



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:50 PM BST

PDB ID : 3J7V
EMDB ID: : EMD-6034
Title : Capsid Expansion Mechanism Of Bacteriophage T7 Revealed By Multi-State Atomic Models Derived From Cryo-EM Reconstructions
Authors : Guo, F.; Liu, Z.; Fang, P.A.; Zhang, Q.; Wright, E.T.; Wu, W.; Zhang, C.; Vago, F.; Ren, Y.; Jakata, J.; Chiu, W.; Serwer, P.; Jiang, W.
Deposited on : 2014-08-12
Resolution : 4.50 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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

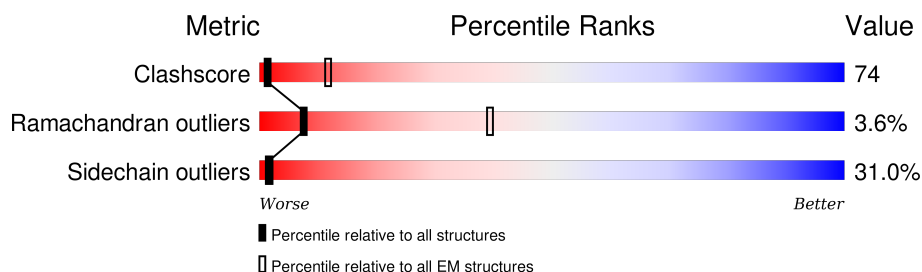
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

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

Mol	Chain	Length	Quality of chain
1	A	345	 30% 42% 13% • 13%
1	B	345	 29% 40% 19% • 10%
1	C	345	 23% 40% 21% • 14%
1	D	345	 31% 37% 17% • 14%
1	E	345	 28% 39% 16% • 15%
1	F	345	 32% 39% 14% • 13%
1	G	345	 31% 43% 17% • 8%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15873 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.

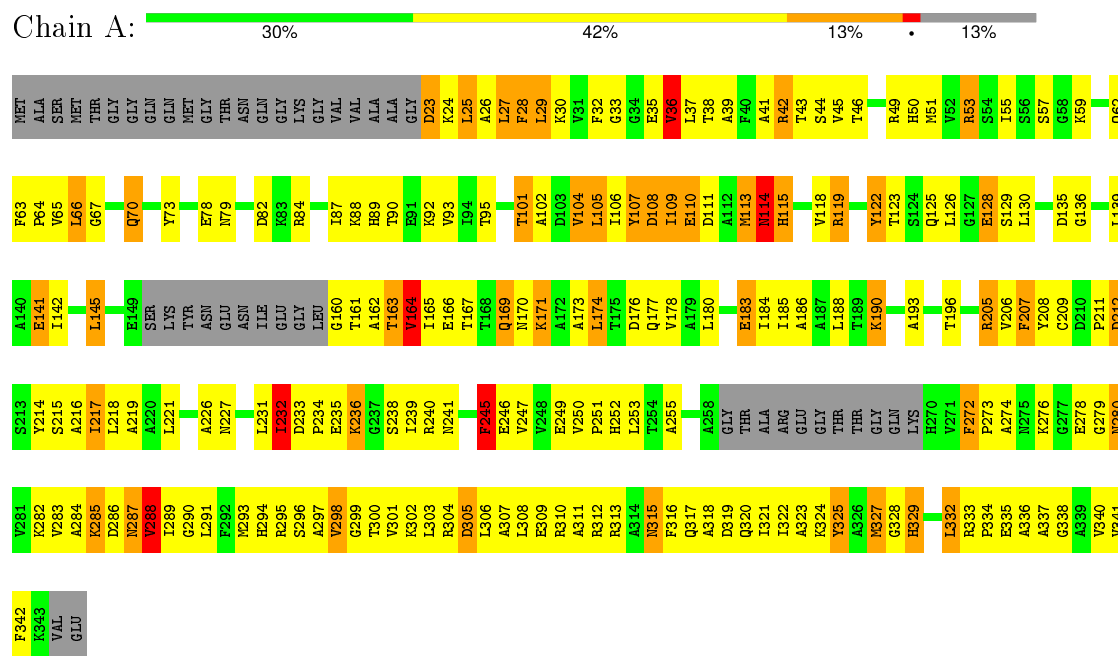
- Molecule 1 is a protein called Major capsid protein 10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	300	Total	C	N	O	S	0	0
			2250	1418	396	427	9		
1	B	309	Total	C	N	O	S	0	0
			2321	1462	406	444	9		
1	C	296	Total	C	N	O	S	0	0
			2234	1411	393	421	9		
1	D	298	Total	C	N	O	S	0	0
			2241	1413	394	425	9		
1	E	293	Total	C	N	O	S	0	0
			2208	1393	387	419	9		
1	F	299	Total	C	N	O	S	0	0
			2245	1415	395	426	9		
1	G	317	Total	C	N	O	S	0	0
			2374	1492	419	454	9		

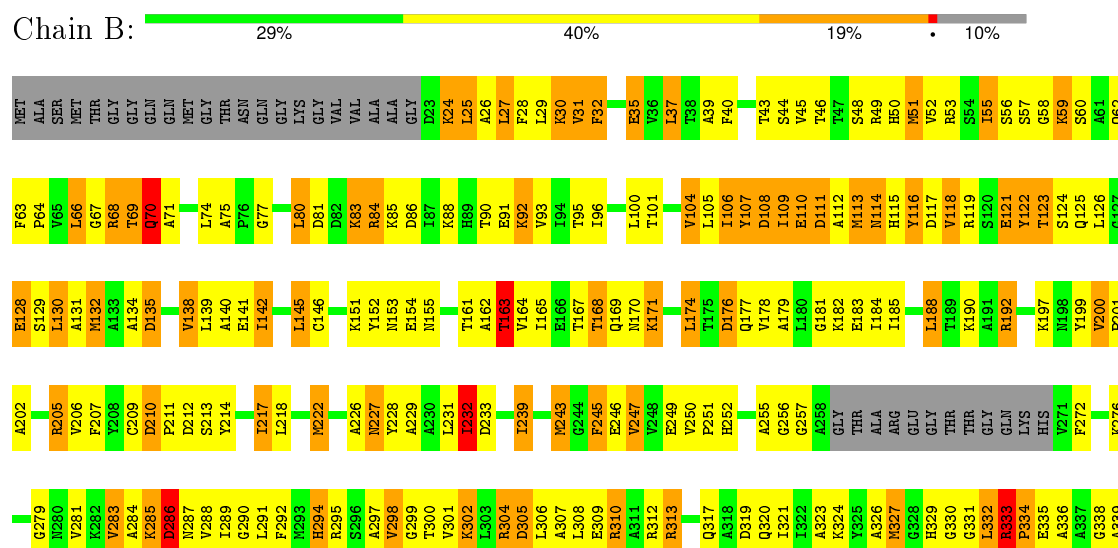
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

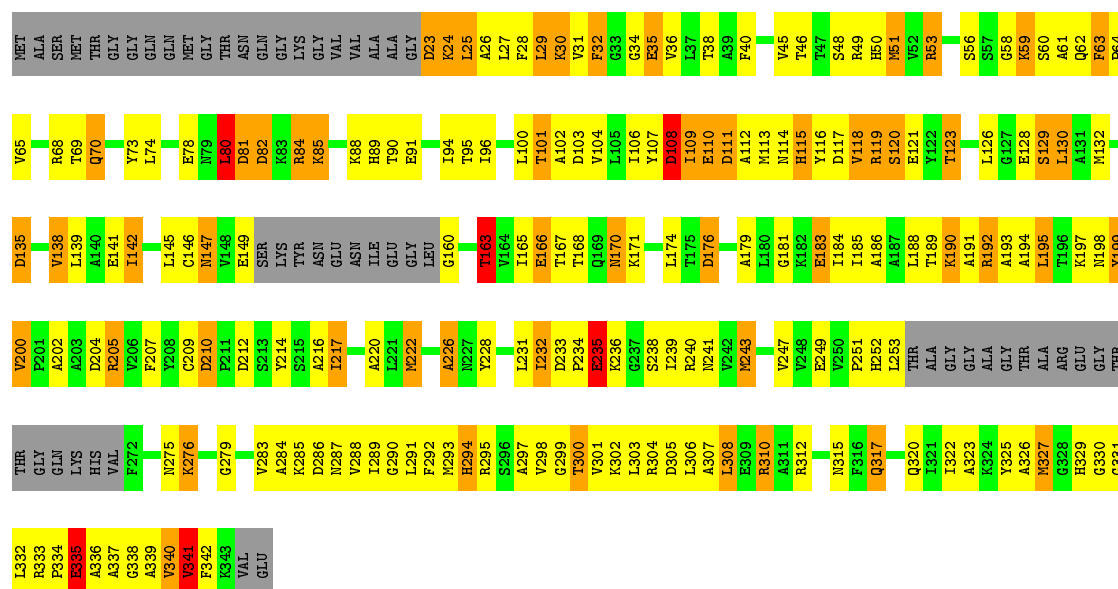
- Molecule 1: Major capsid protein 10A



- Molecule 1: Major capsid protein 10A

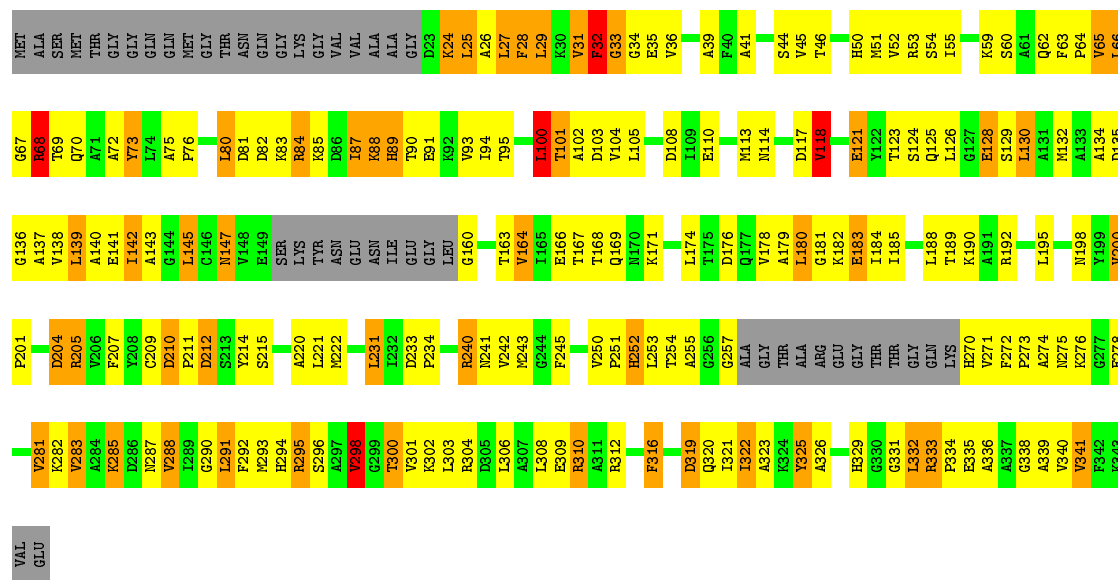






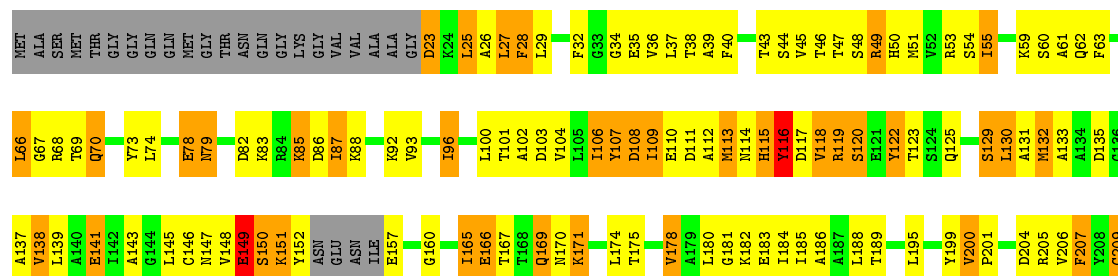
• Molecule 1: Major capsid protein 10A

Chain F: 32% 39% 14% 13%



• Molecule 1: Major capsid protein 10A

Chain G: 31% 43% 17% 8%



D210	E278
P211	
Y214	V281
S215	
A216	A284
I217	K285
L218	D286
A219	L291
A220	F292
L221	M293
M222	H294
P223	R295
N224	S296
	A297
L231	V298
I232	G299
D233	T300
P234	V301
E235	K302
K236	L303
G237	R304
S238	D305
I239	L306
K240	A307
N241	L308
V242	E309
M243	R310
G244	A311
F245	R312
E246	R313
V247	A314
V248	
E249	
V250	A318
P251	D319
H252	Q320
L253	I321
	I322
T254	A323
G255	K324
G256	Y325
G257	A326
A258	M327
G259	G328
T260	H329
A261	
R262	L332
E263	R333
G264	P334
T265	E335
T266	A336
G267	
Q268	
K269	V340
H270	V341
V271	F342
F272	K343
P273	VAL
A274	GLU
N275	

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of images	27520	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	59000	Depositor
Image detector	KODAK SO-163 FILM	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.35	0/2282	0.69	1/3087 (0.0%)
1	B	0.40	0/2354	0.82	3/3185 (0.1%)
1	C	0.45	0/2266	0.82	2/3065 (0.1%)
1	D	0.38	0/2273	0.74	2/3075 (0.1%)
1	E	0.38	0/2239	0.70	2/3028 (0.1%)
1	F	0.37	0/2277	0.70	2/3080 (0.1%)
1	G	0.30	0/2408	0.65	1/3256 (0.0%)
All	All	0.38	0/16099	0.73	13/21776 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	3
1	C	0	6
1	D	0	5
1	E	0	7
1	F	0	3
1	G	0	1
All	All	0	30

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	333	ARG	C-N-CD	-20.55	75.40	120.60
1	B	70	GLN	CB-CA-C	-7.36	95.67	110.40
1	C	200	VAL	C-N-CD	6.03	141.06	128.40
1	E	80	LEU	CA-CB-CG	5.80	128.65	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	331	GLY	N-CA-C	5.50	126.84	113.10
1	B	70	GLN	C-N-CA	5.49	135.41	121.70
1	F	69	THR	N-CA-C	-5.43	96.33	111.00
1	G	23	ASP	CB-CG-OD2	5.24	123.02	118.30
1	D	23	ASP	CB-CG-OD2	5.21	122.99	118.30
1	E	23	ASP	CB-CG-OD2	5.17	122.96	118.30
1	A	305	ASP	CB-CG-OD2	5.16	122.94	118.30
1	D	288	VAL	CB-CA-C	-5.09	101.73	111.40
1	F	100	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

All (30) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	ASP	Peptide
1	A	114	ASN	Peptide
1	A	316	PHE	Peptide
1	A	329	HIS	Peptide
1	A	332	LEU	Peptide
1	B	106	ILE	Peptide
1	B	163	THR	Peptide
1	B	70	GLN	Peptide
1	C	164	VAL	Peptide
1	C	233	ASP	Peptide
1	C	287	ASN	Peptide
1	C	317	GLN	Peptide
1	C	330	GLY	Peptide
1	C	71	ALA	Peptide
1	D	250	VAL	Peptide
1	D	292	PHE	Peptide
1	D	331	GLY	Peptide
1	D	95	THR	Peptide
1	D	98	GLY	Peptide
1	E	107	TYR	Peptide
1	E	108	ASP	Peptide
1	E	146	CYS	Peptide
1	E	163	THR	Peptide
1	E	231	LEU	Peptide
1	E	232	ILE	Peptide
1	E	317	GLN	Peptide
1	F	316	PHE	Peptide
1	F	66	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	F	68	ARG	Peptide
1	G	292	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2250	0	2279	343	0
1	B	2321	0	2348	415	0
1	C	2234	0	2271	465	0
1	D	2241	0	2272	281	0
1	E	2208	0	2240	372	0
1	F	2245	0	2275	229	0
1	G	2374	0	2403	333	0
All	All	15873	0	16088	2351	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 74.

