CG1	1:J:6:LEU:CD2	2.76	0.47
1:D:12:ILE:HA	1:D:15:ILE:HG12	1.95	0.47
1:E:12:ILE:HA	1:E:15:ILE:HG12	1.95	0.47
1:F:113:GLU:HB2	1:F:116:SER:O	2.13	0.47
1:H:79:LYS:O	1:H:80:GLU:HB3	2.14	0.47
1:I:79:LYS:O	1:I:80:GLU:HB3	2.14	0.47
1:N:26:ASP:N	1:N:26:ASP:C	2.63	0.47
1:O:91:THR:OG1	1:O:105:LYS:HD2	2.14	0.47
2:V:1:DT6:H8B	2:V:2:GLA:H61	1.95	0.47
1:C:113:GLU:HB2	1:C:116:SER:O	2.13	0.47
1:E:91:THR:OG1	1:E:105:LYS:HD2	2.15	0.47
1:G:91:THR:OG1	1:G:105:LYS:HD2	2.15	0.47
1:I:91:THR:OG1	1:I:105:LYS:HD2	2.15	0.47
1:J:97:VAL:HG23	1:J:102:LYS:HE2	1.96	0.47
1:K:137:LYS:O	1:K:137:LYS:HG2	2.12	0.47
1:L:91:THR:OG1	1:L:105:LYS:HD2	2.15	0.47
1:L:97:VAL:HG23	1:L:102:LYS:HE2	1.96	0.47
1:M:12:ILE:HA	1:M:15:ILE:HG12	1.95	0.47
1:N:16:LEU:CD2	1:O:9:VAL:HB	2.39	0.47
1:N:65:GLY:HA2	1:Q:145:LYS:HB3	1.95	0.47
1:N:113:GLU:HB2	1:N:116:SER:O	2.13	0.47
1:A:12:ILE:HA	1:A:15:ILE:HG12	1.95	0.47
1:A:38:LEU:O	1:M:10:ILE:HD13	2.13	0.47
1:B:5:GLU:CA	1:C:12:ILE:CD1	2.73	0.47
1:B:53:ASN:CB	1:K:149:SER:CB	2.88	0.47
1:F:6:LEU:C	1:G:16:LEU:HD13	2.37	0.47
1:G:97:VAL:HG23	1:G:102:LYS:HE2	1.96	0.47
1:O:26:ASP:N	1:O:26:ASP:C	2.63	0.47
1:A:91:THR:OG1	1:A:105:LYS:HD2	2.15	0.47
1:B:10:ILE:HD13	1:F:38:LEU:O	2.13	0.47
1:B:44:LYS:HZ3	1:L:14:GLY:HA2	1.59	0.47
1:D:6:LEU:CD1	1:E:16:LEU:HB2	2.40	0.47
1:E:97:VAL:HG23	1:E:102:LYS:HE2	1.96	0.47
1:H:91:THR:OG1	1:H:105:LYS:HD2	2.15	0.47
1:H:97:VAL:HG23	1:H:102:LYS:HE2	1.96	0.47
1:J:16:LEU:HD13	1:K:6:LEU:C	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:84:LYS:HE3	1:J:84:LYS:HB2	1.69	0.47
1:J:113:GLU:HB2	1:J:116:SER:O	2.13	0.47
1:K:77:TYR:O	1:K:93:LEU:N	2.36	0.47
1:K:79:LYS:O	1:K:80:GLU:HB3	2.14	0.47
1:L:16:LEU:HB2	1:M:6:LEU:CD1	2.40	0.47
1:M:16:LEU:CA	1:N:6:LEU:HD11	2.17	0.47
1:M:91:THR:OG1	1:M:105:LYS:HD2	2.14	0.47
1:N:91:THR:OG1	1:N:105:LYS:HD2	2.15	0.47
1:O:71:THR:O	1:O:71:THR:HG22	2.12	0.47
1:O:97:VAL:HG23	1:O:102:LYS:HE2	1.96	0.47
1:P:12:ILE:HA	1:P:15:ILE:HG12	1.95	0.47
1:P:91:THR:OG1	1:P:105:LYS:HD2	2.14	0.47
1:Q:97:VAL:HG23	1:Q:102:LYS:HE2	1.96	0.47
2:Y:1:DT6:H8B	2:Y:2:GLA:H61	1.95	0.47
1:A:1:MEA:CZ	1:B:8:ILE:CD1	2.88	0.47
1:A:97:VAL:HG23	1:A:102:LYS:HE2	1.96	0.47
1:F:91:THR:OG1	1:F:105:LYS:HD2	2.15	0.47
1:J:38:LEU:O	1:N:10:ILE:HD13	2.13	0.47
1:N:16:LEU:HD13	1:O:6:LEU:C	2.37	0.47
1:R:97:VAL:HG23	1:R:102:LYS:HE2	1.96	0.47
2:e:1:DT6:H8B	2:e:2:GLA:H61	1.95	0.47
1:B:79:LYS:O	1:B:80:GLU:HB3	2.14	0.47
1:C:38:LEU:CD1	1:K:10:ILE:HD12	2.26	0.47
1:L:77:TYR:O	1:L:93:LEU:N	2.36	0.47
1:M:116:SER:CB	1:Q:22:PRO:N	2.78	0.47
1:D:38:LEU:O	1:J:10:ILE:HD13	2.13	0.47
1:D:79:LYS:O	1:D:80:GLU:HB3	2.14	0.47
1:F:84:LYS:HB2	1:F:84:LYS:HE3	1.69	0.47
1:G:77:TYR:O	1:G:93:LEU:N	2.36	0.47
1:K:49:GLU:OE2	1:K:49:GLU:CA	2.63	0.47
1:M:97:VAL:HG23	1:M:102:LYS:HE2	1.96	0.47
1:O:49:GLU:OE2	1:O:49:GLU:CA	2.63	0.47
1:P:16:LEU:HB2	1:Q:6:LEU:CD1	2.40	0.47
1:Q:16:LEU:HD13	1:R:6:LEU:C	2.37	0.47
2:h:1:DT6:H8B	2:h:2:GLA:H61	1.95	0.47
1:B:6:LEU:CD2	1:C:15:ILE:CG1	2.76	0.46
1:G:1:MEA:CZ	1:H:8:ILE:CD1	2.88	0.46
1:H:3:LEU:HD11	1:I:12:ILE:HA	1.47	0.46
1:H:26:ASP:N	1:H:26:ASP:C	2.63	0.46
1:H:73:ILE:HG22	1:H:73:ILE:O	2.13	0.46
1:N:79:LYS:O	1:N:80:GLU:HB3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:84:LYS:HE3	1:P:84:LYS:HB2	1.69	0.46
1:Q:91:THR:OG1	1:Q:105:LYS:HD2	2.15	0.46
1:R:84:LYS:HE3	1:R:84:LYS:HB2	1.69	0.46
1:A:1:MEA:CD2	1:B:8:ILE:HD13	2.26	0.46
1:A:77:TYR:O	1:A:93:LEU:N	2.36	0.46
1:B:6:LEU:C	1:C:16:LEU:HD13	2.37	0.46
1:C:49:GLU:OE2	1:C:49:GLU:CA	2.64	0.46
1:I:97:VAL:HG23	1:I:102:LYS:HE2	1.96	0.46
1:J:91:THR:OG1	1:J:105:LYS:HD2	2.15	0.46
1:N:116:SER:HA	1:R:21:LEU:HD13	1.21	0.46
1:A:15:ILE:CG2	1:D:76:LYS:HZ3	2.24	0.46
1:A:116:SER:CB	1:M:22:PRO:N	2.78	0.46
1:E:49:GLU:OE2	1:E:49:GLU:CA	2.64	0.46
1:M:38:LEU:O	1:Q:10:ILE:HD13	2.13	0.46
1:P:97:VAL:HG23	1:P:102:LYS:HE2	1.96	0.46
1:A:49:GLU:OE2	1:A:49:GLU:CA	2.63	0.46
1:A:79:LYS:O	1:A:80:GLU:HB3	2.14	0.46
1:B:38:LEU:HA	1:L:10:ILE:CB	2.37	0.46
1:B:97:VAL:HG23	1:B:102:LYS:HE2	1.96	0.46
1:E:79:LYS:O	1:E:80:GLU:HB3	2.14	0.46
1:J:12:ILE:HA	1:K:3:LEU:HD11	1.47	0.46
1:M:16:LEU:HB2	1:N:6:LEU:CD1	2.40	0.46
1:C:77:TYR:O	1:C:93:LEU:N	2.36	0.46
1:C:116:SER:CB	1:K:22:PRO:N	2.78	0.46
1:F:46:ALA:HB1	1:F:64:ALA:O	2.16	0.46
1:G:6:LEU:CD1	1:H:16:LEU:HB2	2.41	0.46
1:G:9:VAL:HB	1:H:16:LEU:CD2	2.39	0.46
1:I:49:GLU:OE2	1:I:49:GLU:CA	2.64	0.46
1:O:46:ALA:HB1	1:O:64:ALA:O	2.16	0.46
1:C:91:THR:OG1	1:C:105:LYS:HD2	2.14	0.46
1:G:79:LYS:O	1:G:80:GLU:HB3	2.14	0.46
1:N:97:VAL:HG23	1:N:102:LYS:HE2	1.96	0.46
1:Q:49:GLU:OE2	1:Q:49:GLU:CA	2.63	0.46
1:A:16:LEU:HB2	1:J:6:LEU:CD1	2.40	0.46
1:B:46:ALA:HB1	1:B:64:ALA:O	2.16	0.46
1:C:38:LEU:HA	1:K:10:ILE:CD1	2.42	0.46
1:D:97:VAL:HG23	1:D:102:LYS:HE2	1.96	0.46
1:G:46:ALA:HB1	1:G:64:ALA:O	2.16	0.46
1:G:49:GLU:OE2	1:G:49:GLU:CA	2.64	0.46
1:J:46:ALA:HB1	1:J:64:ALA:O	2.16	0.46
1:M:49:GLU:OE2	1:M:49:GLU:CA	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:8:ILE:HD13	1:O:1:MEA:CE2	2.27	0.46
1:Q:16:LEU:HB2	1:R:6:LEU:CD1	2.40	0.46
1:Q:79:LYS:O	1:Q:80:GLU:HB3	2.14	0.46
1:Q:84:LYS:HB2	1:Q:84:LYS:HE3	1.69	0.46
1:C:3:LEU:HD11	1:D:12:ILE:HA	1.47	0.46
1:C:22:PRO:N	1:G:116:SER:CB	2.78	0.46
1:D:10:ILE:HD13	1:H:38:LEU:O	2.13	0.46
1:D:46:ALA:HB1	1:D:64:ALA:O	2.16	0.46
1:L:53:ASN:HB3	1:O:149:SER:HB2	1.91	0.46
1:M:112:ARG:HG2	1:M:112:ARG:NH1	2.31	0.46
1:Q:46:ALA:HB1	1:Q:64:ALA:O	2.16	0.46
1:Q:112:ARG:HG2	1:Q:112:ARG:NH1	2.31	0.46
1:C:21:LEU:HD13	1:G:116:SER:HA	1.20	0.46
1:C:97:VAL:HG23	1:C:102:LYS:HE2	1.96	0.46
1:D:6:LEU:CD2	1:E:15:ILE:HD11	2.23	0.46
1:D:112:ARG:HG2	1:D:112:ARG:NH1	2.31	0.46
1:E:6:LEU:CD1	1:F:16:LEU:HB2	2.40	0.46
1:G:6:LEU:CD2	1:H:15:ILE:CG1	2.76	0.46
1:K:46:ALA:HB1	1:K:64:ALA:O	2.16	0.46
1:K:116:SER:HA	1:O:21:LEU:HD13	1.21	0.46
1:M:46:ALA:HB1	1:M:64:ALA:O	2.16	0.46
1:N:46:ALA:HB1	1:N:64:ALA:O	2.16	0.46
1:Q:12:ILE:CD1	1:R:5:GLU:CA	2.73	0.46
1:Q:26:ASP:N	1:Q:26:ASP:C	2.63	0.46
1:B:116:SER:CB	1:L:22:PRO:N	2.78	0.46
1:C:6:LEU:CD1	1:D:16:LEU:HB2	2.40	0.46
1:G:6:LEU:CA	1:H:16:LEU:CD1	2.58	0.46
1:I:46:ALA:HB1	1:I:64:ALA:O	2.16	0.46
1:M:16:LEU:HD13	1:N:6:LEU:C	2.37	0.46
1:R:49:GLU:OE2	1:R:49:GLU:CA	2.64	0.46
1:C:6:LEU:CD1	1:D:16:LEU:CB	2.67	0.45
1:C:6:LEU:C	1:D:16:LEU:HD13	2.37	0.45
1:C:46:ALA:HB1	1:C:64:ALA:O	2.16	0.45
1:H:6:LEU:CD1	1:I:16:LEU:HB2	2.41	0.45
1:J:34:SER:HB3	1:N:7:MET:CB	2.47	0.45
1:J:116:SER:HA	1:N:21:LEU:HD13	1.21	0.45
1:L:38:LEU:HD21	1:P:10:ILE:H	1.57	0.45
1:L:116:SER:CB	1:P:22:PRO:N	2.78	0.45
1:N:12:ILE:CD1	1:O:5:GLU:CA	2.73	0.45
1:N:16:LEU:HB2	1:O:6:LEU:CD1	2.40	0.45
1:O:53:ASN:CB	1:R:149:SER:CB	2.88	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:PRO:N	1:E:116:SER:CB	2.78	0.45
1:B:77:TYR:O	1:B:93:LEU:N	2.36	0.45
1:C:116:SER:HA	1:K:21:LEU:HD13	1.20	0.45
1:F:9:VAL:HB	1:G:16:LEU:CD2	2.39	0.45
1:H:46:ALA:HB1	1:H:64:ALA:O	2.16	0.45
1:H:49:GLU:OE2	1:H:49:GLU:CA	2.64	0.45
1:M:34:SER:HB3	1:Q:7:MET:CB	2.47	0.45
1:O:16:LEU:HB2	1:P:6:LEU:CD1	2.40	0.45
1:C:121:CYS:C	1:C:151:CYS:SG	3.00	0.45
1:D:34:SER:HB3	1:J:7:MET:CB	2.47	0.45
1:D:121:CYS:C	1:D:151:CYS:SG	3.00	0.45
1:D:149:SER:CB	1:G:53:ASN:CB	2.88	0.45
1:G:3:LEU:HD11	1:H:12:ILE:HA	1.47	0.45
1:G:121:CYS:C	1:G:151:CYS:SG	3.00	0.45
1:J:52:LEU:CG	1:N:25:GLN:CD	2.81	0.45
1:J:121:CYS:C	1:J:151:CYS:SG	3.00	0.45
1:K:26:ASP:N	1:K:26:ASP:C	2.63	0.45
1:L:49:GLU:OE2	1:L:49:GLU:CA	2.63	0.45
1:M:121:CYS:C	1:M:151:CYS:SG	3.00	0.45
1:N:49:GLU:OE2	1:N:49:GLU:CA	2.63	0.45
1:O:84:LYS:HE3	1:O:84:LYS:HB2	1.69	0.45
1:P:46:ALA:HB1	1:P:64:ALA:O	2.16	0.45
1:P:49:GLU:OE2	1:P:49:GLU:CA	2.63	0.45
1:A:34:SER:HB3	1:M:7:MET:CB	2.47	0.45
1:A:46:ALA:HB1	1:A:64:ALA:O	2.16	0.45
1:B:121:CYS:C	1:B:151:CYS:SG	3.00	0.45
1:C:7:MET:CB	1:G:34:SER:HB3	2.47	0.45
1:D:84:LYS:HB2	1:D:84:LYS:HE3	1.69	0.45
1:E:9:VAL:HB	1:F:16:LEU:HD11	1.99	0.45
1:G:6:LEU:C	1:H:16:LEU:HD13	2.37	0.45
1:O:121:CYS:C	1:O:151:CYS:SG	3.00	0.45
1:R:121:CYS:C	1:R:151:CYS:SG	3.00	0.45
1:E:77:TYR:O	1:E:93:LEU:N	2.36	0.45
1:H:121:CYS:C	1:H:151:CYS:SG	3.00	0.45
1:I:121:CYS:C	1:I:151:CYS:SG	3.00	0.45
1:L:116:SER:HA	1:P:21:LEU:HD13	1.21	0.45
1:M:52:LEU:CG	1:Q:25:GLN:CD	2.81	0.45
1:N:16:LEU:HD11	1:O:9:VAL:HB	1.99	0.45
1:N:34:SER:HB3	1:R:7:MET:CB	2.47	0.45
1:Q:121:CYS:C	1:Q:151:CYS:SG	3.00	0.45
1:R:46:ALA:HB1	1:R:64:ALA:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:PRO:N	1:F:116:SER:CB	2.78	0.45
1:D:7:MET:CB	1:H:34:SER:HB3	2.47	0.45
1:E:46:ALA:HB1	1:E:64:ALA:O	2.16	0.45
1:G:1:MEA:HD2	1:H:4:ILE:CG1	2.47	0.45
1:K:38:LEU:HA	1:O:10:ILE:CD1	2.42	0.45
1:M:116:SER:HA	1:Q:21:LEU:HD13	1.21	0.45
1:A:121:CYS:C	1:A:151:CYS:SG	3.00	0.45
1:B:21:LEU:HD13	1:F:116:SER:HA	1.20	0.45
1:C:34:SER:HB3	1:K:7:MET:CB	2.47	0.45
1:F:9:VAL:HB	1:G:16:LEU:HD11	1.99	0.45
1:J:16:LEU:HB2	1:K:6:LEU:CD1	2.40	0.45
1:K:15:ILE:CG1	1:L:6:LEU:CD2	2.76	0.45
1:K:16:LEU:HD11	1:L:9:VAL:HB	1.99	0.45
1:L:8:ILE:CD1	1:M:1:MEA:CZ	2.88	0.45
1:M:4:ILE:CG1	1:N:1:MEA:HD2	2.47	0.45
1:A:1:MEA:HD2	1:B:4:ILE:CG1	2.47	0.45
1:A:16:LEU:HD13	1:J:6:LEU:C	2.37	0.45
1:B:9:VAL:HB	1:C:16:LEU:HD11	1.99	0.45
1:B:49:GLU:OE2	1:B:49:GLU:CA	2.63	0.45
1:D:15:ILE:CG2	1:G:76:LYS:HZ3	2.26	0.45
1:F:121:CYS:C	1:F:151:CYS:SG	3.00	0.45
1:H:67:ALA:C	1:H:69:SER:N	2.75	0.45
1:J:67:ALA:C	1:J:69:SER:N	2.75	0.45
1:M:67:ALA:C	1:M:69:SER:N	2.75	0.45
1:N:4:ILE:CG1	1:O:1:MEA:HD2	2.47	0.45
1:O:4:ILE:CG1	1:P:1:MEA:HD2	2.47	0.45
1:A:4:ILE:CG1	1:J:1:MEA:HD2	2.47	0.45
1:A:6:LEU:CD1	1:B:16:LEU:HB2	2.40	0.45
1:A:9:VAL:HB	1:B:16:LEU:HD11	1.99	0.45
1:B:1:MEA:HD2	1:C:4:ILE:CG1	2.47	0.45
1:F:15:ILE:CG2	1:I:76:LYS:HZ3	2.26	0.45
1:H:9:VAL:HB	1:I:16:LEU:HD11	1.99	0.45
1:L:16:LEU:CD1	1:M:6:LEU:CA	2.58	0.45
1:L:121:CYS:C	1:L:151:CYS:SG	3.00	0.45
1:M:12:ILE:HA	1:N:3:LEU:HD11	1.47	0.45
1:N:121:CYS:C	1:N:151:CYS:SG	3.00	0.45
1:O:16:LEU:HD11	1:P:9:VAL:HB	1.99	0.45
1:P:67:ALA:C	1:P:69:SER:N	2.75	0.45
1:Q:16:LEU:CD1	1:R:6:LEU:CA	2.58	0.45
1:Q:16:LEU:HD11	1:R:9:VAL:HB	1.99	0.45
1:Q:67:ALA:C	1:Q:69:SER:N	2.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:MET:CB	1:E:34:SER:HB3	2.47	0.45
1:B:84:LYS:HE3	1:B:84:LYS:HB2	1.69	0.45
1:F:1:MEA:HD2	1:G:4:ILE:CG1	2.47	0.45
1:H:1:MEA:HD2	1:I:4:ILE:CG1	2.47	0.45
1:H:77:TYR:O	1:H:93:LEU:N	2.36	0.45
1:J:16:LEU:HD11	1:K:9:VAL:HB	1.99	0.45
1:J:49:GLU:OE2	1:J:49:GLU:CA	2.63	0.45
1:L:34:SER:HB3	1:P:7:MET:CB	2.47	0.45
1:L:46:ALA:HB1	1:L:64:ALA:O	2.16	0.45
1:P:121:CYS:C	1:P:151:CYS:SG	3.00	0.45
1:C:1:MEA:HD2	1:D:4:ILE:CG1	2.47	0.44
1:D:67:ALA:C	1:D:69:SER:N	2.75	0.44
1:D:77:TYR:O	1:D:93:LEU:N	2.36	0.44
1:E:1:MEA:HD2	1:F:4:ILE:CG1	2.47	0.44
1:E:121:CYS:C	1:E:151:CYS:SG	3.00	0.44
1:G:5:GLU:CA	1:H:12:ILE:CD1	2.73	0.44
1:K:34:SER:HB3	1:O:7:MET:CB	2.47	0.44
1:L:12:ILE:HA	1:M:3:LEU:HD11	1.47	0.44
1:A:16:LEU:CD1	1:J:6:LEU:O	2.66	0.44
1:K:121:CYS:C	1:K:151:CYS:SG	3.00	0.44
1:L:4:ILE:CG1	1:M:1:MEA:HD2	2.47	0.44
1:N:67:ALA:C	1:N:69:SER:N	2.75	0.44
1:N:116:SER:CB	1:R:22:PRO:N	2.78	0.44
1:P:4:ILE:CG1	1:Q:1:MEA:HD2	2.47	0.44
1:A:4:ILE:CD1	1:J:1:MEA:HD2	2.48	0.44
1:A:12:ILE:HA	1:J:3:LEU:HD11	1.47	0.44
1:B:14:GLY:HA2	1:F:44:LYS:HZ3	1.59	0.44
1:J:4:ILE:CG1	1:K:1:MEA:HD2	2.47	0.44
1:K:158:LYS:OXT	1:K:158:LYS:HG2	2.18	0.44
1:L:16:LEU:HD11	1:M:9:VAL:HB	1.99	0.44
1:N:4:ILE:CD1	1:O:1:MEA:HD2	2.48	0.44
1:P:4:ILE:CD1	1:Q:1:MEA:HD2	2.48	0.44
1:R:158:LYS:HG2	1:R:158:LYS:OXT	2.18	0.44
1:B:1:MEA:HD2	1:C:4:ILE:CD1	2.48	0.44
1:B:6:LEU:O	1:C:16:LEU:CD1	2.66	0.44
1:B:34:SER:HB3	1:L:7:MET:CB	2.47	0.44
1:F:158:LYS:OXT	1:F:158:LYS:HG2	2.18	0.44
1:P:8:ILE:CD1	1:Q:1:MEA:CZ	2.88	0.44
1:P:16:LEU:HD13	1:Q:6:LEU:C	2.37	0.44
1:A:6:LEU:O	1:B:16:LEU:CD1	2.66	0.44
1:A:10:ILE:HD12	1:E:38:LEU:CD1	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:MET:CB	1:F:34:SER:HB3	2.47	0.44
1:D:9:VAL:HB	1:E:16:LEU:HD11	1.99	0.44
1:E:10:ILE:CB	1:I:38:LEU:HA	2.37	0.44
1:E:22:PRO:N	1:I:116:SER:CB	2.78	0.44
1:F:1:MEA:HD2	1:G:4:ILE:CD1	2.48	0.44
1:H:6:LEU:CA	1:I:16:LEU:CD1	2.58	0.44
1:I:84:LYS:HB2	1:I:84:LYS:HE3	1.69	0.44
1:J:16:LEU:CD1	1:K:6:LEU:O	2.66	0.44
1:J:116:SER:CB	1:N:22:PRO:N	2.78	0.44
1:K:4:ILE:CG1	1:L:1:MEA:HD2	2.47	0.44
1:K:16:LEU:CD1	1:L:6:LEU:O	2.66	0.44
1:K:116:SER:CB	1:O:22:PRO:N	2.78	0.44
1:L:8:ILE:HD13	1:M:1:MEA:CD2	2.26	0.44
1:M:16:LEU:CD1	1:N:6:LEU:O	2.66	0.44
1:N:12:ILE:HG21	1:O:3:LEU:HA	1.26	0.44
1:O:4:ILE:CD1	1:P:1:MEA:HD2	2.48	0.44
1:Q:12:ILE:O	1:Q:16:LEU:HB2	2.18	0.44
1:A:1:MEA:HD2	1:B:4:ILE:CD1	2.48	0.44
1:D:1:MEA:HD2	1:E:4:ILE:CD1	2.48	0.44
1:D:116:SER:HA	1:J:21:LEU:HD13	1.20	0.44
1:E:6:LEU:O	1:F:16:LEU:CD1	2.66	0.44
1:E:7:MET:CB	1:I:34:SER:HB3	2.47	0.44
1:F:49:GLU:OE2	1:F:49:GLU:CA	2.64	0.44
1:G:1:MEA:HD2	1:H:4:ILE:CD1	2.48	0.44
1:K:8:ILE:CD1	1:L:1:MEA:CZ	2.88	0.44
1:L:15:ILE:CG1	1:M:6:LEU:CD2	2.76	0.44
1:L:16:LEU:CD1	1:M:6:LEU:O	2.66	0.44
1:M:16:LEU:HD11	1:N:9:VAL:HB	1.99	0.44
1:M:84:LYS:HB2	1:M:84:LYS:HE3	1.70	0.44
1:N:112:ARG:NH2	1:N:114:ASN:HA	2.33	0.44
1:O:15:ILE:CG1	1:P:6:LEU:CD2	2.76	0.44
1:C:6:LEU:O	1:D:16:LEU:CD1	2.66	0.44
1:D:6:LEU:O	1:E:16:LEU:CD1	2.66	0.44
