wwPDB EM Map/Model Validation Report (i)

Apr 10, 2016 – 02:11 PM BST

PDB ID	:	3C92
EMDB ID:	:	EMD-1740
Title	:	Thermoplasma acidophilum 20S proteasome with a closed gate
Authors	:	Rabl, J.; Smith, D.M.; Yu, Y.; Chang, S.C.; Goldberg, A.L.; Cheng, Y.
Deposited on	:	2008-02-14
Resolution	:	6.80 Å(reported)
Based on PDB ID	:	1PMA 3C91

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

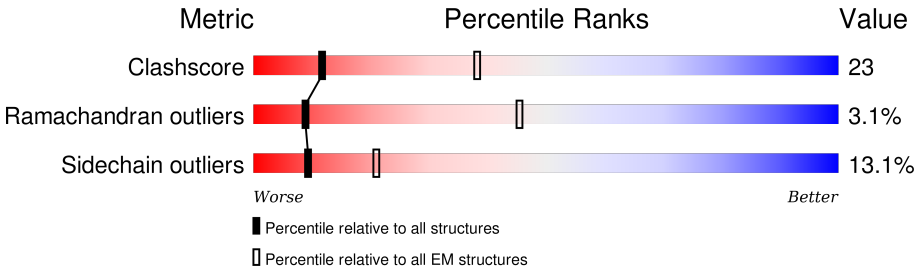
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 6.80 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)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	233	48% 41% 6%
1	B	233	48% 42% 6%
1	C	233	47% 42% 6%
1	D	233	48% 41% 6%
1	E	233	46% 43% 6%
1	F	233	48% 41% 6%
1	G	233	48% 40% 6%
1	O	233	48% 41% 6%
1	P	233	48% 42% 6%

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Mol	Chain	Length	Quality of chain
1	Q	233	47% 42% 6%
1	R	233	47% 42% 6%
1	S	233	46% 43% 6%
1	T	233	47% 42% 6%
1	U	233	48% 41% 6%
2	1	203	59% 34% 7%
2	2	203	55% 37% 8%
2	H	203	53% 38% 9%
2	I	203	61% 31% 8%
2	J	203	60% 32% 8%
2	K	203	54% 38% 8%
2	L	203	53% 38% 8%
2	M	203	58% 35% 7%
2	N	203	54% 39% 7%
2	V	203	53% 38% 9%
2	W	203	60% 32% 8%
2	X	203	60% 33% 7%
2	Y	203	52% 40% 8%
2	Z	203	54% 38% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 46228 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 Proteasome subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	B	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	C	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	D	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	E	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	F	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	G	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	O	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	P	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	Q	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	R	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	S	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	T	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		
1	U	224	Total	C	N	O	S	0	0
			1744	1107	296	338	3		

- Molecule 2 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		

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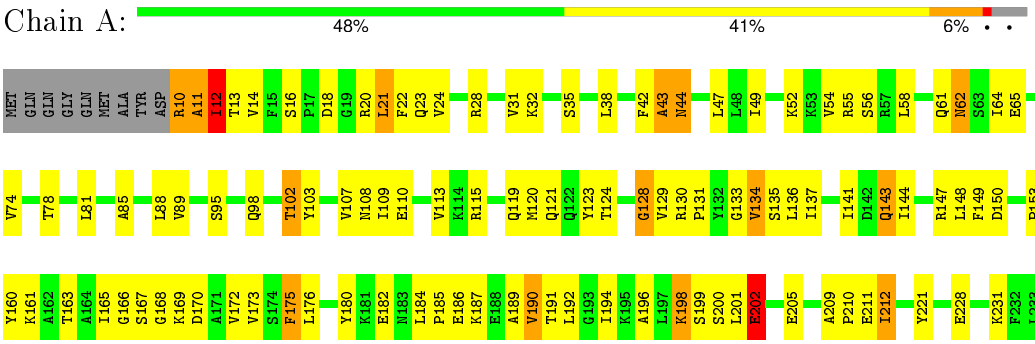
Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	J	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	K	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	L	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	M	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	N	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	V	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	W	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	X	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	Y	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	Z	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	1	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	2	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

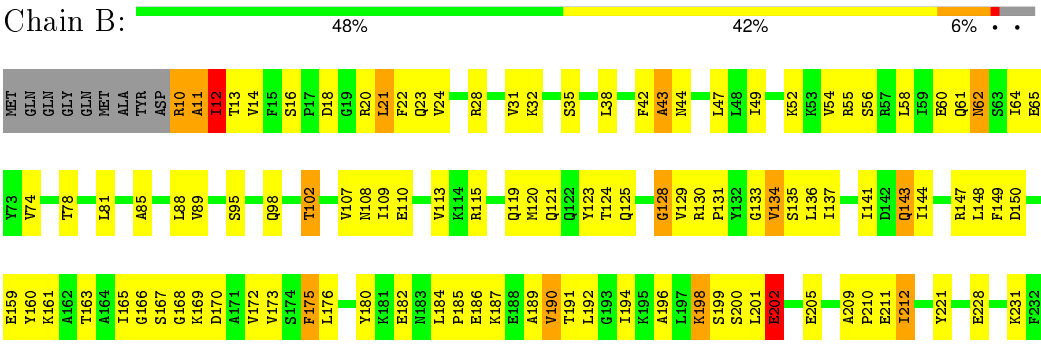
- Molecule 1: Proteasome subunit alpha

Chain A:



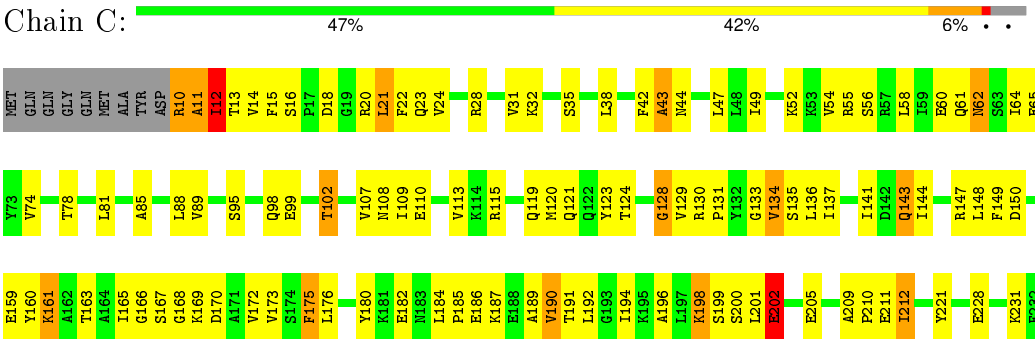
- Molecule 1: Proteasome subunit alpha

Chain B:



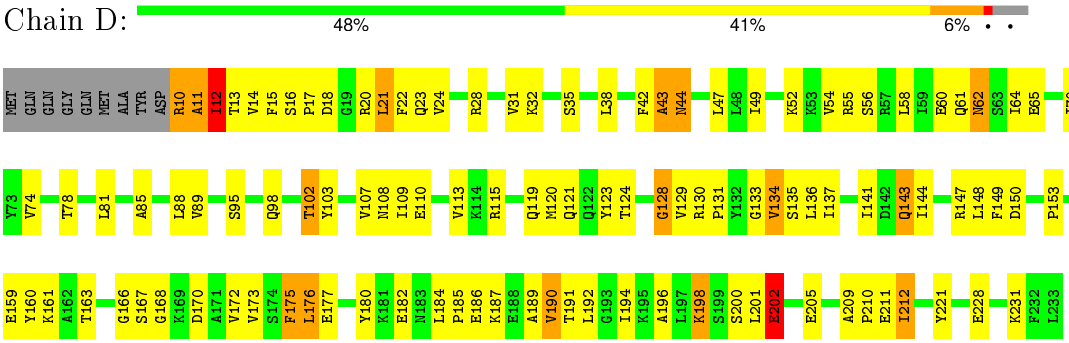
- Molecule 1: Proteasome subunit alpha

Chain C:



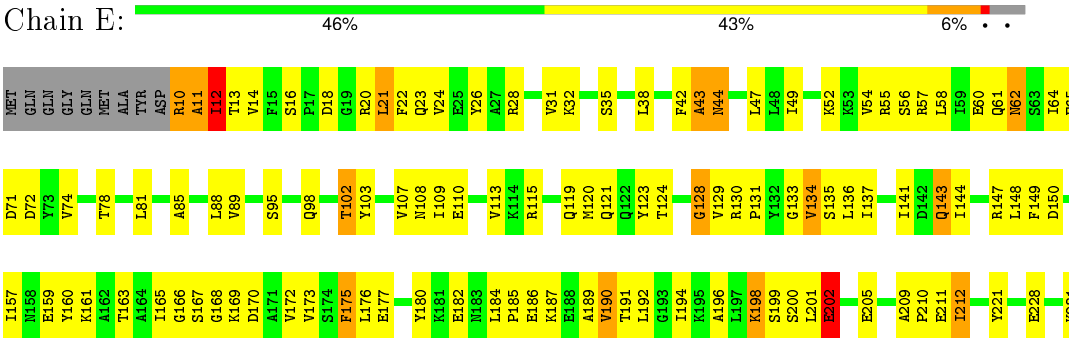
- Molecule 1: Proteasome subunit alpha

Chain D:



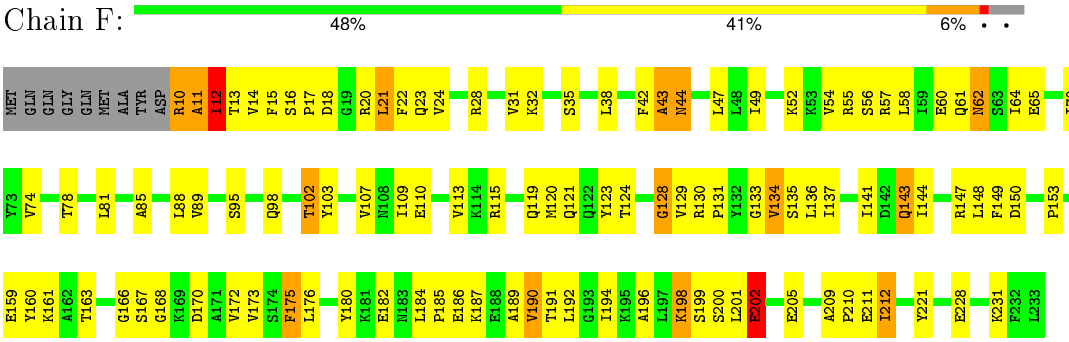
- Molecule 1: Proteasome subunit alpha

Chain E:



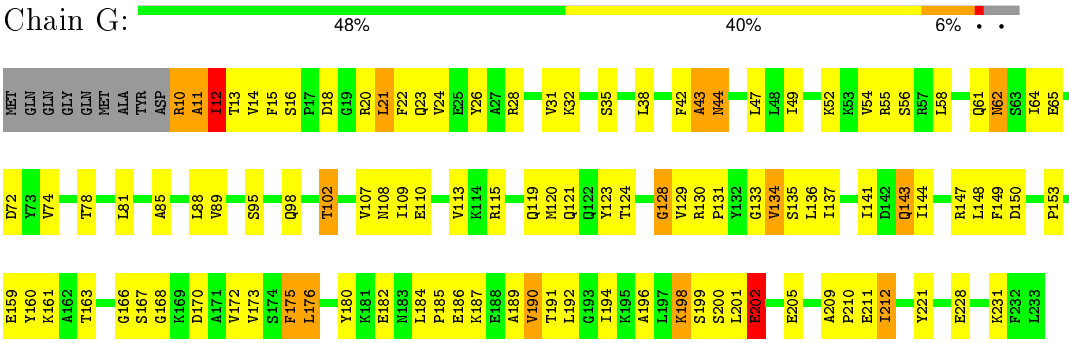
- Molecule 1: Proteasome subunit alpha

Chain F:



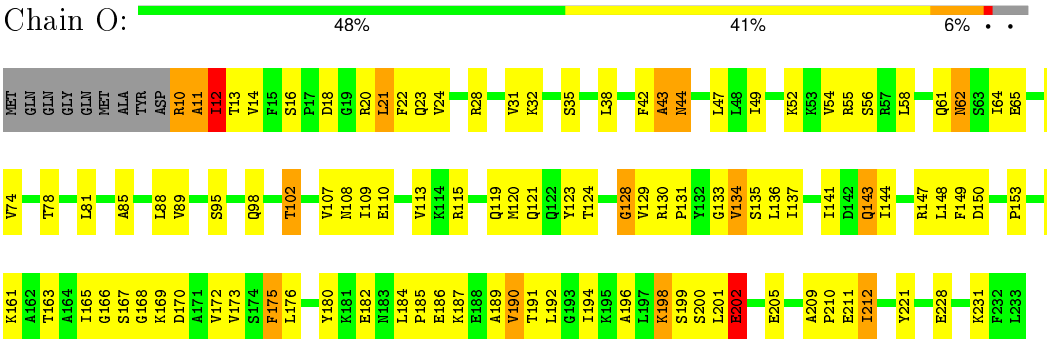
- Molecule 1: Proteasome subunit alpha

Chain G:



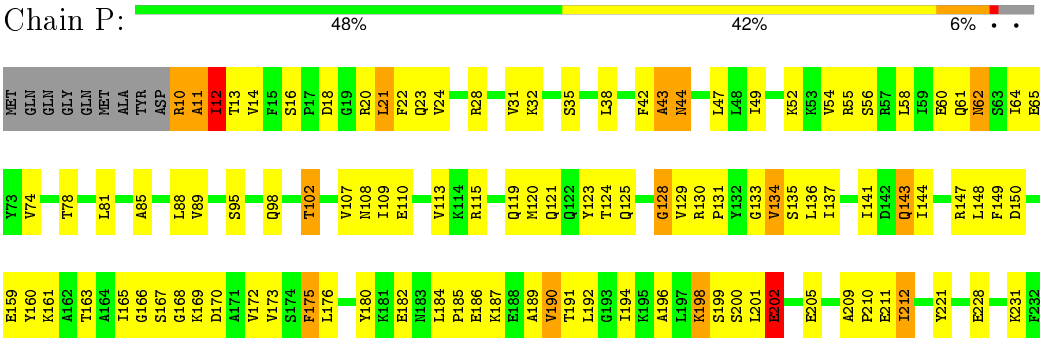
- Molecule 1: Proteasome subunit alpha

Chain O:



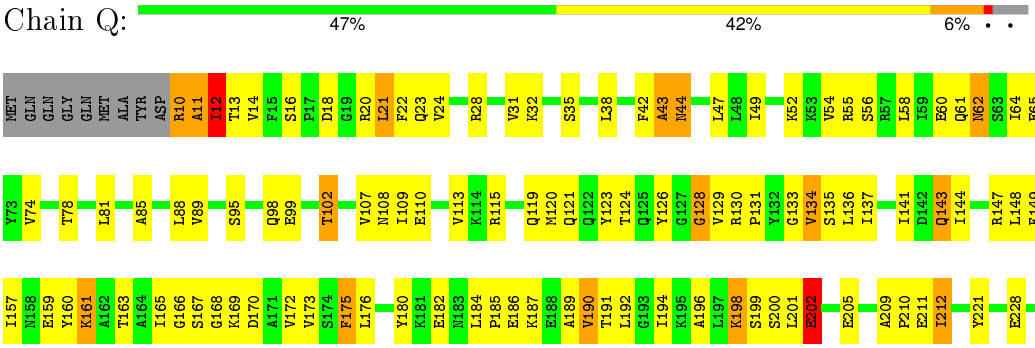
- Molecule 1: Proteasome subunit alpha

Chain P:



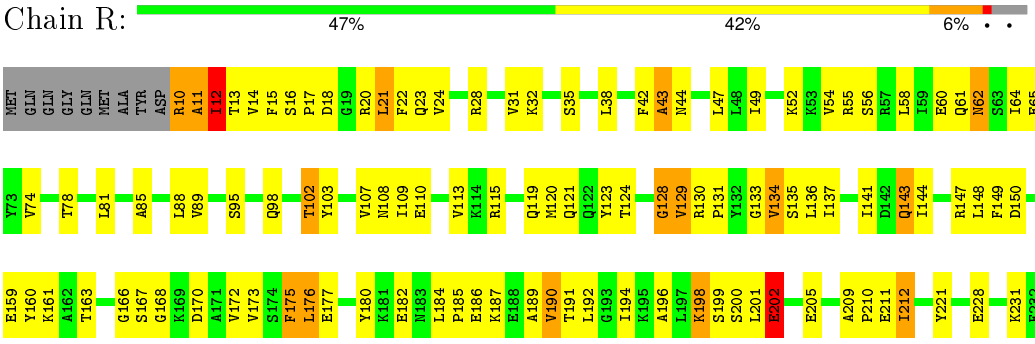
- Molecule 1: Proteasome subunit alpha

Chain Q:



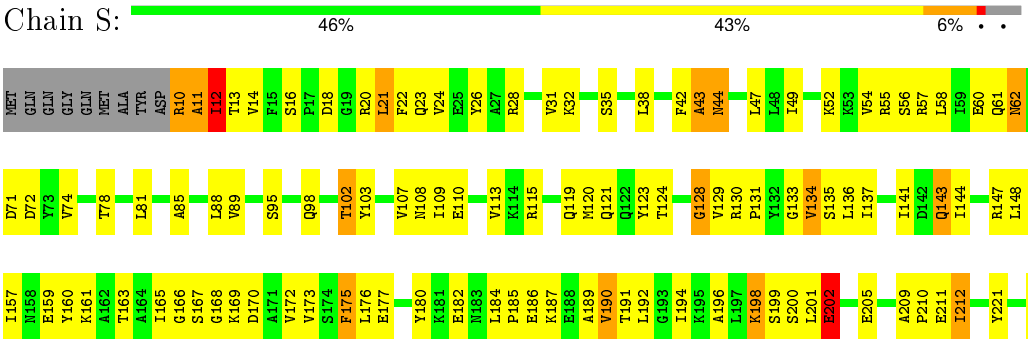
- Molecule 1: Proteasome subunit alpha

Chain R:



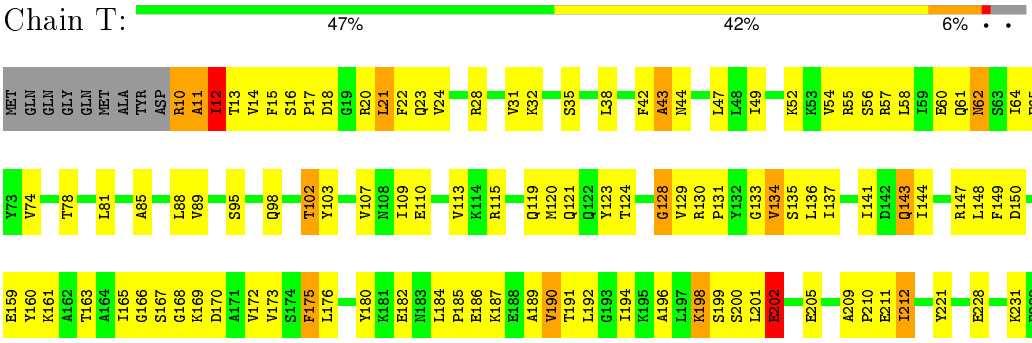
- Molecule 1: Proteasome subunit alpha

Chain S:



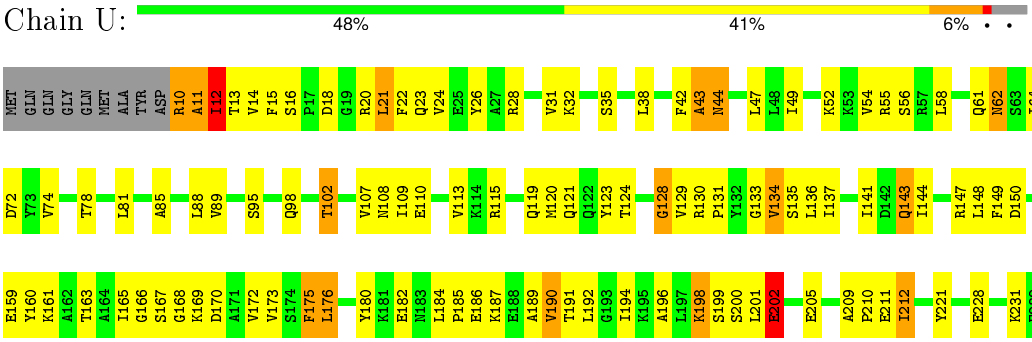
• Molecule 1: Proteasome subunit alpha

Chain T:



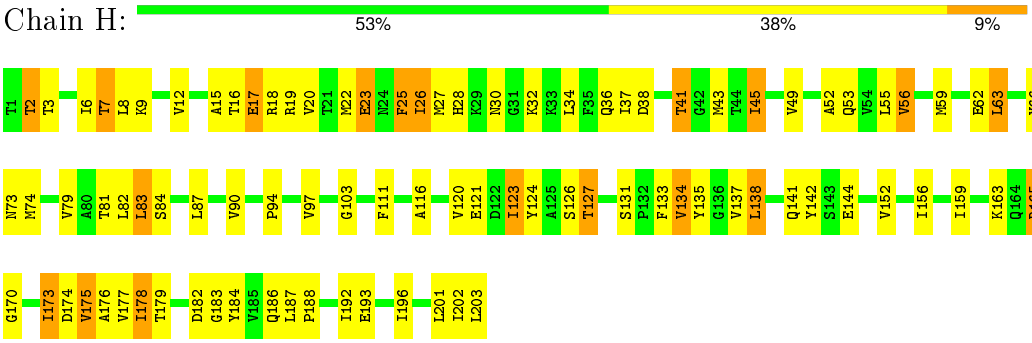
• Molecule 1: Proteasome subunit alpha

Chain U:



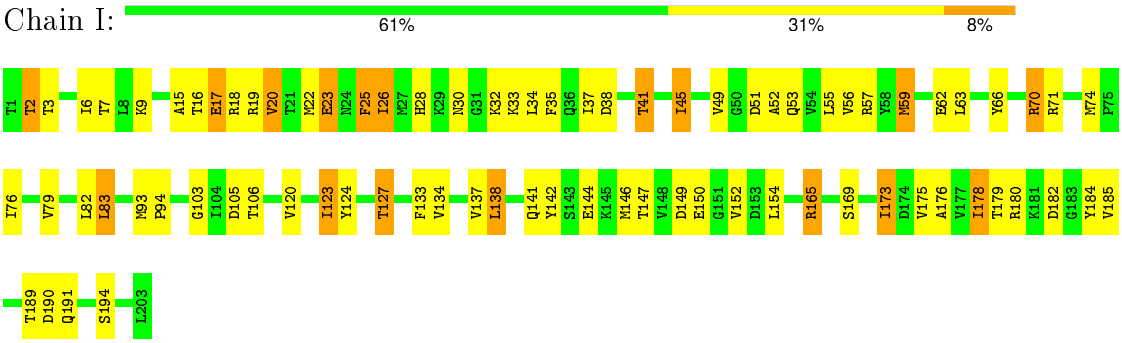
• Molecule 2: Proteasome subunit beta

Chain H:



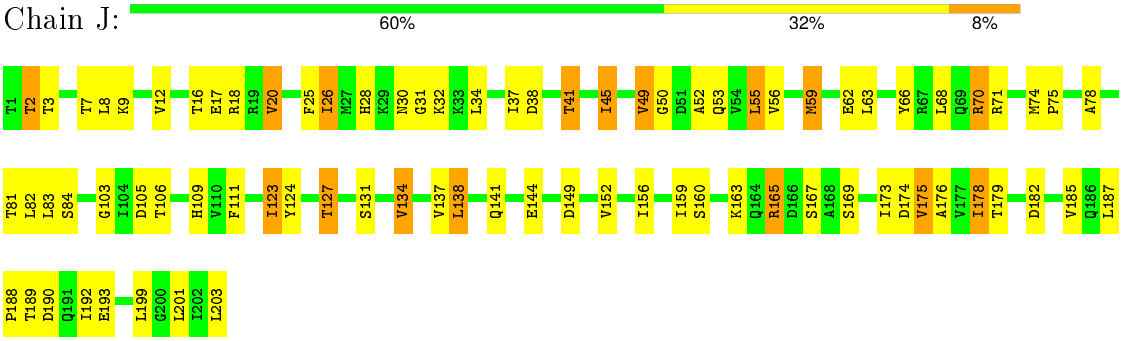
• Molecule 2: Proteasome subunit beta

Chain I:



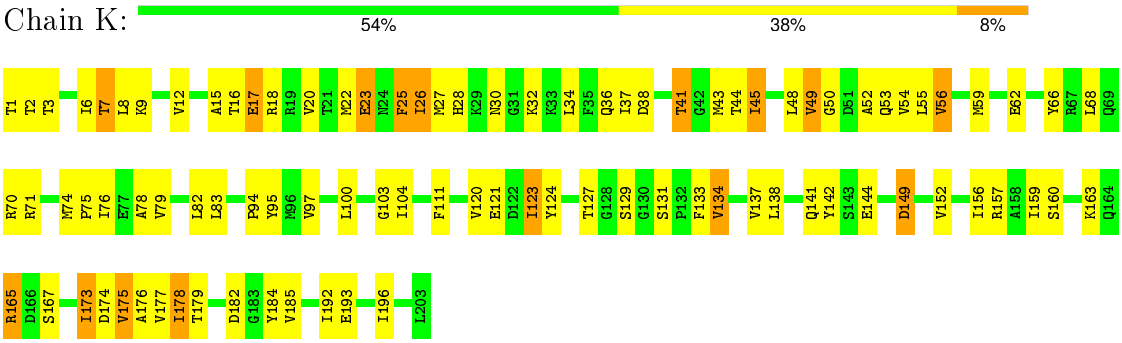
- Molecule 2: Proteasome subunit beta

Chain J:



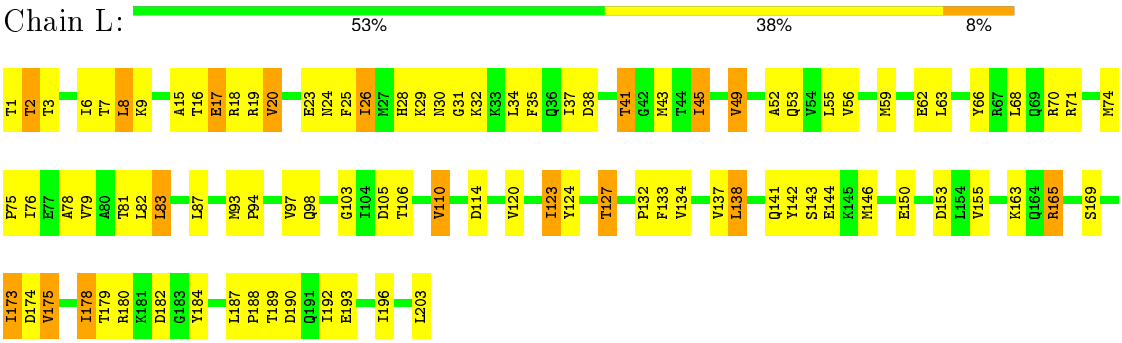
- Molecule 2: Proteasome subunit beta

Chain K:



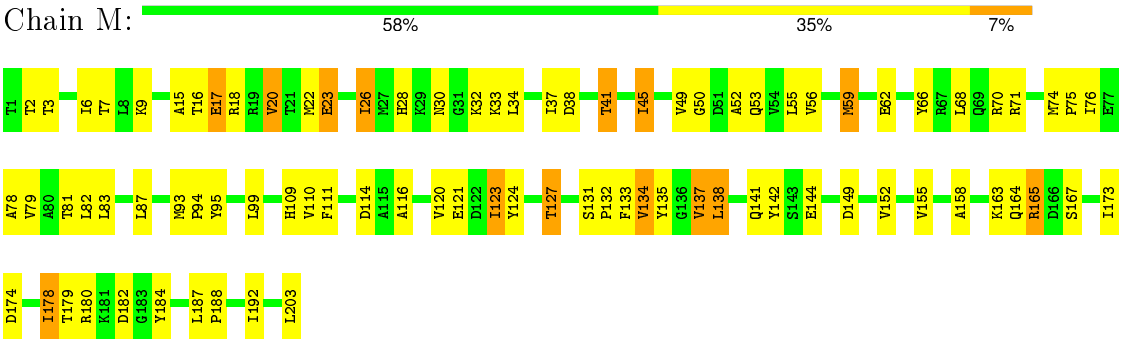
- Molecule 2: Proteasome subunit beta

Chain L:



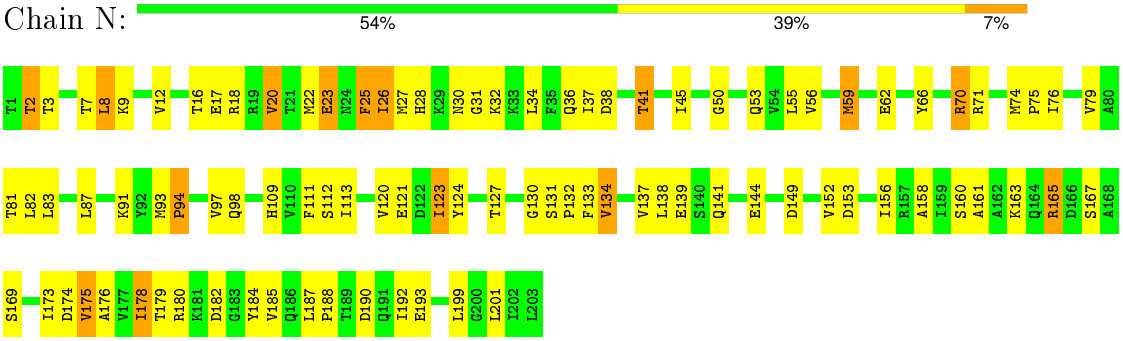
- Molecule 2: Proteasome subunit beta

Chain M:



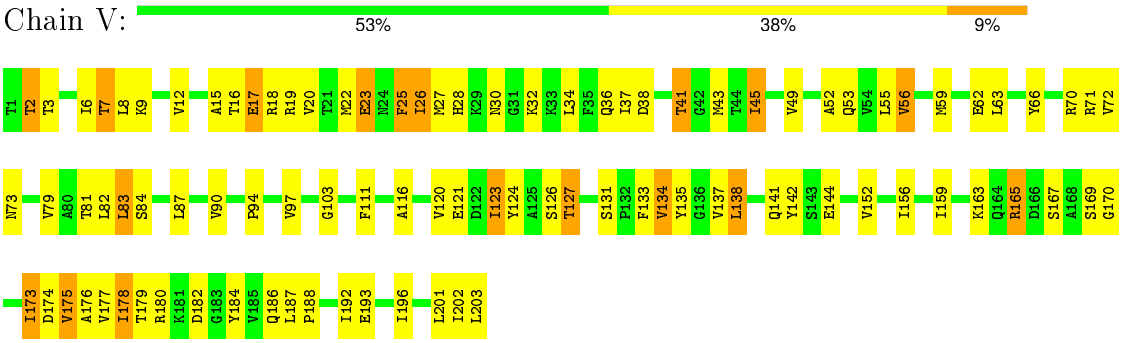
• Molecule 2: Proteasome subunit beta

Chain N:



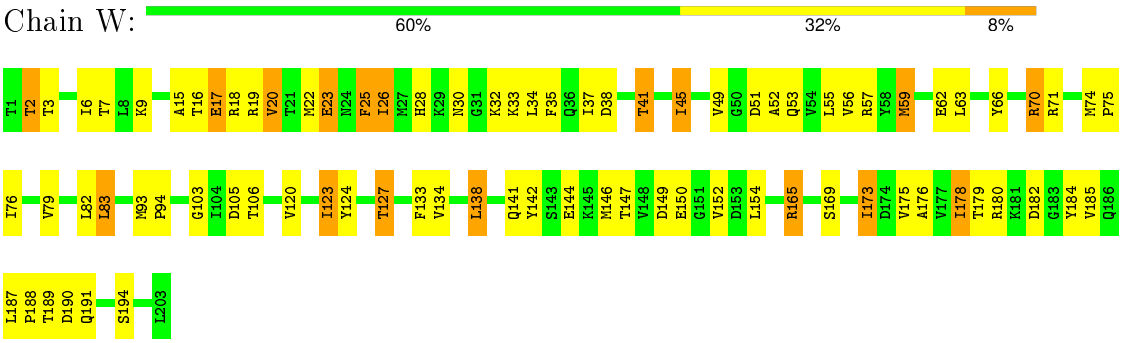
• Molecule 2: Proteasome subunit beta

Chain V:



