



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 02:47 AM UTC

PDB ID : 6TUI / pdb_00006tui
EMDB ID : EMD-10592
Title : Virion of empty GTA particle
Authors : Bardy, P.; Fuzik, T.; Hrebik, D.; Pantucek, R.; Beatty, J.T.; Plevka, P.
Deposited on : 2020-01-07
Resolution : 10.47 Å(reported)

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

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

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

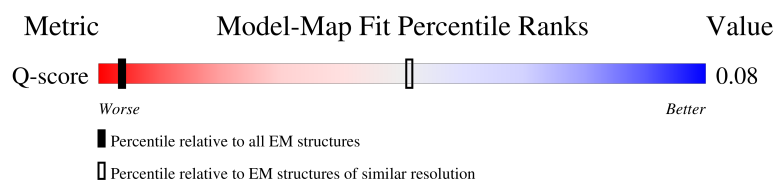
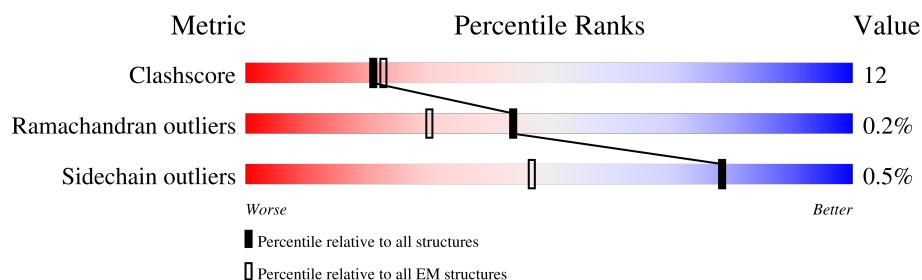
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.47 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.



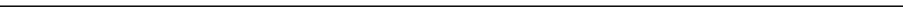
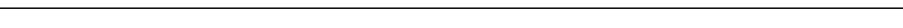
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	100 (10.00 - 10.90)

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	A4	385	 59% 16% 24%
1	A5	385	 55% 21% • 24%
1	B4	385	 58% 19% • 23%
1	B5	385	 49% 20% • 30%

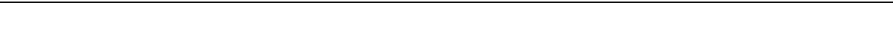
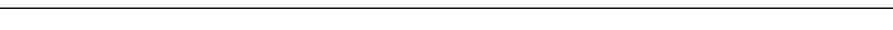
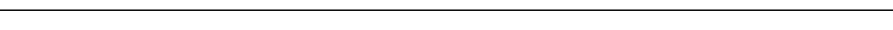
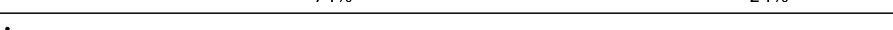
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Mol	Chain	Length	Quality of chain
1	C4	385	
1	C5	385	
1	D4	385	
1	E4	385	
1	F4	385	
1	G4	385	
1	H4	385	
1	I4	385	
1	J4	385	
1	K4	385	
1	L4	385	
1	M4	385	
1	N4	385	
1	O4	385	
1	P4	385	
1	Q4	385	
1	R4	385	
1	S4	385	
1	T4	385	
1	U4	385	
1	V4	385	
1	W4	385	
1	X4	385	
1	Y4	385	
1	Z4	385	

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Mol	Chain	Length	Quality of chain
2	A1	84	 88% 12%
2	A2	84	 88% 12%
2	A3	84	 83% 17%
2	B2	84	 86% 14%
2	B3	84	 89% 11%
2	C2	84	 86% 14%
2	C3	84	 88% 12%
2	D2	84	 86% 14%
2	D3	84	 85% 15%
2	E2	84	 81% 19%
2	E3	84	 83% 17%
3	F2	325	 97%
3	F3	325	 97%
4	G	137	 74% 24% .
4	H	137	 73% 25% .
4	I	137	 72% 26% .
4	J	137	 72% 26% .
5	C	197	 74% 24% .
5	D	197	 79% 20% .
6	A	396	 76% 17% 7%
6	B	396	 78% 14% . 8%
7	F	135	 75% 23% ..
8	E	112	 73% 25% .

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 84902 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 Phage major capsid protein, HK97 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C5	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	X4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	Y4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	Z4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	A5	294	Total	C	N	O	S	0	0
			2184	1385	373	420	6		
1	B5	270	Total	C	N	O	S	0	0
			2012	1281	344	381	6		
1	N4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	R4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	M4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	Q4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	O4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	P4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	W4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	U4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	T4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	S4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	K4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	J4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	V4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	L4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	H4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	I4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	A4	291	Total	C	N	O	S	0	0
			2173	1379	371	417	6		
1	D4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	E4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	F4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	G4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	B4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		
1	C4	297	Total	C	N	O	S	0	0
			2209	1400	377	426	6		

- Molecule 2 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D2	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	A2	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	C2	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	B2	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	E2	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	E3	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	B3	84	Total	C	N	O	S	0	0
			640	403	115	121	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	D3	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	C3	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	A3	84	Total	C	N	O	S	0	0
			640	403	115	121	1		
2	A1	84	Total	C	N	O	S	0	0
			640	403	115	121	1		

- Molecule 3 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	F2	10	Total	C	N	O	0	0
			62	42	10	10		
3	F3	10	Total	C	N	O	0	0
			62	42	10	10		

- Molecule 4 is a protein called Tail tube protein Rcc01691.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	134	Total	C	N	O	S	0	0
			993	623	167	201	2		
4	I	134	Total	C	N	O	S	0	0
			993	623	167	201	2		
4	J	134	Total	C	N	O	S	0	0
			993	623	167	201	2		
4	G	134	Total	C	N	O	S	0	0
			993	623	167	201	2		

- Molecule 5 is a protein called Adaptor protein Rcc01688.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	192	Total	C	N	O	S	0	0
			1440	926	257	249	8		
5	D	195	Total	C	N	O	S	0	0
			1460	938	260	254	8		

- Molecule 6 is a protein called Portal protein Rcc01684.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	370	Total	C	N	O	S	0	0
			2815	1789	505	508	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	366	Total	C	N	O	S	0	0
			2781	1767	499	502	13		

- Molecule 7 is a protein called Tail terminator protein Rcc01690.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	134	Total	C	N	O	S	0	0
			968	613	174	180	1		

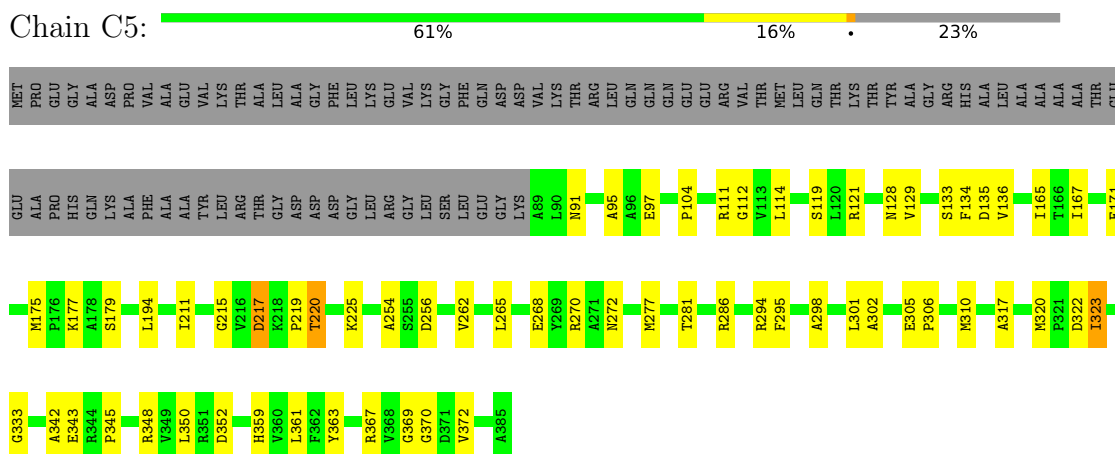
- Molecule 8 is a protein called Stopper protein Rcc01689.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	110	Total	C	N	O	S	0	0
			859	536	171	151	1		

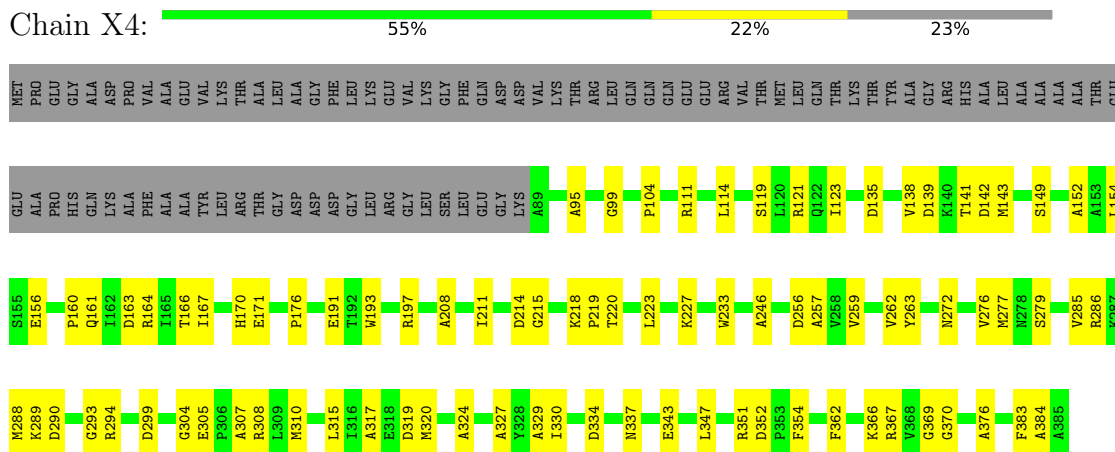
3 Residue-property plots

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

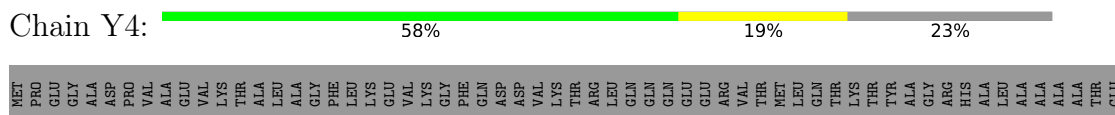
- Molecule 1: Phage major capsid protein, HK97 family

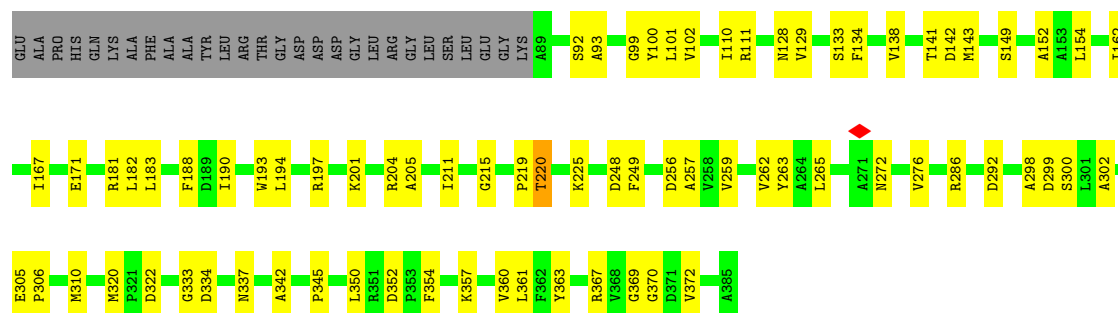


- Molecule 1: Phage major capsid protein, HK97 family



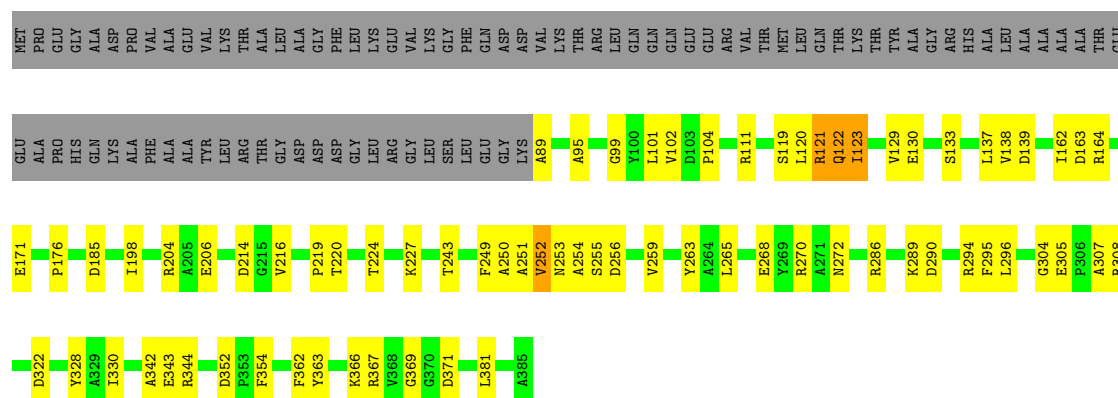
- Molecule 1: Phage major capsid protein, HK97 family





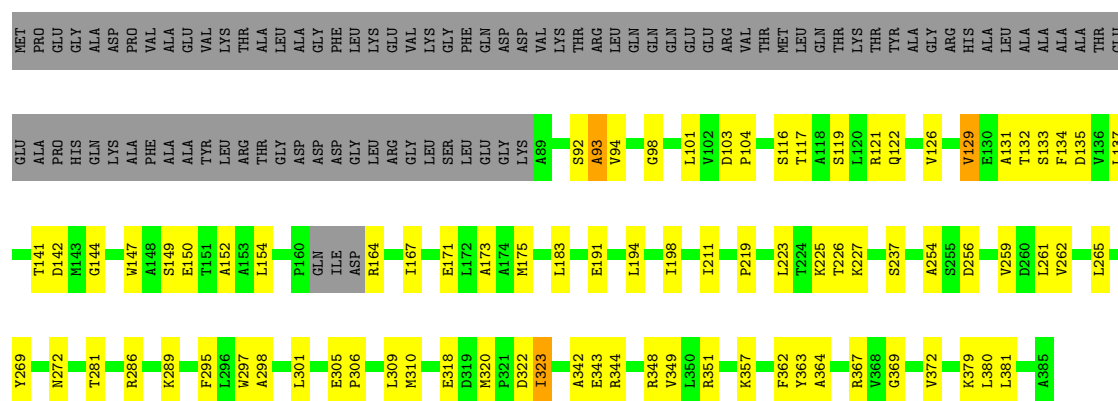
- Molecule 1: Phage major capsid protein, HK97 family

Chain Z4: 58% 18% 23%



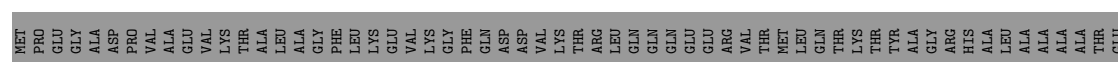
- Molecule 1: Phage major capsid protein, HK97 family

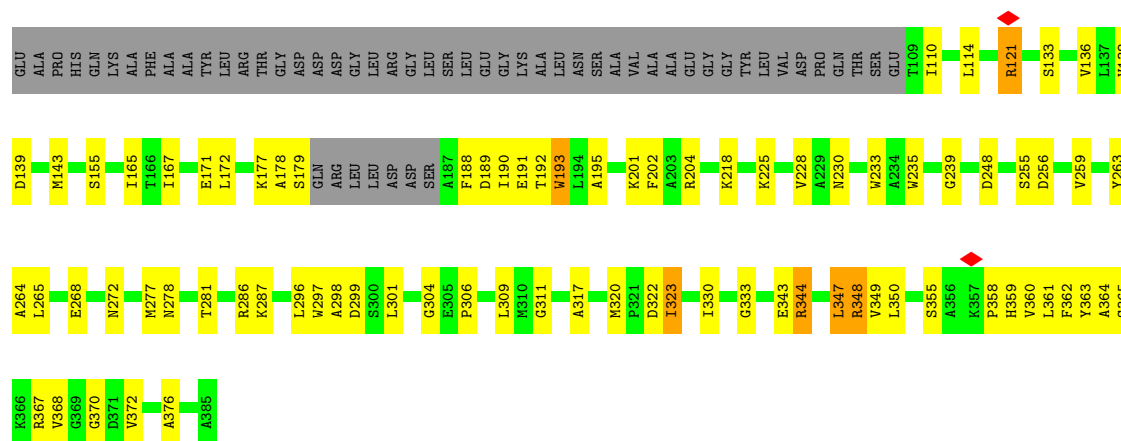
Chain A5: 55% 21% 24%



- Molecule 1: Phage major capsid protein, HK97 family

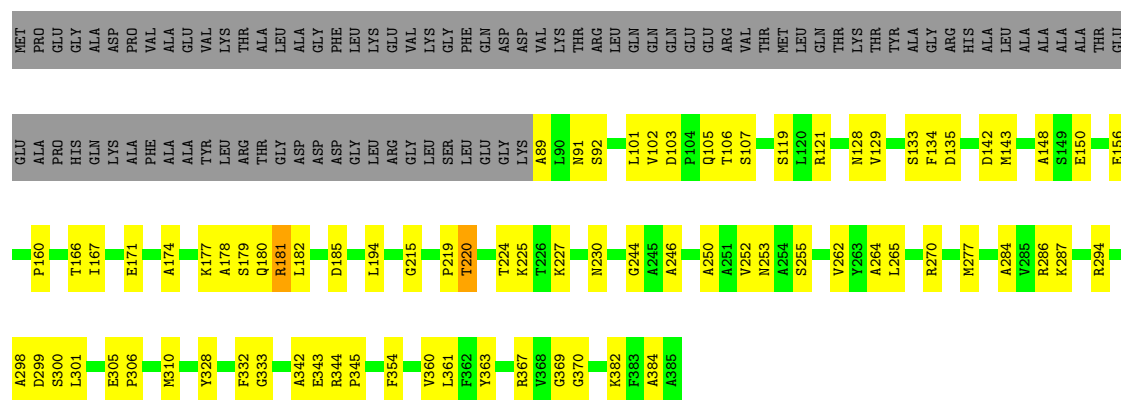
Chain B5: 49% 20% 30%





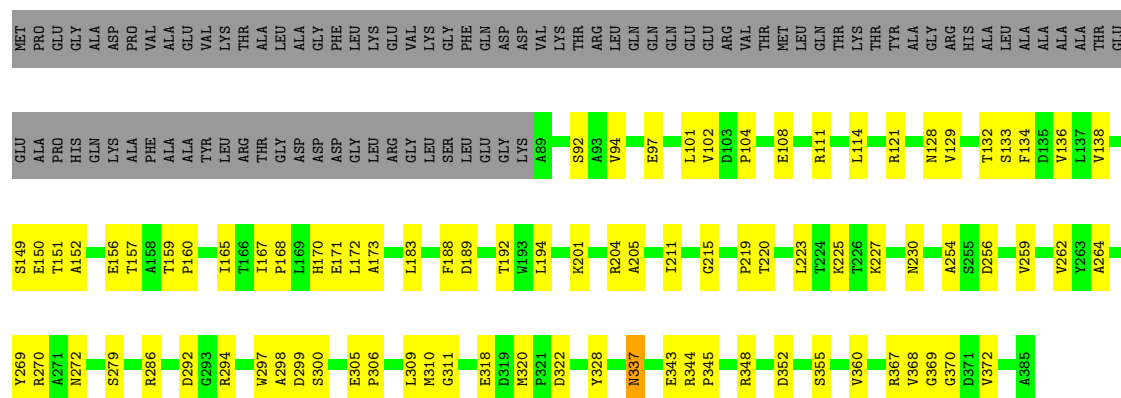
- Molecule 1: Phage major capsid protein, HK97 family

Chain N4:



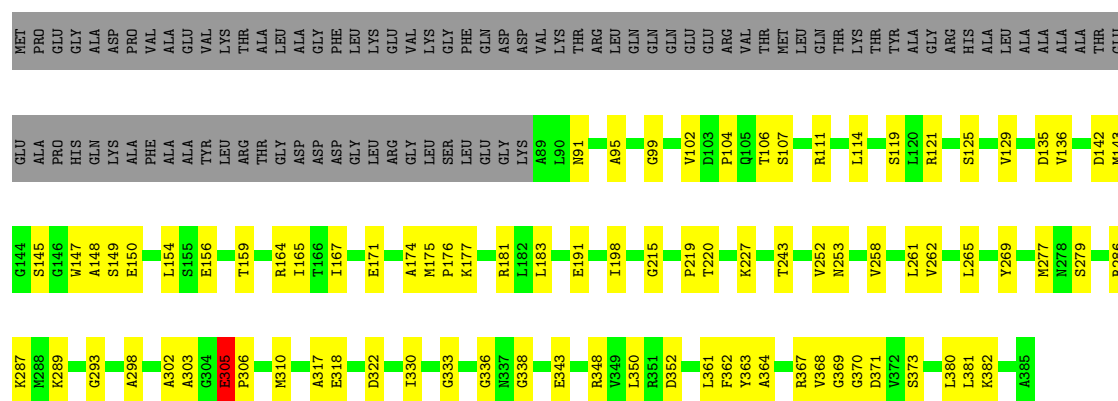
- Molecule 1: Phage major capsid protein, HK97 family

Chain R4:



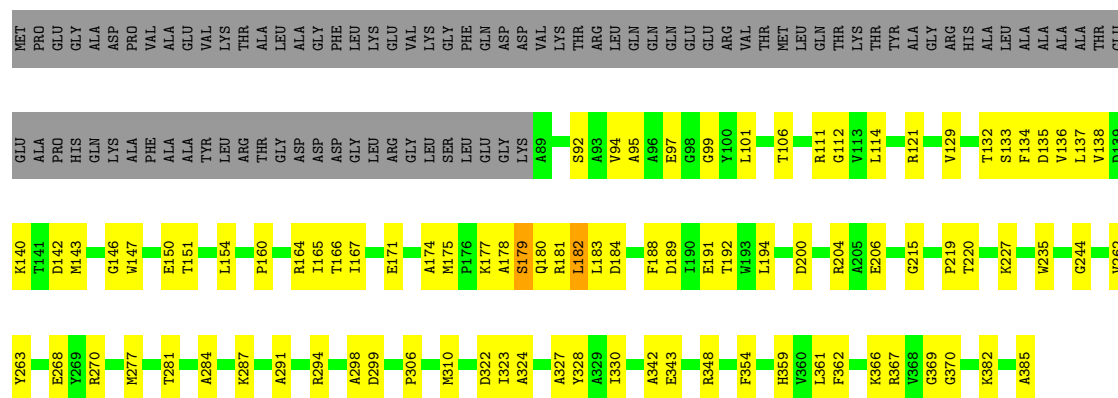
- Molecule 1: Phage major capsid protein, HK97 family

Chain M4:



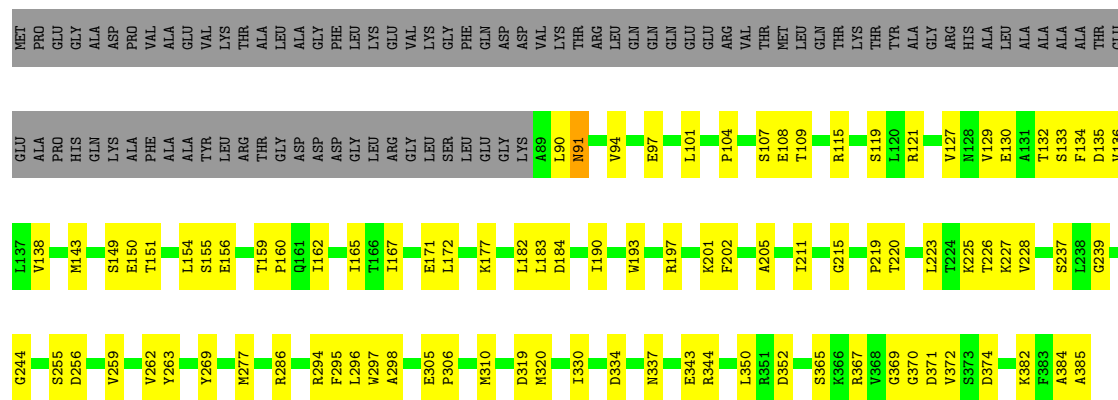
- Molecule 1: Phage major capsid protein, HK97 family

Chain Q4: 54% 23% 23%



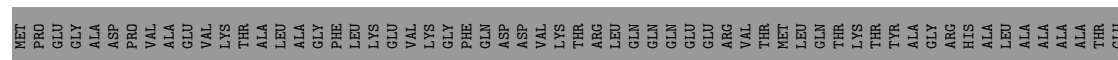
- Molecule 1: Phage major capsid protein, HK97 family

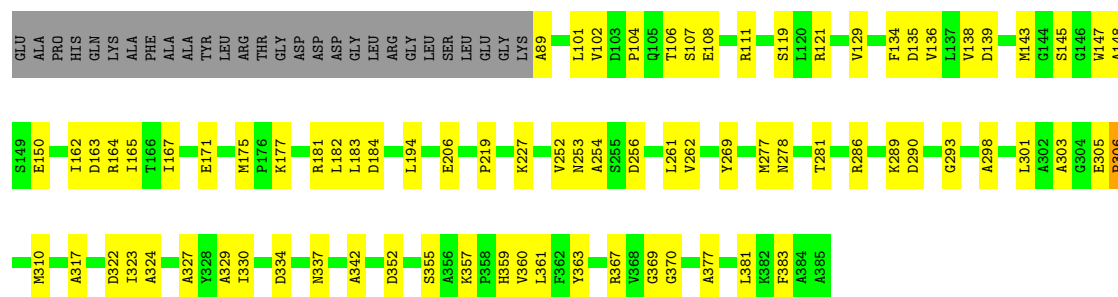
Chain O4: 53% 24% 23%



- Molecule 1: Phage major capsid protein, HK97 family

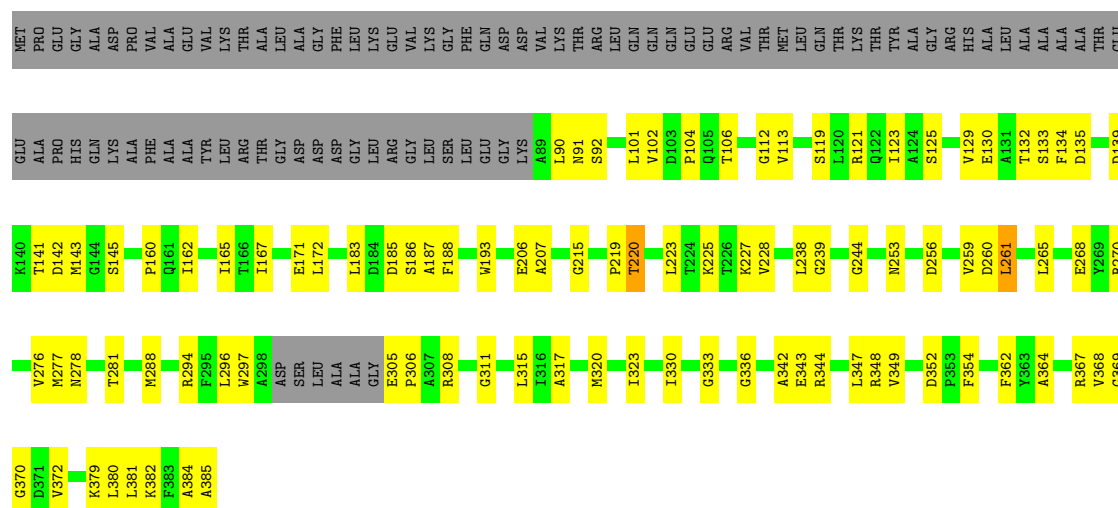
Chain P4: 56% 21% 23%





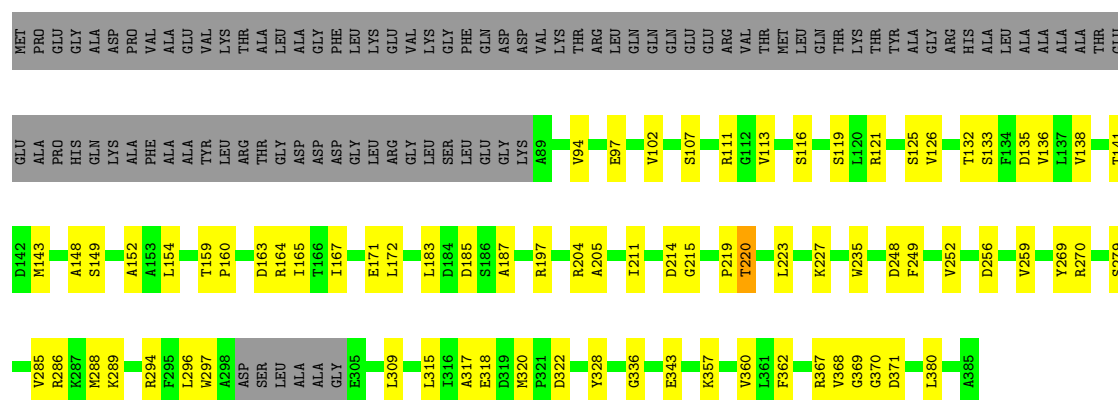
- Molecule 1: Phage major capsid protein, HK97 family

Chain W4: 51% 24% 24%



- Molecule 1: Phage major capsid protein, HK97 family

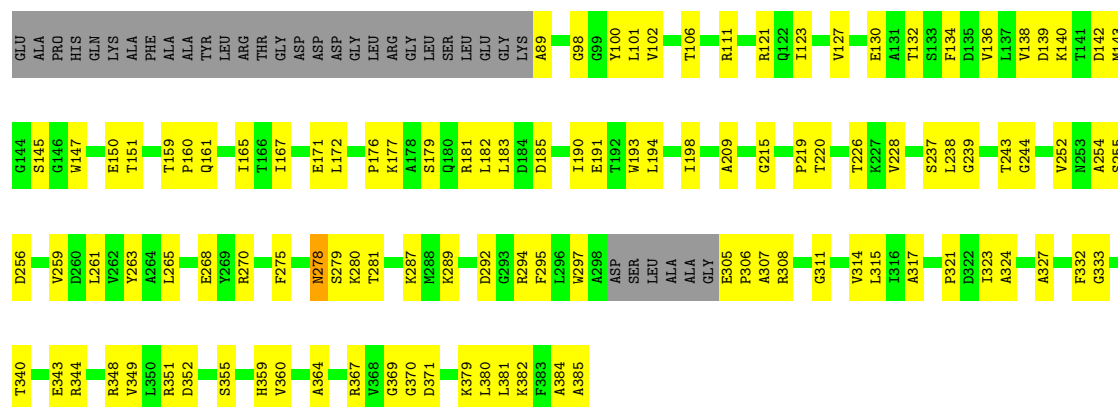
Chain U4: 56% 20% 24%



- Molecule 1: Phage major capsid protein, HK97 family

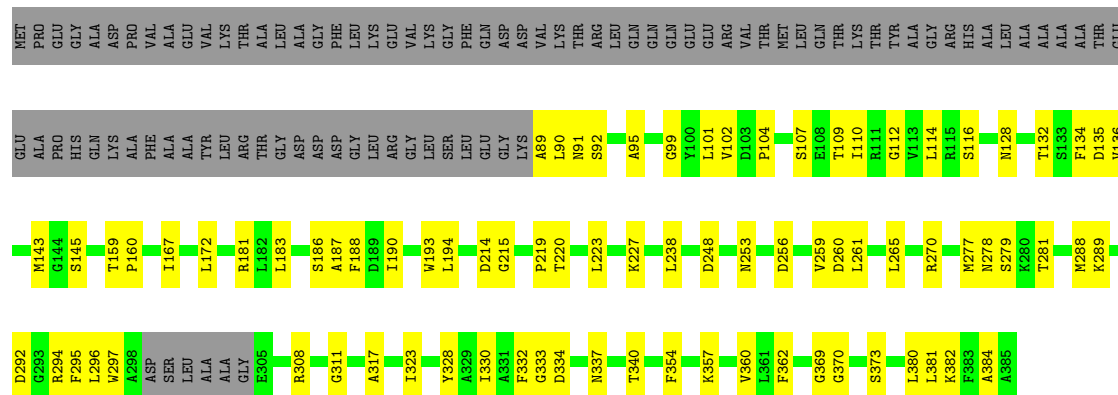
Chain T4: 47% 28% 24%





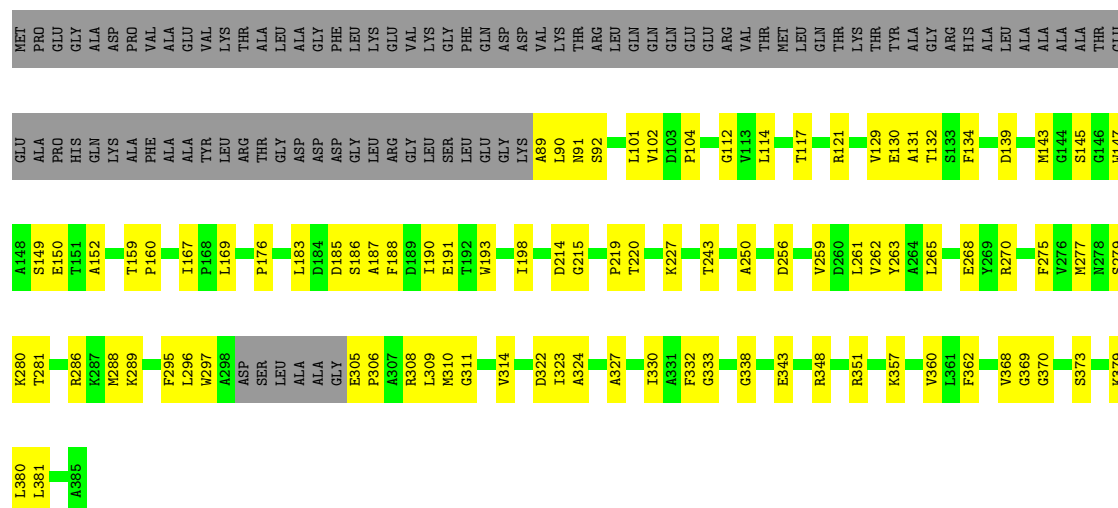
- Molecule 1: Phage major capsid protein, HK97 family