1:D:112:ARG:NH2	1:D:114:ASN:HA	2.33	0.44
1:G:6:LEU:O	1:H:16:LEU:CD1	2.66	0.44
1:H:1:MEA:CD2	1:I:8:ILE:HD13	2.26	0.44
1:H:112:ARG:NH2	1:H:114:ASN:HA	2.33	0.44
1:I:12:ILE:O	1:I:16:LEU:HB2	2.18	0.44
1:I:158:LYS:OXT	1:I:158:LYS:HG2	2.18	0.44
1:J:4:ILE:CD1	1:K:1:MEA:HD2	2.48	0.44
1:J:38:LEU:CD1	1:N:10:ILE:HD12	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:112:ARG:NH2	1:J:114:ASN:HA	2.33	0.44
1:K:12:ILE:O	1:K:16:LEU:HB2	2.18	0.44
1:K:16:LEU:HD13	1:L:6:LEU:C	2.37	0.44
1:K:16:LEU:CD1	1:L:6:LEU:CA	2.58	0.44
1:L:4:ILE:CD1	1:M:1:MEA:HD2	2.48	0.44
1:N:16:LEU:CD1	1:O:6:LEU:O	2.66	0.44
1:C:9:VAL:HB	1:D:16:LEU:HD11	1.99	0.44
1:D:1:MEA:HD2	1:E:4:ILE:CG1	2.47	0.44
1:E:6:LEU:C	1:F:16:LEU:HD13	2.37	0.44
1:F:6:LEU:O	1:G:16:LEU:CD1	2.66	0.44
1:J:16:LEU:CD2	1:K:9:VAL:HB	2.39	0.44
1:L:67:ALA:C	1:L:69:SER:N	2.75	0.44
1:M:12:ILE:O	1:M:16:LEU:HB2	2.18	0.44
1:O:16:LEU:CD1	1:P:6:LEU:O	2.66	0.44
1:O:112:ARG:NH2	1:O:114:ASN:HA	2.33	0.44
1:Q:4:ILE:CG1	1:R:1:MEA:HD2	2.47	0.44
1:Q:4:ILE:CD1	1:R:1:MEA:HD2	2.48	0.44
1:A:3:LEU:HD11	1:B:12:ILE:HA	1.47	0.44
1:A:12:ILE:CD1	1:J:5:GLU:CA	2.73	0.44
1:A:76:LYS:HZ3	1:L:15:ILE:CG2	2.27	0.44
1:B:158:LYS:HG2	1:B:158:LYS:OXT	2.18	0.44
1:D:22:PRO:N	1:H:116:SER:CB	2.78	0.44
1:D:116:SER:CB	1:J:22:PRO:N	2.78	0.44
1:D:158:LYS:OXT	1:D:158:LYS:HG2	2.18	0.44
1:E:1:MEA:HD2	1:F:4:ILE:CD1	2.48	0.44
1:F:1:MEA:HD2	1:G:4:ILE:HD13	2.00	0.44
1:G:67:ALA:C	1:G:69:SER:N	2.75	0.44
1:H:1:MEA:CZ	1:I:8:ILE:CD1	2.88	0.44
1:L:112:ARG:NH2	1:L:114:ASN:HA	2.33	0.44
1:O:12:ILE:O	1:O:16:LEU:HB2	2.18	0.44
1:P:16:LEU:HD11	1:Q:9:VAL:HB	1.99	0.44
1:P:112:ARG:NH2	1:P:114:ASN:HA	2.33	0.44
1:Q:4:ILE:HD13	1:R:1:MEA:HD2	2.00	0.44
1:R:112:ARG:NH2	1:R:114:ASN:HA	2.33	0.44
1:A:16:LEU:HD11	1:J:9:VAL:HB	1.99	0.43
1:A:21:LEU:CD2	1:E:117:VAL:HG22	2.42	0.43
1:C:1:MEA:HD2	1:D:4:ILE:HD13	2.00	0.43
1:C:50:TYR:CD1	1:C:50:TYR:C	2.96	0.43
1:C:67:ALA:C	1:C:69:SER:N	2.75	0.43
1:C:158:LYS:OXT	1:C:158:LYS:HG2	2.18	0.43
1:D:3:LEU:HD11	1:E:12:ILE:HA	1.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:GLU:OE2	1:D:49:GLU:CA	2.64	0.43
1:D:118:LYS:HE3	1:D:120:PHE:CE1	2.53	0.43
1:H:1:MEA:HD2	1:I:4:ILE:CD1	2.48	0.43
1:H:6:LEU:O	1:I:16:LEU:CD1	2.66	0.43
1:H:6:LEU:HD21	1:I:15:ILE:HD12	1.93	0.43
1:I:77:TYR:O	1:I:93:LEU:N	2.36	0.43
1:J:118:LYS:HE3	1:J:120:PHE:CE1	2.53	0.43
1:K:50:TYR:CD1	1:K:50:TYR:C	2.96	0.43
1:K:84:LYS:HB2	1:K:84:LYS:HE3	1.69	0.43
1:K:118:LYS:HE3	1:K:120:PHE:CE1	2.53	0.43
1:N:4:ILE:HD13	1:O:1:MEA:HD2	2.00	0.43
1:O:50:TYR:CD1	1:O:50:TYR:C	2.96	0.43
1:O:158:LYS:HG2	1:O:158:LYS:OXT	2.18	0.43
1:P:12:ILE:O	1:P:16:LEU:HB2	2.18	0.43
1:Q:16:LEU:CD1	1:R:6:LEU:O	2.66	0.43
1:Q:118:LYS:HE3	1:Q:120:PHE:CE1	2.53	0.43
1:B:118:LYS:HE3	1:B:120:PHE:CE1	2.54	0.43
1:C:118:LYS:HE3	1:C:120:PHE:CE1	2.54	0.43
1:D:3:LEU:HA	1:E:12:ILE:HG21	1.26	0.43
1:H:12:ILE:O	1:H:16:LEU:HB2	2.18	0.43
1:K:112:ARG:NH2	1:K:114:ASN:HA	2.33	0.43
1:L:12:ILE:O	1:L:16:LEU:HB2	2.18	0.43
1:L:84:LYS:HB2	1:L:84:LYS:HE3	1.69	0.43
1:L:118:LYS:HE3	1:L:120:PHE:CE1	2.53	0.43
1:N:12:ILE:O	1:N:16:LEU:HB2	2.18	0.43
1:O:16:LEU:HD13	1:P:6:LEU:C	2.37	0.43
1:A:4:ILE:HD13	1:J:1:MEA:HD2	2.00	0.43
1:B:12:ILE:O	1:B:16:LEU:HB2	2.18	0.43
1:C:147:LEU:HA	1:C:148:PRO:HD3	1.93	0.43
1:E:118:LYS:HE3	1:E:120:PHE:CE1	2.53	0.43
1:F:112:ARG:HG2	1:F:112:ARG:NH1	2.31	0.43
1:G:1:MEA:HD2	1:H:4:ILE:HD13	2.00	0.43
1:G:9:VAL:HB	1:H:16:LEU:HD11	1.99	0.43
1:G:118:LYS:HE3	1:G:120:PHE:CE1	2.53	0.43
1:L:50:TYR:CD1	1:L:50:TYR:C	2.96	0.43
1:L:112:ARG:HG2	1:L:112:ARG:NH1	2.31	0.43
1:M:118:LYS:HE3	1:M:120:PHE:CE1	2.53	0.43
1:Q:112:ARG:NH2	1:Q:114:ASN:HA	2.33	0.43
1:Q:158:LYS:OXT	1:Q:158:LYS:HG2	2.18	0.43
1:B:50:TYR:C	1:B:50:TYR:CD1	2.96	0.43
1:C:52:LEU:CG	1:K:25:GLN:CD	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:50:TYR:CD1	1:D:50:TYR:C	2.96	0.43
1:E:67:ALA:C	1:E:69:SER:N	2.75	0.43
1:F:118:LYS:HE3	1:F:120:PHE:CE1	2.53	0.43
1:H:158:LYS:OXT	1:H:158:LYS:HG2	2.17	0.43
1:I:67:ALA:C	1:I:69:SER:N	2.75	0.43
1:I:112:ARG:HG2	1:I:112:ARG:NH1	2.31	0.43
1:K:4:ILE:CD1	1:L:1:MEA:HD2	2.48	0.43
1:K:112:ARG:HG2	1:K:112:ARG:NH1	2.31	0.43
1:M:4:ILE:HD13	1:N:1:MEA:HD2	2.00	0.43
1:M:147:LEU:HA	1:M:148:PRO:HD3	1.94	0.43
1:O:112:ARG:HG2	1:O:112:ARG:NH1	2.31	0.43
1:P:50:TYR:CD1	1:P:50:TYR:C	2.96	0.43
1:A:6:LEU:C	1:B:16:LEU:HD13	2.37	0.43
1:A:67:ALA:C	1:A:69:SER:N	2.75	0.43
1:B:112:ARG:NH2	1:B:114:ASN:HA	2.33	0.43
1:C:1:MEA:HD2	1:D:4:ILE:CD1	2.48	0.43
1:C:112:ARG:NH2	1:C:114:ASN:HA	2.33	0.43
1:E:112:ARG:HG2	1:E:112:ARG:NH1	2.31	0.43
1:F:50:TYR:CD1	1:F:50:TYR:C	2.97	0.43
1:G:112:ARG:NH2	1:G:114:ASN:HA	2.33	0.43
1:H:84:LYS:HE3	1:H:84:LYS:HB2	1.69	0.43
1:J:12:ILE:O	1:J:16:LEU:HB2	2.18	0.43
1:J:158:LYS:HG2	1:J:158:LYS:OXT	2.18	0.43
1:M:4:ILE:CD1	1:N:1:MEA:HD2	2.48	0.43
1:N:118:LYS:HE3	1:N:120:PHE:CE1	2.53	0.43
1:P:16:LEU:CD1	1:Q:6:LEU:O	2.66	0.43
1:R:50:TYR:C	1:R:50:TYR:CD1	2.96	0.43
1:E:3:LEU:HD11	1:F:12:ILE:HA	1.47	0.43
1:G:50:TYR:C	1:G:50:TYR:CD1	2.97	0.43
1:G:158:LYS:HG2	1:G:158:LYS:OXT	2.18	0.43
1:I:112:ARG:NH2	1:I:114:ASN:HA	2.33	0.43
1:I:118:LYS:HE3	1:I:120:PHE:CE1	2.53	0.43
1:J:77:TYR:HB3	1:J:97:VAL:HG12	2.01	0.43
1:J:77:TYR:O	1:J:93:LEU:N	2.36	0.43
1:M:77:TYR:HB3	1:M:97:VAL:HG12	2.01	0.43
1:N:158:LYS:OXT	1:N:158:LYS:HG2	2.18	0.43
1:O:118:LYS:HE3	1:O:120:PHE:CE1	2.54	0.43
1:R:118:LYS:HE3	1:R:120:PHE:CE1	2.53	0.43
1:B:112:ARG:HG2	1:B:112:ARG:NH1	2.31	0.43
1:C:52:LEU:HD12	1:C:52:LEU:HA	1.86	0.43
1:H:77:TYR:HB3	1:H:97:VAL:HG12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:4:ILE:HD13	1:K:1:MEA:HD2	2.00	0.43
1:J:66:VAL:O	1:J:68:SER:N	2.52	0.43
1:K:16:LEU:HB2	1:L:6:LEU:CD1	2.40	0.43
1:K:67:ALA:C	1:K:69:SER:N	2.75	0.43
1:M:66:VAL:O	1:M:68:SER:N	2.52	0.43
1:M:102:LYS:HB3	1:M:102:LYS:HE2	1.82	0.43
1:N:102:LYS:HB3	1:N:102:LYS:HE2	1.82	0.43
1:P:4:ILE:HD13	1:Q:1:MEA:HD2	2.00	0.43
1:P:77:TYR:HB3	1:P:97:VAL:HG12	2.01	0.43
1:Q:8:ILE:CD1	1:R:1:MEA:CZ	2.88	0.43
1:R:112:ARG:HG2	1:R:112:ARG:NH1	2.31	0.43
1:A:84:LYS:HE3	1:A:84:LYS:HB2	1.69	0.43
1:A:158:LYS:OXT	1:A:158:LYS:HG2	2.18	0.43
1:B:38:LEU:CG	1:L:6:LEU:O	2.67	0.43
1:C:66:VAL:O	1:C:68:SER:N	2.52	0.43
1:D:147:LEU:HA	1:D:148:PRO:HD3	1.93	0.43
1:F:12:ILE:O	1:F:16:LEU:HB2	2.18	0.43
1:H:6:LEU:C	1:I:16:LEU:HD13	2.37	0.43
1:L:4:ILE:HD13	1:M:1:MEA:HD2	2.00	0.43
1:M:112:ARG:NH2	1:M:114:ASN:HA	2.33	0.43
1:M:117:VAL:HG22	1:Q:21:LEU:CD2	2.42	0.43
1:N:50:TYR:CD1	1:N:50:TYR:C	2.96	0.43
1:O:8:ILE:HD12	1:P:2:THR:HG23	0.92	0.43
1:P:12:ILE:CD1	1:Q:5:GLU:CA	2.73	0.43
1:P:12:ILE:HA	1:Q:3:LEU:HD11	1.47	0.43
1:P:66:VAL:O	1:P:68:SER:N	2.52	0.43
1:P:112:ARG:HG2	1:P:112:ARG:NH1	2.31	0.43
1:P:118:LYS:HE3	1:P:120:PHE:CE1	2.54	0.43
1:R:66:VAL:O	1:R:68:SER:N	2.52	0.43
1:A:6:LEU:HD11	1:B:16:LEU:CA	2.17	0.43
1:A:102:LYS:HB3	1:A:102:LYS:HE2	1.82	0.43
1:A:149:SER:HG	1:D:53:ASN:HB3	1.80	0.43
1:C:12:ILE:O	1:C:16:LEU:HB2	2.18	0.43
1:E:52:LEU:HD12	1:E:52:LEU:HA	1.86	0.43
1:E:77:TYR:HB3	1:E:97:VAL:HG12	2.01	0.43
1:G:12:ILE:O	1:G:16:LEU:HB2	2.18	0.43
1:H:118:LYS:HE3	1:H:120:PHE:CE1	2.53	0.43
1:J:38:LEU:HD21	1:N:10:ILE:H	1.57	0.43
1:J:116:SER:CA	1:N:25:GLN:CD	2.92	0.43
1:K:8:ILE:HD12	1:L:2:THR:HG23	0.92	0.43
1:N:66:VAL:O	1:N:68:SER:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:66:VAL:O	1:Q:68:SER:N	2.52	0.43
1:A:112:ARG:NH2	1:A:114:ASN:HA	2.33	0.43
1:C:25:GLN:CD	1:G:116:SER:CA	2.92	0.43
1:C:77:TYR:HB3	1:C:97:VAL:HG12	2.01	0.43
1:D:6:LEU:C	1:E:16:LEU:HD13	2.37	0.43
1:D:12:ILE:O	1:D:16:LEU:HB2	2.18	0.43
1:D:21:LEU:HD13	1:H:116:SER:HA	1.20	0.43
1:D:66:VAL:O	1:D:68:SER:N	2.52	0.43
1:E:10:ILE:H	1:I:38:LEU:HD21	1.57	0.43
1:E:12:ILE:O	1:E:16:LEU:HB2	2.18	0.43
1:E:66:VAL:O	1:E:68:SER:N	2.52	0.43
1:E:112:ARG:NH2	1:E:114:ASN:HA	2.33	0.43
1:F:66:VAL:O	1:F:68:SER:N	2.52	0.43
1:H:1:MEA:HD2	1:I:4:ILE:HD13	2.00	0.43
1:H:50:TYR:CD1	1:H:50:TYR:C	2.97	0.43
1:I:50:TYR:CD1	1:I:50:TYR:C	2.97	0.43
1:J:50:TYR:C	1:J:50:TYR:CD1	2.96	0.43
1:L:66:VAL:O	1:L:68:SER:N	2.52	0.43
1:M:158:LYS:HG2	1:M:158:LYS:OXT	2.18	0.43
1:N:8:ILE:HD12	1:O:2:THR:HG23	0.92	0.43
1:P:29:ALA:HB2	1:P:98:ASN:HB2	2.01	0.43
1:Q:12:ILE:HA	1:R:3:LEU:HD11	1.47	0.43
1:A:66:VAL:O	1:A:68:SER:N	2.52	0.42
1:B:1:MEA:HD2	1:C:4:ILE:HD13	2.00	0.42
1:B:66:VAL:O	1:B:68:SER:N	2.52	0.42
1:B:67:ALA:C	1:B:69:SER:N	2.75	0.42
1:E:6:LEU:O	1:I:38:LEU:CG	2.67	0.42
1:E:50:TYR:C	1:E:50:TYR:CD1	2.96	0.42
1:H:32:GLN:OE1	1:H:101:ILE:HD11	2.19	0.42
1:I:69:SER:HB3	1:I:72:ASP:CG	2.45	0.42
1:L:4:ILE:O	1:M:2:THR:HG21	2.16	0.42
1:M:32:GLN:OE1	1:M:101:ILE:HD11	2.19	0.42
1:N:117:VAL:HG22	1:R:21:LEU:CD2	2.42	0.42
1:R:67:ALA:C	1:R:69:SER:N	2.75	0.42
1:A:12:ILE:O	1:A:16:LEU:HB2	2.18	0.42
1:A:32:GLN:OE1	1:A:101:ILE:HD11	2.19	0.42
1:A:118:LYS:HE3	1:A:120:PHE:CE1	2.53	0.42
1:C:14:GLY:HA2	1:G:44:LYS:HZ1	1.59	0.42
1:D:1:MEA:HD2	1:E:4:ILE:HD13	2.00	0.42
1:D:6:LEU:CD2	1:E:15:ILE:CG1	2.76	0.42
1:D:32:GLN:OE1	1:D:101:ILE:HD11	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:VAL:HG21	1:D:102:LYS:CB	2.44	0.42
1:E:158:LYS:OXT	1:E:158:LYS:HG2	2.18	0.42
1:G:66:VAL:O	1:G:68:SER:N	2.52	0.42
1:N:32:GLN:OE1	1:N:101:ILE:HD11	2.19	0.42
1:O:67:ALA:C	1:O:69:SER:N	2.75	0.42
1:R:12:ILE:O	1:R:16:LEU:HB2	2.18	0.42
1:A:77:TYR:HB3	1:A:97:VAL:HG12	2.01	0.42
1:B:6:LEU:CD1	1:C:16:LEU:HB2	2.40	0.42
1:B:77:TYR:HB3	1:B:97:VAL:HG12	2.01	0.42
1:C:32:GLN:OE1	1:C:101:ILE:HD11	2.19	0.42
1:C:112:ARG:HG2	1:C:112:ARG:NH1	2.31	0.42
1:D:52:LEU:HD12	1:D:52:LEU:HA	1.86	0.42
1:F:112:ARG:NH2	1:F:114:ASN:HA	2.33	0.42
1:I:66:VAL:O	1:I:68:SER:N	2.52	0.42
1:J:8:ILE:HD12	1:K:2:THR:HG23	0.92	0.42
1:L:158:LYS:OXT	1:L:158:LYS:HG2	2.18	0.42
1:M:69:SER:HB3	1:M:72:ASP:CG	2.45	0.42
1:O:4:ILE:HD13	1:P:1:MEA:HD2	2.00	0.42
1:O:76:LYS:HZ3	1:R:15:ILE:CG2	2.28	0.42
1:P:32:GLN:OE1	1:P:101:ILE:HD11	2.19	0.42
1:Q:32:GLN:OE1	1:Q:101:ILE:HD11	2.19	0.42
1:B:69:SER:HB3	1:B:72:ASP:CG	2.45	0.42
1:D:69:SER:HB3	1:D:72:ASP:CG	2.45	0.42
1:E:1:MEA:HD2	1:F:4:ILE:HD13	2.00	0.42
1:F:6:LEU:CA	1:G:16:LEU:CD1	2.58	0.42
1:G:6:LEU:HD12	1:H:16:LEU:CG	2.48	0.42
1:H:69:SER:HB3	1:H:72:ASP:CG	2.44	0.42
1:K:4:ILE:HD13	1:L:1:MEA:HD2	2.00	0.42
1:M:8:ILE:CD1	1:N:1:MEA:CZ	2.88	0.42
1:O:69:SER:HB3	1:O:72:ASP:CG	2.45	0.42
1:P:158:LYS:OXT	1:P:158:LYS:HG2	2.18	0.42
1:Q:29:ALA:HB2	1:Q:98:ASN:HB2	2.01	0.42
1:Q:50:TYR:CD1	1:Q:50:TYR:C	2.96	0.42
1:Q:147:LEU:HA	1:Q:148:PRO:HD3	1.93	0.42
1:R:29:ALA:HB2	1:R:98:ASN:HB2	2.01	0.42
1:R:77:TYR:HB3	1:R:97:VAL:HG12	2.01	0.42
1:E:32:GLN:OE1	1:E:101:ILE:HD11	2.19	0.42
1:F:6:LEU:CD1	1:G:16:LEU:HB2	2.40	0.42
1:J:32:GLN:OE1	1:J:101:ILE:HD11	2.19	0.42
1:M:29:ALA:HB2	1:M:98:ASN:HB2	2.02	0.42
1:M:97:VAL:HG21	1:M:102:LYS:CB	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:69:SER:HB3	1:N:72:ASP:CG	2.45	0.42
1:N:112:ARG:HG2	1:N:112:ARG:NH1	2.31	0.42
1:N:116:SER:CA	1:R:25:GLN:CD	2.92	0.42
1:O:12:ILE:HA	1:P:3:LEU:HD11	1.47	0.42
1:O:16:LEU:CD1	1:P:6:LEU:CA	2.58	0.42
1:A:50:TYR:CD1	1:A:50:TYR:C	2.96	0.42
1:C:29:ALA:HB2	1:C:98:ASN:HB2	2.02	0.42
1:C:69:SER:HB3	1:C:72:ASP:CG	2.45	0.42
1:E:102:LYS:HB3	1:E:102:LYS:HE2	1.82	0.42
1:G:2:THR:HG21	1:H:4:ILE:O	2.15	0.42
1:K:29:ALA:HB2	1:K:98:ASN:HB2	2.02	0.42
1:K:66:VAL:O	1:K:68:SER:N	2.52	0.42
1:L:29:ALA:HB2	1:L:98:ASN:HB2	2.02	0.42
1:L:32:GLN:OE1	1:L:101:ILE:HD11	2.19	0.42
1:M:50:TYR:C	1:M:50:TYR:CD1	2.96	0.42
1:N:29:ALA:HB2	1:N:98:ASN:HB2	2.02	0.42
1:O:29:ALA:HB2	1:O:98:ASN:HB2	2.02	0.42
1:A:29:ALA:HB2	1:A:98:ASN:HB2	2.02	0.42
1:A:38:LEU:HA	1:M:10:ILE:CB	2.37	0.42
1:B:1:MEA:CZ	1:C:8:ILE:CD1	2.88	0.42
1:B:3:LEU:CA	1:C:8:ILE:HG22	2.50	0.42
1:B:67:ALA:O	1:B:69:SER:N	2.53	0.42
1:D:1:MEA:CZ	1:E:8:ILE:CD1	2.88	0.42
1:D:77:TYR:HB3	1:D:97:VAL:HG12	2.01	0.42
1:E:2:THR:HG23	1:F:8:ILE:HD12	0.92	0.42
1:F:29:ALA:HB2	1:F:98:ASN:HB2	2.02	0.42
1:G:32:GLN:OE1	1:G:101:ILE:HD11	2.19	0.42
1:I:102:LYS:HB3	1:I:102:LYS:HE2	1.82	0.42
1:L:16:LEU:HD13	1:M:6:LEU:C	2.37	0.42
1:M:16:LEU:CD1	1:N:6:LEU:CA	2.58	0.42
1:N:8:ILE:HG22	1:O:3:LEU:CA	2.50	0.42
1:O:8:ILE:HD13	1:P:1:MEA:CD2	2.26	0.42
1:F:67:ALA:C	1:F:69:SER:N	2.75	0.42
1:F:67:ALA:O	1:F:69:SER:N	2.53	0.42
1:H:66:VAL:O	1:H:68:SER:N	2.52	0.42
1:J:147:LEU:HA	1:J:148:PRO:HD3	1.93	0.42
1:L:44:LYS:HZ3	1:P:14:GLY:HA2	1.64	0.42
1:L:67:ALA:O	1:L:69:SER:N	2.53	0.42
1:M:44:LYS:CE	1:Q:14:GLY:HA2	2.50	0.42
1:A:1:MEA:HD2	1:B:4:ILE:HD13	2.00	0.42
1:A:16:LEU:CG	1:J:6:LEU:HD12	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:SER:HB3	1:A:72:ASP:CG	2.45	0.42
1:A:112:ARG:HG2	1:A:112:ARG:NH1	2.31	0.42
1:B:29:ALA:HB2	1:B:98:ASN:HB2	2.02	0.42
1:G:29:ALA:HB2	1:G:98:ASN:HB2	2.02	0.42
1:H:112:ARG:HG2	1:H:112:ARG:NH1	2.31	0.42
1:I:32:GLN:OE1	1:I:101:ILE:HD11	2.19	0.42
1:K:77:TYR:HB3	1:K:97:VAL:HG12	2.01	0.42
1:K:147:LEU:HA	1:K:148:PRO:HD3	1.93	0.42
1:L:69:SER:HB3	1:L:72:ASP:CG	2.45	0.42
1:O:8:ILE:CD1	1:P:1:MEA:CZ	2.88	0.42
1:A:8:ILE:CD1	1:J:1:MEA:CZ	2.88	0.42
1:A:8:ILE:HG22	1:J:3:LEU:CA	2.50	0.42
1:B:32:GLN:OE1	1:B:101:ILE:HD11	2.19	0.42
1:B:38:LEU:HD21	1:L:10:ILE:H	1.57	0.42