All (2351) 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:B:28:PHE:CE1	1:B:112:ALA:HA	1.24	1.71
1:B:251:PRO:HB2	1:C:199:TYR:CZ	1.09	1.60
1:E:298:VAL:C	1:E:333:ARG:HH12	1.06	1.57
1:E:189:THR:HG22	1:E:243:MET:SD	1.45	1.55
1:E:25:LEU:HD21	1:E:310:ARG:CZ	1.08	1.55
1:A:207:PHE:CZ	1:A:209:CYS:HB2	1.36	1.54
1:A:309:GLU:CB	1:A:322:ILE:HG13	1.38	1.53
1:D:142:ILE:CA	1:D:145:LEU:HD23	1.31	1.53
1:B:251:PRO:CB	1:C:199:TYR:CE1	1.93	1.52
1:B:251:PRO:CG	1:C:199:TYR:CE1	1.92	1.52
1:E:25:LEU:CD2	1:E:310:ARG:NH2	1.70	1.51
1:B:28:PHE:CZ	1:B:112:ALA:HA	1.44	1.51
1:E:25:LEU:CD2	1:E:310:ARG:CZ	1.89	1.50
1:B:251:PRO:CB	1:C:199:TYR:CZ	1.93	1.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:ILE:HA	1:D:145:LEU:CD2	1.40	1.49
1:E:189:THR:CG2	1:E:243:MET:CE	1.91	1.49
1:G:110:GLU:HA	1:G:114:ASN:CG	1.35	1.48
1:E:189:THR:CG2	1:E:243:MET:SD	2.04	1.45
1:C:195:LEU:CD2	1:C:205:ARG:NH2	1.78	1.44
1:B:141:GLU:OE1	1:B:330:GLY:CA	1.65	1.43
1:E:145:LEU:CB	1:E:332:LEU:HD23	1.45	1.43
1:C:161:THR:OG1	1:C:336:ALA:CB	1.64	1.42
1:D:138:VAL:HG23	1:D:139:LEU:CD1	1.51	1.40
1:E:25:LEU:HD21	1:E:310:ARG:NH2	1.10	1.38
1:E:192:ARG:HA	1:E:195:LEU:CD1	1.53	1.38
1:D:130:LEU:HD12	1:D:131:ALA:N	1.38	1.36
1:C:195:LEU:CD2	1:C:202:ALA:HB1	1.54	1.36
1:B:145:LEU:HD21	1:B:332:LEU:CD1	1.53	1.36
1:F:25:LEU:HA	1:F:28:PHE:CD2	1.61	1.36
1:E:192:ARG:CA	1:E:195:LEU:HD11	1.53	1.35
1:B:145:LEU:CD2	1:B:332:LEU:HG	1.55	1.35
1:D:29:LEU:HD13	1:D:30:LYS:N	1.36	1.34
1:C:25:LEU:HD23	1:C:26:ALA:N	1.41	1.33
1:A:289:ILE:HG13	1:A:340:VAL:CG2	1.57	1.33
1:B:109:ILE:HD13	1:B:110:GLU:N	1.37	1.33
1:E:25:LEU:CG	1:E:310:ARG:NH2	1.89	1.33
1:B:40:PHE:HE1	1:B:130:LEU:CD1	1.11	1.33
1:B:40:PHE:CE1	1:B:130:LEU:HD11	1.41	1.33
1:A:27:LEU:HD12	1:A:28:PHE:N	1.41	1.32
1:B:113:MET:HA	1:B:115:HIS:NE2	1.42	1.32
1:A:309:GLU:CB	1:A:322:ILE:CG1	2.07	1.31
1:E:145:LEU:HD22	1:E:332:LEU:CD2	1.58	1.31
1:E:40:PHE:HA	1:E:130:LEU:CD2	1.35	1.31
1:E:181:GLY:O	1:E:185:ILE:CD1	1.75	1.31
1:B:28:PHE:CE1	1:B:112:ALA:CA	2.14	1.30
1:E:25:LEU:CD2	1:E:310:ARG:NH1	1.91	1.29
1:C:195:LEU:HD23	1:C:205:ARG:CZ	1.60	1.29
1:A:309:GLU:CA	1:A:322:ILE:HG13	1.59	1.29
1:B:251:PRO:HG3	1:C:199:TYR:CE1	1.59	1.28
1:C:188:LEU:HD22	1:C:207:PHE:CE1	1.69	1.28
1:A:119:ARG:CB	1:A:119:ARG:HH11	1.46	1.28
1:G:149:GLU:CG	1:G:150:SER:H	1.45	1.27
1:C:26:ALA:CA	1:C:29:LEU:HD13	1.62	1.27
1:C:195:LEU:HD21	1:C:202:ALA:CB	1.63	1.27
1:C:206:VAL:HA	1:C:246:GLU:O	1.20	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:106:ILE:C	1:G:106:ILE:HD13	1.54	1.27
1:E:189:THR:HG22	1:E:243:MET:CE	1.54	1.26
1:A:26:ALA:O	1:A:29:LEU:HD12	1.36	1.26
1:E:145:LEU:HD22	1:E:332:LEU:CG	1.66	1.26
1:E:145:LEU:HB2	1:E:332:LEU:CD2	1.65	1.26
1:A:309:GLU:HB3	1:A:322:ILE:CD1	1.66	1.26
1:A:309:GLU:O	1:A:322:ILE:HG12	1.26	1.26
1:E:25:LEU:HD22	1:E:310:ARG:NH1	1.45	1.25
1:C:26:ALA:HA	1:C:29:LEU:CD1	1.65	1.25
1:C:27:LEU:HD23	1:C:27:LEU:C	1.53	1.25
1:B:113:MET:SD	1:B:115:HIS:CE1	2.30	1.25
1:E:298:VAL:C	1:E:333:ARG:NH1	1.86	1.25
1:D:36:VAL:O	1:D:39:ALA:N	1.69	1.25
1:A:289:ILE:CG1	1:A:340:VAL:HG22	1.64	1.24
1:E:181:GLY:O	1:E:185:ILE:HD12	1.10	1.24
1:C:109:ILE:C	1:C:109:ILE:HD13	1.54	1.24
1:B:130:LEU:HD12	1:B:130:LEU:C	1.53	1.23
1:A:207:PHE:CZ	1:A:209:CYS:CB	2.21	1.23
1:G:25:LEU:O	1:G:29:LEU:HG	1.39	1.23
1:G:110:GLU:HA	1:G:114:ASN:CB	1.68	1.23
1:C:207:PHE:CD2	1:C:247:VAL:HG22	1.72	1.23
1:C:195:LEU:HD23	1:C:205:ARG:NH2	0.90	1.23
1:D:144:GLY:O	1:D:146:CYS:N	1.69	1.22
1:B:139:LEU:O	1:B:142:ILE:HG23	1.34	1.22
1:D:142:ILE:O	1:D:145:LEU:HB2	1.36	1.22
1:G:146:CYS:CB	1:G:336:ALA:HB3	1.69	1.22
1:B:31:VAL:CG1	1:B:35:GLU:OE2	1.87	1.21
1:E:142:ILE:HD12	1:E:142:ILE:C	1.59	1.21
1:B:145:LEU:CD2	1:B:332:LEU:CD1	2.17	1.21
1:E:40:PHE:CA	1:E:130:LEU:HD22	1.52	1.21
1:C:116:TYR:O	1:C:118:VAL:N	1.73	1.21
1:E:142:ILE:HD12	1:E:142:ILE:O	1.37	1.21
1:G:25:LEU:HA	1:G:28:PHE:CD2	1.77	1.20
1:A:27:LEU:C	1:A:27:LEU:HD12	1.58	1.20
1:A:309:GLU:O	1:A:322:ILE:CG1	1.90	1.20
1:G:109:ILE:CD1	1:G:109:ILE:H	1.51	1.20
1:G:130:LEU:C	1:G:130:LEU:HD23	1.59	1.20
1:G:110:GLU:OE2	1:G:118:VAL:CG1	1.90	1.19
1:B:145:LEU:CD2	1:B:332:LEU:CG	2.19	1.19
1:B:132:MET:HE2	1:B:132:MET:HA	1.21	1.19
1:B:113:MET:HA	1:B:115:HIS:CD2	1.78	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:PHE:CE1	1:B:130:LEU:CD1	1.86	1.19
1:G:113:MET:HE3	1:G:113:MET:CA	1.72	1.19
1:A:119:ARG:HB2	1:A:119:ARG:HH11	1.07	1.18
1:A:114:ASN:N	1:A:115:HIS:CD2	2.09	1.18
1:C:25:LEU:CD2	1:C:26:ALA:H	1.58	1.17
1:B:132:MET:CE	1:B:132:MET:HA	1.64	1.17
1:E:25:LEU:HD12	1:E:25:LEU:C	1.54	1.17
1:D:46:THR:HG23	1:D:135:ASP:OD1	1.41	1.17
1:A:25:LEU:O	1:A:25:LEU:HD13	1.39	1.16
1:E:145:LEU:CD2	1:E:332:LEU:CD2	2.24	1.16
1:F:25:LEU:HA	1:F:28:PHE:CE2	1.80	1.16
1:G:110:GLU:O	1:G:114:ASN:HB3	1.41	1.16
1:G:106:ILE:HD13	1:G:107:TYR:N	1.59	1.16
1:G:28:PHE:CE1	1:G:111:ASP:OD2	1.99	1.16
1:A:289:ILE:HG12	1:A:340:VAL:O	1.42	1.16
1:A:309:GLU:CB	1:A:322:ILE:CD1	2.23	1.16
1:E:63:PHE:CE2	1:E:333:ARG:NH2	2.13	1.16
1:A:309:GLU:O	1:A:322:ILE:N	1.78	1.16
1:B:24:LYS:HD2	1:B:24:LYS:C	1.64	1.15
1:C:26:ALA:C	1:C:29:LEU:HD13	1.65	1.15
1:A:294:HIS:CD2	1:A:337:ALA:HA	1.81	1.15
1:B:138:VAL:O	1:B:142:ILE:HG22	1.43	1.15
1:C:26:ALA:HA	1:C:29:LEU:HD13	1.15	1.15
1:E:40:PHE:CA	1:E:130:LEU:CD2	2.03	1.15
1:E:24:LYS:HZ1	1:E:112:ALA:HB1	1.01	1.15
1:D:130:LEU:C	1:D:130:LEU:HD12	1.60	1.14
1:A:109:ILE:N	1:A:109:ILE:HD13	1.55	1.14
1:E:298:VAL:CA	1:E:333:ARG:HH12	1.59	1.14
1:F:25:LEU:CA	1:F:28:PHE:CE2	2.30	1.14
1:C:25:LEU:N	1:C:25:LEU:HD22	1.58	1.14
1:C:116:TYR:CD2	1:C:117:ASP:N	2.15	1.14
1:E:25:LEU:CD1	1:E:310:ARG:NH2	2.10	1.14
1:A:309:GLU:HB2	1:A:322:ILE:CG1	1.72	1.14
1:G:270:HIS:O	1:G:272:PHE:N	1.78	1.14
1:E:145:LEU:HD22	1:E:332:LEU:HG	1.30	1.14
1:E:119:ARG:HG2	1:E:119:ARG:HH11	1.03	1.14
1:B:251:PRO:HB2	1:C:199:TYR:CE2	1.83	1.14
1:A:110:GLU:OE1	1:A:118:VAL:HG11	1.46	1.14
1:F:29:LEU:HD23	1:F:29:LEU:O	1.45	1.13
1:E:40:PHE:CZ	1:E:130:LEU:CD1	2.24	1.13
1:A:119:ARG:O	1:A:123:THR:HG23	1.46	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:27:LEU:HD13	1:F:27:LEU:O	1.45	1.13
1:E:128:GLU:OE2	1:F:201:PRO:HG3	1.45	1.13
1:B:334:PRO:HA	1:B:335:GLU:HB2	1.23	1.13
1:C:205:ARG:O	1:C:246:GLU:HB3	1.49	1.12
1:F:25:LEU:HD12	1:F:26:ALA:H	1.00	1.12
1:D:27:LEU:C	1:D:27:LEU:HD12	1.69	1.12
1:A:308:LEU:HA	1:A:323:ALA:HA	1.15	1.12
1:E:109:ILE:N	1:E:109:ILE:HD12	1.55	1.12
1:G:110:GLU:HA	1:G:114:ASN:ND2	1.62	1.12
1:E:119:ARG:CG	1:E:119:ARG:HH11	1.63	1.12
1:E:189:THR:HG21	1:E:243:MET:CE	1.67	1.12
1:A:309:GLU:HB2	1:A:322:ILE:HG13	1.16	1.12
1:C:207:PHE:CZ	1:C:245:PHE:CD2	2.37	1.12
1:G:257:GLY:HA3	1:G:268:GLN:OE1	1.47	1.12
1:B:113:MET:SD	1:B:115:HIS:NE2	2.22	1.11
1:D:25:LEU:HD12	1:D:25:LEU:C	1.70	1.11
1:C:208:TYR:HB2	1:C:291:LEU:HG	1.31	1.11
1:B:141:GLU:OE1	1:B:330:GLY:HA2	0.95	1.10
1:C:161:THR:OG1	1:C:336:ALA:HB2	1.38	1.10
1:A:205:ARG:NH1	1:A:293:MET:SD	2.24	1.10
1:G:25:LEU:N	1:G:25:LEU:HD23	1.56	1.10
1:G:113:MET:CE	1:G:113:MET:CA	2.30	1.10
1:C:208:TYR:HB3	1:C:291:LEU:HD11	1.27	1.10
1:G:132:MET:SD	1:G:132:MET:C	2.30	1.10
1:B:132:MET:CA	1:B:132:MET:CE	2.30	1.10
1:C:204:ASP:O	1:C:205:ARG:HG3	1.50	1.10
1:C:206:VAL:HG21	1:C:248:VAL:HG23	1.28	1.10
1:D:138:VAL:HG23	1:D:139:LEU:HD13	1.20	1.10
1:E:110:GLU:CG	1:E:118:VAL:HG21	1.78	1.10
1:D:110:GLU:HB2	1:D:114:ASN:HB2	1.25	1.10
1:B:132:MET:HA	1:B:135:ASP:OD2	1.52	1.09
1:E:145:LEU:CD2	1:E:332:LEU:HD21	1.82	1.09
1:G:109:ILE:N	1:G:109:ILE:HD13	1.54	1.09
1:C:201:PRO:HA	1:C:202:ALA:HB3	1.34	1.09
1:A:302:LYS:HE2	1:A:327:MET:HG2	1.34	1.09
1:E:109:ILE:H	1:E:109:ILE:CD1	1.51	1.09
1:C:33:GLY:HA2	1:C:36:VAL:CG2	1.82	1.09
1:E:110:GLU:HG3	1:E:118:VAL:CG1	1.83	1.09
1:B:251:PRO:HB2	1:C:199:TYR:CE1	1.72	1.08
1:E:145:LEU:CB	1:E:332:LEU:CD2	2.28	1.08
1:G:110:GLU:CD	1:G:118:VAL:HB	1.74	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:115:HIS:CD2	1:G:119:ARG:HH22	1.70	1.08
1:C:207:PHE:HD2	1:C:247:VAL:CG2	1.65	1.08
1:E:110:GLU:HG2	1:E:118:VAL:HG21	1.34	1.08
1:E:25:LEU:HD11	1:E:310:ARG:NH2	1.64	1.08
1:A:287:ASN:HD22	1:A:288:VAL:N	1.50	1.08
1:A:309:GLU:HB3	1:A:322:ILE:HD11	1.20	1.08
1:B:29:LEU:HD11	1:B:310:ARG:HD3	1.09	1.08
1:D:142:ILE:HD13	1:D:145:LEU:CD2	1.82	1.08
1:C:27:LEU:HD23	1:C:28:PHE:N	1.66	1.08
1:A:208:TYR:HE2	1:A:293:MET:HE3	1.17	1.08
1:C:119:ARG:HH11	1:C:119:ARG:HG3	1.19	1.08
1:B:128:GLU:OE1	1:C:68:ARG:HD3	1.54	1.08
1:B:114:ASN:OD1	1:C:53:ARG:NH2	1.86	1.07
1:C:29:LEU:HD12	1:C:29:LEU:H	0.96	1.07
1:B:114:ASN:H	1:B:115:HIS:CD2	1.72	1.07
1:A:109:ILE:HD13	1:A:109:ILE:H	1.09	1.07
1:G:34:GLY:O	1:G:38:THR:HG23	1.51	1.07
1:A:55:ILE:CG2	1:A:301:VAL:HG23	1.83	1.07
1:G:113:MET:CE	1:G:113:MET:HA	1.81	1.07
1:G:113:MET:HA	1:G:113:MET:HE3	1.09	1.07
1:B:28:PHE:CZ	1:B:112:ALA:CA	2.31	1.06
1:B:114:ASN:N	1:B:115:HIS:HD2	1.54	1.06
1:A:287:ASN:ND2	1:A:288:VAL:H	1.51	1.06
1:B:31:VAL:HG13	1:B:35:GLU:OE2	1.54	1.06
1:B:145:LEU:HD22	1:B:332:LEU:CG	1.82	1.06