Chain S4: 54% 21% 24%



- Molecule 1: Phage major capsid protein, HK97 family

Chain K4: 52% 24% 24%



- Molecule 1: Phage major capsid protein, HK97 family

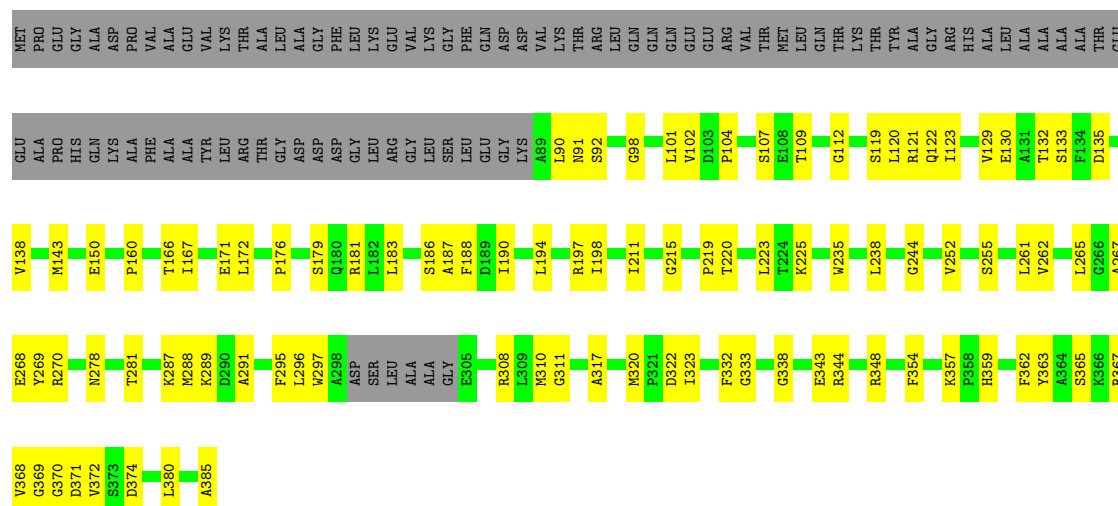
Chain J4: 51% 24% 24%

- Molecule 1: Phage major capsid protein, HK97 family

- Molecule 1: Phage major capsid protein, HK97 family

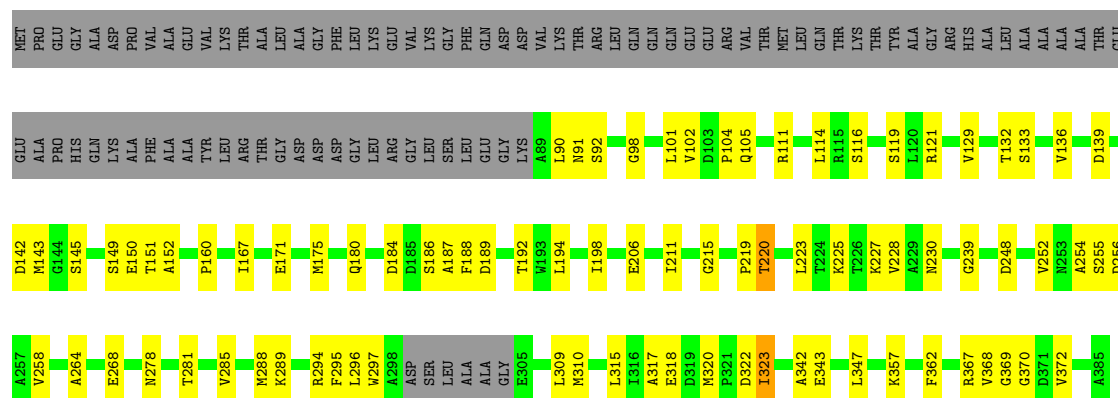
- Molecule 1: Phage major capsid protein, HK97 family





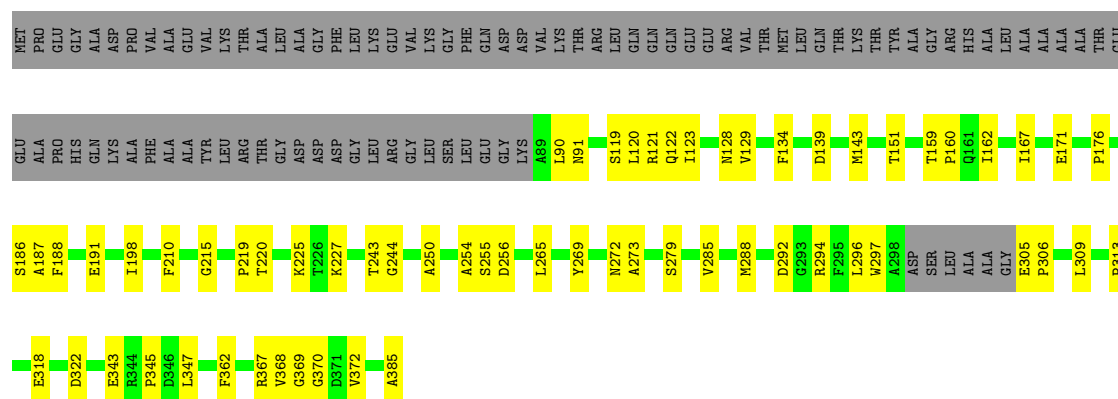
- Molecule 1: Phage major capsid protein, HK97 family

Chain I4: 54% 21% 24%



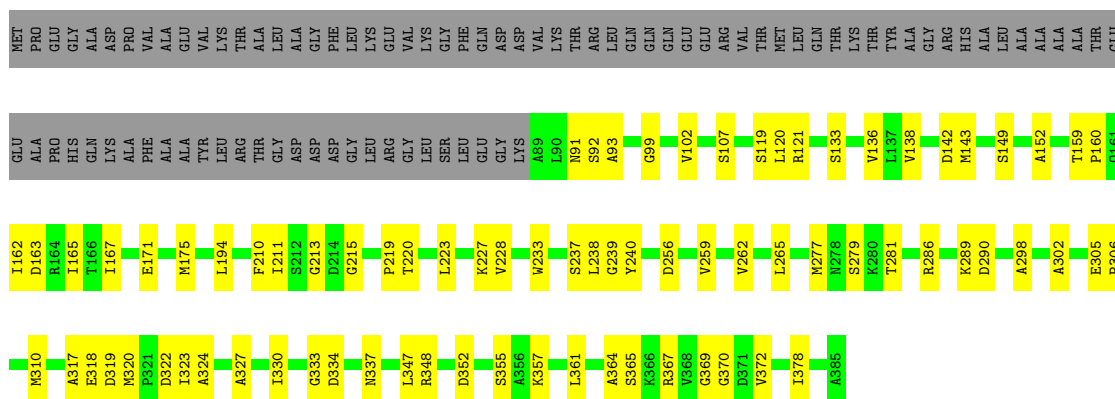
- Molecule 1: Phage major capsid protein, HK97 family

Chain A4: 59% 16% 24%



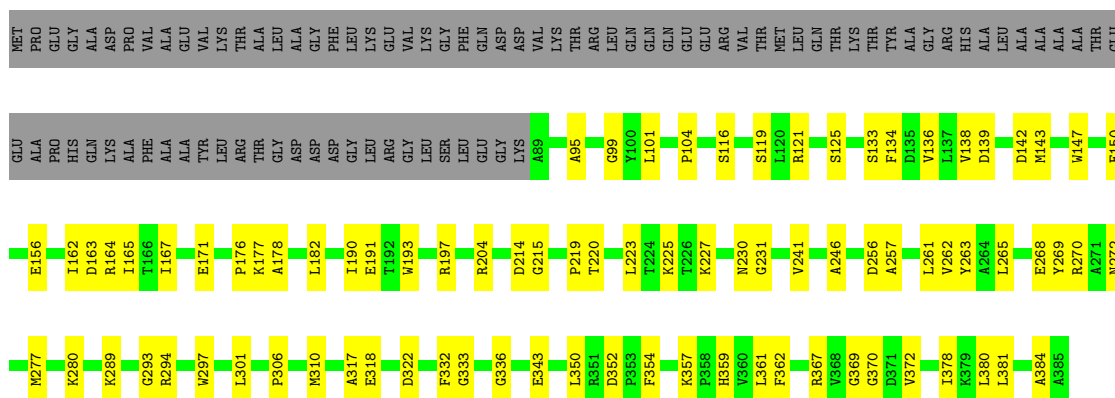
- Molecule 1: Phage major capsid protein, HK97 family

Chain D4: 57% 21% 23%



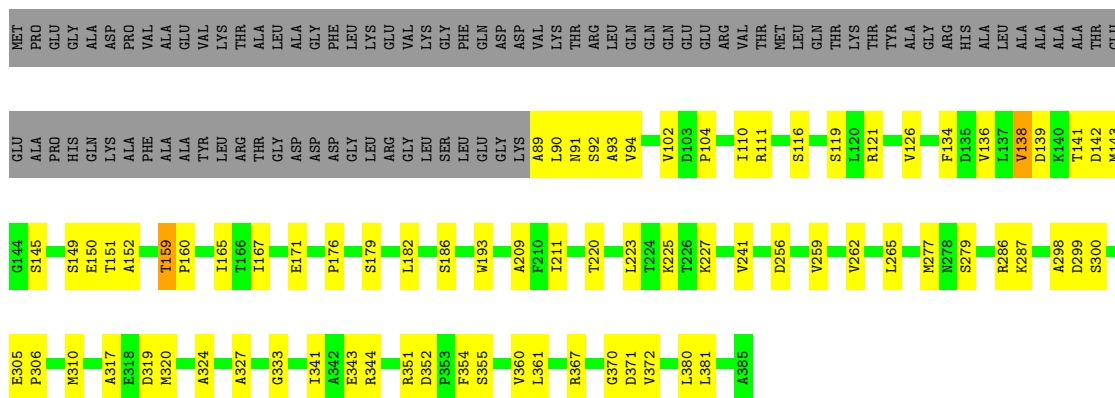
- Molecule 1: Phage major capsid protein, HK97 family

Chain E4: 55% 22% 23%



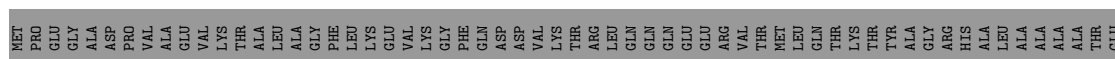
- Molecule 1: Phage major capsid protein, HK97 family

Chain F4: 57% 20% 23%



- Molecule 1: Phage major capsid protein, HK97 family

Chain G4: 56% 21% 23%



Chain A2:  88% 12%



- Molecule 2: Uncharacterized protein

Chain C2:  86% 14%



- Molecule 2: Uncharacterized protein

Chain B2:  86% 14%



- Molecule 2: Uncharacterized protein

Chain E2:  81% 19%



- Molecule 2: Uncharacterized protein

Chain E3:  83% 17%



- Molecule 2: Uncharacterized protein

Chain B3:  89% 11%

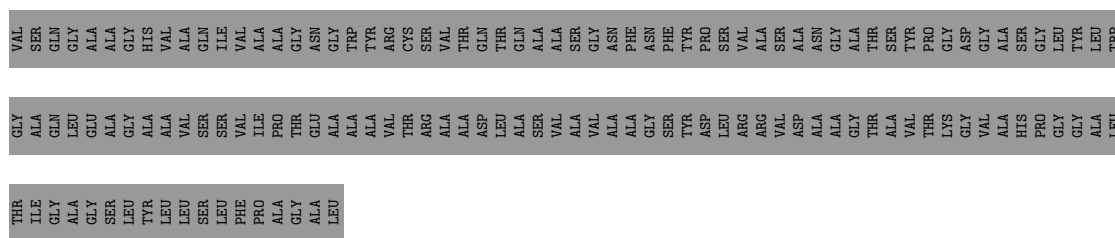


- Molecule 2: Uncharacterized protein

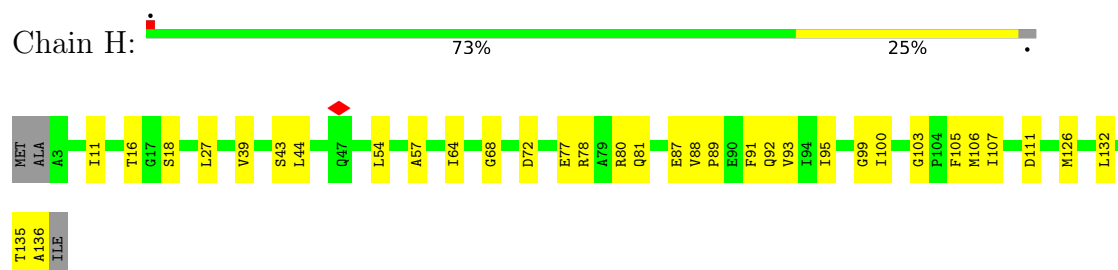
Chain D3:  85% 15%



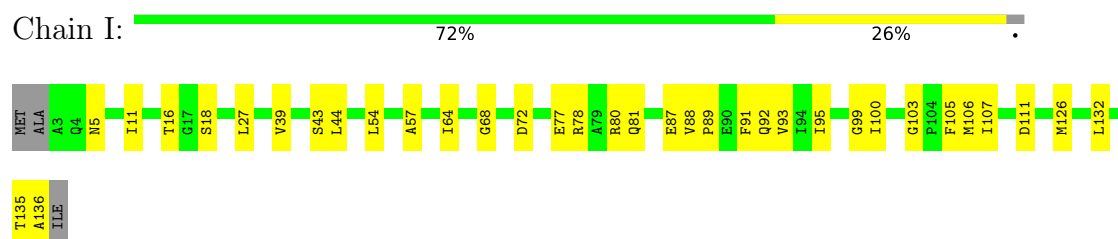
- Molecule 2: Uncharacterized protein



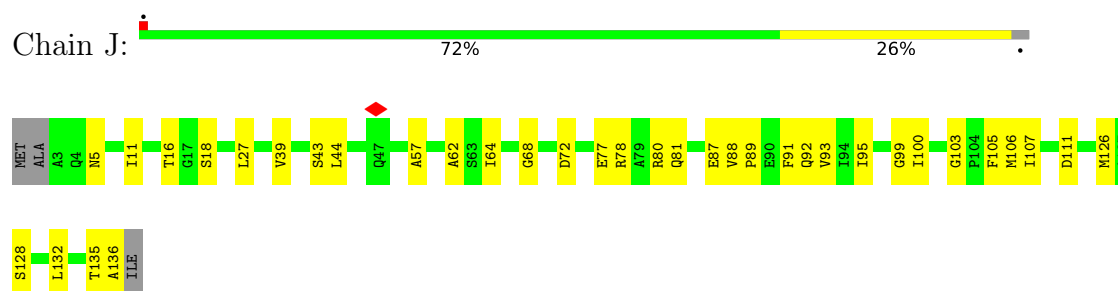
- Molecule 4: Tail tube protein Rcc01691



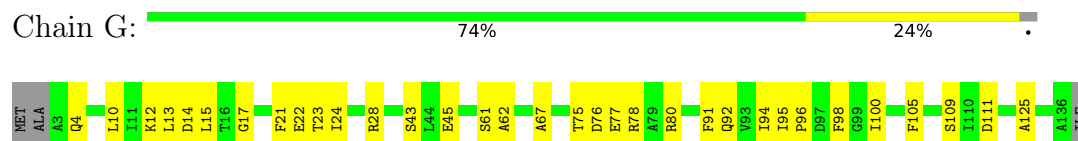
- Molecule 4: Tail tube protein Rcc01691



- Molecule 4: Tail tube protein Rcc01691

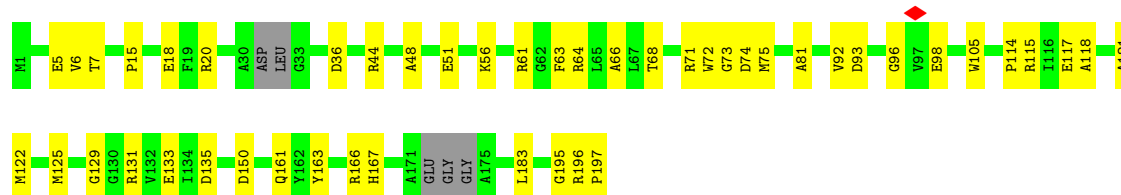


- Molecule 4: Tail tube protein Rcc01691

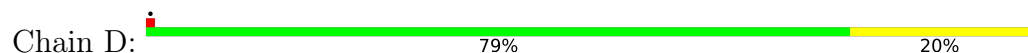


- Molecule 5: Adaptor protein Rcc01688

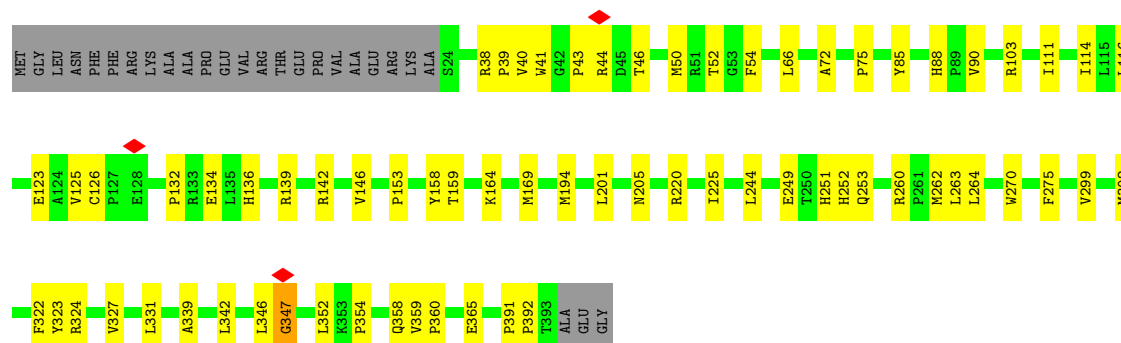
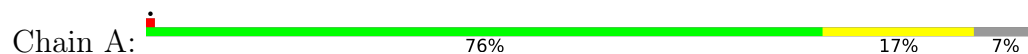




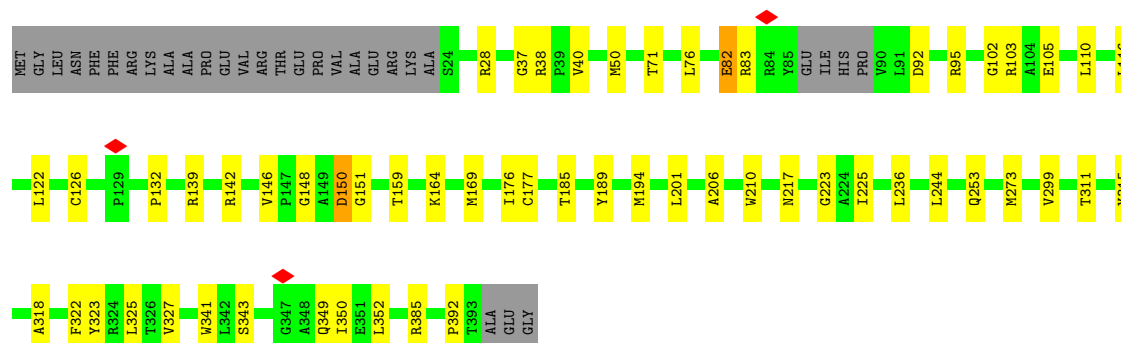
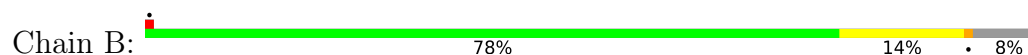
• Molecule 5: Adaptor protein Rcc01688



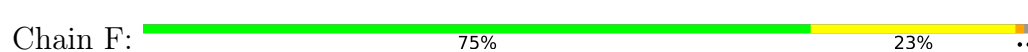
• Molecule 6: Portal protein Rcc01684

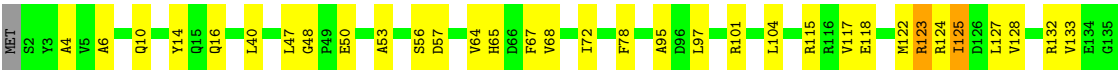


• Molecule 6: Portal protein Rcc01684



• Molecule 7: Tail terminator protein Rcc01690





● Molecule 8: Stopper protein Rcc01689



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	6277	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42.75	Depositor
Minimum defocus (nm)	-1000	Depositor
Maximum defocus (nm)	-3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.176	Depositor
Minimum map value	-0.068	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	1530.72, 1530.72, 1530.72	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	4.252, 4.252, 4.252	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	A4	0.43	0/2216	0.64	0/3012
1	A5	0.38	0/2227	0.59	0/3027
1	B4	0.42	0/2253	0.55	0/3064
1	B5	0.45	0/2053	0.71	4/2789 (0.1%)
1	C4	0.41	0/2253	0.49	2/3064 (0.1%)
1	C5	0.41	0/2253	0.53	0/3064
1	D4	0.39	0/2253	0.48	0/3064
1	E4	0.40	0/2253	0.48	0/3064
1	F4	0.43	0/2253	0.50	0/3064
1	G4	0.47	0/2253	0.65	1/3064 (0.0%)
1	H4	0.39	0/2216	0.48	0/3012
1	I4	0.40	0/2216	0.63	0/3012
1	J4	0.38	0/2216	0.45	0/3012
1	K4	0.37	0/2216	0.45	0/3012
1	L4	0.37	0/2216	0.44	0/3012
1	M4	0.40	0/2253	0.52	2/3064 (0.1%)
1	N4	0.38	0/2253	0.49	1/3064 (0.0%)
1	O4	0.38	0/2253	0.49	0/3064
1	P4	0.41	0/2253	0.52	2/3064 (0.1%)
1	Q4	0.40	0/2253	0.49	2/3064 (0.1%)
1	R4	0.40	0/2253	0.59	0/3064
1	S4	0.35	0/2216	0.44	0/3012
1	T4	0.41	0/2216	0.49	0/3012
1	U4	0.39	0/2216	0.60	0/3012
1	V4	0.36	0/2216	0.45	0/3012
1	W4	0.36	0/2216	0.47	0/3012
1	X4	0.37	0/2253	0.46	2/3064 (0.1%)
1	Y4	0.37	0/2253	0.44	0/3064
1	Z4	0.42	0/2253	0.67	3/3064 (0.1%)
2	A1	0.41	0/652	0.71	0/892
2	A2	0.42	0/652	0.72	0/892
2	A3	0.41	0/652	0.71	0/892
2	B2	0.42	0/652	0.72	0/892
2	B3	0.42	0/652	0.72	0/892

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	C2	0.42	0/652	0.71	0/892
2	C3	0.42	0/652	0.72	0/892
2	D2	0.42	0/652	0.71	0/892
2	D3	0.41	0/652	0.71	0/892
2	E2	0.41	0/652	0.71	0/892
2	E3	0.41	0/652	0.71	0/892
3	F2	0.41	0/61	1.02	0/81
3	F3	0.42	0/61	1.02	0/81
4	G	0.35	0/1009	0.71	1/1363 (0.1%)
4	H	0.49	0/1009	0.71	1/1363 (0.1%)
4	I	0.49	0/1009	0.71	1/1363 (0.1%)
4	J	0.49	0/1009	0.71	1/1363 (0.1%)
5	C	0.40	0/1471	0.73	2/2003 (0.1%)
5	D	0.45	1/1492 (0.1%)	0.80	1/2033 (0.0%)
6	A	0.40	0/2889	0.68	2/3934 (0.1%)
6	B	0.39	0/2852	0.69	1/3881 (0.0%)
7	F	0.39	0/982	0.77	1/1337 (0.1%)
8	E	0.39	0/875	0.67	0/1182
All	All	0.40	1/86595 (0.0%)	0.58	30/117768 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	109	PRO	N-CD	5.33	1.55	1.47

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	150	ASP	N-CA-C	10.04	125.36	109.50
6	A	41	TRP	N-CA-C	9.54	124.72	112.89
1	Z4	121	ARG	N-CA-C	-6.82	104.92	113.18
1	N4	181	ARG	N-CA-C	-6.64	104.54	114.64
1	Z4	122	GLN	N-CA-C	6.62	118.15	111.07
1	Z4	123	ILE	N-CA-CB	-6.59	100.57	111.98
1	P4	305	GLU	CA-C-N	6.25	127.65	119.84
1	P4	305	GLU	C-N-CA	6.25	127.65	119.84
1	M4	305	GLU	CA-C-N	5.86	125.53	119.56
1	M4	305	GLU	C-N-CA	5.86	125.53	119.56
4	G	76	ASP	N-CA-C	5.84	117.72	111.36
6	A	40	VAL	N-CA-C	-5.73	99.50	107.80
7	F	48	GLY	N-CA-C	5.63	123.82	112.34
1	B5	121	ARG	N-CA-C	-5.46	106.58	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B5	323	ILE	N-CA-C	-5.44	100.49	108.54
1	G4	193	TRP	N-CA-C	-5.35	105.89	112.90
4	H	95	ILE	N-CA-C	-5.32	103.74	108.95
4	I	95	ILE	N-CA-C	-5.28	103.77	108.95
1	C4	305	GLU	CA-C-N	5.26	124.92	119.56
1	C4	305	GLU	C-N-CA	5.26	124.92	119.56
5	C	75	MET	CA-C-N	5.26	131.58	121.54
5	C	75	MET	C-N-CA	5.26	131.58	121.54
4	J	95	ILE	N-CA-C	-5.22	103.84	108.95
1	Q4	182	LEU	CA-C-N	5.14	127.17	120.28
1	Q4	182	LEU	C-N-CA	5.14	127.17	120.28
1	X4	305	GLU	CA-C-N	5.08	124.58	119.19
1	X4	305	GLU	C-N-CA	5.08	124.58	119.19
1	B5	344	ARG	CA-C-N	5.03	126.13	119.84
1	B5	344	ARG	C-N-CA	5.03	126.13	119.84
5	D	32	LEU	N-CA-C	5.00	119.23	113.38

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	A4	2173	0	2142	38	0
1	A5	2184	0	2152	89	0
1	B4	2209	0	2176	53	0
1	B5	2012	0	1990	112	0
1	C4	2209	0	2176	52	0
1	C5	2209	0	2176	51	0
1	D4	2209	0	2176	61	0
1	E4	2209	0	2176	68	0
1	F4	2209	0	2176	65	0
1	G4	2209	0	2176	54	0
1	H4	2173	0	2142	76	0
1	I4	2173	0	2142	72	0
1	J4	2173	0	2142	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K4	2173	0	2142	69	0
1	L4	2173	0	2142	69	0
1	M4	2209	0	2176	69	0
1	N4	2209	0	2176	68	0
1	O4	2209	0	2176	68	0
1	P4	2209	0	2176	77	0
1	Q4	2209	0	2176	76	0
1	R4	2209	0	2176	68	0
1	S4	2173	0	2142	67	0
1	T4	2173	0	2142	86	0
1	U4	2173	0	2142	66	0
1	V4	2173	0	2142	69	0
1	W4	2173	0	2142	80	0
1	X4	2209	0	2176	64	0
1	Y4	2209	0	2176	62	0
1	Z4	2209	0	2176	63	0
2	A1	640	0	653	8	0
2	A2	640	0	653	11	0
2	A3	640	0	653	13	0
2	B2	640	0	653	10	0
2	B3	640	0	653	9	0
2	C2	640	0	653	15	0
2	C3	640	0	653	9	0
2	D2	640	0	653	14	0
2	D3	640	0	653	14	0
2	E2	640	0	653	16	0
2	E3	640	0	653	15	0
3	F2	62	0	73	1	0
3	F3	62	0	73	1	0
4	G	993	0	957	22	0
4	H	993	0	957	19	0
4	I	993	0	957	20	0
4	J	993	0	957	20	0
5	C	1440	0	1472	71	0
5	D	1460	0	1493	46	0
6	A	2815	0	2788	51	0
6	B	2781	0	2756	52	0
7	F	968	0	987	30	0
8	E	859	0	861	18	0
All	All	84902	0	84034	2017	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 12.