1:D:5:GLU:CA	1:E:12:ILE:CD1	2.73	0.42
1:D:29:ALA:HB2	1:D:98:ASN:HB2	2.02	0.42
1:F:3:LEU:CA	1:G:8:ILE:HG22	2.50	0.42
1:G:3:LEU:CA	1:H:8:ILE:HG22	2.50	0.42
1:G:69:SER:HB3	1:G:72:ASP:CG	2.45	0.42
1:H:29:ALA:HB2	1:H:98:ASN:HB2	2.02	0.42
1:J:8:ILE:HG22	1:K:3:LEU:CA	2.50	0.42
1:J:29:ALA:HB2	1:J:98:ASN:HB2	2.02	0.42
1:L:77:TYR:HB3	1:L:97:VAL:HG12	2.01	0.42
1:O:32:GLN:OE1	1:O:101:ILE:HD11	2.19	0.42
1:P:8:ILE:HD12	1:Q:2:THR:HG23	0.92	0.42
1:Q:69:SER:HB3	1:Q:72:ASP:CG	2.45	0.42
1:Q:77:TYR:HB3	1:Q:97:VAL:HG12	2.01	0.42
1:R:69:SER:HB3	1:R:72:ASP:CG	2.45	0.42
1:A:6:LEU:HD12	1:B:16:LEU:CG	2.48	0.41
1:A:6:LEU:CD2	1:B:15:ILE:CG1	2.76	0.41
1:D:25:GLN:CD	1:H:116:SER:CA	2.92	0.41
1:E:29:ALA:HB2	1:E:98:ASN:HB2	2.02	0.41
1:G:108:LEU:HD11	1:G:121:CYS:SG	2.60	0.41
1:G:147:LEU:HA	1:G:148:PRO:HD3	1.93	0.41
1:H:4:ILE:N	1:I:12:ILE:CD1	2.72	0.41
1:K:67:ALA:O	1:K:69:SER:N	2.53	0.41
1:K:125:VAL:HG21	1:K:133:VAL:HG23	2.02	0.41
1:L:108:LEU:HD11	1:L:121:CYS:SG	2.60	0.41
1:L:125:VAL:HG21	1:L:133:VAL:HG23	2.02	0.41
1:M:38:LEU:HA	1:Q:10:ILE:CD1	2.42	0.41
1:M:116:SER:CA	1:Q:25:GLN:CD	2.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:38:LEU:HA	1:R:10:ILE:CD1	2.42	0.41
1:O:4:ILE:O	1:P:2:THR:HG21	2.16	0.41
1:P:69:SER:HB3	1:P:72:ASP:CG	2.45	0.41
1:R:32:GLN:OE1	1:R:101:ILE:HD11	2.19	0.41
1:A:38:LEU:CG	1:M:6:LEU:O	2.67	0.41
1:B:67:ALA:C	1:B:69:SER:H	2.29	0.41
1:C:5:GLU:CA	1:D:12:ILE:CD1	2.73	0.41
1:C:84:LYS:HE3	1:C:84:LYS:HB2	1.69	0.41
1:C:116:SER:CA	1:K:25:GLN:CD	2.92	0.41
1:D:1:MEA:CD2	1:E:8:ILE:HD13	2.26	0.41
1:D:4:ILE:H	1:E:12:ILE:CD1	2.22	0.41
1:D:52:LEU:CG	1:J:25:GLN:CD	2.81	0.41
1:E:125:VAL:HG21	1:E:133:VAL:HG23	2.02	0.41
1:F:3:LEU:HA	1:G:12:ILE:HG21	1.26	0.41
1:F:77:TYR:HB3	1:F:97:VAL:HG12	2.01	0.41
1:F:125:VAL:HG21	1:F:133:VAL:HG23	2.03	0.41
1:G:77:TYR:HB3	1:G:97:VAL:HG12	2.01	0.41
1:I:67:ALA:O	1:I:69:SER:N	2.53	0.41
1:K:8:ILE:HD13	1:L:1:MEA:CD2	2.26	0.41
1:K:38:LEU:HA	1:O:10:ILE:CB	2.37	0.41
1:L:38:LEU:CG	1:P:6:LEU:O	2.67	0.41
1:N:8:ILE:CD1	1:O:1:MEA:CZ	2.88	0.41
1:N:16:LEU:CD1	1:O:6:LEU:CA	2.58	0.41
1:N:38:LEU:CG	1:R:6:LEU:O	2.67	0.41
1:N:77:TYR:HB3	1:N:97:VAL:HG12	2.01	0.41
1:P:8:ILE:HG22	1:Q:3:LEU:CA	2.50	0.41
1:P:67:ALA:O	1:P:69:SER:N	2.53	0.41
1:Q:8:ILE:HD12	1:R:2:THR:HG23	0.93	0.41
1:Q:97:VAL:HG21	1:Q:102:LYS:CB	2.44	0.41
1:R:67:ALA:O	1:R:69:SER:N	2.53	0.41
1:R:147:LEU:HA	1:R:148:PRO:HD3	1.93	0.41
1:A:3:LEU:CA	1:B:8:ILE:HG22	2.50	0.41
1:B:3:LEU:HD11	1:C:12:ILE:HA	1.47	0.41
1:D:44:LYS:CE	1:J:14:GLY:HA2	2.50	0.41
1:E:69:SER:HB3	1:E:72:ASP:CG	2.45	0.41
1:H:97:VAL:HG21	1:H:102:LYS:CB	2.44	0.41
1:J:108:LEU:HD11	1:J:121:CYS:SG	2.60	0.41
1:M:125:VAL:HG21	1:M:133:VAL:HG23	2.02	0.41
1:O:66:VAL:O	1:O:68:SER:N	2.52	0.41
1:O:67:ALA:O	1:O:69:SER:N	2.53	0.41
1:A:116:SER:CA	1:M:25:GLN:CD	2.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:LEU:HD12	1:C:121:CYS:HA	2.03	0.41
1:D:6:LEU:O	1:H:38:LEU:CG	2.67	0.41
1:D:51:TYR:OH	1:D:112:ARG:HB2	2.21	0.41
1:D:116:SER:CA	1:J:25:GLN:CD	2.92	0.41
1:D:125:VAL:HG21	1:D:133:VAL:HG23	2.02	0.41
1:F:6:LEU:HD21	1:G:15:ILE:HD12	1.93	0.41
1:F:32:GLN:OE1	1:F:101:ILE:HD11	2.19	0.41
1:F:69:SER:HB3	1:F:72:ASP:CG	2.45	0.41
1:G:108:LEU:HD12	1:G:121:CYS:HA	2.03	0.41
1:I:29:ALA:HB2	1:I:98:ASN:HB2	2.02	0.41
1:K:32:GLN:OE1	1:K:101:ILE:HD11	2.19	0.41
1:K:44:LYS:CE	1:O:14:GLY:HA2	2.50	0.41
1:L:12:ILE:HG21	1:M:3:LEU:HA	1.26	0.41
1:L:125:VAL:HG22	1:L:126:THR:N	2.36	0.41
1:M:8:ILE:HG22	1:N:3:LEU:CA	2.50	0.41
1:O:8:ILE:HG22	1:P:3:LEU:CA	2.50	0.41
1:O:108:LEU:HD11	1:O:121:CYS:SG	2.60	0.41
1:Q:8:ILE:HG22	1:R:3:LEU:CA	2.50	0.41
1:R:125:VAL:HG21	1:R:133:VAL:HG23	2.03	0.41
1:C:38:LEU:CG	1:K:6:LEU:O	2.67	0.41
1:D:67:ALA:C	1:D:69:SER:H	2.29	0.41
1:E:6:LEU:CD2	1:F:15:ILE:CG1	2.76	0.41
1:F:1:MEA:CZ	1:G:8:ILE:CD1	2.88	0.41
1:G:51:TYR:OH	1:G:112:ARG:HB2	2.21	0.41
1:G:112:ARG:HG2	1:G:112:ARG:NH1	2.31	0.41
1:H:51:TYR:OH	1:H:112:ARG:HB2	2.21	0.41
1:H:108:LEU:HD11	1:H:121:CYS:SG	2.60	0.41
1:I:51:TYR:OH	1:I:112:ARG:HB2	2.21	0.41
1:J:44:LYS:HZ1	1:N:14:GLY:HA2	1.60	0.41
1:J:51:TYR:OH	1:J:112:ARG:HB2	2.21	0.41
1:J:108:LEU:HD12	1:J:121:CYS:HA	2.03	0.41
1:K:69:SER:HB3	1:K:72:ASP:CG	2.45	0.41
1:K:125:VAL:HG22	1:K:126:THR:N	2.36	0.41
1:L:12:ILE:CD1	1:M:5:GLU:CA	2.73	0.41
1:M:108:LEU:HD11	1:M:121:CYS:SG	2.60	0.41
1:N:53:ASN:CG	1:Q:149:SER:CB	2.92	0.41
1:N:67:ALA:O	1:N:69:SER:N	2.53	0.41
1:N:147:LEU:HA	1:N:148:PRO:HD3	1.93	0.41
1:P:16:LEU:CG	1:Q:6:LEU:HD12	2.48	0.41
1:R:67:ALA:C	1:R:69:SER:H	2.29	0.41
1:B:116:SER:HA	1:L:21:LEU:HD13	1.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:108:LEU:HD12	1:D:121:CYS:HA	2.03	0.41
1:E:6:LEU:HD12	1:F:16:LEU:CG	2.48	0.41
1:E:108:LEU:HD11	1:E:121:CYS:SG	2.60	0.41
1:F:67:ALA:C	1:F:69:SER:H	2.29	0.41
1:F:125:VAL:HG22	1:F:126:THR:N	2.36	0.41
1:H:3:LEU:CA	1:I:8:ILE:HG22	2.50	0.41
1:H:125:VAL:HG21	1:H:133:VAL:HG23	2.03	0.41
1:J:69:SER:HB3	1:J:72:ASP:CG	2.45	0.41
1:L:38:LEU:HA	1:P:10:ILE:CD1	2.42	0.41
1:M:51:TYR:OH	1:M:112:ARG:HB2	2.21	0.41
1:M:67:ALA:O	1:M:69:SER:N	2.53	0.41
1:N:108:LEU:HD11	1:N:121:CYS:SG	2.60	0.41
1:O:16:LEU:CG	1:P:6:LEU:HD12	2.48	0.41
1:O:77:TYR:HB3	1:O:97:VAL:HG12	2.01	0.41
1:Q:51:TYR:OH	1:Q:112:ARG:HB2	2.21	0.41
1:Q:67:ALA:C	1:Q:69:SER:H	2.29	0.41
1:Q:67:ALA:O	1:Q:69:SER:N	2.53	0.41
1:R:77:TYR:O	1:R:93:LEU:N	2.36	0.41
1:A:4:ILE:N	1:B:12:ILE:CD1	2.72	0.41
1:B:1:MEA:CD2	1:C:8:ILE:HD13	2.26	0.41
1:B:2:THR:HG23	1:C:8:ILE:HD12	0.92	0.41
1:B:125:VAL:HG22	1:B:126:THR:N	2.36	0.41
1:D:117:VAL:HG22	1:J:21:LEU:CD2	2.42	0.41
1:E:67:ALA:O	1:E:69:SER:N	2.53	0.41
1:E:125:VAL:HG22	1:E:126:THR:N	2.36	0.41
1:F:108:LEU:HD11	1:F:121:CYS:SG	2.60	0.41
1:G:67:ALA:O	1:G:69:SER:N	2.53	0.41
1:M:67:ALA:C	1:M:69:SER:H	2.29	0.41
1:Q:108:LEU:HD11	1:Q:121:CYS:SG	2.60	0.41
1:A:51:TYR:OH	1:A:112:ARG:HB2	2.21	0.41
1:A:108:LEU:HD11	1:A:121:CYS:SG	2.60	0.41
1:B:10:ILE:CD1	1:F:38:LEU:HA	2.42	0.41
1:B:14:GLY:HA2	1:F:44:LYS:CE	2.50	0.41
1:C:3:LEU:CA	1:D:8:ILE:HG22	2.50	0.41
1:C:44:LYS:CE	1:K:14:GLY:HA2	2.50	0.41
1:C:51:TYR:OH	1:C:112:ARG:HB2	2.21	0.41
1:D:108:LEU:HD11	1:D:121:CYS:SG	2.60	0.41
1:F:108:LEU:HD12	1:F:121:CYS:HA	2.03	0.41
1:G:6:LEU:HD21	1:H:15:ILE:HD12	1.93	0.41
1:H:6:LEU:HD12	1:I:16:LEU:CG	2.48	0.41
1:H:67:ALA:O	1:H:69:SER:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:77:TYR:HB3	1:I:97:VAL:HG12	2.01	0.41
1:I:108:LEU:HD11	1:I:121:CYS:SG	2.60	0.41
1:I:125:VAL:HG21	1:I:133:VAL:HG23	2.03	0.41
1:J:112:ARG:HG2	1:J:112:ARG:NH1	2.31	0.41
1:J:125:VAL:HG22	1:J:126:THR:N	2.36	0.41
1:K:8:ILE:HG22	1:L:3:LEU:CA	2.50	0.41
1:K:16:LEU:CG	1:L:6:LEU:HD12	2.48	0.41
1:K:108:LEU:HD11	1:K:121:CYS:SG	2.60	0.41
1:K:108:LEU:HD12	1:K:121:CYS:HA	2.03	0.41
1:L:51:TYR:OH	1:L:112:ARG:HB2	2.21	0.41
1:L:67:ALA:C	1:L:69:SER:H	2.29	0.41
1:N:51:TYR:OH	1:N:112:ARG:HB2	2.21	0.41
1:A:6:LEU:O	1:E:38:LEU:CG	2.67	0.41
1:A:67:ALA:O	1:A:69:SER:N	2.53	0.41
1:A:97:VAL:HG21	1:A:102:LYS:CB	2.44	0.41
1:B:44:LYS:CE	1:L:14:GLY:HA2	2.50	0.41
1:B:51:TYR:OH	1:B:112:ARG:HB2	2.21	0.41
1:D:67:ALA:O	1:D:69:SER:N	2.53	0.41
1:E:14:GLY:HA2	1:I:44:LYS:CE	2.50	0.41
1:E:51:TYR:OH	1:E:112:ARG:HB2	2.21	0.41
1:F:106:LEU:HB2	1:F:122:GLY:O	2.21	0.41
1:G:106:LEU:HB2	1:G:122:GLY:O	2.21	0.41
1:H:106:LEU:HB2	1:H:122:GLY:O	2.21	0.41
1:I:125:VAL:HG22	1:I:126:THR:N	2.36	0.41
1:J:106:LEU:HB2	1:J:122:GLY:O	2.21	0.41
1:K:106:LEU:HB2	1:K:122:GLY:O	2.21	0.41
1:L:76:LYS:H	1:L:76:LYS:HG3	1.62	0.41
1:L:147:LEU:HA	1:L:148:PRO:HD3	1.93	0.41
1:M:125:VAL:HG22	1:M:126:THR:N	2.36	0.41
1:N:67:ALA:C	1:N:69:SER:H	2.29	0.41
1:N:77:TYR:O	1:N:93:LEU:N	2.36	0.41
1:N:108:LEU:HD12	1:N:121:CYS:HA	2.03	0.41
1:O:106:LEU:HB2	1:O:122:GLY:O	2.21	0.41
1:P:102:LYS:HB3	1:P:102:LYS:HE2	1.82	0.41
1:P:108:LEU:HD11	1:P:121:CYS:SG	2.60	0.41
1:Q:108:LEU:HD12	1:Q:121:CYS:HA	2.03	0.41
1:R:76:LYS:H	1:R:76:LYS:HG3	1.62	0.41
1:R:108:LEU:HD11	1:R:121:CYS:SG	2.60	0.41
1:R:125:VAL:HG22	1:R:126:THR:N	2.36	0.41
1:A:16:LEU:CA	1:J:6:LEU:HD11	2.17	0.41
1:B:6:LEU:HD12	1:C:16:LEU:CG	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:117:VAL:HG22	1:K:21:LEU:CD2	2.42	0.41
1:C:125:VAL:HG21	1:C:133:VAL:HG23	2.02	0.41
1:J:67:ALA:O	1:J:69:SER:N	2.53	0.41
1:O:125:VAL:HG21	1:O:133:VAL:HG23	2.03	0.41
1:P:41:GLU:C	1:P:43:GLN:N	2.79	0.41
1:P:51:TYR:OH	1:P:112:ARG:HB2	2.21	0.41
1:Q:106:LEU:HB2	1:Q:122:GLY:O	2.21	0.41
1:Q:125:VAL:HG21	1:Q:133:VAL:HG23	2.03	0.41
1:R:106:LEU:HB2	1:R:122:GLY:O	2.21	0.41
1:A:16:LEU:CD1	1:J:6:LEU:CA	2.58	0.40
1:A:125:VAL:HG21	1:A:133:VAL:HG23	2.03	0.40
1:B:38:LEU:HA	1:L:10:ILE:CD1	2.42	0.40
1:B:108:LEU:HD11	1:B:121:CYS:SG	2.60	0.40
1:C:67:ALA:C	1:C:69:SER:H	2.29	0.40
1:C:108:LEU:HD11	1:C:121:CYS:SG	2.60	0.40
1:D:106:LEU:HB2	1:D:122:GLY:O	2.21	0.40
1:E:3:LEU:CA	1:F:8:ILE:HG22	2.50	0.40
1:J:67:ALA:C	1:J:69:SER:H	2.29	0.40
1:K:76:LYS:HZ3	1:N:15:ILE:CG2	2.30	0.40
1:M:108:LEU:HD12	1:M:121:CYS:HA	2.03	0.40
1:O:137:LYS:O	1:O:137:LYS:CG	2.69	0.40
1:A:2:THR:HG23	1:B:8:ILE:HD12	0.92	0.40
1:A:38:LEU:HD21	1:M:10:ILE:H	1.57	0.40
1:A:41:GLU:C	1:A:43:GLN:N	2.79	0.40
1:D:2:THR:HG21	1:E:4:ILE:O	2.16	0.40
1:E:3:LEU:HA	1:F:12:ILE:HG21	1.26	0.40
1:E:6:LEU:CA	1:F:16:LEU:CD1	2.58	0.40
1:F:41:GLU:C	1:F:43:GLN:N	2.79	0.40
1:F:51:TYR:OH	1:F:112:ARG:HB2	2.21	0.40
1:H:108:LEU:HD12	1:H:121:CYS:HA	2.03	0.40
1:I:67:ALA:C	1:I:69:SER:H	2.29	0.40
1:I:106:LEU:HB2	1:I:122:GLY:O	2.21	0.40
1:J:38:LEU:CG	1:N:6:LEU:O	2.67	0.40
1:J:125:VAL:HG21	1:J:133:VAL:HG23	2.02	0.40
1:L:16:LEU:CG	1:M:6:LEU:HD12	2.48	0.40
1:L:41:GLU:C	1:L:43:GLN:N	2.79	0.40
1:L:44:LYS:CE	1:P:14:GLY:HA2	2.50	0.40
1:O:125:VAL:HG22	1:O:126:THR:N	2.36	0.40
1:P:77:TYR:O	1:P:93:LEU:N	2.36	0.40
1:Q:16:LEU:CA	1:R:6:LEU:HD11	2.17	0.40
1:R:51:TYR:OH	1:R:112:ARG:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:VAL:HG21	1:B:133:VAL:HG23	2.02	0.40
1:C:106:LEU:HB2	1:C:122:GLY:O	2.21	0.40
1:D:3:LEU:CA	1:E:8:ILE:HG22	2.50	0.40
1:H:125:VAL:HG22	1:H:126:THR:N	2.36	0.40
1:H:137:LYS:O	1:H:137:LYS:CG	2.69	0.40
1:K:51:TYR:OH	1:K:112:ARG:HB2	2.21	0.40
1:K:67:ALA:C	1:K:69:SER:H	2.29	0.40
1:L:8:ILE:HG22	1:M:3:LEU:CA	2.50	0.40
1:L:43:GLN:NE2	1:L:73:ILE:HD13	2.26	0.40
1:P:106:LEU:HB2	1:P:122:GLY:O	2.21	0.40
1:P:125:VAL:HG21	1:P:133:VAL:HG23	2.02	0.40
1:A:8:ILE:HD12	1:J:2:THR:HG23	0.92	0.40
1:A:137:LYS:O	1:A:137:LYS:CG	2.70	0.40
1:B:108:LEU:HD12	1:B:121:CYS:HA	2.03	0.40
1:C:41:GLU:C	1:C:43:GLN:N	2.79	0.40
1:E:67:ALA:C	1:E:69:SER:H	2.29	0.40
1:E:106:LEU:HB2	1:E:122:GLY:O	2.21	0.40
1:E:137:LYS:O	1:E:137:LYS:CG	2.70	0.40
1:G:125:VAL:HG22	1:G:126:THR:N	2.36	0.40
1:J:12:ILE:HG21	1:K:3:LEU:HA	1.26	0.40
1:K:76:LYS:H	1:K:76:LYS:HG3	1.62	0.40
1:M:41:GLU:C	1:M:43:GLN:N	2.79	0.40
1:N:92:MET:O	1:N:93:LEU:O	2.40	0.40
1:N:94:SER:HA	1:N:102:LYS:HB2	2.04	0.40
1:O:51:TYR:OH	1:O:112:ARG:HB2	2.21	0.40
1:O:67:ALA:C	1:O:69:SER:H	2.29	0.40
1:R:41:GLU:C	1:R:43:GLN:N	2.79	0.40
1:R:108:LEU:HD12	1:R:121:CYS:HA	2.03	0.40
1:A:19:VAL:HG11	1:D:38:LEU:HD12	2.04	0.40
1:A:67:ALA:C	1:A:69:SER:H	2.29	0.40
1:A:106:LEU:HB2	1:A:122:GLY:O	2.21	0.40
1:C:67:ALA:O	1:C:69:SER:N	2.53	0.40
1:D:6:LEU:HD12	1:E:16:LEU:CG	2.48	0.40
1:D:19:VAL:HG11	1:G:38:LEU:HD12	2.04	0.40
1:E:4:ILE:H	1:F:12:ILE:CD1	2.22	0.40
1:E:19:VAL:HG11	1:H:38:LEU:HD12	2.04	0.40
1:F:76:LYS:H	1:F:76:LYS:HG3	1.62	0.40
1:G:41:GLU:C	1:G:43:GLN:N	2.79	0.40
1:G:92:MET:O	1:G:93:LEU:O	2.40	0.40
1:H:102:LYS:HB3	1:H:102:LYS:HE2	1.82	0.40
1:I:76:LYS:H	1:I:76:LYS:HG3	1.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:137:LYS:O	1:I:137:LYS:CG	2.69	0.40
1:J:38:LEU:HD12	1:M:19:VAL:HG11	2.04	0.40
1:K:117:VAL:HG22	1:O:21:LEU:CD2	2.42	0.40
1:M:137:LYS:O	1:M:137:LYS:CG	2.69	0.40
1:N:16:LEU:CG	1:O:6:LEU:HD12	2.48	0.40
1:N:44:LYS:CE	1:R:14:GLY:HA2	2.50	0.40
1:N:125:VAL:HG21	1:N:133:VAL:HG23	2.02	0.40
1:O:41:GLU:C	1:O:43:GLN:N	2.79	0.40
1:O:108:LEU:HD12	1:O:121:CYS:HA	2.03	0.40
1:Q:41:GLU:C	1:Q:43:GLN:N	2.79	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	A	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	B	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	C	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	D	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	E	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	F	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	G	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	H	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	I	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	J	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	K	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	L	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	N	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	O	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	P	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	Q	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
1	R	156/158 (99%)	138 (88%)	9 (6%)	9 (6%)	1	14
All	All	2808/2844 (99%)	2484 (88%)	162 (6%)	162 (6%)	2	14