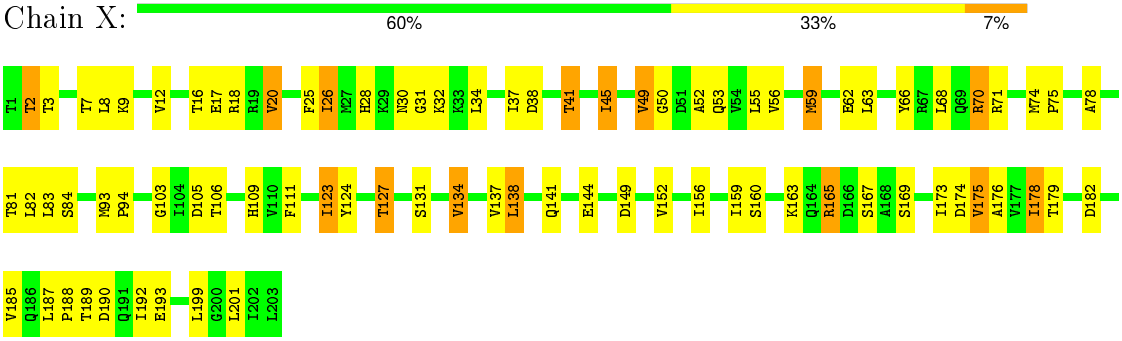
• Molecule 2: Proteasome subunit beta

Chain W:



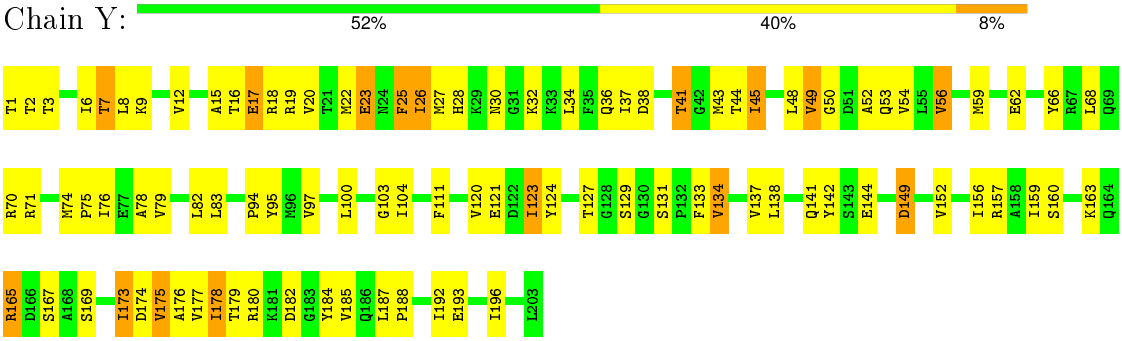
• Molecule 2: Proteasome subunit beta

Chain X:



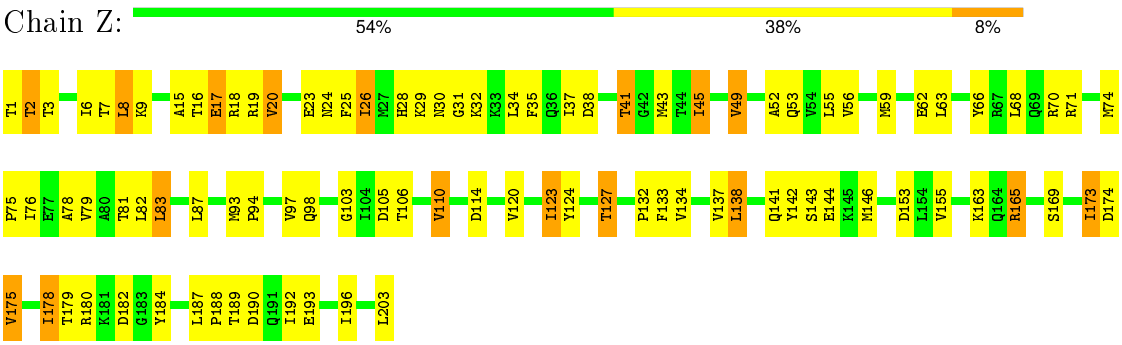
• Molecule 2: Proteasome subunit beta

Chain Y:



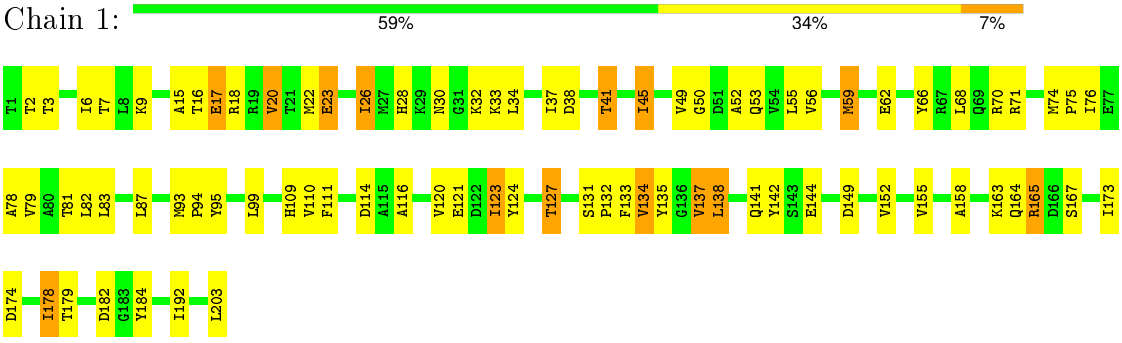
• Molecule 2: Proteasome subunit beta

Chain Z:



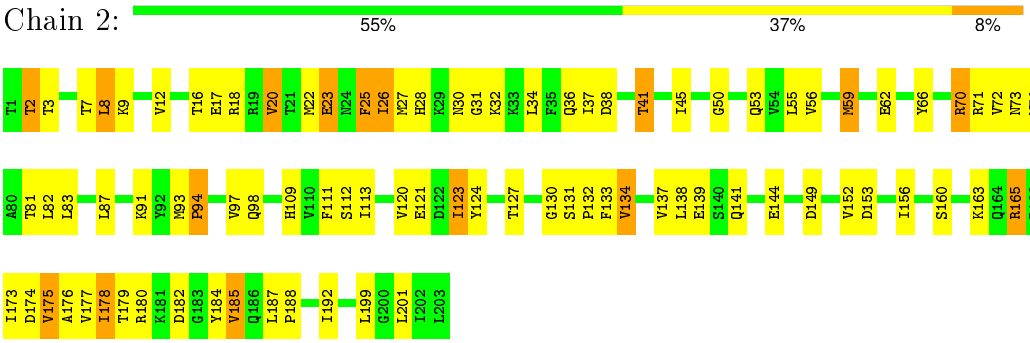
• Molecule 2: Proteasome subunit beta

Chain 1:



• Molecule 2: Proteasome subunit beta

Chain 2:


55%
37%
8%
T1 T2 T3 T7 L8 N9 V12 T16 E17 R18 R19 V20 T21 M22 E23 N24 F25 I26 M27 H28 K29 N30 G31 K32 K33 L34 F35 Q36 I37 D38 T41 I45 G50 Q53 V54 L55 V56 M59 E62 Y66 R70 R71 V72 N73 M74 F75 I76 V79
A80 T81 L82 L83 L87 K91 Y92 N93 P94 V97 Q98 H109 V110 F111 S112 I113 V120 E121 D122 I123 Y124 T127 G130 S131 P132 F133 V134 V137 L138 E139 S140 Q141 E144 D149 V152 D153 I156 S160 K163 Q164 R165 D166 S167 A168 S169
I173 D174 V175 A176 V177 I178 T179 R180 K181 D182 G183 Y184 V185 Q186 L187 P188 I192 L199 G200 L201 I202 L203

4 Experimental information (i)

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PHASE AND AMPLITUDE	Depositor
Microscope	FEI TECNAI TF20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	2000.00	Depositor
Minimum defocus (nm)	-1500.00	Depositor
Maximum defocus (nm)	-3500.00	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	A	0.55	0/1767	0.81	6/2380 (0.3%)
1	B	0.55	0/1767	0.81	6/2380 (0.3%)
1	C	0.55	0/1767	0.81	6/2380 (0.3%)
1	D	0.55	0/1767	0.81	6/2380 (0.3%)
1	E	0.55	0/1767	0.81	6/2380 (0.3%)
1	F	0.56	0/1767	0.81	6/2380 (0.3%)
1	G	0.56	0/1767	0.81	6/2380 (0.3%)
1	O	0.55	0/1767	0.81	6/2380 (0.3%)
1	P	0.56	0/1767	0.81	6/2380 (0.3%)
1	Q	0.56	0/1767	0.81	6/2380 (0.3%)
1	R	0.55	0/1767	0.81	6/2380 (0.3%)
1	S	0.55	0/1767	0.81	6/2380 (0.3%)
1	T	0.56	0/1767	0.82	6/2380 (0.3%)
1	U	0.56	0/1767	0.81	6/2380 (0.3%)
2	1	0.55	0/1577	0.75	1/2129 (0.0%)
2	2	0.54	0/1577	0.75	0/2129
2	H	0.57	0/1577	0.76	0/2129
2	I	0.57	0/1577	0.76	0/2129
2	J	0.54	0/1577	0.75	0/2129
2	K	0.55	0/1577	0.77	2/2129 (0.1%)
2	L	0.57	0/1577	0.77	0/2129
2	M	0.55	0/1577	0.75	1/2129 (0.0%)
2	N	0.54	0/1577	0.75	0/2129
2	V	0.57	0/1577	0.76	0/2129
2	W	0.57	0/1577	0.76	0/2129
2	X	0.54	0/1577	0.75	0/2129
2	Y	0.55	0/1577	0.77	2/2129 (0.1%)
2	Z	0.57	0/1577	0.77	0/2129
All	All	0.56	0/46816	0.79	90/63126 (0.1%)

There are no bond length outliers.

All (90) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	R	12	ILE	CB-CA-C	-10.42	90.76	111.60
1	T	12	ILE	CB-CA-C	-10.41	90.79	111.60
1	C	12	ILE	CB-CA-C	-10.40	90.79	111.60
1	G	12	ILE	CB-CA-C	-10.40	90.79	111.60
1	U	12	ILE	CB-CA-C	-10.40	90.80	111.60
1	D	12	ILE	CB-CA-C	-10.40	90.81	111.60
1	F	12	ILE	CB-CA-C	-10.40	90.81	111.60
1	S	12	ILE	CB-CA-C	-10.40	90.81	111.60
1	A	12	ILE	CB-CA-C	-10.39	90.81	111.60
1	Q	12	ILE	CB-CA-C	-10.39	90.81	111.60
1	B	12	ILE	CB-CA-C	-10.39	90.82	111.60
1	P	12	ILE	CB-CA-C	-10.39	90.82	111.60
1	O	12	ILE	CB-CA-C	-10.38	90.83	111.60
1	E	12	ILE	CB-CA-C	-10.37	90.85	111.60
1	S	13	THR	N-CA-CB	8.32	126.11	110.30
1	E	13	THR	N-CA-CB	8.32	126.10	110.30
1	U	13	THR	N-CA-CB	8.31	126.08	110.30
1	R	13	THR	N-CA-CB	8.31	126.08	110.30
1	T	13	THR	N-CA-CB	8.30	126.07	110.30
1	D	13	THR	N-CA-CB	8.30	126.07	110.30
1	O	13	THR	N-CA-CB	8.30	126.06	110.30
1	A	13	THR	N-CA-CB	8.29	126.06	110.30
1	B	13	THR	N-CA-CB	8.29	126.06	110.30
1	G	13	THR	N-CA-CB	8.29	126.06	110.30
1	C	13	THR	N-CA-CB	8.29	126.05	110.30
1	P	13	THR	N-CA-CB	8.29	126.04	110.30
1	Q	13	THR	N-CA-CB	8.28	126.04	110.30
1	F	13	THR	N-CA-CB	8.28	126.03	110.30
1	U	12	ILE	N-CA-C	6.58	128.77	111.00
1	S	12	ILE	N-CA-C	6.58	128.75	111.00
1	G	12	ILE	N-CA-C	6.57	128.75	111.00
1	A	12	ILE	N-CA-C	6.57	128.73	111.00
1	D	12	ILE	N-CA-C	6.57	128.73	111.00
1	E	12	ILE	N-CA-C	6.57	128.73	111.00
1	B	12	ILE	N-CA-C	6.56	128.71	111.00
1	C	12	ILE	N-CA-C	6.55	128.70	111.00
1	F	12	ILE	N-CA-C	6.55	128.70	111.00
1	O	12	ILE	N-CA-C	6.55	128.69	111.00
1	Q	12	ILE	N-CA-C	6.55	128.69	111.00
1	R	12	ILE	N-CA-C	6.55	128.69	111.00
1	T	12	ILE	N-CA-C	6.54	128.67	111.00
1	P	12	ILE	N-CA-C	6.54	128.66	111.00
1	T	10	ARG	CD-NE-CZ	6.50	132.70	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	10	ARG	CD-NE-CZ	6.49	132.69	123.60
1	F	10	ARG	CD-NE-CZ	6.48	132.67	123.60
1	G	10	ARG	CD-NE-CZ	6.47	132.66	123.60
1	B	10	ARG	CD-NE-CZ	6.47	132.66	123.60
1	U	10	ARG	CD-NE-CZ	6.47	132.66	123.60
1	A	10	ARG	CD-NE-CZ	6.46	132.65	123.60
1	Q	10	ARG	CD-NE-CZ	6.46	132.65	123.60
1	S	10	ARG	CD-NE-CZ	6.46	132.65	123.60
1	P	10	ARG	CD-NE-CZ	6.46	132.65	123.60
1	O	10	ARG	CD-NE-CZ	6.45	132.63	123.60
1	D	10	ARG	CD-NE-CZ	6.45	132.63	123.60
1	R	10	ARG	CD-NE-CZ	6.45	132.63	123.60
1	E	10	ARG	CD-NE-CZ	6.45	132.62	123.60
1	T	11	ALA	C-N-CA	-5.97	106.77	121.70
1	E	11	ALA	C-N-CA	-5.97	106.77	121.70
1	C	11	ALA	C-N-CA	-5.97	106.79	121.70
1	Q	11	ALA	C-N-CA	-5.96	106.79	121.70
1	F	11	ALA	C-N-CA	-5.96	106.80	121.70
1	P	11	ALA	C-N-CA	-5.96	106.81	121.70
1	R	11	ALA	C-N-CA	-5.96	106.81	121.70
1	S	11	ALA	C-N-CA	-5.96	106.81	121.70
1	B	11	ALA	C-N-CA	-5.96	106.81	121.70
1	A	11	ALA	C-N-CA	-5.95	106.81	121.70
1	O	11	ALA	C-N-CA	-5.95	106.82	121.70
1	G	11	ALA	C-N-CA	-5.95	106.83	121.70
1	D	11	ALA	C-N-CA	-5.95	106.84	121.70
1	U	11	ALA	C-N-CA	-5.93	106.87	121.70
2	K	95	TYR	N-CA-C	-5.88	95.13	111.00
2	Y	95	TYR	N-CA-C	-5.87	95.14	111.00
1	R	128	GLY	N-CA-C	5.12	125.91	113.10
1	U	128	GLY	N-CA-C	5.12	125.91	113.10
1	P	128	GLY	N-CA-C	5.12	125.91	113.10
1	D	128	GLY	N-CA-C	5.12	125.89	113.10
1	E	128	GLY	N-CA-C	5.11	125.89	113.10
1	G	128	GLY	N-CA-C	5.11	125.88	113.10
1	Q	128	GLY	N-CA-C	5.11	125.88	113.10
1	A	128	GLY	N-CA-C	5.11	125.87	113.10
1	B	128	GLY	N-CA-C	5.11	125.87	113.10
1	C	128	GLY	N-CA-C	5.11	125.87	113.10
1	S	128	GLY	N-CA-C	5.11	125.86	113.10
1	F	128	GLY	N-CA-C	5.10	125.85	113.10
1	O	128	GLY	N-CA-C	5.10	125.85	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	T	128	GLY	N-CA-C	5.09	125.83	113.10
2	1	95	TYR	N-CA-C	-5.06	97.35	111.00
2	M	95	TYR	N-CA-C	-5.04	97.39	111.00
2	K	8	LEU	CA-CB-CG	5.03	126.87	115.30
2	Y	8	LEU	CA-CB-CG	5.02	126.85	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1744	0	1781	93	0
1	B	1744	0	1781	90	0
1	C	1744	0	1781	91	0
1	D	1744	0	1781	95	0
1	E	1744	0	1781	100	0
1	F	1744	0	1781	93	0
1	G	1744	0	1781	95	0
1	O	1744	0	1781	91	0
1	P	1744	0	1781	91	0
1	Q	1744	0	1781	93	0
1	R	1744	0	1781	97	0
1	S	1744	0	1781	100	0
1	T	1744	0	1781	95	0
1	U	1744	0	1781	94	0
2	1	1558	0	1609	80	0
2	2	1558	0	1609	74	0
2	H	1558	0	1609	81	0
2	I	1558	0	1609	62	0
2	J	1558	0	1609	65	0
2	K	1558	0	1609	71	0
2	L	1558	0	1609	86	0
2	M	1558	0	1609	81	0
2	N	1558	0	1609	75	0
2	V	1558	0	1609	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	W	1558	0	1609	66	0
2	X	1558	0	1609	57	0
2	Y	1558	0	1609	74	0
2	Z	1558	0	1609	82	0
All	All	46228	0	47460	2137	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 23.