All (2017) 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:B5:358:PRO:HG3	5:C:73:GLY:CA	1.56	1.35
1:B5:358:PRO:CG	5:C:73:GLY:N	1.91	1.32
1:B5:358:PRO:CG	5:C:73:GLY:H	1.44	1.30
1:B5:358:PRO:HG3	5:C:73:GLY:N	0.96	1.28
1:B5:358:PRO:CG	5:C:73:GLY:CA	2.19	1.18
1:A5:191:GLU:OE1	6:A:39:PRO:HD2	1.46	1.13
1:B5:359:HIS:HB3	5:C:121:ALA:HB1	1.13	1.13
1:B5:359:HIS:CB	5:C:121:ALA:HB1	1.77	1.13
1:B5:358:PRO:CG	5:C:73:GLY:HA3	1.77	1.12
1:B5:177:LYS:CB	5:C:121:ALA:HB3	1.61	1.11
1:B5:177:LYS:HB2	5:C:121:ALA:HB3	1.31	1.08
1:B5:359:HIS:CE1	5:C:121:ALA:HA	1.90	1.07
1:B5:358:PRO:HG2	5:C:73:GLY:HA3	1.29	1.05
1:B5:359:HIS:ND1	5:C:121:ALA:CA	2.18	1.01
1:A5:126:VAL:CG2	6:B:38:ARG:NH2	2.24	1.00
1:B5:359:HIS:CG	5:C:121:ALA:HB1	1.97	0.99
1:B5:359:HIS:ND1	5:C:121:ALA:HA	1.71	0.97
1:A5:191:GLU:CD	6:A:39:PRO:HD2	1.90	0.96
5:D:101:VAL:HG13	5:D:103:ALA:HB2	1.48	0.94
1:Q4:179:SER:HA	1:Q4:359:HIS:HA	1.49	0.94
1:A5:183:LEU:O	6:A:38:ARG:NH1	1.98	0.94
1:A5:126:VAL:HG22	6:B:38:ARG:NH2	1.81	0.94
1:B5:359:HIS:HB3	5:C:121:ALA:CB	1.98	0.94
1:J4:102:VAL:HB	1:I4:132:THR:HG21	1.47	0.93
1:F4:220:THR:HG23	1:F4:371:ASP:HB3	1.53	0.91
1:B5:348:ARG:NE	1:B5:348:ARG:HA	1.86	0.90
1:A5:121:ARG:O	6:B:38:ARG:NH1	2.05	0.90
1:P4:286:ARG:HH11	1:P4:303:ALA:HB1	1.35	0.88
1:Z4:290:ASP:HB3	1:Z4:296:LEU:HD11	1.55	0.86
1:O4:296:LEU:HB3	1:P4:301:LEU:HG	1.55	0.86
1:A5:126:VAL:CG2	6:B:38:ARG:HH21	1.87	0.86
1:G4:150:GLU:HG3	1:C4:91:ASN:HB2	1.57	0.86
5:D:92:VAL:HG23	5:D:131:ARG:H	1.42	0.85
1:B5:358:PRO:CB	5:C:73:GLY:H	1.90	0.85
1:Z4:289:LYS:HA	1:Z4:295:PHE:HA	1.59	0.85
1:U4:102:VAL:HB	1:T4:132:THR:HG21	1.61	0.83
5:D:3:LEU:HD22	5:D:79:PRO:HG3	1.60	0.83
1:B5:348:ARG:HA	1:B5:348:ARG:CZ	2.08	0.83
6:B:150:ASP:OD1	6:B:151:GLY:N	2.11	0.83
1:B5:359:HIS:ND1	5:C:121:ALA:CB	2.41	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:3:LEU:HD22	5:D:79:PRO:CG	2.09	0.83
1:A5:126:VAL:HG21	6:B:38:ARG:NH2	1.95	0.82
1:A5:191:GLU:OE1	6:A:39:PRO:CD	2.28	0.81
1:O4:286:ARG:HH12	1:O4:305:GLU:HA	1.44	0.81
1:B5:359:HIS:HE2	5:C:73:GLY:C	1.88	0.80
1:B5:359:HIS:CE1	5:C:121:ALA:CA	2.63	0.80
1:B5:359:HIS:CE1	5:C:74:ASP:HB3	2.16	0.79
1:Y4:101:LEU:HD23	1:Q4:188:PHE:HE2	1.47	0.79
1:H4:215:GLY:HA2	1:H4:220:THR:HG22	1.63	0.79
1:C4:215:GLY:HA2	1:C4:220:THR:HG22	1.64	0.78
1:E4:265:LEU:HD21	1:E4:269:TYR:HB2	1.63	0.78
1:U4:294:ARG:HE	1:V4:294:ARG:HH12	1.28	0.78
1:B5:359:HIS:ND1	5:C:121:ALA:HB1	1.98	0.78
1:E4:215:GLY:HA2	1:E4:220:THR:HG22	1.66	0.78
4:G:15:LEU:HD21	4:G:75:THR:HG22	1.66	0.78
7:F:47:LEU:O	7:F:47:LEU:HD12	1.83	0.78
5:D:101:VAL:CG1	5:D:103:ALA:HB2	2.14	0.78
1:A5:309:LEU:HD23	1:A5:310:MET:HG2	1.66	0.77
1:L4:265:LEU:HD11	1:L4:333:GLY:HA2	1.66	0.77
1:B5:286:ARG:HH12	1:B5:304:GLY:H	1.32	0.77
1:B4:140:LYS:HE3	1:B4:163:ASP:HB2	1.67	0.77
1:L4:219:PRO:HG3	1:L4:369:GLY:HA2	1.67	0.77
1:D4:143:MET:HG2	1:D4:160:PRO:HD3	1.65	0.77
1:H4:143:MET:HG2	1:H4:160:PRO:HD3	1.67	0.76
1:Y4:100:TYR:HB2	1:P4:162:ILE:HD11	1.67	0.76
1:W4:102:VAL:HB	1:V4:132:THR:HG21	1.66	0.76
1:U4:116:SER:HA	1:T4:268:GLU:HB2	1.66	0.76
1:R4:149:SER:HB3	1:R4:152:ALA:HB2	1.67	0.76
1:R4:104:PRO:HB3	1:Q4:133:SER:HB2	1.67	0.75
1:H4:268:GLU:HB2	1:I4:116:SER:HA	1.69	0.75
5:D:89:LEU:HD23	5:D:105:TRP:CD1	2.21	0.75
1:O4:143:MET:HG2	1:O4:160:PRO:HD3	1.67	0.75
1:B5:361:LEU:HD13	5:C:122:MET:HB2	1.69	0.75
7:F:117:VAL:HG11	7:F:124:ARG:HB3	1.69	0.74
1:J4:141:THR:HG22	1:J4:142:ASP:H	1.52	0.74
1:J4:180:GLN:NE2	1:J4:184:ASP:OD1	2.21	0.74
1:H4:261:LEU:HD21	1:H4:332:PHE:HB3	1.68	0.74
1:U4:149:SER:HB3	1:U4:152:ALA:HB2	1.70	0.74
6:B:28:ARG:HH11	6:B:150:ASP:HB2	1.51	0.74
1:W4:143:MET:HG2	1:W4:160:PRO:HD3	1.69	0.74
1:H4:288:MET:HE3	1:H4:297:TRP:HE1	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:126:VAL:HG21	6:B:38:ARG:HH21	1.51	0.74
1:B5:191:GLU:HG2	1:B5:362:PHE:HZ	1.53	0.73
1:B5:359:HIS:NE2	5:C:73:GLY:O	2.15	0.73
1:T4:143:MET:HG2	1:T4:160:PRO:HD3	1.67	0.73
5:D:90:ARG:HD3	5:D:98:GLU:OE1	1.89	0.73
1:N4:215:GLY:HA2	1:N4:220:THR:HG22	1.71	0.73
1:A4:162:ILE:HD13	1:C4:101:LEU:HD21	1.70	0.72
1:U4:286:ARG:NH1	1:T4:263:TYR:OH	2.23	0.72
1:Z4:139:ASP:OD1	1:Z4:139:ASP:O	2.07	0.72
1:O4:219:PRO:HG3	1:O4:369:GLY:HA2	1.71	0.72
1:V4:265:LEU:HD11	1:V4:333:GLY:HA2	1.72	0.72
1:C5:265:LEU:HD11	1:C5:333:GLY:HA2	1.71	0.72
1:B5:265:LEU:HD11	1:B5:333:GLY:HA2	1.72	0.72
1:U4:197:ARG:HB3	1:T4:143:MET:HE3	1.72	0.72
5:D:103:ALA:HB3	5:D:105:TRP:HD1	1.53	0.72
1:B4:265:LEU:HD11	1:B4:333:GLY:HA2	1.70	0.72
1:U4:133:SER:HB2	1:V4:104:PRO:HB3	1.73	0.71
1:K4:215:GLY:HA2	1:K4:220:THR:HG22	1.73	0.71
1:W4:145:SER:HB2	1:S4:172:LEU:HD11	1.72	0.71
1:D4:265:LEU:HD11	1:D4:333:GLY:HA2	1.71	0.71
1:O4:184:ASP:OD2	1:K4:348:ARG:NH2	2.24	0.71
1:Y4:162:ILE:HD13	1:W4:101:LEU:HD11	1.74	0.70
4:G:22:GLU:HB3	4:G:75:THR:HG21	1.73	0.70
1:Q4:284:ALA:HA	1:Q4:287:LYS:HD3	1.73	0.70
1:T4:219:PRO:HG3	1:T4:369:GLY:HA2	1.73	0.70
1:S4:265:LEU:HD11	1:S4:333:GLY:HA2	1.73	0.70
6:A:50:MET:HG2	6:A:116:LEU:HD12	1.73	0.70
1:B5:359:HIS:HE1	5:C:74:ASP:HB3	1.56	0.70
1:J4:143:MET:HG2	1:J4:160:PRO:HD3	1.73	0.70
7:F:125:ILE:O	7:F:125:ILE:HG12	1.91	0.70
1:S4:334:ASP:OD2	1:S4:337:ASN:ND2	2.24	0.70
1:F4:150:GLU:HG3	1:F4:151:THR:HG23	1.74	0.70
1:B4:279:SER:HB2	1:B4:318:GLU:OE2	1.92	0.70
1:F4:143:MET:HG2	1:F4:160:PRO:HD3	1.73	0.69
1:Y4:265:LEU:HD11	1:Y4:333:GLY:HA2	1.72	0.69
1:B5:191:GLU:HG2	1:B5:362:PHE:CZ	2.27	0.69
5:C:93:ASP:OD1	5:C:96:GLY:HA2	1.92	0.69
1:X4:263:TYR:OH	1:Y4:286:ARG:NH1	2.25	0.69
1:R4:286:ARG:NH1	1:Q4:263:TYR:OH	2.25	0.69
1:L4:132:THR:HG21	1:H4:102:VAL:HB	1.74	0.69
1:P4:121:ARG:NH2	1:P4:206:GLU:OE2	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z4:256:ASP:HA	1:Z4:259:VAL:HG12	1.75	0.69
1:W4:106:THR:HA	1:V4:135:ASP:HB2	1.75	0.69
1:O4:150:GLU:HG3	1:O4:151:THR:HG23	1.74	0.69
1:W4:265:LEU:HD11	1:W4:333:GLY:HA2	1.75	0.69
1:J4:183:LEU:HD22	1:J4:360:VAL:HG21	1.74	0.68
1:J4:256:ASP:HA	1:J4:259:VAL:HG12	1.74	0.68
1:A4:279:SER:HB2	1:A4:318:GLU:OE2	1.92	0.68
1:E4:223:LEU:O	1:E4:227:LYS:NZ	2.22	0.68
1:H4:262:VAL:HG12	1:H4:270:ARG:HD3	1.76	0.68
4:G:95:ILE:HB	4:G:98:PHE:HB2	1.74	0.68
1:Y4:182:LEU:HB2	1:Q4:92:SER:HB3	1.75	0.68
1:K4:145:SER:HB3	1:L4:172:LEU:HD11	1.74	0.68
1:R4:294:ARG:HH21	1:Q4:294:ARG:HD3	1.58	0.68
1:J4:265:LEU:HD11	1:J4:333:GLY:HA2	1.74	0.68
1:P4:181:ARG:HH21	1:W4:171:GLU:HG2	1.58	0.68
1:N4:133:SER:HB2	1:O4:104:PRO:HB3	1.74	0.68
1:S4:261:LEU:HD21	1:S4:332:PHE:HB3	1.75	0.68
1:C5:286:ARG:NH1	1:C5:305:GLU:OE2	2.27	0.67
1:Z4:121:ARG:NH1	1:Z4:343:GLU:OE1	2.27	0.67
1:Q4:219:PRO:HG3	1:Q4:369:GLY:HA2	1.76	0.67
1:U4:171:GLU:HA	1:U4:367:ARG:HA	1.76	0.67
1:Y4:215:GLY:HA2	1:Y4:220:THR:HG22	1.76	0.67
1:J4:275:PHE:HB2	1:J4:314:VAL:HG22	1.75	0.67
6:B:50:MET:HG2	6:B:116:LEU:HD12	1.75	0.67
1:Y4:286:ARG:NH1	1:Y4:305:GLU:OE1	2.28	0.67
1:V4:215:GLY:HA2	1:V4:220:THR:HG22	1.77	0.67
1:E4:143:MET:HE1	1:F4:176:PRO:HB3	1.76	0.67
1:U4:279:SER:HB2	1:U4:318:GLU:OE1	1.95	0.67
1:V4:289:LYS:HA	1:V4:295:PHE:HA	1.76	0.67
1:D4:142:ASP:OD2	1:E4:204:ARG:NH2	2.28	0.67
1:A5:183:LEU:HB3	6:A:38:ARG:NH1	2.09	0.67
1:R4:204:ARG:NH2	1:Q4:142:ASP:OD1	2.28	0.67
1:K4:104:PRO:HB3	1:J4:133:SER:HB2	1.77	0.66
1:V4:219:PRO:HG3	1:V4:369:GLY:HA2	1.77	0.66
1:G4:220:THR:HB	1:G4:371:ASP:OD2	1.94	0.66
1:F4:211:ILE:HD12	1:F4:319:ASP:HB2	1.78	0.66
1:B4:256:ASP:HA	1:B4:259:VAL:HG12	1.77	0.66
7:F:117:VAL:HG23	7:F:118:GLU:H	1.60	0.66
1:P4:175:MET:HE3	1:P4:363:TYR:HB2	1.77	0.66
1:K4:149:SER:HB3	1:K4:152:ALA:HB2	1.76	0.66
1:L4:145:SER:HB2	1:H4:172:LEU:HD11	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:15:LEU:HD21	4:G:75:THR:CG2	2.25	0.66
1:A5:297:TRP:HB2	1:B5:301:LEU:HD12	1.77	0.66
1:D4:149:SER:HB3	1:D4:152:ALA:HB2	1.78	0.66
1:D4:171:GLU:HA	1:D4:367:ARG:HA	1.76	0.66
1:L4:143:MET:HG2	1:L4:160:PRO:HD3	1.77	0.66
1:H4:133:SER:HB3	1:I4:104:PRO:HB3	1.78	0.66
6:B:253:GLN:HE22	5:D:195:GLY:HA2	1.60	0.66
5:D:163:TYR:O	5:D:166:ARG:NH1	2.29	0.66
1:B5:359:HIS:CG	5:C:121:ALA:CB	2.68	0.66
1:R4:298:ALA:HB2	1:R4:306:PRO:HD3	1.78	0.66
1:B4:219:PRO:HG3	1:B4:369:GLY:HA2	1.78	0.66
1:C5:270:ARG:NH1	1:X4:279:SER:OG	2.29	0.66
1:F4:265:LEU:HD11	1:F4:333:GLY:HA2	1.76	0.66
1:C4:262:VAL:HG21	1:C4:310:MET:HG2	1.77	0.66
1:A5:141:THR:HG22	1:A5:142:ASP:H	1.61	0.66
1:U4:294:ARG:HE	1:V4:294:ARG:NH1	1.93	0.66
1:A5:121:ARG:NH1	1:A5:343:GLU:OE2	2.28	0.66
1:U4:294:ARG:NE	1:V4:294:ARG:HH12	1.95	0.66
1:F4:298:ALA:HB2	1:F4:306:PRO:HD3	1.78	0.66
1:B5:179:SER:H	5:C:121:ALA:CB	2.08	0.65
1:M4:106:THR:HG23	1:M4:107:SER:H	1.61	0.65
1:T4:265:LEU:HD11	1:T4:333:GLY:HA2	1.76	0.65
1:J4:227:LYS:H	1:J4:227:LYS:HE2	1.61	0.65
1:O4:215:GLY:HA2	1:O4:220:THR:HG22	1.79	0.65
1:U4:256:ASP:HA	1:U4:259:VAL:HG12	1.77	0.65
1:S4:143:MET:HG2	1:S4:160:PRO:HD3	1.78	0.65
1:X4:219:PRO:HG3	1:X4:369:GLY:HA2	1.79	0.65
1:J4:289:LYS:HA	1:J4:295:PHE:HA	1.77	0.65
1:H4:132:THR:HG21	1:I4:102:VAL:HB	1.78	0.65
1:W4:215:GLY:HA2	1:W4:220:THR:HG22	1.79	0.65
1:Q4:227:LYS:HD2	1:Q4:328:TYR:CZ	2.32	0.65
1:V4:268:GLU:OE1	1:V4:268:GLU:N	2.29	0.65
1:U4:215:GLY:HA2	1:U4:220:THR:HG22	1.78	0.65
1:N4:284:ALA:HA	1:N4:287:LYS:HD3	1.79	0.65
1:T4:172:LEU:HD11	1:S4:145:SER:HB3	1.77	0.65
1:B4:215:GLY:HA2	1:B4:220:THR:HG22	1.79	0.65
1:N4:150:GLU:OE1	1:S4:181:ARG:HD2	1.97	0.64
1:U4:172:LEU:HD11	1:T4:145:SER:HB3	1.79	0.64
1:X4:352:ASP:HB3	1:Q4:354:PHE:HD1	1.62	0.64
1:Z4:344:ARG:HE	1:Z4:367:ARG:HD3	1.62	0.64
1:O4:298:ALA:HB2	1:O4:306:PRO:HD3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K4:265:LEU:HD11	1:K4:333:GLY:HA2	1.79	0.64
1:D4:171:GLU:OE1	1:D4:348:ARG:NH1	2.30	0.64
1:C5:302:ALA:O	1:B5:311:GLY:N	2.29	0.64
1:R4:223:LEU:O	1:R4:227:LYS:NZ	2.22	0.64
1:D4:279:SER:OG	1:C4:270:ARG:NH1	2.30	0.64
1:A5:149:SER:HB3	1:A5:152:ALA:HB2	1.79	0.64
1:U4:252:VAL:HG21	2:E3:3:VAL:HG21	1.80	0.64
1:K4:289:LYS:HA	1:K4:295:PHE:HA	1.79	0.64
1:T4:100:TYR:O	1:J4:164:ARG:NH1	2.31	0.64
1:L4:186:SER:O	1:L4:188:PHE:N	2.31	0.64
1:I4:281:THR:HG23	1:I4:323:ILE:HD11	1.80	0.64
1:C5:215:GLY:HA2	1:C5:220:THR:HG22	1.80	0.64
1:N4:244:GLY:HA3	1:N4:250:ALA:HB2	1.80	0.64
1:C4:94:VAL:HG13	1:C4:97:GLU:HB2	1.79	0.64
1:Y4:133:SER:HB3	1:Z4:104:PRO:HB3	1.79	0.64
1:R4:286:ARG:HH12	1:R4:305:GLU:HA	1.63	0.63
1:B4:121:ARG:NH1	1:B4:343:GLU:OE1	2.32	0.63
8:E:39:VAL:HG12	8:E:61:ILE:HG12	1.79	0.63
1:Z4:219:PRO:HG3	1:Z4:369:GLY:HA2	1.80	0.63
1:N4:142:ASP:HB3	1:O4:115:ARG:HH12	1.62	0.63
1:W4:141:THR:HG22	1:W4:142:ASP:H	1.62	0.63
1:F4:121:ARG:NH1	1:F4:343:GLU:OE1	2.31	0.63
1:F4:149:SER:HB2	1:F4:152:ALA:HB2	1.80	0.63
1:M4:219:PRO:HG3	1:M4:369:GLY:HA2	1.79	0.63
1:D4:302:ALA:O	1:C4:311:GLY:N	2.32	0.63
1:A5:298:ALA:HB2	1:A5:306:PRO:HD3	1.81	0.63
1:P4:286:ARG:NH1	1:P4:303:ALA:HB1	2.12	0.63
1:V4:186:SER:O	1:V4:188:PHE:N	2.32	0.63
1:L4:171:GLU:HA	1:L4:367:ARG:HA	1.79	0.63
1:E4:219:PRO:HG3	1:E4:369:GLY:HA2	1.80	0.63
1:T4:238:LEU:HD23	1:T4:380:LEU:HD11	1.80	0.63
1:Q4:143:MET:HG2	1:Q4:160:PRO:HD3	1.81	0.63
1:J4:121:ARG:NH1	1:J4:343:GLU:OE2	2.32	0.63
1:L4:163:ASP:OD2	1:L4:235:TRP:NE1	2.29	0.63
4:J:27:LEU:HA	4:J:68:GLY:HA3	1.81	0.63
5:D:92:VAL:HG23	5:D:131:ARG:N	2.14	0.63
1:Z4:253:ASN:HB3	1:Z4:256:ASP:OD2	1.98	0.63
1:M4:298:ALA:HB1	1:M4:303:ALA:HB1	1.81	0.63
1:Q4:281:THR:HG23	1:Q4:323:ILE:HD11	1.80	0.63
1:P4:136:VAL:HG22	1:P4:165:ILE:HB	1.80	0.63
1:N4:178:ALA:HB3	1:N4:360:VAL:HB	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C5:298:ALA:HB2	1:C5:306:PRO:HD3	1.80	0.62
1:X4:171:GLU:HA	1:X4:367:ARG:HA	1.81	0.62
1:Y4:141:THR:HG22	1:Y4:142:ASP:H	1.65	0.62
1:V4:141:THR:HG22	1:V4:142:ASP:H	1.62	0.62
1:G4:223:LEU:O	1:G4:227:LYS:NZ	2.22	0.62
1:M4:352:ASP:HB3	1:F4:354:PHE:HD1	1.64	0.62
1:U4:279:SER:OG	1:T4:270:ARG:NH1	2.33	0.62
4:I:27:LEU:HA	4:I:68:GLY:HA3	1.81	0.62
5:D:81:ALA:HA	5:D:114:PRO:HG3	1.82	0.62
4:H:27:LEU:HA	4:H:68:GLY:HA3	1.80	0.62
1:Q4:324:ALA:HB3	1:Q4:327:ALA:HB2	1.81	0.62
1:S4:289:LYS:HA	1:S4:295:PHE:HA	1.82	0.62
1:I4:219:PRO:HG3	1:I4:369:GLY:HA2	1.79	0.62
1:G4:176:PRO:HD2	1:G4:362:PHE:O	1.99	0.62
1:G4:286:ARG:HH12	1:G4:304:GLY:H	1.45	0.62
1:R4:219:PRO:HG3	1:R4:369:GLY:HA2	1.80	0.62
1:C4:167:ILE:HG23	1:C4:370:GLY:HA2	1.80	0.62
1:B5:178:ALA:HB3	1:B5:360:VAL:HB	1.82	0.62
1:L4:154:LEU:HD13	1:H4:363:TYR:HE1	1.64	0.62
1:T4:102:VAL:HB	1:S4:132:THR:HG21	1.81	0.61
6:B:343:SER:HB3	6:B:350:ILE:HG22	1.80	0.61
1:B5:281:THR:HG23	1:B5:323:ILE:HD11	1.81	0.61
1:U4:204:ARG:NH2	1:T4:142:ASP:OD2	2.33	0.61
1:J4:204:ARG:NH2	1:I4:142:ASP:OD1	2.32	0.61
1:V4:275:PHE:HB2	1:V4:314:VAL:HG22	1.82	0.61
1:R4:94:VAL:HG23	1:R4:97:GLU:HB2	1.81	0.61
1:T4:159:THR:HG22	1:T4:160:PRO:HD2	1.82	0.61
1:V4:159:THR:HG22	1:V4:160:PRO:HD2	1.81	0.61
1:X4:121:ARG:NH1	1:X4:343:GLU:OE2	2.33	0.61
1:A5:281:THR:HG23	1:A5:323:ILE:HD11	1.81	0.61
1:Z4:286:ARG:HH12	1:Z4:304:GLY:H	1.47	0.61
1:B5:358:PRO:HG2	5:C:73:GLY:CA	2.05	0.61
1:N4:129:VAL:HG11	1:N4:342:ALA:HB1	1.83	0.61
1:A4:198:ILE:HG22	1:A4:347:LEU:HD11	1.83	0.61
1:B5:358:PRO:HG3	5:C:73:GLY:H	0.78	0.61
1:M4:215:GLY:HA2	1:M4:220:THR:HG22	1.82	0.61
1:W4:143:MET:HE1	1:S4:194:LEU:HD22	1.83	0.61
1:A5:223:LEU:C	1:A5:223:LEU:HD23	2.25	0.61
5:C:44:ARG:HG3	5:D:149:VAL:HG11	1.83	0.61
6:B:169:MET:HE1	6:B:176:ILE:H	1.66	0.61
1:C5:268:GLU:HG2	1:X4:114:LEU:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N4:265:LEU:HD11	1:N4:333:GLY:HA2	1.83	0.61
1:R4:102:VAL:HB	1:Q4:132:THR:HG21	1.82	0.61
1:O4:171:GLU:HA	1:O4:367:ARG:HA	1.81	0.61
1:X4:95:ALA:HA	1:X4:99:GLY:HA3	1.81	0.61
1:N4:180:GLN:HB2	1:N4:360:VAL:HG23	1.83	0.61
1:K4:132:THR:HG21	1:L4:102:VAL:HB	1.82	0.61
1:H4:98:GLY:HA2	1:D4:162:ILE:HD12	1.83	0.61
1:G4:129:VAL:HG11	1:G4:342:ALA:HB1	1.83	0.61
1:B5:177:LYS:HB2	5:C:121:ALA:CB	2.18	0.61
1:Q4:106:THR:HA	1:P4:135:ASP:HB2	1.82	0.61
1:T4:252:VAL:HG11	2:D3:3:VAL:HG11	1.83	0.61
1:S4:215:GLY:HA2	1:S4:220:THR:HG22	1.80	0.61
1:S4:219:PRO:HG3	1:S4:369:GLY:HA2	1.83	0.61
1:J4:186:SER:O	1:J4:188:PHE:N	2.33	0.61
1:A5:183:LEU:HB3	6:A:38:ARG:HH12	1.64	0.60
1:N4:106:THR:HG23	1:N4:107:SER:H	1.66	0.60
1:P4:182:LEU:HB2	1:S4:92:SER:HB3	1.83	0.60
4:I:77:GLU:OE2	4:I:80:ARG:NH1	2.34	0.60
7:F:40:LEU:HD22	8:E:54:LEU:HD21	1.82	0.60
8:E:80:PHE:HB2	8:E:87:PHE:HB2	1.82	0.60
1:C5:194:LEU:HD23	1:B5:143:MET:HE1	1.81	0.60
1:Y4:211:ILE:HG21	1:Y4:320:MET:HG2	1.82	0.60
1:B5:256:ASP:HA	1:B5:259:VAL:HG12	1.83	0.60
1:B5:359:HIS:CB	5:C:121:ALA:CB	2.68	0.60
1:N4:121:ARG:NH1	1:N4:343:GLU:OE2	2.34	0.60
1:R4:171:GLU:HA	1:R4:367:ARG:HA	1.83	0.60
1:J4:223:LEU:HD11	1:J4:320:MET:HE3	1.82	0.60
1:F4:159:THR:HG22	1:F4:160:PRO:HD2	1.83	0.60
1:F4:171:GLU:HA	1:F4:367:ARG:HA	1.84	0.60
1:O4:223:LEU:O	1:O4:227:LYS:NZ	2.22	0.60
1:S4:281:THR:HG23	1:S4:323:ILE:HD11	1.83	0.60
1:D4:262:VAL:HG21	1:D4:310:MET:HG2	1.83	0.60
5:D:103:ALA:HB1	5:D:124:PRO:HG3	1.82	0.60
1:U4:132:THR:HG21	1:V4:102:VAL:HB	1.82	0.60
1:T4:287:LYS:O	1:T4:289:LYS:NZ	2.34	0.60
1:B4:136:VAL:HG22	1:B4:165:ILE:HB	1.84	0.60
4:J:77:GLU:OE2	4:J:80:ARG:NH1	2.34	0.60
1:A5:219:PRO:HG3	1:A5:369:GLY:HA2	1.82	0.60
1:N4:344:ARG:NH1	1:L4:185:ASP:OD1	2.34	0.60
1:R4:256:ASP:HA	1:R4:259:VAL:HG12	1.82	0.60
1:Q4:206:GLU:OE1	1:Q4:366:LYS:NZ	2.25	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H4:308:ARG:NH2	1:H4:311:GLY:O	2.35	0.60
1:F4:344:ARG:HE	1:F4:367:ARG:HD3	1.65	0.60
4:H:77:GLU:OE2	4:H:80:ARG:NH1	2.34	0.60
1:Y4:171:GLU:HA	1:Y4:367:ARG:HA	1.83	0.60
1:O4:159:THR:HG21	1:S4:90:LEU:HB2	1.84	0.60
1:A4:215:GLY:HA2	1:A4:220:THR:HG22	1.84	0.60
1:G4:106:THR:OG1	1:G4:107:SER:N	2.33	0.60
1:P4:89:ALA:HB2	1:S4:193:TRP:HZ3	1.66	0.60
1:K4:288:MET:HE3	1:K4:297:TRP:HE1	1.67	0.60
5:D:92:VAL:HG12	5:D:98:GLU:HG2	1.84	0.60
1:N4:182:LEU:HB2	1:F4:92:SER:CB	2.32	0.60
6:A:85:TYR:HB3	6:A:88:HIS:HB2	1.83	0.60
1:A5:92:SER:O	1:A5:94:VAL:N	2.35	0.59
1:E4:139:ASP:HA	1:E4:162:ILE:HA	1.84	0.59
1:G4:281:THR:HG23	1:G4:323:ILE:HD11	1.83	0.59
1:C4:256:ASP:HA	1:C4:259:VAL:HG12	1.83	0.59
1:O4:334:ASP:OD2	1:O4:337:ASN:ND2	2.35	0.59
1:S4:238:LEU:HD23	1:S4:380:LEU:HD11	1.84	0.59
1:D4:133:SER:HB2	1:E4:104:PRO:HB3	1.83	0.59
8:E:61:ILE:HB	8:E:104:CYS:HB2	1.84	0.59
1:R4:149:SER:OG	1:R4:150:GLU:N	2.33	0.59
1:O4:132:THR:HG21	1:P4:102:VAL:HB	1.84	0.59
1:S4:256:ASP:HA	1:S4:259:VAL:HG12	1.84	0.59
1:L4:149:SER:HB3	1:L4:152:ALA:HB2	1.84	0.59
1:Z4:130:GLU:OE2	1:Z4:344:ARG:NH2	2.35	0.59
1:W4:219:PRO:HG3	1:W4:369:GLY:HA2	1.84	0.59
1:A4:285:VAL:HG11	1:A4:309:LEU:HD11	1.83	0.59
1:K4:183:LEU:HD22	1:K4:360:VAL:HG21	1.83	0.59
1:K4:263:TYR:OH	1:L4:286:ARG:NH1	2.35	0.59
1:I4:98:GLY:HA2	1:I4:101:LEU:HD13	1.83	0.59
1:E4:265:LEU:HD22	1:E4:270:ARG:HG3	1.83	0.59
6:A:220:ARG:HE	6:A:275:PHE:HB2	1.68	0.59
1:H4:265:LEU:HD11	1:H4:333:GLY:HA2	1.83	0.59
1:D4:223:LEU:O	1:D4:227:LYS:NZ	2.29	0.59
1:O4:286:ARG:NH2	1:O4:305:GLU:H	2.01	0.59
1:W4:129:VAL:HG11	1:W4:342:ALA:HB1	1.85	0.59
1:V4:183:LEU:HD21	1:V4:362:PHE:HZ	1.68	0.59
1:I4:288:MET:HG2	2:C2:6:LYS:HD2	1.84	0.59
5:C:163:TYR:O	5:C:166:ARG:NH1	2.36	0.59
1:W4:186:SER:O	1:W4:188:PHE:N	2.35	0.59
1:K4:275:PHE:HB2	1:K4:314:VAL:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I4:186:SER:O	1:I4:188:PHE:N	2.36	0.59
1:Y4:256:ASP:HA	1:Y4:259:VAL:HG12	1.84	0.59
1:R4:215:GLY:HA2	1:R4:220:THR:HG22	1.85	0.59
1:M4:154:LEU:HD23	1:L4:357:LYS:HB3	1.84	0.59
1:W4:104:PRO:HB3	1:V4:133:SER:HB2	1.84	0.59
5:C:20:ARG:NH2	5:C:36:ASP:OD1	2.35	0.59
1:X4:352:ASP:HB3	1:Q4:354:PHE:CD1	2.38	0.58
1:A5:344:ARG:HG3	1:A5:367:ARG:HB2	1.85	0.58
1:K4:143:MET:HG2	1:K4:160:PRO:HD3	1.84	0.58
6:A:139:ARG:NH2	6:B:185:THR:O	2.36	0.58
1:Z4:171:GLU:HA	1:Z4:367:ARG:HA	1.83	0.58
1:M4:171:GLU:HA	1:M4:367:ARG:HA	1.85	0.58
1:W4:253:ASN:ND2	2:B3:3:VAL:O	2.34	0.58
1:T4:278:ASN:OD1	1:T4:278:ASN:N	2.36	0.58
1:K4:305:GLU:HG3	1:K4:306:PRO:HD3	1.86	0.58
1:D4:219:PRO:HG3	1:D4:369:GLY:HA2	1.85	0.58
1:U4:248:ASP:OD1	1:U4:249:PHE:N	2.36	0.58
1:I4:215:GLY:HA2	1:I4:220:THR:HG22	1.85	0.58
1:C5:171:GLU:HA	1:C5:367:ARG:HA	1.86	0.58
1:C5:286:ARG:NH1	1:B5:263:TYR:OH	2.36	0.58
1:E4:171:GLU:HA	1:E4:367:ARG:HA	1.85	0.58
1:E4:354:PHE:O	1:E4:357:LYS:NZ	2.33	0.58
1:W4:119:SER:HB2	1:W4:207:ALA:HB2	1.85	0.58
1:P4:334:ASP:OD2	1:P4:337:ASN:ND2	2.36	0.58
1:J4:159:THR:HG22	1:J4:160:PRO:HD2	1.85	0.58
1:D4:256:ASP:HA	1:D4:259:VAL:HG12	1.86	0.58
1:E4:133:SER:HB2	1:F4:104:PRO:HB3	1.86	0.58
1:G4:220:THR:HB	1:G4:371:ASP:CG	2.29	0.58
1:C5:136:VAL:HG22	1:C5:165:ILE:HB	1.86	0.58
1:Q4:328:TYR:OH	1:Q4:382:LYS:NZ	2.37	0.58
1:K4:324:ALA:HB3	1:K4:327:ALA:HB2	1.86	0.58
4:G:10:LEU:HD12	4:G:94:ILE:HD11	1.85	0.58
1:X4:286:ARG:HH12	1:X4:304:GLY:H	1.52	0.58
1:L4:150:GLU:HG2	1:I4:91:ASN:HB2	1.85	0.58
1:A4:186:SER:O	1:A4:188:PHE:N	2.37	0.58
1:X4:256:ASP:HA	1:X4:259:VAL:HG12	1.86	0.58
1:P4:261:LEU:HD22	1:P4:381:LEU:HB2	1.86	0.58
1:A5:126:VAL:CG1	6:B:38:ARG:HH22	2.17	0.57
1:T4:193:TRP:HZ3	1:K4:89:ALA:HB2	1.69	0.57
1:K4:134:PHE:HB3	1:K4:167:ILE:HB	1.86	0.57
5:D:92:VAL:HG21	5:D:131:ARG:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X4:141:THR:HG22	1:X4:161:GLN:HG2	1.86	0.57
1:X4:142:ASP:OD2	1:Y4:204:ARG:NH2	2.37	0.57
1:W4:288:MET:HE3	1:W4:297:TRP:HE1	1.69	0.57
1:H4:219:PRO:HG3	1:H4:369:GLY:HA2	1.86	0.57
1:F4:90:LEU:O	1:F4:90:LEU:HD23	2.04	0.57
1:F4:286:ARG:HH22	1:F4:305:GLU:H	1.52	0.57
1:P4:359:HIS:HE1	1:V4:151:THR:HG22	1.69	0.57
1:T4:349:VAL:HG12	1:T4:364:ALA:HB2	1.86	0.57
1:W4:125:SER:OG	1:W4:336:GLY:O	2.22	0.57
1:L4:143:MET:HE1	1:H4:194:LEU:HD22	1.85	0.57
1:D4:194:LEU:HD23	1:C4:143:MET:HE1	1.87	0.57
6:A:146:VAL:O	6:A:153:PRO:HA	2.05	0.57
1:X4:143:MET:HE3	1:Y4:197:ARG:HB2	1.86	0.57
1:Y4:101:LEU:HD23	1:Q4:188:PHE:CE2	2.34	0.57
1:N4:182:LEU:HD22	1:F4:92:SER:HA	1.85	0.57
1:P4:262:VAL:HG21	1:P4:310:MET:HG2	1.87	0.57
1:P4:277:MET:HG2	1:P4:330:ILE:HG12	1.86	0.57
1:J4:114:LEU:HG	1:I4:268:GLU:HG3	1.87	0.57
5:C:105:TRP:HA	5:C:118:ALA:HA	1.87	0.57
5:D:92:VAL:HG22	5:D:131:ARG:O	2.04	0.57
1:A5:269:TYR:CE1	1:B5:114:LEU:HB2	2.39	0.57
1:K4:286:ARG:NH1	1:J4:263:TYR:OH	2.37	0.57
1:L4:275:PHE:HB2	1:L4:314:VAL:HG22	1.87	0.57
1:I4:288:MET:HB3	1:I4:296:LEU:HD21	1.87	0.57
1:B5:179:SER:N	5:C:121:ALA:HB2	2.20	0.57
1:B5:359:HIS:CE1	5:C:121:ALA:C	2.73	0.57
1:P4:281:THR:HG23	1:P4:323:ILE:HD11	1.86	0.57
1:H4:181:ARG:HG3	1:D4:367:ARG:HH12	1.69	0.57
1:H4:255:SER:O	1:H4:255:SER:OG	2.23	0.57
1:H4:354:PHE:CD1	1:D4:352:ASP:HB3	2.40	0.57
5:D:94:ALA:HA	5:D:129:GLY:O	2.05	0.57
1:C5:281:THR:HG23	1:C5:323:ILE:HD11	1.86	0.57
1:C5:286:ARG:NH2	1:C5:305:GLU:H	2.02	0.57
1:T4:89:ALA:HB2	1:K4:193:TRP:HZ3	1.70	0.57
1:V4:268:GLU:CD	1:V4:268:GLU:H	2.09	0.57
1:L4:261:LEU:HD21	1:L4:332:PHE:HB3	1.87	0.57
1:G4:94:VAL:HG23	1:G4:97:GLU:HB2	1.87	0.57
1:C4:281:THR:HG23	1:C4:323:ILE:HD11	1.86	0.57
7:F:10:GLN:HE21	7:F:47:LEU:HD12	1.69	0.57
1:P4:101:LEU:HD21	1:W4:162:ILE:HD13	1.86	0.57
1:V4:334:ASP:OD2	1:V4:337:ASN:ND2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:66:LEU:HD11	6:B:325:LEU:HD22	1.87	0.57
1:Y4:138:VAL:HA	1:Z4:111:ARG:O	2.05	0.57
1:O4:211:ILE:HD13	1:O4:320:MET:HG2	1.87	0.57
1:W4:256:ASP:HA	1:W4:259:VAL:HG22	1.85	0.57
1:T4:279:SER:OG	1:S4:270:ARG:NH1	2.38	0.57
1:K4:91:ASN:HB2	1:I4:150:GLU:HG2	1.87	0.57
1:V4:288:MET:HE3	1:V4:297:TRP:HE1	1.70	0.57
1:H4:289:LYS:HA	1:H4:295:PHE:HA	1.86	0.57
6:A:262:MET:HE2	6:A:264:LEU:HD21	1.87	0.57
1:R4:286:ARG:NH2	1:R4:305:GLU:H	2.03	0.56
1:S4:183:LEU:HD22	1:S4:360:VAL:HG21	1.86	0.56
1:I4:318:GLU:OE1	1:I4:318:GLU:HA	2.04	0.56
1:G4:289:LYS:HA	1:G4:295:PHE:HA	1.87	0.56
5:D:103:ALA:HB3	5:D:105:TRP:CD1	2.38	0.56
4:G:109:SER:HB2	4:G:125:ALA:HB3	1.87	0.56
1:U4:107:SER:OG	1:T4:136:VAL:HA	2.05	0.56
1:T4:171:GLU:HG3	1:T4:367:ARG:HG2	1.86	0.56
1:D4:167:ILE:HG23	1:D4:370:GLY:HA2	1.87	0.56
1:E4:246:ALA:HA	1:E4:384:ALA:HA	1.87	0.56
1:F4:299:ASP:OD1	1:F4:300:SER:N	2.36	0.56
1:B4:298:ALA:HB2	1:B4:306:PRO:HD3	1.87	0.56
1:C4:176:PRO:HD2	1:C4:362:PHE:O	2.05	0.56
4:I:64:ILE:HB	4:I:126:MET:HB2	1.87	0.56
7:F:4:ALA:O	7:F:101:ARG:NH2	2.38	0.56
1:X4:170:HIS:HA	1:Q4:181:ARG:NH2	2.20	0.56
1:A5:142:ASP:OD2	1:B5:204:ARG:NH2	2.38	0.56
1:A5:286:ARG:NH2	1:A5:305:GLU:H	2.03	0.56
1:N4:367:ARG:NH2	1:L4:181:ARG:HG3	2.21	0.56
1:P4:106:THR:HG23	1:P4:107:SER:H	1.70	0.56
1:I4:294:ARG:HG3	1:I4:295:PHE:N	2.20	0.56
1:B4:136:VAL:HG12	1:C4:111:ARG:HH21	1.69	0.56
1:B4:286:ARG:NH1	1:B4:305:GLU:HA	2.20	0.56
6:A:252:HIS:NE2	5:D:192:VAL:O	2.37	0.56
5:D:92:VAL:CG2	5:D:131:ARG:H	2.15	0.56
1:A5:126:VAL:CG2	6:B:38:ARG:HH22	2.12	0.56
1:P4:171:GLU:HA	1:P4:367:ARG:HA	1.86	0.56
1:D4:286:ARG:HH12	1:D4:305:GLU:HA	1.70	0.56
4:H:64:ILE:HB	4:H:126:MET:HB2	1.87	0.56
1:R4:129:VAL:HG11	1:R4:134:PHE:CD1	2.40	0.56
5:C:71:ARG:NH1	5:C:196:ARG:O	2.38	0.56
1:Y4:352:ASP:HB3	1:W4:354:PHE:CD1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T4:359:HIS:HE1	1:I4:151:THR:HG22	1.70	0.56
1:I4:278:ASN:ND2	1:I4:322:ASP:OD1	2.39	0.56
4:J:64:ILE:HB	4:J:126:MET:HB2	1.87	0.56
1:M4:135:ASP:OD2	1:M4:164:ARG:NE	2.39	0.56
1:O4:167:ILE:HG23	1:O4:370:GLY:HA2	1.87	0.56
1:G4:219:PRO:HG3	1:G4:369:GLY:HA2	1.88	0.56
1:C4:95:ALA:HA	1:C4:99:GLY:HA3	1.86	0.56
6:A:142:ARG:NH2	6:A:158:TYR:OH	2.38	0.56
6:B:76:LEU:HD13	6:B:352:LEU:HD21	1.88	0.56
1:W4:227:LYS:HG2	1:W4:380:LEU:HD22	1.88	0.56
1:V4:149:SER:HB2	1:V4:152:ALA:HB2	1.87	0.56
1:L4:215:GLY:HA2	1:L4:220:THR:HG22	1.87	0.56
6:B:38:ARG:N	6:B:146:VAL:HG23	2.21	0.56
1:Z4:243:THR:O	1:Z4:250:ALA:HB2	2.06	0.56
1:B5:344:ARG:NH1	1:B5:367:ARG:HH11	2.04	0.56
1:M4:289:LYS:HD3	1:M4:293:GLY:HA2	1.88	0.56
1:S4:107:SER:OG	1:S4:109:THR:O	2.22	0.56
1:I4:129:VAL:HG11	1:I4:342:ALA:HB1	1.88	0.56
1:A5:191:GLU:OE2	6:A:38:ARG:HB2	2.06	0.55
1:J4:129:VAL:HG11	1:J4:134:PHE:CD1	2.40	0.55
1:X4:139:ASP:N	1:X4:139:ASP:OD1	2.37	0.55
1:W4:132:THR:HG21	1:S4:102:VAL:HB	1.87	0.55
1:J4:116:SER:HA	1:I4:268:GLU:HB2	1.88	0.55
1:L4:238:LEU:HD23	1:L4:380:LEU:HD11	1.89	0.55
1:Y4:262:VAL:HG21	1:Y4:310:MET:HG2	1.87	0.55
1:A5:154:LEU:HD11	1:B5:363:TYR:HE1	1.71	0.55
1:T4:167:ILE:HG23	1:T4:370:GLY:HA2	1.89	0.55
1:J4:252:VAL:HG13	1:J4:253:ASN:H	1.70	0.55
1:A4:129:VAL:HG11	1:A4:134:PHE:CD1	2.42	0.55
4:J:43:SER:OG	4:J:44:LEU:N	2.40	0.55
5:C:161:GLN:OE1	5:D:176:MET:HB2	2.06	0.55
1:Z4:139:ASP:HA	1:Z4:162:ILE:HA	1.88	0.55
1:R4:211:ILE:HG21	1:R4:320:MET:HG2	1.87	0.55
1:D4:298:ALA:HB2	1:D4:306:PRO:HD3	1.89	0.55
1:E4:134:PHE:HB3	1:E4:167:ILE:HB	1.89	0.55
1:G4:171:GLU:HA	1:G4:367:ARG:HA	1.89	0.55
1:B5:179:SER:H	5:C:121:ALA:HB2	1.71	0.55
1:W4:133:SER:HB3	1:S4:104:PRO:HB3	1.86	0.55
1:I4:252:VAL:HG21	2:D2:3:VAL:HG21	1.88	0.55
1:A5:126:VAL:HG22	6:B:38:ARG:HH21	1.57	0.55
1:N4:194:LEU:HD22	1:M4:143:MET:HE1	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P4:329:ALA:HB3	1:P4:383:PHE:HE2	1.71	0.55
1:W4:296:LEU:HB2	1:S4:294:ARG:HG3	1.89	0.55
1:J4:305:GLU:HG2	1:J4:306:PRO:HD3	1.89	0.55
1:V4:121:ARG:NH1	1:V4:343:GLU:OE2	2.39	0.55
1:V4:183:LEU:HD22	1:V4:360:VAL:HG21	1.89	0.55
1:B4:171:GLU:HA	1:B4:367:ARG:HA	1.89	0.55
1:C5:348:ARG:HH12	1:C5:367:ARG:HD3	1.72	0.55
1:R4:337:ASN:HD22	1:R4:337:ASN:N	2.05	0.55
4:H:43:SER:OG	4:H:44:LEU:N	2.40	0.55
1:C5:167:ILE:HG23	1:C5:370:GLY:HA2	1.88	0.55
1:A5:223:LEU:HD23	1:A5:223:LEU:O	2.07	0.55
1:A5:286:ARG:HH12	1:A5:305:GLU:HA	1.71	0.55
1:N4:182:LEU:HB2	1:F4:92:SER:HB2	1.89	0.55
1:Q4:138:VAL:HG11	1:Q4:235:TRP:CH2	2.42	0.55
1:Q4:150:GLU:HG3	1:Q4:151:THR:HG23	1.88	0.55
1:J4:253:ASN:ND2	2:E2:3:VAL:O	2.39	0.55
6:A:302:MET:HG3	6:B:311:THR:HB	1.88	0.55
6:B:92:ASP:OD1	6:B:95:ARG:NH1	2.39	0.55
8:E:66:ALA:HB3	8:E:73:ARG:HG2	1.87	0.55
1:P4:298:ALA:HB2	1:P4:306:PRO:CG	2.37	0.55
1:W4:260:ASP:OD1	1:W4:261:LEU:N	2.40	0.55
1:U4:223:LEU:O	1:U4:227:LYS:NZ	2.29	0.55
1:T4:182:LEU:HD13	1:K4:92:SER:HB2	1.88	0.55
1:J4:262:VAL:O	1:J4:270:ARG:HD3	2.06	0.55
4:G:13:LEU:HD23	4:G:24:ILE:HG12	1.90	0.54
1:W4:171:GLU:HA	1:W4:367:ARG:HA	1.89	0.54
1:U4:94:VAL:HG13	1:U4:97:GLU:HB2	1.90	0.54
1:U4:111:ARG:NH1	1:T4:340:THR:OG1	2.38	0.54
1:K4:167:ILE:HG23	1:K4:370:GLY:HA2	1.88	0.54
1:K4:338:GLY:O	1:K4:373:SER:N	2.36	0.54
1:H4:107:SER:OG	1:H4:109:THR:O	2.23	0.54
1:C5:219:PRO:HG3	1:C5:369:GLY:HA2	1.88	0.54
1:R4:111:ARG:O	1:Q4:138:VAL:HA	2.08	0.54
1:O4:149:SER:OG	1:O4:150:GLU:N	2.40	0.54
1:W4:288:MET:HA	2:A3:6:LYS:HB3	1.90	0.54
1:H4:176:PRO:HG3	1:H4:198:ILE:HD11	1.89	0.54
7:F:117:VAL:CG1	7:F:124:ARG:HB3	2.37	0.54
1:C5:136:VAL:HG12	1:X4:111:ARG:HH21	1.72	0.54
1:P4:289:LYS:HD3	1:P4:293:GLY:HA2	1.89	0.54
1:U4:183:LEU:HD22	1:U4:360:VAL:HG21	1.89	0.54
1:T4:101:LEU:HD23	1:K4:190:ILE:HD11	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T4:382:LYS:HE2	1:T4:384:ALA:HB2	1.89	0.54
1:C4:246:ALA:HA	1:C4:384:ALA:HA	1.90	0.54
4:I:43:SER:OG	4:I:44:LEU:N	2.40	0.54
6:A:90:VAL:HG13	6:A:342:LEU:HD13	1.89	0.54
4:G:111:ASP:N	4:G:111:ASP:OD1	2.40	0.54
1:X4:154:LEU:HD21	1:Y4:363:TYR:HE1	1.73	0.54
1:A5:137:LEU:HD13	1:B5:188:PHE:CE1	2.42	0.54
1:B5:278:ASN:ND2	1:B5:322:ASP:OD1	2.39	0.54
1:M4:175:MET:HG3	1:M4:363:TYR:HD1	1.73	0.54
1:Q4:121:ARG:NH2	1:Q4:343:GLU:OE1	2.34	0.54
1:U4:125:SER:OG	1:U4:336:GLY:O	2.22	0.54
1:U4:288:MET:HB3	1:U4:296:LEU:HD21	1.89	0.54
1:V4:305:GLU:HB2	1:V4:306:PRO:HD3	1.88	0.54
1:E4:167:ILE:HG23	1:E4:370:GLY:HA2	1.89	0.54
2:D3:32:ARG:NH2	2:D3:67:ARG:O	2.40	0.54
5:D:20:ARG:HG3	5:D:25:LEU:HD12	1.90	0.54
1:A5:121:ARG:NH2	1:A5:343:GLU:OE1	2.41	0.54
1:U4:159:THR:HG22	1:U4:160:PRO:HD2	1.88	0.54
1:F4:145:SER:HB3	1:G4:172:LEU:HD11	1.88	0.54
5:C:81:ALA:HA	5:C:114:PRO:HG3	1.90	0.54
1:J4:149:SER:OG	1:J4:150:GLU:N	2.39	0.54
1:V4:167:ILE:HD12	1:V4:370:GLY:HA2	1.90	0.54
1:H4:287:LYS:O	1:H4:289:LYS:NZ	2.40	0.54
2:A2:32:ARG:NH2	2:A2:67:ARG:O	2.40	0.54
1:Z4:101:LEU:HD21	1:V4:162:ILE:HD13	1.89	0.54
1:O4:138:VAL:HA	1:P4:111:ARG:O	2.08	0.54
1:O4:262:VAL:HG21	1:O4:310:MET:HG2	1.89	0.54
1:K4:279:SER:OG	1:J4:270:ARG:NH1	2.41	0.54
1:L4:288:MET:HE2	1:L4:297:TRP:HE1	1.73	0.54
5:D:101:VAL:HG13	5:D:101:VAL:O	2.06	0.54
1:C5:121:ARG:NH1	1:C5:343:GLU:OE1	2.32	0.54
1:C5:134:PHE:O	1:C5:167:ILE:N	2.39	0.54
1:P4:177:LYS:HE3	1:P4:361:LEU:HD11	1.90	0.54
1:S4:223:LEU:O	1:S4:227:LYS:NZ	2.27	0.54
1:C5:91:ASN:HB3	1:C5:95:ALA:HB2	1.90	0.54
1:M4:121:ARG:HH12	1:M4:343:GLU:CD	2.17	0.54
1:P4:286:ARG:HH11	1:P4:303:ALA:CB	2.15	0.54
1:J4:252:VAL:HG11	2:E2:3:VAL:HG21	1.89	0.54
1:V4:134:PHE:HB3	1:V4:167:ILE:HB	1.90	0.54
1:L4:256:ASP:HA	1:L4:259:VAL:HG12	1.90	0.54
2:B2:32:ARG:NH2	2:B2:67:ARG:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:B:225:ILE:HD13	6:B:244:LEU:HD11	1.90	0.54
5:D:3:LEU:HD22	5:D:79:PRO:HG2	1.88	0.54
1:C5:104:PRO:HB3	1:B5:133:SER:HB2	1.90	0.53
1:A5:135:ASP:OD2	1:A5:164:ARG:NH1	2.40	0.53
1:I4:285:VAL:HG11	1:I4:309:LEU:HD11	1.90	0.53
7:F:68:VAL:HG22	7:F:128:VAL:HG22	1.89	0.53
7:F:95:ALA:HB1	7:F:97:LEU:HG	1.90	0.53
1:X4:294:ARG:NH2	1:X4:299:ASP:OD2	2.42	0.53
1:T4:181:ARG:NH2	1:J4:171:GLU:OE2	2.39	0.53
1:A4:171:GLU:HA	1:A4:367:ARG:HA	1.89	0.53
1:N4:106:THR:HA	1:M4:135:ASP:HB2	1.91	0.53
1:J4:104:PRO:HB3	1:I4:133:SER:HB2	1.90	0.53
1:D4:215:GLY:HA2	1:D4:220:THR:HG22	1.91	0.53
1:F4:182:LEU:O	1:F4:186:SER:OG	2.22	0.53
5:C:129:GLY:O	5:D:106:ARG:NH2	2.41	0.53
1:A5:227:LYS:HG2	1:A5:380:LEU:HD12	1.91	0.53
1:R4:132:THR:HG21	1:M4:102:VAL:HB	1.90	0.53
5:C:6:VAL:HG12	5:C:7:THR:HG23	1.89	0.53
1:C5:211:ILE:HG21	1:C5:320:MET:HG2	1.90	0.53
1:N4:354:PHE:CD1	1:E4:352:ASP:HB3	2.43	0.53
1:N4:363:TYR:CE1	1:M4:154:LEU:HD21	2.44	0.53
1:P4:139:ASP:HA	1:P4:162:ILE:HA	1.90	0.53
1:W4:183:LEU:HD21	1:W4:362:PHE:HZ	1.74	0.53
1:T4:275:PHE:HB2	1:T4:314:VAL:HG22	1.89	0.53
1:J4:171:GLU:HA	1:J4:367:ARG:HA	1.90	0.53
1:H4:92:SER:HB2	1:E4:182:LEU:HB2	1.90	0.53
1:E4:227:LYS:HG2	1:E4:380:LEU:HD22	1.91	0.53
1:G4:349:VAL:HG23	1:G4:364:ALA:HB2	1.91	0.53
7:F:50:GLU:HG3	7:F:67:PHE:HB3	1.91	0.53
1:Y4:181:ARG:HB3	1:O4:150:GLU:OE2	2.09	0.53
1:M4:287:LYS:O	1:M4:289:LYS:NZ	2.29	0.53
1:O4:297:TRP:HB2	1:P4:301:LEU:HD12	1.90	0.53
1:L4:256:ASP:OD1	1:L4:257:ALA:N	2.41	0.53
1:H4:181:ARG:HH21	1:D4:171:GLU:HG2	1.74	0.53
1:M4:148:ALA:O	1:M4:149:SER:HB3	2.09	0.53
1:G4:135:ASP:OD1	1:G4:166:THR:HG22	2.08	0.53
5:C:92:VAL:CG2	5:C:96:GLY:HA3	2.39	0.53
1:D4:107:SER:OG	1:C4:136:VAL:HA	2.09	0.53
1:D4:119:SER:C	1:D4:121:ARG:H	2.17	0.53
1:E4:263:TYR:OH	1:F4:286:ARG:NH1	2.25	0.53
4:J:107:ILE:HA	4:J:126:MET:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z4:296:LEU:HD23	1:A5:295:PHE:CE2	2.44	0.53
1:W4:278:ASN:HA	1:W4:317:ALA:O	2.09	0.53
1:T4:359:HIS:CE1	1:I4:151:THR:HG22	2.44	0.53
1:J4:281:THR:HG23	1:J4:323:ILE:HD11	1.90	0.53
1:I4:255:SER:HB3	1:I4:296:LEU:HD11	1.91	0.53
1:F4:225:LYS:HE2	1:F4:372:VAL:HG22	1.90	0.53
1:C4:121:ARG:NH1	1:C4:343:GLU:OE2	2.37	0.53
2:A1:32:ARG:NH2	2:A1:67:ARG:O	2.40	0.53
5:D:90:ARG:CD	5:D:98:GLU:OE1	2.57	0.53
1:X4:211:ILE:HD12	1:X4:319:ASP:HB2	1.90	0.53
1:B5:359:HIS:NE2	5:C:73:GLY:C	2.65	0.53
1:T4:190:ILE:HD11	1:K4:101:LEU:HD23	1.89	0.53
1:I4:175:MET:HG3	1:I4:362:PHE:O	2.09	0.53
4:G:77:GLU:OE2	4:G:80:ARG:NH1	2.41	0.53
1:X4:149:SER:HB2	1:X4:152:ALA:HB2	1.91	0.52
1:M4:121:ARG:NH2	1:M4:343:GLU:OE1	2.38	0.52
1:O4:190:ILE:HD11	1:L4:101:LEU:HD23	1.91	0.52
1:U4:285:VAL:HG11	1:U4:309:LEU:HD11	1.91	0.52
1:U4:343:GLU:HB3	1:U4:368:VAL:HG23	1.91	0.52
1:L4:288:MET:HG2	2:A2:6:LYS:HD2	1.91	0.52
1:B4:92:SER:OG	1:B4:93:ALA:N	2.42	0.52
1:C4:139:ASP:HA	1:C4:162:ILE:HA	1.91	0.52
4:I:107:ILE:HA	4:I:126:MET:HG2	1.90	0.52
1:C5:134:PHE:HB3	1:C5:167:ILE:HB	1.91	0.52
1:C5:175:MET:HE2	1:B5:155:SER:HA	1.92	0.52
1:N4:227:LYS:HD2	1:N4:328:TYR:CZ	2.44	0.52
1:O4:182:LEU:HB2	1:L4:92:SER:HB3	1.91	0.52
1:D4:277:MET:HG2	1:D4:330:ILE:HG12	1.91	0.52
5:D:101:VAL:HG13	5:D:103:ALA:CB	2.33	0.52
1:X4:143:MET:HG2	1:X4:160:PRO:HD3	1.90	0.52
1:B5:298:ALA:HB2	1:B5:306:PRO:HD3	1.91	0.52
1:Q4:179:SER:CA	1:Q4:359:HIS:HA	2.32	0.52
1:T4:151:THR:O	1:T4:151:THR:OG1	2.25	0.52
1:K4:102:VAL:HB	1:J4:132:THR:HG21	1.90	0.52
1:I4:230:ASN:ND2	1:I4:264:ALA:HB1	2.25	0.52