All (162) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	93	LEU
1	A	98	ASN
1	B	93	LEU
1	B	98	ASN
1	C	93	LEU
1	C	98	ASN
1	D	93	LEU
1	D	98	ASN
1	E	93	LEU
1	E	98	ASN
1	F	93	LEU
1	F	98	ASN
1	G	93	LEU
1	G	98	ASN
1	H	93	LEU
1	H	98	ASN
1	I	93	LEU
1	I	98	ASN
1	J	93	LEU
1	J	98	ASN
1	K	93	LEU
1	K	98	ASN
1	L	93	LEU
1	L	98	ASN
1	M	93	LEU
1	M	98	ASN
1	N	93	LEU
1	N	98	ASN
1	O	93	LEU

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Mol	Chain	Res	Type
1	O	98	ASN
1	P	93	LEU
1	P	98	ASN
1	Q	93	LEU
1	Q	98	ASN
1	R	93	LEU
1	R	98	ASN
1	A	99	ASN
1	B	99	ASN
1	C	99	ASN
1	D	99	ASN
1	E	99	ASN
1	F	99	ASN
1	G	99	ASN
1	H	99	ASN
1	I	99	ASN
1	J	99	ASN
1	K	99	ASN
1	L	99	ASN
1	M	99	ASN
1	N	99	ASN
1	O	99	ASN
1	P	99	ASN
1	Q	99	ASN
1	R	99	ASN
1	A	67	ALA
1	A	68	SER
1	A	114	ASN
1	A	124	PRO
1	B	67	ALA
1	B	68	SER
1	B	114	ASN
1	B	124	PRO
1	C	67	ALA
1	C	68	SER
1	C	114	ASN
1	C	124	PRO
1	D	67	ALA
1	D	68	SER
1	D	114	ASN
1	D	124	PRO
1	E	67	ALA