All (2137) 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:D:12:ILE:HG21	1:D:14:VAL:CG2	1.50	1.41
1:E:12:ILE:HG21	1:E:14:VAL:CG2	1.50	1.40
1:C:12:ILE:HG21	1:C:14:VAL:CG2	1.50	1.39
1:O:12:ILE:HG21	1:O:14:VAL:CG2	1.50	1.39
1:P:12:ILE:HG21	1:P:14:VAL:CG2	1.50	1.39
1:U:12:ILE:HG21	1:U:14:VAL:CG2	1.50	1.39
1:R:12:ILE:HG21	1:R:14:VAL:CG2	1.50	1.38
1:Q:12:ILE:HG21	1:Q:14:VAL:CG2	1.50	1.38
1:B:12:ILE:HG21	1:B:14:VAL:CG2	1.50	1.38
1:G:12:ILE:HG21	1:G:14:VAL:CG2	1.50	1.38
1:T:12:ILE:HG21	1:T:14:VAL:CG2	1.50	1.38
1:F:12:ILE:HG21	1:F:14:VAL:CG2	1.50	1.38
1:S:12:ILE:HG21	1:S:14:VAL:CG2	1.50	1.37
1:A:12:ILE:HG21	1:A:14:VAL:CG2	1.50	1.37
1:C:12:ILE:CG2	1:C:14:VAL:HG22	1.63	1.29
1:P:12:ILE:CG2	1:P:14:VAL:HG22	1.63	1.29
1:U:12:ILE:CG2	1:U:14:VAL:HG22	1.63	1.29
1:T:12:ILE:CG2	1:T:14:VAL:HG22	1.63	1.29
1:E:12:ILE:CG2	1:E:14:VAL:HG22	1.63	1.28
1:B:12:ILE:CG2	1:B:14:VAL:HG22	1.63	1.28
1:R:12:ILE:CG2	1:R:14:VAL:HG22	1.63	1.28
1:F:12:ILE:CG2	1:F:14:VAL:HG22	1.63	1.27
1:A:12:ILE:CG2	1:A:14:VAL:HG22	1.63	1.27
1:D:12:ILE:CG2	1:D:14:VAL:HG22	1.63	1.27
1:S:12:ILE:CG2	1:S:14:VAL:HG22	1.63	1.27
1:Q:12:ILE:CG2	1:Q:14:VAL:HG22	1.63	1.27
1:G:12:ILE:CG2	1:G:14:VAL:HG22	1.63	1.27
1:O:12:ILE:CG2	1:O:14:VAL:HG22	1.63	1.26
2:V:38:ASP:HB3	2:V:41:THR:HG23	1.38	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:38:ASP:HB3	2:H:41:THR:HG23	1.38	1.04
1:G:107:VAL:HG11	2:H:66:TYR:OH	1.58	1.04
1:S:107:VAL:HG11	2:1:66:TYR:OH	1.60	1.00
1:U:107:VAL:HG11	2:V:66:TYR:OH	1.58	1.00
1:E:107:VAL:HG11	2:M:66:TYR:OH	1.60	1.00
2:M:38:ASP:HB3	2:M:41:THR:HG23	1.44	1.00
2:X:45:ILE:HG12	2:X:52:ALA:HB1	1.44	0.99
2:K:38:ASP:HB3	2:K:41:THR:HG23	1.45	0.98
2:1:38:ASP:HB3	2:1:41:THR:HG23	1.44	0.98
2:M:45:ILE:HG12	2:M:52:ALA:HB1	1.46	0.97
2:1:45:ILE:HG12	2:1:52:ALA:HB1	1.46	0.97
2:J:45:ILE:HG12	2:J:52:ALA:HB1	1.44	0.96
1:D:107:VAL:HG11	2:L:66:TYR:OH	1.66	0.96
2:Y:38:ASP:HB3	2:Y:41:THR:HG23	1.45	0.96
2:J:38:ASP:HB3	2:J:41:THR:HG23	1.46	0.95
1:R:107:VAL:HG11	2:Z:66:TYR:OH	1.66	0.95
2:W:38:ASP:HB3	2:W:41:THR:HG23	1.49	0.95
2:X:38:ASP:HB3	2:X:41:THR:HG23	1.46	0.94
2:2:38:ASP:HB3	2:2:41:THR:HG23	1.47	0.94
1:Q:107:VAL:HG11	2:Y:66:TYR:OH	1.68	0.94
2:N:38:ASP:HB3	2:N:41:THR:HG23	1.47	0.94
2:I:38:ASP:HB3	2:I:41:THR:HG23	1.49	0.94
1:C:107:VAL:HG11	2:K:66:TYR:OH	1.68	0.93
1:A:107:VAL:HG11	2:I:66:TYR:OH	1.69	0.93
1:O:107:VAL:HG11	2:W:66:TYR:OH	1.69	0.93
1:R:124:THR:HG22	1:S:130:ARG:HH21	1.35	0.92
1:D:124:THR:HG22	1:E:130:ARG:HH21	1.35	0.90
1:U:12:ILE:HG13	1:U:14:VAL:N	1.84	0.89
1:B:107:VAL:HG11	2:J:66:TYR:OH	1.73	0.89
1:P:107:VAL:HG11	2:X:66:TYR:OH	1.73	0.89
2:1:37:ILE:HD11	2:1:59:MET:HB3	1.56	0.88
1:C:12:ILE:HG13	1:C:14:VAL:N	1.84	0.87
1:O:12:ILE:HG13	1:O:14:VAL:N	1.84	0.87
1:T:12:ILE:HG13	1:T:14:VAL:N	1.84	0.87
1:F:12:ILE:HG13	1:F:14:VAL:N	1.84	0.86
1:O:130:ARG:HH21	1:U:124:THR:HG22	1.39	0.86
1:A:130:ARG:HH21	1:G:124:THR:HG22	1.39	0.86
1:Q:12:ILE:HG13	1:Q:14:VAL:N	1.84	0.86
1:D:12:ILE:HG13	1:D:14:VAL:N	1.84	0.86
1:B:12:ILE:HG13	1:B:14:VAL:N	1.84	0.86
2:M:37:ILE:HD11	2:M:59:MET:HB3	1.56	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:12:ILE:HG21	1:G:14:VAL:HG22	0.85	0.85
1:A:12:ILE:HG21	1:A:14:VAL:HG22	0.85	0.85
2:L:38:ASP:HB3	2:L:41:THR:HG23	1.59	0.85
1:B:12:ILE:HG21	1:B:14:VAL:HG22	0.85	0.85
1:T:107:VAL:HG11	2:2:66:TYR:OH	1.77	0.85
1:R:12:ILE:HG13	1:R:14:VAL:N	1.84	0.84
2:Z:38:ASP:HB3	2:Z:41:THR:HG23	1.59	0.84
1:D:12:ILE:HG21	1:D:14:VAL:HG22	0.85	0.84
1:S:12:ILE:HG13	1:S:14:VAL:N	1.84	0.84
1:O:12:ILE:HG21	1:O:14:VAL:HG22	0.85	0.84
1:T:124:THR:HG22	1:U:130:ARG:HH21	1.42	0.84
1:G:12:ILE:HG13	1:G:14:VAL:N	1.84	0.83
1:A:12:ILE:HG13	1:A:14:VAL:N	1.84	0.83
1:F:107:VAL:HG11	2:N:66:TYR:OH	1.77	0.83
1:U:12:ILE:HG21	1:U:14:VAL:HG22	0.85	0.83
1:P:12:ILE:HG21	1:P:14:VAL:HG22	0.85	0.83
1:E:12:ILE:HG21	1:E:14:VAL:HG22	0.85	0.83
1:C:12:ILE:HG21	1:C:14:VAL:HG22	0.85	0.83
1:P:12:ILE:HG13	1:P:14:VAL:N	1.84	0.83
2:2:53:GLN:O	2:2:56:VAL:HG12	1.78	0.83
2:N:53:GLN:O	2:N:56:VAL:HG12	1.78	0.83
1:Q:12:ILE:HG21	1:Q:14:VAL:HG22	0.85	0.83
2:W:123:ILE:HG12	2:W:124:TYR:HD1	1.44	0.83
1:R:12:ILE:HG21	1:R:14:VAL:HG22	0.85	0.82
1:F:12:ILE:HG21	1:F:14:VAL:HG22	0.85	0.82
1:S:12:ILE:HG21	1:S:14:VAL:HG22	0.85	0.82
1:T:12:ILE:HG21	1:T:14:VAL:HG22	0.85	0.82
1:F:124:THR:HG22	1:G:130:ARG:HH21	1.43	0.82
1:Q:124:THR:HG22	1:R:130:ARG:HH21	1.45	0.81
1:E:12:ILE:HG13	1:E:14:VAL:N	1.84	0.81
2:J:37:ILE:HD11	2:J:59:MET:HB3	1.61	0.81
2:1:20:VAL:HG13	2:1:28:HIS:HB2	1.62	0.81
1:T:52:LYS:NZ	1:T:62:ASN:HA	1.96	0.81
1:A:52:LYS:NZ	1:A:62:ASN:HA	1.96	0.81
1:B:52:LYS:NZ	1:B:62:ASN:HA	1.96	0.81
2:I:123:ILE:HG12	2:I:124:TYR:HD1	1.44	0.81
1:S:52:LYS:NZ	1:S:62:ASN:HA	1.96	0.81
2:M:20:VAL:HG13	2:M:28:HIS:HB2	1.62	0.81
2:X:37:ILE:HD11	2:X:59:MET:HB3	1.61	0.81
1:P:52:LYS:NZ	1:P:62:ASN:HA	1.96	0.80
1:Q:52:LYS:NZ	1:Q:62:ASN:HA	1.96	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:LYS:NZ	1:C:62:ASN:HA	1.96	0.80
1:U:52:LYS:NZ	1:U:62:ASN:HA	1.96	0.80
1:F:52:LYS:NZ	1:F:62:ASN:HA	1.96	0.80
1:O:52:LYS:NZ	1:O:62:ASN:HA	1.96	0.80
1:E:52:LYS:NZ	1:E:62:ASN:HA	1.96	0.80
1:G:52:LYS:NZ	1:G:62:ASN:HA	1.96	0.80
1:D:52:LYS:NZ	1:D:62:ASN:HA	1.96	0.80
1:R:52:LYS:NZ	1:R:62:ASN:HA	1.96	0.80
1:C:124:THR:HG22	1:D:130:ARG:HH21	1.45	0.79
2:Y:123:ILE:HG12	2:Y:124:TYR:HD1	1.48	0.79
2:K:123:ILE:HG12	2:K:124:TYR:HD1	1.48	0.78
2:V:123:ILE:HG12	2:V:124:TYR:HD1	1.49	0.78
1:A:124:THR:HG22	1:B:130:ARG:HH21	1.48	0.78
1:D:186:GLU:O	1:D:190:VAL:HG12	1.84	0.78
2:W:53:GLN:O	2:W:56:VAL:HG12	1.83	0.78
1:O:186:GLU:O	1:O:190:VAL:HG12	1.84	0.78
1:A:52:LYS:HZ1	1:A:62:ASN:HA	1.48	0.77
1:E:124:THR:HG22	1:F:130:ARG:HH21	1.48	0.77
1:F:21:LEU:HD11	1:G:130:ARG:HD2	1.67	0.77
1:G:186:GLU:O	1:G:190:VAL:HG12	1.84	0.77
1:F:186:GLU:O	1:F:190:VAL:HG12	1.84	0.77
1:O:124:THR:HG22	1:P:130:ARG:HH21	1.48	0.77
2:H:43:MET:HE1	2:H:56:VAL:HG23	1.65	0.77
1:A:186:GLU:O	1:A:190:VAL:HG12	1.84	0.77
2:N:32:LYS:HE2	2:N:34:LEU:O	1.85	0.77
2:N:167:SER:HB2	2:Y:167:SER:HB2	1.65	0.77
1:S:124:THR:HG22	1:T:130:ARG:HH21	1.48	0.77
1:R:186:GLU:O	1:R:190:VAL:HG12	1.84	0.77
2:I:53:GLN:O	2:I:56:VAL:HG12	1.83	0.77
2:H:123:ILE:HG12	2:H:124:TYR:HD1	1.49	0.77
1:S:186:GLU:O	1:S:190:VAL:HG12	1.84	0.77
2:X:123:ILE:H	2:X:123:ILE:HD13	1.49	0.77
1:Q:186:GLU:O	1:Q:190:VAL:HG12	1.84	0.76
1:B:186:GLU:O	1:B:190:VAL:HG12	1.84	0.76
1:U:186:GLU:O	1:U:190:VAL:HG12	1.84	0.76
1:E:186:GLU:O	1:E:190:VAL:HG12	1.84	0.76
1:T:21:LEU:HD11	1:U:130:ARG:HD2	1.67	0.76
2:2:32:LYS:HE2	2:2:34:LEU:O	1.85	0.76
1:E:12:ILE:CG2	1:E:14:VAL:CG2	2.42	0.76
1:P:186:GLU:O	1:P:190:VAL:HG12	1.84	0.76
2:K:167:SER:HB2	2:2:167:SER:HB2	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:186:GLU:O	1:T:190:VAL:HG12	1.84	0.76
2:J:123:ILE:HD13	2:J:123:ILE:H	1.49	0.76
1:C:186:GLU:O	1:C:190:VAL:HG12	1.84	0.76
1:S:52:LYS:HZ3	1:S:62:ASN:HA	1.49	0.75
1:T:12:ILE:CG2	1:T:14:VAL:CG2	2.42	0.75
1:P:12:ILE:CG2	1:P:14:VAL:CG2	2.42	0.75
2:Z:53:GLN:O	2:Z:56:VAL:HG12	1.87	0.75
2:2:62:GLU:HG2	2:2:82:LEU:HD21	1.70	0.74
2:2:123:ILE:HD13	2:2:123:ILE:H	1.52	0.74
2:M:123:ILE:HG12	2:M:124:TYR:HD1	1.53	0.74
1:B:12:ILE:CG2	1:B:14:VAL:CG2	2.42	0.74
2:L:53:GLN:O	2:L:56:VAL:HG12	1.87	0.73
2:Z:2:THR:HG22	2:Z:169:SER:OG	1.89	0.73
1:P:78:THR:HG21	1:P:85:ALA:HB1	1.70	0.73
1:E:78:THR:HG21	1:E:85:ALA:HB1	1.70	0.73
2:L:2:THR:HG22	2:L:169:SER:OG	1.89	0.73
1:F:78:THR:HG21	1:F:85:ALA:HB1	1.70	0.73
1:T:168:GLY:O	1:T:172:VAL:HG12	1.89	0.73
1:Q:78:THR:HG21	1:Q:85:ALA:HB1	1.70	0.73
2:W:103:GLY:HA2	2:W:178:ILE:HD11	1.71	0.73
1:A:168:GLY:O	1:A:172:VAL:HG12	1.89	0.73
1:B:168:GLY:O	1:B:172:VAL:HG12	1.89	0.73
2:Z:20:VAL:HG13	2:Z:28:HIS:HB2	1.71	0.73
1:C:52:LYS:HZ3	1:C:62:ASN:HA	1.54	0.72
2:V:32:LYS:HE2	2:V:34:LEU:O	1.89	0.72
1:O:168:GLY:O	1:O:172:VAL:HG12	1.89	0.72
2:V:53:GLN:O	2:V:56:VAL:HG12	1.89	0.72
1:D:168:GLY:O	1:D:172:VAL:HG12	1.89	0.72
1:T:78:THR:HG21	1:T:85:ALA:HB1	1.70	0.72
1:S:168:GLY:O	1:S:172:VAL:HG12	1.89	0.72
1:D:78:THR:HG21	1:D:85:ALA:HB1	1.70	0.72
2:1:18:ARG:HE	2:1:30:ASN:HD22	1.37	0.72
1:Q:12:ILE:HG12	1:Q:14:VAL:HG13	1.71	0.72
2:W:38:ASP:HB3	2:W:41:THR:CG2	2.18	0.72
2:N:62:GLU:HG2	2:N:82:LEU:HD21	1.69	0.72
2:L:20:VAL:HG13	2:L:28:HIS:HB2	1.71	0.72
1:G:12:ILE:HG12	1:G:14:VAL:HG13	1.71	0.72
1:F:12:ILE:HG12	1:F:14:VAL:HG13	1.71	0.72
1:E:168:GLY:O	1:E:172:VAL:HG12	1.89	0.72
1:G:78:THR:HG21	1:G:85:ALA:HB1	1.70	0.72
1:G:168:GLY:O	1:G:172:VAL:HG12	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:18:ARG:HE	2:M:30:ASN:HD22	1.37	0.72
1:D:12:ILE:HG12	1:D:14:VAL:HG13	1.71	0.72
1:C:12:ILE:HG12	1:C:14:VAL:HG13	1.71	0.72
2:H:53:GLN:O	2:H:56:VAL:HG12	1.89	0.72
1:O:78:THR:HG21	1:O:85:ALA:HB1	1.70	0.72
2:1:123:ILE:HG12	2:1:124:TYR:HD1	1.53	0.72
1:S:78:THR:HG21	1:S:85:ALA:HB1	1.70	0.72
1:R:12:ILE:HG12	1:R:14:VAL:HG13	1.71	0.72
1:A:78:THR:HG21	1:A:85:ALA:HB1	1.70	0.72
1:B:78:THR:HG21	1:B:85:ALA:HB1	1.70	0.72
1:Q:168:GLY:O	1:Q:172:VAL:HG12	1.89	0.72
1:P:168:GLY:O	1:P:172:VAL:HG12	1.89	0.72
2:I:38:ASP:HB3	2:I:41:THR:CG2	2.19	0.72
2:N:123:ILE:HD13	2:N:123:ILE:H	1.52	0.72
1:U:168:GLY:O	1:U:172:VAL:HG12	1.89	0.72
1:R:78:THR:HG21	1:R:85:ALA:HB1	1.70	0.72
1:U:12:ILE:HG12	1:U:14:VAL:HG13	1.71	0.72
1:F:168:GLY:O	1:F:172:VAL:HG12	1.89	0.72
1:R:168:GLY:O	1:R:172:VAL:HG12	1.89	0.72
1:B:12:ILE:HG12	1:B:14:VAL:HG13	1.71	0.71
1:C:168:GLY:O	1:C:172:VAL:HG12	1.89	0.71
1:U:52:LYS:HZ3	1:U:62:ASN:HA	1.56	0.71
1:O:12:ILE:HG12	1:O:14:VAL:HG13	1.71	0.71
1:U:78:THR:HG21	1:U:85:ALA:HB1	1.70	0.71
1:Q:108:ASN:HB3	2:Y:70:ARG:HG2	1.73	0.71
1:P:12:ILE:HG12	1:P:14:VAL:HG13	1.71	0.71
1:G:108:ASN:HB3	2:H:70:ARG:HG2	1.72	0.71
2:I:103:GLY:HA2	2:I:178:ILE:HD11	1.71	0.71
1:T:12:ILE:HG12	1:T:14:VAL:HG13	1.71	0.71
2:L:7:THR:HB	2:L:123:ILE:O	1.90	0.71
1:S:12:ILE:CG2	1:S:14:VAL:CG2	2.42	0.71
1:C:78:THR:HG21	1:C:85:ALA:HB1	1.70	0.71
1:E:12:ILE:HG12	1:E:14:VAL:HG13	1.71	0.71
1:F:12:ILE:CG2	1:F:14:VAL:CG2	2.42	0.71
1:S:12:ILE:HG12	1:S:14:VAL:HG13	1.71	0.71
1:D:21:LEU:HD11	1:E:130:ARG:HD2	1.73	0.71
2:Z:7:THR:HB	2:Z:123:ILE:O	1.90	0.71
2:H:59:MET:HE2	2:H:79:VAL:HG23	1.72	0.71
1:A:12:ILE:HG12	1:A:14:VAL:HG13	1.71	0.71
1:E:52:LYS:HZ1	1:E:62:ASN:HA	1.53	0.70
2:H:32:LYS:HE2	2:H:34:LEU:O	1.89	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:12:ILE:CG2	1:Q:14:VAL:CG2	2.42	0.70
1:R:21:LEU:HD11	1:S:130:ARG:HD2	1.73	0.70
1:U:108:ASN:HB3	2:V:70:ARG:HG2	1.72	0.70
2:N:38:ASP:HB3	2:N:41:THR:CG2	2.21	0.70
2:X:53:GLN:O	2:X:56:VAL:HG12	1.91	0.70
1:A:12:ILE:CG2	1:A:14:VAL:CG2	2.42	0.70
1:E:107:VAL:HG11	2:M:66:TYR:HH	1.57	0.70
2:V:59:MET:HE2	2:V:79:VAL:HG23	1.72	0.70
1:G:107:VAL:HG11	2:H:66:TYR:HH	1.57	0.70
1:R:12:ILE:CG2	1:R:14:VAL:CG2	2.42	0.70
1:C:108:ASN:CB	2:K:70:ARG:HG2	2.22	0.70
2:I:62:GLU:HG2	2:I:82:LEU:HD21	1.74	0.70
2:V:38:ASP:HB3	2:V:41:THR:CG2	2.20	0.69
2:W:62:GLU:HG2	2:W:82:LEU:HD21	1.74	0.69
2:Y:12:VAL:HG13	2:Y:178:ILE:HG23	1.74	0.69
2:H:45:ILE:HG12	2:H:52:ALA:HB1	1.74	0.69
2:W:103:GLY:HA2	2:W:178:ILE:CD1	2.22	0.69
1:F:52:LYS:HZ3	1:F:62:ASN:HA	1.58	0.69
2:N:37:ILE:HD11	2:N:59:MET:HB3	1.73	0.69
1:C:108:ASN:HB3	2:K:70:ARG:HG2	1.73	0.69
2:J:45:ILE:CG1	2:J:52:ALA:HB1	2.22	0.69
2:K:7:THR:HB	2:K:123:ILE:O	1.93	0.69
2:V:43:MET:HE1	2:V:56:VAL:HG23	1.75	0.69
2:M:141:GLN:NE2	2:1:141:GLN:NE2	2.41	0.69
1:A:184:LEU:HD23	1:A:189:ALA:HA	1.75	0.69
1:G:184:LEU:HD23	1:G:189:ALA:HA	1.75	0.69
2:I:103:GLY:HA2	2:I:178:ILE:CD1	2.22	0.69
2:J:53:GLN:O	2:J:56:VAL:HG12	1.91	0.69
2:K:12:VAL:HG13	2:K:178:ILE:HG23	1.74	0.69
1:S:184:LEU:HD23	1:S:189:ALA:HA	1.75	0.69
1:Q:108:ASN:CB	2:Y:70:ARG:HG2	2.22	0.69
1:B:52:LYS:HZ3	1:B:62:ASN:HA	1.56	0.68
2:V:45:ILE:HG12	2:V:52:ALA:HB1	1.74	0.68
1:T:184:LEU:HD23	1:T:189:ALA:HA	1.75	0.68
1:S:12:ILE:CG1	1:S:14:VAL:N	2.52	0.68
1:Q:184:LEU:HD23	1:Q:189:ALA:HA	1.75	0.68
1:R:184:LEU:HD23	1:R:189:ALA:HA	1.75	0.68
2:L:193:GLU:HA	2:L:196:ILE:HD12	1.74	0.68
2:1:3:THR:OG1	2:1:127:THR:HG22	1.93	0.68
2:X:149:ASP:O	2:X:152:VAL:HG12	1.94	0.68
1:B:184:LEU:HD23	1:B:189:ALA:HA	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:12:ILE:CG2	1:G:14:VAL:CG2	2.42	0.68
2:Y:7:THR:HB	2:Y:123:ILE:O	1.93	0.68
2:1:53:GLN:O	2:1:56:VAL:HG12	1.93	0.68
2:2:37:ILE:HD11	2:2:59:MET:HB3	1.73	0.68
1:P:159:GLU:HG2	1:Q:60:GLU:HG3	1.76	0.68
2:J:149:ASP:O	2:J:152:VAL:HG12	1.94	0.68
1:D:184:LEU:HD23	1:D:189:ALA:HA	1.75	0.68
1:F:184:LEU:HD23	1:F:189:ALA:HA	1.75	0.68
2:X:18:ARG:HE	2:X:30:ASN:HD22	1.41	0.68
2:Z:193:GLU:HA	2:Z:196:ILE:HD12	1.74	0.68
1:A:12:ILE:CG1	1:A:14:VAL:N	2.51	0.67
1:Q:52:LYS:HZ1	1:Q:62:ASN:HA	1.59	0.67
2:M:3:THR:OG1	2:M:127:THR:HG22	1.93	0.67
1:T:52:LYS:HZ3	1:T:62:ASN:HA	1.57	0.67
2:H:59:MET:SD	2:H:83:LEU:HD13	2.35	0.67
1:O:184:LEU:HD23	1:O:189:ALA:HA	1.75	0.67
1:D:12:ILE:CG1	1:D:14:VAL:N	2.51	0.67
1:U:184:LEU:HD23	1:U:189:ALA:HA	1.75	0.67
1:C:184:LEU:HD23	1:C:189:ALA:HA	1.75	0.67
2:M:53:GLN:O	2:M:56:VAL:HG12	1.93	0.67
1:P:184:LEU:HD23	1:P:189:ALA:HA	1.75	0.67
1:T:12:ILE:O	1:T:23:GLN:HG2	1.95	0.67
2:X:45:ILE:CG1	2:X:52:ALA:HB1	2.22	0.67
1:E:184:LEU:HD23	1:E:189:ALA:HA	1.75	0.67
1:B:159:GLU:HG2	1:C:60:GLU:HG3	1.76	0.67
1:T:12:ILE:CG1	1:T:14:VAL:N	2.51	0.67
1:Q:12:ILE:O	1:Q:23:GLN:HG2	1.95	0.67
1:F:12:ILE:O	1:F:23:GLN:HG2	1.95	0.67
1:A:12:ILE:O	1:A:23:GLN:HG2	1.95	0.67
2:I:133:PHE:CZ	2:I:165:ARG:HB3	2.30	0.67
1:O:12:ILE:O	1:O:23:GLN:HG2	1.95	0.66
2:2:38:ASP:HB3	2:2:41:THR:CG2	2.21	0.66
1:D:52:LYS:HZ1	1:D:62:ASN:HA	1.59	0.66
1:D:12:ILE:O	1:D:23:GLN:HG2	1.95	0.66
1:U:12:ILE:O	1:U:23:GLN:HG2	1.95	0.66
1:S:12:ILE:O	1:S:23:GLN:HG2	1.95	0.66
2:M:123:ILE:HD13	2:M:123:ILE:H	1.60	0.66
2:H:38:ASP:HB3	2:H:41:THR:CG2	2.20	0.66
1:E:12:ILE:CG1	1:E:14:VAL:N	2.51	0.66
1:C:12:ILE:O	1:C:23:GLN:HG2	1.95	0.66
1:P:12:ILE:O	1:P:23:GLN:HG2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:ILE:O	1:B:23:GLN:HG2	1.95	0.66
2:W:7:THR:HB	2:W:123:ILE:O	1.96	0.66
2:I:7:THR:HB	2:I:123:ILE:O	1.96	0.66
2:L:59:MET:SD	2:L:83:LEU:HD13	2.36	0.66
2:W:133:PHE:CZ	2:W:165:ARG:HB3	2.30	0.66
1:P:12:ILE:CG1	1:P:14:VAL:N	2.51	0.66
1:G:12:ILE:O	1:G:23:GLN:HG2	1.95	0.66
1:T:61:GLN:O	1:T:64:ILE:HG22	1.95	0.66
2:V:59:MET:SD	2:V:83:LEU:HD13	2.35	0.66
1:E:12:ILE:O	1:E:23:GLN:HG2	1.95	0.66
1:C:61:GLN:O	1:C:64:ILE:HG22	1.95	0.66
1:R:12:ILE:O	1:R:23:GLN:HG2	1.95	0.66
2:X:2:THR:HG22	2:X:169:SER:OG	1.96	0.66
2:X:75:PRO:O	2:X:78:ALA:HB3	1.96	0.66
2:J:18:ARG:HE	2:J:30:ASN:HD22	1.41	0.66
1:D:198:LYS:O	1:D:202:GLU:HB2	1.96	0.66
1:Q:198:LYS:O	1:Q:202:GLU:HB2	1.96	0.66
2:M:164:GLN:NE2	2:Z:29:LYS:NZ	2.44	0.66
2:Z:59:MET:SD	2:Z:83:LEU:HD13	2.36	0.66
1:F:198:LYS:O	1:F:202:GLU:HB2	1.96	0.66
1:O:61:GLN:O	1:O:64:ILE:HG22	1.96	0.66
1:D:61:GLN:O	1:D:64:ILE:HG22	1.95	0.66
1:R:198:LYS:O	1:R:202:GLU:HB2	1.96	0.66
1:G:198:LYS:O	1:G:202:GLU:HB2	1.96	0.66
1:U:61:GLN:O	1:U:64:ILE:HG22	1.96	0.66
1:R:61:GLN:O	1:R:64:ILE:HG22	1.95	0.66
2:J:2:THR:HG22	2:J:169:SER:OG	1.96	0.66
1:B:61:GLN:O	1:B:64:ILE:HG22	1.95	0.65
1:S:61:GLN:O	1:S:64:ILE:HG22	1.95	0.65
1:Q:61:GLN:O	1:Q:64:ILE:HG22	1.96	0.65
2:1:123:ILE:HD13	2:1:123:ILE:H	1.60	0.65
1:P:198:LYS:O	1:P:202:GLU:HB2	1.96	0.65
1:O:198:LYS:O	1:O:202:GLU:HB2	1.96	0.65
1:B:12:ILE:CG1	1:B:14:VAL:N	2.51	0.65
2:M:124:TYR:CD2	2:M:138:LEU:HD23	2.31	0.65
2:L:123:ILE:HG12	2:L:124:TYR:HD1	1.61	0.65
2:Y:28:HIS:CD2	2:Z:120:VAL:HG11	2.31	0.65
1:A:61:GLN:O	1:A:64:ILE:HG22	1.96	0.65
1:F:61:GLN:O	1:F:64:ILE:HG22	1.95	0.65
1:G:61:GLN:O	1:G:64:ILE:HG22	1.95	0.65
2:M:164:GLN:NE2	2:Z:29:LYS:HZ1	1.93	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:198:LYS:O	1:C:202:GLU:HB2	1.96	0.65
2:L:29:LYS:NZ	2:1:164:GLN:NE2	2.45	0.65
1:P:61:GLN:O	1:P:64:ILE:HG22	1.95	0.65
2:W:45:ILE:HG12	2:W:52:ALA:HB1	1.79	0.65
1:A:198:LYS:O	1:A:202:GLU:HB2	1.96	0.65
2:Z:123:ILE:HG12	2:Z:124:TYR:HD1	1.62	0.65
1:E:61:GLN:O	1:E:64:ILE:HG22	1.95	0.65
2:K:28:HIS:CD2	2:L:120:VAL:HG11	2.31	0.65
1:U:198:LYS:O	1:U:202:GLU:HB2	1.96	0.65
1:E:198:LYS:O	1:E:202:GLU:HB2	1.96	0.65
2:W:123:ILE:H	2:W:123:ILE:HD13	1.62	0.65
1:O:12:ILE:HG21	1:O:14:VAL:HG21	1.72	0.65
1:T:198:LYS:O	1:T:202:GLU:HB2	1.96	0.65
2:I:124:TYR:CD2	2:I:138:LEU:HD23	2.32	0.65
2:W:20:VAL:HG13	2:W:28:HIS:HB2	1.79	0.65
1:S:198:LYS:O	1:S:202:GLU:HB2	1.96	0.65
2:I:20:VAL:HG13	2:I:28:HIS:HB2	1.79	0.64
2:K:59:MET:HE2	2:K:79:VAL:HG23	1.79	0.64
2:Y:123:ILE:HG12	2:Y:124:TYR:CD1	2.31	0.64
2:1:124:TYR:CD2	2:1:138:LEU:HD23	2.31	0.64
2:N:123:ILE:HG12	2:N:124:TYR:HD2	1.61	0.64
1:B:198:LYS:O	1:B:202:GLU:HB2	1.96	0.64
2:1:49:VAL:HG23	2:1:50:GLY:H	1.63	0.64
2:J:75:PRO:O	2:J:78:ALA:HB3	1.96	0.64
1:A:130:ARG:HD2	1:G:21:LEU:HD11	1.79	0.64
2:W:124:TYR:CD2	2:W:138:LEU:HD23	2.32	0.64
2:L:124:TYR:CD2	2:L:138:LEU:HD23	2.33	0.64
2:V:124:TYR:CD2	2:V:138:LEU:HD23	2.33	0.64
2:I:45:ILE:HG12	2:I:52:ALA:HB1	1.79	0.64
2:1:45:ILE:CG1	2:1:52:ALA:HB1	2.26	0.64
2:M:123:ILE:HG12	2:M:124:TYR:CD1	2.33	0.64
2:2:123:ILE:HG12	2:2:124:TYR:HD2	1.61	0.64
2:V:55:LEU:HD21	2:V:87:LEU:HD11	1.80	0.64
2:L:18:ARG:HB2	2:L:31:GLY:O	1.98	0.64
1:G:52:LYS:HZ1	1:G:62:ASN:HA	1.61	0.64
2:1:123:ILE:HG12	2:1:124:TYR:CD1	2.33	0.64
2:K:3:THR:HB	2:K:16:THR:HG22	1.80	0.64
2:I:123:ILE:H	2:I:123:ILE:HD13	1.62	0.64
1:S:159:GLU:HG2	1:T:60:GLU:HG3	1.80	0.64
1:O:130:ARG:HD2	1:U:21:LEU:HD11	1.79	0.63
1:O:52:LYS:HZ3	1:O:62:ASN:HA	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:123:ILE:H	2:V:123:ILE:HD13	1.62	0.63
2:I:123:ILE:HG12	2:I:124:TYR:CD1	2.32	0.63
2:M:141:GLN:NE2	2:1:141:GLN:HE21	1.96	0.63
2:Z:37:ILE:HD11	2:Z:59:MET:HB3	1.79	0.63
1:E:159:GLU:HG2	1:F:60:GLU:HG3	1.80	0.63
2:M:45:ILE:CG1	2:M:52:ALA:HB1	2.26	0.63
2:Z:124:TYR:CD2	2:Z:138:LEU:HD23	2.33	0.63
2:J:103:GLY:HA2	2:J:178:ILE:HD13	1.81	0.63
2:K:193:GLU:HA	2:K:196:ILE:HD12	1.81	0.63
2:Z:18:ARG:HB2	2:Z:31:GLY:O	1.98	0.63
2:Y:193:GLU:HA	2:Y:196:ILE:HD12	1.81	0.63
2:M:49:VAL:HG23	2:M:50:GLY:H	1.62	0.63
1:C:12:ILE:HG21	1:C:14:VAL:HG21	1.72	0.63
1:O:12:ILE:CG1	1:O:14:VAL:N	2.52	0.63
1:Q:12:ILE:CG1	1:Q:14:VAL:N	2.51	0.63
2:H:167:SER:HB2	2:X:167:SER:HB2	1.79	0.63
2:X:103:GLY:HA2	2:X:178:ILE:HD13	1.81	0.63
2:N:179:THR:HG23	2:N:182:ASP:H	1.63	0.63
2:H:124:TYR:CD2	2:H:138:LEU:HD23	2.33	0.63
1:B:12:ILE:HG21	1:B:14:VAL:HG21	1.72	0.63
1:F:12:ILE:CG1	1:F:14:VAL:N	2.51	0.63
1:O:52:LYS:HZ1	1:O:62:ASN:HA	1.62	0.63
1:R:52:LYS:HZ1	1:R:62:ASN:HA	1.61	0.63
1:S:177:GLU:O	1:T:57:ARG:NE	2.31	0.63
1:U:12:ILE:CG1	1:U:14:VAL:N	2.52	0.63
2:H:123:ILE:H	2:H:123:ILE:HD13	1.62	0.63
2:N:133:PHE:CZ	2:N:165:ARG:HB3	2.34	0.63
2:J:103:GLY:HA2	2:J:178:ILE:CD1	2.29	0.62
2:2:133:PHE:CZ	2:2:165:ARG:HB3	2.34	0.62
1:R:52:LYS:HZ3	1:R:62:ASN:HA	1.64	0.62
2:L:37:ILE:HD11	2:L:59:MET:HB3	1.79	0.62
1:P:52:LYS:HZ3	1:P:62:ASN:HA	1.61	0.62
1:G:52:LYS:HZ3	1:G:62:ASN:HA	1.63	0.62
2:Z:15:ALA:HB2	2:Z:175:VAL:HB	1.82	0.62
1:T:15:PHE:HB2	1:U:23:GLN:HE22	1.65	0.62
2:K:123:ILE:HD13	2:K:123:ILE:H	1.63	0.62
1:C:121:GLN:O	1:C:124:THR:HB	2.00	0.62
2:I:76:ILE:O	2:I:79:VAL:HG12	2.00	0.62
1:F:15:PHE:HB2	1:G:23:GLN:HE22	1.65	0.62
1:U:121:GLN:O	1:U:124:THR:HB	2.00	0.62
2:M:141:GLN:HE21	2:1:141:GLN:NE2	1.97	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:3:THR:HB	2:Y:16:THR:HG22	1.80	0.62
1:U:12:ILE:HG21	1:U:14:VAL:HG21	1.72	0.62
1:A:12:ILE:HG21	1:A:14:VAL:HG21	1.72	0.62
2:V:43:MET:CE	2:V:56:VAL:HG23	2.29	0.62
2:X:103:GLY:HA2	2:X:178:ILE:CD1	2.29	0.62
2:J:167:SER:HB2	2:V:167:SER:HB2	1.82	0.62
2:H:2:THR:HG22	2:H:169:SER:OG	2.00	0.62
2:H:55:LEU:HD21	2:H:87:LEU:HD11	1.80	0.62
1:C:12:ILE:CG1	1:C:14:VAL:N	2.51	0.62
2:1:149:ASP:O	2:1:152:VAL:HG12	1.99	0.62
2:H:123:ILE:HG12	2:H:124:TYR:CD1	2.33	0.62
2:2:179:THR:HG23	2:2:182:ASP:H	1.63	0.62
1:D:121:GLN:O	1:D:124:THR:HB	2.00	0.61
1:Q:21:LEU:HD11	1:R:130:ARG:HD2	1.82	0.61
2:M:149:ASP:O	2:M:152:VAL:HG12	1.99	0.61
1:B:124:THR:HG22	1:C:130:ARG:HH21	1.65	0.61
1:P:121:GLN:O	1:P:124:THR:HB	2.00	0.61
1:P:124:THR:HG22	1:Q:130:ARG:HH21	1.65	0.61
2:K:38:ASP:HB3	2:K:41:THR:CG2	2.26	0.61
2:V:2:THR:HG22	2:V:169:SER:OG	2.00	0.61
1:A:49:ILE:HD12	1:A:211:GLU:O	2.01	0.61
2:W:76:ILE:O	2:W:79:VAL:HG12	1.99	0.61
1:D:88:LEU:HD21	1:D:120:MET:SD	2.41	0.61
1:E:49:ILE:HD12	1:E:211:GLU:O	2.01	0.61
1:D:108:ASN:HB3	2:L:70:ARG:HG2	1.83	0.61
1:B:88:LEU:HD21	1:B:120:MET:SD	2.41	0.61
1:S:49:ILE:HD12	1:S:211:GLU:O	2.01	0.61
1:R:121:GLN:O	1:R:124:THR:HB	2.00	0.61
2:Y:123:ILE:HD13	2:Y:123:ILE:H	1.63	0.61
2:N:76:ILE:O	2:N:79:VAL:HG12	2.00	0.61
1:T:88:LEU:HD21	1:T:120:MET:SD	2.41	0.61
1:P:88:LEU:HD21	1:P:120:MET:SD	2.41	0.61
1:E:88:LEU:HD21	1:E:120:MET:SD	2.41	0.61
1:G:121:GLN:O	1:G:124:THR:HB	2.00	0.61
1:F:61:GLN:OE1	1:F:62:ASN:HB3	2.00	0.61
2:K:123:ILE:HG12	2:K:124:TYR:CD1	2.31	0.61
1:E:121:GLN:O	1:E:124:THR:HB	2.00	0.61
1:O:121:GLN:O	1:O:124:THR:HB	2.00	0.61
1:P:49:ILE:HD12	1:P:211:GLU:O	2.01	0.61
1:D:49:ILE:HD12	1:D:211:GLU:O	2.01	0.61
1:O:88:LEU:HD21	1:O:120:MET:SD	2.41	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:88:LEU:HD21	1:C:120:MET:SD	2.41	0.61
2:W:123:ILE:HG12	2:W:124:TYR:CD1	2.32	0.61
1:Q:121:GLN:O	1:Q:124:THR:HB	2.00	0.61
1:A:61:GLN:OE1	1:A:62:ASN:HB3	2.00	0.61
1:S:61:GLN:OE1	1:S:62:ASN:HB3	2.00	0.61
1:P:61:GLN:OE1	1:P:62:ASN:HB3	2.00	0.61
1:A:121:GLN:O	1:A:124:THR:HB	2.00	0.61
1:Q:49:ILE:HD12	1:Q:211:GLU:O	2.01	0.61
1:U:88:LEU:HD21	1:U:120:MET:SD	2.41	0.61
1:F:88:LEU:HD21	1:F:120:MET:SD	2.41	0.61
1:Q:61:GLN:OE1	1:Q:62:ASN:HB3	2.00	0.61
1:S:121:GLN:O	1:S:124:THR:HB	2.00	0.61
1:F:49:ILE:HD12	1:F:211:GLU:O	2.01	0.61
1:T:121:GLN:O	1:T:124:THR:HB	2.00	0.61
1:F:121:GLN:O	1:F:124:THR:HB	2.00	0.61
1:C:21:LEU:HD11	1:D:130:ARG:HD2	1.82	0.61
1:B:121:GLN:O	1:B:124:THR:HB	2.00	0.61
2:L:15:ALA:HB2	2:L:175:VAL:HB	1.82	0.61
1:C:49:ILE:HD12	1:C:211:GLU:O	2.01	0.61
1:U:49:ILE:HD12	1:U:211:GLU:O	2.01	0.61
1:R:61:GLN:OE1	1:R:62:ASN:HB3	2.00	0.61
2:W:37:ILE:HD11	2:W:59:MET:HB3	1.82	0.61
1:O:49:ILE:HD12	1:O:211:GLU:O	2.01	0.61
2:N:3:THR:HB	2:N:16:THR:HG22	1.83	0.61
1:E:177:GLU:O	1:F:57:ARG:NE	2.31	0.61
1:G:12:ILE:HG21	1:G:14:VAL:HG21	1.72	0.60
2:I:37:ILE:HD11	2:I:59:MET:HB3	1.83	0.60
1:Q:88:LEU:HD21	1:Q:120:MET:SD	2.41	0.60
1:T:12:ILE:HG21	1:T:14:VAL:HG21	1.72	0.60
1:S:12:ILE:HG21	1:S:14:VAL:HG21	1.72	0.60
1:T:61:GLN:OE1	1:T:62:ASN:HB3	2.00	0.60
1:Q:52:LYS:HZ3	1:Q:62:ASN:HA	1.66	0.60
1:E:61:GLN:OE1	1:E:62:ASN:HB3	2.00	0.60
2:L:3:THR:HB	2:L:16:THR:HG22	1.83	0.60
1:R:12:ILE:CG1	1:R:14:VAL:N	2.51	0.60
1:U:61:GLN:OE1	1:U:62:ASN:HB3	2.00	0.60
2:Z:32:LYS:HE2	2:Z:34:LEU:O	2.01	0.60
1:R:28:ARG:O	1:R:31:VAL:HG22	2.02	0.60
1:D:28:ARG:O	1:D:31:VAL:HG22	2.02	0.60
2:L:133:PHE:HE1	2:2:132:PRO:HA	1.65	0.60
1:C:61:GLN:OE1	1:C:62:ASN:HB3	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:61:GLN:OE1	1:G:62:ASN:HB3	2.00	0.60
2:2:76:ILE:O	2:2:79:VAL:HG12	2.00	0.60
1:R:108:ASN:HB3	2:Z:70:ARG:HG2	1.83	0.60
1:G:28:ARG:O	1:G:31:VAL:HG22	2.02	0.60
2:K:124:TYR:CD2	2:K:138:LEU:HD23	2.37	0.60
1:O:28:ARG:O	1:O:31:VAL:HG22	2.02	0.60
1:G:42:PHE:HD1	1:G:43:ALA:N	2.00	0.60
1:T:42:PHE:HD1	1:T:43:ALA:N	2.00	0.60
1:R:42:PHE:HD1	1:R:43:ALA:N	2.00	0.60
1:B:42:PHE:HD1	1:B:43:ALA:N	2.00	0.60
1:T:49:ILE:HD12	1:T:211:GLU:O	2.01	0.60
1:G:49:ILE:HD12	1:G:211:GLU:O	2.01	0.60
1:R:49:ILE:HD12	1:R:211:GLU:O	2.01	0.60
1:R:88:LEU:HD21	1:R:120:MET:SD	2.41	0.60
1:D:12:ILE:CG2	1:D:14:VAL:CG2	2.42	0.60
1:B:61:GLN:OE1	1:B:62:ASN:HB3	2.00	0.60
1:P:52:LYS:HZ1	1:P:62:ASN:HA	1.64	0.60
2:1:133:PHE:CZ	2:1:165:ARG:HB3	2.37	0.60
2:Y:159:ILE:O	2:Y:163:LYS:HG3	2.02	0.60
1:D:107:VAL:HG11	2:L:66:TYR:HH	1.67	0.60
1:F:28:ARG:O	1:F:31:VAL:HG22	2.02	0.60
1:O:61:GLN:OE1	1:O:62:ASN:HB3	2.00	0.60
1:D:61:GLN:OE1	1:D:62:ASN:HB3	2.00	0.60
2:H:43:MET:CE	2:H:56:VAL:HG23	2.30	0.60
2:2:3:THR:HB	2:2:16:THR:HG22	1.83	0.60
1:A:88:LEU:HD21	1:A:120:MET:SD	2.41	0.60
1:G:12:ILE:CG1	1:G:14:VAL:N	2.51	0.60
1:G:108:ASN:CB	2:H:70:ARG:HG2	2.31	0.60
1:F:42:PHE:HD1	1:F:43:ALA:N	2.00	0.60
1:P:42:PHE:HD1	1:P:43:ALA:N	2.00	0.60
1:B:49:ILE:HD12	1:B:211:GLU:O	2.01	0.60
1:U:108:ASN:CB	2:V:70:ARG:HG2	2.31	0.59
1:S:88:LEU:HD21	1:S:120:MET:SD	2.41	0.59
1:G:88:LEU:HD21	1:G:120:MET:SD	2.41	0.59
1:U:12:ILE:CG2	1:U:14:VAL:CG2	2.42	0.59
2:X:38:ASP:HB2	2:X:63:LEU:HD23	1.84	0.59
1:Q:28:ARG:O	1:Q:31:VAL:HG22	2.02	0.59
2:V:123:ILE:HG12	2:V:124:TYR:CD1	2.33	0.59
1:A:42:PHE:HD1	1:A:43:ALA:N	2.00	0.59
2:Z:3:THR:HB	2:Z:16:THR:HG22	1.83	0.59
2:V:37:ILE:HD11	2:V:59:MET:HB3	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:42:PHE:HD1	1:D:43:ALA:N	2.00	0.59
1:O:42:PHE:HD1	1:O:43:ALA:N	2.00	0.59
1:U:42:PHE:HD1	1:U:43:ALA:N	2.00	0.59
1:E:42:PHE:HD1	1:E:43:ALA:N	2.00	0.59
2:K:32:LYS:HE2	2:K:34:LEU:O	2.02	0.59
2:M:133:PHE:CZ	2:M:165:ARG:HB3	2.37	0.59
1:C:12:ILE:CG2	1:C:14:VAL:CG2	2.42	0.59
1:S:42:PHE:HD1	1:S:43:ALA:N	2.00	0.59
2:Y:18:ARG:HE	2:Y:30:ASN:HD22	1.51	0.59
2:W:149:ASP:O	2:W:152:VAL:HG12	2.03	0.59
1:P:28:ARG:O	1:P:31:VAL:HG22	2.02	0.59
1:R:12:ILE:HG21	1:R:14:VAL:HG21	1.72	0.59
1:C:28:ARG:O	1:C:31:VAL:HG22	2.02	0.59
1:S:28:ARG:O	1:S:31:VAL:HG22	2.02	0.59
1:Q:42:PHE:HD1	1:Q:43:ALA:N	2.00	0.59
1:C:49:ILE:HD11	1:C:210:PRO:HB3	1.85	0.59
1:U:49:ILE:HD11	1:U:210:PRO:HB3	1.85	0.59
2:K:152:VAL:O	2:K:156:ILE:HG13	2.03	0.59
1:O:49:ILE:HD11	1:O:210:PRO:HB3	1.85	0.59
1:B:28:ARG:O	1:B:31:VAL:HG22	2.02	0.59
2:1:38:ASP:HB3	2:1:41:THR:CG2	2.28	0.59
1:D:52:LYS:HZ3	1:D:62:ASN:HA	1.66	0.59
1:E:28:ARG:O	1:E:31:VAL:HG22	2.02	0.59
1:C:42:PHE:HD1	1:C:43:ALA:N	2.00	0.59
1:B:49:ILE:HD11	1:B:210:PRO:HB3	1.85	0.59
2:L:32:LYS:HE2	2:L:34:LEU:O	2.01	0.59
2:J:66:TYR:CD2	2:J:74:MET:HE2	2.37	0.59
1:A:28:ARG:O	1:A:31:VAL:HG22	2.02	0.59
1:A:21:LEU:HD11	1:B:130:ARG:HD2	1.85	0.59
2:H:37:ILE:HD11	2:H:59:MET:HB3	1.82	0.59
2:X:66:TYR:CD2	2:X:74:MET:HE2	2.37	0.59
1:U:28:ARG:O	1:U:31:VAL:HG22	2.02	0.59
2:L:38:ASP:HB3	2:L:41:THR:CG2	2.31	0.59
1:T:28:ARG:O	1:T:31:VAL:HG22	2.02	0.59
1:D:49:ILE:HD11	1:D:210:PRO:HB3	1.85	0.59
1:F:52:LYS:HZ1	1:F:62:ASN:HA	1.67	0.58
2:Y:124:TYR:CD2	2:Y:138:LEU:HD23	2.37	0.58
1:O:21:LEU:HD11	1:P:130:ARG:HD2	1.85	0.58
2:J:7:THR:HB	2:J:123:ILE:O	2.03	0.58
2:J:38:ASP:HB2	2:J:63:LEU:HD23	1.84	0.58
2:Z:123:ILE:HD13	2:Z:123:ILE:H	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:49:ILE:HD11	1:P:210:PRO:HB3	1.85	0.58
2:N:132:PRO:HA	2:Z:133:PHE:HE1	1.67	0.58
2:Z:38:ASP:HB3	2:Z:41:THR:CG2	2.31	0.58
1:T:49:ILE:HD11	1:T:210:PRO:HB3	1.85	0.58
2:2:178:ILE:HB	2:2:184:TYR:HA	1.84	0.58
2:X:7:THR:HB	2:X:123:ILE:O	2.03	0.58
2:L:123:ILE:HD13	2:L:123:ILE:H	1.67	0.58
2:Y:152:VAL:O	2:Y:156:ILE:HG13	2.03	0.58
2:K:159:ILE:O	2:K:163:LYS:HG3	2.02	0.58
2:X:199:LEU:HB3	2:X:201:LEU:HD13	1.85	0.58
1:U:35:SER:O	1:U:166:GLY:HA3	2.03	0.58
2:L:28:HIS:CD2	2:M:120:VAL:HG11	2.39	0.58
2:Y:20:VAL:HG22	2:Y:28:HIS:HB2	1.86	0.58
1:A:49:ILE:HD11	1:A:210:PRO:HB3	1.85	0.58
1:P:135:SER:OG	1:P:153:PRO:HD3	2.04	0.58
1:T:35:SER:O	1:T:166:GLY:HA3	2.03	0.58
1:C:35:SER:O	1:C:166:GLY:HA3	2.03	0.58
2:Y:59:MET:HE3	2:Y:82:LEU:HD23	1.83	0.58
1:Q:135:SER:OG	1:Q:153:PRO:HD3	2.04	0.58
1:E:135:SER:OG	1:E:153:PRO:HD3	2.04	0.58
1:O:12:ILE:CG2	1:O:14:VAL:CG2	2.42	0.58
2:Y:32:LYS:HE2	2:Y:34:LEU:O	2.02	0.58
2:V:152:VAL:O	2:V:156:ILE:HG13	2.04	0.58
1:E:49:ILE:HD11	1:E:210:PRO:HB3	1.85	0.58
1:B:35:SER:O	1:B:166:GLY:HA3	2.03	0.58
1:O:35:SER:O	1:O:166:GLY:HA3	2.03	0.58
1:F:135:SER:OG	1:F:153:PRO:HD3	2.04	0.58
2:H:8:LEU:O	2:H:8:LEU:HD12	2.03	0.58
1:F:12:ILE:HG21	1:F:14:VAL:HG21	1.72	0.58
2:Y:38:ASP:HB3	2:Y:41:THR:CG2	2.26	0.58
1:T:52:LYS:HZ1	1:T:62:ASN:HA	1.68	0.58
1:Q:49:ILE:HD11	1:Q:210:PRO:HB3	1.85	0.58
1:O:135:SER:OG	1:O:153:PRO:HD3	2.04	0.58
2:I:149:ASP:O	2:I:152:VAL:HG12	2.03	0.58
1:P:108:ASN:HB3	2:X:70:ARG:HG2	1.86	0.58
1:D:135:SER:OG	1:D:153:PRO:HD3	2.04	0.58
2:X:123:ILE:HG12	2:X:124:TYR:HD1	1.69	0.58
2:K:18:ARG:HE	2:K:30:ASN:HD22	1.51	0.58
1:S:49:ILE:HD11	1:S:210:PRO:HB3	1.85	0.57
1:G:49:ILE:HD11	1:G:210:PRO:HB3	1.85	0.57
2:M:28:HIS:CD2	2:N:120:VAL:HG11	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:49:ILE:HD11	1:F:210:PRO:HB3	1.85	0.57
2:X:160:SER:O	2:X:163:LYS:HB2	2.04	0.57
2:J:3:THR:OG1	2:J:127:THR:HG22	2.05	0.57
2:N:178:ILE:HB	2:N:184:TYR:HA	1.84	0.57
1:D:35:SER:O	1:D:166:GLY:HA3	2.03	0.57
1:S:108:ASN:HB3	2:1:70:ARG:HG2	1.86	0.57
1:E:108:ASN:HB3	2:M:70:ARG:HG2	1.86	0.57
2:1:28:HIS:CD2	2:2:120:VAL:HG11	2.39	0.57
2:I:51:ASP:O	2:I:55:LEU:HB2	2.04	0.57
1:A:35:SER:O	1:A:166:GLY:HA3	2.03	0.57
1:S:35:SER:O	1:S:166:GLY:HA3	2.03	0.57
2:Z:28:HIS:CD2	2:1:120:VAL:HG11	2.39	0.57
1:R:135:SER:OG	1:R:153:PRO:HD3	2.04	0.57
2:X:3:THR:OG1	2:X:127:THR:HG22	2.05	0.57
2:M:75:PRO:O	2:M:78:ALA:HB3	2.05	0.57
1:P:143:GLN:HA	1:P:143:GLN:HE21	1.70	0.57
2:N:124:TYR:CD1	2:N:138:LEU:HD23	2.40	0.57
2:K:20:VAL:HG22	2:K:28:HIS:HB2	1.86	0.57
2:Y:131:SER:O	2:Y:134:VAL:HG13	2.04	0.57
2:V:8:LEU:O	2:V:8:LEU:HD12	2.03	0.57
1:R:49:ILE:HD11	1:R:210:PRO:HB3	1.85	0.57
2:K:131:SER:O	2:K:134:VAL:HG13	2.04	0.57
1:E:143:GLN:HE21	1:E:143:GLN:HA	1.70	0.57
1:S:21:LEU:HD11	1:T:130:ARG:HD2	1.87	0.57
1:R:35:SER:O	1:R:166:GLY:HA3	2.03	0.57
1:G:135:SER:OG	1:G:153:PRO:HD3	2.04	0.57
2:W:51:ASP:O	2:W:55:LEU:HB2	2.05	0.57
1:F:35:SER:O	1:F:166:GLY:HA3	2.03	0.57
2:H:152:VAL:O	2:H:156:ILE:HG13	2.04	0.57
1:U:135:SER:OG	1:U:153:PRO:HD3	2.04	0.57
1:U:52:LYS:HZ1	1:U:62:ASN:HA	1.69	0.57
2:Y:59:MET:HE2	2:Y:79:VAL:HG23	1.85	0.57
2:M:178:ILE:HB	2:M:184:TYR:HA	1.87	0.57
2:H:37:ILE:HD11	2:H:59:MET:CG	2.35	0.57
1:D:102:THR:O	2:L:81:THR:HG22	2.05	0.57
1:B:108:ASN:HB3	2:J:70:ARG:HG2	1.86	0.57
1:C:135:SER:OG	1:C:153:PRO:HD3	2.04	0.57
1:G:35:SER:O	1:G:166:GLY:HA3	2.03	0.57
1:O:143:GLN:HE21	1:O:143:GLN:HA	1.70	0.57
1:B:52:LYS:HZ1	1:B:62:ASN:HA	1.69	0.57
2:L:43:MET:CE	2:L:56:VAL:HG23	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:62:GLU:HG2	2:V:82:LEU:HD21	1.87	0.57
1:P:35:SER:O	1:P:166:GLY:HA3	2.03	0.57
2:2:152:VAL:O	2:2:156:ILE:HG13	2.05	0.57
2:1:178:ILE:HB	2:1:184:TYR:HA	1.87	0.57
2:K:45:ILE:HG12	2:K:52:ALA:HB1	1.87	0.56
2:2:124:TYR:CD1	2:2:138:LEU:HD23	2.40	0.56
2:L:179:THR:HG23	2:L:182:ASP:H	1.70	0.56
2:M:76:ILE:HG21	2:M:109:HIS:HB2	1.88	0.56
1:D:143:GLN:HA	1:D:143:GLN:HE21	1.70	0.56
2:M:38:ASP:HB3	2:M:41:THR:CG2	2.28	0.56
1:E:35:SER:O	1:E:166:GLY:HA3	2.04	0.56
1:Q:35:SER:O	1:Q:166:GLY:HA3	2.03	0.56
2:N:152:VAL:O	2:N:156:ILE:HG13	2.05	0.56
1:F:143:GLN:HE21	1:F:143:GLN:HA	1.70	0.56
2:H:174:ASP:HA	2:H:192:ILE:HD13	1.88	0.56
2:J:160:SER:O	2:J:163:LYS:HB2	2.04	0.56
2:Z:43:MET:HE1	2:Z:56:VAL:HG23	1.88	0.56
2:V:37:ILE:HD11	2:V:59:MET:CG	2.35	0.56
2:J:199:LEU:HB3	2:J:201:LEU:HD13	1.85	0.56
1:C:52:LYS:HZ1	1:C:62:ASN:HA	1.70	0.56
1:R:102:THR:O	2:Z:81:THR:HG22	2.05	0.56
2:V:174:ASP:HA	2:V:192:ILE:HD13	1.88	0.56
1:Q:143:GLN:HE21	1:Q:143:GLN:HA	1.70	0.56
1:U:12:ILE:O	1:U:23:GLN:CG	2.54	0.56
1:Q:12:ILE:HG21	1:Q:14:VAL:HG21	1.72	0.56
1:E:21:LEU:HD11	1:F:130:ARG:HD2	1.86	0.56
1:T:135:SER:OG	1:T:153:PRO:HD3	2.04	0.56
1:S:135:SER:OG	1:S:153:PRO:HD3	2.04	0.56
2:Z:179:THR:HG23	2:Z:182:ASP:H	1.70	0.56
1:D:12:ILE:O	1:D:23:GLN:CG	2.54	0.56
1:C:12:ILE:O	1:C:23:GLN:CG	2.54	0.56
1:O:12:ILE:O	1:O:23:GLN:CG	2.54	0.56
1:T:43:ALA:HB2	1:T:185:PRO:HA	1.88	0.56
2:N:174:ASP:HA	2:N:192:ILE:HD13	1.87	0.56
1:B:143:GLN:HA	1:B:143:GLN:HE21	1.70	0.56
1:B:135:SER:OG	1:B:153:PRO:HD3	2.04	0.56
2:M:32:LYS:HE2	2:M:34:LEU:O	2.06	0.56
1:T:143:GLN:HE21	1:T:143:GLN:HA	1.70	0.56
