



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 10:04 PM UTC

PDB ID : 3C92 / pdb_00003c92
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 initial models : 3C91, 1PMA

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

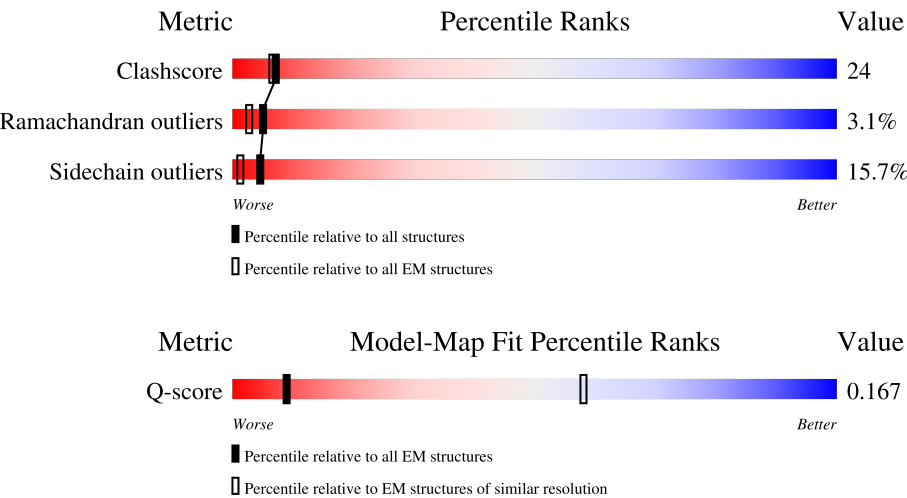
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	503 (6.30 - 7.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	233	
1	B	233	
1	C	233	
1	D	233	

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Mol	Chain	Length	Quality of chain
1	E	233	
1	F	233	
1	G	233	
1	O	233	
1	P	233	
1	Q	233	
1	R	233	
1	S	233	
1	T	233	
1	U	233	
2	1	203	
2	2	203	
2	H	203	
2	I	203	
2	J	203	
2	K	203	
2	L	203	
2	M	203	
2	N	203	
2	V	203	
2	W	203	
2	X	203	
2	Y	203	
2	Z	203	

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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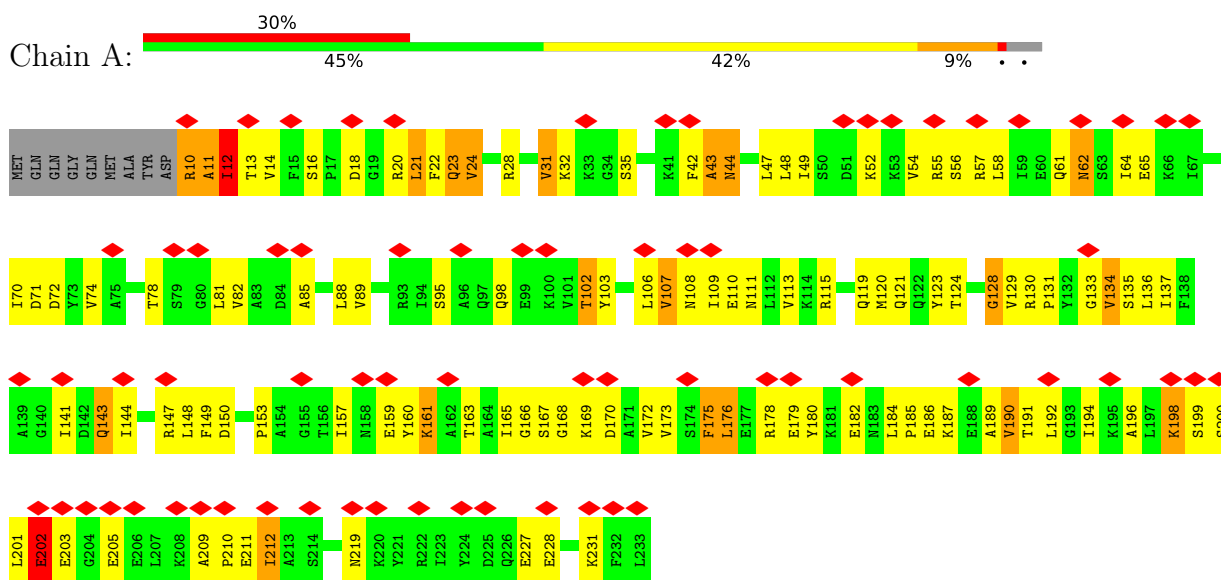
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	J	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	K	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	L	203	Total	C	N	O	S	0	0
			1558	985	264	298	11		
2	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		

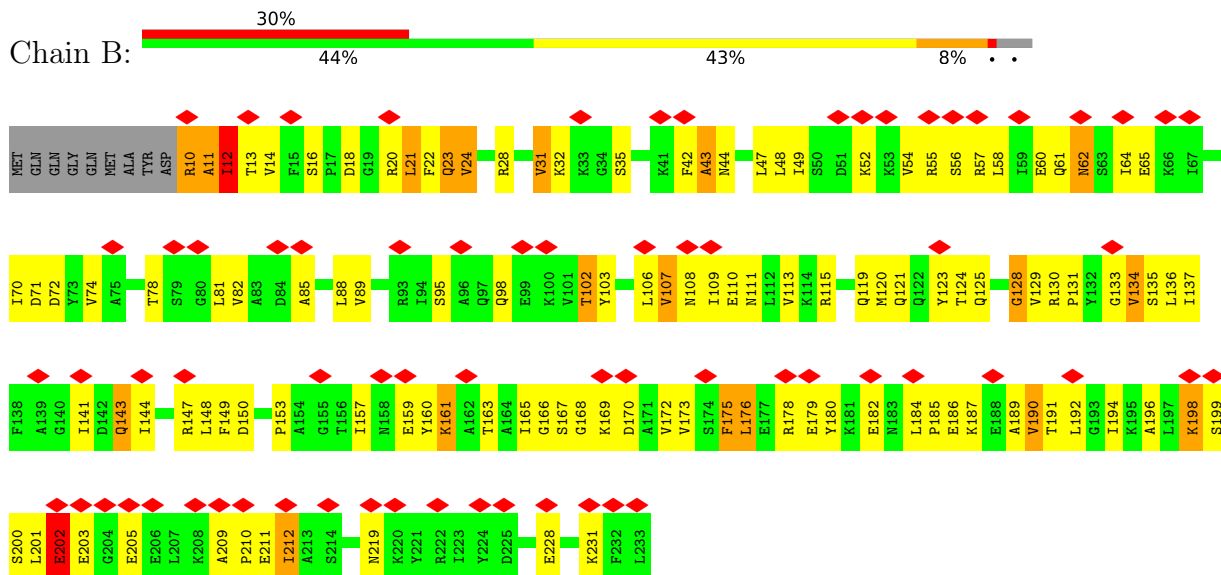
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

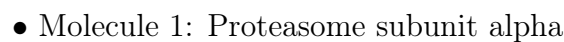
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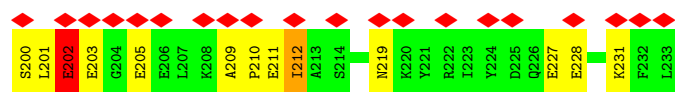


- Molecule 1: Proteasome subunit alpha

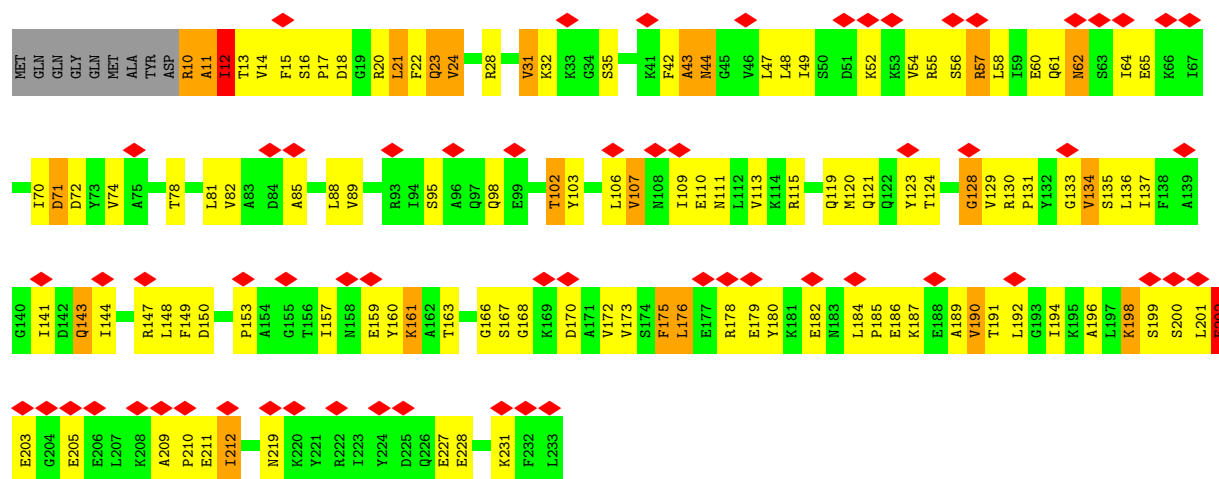
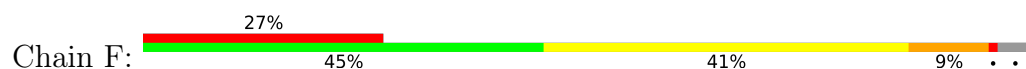


- Molecule 1: Proteasome subunit alpha

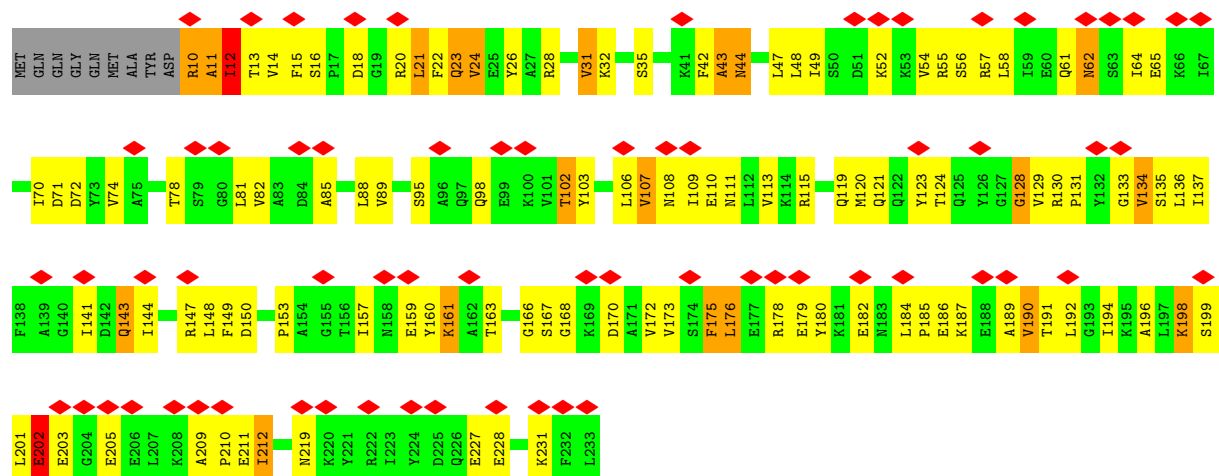
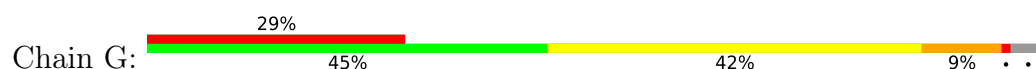




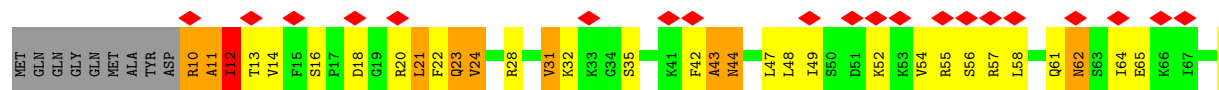
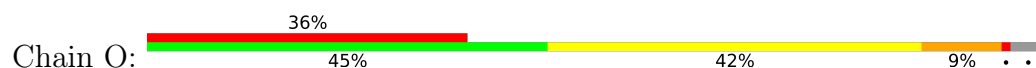
• Molecule 1: Proteasome subunit alpha

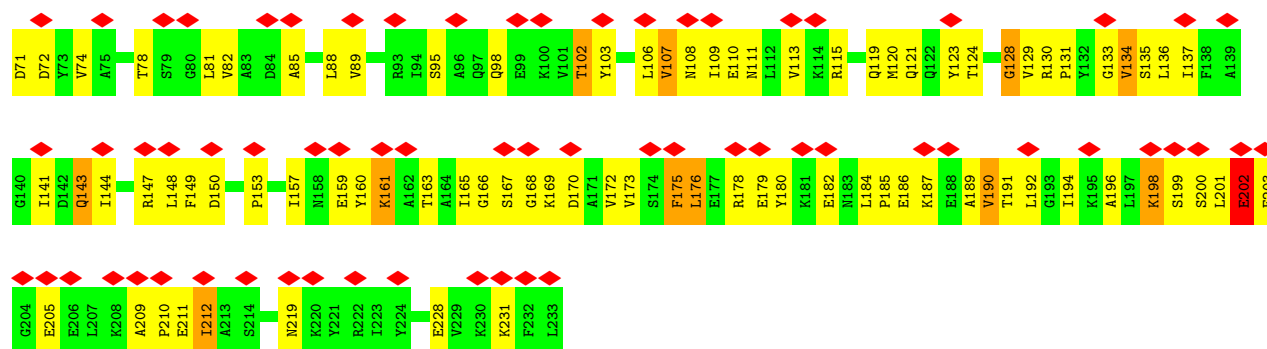


• Molecule 1: Proteasome subunit alpha

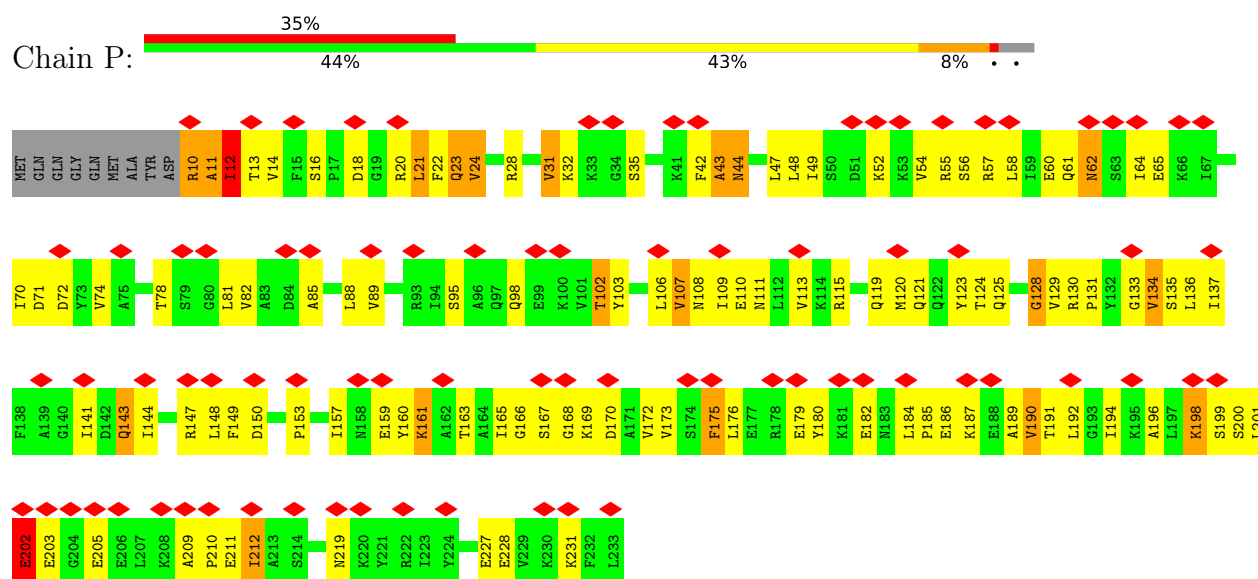


• Molecule 1: Proteasome subunit alpha

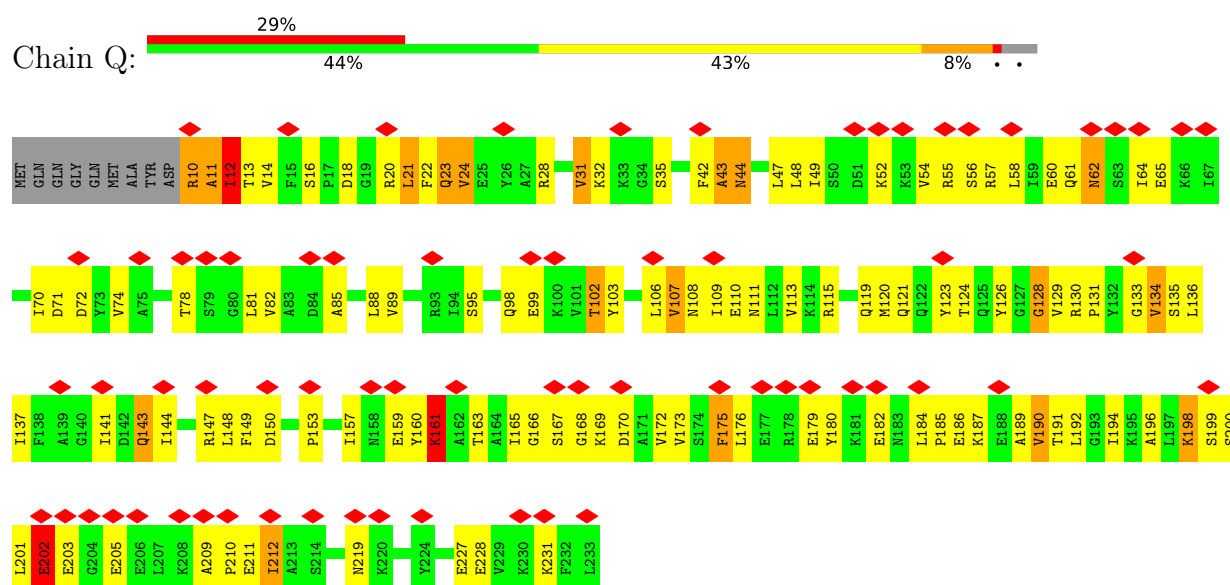




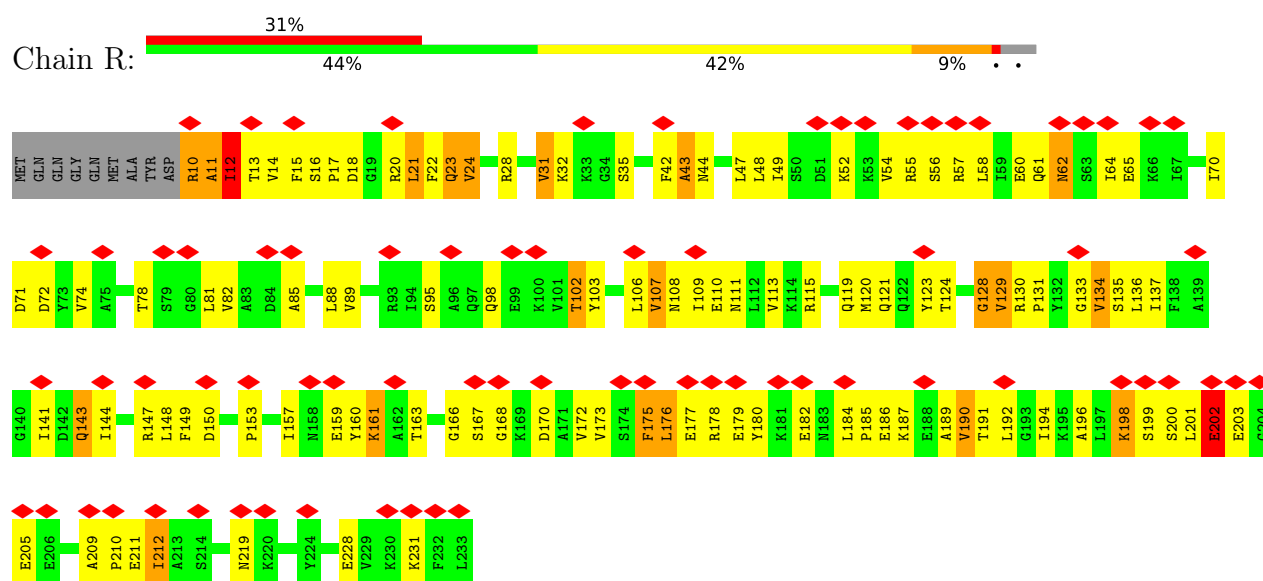
• Molecule 1: Proteasome subunit alpha



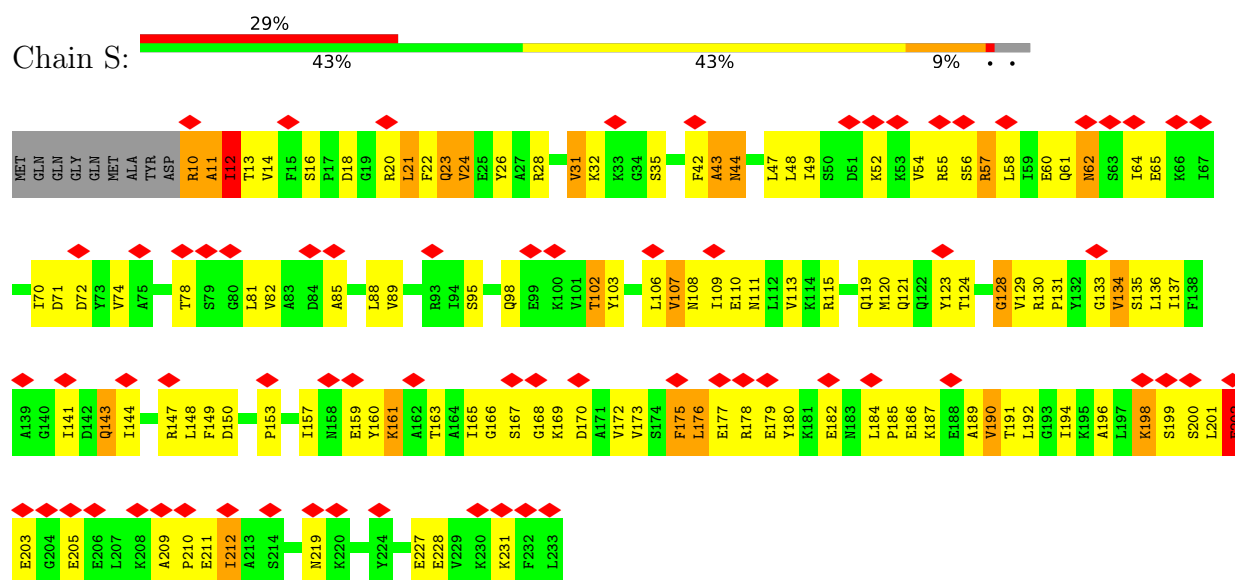
• Molecule 1: Proteasome subunit alpha



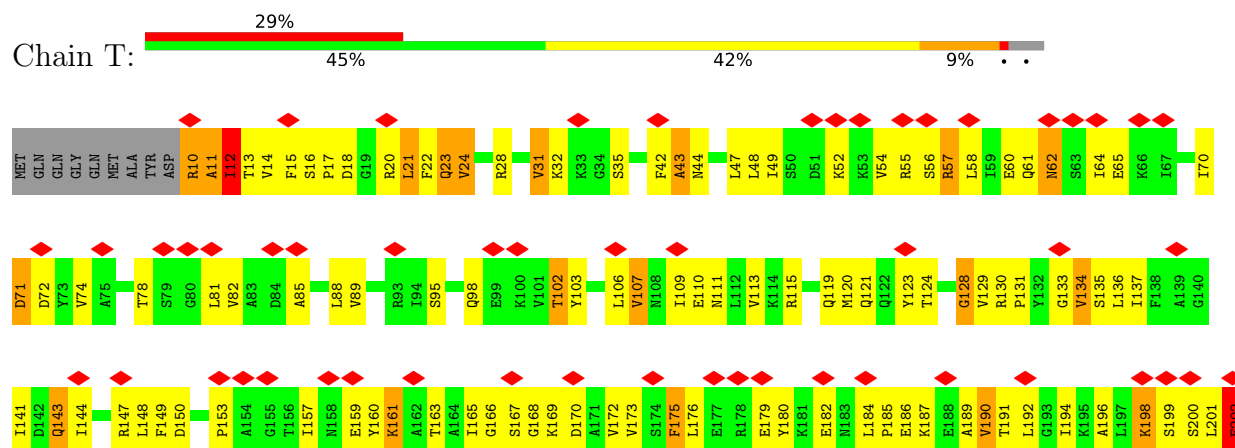
• Molecule 1: Proteasome subunit alpha



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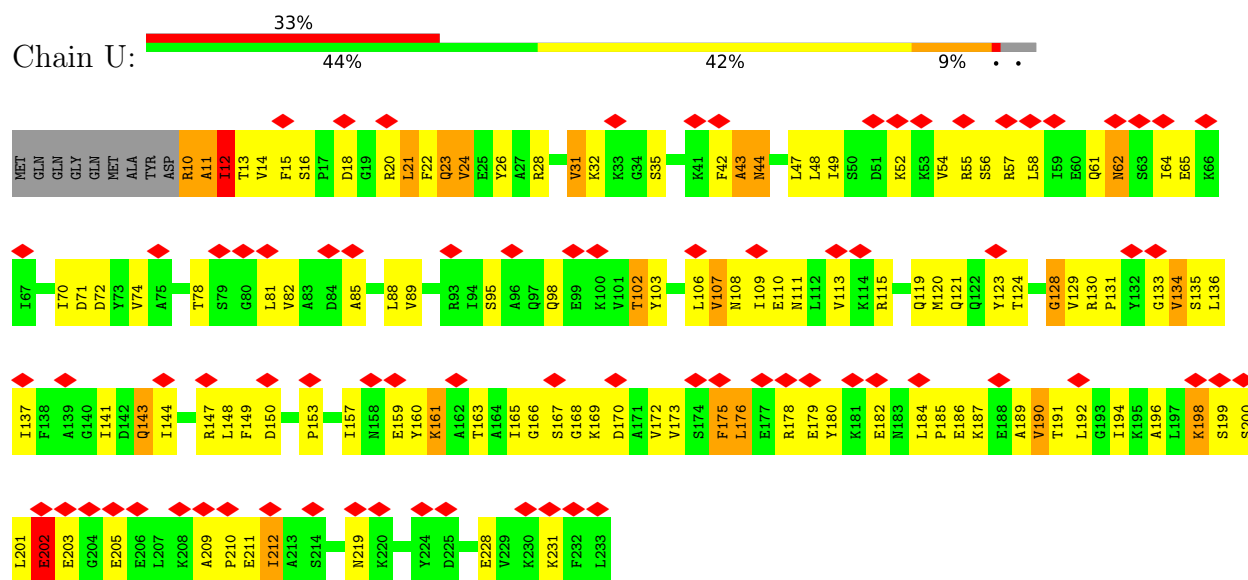