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Mol	Chain	Res	Type
1	E	68	SER
1	E	114	ASN
1	E	124	PRO
1	F	67	ALA
1	F	68	SER
1	F	114	ASN
1	F	124	PRO
1	G	67	ALA
1	G	68	SER
1	G	114	ASN
1	G	124	PRO
1	H	67	ALA
1	H	68	SER
1	H	114	ASN
1	H	124	PRO
1	I	67	ALA
1	I	68	SER
1	I	114	ASN
1	I	124	PRO
1	J	67	ALA
1	J	68	SER
1	J	114	ASN
1	J	124	PRO
1	K	67	ALA
1	K	68	SER
1	K	114	ASN
1	K	124	PRO
1	L	67	ALA
1	L	68	SER
1	L	114	ASN
1	L	124	PRO
1	M	67	ALA
1	M	68	SER
1	M	114	ASN
1	M	124	PRO
1	N	67	ALA
1	N	68	SER
1	N	114	ASN
1	N	124	PRO
1	O	67	ALA
1	O	68	SER
1	O	114	ASN

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Mol	Chain	Res	Type
1	O	124	PRO
1	P	67	ALA
1	P	68	SER
1	P	114	ASN
1	P	124	PRO
1	Q	67	ALA
1	Q	68	SER
1	Q	114	ASN
1	Q	124	PRO
1	R	67	ALA
1	R	68	SER
1	R	114	ASN
1	R	124	PRO
1	A	80	GLU
1	B	80	GLU
1	C	80	GLU
1	D	80	GLU
1	E	80	GLU
1	F	80	GLU
1	G	80	GLU
1	H	80	GLU
1	I	80	GLU
1	J	80	GLU
1	K	80	GLU
1	L	80	GLU
1	M	80	GLU
1	N	80	GLU
1	O	80	GLU
1	P	80	GLU
1	Q	80	GLU
1	R	80	GLU
1	A	138	ASP
1	B	138	ASP
1	C	138	ASP
1	D	138	ASP
1	E	138	ASP
1	F	138	ASP
1	G	138	ASP
1	H	138	ASP
1	I	138	ASP
1	J	138	ASP
1	K	138	ASP

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Mol	Chain	Res	Type
1	L	138	ASP
1	M	138	ASP
1	N	138	ASP
1	O	138	ASP
1	P	138	ASP
1	Q	138	ASP
1	R	138	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	A	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	B	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	C	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	D	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	E	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	F	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	G	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	H	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	I	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	J	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	K	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	L	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	M	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	N	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	O	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	P	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	Q	128/129 (99%)	113 (88%)	15 (12%)	5	18
1	R	128/129 (99%)	113 (88%)	15 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2304/2322 (99%)	2034 (88%)	270 (12%)	7 18

All (270) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU
1	A	21	LEU
1	A	25	GLN
1	A	28	THR
1	A	38	LEU
1	A	39	LEU
1	A	49	GLU
1	A	52	LEU
1	A	88	VAL
1	A	93	LEU
1	A	105	LYS
1	A	106	LEU
1	A	108	LEU
1	A	137	LYS
1	A	140	LYS
1	B	5	GLU
1	B	21	LEU
1	B	25	GLN
1	B	28	THR
1	B	38	LEU
1	B	39	LEU
1	B	49	GLU
1	B	52	LEU
1	B	88	VAL
1	B	93	LEU
1	B	105	LYS
1	B	106	LEU
1	B	108	LEU
1	B	137	LYS
1	B	140	LYS
1	C	5	GLU
1	C	21	LEU
1	C	25	GLN
1	C	28	THR
1	C	38	LEU
1	C	39	LEU
1	C	49	GLU

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Mol	Chain	Res	Type
1	C	52	LEU
1	C	88	VAL
1	C	93	LEU
1	C	105	LYS
1	C	106	LEU
1	C	108	LEU
1	C	137	LYS
1	C	140	LYS
1	D	5	GLU
1	D	21	LEU
1	D	25	GLN
1	D	28	THR
1	D	38	LEU
1	D	39	LEU
1	D	49	GLU
1	D	52	LEU
1	D	88	VAL
1	D	93	LEU
1	D	105	LYS
1	D	106	LEU
1	D	108	LEU
1	D	137	LYS
1	D	140	LYS
1	E	5	GLU
1	E	21	LEU
1	E	25	GLN
1	E	28	THR
1	E	38	LEU
1	E	39	LEU
1	E	49	GLU
1	E	52	LEU
1	E	88	VAL
1	E	93	LEU
1	E	105	LYS
1	E	106	LEU
1	E	108	LEU
1	E	137	LYS
1	E	140	LYS
1	F	5	GLU
1	F	21	LEU
1	F	25	GLN
1	F	28	THR

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Mol	Chain	Res	Type
1	F	38	LEU
1	F	39	LEU
1	F	49	GLU
1	F	52	LEU
1	F	88	VAL
1	F	93	LEU
1	F	105	LYS
1	F	106	LEU
1	F	108	LEU
1	F	137	LYS
1	F	140	LYS
1	G	5	GLU
1	G	21	LEU
1	G	25	GLN
1	G	28	THR
1	G	38	LEU
1	G	39	LEU
1	G	49	GLU
1	G	52	LEU
1	G	88	VAL
1	G	93	LEU
1	G	105	LYS
1	G	106	LEU
1	G	108	LEU
1	G	137	LYS
1	G	140	LYS
1	H	5	GLU
1	H	21	LEU
1	H	25	GLN
1	H	28	THR
1	H	38	LEU
1	H	39	LEU
1	H	49	GLU
1	H	52	LEU
1	H	88	VAL
1	H	93	LEU
1	H	105	LYS
1	H	106	LEU
1	H	108	LEU
1	H	137	LYS
1	H	140	LYS
1	I	5	GLU

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Mol	Chain	Res	Type
1	I	21	LEU
1	I	25	GLN
1	I	28	THR
1	I	38	LEU
1	I	39	LEU
1	I	49	GLU
1	I	52	LEU
1	I	88	VAL
1	I	93	LEU
1	I	105	LYS
1	I	106	LEU
1	I	108	LEU
1	I	137	LYS
1	I	140	LYS
1	J	5	GLU
1	J	21	LEU
1	J	25	GLN
1	J	28	THR
1	J	38	LEU
1	J	39	LEU
1	J	49	GLU
1	J	52	LEU
1	J	88	VAL
1	J	93	LEU
1	J	105	LYS
1	J	106	LEU
1	J	108	LEU
1	J	137	LYS
1	J	140	LYS
1	K	5	GLU
1	K	21	LEU
1	K	25	GLN
1	K	28	THR
1	K	38	LEU
1	K	39	LEU
1	K	49	GLU
1	K	52	LEU
1	K	88	VAL
1	K	93	LEU
1	K	105	LYS
1	K	106	LEU
1	K	108	LEU

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Mol	Chain	Res	Type
1	K	137	LYS
1	K	140	LYS
1	L	5	GLU
1	L	21	LEU
1	L	25	GLN
1	L	28	THR
1	L	38	LEU
1	L	39	LEU
1	L	49	GLU
1	L	52	LEU
1	L	88	VAL
1	L	93	LEU
1	L	105	LYS
1	L	106	LEU
1	L	108	LEU
1	L	137	LYS
1	L	140	LYS
1	M	5	GLU
1	M	21	LEU
1	M	25	GLN
1	M	28	THR
1	M	38	LEU
1	M	39	LEU
1	M	49	GLU
1	M	52	LEU
1	M	88	VAL
1	M	93	LEU
1	M	105	LYS
1	M	106	LEU
1	M	108	LEU
1	M	137	LYS
1	M	140	LYS
1	N	5	GLU
1	N	21	LEU
1	N	25	GLN
1	N	28	THR
1	N	38	LEU
1	N	39	LEU
1	N	49	GLU
1	N	52	LEU
1	N	88	VAL
1	N	93	LEU

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Mol	Chain	Res	Type
1	N	105	LYS
1	N	106	LEU
1	N	108	LEU
1	N	137	LYS
1	N	140	LYS
1	O	5	GLU
1	O	21	LEU
1	O	25	GLN
1	O	28	THR
1	O	38	LEU
1	O	39	LEU
1	O	49	GLU
1	O	52	LEU
1	O	88	VAL
1	O	93	LEU
1	O	105	LYS
1	O	106	LEU
1	O	108	LEU
1	O	137	LYS
1	O	140	LYS
1	P	5	GLU
1	P	21	LEU
1	P	25	GLN
1	P	28	THR
1	P	38	LEU
1	P	39	LEU
1	P	49	GLU
1	P	52	LEU
1	P	88	VAL
1	P	93	LEU
1	P	105	LYS
1	P	106	LEU
1	P	108	LEU
1	P	137	LYS
1	P	140	LYS
1	Q	5	GLU
1	Q	21	LEU
1	Q	25	GLN
1	Q	28	THR
1	Q	38	LEU
1	Q	39	LEU
1	Q	49	GLU

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Mol	Chain	Res	Type
1	Q	52	LEU
1	Q	88	VAL
1	Q	93	LEU
1	Q	105	LYS
1	Q	106	LEU
1	Q	108	LEU
1	Q	137	LYS
1	Q	140	LYS
1	R	5	GLU
1	R	21	LEU
1	R	25	GLN
1	R	28	THR
1	R	38	LEU
1	R	39	LEU
1	R	49	GLU
1	R	52	LEU
1	R	88	VAL
1	R	93	LEU
1	R	105	LYS
1	R	106	LEU
1	R	108	LEU
1	R	137	LYS
1	R	140	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (101) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	53	ASN
1	A	98	ASN
1	A	99	ASN
1	A	146	HIS
1	A	154	ASN
1	B	25	GLN
1	B	53	ASN
1	B	98	ASN
1	B	99	ASN
1	B	146	HIS
1	B	154	ASN
1	C	25	GLN
1	C	53	ASN
1	C	98	ASN

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Mol	Chain	Res	Type
1	C	99	ASN
1	C	146	HIS
1	C	154	ASN
1	D	25	GLN
1	D	53	ASN
1	D	98	ASN
1	D	99	ASN
1	D	146	HIS
1	D	154	ASN
1	E	25	GLN
1	E	43	GLN
1	E	53	ASN
1	E	98	ASN
1	E	99	ASN
1	E	146	HIS
1	E	154	ASN
1	F	53	ASN
1	F	98	ASN
1	F	146	HIS
1	F	154	ASN
1	G	53	ASN
1	G	98	ASN
1	G	146	HIS
1	G	154	ASN
1	H	53	ASN
1	H	98	ASN
1	H	146	HIS
1	H	154	ASN
1	I	53	ASN
1	I	98	ASN
1	I	146	HIS
1	I	154	ASN
1	J	25	GLN
1	J	53	ASN
1	J	98	ASN
1	J	99	ASN
1	J	146	HIS
1	J	154	ASN
1	K	25	GLN
1	K	53	ASN
1	K	98	ASN
1	K	99	ASN

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Mol	Chain	Res	Type
1	K	146	HIS
1	K	154	ASN
1	L	25	GLN
1	L	53	ASN
1	L	98	ASN
1	L	99	ASN
1	L	146	HIS
1	L	154	ASN
1	M	25	GLN
1	M	53	ASN
1	M	98	ASN
1	M	99	ASN
1	M	146	HIS
1	M	154	ASN
1	N	25	GLN
1	N	53	ASN
1	N	98	ASN
1	N	99	ASN
1	N	146	HIS
1	N	154	ASN
1	O	25	GLN
1	O	53	ASN
1	O	98	ASN
1	O	99	ASN
1	O	146	HIS
1	O	154	ASN
1	P	25	GLN
1	P	43	GLN
1	P	53	ASN
1	P	98	ASN
1	P	99	ASN
1	P	146	HIS
1	P	154	ASN
1	Q	25	GLN
1	Q	53	ASN
1	Q	98	ASN
1	Q	99	ASN
1	Q	146	HIS
1	Q	154	ASN
1	R	25	GLN
1	R	53	ASN
1	R	98	ASN

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Mol	Chain	Res	Type
1	R	146	HIS
1	R	154	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

18 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	MEA	A	1	1	10,11,13	0.62	0	8,13,16	0.21	0
1	MEA	G	1	1	10,11,13	0.63	0	8,13,16	0.22	0
1	MEA	O	1	1	10,11,13	0.64	0	8,13,16	0.25	0
1	MEA	Q	1	1	10,11,13	0.64	0	8,13,16	0.25	0
1	MEA	D	1	1	10,11,13	0.63	0	8,13,16	0.22	0
1	MEA	C	1	1	10,11,13	0.62	0	8,13,16	0.21	0
1	MEA	I	1	1	10,11,13	0.63	0	8,13,16	0.22	0
1	MEA	J	1	1	10,11,13	0.62	0	8,13,16	0.22	0
1	MEA	K	1	1	10,11,13	0.62	0	8,13,16	0.22	0
1	MEA	M	1	1	10,11,13	0.63	0	8,13,16	0.24	0
1	MEA	N	1	1	10,11,13	0.64	0	8,13,16	0.24	0
1	MEA	L	1	1	10,11,13	0.63	0	8,13,16	0.22	0
1	MEA	R	1	1	10,11,13	0.64	0	8,13,16	0.23	0
1	MEA	B	1	1	10,11,13	0.62	0	8,13,16	0.21	0
1	MEA	F	1	1	10,11,13	0.63	0	8,13,16	0.21	0
1	MEA	E	1	1	10,11,13	0.63	0	8,13,16	0.22	0
1	MEA	P	1	1	10,11,13	0.64	0	8,13,16	0.25	0
1	MEA	H	1	1	10,11,13	0.63	0	8,13,16	0.22	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MEA	A	1	1	-	0/5/6/10	0/1/1/1
1	MEA	G	1	1	-	0/5/6/10	0/1/1/1
1	MEA	O	1	1	-	0/5/6/10	0/1/1/1
1	MEA	Q	1	1	-	0/5/6/10	0/1/1/1
1	MEA	D	1	1	-	0/5/6/10	0/1/1/1
1	MEA	C	1	1	-	0/5/6/10	0/1/1/1
1	MEA	I	1	1	-	0/5/6/10	0/1/1/1
1	MEA	J	1	1	-	0/5/6/10	0/1/1/1
1	MEA	K	1	1	-	0/5/6/10	0/1/1/1
1	MEA	M	1	1	-	0/5/6/10	0/1/1/1
1	MEA	N	1	1	-	0/5/6/10	0/1/1/1
1	MEA	L	1	1	-	0/5/6/10	0/1/1/1
1	MEA	R	1	1	-	0/5/6/10	0/1/1/1
1	MEA	B	1	1	-	0/5/6/10	0/1/1/1
1	MEA	F	1	1	-	0/5/6/10	0/1/1/1
1	MEA	E	1	1	-	0/5/6/10	0/1/1/1
1	MEA	P	1	1	-	0/5/6/10	0/1/1/1
1	MEA	H	1	1	-	0/5/6/10	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

17 monomers are involved in 279 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1	MEA	17	0
1	G	1	MEA	16	0
1	O	1	MEA	17	0
1	Q	1	MEA	16	0
1	D	1	MEA	17	0
1	C	1	MEA	15	0
1	J	1	MEA	16	0
1	K	1	MEA	15	0
1	M	1	MEA	17	0
1	N	1	MEA	16	0
1	L	1	MEA	17	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	R	1	MEA	17	0
1	B	1	MEA	17	0
1	F	1	MEA	17	0
1	E	1	MEA	15	0
1	P	1	MEA	17	0
1	H	1	MEA	17	0

5.5 Carbohydrates

36 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	DT6	S	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	S	2	2	11,11,12	0.39	0	15,15,17	0.71	0
2	DT6	T	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	T	2	2	11,11,12	0.38	0	15,15,17	0.71	0
2	DT6	U	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	U	2	2	11,11,12	0.38	0	15,15,17	0.71	0
2	DT6	V	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	V	2	2	11,11,12	0.38	0	15,15,17	0.71	0
2	DT6	W	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	W	2	2	11,11,12	0.37	0	15,15,17	0.71	0
2	DT6	X	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	X	2	2	11,11,12	0.36	0	15,15,17	0.72	0
2	DT6	Y	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	Y	2	2	11,11,12	0.38	0	15,15,17	0.71	0
2	DT6	Z	1	2,1	17,17,18	0.63	0	17,23,25	0.72	1 (5%)
2	GLA	Z	2	2	11,11,12	0.38	0	15,15,17	0.71	0
2	DT6	a	1	2,1	17,17,18	0.62	0	17,23,25	0.72	1 (5%)
2	GLA	a	2	2	11,11,12	0.37	0	15,15,17	0.71	0
2	DT6	b	1	2,1	17,17,18	0.62	0	17,23,25	0.73	1 (5%)
2	GLA	b	2	2	11,11,12	0.38	0	15,15,17	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	DT6	c	1	2,1	17,17,18	0.63	0	17,23,25	0.73	1 (5%)
2	GLA	c	2	2	11,11,12	0.37	0	15,15,17	0.71	0
2	DT6	d	1	2,1	17,17,18	0.63	0	17,23,25	0.74	1 (5%)
2	GLA	d	2	2	11,11,12	0.38	0	15,15,17	0.71	0
2	DT6	e	1	2,1	17,17,18	0.63	0	17,23,25	0.73	1 (5%)
2	GLA	e	2	2	11,11,12	0.37	0	15,15,17	0.71	0
2	DT6	f	1	2,1	17,17,18	0.63	0	17,23,25	0.72	1 (5%)
2	GLA	f	2	2	11,11,12	0.38	0	15,15,17	0.71	0
2	DT6	g	1	2,1	17,17,18	0.63	0	17,23,25	0.72	1 (5%)
2	GLA	g	2	2	11,11,12	0.37	0	15,15,17	0.71	0
2	DT6	h	1	2,1	17,17,18	0.63	0	17,23,25	0.71	1 (5%)
2	GLA	h	2	2	11,11,12	0.37	0	15,15,17	0.72	0
2	DT6	i	1	2,1	17,17,18	0.64	0	17,23,25	0.70	1 (5%)
2	GLA	i	2	2	11,11,12	0.36	0	15,15,17	0.72	0
2	DT6	j	1	2,1	17,17,18	0.64	0	17,23,25	0.70	1 (5%)
2	GLA	j	2	2	11,11,12	0.37	0	15,15,17	0.72	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DT6	S	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	S	2	2	-	1/2/19/22	0/1/1/1
2	DT6	T	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	T	2	2	-	1/2/19/22	0/1/1/1
2	DT6	U	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	U	2	2	-	1/2/19/22	0/1/1/1
2	DT6	V	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	V	2	2	-	1/2/19/22	0/1/1/1
2	DT6	W	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	W	2	2	-	1/2/19/22	0/1/1/1
2	DT6	X	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	X	2	2	-	1/2/19/22	0/1/1/1
2	DT6	Y	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	Y	2	2	-	1/2/19/22	0/1/1/1
2	DT6	Z	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	Z	2	2	-	1/2/19/22	0/1/1/1
2	DT6	a	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	a	2	2	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DT6	b	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	b	2	2	-	1/2/19/22	0/1/1/1
2	DT6	c	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	c	2	2	-	1/2/19/22	0/1/1/1
2	DT6	d	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	d	2	2	-	1/2/19/22	0/1/1/1
2	DT6	e	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	e	2	2	-	1/2/19/22	0/1/1/1
2	DT6	f	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	f	2	2	-	1/2/19/22	0/1/1/1
2	DT6	g	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	g	2	2	-	1/2/19/22	0/1/1/1
2	DT6	h	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	h	2	2	-	1/2/19/22	0/1/1/1
2	DT6	i	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	i	2	2	-	1/2/19/22	0/1/1/1
2	DT6	j	1	2,1	-	1/10/27/30	0/1/1/1
2	GLA	j	2	2	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	d	1	DT6	C2-N2-C7	-2.19	119.96	122.90
2	b	1	DT6	C2-N2-C7	-2.18	119.98	122.90
2	e	1	DT6	C2-N2-C7	-2.17	120.00	122.90
2	f	1	DT6	C2-N2-C7	-2.17	120.00	122.90
2	c	1	DT6	C2-N2-C7	-2.16	120.01	122.90
2	U	1	DT6	C2-N2-C7	-2.15	120.02	122.90
2	Y	1	DT6	C2-N2-C7	-2.15	120.02	122.90
2	S	1	DT6	C2-N2-C7	-2.15	120.02	122.90
2	W	1	DT6	C2-N2-C7	-2.15	120.02	122.90
2	X	1	DT6	C2-N2-C7	-2.14	120.03	122.90
2	Z	1	DT6	C2-N2-C7	-2.14	120.03	122.90
2	g	1	DT6	C2-N2-C7	-2.14	120.03	122.90
2	V	1	DT6	C2-N2-C7	-2.13	120.04	122.90
2	T	1	DT6	C2-N2-C7	-2.13	120.04	122.90
2	a	1	DT6	C2-N2-C7	-2.12	120.06	122.90
2	h	1	DT6	C2-N2-C7	-2.12	120.06	122.90
2	j	1	DT6	C2-N2-C7	-2.10	120.08	122.90
2	i	1	DT6	C2-N2-C7	-2.10	120.09	122.90

There are no chirality outliers.