1:T:12:ILE:O	1:T:23:GLN:CG	2.54	0.56
2:1:75:PRO:O	2:1:78:ALA:HB3	2.04	0.56
2:V:120:VAL:HG11	2:2:28:HIS:CD2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:ALA:HB2	1:B:185:PRO:HA	1.88	0.56
1:A:135:SER:OG	1:A:153:PRO:HD3	2.04	0.56
1:O:130:ARG:NH2	1:U:124:THR:HG22	2.17	0.55
2:N:66:TYR:CZ	2:N:70:ARG:HD2	2.41	0.55
2:Z:43:MET:CE	2:Z:56:VAL:HG23	2.35	0.55
2:N:26:ILE:C	2:N:26:ILE:HD13	2.27	0.55
1:E:12:ILE:O	1:E:23:GLN:CG	2.54	0.55
1:A:12:ILE:O	1:A:23:GLN:CG	2.54	0.55
1:R:124:THR:HG22	1:S:130:ARG:NH2	2.14	0.55
2:J:123:ILE:HG12	2:J:124:TYR:HD1	1.69	0.55
2:H:62:GLU:HG2	2:H:82:LEU:HD21	1.87	0.55
2:V:6:ILE:HD11	2:V:142:TYR:CD1	2.42	0.55
1:R:143:GLN:HA	1:R:143:GLN:HE21	1.70	0.55
1:G:143:GLN:HE21	1:G:143:GLN:HA	1.70	0.55
2:2:174:ASP:HA	2:2:192:ILE:HD13	1.87	0.55
1:U:143:GLN:HE21	1:U:143:GLN:HA	1.70	0.55
1:C:143:GLN:HE21	1:C:143:GLN:HA	1.70	0.55
1:B:12:ILE:O	1:B:23:GLN:CG	2.54	0.55
1:A:43:ALA:HB2	1:A:185:PRO:HA	1.88	0.55
1:S:43:ALA:HB2	1:S:185:PRO:HA	1.88	0.55
1:S:143:GLN:HA	1:S:143:GLN:HE21	1.70	0.55
1:A:143:GLN:HE21	1:A:143:GLN:HA	1.70	0.55
1:S:12:ILE:O	1:S:23:GLN:CG	2.54	0.55
1:U:43:ALA:HB2	1:U:185:PRO:HA	1.88	0.55
1:U:70:ILE:HD12	1:U:74:VAL:HG22	1.88	0.55
2:1:76:ILE:HG21	2:1:109:HIS:HB2	1.88	0.55
1:O:70:ILE:HD12	1:O:74:VAL:HG22	1.88	0.55
2:M:167:SER:OG	2:Z:24:ASN:HA	2.07	0.55
2:H:120:VAL:HG11	2:N:28:HIS:CD2	2.41	0.55
1:P:12:ILE:O	1:P:23:GLN:CG	2.54	0.55
2:2:66:TYR:CZ	2:2:70:ARG:HD2	2.41	0.55
1:F:12:ILE:O	1:F:23:GLN:CG	2.54	0.55
1:T:198:LYS:HG2	1:T:202:GLU:HG2	1.88	0.55
1:S:198:LYS:HG2	1:S:202:GLU:HG2	1.88	0.55
1:G:12:ILE:CB	1:G:14:VAL:HG22	2.36	0.55
1:G:12:ILE:O	1:G:23:GLN:CG	2.54	0.55
1:D:124:THR:HG22	1:E:130:ARG:NH2	2.14	0.55
1:B:198:LYS:HG2	1:B:202:GLU:HG2	1.88	0.55
2:Y:45:ILE:HG12	2:Y:52:ALA:HB1	1.87	0.55
2:H:179:THR:HG23	2:H:182:ASP:H	1.72	0.55
1:F:70:ILE:HD12	1:F:74:VAL:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:12:ILE:CB	1:R:14:VAL:HG22	2.36	0.55
1:D:43:ALA:HB2	1:D:185:PRO:HA	1.88	0.55
1:C:43:ALA:HB2	1:C:185:PRO:HA	1.88	0.55
1:A:198:LYS:HG2	1:A:202:GLU:HG2	1.88	0.55
1:C:70:ILE:HD12	1:C:74:VAL:HG22	1.88	0.55
1:D:95:SER:OG	1:D:115:ARG:HD3	2.07	0.55
1:Q:70:ILE:HD12	1:Q:74:VAL:HG22	1.88	0.55
2:I:17:GLU:O	2:I:33:LYS:HD2	2.07	0.55
1:R:12:ILE:O	1:R:23:GLN:CG	2.54	0.55
1:Q:12:ILE:CB	1:Q:14:VAL:HG22	2.36	0.55
1:S:12:ILE:CB	1:S:14:VAL:HG22	2.36	0.55
1:B:95:SER:OG	1:B:115:ARG:HD3	2.07	0.55
1:E:95:SER:OG	1:E:115:ARG:HD3	2.07	0.55
1:G:70:ILE:HD12	1:G:74:VAL:HG22	1.88	0.55
1:E:12:ILE:HG21	1:E:14:VAL:HG21	1.72	0.55
1:E:43:ALA:HB2	1:E:185:PRO:HA	1.88	0.55
1:P:95:SER:OG	1:P:115:ARG:HD3	2.07	0.55
1:P:70:ILE:HD12	1:P:74:VAL:HG22	1.88	0.55
1:D:70:ILE:HD12	1:D:74:VAL:HG22	1.88	0.55
1:E:70:ILE:HD12	1:E:74:VAL:HG22	1.88	0.55
1:S:95:SER:OG	1:S:115:ARG:HD3	2.07	0.55
1:A:95:SER:OG	1:A:115:ARG:HD3	2.07	0.55
1:T:70:ILE:HD12	1:T:74:VAL:HG22	1.88	0.55
1:Q:12:ILE:O	1:Q:23:GLN:CG	2.54	0.54
1:A:12:ILE:CB	1:A:14:VAL:HG22	2.36	0.54
2:V:179:THR:HG23	2:V:182:ASP:H	1.71	0.54
2:2:26:ILE:C	2:2:26:ILE:HD13	2.27	0.54
1:F:12:ILE:CB	1:F:14:VAL:HG22	2.36	0.54
1:R:198:LYS:HG2	1:R:202:GLU:HG2	1.88	0.54
1:G:198:LYS:HG2	1:G:202:GLU:HG2	1.88	0.54
1:O:95:SER:OG	1:O:115:ARG:HD3	2.07	0.54
1:R:95:SER:OG	1:R:115:ARG:HD3	2.07	0.54
1:G:43:ALA:HB2	1:G:185:PRO:HA	1.88	0.54
1:R:43:ALA:HB2	1:R:185:PRO:HA	1.88	0.54
2:W:17:GLU:O	2:W:33:LYS:HD2	2.07	0.54
2:H:6:ILE:HD11	2:H:142:TYR:CD1	2.42	0.54
1:F:95:SER:OG	1:F:115:ARG:HD3	2.07	0.54
1:R:70:ILE:HD12	1:R:74:VAL:HG22	1.88	0.54
1:U:198:LYS:HG2	1:U:202:GLU:HG2	1.88	0.54
1:C:95:SER:OG	1:C:115:ARG:HD3	2.07	0.54
1:Q:95:SER:OG	1:Q:115:ARG:HD3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:95:SER:OG	1:T:115:ARG:HD3	2.07	0.54
1:S:70:ILE:HD12	1:S:74:VAL:HG22	1.88	0.54
1:Q:43:ALA:HB2	1:Q:185:PRO:HA	1.88	0.54
1:C:198:LYS:HG2	1:C:202:GLU:HG2	1.88	0.54
2:M:37:ILE:HD11	2:M:59:MET:CB	2.35	0.54
1:F:43:ALA:HB2	1:F:185:PRO:HA	1.88	0.54
1:O:43:ALA:HB2	1:O:185:PRO:HA	1.88	0.54
2:M:164:GLN:HE21	2:Z:29:LYS:HZ1	1.54	0.54
2:K:62:GLU:HG2	2:K:82:LEU:HD21	1.90	0.54
2:I:3:THR:HB	2:I:16:THR:HG22	1.90	0.54
2:1:32:LYS:HE2	2:1:34:LEU:O	2.06	0.54
2:L:43:MET:HE2	2:L:56:VAL:HG23	1.89	0.54
1:P:43:ALA:HB2	1:P:185:PRO:HA	1.88	0.54
2:L:29:LYS:HZ3	2:1:164:GLN:NE2	2.05	0.54
1:E:198:LYS:HG2	1:E:202:GLU:HG2	1.88	0.54
2:K:37:ILE:HD11	2:K:59:MET:HB3	1.90	0.54
2:N:165:ARG:C	2:Y:26:ILE:HG22	2.28	0.54
2:Y:37:ILE:HD11	2:Y:59:MET:HB3	1.90	0.54
1:B:70:ILE:HD12	1:B:74:VAL:HG22	1.88	0.54
1:U:95:SER:OG	1:U:115:ARG:HD3	2.07	0.54
2:H:159:ILE:O	2:H:163:LYS:HG3	2.08	0.54
2:W:3:THR:HB	2:W:16:THR:HG22	1.90	0.54
2:K:141:GLN:NE2	2:V:141:GLN:NE2	2.55	0.54
1:G:95:SER:OG	1:G:115:ARG:HD3	2.07	0.54
1:A:70:ILE:HD12	1:A:74:VAL:HG22	1.88	0.54
1:D:42:PHE:HB2	1:D:184:LEU:O	2.08	0.54
1:S:49:ILE:HD13	1:S:212:ILE:HB	1.89	0.54
1:R:49:ILE:HD13	1:R:212:ILE:HB	1.89	0.54
2:I:63:LEU:HD11	2:I:74:MET:SD	2.48	0.54
2:L:45:ILE:HG12	2:L:52:ALA:HB1	1.90	0.54
2:V:26:ILE:C	2:V:26:ILE:HD13	2.28	0.54
1:T:12:ILE:CB	1:T:14:VAL:HG22	2.36	0.54
1:Q:42:PHE:HB2	1:Q:184:LEU:O	2.08	0.54
1:P:42:PHE:HB2	1:P:184:LEU:O	2.08	0.54
1:A:49:ILE:HD13	1:A:212:ILE:HB	1.89	0.54
2:K:141:GLN:HE21	2:V:141:GLN:NE2	2.06	0.54
2:W:63:LEU:HD11	2:W:74:MET:SD	2.48	0.54
2:Z:35:PHE:CE2	2:Z:45:ILE:HD12	2.43	0.54
1:P:12:ILE:CB	1:P:14:VAL:HG22	2.36	0.54
2:1:37:ILE:HD11	2:1:59:MET:CB	2.35	0.54
1:O:42:PHE:HB2	1:O:184:LEU:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:198:LYS:HG2	1:O:202:GLU:HG2	1.88	0.54
2:L:141:GLN:NE2	2:2:141:GLN:NE2	2.56	0.54
2:Y:36:GLN:HB2	2:Y:184:TYR:CE1	2.43	0.54
2:H:26:ILE:HD13	2:H:26:ILE:C	2.28	0.54
2:J:32:LYS:HE2	2:J:34:LEU:O	2.08	0.54
1:F:42:PHE:HB2	1:F:184:LEU:O	2.08	0.53
1:E:42:PHE:HB2	1:E:184:LEU:O	2.08	0.53
1:E:49:ILE:HD13	1:E:212:ILE:HB	1.89	0.53
1:O:49:ILE:HD13	1:O:212:ILE:HB	1.89	0.53
1:B:49:ILE:HD13	1:B:212:ILE:HB	1.89	0.53
2:H:3:THR:HB	2:H:16:THR:HG22	1.90	0.53
2:J:131:SER:O	2:J:134:VAL:HG13	2.08	0.53
2:V:159:ILE:O	2:V:163:LYS:HG3	2.08	0.53
1:B:12:ILE:CB	1:B:14:VAL:HG22	2.36	0.53
1:D:198:LYS:HG2	1:D:202:GLU:HG2	1.88	0.53
1:F:198:LYS:HG2	1:F:202:GLU:HG2	1.88	0.53
1:P:198:LYS:HG2	1:P:202:GLU:HG2	1.88	0.53
1:P:49:ILE:HD13	1:P:212:ILE:HB	1.89	0.53
1:D:49:ILE:HD13	1:D:212:ILE:HB	1.89	0.53
1:Q:49:ILE:HD13	1:Q:212:ILE:HB	1.89	0.53
1:G:49:ILE:HD13	1:G:212:ILE:HB	1.89	0.53
2:2:199:LEU:HB3	2:2:201:LEU:HD13	1.90	0.53
2:M:55:LEU:HD23	2:M:99:LEU:HD11	1.91	0.53
1:E:52:LYS:HZ3	1:E:62:ASN:HA	1.71	0.53
1:C:42:PHE:HB2	1:C:184:LEU:O	2.08	0.53
1:F:49:ILE:HD13	1:F:212:ILE:HB	1.89	0.53
2:K:36:GLN:HB2	2:K:184:TYR:CE1	2.43	0.53
1:E:144:ILE:HD12	1:E:147:ARG:NH1	2.24	0.53
2:Y:25:PHE:CD1	2:Y:25:PHE:C	2.80	0.53
1:G:42:PHE:HB2	1:G:184:LEU:O	2.09	0.53
1:T:49:ILE:HD13	1:T:212:ILE:HB	1.89	0.53
2:M:135:TYR:HB3	2:1:165:ARG:HG2	1.90	0.53
2:J:3:THR:HB	2:J:16:THR:HG22	1.90	0.53
2:N:149:ASP:O	2:N:152:VAL:HG12	2.08	0.53
1:U:144:ILE:HD12	1:U:147:ARG:NH1	2.24	0.53
1:C:144:ILE:HD12	1:C:147:ARG:NH1	2.23	0.53
1:P:144:ILE:HD12	1:P:147:ARG:NH1	2.24	0.53
1:P:12:ILE:HG21	1:P:14:VAL:HG21	1.72	0.53
1:R:42:PHE:HB2	1:R:184:LEU:O	2.08	0.53
2:1:55:LEU:HD23	2:1:99:LEU:HD11	1.91	0.53
2:H:133:PHE:CZ	2:H:165:ARG:HB3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:103:GLY:HA2	2:Z:178:ILE:CD1	2.39	0.53
1:E:12:ILE:CB	1:E:14:VAL:HG22	2.36	0.53
1:U:42:PHE:HB2	1:U:184:LEU:O	2.08	0.53
2:X:3:THR:HB	2:X:16:THR:HG22	1.90	0.53
2:2:149:ASP:O	2:2:152:VAL:HG12	2.08	0.53
2:L:35:PHE:CE2	2:L:45:ILE:HD12	2.43	0.53
2:Z:45:ILE:HG12	2:Z:52:ALA:HB1	1.90	0.53
1:D:12:ILE:HG21	1:D:14:VAL:HG21	1.72	0.53
2:2:123:ILE:HG12	2:2:124:TYR:CD2	2.44	0.53
1:Q:198:LYS:HG2	1:Q:202:GLU:HG2	1.88	0.53
2:L:103:GLY:HA2	2:L:178:ILE:CD1	2.39	0.53
2:J:26:ILE:C	2:J:26:ILE:HD13	2.30	0.53
2:V:133:PHE:CZ	2:V:165:ARG:HB3	2.43	0.53
2:K:26:ILE:HG22	2:2:165:ARG:C	2.30	0.53
2:K:26:ILE:HD13	2:K:26:ILE:C	2.29	0.53
2:Y:15:ALA:HB2	2:Y:175:VAL:HB	1.91	0.53
2:X:32:LYS:HE2	2:X:34:LEU:O	2.08	0.53
2:Z:26:ILE:HD13	2:Z:26:ILE:O	2.09	0.53
2:1:6:ILE:HD11	2:1:142:TYR:CD1	2.44	0.53
1:B:12:ILE:HG13	1:B:14:VAL:H	1.73	0.53
1:F:12:ILE:HG13	1:F:14:VAL:H	1.73	0.53
1:C:49:ILE:HD13	1:C:212:ILE:HB	1.89	0.53
2:V:3:THR:HB	2:V:16:THR:HG22	1.90	0.53
1:B:42:PHE:HB2	1:B:184:LEU:O	2.08	0.52
1:O:159:GLU:HG2	1:P:60:GLU:HG3	1.92	0.52
1:O:12:ILE:CB	1:O:14:VAL:HG22	2.36	0.52
1:U:12:ILE:CB	1:U:14:VAL:HG22	2.36	0.52
1:A:42:PHE:CD1	1:A:43:ALA:N	2.78	0.52
2:K:103:GLY:HA2	2:K:178:ILE:HD13	1.91	0.52
1:G:144:ILE:HD12	1:G:147:ARG:NH1	2.24	0.52
1:A:144:ILE:HD12	1:A:147:ARG:NH1	2.24	0.52
2:N:131:SER:O	2:N:134:VAL:HG13	2.09	0.52
2:X:28:HIS:CD2	2:Y:120:VAL:HG11	2.44	0.52
2:2:131:SER:O	2:2:134:VAL:HG13	2.09	0.52
2:N:199:LEU:HB3	2:N:201:LEU:HD13	1.90	0.52
2:K:173:ILE:HD13	2:K:173:ILE:C	2.30	0.52
2:X:131:SER:O	2:X:134:VAL:HG13	2.08	0.52
2:M:131:SER:O	2:M:134:VAL:HG13	2.10	0.52
1:C:12:ILE:CB	1:C:14:VAL:HG22	2.36	0.52
2:J:124:TYR:CD2	2:J:138:LEU:HD23	2.45	0.52
1:A:42:PHE:HB2	1:A:184:LEU:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:42:PHE:CD1	1:S:43:ALA:N	2.78	0.52
2:V:45:ILE:CG1	2:V:52:ALA:HB1	2.39	0.52
1:B:159:GLU:HG2	1:C:60:GLU:CG	2.39	0.52
1:U:49:ILE:HD13	1:U:212:ILE:HB	1.89	0.52
2:K:15:ALA:HB2	2:K:175:VAL:HB	1.91	0.52
1:R:144:ILE:HD12	1:R:147:ARG:NH1	2.24	0.52
2:L:26:ILE:HD13	2:L:26:ILE:O	2.09	0.52
1:O:144:ILE:HD12	1:O:147:ARG:NH1	2.24	0.52
1:G:42:PHE:CD1	1:G:43:ALA:N	2.78	0.52
2:K:59:MET:HE3	2:K:82:LEU:HD23	1.91	0.52
2:Y:26:ILE:HD13	2:Y:26:ILE:C	2.29	0.52
2:X:26:ILE:HD13	2:X:26:ILE:C	2.30	0.52
2:H:141:GLN:NE2	2:Y:141:GLN:NE2	2.58	0.52
1:S:144:ILE:HD12	1:S:147:ARG:NH1	2.23	0.52
1:F:160:TYR:CD2	1:F:163:THR:HB	2.45	0.52
1:Q:144:ILE:HD12	1:Q:147:ARG:NH1	2.23	0.52
2:X:124:TYR:CD2	2:X:138:LEU:HD23	2.44	0.52
1:S:42:PHE:HB2	1:S:184:LEU:O	2.08	0.52
2:J:28:HIS:CD2	2:K:120:VAL:HG11	2.44	0.52
1:Q:160:TYR:CD2	1:Q:163:THR:HB	2.45	0.52
2:J:37:ILE:HD11	2:J:59:MET:CB	2.38	0.52
2:1:20:VAL:CG1	2:1:28:HIS:HB2	2.36	0.52
1:R:42:PHE:CD1	1:R:43:ALA:N	2.78	0.52
1:O:42:PHE:CD1	1:O:43:ALA:N	2.78	0.52
2:I:45:ILE:CG1	2:I:52:ALA:HB1	2.39	0.52
1:P:108:ASN:CB	2:X:70:ARG:HG2	2.40	0.52
1:R:160:TYR:CD2	1:R:163:THR:HB	2.45	0.52
2:Y:173:ILE:HD13	2:Y:173:ILE:C	2.30	0.52
2:X:189:THR:HG23	2:X:190:ASP:N	2.25	0.52
1:G:160:TYR:CD2	1:G:163:THR:HB	2.45	0.52
1:B:144:ILE:HD12	1:B:147:ARG:NH1	2.24	0.52
2:M:6:ILE:HD11	2:M:142:TYR:CD1	2.44	0.52
1:U:12:ILE:HG13	1:U:14:VAL:H	1.73	0.52
1:O:21:LEU:O	1:O:24:VAL:HG12	2.10	0.52
2:H:45:ILE:CG1	2:H:52:ALA:HB1	2.39	0.52
1:T:42:PHE:CD1	1:T:43:ALA:N	2.78	0.52
1:D:42:PHE:CD1	1:D:43:ALA:N	2.78	0.52
2:2:18:ARG:HE	2:2:30:ASN:HD22	1.57	0.52
1:D:144:ILE:HD12	1:D:147:ARG:NH1	2.24	0.52
1:F:144:ILE:HD12	1:F:147:ARG:NH1	2.24	0.52
2:L:24:ASN:HA	2:1:167:SER:OG	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:160:TYR:CD2	1:P:163:THR:HB	2.45	0.52
2:L:62:GLU:HG2	2:L:82:LEU:HD21	1.91	0.52
1:E:160:TYR:CD2	1:E:163:THR:HB	2.45	0.52
1:P:12:ILE:HG13	1:P:14:VAL:H	1.73	0.52
1:D:21:LEU:O	1:D:24:VAL:HG12	2.10	0.52
1:F:21:LEU:O	1:F:24:VAL:HG12	2.10	0.52
1:B:42:PHE:CD1	1:B:43:ALA:N	2.78	0.52
2:W:45:ILE:CG1	2:W:52:ALA:HB1	2.39	0.52
2:H:141:GLN:NE2	2:Y:141:GLN:HE21	2.08	0.52
1:D:12:ILE:CB	1:D:14:VAL:HG22	2.36	0.52
1:C:12:ILE:HG13	1:C:14:VAL:H	1.73	0.52
1:Q:21:LEU:O	1:Q:24:VAL:HG12	2.10	0.52
2:Y:103:GLY:HA2	2:Y:178:ILE:HD13	1.91	0.52
1:T:42:PHE:HB2	1:T:184:LEU:O	2.08	0.52
2:Y:62:GLU:HG2	2:Y:82:LEU:HD21	1.90	0.52
1:S:160:TYR:CD2	1:S:163:THR:HB	2.45	0.52
2:Z:55:LEU:HD21	2:Z:87:LEU:HD11	1.92	0.52
1:D:85:ALA:O	1:D:89:VAL:HG23	2.10	0.52
1:S:85:ALA:O	1:S:89:VAL:HG23	2.10	0.52
1:A:85:ALA:O	1:A:89:VAL:HG23	2.10	0.52
1:O:70:ILE:HB	1:O:74:VAL:HG13	1.92	0.52
2:Z:62:GLU:HG2	2:Z:82:LEU:HD21	1.91	0.52
1:T:144:ILE:HD12	1:T:147:ARG:NH1	2.24	0.52
2:2:2:THR:HG22	2:2:169:SER:OG	2.10	0.52
1:O:85:ALA:O	1:O:89:VAL:HG23	2.11	0.51
1:U:42:PHE:CD1	1:U:43:ALA:N	2.78	0.51
1:C:42:PHE:CD1	1:C:43:ALA:N	2.78	0.51
1:B:21:LEU:O	1:B:24:VAL:HG12	2.10	0.51
1:B:108:ASN:CB	2:J:70:ARG:HG2	2.40	0.51
1:A:160:TYR:CD2	1:A:163:THR:HB	2.45	0.51
2:V:176:ALA:HA	2:V:186:GLN:HA	1.92	0.51
1:C:21:LEU:O	1:C:24:VAL:HG12	2.10	0.51
1:A:21:LEU:O	1:A:24:VAL:HG12	2.10	0.51
1:P:159:GLU:HG2	1:Q:60:GLU:CG	2.39	0.51
2:N:165:ARG:HA	2:Y:26:ILE:HG23	1.92	0.51
2:M:165:ARG:HG2	2:1:135:TYR:HB3	1.91	0.51
1:D:70:ILE:HB	1:D:74:VAL:HG13	1.92	0.51
2:J:189:THR:HG23	2:J:190:ASP:N	2.25	0.51
2:K:174:ASP:HA	2:K:192:ILE:HD13	1.92	0.51
2:N:141:GLN:NE2	2:Z:141:GLN:NE2	2.58	0.51
2:Y:174:ASP:HA	2:Y:192:ILE:HD13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:160:TYR:CD2	1:C:163:THR:HB	2.45	0.51
1:D:160:TYR:CD2	1:D:163:THR:HB	2.45	0.51
1:G:85:ALA:O	1:G:89:VAL:HG23	2.10	0.51
2:1:124:TYR:HD2	2:1:138:LEU:HD23	1.76	0.51
2:L:29:LYS:NZ	2:1:164:GLN:HE21	2.08	0.51
1:P:70:ILE:HB	1:P:74:VAL:HG13	1.92	0.51
1:E:70:ILE:HB	1:E:74:VAL:HG13	1.92	0.51
2:W:18:ARG:HE	2:W:30:ASN:HD22	1.57	0.51
1:U:160:TYR:CD2	1:U:163:THR:HB	2.45	0.51
1:U:191:THR:O	1:U:194:ILE:HG22	2.11	0.51
2:K:25:PHE:C	2:K:25:PHE:CD1	2.80	0.51
1:R:21:LEU:O	1:R:24:VAL:HG12	2.10	0.51
1:U:21:LEU:O	1:U:24:VAL:HG12	2.10	0.51
1:G:21:LEU:O	1:G:24:VAL:HG12	2.10	0.51
1:T:21:LEU:O	1:T:24:VAL:HG12	2.10	0.51
1:S:21:LEU:O	1:S:24:VAL:HG12	2.10	0.51
1:Q:85:ALA:O	1:Q:89:VAL:HG23	2.10	0.51
1:T:85:ALA:O	1:T:89:VAL:HG23	2.10	0.51
1:D:191:THR:O	1:D:194:ILE:HG22	2.11	0.51
2:I:179:THR:HG23	2:I:182:ASP:H	1.75	0.51
2:N:2:THR:HG22	2:N:169:SER:OG	2.10	0.51
1:E:12:ILE:HG13	1:E:14:VAL:H	1.74	0.51
1:O:12:ILE:HG13	1:O:14:VAL:H	1.73	0.51
1:E:85:ALA:O	1:E:89:VAL:HG23	2.10	0.51
1:R:85:ALA:O	1:R:89:VAL:HG23	2.11	0.51
2:Z:124:TYR:HD2	2:Z:138:LEU:HD23	1.76	0.51
1:P:42:PHE:CD1	1:P:43:ALA:N	2.78	0.51
1:C:70:ILE:HB	1:C:74:VAL:HG13	1.92	0.51
1:A:159:GLU:HG2	1:B:60:GLU:HG3	1.92	0.51
1:E:191:THR:O	1:E:194:ILE:HG22	2.11	0.51
1:T:160:TYR:CD2	1:T:163:THR:HB	2.45	0.51
1:T:191:THR:O	1:T:194:ILE:HG22	2.11	0.51
1:O:191:THR:O	1:O:194:ILE:HG22	2.11	0.51
1:C:85:ALA:O	1:C:89:VAL:HG23	2.10	0.51
2:M:164:GLN:HE21	2:Z:29:LYS:NZ	2.07	0.51
1:U:70:ILE:HB	1:U:74:VAL:HG13	1.92	0.51
2:L:141:GLN:NE2	2:2:141:GLN:HE21	2.09	0.51
1:D:180:TYR:HA	1:D:192:LEU:HD21	1.93	0.51
1:P:191:THR:O	1:P:194:ILE:HG22	2.11	0.51
2:V:116:ALA:O	2:2:50:GLY:HA3	2.11	0.51
1:C:191:THR:O	1:C:194:ILE:HG22	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:149:PHE:CE1	1:U:159:GLU:HB2	2.46	0.51
1:C:149:PHE:CE1	1:C:159:GLU:HB2	2.46	0.51
1:O:160:TYR:CD2	1:O:163:THR:HB	2.45	0.51
2:V:173:ILE:C	2:V:173:ILE:HD13	2.31	0.51
1:F:85:ALA:O	1:F:89:VAL:HG23	2.10	0.51
1:E:42:PHE:CD1	1:E:43:ALA:N	2.78	0.51
1:P:21:LEU:O	1:P:24:VAL:HG12	2.10	0.51
2:2:36:GLN:HB2	2:2:184:TYR:CE1	2.46	0.51
1:F:149:PHE:CE1	1:F:159:GLU:HB2	2.46	0.51
2:K:53:GLN:O	2:K:56:VAL:HG12	2.10	0.51
1:F:191:THR:O	1:F:194:ILE:HG22	2.11	0.51
1:B:160:TYR:CD2	1:B:163:THR:HB	2.45	0.51
2:L:55:LEU:HD21	2:L:87:LEU:HD11	1.92	0.51
1:B:191:THR:O	1:B:194:ILE:HG22	2.11	0.51
1:O:180:TYR:HA	1:O:192:LEU:HD21	1.93	0.51
2:I:18:ARG:HE	2:I:30:ASN:HD22	1.57	0.51
1:C:180:TYR:HA	1:C:192:LEU:HD21	1.93	0.51
1:B:85:ALA:O	1:B:89:VAL:HG23	2.11	0.51
2:W:59:MET:CE	2:W:82:LEU:HD23	2.41	0.51
2:N:36:GLN:HB2	2:N:184:TYR:CE1	2.46	0.51
1:F:70:ILE:HB	1:F:74:VAL:HG13	1.92	0.51
1:Q:191:THR:O	1:Q:194:ILE:HG22	2.11	0.51
1:G:149:PHE:CE1	1:G:159:GLU:HB2	2.46	0.51
1:T:149:PHE:CE1	1:T:159:GLU:HB2	2.46	0.51
2:1:131:SER:O	2:1:134:VAL:HG13	2.10	0.51
1:S:175:PHE:C	1:S:175:PHE:CD1	2.84	0.51
1:T:180:TYR:HA	1:T:192:LEU:HD21	1.93	0.51
1:O:175:PHE:C	1:O:175:PHE:CD1	2.85	0.51
2:H:116:ALA:O	2:N:50:GLY:HA3	2.11	0.51
1:A:130:ARG:NH2	1:G:124:THR:HG22	2.17	0.51
2:N:123:ILE:HG12	2:N:124:TYR:CD2	2.44	0.51
2:I:59:MET:CE	2:I:82:LEU:HD23	2.41	0.51
1:Q:42:PHE:CD1	1:Q:43:ALA:N	2.78	0.51
1:S:149:PHE:CE1	1:S:159:GLU:HB2	2.46	0.51
1:Q:70:ILE:HB	1:Q:74:VAL:HG13	1.92	0.51
1:R:149:PHE:CE1	1:R:159:GLU:HB2	2.46	0.51
1:S:191:THR:O	1:S:194:ILE:HG22	2.11	0.51
2:M:62:GLU:HG2	2:M:82:LEU:HD21	1.93	0.51
1:D:12:ILE:HG13	1:D:14:VAL:H	1.73	0.51
1:E:21:LEU:O	1:E:24:VAL:HG12	2.10	0.51
1:P:85:ALA:O	1:P:89:VAL:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:85:ALA:O	1:U:89:VAL:HG23	2.10	0.51
2:2:20:VAL:HG13	2:2:28:HIS:HB2	1.93	0.51
2:W:15:ALA:HB2	2:W:175:VAL:HB	1.93	0.51
1:P:175:PHE:C	1:P:175:PHE:CD1	2.85	0.51
1:R:191:THR:O	1:R:194:ILE:HG22	2.11	0.51
2:H:173:ILE:C	2:H:173:ILE:HD13	2.31	0.51
1:G:191:THR:O	1:G:194:ILE:HG22	2.11	0.51
1:A:191:THR:O	1:A:194:ILE:HG22	2.11	0.51
2:Y:53:GLN:O	2:Y:56:VAL:HG12	2.10	0.51
1:U:180:TYR:HA	1:U:192:LEU:HD21	1.93	0.51
1:R:108:ASN:CB	2:Z:70:ARG:HG2	2.41	0.50
2:L:173:ILE:HD13	2:L:173:ILE:C	2.32	0.50
1:B:149:PHE:CE1	1:B:159:GLU:HB2	2.46	0.50
2:L:29:LYS:HZ1	2:1:164:GLN:NE2	2.10	0.50
2:J:160:SER:HA	2:J:163:LYS:HD3	1.93	0.50
1:S:70:ILE:HB	1:S:74:VAL:HG13	1.92	0.50
1:A:149:PHE:CE1	1:A:159:GLU:HB2	2.46	0.50
1:Q:175:PHE:HD1	1:Q:175:PHE:C	2.15	0.50
1:R:175:PHE:CD1	1:R:175:PHE:C	2.85	0.50
1:T:102:THR:O	2:2:81:THR:HG22	2.12	0.50
1:E:175:PHE:CD1	1:E:175:PHE:C	2.84	0.50
1:E:175:PHE:C	1:E:175:PHE:HD1	2.15	0.50
1:A:175:PHE:CD1	1:A:175:PHE:C	2.85	0.50
2:H:176:ALA:HA	2:H:186:GLN:HA	1.92	0.50
1:B:180:TYR:HA	1:B:192:LEU:HD21	1.93	0.50
2:N:20:VAL:HG13	2:N:28:HIS:HB2	1.93	0.50
2:W:3:THR:OG1	2:W:127:THR:HG22	2.12	0.50
2:W:179:THR:HG23	2:W:182:ASP:H	1.75	0.50
1:D:175:PHE:C	1:D:175:PHE:CD1	2.85	0.50
1:G:175:PHE:C	1:G:175:PHE:CD1	2.85	0.50
1:G:175:PHE:C	1:G:175:PHE:HD1	2.15	0.50
1:U:175:PHE:CD1	1:U:175:PHE:C	2.85	0.50
1:T:175:PHE:C	1:T:175:PHE:CD1	2.85	0.50
1:B:175:PHE:CD1	1:B:175:PHE:C	2.85	0.50
2:N:25:PHE:C	2:N:25:PHE:CD1	2.84	0.50
2:V:124:TYR:HD2	2:V:138:LEU:HD23	1.76	0.50
2:M:49:VAL:HG23	2:M:50:GLY:N	2.25	0.50
1:A:70:ILE:HB	1:A:74:VAL:HG13	1.92	0.50
1:Q:175:PHE:C	1:Q:175:PHE:CD1	2.84	0.50
2:1:62:GLU:HG2	2:1:82:LEU:HD21	1.93	0.50
1:F:175:PHE:HD1	1:F:175:PHE:C	2.15	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:175:PHE:CD1	1:C:175:PHE:C	2.85	0.50
1:D:108:ASN:CB	2:L:70:ARG:HG2	2.41	0.50
1:F:42:PHE:CD1	1:F:43:ALA:N	2.78	0.50
1:T:70:ILE:HB	1:T:74:VAL:HG13	1.92	0.50
1:F:175:PHE:C	1:F:175:PHE:CD1	2.85	0.50
1:E:180:TYR:HA	1:E:192:LEU:HD21	1.93	0.50
2:2:112:SER:O	2:2:113:ILE:HD13	2.12	0.50
1:S:180:TYR:HA	1:S:192:LEU:HD21	1.93	0.50
1:P:180:TYR:HA	1:P:192:LEU:HD21	1.93	0.50
1:Q:149:PHE:CE1	1:Q:159:GLU:HB2	2.46	0.50
2:H:124:TYR:HD2	2:H:138:LEU:HD23	1.76	0.50
2:1:49:VAL:HG23	2:1:50:GLY:N	2.25	0.50
1:B:70:ILE:HB	1:B:74:VAL:HG13	1.92	0.50
1:P:175:PHE:C	1:P:175:PHE:HD1	2.15	0.50
2:J:174:ASP:HA	2:J:192:ILE:HD13	1.94	0.50
2:2:25:PHE:C	2:2:25:PHE:CD1	2.84	0.50
2:M:20:VAL:CG1	2:M:28:HIS:HB2	2.36	0.50
1:P:149:PHE:CE1	1:P:159:GLU:HB2	2.46	0.50
2:Z:133:PHE:CZ	2:Z:165:ARG:HB3	2.47	0.50
2:X:160:SER:HA	2:X:163:LYS:HD3	1.94	0.50
1:R:70:ILE:HB	1:R:74:VAL:HG13	1.92	0.50
1:A:180:TYR:HA	1:A:192:LEU:HD21	1.93	0.50
1:D:149:PHE:CE1	1:D:159:GLU:HB2	2.46	0.50
2:X:123:ILE:H	2:X:123:ILE:CD1	2.23	0.50
2:M:132:PRO:HA	2:1:133:PHE:CE1	2.47	0.50
2:M:133:PHE:CE1	2:1:132:PRO:HA	2.47	0.50
1:G:70:ILE:HB	1:G:74:VAL:HG13	1.92	0.50
2:I:15:ALA:HB2	2:I:175:VAL:HB	1.93	0.50
2:W:66:TYR:CZ	2:W:70:ARG:HD2	2.46	0.50
2:Z:173:ILE:C	2:Z:173:ILE:HD13	2.32	0.50
2:N:123:ILE:CD1	2:N:123:ILE:H	2.24	0.50
1:R:175:PHE:HD1	1:R:175:PHE:C	2.15	0.50
1:E:149:PHE:CE1	1:E:159:GLU:HB2	2.46	0.50
2:M:26:ILE:O	2:M:26:ILE:HD13	2.11	0.50
2:I:66:TYR:CZ	2:I:70:ARG:HD2	2.46	0.49
1:O:62:ASN:O	1:O:65:GLU:HG2	2.13	0.49
1:S:175:PHE:C	1:S:175:PHE:HD1	2.15	0.49
1:O:175:PHE:HD1	1:O:175:PHE:C	2.15	0.49
1:R:180:TYR:HA	1:R:192:LEU:HD21	1.93	0.49
1:O:137:ILE:HG22	1:O:150:ASP:HB2	1.94	0.49
2:N:18:ARG:HE	2:N:30:ASN:HD22	1.57	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:26:ILE:HD13	2:1:26:ILE:O	2.11	0.49
2:L:133:PHE:CZ	2:L:165:ARG:HB3	2.47	0.49
1:O:149:PHE:CE1	1:O:159:GLU:HB2	2.46	0.49
1:A:137:ILE:HG22	1:A:150:ASP:HB2	1.94	0.49
1:B:137:ILE:HG22	1:B:150:ASP:HB2	1.94	0.49
2:V:178:ILE:HB	2:V:184:TYR:HA	1.93	0.49
1:T:137:ILE:HG22	1:T:150:ASP:HB2	1.95	0.49
1:F:102:THR:O	2:N:81:THR:HG22	2.12	0.49
1:S:137:ILE:HG22	1:S:150:ASP:HB2	1.94	0.49
1:C:62:ASN:O	1:C:65:GLU:HG2	2.13	0.49
2:L:132:PRO:HA	2:2:133:PHE:CE1	2.47	0.49
2:I:3:THR:OG1	2:I:127:THR:HG22	2.12	0.49
1:A:175:PHE:HD1	1:A:175:PHE:C	2.15	0.49
1:D:175:PHE:HD1	1:D:175:PHE:C	2.15	0.49
1:U:137:ILE:HG22	1:U:150:ASP:HB2	1.95	0.49
1:C:137:ILE:HG22	1:C:150:ASP:HB2	1.95	0.49
1:P:137:ILE:HG22	1:P:150:ASP:HB2	1.94	0.49
1:C:175:PHE:C	1:C:175:PHE:HD1	2.15	0.49
1:F:170:ASP:O	1:F:173:VAL:HG12	2.13	0.49
1:F:180:TYR:HA	1:F:192:LEU:HD21	1.93	0.49
1:S:170:ASP:O	1:S:173:VAL:HG12	2.13	0.49
2:X:174:ASP:HA	2:X:192:ILE:HD13	1.94	0.49
1:A:170:ASP:O	1:A:173:VAL:HG12	2.13	0.49
1:G:180:TYR:HA	1:G:192:LEU:HD21	1.93	0.49
1:E:137:ILE:HG22	1:E:150:ASP:HB2	1.94	0.49
1:S:62:ASN:O	1:S:65:GLU:HG2	2.13	0.49
1:U:62:ASN:O	1:U:65:GLU:HG2	2.13	0.49
1:D:62:ASN:O	1:D:65:GLU:HG2	2.13	0.49
2:Z:189:THR:HG23	2:Z:190:ASP:N	2.28	0.49
1:U:175:PHE:HD1	1:U:175:PHE:C	2.15	0.49
1:Q:180:TYR:HA	1:Q:192:LEU:HD21	1.93	0.49
2:K:179:THR:HG23	2:K:182:ASP:H	1.77	0.49
1:S:102:THR:O	2:1:81:THR:HG22	2.13	0.49
1:D:137:ILE:HG22	1:D:150:ASP:HB2	1.95	0.49
1:B:170:ASP:O	1:B:173:VAL:HG12	2.13	0.49
1:E:108:ASN:CB	2:M:70:ARG:HG2	2.43	0.49
1:A:62:ASN:O	1:A:65:GLU:HG2	2.13	0.49
1:S:52:LYS:HZ1	1:S:62:ASN:HA	1.76	0.49
1:Q:170:ASP:O	1:Q:173:VAL:HG12	2.13	0.49
1:D:110:GLU:O	1:D:113:VAL:HG12	2.13	0.49
1:Q:110:GLU:O	1:Q:113:VAL:HG12	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:102:THR:O	2:M:81:THR:HG22	2.13	0.49
1:R:110:GLU:O	1:R:113:VAL:HG12	2.13	0.49
1:D:228:GLU:O	1:D:231:LYS:HB3	2.13	0.49
1:T:175:PHE:C	1:T:175:PHE:HD1	2.15	0.49
1:O:228:GLU:O	1:O:231:LYS:HB3	2.13	0.49
1:T:170:ASP:O	1:T:173:VAL:HG12	2.13	0.49
1:F:110:GLU:O	1:F:113:VAL:HG12	2.13	0.49
2:X:62:GLU:HG2	2:X:82:LEU:HD21	1.94	0.49
1:C:170:ASP:O	1:C:173:VAL:HG12	2.13	0.49
1:E:228:GLU:O	1:E:231:LYS:HB3	2.13	0.49
1:R:137:ILE:HG22	1:R:150:ASP:HB2	1.95	0.49
1:G:110:GLU:O	1:G:113:VAL:HG12	2.13	0.49
1:P:170:ASP:O	1:P:173:VAL:HG12	2.13	0.49
1:P:62:ASN:O	1:P:65:GLU:HG2	2.13	0.49
1:E:62:ASN:O	1:E:65:GLU:HG2	2.13	0.49
2:K:26:ILE:HG23	2:2:165:ARG:HA	1.94	0.49
2:Y:59:MET:CE	2:Y:82:LEU:HD23	2.43	0.49
1:D:170:ASP:O	1:D:173:VAL:HG12	2.13	0.49
1:G:137:ILE:HG22	1:G:150:ASP:HB2	1.95	0.49
1:C:228:GLU:O	1:C:231:LYS:HB3	2.13	0.49
1:F:137:ILE:HG22	1:F:150:ASP:CB	2.43	0.49
2:W:124:TYR:HD2	2:W:138:LEU:HD23	1.78	0.49
1:C:108:ASN:HB2	2:K:70:ARG:HG2	1.94	0.49
2:H:26:ILE:HG23	2:X:165:ARG:HA	1.94	0.49
1:R:159:GLU:HG2	1:S:60:GLU:HG3	1.95	0.49
1:B:175:PHE:HD1	1:B:175:PHE:C	2.15	0.49
1:P:137:ILE:HG22	1:P:150:ASP:CB	2.43	0.49
1:R:137:ILE:HG22	1:R:150:ASP:CB	2.43	0.49
1:O:110:GLU:O	1:O:113:VAL:HG12	2.13	0.49
1:C:110:GLU:O	1:C:113:VAL:HG12	2.13	0.49
1:Q:137:ILE:HG22	1:Q:150:ASP:CB	2.43	0.49
2:H:178:ILE:HB	2:H:184:TYR:HA	1.93	0.49
1:U:170:ASP:O	1:U:173:VAL:HG12	2.13	0.49
1:A:110:GLU:O	1:A:113:VAL:HG12	2.13	0.49
1:B:62:ASN:O	1:B:65:GLU:HG2	2.13	0.49
1:F:62:ASN:O	1:F:65:GLU:HG2	2.13	0.49
1:C:137:ILE:HG22	1:C:150:ASP:CB	2.43	0.49
1:G:137:ILE:HG22	1:G:150:ASP:CB	2.43	0.49
1:G:228:GLU:O	1:G:231:LYS:HB3	2.13	0.49
1:E:170:ASP:O	1:E:173:VAL:HG12	2.13	0.49
1:U:228:GLU:O	1:U:231:LYS:HB3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:228:GLU:O	1:R:231:LYS:HB3	2.13	0.49
1:U:107:VAL:HG11	2:V:66:TYR:HH	1.70	0.48
1:R:107:VAL:HG11	2:Z:66:TYR:HH	1.72	0.48
2:J:18:ARG:HB2	2:J:31:GLY:O	2.13	0.48
2:M:76:ILE:O	2:M:79:VAL:HG12	2.13	0.48
2:N:141:GLN:HE21	2:Z:141:GLN:NE2	2.11	0.48
1:T:137:ILE:HG22	1:T:150:ASP:CB	2.43	0.48
1:U:137:ILE:HG22	1:U:150:ASP:CB	2.43	0.48
1:F:137:ILE:HG22	1:F:150:ASP:HB2	1.95	0.48
1:Q:137:ILE:HG22	1:Q:150:ASP:HB2	1.95	0.48
1:U:110:GLU:O	1:U:113:VAL:HG12	2.13	0.48
1:P:110:GLU:O	1:P:113:VAL:HG12	2.13	0.48
1:B:228:GLU:O	1:B:231:LYS:HB3	2.13	0.48
1:F:228:GLU:O	1:F:231:LYS:HB3	2.13	0.48
2:N:112:SER:O	2:N:113:ILE:HD13	2.12	0.48
1:R:62:ASN:O	1:R:65:GLU:HG2	2.13	0.48
2:Y:175:VAL:CG2	2:Y:176:ALA:N	2.75	0.48
2:1:76:ILE:O	2:1:79:VAL:HG12	2.13	0.48
1:A:137:ILE:HG22	1:A:150:ASP:CB	2.43	0.48
1:R:170:ASP:O	1:R:173:VAL:HG12	2.13	0.48
1:P:228:GLU:O	1:P:231:LYS:HB3	2.13	0.48
1:Q:228:GLU:O	1:Q:231:LYS:HB3	2.13	0.48
1:T:62:ASN:O	1:T:65:GLU:HG2	2.12	0.48
1:Q:62:ASN:O	1:Q:65:GLU:HG2	2.13	0.48
1:A:228:GLU:O	1:A:231:LYS:HB3	2.13	0.48
2:Y:179:THR:HG23	2:Y:182:ASP:H	1.77	0.48
1:S:110:GLU:O	1:S:113:VAL:HG12	2.13	0.48
1:F:148:LEU:O	1:F:159:GLU:HG3	2.14	0.48
1:B:137:ILE:HG22	1:B:150:ASP:CB	2.43	0.48
2:V:36:GLN:HB2	2:V:184:TYR:CE1	2.48	0.48
1:D:137:ILE:HG22	1:D:150:ASP:CB	2.43	0.48
2:H:12:VAL:HG13	2:H:178:ILE:HG23	1.96	0.48
1:B:110:GLU:O	1:B:113:VAL:HG12	2.13	0.48
2:I:189:THR:HG23	2:I:190:ASP:N	2.28	0.48
1:O:170:ASP:O	1:O:173:VAL:HG12	2.13	0.48
1:S:108:ASN:CB	2:1:70:ARG:HG2	2.43	0.48
1:A:108:ASN:HB3	2:I:70:ARG:HG2	1.95	0.48
1:G:62:ASN:O	1:G:65:GLU:HG2	2.13	0.48
2:2:123:ILE:HD13	2:2:123:ILE:N	2.26	0.48
2:K:175:VAL:CG2	2:K:176:ALA:N	2.75	0.48
1:G:148:LEU:O	1:G:159:GLU:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:137:ILE:HG22	1:S:150:ASP:CB	2.43	0.48
1:E:137:ILE:HG22	1:E:150:ASP:CB	2.43	0.48
2:H:36:GLN:HB2	2:H:184:TYR:CE1	2.48	0.48
1:E:110:GLU:O	1:E:113:VAL:HG12	2.13	0.48
1:Q:107:VAL:HG11	2:Y:66:TYR:HH	1.74	0.48
1:Q:108:ASN:HB2	2:Y:70:ARG:HG2	1.94	0.48
2:L:189:THR:HG23	2:L:190:ASP:N	2.28	0.48
2:L:18:ARG:HE	2:L:30:ASN:HD22	1.61	0.48
2:N:139:GLU:OE1	2:Z:165:ARG:NE	2.46	0.48
1:A:148:LEU:O	1:A:159:GLU:HG3	2.14	0.48
1:R:148:LEU:O	1:R:159:GLU:HG3	2.14	0.48
2:H:17:GLU:HB2	2:H:170:GLY:O	2.14	0.48
1:Q:148:LEU:O	1:Q:159:GLU:HG3	2.14	0.48
1:S:228:GLU:O	1:S:231:LYS:HB3	2.13	0.48
1:T:228:GLU:O	1:T:231:LYS:HB3	2.13	0.48
1:P:148:LEU:O	1:P:159:GLU:HG3	2.14	0.48
1:B:148:LEU:O	1:B:159:GLU:HG3	2.14	0.48
2:K:59:MET:CE	2:K:82:LEU:HD23	2.43	0.48
1:S:148:LEU:O	1:S:159:GLU:HG3	2.14	0.48
2:M:26:ILE:C	2:M:26:ILE:HD13	2.34	0.48
1:T:110:GLU:O	1:T:113:VAL:HG12	2.12	0.48
1:G:170:ASP:O	1:G:173:VAL:HG12	2.13	0.48
2:H:59:MET:HE2	2:H:79:VAL:CG2	2.42	0.48
1:E:148:LEU:O	1:E:159:GLU:HG3	2.14	0.48
1:D:159:GLU:HG2	1:E:60:GLU:HG3	1.95	0.48
2:V:103:GLY:HA2	2:V:178:ILE:CD1	2.44	0.48
2:Z:174:ASP:HA	2:Z:192:ILE:HD13	1.96	0.48
1:D:103:TYR:HE1	2:L:74:MET:HE2	1.78	0.48
2:J:45:ILE:HD11	2:J:52:ALA:O	2.14	0.48
2:J:165:ARG:HA	2:V:26:ILE:HG23	1.96	0.48
1:T:148:LEU:O	1:T:159:GLU:HG3	2.14	0.48
1:O:137:ILE:HG22	1:O:150:ASP:CB	2.43	0.48
2:X:109:HIS:HB3	2:X:111:PHE:HE1	1.79	0.48
2:K:1:THR:H3	2:K:129:SER:HB3	1.79	0.48
1:T:134:VAL:O	1:T:153:PRO:HG3	2.14	0.48
1:S:134:VAL:O	1:S:153:PRO:HG3	2.14	0.48
1:A:134:VAL:O	1:A:153:PRO:HG3	2.14	0.48
2:Z:178:ILE:O	2:Z:178:ILE:HG12	2.14	0.48
1:C:148:LEU:O	1:C:159:GLU:HG3	2.14	0.48
2:W:22:MET:O	2:W:23:GLU:HB2	2.14	0.48
2:K:44:THR:OG1	2:K:100:LEU:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:32:LYS:HE2	2:I:34:LEU:O	2.14	0.48
2:1:179:THR:HG23	2:1:182:ASP:H	1.79	0.48
2:J:152:VAL:O	2:J:156:ILE:HG13	2.14	0.47
1:Q:134:VAL:O	1:Q:153:PRO:HG3	2.14	0.47
1:F:134:VAL:O	1:F:153:PRO:HG3	2.14	0.47
2:1:74:MET:HG2	2:1:78:ALA:HB3	1.96	0.47
2:1:26:ILE:HD13	2:1:26:ILE:C	2.34	0.47
2:J:141:GLN:NE2	2:W:141:GLN:HE21	2.11	0.47
2:V:66:TYR:CZ	2:V:70:ARG:HD2	2.49	0.47
2:X:45:ILE:HD11	2:X:52:ALA:O	2.14	0.47
1:B:134:VAL:O	1:B:153:PRO:HG3	2.14	0.47
1:O:148:LEU:O	1:O:159:GLU:HG3	2.14	0.47
1:U:148:LEU:O	1:U:159:GLU:HG3	2.14	0.47
2:W:26:ILE:HD13	2:W:26:ILE:C	2.35	0.47
2:W:32:LYS:HE2	2:W:34:LEU:O	2.14	0.47
2:W:189:THR:HG23	2:W:190:ASP:N	2.28	0.47
2:V:126:SER:HB3	2:V:135:TYR:CE2	2.49	0.47
2:Y:44:THR:OG1	2:Y:100:LEU:HB3	2.14	0.47
2:Y:124:TYR:HD2	2:Y:138:LEU:HD23	1.80	0.47
2:K:103:GLY:HA2	2:K:178:ILE:CD1	2.44	0.47
2:2:76:ILE:HG21	2:2:109:HIS:HB2	1.96	0.47
2:J:159:ILE:O	2:J:163:LYS:HG3	2.14	0.47
2:Y:43:MET:HE2	2:Y:56:VAL:HG23	1.96	0.47
1:D:148:LEU:O	1:D:159:GLU:HG3	2.14	0.47
2:J:62:GLU:HG2	2:J:82:LEU:HD21	1.94	0.47
2:M:7:THR:HB	2:M:123:ILE:O	2.14	0.47
2:V:55:LEU:HA	2:V:55:LEU:HD12	1.50	0.47
2:M:74:MET:HG2	2:M:78:ALA:HB3	1.95	0.47
1:U:134:VAL:O	1:U:153:PRO:HG3	2.14	0.47
2:K:133:PHE:CZ	2:K:165:ARG:HB3	2.48	0.47
1:D:12:ILE:CG1	1:D:14:VAL:HG22	2.44	0.47
1:E:12:ILE:CG1	1:E:14:VAL:HG22	2.44	0.47
1:R:12:ILE:CG1	1:R:14:VAL:HG22	2.44	0.47
1:F:12:ILE:CG1	1:F:14:VAL:HG22	2.44	0.47
1:O:108:ASN:HB3	2:W:70:ARG:HG2	1.95	0.47
2:I:124:TYR:HD2	2:I:138:LEU:HD23	1.78	0.47
2:N:133:PHE:CE1	2:Z:132:PRO:HA	2.50	0.47
1:O:134:VAL:O	1:O:153:PRO:HG3	2.14	0.47
1:D:134:VAL:O	1:D:153:PRO:HG3	2.14	0.47
2:X:159:ILE:O	2:X:163:LYS:HG3	2.14	0.47
2:H:6:ILE:HD11	2:H:142:TYR:HD1	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:12:VAL:HG13	2:V:178:ILE:HG23	1.96	0.47
2:H:103:GLY:HA2	2:H:178:ILE:CD1	2.44	0.47
2:I:22:MET:O	2:I:23:GLU:HB2	2.14	0.47
2:I:26:ILE:C	2:I:26:ILE:HD13	2.35	0.47
1:C:134:VAL:O	1:C:153:PRO:HG3	2.14	0.47
2:Y:133:PHE:CZ	2:Y:165:ARG:HB3	2.49	0.47
2:Y:50:GLY:O	2:Y:54:VAL:HG12	2.14	0.47
1:C:12:ILE:CG1	1:C:14:VAL:HG22	2.44	0.47
1:P:12:ILE:CG1	1:P:14:VAL:HG22	2.44	0.47
1:Q:12:ILE:CG1	1:Q:14:VAL:HG22	2.44	0.47
1:G:12:ILE:CG1	1:G:14:VAL:HG22	2.44	0.47
2:H:66:TYR:CZ	2:H:70:ARG:HD2	2.49	0.47
2:Y:74:MET:HG2	2:Y:78:ALA:HB3	1.97	0.47
2:X:37:ILE:HD11	2:X:59:MET:CB	2.37	0.47
2:Y:103:GLY:HA2	2:Y:178:ILE:CD1	2.44	0.47
2:2:59:MET:HE2	2:2:79:VAL:HG23	1.96	0.47
2:X:18:ARG:HB2	2:X:31:GLY:O	2.13	0.47
2:Z:18:ARG:HE	2:Z:30:ASN:HD22	1.61	0.47
2:L:178:ILE:HG12	2:L:178:ILE:O	2.14	0.47
2:X:175:VAL:CG2	2:X:176:ALA:N	2.78	0.47
2:V:17:GLU:HB2	2:V:170:GLY:O	2.14	0.47
1:S:175:PHE:CD2	1:S:196:ALA:HA	2.50	0.47
1:O:175:PHE:CD2	1:O:196:ALA:HA	2.50	0.47
1:A:175:PHE:CD2	1:A:196:ALA:HA	2.50	0.47
1:U:175:PHE:CD2	1:U:196:ALA:HA	2.50	0.47
2:W:189:THR:HG23	2:W:190:ASP:H	1.79	0.47
2:J:109:HIS:HB3	2:J:111:PHE:HE1	1.79	0.47
2:I:141:GLN:HE21	2:X:141:GLN:NE2	2.12	0.47
2:H:126:SER:HB3	2:H:135:TYR:CE2	2.49	0.47
2:H:20:VAL:HG22	2:H:28:HIS:HB2	1.97	0.47
1:S:12:ILE:CG1	1:S:14:VAL:HG22	2.44	0.47
2:N:76:ILE:HG21	2:N:109:HIS:HB2	1.96	0.47
2:N:18:ARG:HB2	2:N:31:GLY:O	2.15	0.47
2:N:91:LYS:O	2:N:94:PRO:HD3	2.15	0.47
2:L:174:ASP:HA	2:L:192:ILE:HD13	1.96	0.47
1:B:12:ILE:CG1	1:B:14:VAL:HG22	2.44	0.47
2:L:124:TYR:HD2	2:L:138:LEU:HD23	1.76	0.47
2:V:37:ILE:HD11	2:V:59:MET:CB	2.45	0.47
1:G:134:VAL:O	1:G:153:PRO:HG3	2.14	0.47
2:K:141:GLN:NE2	2:V:141:GLN:HE21	2.13	0.47
2:W:175:VAL:CG2	2:W:176:ALA:N	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:175:PHE:CD2	1:P:196:ALA:HA	2.50	0.47
1:C:175:PHE:CD2	1:C:196:ALA:HA	2.50	0.47
2:M:179:THR:HG23	2:M:182:ASP:H	1.79	0.47
2:N:175:VAL:CG2	2:N:176:ALA:N	2.78	0.47
2:2:55:LEU:HD21	2:2:87:LEU:HD11	1.97	0.47
2:2:93:MET:N	2:2:94:PRO:CD	2.77	0.47
1:O:12:ILE:CG1	1:O:14:VAL:HG22	2.44	0.47
1:U:12:ILE:CG1	1:U:14:VAL:HG22	2.44	0.47
1:A:12:ILE:CG1	1:A:14:VAL:HG22	2.44	0.47
2:1:7:THR:HB	2:1:123:ILE:O	2.14	0.47
2:I:35:PHE:CE2	2:I:45:ILE:HD12	2.50	0.47
2:K:43:MET:CE	2:K:56:VAL:HG23	2.45	0.47
1:E:175:PHE:CD2	1:E:196:ALA:HA	2.50	0.47
1:D:175:PHE:CD2	1:D:196:ALA:HA	2.50	0.47
1:G:175:PHE:CD2	1:G:196:ALA:HA	2.50	0.47
1:T:175:PHE:CD2	1:T:196:ALA:HA	2.50	0.47
2:I:189:THR:HG23	2:I:190:ASP:H	1.79	0.47
1:R:103:TYR:HE1	2:Z:74:MET:HE2	1.80	0.47
2:N:123:ILE:N	2:N:123:ILE:HD13	2.26	0.46
1:R:134:VAL:O	1:R:153:PRO:HG3	2.14	0.46
2:X:20:VAL:HG13	2:X:28:HIS:HB2	1.97	0.46
2:Y:43:MET:CE	2:Y:56:VAL:HG23	2.45	0.46
1:B:175:PHE:CD2	1:B:196:ALA:HA	2.50	0.46
2:M:22:MET:O	2:M:23:GLU:HB2	2.15	0.46