1:A4:322:ASP:OD1	1:A4:322:ASP:N	2.39	0.52
1:X4:289:LYS:HD3	1:X4:293:GLY:HA2	1.91	0.52
1:Y4:219:PRO:HG3	1:Y4:369:GLY:HA2	1.92	0.52
1:O4:133:SER:HB3	1:P4:104:PRO:HB3	1.91	0.52
1:T4:179:SER:OG	1:I4:150:GLU:OE2	2.26	0.52
1:K4:308:ARG:NH2	1:K4:311:GLY:O	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H4:121:ARG:NH1	1:H4:343:GLU:OE2	2.43	0.52
1:H4:281:THR:HA	1:H4:323:ILE:HD11	1.90	0.52
1:A4:90:LEU:HG	1:A4:91:ASN:H	1.74	0.52
4:I:54:LEU:HD21	4:J:5:ASN:HA	1.91	0.52
1:A5:191:GLU:OE2	6:A:39:PRO:HD2	2.09	0.52
1:L4:278:ASN:HA	1:L4:317:ALA:O	2.10	0.52
1:E4:163:ASP:OD1	1:E4:164:ARG:N	2.43	0.52
1:F4:167:ILE:HG23	1:F4:370:GLY:HA2	1.92	0.52
6:A:54:PHE:HB2	6:A:194:MET:HE1	1.92	0.52
6:B:102:GLY:HA3	6:B:105:GLU:OE1	2.09	0.52
1:A5:265:LEU:HD12	1:A5:379:LYS:HG2	1.90	0.52
1:N4:171:GLU:HG2	1:L4:181:ARG:HH21	1.75	0.52
1:Q4:134:PHE:HB3	1:Q4:167:ILE:HB	1.91	0.52
1:U4:135:ASP:OD2	1:U4:164:ARG:NH2	2.43	0.52
1:F4:256:ASP:HA	1:F4:259:VAL:HG12	1.91	0.52
4:I:39:VAL:HG11	4:I:57:ALA:HB3	1.92	0.52
7:F:132:ARG:NH1	7:F:133:VAL:O	2.42	0.52
1:X4:285:VAL:HG13	1:X4:288:MET:HE2	1.91	0.52
1:M4:191:GLU:HG3	1:M4:362:PHE:CE1	2.45	0.52
1:M4:262:VAL:HG21	1:M4:310:MET:HG3	1.92	0.52
1:Q4:277:MET:HG2	1:Q4:330:ILE:HG12	1.91	0.52
1:U4:167:ILE:HG23	1:U4:370:GLY:HA2	1.92	0.52
1:S4:308:ARG:NH2	1:S4:311:GLY:O	2.43	0.52
1:I4:288:MET:HA	2:C2:6:LYS:HB3	1.91	0.52
1:F4:110:ILE:HD11	1:F4:193:TRP:CE2	2.45	0.52
1:B4:107:SER:OG	1:B4:109:THR:O	2.27	0.52
4:H:39:VAL:HG11	4:H:57:ALA:HB3	1.92	0.52
4:H:107:ILE:HA	4:H:126:MET:HG2	1.90	0.52
4:J:39:VAL:HG11	4:J:57:ALA:HB3	1.92	0.52
5:C:64:ARG:HG2	5:C:135:ASP:HB3	1.90	0.52
4:G:91:PHE:HB2	4:G:105:PHE:HD2	1.75	0.52
1:C5:305:GLU:OE2	1:B5:263:TYR:OH	2.27	0.52
1:Z4:120:LEU:HD12	1:Z4:123:ILE:HD11	1.91	0.52
1:R4:159:THR:HG22	1:R4:160:PRO:HD2	1.92	0.52
1:O4:352:ASP:OD1	1:O4:352:ASP:N	2.39	0.52
1:E4:262:VAL:HG21	1:E4:310:MET:HG2	1.92	0.52
1:G4:201:LYS:HZ3	1:G4:205:ALA:HB2	1.74	0.52
1:C4:277:MET:O	1:C4:317:ALA:N	2.43	0.52
2:A2:63:ILE:O	2:A2:63:ILE:HG13	2.10	0.52
2:A3:63:ILE:HG13	2:A3:63:ILE:O	2.10	0.52
6:A:72:ALA:O	6:A:103:ARG:NH2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X4:290:ASP:OD1	1:X4:290:ASP:N	2.43	0.52
1:Y4:354:PHE:CD1	1:P4:352:ASP:HB3	2.45	0.52
1:M4:265:LEU:HD11	1:M4:333:GLY:HA2	1.92	0.52
1:M4:348:ARG:O	1:M4:364:ALA:HA	2.10	0.52
1:O4:352:ASP:HB3	1:S4:354:PHE:CD1	2.44	0.52
1:T4:111:ARG:NH1	1:S4:340:THR:OG1	2.43	0.52
1:L4:128:ASN:OD1	1:L4:345:PRO:HG3	2.10	0.52
1:D4:159:THR:HG22	1:D4:160:PRO:HD2	1.92	0.52
1:E4:116:SER:HB3	1:E4:318:GLU:HG3	1.90	0.52
5:C:48:ALA:HA	5:C:51:GLU:HG2	1.91	0.52
6:B:83:ARG:HG2	6:B:83:ARG:O	2.10	0.52
1:W4:112:GLY:HA2	1:V4:139:ASP:H	1.75	0.52
1:T4:215:GLY:HA2	1:T4:220:THR:HG22	1.90	0.52
1:K4:227:LYS:HG2	1:K4:380:LEU:HD22	1.92	0.52
1:L4:143:MET:HE3	1:H4:197:ARG:HB3	1.92	0.52
1:A4:292:ASP:OD2	1:A4:294:ARG:NH1	2.43	0.52
1:R4:128:ASN:ND2	1:R4:345:PRO:HG3	2.24	0.51
1:P4:219:PRO:HG3	1:P4:369:GLY:HA2	1.92	0.51
1:J4:155:SER:OG	1:J4:156:GLU:N	2.43	0.51
2:D2:63:ILE:O	2:D2:63:ILE:HG13	2.10	0.51
2:B3:32:ARG:NH2	2:B3:67:ARG:O	2.40	0.51
1:A5:147:TRP:CD1	1:B5:218:LYS:HE3	2.45	0.51
1:R4:133:SER:HB2	1:M4:104:PRO:HB3	1.91	0.51
1:R4:322:ASP:OD1	1:R4:322:ASP:N	2.38	0.51
1:D4:120:LEU:HD23	1:D4:210:PHE:HB3	1.93	0.51
1:B4:262:VAL:HG21	1:B4:310:MET:HG2	1.91	0.51
1:B5:177:LYS:HA	1:B5:361:LEU:HA	1.92	0.51
1:K4:186:SER:O	1:K4:188:PHE:N	2.43	0.51
2:D2:32:ARG:NH2	2:D2:67:ARG:O	2.40	0.51
7:F:117:VAL:HG23	7:F:118:GLU:N	2.24	0.51
4:G:43:SER:OG	4:G:45:GLU:O	2.27	0.51
1:S4:260:ASP:OD1	1:S4:261:LEU:N	2.44	0.51
1:I4:121:ARG:NH1	1:I4:343:GLU:OE1	2.43	0.51
1:X4:191:GLU:OE2	1:X4:351:ARG:NH1	2.42	0.51
1:T4:194:LEU:HD22	1:S4:143:MET:HE1	1.93	0.51
1:H4:269:TYR:OH	1:H4:374:ASP:OD2	2.20	0.51
1:B5:349:VAL:HA	1:B5:364:ALA:HA	1.93	0.51
1:Q4:194:LEU:HD22	1:P4:143:MET:HE1	1.92	0.51
1:V4:135:ASP:OD1	1:V4:166:THR:HG22	2.11	0.51
1:H4:252:VAL:HG11	2:C2:3:VAL:HG13	1.92	0.51
1:I4:198:ILE:HG22	1:I4:347:LEU:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E2:63:ILE:HG13	2:E2:63:ILE:O	2.10	0.51
2:A1:63:ILE:HG13	2:A1:63:ILE:O	2.10	0.51
5:C:92:VAL:CG2	5:C:96:GLY:CA	2.88	0.51
1:A5:261:LEU:CD1	1:A5:381:LEU:HB2	2.41	0.51
1:P4:290:ASP:OD1	1:P4:290:ASP:N	2.42	0.51
1:J4:277:MET:HG2	1:J4:330:ILE:HG12	1.92	0.51
1:L4:154:LEU:HD13	1:H4:363:TYR:CE1	2.46	0.51
1:C4:219:PRO:HG3	1:C4:369:GLY:HA2	1.93	0.51
2:B3:63:ILE:HG13	2:B3:63:ILE:O	2.10	0.51
6:A:123:GLU:HB3	6:A:136:HIS:HB2	1.92	0.51
1:B5:350:LEU:N	1:B5:363:TYR:O	2.36	0.51
1:K4:143:MET:HE3	1:L4:197:ARG:HB3	1.93	0.51
1:H4:269:TYR:CZ	1:I4:114:LEU:HB2	2.46	0.51
4:H:99:GLY:HA3	4:H:136:ALA:HA	1.92	0.51
1:Y4:110:ILE:HD11	1:Y4:193:TRP:CE2	2.46	0.51
1:B5:347:LEU:O	1:B5:347:LEU:HD13	2.10	0.51
1:M4:352:ASP:HB3	1:F4:354:PHE:CD1	2.46	0.51
1:J4:107:SER:OG	1:I4:136:VAL:HA	2.11	0.51
4:I:92:GLN:HG3	4:I:100:ILE:HG23	1.92	0.51
1:X4:156:GLU:HG2	1:Y4:361:LEU:HD11	1.93	0.51
1:R4:157:THR:HG21	1:M4:174:ALA:HA	1.93	0.51
1:O4:286:ARG:HH22	1:O4:305:GLU:H	1.59	0.51
1:P4:277:MET:O	1:P4:317:ALA:N	2.44	0.51
1:K4:219:PRO:HG3	1:K4:369:GLY:HA2	1.93	0.51
1:L4:343:GLU:HB3	1:L4:368:VAL:HG23	1.92	0.51
1:D4:347:LEU:HD21	1:D4:364:ALA:HB1	1.93	0.51
1:C4:248:ASP:OD1	1:C4:249:PHE:N	2.43	0.51
2:C3:63:ILE:O	2:C3:63:ILE:HG13	2.10	0.51
4:H:92:GLN:HG3	4:H:100:ILE:HG23	1.92	0.51
4:I:99:GLY:HA3	4:I:136:ALA:HA	1.92	0.51
6:A:52:THR:O	6:A:205:ASN:ND2	2.44	0.51
7:F:104:LEU:HA	7:F:133:VAL:HA	1.93	0.51
8:E:8:ARG:NH2	8:E:82:GLU:OE1	2.36	0.51
1:R4:299:ASP:OD1	1:R4:300:SER:N	2.44	0.50
1:Q4:184:ASP:OD1	1:Q4:184:ASP:N	2.42	0.50
1:U4:111:ARG:O	1:T4:138:VAL:HA	2.10	0.50
1:S4:186:SER:O	1:S4:188:PHE:N	2.44	0.50
1:K4:149:SER:OG	1:K4:150:GLU:N	2.43	0.50
1:K4:288:MET:HA	2:E2:6:LYS:HB3	1.92	0.50
1:I4:167:ILE:HG23	1:I4:370:GLY:HA2	1.93	0.50
4:J:99:GLY:HA3	4:J:136:ALA:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:68:THR:HA	5:C:131:ARG:HB2	1.94	0.50
1:X4:193:TRP:HE1	1:X4:197:ARG:NH1	2.10	0.50
1:A5:98:GLY:HA2	1:A5:101:LEU:HD12	1.93	0.50
1:N4:142:ASP:HB3	1:O4:115:ARG:NH1	2.26	0.50
1:U4:121:ARG:NH1	1:U4:343:GLU:OE2	2.44	0.50
1:I4:223:LEU:O	1:I4:227:LYS:NZ	2.28	0.50
2:B2:63:ILE:HG13	2:B2:63:ILE:O	2.10	0.50
2:A3:44:LEU:HA	2:A3:76:THR:HA	1.94	0.50
2:A1:44:LEU:HA	2:A1:76:THR:HA	1.94	0.50
1:X4:154:LEU:HD21	1:Y4:363:TYR:CE1	2.46	0.50
1:B5:348:ARG:CZ	1:B5:348:ARG:CA	2.87	0.50
1:N4:265:LEU:CD1	1:N4:333:GLY:HA2	2.41	0.50
1:O4:156:GLU:OE1	1:P4:177:LYS:HD2	2.12	0.50
1:A4:119:SER:C	1:A4:121:ARG:H	2.19	0.50
4:J:92:GLN:HG3	4:J:100:ILE:HG23	1.93	0.50
7:F:72:ILE:CD1	7:F:124:ARG:HB2	2.41	0.50
1:U4:136:VAL:HA	1:V4:107:SER:OG	2.11	0.50
2:D2:44:LEU:HA	2:D2:76:THR:HA	1.94	0.50
2:D3:63:ILE:HG13	2:D3:63:ILE:O	2.10	0.50
1:P4:107:SER:OG	1:P4:108:GLU:N	2.45	0.50
2:C2:44:LEU:HA	2:C2:76:THR:HA	1.94	0.50
2:C2:63:ILE:HG13	2:C2:63:ILE:O	2.10	0.50
2:A1:25:ASP:OD1	2:A1:74:THR:HG23	2.12	0.50
4:H:111:ASP:OD1	4:H:111:ASP:N	2.44	0.50
1:M4:305:GLU:HA	1:M4:305:GLU:OE2	2.12	0.50
1:P4:298:ALA:HB2	1:P4:306:PRO:CD	2.41	0.50
1:T4:321:PRO:HB2	1:T4:327:ALA:HB1	1.93	0.50
1:L4:162:ILE:HD13	1:E4:101:LEU:HD21	1.94	0.50
1:L4:244:GLY:O	1:L4:385:ALA:HA	2.12	0.50
1:F4:310:MET:HE2	1:G4:301:LEU:HD22	1.93	0.50
1:B4:129:VAL:HG13	1:B4:169:LEU:HD22	1.93	0.50
1:C4:121:ARG:HH12	1:C4:343:GLU:CD	2.19	0.50
2:E2:25:ASP:OD1	2:E2:74:THR:HG23	2.12	0.50
4:H:103:GLY:HA3	4:H:132:LEU:HD13	1.93	0.50
1:B5:190:ILE:HG13	1:B5:193:TRP:CE3	2.46	0.50
1:Q4:215:GLY:HA2	1:Q4:220:THR:HG23	1.93	0.50
1:O4:162:ILE:HD13	1:S4:101:LEU:HD11	1.93	0.50
1:O4:263:TYR:HE2	1:P4:286:ARG:HD3	1.76	0.50
1:V4:343:GLU:HB3	1:V4:368:VAL:HG23	1.94	0.50
1:H4:278:ASN:ND2	1:H4:322:ASP:OD1	2.44	0.50
1:A4:254:ALA:C	1:A4:256:ASP:H	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E2:32:ARG:NH2	2:E2:67:ARG:O	2.40	0.50
2:B3:44:LEU:HA	2:B3:76:THR:HA	1.94	0.50
2:A3:25:ASP:OD1	2:A3:74:THR:HG23	2.12	0.50
5:D:23:LEU:O	8:E:64:ARG:NH1	2.44	0.50
8:E:11:VAL:HG22	8:E:34:GLU:HG2	1.93	0.50
1:C5:301:LEU:HD11	1:B5:255:SER:HB2	1.94	0.50
1:Z4:176:PRO:HD2	1:Z4:362:PHE:O	2.12	0.50
1:A5:171:GLU:OE2	1:A5:173:ALA:HB2	2.11	0.50
1:B5:355:SER:HB2	5:C:125:MET:SD	2.51	0.50
1:K4:191:GLU:OE1	1:K4:351:ARG:NE	2.44	0.50
1:C4:171:GLU:HA	1:C4:367:ARG:HA	1.93	0.50
2:A3:32:ARG:NH2	2:A3:67:ARG:O	2.40	0.50
1:Y4:298:ALA:HB2	1:Y4:306:PRO:HD3	1.94	0.50
1:A5:342:ALA:O	1:A5:369:GLY:N	2.43	0.50
1:Q4:177:LYS:HG2	1:Q4:361:LEU:HD13	1.94	0.50
1:T4:255:SER:HB2	1:T4:297:TRP:CZ2	2.46	0.50
1:V4:225:LYS:HE2	1:V4:372:VAL:HG22	1.94	0.50
1:V4:324:ALA:HB3	1:V4:327:ALA:HB2	1.94	0.50
1:D4:286:ARG:NH1	1:C4:263:TYR:OH	2.45	0.50
2:A2:44:LEU:HA	2:A2:76:THR:HA	1.94	0.50
4:I:103:GLY:HA3	4:I:132:LEU:HD13	1.93	0.50
7:F:14:TYR:HD1	7:F:47:LEU:HD21	1.76	0.50
1:Z4:220:THR:HB	1:Z4:371:ASP:HB3	1.94	0.49
1:A5:183:LEU:HD21	1:A5:362:PHE:HZ	1.76	0.49
1:A5:322:ASP:OD1	1:A5:322:ASP:N	2.37	0.49
1:N4:185:ASP:OD1	1:N4:185:ASP:N	2.42	0.49
1:S4:167:ILE:HD12	1:S4:370:GLY:HA2	1.94	0.49
1:D4:322:ASP:N	1:D4:322:ASP:OD1	2.40	0.49
1:E4:121:ARG:NH1	1:E4:343:GLU:OE1	2.45	0.49
2:D3:44:LEU:HA	2:D3:76:THR:HA	1.94	0.49
1:B5:297:TRP:CE2	1:B5:309:LEU:HD13	2.47	0.49
1:H4:211:ILE:HG21	1:H4:320:MET:HG2	1.93	0.49
1:I4:119:SER:C	1:I4:121:ARG:H	2.20	0.49
1:D4:334:ASP:OD2	1:D4:337:ASN:ND2	2.45	0.49
1:E4:150:GLU:HG3	1:G4:91:ASN:HB2	1.93	0.49
1:G4:307:ALA:O	1:G4:308:ARG:HG2	2.13	0.49
4:H:16:THR:HG23	4:H:18:SER:H	1.77	0.49
1:X4:352:ASP:N	1:X4:352:ASP:OD1	2.43	0.49
1:P4:357:LYS:NZ	1:W4:352:ASP:OD2	2.40	0.49
1:K4:262:VAL:HG12	1:K4:270:ARG:HD3	1.94	0.49
1:J4:326:ASN:HB3	1:J4:382:LYS:HE2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J4:334:ASP:OD2	1:J4:337:ASN:ND2	2.45	0.49
1:H4:90:LEU:HG	1:H4:91:ASN:H	1.77	0.49
1:H4:179:SER:HA	1:H4:359:HIS:HA	1.94	0.49
1:A4:143:MET:HG3	1:A4:160:PRO:HD3	1.94	0.49
1:F4:138:VAL:HG12	1:F4:139:ASP:H	1.77	0.49
2:E2:44:LEU:HA	2:E2:76:THR:HA	1.94	0.49
4:I:16:THR:HG23	4:I:18:SER:H	1.77	0.49
5:D:70:TRP:HE3	5:D:76:GLN:HE21	1.61	0.49
1:Z4:344:ARG:NE	1:Z4:367:ARG:HD3	2.27	0.49
1:N4:134:PHE:HB3	1:N4:167:ILE:HB	1.95	0.49
1:P4:181:ARG:NH2	1:W4:171:GLU:HG2	2.26	0.49
1:T4:305:GLU:HG2	1:T4:306:PRO:HD3	1.95	0.49
1:S4:186:SER:O	1:S4:186:SER:OG	2.30	0.49
2:E3:63:ILE:O	2:E3:63:ILE:HG13	2.10	0.49
2:C3:44:LEU:HA	2:C3:76:THR:HA	1.94	0.49
4:J:111:ASP:N	4:J:111:ASP:OD1	2.44	0.49
1:Z4:290:ASP:HB3	1:Z4:296:LEU:CD1	2.35	0.49
1:B5:190:ILE:HG13	1:B5:193:TRP:CZ3	2.48	0.49
1:Q4:167:ILE:HG23	1:Q4:370:GLY:HA2	1.95	0.49
1:U4:113:VAL:HG23	1:T4:139:ASP:O	2.12	0.49
1:S4:90:LEU:HG	1:S4:91:ASN:H	1.77	0.49
1:K4:265:LEU:HD13	1:K4:332:PHE:CD2	2.46	0.49
1:J4:215:GLY:HA2	1:J4:220:THR:HG22	1.95	0.49
1:V4:167:ILE:HG23	1:V4:370:GLY:HA2	1.93	0.49
1:D4:352:ASP:OD1	1:D4:352:ASP:N	2.45	0.49
3:F2:2:ILE:HG13	3:F2:11:ALA:HB1	1.94	0.49
2:C2:32:ARG:NH2	2:C2:67:ARG:O	2.40	0.49
4:J:103:GLY:HA3	4:J:132:LEU:HD13	1.93	0.49
6:A:43:PRO:HB2	6:A:46:THR:HG23	1.94	0.49
1:A5:348:ARG:NE	1:A5:348:ARG:HA	2.28	0.49
1:Q4:121:ARG:HH12	1:Q4:343:GLU:CD	2.20	0.49
1:T4:209:ALA:HB1	1:T4:219:PRO:HD2	1.95	0.49
1:K4:309:LEU:HD23	1:K4:310:MET:HB2	1.94	0.49
1:B4:175:MET:HE3	1:B4:361:LEU:HD11	1.93	0.49
1:C4:136:VAL:HG22	1:C4:165:ILE:HB	1.94	0.49
1:R4:167:ILE:HG23	1:R4:370:GLY:HA2	1.94	0.49
1:T4:121:ARG:NH1	1:T4:343:GLU:OE2	2.45	0.49
1:H4:138:VAL:HA	1:I4:111:ARG:O	2.13	0.49
1:I4:149:SER:OG	1:I4:150:GLU:N	2.46	0.49
1:D4:211:ILE:HD12	1:D4:319:ASP:HB2	1.95	0.49
1:E4:95:ALA:HA	1:E4:99:GLY:HA3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:100:ILE:HB	4:J:135:THR:HB	1.95	0.49
6:A:50:MET:HE2	6:A:116:LEU:HB3	1.95	0.49
1:A5:131:ALA:C	1:A5:133:SER:H	2.21	0.49
1:B5:248:ASP:OD1	1:B5:248:ASP:N	2.46	0.49
1:N4:179:SER:O	1:N4:181:ARG:N	2.36	0.49
1:N4:219:PRO:HG3	1:N4:369:GLY:HA2	1.94	0.49
1:R4:134:PHE:HB3	1:R4:167:ILE:HB	1.93	0.49
1:Q4:167:ILE:HD12	1:Q4:370:GLY:HA2	1.95	0.49
1:O4:269:TYR:OH	1:O4:374:ASP:OD2	2.24	0.49
1:J4:261:LEU:HD21	1:J4:332:PHE:HB3	1.93	0.49
3:F3:2:ILE:HG13	3:F3:11:ALA:HB1	1.94	0.49
4:J:78:ARG:HD2	4:J:81:GLN:HE21	1.78	0.49
1:A5:254:ALA:C	1:A5:256:ASP:H	2.21	0.49
1:N4:382:LYS:HE2	1:N4:384:ALA:HB2	1.95	0.49
1:R4:344:ARG:HE	1:R4:367:ARG:HD3	1.78	0.49
1:P4:183:LEU:HD12	1:P4:360:VAL:HG21	1.95	0.49
1:H4:348:ARG:NH1	1:H4:365:SER:O	2.46	0.49
4:H:78:ARG:HD2	4:H:81:GLN:HE21	1.78	0.49
6:B:102:GLY:CA	6:B:105:GLU:OE1	2.61	0.49
8:E:88:ARG:HH21	8:E:107:ARG:HG3	1.78	0.49
1:M4:265:LEU:CD1	1:M4:333:GLY:HA2	2.43	0.49
1:P4:119:SER:O	1:P4:119:SER:OG	2.30	0.49
1:S4:277:MET:O	1:S4:317:ALA:N	2.46	0.49
1:J4:294:ARG:NH1	1:I4:294:ARG:HG2	2.28	0.49
1:H4:343:GLU:HB3	1:H4:368:VAL:HG23	1.95	0.49
1:D4:175:MET:HE3	1:D4:361:LEU:HD11	1.94	0.49
1:B4:159:THR:HG22	1:B4:160:PRO:HD2	1.94	0.49
2:E3:44:LEU:HA	2:E3:76:THR:HA	1.94	0.49
6:A:323:TYR:HA	6:A:327:VAL:HB	1.95	0.49
1:Y4:92:SER:HA	1:Q4:182:LEU:HD13	1.96	0.48
1:M4:121:ARG:NH1	1:M4:343:GLU:OE2	2.40	0.48
1:O4:134:PHE:HB3	1:O4:167:ILE:HB	1.95	0.48
1:P4:134:PHE:HB3	1:P4:167:ILE:HB	1.94	0.48
1:W4:90:LEU:HG	1:W4:91:ASN:H	1.77	0.48
1:K4:130:GLU:OE1	1:K4:130:GLU:N	2.45	0.48
1:V4:289:LYS:O	2:E3:7:HIS:HA	2.13	0.48
1:L4:214:ASP:OD2	1:L4:216:VAL:HG22	2.13	0.48
6:B:82:GLU:OE1	6:B:82:GLU:N	2.46	0.48
4:G:10:LEU:HD13	4:G:23:THR:HG21	1.93	0.48
1:Z4:214:ASP:OD1	1:Z4:214:ASP:N	2.42	0.48
1:R4:134:PHE:O	1:R4:167:ILE:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R4:188:PHE:CZ	1:Q4:137:LEU:HD12	2.48	0.48
1:W4:134:PHE:HB3	1:W4:167:ILE:HB	1.95	0.48
1:V4:308:ARG:NH2	1:V4:311:GLY:O	2.43	0.48
1:E4:268:GLU:HG2	1:F4:116:SER:HA	1.95	0.48
2:C3:32:ARG:NH2	2:C3:67:ARG:O	2.40	0.48
4:I:78:ARG:HD2	4:I:81:GLN:HE21	1.78	0.48
4:I:100:ILE:HB	4:I:135:THR:HB	1.95	0.48
6:A:44:ARG:HD2	6:A:44:ARG:C	2.38	0.48
5:D:108:VAL:HG21	5:D:115:ARG:CZ	2.42	0.48
7:F:78:PHE:HB3	7:F:123:ARG:CD	2.42	0.48
4:G:15:LEU:CD2	4:G:75:THR:HG22	2.40	0.48
1:P4:184:ASP:O	1:W4:344:ARG:NH1	2.46	0.48
1:S4:253:ASN:ND2	2:C3:3:VAL:O	2.46	0.48
1:K4:176:PRO:HG3	1:K4:198:ILE:HD11	1.95	0.48
1:V4:289:LYS:HD3	1:V4:293:GLY:HA2	1.95	0.48
1:B4:92:SER:O	1:B4:94:VAL:N	2.46	0.48
1:B4:357:LYS:HB3	1:B4:358:PRO:HD3	1.95	0.48
4:J:16:THR:HG23	4:J:18:SER:H	1.77	0.48
1:C5:129:VAL:HG11	1:C5:342:ALA:HB1	1.96	0.48
1:Z4:119:SER:C	1:Z4:121:ARG:H	2.21	0.48
1:J4:288:MET:HG2	2:D2:6:LYS:HD2	1.95	0.48
1:L4:141:THR:OG1	1:L4:161:GLN:HG2	2.14	0.48
1:I4:211:ILE:HG21	1:I4:320:MET:HG2	1.95	0.48
1:F4:142:ASP:OD2	1:G4:204:ARG:NH2	2.47	0.48
1:F4:286:ARG:HH12	1:F4:305:GLU:N	2.12	0.48
4:G:28:ARG:N	4:G:67:ALA:O	2.47	0.48
1:C5:295:PHE:CE2	1:C5:301:LEU:HD12	2.48	0.48
1:Z4:307:ALA:O	1:Z4:308:ARG:HG2	2.14	0.48
1:M4:305:GLU:OE2	1:M4:305:GLU:CA	2.61	0.48
1:M4:305:GLU:HG3	1:M4:305:GLU:O	2.13	0.48
1:A4:255:SER:HB3	1:A4:296:LEU:HD21	1.96	0.48
4:I:111:ASP:OD1	4:I:111:ASP:N	2.44	0.48
1:C5:133:SER:HB2	1:X4:104:PRO:HB3	1.95	0.48
1:R4:227:LYS:HE3	1:R4:328:TYR:CE2	2.49	0.48
1:O4:382:LYS:HE2	1:O4:384:ALA:HB2	1.95	0.48
1:T4:98:GLY:HA2	1:J4:162:ILE:HD12	1.96	0.48
1:K4:112:GLY:HA2	1:J4:139:ASP:H	1.78	0.48
1:H4:171:GLU:HA	1:H4:367:ARG:HA	1.96	0.48
2:B2:44:LEU:HA	2:B2:76:THR:HA	1.94	0.48
1:C5:111:ARG:O	1:B5:138:VAL:HA	2.14	0.48
1:Z4:137:LEU:HD23	1:Z4:164:ARG:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U4:119:SER:C	1:U4:121:ARG:H	2.22	0.48
1:U4:296:LEU:HA	1:V4:294:ARG:CD	2.43	0.48
1:A4:167:ILE:HG23	1:A4:370:GLY:HA2	1.94	0.48
1:C4:258:VAL:O	1:C4:262:VAL:HG23	2.14	0.48
4:J:72:ASP:N	4:J:72:ASP:OD1	2.46	0.48
5:D:89:LEU:CD2	5:D:105:TRP:CD1	2.96	0.48
1:A5:134:PHE:HD2	1:A5:167:ILE:HD12	1.78	0.48
1:R4:136:VAL:HG22	1:R4:165:ILE:HB	1.95	0.48
1:R4:156:GLU:HG2	1:M4:177:LYS:HD2	1.95	0.48
1:O4:244:GLY:O	1:O4:385:ALA:HA	2.14	0.48
1:U4:148:ALA:HB2	1:U4:154:LEU:HD13	1.96	0.48
1:S4:134:PHE:HB3	1:S4:167:ILE:HB	1.96	0.48
1:S4:183:LEU:HD21	1:S4:362:PHE:HZ	1.78	0.48
1:V4:214:ASP:OD1	1:V4:214:ASP:N	2.44	0.48
1:I4:254:ALA:C	1:I4:256:ASP:H	2.21	0.48
4:H:100:ILE:HB	4:H:135:THR:HB	1.95	0.48
4:I:72:ASP:OD1	4:I:72:ASP:N	2.46	0.48
6:B:102:GLY:N	6:B:105:GLU:HB2	2.28	0.48
1:Y4:286:ARG:NH2	1:Y4:305:GLU:H	2.10	0.48
1:N4:148:ALA:O	1:S4:181:ARG:NH2	2.46	0.48
1:Q4:95:ALA:HA	1:Q4:99:GLY:HA3	1.95	0.48
1:Q4:200:ASP:OD2	1:Q4:204:ARG:NH1	2.47	0.48
1:T4:278:ASN:HA	1:T4:317:ALA:O	2.14	0.48
1:S4:159:THR:HG22	1:S4:160:PRO:HD2	1.95	0.48
1:K4:296:LEU:H	1:K4:296:LEU:HD23	1.79	0.48
1:A4:225:LYS:HE2	1:A4:372:VAL:HG22	1.95	0.48
7:F:50:GLU:HA	7:F:67:PHE:HA	1.96	0.48
1:C5:112:GLY:HA2	1:B5:139:ASP:OD2	2.14	0.48
1:X4:290:ASP:HB2	1:Y4:292:ASP:O	2.12	0.48
1:Y4:263:TYR:OH	1:Z4:305:GLU:OE1	2.31	0.48
1:Y4:322:ASP:OD1	1:Y4:322:ASP:N	2.41	0.48
1:Y4:334:ASP:OD2	1:Y4:337:ASN:ND2	2.47	0.48
1:Z4:119:SER:N	1:Z4:122:GLN:HE22	2.12	0.48
1:W4:113:VAL:HG23	1:V4:139:ASP:O	2.13	0.48
1:W4:193:TRP:CH2	1:V4:162:ILE:HD11	2.49	0.48
1:T4:140:LYS:HG3	1:T4:161:GLN:HG3	1.96	0.48
1:K4:130:GLU:HG2	1:K4:130:GLU:O	2.14	0.48
1:K4:281:THR:HG23	1:K4:323:ILE:HD11	1.96	0.48
1:D4:238:LEU:HD11	1:D4:372:VAL:HG11	1.94	0.48
1:E4:139:ASP:OD1	1:E4:139:ASP:N	2.45	0.48
4:H:72:ASP:OD1	4:H:72:ASP:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:263:LEU:HD11	6:B:236:LEU:HD21	1.96	0.48
6:B:110:LEU:HD11	6:B:122:LEU:HD11	1.96	0.48
7:F:40:LEU:HB2	8:E:111:VAL:HB	1.96	0.48
1:T4:176:PRO:HG3	1:T4:198:ILE:HD11	1.96	0.47
1:H4:167:ILE:HG23	1:H4:370:GLY:HA2	1.96	0.47
1:H4:186:SER:OG	1:E4:101:LEU:HB3	2.14	0.47
1:D4:92:SER:OG	1:D4:93:ALA:N	2.47	0.47
1:E4:277:MET:O	1:E4:317:ALA:N	2.47	0.47
1:C4:289:LYS:HD3	1:C4:293:GLY:HA2	1.95	0.47
5:D:108:VAL:HG11	5:D:117:GLU:OE1	2.14	0.47
7:F:117:VAL:CG2	7:F:122:MET:HB2	2.44	0.47
1:C5:128:ASN:ND2	1:C5:345:PRO:HG3	2.29	0.47
1:Y4:167:ILE:HG23	1:Y4:370:GLY:HA2	1.96	0.47
1:I4:343:GLU:HB3	1:I4:368:VAL:HG23	1.95	0.47
1:F4:286:ARG:HH12	1:F4:305:GLU:H	1.61	0.47
1:B4:211:ILE:HG21	1:B4:320:MET:HG2	1.96	0.47
6:B:150:ASP:OD1	6:B:150:ASP:C	2.57	0.47
1:Y4:142:ASP:OD2	1:Z4:204:ARG:NH2	2.45	0.47
1:R4:225:LYS:HE2	1:R4:372:VAL:HG22	1.96	0.47
1:T4:289:LYS:HA	1:T4:295:PHE:HA	1.96	0.47
1:I4:180:GLN:NE2	1:I4:184:ASP:OD1	2.46	0.47
1:A4:244:GLY:O	1:A4:385:ALA:HA	2.14	0.47
1:C4:223:LEU:O	1:C4:227:LYS:NZ	2.27	0.47
1:C4:322:ASP:OD1	1:C4:322:ASP:N	2.38	0.47
1:B5:358:PRO:HB3	5:C:73:GLY:H	1.78	0.47
1:M4:265:LEU:HD21	1:M4:269:TYR:HB2	1.96	0.47
1:O4:119:SER:O	1:O4:119:SER:OG	2.29	0.47
1:V4:278:ASN:ND2	1:V4:322:ASP:OD1	2.47	0.47
1:B4:119:SER:C	1:B4:121:ARG:H	2.20	0.47
1:B5:167:ILE:HG23	1:B5:370:GLY:HA2	1.96	0.47
1:N4:167:ILE:HD12	1:N4:370:GLY:HA2	1.97	0.47
1:Q4:136:VAL:HG22	1:Q4:165:ILE:HB	1.96	0.47
1:Q4:298:ALA:HB2	1:Q4:306:PRO:HD3	1.95	0.47
1:J4:252:VAL:HG13	1:J4:253:ASN:N	2.29	0.47
5:C:92:VAL:HG22	5:C:96:GLY:HA2	1.95	0.47
1:Z4:286:ARG:HH12	1:Z4:304:GLY:N	2.10	0.47
1:B5:202:PHE:HD2	1:B5:347:LEU:HD21	1.79	0.47
1:Q4:348:ARG:HH12	1:Q4:367:ARG:HD2	1.79	0.47
1:O4:136:VAL:HG22	1:O4:165:ILE:HB	1.97	0.47
1:W4:244:GLY:O	1:W4:385:ALA:HA	2.15	0.47
1:W4:343:GLU:HB3	1:W4:368:VAL:HG23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K4:147:TRP:H	1:L4:172:LEU:HD12	1.79	0.47
1:H4:278:ASN:HA	1:H4:317:ALA:O	2.15	0.47
1:A4:219:PRO:HG3	1:A4:369:GLY:HA2	1.97	0.47
1:D4:348:ARG:HG2	1:D4:365:SER:O	2.14	0.47
5:C:196:ARG:HG3	6:A:249:GLU:HG3	1.97	0.47
1:Y4:143:MET:HE1	1:Z4:198:ILE:HG13	1.96	0.47
1:B5:121:ARG:NH1	1:B5:343:GLU:OE2	2.47	0.47
1:N4:91:ASN:H	1:F4:179:SER:HB2	1.79	0.47
1:M4:277:MET:O	1:M4:317:ALA:N	2.46	0.47
1:Q4:178:ALA:HB1	1:Q4:183:LEU:HD21	1.97	0.47
1:P4:101:LEU:HG	1:S4:190:ILE:HD11	1.97	0.47
1:W4:277:MET:HG2	1:W4:330:ILE:HG12	1.96	0.47
1:W4:281:THR:HG23	1:W4:323:ILE:HD11	1.96	0.47
1:T4:265:LEU:HD12	1:T4:379:LYS:HG2	1.97	0.47
1:V4:136:VAL:HG11	1:V4:373:SER:HB2	1.96	0.47
1:L4:176:PRO:HG3	1:L4:198:ILE:HD11	1.96	0.47
1:A4:151:THR:O	1:A4:151:THR:OG1	2.33	0.47
1:D4:93:ALA:HB2	1:D4:102:VAL:HG21	1.97	0.47
1:E4:256:ASP:OD2	1:E4:257:ALA:N	2.48	0.47
1:F4:138:VAL:HA	1:G4:111:ARG:O	2.15	0.47
5:C:5:GLU:OE1	5:C:61:ARG:NH2	2.48	0.47
6:B:71:THR:HG22	6:B:327:VAL:HG13	1.96	0.47
6:B:206:ALA:O	6:B:210:TRP:N	2.48	0.47
5:D:101:VAL:HG22	5:D:103:ALA:HB2	1.95	0.47
8:E:54:LEU:HD23	8:E:111:VAL:HA	1.96	0.47
1:C5:217:ASP:OD1	1:C5:217:ASP:N	2.47	0.47
1:X4:208:ALA:HB2	1:X4:319:ASP:OD2	2.14	0.47
1:X4:289:LYS:HB2	1:X4:293:GLY:HA2	1.96	0.47
1:Y4:128:ASN:ND2	1:Y4:345:PRO:HG3	2.30	0.47
1:A5:256:ASP:OD1	1:B5:287:LYS:HE3	2.15	0.47
1:R4:310:MET:HE2	1:R4:310:MET:HB2	1.68	0.47
1:M4:338:GLY:O	1:M4:373:SER:N	2.46	0.47
1:B4:126:VAL:HG12	1:B4:341:ILE:HB	1.97	0.47
7:F:117:VAL:HG23	7:F:122:MET:HB2	1.97	0.47
1:C5:177:LYS:HB2	1:C5:361:LEU:HD13	1.97	0.47
1:Y4:134:PHE:HB3	1:Y4:167:ILE:HB	1.96	0.47
1:A5:137:LEU:CD1	1:B5:188:PHE:CE1	2.98	0.47
1:P4:129:VAL:HG11	1:P4:342:ALA:HB1	1.96	0.47
1:W4:348:ARG:HH11	1:W4:367:ARG:HG3	1.79	0.47
1:S4:128:ASN:OD1	1:S4:128:ASN:C	2.58	0.47
1:L4:305:GLU:HB2	1:L4:306:PRO:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H4:188:PHE:O	1:H4:190:ILE:N	2.48	0.47
6:B:323:TYR:HA	6:B:327:VAL:HB	1.97	0.47
1:C5:179:SER:HA	1:C5:359:HIS:HA	1.97	0.47
1:N4:181:ARG:HG3	1:E4:367:ARG:HH22	1.79	0.47
1:R4:297:TRP:CE2	1:R4:309:LEU:HD13	2.49	0.47
1:M4:125:SER:OG	1:M4:336:GLY:O	2.25	0.47
1:L4:94:VAL:HG13	1:L4:97:GLU:HB2	1.96	0.47
1:H4:338:GLY:HA2	1:H4:374:ASP:HB3	1.96	0.47
1:D4:352:ASP:OD2	1:D4:355:SER:OG	2.25	0.47
7:F:16:GLN:HB2	7:F:97:LEU:HD21	1.97	0.47
1:I4:258:VAL:HG12	1:I4:310:MET:HE1	1.97	0.46
5:C:150:ASP:HB2	5:C:183:LEU:HD22	1.97	0.46
6:A:159:THR:HG22	6:A:164:LYS:HD3	1.97	0.46
1:Z4:119:SER:H	1:Z4:122:GLN:HE22	1.62	0.46
1:Z4:296:LEU:HB3	1:A5:301:LEU:HB2	1.97	0.46
1:M4:95:ALA:HA	1:M4:99:GLY:HA3	1.98	0.46
1:W4:305:GLU:HB2	1:W4:306:PRO:HD3	1.97	0.46
1:S4:265:LEU:HD13	1:S4:332:PHE:CD2	2.50	0.46
1:J4:278:ASN:HA	1:J4:317:ALA:O	2.14	0.46
1:H4:130:GLU:OE1	1:H4:344:ARG:NH2	2.48	0.46
1:I4:143:MET:HG2	1:I4:160:PRO:HD3	1.96	0.46
1:I4:248:ASP:OD1	1:I4:323:ILE:HG21	2.15	0.46
1:F4:211:ILE:HG21	1:F4:320:MET:HG2	1.97	0.46
6:B:194:MET:HG3	6:B:201:LEU:HD11	1.97	0.46
6:B:385:ARG:HE	6:B:392:PRO:HA	1.80	0.46
1:X4:246:ALA:HA	1:X4:384:ALA:HA	1.97	0.46
1:Y4:183:LEU:HD13	1:Y4:360:VAL:HG21	1.96	0.46
1:Y4:248:ASP:CG	1:Y4:249:PHE:H	2.23	0.46
1:R4:279:SER:OG	1:R4:318:GLU:OE2	2.24	0.46
1:U4:357:LYS:HB2	1:U4:357:LYS:HE2	1.74	0.46
1:S4:296:LEU:H	1:S4:296:LEU:HD23	1.80	0.46
1:G4:140:LYS:HG3	1:G4:235:TRP:CD1	2.51	0.46
1:G4:279:SER:HB2	1:G4:318:GLU:OE2	2.15	0.46
2:E3:32:ARG:NH2	2:E3:67:ARG:O	2.40	0.46
5:D:101:VAL:HG22	5:D:103:ALA:CA	2.46	0.46
7:F:125:ILE:HD11	7:F:127:LEU:HD11	1.97	0.46
1:Z4:322:ASP:OD1	1:Z4:322:ASP:N	2.39	0.46
1:O4:255:SER:HB2	1:P4:301:LEU:HD21	1.97	0.46
1:P4:167:ILE:HG23	1:P4:370:GLY:HA2	1.97	0.46
1:S4:278:ASN:HA	1:S4:317:ALA:O	2.15	0.46
1:K4:92:SER:O	1:K4:92:SER:OG	2.25	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G4:129:VAL:HG13	1:G4:169:LEU:HD22	1.98	0.46
2:A2:32:ARG:HG2	2:B2:2:ASP:HB3	1.97	0.46
7:F:78:PHE:CD1	7:F:123:ARG:HD3	2.51	0.46
1:Y4:225:LYS:HE2	1:Y4:372:VAL:HG22	1.98	0.46
1:N4:135:ASP:OD1	1:N4:166:THR:HG22	2.16	0.46
1:R4:150:GLU:HG3	1:R4:151:THR:HG23	1.98	0.46
1:W4:347:LEU:HD23	1:W4:349:VAL:HG23	1.97	0.46
1:T4:352:ASP:OD2	1:T4:355:SER:OG	2.26	0.46
1:A4:120:LEU:HD12	1:A4:123:ILE:HD11	1.98	0.46
1:G4:150:GLU:HA	1:G4:150:GLU:OE1	2.16	0.46
1:X4:176:PRO:HD2	1:X4:362:PHE:O	2.16	0.46
1:A5:131:ALA:O	1:A5:133:SER:N	2.49	0.46
1:A5:144:GLY:HA2	1:B5:201:LYS:NZ	2.30	0.46
1:B5:343:GLU:HB3	1:B5:368:VAL:HG23	1.96	0.46
1:N4:128:ASN:ND2	1:N4:345:PRO:HG3	2.31	0.46
1:M4:136:VAL:CG2	1:M4:165:ILE:HB	2.46	0.46
1:Q4:112:GLY:HA2	1:P4:138:VAL:HG23	1.98	0.46
1:O4:256:ASP:HA	1:O4:259:VAL:HG12	1.97	0.46
1:W4:265:LEU:HD12	1:W4:379:LYS:HG2	1.97	0.46
1:L4:186:SER:O	1:L4:186:SER:OG	2.30	0.46
1:G4:121:ARG:HH12	1:G4:343:GLU:CD	2.24	0.46
1:C4:201:LYS:NZ	1:C4:205:ALA:HB2	2.31	0.46
1:C4:285:VAL:HG13	1:C4:288:MET:HE2	1.98	0.46
5:D:110:ASP:N	5:D:110:ASP:OD1	2.48	0.46
1:X4:262:VAL:HG21	1:X4:310:MET:HG2	1.98	0.46
1:Y4:256:ASP:OD2	1:Y4:257:ALA:N	2.49	0.46
1:N4:224:THR:O	1:N4:225:LYS:HD2	2.16	0.46
1:P4:301:LEU:HD23	1:P4:301:LEU:HA	1.77	0.46
1:W4:294:ARG:HH12	1:V4:294:ARG:HG3	1.81	0.46
6:A:111:ILE:HD13	6:A:114:ILE:HD12	1.96	0.46
8:E:9:LEU:HD11	8:E:34:GLU:HB3	1.98	0.46
4:G:61:SER:OG	4:G:62:ALA:N	2.46	0.46
1:X4:310:MET:H	1:Y4:302:ALA:HA	1.81	0.46
1:Z4:163:ASP:OD1	1:Z4:164:ARG:N	2.48	0.46
1:B5:225:LYS:HE2	1:B5:372:VAL:HG22	1.98	0.46
1:P4:254:ALA:C	1:P4:256:ASP:H	2.23	0.46
1:K4:268:GLU:HG2	1:L4:114:LEU:HG	1.98	0.46
1:K4:343:GLU:HB3	1:K4:368:VAL:HG23	1.98	0.46
6:A:299:VAL:HG12	6:A:322:PHE:HE1	1.80	0.46
4:G:94:ILE:O	4:G:94:ILE:HG13	2.16	0.46
1:Z4:251:ALA:O	1:Z4:252:VAL:HG22	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A5:262:VAL:HG21	1:A5:310:MET:HG3	1.98	0.46
1:B5:171:GLU:HA	1:B5:367:ARG:HA	1.98	0.46
1:U4:172:LEU:HD21	1:U4:205:ALA:HB3	1.97	0.46
1:S4:382:LYS:HE2	1:S4:384:ALA:HB2	1.98	0.46
1:K4:150:GLU:HG2	1:H4:91:ASN:HB2	1.97	0.46
1:J4:227:LYS:H	1:J4:227:LYS:CE	2.26	0.46
1:I4:228:VAL:O	1:I4:239:GLY:HA2	2.16	0.46
1:D4:286:ARG:NH2	1:D4:305:GLU:H	2.13	0.46
1:E4:297:TRP:CE2	1:E4:306:PRO:HG2	2.51	0.46
1:B4:121:ARG:NH2	1:B4:206:GLU:OE2	2.48	0.46
1:C4:193:TRP:HE1	1:C4:197:ARG:HH11	1.62	0.46
6:B:82:GLU:OE1	6:B:82:GLU:CA	2.64	0.46
4:G:14:ASP:O	4:G:78:ARG:NE	2.49	0.46
4:G:94:ILE:HG22	4:G:100:ILE:HG13	1.98	0.46
1:X4:277:MET:HG2	1:X4:330:ILE:HG12	1.97	0.46
1:Z4:129:VAL:HG11	1:Z4:342:ALA:HB1	1.98	0.46
1:A5:147:TRP:CZ3	1:B5:172:LEU:HB2	2.51	0.46
1:B5:121:ARG:NH2	1:B5:343:GLU:OE1	2.48	0.46
1:R4:352:ASP:OD2	1:R4:355:SER:OG	2.26	0.46
1:O4:121:ARG:NH2	1:O4:343:GLU:OE1	2.28	0.46
1:W4:186:SER:O	1:W4:186:SER:OG	2.26	0.46
1:T4:244:GLY:O	1:T4:385:ALA:HA	2.16	0.46
1:S4:227:LYS:HE3	1:S4:328:TYR:CE2	2.50	0.46
1:J4:112:GLY:HA2	1:I4:139:ASP:H	1.80	0.46
1:J4:288:MET:HE2	1:J4:297:TRP:HE1	1.81	0.46
1:A4:128:ASN:ND2	1:A4:345:PRO:HG3	2.30	0.46
1:E4:263:TYR:O	1:F4:279:SER:OG	2.34	0.46
1:F4:277:MET:O	1:F4:317:ALA:N	2.49	0.46
2:B3:32:ARG:HG2	2:C3:2:ASP:HB3	1.97	0.46
2:B3:37:ARG:HB3	2:B3:81:VAL:HG13	1.98	0.46
4:G:14:ASP:HB3	4:G:17:GLY:HA2	1.98	0.46
1:B5:230:ASN:ND2	1:B5:264:ALA:HB1	2.31	0.45
1:R4:201:LYS:HZ2	1:R4:205:ALA:HB2	1.79	0.45
1:H4:143:MET:HE1	1:I4:194:LEU:HD22	1.98	0.45
1:E4:176:PRO:HD2	1:E4:362:PHE:O	2.15	0.45
1:G4:168:PRO:HB2	1:G4:170:HIS:CE1	2.50	0.45
1:B4:133:SER:HB2	1:C4:104:PRO:HB3	1.98	0.45
2:E3:37:ARG:HD2	2:E3:63:ILE:HG22	1.98	0.45
6:A:225:ILE:HD13	6:A:244:LEU:HD11	1.98	0.45
1:B5:172:LEU:O	1:B5:365:SER:HA	2.16	0.45
1:T4:265:LEU:HD13	1:T4:332:PHE:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H4:129:VAL:HG23	1:I4:105:GLN:CD	2.41	0.45
1:A4:272:ASN:OD1	1:A4:272:ASN:N	2.49	0.45
1:B4:140:LYS:HE2	1:B4:235:TRP:CD1	2.51	0.45
2:A1:37:ARG:HB3	2:A1:81:VAL:HG13	1.99	0.45
5:D:58:LEU:HA	5:D:140:PHE:HD2	1.81	0.45
1:A5:289:LYS:HZ2	1:A5:295:PHE:HE1	1.61	0.45
1:B5:348:ARG:NE	1:B5:348:ARG:CA	2.66	0.45
1:R4:183:LEU:HD12	1:R4:360:VAL:HG21	1.98	0.45
1:W4:225:LYS:HE2	1:W4:372:VAL:HG22	1.99	0.45
1:T4:307:ALA:O	1:T4:314:VAL:HB	2.16	0.45
1:E4:142:ASP:OD1	1:E4:142:ASP:N	2.39	0.45
1:G4:175:MET:HG3	1:G4:363:TYR:HB2	1.98	0.45
2:D2:37:ARG:HB3	2:D2:81:VAL:HG13	1.99	0.45
6:B:343:SER:HB2	6:B:349:GLN:HA	1.99	0.45
1:C5:194:LEU:CD2	1:B5:143:MET:HE1	2.46	0.45
1:X4:272:ASN:OD1	1:X4:272:ASN:N	2.50	0.45
1:N4:106:THR:HG23	1:N4:107:SER:N	2.30	0.45
1:J4:194:LEU:HD22	1:I4:143:MET:CE	2.47	0.45
1:A4:159:THR:HG22	1:A4:160:PRO:HD2	1.97	0.45
1:D4:324:ALA:HB3	1:D4:327:ALA:HB2	1.98	0.45
1:E4:191:GLU:HG3	1:E4:362:PHE:CE1	2.52	0.45
1:B4:225:LYS:HE2	1:B4:372:VAL:HG22	1.98	0.45
2:D2:37:ARG:HD2	2:D2:63:ILE:HG22	1.98	0.45
6:A:346:LEU:O	6:A:347:GLY:C	2.59	0.45
1:X4:286:ARG:NH1	1:X4:304:GLY:H	2.15	0.45
1:X4:347:LEU:HD13	1:X4:366:LYS:HB2	1.98	0.45
1:B5:228:VAL:O	1:B5:239:GLY:HA2	2.15	0.45
1:R4:343:GLU:HB3	1:R4:368:VAL:HG23	1.98	0.45
1:M4:277:MET:HG2	1:M4:330:ILE:HG12	1.99	0.45
1:W4:261:LEU:HD13	1:W4:381:LEU:HB2	1.98	0.45
1:W4:268:GLU:HG2	1:S4:114:LEU:HG	1.98	0.45
1:K4:261:LEU:HD22	1:K4:381:LEU:HB2	1.99	0.45
1:H4:269:TYR:CE1	1:I4:114:LEU:HB2	2.51	0.45
1:I4:171:GLU:HA	1:I4:367:ARG:HA	1.99	0.45
1:A4:343:GLU:HB3	1:A4:368:VAL:HG23	1.97	0.45
2:C3:37:ARG:HD2	2:C3:63:ILE:HG22	1.98	0.45
2:A1:37:ARG:HD2	2:A1:63:ILE:HG22	1.98	0.45
6:A:324:ARG:NH1	6:A:365:GLU:OE1	2.49	0.45
8:E:37:ALA:HB2	8:E:63:VAL:HG12	1.99	0.45
1:C5:294:ARG:HH12	1:B5:296:LEU:HA	1.81	0.45
1:Y4:201:LYS:HZ2	1:Y4:205:ALA:HB2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z4:294:ARG:O	1:Z4:295:PHE:HB2	2.17	0.45
1:N4:255:SER:OG	1:O4:295:PHE:HZ	2.00	0.45
1:M4:279:SER:HB2	1:M4:318:GLU:OE2	2.17	0.45
1:M4:350:LEU:HD11	1:F4:354:PHE:CE1	2.52	0.45
1:Q4:189:ASP:HB3	1:Q4:192:THR:HG22	1.99	0.45
1:W4:121:ARG:NH2	1:W4:206:GLU:OE2	2.50	0.45
1:H4:225:LYS:HE2	1:H4:372:VAL:HG22	1.97	0.45
1:A4:191:GLU:HG2	1:A4:362:PHE:CZ	2.51	0.45
2:A2:32:ARG:HE	2:A2:67:ARG:HG2	1.82	0.45
2:E3:32:ARG:HE	2:E3:67:ARG:HG2	1.82	0.45
1:Z4:220:THR:HG23	1:Z4:224:THR:HG23	1.99	0.45
1:A5:137:LEU:O	1:B5:110:ILE:HG13	2.16	0.45
1:A5:225:LYS:HE3	1:A5:372:VAL:HG22	1.98	0.45
1:M4:167:ILE:HG23	1:M4:370:GLY:HA2	1.98	0.45
1:U4:252:VAL:CG2	2:E3:3:VAL:HG21	2.45	0.45
1:T4:292:ASP:OD2	1:T4:294:ARG:NH2	2.35	0.45
1:V4:211:ILE:HG21	1:V4:320:MET:HG2	1.98	0.45
1:I4:121:ARG:NH2	1:I4:206:GLU:OE2	2.50	0.45
1:E4:136:VAL:CG2	1:E4:165:ILE:HB	2.46	0.45
1:G4:119:SER:C	1:G4:121:ARG:H	2.25	0.45
2:A2:37:ARG:HB3	2:A2:81:VAL:HG13	1.99	0.45
2:D3:32:ARG:HE	2:D3:67:ARG:HG2	1.82	0.45
2:A3:32:ARG:HE	2:A3:67:ARG:HG2	1.82	0.45
4:H:91:PHE:HB2	4:H:105:PHE:HD2	1.82	0.45
4:J:88:VAL:HG12	4:J:106:MET:HB2	1.99	0.45
6:B:223:GLY:HA2	6:B:273:MET:H	1.82	0.45
8:E:79:ARG:HD2	8:E:86:ILE:HG23	1.98	0.45
1:X4:324:ALA:HB3	1:X4:327:ALA:HB2	1.99	0.45
1:X4:352:ASP:C	1:X4:354:PHE:H	2.24	0.45
1:A5:149:SER:OG	1:A5:150:GLU:N	2.50	0.45
1:A5:310:MET:HE1	1:B5:301:LEU:HD22	1.99	0.45
1:P4:106:THR:HG23	1:P4:107:SER:N	2.31	0.45
1:T4:106:THR:HA	1:S4:135:ASP:HB2	1.99	0.45
1:J4:366:LYS:HZ2	1:J4:368:VAL:HB	1.82	0.45
1:V4:227:LYS:HG2	1:V4:380:LEU:HD22	1.99	0.45
1:L4:265:LEU:HD12	1:L4:379:LYS:HG2	1.99	0.45
2:D3:37:ARG:HB3	2:D3:81:VAL:HG13	1.98	0.45
7:F:4:ALA:HB1	7:F:101:ARG:HH12	1.82	0.45
1:X4:119:SER:O	1:X4:119:SER:OG	2.29	0.45
1:Z4:101:LEU:HD21	1:V4:162:ILE:CD1	2.47	0.45
1:B5:189:ASP:O	1:B5:190:ILE:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N4:294:ARG:HD3	1:O4:294:ARG:NH2	2.32	0.45
1:N4:301:LEU:HG	1:M4:310:MET:HE2	1.99	0.45
1:R4:189:ASP:HB3	1:R4:192:THR:HG22	1.98	0.45
1:O4:277:MET:HG2	1:O4:330:ILE:HG12	1.98	0.45
1:P4:167:ILE:HD12	1:P4:370:GLY:HA2	1.98	0.45
1:U4:288:MET:HA	2:D3:6:LYS:HB3	1.98	0.45
1:T4:183:LEU:HD22	1:T4:360:VAL:HG21	1.97	0.45
1:V4:291:ALA:O	2:D3:10:SER:HB2	2.17	0.45
1:A4:139:ASP:HB2	1:A4:160:PRO:HB2	1.99	0.45
1:E4:156:GLU:HG2	1:F4:361:LEU:HD11	1.97	0.45
1:E4:177:LYS:HD2	1:E4:359:HIS:CD2	2.52	0.45
2:B2:37:ARG:HD2	2:B2:63:ILE:HG22	1.98	0.45
2:B3:37:ARG:HD2	2:B3:63:ILE:HG22	1.98	0.45
2:A3:72:LEU:O	2:A3:76:THR:OG1	2.29	0.45
1:X4:277:MET:O	1:X4:317:ALA:N	2.50	0.45
1:N4:252:VAL:HG23	1:N4:253:ASN:H	1.81	0.45
1:R4:311:GLY:N	1:M4:302:ALA:O	2.50	0.45
1:U4:219:PRO:HG3	1:U4:369:GLY:HA2	1.98	0.45
1:U4:227:LYS:HG2	1:U4:380:LEU:HD22	1.99	0.45
1:A4:243:THR:O	1:A4:250:ALA:HB2	2.17	0.45
1:G4:255:SER:HB3	1:G4:296:LEU:HD13	1.99	0.45
1:B4:129:VAL:HG11	1:B4:342:ALA:HB1	1.99	0.45
2:D2:32:ARG:HE	2:D2:67:ARG:HG2	1.82	0.45
2:B2:37:ARG:HB3	2:B2:81:VAL:HG13	1.99	0.45
2:E2:37:ARG:HD2	2:E2:63:ILE:HG22	1.98	0.45
2:E3:37:ARG:HB3	2:E3:81:VAL:HG13	1.99	0.45
2:A1:32:ARG:HE	2:A1:67:ARG:HG2	1.82	0.45
1:N4:286:ARG:NH1	1:N4:305:GLU:H	2.15	0.44
1:R4:230:ASN:ND2	1:R4:264:ALA:HB1	2.32	0.44
1:R4:272:ASN:OD1	1:R4:272:ASN:N	2.50	0.44
1:T4:226:THR:O	1:T4:237:SER:HB2	2.17	0.44
1:L4:288:MET:HA	2:A2:6:LYS:HB3	1.98	0.44
1:D4:277:MET:O	1:D4:317:ALA:N	2.50	0.44
1:F4:223:LEU:HD11	1:F4:320:MET:HE3	1.99	0.44
1:F4:352:ASP:OD2	1:F4:355:SER:OG	2.33	0.44