• Molecule 1: Proteasome subunit alpha

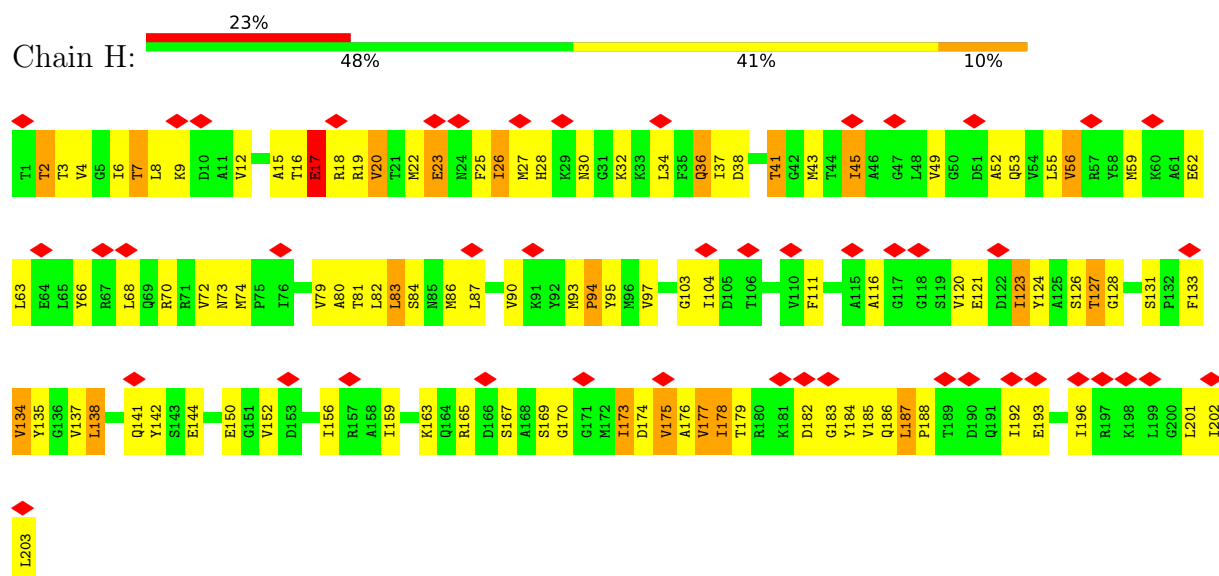




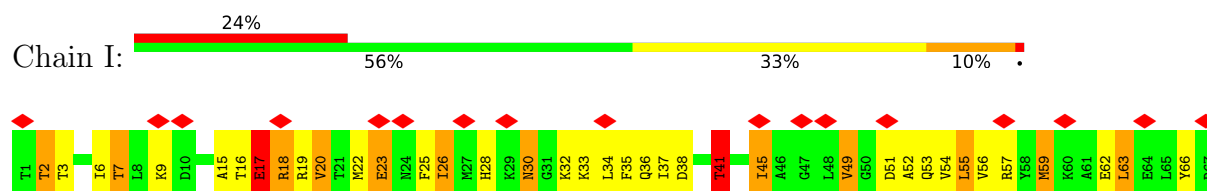
• Molecule 1: Proteasome subunit alpha

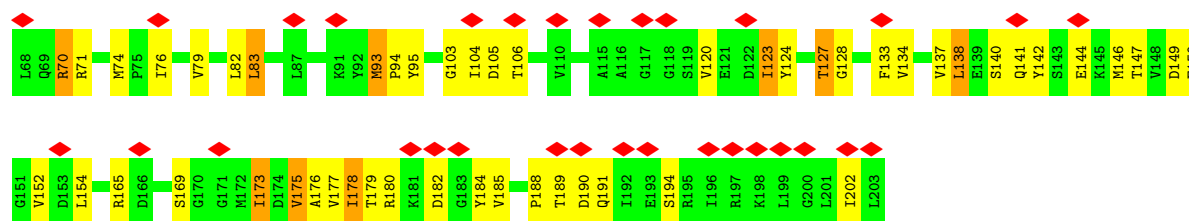


• Molecule 2: Proteasome subunit beta

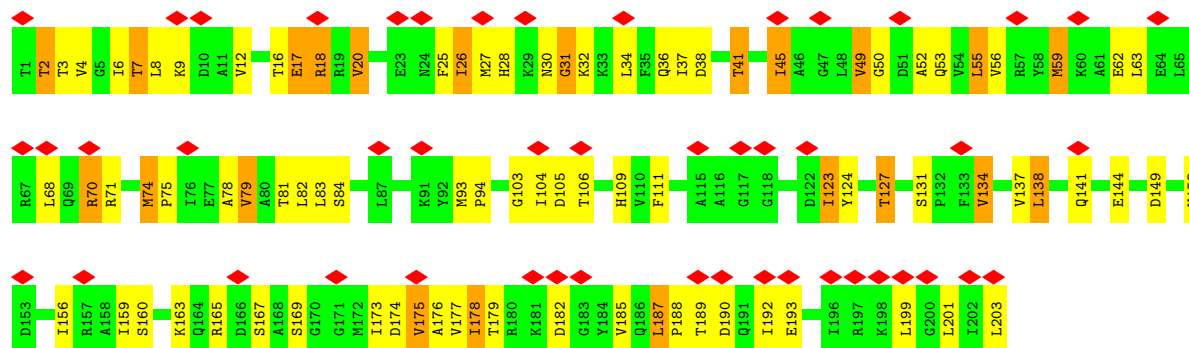


• Molecule 2: Proteasome subunit beta

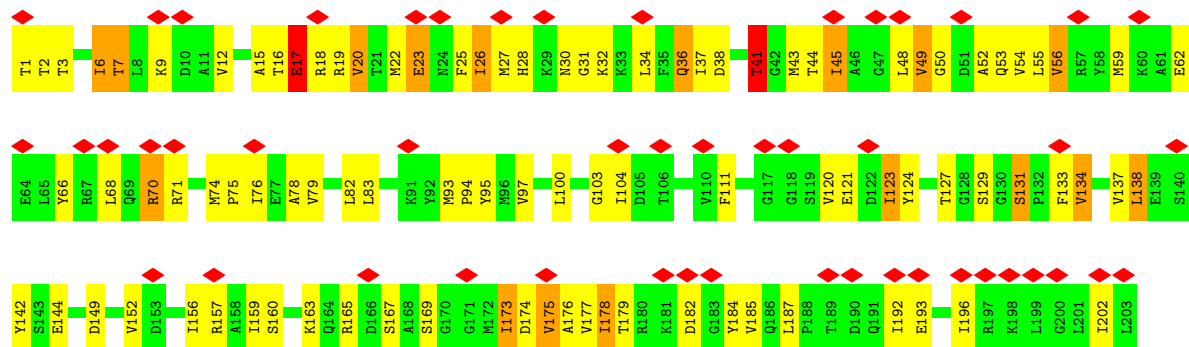




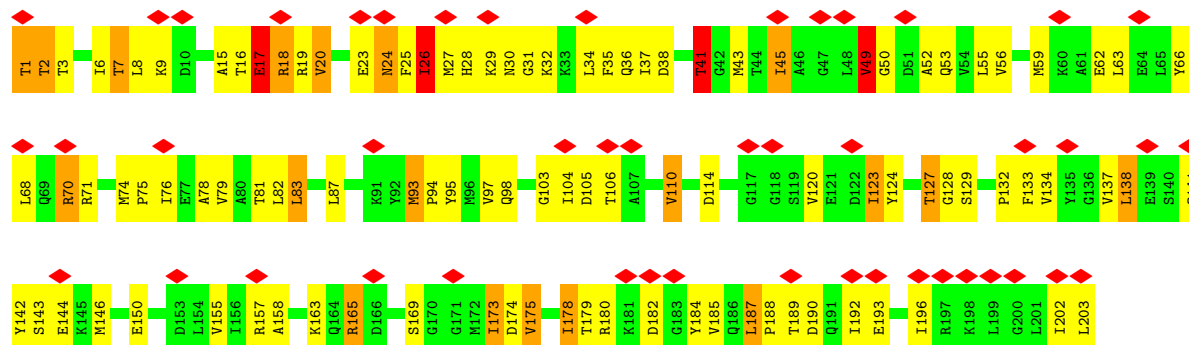
• Molecule 2: Proteasome subunit beta



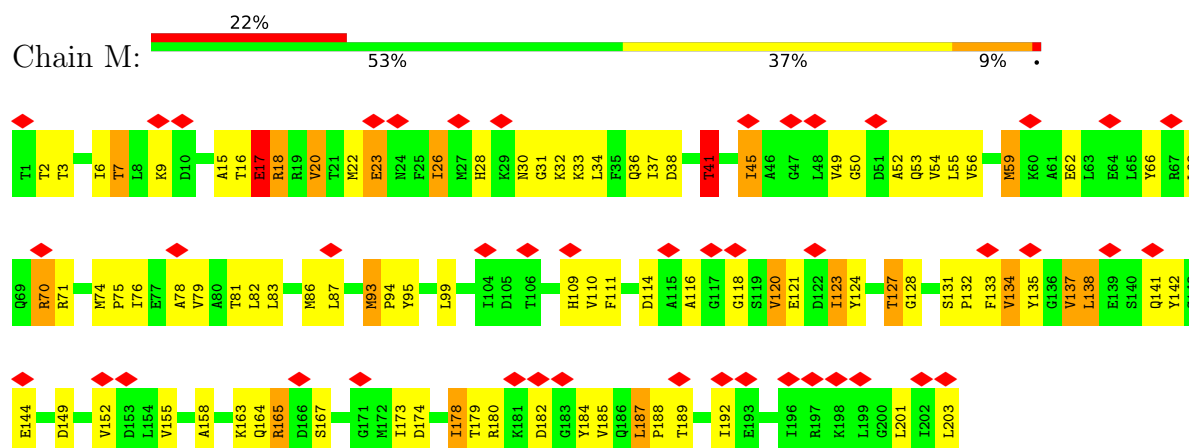
• Molecule 2: Proteasome subunit beta



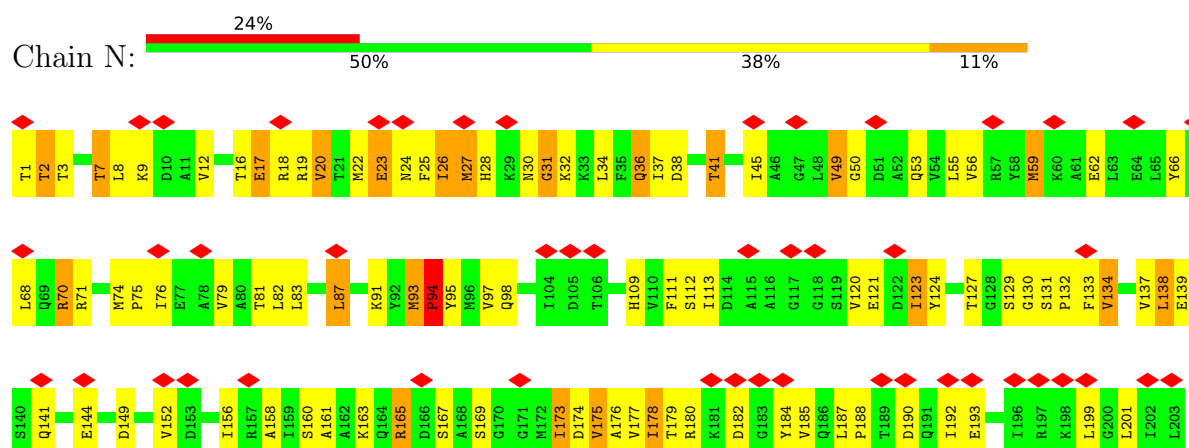
• Molecule 2: Proteasome subunit beta



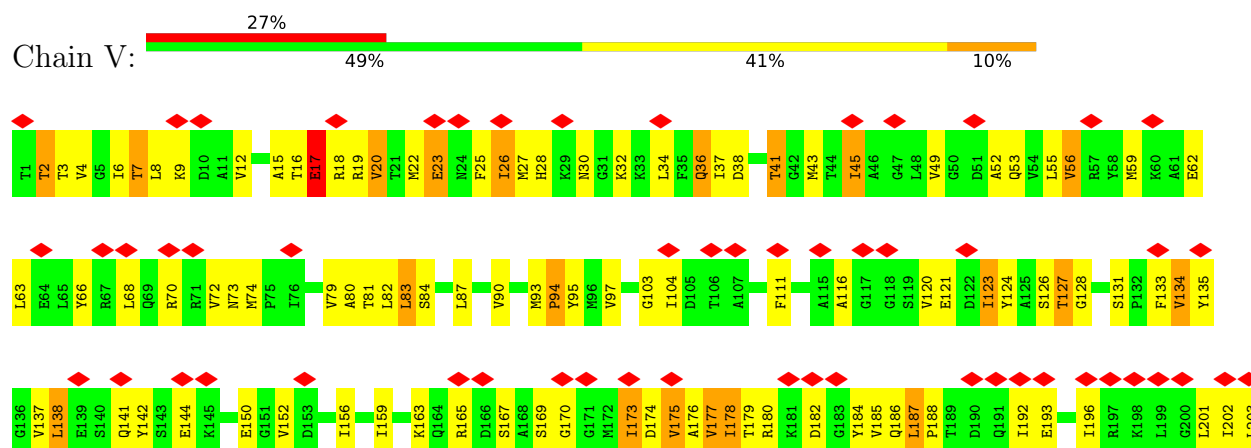
- Molecule 2: Proteasome subunit beta



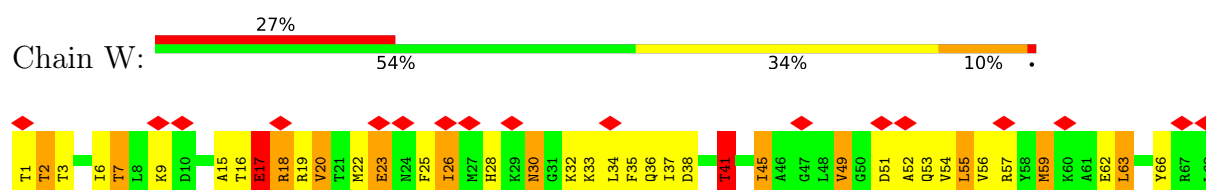
- Molecule 2: Proteasome subunit beta

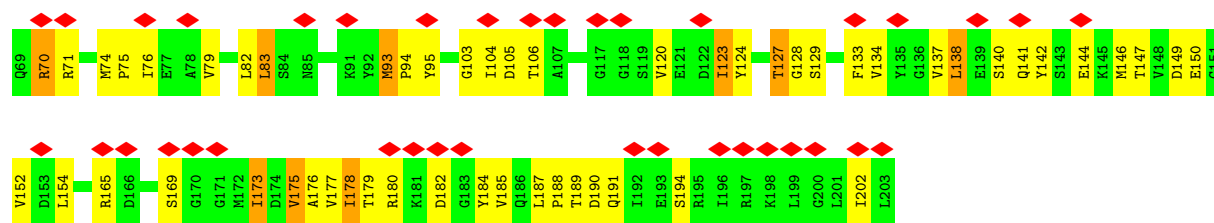


- Molecule 2: Proteasome subunit beta

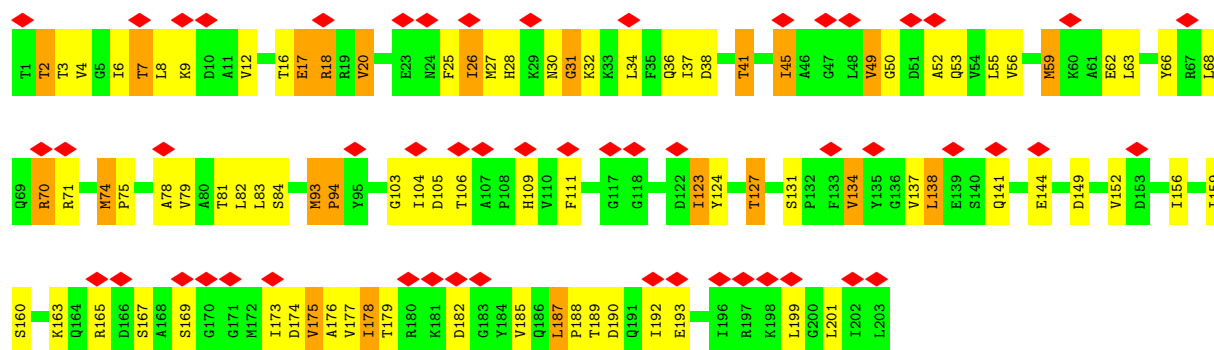


- Molecule 2: Proteasome subunit beta

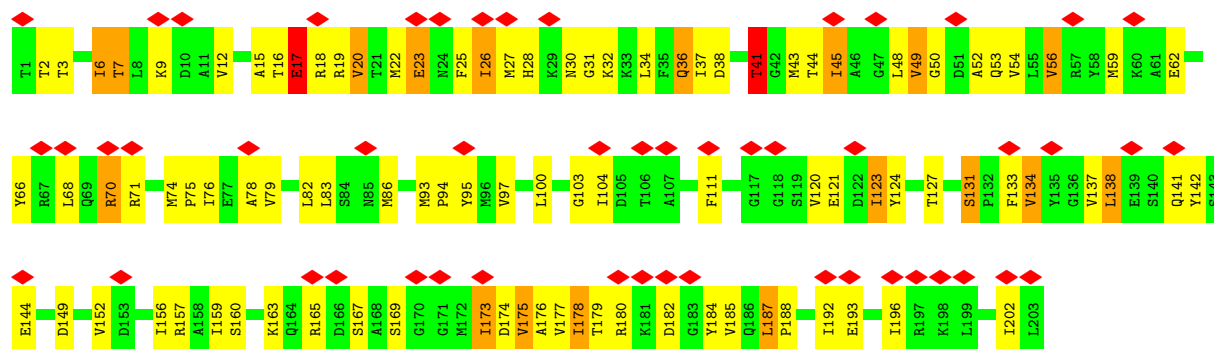




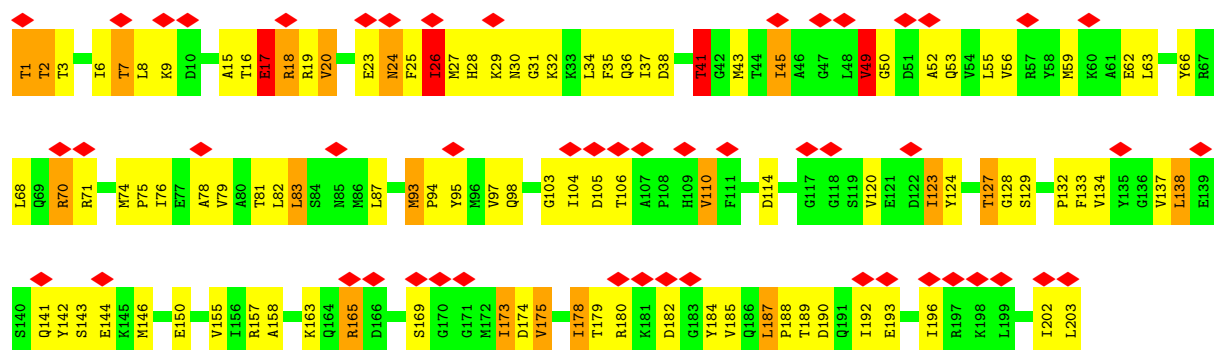
• Molecule 2: Proteasome subunit beta



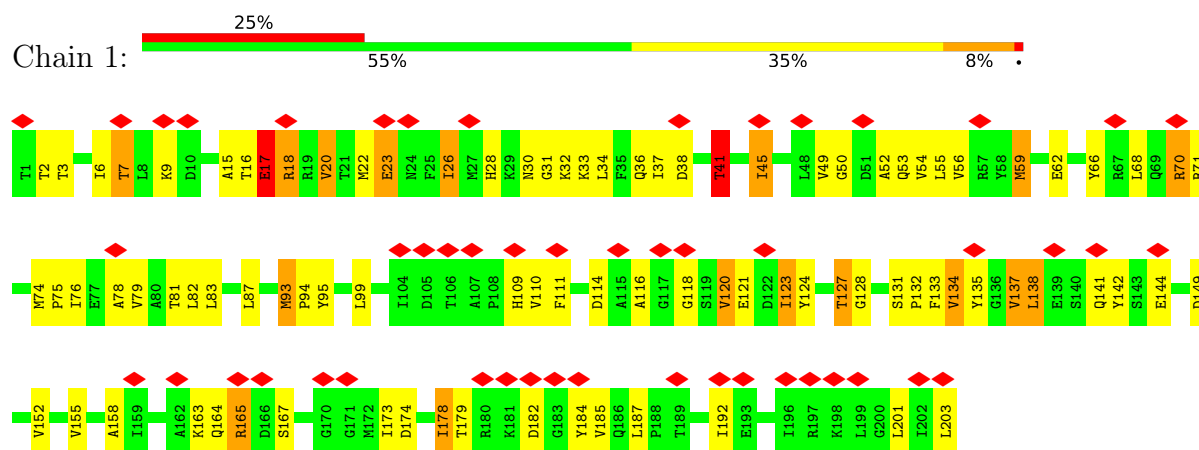
• Molecule 2: Proteasome subunit beta



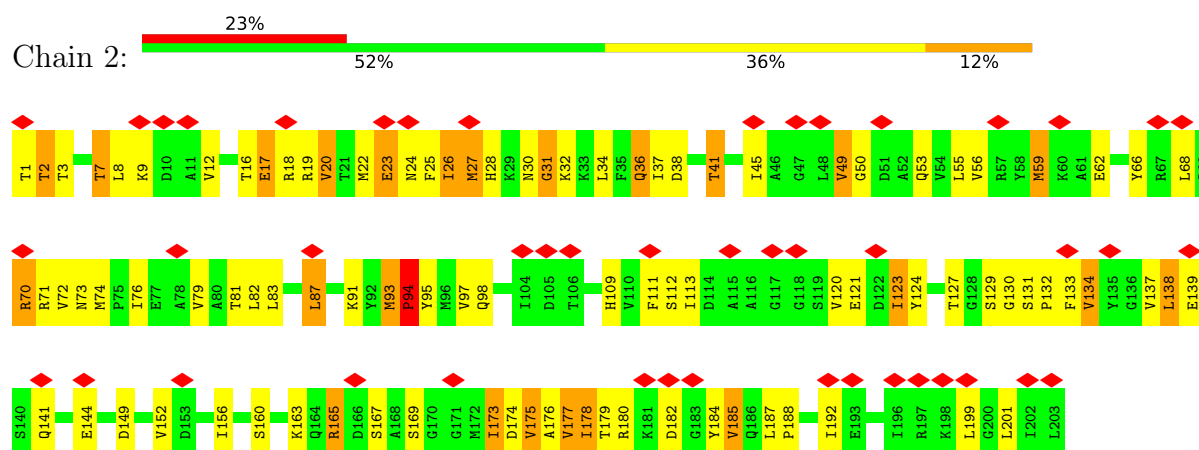
• Molecule 2: Proteasome subunit beta



● Molecule 2: Proteasome subunit beta



● Molecule 2: Proteasome subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D7	Depositor
Number of particles used	41546	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE AND AMPLITUDE	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	-1500.00	Depositor
Maximum defocus (nm)	-3500.00	Depositor
Magnification	51159	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	8.466	Depositor
Minimum map value	-4.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	197.028, 197.028, 197.028	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	1.36825, 1.36825, 1.36825	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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.67	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	B	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	C	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	D	0.67	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	E	0.67	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	F	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	G	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	O	0.67	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	P	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	Q	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	R	0.67	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	S	0.67	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	T	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
1	U	0.68	1/1767 (0.1%)	1.09	12/2380 (0.5%)
2	1	0.73	0/1577	1.11	12/2129 (0.6%)
2	2	0.72	0/1577	1.11	11/2129 (0.5%)
2	H	0.75	0/1577	1.12	11/2129 (0.5%)
2	I	0.72	1/1577 (0.1%)	1.14	12/2129 (0.6%)
2	J	0.71	0/1577	1.15	13/2129 (0.6%)
2	K	0.74	0/1577	1.13	11/2129 (0.5%)
2	L	0.75	1/1577 (0.1%)	1.14	15/2129 (0.7%)
2	M	0.73	0/1577	1.11	12/2129 (0.6%)
2	N	0.72	0/1577	1.11	11/2129 (0.5%)
2	V	0.75	0/1577	1.12	11/2129 (0.5%)
2	W	0.72	1/1577 (0.1%)	1.14	12/2129 (0.6%)
2	X	0.71	0/1577	1.14	13/2129 (0.6%)
2	Y	0.74	0/1577	1.13	11/2129 (0.5%)
2	Z	0.75	1/1577 (0.1%)	1.14	15/2129 (0.7%)
All	All	0.70	18/46816 (0.0%)	1.11	338/63126 (0.5%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Z	26	ILE	CA-CB	6.71	1.60	1.53
2	L	26	ILE	CA-CB	6.69	1.60	1.53
1	D	12	ILE	N-CA	6.03	1.53	1.46
1	Q	12	ILE	N-CA	6.02	1.53	1.46
1	R	12	ILE	N-CA	6.01	1.53	1.46
1	E	12	ILE	N-CA	6.01	1.53	1.46
1	A	12	ILE	N-CA	5.99	1.53	1.46
1	O	12	ILE	N-CA	5.98	1.53	1.46
1	S	12	ILE	N-CA	5.98	1.53	1.46
1	C	12	ILE	N-CA	5.98	1.53	1.46
1	F	12	ILE	N-CA	5.98	1.53	1.46
1	T	12	ILE	N-CA	5.97	1.53	1.46
1	B	12	ILE	N-CA	5.96	1.53	1.46
1	U	12	ILE	N-CA	5.94	1.53	1.46
1	G	12	ILE	N-CA	5.94	1.53	1.46
1	P	12	ILE	N-CA	5.93	1.53	1.46
2	I	93	MET	SD-CE	5.13	1.92	1.79
2	W	93	MET	SD-CE	5.10	1.92	1.79

All (338) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	12	ILE	CB-CA-C	-12.52	90.76	111.29
1	T	12	ILE	CB-CA-C	-12.50	90.79	111.29
1	G	12	ILE	CB-CA-C	-12.50	90.79	111.29
1	C	12	ILE	CB-CA-C	-12.50	90.79	111.29
1	U	12	ILE	CB-CA-C	-12.49	90.80	111.29
1	D	12	ILE	CB-CA-C	-12.49	90.81	111.29
1	F	12	ILE	CB-CA-C	-12.49	90.81	111.29
1	S	12	ILE	CB-CA-C	-12.49	90.81	111.29
1	A	12	ILE	CB-CA-C	-12.49	90.81	111.29
1	B	12	ILE	CB-CA-C	-12.48	90.82	111.29
1	P	12	ILE	CB-CA-C	-12.48	90.82	111.29
1	Q	12	ILE	CB-CA-C	-12.48	90.81	111.29
1	O	12	ILE	CB-CA-C	-12.47	90.83	111.29
1	E	12	ILE	CB-CA-C	-12.46	90.85	111.29
1	B	203	GLU	N-CA-C	-9.92	100.32	111.82
1	P	203	GLU	N-CA-C	-9.91	100.32	111.82
1	F	203	GLU	N-CA-C	-9.90	100.33	111.82
1	T	203	GLU	N-CA-C	-9.90	100.33	111.82
2	J	93	MET	CA-C-N	9.89	130.51	119.92
2	J	93	MET	C-N-CA	9.89	130.51	119.92
1	E	203	GLU	N-CA-C	-9.88	100.35	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	93	MET	CA-C-N	9.88	130.49	119.92
2	X	93	MET	C-N-CA	9.88	130.49	119.92
1	S	203	GLU	N-CA-C	-9.88	100.36	111.82
1	A	203	GLU	N-CA-C	-9.87	100.37	111.82
1	C	203	GLU	N-CA-C	-9.87	100.37	111.82
1	Q	203	GLU	N-CA-C	-9.87	100.37	111.82
1	G	203	GLU	N-CA-C	-9.87	100.38	111.82
1	O	203	GLU	N-CA-C	-9.86	100.38	111.82
1	U	203	GLU	N-CA-C	-9.85	100.39	111.82
1	D	203	GLU	N-CA-C	-9.84	100.41	111.82
1	R	203	GLU	N-CA-C	-9.84	100.41	111.82
2	I	93	MET	CA-C-N	9.68	130.28	119.92
2	I	93	MET	C-N-CA	9.68	130.28	119.92
2	W	93	MET	CA-C-N	9.65	130.24	119.92
2	W	93	MET	C-N-CA	9.65	130.24	119.92
2	1	18	ARG	N-CA-C	9.58	121.72	110.41
2	Z	18	ARG	N-CA-C	9.56	121.69	110.41
2	L	18	ARG	N-CA-C	9.55	121.68	110.41
2	M	18	ARG	N-CA-C	9.55	121.67	110.41
1	U	12	ILE	N-CA-C	9.34	128.77	109.34
1	S	12	ILE	N-CA-C	9.33	128.75	109.34
1	G	12	ILE	N-CA-C	9.33	128.75	109.34
1	A	12	ILE	N-CA-C	9.32	128.73	109.34
1	D	12	ILE	N-CA-C	9.32	128.73	109.34
1	E	12	ILE	N-CA-C	9.32	128.73	109.34
1	B	12	ILE	N-CA-C	9.31	128.71	109.34
1	C	12	ILE	N-CA-C	9.31	128.70	109.34
1	F	12	ILE	N-CA-C	9.31	128.70	109.34
1	O	12	ILE	N-CA-C	9.30	128.69	109.34
1	Q	12	ILE	N-CA-C	9.30	128.69	109.34
1	R	12	ILE	N-CA-C	9.30	128.69	109.34
1	T	12	ILE	N-CA-C	9.29	128.67	109.34
1	P	12	ILE	N-CA-C	9.29	128.66	109.34
2	X	18	ARG	N-CA-C	8.52	120.47	110.41
2	J	18	ARG	N-CA-C	8.50	120.44	110.41
1	B	161	LYS	N-CA-C	-8.47	103.07	113.41
1	O	161	LYS	N-CA-C	-8.46	103.09	113.41
1	U	161	LYS	N-CA-C	-8.45	103.10	113.41
1	P	161	LYS	N-CA-C	-8.45	103.10	113.41
1	A	161	LYS	N-CA-C	-8.45	103.11	113.41
1	T	11	ALA	CA-C-N	-8.45	106.77	121.97
1	T	11	ALA	C-N-CA	-8.45	106.77	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	11	ALA	CA-C-N	-8.44	106.77	121.97
1	E	11	ALA	C-N-CA	-8.44	106.77	121.97
1	C	11	ALA	CA-C-N	-8.44	106.79	121.97
1	C	11	ALA	C-N-CA	-8.44	106.79	121.97
1	C	161	LYS	N-CA-C	-8.44	103.12	113.41
1	F	161	LYS	N-CA-C	-8.44	103.12	113.41
1	T	161	LYS	N-CA-C	-8.44	103.12	113.41
1	D	161	LYS	N-CA-C	-8.43	103.12	113.41
1	S	161	LYS	N-CA-C	-8.43	103.12	113.41
1	E	161	LYS	N-CA-C	-8.43	103.12	113.41
1	G	161	LYS	N-CA-C	-8.43	103.12	113.41
1	Q	11	ALA	CA-C-N	-8.43	106.79	121.97
1	Q	11	ALA	C-N-CA	-8.43	106.79	121.97
1	Q	161	LYS	N-CA-C	-8.43	103.12	113.41
1	F	11	ALA	CA-C-N	-8.43	106.80	121.97
1	F	11	ALA	C-N-CA	-8.43	106.80	121.97
1	P	11	ALA	CA-C-N	-8.42	106.81	121.97
1	P	11	ALA	C-N-CA	-8.42	106.81	121.97
1	R	11	ALA	CA-C-N	-8.42	106.81	121.97
1	R	11	ALA	C-N-CA	-8.42	106.81	121.97
1	S	11	ALA	CA-C-N	-8.42	106.81	121.97
1	S	11	ALA	C-N-CA	-8.42	106.81	121.97
1	B	11	ALA	CA-C-N	-8.42	106.81	121.97
1	B	11	ALA	C-N-CA	-8.42	106.81	121.97
1	A	11	ALA	CA-C-N	-8.42	106.81	121.97
1	A	11	ALA	C-N-CA	-8.42	106.81	121.97
1	O	11	ALA	CA-C-N	-8.42	106.82	121.97
1	O	11	ALA	C-N-CA	-8.42	106.82	121.97
1	R	161	LYS	N-CA-C	-8.41	103.15	113.41
1	G	11	ALA	CA-C-N	-8.41	106.83	121.97
1	G	11	ALA	C-N-CA	-8.41	106.83	121.97
1	D	11	ALA	CA-C-N	-8.41	106.84	121.97
1	D	11	ALA	C-N-CA	-8.41	106.84	121.97
1	U	11	ALA	CA-C-N	-8.39	106.87	121.97
1	U	11	ALA	C-N-CA	-8.39	106.87	121.97
2	K	95	TYR	N-CA-C	-8.25	95.13	108.41
2	Y	95	TYR	N-CA-C	-8.24	95.14	108.41
2	N	93	MET	CA-C-N	8.03	128.52	119.92
2	N	93	MET	C-N-CA	8.03	128.52	119.92
2	2	93	MET	CA-C-N	8.03	128.51	119.92
2	2	93	MET	C-N-CA	8.03	128.51	119.92
2	H	93	MET	CA-C-N	8.03	128.51	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	93	MET	C-N-CA	8.03	128.51	119.92
2	I	18	ARG	N-CA-C	8.01	119.86	110.41
2	V	93	MET	CA-C-N	8.00	128.48	119.92
2	V	93	MET	C-N-CA	8.00	128.48	119.92
1	S	13	THR	N-CA-CB	7.98	126.11	111.11
2	W	18	ARG	N-CA-C	7.97	119.82	110.41
1	E	13	THR	N-CA-CB	7.97	126.10	111.11
1	R	13	THR	N-CA-CB	7.96	126.08	111.11
1	U	13	THR	N-CA-CB	7.96	126.08	111.11
1	T	13	THR	N-CA-CB	7.96	126.07	111.11
1	D	13	THR	N-CA-CB	7.96	126.07	111.11
1	O	13	THR	N-CA-CB	7.95	126.06	111.11
1	B	13	THR	N-CA-CB	7.95	126.06	111.11
1	A	13	THR	N-CA-CB	7.95	126.06	111.11
1	G	13	THR	N-CA-CB	7.95	126.06	111.11
1	C	13	THR	N-CA-CB	7.95	126.05	111.11
1	P	13	THR	N-CA-CB	7.94	126.04	111.11
1	Q	13	THR	N-CA-CB	7.94	126.04	111.11
1	F	13	THR	N-CA-CB	7.93	126.03	111.11
2	M	31	GLY	N-CA-C	-7.79	101.90	112.57
2	1	31	GLY	N-CA-C	-7.78	101.91	112.57
2	J	31	GLY	N-CA-C	-7.50	100.73	112.58
2	1	93	MET	CA-C-N	7.44	129.14	119.84
2	1	93	MET	C-N-CA	7.44	129.14	119.84
2	M	93	MET	CA-C-N	7.43	129.13	119.84
2	M	93	MET	C-N-CA	7.43	129.13	119.84
2	X	36	GLN	N-CA-C	-7.27	99.72	110.48
2	J	36	GLN	N-CA-C	-7.25	99.74	110.48
2	K	36	GLN	N-CA-C	-7.18	98.86	110.20
2	Y	36	GLN	N-CA-C	-7.17	98.87	110.20
2	J	17	GLU	N-CA-C	-7.01	99.36	109.31
2	X	17	GLU	N-CA-C	-7.00	99.36	109.31
2	L	17	GLU	N-CA-C	-7.00	98.96	109.94
2	N	17	GLU	N-CA-C	-6.99	99.38	109.31
2	2	17	GLU	N-CA-C	-6.99	99.39	109.31
2	Z	17	GLU	N-CA-C	-6.97	98.99	109.94
2	Y	17	GLU	N-CA-C	-6.93	99.47	109.31
2	L	93	MET	CA-C-N	6.91	128.48	119.84
2	L	93	MET	C-N-CA	6.91	128.48	119.84
2	Z	93	MET	CA-C-N	6.91	128.48	119.84
2	Z	93	MET	C-N-CA	6.91	128.48	119.84
2	X	31	GLY	N-CA-C	-6.91	100.70	112.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	17	GLU	N-CA-C	-6.91	99.50	109.31
2	1	95	TYR	N-CA-C	-6.87	97.35	108.41
2	M	95	TYR	N-CA-C	-6.85	97.39	108.41
2	V	36	GLN	N-CA-C	-6.80	99.46	110.20
2	H	36	GLN	N-CA-C	-6.79	99.47	110.20
2	N	36	GLN	N-CA-C	-6.79	99.47	110.20
2	2	36	GLN	N-CA-C	-6.78	99.49	110.20
2	1	17	GLU	N-CA-C	-6.68	99.45	109.94
2	M	17	GLU	N-CA-C	-6.67	99.47	109.94
2	X	94	PRO	N-CA-C	6.63	121.62	111.34
2	J	94	PRO	N-CA-C	6.61	121.59	111.34
1	F	57	ARG	N-CA-C	-6.57	104.75	112.89
1	G	57	ARG	N-CA-C	-6.57	104.75	112.89
1	C	57	ARG	N-CA-C	-6.56	104.75	112.89
1	S	57	ARG	N-CA-C	-6.56	104.76	112.89
1	A	57	ARG	N-CA-C	-6.55	104.77	112.89
1	T	57	ARG	N-CA-C	-6.55	104.77	112.89
1	U	57	ARG	N-CA-C	-6.55	104.77	112.89
1	R	57	ARG	N-CA-C	-6.54	104.78	112.89
1	B	57	ARG	N-CA-C	-6.54	104.78	112.89
2	K	93	MET	CA-C-N	6.54	128.02	119.84
2	K	93	MET	C-N-CA	6.54	128.02	119.84
1	Q	57	ARG	N-CA-C	-6.54	104.78	112.89
1	D	57	ARG	N-CA-C	-6.54	104.78	112.89
1	P	57	ARG	N-CA-C	-6.54	104.78	112.89
1	O	57	ARG	N-CA-C	-6.53	104.79	112.89
2	Y	93	MET	CA-C-N	6.53	128.00	119.84
2	Y	93	MET	C-N-CA	6.53	128.00	119.84
1	E	57	ARG	N-CA-C	-6.53	104.80	112.89
2	V	80	ALA	N-CA-C	-6.53	103.86	110.97
2	L	187	LEU	CA-C-N	6.53	126.88	119.83
2	L	187	LEU	C-N-CA	6.53	126.88	119.83
2	H	80	ALA	N-CA-C	-6.51	103.87	110.97
2	Z	187	LEU	CA-C-N	6.51	126.86	119.83
2	Z	187	LEU	C-N-CA	6.51	126.86	119.83
2	I	128	GLY	N-CA-C	6.41	118.58	112.04
2	W	128	GLY	N-CA-C	6.39	118.56	112.04
2	1	36	GLN	N-CA-C	-6.39	101.02	110.48
2	M	36	GLN	N-CA-C	-6.39	101.02	110.48
2	H	128	GLY	N-CA-C	6.32	118.49	112.04
2	W	95	TYR	N-CA-C	-6.32	98.87	108.67
2	I	95	TYR	N-CA-C	-6.32	98.88	108.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	128	GLY	N-CA-C	6.30	118.46	112.04
2	L	128	GLY	N-CA-C	6.06	119.46	111.70
2	Z	128	GLY	N-CA-C	6.04	119.43	111.70
2	2	94	PRO	N-CA-C	6.00	120.64	111.34
2	I	30	ASN	N-CA-C	5.99	116.99	108.54
2	N	94	PRO	N-CA-C	5.99	120.62	111.34
2	W	30	ASN	N-CA-C	5.98	116.97	108.54
1	T	10	ARG	CD-NE-CZ	5.93	132.70	124.40
1	C	10	ARG	CD-NE-CZ	5.92	132.69	124.40
1	F	10	ARG	CD-NE-CZ	5.91	132.67	124.40
1	G	10	ARG	CD-NE-CZ	5.90	132.66	124.40
1	B	10	ARG	CD-NE-CZ	5.90	132.66	124.40
1	U	10	ARG	CD-NE-CZ	5.90	132.66	124.40
1	A	10	ARG	CD-NE-CZ	5.89	132.65	124.40
1	Q	10	ARG	CD-NE-CZ	5.89	132.65	124.40
1	P	10	ARG	CD-NE-CZ	5.89	132.65	124.40
1	S	10	ARG	CD-NE-CZ	5.89	132.65	124.40
2	M	118	GLY	N-CA-C	-5.88	100.80	111.15
1	O	10	ARG	CD-NE-CZ	5.88	132.63	124.40
1	D	10	ARG	CD-NE-CZ	5.88	132.63	124.40
1	R	10	ARG	CD-NE-CZ	5.88	132.63	124.40
1	E	10	ARG	CD-NE-CZ	5.87	132.62	124.40
2	1	118	GLY	N-CA-C	-5.86	100.83	111.15
2	L	95	TYR	N-CA-C	-5.85	98.20	108.20
2	V	150	GLU	N-CA-C	-5.85	104.90	111.28
2	X	187	LEU	CA-C-N	5.85	126.04	119.90
2	X	187	LEU	C-N-CA	5.85	126.04	119.90
2	Z	95	TYR	N-CA-C	-5.84	98.21	108.20
2	H	150	GLU	N-CA-C	-5.82	104.94	111.28
2	J	187	LEU	CA-C-N	5.82	126.01	119.90
2	J	187	LEU	C-N-CA	5.82	126.01	119.90
2	M	187	LEU	CA-C-N	5.81	126.72	119.98
2	M	187	LEU	C-N-CA	5.81	126.72	119.98
2	W	17	GLU	N-CA-C	-5.81	100.97	109.63
2	H	95	TYR	N-CA-C	-5.81	97.77	107.99
2	1	187	LEU	CA-C-N	5.81	126.72	119.98
2	1	187	LEU	C-N-CA	5.81	126.72	119.98
2	V	95	TYR	N-CA-C	-5.80	97.78	107.99
2	I	17	GLU	N-CA-C	-5.80	100.99	109.63
2	Y	131	SER	N-CA-C	5.79	120.78	113.25
2	J	4	VAL	N-CA-C	5.78	116.19	108.27
2	K	131	SER	N-CA-C	5.76	120.74	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	4	VAL	N-CA-C	5.75	116.15	108.27
2	2	27	MET	N-CA-C	5.75	120.43	112.90
2	X	74	MET	CA-C-N	5.74	125.69	119.78
2	X	74	MET	C-N-CA	5.74	125.69	119.78
2	N	27	MET	N-CA-C	5.74	120.42	112.90
2	J	74	MET	CA-C-N	5.74	125.69	119.78
2	J	74	MET	C-N-CA	5.74	125.69	119.78
2	K	187	LEU	CA-C-N	5.73	125.91	119.90
2	K	187	LEU	C-N-CA	5.73	125.91	119.90
2	Y	187	LEU	CA-C-N	5.72	125.91	119.90
2	Y	187	LEU	C-N-CA	5.72	125.91	119.90
2	N	31	GLY	N-CA-C	-5.65	103.65	112.58
2	2	31	GLY	N-CA-C	-5.65	103.66	112.58
2	W	202	ILE	N-CA-C	5.64	116.49	108.42
2	I	202	ILE	N-CA-C	5.64	116.48	108.42
1	R	219	ASN	N-CA-C	5.60	116.47	108.74
1	C	219	ASN	N-CA-C	5.59	116.45	108.74
1	A	219	ASN	N-CA-C	5.58	116.44	108.74
1	O	219	ASN	N-CA-C	5.58	116.44	108.74
1	E	219	ASN	N-CA-C	5.58	116.44	108.74
1	Q	219	ASN	N-CA-C	5.58	116.43	108.74
1	S	219	ASN	N-CA-C	5.57	116.43	108.74
1	P	179	GLU	N-CA-C	5.57	119.17	112.93
1	D	219	ASN	N-CA-C	5.56	116.42	108.74
1	P	219	ASN	N-CA-C	5.56	116.41	108.74
1	F	219	ASN	N-CA-C	5.56	116.41	108.74
1	G	219	ASN	N-CA-C	5.55	116.41	108.74
1	T	219	ASN	N-CA-C	5.55	116.40	108.74
1	B	179	GLU	N-CA-C	5.55	119.15	112.93
1	F	179	GLU	N-CA-C	5.55	119.14	112.93
1	U	219	ASN	N-CA-C	5.55	116.40	108.74
1	D	179	GLU	N-CA-C	5.55	119.14	112.93
2	W	36	GLN	N-CA-C	-5.54	101.44	110.20
1	B	219	ASN	N-CA-C	5.54	116.38	108.74
1	O	179	GLU	N-CA-C	5.54	119.13	112.93
1	T	179	GLU	N-CA-C	5.54	119.13	112.93
1	G	179	GLU	N-CA-C	5.53	119.12	112.93
2	Z	26	ILE	CB-CA-C	5.53	117.66	111.80
2	I	36	GLN	N-CA-C	-5.52	101.47	110.20
1	S	179	GLU	N-CA-C	5.52	119.11	112.93
1	E	179	GLU	N-CA-C	5.52	119.11	112.93
1	A	179	GLU	N-CA-C	5.52	119.11	112.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	179	GLU	N-CA-C	5.51	119.10	112.93
1	U	179	GLU	N-CA-C	5.51	119.10	112.93
1	C	179	GLU	N-CA-C	5.50	119.09	112.93
2	L	26	ILE	CB-CA-C	5.50	117.64	111.80
2	K	41	THR	N-CA-C	5.49	117.43	108.76
2	L	202	ILE	N-CA-C	5.49	117.70	108.81
2	Y	41	THR	N-CA-C	5.48	117.42	108.76
2	K	31	GLY	N-CA-C	-5.48	104.22	112.60
2	Y	31	GLY	N-CA-C	-5.47	104.23	112.60
2	Z	202	ILE	N-CA-C	5.47	117.67	108.81
2	2	95	TYR	N-CA-C	-5.46	100.20	108.67
2	N	95	TYR	N-CA-C	-5.46	100.21	108.67
1	Q	179	GLU	N-CA-C	5.46	119.04	112.93
2	V	94	PRO	N-CA-C	5.42	119.75	111.34
2	N	49	VAL	N-CA-C	5.41	115.86	110.23
2	H	94	PRO	N-CA-C	5.41	119.72	111.34
2	Z	27	MET	N-CA-C	5.39	118.32	111.69
2	2	49	VAL	N-CA-C	5.39	115.83	110.23
2	W	41	THR	N-CA-C	5.38	117.26	108.76
2	I	41	THR	N-CA-C	5.38	117.26	108.76
1	R	128	GLY	N-CA-C	5.37	125.91	113.18
1	U	128	GLY	N-CA-C	5.37	125.91	113.18
1	P	128	GLY	N-CA-C	5.37	125.91	113.18
1	D	128	GLY	N-CA-C	5.36	125.89	113.18
1	E	128	GLY	N-CA-C	5.36	125.89	113.18
1	G	128	GLY	N-CA-C	5.36	125.88	113.18
2	L	27	MET	N-CA-C	5.36	118.28	111.69
1	Q	128	GLY	N-CA-C	5.36	125.88	113.18
1	A	128	GLY	N-CA-C	5.36	125.87	113.18
1	B	128	GLY	N-CA-C	5.36	125.87	113.18
1	C	128	GLY	N-CA-C	5.35	125.87	113.18
1	S	128	GLY	N-CA-C	5.35	125.86	113.18
1	F	128	GLY	N-CA-C	5.35	125.85	113.18
1	O	128	GLY	N-CA-C	5.34	125.85	113.18
2	L	41	THR	N-CA-C	5.33	117.37	108.99
1	T	128	GLY	N-CA-C	5.33	125.83	113.18
2	H	187	LEU	CA-C-N	5.33	125.09	119.76
2	H	187	LEU	C-N-CA	5.33	125.09	119.76
2	Z	41	THR	N-CA-C	5.32	117.35	108.99
2	V	187	LEU	CA-C-N	5.30	125.06	119.76
2	V	187	LEU	C-N-CA	5.30	125.06	119.76
2	J	27	MET	N-CA-C	5.29	118.89	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	17	GLU	N-CA-C	-5.28	99.55	110.80
2	X	27	MET	N-CA-C	5.28	118.89	112.23
2	H	17	GLU	N-CA-C	-5.28	99.55	110.80
2	N	24	ASN	N-CA-C	-5.23	107.06	113.50
2	M	128	GLY	N-CA-C	5.22	118.38	111.70
2	2	24	ASN	N-CA-C	-5.21	107.10	113.50
2	K	202	ILE	N-CA-C	5.19	117.21	108.81
2	1	128	GLY	N-CA-C	5.18	118.33	111.70
2	Y	202	ILE	N-CA-C	5.18	117.20	108.81
2	Z	24	ASN	N-CA-C	-5.17	107.35	113.97
2	L	24	ASN	N-CA-C	-5.17	107.35	113.97
2	Z	150	GLU	N-CA-C	-5.13	105.68	111.28
2	L	150	GLU	N-CA-C	-5.12	105.70	111.28
2	L	36	GLN	N-CA-C	-5.11	102.13	110.20
2	M	41	THR	N-CA-C	5.10	116.81	108.55
2	Z	36	GLN	N-CA-C	-5.10	102.15	110.20
2	1	41	THR	N-CA-C	5.07	116.77	108.55
2	W	140	SER	N-CA-C	5.04	117.89	111.69
2	2	87	LEU	N-CA-C	5.04	116.77	111.28
2	N	87	LEU	N-CA-C	5.02	116.75	111.28
2	I	140	SER	N-CA-C	5.01	117.86	111.69
2	W	49	VAL	N-CA-C	5.00	115.61	110.36
2	I	49	VAL	N-CA-C	5.00	115.61	110.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1744	0	1781	97	0
1	B	1744	0	1781	94	0
1	C	1744	0	1781	93	0
1	D	1744	0	1781	96	0
1	E	1744	0	1781	103	0
1	F	1744	0	1781	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1744	0	1781	98	0
1	O	1744	0	1781	93	0
1	P	1744	0	1781	94	0
1	Q	1744	0	1781	95	0
1	R	1744	0	1781	98	0
1	S	1744	0	1781	104	0
1	T	1744	0	1781	95	0
1	U	1744	0	1781	96	0
2	1	1558	0	1609	83	0
2	2	1558	0	1609	79	0
2	H	1558	0	1609	82	0
2	I	1558	0	1609	68	0
2	J	1558	0	1609	72	0
2	K	1558	0	1609	71	0
2	L	1558	0	1609	88	0
2	M	1558	0	1609	87	0
2	N	1558	0	1609	81	0
2	V	1558	0	1609	83	0
2	W	1558	0	1609	71	0
2	X	1558	0	1609	62	0
2	Y	1558	0	1609	75	0
2	Z	1558	0	1609	87	0
All	All	46228	0	47460	2208	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 24.