1:C:110:GLU:OE2	1:C:118:VAL:HG21	1.52	1.06
1:E:303:LEU:HB2	1:E:327:MET:HG2	1.32	1.06
1:B:130:LEU:O	1:B:130:LEU:HD12	1.54	1.05
1:A:302:LYS:HG2	1:A:327:MET:CB	1.84	1.05
1:G:119:ARG:CG	1:G:119:ARG:HH11	1.69	1.05
1:G:25:LEU:H	1:G:25:LEU:HD23	0.90	1.05
1:B:24:LYS:NZ	1:B:24:LYS:HB3	1.69	1.05
1:G:132:MET:HE3	1:G:252:HIS:NE2	1.71	1.05
1:C:161:THR:OG1	1:C:336:ALA:HB1	1.30	1.05
1:G:149:GLU:HG2	1:G:150:SER:N	1.70	1.05
1:G:132:MET:SD	1:G:133:ALA:N	2.30	1.05
1:B:29:LEU:CD1	1:B:310:ARG:HD3	1.85	1.05
1:G:113:MET:HE1	1:G:115:HIS:HB2	1.36	1.04
1:C:28:PHE:C	1:C:28:PHE:CD2	2.30	1.04
1:G:25:LEU:HA	1:G:28:PHE:CE2	1.92	1.04
1:C:33:GLY:CA	1:C:36:VAL:HG23	1.88	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:146:CYS:SG	1:G:336:ALA:N	2.30	1.04
1:B:35:GLU:HB2	1:B:123:THR:HG23	1.36	1.04
1:E:298:VAL:CA	1:E:333:ARG:NH1	2.17	1.04
1:E:25:LEU:HD12	1:E:25:LEU:O	1.58	1.04
1:G:113:MET:C	1:G:113:MET:HE2	1.78	1.04
1:A:208:TYR:CE2	1:A:293:MET:HE3	1.92	1.04
1:D:141:GLU:O	1:D:145:LEU:HD22	1.56	1.04
1:B:108:ASP:HA	1:B:111:ASP:OD2	1.57	1.04
1:B:40:PHE:CE1	1:B:130:LEU:HD13	1.92	1.04
1:D:139:LEU:N	1:D:139:LEU:HD13	1.73	1.03
1:B:132:MET:CA	1:B:132:MET:HE2	1.84	1.03
1:G:146:CYS:CB	1:G:336:ALA:CB	2.35	1.03
1:B:30:LYS:HD3	1:B:30:LYS:C	1.76	1.03
1:D:142:ILE:HD13	1:D:145:LEU:HD21	1.35	1.03
1:D:26:ALA:O	1:D:29:LEU:HD12	1.56	1.03
1:E:110:GLU:OE2	1:E:111:ASP:HA	1.56	1.03
1:E:299:GLY:N	1:E:331:GLY:O	1.91	1.03
1:G:110:GLU:OE2	1:G:118:VAL:HG12	1.59	1.02
1:A:302:LYS:HG2	1:A:327:MET:HB3	1.39	1.02
1:A:36:VAL:O	1:A:39:ALA:N	1.91	1.02
1:G:119:ARG:HH11	1:G:119:ARG:HG3	0.86	1.02
1:D:139:LEU:H	1:D:139:LEU:HD13	1.23	1.02
1:A:207:PHE:HE1	1:A:290:GLY:HA3	1.23	1.02
1:C:33:GLY:HA2	1:C:36:VAL:HG23	1.40	1.01
1:E:189:THR:HG21	1:E:243:MET:HE3	1.02	1.01
1:A:309:GLU:C	1:A:322:ILE:HG12	1.81	1.01
1:F:25:LEU:CA	1:F:28:PHE:CD2	2.41	1.01
1:G:141:GLU:N	1:G:270:HIS:ND1	2.06	1.01
1:F:25:LEU:HD12	1:F:26:ALA:N	1.76	1.01
1:B:116:TYR:H	1:B:116:TYR:HD1	1.07	1.01
1:A:309:GLU:C	1:A:322:ILE:CG1	2.27	1.01
1:G:141:GLU:N	1:G:270:HIS:CE1	2.29	1.01
1:G:113:MET:CE	1:G:115:HIS:HB2	1.91	1.00
1:G:26:ALA:HA	1:G:29:LEU:HD12	1.37	1.00
1:E:110:GLU:HG3	1:E:118:VAL:HG11	1.04	1.00
1:G:110:GLU:CA	1:G:114:ASN:CG	2.30	1.00
1:B:27:LEU:HD23	1:B:30:LYS:HB3	1.40	1.00
1:B:141:GLU:CD	1:B:330:GLY:HA2	1.82	1.00
1:D:25:LEU:O	1:D:25:LEU:HD12	1.62	1.00
1:G:149:GLU:HG2	1:G:150:SER:H	0.87	1.00
1:F:27:LEU:C	1:F:27:LEU:CD1	2.30	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:C	1:A:27:LEU:CD1	2.30	1.00
1:E:24:LYS:NZ	1:E:112:ALA:HB1	1.76	1.00
1:A:302:LYS:HG2	1:A:327:MET:CG	1.90	0.99
1:E:189:THR:HG23	1:E:243:MET:SD	1.96	0.99
1:C:26:ALA:O	1:C:29:LEU:HD13	1.60	0.99
1:C:29:LEU:O	1:C:32:PHE:HB3	1.61	0.99
1:G:25:LEU:H	1:G:25:LEU:CD2	1.71	0.99
1:E:115:HIS:CE1	1:E:119:ARG:NH2	2.30	0.99
1:G:113:MET:CE	1:G:113:MET:C	2.30	0.99
1:B:141:GLU:OE2	1:B:331:GLY:N	1.94	0.99
1:F:28:PHE:CD1	1:F:29:LEU:N	2.30	0.99
1:D:45:VAL:HG23	1:D:135:ASP:OD2	1.62	0.99
1:D:130:LEU:HD12	1:D:131:ALA:CA	1.93	0.99
1:C:29:LEU:CD1	1:C:29:LEU:H	1.76	0.99
1:B:116:TYR:N	1:B:116:TYR:HD1	1.60	0.99
1:F:25:LEU:CD1	1:F:26:ALA:H	1.75	0.99
1:G:106:ILE:CD1	1:G:106:ILE:C	2.30	0.99
1:A:25:LEU:C	1:A:25:LEU:HD13	1.84	0.99
1:E:25:LEU:CD1	1:E:25:LEU:C	2.30	0.99
1:C:26:ALA:CA	1:C:29:LEU:CD1	2.30	0.99
1:A:287:ASN:OD1	1:A:341:VAL:HB	1.63	0.98
1:G:130:LEU:CD2	1:G:130:LEU:C	2.30	0.98
1:E:115:HIS:CE1	1:E:119:ARG:HH22	1.81	0.98
1:C:27:LEU:CD2	1:C:27:LEU:C	2.30	0.98
1:F:27:LEU:HD13	1:F:27:LEU:C	1.79	0.98
1:C:28:PHE:HD2	1:C:29:LEU:N	1.61	0.98
1:D:138:VAL:CG2	1:D:139:LEU:CD1	2.41	0.98
1:G:148:VAL:HG23	1:G:148:VAL:O	1.59	0.98
1:G:149:GLU:OE1	1:G:150:SER:N	1.96	0.98
1:B:107:TYR:HD2	1:B:107:TYR:N	1.61	0.98
1:G:147:ASN:ND2	1:G:273:PRO:HG3	1.78	0.98
1:C:113:MET:HE1	1:C:119:ARG:NH2	1.79	0.97
1:G:146:CYS:HB2	1:G:336:ALA:CB	1.94	0.97
1:E:114:ASN:O	1:E:115:HIS:HB2	1.62	0.97
1:G:27:LEU:C	1:G:27:LEU:HD12	1.84	0.97
1:C:207:PHE:HD2	1:C:247:VAL:HG22	0.82	0.97
1:G:146:CYS:SG	1:G:336:ALA:HB3	2.04	0.97
1:G:110:GLU:OE2	1:G:118:VAL:HG11	1.63	0.97
1:D:138:VAL:CG2	1:D:139:LEU:HD13	1.95	0.97
1:D:130:LEU:C	1:D:130:LEU:CD1	2.30	0.97
1:C:109:ILE:O	1:C:109:ILE:HD13	1.65	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:32:PHE:C	1:D:32:PHE:CD1	2.37	0.97
1:B:24:LYS:CD	1:B:24:LYS:C	2.30	0.97
1:B:145:LEU:HD21	1:B:332:LEU:HD12	1.00	0.97
1:C:109:ILE:CD1	1:C:109:ILE:C	2.30	0.97
1:C:28:PHE:HD2	1:C:28:PHE:C	1.67	0.96
1:B:31:VAL:HG12	1:B:35:GLU:OE2	1.65	0.96
1:G:146:CYS:SG	1:G:336:ALA:CB	2.53	0.96
1:C:119:ARG:HH11	1:C:119:ARG:CG	1.77	0.96
1:C:107:TYR:N	1:C:107:TYR:CD2	2.30	0.96
1:B:69:THR:HG22	1:B:70:GLN:H	1.30	0.96
1:C:207:PHE:HZ	1:C:245:PHE:CD2	1.83	0.96
1:B:24:LYS:O	1:B:24:LYS:HD2	1.63	0.96
1:G:110:GLU:HG2	1:G:118:VAL:HG21	1.43	0.96
1:C:117:ASP:OD2	1:D:51:MET:CE	2.13	0.96
1:A:55:ILE:CG2	1:A:301:VAL:CG2	2.44	0.96
1:A:302:LYS:CE	1:A:327:MET:HG2	1.96	0.95
1:B:30:LYS:O	1:B:30:LYS:HE2	1.66	0.95
1:B:35:GLU:HB2	1:B:123:THR:CG2	1.95	0.95
1:B:130:LEU:C	1:B:130:LEU:CD1	2.30	0.95
1:E:189:THR:CG2	1:E:243:MET:HE3	1.67	0.95
1:G:110:GLU:CA	1:G:114:ASN:ND2	2.30	0.95
1:A:119:ARG:CB	1:A:119:ARG:NH1	2.30	0.95
1:B:24:LYS:CE	1:B:25:LEU:N	2.30	0.95
1:C:40:PHE:HE1	1:C:131:ALA:HA	1.32	0.95
1:D:139:LEU:N	1:D:139:LEU:CD1	2.30	0.95
1:D:28:PHE:CD2	1:D:29:LEU:N	2.34	0.95
1:C:188:LEU:CD2	1:C:207:PHE:CE1	2.49	0.95
1:C:29:LEU:N	1:C:29:LEU:HD12	1.78	0.95
1:D:29:LEU:CD1	1:D:30:LYS:N	2.30	0.94
1:B:29:LEU:HD11	1:B:310:ARG:CD	1.98	0.94
1:G:141:GLU:OE1	1:G:141:GLU:HA	1.63	0.94
1:G:109:ILE:O	1:G:114:ASN:HB2	1.67	0.94
1:C:207:PHE:CD2	1:C:247:VAL:CG2	2.45	0.94
1:A:109:ILE:N	1:A:109:ILE:CD1	2.30	0.94
1:G:110:GLU:CA	1:G:114:ASN:CB	2.45	0.94
1:C:195:LEU:HD21	1:C:202:ALA:HB1	0.95	0.94
1:F:29:LEU:CD2	1:F:29:LEU:C	2.33	0.94
1:A:119:ARG:HB2	1:A:119:ARG:NH1	1.81	0.94
1:G:149:GLU:CG	1:G:150:SER:N	2.17	0.94
1:B:24:LYS:HZ2	1:B:24:LYS:HB3	1.28	0.94
1:E:40:PHE:HA	1:E:130:LEU:HD22	1.07	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:130:LEU:CD2	1:G:131:ALA:N	2.30	0.94
1:D:46:THR:CG2	1:D:135:ASP:OD1	2.16	0.94
1:C:27:LEU:CD2	1:C:28:PHE:N	2.30	0.93
1:G:106:ILE:CD1	1:G:107:TYR:N	2.30	0.93
1:A:205:ARG:HE	1:A:295:ARG:HA	1.31	0.93
1:B:24:LYS:CB	1:B:24:LYS:NZ	2.30	0.93
1:B:30:LYS:HD3	1:B:30:LYS:O	1.67	0.93
1:B:114:ASN:H	1:B:115:HIS:HD2	0.97	0.93
1:C:41:ALA:O	1:C:42:ARG:HB2	1.64	0.93
1:B:132:MET:HE2	1:B:135:ASP:OD2	1.67	0.93
1:F:29:LEU:HD23	1:F:29:LEU:C	1.84	0.93
1:B:28:PHE:HZ	1:B:111:ASP:O	1.50	0.93
1:D:142:ILE:CD1	1:D:145:LEU:CD2	2.46	0.93
1:F:25:LEU:HA	1:F:28:PHE:HD2	1.32	0.93
1:A:107:TYR:OH	1:B:90:THR:HG21	1.68	0.93
1:C:25:LEU:N	1:C:25:LEU:CD2	2.30	0.93
1:B:113:MET:CA	1:B:115:HIS:NE2	2.30	0.93
1:C:25:LEU:H	1:C:25:LEU:HD22	1.16	0.93
1:A:115:HIS:CD2	1:A:115:HIS:H	1.83	0.93
1:A:57:SER:H	1:A:303:LEU:HD13	1.30	0.93
1:E:25:LEU:HD22	1:E:310:ARG:HH12	0.99	0.93
1:C:188:LEU:HD22	1:C:207:PHE:CZ	2.03	0.92
1:G:113:MET:HE1	1:G:115:HIS:CB	2.00	0.92
1:E:186:ALA:O	1:E:190:LYS:HD3	1.70	0.92
1:D:252:HIS:HE1	1:E:192:ARG:HH21	1.16	0.92
1:E:63:PHE:HE2	1:E:333:ARG:NH2	1.59	0.92
1:G:119:ARG:NH1	1:G:119:ARG:HG3	1.69	0.92
1:D:40:PHE:CE1	1:D:131:ALA:HA	2.03	0.92
1:A:27:LEU:CD1	1:A:28:PHE:N	2.33	0.92
1:E:40:PHE:HA	1:E:130:LEU:HD23	1.50	0.92
1:C:162:ALA:HB3	1:C:337:ALA:O	1.70	0.92
1:A:119:ARG:CG	1:A:119:ARG:HH11	1.81	0.92
1:G:130:LEU:HD23	1:G:131:ALA:N	1.85	0.92
1:E:24:LYS:HZ1	1:E:112:ALA:CB	1.81	0.92
1:E:145:LEU:CG	1:E:332:LEU:HD23	1.99	0.92
1:D:141:GLU:C	1:D:145:LEU:HD22	1.90	0.92
1:A:302:LYS:HG2	1:A:327:MET:HG2	1.48	0.92
1:B:109:ILE:CD1	1:B:110:GLU:N	2.30	0.91
1:A:207:PHE:HZ	1:A:209:CYS:HB2	1.16	0.91
1:G:113:MET:HE2	1:G:114:ASN:N	1.83	0.91
1:C:113:MET:CE	1:C:119:ARG:CZ	2.48	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:109:ILE:H	1:E:109:ILE:HD12	0.75	0.91
1:C:107:TYR:N	1:C:107:TYR:HD2	1.67	0.91
1:D:135:ASP:O	1:D:139:LEU:HD22	1.70	0.91
1:C:208:TYR:HB3	1:C:291:LEU:CD1	2.00	0.91
1:E:142:ILE:HA	1:E:332:LEU:HD22	1.52	0.91
1:D:92:LYS:HD2	1:D:332:LEU:H	1.36	0.91
1:E:28:PHE:CE1	1:E:111:ASP:O	2.24	0.91
1:A:106:ILE:C	1:A:107:TYR:HD2	1.72	0.91
1:D:33:GLY:O	1:D:36:VAL:HG12	1.70	0.91
1:B:24:LYS:CA	1:B:24:LYS:HZ3	1.83	0.91
1:A:106:ILE:HG22	1:A:122:TYR:CE2	2.06	0.91
1:D:32:PHE:O	1:D:32:PHE:HD1	1.53	0.90
1:E:299:GLY:CA	1:E:333:ARG:HH22	1.84	0.90
1:D:130:LEU:CD1	1:D:131:ALA:N	2.30	0.90
1:A:107:TYR:HD2	1:A:107:TYR:N	1.69	0.90
1:G:114:ASN:O	1:G:116:TYR:N	2.04	0.90
1:C:117:ASP:OD2	1:D:51:MET:HE3	1.69	0.90
1:C:208:TYR:HB2	1:C:291:LEU:CG	2.01	0.90
1:E:141:GLU:HG3	1:E:330:GLY:C	1.91	0.90
1:G:110:GLU:CD	1:G:118:VAL:CB	2.40	0.90
1:F:25:LEU:CB	1:F:28:PHE:CE2	2.54	0.90
1:E:142:ILE:CD1	1:E:142:ILE:C	2.34	0.90
1:D:135:ASP:O	1:D:139:LEU:HD13	1.72	0.90
1:B:251:PRO:HB2	1:C:199:TYR:OH	1.72	0.90
1:B:251:PRO:HG3	1:C:199:TYR:HE1	1.02	0.90
1:C:206:VAL:CG2	1:C:246:GLU:OE1	2.20	0.90
1:C:206:VAL:CA	1:C:246:GLU:O	2.16	0.90
1:B:63:PHE:O	1:B:333:ARG:NH2	2.04	0.90