2:X:81:THR:O	2:X:84:SER:HB3	2.15	0.46
2:H:193:GLU:HA	2:H:196:ILE:HD12	1.98	0.46
2:1:22:MET:O	2:1:23:GLU:HB2	2.15	0.46
2:N:55:LEU:HD21	2:N:87:LEU:HD11	1.97	0.46
1:Q:44:ASN:HA	1:Q:44:ASN:HD22	1.56	0.46
1:F:44:ASN:HD22	1:F:44:ASN:HA	1.56	0.46
1:T:12:ILE:CG1	1:T:14:VAL:HG22	2.44	0.46
2:J:138:LEU:HD12	2:J:138:LEU:HA	1.68	0.46
2:M:124:TYR:HD2	2:M:138:LEU:HD23	1.76	0.46
2:H:37:ILE:HD11	2:H:59:MET:CB	2.45	0.46
1:E:134:VAL:O	1:E:153:PRO:HG3	2.14	0.46
1:T:98:GLN:O	1:T:102:THR:HG23	2.15	0.46
2:K:50:GLY:O	2:K:54:VAL:HG12	2.14	0.46
1:O:98:GLN:O	1:O:102:THR:HG23	2.15	0.46
2:V:177:VAL:HG12	2:V:187:LEU:CD1	2.46	0.46
2:K:27:MET:HG2	2:K:27:MET:O	2.16	0.46
2:W:35:PHE:CE2	2:W:45:ILE:HD12	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:134:VAL:O	1:P:153:PRO:HG3	2.14	0.46
2:2:18:ARG:HB2	2:2:31:GLY:O	2.15	0.46
1:R:175:PHE:CD2	1:R:196:ALA:HA	2.50	0.46
2:I:175:VAL:CG2	2:I:176:ALA:N	2.78	0.46
2:N:93:MET:N	2:N:94:PRO:CD	2.77	0.46
1:C:98:GLN:O	1:C:102:THR:HG23	2.15	0.46
2:K:74:MET:HG2	2:K:78:ALA:HB3	1.97	0.46
2:H:177:VAL:HG12	2:H:187:LEU:CD1	2.46	0.46
2:M:110:VAL:HG13	2:M:110:VAL:O	2.16	0.46
2:2:175:VAL:CG2	2:2:176:ALA:N	2.78	0.46
1:O:107:VAL:HG11	2:W:66:TYR:HH	1.72	0.46
2:X:138:LEU:HD12	2:X:138:LEU:HA	1.68	0.46
2:N:109:HIS:HB3	2:N:111:PHE:HE1	1.81	0.46
2:J:175:VAL:CG2	2:J:176:ALA:N	2.78	0.46
2:2:91:LYS:O	2:2:94:PRO:HD3	2.15	0.46
2:K:48:LEU:HD12	2:K:49:VAL:N	2.31	0.46
2:J:179:THR:HG23	2:J:182:ASP:H	1.80	0.46
1:S:107:VAL:HG11	2:1:66:TYR:HH	1.76	0.46
2:N:37:ILE:HD11	2:N:59:MET:CG	2.46	0.46
2:X:152:VAL:O	2:X:156:ILE:HG13	2.14	0.46
2:2:109:HIS:HB3	2:2:111:PHE:HE1	1.81	0.46
2:I:20:VAL:CG1	2:I:28:HIS:HB2	2.44	0.46
2:L:132:PRO:HA	2:2:133:PHE:HE1	1.81	0.46
2:K:43:MET:HE1	2:K:56:VAL:HG23	1.97	0.46
1:Q:175:PHE:CD2	1:Q:196:ALA:HA	2.50	0.46
2:H:63:LEU:HD12	2:H:74:MET:HE3	1.98	0.46
2:Y:1:THR:H3	2:Y:129:SER:HB3	1.81	0.46
2:I:138:LEU:HD12	2:I:154:LEU:HD11	1.98	0.46
2:V:7:THR:HB	2:V:123:ILE:O	2.16	0.46
2:2:37:ILE:HD11	2:2:59:MET:CG	2.46	0.46
1:F:175:PHE:CD2	1:F:196:ALA:HA	2.50	0.46
1:E:98:GLN:O	1:E:102:THR:HG23	2.15	0.46
1:U:98:GLN:O	1:U:102:THR:HG23	2.16	0.46
2:V:193:GLU:HA	2:V:196:ILE:HD12	1.97	0.46
1:Q:98:GLN:O	1:Q:102:THR:HG23	2.15	0.46
2:W:20:VAL:CG1	2:W:28:HIS:HB2	2.44	0.46
2:L:165:ARG:NE	2:2:139:GLU:OE1	2.49	0.46
2:L:103:GLY:HA2	2:L:178:ILE:HD11	1.98	0.46
1:G:98:GLN:O	1:G:102:THR:HG23	2.16	0.46
1:R:177:GLU:O	1:S:57:ARG:NE	2.46	0.46
2:X:179:THR:HG23	2:X:182:ASP:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:72:VAL:HG22	2:V:73:ASN:N	2.31	0.46
1:D:98:GLN:O	1:D:102:THR:HG23	2.16	0.46
1:B:98:GLN:O	1:B:102:THR:HG23	2.16	0.46
2:1:174:ASP:HA	2:1:192:ILE:HD13	1.98	0.46
2:N:27:MET:HG2	2:N:27:MET:O	2.15	0.46
2:K:160:SER:HA	2:K:163:LYS:HD3	1.98	0.46
1:R:98:GLN:O	1:R:102:THR:HG23	2.16	0.46
2:K:17:GLU:HA	2:K:173:ILE:HA	1.98	0.46
2:X:189:THR:HG23	2:X:190:ASP:H	1.81	0.46
1:F:98:GLN:O	1:F:102:THR:HG23	2.15	0.46
1:A:98:GLN:O	1:A:102:THR:HG23	2.16	0.46
2:2:27:MET:O	2:2:27:MET:HG2	2.15	0.46
1:F:21:LEU:HD11	1:G:130:ARG:CD	2.44	0.46
2:V:20:VAL:HG22	2:V:28:HIS:HB2	1.96	0.46
1:P:44:ASN:HA	1:P:44:ASN:HD22	1.56	0.46
1:T:52:LYS:HE3	1:T:64:ILE:HG23	1.99	0.45
1:S:98:GLN:O	1:S:102:THR:HG23	2.16	0.45
2:I:105:ASP:OD1	2:I:106:THR:N	2.49	0.45
2:N:97:VAL:HG22	2:N:98:GLN:H	1.81	0.45
1:C:161:LYS:HD2	1:D:60:GLU:OE2	2.17	0.45
2:Y:17:GLU:HA	2:Y:173:ILE:HA	1.98	0.45
2:M:6:ILE:HG23	2:M:6:ILE:O	2.16	0.45
1:G:102:THR:O	2:H:81:THR:HG22	2.17	0.45
2:H:111:PHE:CE2	2:H:121:GLU:HB2	2.51	0.45
2:M:15:ALA:HB3	2:M:155:VAL:HG11	1.98	0.45
2:J:81:THR:O	2:J:84:SER:HB3	2.15	0.45
2:K:111:PHE:CE2	2:K:121:GLU:HB2	2.51	0.45
2:2:97:VAL:HG22	2:2:98:GLN:N	2.32	0.45
1:E:44:ASN:HD22	1:E:44:ASN:HA	1.56	0.45
2:Y:27:MET:HG2	2:Y:27:MET:O	2.16	0.45
1:T:24:VAL:O	1:T:28:ARG:HG3	2.17	0.45
1:B:52:LYS:HE3	1:B:64:ILE:HG23	1.99	0.45
1:S:52:LYS:HE3	1:S:64:ILE:HG23	1.99	0.45
1:R:52:LYS:HE3	1:R:64:ILE:HG23	1.99	0.45
2:2:123:ILE:CD1	2:2:123:ILE:H	2.24	0.45
2:N:124:TYR:HD1	2:N:138:LEU:HD23	1.81	0.45
2:L:19:ARG:HE	2:L:26:ILE:HG13	1.81	0.45
2:J:105:ASP:OD1	2:J:106:THR:N	2.50	0.45
2:Y:48:LEU:HD12	2:Y:49:VAL:N	2.31	0.45
1:P:98:GLN:O	1:P:102:THR:HG23	2.16	0.45
2:M:174:ASP:HA	2:M:192:ILE:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:LYS:HE3	1:C:64:ILE:HG23	1.99	0.45
1:U:52:LYS:HE3	1:U:64:ILE:HG23	1.99	0.45
1:C:99:GLU:OE2	2:K:70:ARG:NH1	2.49	0.45
2:2:37:ILE:HD11	2:2:59:MET:CB	2.43	0.45
2:Y:149:ASP:O	2:Y:152:VAL:HG12	2.17	0.45
2:L:19:ARG:NE	2:L:26:ILE:HG13	2.32	0.45
2:L:75:PRO:O	2:L:78:ALA:HB3	2.16	0.45
2:V:111:PHE:CE2	2:V:121:GLU:HB2	2.51	0.45
2:X:105:ASP:OD1	2:X:106:THR:N	2.50	0.45
2:1:110:VAL:O	2:1:110:VAL:HG13	2.16	0.45
2:Y:75:PRO:O	2:Y:78:ALA:HB3	2.16	0.45
1:A:52:LYS:HE3	1:A:64:ILE:HG23	1.99	0.45
1:C:24:VAL:O	1:C:28:ARG:HG3	2.17	0.45
2:M:55:LEU:HA	2:M:55:LEU:HD12	1.76	0.45
2:H:141:GLN:HE21	2:Y:141:GLN:NE2	2.15	0.45
2:J:20:VAL:HG13	2:J:28:HIS:HB2	1.97	0.45
2:H:22:MET:O	2:H:23:GLU:HB2	2.17	0.45
2:W:173:ILE:HD13	2:W:173:ILE:C	2.37	0.45
2:2:180:ARG:HD2	2:2:180:ARG:HA	1.80	0.45
2:I:173:ILE:HD13	2:I:173:ILE:C	2.37	0.45
2:N:8:LEU:O	2:N:8:LEU:HD12	2.17	0.45
1:U:24:VAL:O	1:U:28:ARG:HG3	2.17	0.45
1:T:21:LEU:HD11	1:U:130:ARG:CD	2.43	0.45
1:Q:52:LYS:HE3	1:Q:64:ILE:HG23	1.99	0.45
1:S:24:VAL:O	1:S:28:ARG:HG3	2.17	0.45
2:H:7:THR:HB	2:H:123:ILE:O	2.16	0.45
1:G:49:ILE:HD11	1:G:210:PRO:CB	2.47	0.45
1:B:24:VAL:O	1:B:28:ARG:HG3	2.17	0.45
2:Z:19:ARG:HE	2:Z:26:ILE:HG13	1.82	0.45
2:K:75:PRO:O	2:K:78:ALA:HB3	2.16	0.45
2:H:72:VAL:HG22	2:H:73:ASN:N	2.31	0.45
2:L:6:ILE:HD11	2:L:142:TYR:CD1	2.52	0.45
2:W:105:ASP:OD1	2:W:106:THR:N	2.49	0.45
1:Q:18:ASP:OD2	1:Q:20:ARG:HD3	2.17	0.45
2:Z:187:LEU:HA	2:Z:188:PRO:HD3	1.77	0.45
2:Z:110:VAL:O	2:Z:110:VAL:HG13	2.16	0.45
2:L:110:VAL:O	2:L:110:VAL:HG13	2.16	0.45
1:A:23:GLN:HE22	1:G:15:PHE:HB2	1.82	0.45
1:G:52:LYS:HE3	1:G:64:ILE:HG23	1.99	0.45
1:E:78:THR:CG2	1:E:85:ALA:HB1	2.45	0.45
1:Q:99:GLU:OE2	2:Y:70:ARG:NH1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:49:ILE:HD11	1:Q:210:PRO:CB	2.47	0.45
1:F:49:ILE:HD11	1:F:210:PRO:CB	2.47	0.45
1:U:102:THR:O	2:V:81:THR:HG22	2.17	0.45
2:N:97:VAL:HG22	2:N:98:GLN:N	2.32	0.45
2:2:97:VAL:HG22	2:2:98:GLN:H	1.81	0.45
2:W:2:THR:HG22	2:W:169:SER:OG	2.17	0.45
1:T:18:ASP:OD2	1:T:20:ARG:HD3	2.17	0.45
1:B:18:ASP:OD2	1:B:20:ARG:HD3	2.17	0.45
2:N:180:ARG:HA	2:N:180:ARG:HD2	1.80	0.45
1:R:49:ILE:HD11	1:R:210:PRO:CB	2.47	0.45
2:K:149:ASP:O	2:K:152:VAL:HG12	2.17	0.45
2:1:6:ILE:O	2:1:6:ILE:HG23	2.16	0.45
1:E:18:ASP:OD2	1:E:20:ARG:HD3	2.17	0.45
1:F:18:ASP:OD2	1:F:20:ARG:HD3	2.17	0.45
1:C:18:ASP:OD2	1:C:20:ARG:HD3	2.17	0.45
2:W:146:MET:HA	2:W:150:GLU:OE1	2.17	0.45
1:P:18:ASP:OD2	1:P:20:ARG:HD3	2.17	0.45
2:K:55:LEU:HA	2:K:55:LEU:HD12	1.79	0.45
2:M:180:ARG:HD2	2:M:180:ARG:HA	1.77	0.45
2:L:141:GLN:HE21	2:2:141:GLN:NE2	2.14	0.45
2:X:49:VAL:HG23	2:X:50:GLY:H	1.82	0.45
2:1:15:ALA:HB3	2:1:155:VAL:HG11	1.98	0.45
1:F:52:LYS:HE3	1:F:64:ILE:HG23	1.99	0.45
1:O:52:LYS:HE3	1:O:64:ILE:HG23	1.99	0.45
1:D:52:LYS:HE3	1:D:64:ILE:HG23	1.99	0.45
1:A:24:VAL:O	1:A:28:ARG:HG3	2.17	0.45
2:L:17:GLU:HA	2:L:173:ILE:HA	1.99	0.45
2:N:37:ILE:HD11	2:N:59:MET:CB	2.43	0.45
1:A:49:ILE:HD11	1:A:210:PRO:CB	2.47	0.45
2:Y:160:SER:HA	2:Y:163:LYS:HD3	1.98	0.45
2:V:6:ILE:HD11	2:V:142:TYR:HD1	1.79	0.45
2:Z:75:PRO:O	2:Z:78:ALA:HB3	2.16	0.45
1:U:18:ASP:OD2	1:U:20:ARG:HD3	2.17	0.45
2:I:2:THR:HG22	2:I:169:SER:OG	2.17	0.45
2:V:22:MET:O	2:V:23:GLU:HB2	2.17	0.45
2:V:27:MET:HG2	2:V:27:MET:O	2.17	0.45
2:J:123:ILE:HG12	2:J:124:TYR:CD1	2.51	0.44
1:C:49:ILE:HD11	1:C:210:PRO:CB	2.47	0.44
2:Z:19:ARG:NE	2:Z:26:ILE:HG13	2.32	0.44
2:J:189:THR:HG23	2:J:190:ASP:H	1.81	0.44
2:Y:111:PHE:CE2	2:Y:121:GLU:HB2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:44:ASN:HA	1:O:44:ASN:HD22	1.56	0.44
2:Z:8:LEU:O	2:Z:8:LEU:HD12	2.17	0.44
1:A:130:ARG:HH21	1:G:124:THR:CG2	2.21	0.44
1:P:78:THR:CG2	1:P:85:ALA:HB1	2.45	0.44
2:N:7:THR:HB	2:N:123:ILE:O	2.18	0.44
1:U:49:ILE:HD11	1:U:210:PRO:CB	2.47	0.44
1:Q:161:LYS:HD2	1:R:60:GLU:OE2	2.16	0.44
1:S:18:ASP:OD2	1:S:20:ARG:HD3	2.17	0.44
2:Y:187:LEU:HA	2:Y:188:PRO:HD3	1.76	0.44
2:V:15:ALA:HB2	2:V:175:VAL:HB	1.99	0.44
2:2:8:LEU:O	2:2:8:LEU:HD12	2.17	0.44
2:L:8:LEU:HD12	2:L:8:LEU:O	2.17	0.44
1:D:24:VAL:O	1:D:28:ARG:HG3	2.17	0.44
1:Q:124:THR:HG22	1:R:130:ARG:NH2	2.24	0.44
1:P:52:LYS:HE3	1:P:64:ILE:HG23	1.99	0.44
2:I:59:MET:HE1	2:I:82:LEU:HD23	1.99	0.44
1:P:49:ILE:HD11	1:P:210:PRO:CB	2.47	0.44
1:R:176:LEU:HB3	1:S:58:LEU:HD21	1.99	0.44
1:D:18:ASP:OD2	1:D:20:ARG:HD3	2.17	0.44
2:L:93:MET:N	2:L:94:PRO:CD	2.81	0.44
2:W:138:LEU:HD12	2:W:154:LEU:HD11	1.98	0.44
2:K:124:TYR:HD2	2:K:138:LEU:HD23	1.80	0.44
1:O:24:VAL:O	1:O:28:ARG:HG3	2.17	0.44
1:S:49:ILE:HD11	1:S:210:PRO:CB	2.47	0.44
1:P:24:VAL:O	1:P:28:ARG:HG3	2.17	0.44
2:Y:76:ILE:O	2:Y:79:VAL:HG12	2.18	0.44
2:Z:103:GLY:HA2	2:Z:178:ILE:HD11	1.98	0.44
2:2:130:GLY:O	2:2:134:VAL:HG12	2.17	0.44
1:D:177:GLU:O	1:E:57:ARG:NE	2.46	0.44
1:R:18:ASP:OD2	1:R:20:ARG:HD3	2.17	0.44
1:A:18:ASP:OD2	1:A:20:ARG:HD3	2.17	0.44
2:W:25:PHE:CD1	2:W:25:PHE:C	2.91	0.44
2:H:27:MET:HG2	2:H:27:MET:O	2.17	0.44
1:O:23:GLN:HE22	1:U:15:PHE:HB2	1.82	0.44
1:R:24:VAL:O	1:R:28:ARG:HG3	2.17	0.44
1:E:52:LYS:HE3	1:E:64:ILE:HG23	1.99	0.44
2:N:59:MET:HE2	2:N:79:VAL:HG23	1.99	0.44
1:D:15:PHE:HB2	1:E:23:GLN:HE22	1.82	0.44
1:A:12:ILE:HG13	1:A:14:VAL:H	1.73	0.44
1:E:24:VAL:O	1:E:28:ARG:HG3	2.17	0.44
2:J:123:ILE:CD1	2:J:123:ILE:H	2.23	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:17:GLU:HA	2:Z:173:ILE:HA	1.99	0.44
1:E:49:ILE:HD11	1:E:210:PRO:CB	2.47	0.44
2:N:130:GLY:O	2:N:134:VAL:HG12	2.17	0.44
2:L:74:MET:HG2	2:L:78:ALA:HB3	2.00	0.44
2:H:187:LEU:HA	2:H:188:PRO:HD3	1.77	0.44
2:I:6:ILE:HD11	2:I:142:TYR:CD1	2.52	0.44
1:F:71:ASP:HA	2:M:68:LEU:HD21	2.00	0.44
1:S:81:LEU:HD23	1:S:133:GLY:HA3	2.00	0.44
1:R:81:LEU:HD23	1:R:133:GLY:HA3	2.00	0.44
2:I:25:PHE:CD1	2:I:25:PHE:C	2.91	0.44
1:R:15:PHE:HB2	1:S:23:GLN:HE22	1.82	0.44
1:O:78:THR:CG2	1:O:85:ALA:HB1	2.45	0.44
2:Z:74:MET:HG2	2:Z:78:ALA:HB3	2.00	0.44
1:A:81:LEU:HD23	1:A:133:GLY:HA3	2.00	0.44
1:S:32:LYS:O	1:S:167:SER:HA	2.18	0.44
2:W:6:ILE:HD11	2:W:142:TYR:CD1	2.53	0.44
1:G:18:ASP:OD2	1:G:20:ARG:HD3	2.17	0.44
1:D:44:ASN:HD22	1:D:44:ASN:HA	1.56	0.44
1:Q:24:VAL:O	1:Q:28:ARG:HG3	2.17	0.44
1:S:124:THR:HG22	1:T:130:ARG:NH2	2.25	0.44
2:V:59:MET:HE2	2:V:79:VAL:CG2	2.43	0.44
1:B:49:ILE:HD11	1:B:210:PRO:CB	2.47	0.44
1:G:81:LEU:HD23	1:G:133:GLY:HA3	2.00	0.44
1:G:16:SER:HB3	1:G:22:PHE:CE2	2.53	0.44
1:A:32:LYS:O	1:A:167:SER:HA	2.18	0.44
1:Q:81:LEU:HD23	1:Q:133:GLY:HA3	2.00	0.44
1:B:32:LYS:O	1:B:167:SER:HA	2.18	0.44
2:Z:76:ILE:HA	2:Z:79:VAL:HG12	2.00	0.44
2:V:90:VAL:HG22	2:V:90:VAL:O	2.18	0.44
1:F:24:VAL:O	1:F:28:ARG:HG3	2.17	0.44
2:2:124:TYR:HD1	2:2:138:LEU:HD23	1.81	0.44
2:K:76:ILE:O	2:K:79:VAL:HG12	2.18	0.44
2:Y:34:LEU:HD21	2:Y:176:ALA:HB3	2.00	0.44
1:R:16:SER:HB3	1:R:22:PHE:CE2	2.53	0.44
2:2:160:SER:HA	2:2:163:LYS:HD3	2.00	0.44
1:T:32:LYS:O	1:T:167:SER:HA	2.18	0.44
1:P:81:LEU:HD23	1:P:133:GLY:HA3	2.00	0.44
2:H:15:ALA:HB2	2:H:175:VAL:HB	1.99	0.44
1:G:24:VAL:O	1:G:28:ARG:HG3	2.17	0.43
1:U:130:ARG:NH1	1:U:131:PRO:O	2.51	0.43
2:N:83:LEU:HA	2:N:83:LEU:HD12	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:130:ARG:NH1	1:C:131:PRO:O	2.51	0.43
2:M:93:MET:N	2:M:94:PRO:CD	2.81	0.43
1:E:16:SER:HB3	1:E:22:PHE:CE2	2.53	0.43
1:D:17:PRO:HA	1:E:26:TYR:CD1	2.53	0.43
2:W:187:LEU:HA	2:W:188:PRO:HD3	1.83	0.43
1:T:81:LEU:HD23	1:T:133:GLY:HA3	2.00	0.43
1:B:81:LEU:HD23	1:B:133:GLY:HA3	2.00	0.43
1:T:71:ASP:HA	2:1:68:LEU:HD21	2.00	0.43
1:O:18:ASP:OD2	1:O:20:ARG:HD3	2.17	0.43
1:F:81:LEU:HD23	1:F:133:GLY:HA3	2.00	0.43
1:P:16:SER:HB3	1:P:22:PHE:CE2	2.53	0.43
1:S:12:ILE:HG13	1:S:14:VAL:H	1.74	0.43
1:O:130:ARG:NH1	1:O:131:PRO:O	2.51	0.43
2:2:111:PHE:CE2	2:2:121:GLU:HB2	2.53	0.43
2:N:165:ARG:HA	2:Y:26:ILE:CG2	2.48	0.43
2:L:178:ILE:HB	2:L:184:TYR:HA	2.00	0.43
1:D:109:ILE:CG2	1:D:147:ARG:HD3	2.48	0.43
2:I:146:MET:HA	2:I:150:GLU:OE1	2.17	0.43
2:L:76:ILE:HA	2:L:79:VAL:HG12	2.00	0.43
1:D:130:ARG:NH1	1:D:131:PRO:O	2.51	0.43
2:N:138:LEU:HA	2:N:138:LEU:HD12	1.71	0.43
2:M:133:PHE:HE1	2:1:132:PRO:HA	1.81	0.43
1:E:109:ILE:CG2	1:E:147:ARG:HD3	2.49	0.43
1:P:109:ILE:CG2	1:P:147:ARG:HD3	2.48	0.43
1:G:109:ILE:CG2	1:G:147:ARG:HD3	2.49	0.43
2:V:17:GLU:HA	2:V:173:ILE:HA	2.01	0.43
2:J:49:VAL:HG23	2:J:50:GLY:H	1.82	0.43
1:D:176:LEU:HB3	1:E:58:LEU:HD21	1.99	0.43
1:S:44:ASN:HA	1:S:44:ASN:HD22	1.56	0.43
2:V:25:PHE:C	2:V:25:PHE:CD1	2.90	0.43
1:A:52:LYS:HZ3	1:A:62:ASN:HA	1.77	0.43
1:S:52:LYS:HB3	1:S:209:ALA:O	2.19	0.43
1:E:187:LYS:O	1:E:190:VAL:HG13	2.19	0.43
1:P:187:LYS:O	1:P:190:VAL:HG13	2.19	0.43
2:L:189:THR:HG23	2:L:190:ASP:H	1.83	0.43
1:S:159:GLU:O	1:T:60:GLU:HB2	2.18	0.43
1:T:49:ILE:HD11	1:T:210:PRO:CB	2.47	0.43
2:V:19:ARG:HE	2:V:26:ILE:HG13	1.84	0.43
1:R:109:ILE:CG2	1:R:147:ARG:HD3	2.48	0.43
2:N:141:GLN:NE2	2:Z:141:GLN:HE21	2.15	0.43
2:Z:6:ILE:HD11	2:Z:142:TYR:CD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:90:VAL:O	2:H:90:VAL:HG22	2.18	0.43
2:M:66:TYR:CZ	2:M:70:ARG:HD2	2.54	0.43
1:A:52:LYS:HB3	1:A:209:ALA:O	2.19	0.43
1:B:52:LYS:HB3	1:B:209:ALA:O	2.19	0.43
1:B:130:ARG:NH1	1:B:131:PRO:O	2.51	0.43
1:D:49:ILE:HD11	1:D:210:PRO:CB	2.47	0.43
1:O:49:ILE:HD11	1:O:210:PRO:CB	2.47	0.43
1:O:109:ILE:CG2	1:O:147:ARG:HD3	2.49	0.43
2:H:17:GLU:HA	2:H:173:ILE:HA	2.01	0.43
1:R:32:LYS:O	1:R:167:SER:HA	2.18	0.43
1:G:32:LYS:O	1:G:167:SER:HA	2.18	0.43
2:1:66:TYR:CZ	2:1:70:ARG:HD2	2.53	0.43
1:T:52:LYS:HB3	1:T:209:ALA:O	2.19	0.43
1:O:187:LYS:O	1:O:190:VAL:HG13	2.19	0.43
1:T:130:ARG:NH1	1:T:131:PRO:O	2.51	0.43
2:Z:189:THR:HG23	2:Z:190:ASP:H	1.84	0.43
2:L:3:THR:OG1	2:L:127:THR:HG22	2.19	0.43
2:H:19:ARG:HE	2:H:26:ILE:HG13	1.84	0.43
1:U:81:LEU:HD23	1:U:133:GLY:HA3	2.00	0.43
2:1:93:MET:N	2:1:94:PRO:CD	2.81	0.43
2:Y:6:ILE:HD11	2:Y:142:TYR:CD1	2.53	0.43
1:E:81:LEU:HD23	1:E:133:GLY:HA3	2.00	0.43
2:Z:105:ASP:OD1	2:Z:106:THR:N	2.52	0.43
2:V:83:LEU:HD12	2:V:83:LEU:HA	1.69	0.43
1:E:159:GLU:O	1:F:60:GLU:HB2	2.18	0.43
1:S:103:TYR:HE1	2:1:74:MET:CE	2.32	0.43
1:Q:109:ILE:CG2	1:Q:147:ARG:HD3	2.48	0.43
2:Z:55:LEU:HA	2:Z:55:LEU:HD12	1.67	0.43
2:V:103:GLY:HA2	2:V:178:ILE:HD13	2.01	0.43
2:H:103:GLY:HA2	2:H:178:ILE:HD13	2.01	0.43
1:O:81:LEU:HD23	1:O:133:GLY:HA3	2.00	0.43
1:B:16:SER:HB3	1:B:22:PHE:CE2	2.53	0.43
1:A:130:ARG:NH1	1:A:131:PRO:O	2.51	0.43
1:G:130:ARG:NH1	1:G:131:PRO:O	2.51	0.43
1:R:130:ARG:NH1	1:R:131:PRO:O	2.51	0.43
1:Q:61:GLN:CD	1:Q:62:ASN:H	2.22	0.43
1:F:187:LYS:O	1:F:190:VAL:HG13	2.19	0.43
2:I:45:ILE:CD1	2:I:52:ALA:HB1	2.49	0.43
2:Z:15:ALA:HB3	2:Z:155:VAL:HG11	2.00	0.43
2:M:132:PRO:HA	2:1:133:PHE:HE1	1.81	0.43
2:Y:157:ARG:O	2:Y:160:SER:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:109:HIS:HB3	2:M:111:PHE:HE1	1.84	0.43
1:C:109:ILE:CG2	1:C:147:ARG:HD3	2.48	0.43
2:Z:178:ILE:HB	2:Z:184:TYR:HA	2.01	0.43
1:F:109:ILE:CG2	1:F:147:ARG:HD3	2.49	0.43
2:H:131:SER:O	2:H:134:VAL:HG13	2.19	0.43
2:L:187:LEU:HA	2:L:188:PRO:HD3	1.77	0.43
2:N:160:SER:HA	2:N:163:LYS:HD3	2.00	0.43
1:C:32:LYS:O	1:C:167:SER:HA	2.18	0.43
2:L:180:ARG:HA	2:L:180:ARG:HD2	1.72	0.43
1:Q:12:ILE:HG13	1:Q:14:VAL:H	1.73	0.43
1:Q:187:LYS:O	1:Q:190:VAL:HG13	2.19	0.43
2:2:7:THR:HB	2:2:123:ILE:O	2.18	0.43
2:V:59:MET:HE3	2:V:82:LEU:HD23	2.01	0.43
2:W:59:MET:HE1	2:W:82:LEU:HD23	2.00	0.43
2:K:34:LEU:HD21	2:K:176:ALA:HB3	2.00	0.43
2:V:3:THR:OG1	2:V:127:THR:HG22	2.19	0.43
1:A:109:ILE:CG2	1:A:147:ARG:HD3	2.49	0.43
1:T:109:ILE:CG2	1:T:147:ARG:HD3	2.48	0.43
2:V:28:HIS:CD2	2:W:120:VAL:HG11	2.54	0.43
1:O:58:LEU:HD21	1:U:176:LEU:HB3	2.01	0.43
2:V:18:ARG:HE	2:V:30:ASN:HD22	1.67	0.43
1:R:17:PRO:HA	1:S:26:TYR:CD1	2.53	0.43
1:C:81:LEU:HD23	1:C:133:GLY:HA3	2.00	0.43
1:T:16:SER:HB3	1:T:22:PHE:CE2	2.53	0.43
2:M:87:LEU:HD23	2:M:114:ASP:O	2.19	0.43
2:H:202:ILE:HG12	2:H:203:LEU:N	2.34	0.43
1:E:32:LYS:O	1:E:167:SER:HA	2.18	0.43
2:Y:180:ARG:HA	2:Y:180:ARG:HD2	1.78	0.43
1:R:12:ILE:HG13	1:R:14:VAL:H	1.73	0.43
1:S:130:ARG:NH1	1:S:131:PRO:O	2.51	0.43
1:F:61:GLN:CD	1:F:62:ASN:H	2.23	0.43
1:D:187:LYS:O	1:D:190:VAL:HG13	2.19	0.43
1:U:187:LYS:O	1:U:190:VAL:HG13	2.19	0.43
2:Z:15:ALA:HB3	2:Z:155:VAL:CG1	2.49	0.43
2:L:55:LEU:HA	2:L:55:LEU:HD12	1.68	0.43
1:Q:16:SER:HB3	1:Q:22:PHE:CE2	2.53	0.43
1:F:16:SER:HB3	1:F:22:PHE:CE2	2.53	0.43
2:L:25:PHE:CD1	2:L:25:PHE:C	2.91	0.43
1:G:12:ILE:HG13	1:G:14:VAL:H	1.73	0.42
1:P:61:GLN:CD	1:P:62:ASN:H	2.23	0.42
1:E:61:GLN:CD	1:E:62:ASN:H	2.22	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:187:LYS:O	1:G:190:VAL:HG13	2.19	0.42
1:A:103:TYR:HE1	2:I:74:MET:HE2	1.82	0.42
1:U:109:ILE:CG2	1:U:147:ARG:HD3	2.49	0.42
1:A:16:SER:HB3	1:A:22:PHE:CE2	2.53	0.42
1:C:16:SER:HB3	1:C:22:PHE:CE2	2.53	0.42
1:U:32:LYS:O	1:U:167:SER:HA	2.18	0.42
2:W:180:ARG:HD2	2:W:180:ARG:HA	1.81	0.42
1:O:124:THR:HG22	1:P:130:ARG:NH2	2.26	0.42
1:P:130:ARG:NH1	1:P:131:PRO:O	2.51	0.42
1:R:187:LYS:O	1:R:190:VAL:HG13	2.19	0.42
1:Q:130:ARG:NH1	1:Q:131:PRO:O	2.51	0.42
1:E:103:TYR:HE1	2:M:74:MET:CE	2.32	0.42
2:1:74:MET:HA	2:1:75:PRO:HD3	1.87	0.42
1:S:109:ILE:CG2	1:S:147:ARG:HD3	2.48	0.42
2:H:28:HIS:CD2	2:I:120:VAL:HG11	2.54	0.42
1:P:32:LYS:O	1:P:167:SER:HA	2.18	0.42
2:K:6:ILE:HD11	2:K:142:TYR:CD1	2.53	0.42
1:R:61:GLN:CD	1:R:62:ASN:H	2.23	0.42
2:N:111:PHE:CE2	2:N:121:GLU:HB2	2.53	0.42
2:L:29:LYS:HZ1	2:1:164:GLN:HE21	1.67	0.42
2:H:55:LEU:HD12	2:H:55:LEU:HA	1.50	0.42
2:L:15:ALA:HB3	2:L:155:VAL:HG11	2.00	0.42
2:M:114:ASP:OD1	2:M:116:ALA:HB3	2.20	0.42
1:F:32:LYS:O	1:F:167:SER:HA	2.18	0.42
1:D:81:LEU:HD23	1:D:133:GLY:HA3	2.00	0.42
1:U:16:SER:HB3	1:U:22:PHE:CE2	2.53	0.42
1:G:54:VAL:HG22	1:G:55:ARG:N	2.34	0.42
1:A:58:LEU:CD1	1:A:58:LEU:N	2.82	0.42
1:A:58:LEU:HD21	1:G:176:LEU:HB3	2.01	0.42
1:B:54:VAL:HG22	1:B:55:ARG:N	2.35	0.42
2:I:123:ILE:H	2:I:123:ILE:CD1	2.31	0.42
1:U:61:GLN:CD	1:U:62:ASN:H	2.23	0.42
1:R:52:LYS:HB3	1:R:209:ALA:O	2.19	0.42
1:T:187:LYS:O	1:T:190:VAL:HG13	2.19	0.42
1:C:187:LYS:O	1:C:190:VAL:HG13	2.18	0.42
2:L:15:ALA:HB3	2:L:155:VAL:CG1	2.49	0.42
2:K:157:ARG:O	2:K:160:SER:HB2	2.19	0.42
2:M:184:TYR:CD1	2:M:184:TYR:C	2.93	0.42
1:B:109:ILE:CG2	1:B:147:ARG:HD3	2.48	0.42
1:Q:32:LYS:O	1:Q:167:SER:HA	2.18	0.42
2:Z:93:MET:N	2:Z:94:PRO:CD	2.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:202:ILE:HG12	2:V:203:LEU:N	2.34	0.42
1:Q:58:LEU:CD1	1:Q:58:LEU:N	2.82	0.42
1:S:16:SER:HB3	1:S:22:PHE:CE2	2.53	0.42
2:V:131:SER:O	2:V:134:VAL:HG13	2.19	0.42
2:N:22:MET:O	2:N:23:GLU:HB2	2.20	0.42
1:O:16:SER:HB3	1:O:22:PHE:CE2	2.53	0.42
1:U:54:VAL:HG22	1:U:55:ARG:N	2.34	0.42
1:T:54:VAL:HG22	1:T:55:ARG:N	2.35	0.42
1:A:44:ASN:HA	1:A:44:ASN:HD22	1.56	0.42
1:E:130:ARG:NH1	1:E:131:PRO:O	2.51	0.42
1:S:61:GLN:CD	1:S:62:ASN:H	2.23	0.42
1:C:52:LYS:HB3	1:C:209:ALA:O	2.19	0.42
1:G:61:GLN:CD	1:G:62:ASN:H	2.23	0.42
2:1:138:LEU:HA	2:1:138:LEU:HD12	1.86	0.42
2:H:83:LEU:HD12	2:H:83:LEU:HA	1.69	0.42
2:1:109:HIS:HB3	2:1:111:PHE:HE1	1.84	0.42
2:H:179:THR:O	2:H:183:GLY:N	2.50	0.42
2:J:34:LEU:HD21	2:J:176:ALA:CB	2.50	0.42
1:Q:54:VAL:HG22	1:Q:55:ARG:N	2.34	0.42
1:R:58:LEU:N	1:R:58:LEU:CD1	2.82	0.42
2:W:93:MET:N	2:W:94:PRO:CD	2.82	0.42
1:T:17:PRO:HA	1:U:26:TYR:CD1	2.55	0.42
1:U:56:SER:OG	1:U:58:LEU:HB2	2.20	0.42
2:Z:25:PHE:C	2:Z:25:PHE:CD1	2.91	0.42
2:H:25:PHE:CD1	2:H:25:PHE:C	2.90	0.42
1:C:61:GLN:CD	1:C:62:ASN:H	2.23	0.42
1:D:61:GLN:CD	1:D:62:ASN:H	2.23	0.42
1:F:130:ARG:NH1	1:F:131:PRO:O	2.51	0.42
1:A:187:LYS:O	1:A:190:VAL:HG13	2.19	0.42
1:S:187:LYS:O	1:S:190:VAL:HG13	2.19	0.42
2:Z:3:THR:OG1	2:Z:127:THR:HG22	2.19	0.42
2:J:199:LEU:CB	2:J:201:LEU:HD13	2.50	0.42
2:H:3:THR:OG1	2:H:127:THR:HG22	2.19	0.42
2:H:165:ARG:C	2:X:26:ILE:HG22	2.39	0.42
2:X:109:HIS:HB3	2:X:111:PHE:CE1	2.54	0.42
1:C:54:VAL:HG22	1:C:55:ARG:N	2.34	0.42
2:2:187:LEU:HA	2:2:188:PRO:HD3	1.81	0.42
1:R:54:VAL:HG22	1:R:55:ARG:N	2.35	0.42
2:L:105:ASP:OD1	2:L:106:THR:N	2.52	0.42
1:G:58:LEU:N	1:G:58:LEU:CD1	2.82	0.42
2:J:55:LEU:HA	2:J:55:LEU:HD12	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:123:TYR:N	1:R:123:TYR:CD1	2.88	0.42
1:F:123:TYR:CD1	1:F:123:TYR:N	2.88	0.42
1:T:61:GLN:CD	1:T:62:ASN:H	2.23	0.42
1:A:61:GLN:CD	1:A:62:ASN:H	2.23	0.42
1:B:187:LYS:O	1:B:190:VAL:HG13	2.19	0.42
2:Z:190:ASP:HA	2:Z:193:GLU:HG2	2.02	0.42
1:C:56:SER:OG	1:C:58:LEU:HB2	2.20	0.42
2:W:191:GLN:O	2:W:194:SER:HB3	2.20	0.42
2:Z:143:SER:O	2:Z:146:MET:HG3	2.20	0.42
2:X:187:LEU:HA	2:X:188:PRO:HD3	1.79	0.42
1:F:17:PRO:HA	1:G:26:TYR:CD1	2.55	0.42
1:F:58:LEU:N	1:F:58:LEU:CD1	2.82	0.42
1:G:123:TYR:N	1:G:123:TYR:CD1	2.88	0.42
2:J:187:LEU:HA	2:J:188:PRO:HD3	1.79	0.42
1:B:61:GLN:CD	1:B:62:ASN:H	2.23	0.42
1:U:52:LYS:HB3	1:U:209:ALA:O	2.19	0.42
1:O:52:LYS:HB3	1:O:209:ALA:O	2.19	0.42
2:L:2:THR:HG23	2:L:17:GLU:HG3	2.02	0.42
1:F:52:LYS:HB3	1:F:209:ALA:O	2.19	0.42
1:O:61:GLN:CD	1:O:62:ASN:H	2.23	0.42
1:E:52:LYS:HB3	1:E:209:ALA:O	2.19	0.42
1:G:52:LYS:HB3	1:G:209:ALA:O	2.19	0.42
2:I:191:GLN:O	2:I:194:SER:HB3	2.20	0.42
1:P:58:LEU:CD1	1:P:58:LEU:N	2.82	0.42
1:D:32:LYS:O	1:D:167:SER:HA	2.18	0.42
1:D:16:SER:HB3	1:D:22:PHE:CE2	2.53	0.42
1:B:58:LEU:CD1	1:B:58:LEU:N	2.83	0.42
1:Q:123:TYR:CD1	1:Q:123:TYR:N	2.88	0.42
2:I:180:ARG:HA	2:I:180:ARG:HD2	1.81	0.42
2:2:22:MET:O	2:2:23:GLU:HB2	2.20	0.42
2:J:74:MET:HA	2:J:75:PRO:HD3	1.88	0.42
1:E:124:THR:HG22	1:F:130:ARG:NH2	2.25	0.42
1:R:198:LYS:O	1:R:199:SER:C	2.59	0.42
1:R:198:LYS:CG	1:R:202:GLU:HG2	2.50	0.42
1:T:198:LYS:CG	1:T:202:GLU:HG2	2.50	0.42
1:O:56:SER:OG	1:O:58:LEU:HB2	2.20	0.42
2:Z:163:LYS:CE	2:Z:203:LEU:HD23	2.50	0.42
1:F:54:VAL:HG22	1:F:55:ARG:N	2.35	0.42
2:X:123:ILE:HG12	2:X:124:TYR:CD1	2.51	0.41
1:Q:198:LYS:O	1:Q:199:SER:C	2.59	0.41
1:F:198:LYS:O	1:F:199:SER:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:198:LYS:O	1:G:199:SER:C	2.59	0.41
1:G:198:LYS:CG	1:G:202:GLU:HG2	2.50	0.41
2:W:45:ILE:CD1	2:W:52:ALA:HB1	2.49	0.41
1:A:198:LYS:O	1:A:199:SER:C	2.59	0.41
1:S:198:LYS:O	1:S:199:SER:C	2.59	0.41
2:X:34:LEU:HD21	2:X:176:ALA:CB	2.50	0.41
1:S:56:SER:OG	1:S:58:LEU:HB2	2.20	0.41
1:S:58:LEU:N	1:S:58:LEU:CD1	2.83	0.41
1:A:56:SER:OG	1:A:58:LEU:HB2	2.20	0.41
2:M:17:GLU:O	2:M:33:LYS:HD2	2.20	0.41
1:E:54:VAL:HG22	1:E:55:ARG:N	2.34	0.41
1:T:103:TYR:HE1	2:2:74:MET:HE2	1.85	0.41
1:A:54:VAL:HG22	1:A:55:ARG:N	2.34	0.41
2:Z:180:ARG:HD2	2:Z:180:ARG:HA	1.71	0.41
2:Y:66:TYR:CD2	2:Y:74:MET:HE2	2.55	0.41
1:Q:52:LYS:HB3	1:Q:209:ALA:O	2.19	0.41
1:B:198:LYS:CG	1:B:202:GLU:HG2	2.50	0.41
2:M:111:PHE:CE2	2:M:121:GLU:HB2	2.55	0.41
2:I:147:THR:OG1	2:I:150:GLU:HG3	2.21	0.41
1:E:58:LEU:N	1:E:58:LEU:CD1	2.83	0.41
1:P:56:SER:OG	1:P:58:LEU:HB2	2.20	0.41
2:1:87:LEU:HD23	2:1:114:ASP:O	2.19	0.41
1:A:123:TYR:N	1:A:123:TYR:CD1	2.88	0.41
2:W:123:ILE:CD1	2:W:123:ILE:H	2.31	0.41
2:J:190:ASP:HA	2:J:193:GLU:HG2	2.02	0.41
1:R:56:SER:OG	1:R:58:LEU:HB2	2.20	0.41
1:C:58:LEU:CD1	1:C:58:LEU:N	2.82	0.41
1:B:56:SER:OG	1:B:58:LEU:HB2	2.20	0.41
1:S:54:VAL:HG22	1:S:55:ARG:N	2.34	0.41
2:M:163:LYS:CE	2:M:203:LEU:HD23	2.50	0.41
1:T:56:SER:OG	1:T:58:LEU:HB2	2.20	0.41
1:P:52:LYS:HB3	1:P:209:ALA:O	2.19	0.41
1:D:52:LYS:HB3	1:D:209:ALA:O	2.19	0.41
1:T:78:THR:CG2	1:T:85:ALA:HB1	2.45	0.41
2:M:3:THR:HB	2:M:16:THR:HG22	2.03	0.41
1:P:198:LYS:O	1:P:199:SER:C	2.59	0.41
1:B:198:LYS:O	1:B:199:SER:C	2.59	0.41
1:P:125:GLN:HB3	1:Q:130:ARG:CZ	2.50	0.41
2:Y:59:MET:CE	2:Y:79:VAL:HG23	2.49	0.41
2:J:26:ILE:HG22	2:V:165:ARG:C	2.40	0.41
2:I:175:VAL:HG22	2:I:176:ALA:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:19:ARG:NE	2:I:26:ILE:HG13	2.36	0.41
1:O:58:LEU:CD1	1:O:58:LEU:N	2.82	0.41
1:G:56:SER:OG	1:G:58:LEU:HB2	2.20	0.41
1:F:56:SER:OG	1:F:58:LEU:HB2	2.20	0.41
2:1:114:ASP:OD1	2:1:116:ALA:HB3	2.20	0.41
1:T:58:LEU:CD1	1:T:58:LEU:N	2.82	0.41
1:P:54:VAL:HG22	1:P:55:ARG:N	2.35	0.41
1:D:54:VAL:HG22	1:D:55:ARG:N	2.35	0.41
1:D:56:SER:OG	1:D:58:LEU:HB2	2.20	0.41
2:L:143:SER:O	2:L:146:MET:HG3	2.20	0.41
2:I:93:MET:N	2:I:94:PRO:CD	2.82	0.41
2:L:163:LYS:CE	2:L:203:LEU:HD23	2.50	0.41
1:O:32:LYS:O	1:O:167:SER:HA	2.18	0.41
2:V:180:ARG:HA	2:V:180:ARG:HD2	1.79	0.41
1:T:12:ILE:HG13	1:T:14:VAL:H	1.73	0.41
1:R:130:ARG:HA	1:R:131:PRO:HD3	1.96	0.41
2:N:59:MET:SD	2:N:83:LEU:HD13	2.60	0.41
2:K:26:ILE:CG2	2:2:165:ARG:HA	2.50	0.41
2:1:184:TYR:C	2:1:184:TYR:CD1	2.93	0.41
1:Q:56:SER:OG	1:Q:58:LEU:HB2	2.20	0.41
1:O:54:VAL:HG22	1:O:55:ARG:N	2.34	0.41
2:1:163:LYS:CE	2:1:203:LEU:HD23	2.50	0.41
2:N:158:ALA:O	2:N:161:ALA:HB3	2.21	0.41
2:1:137:VAL:HG21	2:1:158:ALA:HA	2.01	0.41
2:M:187:LEU:HA	2:M:188:PRO:HD3	1.82	0.41
1:F:103:TYR:HE1	2:N:74:MET:CE	2.34	0.41
2:L:66:TYR:CZ	2:L:70:ARG:HD2	2.56	0.41
1:A:198:LYS:CG	1:A:202:GLU:HG2	2.50	0.41
1:E:198:LYS:O	1:E:199:SER:C	2.59	0.41
2:1:111:PHE:CE2	2:1:121:GLU:HB2	2.55	0.41
2:W:175:VAL:HG22	2:W:176:ALA:N	2.35	0.41
2:V:187:LEU:HA	2:V:188:PRO:HD3	1.77	0.41
1:U:58:LEU:CD1	1:U:58:LEU:N	2.83	0.41
1:T:103:TYR:HE1	2:2:74:MET:CE	2.34	0.41
2:1:17:GLU:O	2:1:33:LYS:HD2	2.20	0.41
1:O:123:TYR:CD1	1:O:123:TYR:N	2.88	0.41
2:L:43:MET:HE1	2:L:56:VAL:HA	2.02	0.41
2:L:20:VAL:CG1	2:L:28:HIS:HB2	2.44	0.41
2:1:3:THR:HB	2:1:16:THR:HG22	2.03	0.41
1:T:198:LYS:O	1:T:199:SER:C	2.59	0.41
2:M:165:ARG:NH2	2:1:135:TYR:HE1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:49:VAL:HG23	2:K:50:GLY:H	1.86	0.41
1:D:58:LEU:CD1	1:D:58:LEU:N	2.82	0.41
2:K:22:MET:O	2:K:23:GLU:HB2	2.21	0.41
2:2:177:VAL:HG13	2:2:185:VAL:HG13	2.03	0.41
2:H:18:ARG:HE	2:H:30:ASN:HD22	1.67	0.41
2:L:97:VAL:HG22	2:L:98:GLN:N	2.36	0.41
1:Q:126:TYR:HA	1:R:129:VAL:HG23	2.03	0.41
1:C:123:TYR:N	1:C:123:TYR:CD1	2.88	0.41
1:P:123:TYR:CD1	1:P:123:TYR:N	2.88	0.41
1:D:123:TYR:N	1:D:123:TYR:CD1	2.88	0.41
1:A:124:THR:HG22	1:B:130:ARG:NH2	2.26	0.41
2:W:56:VAL:CG1	2:W:57:ARG:N	2.84	0.41
2:I:56:VAL:CG1	2:I:57:ARG:N	2.84	0.41
2:Z:20:VAL:CG1	2:Z:28:HIS:HB2	2.44	0.41
1:C:198:LYS:CG	1:C:202:GLU:HG2	2.50	0.41
2:N:133:PHE:HE1	2:Z:132:PRO:HA	1.83	0.41
2:Z:97:VAL:HG22	2:Z:98:GLN:N	2.36	0.41
2:N:187:LEU:HA	2:N:188:PRO:HD3	1.81	0.41
2:J:203:LEU:HA	2:J:203:LEU:HD12	1.86	0.41
2:Z:66:TYR:CZ	2:Z:70:ARG:HD2	2.56	0.41
2:L:138:LEU:HD12	2:L:138:LEU:HA	1.90	0.41
1:U:198:LYS:CG	1:U:202:GLU:HG2	2.50	0.41
1:S:198:LYS:CG	1:S:202:GLU:HG2	2.50	0.41
2:M:135:TYR:HE1	2:1:165:ARG:NH2	2.19	0.41
2:J:190:ASP:O	2:J:193:GLU:HG2	2.21	0.41
2:J:141:GLN:HE21	2:W:141:GLN:HE21	1.69	0.41
2:W:19:ARG:NE	2:W:26:ILE:HG13	2.36	0.41
1:E:56:SER:OG	1:E:58:LEU:HB2	2.20	0.41
2:N:74:MET:HA	2:N:75:PRO:HD3	1.95	0.41
2:M:137:VAL:HG21	2:M:158:ALA:HA	2.01	0.41
2:Y:19:ARG:NH1	2:Y:169:SER:O	2.54	0.41
1:T:165:ILE:HD12	1:T:169:LYS:HD2	2.03	0.41
1:B:165:ILE:HD12	1:B:169:LYS:HD2	2.03	0.41
1:U:165:ILE:HD12	1:U:169:LYS:HD2	2.03	0.41
2:2:72:VAL:HG22	2:2:73:ASN:N	2.36	0.41
1:C:165:ILE:HD12	1:C:169:LYS:HD2	2.03	0.41
1:S:123:TYR:N	1:S:123:TYR:CD1	2.88	0.41
1:S:78:THR:CG2	1:S:85:ALA:HB1	2.45	0.41
2:V:59:MET:CE	2:V:82:LEU:HD23	2.51	0.41
2:K:59:MET:CE	2:K:79:VAL:HG23	2.49	0.41
2:M:165:ARG:CZ	2:1:135:TYR:CD1	3.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:34:LEU:HD21	2:Y:176:ALA:CB	2.51	0.41
2:J:26:ILE:HG23	2:V:165:ARG:HA	2.03	0.41
2:J:109:HIS:HB3	2:J:111:PHE:CE1	2.55	0.41
2:H:81:THR:O	2:H:84:SER:HB3	2.21	0.41
2:Z:2:THR:HG23	2:Z:17:GLU:HG3	2.02	0.40
2:W:178:ILE:HB	2:W:184:TYR:HA	2.03	0.40
2:I:178:ILE:HB	2:I:184:TYR:HA	2.03	0.40
2:H:59:MET:CE	2:H:82:LEU:HD23	2.51	0.40
1:F:198:LYS:CG	1:F:202:GLU:HG2	2.50	0.40
2:J:103:GLY:HA2	2:J:178:ILE:HD11	2.02	0.40
1:B:125:GLN:HB3	1:C:130:ARG:CZ	2.50	0.40
2:K:34:LEU:HD21	2:K:176:ALA:CB	2.51	0.40
2:M:76:ILE:HA	2:M:79:VAL:HG12	2.04	0.40
2:Z:87:LEU:HD23	2:Z:114:ASP:O	2.20	0.40
1:D:103:TYR:CE1	2:L:74:MET:HE2	2.56	0.40
2:L:146:MET:HE3	2:L:150:GLU:HB3	2.03	0.40
1:Q:165:ILE:HD12	1:Q:169:LYS:HD2	2.03	0.40
2:Y:22:MET:O	2:Y:23:GLU:HB2	2.21	0.40
2:X:93:MET:N	2:X:94:PRO:CD	2.85	0.40
1:U:123:TYR:CD1	1:U:123:TYR:N	2.88	0.40
1:C:15:PHE:HB2	1:D:23:GLN:HE22	1.86	0.40
2:H:66:TYR:CD1	2:H:66:TYR:C	2.94	0.40
1:G:130:ARG:HA	1:G:131:PRO:HD3	1.96	0.40
1:A:78:THR:CG2	1:A:85:ALA:HB1	2.45	0.40
1:B:78:THR:CG2	1:B:85:ALA:HB1	2.45	0.40
2:L:190:ASP:HA	2:L:193:GLU:HG2	2.02	0.40
2:2:59:MET:SD	2:2:83:LEU:HD13	2.60	0.40
2:M:135:TYR:CD1	2:1:165:ARG:CZ	3.04	0.40
2:W:26:ILE:HD13	2:W:26:ILE:O	2.22	0.40
1:O:165:ILE:HD12	1:O:169:LYS:HD2	2.03	0.40
1:P:165:ILE:HD12	1:P:169:LYS:HD2	2.03	0.40
1:T:123:TYR:CD1	1:T:123:TYR:N	2.88	0.40
1:B:123:TYR:N	1:B:123:TYR:CD1	2.88	0.40
2:I:59:MET:SD	2:I:83:LEU:HD13	2.61	0.40
2:W:59:MET:SD	2:W:83:LEU:HD13	2.61	0.40
1:O:198:LYS:O	1:O:199:SER:C	2.59	0.40
1:E:198:LYS:CG	1:E:202:GLU:HG2	2.50	0.40
2:X:190:ASP:HA	2:X:193:GLU:HG2	2.02	0.40
2:V:81:THR:O	2:V:84:SER:HB3	2.21	0.40
2:W:147:THR:OG1	2:W:150:GLU:HG3	2.21	0.40
1:A:165:ILE:HD12	1:A:169:LYS:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:190:ASP:HA	2:N:193:GLU:HG2	2.04	0.40
1:U:44:ASN:HA	1:U:44:ASN:HD22	1.56	0.40
2:V:66:TYR:CD1	2:V:66:TYR:C	2.94	0.40
1:P:198:LYS:CG	1:P:202:GLU:HG2	2.50	0.40
1:C:198:LYS:O	1:C:199:SER:C	2.59	0.40
1:U:198:LYS:O	1:U:199:SER:C	2.59	0.40
2:L:87:LEU:HD23	2:L:114:ASP:O	2.20	0.40
2:V:202:ILE:CG1	2:V:203:LEU:N	2.85	0.40
2:Z:43:MET:HE1	2:Z:56:VAL:HA	2.02	0.40
2:2:76:ILE:O	2:2:79:VAL:CG1	2.69	0.40
2:W:74:MET:HA	2:W:75:PRO:HD3	1.94	0.40
2:J:141:GLN:HE21	2:W:141:GLN:NE2	2.19	0.40
2:I:26:ILE:O	2:I:26:ILE:HD13	2.22	0.40
1:S:165:ILE:HD12	1:S:169:LYS:HD2	2.03	0.40
1:E:165:ILE:HD12	1:E:169:LYS:HD2	2.03	0.40
1:E:123:TYR:CD1	1:E:123:TYR:N	2.88	0.40
1:G:44:ASN:HD22	1:G:44:ASN:HA	1.56	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	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3 31
1	B	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3 31
1	C	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3 31
1	D	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3 31
1	E	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3 31
1	F	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3 31
1	G	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3 31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3	31
1	P	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3	31
1	Q	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3	31
1	R	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3	31
1	S	222/233 (95%)	183 (82%)	28 (13%)	11 (5%)	3	31
1	T	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3	31
1	U	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	3	31
2	1	201/203 (99%)	176 (88%)	23 (11%)	2 (1%)	19	65
2	2	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	19	65
2	H	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	19	65
2	I	201/203 (99%)	183 (91%)	16 (8%)	2 (1%)	19	65
2	J	201/203 (99%)	180 (90%)	20 (10%)	1 (0%)	34	77
2	K	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	19	65
2	L	201/203 (99%)	181 (90%)	16 (8%)	4 (2%)	9	51
2	M	201/203 (99%)	176 (88%)	23 (11%)	2 (1%)	19	65
2	N	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	19	65
2	V	201/203 (99%)	185 (92%)	14 (7%)	2 (1%)	19	65
2	W	201/203 (99%)	183 (91%)	16 (8%)	2 (1%)	19	65
2	X	201/203 (99%)	180 (90%)	20 (10%)	1 (0%)	34	77
2	Y	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	19	65
2	Z	201/203 (99%)	181 (90%)	16 (8%)	4 (2%)	9	51
All	All	5922/6104 (97%)	5120 (86%)	618 (10%)	184 (3%)	9	42