All (2208) 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:B:12:ILE:HG21	1:B:14:VAL:CG2	1.50	1.38
1:Q:12:ILE:HG21	1:Q:14:VAL:CG2	1.50	1.38
1:R:12:ILE:HG21	1:R: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:T:12:ILE:CG2	1:T:14:VAL:HG22	1.63	1.29
1:U:12:ILE:CG2	1:U: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:A:12:ILE:CG2	1:A:14:VAL:HG22	1.63	1.27
1:F:12:ILE:CG2	1:F: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:G:12:ILE:CG2	1:G:14:VAL:HG22	1.63	1.27
1:Q:12:ILE:CG2	1:Q: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
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:E:107:VAL:HG11	2:M:66:TYR:OH	1.60	1.00
1:U:107:VAL:HG11	2:V:66:TYR:OH	1.58	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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: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
1:A:12:ILE:HG21	1:A:14:VAL:HG22	0.85	0.85
1:G:12:ILE:HG21	1:G: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: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:G:12:ILE:HG13	1:G:14:VAL:N	1.84	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:C:12:ILE:HG21	1:C:14:VAL:HG22	0.85	0.83
1:E:12:ILE:HG21	1:E: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:T:52:LYS:NZ	1:T: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
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
2:K:59:MET:HE2	2:K:79:VAL:HG23	1.64	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
2:Y:59:MET:HE1	2:Y:82:LEU:HD23	1.63	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:Y:59:MET:HE2	2:Y:79:VAL:HG23	1.64	0.78
2:K:59:MET:HE1	2:K:82:LEU:HD23	1.63	0.78
1:A:124:THR:HG22	1:B:130:ARG:HH21	1.48	0.78
2:V:43:MET:HE2	2:V:56:VAL:HG23	1.66	0.78
2:V:123:ILE:HG12	2:V:124:TYR:HD1	1.49	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:124:THR:HG22	1:P:130:ARG:HH21	1.48	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:R:186:GLU:O	1:R:190:VAL:HG12	1.84	0.77
1:S:124:THR:HG22	1:T:130:ARG:HH21	1.48	0.77
2:H:123:ILE:HG12	2:H:124:TYR:HD1	1.49	0.77
2:I:53:GLN:O	2:I:56:VAL:HG12	1.83	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
2:K:167:SER:HB2	2:2:167:SER:HB2	1.68	0.76
1:P:186:GLU:O	1:P:190:VAL:HG12	1.84	0.76
1:T:186:GLU:O	1:T:190:VAL:HG12	1.84	0.76
2:H:43:MET:HE2	2:H:56:VAL:HG23	1.66	0.76
2:J:123:ILE:H	2:J:123:ILE:HD13	1.49	0.76
1:C:186:GLU:O	1:C:190:VAL:HG12	1.84	0.76
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
1:D:12:ILE:HG13	1:D:14:VAL:N	1.84	0.74
2:2:62:GLU:HG2	2:2:82:LEU:HD21	1.70	0.74
2:2:123:ILE:H	2:2:123:ILE:HD13	1.52	0.74
2:M:123:ILE:HG12	2:M:124:TYR:HD1	1.53	0.74
1:O:12:ILE:HG13	1:O:14:VAL:N	1.84	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
1:E:78:THR:HG21	1:E:85:ALA:HB1	1.70	0.73
1:P:78:THR:HG21	1:P:85:ALA:HB1	1.70	0.73
2:Z:2:THR:HG22	2:Z:169:SER:OG	1.89	0.73
1:F:78:THR:HG21	1:F:85:ALA:HB1	1.70	0.73
2:L:2:THR:HG22	2:L:169:SER:OG	1.89	0.73
1:Q:78:THR:HG21	1:Q:85:ALA:HB1	1.70	0.73
1:T:168:GLY:O	1:T:172:VAL:HG12	1.89	0.73
1:A:168:GLY:O	1:A:172:VAL:HG12	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:GLY:O	1:B:172:VAL:HG12	1.89	0.73
2:W:103:GLY:HA2	2:W:178:ILE:HD11	1.71	0.73
2:Z:20:VAL:HG13	2:Z:28:HIS:HB2	1.71	0.73
1:O:168:GLY:O	1:O:172:VAL:HG12	1.89	0.72
2:V:32:LYS:HE2	2:V:34:LEU:O	1.89	0.72
1:D:78:THR:HG21	1:D:85:ALA:HB1	1.70	0.72
1:D:168:GLY:O	1:D:172:VAL:HG12	1.89	0.72
1:S:168:GLY:O	1:S:172:VAL:HG12	1.89	0.72
1:T:78:THR:HG21	1:T:85:ALA:HB1	1.70	0.72
2:V:53:GLN:O	2:V:56:VAL:HG12	1.89	0.72
2:1:18:ARG:HE	2:1:30:ASN:HD22	1.37	0.72
2:L:20:VAL:HG13	2:L:28:HIS:HB2	1.71	0.72
2:N:62:GLU:HG2	2:N:82:LEU:HD21	1.69	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
1:E:168:GLY:O	1:E:172:VAL:HG12	1.89	0.72
1:F:12:ILE:HG12	1:F:14:VAL:HG13	1.71	0.72
1:G:12:ILE:HG12	1:G:14:VAL:HG13	1.71	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
2:M:18:ARG:HE	2:M:30:ASN:HD22	1.37	0.72
1:C:12:ILE:HG12	1:C:14:VAL:HG13	1.71	0.72
1:D:12:ILE:HG12	1:D: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
1:S:78:THR:HG21	1:S:85:ALA:HB1	1.70	0.72
1:U:12:ILE:HG13	1:U:14:VAL:N	1.84	0.72
2:1:123:ILE:HG12	2:1:124:TYR:HD1	1.53	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:P:52:LYS:HZ1	1:P:62:ASN:HA	1.52	0.72
1:P:168:GLY:O	1:P:172:VAL:HG12	1.89	0.72
1:Q:168:GLY:O	1:Q:172:VAL:HG12	1.89	0.72
1:R:12:ILE:HG12	1:R:14:VAL:HG13	1.71	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:R:78:THR:HG21	1:R:85:ALA:HB1	1.70	0.72
1:U:168:GLY:O	1:U:172:VAL:HG12	1.89	0.72
1:F:168:GLY:O	1:F:172:VAL:HG12	1.89	0.72
1:U:12:ILE:HG12	1:U:14:VAL:HG13	1.71	0.72
1:R:168:GLY:O	1:R:172:VAL:HG12	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:Q:108:ASN:HB3	2:Y:70:ARG:HG2	1.73	0.71
1:U:78:THR:HG21	1:U:85:ALA:HB1	1.70	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:P:12:ILE:HG12	1:P:14:VAL:HG13	1.71	0.71
2:L:7:THR:HB	2:L:123:ILE:O	1.90	0.71
1:T:12:ILE:HG12	1:T:14:VAL:HG13	1.71	0.71
1:C:78:THR:HG21	1:C:85:ALA:HB1	1.70	0.71
1:S:12:ILE:CG2	1:S:14:VAL:CG2	2.42	0.71
1:D:21:LEU:HD11	1:E:130:ARG:HD2	1.73	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
2:Z:7:THR:HB	2:Z:123:ILE:O	1.90	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
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
2:N:38:ASP:HB3	2:N:41:THR:CG2	2.21	0.70
1:T:52:LYS:HZ1	1:T:62:ASN:HA	1.54	0.70
1:U:108:ASN:HB3	2:V:70:ARG:HG2	1.72	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
2:V:59:MET:HE1	2:V:82:LEU:HD23	1.73	0.70
1:G:107:VAL:HG11	2:H:66:TYR:HH	1.57	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
1:R:12:ILE:CG2	1:R:14:VAL:CG2	2.42	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:H:45:ILE:HG12	2:H:52:ALA:HB1	1.74	0.69
2:Y:12:VAL:HG13	2:Y:178:ILE:HG23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:M:141:GLN:NE2	2:1:141:GLN:NE2	2.41	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
2:H:59:MET:HE1	2:H:82:LEU:HD23	1.73	0.69
1:Q:108:ASN:CB	2:Y:70:ARG:HG2	2.22	0.69
1:T:103:TYR:HE1	2:2:74:MET:HE2	1.58	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
2:L:193:GLU:HA	2:L:196:ILE:HD12	1.74	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
2:1:3:THR:OG1	2:1:127:THR:HG22	1.93	0.68
1:B:184:LEU:HD23	1:B:189:ALA:HA	1.75	0.68
2:X:149:ASP:O	2:X:152:VAL:HG12	1.94	0.68
1:G:12:ILE:CG2	1:G:14:VAL:CG2	2.42	0.68
1:P:159:GLU:HG2	1:Q:60:GLU:HG3	1.76	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
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:S:52:LYS:HZ1	1:S:62:ASN:HA	1.58	0.68
2:M:3:THR:OG1	2:M:127:THR:HG22	1.93	0.67
1:Q:52:LYS:HZ1	1:Q:62:ASN:HA	1.59	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:C:184:LEU:HD23	1:C: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:52:LYS:HZ1	1:C:62:ASN:HA	1.58	0.67
2:M:53:GLN:O	2:M:56:VAL:HG12	1.93	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:184:LEU:HD23	1:P:189:ALA:HA	1.75	0.67
1:B:159:GLU:HG2	1:C:60:GLU:HG3	1.76	0.67
1:E:184:LEU:HD23	1:E:189:ALA:HA	1.75	0.67
1:F:103:TYR:HE1	2:N:74:MET:HE2	1.58	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:A:12:ILE:O	1:A:23:GLN:HG2	1.95	0.67
1:F:12:ILE:O	1:F:23:GLN:HG2	1.95	0.67
2:I:133:PHE:CZ	2:I:165:ARG:HB3	2.30	0.67
1:Q:12:ILE:O	1:Q:23:GLN:HG2	1.95	0.67
1:D:52:LYS:HZ1	1:D:62:ASN:HA	1.59	0.66
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:12:ILE:O	1:D:23:GLN:HG2	1.95	0.66
2:M:123:ILE:H	2:M:123:ILE:HD13	1.60	0.66
1:S:12:ILE:O	1:S:23:GLN:HG2	1.95	0.66
1:U:12:ILE:O	1:U:23:GLN:HG2	1.95	0.66
2:H:38:ASP:HB3	2:H:41:THR:CG2	2.20	0.66
1:B:12:ILE:O	1:B:23:GLN:HG2	1.95	0.66
1:C:12:ILE:O	1:C:23:GLN:HG2	1.95	0.66
1:E:12:ILE:CG1	1:E:14:VAL:N	2.51	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
1:P:12:ILE:O	1:P:23:GLN:HG2	1.95	0.66
2:W:7:THR:HB	2:W:123:ILE:O	1.96	0.66
2:W:133:PHE:CZ	2:W:165:ARG:HB3	2.30	0.66
1:G:12:ILE:O	1:G:23:GLN:HG2	1.95	0.66
1:P:12:ILE:CG1	1:P:14:VAL:N	2.51	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:C:61:GLN:O	1:C:64:ILE:HG22	1.95	0.66
1:E:12:ILE:O	1:E:23:GLN:HG2	1.95	0.66
1:S:103:TYR:HE1	2:1:74:MET:HE2	1.60	0.66
2:Z:43:MET:HE2	2:Z:56:VAL:HG23	1.78	0.66
2:J:18:ARG:HE	2:J:30:ASN:HD22	1.41	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
1:D:198:LYS:O	1:D:202:GLU:HB2	1.96	0.66
1:F:198:LYS:O	1:F:202:GLU:HB2	1.96	0.66
2:M:164:GLN:NE2	2:Z:29:LYS:NZ	2.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:198:LYS:O	1:Q:202:GLU:HB2	1.96	0.66
2:Z:59:MET:SD	2:Z:83:LEU:HD13	2.36	0.66
1:D:61:GLN:O	1:D:64:ILE:HG22	1.95	0.66
1:G:198:LYS:O	1:G:202:GLU:HB2	1.96	0.66
1:O:61:GLN:O	1:O:64:ILE:HG22	1.96	0.66
1:R:198:LYS:O	1:R:202:GLU:HB2	1.96	0.66
2:J:2:THR:HG22	2:J:169:SER:OG	1.96	0.66
1:R:61:GLN:O	1:R:64:ILE:HG22	1.95	0.66
1:U:61:GLN:O	1:U:64:ILE:HG22	1.96	0.66
1:B:61:GLN:O	1:B:64:ILE:HG22	1.95	0.65
1:Q:61:GLN:O	1:Q:64:ILE:HG22	1.96	0.65
1:S:61:GLN:O	1:S:64:ILE:HG22	1.95	0.65
2:1:123:ILE:HD13	2:1:123:ILE:H	1.60	0.65
1:O:198:LYS:O	1:O:202:GLU:HB2	1.96	0.65
1:P:198:LYS:O	1:P:202:GLU:HB2	1.96	0.65
2:L:123:ILE:HG12	2:L:124:TYR:HD1	1.61	0.65
2:M:124:TYR:CD2	2:M:138:LEU:HD23	2.31	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:C:198:LYS:O	1:C:202:GLU:HB2	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:L:29:LYS:NZ	2:1:164:GLN:NE2	2.45	0.65
2:M:164:GLN:NE2	2:Z:29:LYS:HZ1	1.93	0.65
1:A:198:LYS:O	1:A:202:GLU:HB2	1.96	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:G:52:LYS:HZ1	1:G:62:ASN:HA	1.60	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
1:E:198:LYS:O	1:E:202:GLU:HB2	1.96	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
2:W:123:ILE:HD13	2:W:123:ILE:H	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
1:S:198:LYS:O	1:S:202:GLU:HB2	1.96	0.65
2:W:20:VAL:HG13	2:W:28:HIS:HB2	1.79	0.65
1:E:103:TYR:HE1	2:M:74:MET:HE2	1.61	0.64
2:I:20:VAL:HG13	2:I:28:HIS:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:LYS:O	1:B:202:GLU:HB2	1.96	0.64
2:N:123:ILE:HG12	2:N:124:TYR:HD2	1.61	0.64
2:Y:123:ILE:HG12	2:Y:124:TYR:CD1	2.31	0.64
2:1:49:VAL:HG23	2:1:50:GLY:H	1.63	0.64
2:1:124:TYR:CD2	2:1:138:LEU:HD23	2.31	0.64
1:A:130:ARG:HD2	1:G:21:LEU:HD11	1.79	0.64
2:J:75:PRO:O	2:J:78:ALA:HB3	1.96	0.64
2:L:124:TYR:CD2	2:L:138:LEU:HD23	2.33	0.64
2:W:124:TYR:CD2	2:W:138:LEU:HD23	2.32	0.64
2:I:45:ILE:HG12	2:I:52:ALA:HB1	1.79	0.64
2:V:124:TYR:CD2	2:V:138:LEU:HD23	2.33	0.64
2:M:123:ILE:HG12	2:M:124:TYR:CD1	2.33	0.64
2:1:45:ILE:CG1	2:1:52:ALA:HB1	2.26	0.64
2:L:18:ARG:HB2	2:L:31:GLY:O	1.98	0.64
2:V:55:LEU:HD21	2:V:87:LEU:HD11	1.80	0.64
2:2:123:ILE:HG12	2:2:124:TYR:HD2	1.61	0.64
2:K:3:THR:HB	2:K:16:THR:HG22	1.80	0.64
2:1:123:ILE:HG12	2:1:124:TYR:CD1	2.33	0.64
2:I:123:ILE:HD13	2:I:123:ILE:H	1.62	0.64
2:L:29:LYS:HZ1	2:1:164:GLN:NE2	1.96	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
2:L:43:MET:HE2	2:L:56:VAL:HG23	1.78	0.63
1:O:52:LYS:HZ3	1:O:62:ASN:HA	1.62	0.63
2:V:123:ILE:HD13	2:V:123:ILE:H	1.62	0.63
1:E:159:GLU:HG2	1:F:60:GLU:HG3	1.80	0.63
2:I:59:MET:HE1	2:I:82:LEU:HD23	1.79	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:W:59:MET:HE1	2:W:82:LEU:HD23	1.79	0.63
2:Z:37:ILE:HD11	2:Z:59:MET:HB3	1.79	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:M:45:ILE:CG1	2:M:52:ALA:HB1	2.26	0.63
2:M:49:VAL:HG23	2:M:50:GLY:H	1.62	0.63
2:Y:193:GLU:HA	2:Y:196:ILE:HD12	1.81	0.63
2:Z:18:ARG:HB2	2:Z:31:GLY:O	1.98	0.63
2:Z:124:TYR:CD2	2:Z:138:LEU:HD23	2.33	0.63
1:C:12:ILE:HG21	1:C:14:VAL:HG21	1.72	0.63
2:H:167:SER:HB2	2:X:167:SER:HB2	1.79	0.63
2:N:179:THR:HG23	2:N:182:ASP:H	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:X:103:GLY:HA2	2:X:178:ILE:HD13	1.81	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
2:H:123:ILE:HD13	2:H:123:ILE:H	1.62	0.63
2:N:133:PHE:CZ	2:N:165:ARG:HB3	2.34	0.63
1:U:12:ILE:CG1	1:U:14:VAL:N	2.52	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
2:L:37:ILE:HD11	2:L:59:MET:HB3	1.79	0.62
1:R:52:LYS:HZ3	1:R:62:ASN:HA	1.64	0.62
2:Z:15:ALA:HB2	2:Z:175:VAL:HB	1.82	0.62
2:K:123:ILE:HD13	2:K:123:ILE:H	1.63	0.62
1:T:15:PHE:HB2	1:U:23:GLN:HE22	1.65	0.62
2:W:1:THR:H3	2:W:129:SER:HB3	1.65	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
2:M:141:GLN:HE21	2:1:141:GLN:NE2	1.97	0.62
1:U:121:GLN:O	1:U:124:THR:HB	2.00	0.62
2:Y:3:THR:HB	2:Y:16:THR:HG22	1.80	0.62
1:A:12:ILE:HG21	1:A:14:VAL:HG21	1.72	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
2:J:167:SER:HB2	2:V:167:SER:HB2	1.82	0.62
1:U:12:ILE:HG21	1:U: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
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:B:124:THR:HG22	1:C:130:ARG:HH21	1.65	0.61
1:D:121:GLN:O	1:D:124:THR:HB	2.00	0.61
1:E:107:VAL:HG11	2:M:66:TYR:HH	1.65	0.61
2:M:149:ASP:O	2:M:152:VAL:HG12	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:21:LEU:HD11	1:R:130:ARG:HD2	1.82	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
1:A:49:ILE:HD12	1:A:211:GLU:O	2.01	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
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
2:W:76:ILE:O	2:W:79:VAL:HG12	1.99	0.61
1:B:88:LEU:HD21	1:B:120:MET:SD	2.41	0.61
1:D:108:ASN:HB3	2:L:70:ARG:HG2	1.83	0.61
1:G:52:LYS:HZ3	1:G:62:ASN:HA	1.65	0.61
1:S:49:ILE:HD12	1:S:211:GLU:O	2.01	0.61
1:E:88:LEU:HD21	1:E:120:MET:SD	2.41	0.61
2:N:76:ILE:O	2:N:79:VAL:HG12	2.00	0.61
1:P:88:LEU:HD21	1:P:120:MET:SD	2.41	0.61
1:R:121:GLN:O	1:R:124:THR:HB	2.00	0.61
1:T:88:LEU:HD21	1:T:120:MET:SD	2.41	0.61
2:Y:123:ILE:HD13	2:Y:123:ILE:H	1.63	0.61
1:C:88:LEU:HD21	1:C:120:MET:SD	2.41	0.61
1:D:49:ILE:HD12	1:D:211:GLU:O	2.01	0.61
1:E:121:GLN:O	1:E:124:THR:HB	2.00	0.61
1:F:61:GLN:OE1	1:F:62:ASN:HB3	2.00	0.61
1:G:121:GLN:O	1:G:124:THR:HB	2.00	0.61
2:K:123:ILE:HG12	2:K:124:TYR:CD1	2.31	0.61
1:O:88:LEU:HD21	1:O:120:MET:SD	2.41	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:A:61:GLN:OE1	1:A:62:ASN:HB3	2.00	0.61
1:A:121:GLN:O	1:A:124:THR:HB	2.00	0.61
1:F:88:LEU:HD21	1:F:120:MET:SD	2.41	0.61
1:P:61:GLN:OE1	1:P:62:ASN:HB3	2.00	0.61
1:Q:49:ILE:HD12	1:Q:211:GLU:O	2.01	0.61
1:Q:121:GLN:O	1:Q:124:THR:HB	2.00	0.61
1:S:61:GLN:OE1	1:S:62:ASN:HB3	2.00	0.61
1:U:88:LEU:HD21	1:U:120:MET:SD	2.41	0.61
2:W:123:ILE:HG12	2:W:124:TYR:CD1	2.32	0.61
1:F:49:ILE:HD12	1:F:211:GLU:O	2.01	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:B:121:GLN:O	1:B:124:THR:HB	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:21:LEU:HD11	1:D:130:ARG:HD2	1.82	0.61
1:C:49:ILE:HD12	1:C:211:GLU:O	2.01	0.61
1:F:121:GLN:O	1:F:124:THR:HB	2.00	0.61
2:L:15:ALA:HB2	2:L:175:VAL:HB	1.82	0.61
1:T:121:GLN:O	1:T:124:THR:HB	2.00	0.61
1:U:49:ILE:HD12	1:U:211:GLU:O	2.01	0.61
1:E:177:GLU:O	1:F:57:ARG:NE	2.31	0.61
2:N:3:THR:HB	2:N:16:THR:HG22	1.83	0.61
1:O:49:ILE:HD12	1:O: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: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: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:Q:52:LYS:HZ3	1:Q:62:ASN:HA	1.66	0.60
1:S:12:ILE:HG21	1:S:14:VAL:HG21	1.72	0.60
1:T:12:ILE:HG21	1:T:14:VAL:HG21	1.72	0.60
1:T:61:GLN:OE1	1:T:62:ASN:HB3	2.00	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:D:28:ARG:O	1:D:31:VAL:HG22	2.02	0.60
2:H:43:MET:CE	2:H:56:VAL:HG23	2.30	0.60
2:L:133:PHE:HE1	2:2:132:PRO:HA	1.65	0.60
1:R:28:ARG:O	1:R:31:VAL:HG22	2.02	0.60
1:C:61:GLN:OE1	1:C:62:ASN:HB3	2.00	0.60
1:G:61:GLN:OE1	1:G:62:ASN:HB3	2.00	0.60
2:N:26:ILE:HD13	2:N:26:ILE:C	2.27	0.60
1:R:103:TYR:HE1	2:Z:74:MET:HE2	1.66	0.60
1:T:12:ILE:CG1	1:T:14:VAL:N	2.51	0.60
2:2:76:ILE:O	2:2:79:VAL:HG12	2.00	0.60
1:B:42:PHE:HD1	1:B:43:ALA:N	2.00	0.60
1:G:28:ARG:O	1:G:31:VAL:HG22	2.02	0.60
1:G:42:PHE:HD1	1:G:43:ALA:N	2.00	0.60
1:G:49:ILE:HD12	1:G:211:GLU:O	2.01	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:R:42:PHE:HD1	1:R:43:ALA:N	2.00	0.60
1:R:49:ILE:HD12	1:R:211:GLU:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:88:LEU:HD21	1:R:120:MET:SD	2.41	0.60
1:R:108:ASN:HB3	2:Z:70:ARG:HG2	1.83	0.60
1:T:42:PHE:HD1	1:T:43:ALA:N	2.00	0.60
1:T:49:ILE:HD12	1:T:211:GLU:O	2.01	0.60
1:B:61:GLN:OE1	1:B:62:ASN:HB3	2.00	0.60
1:D:12:ILE:CG2	1:D:14:VAL:CG2	2.42	0.60
2:1:133:PHE:CZ	2:1:165:ARG:HB3	2.37	0.60
1:D:103:TYR:HE1	2:L:74:MET:HE2	1.66	0.60
2:Y:159:ILE:O	2:Y:163:LYS:HG3	2.02	0.60
1:A:88:LEU:HD21	1:A:120:MET:SD	2.41	0.60
1:D:61:GLN:OE1	1:D:62:ASN:HB3	2.00	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:S:52:LYS:HZ3	1:S:62:ASN:HA	1.67	0.60
2:2:3:THR:HB	2:2:16:THR:HG22	1.83	0.60
1:B:49:ILE:HD12	1:B:211:GLU:O	2.01	0.60
1:F:42:PHE:HD1	1:F:43:ALA:N	2.00	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:P:42:PHE:HD1	1:P:43:ALA:N	2.00	0.60
1:E:103:TYR:CE1	2:M:74:MET:HE2	2.37	0.59
1:G:88:LEU:HD21	1:G:120:MET:SD	2.41	0.59
1:S:88:LEU:HD21	1:S:120:MET:SD	2.41	0.59
1:U:108:ASN:CB	2:V:70:ARG:HG2	2.31	0.59
1:A:42:PHE:HD1	1:A:43:ALA:N	2.00	0.59
1:B:12:ILE:CG1	1:B:14:VAL:N	2.51	0.59
1:C:52:LYS:HZ3	1:C:62:ASN:HA	1.67	0.59
1:Q:28:ARG:O	1:Q:31:VAL:HG22	2.02	0.59
1:U:12:ILE:CG2	1:U:14:VAL:CG2	2.42	0.59
2:V:123:ILE:HG12	2:V:124:TYR:CD1	2.33	0.59
2:X:38:ASP:HB2	2:X:63:LEU:HD23	1.84	0.59
2:Z:3:THR:HB	2:Z:16:THR:HG22	1.83	0.59
1:D:42:PHE:HD1	1:D: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: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
2:V:37:ILE:HD11	2:V:59:MET:HB3	1.82	0.59
1:C:12:ILE:CG2	1:C:14:VAL:CG2	2.42	0.59
2:K:1:THR:H3	2:K:129:SER:HB3	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:28:ARG:O	1:P:31:VAL:HG22	2.02	0.59
1:S:42:PHE:HD1	1:S:43:ALA:N	2.00	0.59
2:W:149:ASP:O	2:W:152:VAL:HG12	2.03	0.59
2:Y:18:ARG:HE	2:Y:30:ASN:HD22	1.51	0.59
2:2:26:ILE:C	2:2:26:ILE:HD13	2.27	0.59
1:C:28:ARG:O	1:C:31:VAL:HG22	2.02	0.59
1:C:49:ILE:HD11	1:C:210:PRO:HB3	1.85	0.59
2:K:152:VAL:O	2:K:156:ILE:HG13	2.03	0.59
1:Q:42:PHE:HD1	1:Q:43:ALA:N	2.00	0.59
1:R:12:ILE:HG21	1:R:14:VAL:HG21	1.72	0.59
1:S:28:ARG:O	1:S:31:VAL:HG22	2.02	0.59
1:U:49:ILE:HD11	1:U:210:PRO:HB3	1.85	0.59
1:B:28:ARG:O	1:B:31:VAL:HG22	2.02	0.59
1:O:49:ILE:HD11	1:O:210:PRO:HB3	1.85	0.59
2:V:59:MET:HE2	2:V:79:VAL:HG23	1.83	0.59
1:B:49:ILE:HD11	1:B:210:PRO:HB3	1.85	0.59
1:C:42:PHE:HD1	1:C:43:ALA:N	2.00	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
2:L:32:LYS:HE2	2:L:34:LEU:O	2.01	0.59
2:1:38:ASP:HB3	2:1:41:THR:CG2	2.28	0.59
1:A:28:ARG:O	1:A:31:VAL:HG22	2.02	0.59
2:H:59:MET:HE2	2:H:79:VAL:HG23	1.83	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
1:S:12:ILE:CG1	1:S:14:VAL:N	2.52	0.59
1:D:49:ILE:HD11	1:D:210:PRO:HB3	1.85	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:U:28:ARG:O	1:U:31:VAL:HG22	2.02	0.59
1:F:52:LYS:HZ1	1:F:62:ASN:HA	1.67	0.58
2:J:7:THR:HB	2:J:123:ILE:O	2.03	0.58
2:N:165:ARG:C	2:Y:26:ILE:HG22	2.28	0.58
1:O:21:LEU:HD11	1:P:130:ARG:HD2	1.85	0.58
2:Y:124:TYR:CD2	2:Y:138:LEU:HD23	2.37	0.58
2:J:38:ASP:HB2	2:J:63:LEU:HD23	1.84	0.58
2:N:132:PRO:HA	2:Z:133:PHE:HE1	1.67	0.58
1:O:103:TYR:HE1	2:W:74:MET:HE2	1.68	0.58
1:P:49:ILE:HD11	1:P:210:PRO:HB3	1.85	0.58
2:V:26:ILE:HD13	2:V:26:ILE:C	2.28	0.58
2:Z:123:ILE:H	2:Z:123:ILE:HD13	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:49:ILE:HD11	1:T:210:PRO:HB3	1.85	0.58
2:Z:38:ASP:HB3	2:Z:41:THR:CG2	2.31	0.58
2:2:178:ILE:HB	2:2:184:TYR:HA	1.84	0.58
1:A:12:ILE:CG1	1:A:14:VAL:N	2.51	0.58
1:F:103:TYR:CE1	2:N:74:MET:HE2	2.38	0.58
2:H:26:ILE:C	2:H:26:ILE:HD13	2.28	0.58
2:K:159:ILE:O	2:K:163:LYS:HG3	2.02	0.58
2:L:123:ILE:HD13	2:L:123:ILE:H	1.67	0.58
1:S:103:TYR:CE1	2:1:74:MET:HE2	2.37	0.58
1:U:35:SER:O	1:U:166:GLY:HA3	2.03	0.58
2:X:7:THR:HB	2:X:123:ILE:O	2.03	0.58
2:X:199:LEU:HB3	2:X:201:LEU:HD13	1.85	0.58
2:Y:152:VAL:O	2:Y:156:ILE:HG13	2.03	0.58
1:A:103:TYR:HE1	2:I:74:MET:HE2	1.68	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:C:35:SER:O	1:C:166:GLY:HA3	2.03	0.58
1:E:135:SER:OG	1:E:153:PRO:HD3	2.04	0.58
1:P:135:SER:OG	1:P:153:PRO:HD3	2.04	0.58
1:Q:135:SER:OG	1:Q:153:PRO:HD3	2.04	0.58
1:T:35:SER:O	1:T:166:GLY:HA3	2.03	0.58
1:T:103:TYR:CE1	2:2:74:MET:HE2	2.38	0.58
1:O:12:ILE:CG2	1:O:14:VAL:CG2	2.42	0.58
2:V:152:VAL:O	2:V:156:ILE:HG13	2.04	0.58
2:Y:25:PHE:C	2:Y:25:PHE:CD1	2.80	0.58
2:Y:32:LYS:HE2	2:Y:34:LEU:O	2.02	0.58
1:B:35:SER:O	1:B:166:GLY:HA3	2.03	0.58
1:E:49:ILE:HD11	1:E:210:PRO:HB3	1.85	0.58
1:F:135:SER:OG	1:F:153:PRO:HD3	2.04	0.58
2:H:8:LEU:HD12	2:H:8:LEU:O	2.03	0.58
1:O:35:SER:O	1:O:166:GLY:HA3	2.03	0.58
1:D:135:SER:OG	1:D:153:PRO:HD3	2.04	0.58
1:F:12:ILE:HG21	1:F:14:VAL:HG21	1.72	0.58
2:I:149:ASP:O	2:I:152:VAL:HG12	2.03	0.58
1:O:135:SER:OG	1:O:153:PRO:HD3	2.04	0.58
1:P:108:ASN:HB3	2:X:70:ARG:HG2	1.86	0.58
1:Q:49:ILE:HD11	1:Q:210:PRO:HB3	1.85	0.58
2:X:59:MET:HE1	2:X:82:LEU:HD23	1.86	0.58
2:Y:38:ASP:HB3	2:Y:41:THR:CG2	2.26	0.58
2:K:18:ARG:HE	2:K:30:ASN:HD22	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:123:ILE:HG12	2:X:124:TYR:HD1	1.69	0.58
1:G:49:ILE:HD11	1:G:210:PRO:HB3	1.85	0.57
1:S:49:ILE:HD11	1:S:210:PRO:HB3	1.85	0.57
1:D:35:SER:O	1:D:166:GLY:HA3	2.03	0.57