1:E:303:LEU:CB	1:E:327:MET:HG2	2.02	0.90
1:E:192:ARG:O	1:E:195:LEU:HD12	1.72	0.90
1:B:145:LEU:HD22	1:B:332:LEU:HG	0.90	0.90
1:D:110:GLU:CB	1:D:114:ASN:HB2	2.01	0.90
1:D:201:PRO:O	1:D:205:ARG:NH2	2.05	0.90
1:B:28:PHE:HE1	1:B:112:ALA:HA	1.17	0.89
1:E:192:ARG:HA	1:E:195:LEU:CG	2.02	0.89
1:C:113:MET:HE2	1:C:119:ARG:CZ	2.02	0.89
1:A:27:LEU:HD12	1:A:28:PHE:CA	2.02	0.89
1:E:119:ARG:HG2	1:E:119:ARG:NH1	1.84	0.89
1:B:107:TYR:CD2	1:B:107:TYR:N	2.37	0.89
1:C:32:PHE:CE2	1:C:123:THR:HG22	2.07	0.89
1:C:42:ARG:HH11	1:C:42:ARG:HG3	1.35	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:297:ALA:O	1:E:333:ARG:N	2.06	0.89
1:F:25:LEU:CB	1:F:28:PHE:HE2	1.84	0.89
1:E:110:GLU:C	1:E:110:GLU:CD	2.30	0.89
1:E:145:LEU:HD22	1:E:332:LEU:HD21	1.42	0.89
1:E:25:LEU:CD2	1:E:310:ARG:HH12	1.69	0.88
1:D:128:GLU:C	1:D:128:GLU:CD	2.30	0.88
1:F:25:LEU:CD1	1:F:26:ALA:N	2.35	0.88
1:C:119:ARG:O	1:C:123:THR:HG23	1.74	0.88
1:C:35:GLU:HA	1:C:38:THR:OG1	1.72	0.88
1:A:114:ASN:N	1:A:115:HIS:HD2	1.69	0.88
1:F:143:ALA:O	1:F:147:ASN:CG	2.11	0.88
1:G:146:CYS:HB3	1:G:336:ALA:HB3	1.52	0.88
1:D:132:MET:HE1	1:D:251:PRO:CG	2.03	0.88
1:A:308:LEU:HA	1:A:323:ALA:CA	2.03	0.88
1:E:110:GLU:CG	1:E:118:VAL:HG11	2.00	0.88
1:B:116:TYR:CD1	1:B:116:TYR:N	2.35	0.88
1:C:206:VAL:HB	1:C:246:GLU:OE1	1.74	0.88
1:E:192:ARG:CA	1:E:195:LEU:CD1	2.30	0.88
1:B:251:PRO:CG	1:C:199:TYR:HE1	1.52	0.88
1:A:49:ARG:HD3	1:A:206:VAL:HG21	1.55	0.88
1:B:251:PRO:HB3	1:C:199:TYR:CE1	2.06	0.87
1:G:110:GLU:CD	1:G:118:VAL:CG1	2.41	0.87
1:C:33:GLY:C	1:C:36:VAL:HG23	1.94	0.87
1:A:294:HIS:HD2	1:A:337:ALA:HA	1.37	0.87
1:B:145:LEU:O	1:B:145:LEU:HD12	1.72	0.87
1:B:332:LEU:HD12	1:B:334:PRO:HD2	1.54	0.87
1:A:207:PHE:CE2	1:A:247:VAL:HG23	2.09	0.87
1:C:207:PHE:HE2	1:C:242:VAL:HG21	1.39	0.87
1:E:110:GLU:CD	1:E:111:ASP:HA	1.93	0.87
1:G:109:ILE:HD13	1:G:109:ILE:H	0.71	0.87
1:C:26:ALA:HA	1:C:29:LEU:HD11	1.56	0.87
1:C:161:THR:O	1:C:336:ALA:HB1	1.73	0.87
1:G:25:LEU:N	1:G:25:LEU:CD2	2.30	0.87
1:A:302:LYS:HE2	1:A:327:MET:CE	2.05	0.87
1:G:135:ASP:O	1:G:138:VAL:HG23	1.74	0.87
1:D:132:MET:HE1	1:D:251:PRO:CB	2.04	0.87
1:C:207:PHE:CZ	1:C:245:PHE:HD2	1.88	0.87
1:A:115:HIS:CD2	1:A:115:HIS:N	2.42	0.87
1:A:115:HIS:HD2	1:A:115:HIS:H	1.22	0.87
1:G:165:ILE:HD13	1:G:166:GLU:N	1.90	0.87
1:B:117:ASP:OD2	1:C:51:MET:CE	2.23	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ILE:CG1	1:A:340:VAL:O	2.23	0.86
1:C:26:ALA:C	1:C:29:LEU:CD1	2.42	0.86
1:G:115:HIS:O	1:G:119:ARG:HB3	1.74	0.86
1:C:204:ASP:O	1:C:205:ARG:CG	2.23	0.86
1:D:40:PHE:HE1	1:D:131:ALA:HA	1.36	0.86
1:B:24:LYS:HE2	1:B:25:LEU:CA	2.04	0.86
1:A:207:PHE:HZ	1:A:209:CYS:CB	1.75	0.86
1:A:207:PHE:CE1	1:A:209:CYS:HB2	2.08	0.86
1:C:114:ASN:O	1:C:115:HIS:CG	2.29	0.86
1:G:28:PHE:CZ	1:G:111:ASP:OD1	2.27	0.86
1:A:55:ILE:HG22	1:A:301:VAL:HG23	1.57	0.86
1:C:146:CYS:HG	1:C:161:THR:N	1.73	0.86
1:C:195:LEU:CD2	1:C:202:ALA:CB	2.36	0.86
1:G:150:SER:O	1:G:151:LYS:O	1.93	0.86
1:D:128:GLU:OE2	1:D:129:SER:HA	1.76	0.86
1:C:195:LEU:HD23	1:C:205:ARG:HH22	1.03	0.85
1:C:206:VAL:CG2	1:C:248:VAL:N	2.39	0.85
1:E:128:GLU:OE2	1:F:201:PRO:CG	2.23	0.85
1:E:189:THR:HG22	1:E:243:MET:HE1	1.55	0.85
1:G:149:GLU:CD	1:G:150:SER:N	2.29	0.85
1:G:27:LEU:O	1:G:27:LEU:HD12	1.76	0.85
1:D:28:PHE:HD2	1:D:29:LEU:N	1.73	0.85
1:D:29:LEU:HD13	1:D:30:LYS:H	1.39	0.85
1:B:106:ILE:HG22	1:B:122:TYR:OH	1.76	0.85
1:E:121:GLU:OE1	1:F:51:MET:SD	2.34	0.85
1:B:131:ALA:C	1:B:132:MET:HE2	1.96	0.85
1:B:132:MET:HE2	1:B:132:MET:N	1.92	0.85
1:D:142:ILE:N	1:D:145:LEU:HD23	1.90	0.85
1:E:191:ALA:O	1:E:195:LEU:HG	1.76	0.85
1:E:31:VAL:HG12	1:E:35:GLU:OE2	1.77	0.85
1:B:109:ILE:HD13	1:B:110:GLU:H	1.42	0.85
1:F:25:LEU:O	1:F:28:PHE:CD2	2.30	0.85
1:G:132:MET:CE	1:G:252:HIS:NE2	2.38	0.85
1:E:189:THR:CG2	1:E:243:MET:HE1	2.07	0.85
1:C:208:TYR:CB	1:C:291:LEU:CG	2.55	0.85
1:B:28:PHE:CZ	1:B:111:ASP:O	2.30	0.84
1:E:298:VAL:O	1:E:333:ARG:NH1	2.08	0.84
1:E:24:LYS:NZ	1:E:112:ALA:CB	2.38	0.84
1:B:29:LEU:HD21	1:B:310:ARG:HG2	1.57	0.84
1:B:206:VAL:HG13	1:B:246:GLU:HB3	1.59	0.84
1:D:128:GLU:CD	1:D:129:SER:N	2.30	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:LEU:HB2	1:B:179:ALA:HB1	1.58	0.84
1:G:147:ASN:HD21	1:G:273:PRO:HG3	1.41	0.84
1:G:132:MET:HE2	1:G:132:MET:O	1.78	0.84
1:B:334:PRO:HA	1:B:335:GLU:CB	2.08	0.84
1:C:116:TYR:O	1:C:118:VAL:HG12	1.76	0.84
1:A:302:LYS:CG	1:A:327:MET:HG2	2.07	0.84
1:A:207:PHE:HE1	1:A:290:GLY:CA	1.90	0.84
1:C:25:LEU:HD23	1:C:26:ALA:H	0.71	0.84
1:C:114:ASN:O	1:C:115:HIS:CD2	2.30	0.84
1:B:24:LYS:CB	1:B:24:LYS:HZ3	1.88	0.84
1:E:298:VAL:CG1	1:E:332:LEU:CD1	2.55	0.84
1:A:288:VAL:O	1:A:289:ILE:HD13	1.78	0.84
1:C:33:GLY:HA2	1:C:36:VAL:HG21	1.58	0.84
1:A:302:LYS:HE2	1:A:327:MET:CG	2.08	0.84
1:B:132:MET:CE	1:B:132:MET:N	2.41	0.83
1:E:96:ILE:HD11	1:E:327:MET:O	1.78	0.83
1:C:42:ARG:HG3	1:C:42:ARG:NH1	1.90	0.83
1:C:110:GLU:OE1	1:C:122:TYR:CD2	2.31	0.83
1:A:309:GLU:HB2	1:A:322:ILE:CD1	1.99	0.83
1:C:40:PHE:HE1	1:C:131:ALA:CA	1.91	0.83
1:E:115:HIS:HE1	1:E:119:ARG:HH22	1.25	0.83
1:B:128:GLU:OE1	1:C:68:ARG:CD	2.26	0.83
1:A:107:TYR:N	1:A:107:TYR:CD2	2.44	0.83
1:D:45:VAL:CG2	1:D:135:ASP:OD2	2.26	0.83
1:D:110:GLU:O	1:D:113:MET:HG3	1.76	0.83
1:B:139:LEU:C	1:B:142:ILE:HG23	1.98	0.83
1:D:40:PHE:HE1	1:D:131:ALA:CA	1.92	0.83
1:A:108:ASP:HB2	1:A:111:ASP:HB2	1.61	0.83
1:B:114:ASN:N	1:B:115:HIS:CD2	2.39	0.83
1:D:29:LEU:C	1:D:29:LEU:HD13	1.98	0.83
1:B:117:ASP:OD1	1:C:53:ARG:HA	1.77	0.83
1:E:333:ARG:HG3	1:E:333:ARG:HH11	1.43	0.83
1:A:286:ASP:N	1:A:287:ASN:O	2.12	0.83
1:E:114:ASN:O	1:E:115:HIS:CB	2.26	0.83
1:C:188:LEU:HD22	1:C:207:PHE:HE1	1.37	0.83
1:G:146:CYS:HB2	1:G:336:ALA:HB2	1.60	0.83
1:E:25:LEU:HG	1:E:310:ARG:NH2	1.94	0.82
1:C:202:ALA:HB1	1:C:205:ARG:NH2	1.94	0.82
1:C:109:ILE:HD13	1:C:110:GLU:N	1.93	0.82
1:G:110:GLU:C	1:G:114:ASN:HB3	1.99	0.82
1:B:192:ARG:NE	1:B:243:MET:SD	2.52	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:107:TYR:N	1:G:107:TYR:HD2	1.75	0.82
1:D:142:ILE:HD12	1:D:145:LEU:HG	1.62	0.82
1:A:308:LEU:CA	1:A:323:ALA:HA	2.06	0.82
1:B:239:ILE:HB	1:B:247:VAL:HG23	1.60	0.82
1:A:110:GLU:OE1	1:A:118:VAL:CG1	2.25	0.82
1:E:119:ARG:CG	1:E:119:ARG:NH1	2.34	0.82
1:A:287:ASN:ND2	1:A:288:VAL:N	2.16	0.82
1:A:309:GLU:C	1:A:322:ILE:HG13	1.92	0.82
1:G:40:PHE:HD1	1:G:131:ALA:HB2	1.44	0.82
1:B:106:ILE:C	1:B:107:TYR:HD2	1.81	0.82
1:C:206:VAL:CG2	1:C:248:VAL:H	1.92	0.82
1:G:107:TYR:N	1:G:107:TYR:CD2	2.45	0.82
1:E:24:LYS:C	1:E:24:LYS:CD	2.46	0.82
1:D:313:ARG:HB2	1:D:318:ALA:HB3	1.60	0.82
1:G:110:GLU:HG2	1:G:118:VAL:CG2	2.09	0.82
1:D:36:VAL:CG1	1:D:37:LEU:N	2.43	0.82
1:C:110:GLU:OE2	1:C:118:VAL:CG2	2.26	0.82
1:G:110:GLU:CG	1:G:118:VAL:HB	2.10	0.82
1:C:110:GLU:OE1	1:C:122:TYR:CE2	2.33	0.81
1:G:28:PHE:CE2	1:G:111:ASP:OD1	2.32	0.81
1:B:92:LYS:HZ1	1:B:333:ARG:HE	1.28	0.81
1:B:332:LEU:HD12	1:B:334:PRO:CD	2.10	0.81
1:C:119:ARG:NH1	1:C:119:ARG:HB2	1.95	0.81
1:D:49:ARG:O	1:D:50:HIS:ND1	2.14	0.81
1:C:106:ILE:C	1:C:107:TYR:CD2	2.54	0.81
1:C:43:THR:HG21	1:C:128:GLU:HG3	1.62	0.81
1:G:113:MET:HG3	1:G:114:ASN:H	1.46	0.81
1:D:27:LEU:HD12	1:D:28:PHE:N	1.95	0.81
1:G:79:ASN:HB2	1:G:82:ASP:HB2	1.62	0.81
1:A:108:ASP:CB	1:A:111:ASP:HB2	2.11	0.81
1:C:110:GLU:CD	1:C:118:VAL:CG2	2.48	0.81
1:G:222:MET:SD	1:G:224:ASN:ND2	2.53	0.81
1:E:53:ARG:HH12	1:E:62:GLN:H	1.29	0.81
1:B:141:GLU:OE1	1:B:330:GLY:C	2.17	0.81
1:A:26:ALA:HA	1:A:29:LEU:HD11	1.60	0.81
1:D:205:ARG:HG2	1:D:245:PHE:HA	1.62	0.81
1:A:302:LYS:CD	1:A:327:MET:HG2	2.09	0.81
1:B:109:ILE:C	1:B:109:ILE:HD13	2.01	0.81
1:B:134:ALA:O	1:B:138:VAL:HG22	1.81	0.81
1:E:116:TYR:O	1:E:120:SER:HB3	1.80	0.81
1:E:298:VAL:CG1	1:E:332:LEU:HD13	2.12	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:LYS:NZ	1:B:25:LEU:N	2.30	0.80
1:B:125:GLN:HG3	1:C:66:LEU:HD13	1.62	0.80
1:D:27:LEU:O	1:D:31:VAL:HG23	1.81	0.80
1:B:30:LYS:O	1:B:30:LYS:CE	2.30	0.80
1:B:332:LEU:CD1	1:B:334:PRO:HG2	2.11	0.80
1:C:108:ASP:OD2	1:C:111:ASP:CB	2.30	0.80
1:E:24:LYS:O	1:E:24:LYS:CD	2.30	0.80
1:A:306:LEU:O	1:A:306:LEU:HD12	1.81	0.80
1:B:28:PHE:HE1	1:B:112:ALA:CA	1.73	0.80
1:E:110:GLU:CD	1:E:111:ASP:N	2.35	0.80
1:D:141:GLU:C	1:D:145:LEU:CD2	2.49	0.80
1:E:194:ALA:O	1:E:197:LYS:HB3	1.81	0.80
1:E:300:THR:OG1	1:E:301:VAL:N	2.13	0.80
1:A:289:ILE:HG13	1:A:340:VAL:HG22	0.81	0.80
1:D:135:ASP:O	1:D:139:LEU:CD2	2.30	0.80
1:D:252:HIS:CE1	1:E:192:ARG:NH2	2.49	0.80
1:E:25:LEU:CD1	1:E:25:LEU:O	2.30	0.80
1:E:135:ASP:OD1	1:E:252:HIS:CE1	2.34	0.80
1:E:119:ARG:O	1:E:123:THR:HG22	1.83	0.79
1:A:26:ALA:O	1:A:29:LEU:CD1	2.25	0.79
1:E:138:VAL:O	1:E:142:ILE:HG22	1.81	0.79
1:D:141:GLU:O	1:D:145:LEU:CD2	2.30	0.79
1:G:148:VAL:CG2	1:G:148:VAL:O	2.30	0.79
1:G:132:MET:CE	1:G:132:MET:O	2.30	0.79
1:B:132:MET:CE	1:B:135:ASP:OD2	2.30	0.79
1:G:137:ALA:O	1:G:270:HIS:CE1	2.35	0.79
1:A:92:LYS:NZ	1:A:93:VAL:O	2.15	0.79
1:B:40:PHE:HE1	1:B:130:LEU:HD11	0.64	0.79
1:A:207:PHE:CE1	1:A:209:CYS:CB	2.65	0.79
1:A:274:ALA:HA	1:A:285:LYS:O	1.82	0.79