1:G4:167:ILE:HG23	1:G4:370:GLY:HA2	1.98	0.44
1:C4:329:ALA:HB3	1:C4:383:PHE:CE2	2.52	0.44
2:C2:32:ARG:HE	2:C2:67:ARG:HG2	1.82	0.44
2:C2:37:ARG:HD2	2:C2:63:ILE:HG22	1.98	0.44
2:B2:72:LEU:O	2:B2:76:THR:OG1	2.30	0.44
2:E2:32:ARG:HE	2:E2:67:ARG:HG2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:J:91:PHE:HB2	4:J:105:PHE:HD2	1.82	0.44
5:C:92:VAL:HG22	5:C:96:GLY:CA	2.47	0.44
5:C:167:HIS:CE1	8:E:3:ARG:HD2	2.51	0.44
6:A:126:CYS:HB3	6:A:132:PRO:HB3	1.99	0.44
4:G:12:LYS:HD3	4:G:21:PHE:HB3	1.99	0.44
1:C5:277:MET:O	1:C5:317:ALA:N	2.50	0.44
1:A5:269:TYR:CZ	1:B5:114:LEU:HB2	2.53	0.44
1:A5:348:ARG:O	1:A5:364:ALA:HA	2.16	0.44
1:O4:90:LEU:HD23	1:K4:159:THR:OG1	2.17	0.44
1:J4:219:PRO:HG3	1:J4:369:GLY:HA2	1.99	0.44
1:I4:315:LEU:HD23	1:I4:317:ALA:HB2	1.99	0.44
1:A4:265:LEU:HG	1:A4:269:TYR:HB2	1.98	0.44
1:D4:138:VAL:HG23	1:D4:163:ASP:HB3	1.98	0.44
1:E4:214:ASP:N	1:E4:214:ASP:OD1	2.46	0.44
1:E4:256:ASP:HB2	1:F4:287:LYS:HE3	1.98	0.44
1:F4:91:ASN:HD21	1:F4:94:VAL:HB	1.81	0.44
1:B4:167:ILE:HG23	1:B4:370:GLY:HA2	1.97	0.44
4:I:88:VAL:HG12	4:I:106:MET:HB2	1.99	0.44
5:D:93:ASP:OD2	5:D:97:VAL:HG23	2.16	0.44
1:N4:167:ILE:HG21	1:N4:342:ALA:HB3	2.00	0.44
1:M4:227:LYS:HG2	1:M4:380:LEU:HD22	1.99	0.44
1:M4:322:ASP:OD1	1:M4:322:ASP:N	2.49	0.44
1:Q4:262:VAL:HG12	1:Q4:270:ARG:HD3	2.00	0.44
1:P4:194:LEU:HD21	1:S4:89:ALA:HB2	1.98	0.44
1:T4:280:LYS:HE2	1:T4:280:LYS:HB2	1.69	0.44
1:V4:142:ASP:N	1:V4:142:ASP:OD1	2.50	0.44
1:L4:150:GLU:CG	1:I4:91:ASN:HB2	2.46	0.44
1:H4:183:LEU:HD21	1:H4:362:PHE:HZ	1.82	0.44
1:H4:238:LEU:HD23	1:H4:380:LEU:HD11	1.99	0.44
1:B4:138:VAL:HG23	1:B4:163:ASP:HB3	1.99	0.44
5:C:66:ALA:HA	5:C:133:GLU:HA	2.00	0.44
6:A:194:MET:HG3	6:A:201:LEU:HD11	2.00	0.44
6:A:331:LEU:HD12	6:A:354:PRO:HB3	1.99	0.44
1:A5:119:SER:C	1:A5:121:ARG:H	2.25	0.44
1:A5:194:LEU:O	1:A5:198:ILE:HG12	2.17	0.44
1:N4:265:LEU:HD13	1:N4:332:PHE:CD2	2.52	0.44
1:K4:117:THR:HG22	1:J4:268:GLU:OE1	2.18	0.44
1:H4:101:LEU:HD23	1:E4:190:ILE:HD11	2.00	0.44
1:H4:267:ALA:HB3	1:I4:116:SER:HB2	1.99	0.44
1:E4:265:LEU:HD11	1:E4:333:GLY:HA2	2.00	0.44
2:D3:37:ARG:HD2	2:D3:63:ILE:HG22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:161:GLN:OE1	5:D:176:MET:HE3	2.17	0.44
1:A5:171:GLU:HB2	1:A5:367:ARG:NE	2.32	0.44
1:Q4:137:LEU:HD21	1:Q4:164:ARG:HB2	1.99	0.44
1:O4:94:VAL:HG23	1:O4:97:GLU:HB2	2.00	0.44
1:S4:95:ALA:HA	1:S4:99:GLY:HA3	1.99	0.44
1:J4:265:LEU:HD13	1:J4:332:PHE:CD2	2.52	0.44
1:D4:265:LEU:CD1	1:D4:333:GLY:HA2	2.45	0.44
1:E4:225:LYS:HE2	1:E4:372:VAL:HG22	1.98	0.44
1:G4:178:ALA:O	1:G4:360:VAL:HG22	2.17	0.44
2:B3:32:ARG:HE	2:B3:67:ARG:HG2	1.82	0.44
4:J:11:ILE:HG22	4:J:93:VAL:HG13	1.99	0.44
6:B:38:ARG:O	6:B:146:VAL:HG23	2.16	0.44
7:F:6:ALA:HB2	7:F:65:HIS:CE1	2.52	0.44
1:Z4:119:SER:H	1:Z4:122:GLN:NE2	2.15	0.44
1:Z4:268:GLU:HG2	1:A5:116:SER:HA	1.99	0.44
1:Z4:272:ASN:N	1:Z4:272:ASN:OD1	2.49	0.44
1:A5:175:MET:HE3	1:A5:363:TYR:HB2	1.99	0.44
1:A5:211:ILE:HG21	1:A5:320:MET:HG2	2.00	0.44
1:M4:136:VAL:HG23	1:M4:165:ILE:HB	1.99	0.44
1:O4:226:THR:O	1:O4:237:SER:HB2	2.17	0.44
1:W4:139:ASP:H	1:S4:112:GLY:HA2	1.82	0.44
1:U4:270:ARG:NH1	1:V4:279:SER:OG	2.51	0.44
1:T4:193:TRP:CZ3	1:K4:89:ALA:HB2	2.52	0.44
1:A4:129:VAL:HG11	1:A4:134:PHE:HD1	1.81	0.44
1:G4:243:THR:O	1:G4:250:ALA:HB2	2.18	0.44
1:B4:136:VAL:O	1:B4:164:ARG:HA	2.17	0.44
1:B4:156:GLU:OE1	1:C4:177:LYS:HE2	2.18	0.44
2:C2:72:LEU:O	2:C2:76:THR:OG1	2.30	0.44
2:B2:32:ARG:HE	2:B2:67:ARG:HG2	1.82	0.44
2:C3:32:ARG:HE	2:C3:67:ARG:HG2	1.82	0.44
2:C3:37:ARG:HB3	2:C3:81:VAL:HG13	1.99	0.44
2:A3:37:ARG:HD2	2:A3:63:ILE:HG22	1.98	0.44
4:I:91:PHE:HB2	4:I:105:PHE:HD2	1.82	0.44
1:A5:92:SER:OG	1:A5:93:ALA:N	2.47	0.44
1:O4:91:ASN:N	1:O4:91:ASN:ND2	2.64	0.44
1:U4:315:LEU:HD23	1:U4:317:ALA:HB2	1.98	0.44
1:H4:122:GLN:HG2	1:H4:123:ILE:HG23	1.99	0.44
1:D4:333:GLY:HA3	1:D4:378:ILE:HA	1.99	0.44
1:F4:141:THR:HG22	1:F4:142:ASP:N	2.32	0.44
2:C2:37:ARG:HB3	2:C2:81:VAL:HG13	1.99	0.44
4:H:88:VAL:HG12	4:H:106:MET:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X4:223:LEU:O	1:X4:227:LYS:NZ	2.35	0.44
1:Y4:190:ILE:HD11	1:Q4:101:LEU:HD13	1.99	0.44
1:W4:238:LEU:HD23	1:W4:380:LEU:HD11	1.99	0.44
1:T4:281:THR:HA	1:T4:323:ILE:HD11	2.00	0.44
1:K4:129:VAL:HG23	1:L4:105:GLN:CD	2.42	0.44
1:H4:138:VAL:HG21	1:H4:235:TRP:HZ2	1.81	0.44
1:H4:252:VAL:HG11	2:C2:3:VAL:CG1	2.48	0.44
2:A2:37:ARG:HD2	2:A2:63:ILE:HG22	1.98	0.44
2:E2:72:LEU:O	2:E2:76:THR:OG1	2.30	0.44
4:I:11:ILE:HG22	4:I:93:VAL:HG13	1.99	0.44
6:B:102:GLY:O	6:B:103:ARG:C	2.61	0.44
6:B:177:CYS:HB2	6:B:341:TRP:CD2	2.53	0.44
1:X4:143:MET:HE2	1:Y4:194:LEU:HD22	2.00	0.44
1:Z4:206:GLU:OE1	1:Z4:366:LYS:NZ	2.35	0.44
1:R4:121:ARG:NH2	1:R4:343:GLU:OE1	2.50	0.44
1:R4:292:ASP:O	1:Q4:291:ALA:HB3	2.17	0.44
1:U4:136:VAL:HG22	1:U4:165:ILE:HB	1.99	0.44
1:T4:127:VAL:HG11	1:T4:134:PHE:CE2	2.52	0.44
1:T4:150:GLU:HG2	1:V4:91:ASN:HB2	1.99	0.44
1:L4:261:LEU:HD21	1:L4:332:PHE:CB	2.48	0.44
1:I4:143:MET:CG	1:I4:160:PRO:HD3	2.48	0.44
1:A4:305:GLU:HB3	1:A4:306:PRO:HD3	1.98	0.44
1:E4:178:ALA:HB3	1:E4:362:PHE:HE2	1.82	0.44
1:E4:310:MET:HE2	1:E4:310:MET:HB2	1.92	0.44
6:B:315:TYR:HA	6:B:318:ALA:HB3	2.00	0.44
1:Y4:350:LEU:HD11	1:W4:354:PHE:HE1	1.83	0.43
1:R4:114:LEU:HD23	1:Q4:268:GLU:HG3	2.00	0.43
1:P4:329:ALA:HB3	1:P4:383:PHE:CE2	2.52	0.43
1:J4:288:MET:HA	2:D2:6:LYS:HB3	1.99	0.43
1:L4:277:MET:HG2	1:L4:330:ILE:HG12	1.99	0.43
1:D4:290:ASP:OD2	1:E4:294:ARG:HD3	2.18	0.43
1:C4:248:ASP:CG	1:C4:249:PHE:H	2.24	0.43
4:H:11:ILE:HG22	4:H:93:VAL:HG13	1.99	0.43
6:A:75:PRO:HG2	6:A:358:GLN:HE22	1.83	0.43
1:Y4:182:LEU:HD11	1:Q4:101:LEU:HD11	2.00	0.43
1:B5:139:ASP:OD2	1:B5:139:ASP:N	2.42	0.43
1:P4:310:MET:HE2	1:P4:310:MET:HB2	1.91	0.43
1:W4:349:VAL:HG22	1:W4:364:ALA:HB2	2.00	0.43
1:I4:225:LYS:HE2	1:I4:372:VAL:HG22	1.99	0.43
1:I4:289:LYS:O	2:C2:7:HIS:HA	2.17	0.43
1:G4:347:LEU:HB3	1:G4:366:LYS:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E2:37:ARG:HB3	2:E2:81:VAL:HG13	1.99	0.43
5:C:56:LYS:HD3	5:C:81:ALA:HB3	2.00	0.43
7:F:56:SER:OG	7:F:57:ASP:N	2.51	0.43
1:C5:322:ASP:OD1	1:C5:322:ASP:N	2.39	0.43
1:A5:256:ASP:HA	1:A5:259:VAL:HG22	2.01	0.43
1:B5:299:ASP:N	1:B5:299:ASP:OD1	2.51	0.43
1:R4:352:ASP:OD1	1:R4:352:ASP:N	2.51	0.43
1:Q4:322:ASP:OD1	1:Q4:322:ASP:N	2.40	0.43
1:E4:147:TRP:CZ2	1:F4:209:ALA:HB2	2.54	0.43
1:F4:134:PHE:HB3	1:F4:167:ILE:HB	2.00	0.43
1:F4:227:LYS:HG2	1:F4:380:LEU:HD22	2.01	0.43
1:G4:133:SER:HB3	1:B4:104:PRO:HB3	1.99	0.43
5:C:92:VAL:CG2	5:C:96:GLY:HA2	2.48	0.43
1:B5:189:ASP:C	1:B5:191:GLU:N	2.77	0.43
1:N4:89:ALA:HB2	1:F4:193:TRP:HZ3	1.83	0.43
1:O4:211:ILE:HD12	1:O4:319:ASP:HB2	2.00	0.43
1:W4:227:LYS:HE2	1:W4:227:LYS:HB2	1.85	0.43
1:T4:265:LEU:CD1	1:T4:333:GLY:HA2	2.46	0.43
1:S4:136:VAL:HG11	1:S4:373:SER:HB2	2.00	0.43
1:H4:167:ILE:HD12	1:H4:370:GLY:HA2	2.01	0.43
1:A4:288:MET:HE3	1:A4:297:TRP:HE1	1.83	0.43
1:D4:93:ALA:HA	1:D4:99:GLY:HA3	2.00	0.43
1:E4:230:ASN:OD1	1:E4:231:GLY:N	2.49	0.43
1:F4:136:VAL:HG22	1:F4:165:ILE:HB	2.00	0.43
2:A3:37:ARG:HB3	2:A3:81:VAL:HG13	1.99	0.43
1:C5:262:VAL:HG21	1:C5:310:MET:HG2	2.01	0.43
1:X4:329:ALA:HB3	1:X4:383:PHE:CE2	2.54	0.43
1:B5:138:VAL:HG21	1:B5:235:TRP:HZ2	1.83	0.43
1:R4:172:LEU:HA	1:Q4:147:TRP:H	1.82	0.43
1:G4:261:LEU:HD22	1:G4:381:LEU:HB2	2.00	0.43
1:B4:90:LEU:O	1:B4:90:LEU:HD23	2.19	0.43
1:B4:136:VAL:CG1	1:C4:111:ARG:HH21	2.31	0.43
1:B4:367:ARG:HE	1:B4:367:ARG:HB2	1.54	0.43
1:C5:272:ASN:OD1	1:C5:272:ASN:N	2.51	0.43
1:X4:276:VAL:HG12	1:X4:320:MET:HG3	1.99	0.43
1:M4:298:ALA:HB2	1:M4:306:PRO:HD3	2.00	0.43
1:Q4:180:GLN:OE1	1:Q4:180:GLN:HA	2.19	0.43
1:P4:334:ASP:N	1:P4:377:ALA:O	2.51	0.43
1:U4:289:LYS:HD2	2:D3:7:HIS:CE1	2.53	0.43
1:T4:185:ASP:CG	1:J4:367:ARG:HH22	2.26	0.43
1:K4:139:ASP:H	1:L4:112:GLY:HA2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H4:223:LEU:HD11	1:H4:320:MET:HE3	2.00	0.43
1:F4:352:ASP:N	1:F4:352:ASP:OD1	2.51	0.43
1:C4:134:PHE:HB3	1:C4:167:ILE:HB	2.00	0.43
5:C:15:PRO:HB2	5:C:18:GLU:HB2	2.00	0.43
6:A:339:ALA:HB2	6:A:352:LEU:H	1.84	0.43
1:N4:171:GLU:HG2	1:L4:181:ARG:NH2	2.33	0.43
1:M4:243:THR:HG23	1:M4:382:LYS:O	2.18	0.43
1:M4:261:LEU:HD22	1:M4:381:LEU:HB2	2.00	0.43
1:Q4:244:GLY:O	1:Q4:385:ALA:HA	2.18	0.43
1:T4:243:THR:HG23	1:T4:382:LYS:O	2.18	0.43
1:K4:277:MET:HG2	1:K4:330:ILE:HG12	2.01	0.43
1:J4:165:ILE:HD12	1:J4:373:SER:HA	1.99	0.43
1:V4:119:SER:C	1:V4:121:ARG:H	2.26	0.43
1:L4:289:LYS:HD3	1:L4:293:GLY:HA2	2.01	0.43
1:G4:310:MET:HE2	1:G4:310:MET:HB2	1.63	0.43
1:G4:322:ASP:OD1	1:G4:322:ASP:N	2.37	0.43
1:A5:131:ALA:C	1:A5:133:SER:N	2.77	0.43
1:B5:233:TRP:CH2	1:B5:376:ALA:HB2	2.54	0.43
1:N4:174:ALA:HB2	1:M4:145:SER:HB2	2.00	0.43
1:R4:254:ALA:C	1:R4:256:ASP:H	2.27	0.43
1:M4:343:GLU:HB3	1:M4:368:VAL:HG23	2.01	0.43
1:W4:308:ARG:NH2	1:W4:311:GLY:O	2.51	0.43
1:J4:172:LEU:HD11	1:I4:145:SER:HB3	2.01	0.43
1:E4:193:TRP:HE1	1:E4:197:ARG:NH1	2.17	0.43
1:F4:241:VAL:O	1:F4:381:LEU:HD12	2.19	0.43
6:A:169:MET:HE2	6:A:169:MET:HB2	1.80	0.43
5:D:176:MET:HG3	5:D:179:GLY:HA2	2.01	0.43
1:Z4:227:LYS:HE2	1:Z4:227:LYS:HB2	1.85	0.43
1:O4:90:LEU:HD22	1:L4:177:LYS:O	2.19	0.43
1:O4:193:TRP:NE1	1:O4:197:ARG:HE	2.17	0.43
1:W4:130:GLU:OE2	1:W4:344:ARG:NH2	2.52	0.43
1:U4:183:LEU:HD21	1:U4:362:PHE:HZ	1.84	0.43
1:K4:191:GLU:HG2	1:K4:362:PHE:CZ	2.53	0.43
1:H4:220:THR:OG1	1:H4:371:ASP:HB3	2.19	0.43
1:E4:289:LYS:HB2	1:E4:293:GLY:HA2	2.01	0.43
1:B4:343:GLU:HB3	1:B4:368:VAL:HG23	2.01	0.43
7:F:53:ALA:HB3	7:F:64:VAL:HB	1.99	0.43
1:Y4:350:LEU:HD11	1:W4:354:PHE:CE1	2.54	0.43
1:B5:177:LYS:HE3	5:C:122:MET:HB2	1.73	0.43
1:Q4:111:ARG:O	1:P4:138:VAL:HA	2.18	0.43
1:Q4:140:LYS:HE3	1:Q4:235:TRP:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U4:211:ILE:HG21	1:U4:320:MET:HG2	2.01	0.43
1:K4:243:THR:O	1:K4:250:ALA:HB2	2.19	0.43
1:V4:127:VAL:HG11	1:V4:134:PHE:CZ	2.54	0.43
1:H4:297:TRP:CH2	1:H4:310:MET:HE2	2.54	0.43
1:I4:90:LEU:HG	1:I4:91:ASN:H	1.82	0.43
1:D4:211:ILE:HG21	1:D4:320:MET:HG2	2.01	0.43
1:E4:241:VAL:HG23	1:E4:381:LEU:HD12	2.01	0.43
1:B4:297:TRP:CE2	1:B4:309:LEU:HD13	2.54	0.43
5:C:196:ARG:HH12	6:B:217:ASN:HB3	1.84	0.43
6:A:244:LEU:HD23	5:D:190:VAL:HG12	2.00	0.43
1:Z4:263:TYR:HE2	1:A5:286:ARG:HE	1.67	0.42
1:A5:310:MET:HA	1:B5:301:LEU:O	2.18	0.42
1:B5:272:ASN:OD1	1:B5:272:ASN:N	2.51	0.42
1:N4:246:ALA:HA	1:N4:384:ALA:O	2.19	0.42
1:R4:92:SER:O	1:R4:92:SER:OG	2.35	0.42
1:Q4:106:THR:HG22	1:P4:164:ARG:HH11	1.84	0.42
1:P4:278:ASN:HD21	1:P4:322:ASP:HB3	1.84	0.42
1:U4:214:ASP:OD2	1:U4:214:ASP:N	2.32	0.42
1:T4:348:ARG:NH1	1:T4:367:ARG:HG3	2.33	0.42
1:V4:262:VAL:HG12	1:V4:270:ARG:HD3	2.01	0.42
1:V4:296:LEU:HD23	1:V4:296:LEU:H	1.84	0.42
1:A4:273:ALA:O	1:A4:313:PRO:HD2	2.18	0.42
1:D4:281:THR:HG23	1:D4:323:ILE:HD11	2.01	0.42
1:C4:136:VAL:CG2	1:C4:165:ILE:HB	2.49	0.42
4:G:92:GLN:HG3	4:G:100:ILE:HG23	2.00	0.42
1:N4:167:ILE:HG23	1:N4:370:GLY:HA2	2.02	0.42
1:O4:172:LEU:HD21	1:O4:202:PHE:HA	2.02	0.42
1:U4:138:VAL:HG21	1:U4:235:TRP:HZ2	1.84	0.42
1:K4:289:LYS:HD2	2:E2:7:HIS:CE1	2.54	0.42
1:J4:309:LEU:HD23	1:J4:310:MET:HB2	2.01	0.42
1:L4:133:SER:HB2	1:H4:104:PRO:HB3	2.02	0.42
1:D4:228:VAL:O	1:D4:239:GLY:HA2	2.18	0.42
1:E4:119:SER:C	1:E4:121:ARG:H	2.27	0.42
2:A1:2:ASP:OD1	2:A1:2:ASP:N	2.49	0.42
5:D:92:VAL:HG22	5:D:131:ARG:C	2.45	0.42
1:C5:350:LEU:HB3	1:C5:363:TYR:HD2	1.84	0.42
1:Y4:99:GLY:O	1:Y4:102:VAL:HG22	2.19	0.42
1:A5:183:LEU:HD21	1:A5:362:PHE:CZ	2.55	0.42
1:B5:179:SER:H	5:C:121:ALA:HB1	1.82	0.42
1:Q4:121:ARG:NH1	1:Q4:343:GLU:OE2	2.44	0.42
1:Q4:183:LEU:HD13	1:Q4:191:GLU:OE2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P4:352:ASP:OD2	1:P4:355:SER:OG	2.30	0.42
1:D4:289:LYS:NZ	1:C4:253:ASN:HD21	2.17	0.42
1:F4:262:VAL:HG21	1:F4:310:MET:HG3	2.02	0.42
1:G4:276:VAL:HG12	1:G4:320:MET:SD	2.60	0.42
5:C:195:GLY:HA2	6:A:253:GLN:HE22	1.83	0.42
5:D:101:VAL:CG2	5:D:103:ALA:HB2	2.48	0.42
1:X4:215:GLY:HA2	1:X4:220:THR:HG22	2.01	0.42
1:Z4:185:ASP:HB3	1:V4:132:THR:HB	2.02	0.42
1:A5:349:VAL:HA	1:A5:363:TYR:O	2.20	0.42
1:R4:194:LEU:HD22	1:Q4:143:MET:HE1	2.01	0.42
1:W4:167:ILE:HD12	1:W4:370:GLY:HA2	1.99	0.42
1:W4:270:ARG:NH1	1:S4:279:SER:OG	2.53	0.42
1:L4:209:ALA:HA	1:L4:213:GLY:HA3	2.00	0.42
1:H4:296:LEU:H	1:H4:296:LEU:HD23	1.83	0.42
1:B4:286:ARG:HH21	1:B4:286:ARG:HG3	1.84	0.42
1:C4:286:ARG:HH12	1:C4:304:GLY:H	1.66	0.42
5:D:108:VAL:HG23	5:D:108:VAL:O	2.18	0.42
1:U4:159:THR:CG2	1:U4:160:PRO:HD2	2.49	0.42
1:U4:315:LEU:CD2	1:U4:317:ALA:HB2	2.49	0.42
1:T4:254:ALA:C	1:T4:256:ASP:H	2.28	0.42
1:J4:348:ARG:HH11	1:J4:367:ARG:HG3	1.84	0.42
1:D4:318:GLU:O	1:D4:318:GLU:HG3	2.19	0.42
1:G4:90:LEU:HB3	1:G4:91:ASN:H	1.65	0.42
1:G4:329:ALA:HB3	1:G4:383:PHE:CE2	2.54	0.42
4:J:87:GLU:HG3	4:J:89:PRO:HD3	2.02	0.42
7:F:72:ILE:HD13	7:F:124:ARG:HB2	2.01	0.42
1:B5:202:PHE:CE2	1:B5:347:LEU:HD11	2.55	0.42
1:N4:156:GLU:HG2	1:O4:177:LYS:HE3	2.00	0.42
1:N4:177:LYS:HG2	1:N4:361:LEU:HD13	2.00	0.42
1:N4:262:VAL:HG12	1:N4:270:ARG:HD3	2.01	0.42
1:M4:119:SER:C	1:M4:121:ARG:H	2.26	0.42
1:O4:154:LEU:HG	1:O4:155:SER:O	2.19	0.42
1:O4:201:LYS:O	1:O4:205:ALA:N	2.47	0.42
1:P4:227:LYS:HD3	1:P4:227:LYS:H	1.85	0.42
1:U4:288:MET:CE	1:U4:297:TRP:HE1	2.32	0.42
1:S4:330:ILE:HD12	1:S4:381:LEU:HD23	2.02	0.42
1:K4:256:ASP:HA	1:K4:259:VAL:HG12	2.01	0.42
1:K4:265:LEU:HD12	1:K4:379:LYS:HG2	2.02	0.42
1:J4:175:MET:HA	1:J4:362:PHE:O	2.20	0.42
1:H4:186:SER:O	1:H4:188:PHE:N	2.52	0.42
1:A4:176:PRO:HD2	1:A4:362:PHE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A4:367:ARG:NH1	1:C4:181:ARG:HD3	2.35	0.42
1:E4:138:VAL:HG12	1:F4:111:ARG:HG3	2.01	0.42
1:F4:351:ARG:HH21	1:F4:360:VAL:HG21	1.83	0.42
1:G4:297:TRP:CE2	1:G4:309:LEU:HD13	2.54	0.42
1:B4:272:ASN:OD1	1:B4:272:ASN:N	2.52	0.42
4:I:87:GLU:HG3	4:I:89:PRO:HD3	2.02	0.42
1:Y4:299:ASP:OD1	1:Y4:300:SER:N	2.52	0.42
1:Z4:265:LEU:HB3	1:Z4:270:ARG:HG3	2.02	0.42
1:Q4:175:MET:HE3	1:Q4:361:LEU:HD11	2.02	0.42
1:O4:183:LEU:HD12	1:O4:190:ILE:HB	2.00	0.42
1:P4:252:VAL:HG13	1:P4:253:ASN:N	2.35	0.42
1:P4:324:ALA:HB3	1:P4:327:ALA:HB2	2.01	0.42
1:W4:92:SER:O	1:W4:92:SER:OG	2.28	0.42
1:U4:322:ASP:OD1	1:U4:322:ASP:N	2.45	0.42
1:S4:248:ASP:OD2	1:S4:248:ASP:N	2.44	0.42
1:K4:214:ASP:OD2	1:K4:214:ASP:N	2.46	0.42
1:I4:149:SER:HB3	1:I4:152:ALA:HB2	2.01	0.42
1:E4:147:TRP:CH2	1:F4:209:ALA:HB2	2.54	0.42
1:E4:322:ASP:OD1	1:E4:322:ASP:N	2.45	0.42
1:C4:297:TRP:NE1	1:C4:306:PRO:HG2	2.35	0.42
6:B:40:VAL:O	6:B:189:TYR:OH	2.32	0.42
1:X4:334:ASP:OD2	1:X4:337:ASN:ND2	2.53	0.42
1:A5:103:ASP:OD2	1:A5:103:ASP:N	2.49	0.42
1:A5:351:ARG:NH2	6:A:38:ARG:HD3	2.35	0.42
1:B5:277:MET:O	1:B5:317:ALA:N	2.52	0.42
1:N4:230:ASN:ND2	1:N4:264:ALA:HB1	2.34	0.42
1:R4:269:TYR:CE1	1:M4:114:LEU:HB2	2.55	0.42
1:P4:163:ASP:OD1	1:P4:164:ARG:N	2.53	0.42
1:W4:288:MET:CE	1:W4:297:TRP:HE1	2.33	0.42
1:J4:285:VAL:HG11	1:J4:309:LEU:HD11	2.01	0.42
1:V4:122:GLN:HG2	1:V4:123:ILE:HG23	2.02	0.42
1:I4:252:VAL:CG2	2:D2:3:VAL:HG21	2.49	0.42
1:G4:220:THR:CB	1:G4:371:ASP:OD2	2.65	0.42
1:G4:227:LYS:HE3	1:G4:328:TYR:CE2	2.55	0.42
4:H:87:GLU:HG3	4:H:89:PRO:HD3	2.02	0.42
6:A:251:HIS:O	6:A:260:ARG:NH1	2.52	0.42
1:C5:310:MET:HE2	1:C5:310:MET:HB2	1.73	0.42
1:X4:163:ASP:OD1	1:X4:164:ARG:N	2.52	0.42
1:Y4:154:LEU:HD11	1:Z4:363:TYR:HE1	1.85	0.42
1:Z4:95:ALA:HA	1:Z4:99:GLY:HA3	2.01	0.42
1:Z4:133:SER:HB2	1:A5:104:PRO:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z4:352:ASP:C	1:Z4:354:PHE:H	2.28	0.42
1:A5:92:SER:C	1:A5:94:VAL:H	2.27	0.42
1:A5:272:ASN:OD1	1:A5:272:ASN:N	2.52	0.42
1:N4:177:LYS:HD2	1:M4:156:GLU:HG2	2.00	0.42
1:N4:182:LEU:HD21	1:F4:89:ALA:N	2.35	0.42
1:R4:173:ALA:H	1:Q4:146:GLY:HA3	1.85	0.42
1:U4:172:LEU:HD12	1:T4:147:TRP:H	1.85	0.42
1:T4:324:ALA:HB3	1:T4:327:ALA:HB2	2.01	0.42
1:V4:328:TYR:CE1	1:V4:382:LYS:HB2	2.54	0.42
1:G4:230:ASN:ND2	1:G4:379:LYS:HD2	2.35	0.42
1:B4:339:TYR:OH	1:B4:370:GLY:O	2.30	0.42
2:D2:67:ARG:NH2	2:E2:4:PHE:HB2	2.35	0.42
6:B:169:MET:HE1	6:B:176:ILE:N	2.34	0.42
1:X4:307:ALA:O	1:X4:308:ARG:HD2	2.20	0.42
1:N4:185:ASP:O	1:F4:102:VAL:HG12	2.20	0.42
1:N4:277:MET:HE3	1:N4:277:MET:HB2	1.89	0.42
1:R4:102:VAL:HB	1:Q4:132:THR:CG2	2.49	0.42
1:M4:147:TRP:H	1:M4:147:TRP:HE3	1.67	0.42
1:O4:365:SER:O	1:O4:365:SER:OG	2.33	0.42
1:P4:177:LYS:HE2	1:P4:359:HIS:CD2	2.55	0.42
1:U4:126:VAL:HG13	1:U4:343:GLU:HG2	2.02	0.42
1:K4:114:LEU:HG	1:J4:268:GLU:HG2	2.01	0.42
1:D4:227:LYS:HB3	1:D4:240:TYR:HD1	1.84	0.42
1:F4:119:SER:C	1:F4:121:ARG:H	2.27	0.42
1:F4:141:THR:HG22	1:F4:142:ASP:H	1.84	0.42
6:B:159:THR:HG22	6:B:164:LYS:HG2	2.02	0.42
1:X4:233:TRP:CH2	1:X4:376:ALA:HB2	2.54	0.41
1:Y4:149:SER:OG	1:Y4:152:ALA:HB2	2.20	0.41
1:B5:277:MET:HG2	1:B5:330:ILE:HG12	2.01	0.41
1:N4:143:MET:HG2	1:N4:160:PRO:HD3	2.01	0.41
1:R4:138:VAL:HA	1:M4:111:ARG:O	2.20	0.41
1:R4:286:ARG:NH1	1:R4:305:GLU:HA	2.33	0.41
1:Q4:94:VAL:HB	1:Q4:97:GLU:OE2	2.20	0.41
1:W4:172:LEU:HD11	1:V4:145:SER:HB3	2.00	0.41
1:W4:268:GLU:HB2	1:S4:116:SER:HA	2.02	0.41
1:T4:255:SER:O	1:T4:259:VAL:HG13	2.20	0.41
1:K4:280:LYS:HE3	1:K4:322:ASP:OD2	2.20	0.41
1:V4:186:SER:O	1:V4:186:SER:OG	2.28	0.41
1:H4:120:LEU:O	1:H4:120:LEU:HD23	2.21	0.41
1:H4:167:ILE:HD13	1:H4:371:ASP:OD1	2.20	0.41
1:D4:136:VAL:CG2	1:D4:165:ILE:HB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G4:357:LYS:HB2	1:G4:358:PRO:HD3	2.00	0.41
6:B:139:ARG:HD3	6:B:142:ARG:HH21	1.85	0.41
1:C5:352:ASP:OD1	1:C5:352:ASP:N	2.46	0.41
1:X4:135:ASP:OD2	1:X4:166:THR:HG22	2.20	0.41
1:X4:256:ASP:OD2	1:X4:257:ALA:N	2.53	0.41
1:N4:119:SER:C	1:N4:121:ARG:H	2.28	0.41
1:M4:352:ASP:OD1	1:M4:352:ASP:N	2.52	0.41
1:T4:191:GLU:OE2	1:T4:351:ARG:NE	2.53	0.41
1:J4:216:VAL:O	1:J4:216:VAL:HG23	2.20	0.41
1:V4:265:LEU:HD13	1:V4:332:PHE:CD2	2.55	0.41
1:D4:286:ARG:NH1	1:D4:305:GLU:HA	2.33	0.41
1:C4:277:MET:HG2	1:C4:330:ILE:HG12	2.03	0.41
5:C:72:TRP:HZ2	5:C:197:PRO:HB2	1.85	0.41
1:R4:348:ARG:NH1	1:R4:367:ARG:HD2	2.36	0.41
1:Q4:299:ASP:OD1	1:Q4:299:ASP:N	2.52	0.41
1:O4:350:LEU:HD11	1:S4:354:PHE:HE1	1.86	0.41
1:U4:167:ILE:HD13	1:U4:371:ASP:OD1	2.21	0.41
1:L4:139:ASP:H	1:H4:112:GLY:HA2	1.84	0.41
1:I4:357:LYS:HB2	1:I4:357:LYS:HE2	1.79	0.41
1:A4:143:MET:CG	1:A4:160:PRO:HD3	2.50	0.41
1:E4:177:LYS:HD3	1:E4:361:LEU:HD11	2.01	0.41
1:E4:280:LYS:HE2	1:E4:280:LYS:HB2	1.83	0.41
1:B4:92:SER:C	1:B4:94:VAL:N	2.78	0.41
1:B4:168:PRO:HB2	1:B4:170:HIS:CE1	2.55	0.41
2:B3:2:ASP:HB3	2:A3:32:ARG:HG2	2.02	0.41
6:B:126:CYS:HB3	6:B:132:PRO:HB3	2.02	0.41
1:C5:119:SER:C	1:C5:121:ARG:H	2.28	0.41
1:C5:136:VAL:CG1	1:X4:111:ARG:HH21	2.32	0.41
1:Z4:252:VAL:HG23	1:Z4:253:ASN:N	2.36	0.41
1:A5:116:SER:HB3	1:A5:318:GLU:CD	2.45	0.41
1:A5:129:VAL:HG21	1:A5:134:PHE:HD1	1.86	0.41
1:A5:191:GLU:OE1	6:A:39:PRO:CG	2.67	0.41
1:B5:347:LEU:HD12	1:B5:349:VAL:HG12	2.01	0.41
1:R4:337:ASN:N	1:R4:337:ASN:ND2	2.68	0.41
1:T4:185:ASP:OD1	1:J4:367:ARG:NH2	2.54	0.41
1:T4:228:VAL:O	1:T4:239:GLY:HA2	2.20	0.41
1:J4:114:LEU:HG	1:I4:268:GLU:CG	2.49	0.41
1:A4:227:LYS:HE2	1:A4:227:LYS:HB2	1.87	0.41
1:C4:167:ILE:HD12	1:C4:370:GLY:HA2	2.02	0.41
1:C4:277:MET:HE3	1:C4:277:MET:HB2	1.83	0.41
2:D2:11:LEU:HD23	2:E2:14:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:115:ARG:HG2	5:C:117:GLU:HG3	2.02	0.41
6:B:37:GLY:H	6:B:148:GLY:HA2	1.85	0.41
6:B:139:ARG:HD3	6:B:142:ARG:NH2	2.35	0.41
6:B:299:VAL:HG12	6:B:322:PHE:CE1	2.55	0.41
1:X4:138:VAL:HA	1:Y4:111:ARG:O	2.20	0.41
1:Y4:129:VAL:HG11	1:Y4:342:ALA:HB1	2.01	0.41
1:Z4:89:ALA:HA	1:V4:159:THR:HG21	2.03	0.41
1:Z4:102:VAL:HG12	1:W4:185:ASP:O	2.20	0.41
1:Z4:251:ALA:O	1:Z4:253:ASN:N	2.54	0.41
1:N4:102:VAL:HG23	1:N4:103:ASP:H	1.85	0.41
1:N4:105:GLN:CD	1:M4:129:VAL:HG23	2.46	0.41
1:Q4:114:LEU:HB2	1:P4:269:TYR:CZ	2.56	0.41
1:U4:143:MET:HG3	1:U4:160:PRO:HD3	2.03	0.41
1:T4:252:VAL:HG11	2:D3:3:VAL:CG1	2.50	0.41
1:J4:346:ASP:N	1:J4:346:ASP:OD2	2.52	0.41
1:L4:138:VAL:HG23	1:L4:163:ASP:HB3	2.02	0.41
1:H4:135:ASP:OD1	1:H4:166:THR:HG22	2.20	0.41
1:I4:289:LYS:HD2	2:C2:7:HIS:CE1	2.56	0.41
1:F4:167:ILE:HD12	1:F4:370:GLY:HA2	2.02	0.41
1:G4:119:SER:O	1:G4:119:SER:OG	2.36	0.41
1:A5:226:THR:O	1:A5:237:SER:OG	2.33	0.41
1:B5:320:MET:HE3	1:B5:320:MET:HB3	1.91	0.41
1:R4:270:ARG:NH1	1:M4:279:SER:OG	2.53	0.41
1:Q4:154:LEU:HD23	1:Q4:154:LEU:H	1.84	0.41
1:O4:107:SER:O	1:O4:109:THR:N	2.54	0.41
1:O4:135:ASP:HB2	1:P4:106:THR:O	2.21	0.41
1:U4:141:THR:HG23	1:U4:160:PRO:HA	2.02	0.41
1:S4:227:LYS:HE2	1:S4:227:LYS:HB2	1.91	0.41
1:J4:134:PHE:HB3	1:J4:167:ILE:HB	2.03	0.41
1:H4:244:GLY:O	1:H4:385:ALA:HA	2.20	0.41
1:E4:265:LEU:HD13	1:E4:332:PHE:CE2	2.56	0.41
5:C:5:GLU:HA	5:C:63:PHE:HA	2.03	0.41
8:E:32:LYS:HG3	8:E:33:GLY:H	1.86	0.41
1:X4:263:TYR:OH	1:Y4:305:GLU:HG2	2.21	0.41
1:B5:136:VAL:CG2	1:B5:165:ILE:HB	2.50	0.41
1:N4:171:GLU:HA	1:N4:367:ARG:HA	2.03	0.41
1:R4:262:VAL:HG21	1:R4:310:MET:HG2	2.03	0.41
1:M4:286:ARG:NH1	1:M4:305:GLU:H	2.19	0.41
1:O4:91:ASN:HD22	1:O4:91:ASN:C	2.26	0.41
1:O4:228:VAL:O	1:O4:239:GLY:HA2	2.21	0.41
1:P4:298:ALA:HB2	1:P4:306:PRO:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T4:220:THR:OG1	1:T4:371:ASP:HB3	2.20	0.41
1:T4:265:LEU:HD13	1:T4:332:PHE:HD2	1.85	0.41
1:T4:294:ARG:NH2	1:S4:292:ASP:OD2	2.54	0.41
1:S4:357:LYS:HB2	1:S4:357:LYS:HE2	1.72	0.41
1:J4:324:ALA:HB3	1:J4:327:ALA:HB2	2.02	0.41
1:L4:352:ASP:OD2	1:L4:355:SER:OG	2.22	0.41
2:C2:14:PRO:HD2	2:B2:11:LEU:HD23	2.03	0.41
2:E3:11:LEU:HD23	2:A3:14:PRO:HD2	2.02	0.41
2:E3:66:VAL:HA	2:A3:15:ALA:HB3	2.03	0.41
2:E3:67:ARG:NH2	2:A3:4:PHE:HB2	2.35	0.41
1:C5:225:LYS:HE2	1:C5:372:VAL:HG22	2.03	0.41
1:C5:254:ALA:C	1:C5:256:ASP:H	2.27	0.41
1:X4:227:LYS:HD3	1:X4:227:LYS:H	1.85	0.41
1:Y4:276:VAL:HG12	1:Y4:320:MET:SD	2.60	0.41
1:Z4:330:ILE:HD12	1:Z4:381:LEU:HD23	2.02	0.41
1:A5:357:LYS:HD3	1:A5:357:LYS:HA	1.94	0.41
1:N4:354:PHE:CE1	1:E4:350:LEU:HD11	2.56	0.41
1:R4:168:PRO:HB2	1:R4:170:HIS:CE1	2.56	0.41
1:Q4:171:GLU:HA	1:Q4:367:ARG:HA	2.03	0.41
1:O4:225:LYS:HE2	1:O4:372:VAL:HG22	2.03	0.41
1:W4:228:VAL:O	1:W4:239:GLY:HA2	2.19	0.41
1:W4:276:VAL:HG12	1:W4:320:MET:SD	2.59	0.41
1:U4:136:VAL:CG2	1:U4:165:ILE:HB	2.50	0.41
1:T4:123:ILE:HD13	1:T4:315:LEU:HD13	2.03	0.41
1:S4:288:MET:HE2	1:S4:297:TRP:HE1	1.85	0.41
1:J4:91:ASN:HB2	1:H4:150:GLU:HG2	2.01	0.41
1:H4:119:SER:C	1:H4:121:ARG:H	2.28	0.41
1:H4:265:LEU:HD13	1:H4:332:PHE:CE2	2.56	0.41
1:H4:354:PHE:HD1	1:D4:352:ASP:HB3	1.84	0.41
1:I4:92:SER:O	1:I4:92:SER:OG	2.26	0.41
1:E4:333:GLY:HA3	1:E4:378:ILE:HA	2.03	0.41
1:F4:92:SER:OG	1:F4:93:ALA:N	2.53	0.41
1:F4:324:ALA:HB3	1:F4:327:ALA:HB2	2.03	0.41
1:B4:149:SER:HB2	1:B4:152:ALA:HB2	2.02	0.41
1:B4:223:LEU:O	1:B4:227:LYS:NZ	2.28	0.41
6:A:262:MET:HE1	6:A:270:TRP:CE3	2.55	0.41
1:C5:114:LEU:HB3	1:B5:268:GLU:HG2	2.03	0.41
1:B5:192:THR:O	1:B5:195:ALA:N	2.51	0.41
1:M4:177:LYS:HG3	1:M4:361:LEU:HD12	2.02	0.41
1:Q4:135:ASP:OD1	1:Q4:166:THR:HG22	2.21	0.41
1:Q4:174:ALA:HB2	1:P4:145:SER:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q4:310:MET:HE3	1:Q4:310:MET:HB2	1.97	0.41
1:O4:127:VAL:O	1:O4:129:VAL:HG23	2.21	0.41
1:P4:147:TRP:O	1:P4:148:ALA:HB3	2.20	0.41
1:P4:181:ARG:HD3	1:W4:367:ARG:NH1	2.36	0.41
1:W4:119:SER:C	1:W4:121:ARG:H	2.29	0.41
1:W4:162:ILE:HD11	1:S4:193:TRP:CH2	2.56	0.41
1:U4:269:TYR:CE1	1:V4:114:LEU:HB2	2.56	0.41
1:K4:121:ARG:NH1	1:K4:343:GLU:OE2	2.53	0.41
1:V4:277:MET:HG2	1:V4:330:ILE:HG12	2.01	0.41
1:L4:162:ILE:HD13	1:E4:101:LEU:CD2	2.49	0.41
1:E4:272:ASN:OD1	1:E4:272:ASN:N	2.53	0.41
1:G4:255:SER:HB2	1:B4:295:PHE:HZ	1.86	0.41
1:B4:131:ALA:O	1:B4:169:LEU:HD23	2.21	0.41
1:B4:142:ASP:HB3	1:C4:115:ARG:NH2	2.35	0.41
1:C4:107:SER:OG	1:C4:108:GLU:N	2.54	0.41
2:E3:4:PHE:HB3	2:D3:11:LEU:HD11	2.03	0.41
2:E3:52:ILE:H	2:E3:52:ILE:HG13	1.72	0.41
6:B:253:GLN:NE2	5:D:195:GLY:HA2	2.32	0.41
7:F:117:VAL:CG1	7:F:124:ARG:HE	2.33	0.41
1:C5:95:ALA:C	1:C5:97:GLU:H	2.29	0.41
1:X4:214:ASP:OD1	1:X4:218:LYS:NZ	2.41	0.41
1:Y4:181:ARG:NH1	1:P4:171:GLU:HG2	2.36	0.41
1:Y4:188:PHE:HD2	1:Q4:101:LEU:HB2	1.86	0.41
1:Z4:138:VAL:O	1:Z4:138:VAL:HG23	2.20	0.41
1:Z4:216:VAL:O	1:Z4:216:VAL:HG23	2.21	0.41
1:Z4:227:LYS:HE3	1:Z4:328:TYR:CE2	2.56	0.41
1:N4:298:ALA:HB2	1:N4:306:PRO:HD3	2.03	0.41
1:R4:157:THR:HG23	1:M4:175:MET:H	1.86	0.41
1:M4:176:PRO:HG3	1:M4:198:ILE:HD11	2.03	0.41
1:P4:101:LEU:HD11	1:S4:110:ILE:HD12	2.02	0.41
1:W4:135:ASP:HA	1:W4:165:ILE:O	2.21	0.41
1:U4:163:ASP:OD1	1:U4:164:ARG:N	2.54	0.41
1:K4:129:VAL:HG23	1:L4:105:GLN:NE2	2.36	0.41
1:K4:357:LYS:HD3	1:K4:357:LYS:HA	1.80	0.41
1:L4:265:LEU:HD13	1:L4:332:PHE:CD2	2.55	0.41
1:A4:120:LEU:HD23	1:A4:210:PHE:HB3	2.02	0.41
1:D4:357:LYS:HD3	1:D4:357:LYS:HA	1.91	0.41
1:E4:125:SER:HB2	1:E4:336:GLY:O	2.21	0.41
1:G4:136:VAL:CG2	1:G4:165:ILE:HB	2.51	0.41
1:G4:309:LEU:HD12	1:G4:309:LEU:HA	1.87	0.41
1:C4:226:THR:O	1:C4:237:SER:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D2:66:VAL:HA	2:E2:15:ALA:HB3	2.03	0.41
2:E3:2:ASP:HB3	2:D3:32:ARG:HG2	2.03	0.41
1:X4:167:ILE:HG23	1:X4:370:GLY:HA2	2.01	0.40
1:Z4:255:SER:HB3	1:A5:295:PHE:HZ	1.87	0.40
1:M4:181:ARG:C	1:M4:183:LEU:H	2.29	0.40
1:M4:220:THR:OG1	1:M4:371:ASP:HB2	2.21	0.40
1:Q4:175:MET:HA	1:Q4:362:PHE:O	2.22	0.40
1:O4:130:GLU:OE2	1:O4:344:ARG:NH2	2.54	0.40
1:W4:268:GLU:CG	1:S4:114:LEU:HG	2.51	0.40
1:T4:177:LYS:O	1:K4:90:LEU:HD12	2.21	0.40
1:T4:308:ARG:NH2	1:T4:311:GLY:O	2.54	0.40
1:J4:305:GLU:N	1:J4:305:GLU:OE1	2.54	0.40
1:J4:357:LYS:HE2	1:J4:357:LYS:HB2	1.92	0.40
1:L4:329:ALA:HB3	1:L4:383:PHE:CE2	2.56	0.40
1:H4:291:ALA:O	2:A2:10:SER:HB2	2.21	0.40
1:H4:357:LYS:HA	1:H4:357:LYS:HD3	1.85	0.40
1:I4:288:MET:CE	1:I4:297:TRP:HE1	2.35	0.40
1:G4:227:LYS:HG2	1:G4:380:LEU:HD22	2.03	0.40
1:G4:294:ARG:HE	1:G4:294:ARG:HB3	1.67	0.40
2:D3:14:PRO:HD2	2:C3:11:LEU:HD23	2.03	0.40
5:C:93:ASP:OD1	5:C:93:ASP:N	2.44	0.40
8:E:15:ALA:HB2	8:E:29:TRP:CD2	2.56	0.40
1:Y4:272:ASN:OD1	1:Y4:272:ASN:N	2.52	0.40
1:M4:142:ASP:OD1	1:M4:142:ASP:N	2.43	0.40
1:M4:252:VAL:HG13	1:M4:253:ASN:N	2.36	0.40
1:M4:258:VAL:HG12	1:M4:310:MET:HE3	2.02	0.40
1:O4:193:TRP:HE1	1:O4:197:ARG:HE	1.68	0.40
1:O4:220:THR:OG1	1:O4:371:ASP:HB3	2.21	0.40
1:T4:261:LEU:HD22	1:T4:381:LEU:HB2	2.03	0.40
1:S4:214:ASP:OD1	1:S4:214:ASP:N	2.48	0.40
1:L4:179:SER:O	1:L4:183:LEU:HD13	2.21	0.40
1:L4:358:PRO:HG2	1:L4:359:HIS:CD2	2.56	0.40
1:C4:177:LYS:HG3	1:C4:359:HIS:HB3	2.04	0.40
4:J:62:ALA:H	4:J:128:SER:HB2	1.86	0.40
6:A:346:LEU:HD23	6:A:346:LEU:N	2.36	0.40
8:E:10:LEU:HD12	8:E:37:ALA:HB3	2.04	0.40
1:X4:123:ILE:HD13	1:X4:315:LEU:HD22	2.03	0.40
1:Y4:92:SER:OG	1:Y4:93:ALA:N	2.53	0.40
1:B5:202:PHE:HE2	1:B5:347:LEU:HD11	1.86	0.40
1:N4:299:ASP:OD1	1:N4:300:SER:N	2.55	0.40
1:M4:91:ASN:HB3	1:Q4:151:THR:CG2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P4:181:ARG:HD2	1:V4:150:GLU:OE1	2.22	0.40
1:W4:123:ILE:HD13	1:W4:315:LEU:HD13	2.03	0.40
1:W4:133:SER:OG	1:W4:167:ILE:O	2.30	0.40
1:W4:141:THR:HG22	1:W4:142:ASP:N	2.31	0.40
1:J4:228:VAL:O	1:J4:239:GLY:HA2	2.21	0.40
1:L4:214:ASP:OD2	1:L4:215:GLY:N	2.54	0.40
1:L4:277:MET:O	1:L4:317:ALA:N	2.54	0.40
1:I4:254:ALA:O	1:I4:255:SER:OG	2.31	0.40
1:D4:119:SER:C	1:D4:121:ARG:N	2.80	0.40
1:D4:310:MET:HE1	1:E4:301:LEU:HD22	2.03	0.40
1:G4:272:ASN:OD1	1:G4:272:ASN:N	2.51	0.40
1:B4:140:LYS:HG3	1:B4:161:GLN:HG3	2.04	0.40
1:B4:227:LYS:HE2	1:B4:227:LYS:HB2	1.92	0.40
6:A:125:VAL:HG22	6:A:134:GLU:HB2	2.03	0.40
6:A:359:VAL:HA	6:A:360:PRO:HD3	1.84	0.40
4:G:4:GLN:HB3	4:G:96:PRO:CB	2.51	0.40
1:N4:119:SER:O	1:N4:119:SER:OG	2.38	0.40
1:Q4:129:VAL:HG11	1:Q4:342:ALA:HB1	2.03	0.40
1:W4:223:LEU:O	1:W4:227:LYS:NZ	2.30	0.40
1:W4:382:LYS:HE2	1:W4:384:ALA:HB2	2.03	0.40
1:U4:227:LYS:HE3	1:U4:328:TYR:CE2	2.56	0.40
1:K4:131:ALA:O	1:K4:169:LEU:HD23	2.22	0.40
1:E4:261:LEU:HD22	1:E4:381:LEU:HB2	2.03	0.40
1:F4:126:VAL:HG12	1:F4:341:ILE:HB	2.03	0.40
1:B4:191:GLU:HG2	1:B4:362:PHE:CZ	2.57	0.40
1:C4:90:LEU:HB3	1:C4:91:ASN:H	1.78	0.40
2:D2:2:ASP:HB3	2:C2:32:ARG:HG2	2.03	0.40
4:H:54:LEU:HD21	4:I:5:ASN:HA	2.04	0.40
5:D:92:VAL:CG2	5:D:131:ARG:HB2	2.51	0.40
1:C5:135:ASP:HA	1:C5:165:ILE:O	2.21	0.40
1:Y4:357:LYS:NZ	1:P4:352:ASP:OD2	2.50	0.40
1:Z4:220:THR:HG23	1:Z4:224:THR:CG2	2.52	0.40
1:Z4:249:PHE:HB3	1:Z4:254:ALA:HB1	2.02	0.40
1:N4:310:MET:HE3	1:N4:310:MET:HB2	1.93	0.40
1:R4:227:LYS:HE2	1:R4:227:LYS:HB2	1.88	0.40
1:W4:102:VAL:HB	1:V4:132:THR:CG2	2.46	0.40
1:U4:138:VAL:HA	1:V4:111:ARG:O	2.21	0.40
1:T4:130:GLU:OE2	1:T4:344:ARG:NH2	2.55	0.40
1:T4:136:VAL:HG13	1:T4:165:ILE:HB	2.04	0.40
1:L4:119:SER:C	1:L4:121:ARG:H	2.30	0.40
1:I4:189:ASP:HB3	1:I4:192:THR:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D4:213:GLY:O	1:D4:220:THR:HA	2.21	0.40
1:D4:233:TRP:NE1	1:D4:237:SER:O	2.54	0.40
1:E4:294:ARG:HD2	1:E4:294:ARG:HA	1.84	0.40
1:B4:227:LYS:HE3	1:B4:328:TYR:CE2	2.57	0.40
1:B4:265:LEU:HD12	1:B4:332:PHE:CE2	2.57	0.40
1:C4:297:TRP:CZ2	1:C4:309:LEU:HB2	2.56	0.40
2:A2:2:ASP:HB3	2:E2:32:ARG:HG2	2.02	0.40
2:B2:19:TYR:OH	2:B2:31:ARG:O	2.30	0.40
6:A:391:PRO:HA	6:A:392:PRO:HD3	1.94	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	A4	287/385 (74%)	258 (90%)	28 (10%)	1 (0%)	36	72
1	A5	290/385 (75%)	259 (89%)	29 (10%)	2 (1%)	18	56
1	B4	295/385 (77%)	260 (88%)	34 (12%)	1 (0%)	36	72
1	B5	266/385 (69%)	227 (85%)	38 (14%)	1 (0%)	30	67
1	C4	295/385 (77%)	262 (89%)	33 (11%)	0	100	100
1	C5	295/385 (77%)	265 (90%)	30 (10%)	0	100	100
1	D4	295/385 (77%)	264 (90%)	30 (10%)	1 (0%)	36	72
1	E4	295/385 (77%)	267 (90%)	28 (10%)	0	100	100
1	F4	295/385 (77%)	265 (90%)	30 (10%)	0	100	100
1	G4	295/385 (77%)	259 (88%)	35 (12%)	1 (0%)	36	72
1	H4	287/385 (74%)	254 (88%)	32 (11%)	1 (0%)	36	72
1	I4	287/385 (74%)	261 (91%)	25 (9%)	1 (0%)	36	72
1	J4	287/385 (74%)	249 (87%)	37 (13%)	1 (0%)	36	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K4	287/385 (74%)	257 (90%)	29 (10%)	1 (0%)	36	72
1	L4	287/385 (74%)	256 (89%)	30 (10%)	1 (0%)	36	72
1	M4	295/385 (77%)	257 (87%)	38 (13%)	0	100	100
1	N4	295/385 (77%)	259 (88%)	35 (12%)	1 (0%)	36	72
1	O4	295/385 (77%)	256 (87%)	38 (13%)	1 (0%)	36	72
1	P4	295/385 (77%)	249 (84%)	45 (15%)	1 (0%)	36	72
1	Q4	295/385 (77%)	259 (88%)	35 (12%)	1 (0%)	36	72
1	R4	295/385 (77%)	254 (86%)	40 (14%)	1 (0%)	36	72
1	S4	287/385 (74%)	253 (88%)	33 (12%)	1 (0%)	36	72
1	T4	287/385 (74%)	261 (91%)	26 (9%)	0	100	100
1	U4	287/385 (74%)	257 (90%)	29 (10%)	1 (0%)	36	72
1	V4	287/385 (74%)	256 (89%)	30 (10%)	1 (0%)	36	72
1	W4	287/385 (74%)	253 (88%)	33 (12%)	1 (0%)	36	72
1	X4	295/385 (77%)	265 (90%)	30 (10%)	0	100	100
1	Y4	295/385 (77%)	265 (90%)	30 (10%)	0	100	100
1	Z4	295/385 (77%)	257 (87%)	38 (13%)	0	100	100
2	A1	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	A2	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	A3	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	B2	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	B3	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	C2	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	C3	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	D2	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	D3	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	E2	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
2	E3	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
3	F2	8/325 (2%)	5 (62%)	3 (38%)	0	100	100
3	F3	8/325 (2%)	5 (62%)	3 (38%)	0	100	100
4	G	132/137 (96%)	116 (88%)	16 (12%)	0	100	100
4	H	132/137 (96%)	118 (89%)	14 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	I	132/137 (96%)	118 (89%)	14 (11%)	0	100	100
4	J	132/137 (96%)	118 (89%)	14 (11%)	0	100	100
5	C	186/197 (94%)	158 (85%)	27 (14%)	1 (0%)	24	63
5	D	191/197 (97%)	161 (84%)	30 (16%)	0	100	100
6	A	368/396 (93%)	330 (90%)	37 (10%)	1 (0%)	36	72
6	B	362/396 (91%)	325 (90%)	37 (10%)	0	100	100
7	F	132/135 (98%)	115 (87%)	17 (13%)	0	100	100
8	E	108/112 (96%)	97 (90%)	11 (10%)	0	100	100
All	All	11226/14720 (76%)	9966 (89%)	1237 (11%)	23 (0%)	44	78