1:F:49:ILE:HD11	1:F:210:PRO:HB3	1.85	0.57
2:J:3:THR:OG1	2:J:127:THR:HG22	2.05	0.57
2:J:26:ILE:C	2:J:26:ILE:HD13	2.30	0.57
2:M:28:HIS:CD2	2:N:120:VAL:HG11	2.39	0.57
2:N:178:ILE:HB	2:N:184:TYR:HA	1.84	0.57
2:X:160:SER:O	2:X:163:LYS:HB2	2.04	0.57
1:A:35:SER:O	1:A:166:GLY:HA3	2.03	0.57
1:E:108:ASN:HB3	2:M:70:ARG:HG2	1.86	0.57
2:I:51:ASP:O	2:I:55:LEU:HB2	2.04	0.57
2:J:59:MET:HE1	2:J:82:LEU:HD23	1.86	0.57
2:K:26:ILE:C	2:K:26:ILE:HD13	2.29	0.57
1:S:35:SER:O	1:S:166:GLY:HA3	2.03	0.57
1:S:108:ASN:HB3	2:1:70:ARG:HG2	1.86	0.57
2:1:28:HIS:CD2	2:2:120:VAL:HG11	2.39	0.57
2:M:75:PRO:O	2:M:78:ALA:HB3	2.05	0.57
1:P:143:GLN:HE21	1:P:143:GLN:HA	1.70	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:Z:28:HIS:CD2	2:1:120:VAL:HG11	2.39	0.57
2:K:20:VAL:HG22	2:K:28:HIS:HB2	1.86	0.57
2:K:173:ILE:HD13	2:K:173:ILE:C	2.30	0.57
2:N:124:TYR:CD1	2:N:138:LEU:HD23	2.40	0.57
2:V:8:LEU:HD12	2:V:8:LEU:O	2.03	0.57
2:Y:26:ILE:HD13	2:Y:26:ILE:C	2.29	0.57
2:Y:131:SER:O	2:Y:134:VAL:HG13	2.04	0.57
1:E:143:GLN:HE21	1:E:143:GLN:HA	1.70	0.57
2:K:26:ILE:HG22	2:2:165:ARG:C	2.30	0.57
2:K:131:SER:O	2:K:134:VAL:HG13	2.04	0.57
1:R:49:ILE:HD11	1:R:210:PRO:HB3	1.85	0.57
1:F:35:SER:O	1:F:166:GLY:HA3	2.03	0.57
1:G:135:SER:OG	1:G:153:PRO:HD3	2.04	0.57
2:H:152:VAL:O	2:H:156:ILE:HG13	2.04	0.57
1:R:35:SER:O	1:R:166:GLY:HA3	2.03	0.57
1:S:21:LEU:HD11	1:T:130:ARG:HD2	1.87	0.57
1:U:135:SER:OG	1:U:153:PRO:HD3	2.04	0.57
2:W:51:ASP:O	2:W:55:LEU:HB2	2.05	0.57
2:X:26:ILE:C	2:X:26:ILE:HD13	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:178:ILE:HB	2:M:184:TYR:HA	1.87	0.57
1:U:52:LYS:HZ1	1:U:62:ASN:HA	1.69	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:D:102:THR:O	2:L:81:THR:HG22	2.05	0.57
1:G:35:SER:O	1:G:166:GLY:HA3	2.03	0.57
2:H:37:ILE:HD11	2:H:59:MET:CG	2.35	0.57
1:O:143:GLN:HA	1:O:143:GLN:HE21	1.70	0.57
1:B:52:LYS:HZ1	1:B:62:ASN:HA	1.69	0.57
1:B:103:TYR:HE1	2:J:74:MET:HE2	1.70	0.57
1:P:35:SER:O	1:P:166:GLY:HA3	2.03	0.57
2:V:62:GLU:HG2	2:V:82:LEU:HD21	1.87	0.57
2:Y:173:ILE:C	2:Y:173:ILE:HD13	2.30	0.57
2:1:178:ILE:HB	2:1:184:TYR:HA	1.87	0.57
2:2:152:VAL:O	2:2:156:ILE:HG13	2.05	0.57
2:K:45:ILE:HG12	2:K:52:ALA:HB1	1.87	0.56
1:D:143:GLN:HA	1:D:143:GLN:HE21	1.70	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
2:2:124:TYR:CD1	2:2:138:LEU:HD23	2.40	0.56
1:E:35:SER:O	1:E:166:GLY:HA3	2.04	0.56
1:F:143:GLN:HA	1:F:143:GLN:HE21	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:L:1:THR:H3	2:L:129:SER:HB3	1.70	0.56
2:M:38:ASP:HB3	2:M:41:THR:CG2	2.28	0.56
2:N:152:VAL:O	2:N:156:ILE:HG13	2.05	0.56
1:Q:35:SER:O	1:Q:166:GLY:HA3	2.03	0.56
2:J:199:LEU:HB3	2:J:201:LEU:HD13	1.85	0.56
2:V:37:ILE:HD11	2:V:59:MET:CG	2.35	0.56
1:Q:143:GLN:HA	1:Q:143:GLN:HE21	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:E:21:LEU:HD11	1:F:130:ARG:HD2	1.86	0.56
2:K:25:PHE:CD1	2:K:25:PHE:C	2.80	0.56
1:Q:12:ILE:HG21	1:Q:14:VAL:HG21	1.72	0.56
1:S:135:SER:OG	1:S:153:PRO:HD3	2.04	0.56
1:T:135:SER:OG	1:T:153:PRO:HD3	2.04	0.56
1:U:12:ILE:O	1:U:23:GLN:CG	2.54	0.56
2:Z:179:THR:HG23	2:Z:182:ASP:H	1.70	0.56
1:B:143:GLN:HA	1:B:143:GLN:HE21	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:ILE:O	1:C:23:GLN:CG	2.54	0.56
1:D:12:ILE:O	1:D:23:GLN:CG	2.54	0.56
2:L:43:MET:CE	2:L:56:VAL:HG23	2.35	0.56
2:N:174:ASP:HA	2:N:192:ILE:HD13	1.87	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
1:B:135:SER:OG	1:B:153:PRO:HD3	2.04	0.56
2:H:173:ILE:HD13	2:H:173:ILE:C	2.31	0.56
2:M:32:LYS:HE2	2:M:34:LEU:O	2.06	0.56
1:T:143:GLN:HA	1:T:143:GLN:HE21	1.70	0.56
1:T:12:ILE:O	1:T:23:GLN:CG	2.54	0.56
2:V:120:VAL:HG11	2:2:28:HIS:CD2	2.41	0.56
2:V:173:ILE:HD13	2:V:173:ILE:C	2.31	0.56
2:1:75:PRO:O	2:1:78:ALA:HB3	2.04	0.56
1:A:135:SER:OG	1:A:153:PRO:HD3	2.04	0.56
1:B:43:ALA:HB2	1:B:185:PRO:HA	1.88	0.56
2:Y:43:MET:HE2	2:Y:56:VAL:HG23	1.88	0.56
2:N:66:TYR:CZ	2:N:70:ARG:HD2	2.41	0.55
1:O:130:ARG:NH2	1:U:124:THR:HG22	2.17	0.55
1:O:175:PHE:CD1	1:O:175:PHE:C	2.85	0.55
1:S:107:VAL:HG11	2:1:66:TYR:HH	1.67	0.55
1:S:175:PHE:C	1:S:175:PHE:CD1	2.84	0.55
2:Z:43:MET:CE	2:Z:56:VAL:HG23	2.35	0.55
1:A:12:ILE:O	1:A:23:GLN:CG	2.54	0.55
1:C:143:GLN:HA	1:C:143:GLN:HE21	1.70	0.55
1:E:12:ILE:O	1:E:23:GLN:CG	2.54	0.55
1:G:143:GLN:HA	1:G:143:GLN:HE21	1.70	0.55
2:H:62:GLU:HG2	2:H:82:LEU:HD21	1.87	0.55
2:J:123:ILE:HG12	2:J:124:TYR:HD1	1.69	0.55
1:R:124:THR:HG22	1:S:130:ARG:NH2	2.14	0.55
1:R:143:GLN:HA	1:R:143:GLN:HE21	1.70	0.55
1:T:52:LYS:HZ3	1:T:62:ASN:HA	1.70	0.55
1:U:143:GLN:HE21	1:U:143:GLN:HA	1.70	0.55
2:V:6:ILE:HD11	2:V:142:TYR:CD1	2.42	0.55
2:2:174:ASP:HA	2:2:192:ILE:HD13	1.87	0.55
1:A:43:ALA:HB2	1:A:185:PRO:HA	1.88	0.55
1:A:143:GLN:HA	1:A:143:GLN:HE21	1.70	0.55
1:B:12:ILE:O	1:B:23:GLN:CG	2.54	0.55
2:L:173:ILE:C	2:L:173:ILE:HD13	2.32	0.55
1:P:175:PHE:CD1	1:P:175:PHE:C	2.85	0.55
1:S:43:ALA:HB2	1:S:185:PRO:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:143:GLN:HE21	1:S:143:GLN:HA	1.70	0.55
1:A:175:PHE:CD1	1:A:175:PHE:C	2.85	0.55
1:E:175:PHE:C	1:E:175:PHE:HD1	2.15	0.55
1:E:175:PHE:C	1:E:175:PHE:CD1	2.84	0.55
2:H:120:VAL:HG11	2:N:28:HIS:CD2	2.41	0.55
2:M:167:SER:OG	2:Z:24:ASN:HA	2.07	0.55
1:O:70:ILE:HD12	1:O:74:VAL:HG22	1.88	0.55
1:Q:175:PHE:HD1	1:Q:175:PHE:C	2.15	0.55
1:R:175:PHE:CD1	1:R:175:PHE:C	2.85	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:D:175:PHE:CD1	1:D:175:PHE:C	2.85	0.55
1:G:175:PHE:HD1	1:G:175:PHE:C	2.15	0.55
1:P:12:ILE:O	1:P:23:GLN:CG	2.54	0.55
1:Q:175:PHE:C	1:Q:175:PHE:CD1	2.84	0.55
1:T:175:PHE:CD1	1:T:175:PHE:C	2.85	0.55
1:U:175:PHE:CD1	1:U:175:PHE:C	2.85	0.55
2:2:66:TYR:CZ	2:2:70:ARG:HD2	2.41	0.55
1:B:175:PHE:CD1	1:B:175:PHE:C	2.85	0.55
1:C:175:PHE:C	1:C:175:PHE:CD1	2.85	0.55
1:F:12:ILE:O	1:F:23:GLN:CG	2.54	0.55
1:F:175:PHE:HD1	1:F:175:PHE:C	2.15	0.55
1:S:198:LYS:HG2	1:S:202:GLU:HG2	1.88	0.55
1:T:198:LYS:HG2	1:T:202:GLU:HG2	1.88	0.55
1:B:198:LYS:HG2	1:B:202:GLU:HG2	1.88	0.55
1:D:124:THR:HG22	1:E:130:ARG:NH2	2.14	0.55
1:F:70:ILE:HD12	1:F:74:VAL:HG22	1.88	0.55
1:F:175:PHE:C	1:F:175:PHE:CD1	2.85	0.55
1:G:12:ILE:O	1:G:23:GLN:CG	2.54	0.55
1:G:12:ILE:CB	1:G:14:VAL:HG22	2.36	0.55
1:G:175:PHE:C	1:G:175:PHE:CD1	2.85	0.55
2:H:179:THR:HG23	2:H:182:ASP:H	1.72	0.55
2:Y:45:ILE:HG12	2:Y:52:ALA:HB1	1.87	0.55
1:A:198:LYS:HG2	1:A:202:GLU:HG2	1.88	0.55
1:C:43:ALA:HB2	1:C:185:PRO:HA	1.88	0.55
1:C:70:ILE:HD12	1:C:74:VAL:HG22	1.88	0.55
1:D:43:ALA:HB2	1:D:185:PRO:HA	1.88	0.55
1:D:95:SER:OG	1:D:115:ARG:HD3	2.07	0.55
2:I:17:GLU:O	2:I:33:LYS:HD2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:43:MET:HE2	2:K:56:VAL:HG23	1.88	0.55
1:Q:70:ILE:HD12	1:Q:74:VAL:HG22	1.88	0.55
1:R:12:ILE:CB	1:R: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:P:175:PHE:C	1:P:175:PHE:HD1	2.15	0.55
1:Q:12:ILE:CB	1:Q:14:VAL:HG22	2.36	0.55
1:R:12:ILE:O	1:R:23:GLN:CG	2.54	0.55
1:S:12:ILE:CB	1:S:14:VAL:HG22	2.36	0.55
1:A:95:SER:OG	1:A:115:ARG:HD3	2.07	0.55
1:D:70:ILE:HD12	1:D: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:E:70:ILE:HD12	1:E:74:VAL:HG22	1.88	0.55
1:P:70:ILE:HD12	1:P:74:VAL:HG22	1.88	0.55
1:P:95:SER:OG	1:P:115:ARG:HD3	2.07	0.55
1:S:95:SER:OG	1:S:115:ARG:HD3	2.07	0.55
1:T:70:ILE:HD12	1:T:74:VAL:HG22	1.88	0.55
1:A:12:ILE:CB	1:A:14:VAL:HG22	2.36	0.54
1:Q:12:ILE:O	1:Q:23:GLN:CG	2.54	0.54
2:V:179:THR:HG23	2:V:182:ASP:H	1.71	0.54
2:Z:173:ILE:C	2:Z:173:ILE:HD13	2.32	0.54
2:2:25:PHE:CD1	2:2:25:PHE:C	2.84	0.54
1:F:12:ILE:CB	1:F:14:VAL:HG22	2.36	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:R:175:PHE:C	1:R:175:PHE:HD1	2.15	0.54
1:R:198:LYS:HG2	1:R:202:GLU:HG2	1.88	0.54
1:F:95:SER:OG	1:F:115:ARG:HD3	2.07	0.54
1:G:43:ALA:HB2	1:G:185:PRO:HA	1.88	0.54
2:H:6:ILE:HD11	2:H:142:TYR:CD1	2.42	0.54
1:O:175:PHE:C	1:O:175:PHE:HD1	2.15	0.54
1:P:103:TYR:HE1	2:X:74:MET:HE2	1.70	0.54
1:R:43:ALA:HB2	1:R:185:PRO:HA	1.88	0.54
1:R:70:ILE:HD12	1:R:74:VAL:HG22	1.88	0.54
2:W:17:GLU:O	2:W:33:LYS:HD2	2.07	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
1:S:70:ILE:HD12	1:S:74:VAL:HG22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:175:PHE:C	1:S:175:PHE:HD1	2.15	0.54
1:T:95:SER:OG	1:T:115:ARG:HD3	2.07	0.54
1:U:198:LYS:HG2	1:U:202:GLU:HG2	1.88	0.54
1:A:175:PHE:C	1:A:175:PHE:HD1	2.15	0.54
1:C:198:LYS:HG2	1:C:202:GLU:HG2	1.88	0.54
1:D:175:PHE:C	1:D:175:PHE:HD1	2.15	0.54
1:Q:43:ALA:HB2	1:Q:185:PRO:HA	1.88	0.54
1:C:175:PHE:C	1:C:175:PHE:HD1	2.15	0.54
1:F:43:ALA:HB2	1:F:185:PRO:HA	1.88	0.54
2:I:3:THR:HB	2:I:16:THR:HG22	1.90	0.54
2:K:62:GLU:HG2	2:K:82:LEU:HD21	1.90	0.54
2:M:37:ILE:HD11	2:M:59:MET:CB	2.35	0.54
2:M:164:GLN:HE21	2:Z:29:LYS:HZ1	1.54	0.54
1:O:43:ALA:HB2	1:O:185:PRO:HA	1.88	0.54
2:1:32:LYS:HE2	2:1:34:LEU:O	2.06	0.54
1:A:70:ILE:HD12	1:A:74:VAL:HG22	1.88	0.54
1:B:70:ILE:HD12	1:B:74:VAL:HG22	1.88	0.54
1:E:198:LYS:HG2	1:E:202:GLU:HG2	1.88	0.54
1:G:95:SER:OG	1:G:115:ARG:HD3	2.07	0.54
2:H:159:ILE:O	2:H:163:LYS:HG3	2.08	0.54
2:K:37:ILE:HD11	2:K:59:MET:HB3	1.90	0.54
2:K:141:GLN:NE2	2:V:141:GLN:NE2	2.55	0.54
1:P:43:ALA:HB2	1:P:185:PRO:HA	1.88	0.54
1:U:95:SER:OG	1:U:115:ARG:HD3	2.07	0.54
1:U:175:PHE:C	1:U:175:PHE:HD1	2.15	0.54
2:W:3:THR:HB	2:W:16:THR:HG22	1.90	0.54
2:Y:37:ILE:HD11	2:Y:59:MET:HB3	1.90	0.54
2:Z:1:THR:H3	2:Z:129:SER:HB3	1.73	0.54
1:D:42:PHE:HB2	1:D:184:LEU:O	2.08	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
1:R:49:ILE:HD13	1:R:212:ILE:HB	1.89	0.54
1:S:49:ILE:HD13	1:S:212:ILE:HB	1.89	0.54
1:T:175:PHE:C	1:T:175:PHE:HD1	2.15	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
1:P:42:PHE:HB2	1:P:184:LEU:O	2.08	0.54
1:Q:42:PHE:HB2	1:Q:184:LEU:O	2.08	0.54
1:T:12:ILE:CB	1:T:14:VAL:HG22	2.36	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:32:LYS:HE2	2:J:34:LEU:O	2.08	0.54
2:L:141:GLN:NE2	2:2:141:GLN:NE2	2.56	0.54
1:O:42:PHE:HB2	1:O:184:LEU:O	2.08	0.54
1:O:198:LYS:HG2	1:O:202:GLU:HG2	1.88	0.54
1:P:12:ILE:CB	1:P:14:VAL:HG22	2.36	0.54
2:Y:36:GLN:HB2	2:Y:184:TYR:CE1	2.43	0.54
2:1:37:ILE:HD11	2:1:59:MET:CB	2.35	0.54
1:B:49:ILE:HD13	1:B:212:ILE:HB	1.89	0.53
1:B:175:PHE:C	1:B:175:PHE:HD1	2.15	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:F:42:PHE:HB2	1:F:184:LEU:O	2.08	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
1:O:49:ILE:HD13	1:O:212:ILE:HB	1.89	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:49:ILE:HD13	1:D:212:ILE:HB	1.89	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:G:49:ILE:HD13	1:G:212:ILE:HB	1.89	0.53
2:M:55:LEU:HD23	2:M:99:LEU:HD11	1.91	0.53
2:N:25:PHE:C	2:N:25:PHE:CD1	2.84	0.53
1:P:49:ILE:HD13	1:P:212:ILE:HB	1.89	0.53
1:P:198:LYS:HG2	1:P:202:GLU:HG2	1.88	0.53
1:Q:49:ILE:HD13	1:Q:212:ILE:HB	1.89	0.53
2:2:199:LEU:HB3	2:2:201:LEU:HD13	1.90	0.53
1:C:42:PHE:HB2	1:C:184:LEU:O	2.08	0.53
1:E:52:LYS:HZ3	1:E:62:ASN:HA	1.71	0.53
1:E:144:ILE:HD12	1:E:147:ARG:NH1	2.24	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:C:144:ILE:HD12	1:C:147:ARG:NH1	2.23	0.53
1:G:42:PHE:HB2	1:G:184:LEU:O	2.09	0.53
2:J:3:THR:HB	2:J:16:THR:HG22	1.90	0.53
2:M:135:TYR:HB3	2:1:165:ARG:HG2	1.90	0.53
2:N:149:ASP:O	2:N:152:VAL:HG12	2.08	0.53
1:P:144:ILE:HD12	1:P:147:ARG:NH1	2.24	0.53
1:T:49:ILE:HD13	1:T:212:ILE:HB	1.89	0.53
1:U:144:ILE:HD12	1:U:147:ARG:NH1	2.24	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)
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:Z:103:GLY:HA2	2:Z:178:ILE:CD1	2.39	0.53
2:1:55:LEU:HD23	2:1:99:LEU:HD11	1.91	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: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
2:2:149:ASP:O	2:2:152:VAL:HG12	2.08	0.53
1:D:12:ILE:HG21	1:D:14:VAL:HG21	1.72	0.53
2:L:103:GLY:HA2	2:L:178:ILE:CD1	2.39	0.53
1:Q:198:LYS:HG2	1:Q:202:GLU:HG2	1.88	0.53
2:V:133:PHE:CZ	2:V:165:ARG:HB3	2.43	0.53
2:2:123:ILE:HG12	2:2:124:TYR:CD2	2.44	0.53
2:X:32:LYS:HE2	2:X:34:LEU:O	2.08	0.53
2:Y:15:ALA:HB2	2:Y:175:VAL:HB	1.91	0.53
2:Z:26:ILE:O	2:Z:26:ILE:HD13	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:C:49:ILE:HD13	1:C:212:ILE:HB	1.89	0.53
1:F:12:ILE:HG13	1:F:14:VAL:H	1.73	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:A:42:PHE:CD1	1:A:43:ALA:N	2.78	0.52
1:A:144:ILE:HD12	1:A:147:ARG:NH1	2.24	0.52
1:G:144:ILE:HD12	1:G:147:ARG:NH1	2.24	0.52
2:K:103:GLY:HA2	2:K:178:ILE:HD13	1.91	0.52
2:M:131:SER:O	2:M:134:VAL:HG13	2.10	0.52
2:N:131:SER:O	2:N:134:VAL:HG13	2.09	0.52
2:N:199:LEU:HB3	2:N:201:LEU:HD13	1.90	0.52
1:O:12:ILE:CB	1:O:14:VAL:HG22	2.36	0.52
1:P:52:LYS:HZ3	1:P:62:ASN:HA	1.73	0.52
1:U:12:ILE:CB	1:U:14:VAL:HG22	2.36	0.52
2:X:28:HIS:CD2	2:Y:120:VAL:HG11	2.44	0.52
2:X:131:SER:O	2:X:134:VAL:HG13	2.08	0.52
2:Z:59:MET:HE1	2:Z:82:LEU:HD23	1.91	0.52
2:2:131:SER:O	2:2:134:VAL:HG13	2.09	0.52
1:A:42:PHE:HB2	1:A:184:LEU:O	2.08	0.52
1:B:159:GLU:HG2	1:C:60:GLU:CG	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:K:15:ALA:HB2	2:K:175:VAL:HB	1.91	0.52
2:L:26:ILE:O	2:L:26:ILE:HD13	2.09	0.52
1:O:144:ILE:HD12	1:O:147:ARG:NH1	2.24	0.52
1:R:144:ILE:HD12	1:R:147:ARG:NH1	2.24	0.52
1:S:42:PHE:CD1	1:S:43:ALA:N	2.78	0.52
1:U:49:ILE:HD13	1:U:212:ILE:HB	1.89	0.52
2:V:45:ILE:CG1	2:V:52:ALA:HB1	2.39	0.52
1:F:160:TYR:CD2	1:F:163:THR:HB	2.45	0.52
1:G:42:PHE:CD1	1:G:43:ALA:N	2.78	0.52
2:H:141:GLN:NE2	2:Y:141:GLN:NE2	2.58	0.52
1:Q:144:ILE:HD12	1:Q:147:ARG:NH1	2.23	0.52
1:S:144:ILE:HD12	1:S:147:ARG:NH1	2.23	0.52
2:W:26:ILE:HD13	2:W:26:ILE:C	2.35	0.52
2:J:28:HIS:CD2	2:K:120:VAL:HG11	2.44	0.52
2:M:26:ILE:C	2:M:26:ILE:HD13	2.34	0.52
1:Q:160:TYR:CD2	1:Q:163:THR:HB	2.45	0.52
1:S:42:PHE:HB2	1:S:184:LEU:O	2.08	0.52
2:X:124:TYR:CD2	2:X:138:LEU:HD23	2.44	0.52
1:B:144:ILE:HD12	1:B:147:ARG:NH1	2.24	0.52
1:G:160:TYR:CD2	1:G:163:THR:HB	2.45	0.52
2:I:45:ILE:CG1	2:I:52:ALA:HB1	2.39	0.52
2:J:37:ILE:HD11	2:J:59:MET:CB	2.38	0.52
2:L:29:LYS:HZ1	2:1:164:GLN:HE21	1.57	0.52
2:M:6:ILE:HD11	2:M:142:TYR:CD1	2.44	0.52
1:O:42:PHE:CD1	1:O:43:ALA:N	2.78	0.52
1:P:108:ASN:CB	2:X:70:ARG:HG2	2.40	0.52
1:R:42:PHE:CD1	1:R:43:ALA:N	2.78	0.52
1:R:160:TYR:CD2	1:R:163:THR:HB	2.45	0.52
2:X:189:THR:HG23	2:X:190:ASP:N	2.25	0.52
2:1:20:VAL:CG1	2:1:28:HIS:HB2	2.36	0.52
1:D:42:PHE:CD1	1:D:43:ALA:N	2.78	0.52
1:D:144:ILE:HD12	1:D:147:ARG:NH1	2.24	0.52
1:E:160:TYR:CD2	1:E:163:THR:HB	2.45	0.52
1:F:144:ILE:HD12	1:F:147:ARG:NH1	2.24	0.52
2:H:45:ILE:CG1	2:H:52:ALA:HB1	2.39	0.52
2:I:26:ILE:HD13	2:I:26:ILE:C	2.35	0.52
2:L:24:ASN:HA	2:1:167:SER:OG	2.09	0.52
2:L:59:MET:HE1	2:L:82:LEU:HD23	1.91	0.52
2:L:62:GLU:HG2	2:L:82:LEU:HD21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:21:LEU:O	1:O:24:VAL:HG12	2.10	0.52
1:P:160:TYR:CD2	1:P:163:THR:HB	2.45	0.52
1:T:42:PHE:CD1	1:T:43:ALA:N	2.78	0.52
1:U:12:ILE:HG13	1:U:14:VAL:H	1.73	0.52
2:2:18:ARG:HE	2:2:30:ASN:HD22	1.57	0.52
1:B:42:PHE:CD1	1:B:43:ALA:N	2.78	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
2:H:141:GLN:NE2	2:Y:141:GLN:HE21	2.08	0.52
1:P:12:ILE:HG13	1:P:14:VAL:H	1.73	0.52
2:W:45:ILE:CG1	2:W:52:ALA:HB1	2.39	0.52
2:1:26:ILE:HD13	2:1:26:ILE:C	2.34	0.52
1:C:12:ILE:HG13	1:C:14:VAL:H	1.73	0.52
1:D:12:ILE:CB	1:D:14:VAL:HG22	2.36	0.52
1:Q:21:LEU:O	1:Q:24:VAL:HG12	2.10	0.52
1:S:160:TYR:CD2	1:S:163:THR:HB	2.45	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
2:Y:103:GLY:HA2	2:Y:178:ILE:HD13	1.91	0.52
2:Z:55:LEU:HD21	2:Z:87:LEU:HD11	1.92	0.52
1:A:85:ALA:O	1:A:89:VAL:HG23	2.10	0.52
1:D:85:ALA:O	1:D:89:VAL:HG23	2.10	0.52
1:O:70:ILE:HB	1:O:74:VAL:HG13	1.92	0.52
1:S:85:ALA:O	1:S:89:VAL:HG23	2.10	0.52
1:T:144:ILE:HD12	1:T:147:ARG:NH1	2.24	0.52
2:Z:62:GLU:HG2	2:Z:82:LEU:HD21	1.91	0.52
2:2:2:THR:HG22	2:2:169:SER:OG	2.10	0.52
1:A:160:TYR:CD2	1:A:163:THR:HB	2.45	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:C:42:PHE:CD1	1:C:43:ALA:N	2.78	0.51
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
2:V:176:ALA:HA	2:V:186:GLN:HA	1.92	0.51
1:A:21:LEU:O	1:A:24:VAL:HG12	2.10	0.51
1:C:21:LEU:O	1:C:24:VAL:HG12	2.10	0.51
1:C:160:TYR:CD2	1:C:163:THR:HB	2.45	0.51
1:D:70:ILE:HB	1:D:74:VAL:HG13	1.92	0.51
1:D:160:TYR:CD2	1:D:163:THR:HB	2.45	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:165:ARG:HG2	2:1:135:TYR:HB3	1.91	0.51
2:N:141:GLN:NE2	2:Z:141:GLN:NE2	2.58	0.51
2:N:165:ARG:HA	2:Y:26:ILE:HG23	1.92	0.51
1:P:159:GLU:HG2	1:Q:60:GLU:CG	2.39	0.51
2:Y:174:ASP:HA	2:Y:192:ILE:HD13	1.92	0.51
1:E:70:ILE:HB	1:E:74:VAL:HG13	1.92	0.51
1:G:85:ALA:O	1:G:89:VAL:HG23	2.10	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: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:W:18:ARG:HE	2:W:30:ASN:HD22	1.57	0.51
2:1:124:TYR:HD2	2:1:138:LEU:HD23	1.76	0.51
1:D:191:THR:O	1:D:194:ILE:HG22	2.11	0.51
1:G:21:LEU:O	1:G:24:VAL:HG12	2.10	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:Q:85:ALA:O	1:Q:89:VAL:HG23	2.10	0.51
1:R:21:LEU:O	1:R:24:VAL:HG12	2.10	0.51
1:S:21:LEU:O	1:S:24:VAL:HG12	2.10	0.51
1:T:21:LEU:O	1:T:24:VAL:HG12	2.10	0.51
1:T:85:ALA:O	1:T:89:VAL:HG23	2.10	0.51
1:U:21:LEU:O	1:U:24:VAL:HG12	2.10	0.51
1:A:159:GLU:HG2	1:B:60:GLU:HG3	1.92	0.51
1:C:70:ILE:HB	1:C:74:VAL:HG13	1.92	0.51
1:D:103:TYR:CE1	2:L:74:MET:HE2	2.46	0.51
1:E:12:ILE:HG13	1:E:14:VAL:H	1.74	0.51
1:E:85:ALA:O	1:E:89:VAL:HG23	2.10	0.51
1:E:191:THR:O	1:E:194:ILE:HG22	2.11	0.51
1:O:12:ILE:HG13	1:O:14:VAL:H	1.73	0.51
1:O:191:THR:O	1:O:194:ILE:HG22	2.11	0.51
1:P:42:PHE:CD1	1:P:43:ALA:N	2.78	0.51
1:R:85:ALA:O	1:R:89:VAL:HG23	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
2:Z:124:TYR:HD2	2:Z:138:LEU:HD23	1.76	0.51
1:C:85:ALA:O	1:C:89:VAL:HG23	2.10	0.51
1:C:149:PHE:CE1	1:C:159:GLU:HB2	2.46	0.51
1:C:191:THR:O	1:C:194:ILE:HG22	2.11	0.51
1:D:180:TYR:HA	1:D:192:LEU:HD21	1.93	0.51
2:L:141:GLN:NE2	2:2:141:GLN:HE21	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:164:GLN:HE21	2:Z:29:LYS:NZ	2.07	0.51
1:O:160:TYR:CD2	1:O:163:THR:HB	2.45	0.51
1:P:191:THR:O	1:P:194:ILE:HG22	2.11	0.51
1:U:70:ILE:HB	1:U:74:VAL:HG13	1.92	0.51
1:U:149:PHE:CE1	1:U:159:GLU:HB2	2.46	0.51
2:V:116:ALA:O	2:2:50:GLY:HA3	2.11	0.51
1:B:160:TYR:CD2	1:B:163:THR:HB	2.45	0.51
1:B:191:THR:O	1:B:194:ILE:HG22	2.11	0.51
1:C:180:TYR:HA	1:C:192:LEU:HD21	1.93	0.51
1:E:42:PHE:CD1	1:E:43:ALA:N	2.78	0.51
1:F:85:ALA:O	1:F:89:VAL:HG23	2.10	0.51
1:F:149:PHE:CE1	1:F:159:GLU:HB2	2.46	0.51
1:F:191:THR:O	1:F:194:ILE:HG22	2.11	0.51
2:I:18:ARG:HE	2:I:30:ASN:HD22	1.57	0.51
2:K:53:GLN:O	2:K:56:VAL:HG12	2.10	0.51
2:L:55:LEU:HD21	2:L:87:LEU:HD11	1.92	0.51
1:O:180:TYR:HA	1:O:192:LEU:HD21	1.93	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:B:85:ALA:O	1:B:89:VAL:HG23	2.11	0.51
1:F:70:ILE:HB	1:F:74:VAL:HG13	1.92	0.51
1:G:149:PHE:CE1	1:G:159:GLU:HB2	2.46	0.51
2:H:116:ALA:O	2:N:50:GLY:HA3	2.11	0.51
2:N:36:GLN:HB2	2:N:184:TYR:CE1	2.46	0.51
1:Q:191:THR:O	1:Q:194:ILE:HG22	2.11	0.51
1:T:149:PHE:CE1	1:T:159:GLU:HB2	2.46	0.51
1:T:180:TYR:HA	1:T:192:LEU:HD21	1.93	0.51
2:W:59:MET:CE	2:W:82:LEU:HD23	2.41	0.51
2:1:131:SER:O	2:1:134:VAL:HG13	2.10	0.51
1:A:130:ARG:NH2	1:G:124:THR:HG22	2.17	0.51
2:I:59:MET:CE	2:I:82:LEU:HD23	2.41	0.51
2:M:62:GLU:HG2	2:M:82:LEU:HD21	1.93	0.51
2:N:123:ILE:HG12	2:N:124:TYR:CD2	2.44	0.51
1:Q:42:PHE:CD1	1:Q:43:ALA:N	2.78	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:149:PHE:CE1	1:S:159:GLU:HB2	2.46	0.51
1:S:191:THR:O	1:S:194:ILE:HG22	2.11	0.51
1:A:191:THR:O	1:A:194:ILE:HG22	2.11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:191:THR:O	1:G:194:ILE:HG22	2.11	0.51
1:P:85:ALA:O	1:P:89:VAL:HG23	2.11	0.51
1:R:191:THR:O	1:R:194:ILE:HG22	2.11	0.51
1:U:85:ALA:O	1:U:89:VAL:HG23	2.10	0.51
1:U:180:TYR:HA	1:U:192:LEU:HD21	1.93	0.51
2:W:15:ALA:HB2	2:W:175:VAL:HB	1.93	0.51
2:Y:53:GLN:O	2:Y:56:VAL:HG12	2.10	0.51
2:2:20:VAL:HG13	2:2:28:HIS:HB2	1.93	0.51
1:A:149:PHE:CE1	1:A:159:GLU:HB2	2.46	0.50
1:B:149:PHE:CE1	1:B:159:GLU:HB2	2.46	0.50
1:B:180:TYR:HA	1:B:192:LEU:HD21	1.93	0.50
2:H:176:ALA:HA	2:H:186:GLN:HA	1.92	0.50
2:J:160:SER:HA	2:J:163:LYS:HD3	1.93	0.50
1:R:108:ASN:CB	2:Z:70:ARG:HG2	2.41	0.50
1:S:70:ILE:HB	1:S:74:VAL:HG13	1.92	0.50
1:T:102:THR:O	2:2:81:THR:HG22	2.12	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:A:70:ILE:HB	1:A:74:VAL:HG13	1.92	0.50
2:M:49:VAL:HG23	2:M:50:GLY:N	2.25	0.50
2:V:124:TYR:HD2	2:V:138:LEU:HD23	1.76	0.50
2:1:62:GLU:HG2	2:1:82:LEU:HD21	1.93	0.50
1:D:108:ASN:CB	2:L:70:ARG:HG2	2.41	0.50
1:E:180:TYR:HA	1:E:192:LEU:HD21	1.93	0.50
1:F:42:PHE:CD1	1:F:43:ALA:N	2.78	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
1:S:180:TYR:HA	1:S:192:LEU:HD21	1.93	0.50
1:T:70:ILE:HB	1:T:74:VAL:HG13	1.92	0.50
2:2:112:SER:O	2:2:113:ILE:HD13	2.12	0.50
1:B:70:ILE:HB	1:B:74:VAL:HG13	1.92	0.50
2:H:124:TYR:HD2	2:H:138:LEU:HD23	1.76	0.50
2:J:174:ASP:HA	2:J:192:ILE:HD13	1.94	0.50
2:1:49:VAL:HG23	2:1:50:GLY:N	2.25	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: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
1:R:70:ILE:HB	1:R:74:VAL:HG13	1.92	0.50