All (184) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	ILE
1	A	128	GLY
1	A	182	GLU
1	A	200	SER
1	B	12	ILE
1	B	128	GLY
1	B	182	GLU
1	B	200	SER
1	C	12	ILE

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Mol	Chain	Res	Type
1	C	128	GLY
1	C	182	GLU
1	C	200	SER
1	D	12	ILE
1	D	128	GLY
1	D	182	GLU
1	D	200	SER
1	E	12	ILE
1	E	128	GLY
1	E	182	GLU
1	E	200	SER
1	F	12	ILE
1	F	128	GLY
1	F	182	GLU
1	F	200	SER
1	G	12	ILE
1	G	128	GLY
1	G	182	GLU
1	G	200	SER
2	I	9	LYS
2	L	9	LYS
2	M	9	LYS
1	O	12	ILE
1	O	128	GLY
1	O	182	GLU
1	O	200	SER
1	P	12	ILE
1	P	128	GLY
1	P	182	GLU
1	P	200	SER
1	Q	12	ILE
1	Q	128	GLY
1	Q	182	GLU
1	Q	200	SER
1	R	12	ILE
1	R	128	GLY
1	R	182	GLU
1	R	200	SER
1	S	12	ILE
1	S	128	GLY
1	S	182	GLU
1	S	200	SER