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P4	306	PRO
1	J4	187	ALA
1	V4	187	ALA
1	L4	187	ALA
1	A5	132	THR
1	Q4	179	SER
1	W4	187	ALA
1	U4	187	ALA
1	S4	187	ALA
1	K4	187	ALA
1	H4	187	ALA
1	I4	187	ALA
1	A4	187	ALA
1	G4	295	PHE
1	A5	93	ALA
1	B5	193	TRP
1	N4	92	SER
1	R4	108	GLU
1	O4	108	GLU
1	D4	91	ASN
5	C	98	GLU
1	B4	93	ALA
6	A	347	GLY

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	A4	215/284 (76%)	214 (100%)	1 (0%)	81	83
1	A5	215/284 (76%)	211 (98%)	4 (2%)	50	67
1	B4	218/284 (77%)	217 (100%)	1 (0%)	81	83
1	B5	197/284 (69%)	195 (99%)	2 (1%)	68	78
1	C4	218/284 (77%)	218 (100%)	0	100	100
1	C5	218/284 (77%)	215 (99%)	3 (1%)	59	72
1	D4	218/284 (77%)	218 (100%)	0	100	100
1	E4	218/284 (77%)	218 (100%)	0	100	100
1	F4	218/284 (77%)	216 (99%)	2 (1%)	70	79
1	G4	218/284 (77%)	216 (99%)	2 (1%)	70	79
1	H4	215/284 (76%)	215 (100%)	0	100	100
1	I4	215/284 (76%)	213 (99%)	2 (1%)	70	79
1	J4	215/284 (76%)	215 (100%)	0	100	100
1	K4	215/284 (76%)	214 (100%)	1 (0%)	81	83
1	L4	215/284 (76%)	214 (100%)	1 (0%)	81	83
1	M4	218/284 (77%)	215 (99%)	3 (1%)	59	72
1	N4	218/284 (77%)	216 (99%)	2 (1%)	70	79
1	O4	218/284 (77%)	216 (99%)	2 (1%)	70	79
1	P4	218/284 (77%)	217 (100%)	1 (0%)	81	83
1	Q4	218/284 (77%)	218 (100%)	0	100	100
1	R4	218/284 (77%)	216 (99%)	2 (1%)	70	79
1	S4	215/284 (76%)	215 (100%)	0	100	100
1	T4	215/284 (76%)	214 (100%)	1 (0%)	81	83
1	U4	215/284 (76%)	213 (99%)	2 (1%)	70	79
1	V4	215/284 (76%)	215 (100%)	0	100	100
1	W4	215/284 (76%)	213 (99%)	2 (1%)	70	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X4	218/284 (77%)	218 (100%)	0	100	100
1	Y4	218/284 (77%)	217 (100%)	1 (0%)	81	83
1	Z4	218/284 (77%)	217 (100%)	1 (0%)	81	83
2	A1	69/69 (100%)	69 (100%)	0	100	100
2	A2	69/69 (100%)	69 (100%)	0	100	100
2	A3	69/69 (100%)	69 (100%)	0	100	100
2	B2	69/69 (100%)	69 (100%)	0	100	100
2	B3	69/69 (100%)	69 (100%)	0	100	100
2	C2	69/69 (100%)	69 (100%)	0	100	100
2	C3	69/69 (100%)	69 (100%)	0	100	100
2	D2	69/69 (100%)	69 (100%)	0	100	100
2	D3	69/69 (100%)	69 (100%)	0	100	100
2	E2	69/69 (100%)	69 (100%)	0	100	100
2	E3	69/69 (100%)	69 (100%)	0	100	100
3	F2	5/224 (2%)	5 (100%)	0	100	100
3	F3	5/224 (2%)	5 (100%)	0	100	100
4	G	101/103 (98%)	101 (100%)	0	100	100
4	H	101/103 (98%)	101 (100%)	0	100	100
4	I	101/103 (98%)	101 (100%)	0	100	100
4	J	101/103 (98%)	101 (100%)	0	100	100
5	C	138/141 (98%)	138 (100%)	0	100	100
5	D	140/141 (99%)	140 (100%)	0	100	100
6	A	283/302 (94%)	283 (100%)	0	100	100
6	B	279/302 (92%)	278 (100%)	1 (0%)	84	84
7	F	91/92 (99%)	88 (97%)	3 (3%)	33	55
8	E	83/85 (98%)	82 (99%)	1 (1%)	63	75
All	All	8452/10918 (77%)	8411 (100%)	41 (0%)	78	83