2:X:160:SER:HA	2:X:163:LYS:HD3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:133:PHE:CZ	2:Z:165:ARG:HB3	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: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:R:103:TYR:CE1	2:Z:74:MET:HE2	2.46	0.50
2:X:123:ILE:H	2:X:123:ILE:CD1	2.23	0.50
2:I:59:MET:HE1	2:I:82:LEU:CD2	2.42	0.50
2:I:173:ILE:C	2:I:173:ILE:HD13	2.37	0.50
2:N:123:ILE:H	2:N:123:ILE:CD1	2.24	0.50
2:W:66:TYR:CZ	2:W:70:ARG:HD2	2.46	0.50
2:W:173:ILE:C	2:W:173:ILE:HD13	2.37	0.50
1:E:149:PHE:CE1	1:E:159:GLU:HB2	2.46	0.50
2:M:26:ILE:HD13	2:M:26:ILE:O	2.11	0.50
2:I:66:TYR:CZ	2:I:70:ARG:HD2	2.46	0.49
2:N:18:ARG:HE	2:N:30:ASN:HD22	1.57	0.49
1:O:62:ASN:O	1:O:65:GLU:HG2	2.13	0.49
1:O:137:ILE:HG22	1:O:150:ASP:HB2	1.94	0.49
1:R:180:TYR:HA	1:R:192:LEU:HD21	1.93	0.49
2:1:26:ILE:HD13	2:1:26:ILE:O	2.11	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
1:F:102:THR:O	2:N:81:THR:HG22	2.12	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:S:137:ILE:HG22	1:S:150:ASP:HB2	1.94	0.49
1:T:137:ILE:HG22	1:T:150:ASP:HB2	1.95	0.49
2:V:178:ILE:HB	2:V:184:TYR:HA	1.93	0.49
1:C:62:ASN:O	1:C:65:GLU:HG2	2.13	0.49
1:C:137:ILE:HG22	1:C:150:ASP:HB2	1.95	0.49
2:I:3:THR:OG1	2:I:127:THR:HG22	2.12	0.49
2:L:132:PRO:HA	2:2:133:PHE:CE1	2.47	0.49
1:P:137:ILE:HG22	1:P:150:ASP:HB2	1.94	0.49
1:U:137:ILE:HG22	1:U:150:ASP:HB2	1.95	0.49
1:A:170:ASP:O	1:A:173:VAL:HG12	2.13	0.49
1:E:137:ILE:HG22	1:E:150:ASP:HB2	1.94	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:G:180:TYR:HA	1:G: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:170:ASP:O	1:B:173:VAL:HG12	2.13	0.49
1:D:62:ASN:O	1:D:65:GLU:HG2	2.13	0.49
1:D:137:ILE:HG22	1:D:150:ASP:HB2	1.95	0.49
2:K:179:THR:HG23	2:K:182:ASP:H	1.77	0.49
1:Q:180:TYR:HA	1:Q:192:LEU:HD21	1.93	0.49
1:S:62:ASN:O	1:S:65:GLU:HG2	2.13	0.49
1:S:102:THR:O	2:1:81:THR:HG22	2.13	0.49
1:U:62:ASN:O	1:U:65:GLU:HG2	2.13	0.49
2:Z:189:THR:HG23	2:Z:190:ASP:N	2.28	0.49
1:A:62:ASN:O	1:A:65:GLU:HG2	2.13	0.49
1:D:110:GLU:O	1:D:113:VAL:HG12	2.13	0.49
1:D:228:GLU:O	1:D:231:LYS:HB3	2.13	0.49
1:E:102:THR:O	2:M:81:THR:HG22	2.13	0.49
1:E:108:ASN:CB	2:M:70:ARG:HG2	2.43	0.49
1:Q:110:GLU:O	1:Q:113:VAL:HG12	2.13	0.49
1:Q:170:ASP:O	1:Q:173:VAL:HG12	2.13	0.49
1:R:110:GLU:O	1:R:113:VAL:HG12	2.13	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:F:110:GLU:O	1:F:113:VAL:HG12	2.13	0.49
1:G:110:GLU:O	1:G:113:VAL:HG12	2.13	0.49
1:O:228:GLU:O	1:O:231:LYS:HB3	2.13	0.49
1:P:103:TYR:CE1	2:X:74:MET:HE2	2.47	0.49
1:P:170:ASP:O	1:P:173:VAL:HG12	2.13	0.49
1:R:137:ILE:HG22	1:R:150:ASP:HB2	1.95	0.49
1:T:170:ASP:O	1:T:173:VAL:HG12	2.13	0.49
2:W:59:MET:HE1	2:W:82:LEU:CD2	2.42	0.49
2:X:62:GLU:HG2	2:X:82:LEU:HD21	1.94	0.49
1:C:228:GLU:O	1:C:231:LYS:HB3	2.13	0.49
1:D:170:ASP:O	1:D:173:VAL:HG12	2.13	0.49
1:E:62:ASN:O	1:E:65:GLU:HG2	2.13	0.49
1:F:137:ILE:HG22	1:F:150:ASP:CB	2.43	0.49
1:G:137:ILE:HG22	1:G:150:ASP:HB2	1.95	0.49
2:K:26:ILE:HG23	2:2:165:ARG:HA	1.94	0.49
1:P:62:ASN:O	1:P:65:GLU:HG2	2.13	0.49
1:A:103:TYR:CE1	2:I:74:MET:HE2	2.48	0.49
1:A:110:GLU:O	1:A:113:VAL:HG12	2.13	0.49
1:C:108:ASN:HB2	2:K:70:ARG:HG2	1.94	0.49
1:C:110:GLU:O	1:C:113:VAL:HG12	2.13	0.49
2:H:26:ILE:HG23	2:X:165:ARG:HA	1.94	0.49
2:H:178:ILE:HB	2:H:184:TYR:HA	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:110:GLU:O	1:O:113:VAL:HG12	2.13	0.49
1:P:137:ILE:HG22	1:P:150:ASP:CB	2.43	0.49
1:Q:137:ILE:HG22	1:Q:150:ASP:CB	2.43	0.49
1:R:137:ILE:HG22	1:R:150:ASP:CB	2.43	0.49
1:R:159:GLU:HG2	1:S:60:GLU:HG3	1.95	0.49
1:U:170:ASP:O	1:U:173:VAL:HG12	2.13	0.49
2:W:124:TYR:HD2	2:W:138:LEU:HD23	1.78	0.49
1:B:62:ASN:O	1:B:65:GLU:HG2	2.13	0.49
1:C:137:ILE:HG22	1:C:150:ASP:CB	2.43	0.49
1:E:170:ASP:O	1:E:173:VAL:HG12	2.13	0.49
1:F:62:ASN:O	1:F:65:GLU:HG2	2.13	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:R:228:GLU:O	1:R:231:LYS:HB3	2.13	0.49
1:U:228:GLU:O	1:U:231:LYS:HB3	2.13	0.49
2:X:66:TYR:CD2	2:X:74:MET:HE2	2.48	0.49
1:B:228:GLU:O	1:B:231:LYS:HB3	2.13	0.48
1:F:137:ILE:HG22	1:F:150:ASP:HB2	1.95	0.48
1:F:228:GLU:O	1:F:231:LYS:HB3	2.13	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:112:SER:O	2:N:113:ILE:HD13	2.12	0.48
2:N:141:GLN:HE21	2:Z:141:GLN:NE2	2.11	0.48
1:P:110:GLU:O	1:P:113:VAL:HG12	2.13	0.48
1:Q:137:ILE:HG22	1:Q:150:ASP:HB2	1.95	0.48
1:T:137:ILE:HG22	1:T:150:ASP:CB	2.43	0.48
1:U:107:VAL:HG11	2:V:66:TYR:HH	1.70	0.48
1:U:110:GLU:O	1:U:113:VAL:HG12	2.13	0.48
1:U:137:ILE:HG22	1:U:150:ASP:CB	2.43	0.48
1:A:137:ILE:HG22	1:A:150:ASP:CB	2.43	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:R:62:ASN:O	1:R:65:GLU:HG2	2.13	0.48
1:R:170:ASP:O	1:R:173:VAL:HG12	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:228:GLU:O	1:A:231:LYS:HB3	2.13	0.48
2:N:1:THR:H3	2:N:129:SER:HB3	1.79	0.48
1:Q:62:ASN:O	1:Q:65:GLU:HG2	2.13	0.48
1:S:110:GLU:O	1:S:113:VAL:HG12	2.13	0.48
1:T:62:ASN:O	1:T:65:GLU:HG2	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:179:THR:HG23	2:Y:182:ASP:H	1.77	0.48
1:B:110:GLU:O	1:B:113:VAL:HG12	2.13	0.48
1:B:137:ILE:HG22	1:B:150:ASP:CB	2.43	0.48
1:D:137:ILE:HG22	1:D:150:ASP:CB	2.43	0.48
1:F:148:LEU:O	1:F:159:GLU:HG3	2.14	0.48
2:H:12:VAL:HG13	2:H:178:ILE:HG23	1.96	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
2:V:36:GLN:HB2	2:V:184:TYR:CE1	2.48	0.48
1:A:108:ASN:HB3	2:I:70:ARG:HG2	1.95	0.48
1:B:103:TYR:CE1	2:J:74:MET:HE2	2.47	0.48
1:E:110:GLU:O	1:E:113:VAL:HG12	2.13	0.48
1:E:137:ILE:HG22	1:E:150:ASP:CB	2.43	0.48
1:G:62:ASN:O	1:G:65:GLU:HG2	2.13	0.48
1:G:148:LEU:O	1:G:159:GLU:HG3	2.14	0.48
2:H:36:GLN:HB2	2:H:184:TYR:CE1	2.48	0.48
2:K:175:VAL:CG2	2:K:176:ALA:N	2.75	0.48
1:S:108:ASN:CB	2:1:70:ARG:HG2	2.43	0.48
1:S:137:ILE:HG22	1:S:150:ASP:CB	2.43	0.48
2:2:123:ILE:HD13	2:2:123:ILE:N	2.26	0.48
1:A:148:LEU:O	1:A:159:GLU:HG3	2.14	0.48
2:H:17:GLU:HB2	2:H:170:GLY:O	2.14	0.48
2:L:18:ARG:HE	2:L:30:ASN:HD22	1.61	0.48
2:L:189:THR:HG23	2:L:190:ASP:N	2.28	0.48
2:N:139:GLU:OE1	2:Z:165:ARG:NE	2.46	0.48
1:O:103:TYR:CE1	2:W:74:MET:HE2	2.48	0.48
1:Q:108:ASN:HB2	2:Y:70:ARG:HG2	1.94	0.48
1:Q:148:LEU:O	1:Q:159:GLU:HG3	2.14	0.48
1:R:148:LEU:O	1:R: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:B:148:LEU:O	1:B:159:GLU:HG3	2.14	0.48
1:G:170:ASP:O	1:G:173:VAL:HG12	2.13	0.48
2:J:66:TYR:CD2	2:J:74:MET:HE2	2.48	0.48
1:P:148:LEU:O	1:P:159:GLU:HG3	2.14	0.48
1:S:148:LEU:O	1:S:159:GLU:HG3	2.14	0.48
1:T:110:GLU:O	1:T:113:VAL:HG12	2.12	0.48
1:D:159:GLU:HG2	1:E:60:GLU:HG3	1.95	0.48
1:E:148:LEU:O	1:E:159:GLU:HG3	2.14	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:O:137:ILE:HG22	1:O:150:ASP:CB	2.43	0.48
1:T:148:LEU:O	1:T:159:GLU:HG3	2.14	0.48
2:X:109:HIS:HB3	2:X:111:PHE:HE1	1.79	0.48
1:A:134:VAL:O	1:A:153:PRO:HG3	2.14	0.48
1:C:148:LEU:O	1:C:159:GLU:HG3	2.14	0.48
2:I:32:LYS:HE2	2:I:34:LEU:O	2.14	0.48
2:K:44:THR:OG1	2:K:100:LEU:HB3	2.14	0.48
1:S:134:VAL:O	1:S:153:PRO:HG3	2.14	0.48
1:T:134:VAL:O	1:T:153:PRO:HG3	2.14	0.48
2:Z:178:ILE:O	2:Z:178:ILE:HG12	2.14	0.48
2:1:179:THR:HG23	2:1:182:ASP:H	1.79	0.48
1:A:107:VAL:HG11	2:I:66:TYR:HH	1.76	0.47
1:F:134:VAL:O	1:F:153:PRO:HG3	2.14	0.47
2:H:25:PHE:CD1	2:H:25:PHE:C	2.90	0.47
2:J:141:GLN:NE2	2:W:141:GLN:HE21	2.11	0.47
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
2:Z:25:PHE:CD1	2:Z:25:PHE:C	2.91	0.47
2:1:74:MET:HG2	2:1:78:ALA:HB3	1.96	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:V:66:TYR:CZ	2:V:70:ARG:HD2	2.49	0.47
2:V:126:SER:HB3	2:V:135:TYR:CE2	2.49	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:X:45:ILE:HD11	2:X:52:ALA:O	2.14	0.47
2:Y:44:THR:OG1	2:Y:100:LEU:HB3	2.14	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:J:159:ILE:O	2:J:163:LYS:HG3	2.14	0.47
2:K:103:GLY:HA2	2:K:178:ILE:CD1	2.44	0.47
2:L:25:PHE:CD1	2:L:25:PHE:C	2.91	0.47
2:W:25:PHE:CD1	2:W:25:PHE:C	2.91	0.47
2:Y:124:TYR:HD2	2:Y:138:LEU:HD23	1.80	0.47
2:2:76:ILE:HG21	2:2:109:HIS:HB2	1.96	0.47
2:K:133:PHE:CZ	2:K:165:ARG:HB3	2.48	0.47
2:M:7:THR:HB	2:M:123:ILE:O	2.14	0.47
2:M:74:MET:HG2	2:M:78:ALA:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:61:GLN:CD	1:R:62:ASN:H	2.23	0.47
1:S:61:GLN:CD	1:S:62:ASN:H	2.23	0.47
1:U:134:VAL:O	1:U:153:PRO:HG3	2.14	0.47
2:V:55:LEU:HD12	2:V:55:LEU:HA	1.50	0.47
2:W:22:MET:O	2:W:23:GLU:HB2	2.14	0.47
1:D:12:ILE:CG1	1:D:14:VAL:HG22	2.44	0.47
1:D:134:VAL:O	1:D:153:PRO:HG3	2.14	0.47
1:E:12:ILE:CG1	1:E:14:VAL:HG22	2.44	0.47
1:F:12:ILE:CG1	1:F:14:VAL:HG22	2.44	0.47
1:G:61:GLN:CD	1:G:62:ASN:H	2.23	0.47
2:H:6:ILE:HD11	2:H:142:TYR:HD1	1.79	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: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:108:ASN:HB3	2:W:70:ARG:HG2	1.95	0.47
1:O:134:VAL:O	1:O:153:PRO:HG3	2.14	0.47
1:R:12:ILE:CG1	1:R:14:VAL:HG22	2.44	0.47
2:V:12:VAL:HG13	2:V:178:ILE:HG23	1.96	0.47
2:X:159:ILE:O	2:X:163:LYS:HG3	2.14	0.47
1:A:61:GLN:CD	1:A:62:ASN:H	2.23	0.47
1:C:134:VAL:O	1:C:153:PRO:HG3	2.14	0.47
2:Y:50:GLY:O	2:Y:54:VAL:HG12	2.14	0.47
2:Y:133:PHE:CZ	2:Y:165:ARG:HB3	2.49	0.47
1:A:175:PHE:CD2	1:A:196:ALA:HA	2.50	0.47
1:C:12:ILE:CG1	1:C:14:VAL:HG22	2.44	0.47
1:E:61:GLN:CD	1:E:62:ASN:H	2.22	0.47
1:F:61:GLN:CD	1:F:62:ASN:H	2.23	0.47
1:G:12:ILE:CG1	1:G:14:VAL:HG22	2.44	0.47
2:H:20:VAL:HG22	2:H:28:HIS:HB2	1.97	0.47
2:H:66:TYR:CZ	2:H:70:ARG:HD2	2.49	0.47
2:H:126:SER:HB3	2:H:135:TYR:CE2	2.49	0.47
2:H:165:ARG:C	2:X:26:ILE:HG22	2.39	0.47
2:I:141:GLN:HE21	2:X:141:GLN:NE2	2.12	0.47
2:J:109:HIS:HB3	2:J:111:PHE:HE1	1.79	0.47
2:L:178:ILE:O	2:L:178:ILE:HG12	2.14	0.47
2:M:184:TYR:CD1	2:M:184:TYR:C	2.93	0.47
1:O:175:PHE:CD2	1:O:196:ALA:HA	2.50	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:S:175:PHE:CD2	1:S:196:ALA:HA	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:61:GLN:CD	1:U:62:ASN:H	2.23	0.47
1:U:175:PHE:CD2	1:U:196:ALA:HA	2.50	0.47
2:V:17:GLU:HB2	2:V:170:GLY:O	2.14	0.47
2:V:25:PHE:C	2:V:25:PHE:CD1	2.90	0.47
2:W:189:THR:HG23	2:W:190:ASP:H	1.79	0.47
2:X:18:ARG:HB2	2:X:31:GLY:O	2.13	0.47
2:X:37:ILE:HD11	2:X:59:MET:CB	2.37	0.47
2:X:175:VAL:CG2	2:X:176:ALA:N	2.78	0.47
2:Y:74:MET:HG2	2:Y:78:ALA:HB3	1.97	0.47
2:Y:103:GLY:HA2	2:Y:178:ILE:CD1	2.44	0.47
2:Z:18:ARG:HE	2:Z:30:ASN:HD22	1.61	0.47
1:C:61:GLN:CD	1:C:62:ASN:H	2.23	0.47
1:D:61:GLN:CD	1:D:62:ASN:H	2.23	0.47
2:L:174:ASP:HA	2:L:192:ILE:HD13	1.96	0.47
2:N:18:ARG:HB2	2:N:31:GLY:O	2.15	0.47
2:N:76:ILE:HG21	2:N:109:HIS:HB2	1.96	0.47
2:N:91:LYS:O	2:N:94:PRO:HD3	2.15	0.47
1:S:12:ILE:CG1	1:S:14:VAL:HG22	2.44	0.47
2:2:1:THR:H3	2:2:129:SER:HB3	1.78	0.47
1:B:12:ILE:CG1	1:B:14:VAL:HG22	2.44	0.47
1:C:175:PHE:CD2	1:C:196:ALA:HA	2.50	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:L:124:TYR:HD2	2:L:138:LEU:HD23	1.76	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
1:P:175:PHE:CD2	1:P:196:ALA:HA	2.50	0.47
2:V:37:ILE:HD11	2:V:59:MET:CB	2.45	0.47
2:W:175:VAL:CG2	2:W: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:A:12:ILE:CG1	1:A:14:VAL:HG22	2.44	0.47
1:B:61:GLN:CD	1:B:62:ASN:H	2.23	0.47
1:D:175:PHE:CD2	1:D:196:ALA:HA	2.50	0.47
1:E:175:PHE:CD2	1:E:196:ALA:HA	2.50	0.47
1:G:175:PHE:CD2	1:G:196:ALA:HA	2.50	0.47
2:I:35:PHE:CE2	2:I:45:ILE:HD12	2.50	0.47
2:I:189:THR:HG23	2:I:190:ASP:H	1.79	0.47
1:O:12:ILE:CG1	1:O:14:VAL:HG22	2.44	0.47
1:P:61:GLN:CD	1:P:62:ASN:H	2.23	0.47
1:Q:61:GLN:CD	1:Q:62:ASN:H	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:61:GLN:CD	1:T:62:ASN:H	2.23	0.47
1:T:175:PHE:CD2	1:T:196:ALA:HA	2.50	0.47
1:U:12:ILE:CG1	1:U:14:VAL:HG22	2.44	0.47
2:1:7:THR:HB	2:1:123:ILE:O	2.14	0.47
1:B:175:PHE:CD2	1:B:196:ALA:HA	2.50	0.46
1:F:44:ASN:HD22	1:F:44:ASN:HA	1.56	0.46
2:H:193:GLU:HA	2:H:196:ILE:HD12	1.98	0.46
2:M:22:MET:O	2:M:23:GLU:HB2	2.15	0.46
2:N:55:LEU:HD21	2:N:87:LEU:HD11	1.97	0.46
2:N:123:ILE:HD13	2:N:123:ILE:N	2.26	0.46
1:Q:44:ASN:HD22	1:Q:44:ASN:HA	1.56	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:X:81:THR:O	2:X:84:SER:HB3	2.15	0.46
2:Y:43:MET:CE	2:Y:56:VAL:HG23	2.45	0.46
2:1:22:MET:O	2:1:23:GLU:HB2	2.15	0.46
1:E:134:VAL:O	1:E:153:PRO:HG3	2.14	0.46
2:H:37:ILE:HD11	2:H:59:MET:CB	2.45	0.46
2:I:25:PHE:C	2:I:25:PHE:CD1	2.91	0.46
2:J:138:LEU:HD12	2:J:138:LEU:HA	1.68	0.46
2:K:27:MET:HG2	2:K:27:MET:O	2.16	0.46
2:K:50:GLY:O	2:K:54:VAL:HG12	2.14	0.46
2:M:124:TYR:HD2	2:M:138:LEU:HD23	1.76	0.46
1:O:98:GLN:O	1:O:102:THR:HG23	2.15	0.46
1:R:198:LYS:O	1:R:199:SER:C	2.59	0.46
1:S:198:LYS:O	1:S:199:SER:C	2.59	0.46
1:T:12:ILE:CG1	1:T:14:VAL:HG22	2.44	0.46
1:T:98:GLN:O	1:T:102:THR:HG23	2.15	0.46
2:V:177:VAL:HG12	2:V:187:LEU:CD1	2.46	0.46
1:A:198:LYS:O	1:A:199:SER:C	2.59	0.46
1:B:107:VAL:HG11	2:J:66:TYR:HH	1.73	0.46
1:C:98:GLN:O	1:C:102:THR:HG23	2.15	0.46
1:F:198:LYS:O	1:F:199:SER:C	2.59	0.46
1:G:198:LYS:O	1:G:199:SER:C	2.59	0.46
2:H:177:VAL:HG12	2:H:187:LEU:CD1	2.46	0.46
2:I:175:VAL:CG2	2:I:176:ALA:N	2.78	0.46
2:K:74:MET:HG2	2:K:78:ALA:HB3	1.97	0.46
2:M:110:VAL:O	2:M:110:VAL:HG13	2.16	0.46
2:N:93:MET:N	2:N:94:PRO:CD	2.77	0.46
1:P:134:VAL:O	1:P:153:PRO:HG3	2.14	0.46
1:Q:198:LYS:O	1:Q:199:SER:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:175:PHE:CD2	1:R:196:ALA:HA	2.50	0.46
2:W:35:PHE:CE2	2:W:45:ILE:HD12	2.50	0.46
2:2:18:ARG:HB2	2:2:31:GLY:O	2.15	0.46
2:2:175:VAL:CG2	2:2:176:ALA:N	2.78	0.46
2:J:175:VAL:CG2	2:J:176:ALA:N	2.78	0.46
2:J:179:THR:HG23	2:J:182:ASP:H	1.80	0.46
2:K:48:LEU:HD12	2:K:49:VAL:N	2.31	0.46
2:N:109:HIS:HB3	2:N:111:PHE:HE1	1.81	0.46
2:X:138:LEU:HD12	2:X:138:LEU:HA	1.68	0.46
2:2:91:LYS:O	2:2:94:PRO:HD3	2.15	0.46
1:B:198:LYS:O	1:B:199:SER:C	2.59	0.46
2:I:20:VAL:CG1	2:I:28:HIS:HB2	2.44	0.46
2:J:26:ILE:HG22	2:V:165:ARG:C	2.40	0.46
2:L:132:PRO:HA	2:2:133:PHE:HE1	1.81	0.46
2:N:37:ILE:HD11	2:N:59:MET:CG	2.46	0.46
1:O:61:GLN:CD	1:O:62:ASN:H	2.23	0.46
1:Q:175:PHE:CD2	1:Q:196:ALA:HA	2.50	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
1:E:98:GLN:O	1:E:102:THR:HG23	2.15	0.46
1:F:175:PHE:CD2	1:F:196:ALA:HA	2.50	0.46
2:I:138:LEU:HD12	2:I:154:LEU:HD11	1.98	0.46
1:P:198:LYS:O	1:P:199:SER:C	2.59	0.46
1:Q:98:GLN:O	1:Q:102:THR:HG23	2.15	0.46
1:U:98:GLN:O	1:U:102:THR:HG23	2.16	0.46
2:V:7:THR:HB	2:V:123:ILE:O	2.16	0.46
2:V:193:GLU:HA	2:V:196:ILE:HD12	1.97	0.46
2:2:37:ILE:HD11	2:2:59:MET:CG	2.46	0.46
1:G:98:GLN:O	1:G:102:THR:HG23	2.16	0.46
2:L:103:GLY:HA2	2:L:178:ILE:HD11	1.98	0.46
2:L:165:ARG:NE	2:2:139:GLU:OE1	2.49	0.46
1:R:177:GLU:O	1:S:57:ARG:NE	2.46	0.46
2:V:72:VAL:HG22	2:V:73:ASN:N	2.31	0.46
2:W:20:VAL:CG1	2:W:28:HIS:HB2	2.44	0.46
2:X:179:THR:HG23	2:X:182:ASP:H	1.80	0.46
2:1:184:TYR:CD1	2:1:184:TYR:C	2.93	0.46
1:B:98:GLN:O	1:B:102:THR:HG23	2.16	0.46
1:D:98:GLN:O	1:D:102:THR:HG23	2.16	0.46
1:E:198:LYS:O	1:E:199:SER:C	2.59	0.46
2:N:27:MET:O	2:N:27:MET:HG2	2.15	0.46
1:T:198:LYS:O	1:T:199:SER:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:174:ASP:HA	2:1:192:ILE:HD13	1.98	0.46
1:A:98:GLN:O	1:A:102:THR:HG23	2.16	0.46
1:F:98:GLN:O	1:F:102:THR:HG23	2.15	0.46
2:K:17:GLU:HA	2:K:173:ILE:HA	1.98	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:X:189:THR:HG23	2:X:190:ASP:H	1.81	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
1:P:44:ASN:HD22	1:P:44:ASN:HA	1.56	0.46
2:V:20:VAL:HG22	2:V:28:HIS:HB2	1.96	0.46
1:C:161:LYS:HD2	1:D:60:GLU:OE2	2.17	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:S:98:GLN:O	1:S:102:THR:HG23	2.16	0.45
1:T:52:LYS:HE3	1:T:64:ILE:HG23	1.99	0.45
1:E:44:ASN:HD22	1:E:44:ASN:HA	1.56	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: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:M:6:ILE:HG23	2:M:6:ILE:O	2.16	0.45
2:M:15:ALA:HB3	2:M:155:VAL:HG11	1.98	0.45
2:Y:17:GLU:HA	2:Y:173:ILE:HA	1.98	0.45
2:Y:27:MET:HG2	2:Y:27:MET:O	2.16	0.45
2:2:97:VAL:HG22	2:2:98:GLN:N	2.32	0.45
1:B:52:LYS:HE3	1:B:64:ILE:HG23	1.99	0.45
2:J:105:ASP:OD1	2:J:106:THR:N	2.50	0.45
2:K:43:MET:CE	2:K:56:VAL:HG23	2.45	0.45
2:L:19:ARG:HE	2:L:26:ILE:HG13	1.81	0.45
2:M:174:ASP:HA	2:M:192:ILE:HD13	1.98	0.45
2:N:124:TYR:HD1	2:N:138:LEU:HD23	1.81	0.45
1:P:98:GLN:O	1:P:102:THR:HG23	2.16	0.45
1:R:52:LYS:HE3	1:R:64:ILE:HG23	1.99	0.45
1:S:52:LYS:HE3	1:S:64:ILE:HG23	1.99	0.45
1:T:24:VAL:O	1:T:28:ARG:HG3	2.17	0.45
2:Y:48:LEU:HD12	2:Y:49:VAL:N	2.31	0.45
2:2:123:ILE:H	2:2:123:ILE:CD1	2.24	0.45
1:C:52:LYS:HE3	1:C:64:ILE:HG23	1.99	0.45
1:C:99:GLU:OE2	2:K:70:ARG:NH1	2.49	0.45
2:L:19:ARG:NE	2:L:26:ILE:HG13	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:75:PRO:O	2:L:78:ALA:HB3	2.16	0.45
1:U:52:LYS:HE3	1:U:64:ILE:HG23	1.99	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:Y:149:ASP:O	2:Y:152:VAL:HG12	2.17	0.45
2:1:110:VAL:O	2:1:110:VAL:HG13	2.16	0.45
2:2:37:ILE:HD11	2:2:59:MET:CB	2.43	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:H:22:MET:O	2:H:23:GLU:HB2	2.17	0.45
2:H:66:TYR:CD1	2:H:66:TYR:C	2.94	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:M:55:LEU:HD12	2:M:55:LEU:HA	1.76	0.45
2:N:8:LEU:HD12	2:N:8:LEU:O	2.17	0.45
2:Y:75:PRO:O	2:Y:78:ALA:HB3	2.16	0.45
2:2:180:ARG:HD2	2:2:180:ARG:HA	1.80	0.45
1:B:24:VAL:O	1:B:28:ARG:HG3	2.17	0.45
1:G:49:ILE:HD11	1:G:210:PRO:CB	2.47	0.45
2:H:7:THR:HB	2:H:123:ILE:O	2.16	0.45
2:H:72:VAL:HG22	2:H:73:ASN:N	2.31	0.45
2:K:75:PRO:O	2:K:78:ALA:HB3	2.16	0.45
2:L:6:ILE:HD11	2:L:142:TYR:CD1	2.52	0.45
2:L:110:VAL:O	2:L:110:VAL:HG13	2.16	0.45
1:O:198:LYS:O	1:O:199:SER:C	2.59	0.45
1:Q:18:ASP:OD2	1:Q:20:ARG:HD3	2.17	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
1:T:21:LEU:HD11	1:U:130:ARG:CD	2.43	0.45
1:U:24:VAL:O	1:U:28:ARG:HG3	2.17	0.45
2:W:105:ASP:OD1	2:W:106:THR:N	2.49	0.45
2:Z:19:ARG:HE	2:Z:26:ILE:HG13	1.82	0.45
2:Z:110:VAL:O	2:Z:110:VAL:HG13	2.16	0.45
2:Z:187:LEU:HA	2:Z:188:PRO:HD3	1.77	0.45
1:A:23:GLN:HE22	1:G:15:PHE:HB2	1.82	0.45
1:B:18:ASP:OD2	1:B:20:ARG:HD3	2.17	0.45
1:C:198:LYS:O	1:C:199:SER:C	2.59	0.45
1:E:78:THR:CG2	1:E:85:ALA:HB1	2.45	0.45
1:F:49:ILE:HD11	1:F:210:PRO:CB	2.47	0.45
1:G:52:LYS:HE3	1:G:64:ILE:HG23	1.99	0.45
2:N:97:VAL:HG22	2:N:98:GLN:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:180:ARG:HD2	2:N:180:ARG:HA	1.80	0.45
1:Q:49:ILE:HD11	1:Q:210:PRO:CB	2.47	0.45
1:Q:99:GLU:OE2	2:Y:70:ARG:NH1	2.49	0.45
1:T:18:ASP:OD2	1:T:20:ARG:HD3	2.17	0.45
1:U:102:THR:O	2:V:81:THR:HG22	2.17	0.45
2:V:66:TYR:CD1	2:V:66:TYR:C	2.94	0.45
2:W:2:THR:HG22	2:W:169:SER:OG	2.17	0.45
2:2:97:VAL:HG22	2:2:98:GLN:H	1.81	0.45
1:C:18:ASP:OD2	1:C:20:ARG:HD3	2.17	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
2:K:55:LEU:HD12	2:K:55:LEU:HA	1.79	0.45
2:K:149:ASP:O	2:K:152:VAL:HG12	2.17	0.45
2:M:180:ARG:HA	2:M:180:ARG:HD2	1.77	0.45
1:P:18:ASP:OD2	1:P:20:ARG:HD3	2.17	0.45
1:R:49:ILE:HD11	1:R:210:PRO:CB	2.47	0.45
2:W:146:MET:HA	2:W:150:GLU:OE1	2.17	0.45
2:1:6:ILE:HG23	2:1:6:ILE:O	2.16	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:A:24:VAL:O	1:A:28:ARG:HG3	2.17	0.45
1:A:49:ILE:HD11	1:A:210:PRO:CB	2.47	0.45
1:D:52:LYS:HE3	1:D:64:ILE:HG23	1.99	0.45
1:F:52:LYS:HE3	1:F:64:ILE:HG23	1.99	0.45
2:I:2:THR:HG22	2:I:169:SER:OG	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:O:52:LYS:HE3	1:O:64:ILE:HG23	1.99	0.45
1:U:18:ASP:OD2	1:U:20:ARG:HD3	2.17	0.45
2:V:6:ILE:HD11	2:V:142:TYR:HD1	1.79	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:Y:160:SER:HA	2:Y:163:LYS:HD3	1.98	0.45
2:Z:75:PRO:O	2:Z:78:ALA:HB3	2.16	0.45
1:C:49:ILE:HD11	1:C:210:PRO:CB	2.47	0.44
2:J:123:ILE:HG12	2:J:124:TYR:CD1	2.51	0.44
2:J:189:THR:HG23	2:J:190:ASP:H	1.81	0.44
1:O:44:ASN:HD22	1:O:44:ASN:HA	1.56	0.44
2:Y:111:PHE:CE2	2:Y:121:GLU:HB2	2.51	0.44
2:Z:8:LEU:HD12	2:Z:8:LEU:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:19:ARG:NE	2:Z:26:ILE:HG13	2.32	0.44
2:2:19:ARG:HD2	2:2:169:SER:C	2.43	0.44
1:A:130:ARG:HH21	1:G:124:THR:CG2	2.21	0.44
2:L:8:LEU:O	2:L:8:LEU:HD12	2.17	0.44
2:N:7:THR:HB	2:N:123:ILE:O	2.18	0.44
1:P:78:THR:CG2	1:P:85:ALA:HB1	2.45	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
1:U:49:ILE:HD11	1:U:210:PRO:CB	2.47	0.44
1:U:198:LYS:O	1:U:199:SER:C	2.59	0.44
2:V:15:ALA:HB2	2:V:175:VAL:HB	1.99	0.44
2:Y:187:LEU:HA	2:Y:188:PRO:HD3	1.76	0.44
2:2:8:LEU:HD12	2:2:8:LEU:O	2.17	0.44
1:D:18:ASP:OD2	1:D:20:ARG:HD3	2.17	0.44
1:D:24:VAL:O	1:D:28:ARG:HG3	2.17	0.44
1:D:198:LYS:O	1:D:199:SER:C	2.59	0.44
2:L:93:MET:N	2:L:94:PRO:CD	2.81	0.44
1:P:49:ILE:HD11	1:P:210:PRO:CB	2.47	0.44
1:P:52:LYS:HE3	1:P:64:ILE:HG23	1.99	0.44
1:Q:124:THR:HG22	1:R:130:ARG:NH2	2.24	0.44
1:R:176:LEU:HB3	1:S:58:LEU:HD21	1.99	0.44
1:A:18:ASP:OD2	1:A:20:ARG:HD3	2.17	0.44
1:D:177:GLU:O	1:E:57:ARG:NE	2.46	0.44
2:H:27:MET:O	2:H:27:MET:HG2	2.17	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:P:24:VAL:O	1:P:28:ARG:HG3	2.17	0.44
1:R:18:ASP:OD2	1:R:20:ARG:HD3	2.17	0.44
1:S:49:ILE:HD11	1:S:210:PRO:CB	2.47	0.44
2:W:138:LEU:HD12	2:W:154:LEU:HD11	1.98	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:E:52:LYS:HE3	1:E:64:ILE:HG23	1.99	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
2:Z:59:MET:HE1	2:Z:82:LEU:CD2	2.48	0.44
2:2:173:ILE:HD13	2:2:173:ILE:C	2.43	0.44
1:A:12:ILE:HG13	1:A:14:VAL:H	1.73	0.44
1:D:15:PHE:HB2	1:E:23:GLN:HE22	1.82	0.44