1:C:25:LEU:O	1:C:29:LEU:CD1	2.30	0.79
1:G:148:VAL:O	1:G:149:GLU:HB3	1.79	0.79
1:A:185:ILE:HD13	1:A:188:LEU:HD12	1.64	0.79
1:G:115:HIS:O	1:G:119:ARG:CB	2.30	0.79
1:D:135:ASP:O	1:D:139:LEU:CD1	2.30	0.79
1:D:25:LEU:CD1	1:D:25:LEU:C	2.47	0.79
1:C:26:ALA:O	1:C:29:LEU:CD1	2.30	0.79
1:G:141:GLU:OE1	1:G:141:GLU:CA	2.30	0.79
1:E:40:PHE:CZ	1:E:130:LEU:HD12	2.18	0.79
1:C:116:TYR:CG	1:C:117:ASP:N	2.42	0.79
1:D:32:PHE:C	1:D:32:PHE:HD1	1.85	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:141:GLU:CD	1:E:330:GLY:O	2.20	0.79
1:C:206:VAL:CB	1:C:246:GLU:OE1	2.31	0.79
1:B:30:LYS:CD	1:B:30:LYS:O	2.30	0.79
1:A:119:ARG:O	1:A:123:THR:CG2	2.30	0.79
1:C:116:TYR:C	1:C:116:TYR:CD2	2.55	0.79
1:E:60:SER:HA	1:E:95:THR:HA	1.65	0.79
1:B:125:GLN:HG3	1:C:66:LEU:CD1	2.12	0.79
1:B:132:MET:CA	1:B:135:ASP:OD2	2.30	0.78
1:E:192:ARG:O	1:E:195:LEU:CD1	2.30	0.78
1:A:205:ARG:NH1	1:A:293:MET:HG2	1.98	0.78
1:B:26:ALA:O	1:B:29:LEU:HB2	1.82	0.78
1:B:113:MET:CA	1:B:115:HIS:CD2	2.63	0.78
1:B:125:GLN:CG	1:C:66:LEU:CD1	2.62	0.78
1:B:109:ILE:HD13	1:B:110:GLU:CA	2.12	0.78
1:E:298:VAL:HG12	1:E:332:LEU:CD1	2.14	0.78
1:C:299:GLY:O	1:C:330:GLY:HA2	1.82	0.78
1:G:87:ILE:HG22	1:G:88:LYS:HG2	1.65	0.78
1:D:252:HIS:CE1	1:E:192:ARG:HH21	1.99	0.78
1:C:112:ALA:HB3	1:C:115:HIS:CE1	2.18	0.78
1:A:308:LEU:HD12	1:A:308:LEU:O	1.84	0.78
1:C:206:VAL:HG22	1:C:248:VAL:H	1.47	0.78
1:G:130:LEU:O	1:G:130:LEU:HD23	1.84	0.78
1:C:208:TYR:CB	1:C:291:LEU:HD11	2.09	0.78
1:A:208:TYR:OH	1:A:293:MET:CE	2.31	0.78
1:B:138:VAL:O	1:B:142:ILE:CG2	2.30	0.78
1:C:205:ARG:O	1:C:246:GLU:CB	2.30	0.78
1:A:55:ILE:HG21	1:A:301:VAL:CG2	2.12	0.78
1:E:191:ALA:O	1:E:195:LEU:CD2	2.31	0.78
1:D:36:VAL:O	1:D:37:LEU:C	2.22	0.77
1:C:25:LEU:O	1:C:29:LEU:HD11	1.83	0.77
1:C:25:LEU:CD2	1:C:26:ALA:N	2.30	0.77
1:G:106:ILE:HD13	1:G:107:TYR:CA	2.13	0.77
1:D:36:VAL:HG13	1:D:37:LEU:N	1.98	0.77
1:E:110:GLU:OE2	1:E:111:ASP:CA	2.30	0.77
1:E:145:LEU:HB2	1:E:332:LEU:HD23	0.78	0.77
1:B:30:LYS:C	1:B:30:LYS:CD	2.52	0.77
1:C:205:ARG:HE	1:C:294:HIS:HB3	1.50	0.77
1:B:68:ARG:O	1:B:69:THR:OG1	2.02	0.77
1:B:251:PRO:CB	1:C:199:TYR:CD1	2.65	0.77
1:C:288:VAL:HG12	1:C:341:VAL:HA	1.66	0.77
1:D:142:ILE:HG21	1:D:293:MET:HE3	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:GLN:HG2	1:C:66:LEU:HD12	1.67	0.77
1:C:53:ARG:NH1	1:C:62:GLN:O	2.17	0.77
1:D:142:ILE:O	1:D:145:LEU:CB	2.28	0.77
1:D:138:VAL:HG23	1:D:139:LEU:HD12	1.64	0.77
1:E:192:ARG:HA	1:E:195:LEU:HD11	0.79	0.77
1:C:208:TYR:CB	1:C:291:LEU:HG	2.13	0.77
1:E:65:VAL:HG12	1:E:333:ARG:HD3	1.67	0.77
1:A:25:LEU:O	1:A:25:LEU:CD1	2.30	0.77
1:E:327:MET:SD	1:E:327:MET:N	2.57	0.76
1:F:300:THR:OG1	1:F:301:VAL:N	2.16	0.76
1:F:29:LEU:O	1:F:29:LEU:CD2	2.30	0.76
1:A:205:ARG:NH1	1:A:293:MET:CG	2.48	0.76
1:F:24:LYS:H	1:F:24:LYS:HD2	1.49	0.76
1:D:142:ILE:C	1:D:145:LEU:HB2	2.05	0.76
1:C:36:VAL:HG11	1:C:126:LEU:HD21	1.66	0.76
1:F:141:GLU:HG2	1:F:329:HIS:NE2	2.01	0.76
1:A:207:PHE:CE1	1:A:290:GLY:HA3	2.15	0.76
1:C:195:LEU:HD23	1:C:202:ALA:HB1	1.63	0.76
1:D:27:LEU:C	1:D:27:LEU:CD1	2.46	0.76
1:D:36:VAL:O	1:D:38:THR:N	2.18	0.76
1:B:68:ARG:N	1:B:68:ARG:HD2	2.00	0.76
1:F:141:GLU:HG2	1:F:329:HIS:CD2	2.20	0.76
1:C:195:LEU:HD23	1:C:205:ARG:HH21	1.43	0.76
1:D:53:ARG:HB3	1:D:301:VAL:HG12	1.67	0.76
1:E:145:LEU:HD23	1:E:332:LEU:HD21	1.68	0.76
1:E:119:ARG:O	1:E:123:THR:CG2	2.33	0.76
1:A:207:PHE:HZ	1:A:209:CYS:SG	2.08	0.76
1:E:119:ARG:NH1	1:E:119:ARG:CB	2.49	0.76
1:E:298:VAL:O	1:E:333:ARG:CZ	2.33	0.76
1:C:225:ALA:HA	1:C:226:ALA:HB3	1.66	0.76
1:F:25:LEU:O	1:F:28:PHE:CE2	2.38	0.75
1:C:288:VAL:HG22	1:C:289:ILE:HG13	1.66	0.75
1:F:136:GLY:O	1:F:140:ALA:N	2.18	0.75
1:D:40:PHE:CE1	1:D:131:ALA:CA	2.67	0.75
1:G:110:GLU:CG	1:G:118:VAL:CB	2.64	0.75
1:E:192:ARG:CB	1:E:195:LEU:HD11	2.16	0.75
1:G:25:LEU:O	1:G:29:LEU:CG	2.29	0.75
1:E:68:ARG:HE	1:E:70:GLN:HE22	1.34	0.75
1:D:138:VAL:HG23	1:D:139:LEU:HD11	1.67	0.75
1:B:145:LEU:HD21	1:B:332:LEU:CG	1.98	0.75
1:B:334:PRO:CA	1:B:335:GLU:HB2	2.12	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:ARG:O	1:C:44:SER:OG	2.01	0.75
1:C:110:GLU:CD	1:C:118:VAL:HG21	2.07	0.75
1:A:106:ILE:C	1:A:107:TYR:CD2	2.58	0.75
1:D:252:HIS:HE1	1:E:192:ARG:NH2	1.84	0.75
1:A:29:LEU:CD2	1:A:310:ARG:HD3	2.17	0.75
1:A:309:GLU:HB3	1:A:322:ILE:CG1	1.93	0.75
1:E:135:ASP:OD1	1:E:252:HIS:NE2	2.19	0.75
1:E:298:VAL:CG1	1:E:332:LEU:HD12	2.17	0.75
1:E:24:LYS:HD2	1:E:24:LYS:O	1.87	0.75
1:E:110:GLU:CG	1:E:118:VAL:CG2	2.62	0.75
1:E:29:LEU:O	1:E:32:PHE:N	2.20	0.75
1:C:43:THR:HG21	1:C:128:GLU:CG	2.17	0.74
1:B:132:MET:SD	1:C:199:TYR:CE1	2.80	0.74
1:B:251:PRO:HB3	1:C:199:TYR:CD1	2.21	0.74
1:B:251:PRO:HG2	1:C:199:TYR:CE1	2.18	0.74
1:D:29:LEU:HD13	1:D:30:LYS:CA	2.16	0.74
1:G:130:LEU:HD22	1:G:131:ALA:N	2.00	0.74
1:E:135:ASP:CG	1:E:252:HIS:CE1	2.61	0.74
1:E:145:LEU:CD2	1:E:332:LEU:HG	2.15	0.74
1:G:110:GLU:O	1:G:114:ASN:CB	2.30	0.74
1:E:96:ILE:CD1	1:E:327:MET:O	2.35	0.74
1:C:40:PHE:CE1	1:C:131:ALA:HA	2.18	0.74
1:E:141:GLU:HG3	1:E:330:GLY:CA	2.18	0.74
1:G:25:LEU:CA	1:G:28:PHE:CE2	2.69	0.74
1:C:33:GLY:O	1:C:36:VAL:HG23	1.87	0.74
1:E:186:ALA:HB1	1:E:190:LYS:HZ2	1.52	0.74
1:B:101:THR:HG21	1:B:323:ALA:H	1.53	0.74
1:A:205:ARG:HH21	1:A:296:SER:H	1.33	0.74
1:F:143:ALA:O	1:F:147:ASN:ND2	2.21	0.73
1:F:24:LYS:HD2	1:F:24:LYS:N	2.02	0.73
1:D:227:ASN:O	1:D:231:LEU:N	2.19	0.73
1:D:142:ILE:CD1	1:D:145:LEU:HD23	2.16	0.73
1:A:32:PHE:O	1:A:36:VAL:HG23	1.87	0.73
1:B:69:THR:HG22	1:B:70:GLN:N	2.02	0.73
1:B:288:VAL:HA	1:B:341:VAL:HG12	1.69	0.73
1:C:206:VAL:HG23	1:C:247:VAL:CA	2.18	0.73
1:A:32:PHE:O	1:A:36:VAL:CG2	2.35	0.73
1:G:165:ILE:HG12	1:G:341:VAL:HG12	1.70	0.73
1:E:32:PHE:O	1:E:32:PHE:HD1	1.71	0.73
1:C:89:HIS:ND1	1:C:89:HIS:O	2.21	0.73
1:E:50:HIS:CE1	1:E:300:THR:HG22	2.23	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:214:TYR:HA	1:E:217:ILE:HG23	1.70	0.73
1:E:110:GLU:CD	1:E:111:ASP:CA	2.56	0.73
1:C:104:VAL:O	1:C:320:GLN:NE2	2.21	0.73
1:C:117:ASP:OD2	1:D:51:MET:HE1	1.86	0.73
1:G:28:PHE:CZ	1:G:111:ASP:CG	2.62	0.73
1:E:117:ASP:HB3	1:F:53:ARG:HD2	1.68	0.73
1:A:160:GLY:N	1:A:334:PRO:O	2.21	0.73
1:E:298:VAL:O	1:E:333:ARG:NH2	2.22	0.73
1:C:35:GLU:CA	1:C:38:THR:OG1	2.37	0.73
1:B:332:LEU:CD1	1:B:334:PRO:CD	2.66	0.73
1:B:24:LYS:HZ3	1:B:25:LEU:N	1.86	0.73
1:F:308:LEU:HB3	1:F:323:ALA:HA	1.69	0.73
1:F:145:LEU:HD21	1:F:334:PRO:HB3	1.69	0.73
1:C:28:PHE:CD2	1:C:29:LEU:N	2.51	0.73
1:B:70:GLN:HA	1:B:70:GLN:NE2	2.02	0.73
1:C:142:ILE:HA	1:C:145:LEU:HD23	1.70	0.73
1:B:209:CYS:SG	1:B:210:ASP:N	2.61	0.72
1:E:145:LEU:CG	1:E:332:LEU:CD2	2.64	0.72
1:C:119:ARG:O	1:C:123:THR:CG2	2.37	0.72
1:B:24:LYS:HE2	1:B:25:LEU:N	2.01	0.72
1:A:306:LEU:HB3	1:A:325:TYR:CZ	2.24	0.72
1:D:28:PHE:C	1:D:28:PHE:CD2	2.63	0.72
1:E:235:GLU:HG2	1:E:236:LYS:HG2	1.70	0.72
1:B:115:HIS:CD2	1:B:115:HIS:N	2.55	0.72
1:A:209:CYS:HA	1:A:290:GLY:CA	2.19	0.72
1:G:115:HIS:CD2	1:G:119:ARG:NH2	2.53	0.72
1:E:147:ASN:N	1:E:147:ASN:OD1	2.19	0.72
1:B:60:SER:HA	1:B:95:THR:HA	1.70	0.72
1:D:293:MET:N	1:D:293:MET:SD	2.60	0.72
1:C:42:ARG:CG	1:C:42:ARG:HH11	2.02	0.72
1:A:114:ASN:H	1:A:115:HIS:CD2	2.08	0.72
1:G:302:LYS:HA	1:G:327:MET:HA	1.71	0.72
1:A:207:PHE:HE2	1:A:247:VAL:HG23	1.51	0.72
1:D:26:ALA:O	1:D:29:LEU:CD1	2.36	0.72
1:A:309:GLU:CA	1:A:322:ILE:CG1	2.46	0.72
1:C:208:TYR:CB	1:C:291:LEU:CD1	2.68	0.72
1:D:113:MET:SD	1:D:114:ASN:ND2	2.63	0.72
1:E:333:ARG:HG3	1:E:333:ARG:NH1	2.03	0.72
1:E:25:LEU:HD12	1:E:26:ALA:N	2.05	0.72
1:G:115:HIS:NE2	1:G:119:ARG:NH2	2.38	0.71
1:C:207:PHE:HZ	1:C:245:PHE:CE2	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:119:ARG:HH11	1:E:119:ARG:CB	2.03	0.71
1:E:28:PHE:CG	1:E:111:ASP:OD1	2.27	0.71
1:A:289:ILE:HG22	1:A:290:GLY:N	2.06	0.71
1:F:25:LEU:C	1:F:28:PHE:CE2	2.63	0.71
1:B:27:LEU:CD2	1:B:30:LYS:HB3	2.18	0.71
1:G:32:PHE:O	1:G:36:VAL:HG23	1.90	0.71
1:B:300:THR:OG1	1:B:301:VAL:N	2.24	0.71
1:F:205:ARG:HG2	1:F:245:PHE:HA	1.73	0.71
1:C:310:ARG:NH2	1:C:319:ASP:OD2	2.23	0.71
1:G:120:SER:O	1:G:123:THR:OG1	2.06	0.71
1:B:108:ASP:CA	1:B:111:ASP:OD2	2.37	0.71
1:B:113:MET:SD	1:B:115:HIS:HE1	2.09	0.71
1:A:287:ASN:HD21	1:A:341:VAL:CG1	2.04	0.71
1:D:27:LEU:HD12	1:D:27:LEU:O	1.91	0.71
1:G:40:PHE:CD1	1:G:131:ALA:HB2	2.26	0.71
1:D:132:MET:HE1	1:D:251:PRO:HB2	1.72	0.71
1:B:49:ARG:NH2	1:B:246:GLU:OE2	2.23	0.71
1:C:207:PHE:CZ	1:C:245:PHE:CE2	2.78	0.71
1:E:115:HIS:ND1	1:E:119:ARG:NH2	2.38	0.71
1:E:117:ASP:HB3	1:F:53:ARG:CD	2.20	0.71
1:B:96:ILE:HG22	1:B:327:MET:HB3	1.73	0.71
1:E:147:ASN:HB3	1:E:283:VAL:H	1.55	0.71
1:E:335:GLU:O	1:E:336:ALA:C	2.28	0.71
1:C:36:VAL:CG1	1:C:126:LEU:HG	2.20	0.71
1:A:109:ILE:H	1:A:109:ILE:CD1	1.79	0.71
1:E:170:ASN:HA	1:E:342:PHE:HB3	1.72	0.71
1:C:38:THR:O	1:C:41:ALA:HB3	1.90	0.71
1:A:240:ARG:NH1	1:A:246:GLU:OE2	2.24	0.71
1:E:80:LEU:HD13	1:E:81:ASP:H	1.54	0.71
1:D:32:PHE:O	1:D:32:PHE:CD1	2.37	0.70
1:B:111:ASP:OD1	1:B:112:ALA:N	2.23	0.70
1:E:202:ALA:HB1	1:E:205:ARG:CZ	2.20	0.70