All (36) torsion outliers are listed below:

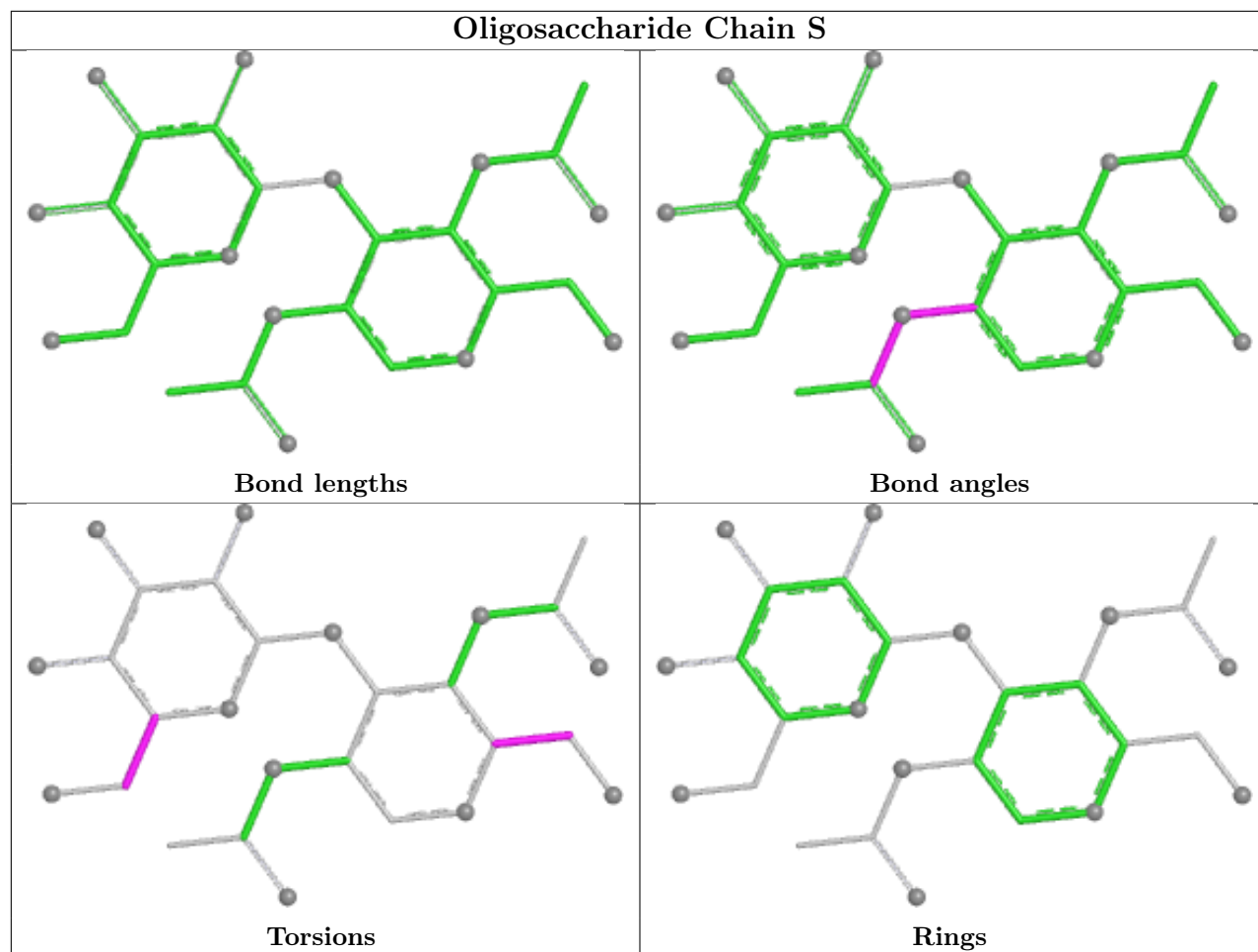
Mol	Chain	Res	Type	Atoms
2	W	2	GLA	O5-C5-C6-O6
2	X	2	GLA	O5-C5-C6-O6
2	h	2	GLA	O5-C5-C6-O6
2	i	2	GLA	O5-C5-C6-O6
2	S	2	GLA	O5-C5-C6-O6
2	T	2	GLA	O5-C5-C6-O6
2	U	2	GLA	O5-C5-C6-O6
2	V	2	GLA	O5-C5-C6-O6
2	Y	2	GLA	O5-C5-C6-O6
2	Z	2	GLA	O5-C5-C6-O6
2	a	2	GLA	O5-C5-C6-O6
2	b	2	GLA	O5-C5-C6-O6
2	c	2	GLA	O5-C5-C6-O6
2	d	2	GLA	O5-C5-C6-O6
2	e	2	GLA	O5-C5-C6-O6
2	f	2	GLA	O5-C5-C6-O6
2	g	2	GLA	O5-C5-C6-O6
2	j	2	GLA	O5-C5-C6-O6
2	X	1	DT6	O5-C5-C6-O6
2	Y	1	DT6	O5-C5-C6-O6
2	Z	1	DT6	O5-C5-C6-O6
2	a	1	DT6	O5-C5-C6-O6
2	W	1	DT6	O5-C5-C6-O6
2	S	1	DT6	O5-C5-C6-O6
2	T	1	DT6	O5-C5-C6-O6
2	U	1	DT6	O5-C5-C6-O6
2	V	1	DT6	O5-C5-C6-O6
2	b	1	DT6	O5-C5-C6-O6
2	c	1	DT6	O5-C5-C6-O6
2	d	1	DT6	O5-C5-C6-O6
2	e	1	DT6	O5-C5-C6-O6
2	f	1	DT6	O5-C5-C6-O6
2	g	1	DT6	O5-C5-C6-O6
2	h	1	DT6	O5-C5-C6-O6
2	i	1	DT6	O5-C5-C6-O6
2	j	1	DT6	O5-C5-C6-O6

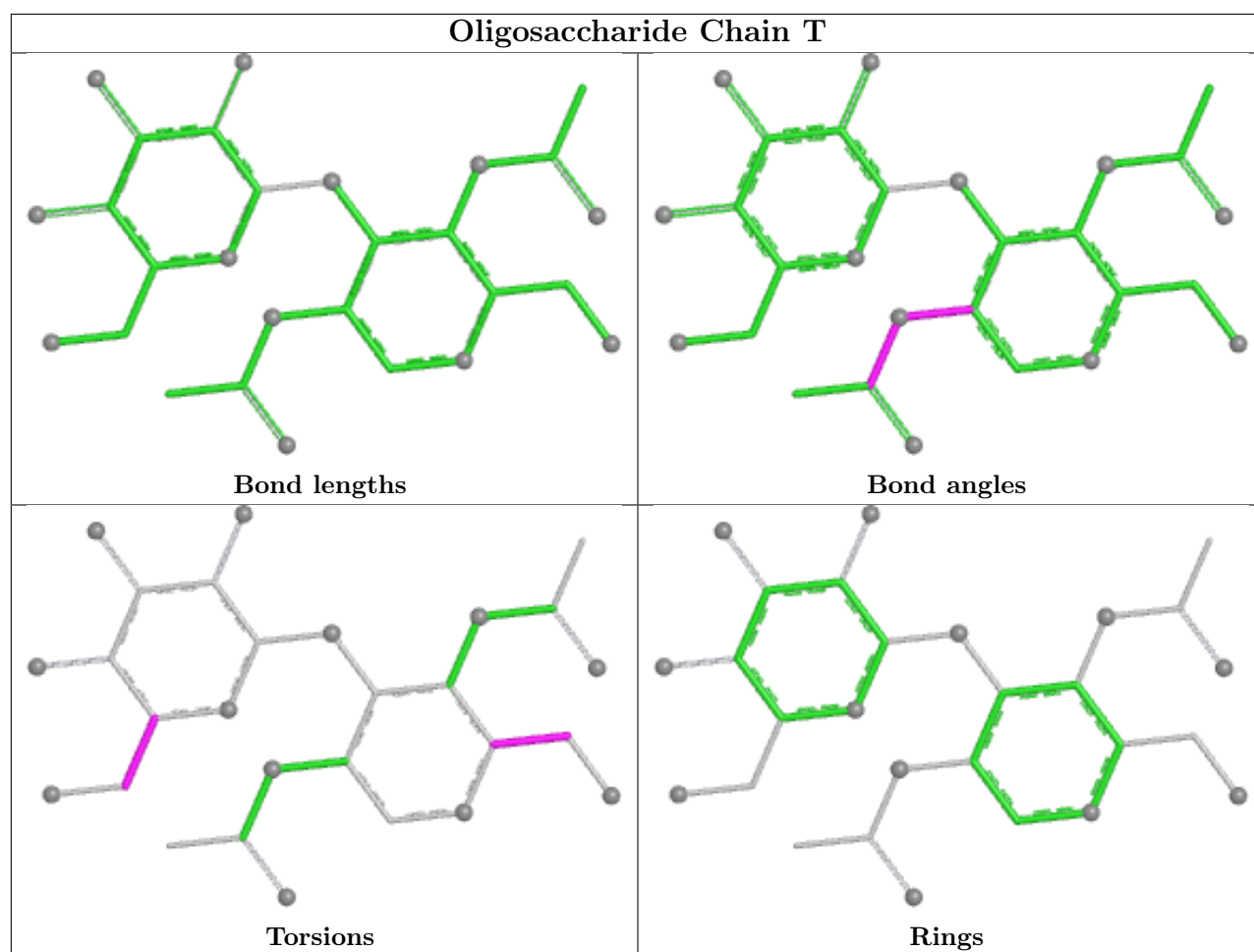
There are no ring outliers.

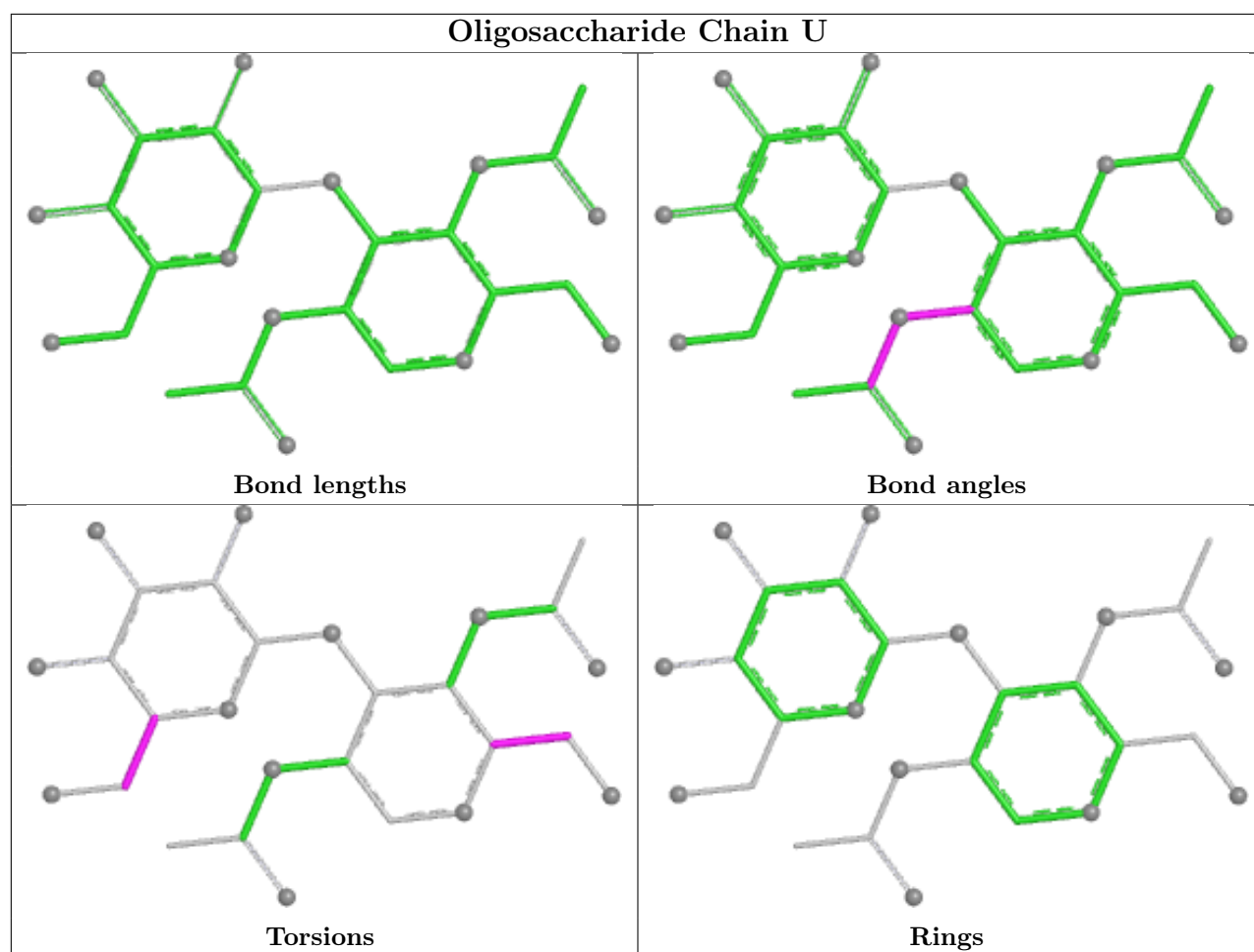
36 monomers are involved in 18 short contacts:

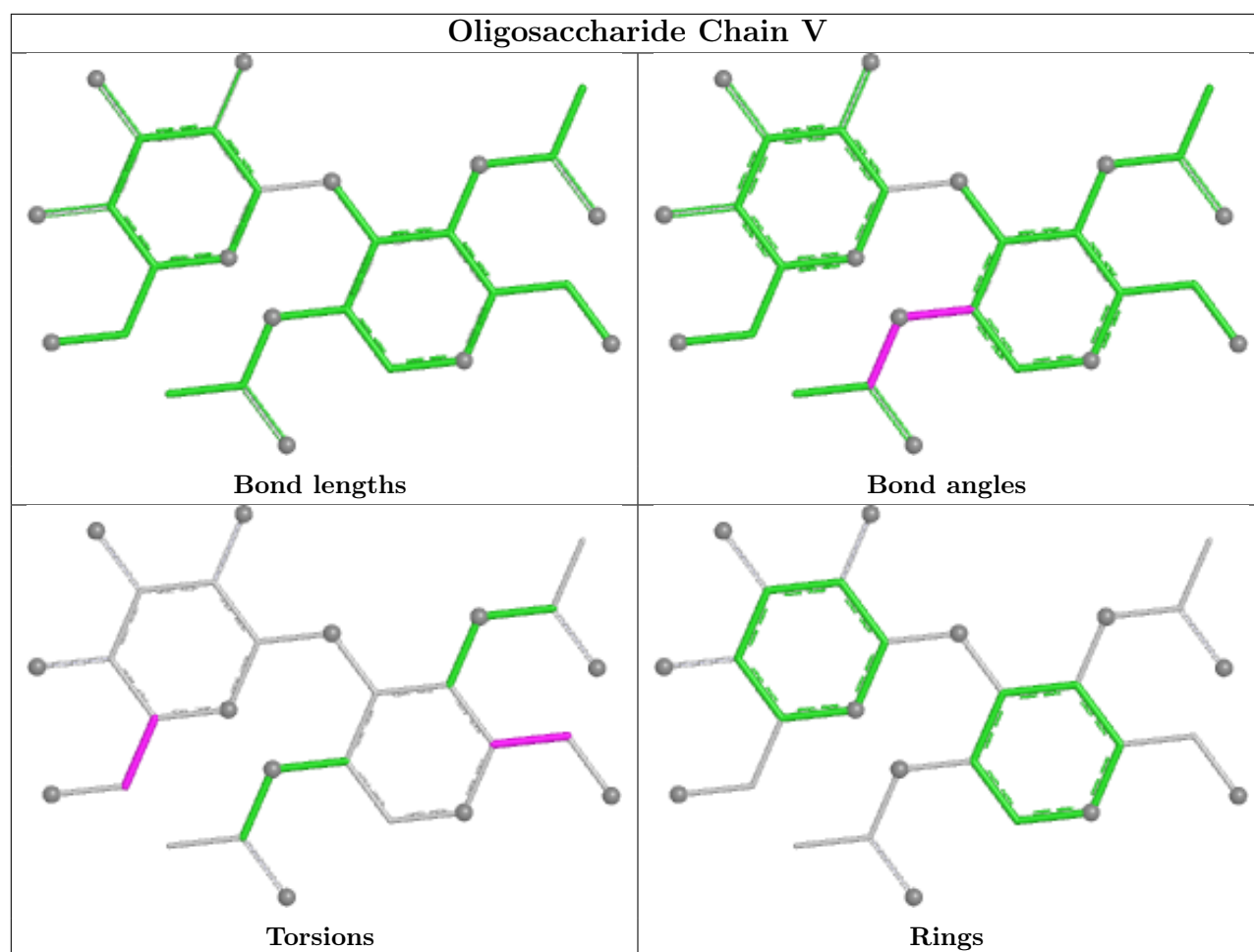
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	T	2	GLA	1	0
2	V	1	DT6	1	0
2	c	2	GLA	1	0
2	T	1	DT6	1	0
2	g	2	GLA	1	0
2	e	2	GLA	1	0
2	U	1	DT6	1	0
2	f	1	DT6	1	0
2	d	2	GLA	1	0
2	b	1	DT6	1	0
2	j	1	DT6	1	0
2	S	1	DT6	1	0
2	h	1	DT6	1	0
2	X	1	DT6	1	0
2	Z	2	GLA	1	0
2	i	2	GLA	1	0
2	Y	1	DT6	1	0
2	h	2	GLA	1	0
2	g	1	DT6	1	0
2	e	1	DT6	1	0
2	j	2	GLA	1	0
2	V	2	GLA	1	0
2	d	1	DT6	1	0
2	S	2	GLA	1	0
2	a	1	DT6	1	0
2	U	2	GLA	1	0
2	f	2	GLA	1	0
2	W	1	DT6	1	0
2	Z	1	DT6	1	0
2	b	2	GLA	1	0
2	c	1	DT6	1	0
2	i	1	DT6	1	0
2	a	2	GLA	1	0
2	W	2	GLA	1	0
2	X	2	GLA	1	0
2	Y	2	GLA	1	0

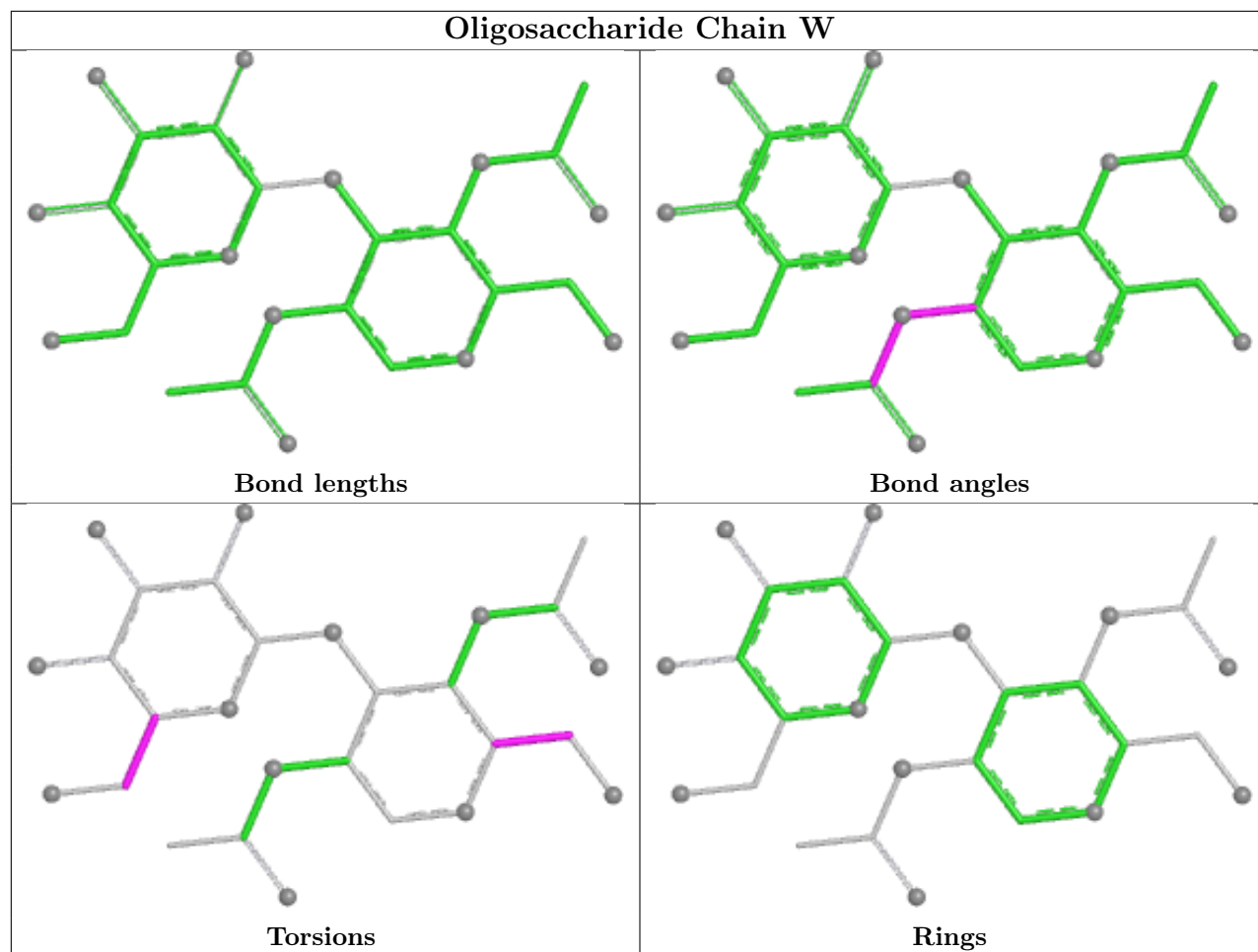
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