1:E:24:VAL:O	1:E:28:ARG:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:49:ILE:HD11	1:E:210:PRO:CB	2.47	0.44
1:F:71:ASP:HA	2:M:68:LEU:HD21	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
2:J:123:ILE:H	2:J:123:ILE:CD1	2.23	0.44
2:L:74:MET:HG2	2:L:78:ALA:HB3	2.00	0.44
2:N:19:ARG:HD2	2:N:169:SER:C	2.42	0.44
2:N:49:VAL:O	2:N:50:GLY:C	2.61	0.44
2:N:130:GLY:O	2:N:134:VAL:HG12	2.17	0.44
1:R:81:LEU:HD23	1:R:133:GLY:HA3	2.00	0.44
1:S:81:LEU:HD23	1:S:133:GLY:HA3	2.00	0.44
2:Z:17:GLU:HA	2:Z:173:ILE:HA	1.99	0.44
1:A:81:LEU:HD23	1:A:133:GLY:HA3	2.00	0.44
1:D:44:ASN:HD22	1:D:44:ASN:HA	1.56	0.44
1:G:18:ASP:OD2	1:G:20:ARG:HD3	2.17	0.44
2:H:59:MET:HE2	2:H:79:VAL:CG2	2.47	0.44
2:N:25:PHE:C	2:N:25:PHE:HD1	2.26	0.44
1:O:78:THR:CG2	1:O:85:ALA:HB1	2.45	0.44
1:R:15:PHE:HB2	1:S:23:GLN:HE22	1.82	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
2:Z:74:MET:HG2	2:Z:78:ALA:HB3	2.00	0.44
1:A:32:LYS:O	1:A:167:SER:HA	2.18	0.44
1:B:32:LYS:O	1:B:167:SER:HA	2.18	0.44
1:B:49:ILE:HD11	1:B:210:PRO:CB	2.47	0.44
1:G:16:SER:HB3	1:G:22:PHE:CE2	2.53	0.44
1:G:81:LEU:HD23	1:G:133:GLY:HA3	2.00	0.44
2:K:19:ARG:HD2	2:K:169:SER:C	2.43	0.44
1:Q:24:VAL:O	1:Q:28:ARG:HG3	2.17	0.44
1:Q:81:LEU:HD23	1:Q:133:GLY:HA3	2.00	0.44
1:S:124:THR:HG22	1:T:130:ARG:NH2	2.25	0.44
2:V:90:VAL:O	2:V:90:VAL:HG22	2.18	0.44
2:Z:76:ILE:HA	2:Z:79:VAL:HG12	2.00	0.44
1:F:24:VAL:O	1:F:28:ARG:HG3	2.17	0.44
2:H:15:ALA:HB2	2:H:175:VAL:HB	1.99	0.44
2:K:76:ILE:O	2:K:79:VAL:HG12	2.18	0.44
1:P:81:LEU:HD23	1:P:133:GLY:HA3	2.00	0.44
1:R:16:SER:HB3	1:R:22:PHE:CE2	2.53	0.44
1:T:32:LYS:O	1:T:167:SER:HA	2.18	0.44
2:Y:34:LEU:HD21	2:Y:176:ALA:HB3	2.00	0.44
2:2:124:TYR:HD1	2:2:138:LEU:HD23	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:160:SER:HA	2:2:163:LYS:HD3	2.00	0.44
1:B:81:LEU:HD23	1:B:133:GLY:HA3	2.00	0.43
1:C:130:ARG:NH1	1:C:131:PRO:O	2.51	0.43
1:D:17:PRO:HA	1:E:26:TYR:CD1	2.53	0.43
1:E:16:SER:HB3	1:E:22:PHE:CE2	2.53	0.43
1:F:81:LEU:HD23	1:F:133:GLY:HA3	2.00	0.43
1:G:24:VAL:O	1:G:28:ARG:HG3	2.17	0.43
2:L:59:MET:HE1	2:L:82:LEU:CD2	2.48	0.43
2:M:93:MET:N	2:M:94:PRO:CD	2.81	0.43
2:N:83:LEU:HD12	2:N:83:LEU:HA	1.85	0.43
1:O:18:ASP:OD2	1:O:20:ARG:HD3	2.17	0.43
1:P:16:SER:HB3	1:P:22:PHE:CE2	2.53	0.43
1:T:71:ASP:HA	2:1:68:LEU:HD21	2.00	0.43
1:T:81:LEU:HD23	1:T:133:GLY:HA3	2.00	0.43
1:U:130:ARG:NH1	1:U:131:PRO:O	2.51	0.43
2:W:187:LEU:HA	2:W:188:PRO:HD3	1.83	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
2:L:178:ILE:HB	2:L:184:TYR:HA	2.00	0.43
2:N:165:ARG:HA	2:Y:26:ILE:CG2	2.48	0.43
1:O:130:ARG:NH1	1:O:131:PRO:O	2.51	0.43
1:S:12:ILE:HG13	1:S:14:VAL:H	1.74	0.43
2:Y:19:ARG:HD2	2:Y:169:SER:C	2.43	0.43
2:2:111:PHE:CE2	2:2:121:GLU:HB2	2.53	0.43
1:D:130:ARG:NH1	1:D:131:PRO:O	2.51	0.43
1:D:176:LEU:HB3	1:E:58:LEU:HD21	1.99	0.43
1:E:109:ILE:CG2	1:E:147:ARG:HD3	2.49	0.43
1:G:109:ILE:CG2	1:G:147:ARG:HD3	2.49	0.43
2:J:49:VAL:HG23	2:J:50:GLY:H	1.82	0.43
2:M:133:PHE:HE1	2:1:132:PRO:HA	1.81	0.43
2:N:138:LEU:HD12	2:N:138:LEU:HA	1.71	0.43
1:P:109:ILE:CG2	1:P:147:ARG:HD3	2.48	0.43
1:S:44:ASN:HD22	1:S:44:ASN:HA	1.56	0.43
2:V:17:GLU:HA	2:V:173:ILE:HA	2.01	0.43
2:W:184:TYR:CD1	2:W:184:TYR:C	2.97	0.43
2:2:49:VAL:O	2:2:50:GLY:C	2.61	0.43
1:A:52:LYS:HZ3	1:A:62:ASN:HA	1.77	0.43
1:E:187:LYS:O	1:E:190:VAL:HG13	2.19	0.43
2:H:90:VAL:O	2:H:90:VAL:HG22	2.18	0.43
2:L:189:THR:HG23	2:L:190:ASP:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:141:GLN:NE2	2:Z:141:GLN:HE21	2.15	0.43
2:N:173:ILE:HD13	2:N:173:ILE:C	2.43	0.43
1:P:187:LYS:O	1:P:190:VAL:HG13	2.19	0.43
1:R:109:ILE:CG2	1:R:147:ARG:HD3	2.48	0.43
1:S:52:LYS:HB3	1:S:209:ALA:O	2.19	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
2:Z:6:ILE:HD11	2:Z:142:TYR:CD1	2.52	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:G:32:LYS:O	1:G:167:SER:HA	2.18	0.43
2:H:17:GLU:HA	2:H:173:ILE:HA	2.01	0.43
2:M:66:TYR:CZ	2:M:70:ARG:HD2	2.54	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
1:R:32:LYS:O	1:R:167:SER:HA	2.18	0.43
2:Y:59:MET:CE	2:Y:82:LEU:HD23	2.43	0.43
1:C:103:TYR:HE1	2:K:74:MET:HE2	1.84	0.43
1:E:81:LEU:HD23	1:E:133:GLY:HA3	2.00	0.43
2:H:19:ARG:HE	2:H:26:ILE:HG13	1.84	0.43
2:L:3:THR:OG1	2:L:127:THR:HG22	2.19	0.43
1:O:187:LYS:O	1:O:190:VAL:HG13	2.19	0.43
1:T:52:LYS:HB3	1:T:209:ALA:O	2.19	0.43
1:T:130:ARG:NH1	1:T:131:PRO:O	2.51	0.43
1:U:81:LEU:HD23	1:U:133:GLY:HA3	2.00	0.43
2:Y:6:ILE:HD11	2:Y:142:TYR:CD1	2.53	0.43
2:Z:105:ASP:OD1	2:Z:106:THR:N	2.52	0.43
2:Z:189:THR:HG23	2:Z:190:ASP:H	1.84	0.43
2:1:66:TYR:CZ	2:1:70:ARG:HD2	2.53	0.43
2:1:93:MET:N	2:1:94:PRO:CD	2.81	0.43
1:B:16:SER:HB3	1:B:22:PHE:CE2	2.53	0.43
1:E:159:GLU:O	1:F:60:GLU:HB2	2.18	0.43
2:H:103:GLY:HA2	2:H:178:ILE:HD13	2.01	0.43
2:J:105:ASP:CG	2:J:106:THR:H	2.26	0.43
2:M:49:VAL:O	2:M:50:GLY:C	2.61	0.43
1:O:81:LEU:HD23	1:O:133:GLY:HA3	2.00	0.43
1:Q:109:ILE:CG2	1:Q:147:ARG:HD3	2.48	0.43
2:V:83:LEU:HD12	2:V:83:LEU:HA	1.69	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:103:GLY:HA2	2:V:178:ILE:HD13	2.01	0.43
2:Z:55:LEU:HD12	2:Z:55:LEU:HA	1.67	0.43
1:A:130:ARG:NH1	1:A:131:PRO:O	2.51	0.43
1:C:32:LYS:O	1:C:167:SER:HA	2.18	0.43
1:C:109:ILE:CG2	1:C:147:ARG:HD3	2.48	0.43
1:F:109:ILE:CG2	1:F:147:ARG:HD3	2.49	0.43
1:F:187:LYS:O	1:F:190:VAL:HG13	2.19	0.43
1:G:130:ARG:NH1	1:G:131:PRO:O	2.51	0.43
2:H:131:SER:O	2:H:134:VAL:HG13	2.19	0.43
2:I:45:ILE:CD1	2:I:52:ALA:HB1	2.49	0.43
2:L:180:ARG:HA	2:L:180:ARG:HD2	1.72	0.43
2:L:187:LEU:HA	2:L:188:PRO:HD3	1.77	0.43
2:M:109:HIS:HB3	2:M:111:PHE:HE1	1.84	0.43
2:M:132:PRO:HA	2:1:133:PHE:HE1	1.81	0.43
2:N:160:SER:HA	2:N:163:LYS:HD3	2.00	0.43
1:R:130:ARG:NH1	1:R:131:PRO:O	2.51	0.43
2:Y:157:ARG:O	2:Y:160:SER:HB2	2.19	0.43
2:Z:15:ALA:HB3	2:Z:155:VAL:HG11	2.00	0.43
2:Z:26:ILE:HD13	2:Z:26:ILE:C	2.44	0.43
2:Z:178:ILE:HB	2:Z:184:TYR:HA	2.01	0.43
1:A:109:ILE:CG2	1:A:147:ARG:HD3	2.49	0.43
1:C:81:LEU:HD23	1:C:133:GLY:HA3	2.00	0.43
1:E:32:LYS:O	1:E:167:SER:HA	2.18	0.43
2:H:202:ILE:HG12	2:H:203:LEU:N	2.34	0.43
2:K:34:LEU:HD21	2:K:176:ALA:HB3	2.00	0.43
2:M:87:LEU:HD23	2:M:114:ASP:O	2.19	0.43
1:O:58:LEU:HD21	1:U:176:LEU:HB3	2.01	0.43
1:Q:12:ILE:HG13	1:Q:14:VAL:H	1.73	0.43
1:Q:103:TYR:HE1	2:Y:74:MET:HE2	1.84	0.43
1:Q:187:LYS:O	1:Q:190:VAL:HG13	2.19	0.43
1:R:17:PRO:HA	1:S:26:TYR:CD1	2.53	0.43
1:T:16:SER:HB3	1:T:22:PHE:CE2	2.53	0.43
1:T:109:ILE:CG2	1:T:147:ARG:HD3	2.48	0.43
2:V:3:THR:OG1	2:V:127:THR:HG22	2.19	0.43
2:V:18:ARG:HE	2:V:30:ASN:HD22	1.67	0.43
2:V:28:HIS:CD2	2:W:120:VAL:HG11	2.54	0.43
2:Y:180:ARG:HD2	2:Y:180:ARG:HA	1.78	0.43
2:2:7:THR:HB	2:2:123:ILE:O	2.18	0.43
1:D:187:LYS:O	1:D:190:VAL:HG13	2.19	0.43
1:F:16:SER:HB3	1:F:22:PHE:CE2	2.53	0.43
2:J:25:PHE:CD1	2:J:25:PHE:C	2.96	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:26:ILE:HD13	2:L:26:ILE:C	2.44	0.43
2:L:55:LEU:HD12	2:L:55:LEU:HA	1.68	0.43
1:Q:16:SER:HB3	1:Q:22:PHE:CE2	2.53	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: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
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:G:12:ILE:HG13	1:G:14:VAL:H	1.73	0.42
1:G:187:LYS:O	1:G:190:VAL:HG13	2.19	0.42
1:U:32:LYS:O	1:U:167:SER:HA	2.18	0.42
1:U:109:ILE:CG2	1:U:147:ARG:HD3	2.49	0.42
2:V:59:MET:HE2	2:V:79:VAL:CG2	2.47	0.42
2:W:180:ARG:HD2	2:W:180:ARG:HA	1.81	0.42
2:2:59:MET:HE1	2:2:82:LEU:HD23	2.01	0.42
2:H:28:HIS:CD2	2:I:120:VAL:HG11	2.54	0.42
2:K:6:ILE:HD11	2:K:142:TYR:CD1	2.53	0.42
1:O:124:THR:HG22	1:P:130:ARG:NH2	2.26	0.42
1:P:32:LYS:O	1:P:167:SER:HA	2.18	0.42
1:P:130:ARG:NH1	1:P:131:PRO:O	2.51	0.42
1:Q:130:ARG:NH1	1:Q:131:PRO:O	2.51	0.42
1:R:187:LYS:O	1:R:190:VAL:HG13	2.19	0.42
1:S:109:ILE:CG2	1:S:147:ARG:HD3	2.48	0.42
2:Z:49:VAL:O	2:Z:50:GLY:C	2.62	0.42
2:Z:157:ARG:O	2:Z:158:ALA:C	2.63	0.42
2:1:74:MET:HA	2:1:75:PRO:HD3	1.87	0.42
1:A:58:LEU:N	1:A:58:LEU:CD1	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
1:D:81:LEU:HD23	1:D:133:GLY:HA3	2.00	0.42
1:F:32:LYS:O	1:F:167:SER:HA	2.18	0.42
1:G:54:VAL:HG22	1:G:55:ARG:N	2.34	0.42
2:H:55:LEU:HA	2:H:55:LEU:HD12	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
2:N:111:PHE:CE2	2:N:121:GLU:HB2	2.53	0.42
1:U:16:SER:HB3	1:U:22:PHE:CE2	2.53	0.42
1:A:44:ASN:HD22	1:A:44:ASN:HA	1.56	0.42
1:B:109:ILE:CG2	1:B:147:ARG:HD3	2.48	0.42
1:C:187:LYS:O	1:C:190:VAL:HG13	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:123:ILE:H	2:I:123:ILE:CD1	2.31	0.42
2:I:184:TYR:CD1	2:I:184:TYR:C	2.97	0.42
2:K:157:ARG:O	2:K:160:SER:HB2	2.19	0.42
2:L:15:ALA:HB3	2:L:155:VAL:CG1	2.49	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:Q:32:LYS:O	1:Q:167:SER:HA	2.18	0.42
1:Q:58:LEU:N	1:Q:58:LEU:CD1	2.82	0.42
1:R:52:LYS:HB3	1:R:209:ALA:O	2.19	0.42
1:S:16:SER:HB3	1:S:22:PHE:CE2	2.53	0.42
1:S:103:TYR:HE1	2:1:74:MET:CE	2.32	0.42
1:T:54:VAL:HG22	1:T:55:ARG:N	2.35	0.42
1:T:187:LYS:O	1:T:190:VAL:HG13	2.19	0.42
1:U:54:VAL:HG22	1:U:55:ARG:N	2.34	0.42
2:V:131:SER:O	2:V:134:VAL:HG13	2.19	0.42
2:V:202:ILE:HG12	2:V:203:LEU:N	2.34	0.42
2:Z:93:MET:N	2:Z:94:PRO:CD	2.81	0.42
1:C:52:LYS:HB3	1:C:209:ALA:O	2.19	0.42
1:E:130:ARG:NH1	1:E:131:PRO:O	2.51	0.42
2:H:83:LEU:HD12	2:H:83:LEU:HA	1.69	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
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:W:93:MET:N	2:W:94:PRO:CD	2.82	0.42
2:1:109:HIS:HB3	2:1:111:PHE:HE1	1.84	0.42
2:1:138:LEU:HD12	2:1:138:LEU:HA	1.86	0.42
1:A:187:LYS:O	1:A:190:VAL:HG13	2.19	0.42
1:C:54:VAL:HG22	1:C:55:ARG:N	2.34	0.42
1:F:123:TYR:CD1	1:F:123:TYR:N	2.88	0.42
1:F:130:ARG:NH1	1:F:131:PRO:O	2.51	0.42
1:G:58:LEU:N	1:G:58:LEU:CD1	2.82	0.42
2:H:3:THR:OG1	2:H:127:THR:HG22	2.19	0.42
2:J:55:LEU:HD12	2:J:55:LEU:HA	1.85	0.42
2:J:199:LEU:CB	2:J:201:LEU:HD13	2.50	0.42
2:L:105:ASP:OD1	2:L:106:THR:N	2.52	0.42
1:R:54:VAL:HG22	1:R:55:ARG:N	2.35	0.42
1:R:123:TYR:N	1:R:123:TYR:CD1	2.88	0.42
1:S:187:LYS:O	1:S:190:VAL:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:109:HIS:HB3	2:X:111:PHE:CE1	2.54	0.42
2:Z:3:THR:OG1	2:Z:127:THR:HG22	2.19	0.42
2:2:187:LEU:HA	2:2:188:PRO:HD3	1.81	0.42
1:B:187:LYS:O	1:B:190:VAL:HG13	2.19	0.42
1:C:56:SER:OG	1:C:58:LEU:HB2	2.20	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:103:TYR:HE1	2:H:74:MET:HE2	1.85	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
2:W:191:GLN:O	2:W:194:SER:HB3	2.20	0.42
2:X:25:PHE:C	2:X:25:PHE:CD1	2.96	0.42
2:X:187:LEU:HA	2:X:188:PRO:HD3	1.79	0.42
2:Z:143:SER:O	2:Z:146:MET:HG3	2.20	0.42
2:Z:190:ASP:HA	2:Z:193:GLU:HG2	2.02	0.42
2:2:25:PHE:C	2:2:25:PHE:HD1	2.26	0.42
2:L:2:THR:HG23	2:L:17:GLU:HG3	2.02	0.42
1:O:52:LYS:HB3	1:O:209:ALA:O	2.19	0.42
1:U:52:LYS:HB3	1:U:209:ALA:O	2.19	0.42
1:B:58:LEU:N	1:B:58:LEU:CD1	2.83	0.42
1:D:16:SER:HB3	1:D:22:PHE:CE2	2.53	0.42
1:D:32:LYS:O	1:D:167:SER:HA	2.18	0.42
1:E:52:LYS:HB3	1:E:209:ALA:O	2.19	0.42
1:F:52:LYS:HB3	1:F:209:ALA:O	2.19	0.42
1:G:52:LYS:HB3	1:G:209:ALA:O	2.19	0.42
2:I:180:ARG:HD2	2:I:180:ARG:HA	1.81	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:Q:123:TYR:N	1:Q:123:TYR:CD1	2.88	0.42
2:W:188:PRO:O	2:W:189:THR:C	2.63	0.42
2:2:22:MET:O	2:2:23:GLU:HB2	2.20	0.42
1:E:124:THR:HG22	1:F:130:ARG:NH2	2.25	0.42
1:F:54:VAL:HG22	1:F:55:ARG:N	2.35	0.42
2:J:74:MET:HA	2:J:75:PRO:HD3	1.88	0.42
1:O:56:SER:OG	1:O:58:LEU:HB2	2.20	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
2:Z:163:LYS:CE	2:Z:203:LEU:HD23	2.50	0.42
1:A:54:VAL:HG22	1:A:55:ARG:N	2.34	0.41
1:A:56:SER:OG	1:A:58:LEU:HB2	2.20	0.41
1:E:54:VAL:HG22	1:E:55:ARG:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:198:LYS:CG	1:G:202:GLU:HG2	2.50	0.41
2:I:188:PRO:O	2:I:189:THR:C	2.63	0.41
2:M:17:GLU:O	2:M:33:LYS:HD2	2.20	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
2:W:45:ILE:CD1	2:W:52:ALA:HB1	2.49	0.41
2:X:34:LEU:HD21	2:X:176:ALA:CB	2.50	0.41
2:X:123:ILE:HG12	2:X:124:TYR:CD1	2.51	0.41
2:Z:180:ARG:HA	2:Z:180:ARG:HD2	1.71	0.41
1:A:123:TYR:N	1:A:123:TYR:CD1	2.88	0.41
1:B:198:LYS:CG	1:B:202:GLU:HG2	2.50	0.41
1:E:58:LEU:CD1	1:E:58:LEU:N	2.83	0.41
2:I:147:THR:OG1	2:I:150:GLU:HG3	2.21	0.41
2:L:157:ARG:O	2:L:158:ALA:C	2.63	0.41
2:M:111:PHE:CE2	2:M:121:GLU:HB2	2.55	0.41
1:P:56:SER:OG	1:P:58:LEU:HB2	2.20	0.41
1:Q:52:LYS:HB3	1:Q:209:ALA:O	2.19	0.41
2:1:87:LEU:HD23	2:1:114:ASP:O	2.19	0.41
1:B:56:SER:OG	1:B:58:LEU:HB2	2.20	0.41
1:C:58:LEU:N	1:C:58:LEU:CD1	2.82	0.41
2:J:190:ASP:HA	2:J:193:GLU:HG2	2.02	0.41
2:M:59:MET:HE1	2:M:82:LEU:HD23	2.01	0.41
2:M:163:LYS:CE	2:M:203:LEU:HD23	2.50	0.41
2:N:59:MET:HE1	2:N:82:LEU:HD23	2.01	0.41
1:R:56:SER:OG	1:R:58:LEU:HB2	2.20	0.41
1:S:54:VAL:HG22	1:S:55:ARG:N	2.34	0.41
1:T:56:SER:OG	1:T:58:LEU:HB2	2.20	0.41
2:W:123:ILE:H	2:W:123:ILE:CD1	2.31	0.41
2:1:59:MET:HE1	2:1:82:LEU:HD23	2.01	0.41
1:D:52:LYS:HB3	1:D:209:ALA:O	2.19	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
1:F:56:SER:OG	1:F:58:LEU:HB2	2.20	0.41
1:G:56:SER:OG	1:G:58:LEU:HB2	2.20	0.41
2:I:19:ARG:NE	2:I:26:ILE:HG13	2.36	0.41
2:I:93:MET:N	2:I:94:PRO:CD	2.82	0.41
2:I:175:VAL:HG22	2:I:176:ALA:N	2.35	0.41
2:L:143:SER:O	2:L:146:MET:HG3	2.20	0.41
2:L:163:LYS:CE	2:L:203:LEU:HD23	2.50	0.41
2:M:3:THR:HB	2:M:16:THR:HG22	2.03	0.41
1:O:32:LYS:O	1:O:167:SER:HA	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:58:LEU:N	1:O:58:LEU:CD1	2.82	0.41
1:P:52:LYS:HB3	1:P:209:ALA:O	2.19	0.41
1:P:54:VAL:HG22	1:P:55:ARG:N	2.35	0.41
1:P:125:GLN:HB3	1:Q:130:ARG:CZ	2.50	0.41
1:T:58:LEU:N	1:T:58:LEU:CD1	2.82	0.41
1:T:78:THR:CG2	1:T:85:ALA:HB1	2.45	0.41
2:V:180:ARG:HA	2:V:180:ARG:HD2	1.79	0.41
2:1:114:ASP:OD1	2:1:116:ALA:HB3	2.20	0.41
1:E:103:TYR:HE1	2:M:74:MET:CE	2.32	0.41
2:K:26:ILE:CG2	2:2:165:ARG:HA	2.50	0.41
2:M:187:LEU:HA	2:M:188:PRO:HD3	1.82	0.41
2:N:59:MET:SD	2:N:83:LEU:HD13	2.60	0.41
2:N:158:ALA:O	2:N:161:ALA:HB3	2.21	0.41
1:O:54:VAL:HG22	1:O:55:ARG:N	2.34	0.41
1:Q:56:SER:OG	1:Q:58:LEU:HB2	2.20	0.41
1:R:130:ARG:HA	1:R:131:PRO:HD3	1.96	0.41
1:T:12:ILE:HG13	1:T:14:VAL:H	1.73	0.41
2:Y:49:VAL:O	2:Y:50:GLY:C	2.64	0.41
2:1:49:VAL:O	2:1:50:GLY:C	2.61	0.41
2:1:137:VAL:HG21	2:1:158:ALA:HA	2.01	0.41
2:1:163:LYS:CE	2:1:203:LEU:HD23	2.50	0.41
1:A:198:LYS:CG	1:A:202:GLU:HG2	2.50	0.41
2:L:66:TYR:CZ	2:L:70:ARG:HD2	2.56	0.41
1:O:123:TYR:CD1	1:O:123:TYR:N	2.88	0.41
1:U:58:LEU:CD1	1:U:58:LEU:N	2.83	0.41
2:V:187:LEU:HA	2:V:188:PRO:HD3	1.77	0.41
2:X:105:ASP:CG	2:X:106:THR:H	2.26	0.41
2:1:17:GLU:O	2:1:33:LYS:HD2	2.20	0.41
2:1:111:PHE:CE2	2:1:121:GLU:HB2	2.55	0.41
1:C:123:TYR:CD1	1:C:123:TYR:N	2.88	0.41
1:D:58:LEU:N	1:D:58:LEU:CD1	2.82	0.41
1:D:123:TYR:CD1	1:D:123:TYR:N	2.88	0.41
2:H:18:ARG:HE	2:H:30:ASN:HD22	1.67	0.41
2:I:105:ASP:CG	2:I:106:THR:H	2.28	0.41
2:K:22:MET:O	2:K:23:GLU:HB2	2.21	0.41
2:K:49:VAL:HG23	2:K:50:GLY:H	1.86	0.41
2:L:20:VAL:CG1	2:L:28:HIS:HB2	2.44	0.41
2:L:97:VAL:HG22	2:L:98:GLN:N	2.36	0.41
2:M:165:ARG:NH2	2:1:135:TYR:HE1	2.18	0.41
1:P:123:TYR:N	1:P:123:TYR:CD1	2.88	0.41
1:Q:126:TYR:HA	1:R:129:VAL:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:86:MET:HE2	2:Y:86:MET:HB3	2.00	0.41
2:1:3:THR:HB	2:1:16:THR:HG22	2.03	0.41
2:2:177:VAL:HG13	2:2:185:VAL:HG13	2.03	0.41
1:A:124:THR:HG22	1:B:130:ARG:NH2	2.26	0.41
1:C:176:LEU:C	1:C:178:ARG:N	2.79	0.41
1:C:198:LYS:CG	1:C:202:GLU:HG2	2.50	0.41
1:G:176:LEU:C	1:G:178:ARG:N	2.79	0.41
2:I:56:VAL:CG1	2:I:57:ARG:N	2.84	0.41
2:J:59:MET:HE2	2:J:79:VAL:HG23	2.03	0.41
2:J:203:LEU:HD12	2:J:203:LEU:HA	1.86	0.41
2:N:133:PHE:HE1	2:Z:132:PRO:HA	1.83	0.41
2:N:187:LEU:HA	2:N:188:PRO:HD3	1.81	0.41
2:W:56:VAL:CG1	2:W:57:ARG:N	2.84	0.41
2:Z:20:VAL:CG1	2:Z:28:HIS:HB2	2.44	0.41
2:Z:97:VAL:HG22	2:Z:98:GLN:N	2.36	0.41
1:B:165:ILE:HD12	1:B:169:LYS:HD2	2.03	0.41
1:C:165:ILE:HD12	1:C:169:LYS:HD2	2.03	0.41
1:E:56:SER:OG	1:E:58:LEU:HB2	2.20	0.41
2:J:141:GLN:HE21	2:W:141:GLN:HE21	1.69	0.41
2:J:190:ASP:O	2:J:193:GLU:HG2	2.21	0.41
2:L:138:LEU:HD12	2:L:138:LEU:HA	1.90	0.41
2:M:86:MET:HE2	2:M:86:MET:HB3	1.91	0.41
2:M:135:TYR:HE1	2:1:165:ARG:NH2	2.19	0.41
2:M:137:VAL:HG21	2:M:158:ALA:HA	2.01	0.41
2:N:74:MET:HA	2:N:75:PRO:HD3	1.95	0.41
1:Q:103:TYR:CE1	2:Y:74:MET:HE2	2.56	0.41
1:R:176:LEU:C	1:R:178:ARG:N	2.79	0.41
1:S:123:TYR:N	1:S:123:TYR:CD1	2.88	0.41
1:S:176:LEU:C	1:S:178:ARG:N	2.79	0.41
1:S:198:LYS:CG	1:S:202:GLU:HG2	2.50	0.41
1:T:165:ILE:HD12	1:T:169:LYS:HD2	2.03	0.41
1:U:103:TYR:HE1	2:V:74:MET:HE2	1.85	0.41
1:U:165:ILE:HD12	1:U:169:LYS:HD2	2.03	0.41
1:U:198:LYS:CG	1:U:202:GLU:HG2	2.50	0.41
2:W:19:ARG:NE	2:W:26:ILE:HG13	2.36	0.41
2:Y:19:ARG:NH1	2:Y:169:SER:O	2.54	0.41
2:Z:66:TYR:CZ	2:Z:70:ARG:HD2	2.56	0.41
2:2:72:VAL:HG22	2:2:73:ASN:N	2.36	0.41
2:H:81:THR:O	2:H:84:SER:HB3	2.21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:165:ARG:CZ	2:1:135:TYR:CD1	3.04	0.41
1:S:78:THR:CG2	1:S:85:ALA:HB1	2.45	0.41
1:U:176:LEU:C	1:U:178:ARG:N	2.79	0.41
2:Y:34:LEU:HD21	2:Y:176:ALA:CB	2.51	0.41
1:B:125:GLN:HB3	1:C:130:ARG:CZ	2.50	0.40
1:F:198:LYS:CG	1:F:202:GLU:HG2	2.50	0.40
2:I:178:ILE:HB	2:I:184:TYR:HA	2.03	0.40
2:J:103:GLY:HA2	2:J:178:ILE:HD11	2.02	0.40
2:K:34:LEU:HD21	2:K:176:ALA:CB	2.51	0.40
2:L:49:VAL:O	2:L:50:GLY:C	2.62	0.40
2:M:76:ILE:HA	2:M:79:VAL:HG12	2.04	0.40
1:O:176:LEU:C	1:O:178:ARG:N	2.79	0.40
1:Q:165:ILE:HD12	1:Q:169:LYS:HD2	2.03	0.40
1:Q:227:GLU:CD	1:Q:227:GLU:N	2.79	0.40
1:S:227:GLU:CD	1:S:227:GLU:N	2.79	0.40
1:U:123:TYR:N	1:U:123:TYR:CD1	2.88	0.40
2:W:178:ILE:HB	2:W:184:TYR:HA	2.03	0.40
2:X:93:MET:N	2:X:94:PRO:CD	2.85	0.40
2:Y:22:MET:O	2:Y:23:GLU:HB2	2.21	0.40
2:Z:2:THR:HG23	2:Z:17:GLU:HG3	2.02	0.40
2:Z:87:LEU:HD23	2:Z:114:ASP:O	2.20	0.40
1:A:78:THR:CG2	1:A:85:ALA:HB1	2.45	0.40
1:A:176:LEU:C	1:A:178:ARG:N	2.79	0.40
1:B:78:THR:CG2	1:B:85:ALA:HB1	2.45	0.40
1:B:123:TYR:N	1:B:123:TYR:CD1	2.88	0.40
1:B:176:LEU:C	1:B:178:ARG:N	2.79	0.40
1:C:15:PHE:HB2	1:D:23:GLN:HE22	1.86	0.40
1:D:227:GLU:N	1:D:227:GLU:CD	2.79	0.40
1:E:227:GLU:N	1:E:227:GLU:CD	2.79	0.40
1:G:130:ARG:HA	1:G:131:PRO:HD3	1.96	0.40
2:L:190:ASP:HA	2:L:193:GLU:HG2	2.02	0.40
2:M:135:TYR:CD1	2:1:165:ARG:CZ	3.04	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:N	1:T:123:TYR:CD1	2.88	0.40
2:W:26:ILE:HD13	2:W:26:ILE:O	2.22	0.40
2:W:105:ASP:CG	2:W:106:THR:H	2.28	0.40
2:2:59:MET:SD	2:2:83:LEU:HD13	2.60	0.40
1:A:165:ILE:HD12	1:A:169:LYS:HD2	2.03	0.40
1:A:227:GLU:CD	1:A:227:GLU:N	2.79	0.40
1:E:198:LYS:CG	1:E:202:GLU:HG2	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:176:LEU:C	1:F:178:ARG:N	2.79	0.40
1:G:227:GLU:CD	1:G:227:GLU:N	2.79	0.40
2:I:59:MET:SD	2:I:83:LEU:HD13	2.61	0.40
2:N:190:ASP:HA	2:N:193:GLU:HG2	2.04	0.40
1:U:44:ASN:HD22	1:U:44:ASN:HA	1.56	0.40
2:V:81:THR:O	2:V:84:SER:HB3	2.21	0.40
2:W:59:MET:SD	2:W:83:LEU:HD13	2.61	0.40
2:W:147:THR:OG1	2:W:150:GLU:HG3	2.21	0.40
2:X:190:ASP:HA	2:X:193:GLU:HG2	2.02	0.40
2:H:86:MET:HE2	2:H:86:MET:HB3	1.97	0.40
2:L:87:LEU:HD23	2:L:114:ASP:O	2.20	0.40
1:P:198:LYS:CG	1:P:202:GLU:HG2	2.50	0.40
2:V:202:ILE:CG1	2:V:203:LEU:N	2.85	0.40
1:E:123:TYR:N	1:E:123:TYR:CD1	2.88	0.40
1:E:165:ILE:HD12	1:E:169:LYS:HD2	2.03	0.40
1:F:227:GLU:CD	1:F:227:GLU:N	2.80	0.40
1:G:44:ASN:HD22	1:G:44:ASN:HA	1.56	0.40
2:I:26:ILE:HD13	2:I:26:ILE:O	2.22	0.40
2:J:141:GLN:HE21	2:W:141:GLN:NE2	2.19	0.40
2:M:188:PRO:O	2:M:189:THR:C	2.65	0.40
1:P:227:GLU:CD	1:P:227:GLU:N	2.79	0.40
1:S:165:ILE:HD12	1:S:169:LYS:HD2	2.03	0.40
2:W:74:MET:HA	2:W:75:PRO:HD3	1.94	0.40
2:2:76:ILE:O	2:2:79:VAL:CG1	2.69	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%)	1 16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	C	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	D	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	E	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	F	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	G	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	O	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	P	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	Q	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	R	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	S	222/233 (95%)	183 (82%)	28 (13%)	11 (5%)	1	16
1	T	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
1	U	222/233 (95%)	184 (83%)	27 (12%)	11 (5%)	1	16
2	1	201/203 (99%)	176 (88%)	23 (11%)	2 (1%)	12	48
2	2	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	12	48
2	H	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	12	48
2	I	201/203 (99%)	183 (91%)	16 (8%)	2 (1%)	12	48
2	J	201/203 (99%)	180 (90%)	20 (10%)	1 (0%)	24	63
2	K	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	12	48
2	L	201/203 (99%)	181 (90%)	16 (8%)	4 (2%)	6	31
2	M	201/203 (99%)	176 (88%)	23 (11%)	2 (1%)	12	48
2	N	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	12	48
2	V	201/203 (99%)	185 (92%)	14 (7%)	2 (1%)	12	48
2	W	201/203 (99%)	183 (91%)	16 (8%)	2 (1%)	12	48
2	X	201/203 (99%)	180 (90%)	20 (10%)	1 (0%)	24	63
2	Y	201/203 (99%)	184 (92%)	15 (8%)	2 (1%)	12	48
2	Z	201/203 (99%)	181 (90%)	16 (8%)	4 (2%)	6	31
All	All	5922/6104 (97%)	5120 (86%)	618 (10%)	184 (3%)	5	22