1:B:110:GLU:C	1:B:110:GLU:OE1	2.30	0.70
1:C:29:LEU:O	1:C:32:PHE:CB	2.39	0.70
1:C:42:ARG:N	1:C:44:SER:OG	2.24	0.70
1:G:150:SER:OG	1:G:334:PRO:O	2.09	0.70
1:E:108:ASP:OD1	1:E:108:ASP:C	2.30	0.70
1:D:142:ILE:N	1:D:145:LEU:CD2	2.53	0.70
1:D:45:VAL:CB	1:D:135:ASP:OD2	2.40	0.70
1:C:27:LEU:HD23	1:C:27:LEU:O	1.91	0.70
1:G:106:ILE:CG1	1:G:107:TYR:N	2.54	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:SER:O	1:B:59:LYS:NZ	2.23	0.70
1:B:130:LEU:HD12	1:B:131:ALA:N	2.05	0.70
1:C:119:ARG:NH1	1:C:119:ARG:CG	2.46	0.70
1:A:110:GLU:OE2	1:A:110:GLU:C	2.30	0.70
1:G:28:PHE:CZ	1:G:111:ASP:OD2	2.45	0.70
1:B:113:MET:O	1:B:114:ASN:CG	2.30	0.70
1:D:144:GLY:C	1:D:146:CYS:H	1.92	0.70
1:G:108:ASP:OD2	1:G:108:ASP:C	2.30	0.70
1:G:149:GLU:OE1	1:G:149:GLU:C	2.30	0.70
1:D:294:HIS:HD2	1:D:297:ALA:HB2	1.56	0.70
1:D:313:ARG:N	1:D:318:ALA:O	2.24	0.70
1:D:300:THR:OG1	1:D:301:VAL:N	2.18	0.70
1:C:195:LEU:HD21	1:C:202:ALA:HB3	1.72	0.70
1:E:40:PHE:CA	1:E:130:LEU:HD21	1.92	0.70
1:E:121:GLU:OE1	1:F:51:MET:HG2	1.92	0.70
1:B:181:GLY:HA2	1:B:184:ILE:HB	1.72	0.70
1:A:55:ILE:HG21	1:A:301:VAL:HG21	1.72	0.70
1:F:143:ALA:O	1:F:147:ASN:OD1	2.09	0.70
1:A:205:ARG:NE	1:A:295:ARG:HA	2.04	0.70
1:B:125:GLN:CG	1:C:66:LEU:HD12	2.22	0.70
1:E:299:GLY:HA2	1:E:333:ARG:HH22	1.56	0.69
1:E:111:ASP:OD1	1:E:111:ASP:C	2.30	0.69
1:C:201:PRO:CA	1:C:202:ALA:HB3	2.16	0.69
1:D:142:ILE:CA	1:D:145:LEU:CD2	2.26	0.69
1:C:37:LEU:HD13	1:C:306:LEU:HD11	1.73	0.69
1:G:132:MET:CE	1:G:132:MET:C	2.61	0.69
1:D:132:MET:CE	1:D:251:PRO:CG	2.71	0.69
1:A:240:ARG:HG3	1:A:241:ASN:H	1.56	0.69
1:C:195:LEU:CD2	1:C:205:ARG:CZ	2.49	0.69
1:C:206:VAL:HG23	1:C:246:GLU:OE1	1.91	0.69
1:F:32:PHE:O	1:F:35:GLU:N	2.25	0.69
1:G:106:ILE:O	1:G:106:ILE:HD13	1.91	0.69
1:A:23:ASP:C	1:A:23:ASP:OD1	2.30	0.69
1:C:117:ASP:CG	1:D:51:MET:HE1	2.13	0.69
1:B:114:ASN:O	1:B:118:VAL:HB	1.93	0.69
1:B:141:GLU:OE1	1:B:329:HIS:O	2.09	0.69
1:B:132:MET:SD	1:B:135:ASP:OD2	2.51	0.69
1:E:191:ALA:O	1:E:195:LEU:CG	2.39	0.69
1:C:108:ASP:OD1	1:C:111:ASP:CG	2.30	0.69
1:C:162:ALA:CB	1:C:337:ALA:O	2.41	0.69
1:E:141:GLU:HG3	1:E:330:GLY:HA3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:165:ILE:HD11	1:D:190:LYS:HD2	1.73	0.69
1:B:110:GLU:OE1	1:B:111:ASP:HA	1.92	0.69
1:F:25:LEU:O	1:F:28:PHE:CG	2.46	0.69
1:A:302:LYS:CG	1:A:327:MET:HB3	2.22	0.69
1:A:59:LYS:O	1:A:95:THR:OG1	2.10	0.69
1:A:311:ALA:O	1:A:319:ASP:OD1	2.11	0.69
1:C:27:LEU:HD23	1:C:28:PHE:CA	2.23	0.69
1:C:40:PHE:O	1:C:44:SER:HB3	1.93	0.69
1:A:29:LEU:HD22	1:A:310:ARG:HD3	1.75	0.69
1:B:28:PHE:CE1	1:B:112:ALA:CB	2.76	0.69
1:D:142:ILE:HG21	1:D:293:MET:CE	2.23	0.68
1:A:208:TYR:CE2	1:A:293:MET:CE	2.75	0.68
1:C:168:THR:O	1:C:169:GLN:NE2	2.26	0.68
1:G:314:ALA:HA	1:G:318:ALA:H	1.57	0.68
1:C:207:PHE:CE2	1:C:242:VAL:HG21	2.27	0.68
1:B:24:LYS:NZ	1:B:25:LEU:H	1.91	0.68
1:G:129:SER:O	1:G:132:MET:HG3	1.93	0.68
1:G:113:MET:CE	1:G:115:HIS:CB	2.66	0.68
1:G:25:LEU:HA	1:G:28:PHE:HD2	1.56	0.68
1:C:208:TYR:CB	1:C:291:LEU:HD21	2.16	0.68
1:C:200:VAL:O	1:C:202:ALA:HB3	1.93	0.68
1:B:145:LEU:CD2	1:B:332:LEU:HD12	1.91	0.68
1:G:106:ILE:C	1:G:107:TYR:CD2	2.67	0.68
1:B:332:LEU:CD1	1:B:334:PRO:CG	2.72	0.68
1:C:108:ASP:O	1:C:111:ASP:HB3	1.93	0.68
1:A:101:THR:C	1:B:71:ALA:HB1	2.14	0.68
1:F:68:ARG:O	1:F:68:ARG:NH1	2.23	0.68
1:B:312:ARG:NH1	1:B:317:GLN:O	2.17	0.68
1:C:195:LEU:CD2	1:C:205:ARG:HH22	1.71	0.68
1:C:206:VAL:CG2	1:C:248:VAL:HG23	2.16	0.68
1:E:135:ASP:OD1	1:E:135:ASP:C	2.30	0.68
1:D:209:CYS:HB2	1:D:249:GLU:HG2	1.75	0.68
1:A:289:ILE:CB	1:A:340:VAL:HG22	2.23	0.68
1:C:113:MET:SD	1:C:113:MET:O	2.51	0.68
1:B:281:VAL:HB	1:B:283:VAL:HG23	1.76	0.68
1:D:36:VAL:CG1	1:D:37:LEU:H	2.05	0.68
1:E:103:ASP:HB2	1:E:322:ILE:HA	1.76	0.68
1:F:163:THR:OG1	1:F:164:VAL:N	2.26	0.68
1:B:214:TYR:HA	1:B:217:ILE:HG23	1.76	0.67
1:A:309:GLU:O	1:A:322:ILE:CA	2.41	0.67
1:C:37:LEU:CD1	1:C:306:LEU:HD21	2.23	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:149:GLU:CD	1:G:150:SER:H	1.91	0.67
1:D:214:TYR:HD1	1:D:249:GLU:HB2	1.59	0.67
1:F:59:LYS:O	1:F:95:THR:OG1	2.09	0.67
1:C:186:ALA:O	1:C:189:THR:OG1	2.12	0.67
1:B:112:ALA:O	1:B:113:MET:SD	2.52	0.67
1:E:298:VAL:HA	1:E:332:LEU:HA	1.77	0.67
1:E:50:HIS:CD2	1:E:51:MET:H	2.12	0.67
1:G:110:GLU:HG2	1:G:118:VAL:CB	2.24	0.67
1:C:124:SER:OG	1:C:125:GLN:N	2.24	0.67
1:C:171:LYS:HE3	1:C:171:LYS:H	1.59	0.67
1:C:32:PHE:O	1:C:35:GLU:N	2.27	0.67
1:G:132:MET:HE2	1:G:132:MET:C	2.15	0.67
1:G:132:MET:SD	1:G:133:ALA:CA	2.83	0.67
1:G:271:VAL:O	1:G:271:VAL:HG22	1.93	0.67
1:D:136:GLY:HA2	1:D:139:LEU:HD22	1.76	0.67
1:E:192:ARG:C	1:E:195:LEU:CD1	2.62	0.67
1:B:327:MET:N	1:B:327:MET:SD	2.68	0.67
1:D:29:LEU:O	1:D:29:LEU:HD22	1.94	0.67
1:A:25:LEU:CD1	1:A:25:LEU:C	2.57	0.67
1:E:110:GLU:OE1	1:E:111:ASP:CA	2.42	0.67
1:A:306:LEU:HB3	1:A:325:TYR:CE1	2.30	0.67
1:A:211:PRO:HG3	1:A:251:PRO:HA	1.75	0.67
1:D:95:THR:HA	1:D:96:ILE:HG23	1.77	0.67
1:B:251:PRO:HG3	1:C:199:TYR:CD1	2.27	0.67
1:A:287:ASN:ND2	1:A:341:VAL:HG12	2.10	0.67
1:C:109:ILE:CD1	1:C:110:GLU:N	2.56	0.67
1:E:110:GLU:OE1	1:E:111:ASP:HA	1.94	0.67
1:E:119:ARG:HB3	1:E:119:ARG:NH1	2.08	0.66
1:A:205:ARG:HG3	1:A:293:MET:O	1.95	0.66
1:B:66:LEU:HD23	1:B:201:PRO:HD2	1.77	0.66
1:E:298:VAL:N	1:E:333:ARG:NH1	2.41	0.66
1:A:207:PHE:CZ	1:A:209:CYS:SG	2.87	0.66
1:E:24:LYS:HD2	1:E:24:LYS:C	2.16	0.66
1:G:300:THR:OG1	1:G:301:VAL:N	2.27	0.66
1:B:66:LEU:CD2	1:B:200:VAL:HB	2.26	0.66
1:F:25:LEU:C	1:F:28:PHE:CD2	2.68	0.66
1:B:24:LYS:HE2	1:B:25:LEU:HA	1.77	0.66
1:E:121:GLU:OE1	1:F:51:MET:CG	2.43	0.66
1:B:88:LYS:NZ	1:B:154:GLU:OE2	2.28	0.66
1:C:290:GLY:HA3	1:C:340:VAL:H	1.61	0.66
1:C:100:LEU:O	1:C:101:THR:OG1	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:HIS:CD2	1:B:115:HIS:H	2.14	0.66
1:A:207:PHE:HB2	1:A:291:LEU:O	1.94	0.66
1:C:119:ARG:NH1	1:C:119:ARG:CB	2.57	0.66
1:C:181:GLY:HA2	1:C:216:ALA:HB1	1.78	0.66
1:G:110:GLU:CA	1:G:114:ASN:HB3	2.22	0.66
1:B:145:LEU:CD2	1:B:332:LEU:HD11	2.21	0.66
1:C:208:TYR:CB	1:C:291:LEU:CD2	2.73	0.66
1:D:218:LEU:HD22	1:D:221:LEU:HD23	1.76	0.66
1:G:217:ILE:HG12	1:G:221:LEU:HB2	1.76	0.66
1:E:299:GLY:N	1:E:333:ARG:HH12	1.86	0.66
1:A:284:ALA:O	1:A:288:VAL:HB	1.94	0.66
1:C:110:GLU:C	1:C:110:GLU:OE2	2.34	0.66
1:G:28:PHE:CD1	1:G:111:ASP:OD2	2.48	0.66
1:B:28:PHE:CZ	1:B:111:ASP:C	2.69	0.66
1:E:298:VAL:C	1:E:333:ARG:CZ	2.63	0.66
1:F:28:PHE:C	1:F:28:PHE:CD1	2.69	0.66
1:E:24:LYS:O	1:E:24:LYS:HD3	1.95	0.66
1:A:205:ARG:HH21	1:A:296:SER:N	1.94	0.66
1:A:36:VAL:CG1	1:A:126:LEU:HD11	2.26	0.66
1:C:107:TYR:HA	1:C:318:ALA:HB3	1.78	0.66
1:F:254:THR:OG1	1:F:285:LYS:NZ	2.29	0.66
1:E:34:GLY:O	1:E:38:THR:HG23	1.96	0.66
1:B:106:ILE:CG2	1:B:122:TYR:OH	2.44	0.66
1:B:66:LEU:H	1:B:66:LEU:CD1	2.08	0.66
1:G:241:ASN:ND2	1:G:245:PHE:O	2.28	0.66
1:F:113:MET:SD	1:F:114:ASN:ND2	2.57	0.66
1:E:298:VAL:HG13	1:E:332:LEU:HD12	1.78	0.65
1:C:195:LEU:CD2	1:C:205:ARG:HH21	2.03	0.65
1:C:205:ARG:NE	1:C:294:HIS:HB3	2.10	0.65
1:D:40:PHE:O	1:D:43:THR:OG1	2.13	0.65
1:C:113:MET:CE	1:C:119:ARG:NH2	2.49	0.65
1:C:108:ASP:O	1:C:111:ASP:CB	2.45	0.65
1:B:27:LEU:HD22	1:B:27:LEU:O	1.96	0.65
1:E:142:ILE:CD1	1:E:142:ILE:O	2.30	0.65
1:F:250:VAL:HG21	1:F:253:LEU:HG	1.77	0.65
1:G:262:ARG:NH2	1:G:263:GLU:OE2	2.29	0.65
1:B:113:MET:O	1:B:114:ASN:ND2	2.30	0.65
1:E:195:LEU:O	1:E:199:TYR:N	2.30	0.65
1:D:36:VAL:HG12	1:D:37:LEU:H	1.61	0.65
1:E:186:ALA:HB1	1:E:190:LYS:NZ	2.12	0.65
1:E:110:GLU:OE1	1:E:111:ASP:N	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:132:MET:HE1	1:D:251:PRO:HG2	1.79	0.65
1:E:45:VAL:HG13	1:E:46:THR:HG23	1.78	0.65
1:E:298:VAL:HG13	1:E:332:LEU:CD1	2.25	0.65
1:A:309:GLU:N	1:A:322:ILE:HG13	2.12	0.65
1:B:64:PRO:O	1:B:333:ARG:NH1	2.26	0.65
1:G:106:ILE:C	1:G:107:TYR:HD2	2.00	0.65
1:A:41:ALA:HA	1:A:44:SER:HB3	1.78	0.65
1:B:45:VAL:HG13	1:B:46:THR:HG23	1.77	0.65
1:C:297:ALA:O	1:C:298:VAL:HG13	1.97	0.65
1:A:297:ALA:HB1	1:A:334:PRO:HB3	1.79	0.65
1:C:211:PRO:HG3	1:C:251:PRO:HA	1.79	0.65
1:D:288:VAL:HG11	1:D:340:VAL:HG13	1.79	0.65
1:G:141:GLU:HB2	1:G:270:HIS:HE1	1.62	0.65
1:A:208:TYR:OH	1:A:293:MET:HE1	1.97	0.65
1:E:291:LEU:HD13	1:E:339:ALA:HB2	1.79	0.65
1:B:110:GLU:OE1	1:B:111:ASP:N	2.30	0.65
1:A:285:LYS:HG2	1:A:286:ASP:N	2.11	0.65
1:F:25:LEU:HB2	1:F:28:PHE:CE2	2.30	0.65
1:B:125:GLN:NE2	1:C:66:LEU:O	2.26	0.65
1:A:53:ARG:NH2	1:F:114:ASN:OD1	2.30	0.65
1:G:115:HIS:CE1	1:G:119:ARG:NH2	2.65	0.64
1:E:195:LEU:O	1:E:199:TYR:O	2.15	0.64
1:G:141:GLU:H	1:G:270:HIS:CE1	2.14	0.64
1:A:57:SER:N	1:A:303:LEU:HD13	2.09	0.64
1:C:329:HIS:CD2	1:C:331:GLY:H	2.15	0.64
1:G:53:ARG:NH1	1:G:62:GLN:O	2.30	0.64
1:F:295:ARG:NH2	1:F:296:SER:OG	2.28	0.64
1:A:70:GLN:NE2	1:F:129:SER:OG	2.30	0.64
1:C:35:GLU:O	1:C:39:ALA:N	2.30	0.64
1:B:24:LYS:HD2	1:B:25:LEU:N	2.11	0.64
1:B:24:LYS:HZ3	1:B:24:LYS:N	1.94	0.64
1:G:49:ARG:HH22	1:G:248:VAL:HG21	1.63	0.64
1:B:55:ILE:O	1:B:304:ARG:NH2	2.31	0.64
1:C:248:VAL:HG12	1:C:249:GLU:H	1.63	0.64
1:A:287:ASN:CG	1:A:341:VAL:HB	2.18	0.64