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Mol	Chain	Res	Type
1	T	12	ILE
1	T	128	GLY
1	T	182	GLU
1	T	200	SER
1	U	12	ILE
1	U	128	GLY
1	U	182	GLU
1	U	200	SER
2	W	9	LYS
2	Z	9	LYS
2	1	9	LYS
1	A	11	ALA
1	A	43	ALA
1	A	72	ASP
1	A	205	GLU
1	B	11	ALA
1	B	43	ALA
1	B	72	ASP
1	B	205	GLU
1	C	11	ALA
1	C	43	ALA
1	C	72	ASP
1	C	205	GLU
1	D	11	ALA
1	D	43	ALA
1	D	72	ASP
1	D	205	GLU
1	E	11	ALA
1	E	43	ALA
1	E	72	ASP
1	E	205	GLU
1	F	11	ALA
1	F	43	ALA
1	F	72	ASP
1	F	205	GLU
1	G	11	ALA
1	G	43	ALA
1	G	72	ASP
1	G	205	GLU
2	H	9	LYS
2	J	9	LYS
2	K	9	LYS

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Mol	Chain	Res	Type
2	N	9	LYS
1	O	11	ALA
1	O	43	ALA
1	O	72	ASP
1	O	205	GLU
1	P	11	ALA
1	P	43	ALA
1	P	72	ASP
1	P	205	GLU
1	Q	11	ALA
1	Q	43	ALA
1	Q	72	ASP
1	Q	205	GLU
1	R	11	ALA
1	R	43	ALA
1	R	72	ASP
1	R	205	GLU
1	S	11	ALA
1	S	43	ALA
1	S	72	ASP
1	S	205	GLU
1	T	11	ALA
1	T	43	ALA
1	T	72	ASP
1	T	205	GLU
1	U	11	ALA
1	U	43	ALA
1	U	72	ASP
1	U	205	GLU
2	V	9	LYS
2	X	9	LYS
2	Y	9	LYS
2	2	9	LYS
2	H	23	GLU
2	K	23	GLU
2	V	23	GLU
2	Y	23	GLU
2	M	23	GLU
2	1	23	GLU
1	A	198	LYS
1	A	202	GLU
1	B	198	LYS