All (184) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	12	ILE

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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 ⓘ

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%)	157 (84%)	29 (16%)	2	12
1	B	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	C	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	D	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	E	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	F	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	G	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	O	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	P	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	Q	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	R	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	S	186/193 (96%)	157 (84%)	29 (16%)	2	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	T	186/193 (96%)	157 (84%)	29 (16%)	2	12
1	U	186/193 (96%)	157 (84%)	29 (16%)	2	12
2	1	170/170 (100%)	146 (86%)	24 (14%)	3	13
2	2	170/170 (100%)	145 (85%)	25 (15%)	3	13
2	H	170/170 (100%)	142 (84%)	28 (16%)	2	10
2	I	170/170 (100%)	143 (84%)	27 (16%)	2	11
2	J	170/170 (100%)	140 (82%)	30 (18%)	2	9
2	K	170/170 (100%)	142 (84%)	28 (16%)	2	10
2	L	170/170 (100%)	144 (85%)	26 (15%)	3	12
2	M	170/170 (100%)	146 (86%)	24 (14%)	3	13
2	N	170/170 (100%)	145 (85%)	25 (15%)	3	13
2	V	170/170 (100%)	142 (84%)	28 (16%)	2	10
2	W	170/170 (100%)	143 (84%)	27 (16%)	2	11
2	X	170/170 (100%)	140 (82%)	30 (18%)	2	9
2	Y	170/170 (100%)	142 (84%)	28 (16%)	2	10
2	Z	170/170 (100%)	144 (85%)	26 (15%)	3	12
All	All	4984/5082 (98%)	4202 (84%)	782 (16%)	4	12

All (782) 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	23	GLN
1	A	24	VAL
1	A	31	VAL
1	A	44	ASN
1	A	47	LEU
1	A	48	LEU
1	A	62	ASN
1	A	71	ASP
1	A	82	VAL
1	A	102	THR
1	A	106	LEU
1	A	107	VAL

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Mol	Chain	Res	Type
1	A	111	ASN
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	B	10	ARG
1	B	12	ILE
1	B	21	LEU
1	B	23	GLN
1	B	24	VAL
1	B	31	VAL
1	B	44	ASN
1	B	47	LEU
1	B	48	LEU
1	B	62	ASN
1	B	71	ASP
1	B	82	VAL
1	B	102	THR
1	B	106	LEU
1	B	107	VAL
1	B	111	ASN
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

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Mol	Chain	Res	Type
1	B	212	ILE
1	C	10	ARG
1	C	12	ILE
1	C	21	LEU
1	C	23	GLN
1	C	24	VAL
1	C	31	VAL
1	C	44	ASN
1	C	47	LEU
1	C	48	LEU
1	C	62	ASN
1	C	71	ASP
1	C	82	VAL
1	C	102	THR
1	C	106	LEU
1	C	107	VAL
1	C	111	ASN
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
1	C	201	LEU
1	C	202	GLU
1	C	212	ILE
1	D	10	ARG
1	D	12	ILE
1	D	21	LEU
1	D	23	GLN
1	D	24	VAL
1	D	31	VAL
1	D	44	ASN
1	D	47	LEU
1	D	48	LEU
1	D	62	ASN
1	D	71	ASP
1	D	82	VAL

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Mol	Chain	Res	Type
1	D	102	THR
1	D	106	LEU
1	D	107	VAL
1	D	111	ASN
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	E	10	ARG
1	E	12	ILE
1	E	21	LEU
1	E	23	GLN
1	E	24	VAL
1	E	31	VAL
1	E	44	ASN
1	E	47	LEU
1	E	48	LEU
1	E	62	ASN
1	E	71	ASP
1	E	82	VAL
1	E	102	THR
1	E	106	LEU
1	E	107	VAL
1	E	111	ASN
1	E	119	GLN
1	E	134	VAL
1	E	136	LEU
1	E	141	ILE
1	E	143	GLN
1	E	157	ILE
1	E	161	LYS
1	E	175	PHE
1	E	176	LEU

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Mol	Chain	Res	Type
1	E	190	VAL
1	E	201	LEU
1	E	202	GLU
1	E	212	ILE
1	F	10	ARG
1	F	12	ILE
1	F	21	LEU
1	F	23	GLN
1	F	24	VAL
1	F	31	VAL
1	F	44	ASN
1	F	47	LEU
1	F	48	LEU
1	F	62	ASN
1	F	71	ASP
1	F	82	VAL
1	F	102	THR
1	F	106	LEU
1	F	107	VAL
1	F	111	ASN
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	G	10	ARG
1	G	12	ILE
1	G	21	LEU
1	G	23	GLN
1	G	24	VAL
1	G	31	VAL
1	G	44	ASN
1	G	47	LEU
1	G	48	LEU

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Mol	Chain	Res	Type
1	G	62	ASN
1	G	71	ASP
1	G	82	VAL
1	G	102	THR
1	G	106	LEU
1	G	107	VAL
1	G	111	ASN
1	G	119	GLN
1	G	134	VAL
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
2	H	2	THR
2	H	4	VAL
2	H	7	THR
2	H	17	GLU
2	H	20	VAL
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	68	LEU
2	H	83	LEU
2	H	94	PRO
2	H	97	VAL
2	H	104	ILE
2	H	123	ILE
2	H	127	THR
2	H	134	VAL
2	H	137	VAL
2	H	138	LEU
2	H	144	GLU

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Mol	Chain	Res	Type
2	H	173	ILE
2	H	175	VAL
2	H	177	VAL
2	H	178	ILE
2	H	185	VAL
2	H	201	LEU
2	I	2	THR
2	I	7	THR
2	I	17	GLU
2	I	20	VAL
2	I	26	ILE
2	I	41	THR
2	I	45	ILE
2	I	49	VAL
2	I	54	VAL
2	I	55	LEU
2	I	59	MET
2	I	63	LEU
2	I	70	ARG
2	I	71	ARG
2	I	83	LEU
2	I	104	ILE
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	173	ILE
2	I	175	VAL
2	I	177	VAL
2	I	178	ILE
2	I	185	VAL
2	J	2	THR
2	J	6	ILE
2	J	7	THR
2	J	8	LEU
2	J	12	VAL
2	J	17	GLU
2	J	20	VAL
2	J	26	ILE
2	J	41	THR

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Mol	Chain	Res	Type
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	79	VAL
2	J	83	LEU
2	J	104	ILE
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	173	ILE
2	J	175	VAL
2	J	177	VAL
2	J	178	ILE
2	J	185	VAL
2	K	2	THR
2	K	6	ILE
2	K	7	THR
2	K	17	GLU
2	K	20	VAL
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	70	ARG
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

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Mol	Chain	Res	Type
2	K	138	LEU
2	K	144	GLU
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	7	THR
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	70	ARG
2	L	71	ARG
2	L	83	LEU
2	L	104	ILE
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	165	ARG
2	L	173	ILE
2	L	175	VAL
2	L	178	ILE
2	L	185	VAL
2	M	2	THR
2	M	7	THR
2	M	17	GLU
2	M	20	VAL
2	M	26	ILE
2	M	41	THR
2	M	45	ILE
2	M	54	VAL
2	M	59	MET

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Mol	Chain	Res	Type
2	M	70	ARG
2	M	71	ARG
2	M	83	LEU
2	M	120	VAL
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	M	185	VAL
2	M	201	LEU
2	N	2	THR
2	N	7	THR
2	N	12	VAL
2	N	17	GLU
2	N	20	VAL
2	N	26	ILE
2	N	41	THR
2	N	45	ILE
2	N	59	MET
2	N	68	LEU
2	N	70	ARG
2	N	71	ARG
2	N	94	PRO
2	N	123	ILE
2	N	127	THR
2	N	134	VAL
2	N	137	VAL
2	N	138	LEU
2	N	144	GLU
2	N	165	ARG
2	N	173	ILE
2	N	175	VAL
2	N	177	VAL
2	N	178	ILE
2	N	185	VAL
1	O	10	ARG
1	O	12	ILE

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Mol	Chain	Res	Type
1	O	21	LEU
1	O	23	GLN
1	O	24	VAL
1	O	31	VAL
1	O	44	ASN
1	O	47	LEU
1	O	48	LEU
1	O	62	ASN
1	O	71	ASP
1	O	82	VAL
1	O	102	THR
1	O	106	LEU
1	O	107	VAL
1	O	111	ASN
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	P	10	ARG
1	P	12	ILE
1	P	21	LEU
1	P	23	GLN
1	P	24	VAL
1	P	31	VAL
1	P	44	ASN
1	P	47	LEU
1	P	48	LEU
1	P	62	ASN
1	P	71	ASP
1	P	82	VAL
1	P	102	THR
1	P	106	LEU
1	P	107	VAL

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Mol	Chain	Res	Type
1	P	111	ASN
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	Q	10	ARG
1	Q	12	ILE
1	Q	21	LEU
1	Q	23	GLN
1	Q	24	VAL
1	Q	31	VAL
1	Q	44	ASN
1	Q	47	LEU
1	Q	48	LEU
1	Q	62	ASN
1	Q	71	ASP
1	Q	82	VAL
1	Q	102	THR
1	Q	106	LEU
1	Q	107	VAL
1	Q	111	ASN
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

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Mol	Chain	Res	Type
1	Q	212	ILE
1	R	10	ARG
1	R	12	ILE
1	R	21	LEU
1	R	23	GLN
1	R	24	VAL
1	R	31	VAL
1	R	44	ASN
1	R	47	LEU
1	R	48	LEU
1	R	62	ASN
1	R	71	ASP
1	R	82	VAL
1	R	102	THR
1	R	106	LEU
1	R	107	VAL
1	R	111	ASN
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	S	10	ARG
1	S	12	ILE
1	S	21	LEU
1	S	23	GLN
1	S	24	VAL
1	S	31	VAL
1	S	44	ASN
1	S	47	LEU
1	S	48	LEU
1	S	62	ASN
1	S	71	ASP
1	S	82	VAL

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Mol	Chain	Res	Type
1	S	102	THR
1	S	106	LEU
1	S	107	VAL
1	S	111	ASN
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	T	10	ARG
1	T	12	ILE
1	T	21	LEU
1	T	23	GLN
1	T	24	VAL
1	T	31	VAL
1	T	44	ASN
1	T	47	LEU
1	T	48	LEU
1	T	62	ASN
1	T	71	ASP
1	T	82	VAL
1	T	102	THR
1	T	106	LEU
1	T	107	VAL
1	T	111	ASN
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

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Mol	Chain	Res	Type
1	T	190	VAL
1	T	201	LEU
1	T	202	GLU
1	T	212	ILE
1	U	10	ARG
1	U	12	ILE
1	U	21	LEU
1	U	23	GLN
1	U	24	VAL
1	U	31	VAL
1	U	44	ASN
1	U	47	LEU
1	U	48	LEU
1	U	62	ASN
1	U	71	ASP
1	U	82	VAL
1	U	102	THR
1	U	106	LEU
1	U	107	VAL
1	U	111	ASN
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
1	U	201	LEU
1	U	202	GLU
1	U	212	ILE
2	V	2	THR
2	V	4	VAL
2	V	7	THR
2	V	17	GLU
2	V	20	VAL
2	V	26	ILE
2	V	41	THR
2	V	45	ILE
2	V	49	VAL

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Mol	Chain	Res	Type
2	V	56	VAL
2	V	63	LEU
2	V	68	LEU
2	V	83	LEU
2	V	94	PRO
2	V	97	VAL
2	V	104	ILE
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	173	ILE
2	V	175	VAL
2	V	177	VAL
2	V	178	ILE
2	V	185	VAL
2	V	201	LEU
2	W	2	THR
2	W	7	THR
2	W	17	GLU
2	W	20	VAL
2	W	26	ILE
2	W	41	THR
2	W	45	ILE
2	W	49	VAL
2	W	54	VAL
2	W	55	LEU
2	W	59	MET
2	W	63	LEU
2	W	70	ARG
2	W	71	ARG
2	W	83	LEU
2	W	104	ILE
2	W	123	ILE
2	W	127	THR
2	W	134	VAL
2	W	137	VAL
2	W	138	LEU
2	W	144	GLU
2	W	173	ILE

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Mol	Chain	Res	Type
2	W	175	VAL
2	W	177	VAL
2	W	178	ILE
2	W	185	VAL
2	X	2	THR
2	X	6	ILE
2	X	7	THR
2	X	8	LEU
2	X	12	VAL
2	X	17	GLU
2	X	20	VAL
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	79	VAL
2	X	83	LEU
2	X	104	ILE
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	173	ILE
2	X	175	VAL
2	X	177	VAL
2	X	178	ILE
2	X	185	VAL
2	Y	2	THR
2	Y	6	ILE
2	Y	7	THR
2	Y	17	GLU
2	Y	20	VAL
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	70	ARG
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	138	LEU
2	Y	144	GLU
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	7	THR
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	70	ARG
2	Z	71	ARG
2	Z	83	LEU
2	Z	104	ILE
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	165	ARG

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Mol	Chain	Res	Type
2	Z	173	ILE
2	Z	175	VAL
2	Z	178	ILE
2	Z	185	VAL
2	1	2	THR
2	1	7	THR
2	1	17	GLU
2	1	20	VAL
2	1	26	ILE
2	1	41	THR
2	1	45	ILE
2	1	54	VAL
2	1	59	MET
2	1	70	ARG
2	1	71	ARG
2	1	83	LEU
2	1	120	VAL
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	1	185	VAL
2	1	201	LEU
2	2	2	THR
2	2	7	THR
2	2	12	VAL
2	2	17	GLU
2	2	20	VAL
2	2	26	ILE
2	2	41	THR
2	2	45	ILE
2	2	59	MET
2	2	68	LEU
2	2	70	ARG
2	2	71	ARG
2	2	94	PRO
2	2	123	ILE

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Mol	Chain	Res	Type
2	2	127	THR
2	2	134	VAL
2	2	137	VAL
2	2	138	LEU
2	2	144	GLU
2	2	165	ARG
2	2	173	ILE
2	2	175	VAL
2	2	177	VAL
2	2	178	ILE
2	2	185	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (167) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	44	ASN
1	A	98	GLN
1	A	119	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	119	GLN
1	B	121	GLN
1	B	125	GLN
1	B	143	GLN
1	C	44	ASN
1	C	98	GLN
1	C	119	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	119	GLN
1	D	121	GLN
1	D	125	GLN
1	D	143	GLN

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Mol	Chain	Res	Type
1	E	23	GLN
1	E	44	ASN
1	E	98	GLN
1	E	119	GLN
1	E	121	GLN
1	E	125	GLN
1	E	143	GLN
1	F	44	ASN
1	F	98	GLN
1	F	119	GLN
1	F	121	GLN
1	F	125	GLN
1	F	143	GLN
1	G	23	GLN
1	G	44	ASN
1	G	98	GLN
1	G	119	GLN
1	G	121	GLN
1	G	125	GLN
1	G	143	GLN
2	H	28	HIS
2	H	30	ASN
2	H	36	GLN
2	H	85	ASN
2	H	164	GLN
2	I	28	HIS
2	I	30	ASN
2	I	36	GLN
2	I	85	ASN
2	I	164	GLN
2	J	30	ASN
2	J	36	GLN
2	J	141	GLN
2	J	164	GLN
2	K	28	HIS
2	K	30	ASN
2	K	36	GLN
2	K	85	ASN
2	K	141	GLN
2	K	164	GLN
2	L	28	HIS
2	L	30	ASN

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Mol	Chain	Res	Type
2	L	36	GLN
2	L	85	ASN
2	L	141	GLN
2	L	164	GLN
2	M	28	HIS
2	M	30	ASN
2	M	85	ASN
2	M	141	GLN
2	M	164	GLN
2	N	30	ASN
2	N	36	GLN
2	N	85	ASN
2	N	141	GLN
2	N	164	GLN
1	O	23	GLN
1	O	44	ASN
1	O	98	GLN
1	O	119	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	119	GLN
1	P	121	GLN
1	P	125	GLN
1	P	143	GLN
1	Q	44	ASN
1	Q	119	GLN
1	Q	121	GLN
1	Q	125	GLN
1	Q	143	GLN
1	R	23	GLN
1	R	44	ASN
1	R	98	GLN
1	R	119	GLN
1	R	121	GLN
1	R	125	GLN
1	R	143	GLN
1	S	23	GLN
1	S	44	ASN

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Mol	Chain	Res	Type
1	S	98	GLN
1	S	119	GLN
1	S	121	GLN
1	S	125	GLN
1	S	143	GLN
1	T	44	ASN
1	T	98	GLN
1	T	119	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	119	GLN
1	U	121	GLN
1	U	125	GLN
1	U	143	GLN
2	V	28	HIS
2	V	30	ASN
2	V	36	GLN
2	V	85	ASN
2	V	164	GLN
2	W	28	HIS
2	W	30	ASN
2	W	36	GLN
2	W	85	ASN
2	W	141	GLN
2	W	164	GLN
2	X	30	ASN
2	X	36	GLN
2	X	141	GLN
2	X	164	GLN
2	Y	28	HIS
2	Y	30	ASN
2	Y	36	GLN
2	Y	85	ASN
2	Y	141	GLN
2	Y	164	GLN
2	Z	28	HIS
2	Z	30	ASN
2	Z	36	GLN

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Mol	Chain	Res	Type
2	Z	85	ASN
2	Z	141	GLN
2	Z	164	GLN
2	1	28	HIS
2	1	30	ASN
2	1	85	ASN
2	1	141	GLN
2	1	164	GLN
2	2	28	HIS
2	2	30	ASN
2	2	36	GLN
2	2	85	ASN
2	2	141	GLN
2	2	164	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

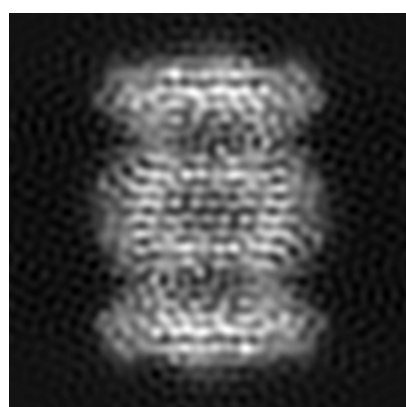
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1740. These allow visual inspection of the internal detail of the map and identification of artifacts.