1:C:110:GLU:OE1	1:C:122:TYR:HD2	1.81	0.64
1:C:110:GLU:HG2	1:C:122:TYR:HE2	1.62	0.64
1:G:25:LEU:HB3	1:G:28:PHE:CE2	2.33	0.64
1:G:28:PHE:C	1:G:28:PHE:CD1	2.70	0.64
1:D:200:VAL:HG22	1:D:201:PRO:HD2	1.79	0.64
1:C:43:THR:CG2	1:C:128:GLU:HG3	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:110:GLU:N	1:G:114:ASN:ND2	2.45	0.64
1:B:50:HIS:NE2	1:B:298:VAL:HB	2.12	0.64
1:B:139:LEU:HA	1:B:142:ILE:CG2	2.28	0.64
1:E:139:LEU:O	1:E:142:ILE:HG23	1.98	0.64
1:G:109:ILE:C	1:G:114:ASN:HD22	2.01	0.64
1:E:106:ILE:HD12	1:E:108:ASP:HA	1.80	0.64
1:A:300:THR:OG1	1:A:301:VAL:N	2.28	0.64
1:B:106:ILE:C	1:B:107:TYR:CD2	2.67	0.64
1:A:45:VAL:HG22	1:A:250:VAL:HG11	1.80	0.64
1:F:332:LEU:HD13	1:F:333:ARG:H	1.62	0.64
1:A:302:LYS:CE	1:A:327:MET:CE	2.76	0.64
1:G:303:LEU:HD22	1:G:304:ARG:HG3	1.80	0.64
1:B:113:MET:CG	1:B:115:HIS:NE2	2.61	0.63
1:B:24:LYS:CD	1:B:25:LEU:N	2.59	0.63
1:A:327:MET:SD	1:A:328:GLY:N	2.66	0.63
1:A:161:THR:H	1:A:336:ALA:HA	1.62	0.63
1:C:129:SER:OG	1:D:70:GLN:O	2.15	0.63
1:C:114:ASN:N	1:C:114:ASN:OD1	2.30	0.63
1:C:49:ARG:NH2	1:C:246:GLU:OE2	2.30	0.63
1:A:294:HIS:NE2	1:A:337:ALA:HA	2.11	0.63
1:G:78:GLU:OE2	1:G:79:ASN:N	2.31	0.63
1:B:53:ARG:NH1	1:B:62:GLN:O	2.23	0.63
1:D:29:LEU:C	1:D:29:LEU:HD22	2.19	0.63
1:G:25:LEU:CA	1:G:28:PHE:CD2	2.70	0.63
1:B:27:LEU:HD23	1:B:30:LYS:CB	2.22	0.63
1:B:92:LYS:HZ1	1:B:333:ARG:NE	1.96	0.63
1:G:54:SER:OG	1:G:302:LYS:N	2.31	0.63
1:F:276:LYS:HZ2	1:F:278:GLU:H	1.46	0.63
1:C:205:ARG:HG2	1:C:294:HIS:HB3	1.80	0.63
1:D:128:GLU:OE1	1:D:129:SER:N	2.30	0.63
1:A:208:TYR:OH	1:A:293:MET:SD	2.57	0.63
1:C:43:THR:CB	1:C:128:GLU:HG3	2.29	0.63
1:G:119:ARG:CG	1:G:119:ARG:NH1	2.39	0.63
1:C:36:VAL:CG1	1:C:126:LEU:HD21	2.28	0.63
1:C:162:ALA:O	1:C:164:VAL:N	2.31	0.63
1:F:167:THR:OG1	1:F:168:THR:N	2.32	0.63
1:B:113:MET:O	1:B:114:ASN:CB	2.47	0.63
1:B:161:THR:OG1	1:B:162:ALA:N	2.32	0.63
1:G:165:ILE:HG12	1:G:341:VAL:CG1	2.28	0.63
1:E:138:VAL:O	1:E:142:ILE:CG2	2.45	0.63
1:B:145:LEU:HD23	1:B:332:LEU:CD1	2.24	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:50:HIS:CD2	1:E:298:VAL:HG23	2.34	0.62
1:C:36:VAL:HG13	1:C:126:LEU:HG	1.80	0.62
1:A:309:GLU:HB2	1:A:322:ILE:HD12	1.81	0.62
1:B:332:LEU:HD12	1:B:334:PRO:HG2	1.80	0.62
1:F:145:LEU:CD2	1:F:334:PRO:HB3	2.29	0.62
1:F:36:VAL:HG21	1:F:126:LEU:HD11	1.81	0.62
1:D:142:ILE:HA	1:D:145:LEU:CG	2.25	0.62
1:D:110:GLU:OE1	1:D:111:ASP:N	2.30	0.62
1:D:59:LYS:O	1:D:96:ILE:HG21	1.98	0.62
1:A:207:PHE:CE1	1:A:209:CYS:CA	2.83	0.62
1:G:110:GLU:C	1:G:114:ASN:CB	2.65	0.62
1:C:40:PHE:CE1	1:C:131:ALA:CA	2.78	0.62
1:B:128:GLU:OE1	1:C:68:ARG:CG	2.47	0.62
1:A:57:SER:H	1:A:303:LEU:CD1	2.07	0.62
1:C:170:ASN:HB3	1:C:172:ALA:H	1.64	0.62
1:D:142:ILE:CD1	1:D:145:LEU:HD21	2.20	0.62
1:G:27:LEU:C	1:G:27:LEU:CD1	2.58	0.62
1:A:207:PHE:HE2	1:A:247:VAL:CG2	2.13	0.62
1:A:209:CYS:HA	1:A:290:GLY:HA3	1.82	0.62
1:E:192:ARG:CA	1:E:195:LEU:CG	2.74	0.62
1:D:128:GLU:OE2	1:D:129:SER:CA	2.47	0.62
1:G:209:CYS:SG	1:G:210:ASP:N	2.73	0.62
1:E:135:ASP:OD2	1:E:252:HIS:CE1	2.52	0.62
1:F:171:LYS:HD2	1:F:174:LEU:HD12	1.82	0.62
1:A:110:GLU:HB2	1:A:114:ASN:ND2	2.15	0.62
1:D:110:GLU:HG2	1:D:113:MET:O	2.00	0.62
1:F:51:MET:SD	1:F:295:ARG:NH2	2.72	0.62
1:F:135:ASP:OD1	1:F:252:HIS:NE2	2.31	0.62
1:D:142:ILE:HD12	1:D:145:LEU:CG	2.29	0.62
1:B:59:LYS:HB2	1:B:96:ILE:HD13	1.81	0.62
1:B:117:ASP:OD2	1:C:51:MET:HE1	1.98	0.62
1:C:24:LYS:CG	1:C:25:LEU:N	2.63	0.62
1:A:27:LEU:HD12	1:A:28:PHE:HA	1.81	0.62
1:A:315:ASN:OD1	1:A:315:ASN:N	2.31	0.62
1:B:251:PRO:CG	1:C:199:TYR:CZ	2.53	0.62
1:E:192:ARG:HG2	1:E:193:ALA:N	2.14	0.62
1:C:98:GLY:HA2	1:D:75:ALA:HB2	1.82	0.62
1:B:28:PHE:HZ	1:B:112:ALA:CA	2.07	0.61
1:A:209:CYS:HA	1:A:290:GLY:HA2	1.82	0.61
1:E:59:LYS:O	1:E:95:THR:OG1	2.12	0.61
1:B:132:MET:HE3	1:B:132:MET:N	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:36:VAL:CG1	1:C:126:LEU:CG	2.78	0.61
1:G:26:ALA:CA	1:G:29:LEU:HD12	2.23	0.61
1:A:294:HIS:HD2	1:A:337:ALA:CA	2.11	0.61
1:B:50:HIS:CD2	1:B:51:MET:H	2.18	0.61
1:C:142:ILE:O	1:C:145:LEU:HB2	2.01	0.61
1:F:288:VAL:HG21	1:F:340:VAL:O	1.99	0.61
1:G:206:VAL:HA	1:G:246:GLU:HG2	1.81	0.61
1:C:33:GLY:O	1:C:37:LEU:N	2.31	0.61
1:C:108:ASP:CG	1:C:111:ASP:CG	2.59	0.61
1:D:104:VAL:HG22	1:D:321:ILE:HD11	1.81	0.61
1:B:276:LYS:HD2	1:B:279:GLY:HA3	1.82	0.61
1:E:299:GLY:HA3	1:E:333:ARG:HH22	1.65	0.61
1:C:115:HIS:CD2	1:C:115:HIS:O	2.53	0.61
1:F:201:PRO:O	1:F:205:ARG:NH2	2.33	0.61
1:A:287:ASN:O	1:A:288:VAL:HG12	2.00	0.61
1:B:110:GLU:OE1	1:B:111:ASP:CA	2.49	0.61
1:C:294:HIS:CE1	1:C:335:GLU:HB2	2.35	0.61
1:A:303:LEU:O	1:A:304:ARG:HB2	1.99	0.61
1:G:275:ASN:OD1	1:G:275:ASN:N	2.33	0.61
1:B:109:ILE:C	1:B:109:ILE:CD1	2.66	0.61
1:D:135:ASP:C	1:D:139:LEU:HD22	2.20	0.61
1:G:178:VAL:O	1:G:182:LYS:NZ	2.28	0.61
1:C:36:VAL:CG1	1:C:126:LEU:CD2	2.79	0.61
1:A:119:ARG:CG	1:A:119:ARG:NH1	2.47	0.61
1:A:128:GLU:OE2	1:A:129:SER:N	2.34	0.61
1:A:102:ALA:HB2	1:B:71:ALA:HA	1.83	0.60
1:B:125:GLN:HG2	1:C:66:LEU:CD1	2.28	0.60
1:C:298:VAL:HG12	1:C:331:GLY:C	2.20	0.60
1:C:125:GLN:HG2	1:D:66:LEU:HB3	1.83	0.60
1:B:214:TYR:O	1:B:217:ILE:HG12	2.01	0.60
1:F:166:GLU:HA	1:F:341:VAL:HG13	1.83	0.60
1:B:118:VAL:CG1	1:B:119:ARG:N	2.64	0.60
1:C:208:TYR:HB3	1:C:291:LEU:CG	2.25	0.60
1:G:180:LEU:O	1:G:184:ILE:N	2.35	0.60
1:F:293:MET:HA	1:F:336:ALA:O	2.01	0.60
1:D:196:THR:O	1:D:199:TYR:N	2.34	0.60
1:E:299:GLY:O	1:E:331:GLY:N	2.33	0.60
1:B:67:GLY:HA3	1:B:68:ARG:NH1	2.16	0.60
1:B:131:ALA:O	1:B:135:ASP:CG	2.40	0.60
1:B:139:LEU:HA	1:B:142:ILE:HG21	1.84	0.60
1:A:288:VAL:O	1:A:289:ILE:CD1	2.50	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206:VAL:HG23	1:C:247:VAL:C	2.21	0.60
1:G:167:THR:C	1:G:169:GLN:H	2.04	0.60
1:B:286:ASP:N	1:B:286:ASP:OD2	2.33	0.60
1:B:108:ASP:O	1:B:111:ASP:CG	2.40	0.60
1:D:45:VAL:HB	1:D:135:ASP:OD2	2.02	0.60
1:F:303:LEU:HB2	1:F:326:ALA:HB2	1.82	0.60
1:B:114:ASN:CB	1:B:118:VAL:HB	2.32	0.60
1:F:253:LEU:O	1:F:285:LYS:NZ	2.27	0.60
1:G:234:PRO:HD2	1:G:236:LYS:HE3	1.82	0.60
1:B:332:LEU:HD12	1:B:334:PRO:CG	2.30	0.60
1:G:167:THR:HG23	1:G:341:VAL:O	2.01	0.60
1:E:50:HIS:CD2	1:E:51:MET:N	2.70	0.60
1:B:92:LYS:NZ	1:B:333:ARG:HE	1.98	0.60
1:C:31:VAL:CG1	1:C:32:PHE:N	2.65	0.60
1:A:29:LEU:HD21	1:A:310:ARG:HD3	1.84	0.60
1:E:109:ILE:N	1:E:109:ILE:CD1	2.30	0.60
1:A:287:ASN:ND2	1:A:341:VAL:CG1	2.64	0.60
1:D:293:MET:HB3	1:D:337:ALA:HB2	1.82	0.60
1:D:290:GLY:O	1:D:339:ALA:HA	2.02	0.60
1:G:232:ILE:HG22	1:G:234:PRO:HD3	1.84	0.60
1:A:163:THR:HB	1:A:338:GLY:HA3	1.83	0.60
1:B:24:LYS:HZ3	1:B:24:LYS:C	2.04	0.59
1:E:141:GLU:HG3	1:E:330:GLY:O	2.02	0.59
1:F:174:LEU:HD22	1:F:180:LEU:HD21	1.84	0.59
1:D:81:ASP:N	1:D:81:ASP:OD1	2.33	0.59
1:B:114:ASN:O	1:B:118:VAL:N	2.31	0.59
1:E:298:VAL:HG12	1:E:332:LEU:HD12	1.82	0.59
1:G:119:ARG:O	1:G:123:THR:HG23	2.01	0.59
1:C:202:ALA:HB1	1:C:205:ARG:HH21	1.63	0.59
1:B:92:LYS:HZ1	1:B:333:ARG:HH21	1.49	0.59
1:D:310:ARG:HG2	1:D:321:ILE:HG22	1.85	0.59
1:C:275:ASN:HA	1:C:285:LYS:HE2	1.85	0.59
1:B:131:ALA:O	1:B:132:MET:HE2	2.02	0.59
1:B:332:LEU:CD1	1:B:334:PRO:HD2	2.29	0.59
1:G:270:HIS:HE2	1:G:329:HIS:HE1	1.49	0.59
1:E:61:ALA:N	1:E:94:ILE:O	2.33	0.59
1:G:113:MET:HE3	1:G:113:MET:C	2.08	0.59
1:B:62:GLN:HB3	1:B:93:VAL:HG12	1.84	0.59
1:F:27:LEU:C	1:F:27:LEU:HD12	2.20	0.59
1:C:24:LYS:HG3	1:C:25:LEU:N	2.18	0.59
1:A:294:HIS:CD2	1:A:337:ALA:CA	2.73	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:LEU:HD11	1:E:310:ARG:CZ	2.30	0.59
1:G:28:PHE:CE1	1:G:29:LEU:HD23	2.37	0.59
1:E:209:CYS:SG	1:E:210:ASP:N	2.75	0.59
1:E:298:VAL:HA	1:E:333:ARG:NH1	2.11	0.59
1:E:239:ILE:HB	1:E:247:VAL:HB	1.84	0.59
1:B:227:ASN:O	1:B:227:ASN:ND2	2.26	0.59
1:C:108:ASP:CG	1:C:111:ASP:HB3	2.23	0.59
1:C:35:GLU:OE1	1:C:119:ARG:O	2.21	0.59
1:G:25:LEU:HB3	1:G:28:PHE:HE2	1.68	0.59
1:E:56:SER:OG	1:E:304:ARG:NH2	2.29	0.59
1:E:110:GLU:HG3	1:E:118:VAL:CB	2.33	0.59
1:C:235:GLU:OE1	1:C:236:LYS:N	2.26	0.59
1:E:284:ALA:H	1:E:288:VAL:HG21	1.68	0.59
1:B:307:ALA:HB3	1:B:324:LYS:HB3	1.85	0.59
1:B:131:ALA:C	1:B:132:MET:CE	2.71	0.58
1:G:110:GLU:N	1:G:114:ASN:HD22	2.01	0.58
1:C:201:PRO:HA	1:C:202:ALA:CB	2.13	0.58
1:B:134:ALA:O	1:B:138:VAL:CG2	2.50	0.58
1:D:142:ILE:HD12	1:D:145:LEU:CD2	2.32	0.58
1:C:188:LEU:HB3	1:C:245:PHE:HE2	1.67	0.58
1:C:294:HIS:NE2	1:C:335:GLU:OE2	2.35	0.58
1:F:28:PHE:HD1	1:F:29:LEU:N	1.95	0.58
1:B:66:LEU:HD22	1:B:66:LEU:O	2.02	0.58
1:C:32:PHE:CE1	1:C:36:VAL:CG2	2.87	0.58
1:C:208:TYR:HB3	1:C:291:LEU:HD21	1.82	0.58
1:C:135:ASP:OD1	1:C:135:ASP:N	2.34	0.58
1:G:113:MET:CG	1:G:114:ASN:H	2.09	0.58
1:B:298:VAL:HA	1:B:332:LEU:HD22	1.86	0.58
1:C:32:PHE:CZ	1:C:126:LEU:HD23	2.39	0.58
1:G:165:ILE:HD13	1:G:166:GLU:CA	2.32	0.58
1:D:161:THR:OG1	1:D:162:ALA:N	2.35	0.58
1:A:41:ALA:C	1:A:43:THR:H	2.07	0.58
1:B:117:ASP:OD2	1:C:51:MET:HE3	2.02	0.58
1:B:63:PHE:CZ	1:B:299:GLY:HA3	2.38	0.58
1:G:132:MET:SD	1:G:133:ALA:HA	2.43	0.58
1:A:279:GLY:O	1:A:280:ASN:ND2	2.37	0.58
1:C:214:TYR:CD1	1:C:249:GLU:HG2	2.39	0.58
1:B:161:THR:HG22	1:B:335:GLU:N	2.18	0.58