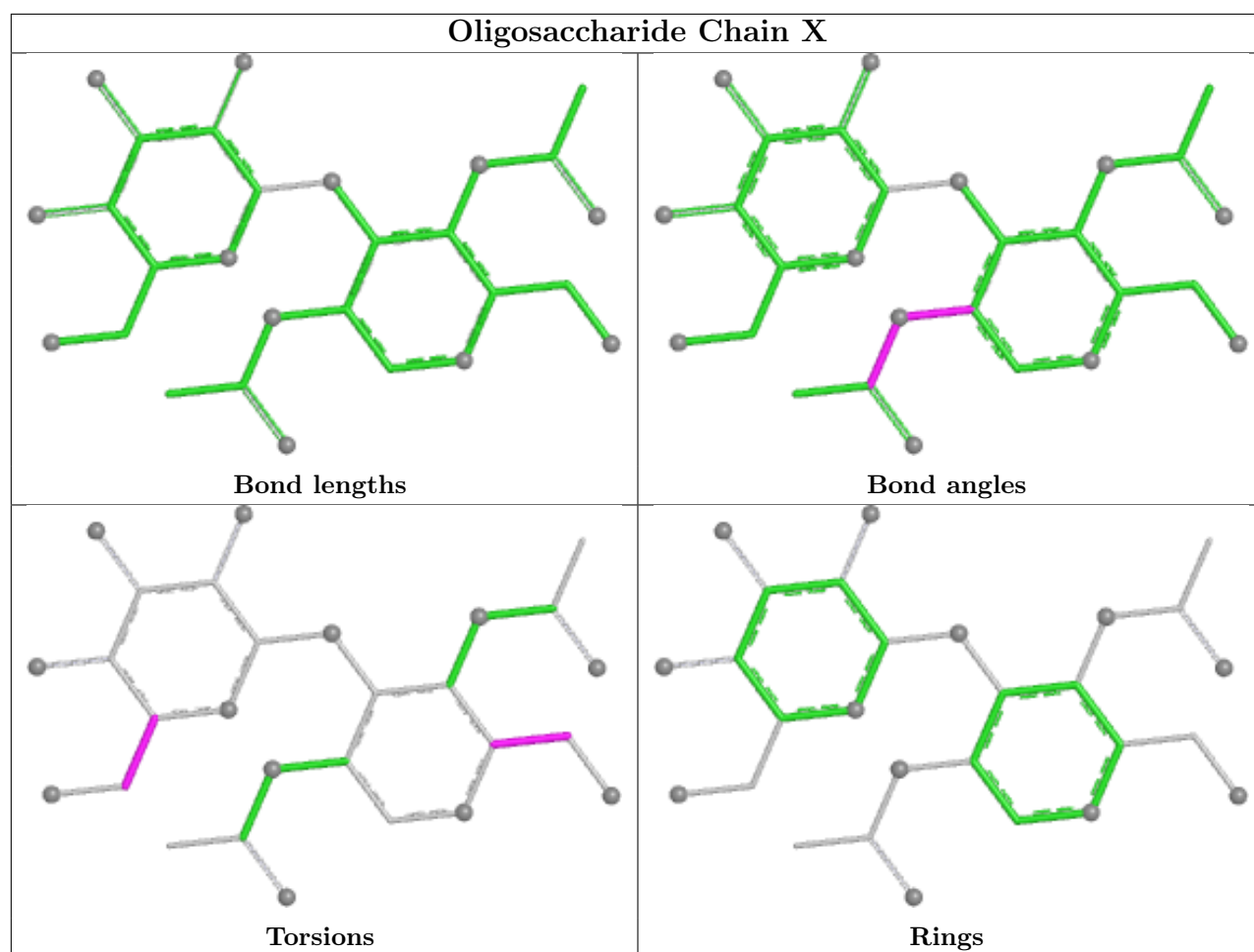


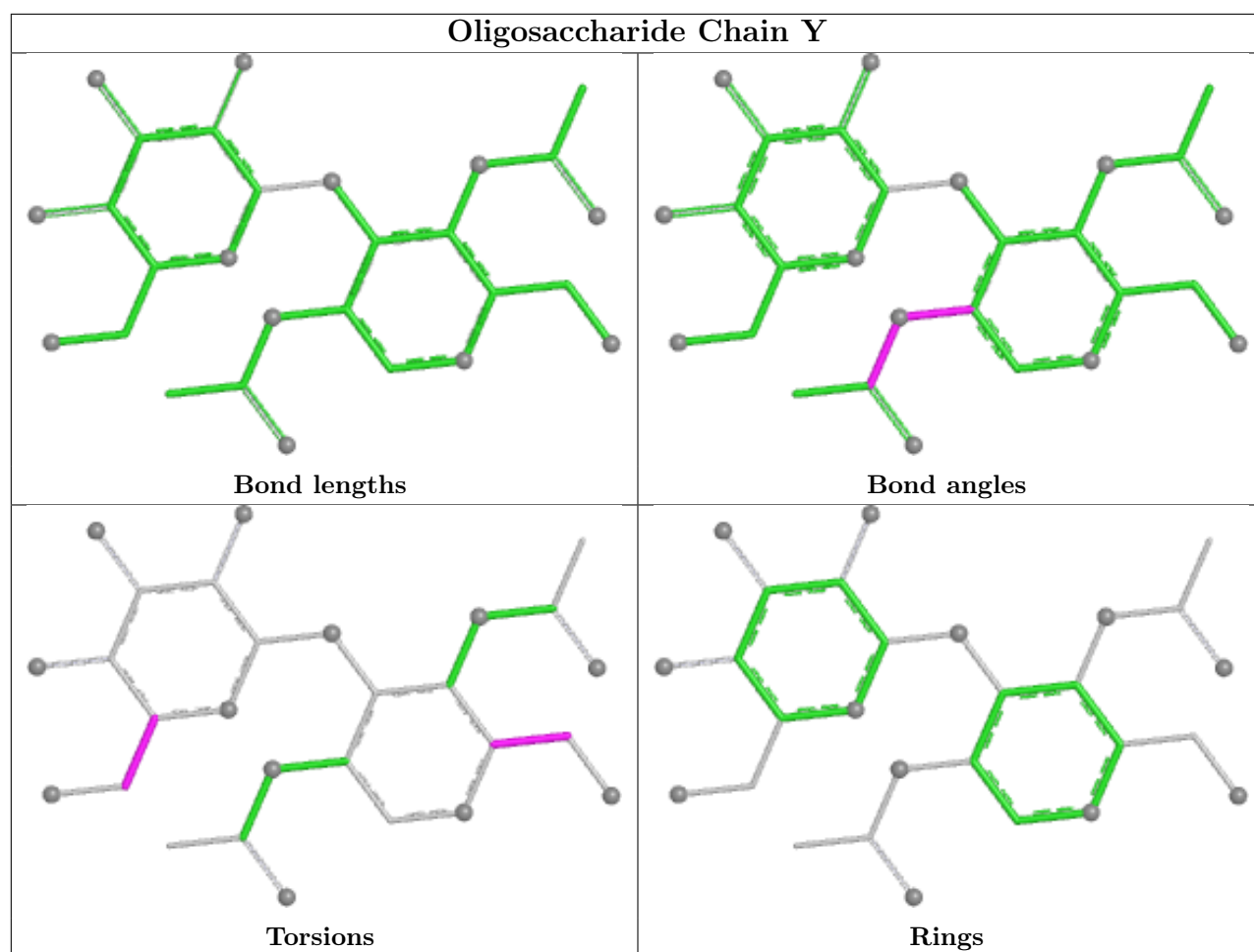


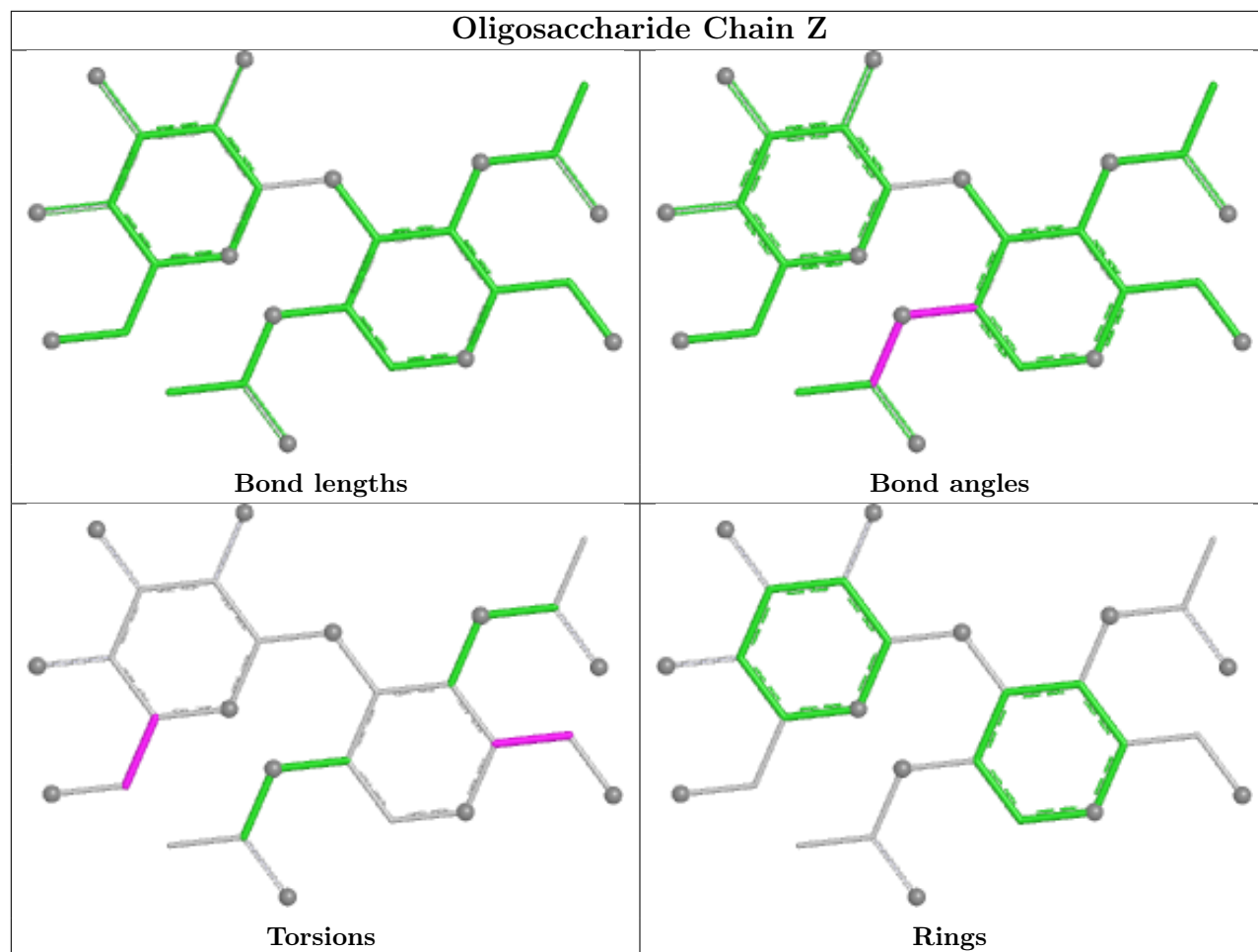


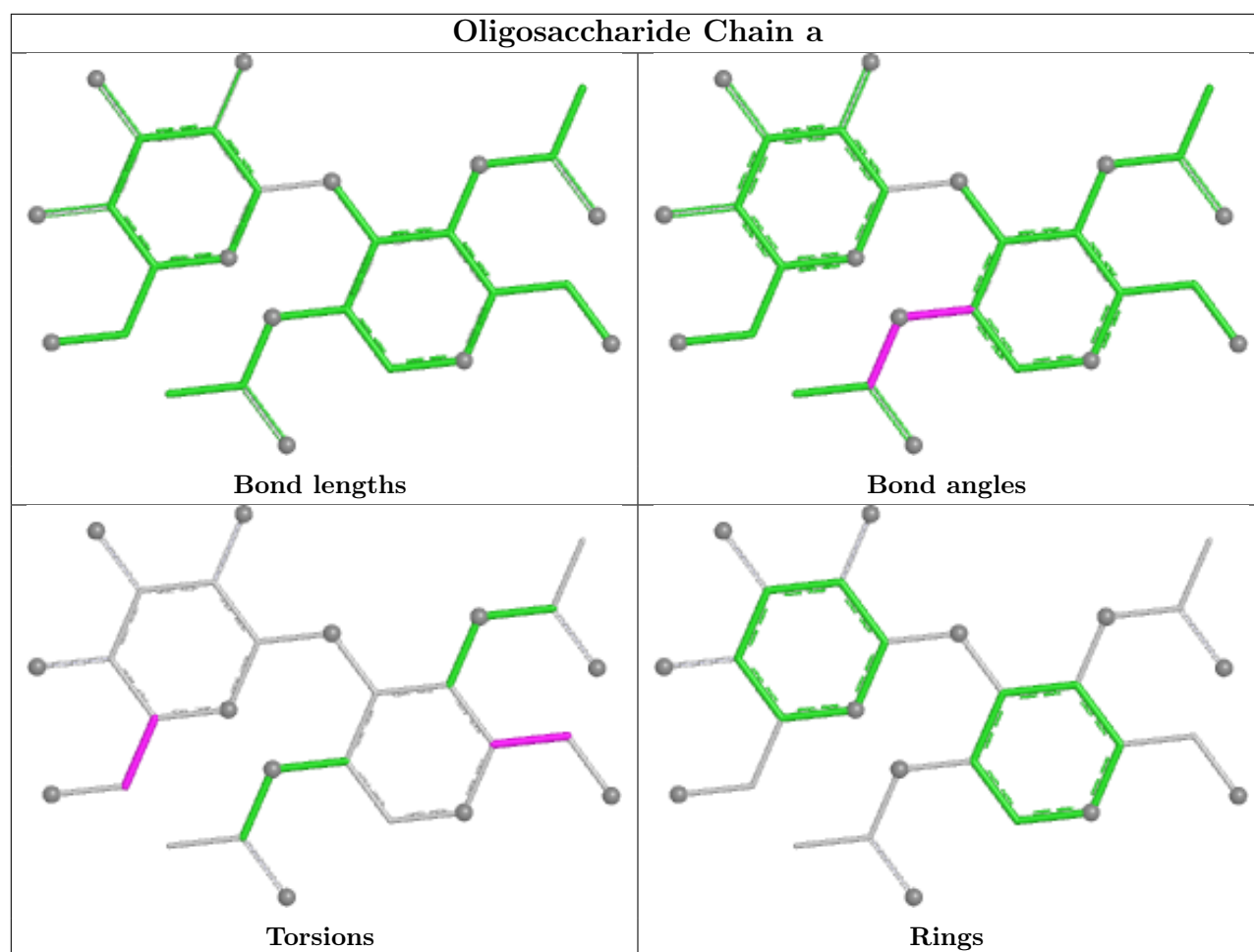


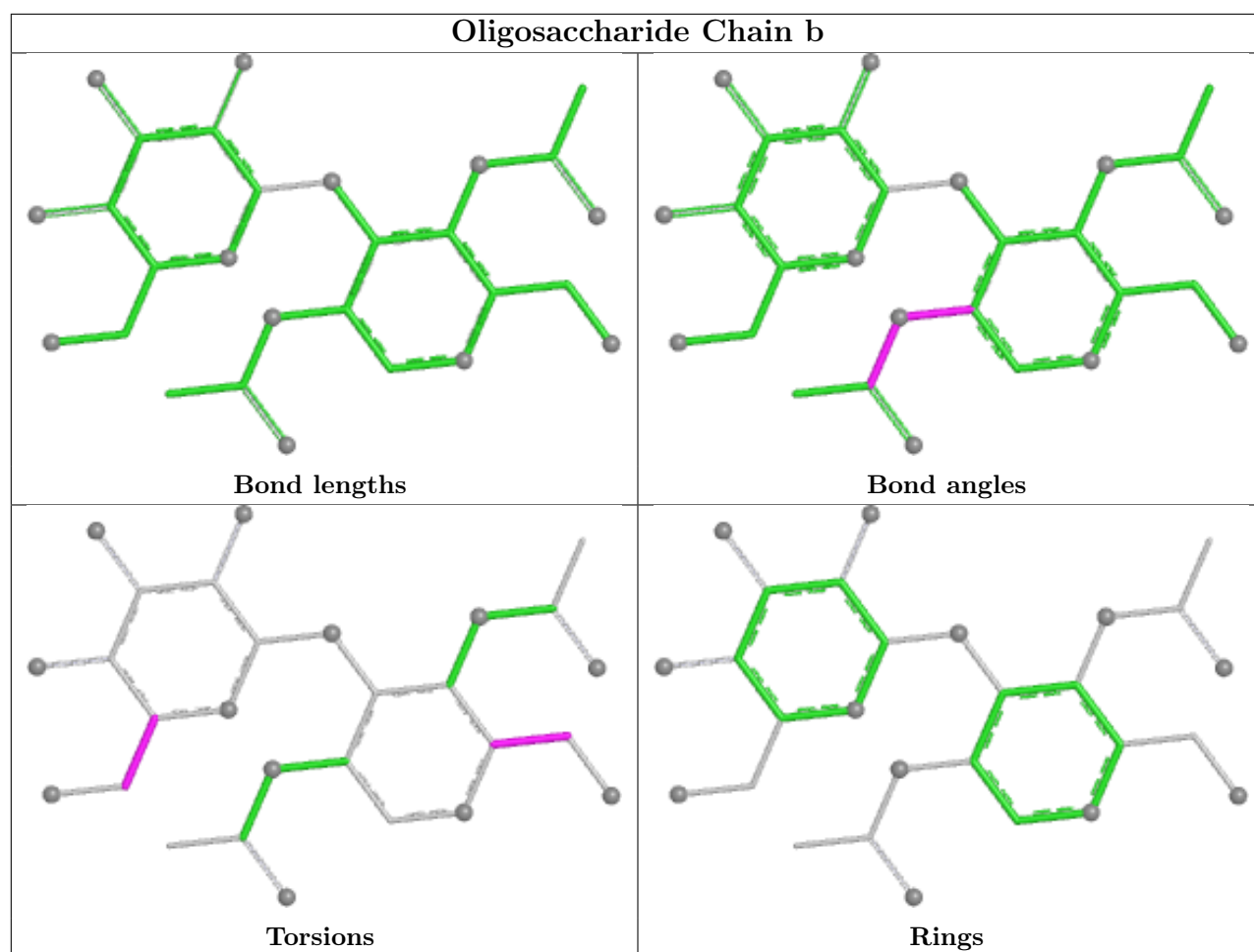


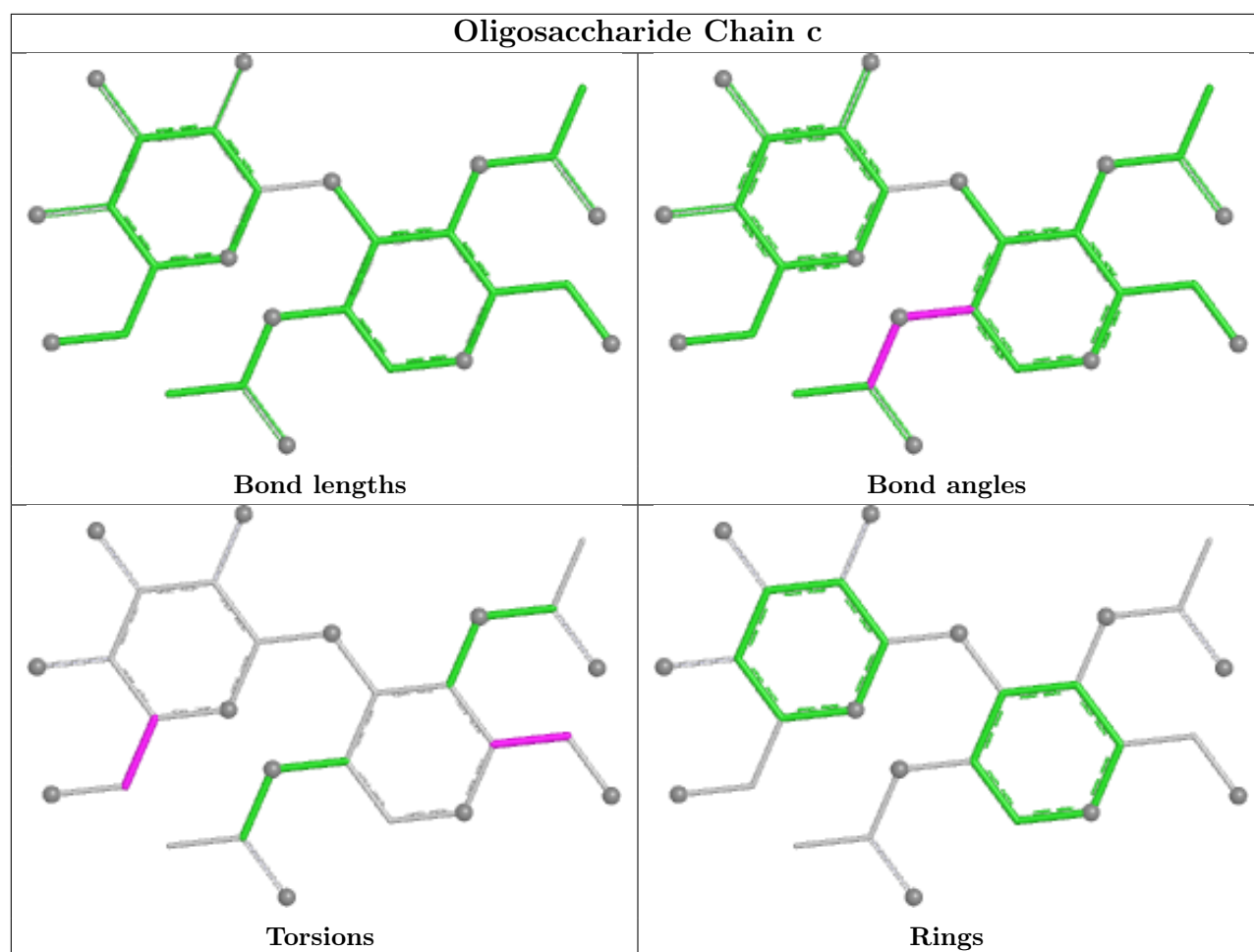


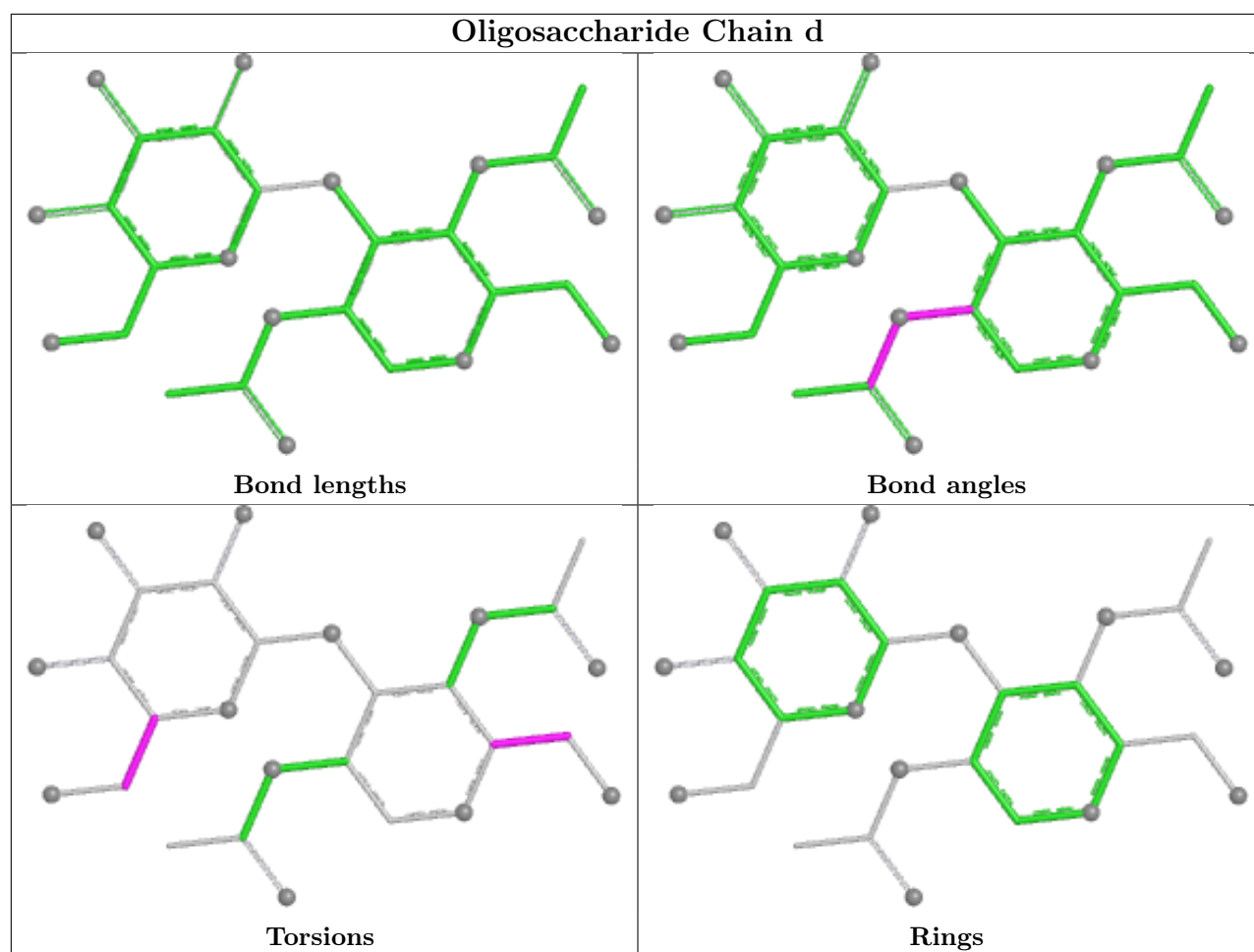


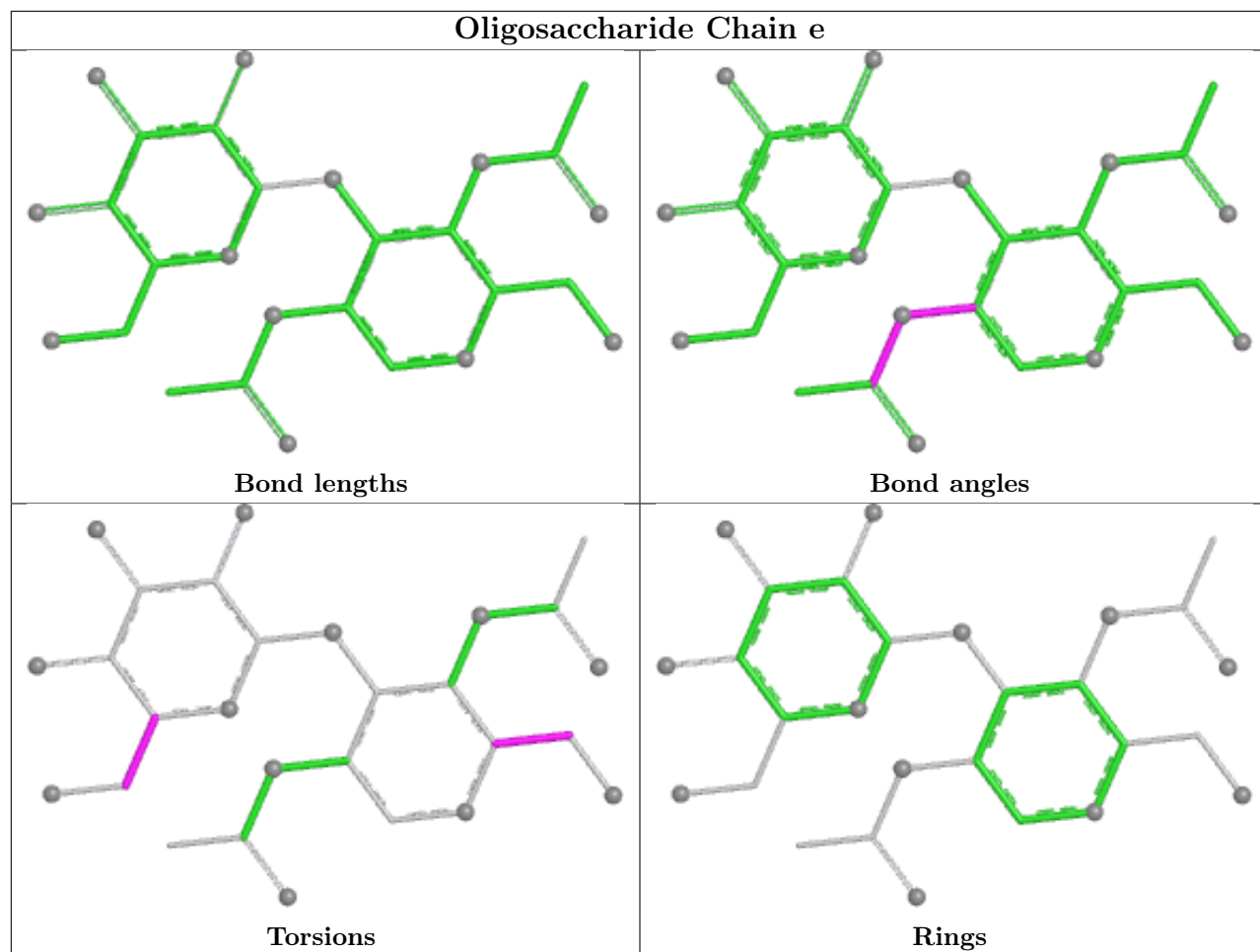


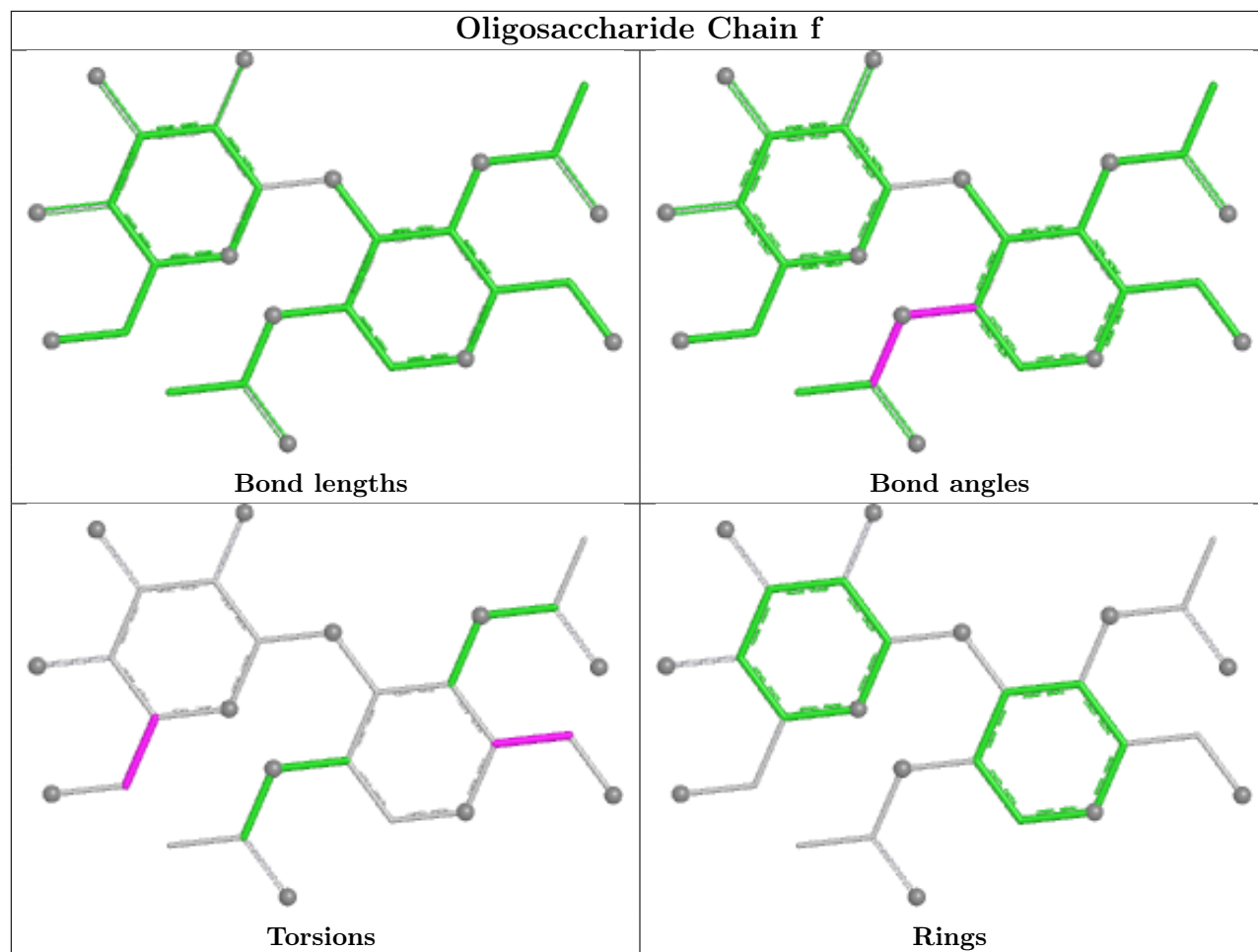


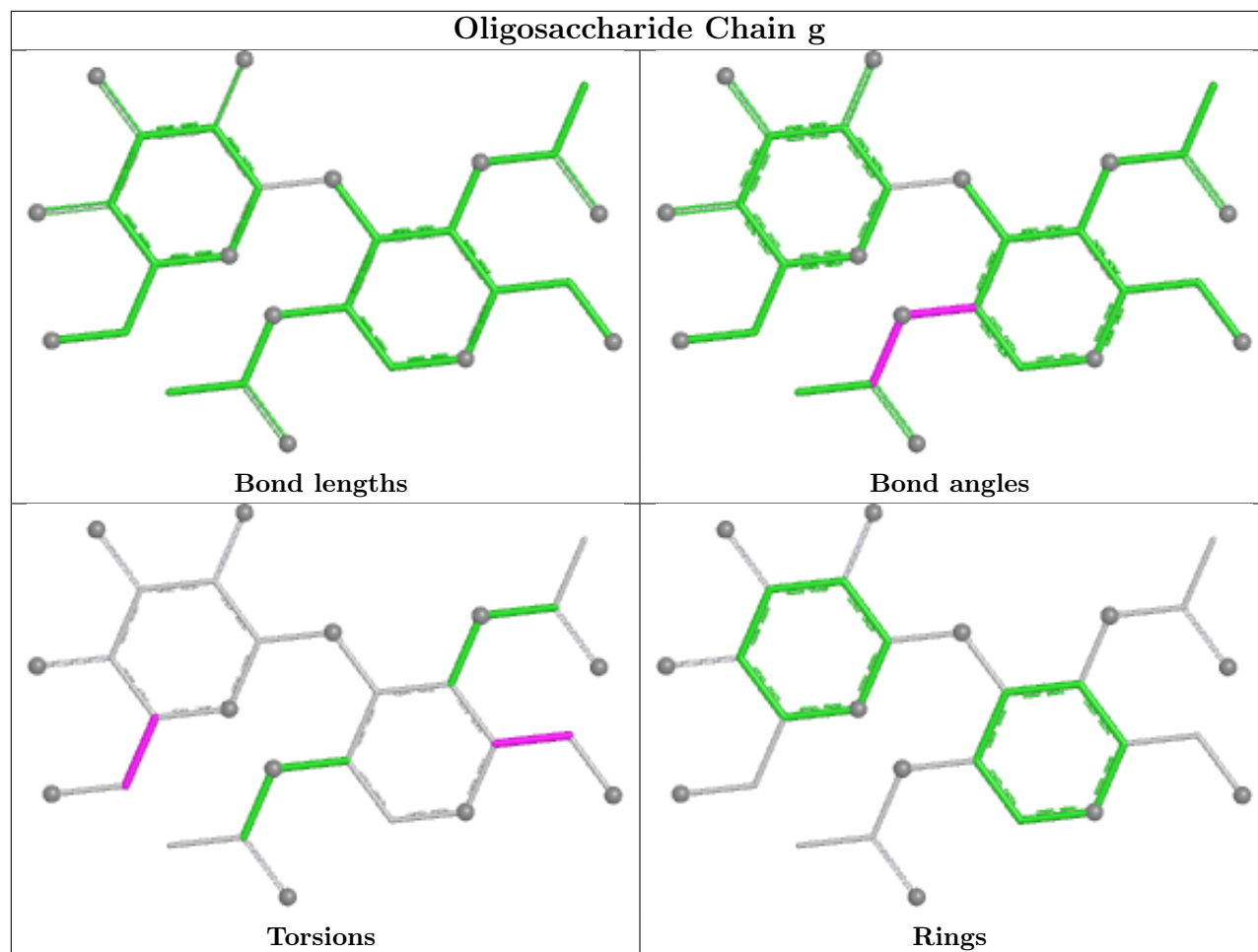


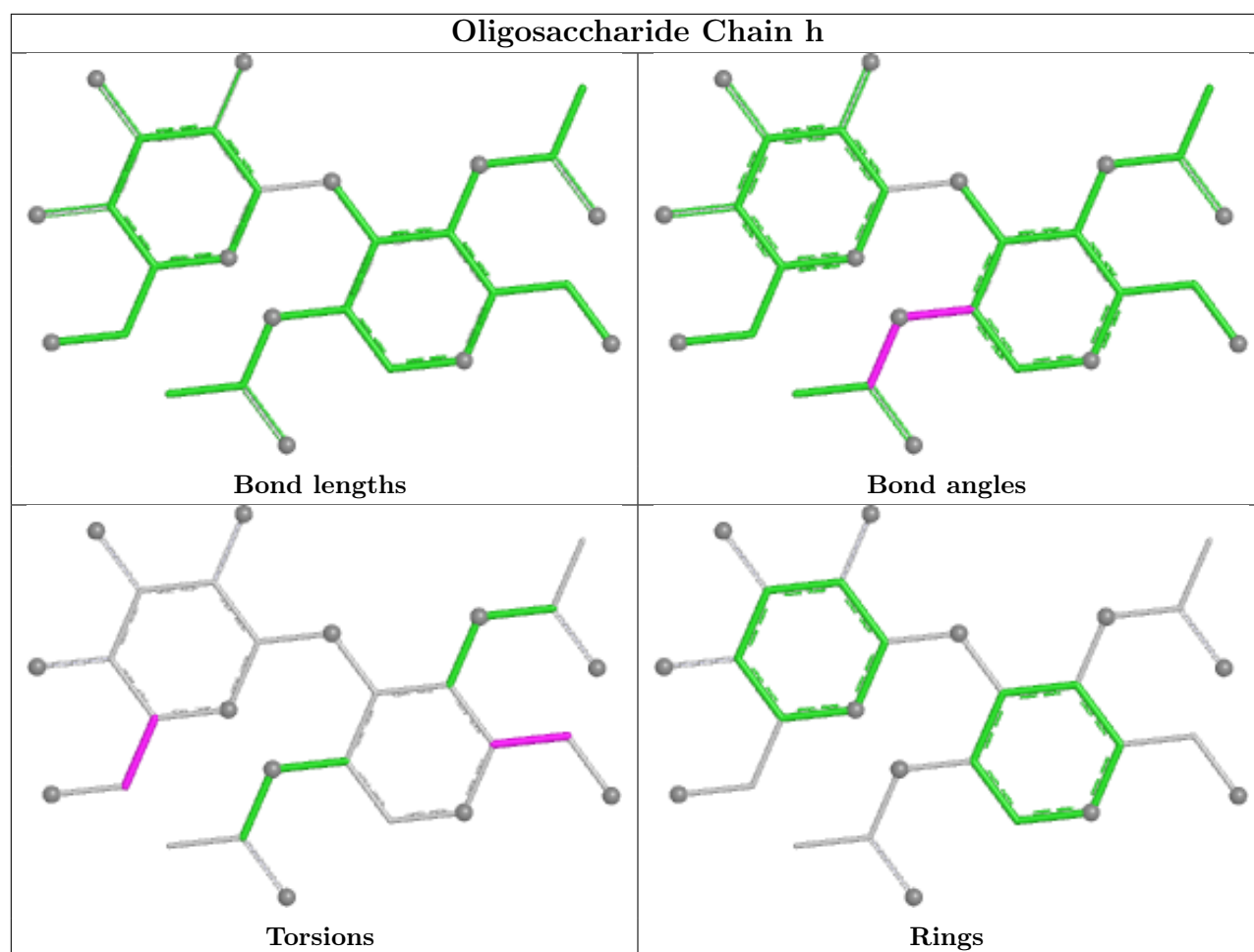


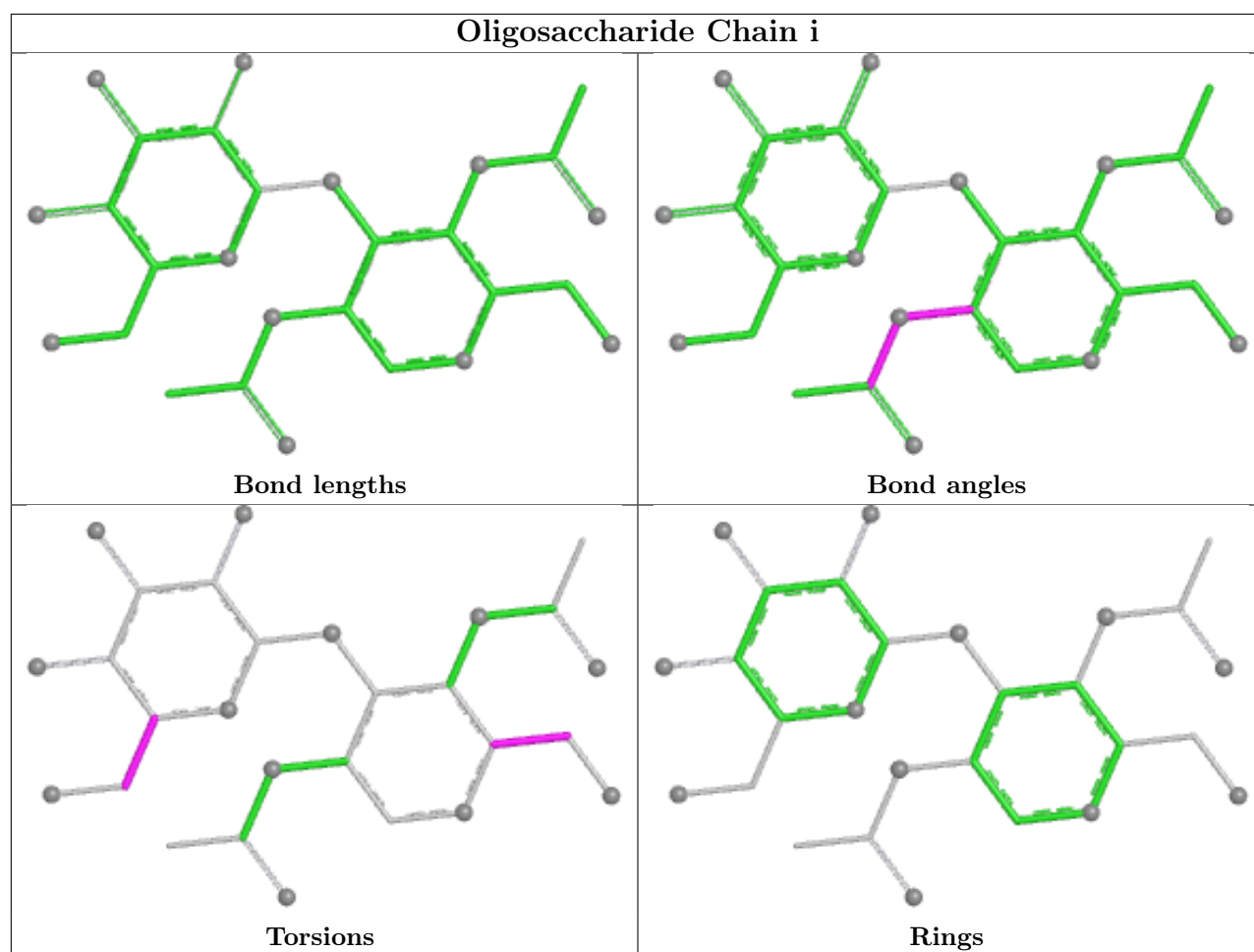


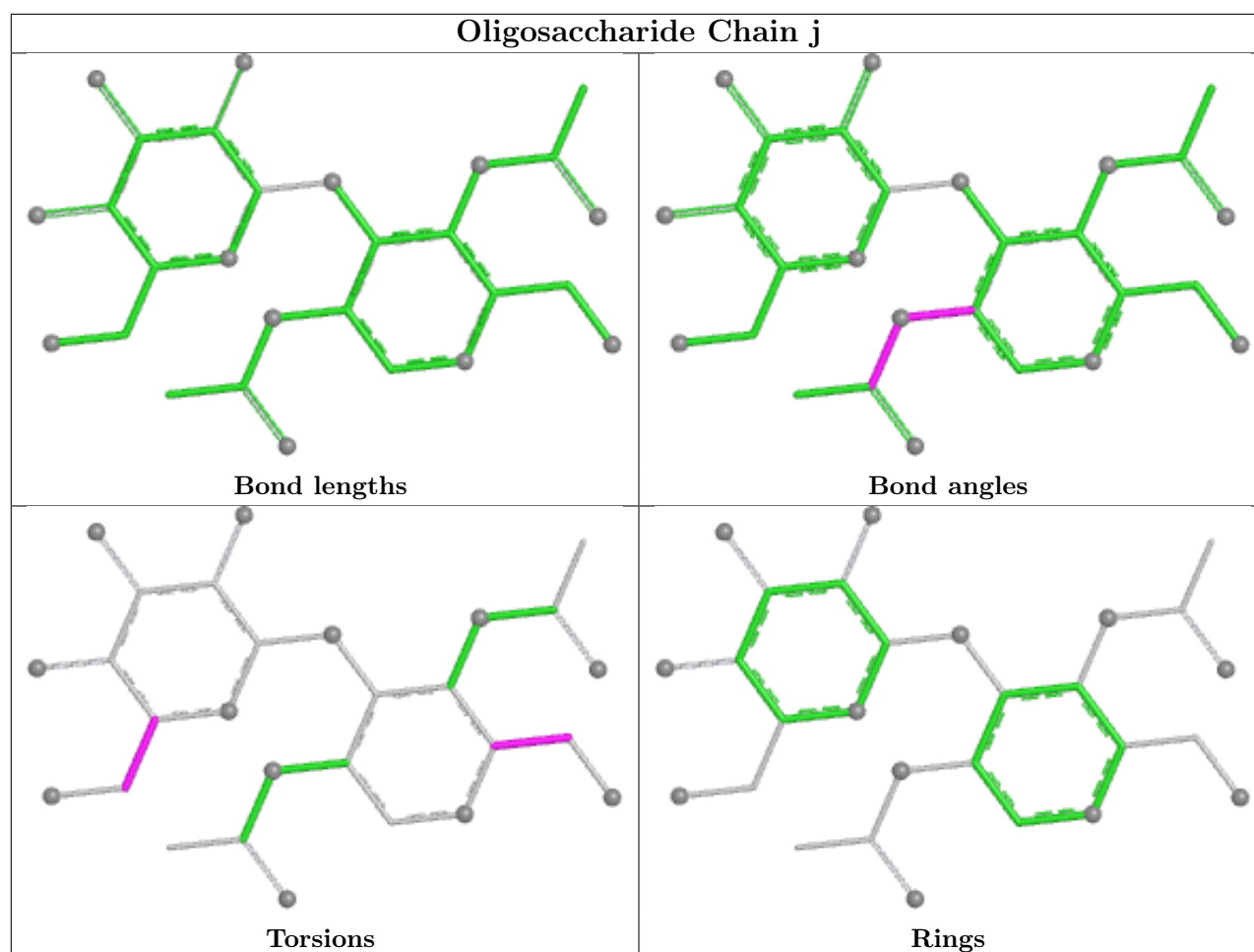












5.6 Ligand geometry [i](#)

18 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	OPE	H	824	1	7,7,7	0.91	0	9,9,9	0.98	0
3	OPE	E	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	J	824	1	7,7,7	0.91	0	9,9,9	0.99	0
3	OPE	C	824	1	7,7,7	0.92	0	9,9,9	0.98	0
3	OPE	L	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	A	824	1	7,7,7	0.92	0	9,9,9	0.99	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OPE	N	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	F	824	1	7,7,7	0.91	0	9,9,9	0.98	0
3	OPE	Q	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	K	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	D	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	M	824	1	7,7,7	0.93	0	9,9,9	0.99	0
3	OPE	R	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	P	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	G	824	1	7,7,7	0.91	0	9,9,9	0.98	0
3	OPE	I	824	1	7,7,7	0.91	0	9,9,9	0.98	0
3	OPE	B	824	1	7,7,7	0.92	0	9,9,9	0.99	0
3	OPE	O	824	1	7,7,7	0.92	0	9,9,9	0.99	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OPE	H	824	1	-	0/5/5/5	-
3	OPE	E	824	1	-	0/5/5/5	-
3	OPE	J	824	1	-	0/5/5/5	-
3	OPE	C	824	1	-	0/5/5/5	-
3	OPE	L	824	1	-	0/5/5/5	-
3	OPE	A	824	1	-	0/5/5/5	-
3	OPE	N	824	1	-	0/5/5/5	-
3	OPE	F	824	1	-	0/5/5/5	-
3	OPE	Q	824	1	-	0/5/5/5	-
3	OPE	K	824	1	-	0/5/5/5	-
3	OPE	D	824	1	-	0/5/5/5	-
3	OPE	M	824	1	-	0/5/5/5	-
3	OPE	R	824	1	-	0/5/5/5	-
3	OPE	P	824	1	-	0/5/5/5	-
3	OPE	G	824	1	-	0/5/5/5	-
3	OPE	I	824	1	-	0/5/5/5	-
3	OPE	B	824	1	-	0/5/5/5	-
3	OPE	O	824	1	-	0/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1236. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