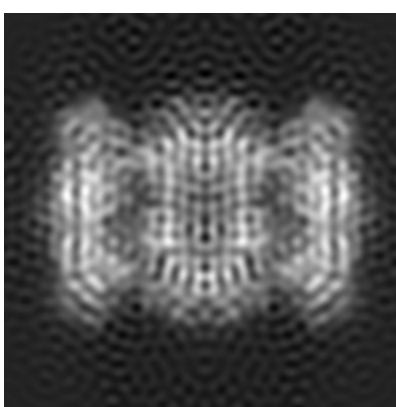
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

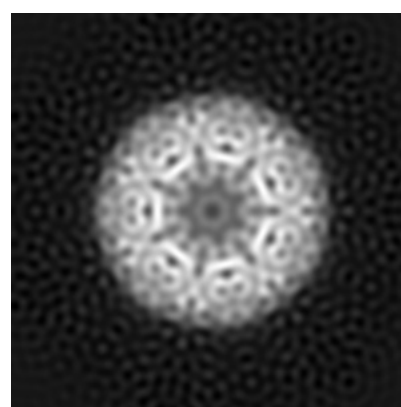
6.1.1 Primary map



X



Y

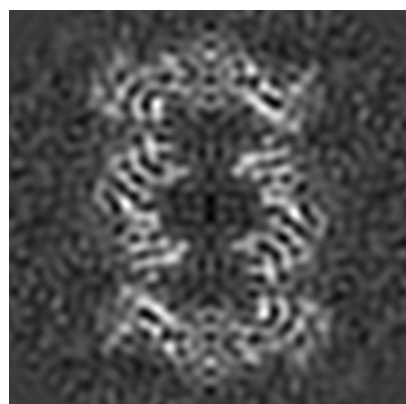


Z

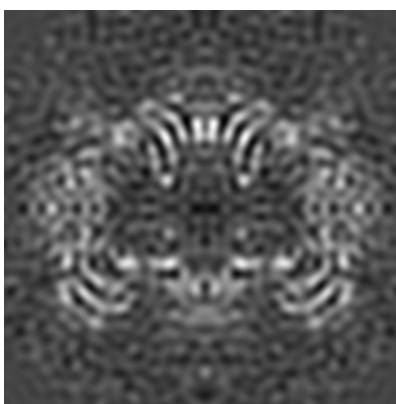
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

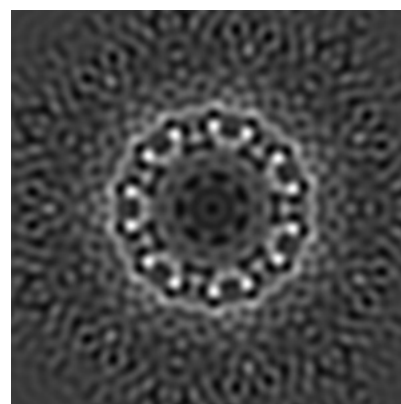
6.2.1 Primary map



X Index: 72



Y Index: 72

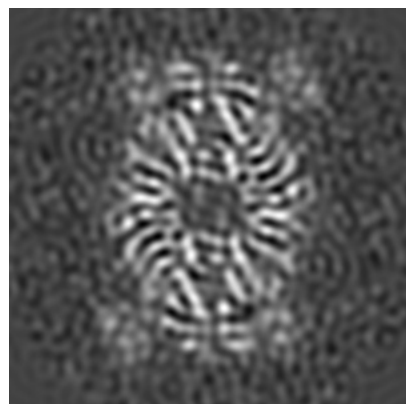


Z Index: 72

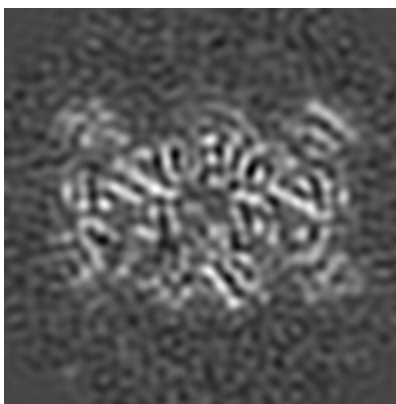
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

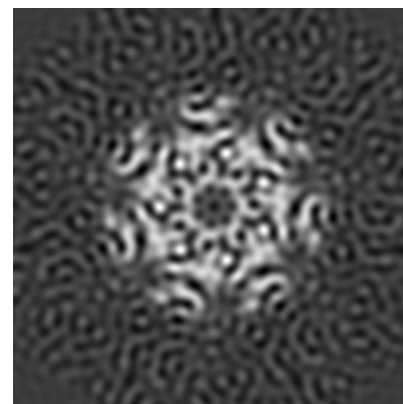
6.3.1 Primary map



X Index: 90



Y Index: 53

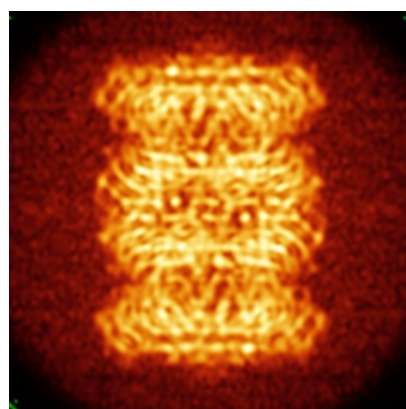


Z Index: 59

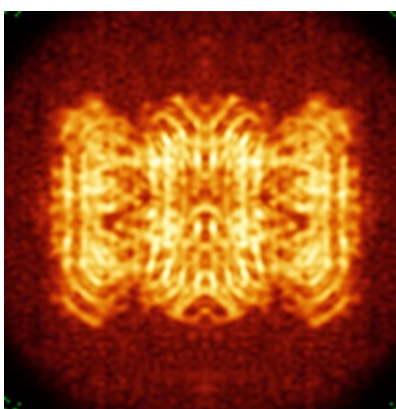
The images above show the largest variance slices of the map in three orthogonal directions.

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

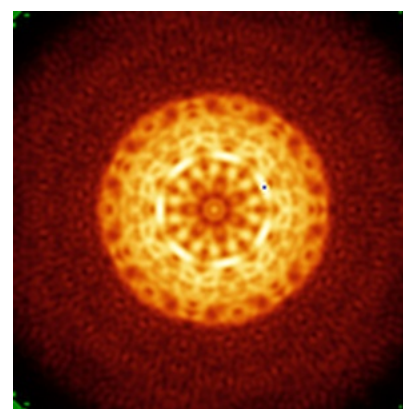
6.4.1 Primary map



X



Y

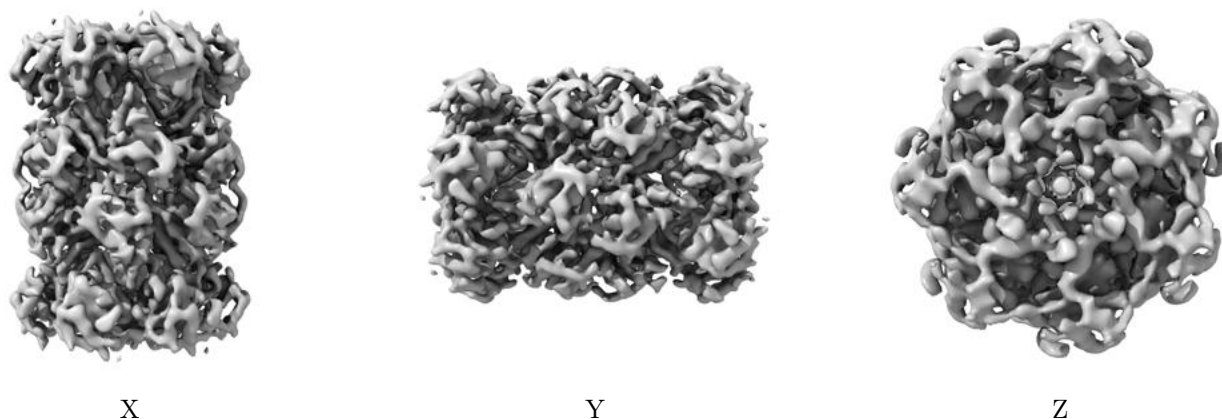


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

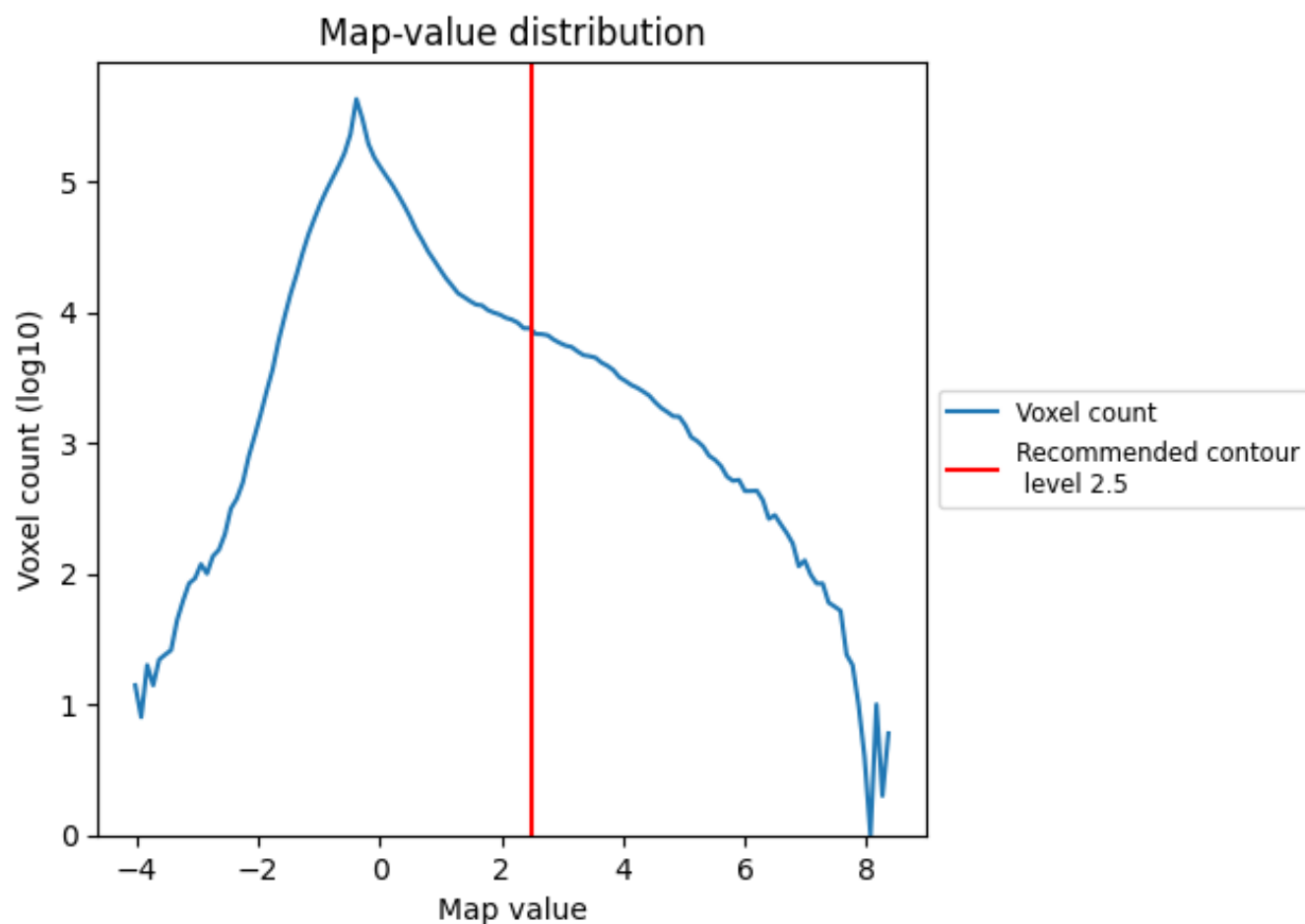
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

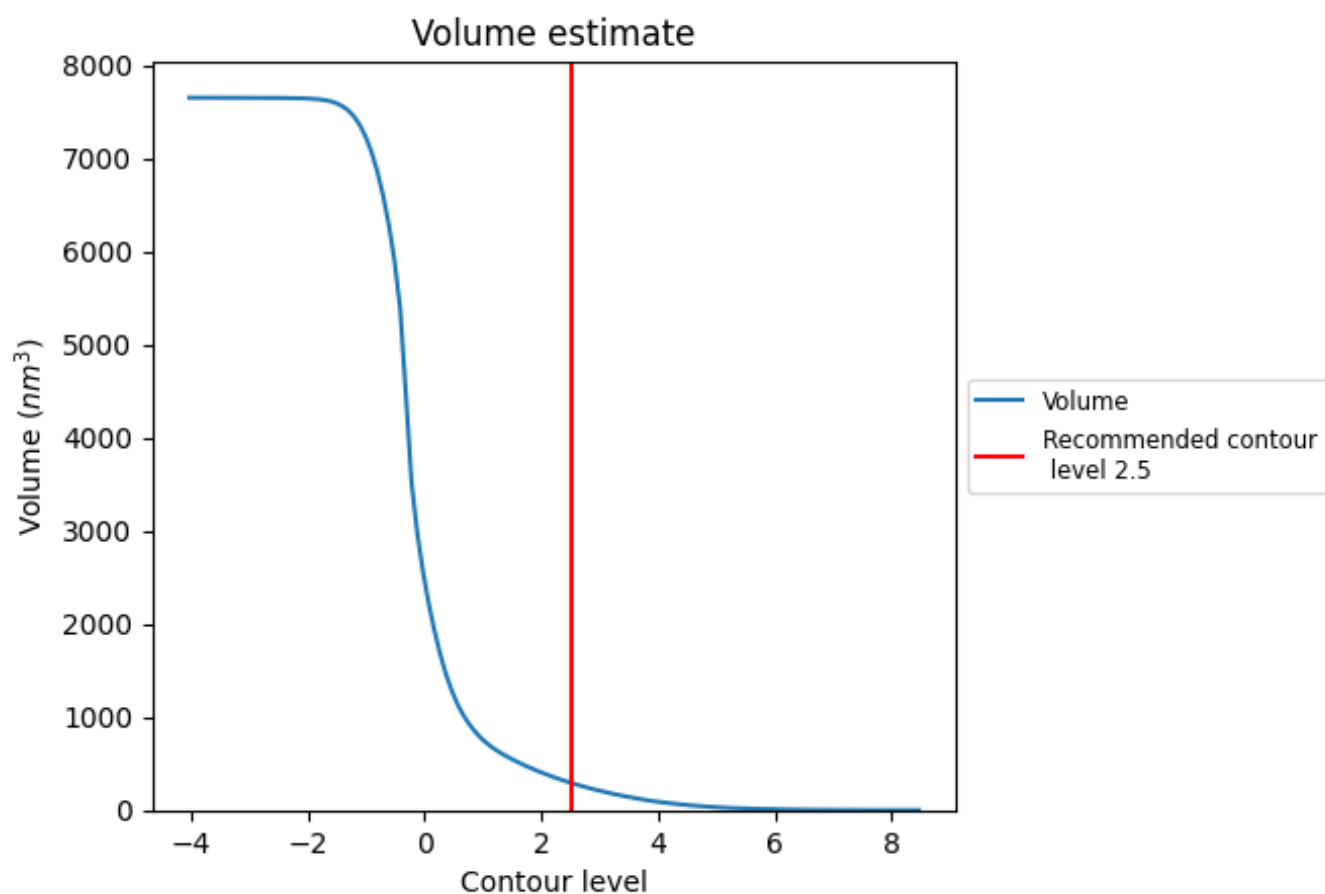
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

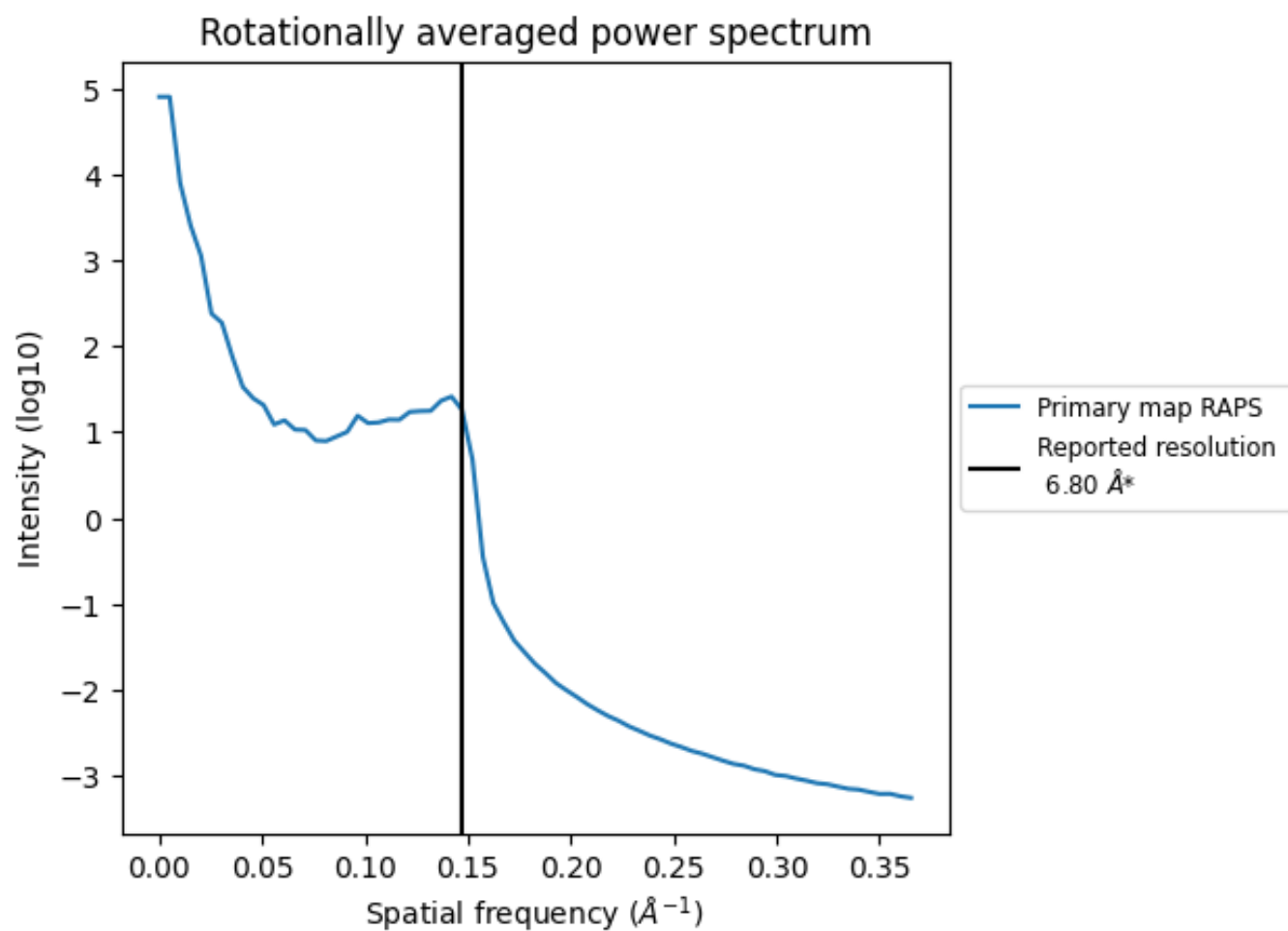
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 295 nm³; this corresponds to an approximate mass of 266 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.147 Å⁻¹

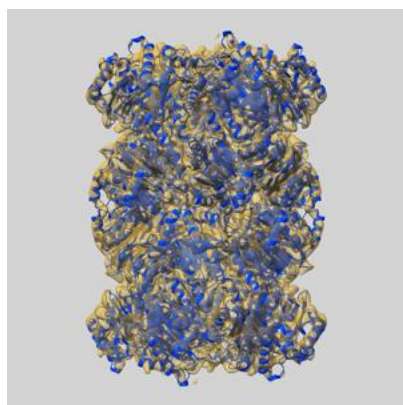
8 Fourier-Shell correlation ⓘ

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

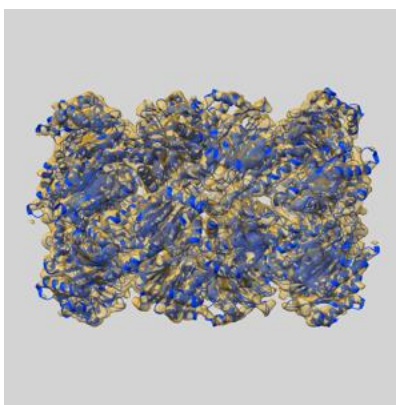
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1740 and PDB model 3C92. Per-residue inclusion information can be found in section [3](#) on page [6](#).

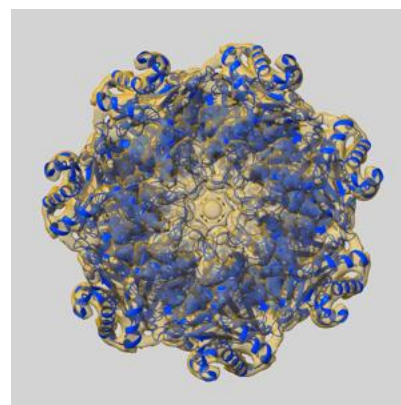
9.1 Map-model overlay [i](#)



X



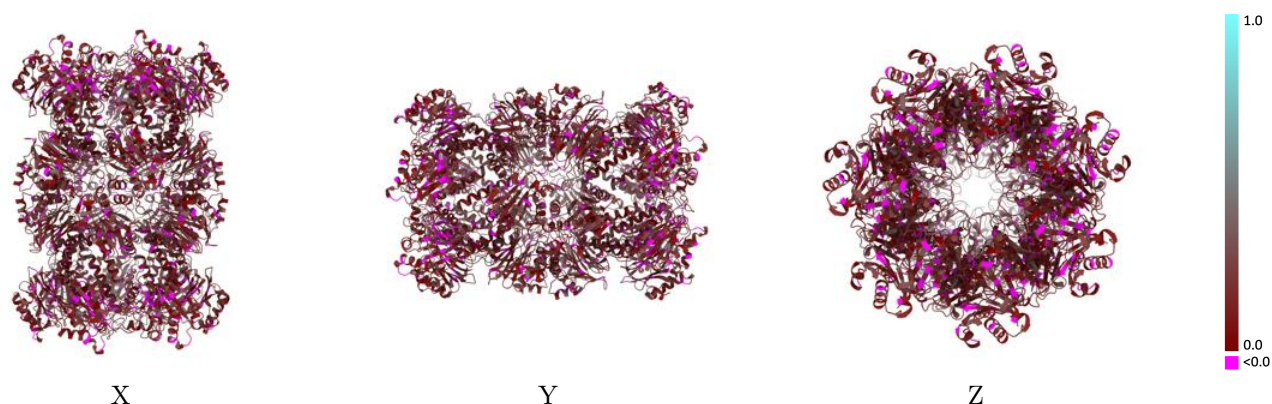
Y



Z

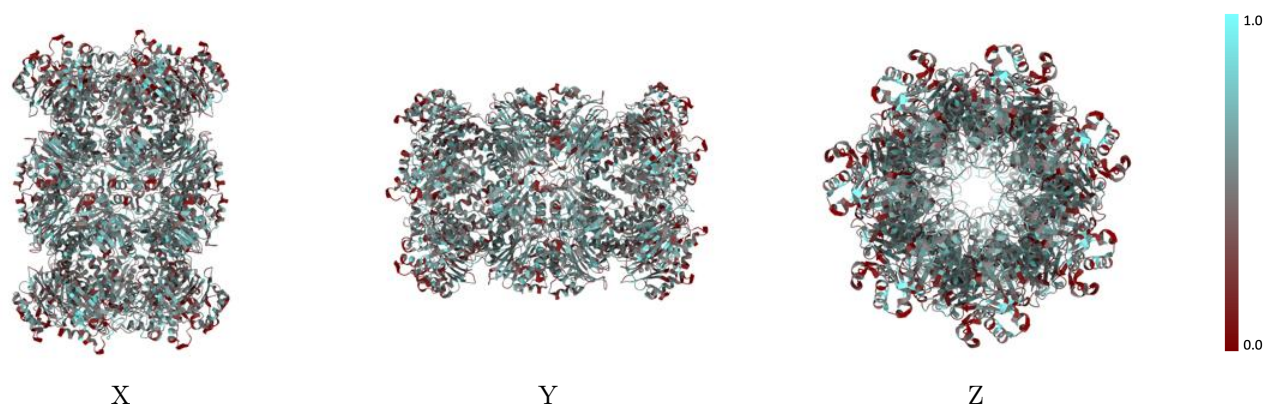
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



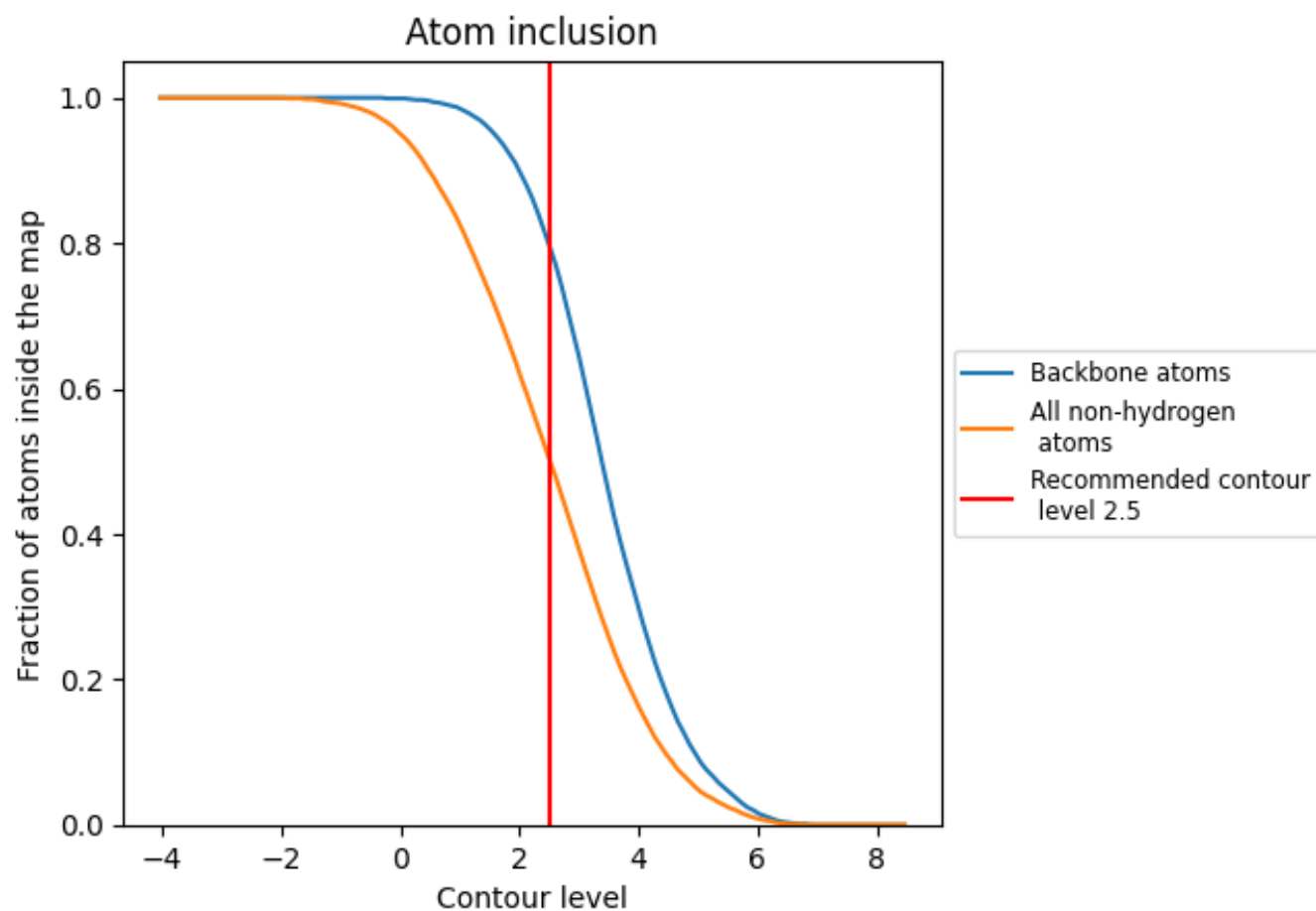
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5030	 0.1670
1	 0.5230	 0.1730
2	 0.5270	 0.1750
A	 0.4800	 0.1580
B	 0.4860	 0.1590
C	 0.4900	 0.1650
D	 0.4810	 0.1560
E	 0.4920	 0.1680
F	 0.4980	 0.1680
G	 0.4860	 0.1620
H	 0.5220	 0.1740
I	 0.5280	 0.1750
J	 0.5300	 0.1790
K	 0.5220	 0.1760
L	 0.5250	 0.1750
M	 0.5280	 0.1780
N	 0.5280	 0.1780
O	 0.4590	 0.1460
P	 0.4730	 0.1530
Q	 0.4890	 0.1660
R	 0.4840	 0.1620
S	 0.4920	 0.1660
T	 0.4920	 0.1660
U	 0.4790	 0.1570
V	 0.5200	 0.1710
W	 0.5210	 0.1670
X	 0.5220	 0.1700
Y	 0.5240	 0.1720
Z	 0.5220	 0.1720