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C5	217	ASP
1	C5	220	THR

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Mol	Chain	Res	Type
1	C5	323	ILE
1	Y4	220	THR
1	Z4	252	VAL
1	A5	117	THR
1	A5	122	GLN
1	A5	129	VAL
1	A5	323	ILE
1	B5	347	LEU
1	B5	348	ARG
1	N4	101	LEU
1	N4	220	THR
1	R4	101	LEU
1	R4	337	ASN
1	M4	150	GLU
1	M4	159	THR
1	M4	305	GLU
1	O4	91	ASN
1	O4	101	LEU
1	P4	150	GLU
1	W4	220	THR
1	W4	261	LEU
1	U4	185	ASP
1	U4	220	THR
1	T4	278	ASN
1	K4	185	ASP
1	L4	272	ASN
1	I4	220	THR
1	I4	323	ILE
1	A4	122	GLN
1	F4	138	VAL
1	F4	159	THR
1	G4	260	ASP
1	G4	323	ILE
1	B4	220	THR
6	B	82	GLU
7	F	115	ARG
7	F	123	ARG
7	F	125	ILE
8	E	59	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (65) such sidechains are listed below:

Mol	Chain	Res	Type
1	C5	170	HIS
1	C5	196	ASN
1	C5	337	ASN
1	X4	337	ASN
1	Y4	128	ASN
1	Y4	180	GLN
1	Y4	337	ASN
1	Z4	91	ASN
1	N4	230	ASN
1	R4	180	GLN
1	R4	337	ASN
1	Q4	359	HIS
1	O4	91	ASN
1	O4	326	ASN
1	P4	359	HIS
1	W4	326	ASN
1	W4	359	HIS
1	U4	326	ASN
1	U4	359	HIS
1	S4	337	ASN
1	J4	326	ASN
1	V4	337	ASN
1	L4	105	GLN
1	L4	128	ASN
1	H4	180	GLN
1	H4	359	HIS
1	I4	230	ASN
1	A4	337	ASN
1	D4	337	ASN
1	F4	337	ASN
1	B4	170	HIS
1	B4	253	ASN
1	B4	337	ASN
1	C4	180	GLN
1	C4	196	ASN
1	C4	253	ASN
2	D2	39	GLN
2	A2	7	HIS
2	A2	39	GLN
2	C2	39	GLN
2	B2	39	GLN
2	E2	7	HIS
2	E2	39	GLN

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Mol	Chain	Res	Type
2	E3	7	HIS
2	E3	39	GLN
2	B3	39	GLN
2	D3	7	HIS
2	D3	39	GLN
2	C3	39	GLN
2	A3	7	HIS
2	A3	39	GLN
2	A1	7	HIS
2	A1	39	GLN
4	H	116	HIS
4	I	116	HIS
4	J	116	HIS
6	A	283	HIS
6	B	172	HIS
6	B	188	HIS
6	B	195	GLN
6	B	204	HIS
6	B	253	GLN
5	D	76	GLN
7	F	10	GLN
7	F	15	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.