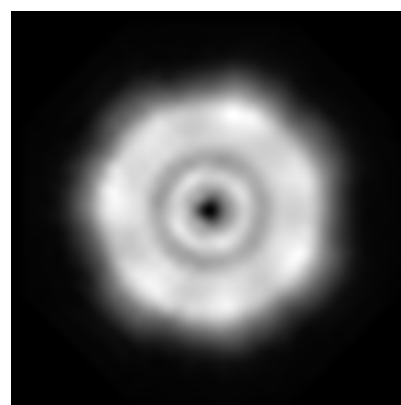
6.1.1 Primary map



X



Y

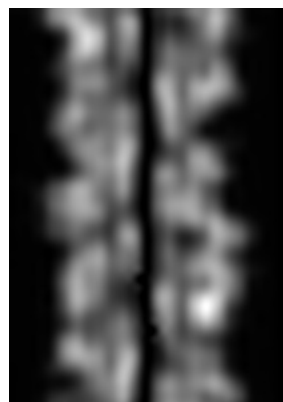


Z

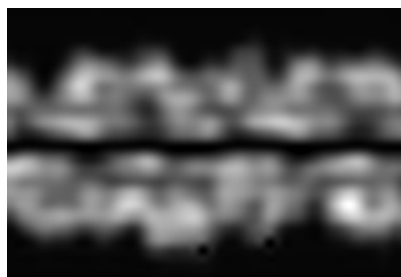
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

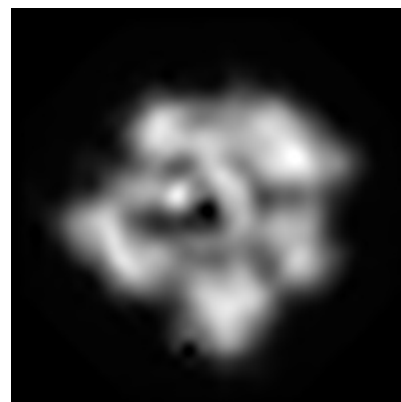
6.2.1 Primary map



X Index: 18



Y Index: 18



Z Index: 27

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: 26



Y Index: 26

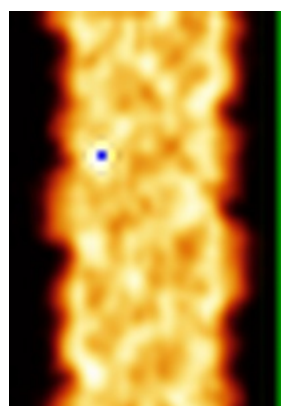


Z Index: 52

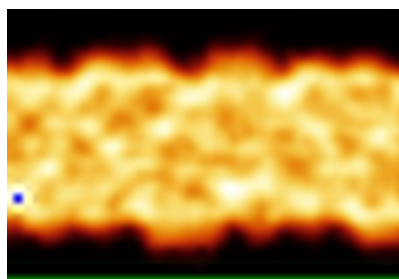
The images above show the largest variance slices of the map in three orthogonal directions.

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

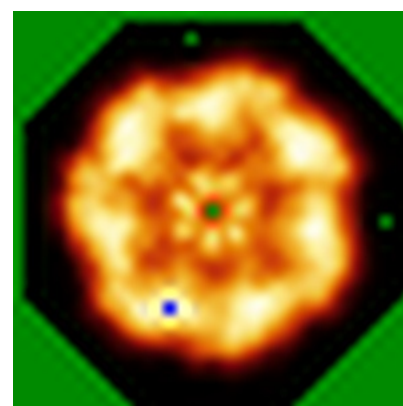
6.4.1 Primary map



X



Y

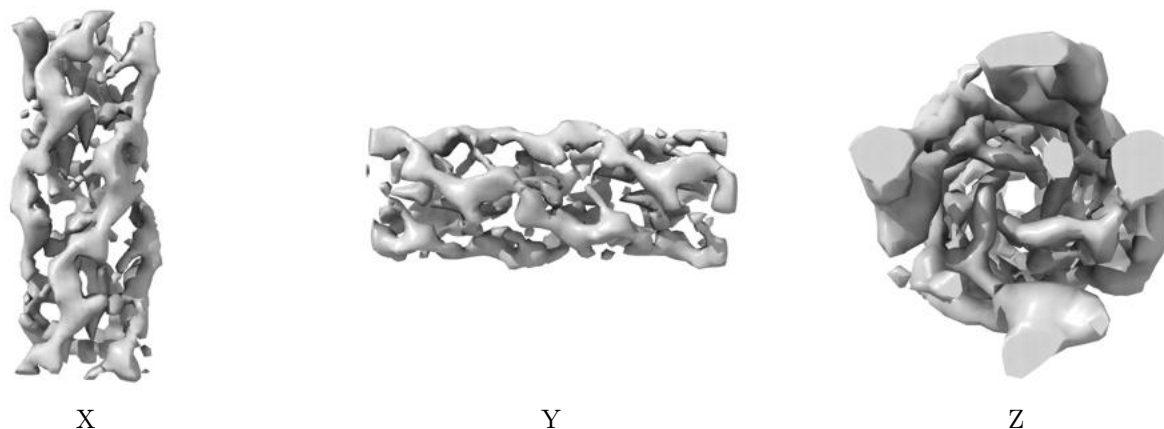


Z

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 2.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

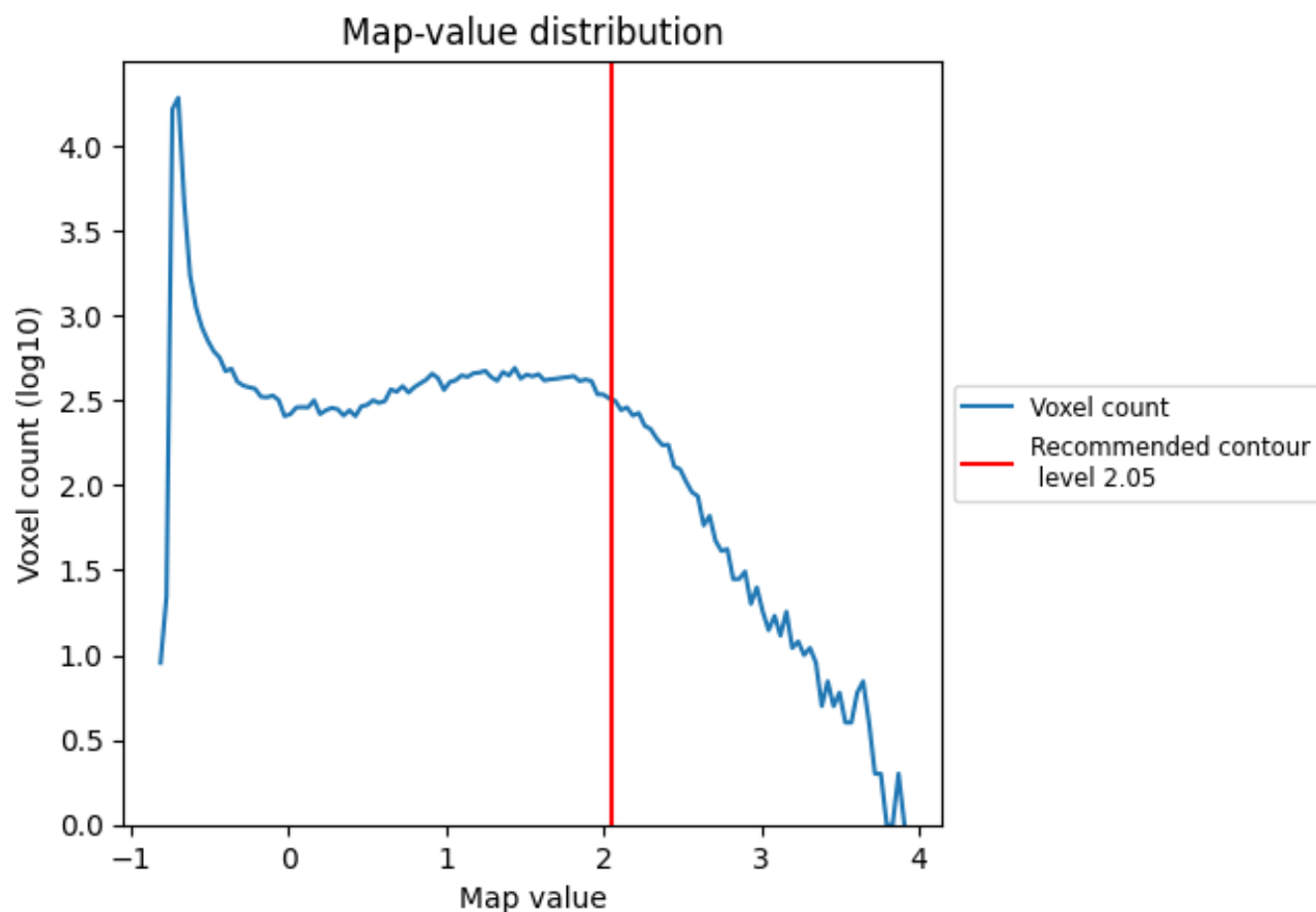
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

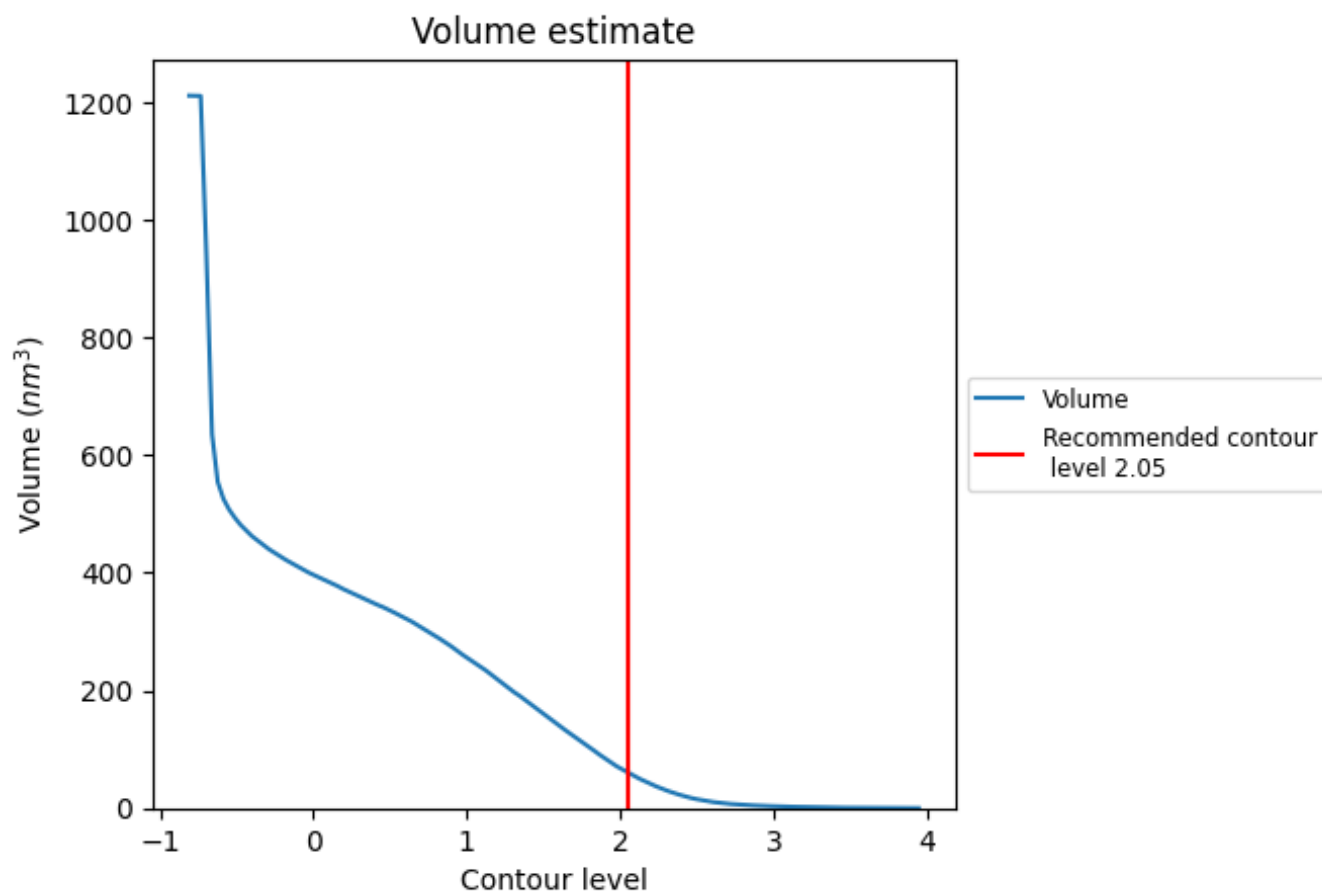
This section contains the results of statistical analysis of the map.

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 60 nm³; this corresponds to an approximate mass of 55 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

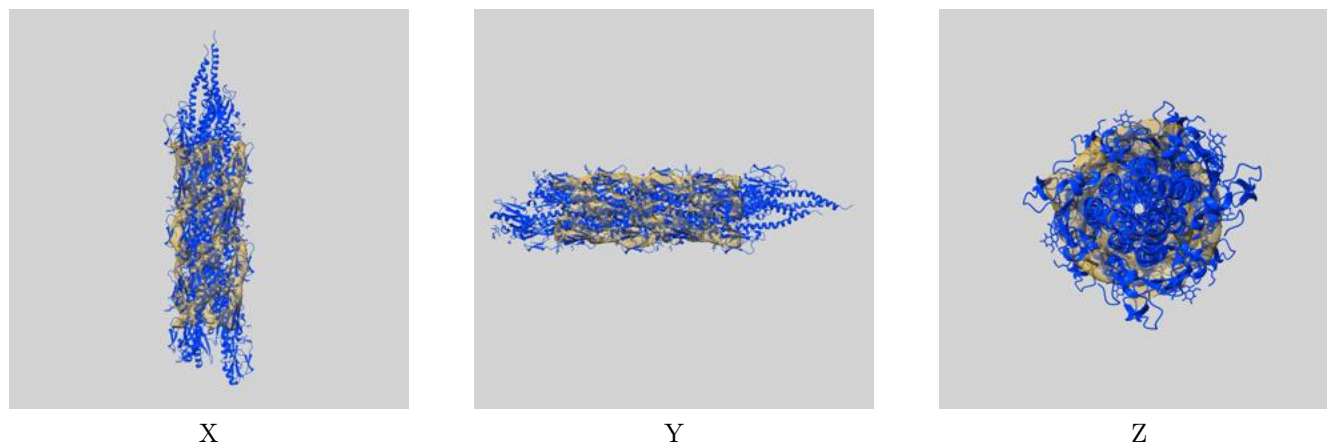
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

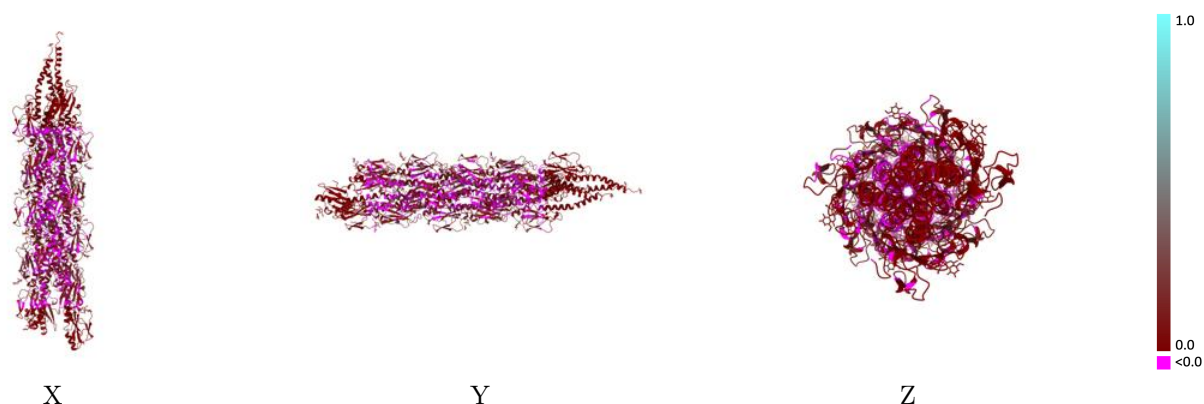
This section contains information regarding the fit between EMDB map EMD-1236 and PDB model 2HIL. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



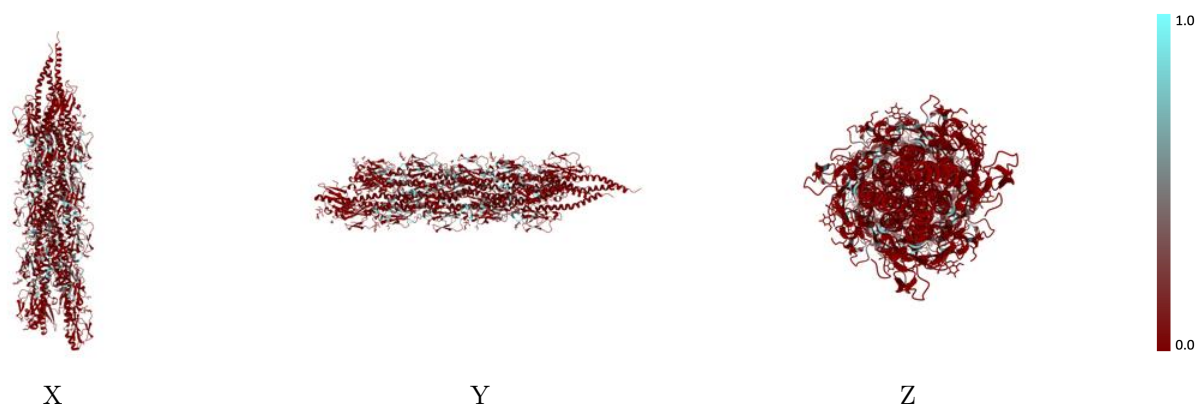
The images above show the 3D surface view of the map at the recommended contour level 2.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



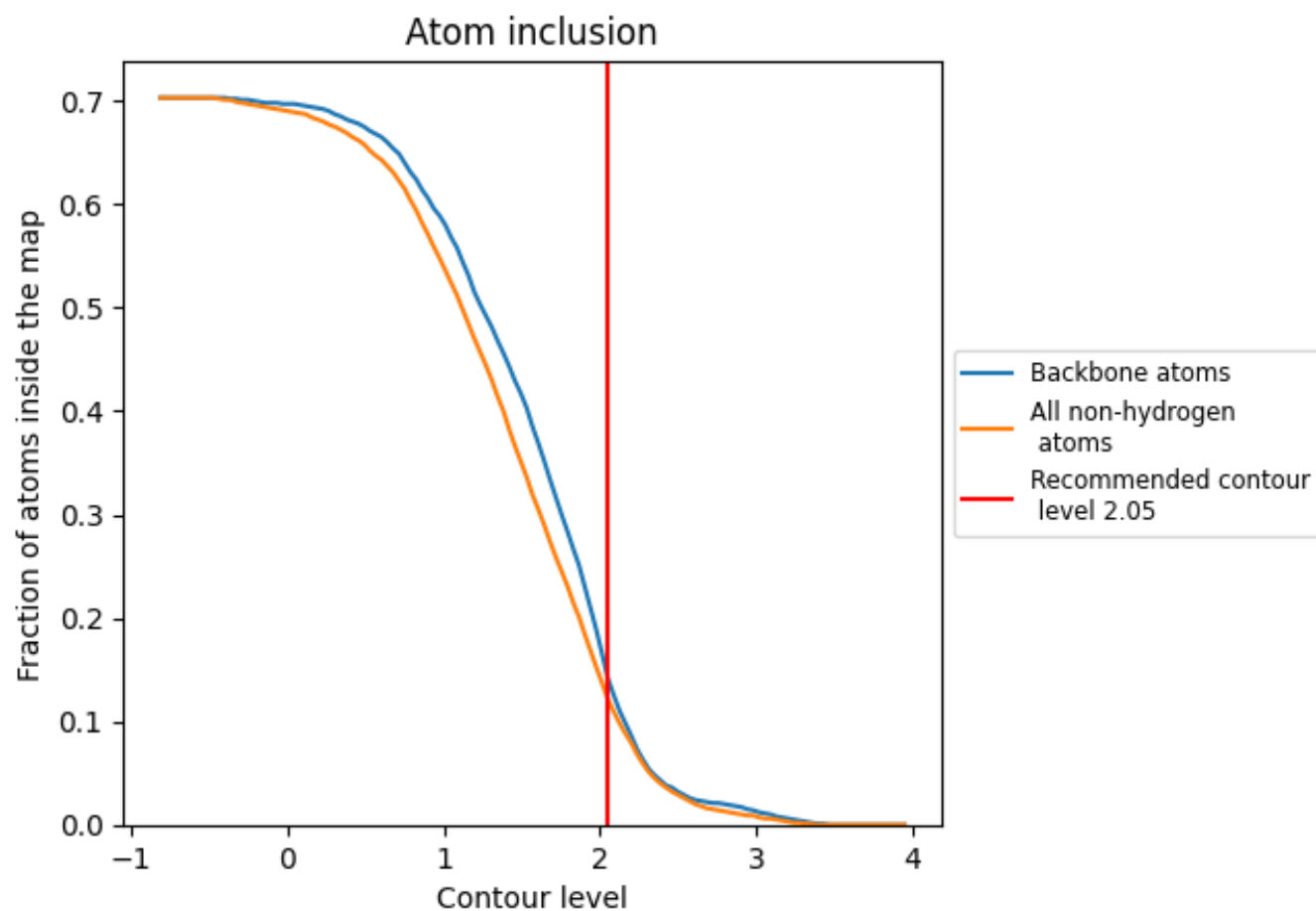
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 14% of all backbone atoms, 12% 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 (2.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.1220	0.0340
A	0.1750	0.0520
B	0.1780	0.0520
C	0.1760	0.0470
D	0.1670	0.0560
E	0.1660	0.0530
F	0.1400	0.0400
G	0.1010	0.0250
H	0.0640	0.0070
I	0.0080	-0.0050
J	0.1760	0.0520
K	0.1740	0.0480
L	0.1710	0.0470
M	0.1800	0.0520
N	0.1680	0.0500
O	0.1030	0.0310
P	0.0670	0.0190
Q	0.0240	-0.0100
R	0.0010	-0.0050
S	0.0000	0.0700
T	0.0000	0.0790
U	0.0000	0.0680
V	0.0000	0.0810
W	0.0000	0.0730
X	0.0000	0.0860
Y	0.0000	0.1040
Z	0.0360	0.0940
a	0.0000	0.0140
b	0.0000	0.0590
c	0.0000	0.0710
d	0.0000	0.0460
e	0.0000	0.0390
f	0.0000	-0.0740
g	0.0000	0.0000
h	0.0000	0.0000



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Chain	Atom inclusion	Q-score
i	 0.0000	 0.0000
j	 0.0000	 0.0000