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Mol	Chain	Res	Type
1	B	202	GLU
1	C	198	LYS
1	C	202	GLU
1	D	198	LYS
1	D	202	GLU
1	E	198	LYS
1	E	202	GLU
1	F	198	LYS
1	F	202	GLU
1	G	198	LYS
1	G	202	GLU
2	L	23	GLU
2	N	23	GLU
1	O	198	LYS
1	O	202	GLU
1	P	198	LYS
1	P	202	GLU
1	Q	198	LYS
1	Q	202	GLU
1	R	198	LYS
1	R	202	GLU
1	S	198	LYS
1	S	202	GLU
1	T	198	LYS
1	T	202	GLU
1	U	198	LYS
1	U	202	GLU
2	Z	23	GLU
2	2	23	GLU
2	I	23	GLU
2	L	49	VAL
2	W	23	GLU
2	Z	49	VAL
2	L	110	VAL
2	Z	110	VAL
1	A	129	VAL
1	B	129	VAL
1	C	129	VAL
1	D	129	VAL
1	E	129	VAL
1	F	129	VAL
1	G	129	VAL

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Mol	Chain	Res	Type
1	O	129	VAL
1	P	129	VAL
1	Q	129	VAL
1	R	129	VAL
1	S	129	VAL
1	T	129	VAL
1	U	129	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	B	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	C	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	D	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	E	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	F	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	G	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	O	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	P	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	Q	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	R	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	S	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	T	186/193 (96%)	163 (88%)	23 (12%)	6 30
1	U	186/193 (96%)	163 (88%)	23 (12%)	6 30
2	1	170/170 (100%)	152 (89%)	18 (11%)	8 36
2	2	170/170 (100%)	146 (86%)	24 (14%)	4 26
2	H	170/170 (100%)	145 (85%)	25 (15%)	4 24
2	I	170/170 (100%)	148 (87%)	22 (13%)	5 28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	J	170/170 (100%)	143 (84%)	27 (16%)	3 21
2	K	170/170 (100%)	143 (84%)	27 (16%)	3 21
2	L	170/170 (100%)	146 (86%)	24 (14%)	4 26
2	M	170/170 (100%)	152 (89%)	18 (11%)	8 36
2	N	170/170 (100%)	146 (86%)	24 (14%)	4 26
2	V	170/170 (100%)	145 (85%)	25 (15%)	4 24
2	W	170/170 (100%)	149 (88%)	21 (12%)	6 30
2	X	170/170 (100%)	143 (84%)	27 (16%)	3 21
2	Y	170/170 (100%)	143 (84%)	27 (16%)	3 21
2	Z	170/170 (100%)	146 (86%)	24 (14%)	4 26
All	All	4984/5082 (98%)	4329 (87%)	655 (13%)	9 28

All (655) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	12	ILE
1	A	21	LEU
1	A	38	LEU
1	A	44	ASN
1	A	47	LEU
1	A	62	ASN
1	A	71	ASP
1	A	102	THR
1	A	119	GLN
1	A	134	VAL
1	A	136	LEU
1	A	141	ILE
1	A	143	GLN
1	A	157	ILE
1	A	161	LYS
1	A	175	PHE
1	A	176	LEU
1	A	190	VAL
1	A	201	LEU
1	A	202	GLU
1	A	212	ILE
1	A	221	TYR

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Mol	Chain	Res	Type
1	B	10	ARG
1	B	12	ILE
1	B	21	LEU
1	B	38	LEU
1	B	44	ASN
1	B	47	LEU
1	B	62	ASN
1	B	71	ASP
1	B	102	THR
1	B	119	GLN
1	B	134	VAL
1	B	136	LEU
1	B	141	ILE
1	B	143	GLN
1	B	157	ILE
1	B	161	LYS
1	B	175	PHE
1	B	176	LEU
1	B	190	VAL
1	B	201	LEU
1	B	202	GLU
1	B	212	ILE
1	B	221	TYR
1	C	10	ARG
1	C	12	ILE
1	C	21	LEU
1	C	38	LEU
1	C	44	ASN
1	C	47	LEU
1	C	62	ASN
1	C	71	ASP
1	C	102	THR
1	C	119	GLN
1	C	134	VAL
1	C	136	LEU
1	C	141	ILE
1	C	143	GLN
1	C	157	ILE
1	C	161	LYS
1	C	175	PHE
1	C	176	LEU
1	C	190	VAL

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Mol	Chain	Res	Type
1	C	201	LEU
1	C	202	GLU
1	C	212	ILE
1	C	221	TYR
1	D	10	ARG
1	D	12	ILE
1	D	21	LEU
1	D	38	LEU
1	D	44	ASN
1	D	47	LEU
1	D	62	ASN
1	D	71	ASP
1	D	102	THR
1	D	119	GLN
1	D	134	VAL
1	D	136	LEU
1	D	141	ILE
1	D	143	GLN
1	D	157	ILE
1	D	161	LYS
1	D	175	PHE
1	D	176	LEU
1	D	190	VAL
1	D	201	LEU
1	D	202	GLU
1	D	212	ILE
1	D	221	TYR
1	E	10	ARG
1	E	12	ILE
1	E	21	LEU
1	E	38	LEU
1	E	44	ASN
1	E	47	LEU
1	E	62	ASN
1	E	71	ASP
1	E	102	THR
1	E	119	GLN
1	E	134	VAL
1	E	136	LEU
1	E	141	ILE
1	E	143	GLN
1	E	157	ILE

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Mol	Chain	Res	Type
1	E	161	LYS
1	E	175	PHE
1	E	176	LEU
1	E	190	VAL
1	E	201	LEU
1	E	202	GLU
1	E	212	ILE
1	E	221	TYR
1	F	10	ARG
1	F	12	ILE
1	F	21	LEU
1	F	38	LEU
1	F	44	ASN
1	F	47	LEU
1	F	62	ASN
1	F	71	ASP
1	F	102	THR
1	F	119	GLN
1	F	134	VAL
1	F	136	LEU
1	F	141	ILE
1	F	143	GLN
1	F	157	ILE
1	F	161	LYS
1	F	175	PHE
1	F	176	LEU
1	F	190	VAL
1	F	201	LEU
1	F	202	GLU
1	F	212	ILE
1	F	221	TYR
1	G	10	ARG
1	G	12	ILE
1	G	21	LEU
1	G	38	LEU
1	G	44	ASN
1	G	47	LEU
1	G	62	ASN
1	G	71	ASP
1	G	102	THR
1	G	119	GLN
1	G	134	VAL

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Mol	Chain	Res	Type
1	G	136	LEU
1	G	141	ILE
1	G	143	GLN
1	G	157	ILE
1	G	161	LYS
1	G	175	PHE
1	G	176	LEU
1	G	190	VAL
1	G	201	LEU
1	G	202	GLU
1	G	212	ILE
1	G	221	TYR
2	H	2	THR
2	H	7	THR
2	H	17	GLU
2	H	25	PHE
2	H	26	ILE
2	H	41	THR
2	H	45	ILE
2	H	49	VAL
2	H	56	VAL
2	H	63	LEU
2	H	71	ARG
2	H	83	LEU
2	H	94	PRO
2	H	97	VAL
2	H	123	ILE
2	H	127	THR
2	H	134	VAL
2	H	137	VAL
2	H	138	LEU
2	H	144	GLU
2	H	165	ARG
2	H	173	ILE
2	H	175	VAL
2	H	178	ILE
2	H	201	LEU
2	I	2	THR
2	I	17	GLU
2	I	20	VAL
2	I	25	PHE
2	I	26	ILE

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Mol	Chain	Res	Type
2	I	41	THR
2	I	45	ILE
2	I	49	VAL
2	I	59	MET
2	I	70	ARG
2	I	71	ARG
2	I	83	LEU
2	I	123	ILE
2	I	127	THR
2	I	134	VAL
2	I	137	VAL
2	I	138	LEU
2	I	144	GLU
2	I	165	ARG
2	I	173	ILE
2	I	178	ILE
2	I	185	VAL
2	J	2	THR
2	J	8	LEU
2	J	12	VAL
2	J	17	GLU
2	J	20	VAL
2	J	25	PHE
2	J	26	ILE
2	J	41	THR
2	J	45	ILE
2	J	49	VAL
2	J	55	LEU
2	J	59	MET
2	J	68	LEU
2	J	70	ARG
2	J	71	ARG
2	J	83	LEU
2	J	123	ILE
2	J	127	THR
2	J	134	VAL
2	J	137	VAL
2	J	138	LEU
2	J	144	GLU
2	J	165	ARG
2	J	173	ILE
2	J	175	VAL

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Mol	Chain	Res	Type
2	J	178	ILE
2	J	185	VAL
2	K	2	THR
2	K	7	THR
2	K	17	GLU
2	K	25	PHE
2	K	26	ILE
2	K	41	THR
2	K	45	ILE
2	K	49	VAL
2	K	56	VAL
2	K	68	LEU
2	K	71	ARG
2	K	83	LEU
2	K	94	PRO
2	K	97	VAL
2	K	104	ILE
2	K	123	ILE
2	K	127	THR
2	K	134	VAL
2	K	137	VAL
2	K	144	GLU
2	K	149	ASP
2	K	165	ARG
2	K	173	ILE
2	K	175	VAL
2	K	177	VAL
2	K	178	ILE
2	K	185	VAL
2	L	1	THR
2	L	2	THR
2	L	8	LEU
2	L	17	GLU
2	L	20	VAL
2	L	26	ILE
2	L	41	THR
2	L	45	ILE
2	L	49	VAL
2	L	63	LEU
2	L	68	LEU
2	L	71	ARG
2	L	83	LEU

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Mol	Chain	Res	Type
2	L	123	ILE
2	L	127	THR
2	L	134	VAL
2	L	137	VAL
2	L	138	LEU
2	L	144	GLU
2	L	153	ASP
2	L	165	ARG
2	L	173	ILE
2	L	175	VAL
2	L	178	ILE
2	M	2	THR
2	M	17	GLU
2	M	20	VAL
2	M	26	ILE
2	M	41	THR
2	M	45	ILE
2	M	59	MET
2	M	71	ARG
2	M	83	LEU
2	M	123	ILE
2	M	127	THR
2	M	134	VAL
2	M	137	VAL
2	M	138	LEU
2	M	144	GLU
2	M	165	ARG
2	M	173	ILE
2	M	178	ILE
2	N	2	THR
2	N	8	LEU
2	N	12	VAL
2	N	17	GLU
2	N	20	VAL
2	N	25	PHE
2	N	26	ILE
2	N	41	THR
2	N	45	ILE
2	N	59	MET
2	N	70	ARG
2	N	71	ARG
2	N	94	PRO

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Mol	Chain	Res	Type
2	N	123	ILE
2	N	127	THR
2	N	134	VAL
2	N	137	VAL
2	N	144	GLU
2	N	153	ASP
2	N	165	ARG
2	N	173	ILE
2	N	175	VAL
2	N	178	ILE
2	N	185	VAL
1	O	10	ARG
1	O	12	ILE
1	O	21	LEU
1	O	38	LEU
1	O	44	ASN
1	O	47	LEU
1	O	62	ASN
1	O	71	ASP
1	O	102	THR
1	O	119	GLN
1	O	134	VAL
1	O	136	LEU
1	O	141	ILE
1	O	143	GLN
1	O	157	ILE
1	O	161	LYS
1	O	175	PHE
1	O	176	LEU
1	O	190	VAL
1	O	201	LEU
1	O	202	GLU
1	O	212	ILE
1	O	221	TYR
1	P	10	ARG
1	P	12	ILE
1	P	21	LEU
1	P	38	LEU
1	P	44	ASN
1	P	47	LEU
1	P	62	ASN
1	P	71	ASP

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Mol	Chain	Res	Type
1	P	102	THR
1	P	119	GLN
1	P	134	VAL
1	P	136	LEU
1	P	141	ILE
1	P	143	GLN
1	P	157	ILE
1	P	161	LYS
1	P	175	PHE
1	P	176	LEU
1	P	190	VAL
1	P	201	LEU
1	P	202	GLU
1	P	212	ILE
1	P	221	TYR
1	Q	10	ARG
1	Q	12	ILE
1	Q	21	LEU
1	Q	38	LEU
1	Q	44	ASN
1	Q	47	LEU
1	Q	62	ASN
1	Q	71	ASP
1	Q	102	THR
1	Q	119	GLN
1	Q	134	VAL
1	Q	136	LEU
1	Q	141	ILE
1	Q	143	GLN
1	Q	157	ILE
1	Q	161	LYS
1	Q	175	PHE
1	Q	176	LEU
1	Q	190	VAL
1	Q	201	LEU
1	Q	202	GLU
1	Q	212	ILE
1	Q	221	TYR
1	R	10	ARG
1	R	12	ILE
1	R	21	LEU
1	R	38	LEU

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Mol	Chain	Res	Type
1	R	44	ASN
1	R	47	LEU
1	R	62	ASN
1	R	71	ASP
1	R	102	THR
1	R	119	GLN
1	R	134	VAL
1	R	136	LEU
1	R	141	ILE
1	R	143	GLN
1	R	157	ILE
1	R	161	LYS
1	R	175	PHE
1	R	176	LEU
1	R	190	VAL
1	R	201	LEU
1	R	202	GLU
1	R	212	ILE
1	R	221	TYR
1	S	10	ARG
1	S	12	ILE
1	S	21	LEU
1	S	38	LEU
1	S	44	ASN
1	S	47	LEU
1	S	62	ASN
1	S	71	ASP
1	S	102	THR
1	S	119	GLN
1	S	134	VAL
1	S	136	LEU
1	S	141	ILE
1	S	143	GLN
1	S	157	ILE
1	S	161	LYS
1	S	175	PHE
1	S	176	LEU
1	S	190	VAL
1	S	201	LEU
1	S	202	GLU
1	S	212	ILE
1	S	221	TYR

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Mol	Chain	Res	Type
1	T	10	ARG
1	T	12	ILE
1	T	21	LEU
1	T	38	LEU
1	T	44	ASN
1	T	47	LEU
1	T	62	ASN
1	T	71	ASP
1	T	102	THR
1	T	119	GLN
1	T	134	VAL
1	T	136	LEU
1	T	141	ILE
1	T	143	GLN
1	T	157	ILE
1	T	161	LYS
1	T	175	PHE
1	T	176	LEU
1	T	190	VAL
1	T	201	LEU
1	T	202	GLU
1	T	212	ILE
1	T	221	TYR
1	U	10	ARG
1	U	12	ILE
1	U	21	LEU
1	U	38	LEU
1	U	44	ASN
1	U	47	LEU
1	U	62	ASN
1	U	71	ASP
1	U	102	THR
1	U	119	GLN
1	U	134	VAL
1	U	136	LEU
1	U	141	ILE
1	U	143	GLN
1	U	157	ILE
1	U	161	LYS
1	U	175	PHE
1	U	176	LEU
1	U	190	VAL

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Mol	Chain	Res	Type
1	U	201	LEU
1	U	202	GLU
1	U	212	ILE
1	U	221	TYR
2	V	2	THR
2	V	7	THR
2	V	17	GLU
2	V	25	PHE
2	V	26	ILE
2	V	41	THR
2	V	45	ILE
2	V	49	VAL
2	V	56	VAL
2	V	63	LEU
2	V	71	ARG
2	V	83	LEU
2	V	94	PRO
2	V	97	VAL
2	V	123	ILE
2	V	127	THR
2	V	134	VAL
2	V	137	VAL
2	V	138	LEU
2	V	144	GLU
2	V	165	ARG
2	V	173	ILE
2	V	175	VAL
2	V	178	ILE
2	V	201	LEU
2	W	2	THR
2	W	17	GLU
2	W	20	VAL
2	W	25	PHE
2	W	26	ILE
2	W	41	THR
2	W	45	ILE
2	W	49	VAL
2	W	59	MET
2	W	70	ARG
2	W	71	ARG
2	W	83	LEU
2	W	123	ILE

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Mol	Chain	Res	Type
2	W	127	THR
2	W	134	VAL
2	W	138	LEU
2	W	144	GLU
2	W	165	ARG
2	W	173	ILE
2	W	178	ILE
2	W	185	VAL
2	X	2	THR
2	X	8	LEU
2	X	12	VAL
2	X	17	GLU
2	X	20	VAL
2	X	25	PHE
2	X	26	ILE
2	X	41	THR
2	X	45	ILE
2	X	49	VAL
2	X	55	LEU
2	X	59	MET
2	X	68	LEU
2	X	70	ARG
2	X	71	ARG
2	X	83	LEU
2	X	123	ILE
2	X	127	THR
2	X	134	VAL
2	X	137	VAL
2	X	138	LEU
2	X	144	GLU
2	X	165	ARG
2	X	173	ILE
2	X	175	VAL
2	X	178	ILE
2	X	185	VAL
2	Y	2	THR
2	Y	7	THR
2	Y	17	GLU
2	Y	25	PHE
2	Y	26	ILE
2	Y	41	THR
2	Y	45	ILE

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Mol	Chain	Res	Type
2	Y	49	VAL
2	Y	56	VAL
2	Y	68	LEU
2	Y	71	ARG
2	Y	83	LEU
2	Y	94	PRO
2	Y	97	VAL
2	Y	104	ILE
2	Y	123	ILE
2	Y	127	THR
2	Y	134	VAL
2	Y	137	VAL
2	Y	144	GLU
2	Y	149	ASP
2	Y	165	ARG
2	Y	173	ILE
2	Y	175	VAL
2	Y	177	VAL
2	Y	178	ILE
2	Y	185	VAL
2	Z	1	THR
2	Z	2	THR
2	Z	8	LEU
2	Z	17	GLU
2	Z	20	VAL
2	Z	26	ILE
2	Z	41	THR
2	Z	45	ILE
2	Z	49	VAL
2	Z	63	LEU
2	Z	68	LEU
2	Z	71	ARG
2	Z	83	LEU
2	Z	123	ILE
2	Z	127	THR
2	Z	134	VAL
2	Z	137	VAL
2	Z	138	LEU
2	Z	144	GLU
2	Z	153	ASP
2	Z	165	ARG
2	Z	173	ILE

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Mol	Chain	Res	Type
2	Z	175	VAL
2	Z	178	ILE
2	1	2	THR
2	1	17	GLU
2	1	20	VAL
2	1	26	ILE
2	1	41	THR
2	1	45	ILE
2	1	59	MET
2	1	71	ARG
2	1	83	LEU
2	1	123	ILE
2	1	127	THR
2	1	134	VAL
2	1	137	VAL
2	1	138	LEU
2	1	144	GLU
2	1	165	ARG
2	1	173	ILE
2	1	178	ILE
2	2	2	THR
2	2	8	LEU
2	2	12	VAL
2	2	17	GLU
2	2	20	VAL
2	2	25	PHE
2	2	26	ILE
2	2	41	THR
2	2	45	ILE
2	2	59	MET
2	2	70	ARG
2	2	71	ARG
2	2	94	PRO
2	2	123	ILE
2	2	127	THR
2	2	134	VAL
2	2	137	VAL
2	2	144	GLU
2	2	153	ASP
2	2	165	ARG
2	2	173	ILE
2	2	175	VAL

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Mol	Chain	Res	Type
2	2	178	ILE
2	2	185	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	44	ASN
1	A	98	GLN
1	A	121	GLN
1	A	125	GLN
1	A	143	GLN
1	B	23	GLN
1	B	44	ASN
1	B	98	GLN
1	B	121	GLN
1	B	125	GLN
1	B	143	GLN
1	C	44	ASN
1	C	98	GLN
1	C	121	GLN
1	C	125	GLN
1	C	143	GLN
1	D	23	GLN
1	D	44	ASN
1	D	98	GLN
1	D	121	GLN
1	D	125	GLN
1	D	143	GLN
1	E	23	GLN
1	E	44	ASN
1	E	98	GLN
1	E	121	GLN
1	E	125	GLN
1	E	143	GLN
1	F	44	ASN
1	F	98	GLN
1	F	121	GLN
1	F	125	GLN
1	F	143	GLN
1	G	23	GLN
1	G	44	ASN

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Mol	Chain	Res	Type
1	G	98	GLN
1	G	121	GLN
1	G	125	GLN
1	G	143	GLN
2	H	30	ASN
2	H	36	GLN
2	H	164	GLN
2	I	30	ASN
2	I	36	GLN
2	I	73	ASN
2	I	164	GLN
2	J	30	ASN
2	J	36	GLN
2	J	141	GLN
2	J	164	GLN
2	K	30	ASN
2	K	85	ASN
2	K	141	GLN
2	K	164	GLN
2	L	30	ASN
2	L	141	GLN
2	L	164	GLN
2	M	30	ASN
2	M	141	GLN
2	M	164	GLN
2	N	30	ASN
2	N	164	GLN
1	O	23	GLN
1	O	44	ASN
1	O	98	GLN
1	O	121	GLN
1	O	125	GLN
1	O	143	GLN
1	P	23	GLN
1	P	44	ASN
1	P	98	GLN
1	P	121	GLN
1	P	125	GLN
1	P	143	GLN
1	Q	44	ASN
1	Q	98	GLN
1	Q	121	GLN

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Mol	Chain	Res	Type
1	Q	125	GLN
1	Q	143	GLN
1	R	23	GLN
1	R	44	ASN
1	R	98	GLN
1	R	121	GLN
1	R	125	GLN
1	R	143	GLN
1	S	23	GLN
1	S	44	ASN
1	S	98	GLN
1	S	121	GLN
1	S	125	GLN
1	S	143	GLN
1	T	44	ASN
1	T	98	GLN
1	T	121	GLN
1	T	125	GLN
1	T	143	GLN
1	U	23	GLN
1	U	44	ASN
1	U	98	GLN
1	U	121	GLN
1	U	125	GLN
1	U	143	GLN
2	V	30	ASN
2	V	36	GLN
2	V	164	GLN
2	W	30	ASN
2	W	36	GLN
2	W	73	ASN
2	W	164	GLN
2	X	30	ASN
2	X	36	GLN
2	X	141	GLN
2	X	164	GLN
2	Y	30	ASN
2	Y	85	ASN
2	Y	141	GLN
2	Y	164	GLN
2	Z	30	ASN
2	Z	141	GLN

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Mol	Chain	Res	Type
2	Z	164	GLN
2	1	30	ASN
2	1	164	GLN
2	2	30	ASN
2	2	164	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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.