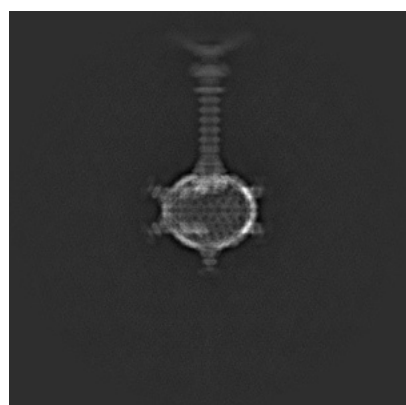
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10592. These allow visual inspection of the internal detail of the map and identification of artifacts.

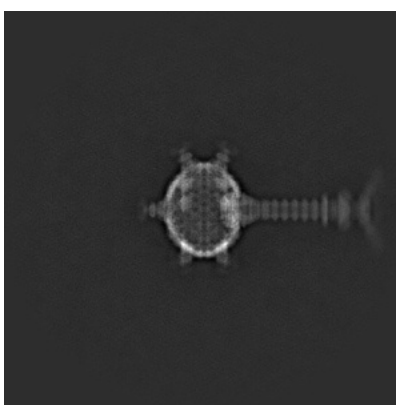
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

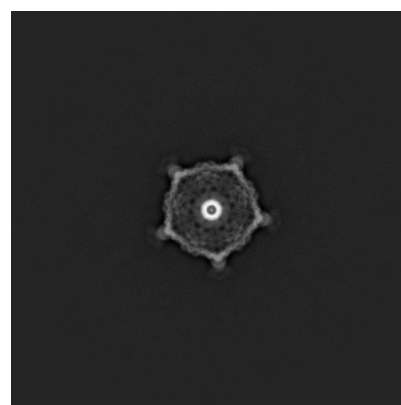
6.1.1 Primary map



X



Y

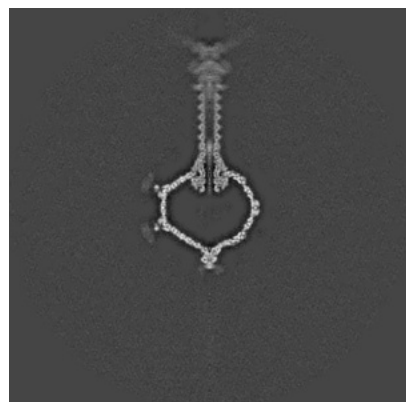


Z

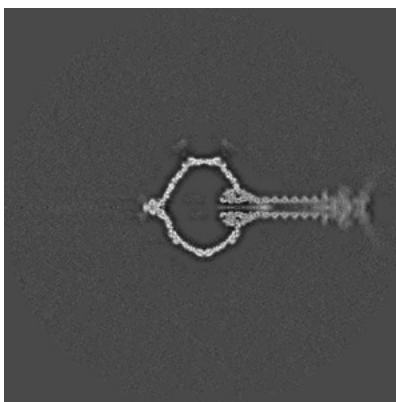
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

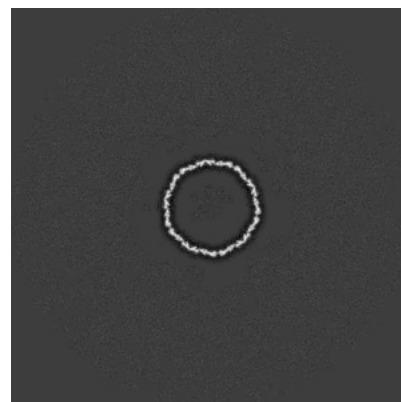
6.2.1 Primary map



X Index: 180



Y Index: 180

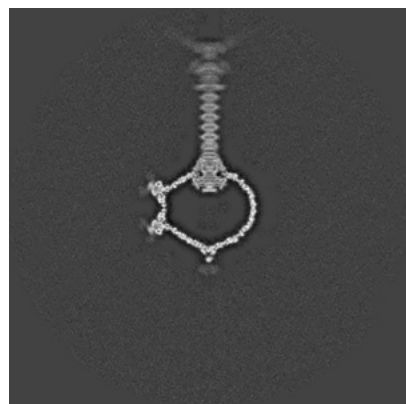


Z Index: 180

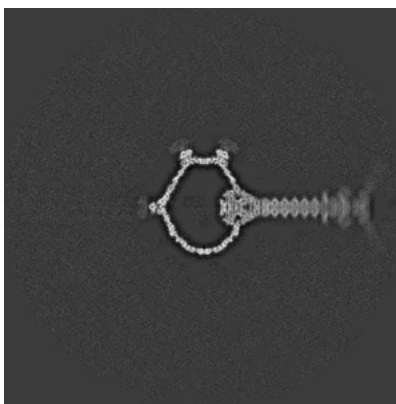
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

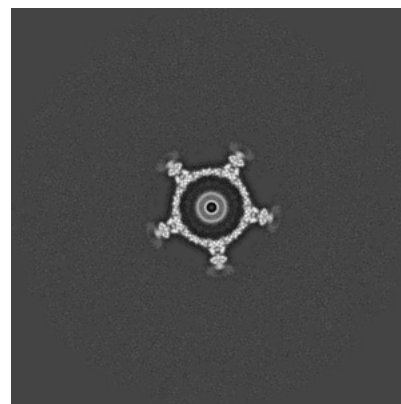
6.3.1 Primary map



X Index: 186



Y Index: 175

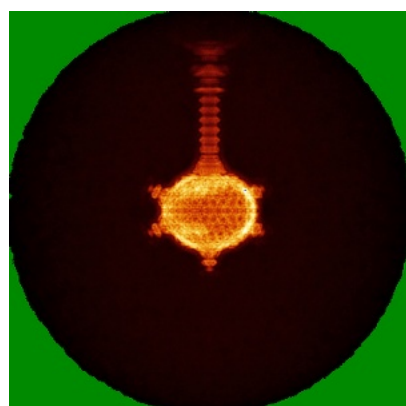


Z Index: 199

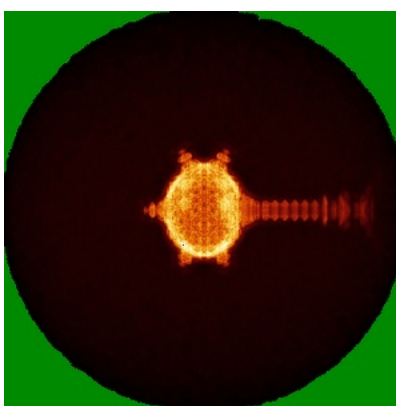
The images above show the largest variance slices of the map in three orthogonal directions.

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

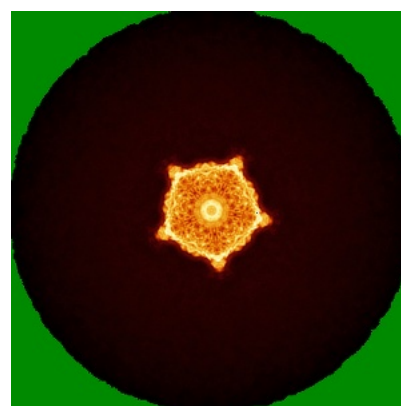
6.4.1 Primary map



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](#)

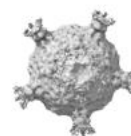
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

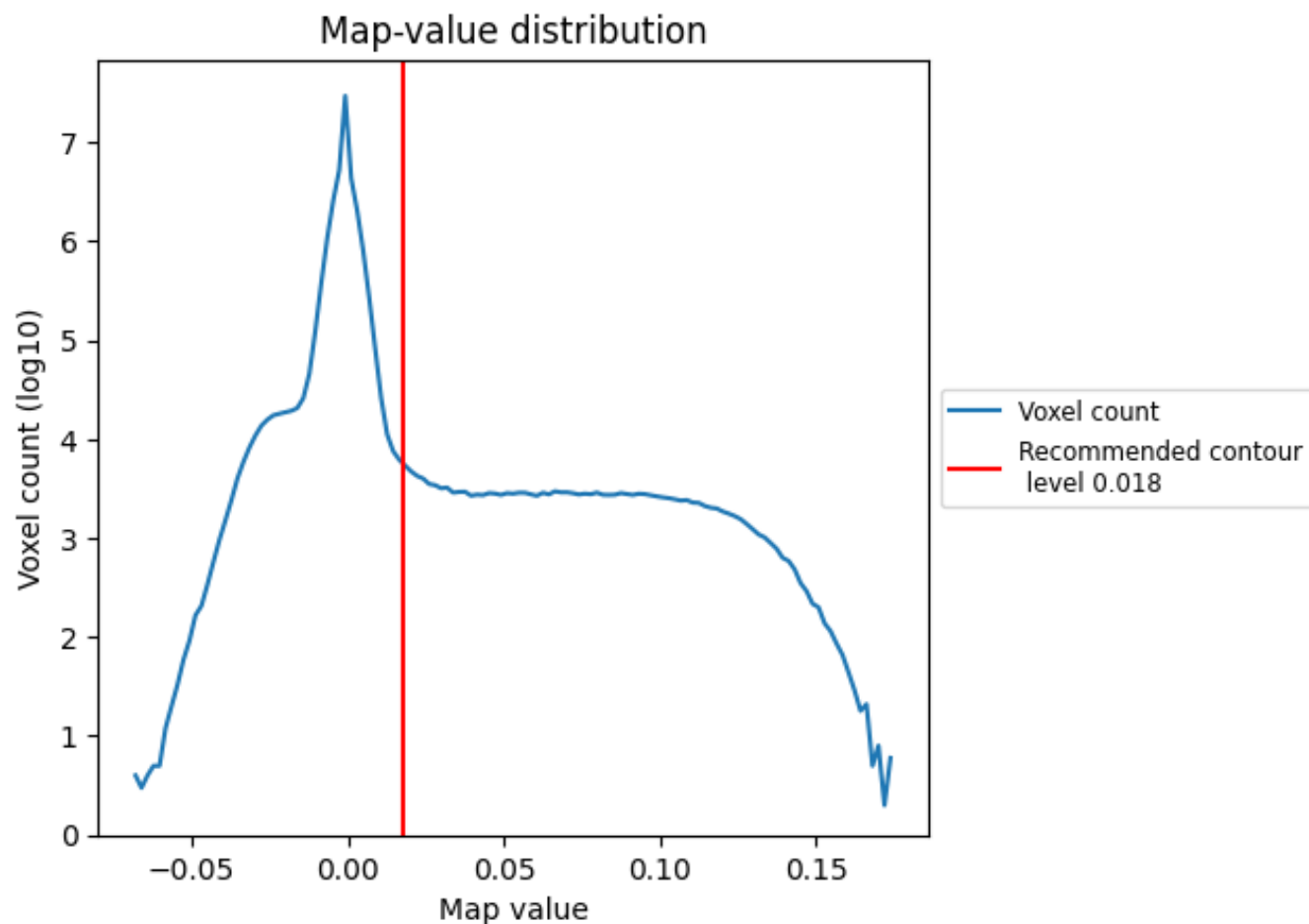
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

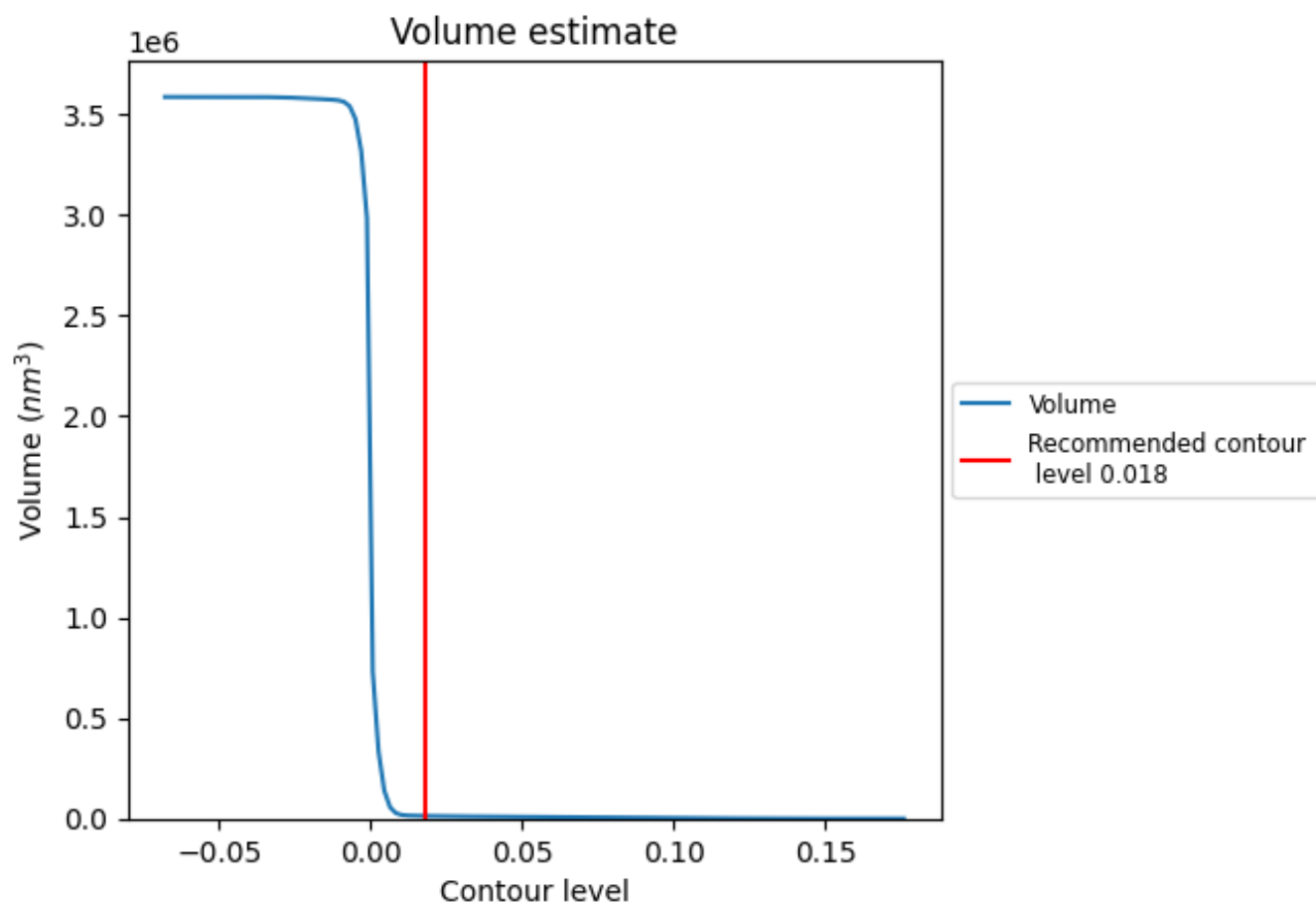
This section contains the results of statistical analysis of the map.

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.

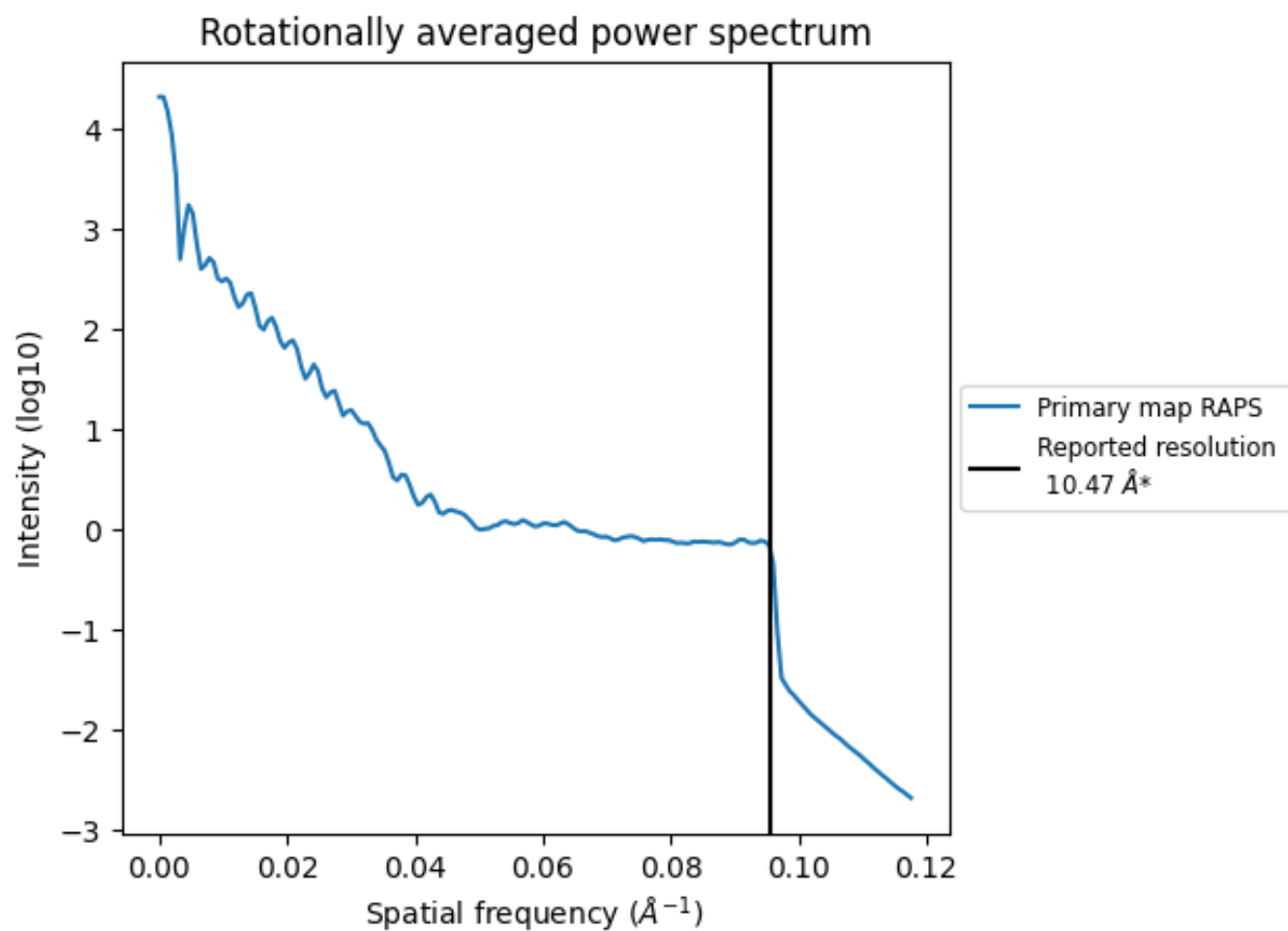
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 13130 nm³; this corresponds to an approximate mass of 11861 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 ⓘ

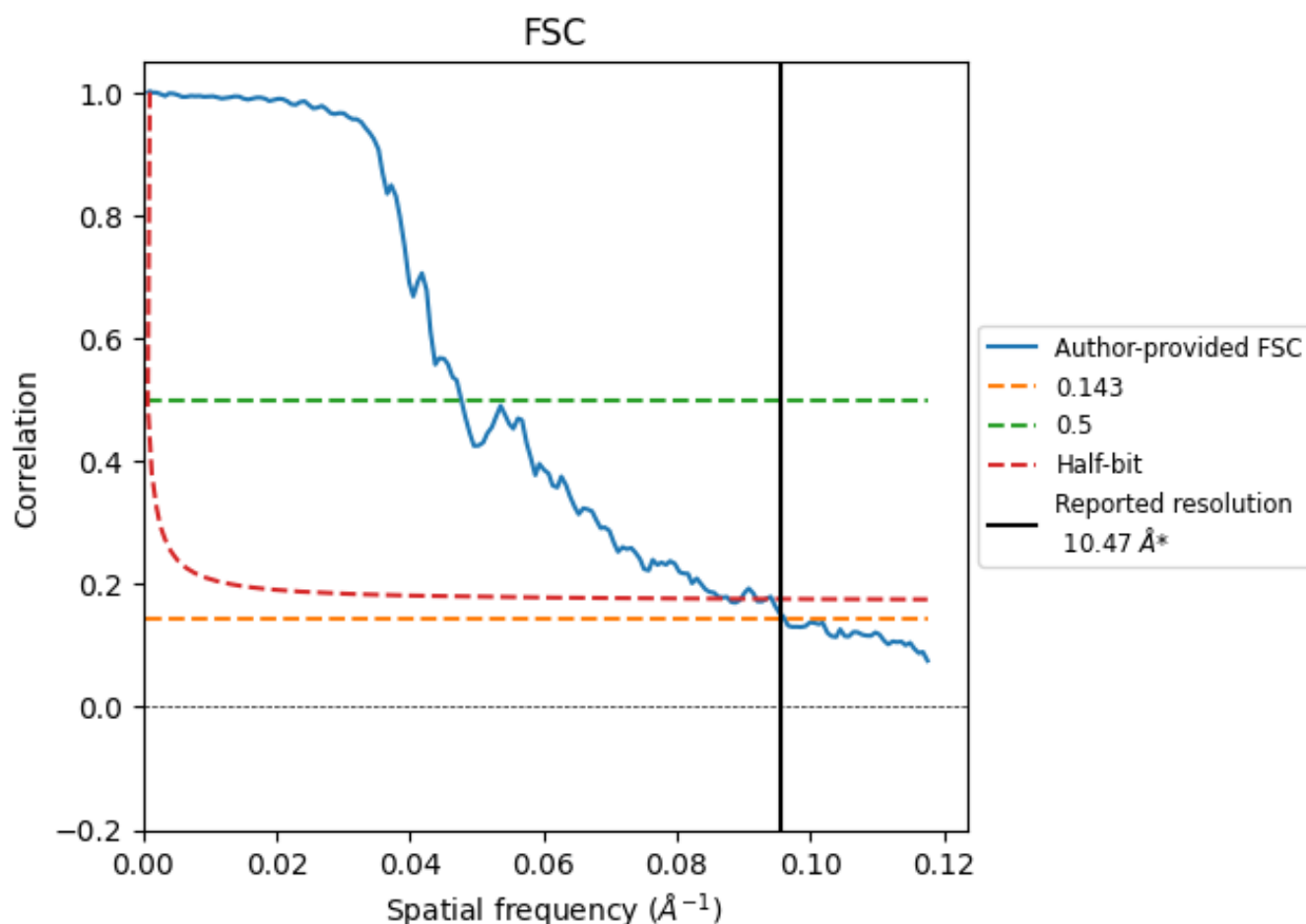


*Reported resolution corresponds to spatial frequency of 0.096 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.096 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.47	-	-
Author-provided FSC curve	10.40	20.96	11.39
Unmasked-calculated*	-	-	-

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

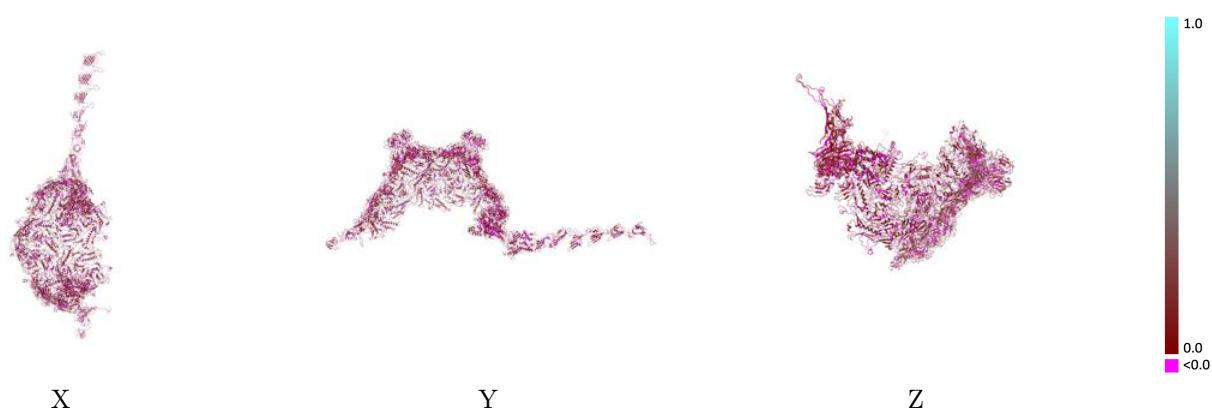
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10592 and PDB model 6TUI. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

This section was not generated.

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

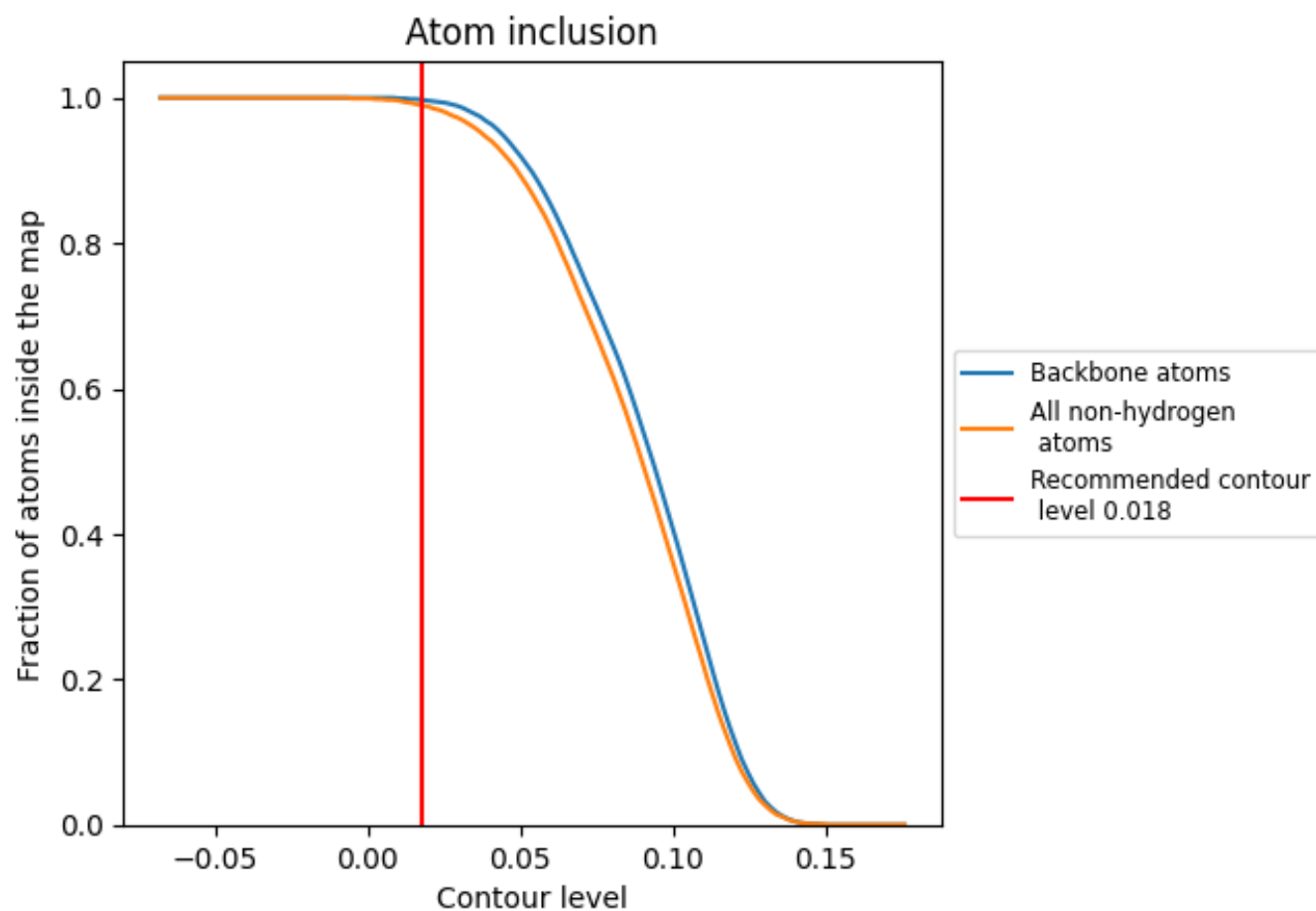


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9890	 0.0800
A	 0.9750	 0.0660
A1	 0.9980	 0.0980
A2	 1.0000	 0.0930
A3	 1.0000	 0.0770
A4	 0.9920	 0.0930
A5	 0.9900	 0.0750
B	 0.9810	 0.0660
B2	 1.0000	 0.0890
B3	 1.0000	 0.0880
B4	 0.9880	 0.0800
B5	 0.9750	 0.0810
C	 0.9820	 0.0560
C2	 1.0000	 0.0930
C3	 0.9940	 0.0790
C4	 0.9950	 0.0860
C5	 0.9890	 0.0760
D	 0.9790	 0.0480
D2	 0.9970	 0.0820
D3	 0.9970	 0.0950
D4	 0.9910	 0.0820
E	 0.9490	 0.0500
E2	 0.9980	 0.0860
E3	 0.9950	 0.0770
E4	 0.9910	 0.0840
F	 0.9820	 0.0710
F2	 1.0000	 -0.0400
F3	 1.0000	 -0.0130
F4	 0.9870	 0.0850
G	 0.9770	 0.0770
G4	 0.9900	 0.0840
H	 0.9840	 0.0780
H4	 0.9900	 0.0800
I	 0.9910	 0.0780
I4	 0.9930	 0.0770



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Chain	Atom inclusion	Q-score
J	 0.9890	 0.0870
J4	 0.9910	 0.0820
K4	 0.9910	 0.0720
L4	 0.9900	 0.0830
M4	 0.9870	 0.0840
N4	 0.9890	 0.0850
O4	 0.9930	 0.0820
P4	 0.9910	 0.0870
Q4	 0.9920	 0.0830
R4	 0.9910	 0.0840
S4	 0.9900	 0.0800
T4	 0.9950	 0.0820
U4	 0.9950	 0.0780
V4	 0.9950	 0.0840
W4	 0.9930	 0.0780
X4	 0.9890	 0.0910
Y4	 0.9890	 0.0820
Z4	 0.9900	 0.0840