1:A:26:ALA:HA	1:A:29:LEU:CD1	2.31	0.58
1:A:250:VAL:HB	1:A:251:PRO:HD2	1.86	0.58
1:G:146:CYS:SG	1:G:336:ALA:CA	2.92	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:28:PHE:CD2	1:E:111:ASP:OD2	2.56	0.58
1:E:100:LEU:HA	1:F:72:ALA:O	2.03	0.58
1:D:57:SER:O	1:D:59:LYS:NZ	2.35	0.58
1:G:101:THR:O	1:G:262:ARG:NH1	2.34	0.58
1:B:214:TYR:OH	1:C:192:ARG:NE	2.36	0.57
1:C:116:TYR:C	1:C:116:TYR:HD2	2.03	0.57
1:G:143:ALA:HB1	1:G:272:PHE:CB	2.34	0.57
1:D:295:ARG:NE	1:D:296:SER:OG	2.38	0.57
1:C:240:ARG:HG3	1:C:241:ASN:H	1.69	0.57
1:F:310:ARG:HB3	1:F:321:ILE:HG22	1.86	0.57
1:A:139:LEU:HD21	1:A:291:LEU:HD11	1.85	0.57
1:C:32:PHE:CE1	1:C:36:VAL:HG22	2.39	0.57
1:G:45:VAL:HG22	1:G:46:THR:HG23	1.86	0.57
1:F:141:GLU:CG	1:F:329:HIS:CD2	2.87	0.57
1:F:212:ASP:O	1:F:215:SER:OG	2.22	0.57
1:C:206:VAL:HA	1:C:246:GLU:C	2.17	0.57
1:E:293:MET:HA	1:E:337:ALA:H	1.69	0.57
1:C:71:ALA:HB1	1:C:72:ALA:HA	1.85	0.57
1:C:271:VAL:H	1:C:274:ALA:HB2	1.69	0.57
1:E:189:THR:HG23	1:E:243:MET:CG	2.35	0.57
1:A:302:LYS:HE2	1:A:327:MET:SD	2.45	0.57
1:F:147:ASN:N	1:F:147:ASN:OD1	2.36	0.57
1:B:285:LYS:O	1:B:288:VAL:N	2.32	0.57
1:C:171:LYS:HB3	1:C:342:PHE:CZ	2.39	0.57
1:A:141:GLU:OE1	1:A:142:ILE:HG12	2.05	0.57
1:B:115:HIS:N	1:B:115:HIS:HD2	2.01	0.57
1:A:287:ASN:HD22	1:A:287:ASN:C	2.04	0.57
1:C:108:ASP:CG	1:C:111:ASP:CB	2.73	0.57
1:C:110:GLU:OE1	1:C:122:TYR:HE2	1.85	0.57
1:B:28:PHE:HE1	1:B:112:ALA:CB	2.17	0.57
1:G:171:LYS:H	1:G:342:PHE:HE2	1.50	0.57
1:E:29:LEU:O	1:E:30:LYS:C	2.42	0.57
1:F:183:GLU:OE1	1:F:184:ILE:N	2.38	0.57
1:G:115:HIS:HA	1:G:119:ARG:NH1	2.20	0.57
1:E:29:LEU:O	1:E:31:VAL:N	2.37	0.57
1:C:188:LEU:HD13	1:C:207:PHE:CZ	2.40	0.57
1:B:24:LYS:HZ3	1:B:24:LYS:HB3	1.52	0.57
1:C:312:ARG:NH1	1:C:318:ALA:O	2.37	0.57
1:D:290:GLY:HA3	1:D:340:VAL:H	1.70	0.57
1:A:207:PHE:CE1	1:A:290:GLY:CA	2.81	0.57
1:B:141:GLU:CD	1:B:330:GLY:CA	2.58	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:ARG:HH11	1:C:119:ARG:CB	2.15	0.57
1:A:108:ASP:HB3	1:A:111:ASP:HB2	1.85	0.57
1:A:55:ILE:HG23	1:A:301:VAL:CG2	2.35	0.57
1:B:206:VAL:HA	1:B:246:GLU:H	1.70	0.57
1:B:139:LEU:C	1:B:142:ILE:CG2	2.71	0.56
1:D:28:PHE:HD2	1:D:29:LEU:H	1.49	0.56
1:C:119:ARG:NH1	1:C:119:ARG:HG3	2.01	0.56
1:C:41:ALA:O	1:C:42:ARG:CB	2.41	0.56
1:E:110:GLU:CD	1:E:118:VAL:HG21	2.25	0.56
1:F:242:VAL:HG22	1:F:243:MET:H	1.70	0.56
1:E:25:LEU:CD1	1:E:310:ARG:CZ	2.79	0.56
1:F:143:ALA:CB	1:F:272:PHE:CD2	2.89	0.56
1:F:272:PHE:O	1:F:274:ALA:N	2.37	0.56
1:F:141:GLU:CG	1:F:329:HIS:NE2	2.69	0.56
1:B:319:ASP:OD2	1:B:320:GLN:N	2.38	0.56
1:E:294:HIS:NE2	1:E:295:ARG:O	2.37	0.56
1:F:181:GLY:HA3	1:F:220:ALA:HB2	1.87	0.56
1:B:139:LEU:CA	1:B:142:ILE:CG2	2.84	0.56
1:A:289:ILE:HG13	1:A:340:VAL:HG23	1.77	0.56
1:A:309:GLU:CB	1:A:322:ILE:HD12	2.27	0.56
1:C:207:PHE:O	1:C:248:VAL:O	2.23	0.56
1:F:32:PHE:O	1:F:34:GLY:N	2.38	0.56
1:E:141:GLU:CG	1:E:330:GLY:O	2.52	0.56
1:F:308:LEU:CB	1:F:323:ALA:HA	2.34	0.56
1:E:234:PRO:O	1:E:236:LYS:N	2.38	0.56
1:C:271:VAL:HG23	1:C:274:ALA:HA	1.86	0.56
1:C:137:ALA:O	1:C:140:ALA:N	2.37	0.56
1:A:212:ASP:N	1:A:212:ASP:OD2	2.30	0.56
1:B:121:GLU:HA	1:B:121:GLU:OE1	2.05	0.56
1:G:44:SER:OG	1:G:135:ASP:HB2	2.05	0.56
1:A:276:LYS:HZ2	1:A:278:GLU:H	1.52	0.56
1:B:210:ASP:OD2	1:B:213:SER:OG	2.23	0.56
1:G:110:GLU:OE1	1:G:118:VAL:HB	2.05	0.56
1:C:188:LEU:CD2	1:C:207:PHE:CZ	2.85	0.56
1:F:29:LEU:O	1:F:32:PHE:HB3	2.05	0.56
1:A:114:ASN:O	1:A:114:ASN:CG	2.43	0.56
1:D:205:ARG:HB3	1:D:205:ARG:CZ	2.35	0.56
1:D:164:VAL:HA	1:D:339:ALA:H	1.70	0.56
1:A:307:ALA:O	1:A:324:LYS:N	2.38	0.56
1:B:115:HIS:O	1:B:119:ARG:HB2	2.05	0.56
1:E:299:GLY:CA	1:E:333:ARG:NH2	2.63	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:GLN:NE2	1:A:321:ILE:O	2.32	0.56
1:B:121:GLU:CD	1:B:121:GLU:O	2.44	0.56
1:A:73:TYR:HE1	1:F:102:ALA:HB2	1.70	0.56
1:D:136:GLY:CA	1:D:139:LEU:HD22	2.35	0.56
1:E:233:ASP:OD2	1:E:238:SER:N	2.37	0.56
1:F:130:LEU:HD11	1:F:325:TYR:HD2	1.71	0.56
1:G:113:MET:O	1:G:115:HIS:N	2.39	0.56
1:B:25:LEU:HD13	1:B:25:LEU:C	2.26	0.56
1:B:28:PHE:CZ	1:B:112:ALA:N	2.74	0.56
1:E:53:ARG:HD3	1:E:63:PHE:CD1	2.41	0.56
1:C:202:ALA:CB	1:C:205:ARG:HH21	2.19	0.56
1:C:48:SER:OG	1:C:49:ARG:N	2.36	0.56
1:G:106:ILE:HD11	1:G:107:TYR:O	2.05	0.56
1:B:132:MET:HE2	1:B:135:ASP:CG	2.25	0.56
1:G:110:GLU:CD	1:G:118:VAL:HG11	2.18	0.56
1:A:66:LEU:HD23	1:A:89:HIS:HE1	1.69	0.56
1:G:130:LEU:HD23	1:G:131:ALA:CA	2.36	0.56
1:F:147:ASN:HA	1:F:283:VAL:HG21	1.87	0.56
1:D:225:ALA:HB1	1:D:226:ALA:C	2.25	0.56
1:C:290:GLY:HA2	1:C:340:VAL:HG22	1.87	0.56
1:E:50:HIS:HE2	1:E:299:GLY:HA2	1.71	0.55
1:E:297:ALA:O	1:E:332:LEU:HD12	2.06	0.55
1:C:29:LEU:O	1:C:32:PHE:N	2.39	0.55
1:D:36:VAL:HG22	1:D:39:ALA:HB3	1.87	0.55
1:F:32:PHE:O	1:F:33:GLY:C	2.43	0.55
1:E:167:THR:OG1	1:E:168:THR:N	2.39	0.55
1:C:162:ALA:C	1:C:164:VAL:H	2.09	0.55
1:C:183:GLU:OE1	1:C:183:GLU:N	2.39	0.55
1:C:49:ARG:HH12	1:C:248:VAL:HG21	1.69	0.55
1:E:110:GLU:OE2	1:E:110:GLU:C	2.43	0.55
1:E:28:PHE:HE1	1:E:111:ASP:O	1.85	0.55
1:C:299:GLY:H	1:C:330:GLY:C	2.09	0.55
1:E:232:ILE:HG22	1:E:240:ARG:HB2	1.88	0.55
1:A:312:ARG:NH1	1:A:318:ALA:O	2.40	0.55
1:F:164:VAL:HG12	1:F:339:ALA:H	1.72	0.55
1:D:46:THR:CB	1:D:135:ASP:OD1	2.54	0.55
1:D:128:GLU:OE2	1:D:128:GLU:C	2.44	0.55
1:C:108:ASP:OD2	1:C:111:ASP:HB3	2.06	0.55
1:C:108:ASP:O	1:C:111:ASP:CG	2.45	0.55
1:F:272:PHE:HE1	1:F:285:LYS:HB2	1.71	0.55
1:B:66:LEU:HD12	1:B:66:LEU:H	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:GLN:O	1:A:129:SER:OG	2.25	0.55
1:F:25:LEU:HD13	1:F:26:ALA:N	2.20	0.55
1:E:325:TYR:CG	1:E:326:ALA:N	2.75	0.55
1:D:300:THR:HG21	1:D:329:HIS:N	2.21	0.55
1:E:226:ALA:O	1:E:228:TYR:N	2.40	0.55
1:E:298:VAL:HG12	1:E:332:LEU:HA	1.87	0.55
1:F:32:PHE:CE1	1:F:123:THR:HG22	2.41	0.55
1:G:102:ALA:HB2	1:G:262:ARG:CZ	2.37	0.55
1:F:124:SER:OG	1:F:125:GLN:N	2.39	0.55
1:F:29:LEU:HD22	1:F:29:LEU:C	2.21	0.55
1:F:200:VAL:HG22	1:F:201:PRO:HD2	1.87	0.55
1:C:103:ASP:HB3	1:C:321:ILE:HD12	1.87	0.55
1:B:181:GLY:O	1:B:185:ILE:HG13	2.06	0.55
1:F:36:VAL:HA	1:F:39:ALA:HB3	1.89	0.55
1:B:39:ALA:O	1:B:43:THR:OG1	2.21	0.55
1:G:92:LYS:HD3	1:G:332:LEU:N	2.22	0.55
1:A:287:ASN:HD21	1:A:341:VAL:HG12	1.70	0.55
1:C:206:VAL:HG23	1:C:248:VAL:N	2.19	0.55
1:B:141:GLU:CD	1:B:331:GLY:N	2.59	0.55
1:B:63:PHE:HZ	1:B:299:GLY:HA3	1.72	0.55
1:G:268:GLN:O	1:G:271:VAL:HG12	2.06	0.55
1:F:291:LEU:H	1:F:291:LEU:HD13	1.71	0.55
1:D:254:THR:HG22	1:D:255:ALA:H	1.72	0.55
1:A:289:ILE:CG2	1:A:290:GLY:N	2.70	0.54
1:A:119:ARG:NH1	1:A:119:ARG:HG3	2.22	0.54
1:C:108:ASP:O	1:C:108:ASP:CG	2.45	0.54
1:A:36:VAL:O	1:A:37:LEU:C	2.45	0.54
1:C:285:LYS:NZ	1:C:286:ASP:OD2	2.27	0.54
1:B:32:PHE:O	1:B:35:GLU:HG2	2.07	0.54
1:A:285:LYS:HA	1:A:287:ASN:O	2.08	0.54
1:C:204:ASP:C	1:C:205:ARG:HG3	2.24	0.54
1:A:113:MET:O	1:A:114:ASN:HB3	2.06	0.54
1:D:113:MET:HA	1:D:115:HIS:CE1	2.42	0.54
1:D:112:ALA:O	1:D:115:HIS:NE2	2.40	0.54
1:A:303:LEU:HG	1:A:304:ARG:HG3	1.89	0.54
1:G:171:LYS:HA	1:G:174:LEU:HB2	1.89	0.54
1:F:24:LYS:H	1:F:24:LYS:CD	2.16	0.54
1:A:90:THR:HG21	1:A:333:ARG:HH22	1.72	0.54
1:A:289:ILE:HG22	1:A:290:GLY:H	1.73	0.54
1:D:138:VAL:CG2	1:D:139:LEU:HD11	2.33	0.54
1:A:28:PHE:C	1:A:28:PHE:CD2	2.81	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:GLU:OE1	1:B:310:ARG:NE	2.35	0.54
1:C:235:GLU:HG2	1:C:236:LYS:HG3	1.89	0.54
1:B:118:VAL:HG12	1:B:119:ARG:N	2.21	0.54
1:B:25:LEU:O	1:B:25:LEU:HD22	2.08	0.54
1:G:137:ALA:HB2	1:G:258:ALA:HB2	1.88	0.54
1:E:216:ALA:O	1:E:220:ALA:N	2.33	0.54
1:A:235:GLU:O	1:A:236:LYS:NZ	2.32	0.54
1:B:81:ASP:HA	1:B:84:ARG:HB2	1.88	0.54
1:A:207:PHE:CB	1:A:291:LEU:O	2.55	0.54
1:C:25:LEU:O	1:C:29:LEU:HD12	2.07	0.54
1:E:24:LYS:NZ	1:E:112:ALA:HB2	2.22	0.54
1:A:328:GLY:O	1:A:329:HIS:HB3	2.08	0.54
1:D:132:MET:CE	1:D:251:PRO:HG2	2.35	0.54
1:B:232:ILE:HA	1:B:239:ILE:HA	1.89	0.54
1:C:36:VAL:HG13	1:C:126:LEU:CD2	2.38	0.54
1:G:141:GLU:HG2	1:G:329:HIS:ND1	2.22	0.54
1:E:307:ALA:H	1:E:325:TYR:HB2	1.73	0.54
1:F:298:VAL:HA	1:F:332:LEU:HB2	1.89	0.54
1:B:28:PHE:CZ	1:B:111:ASP:OD1	2.60	0.54
1:B:40:PHE:HE1	1:B:130:LEU:HD13	1.32	0.54
1:D:298:VAL:HG12	1:D:332:LEU:HB2	1.89	0.54
1:B:35:GLU:CB	1:B:123:THR:CG2	2.80	0.54
1:C:206:VAL:HG23	1:C:247:VAL:HA	1.87	0.54
1:C:110:GLU:CD	1:C:118:VAL:HG23	2.29	0.54
1:A:302:LYS:HE2	1:A:327:MET:HE2	1.86	0.54
1:D:196:THR:OG1	1:D:197:LYS:N	2.40	0.54
1:E:50:HIS:HE1	1:E:300:THR:HG22	1.73	0.54
1:C:28:PHE:CD2	1:C:28:PHE:O	2.61	0.54
1:E:24:LYS:HZ3	1:E:112:ALA:HB2	1.71	0.54
1:E:306:LEU:HA	1:E:325:TYR:CD1	2.43	0.54
1:E:50:HIS:HD2	1:E:51:MET:H	1.56	0.54
1:B:145:LEU:HD23	1:B:332:LEU:HD11	1.85	0.54
1:C:113:MET:HE2	1:C:119:ARG:NE	2.23	0.54
1:G:303:LEU:HB2	1:G:326:ALA:HB3	1.89	0.54
1:E:104:VAL:HG21	1:F:66:LEU:HD21	1.90	0.54
1:C:205:ARG:CG	1:C:294:HIS:HB3	2.37	0.53
1:D:50:HIS:CD2	1:D:298:VAL:HG23	2.43	0.53
1:A:208:TYR:CZ	1:A:293:MET:CE	2.91	0.53
1:C:162:ALA:HB3	1:C:338:GLY:HA3	1.90	0.53
1:B:167:THR:OG1	1:B:168:THR:N	2.38	0.53
1:A:186:ALA:O	1:A:190:LYS:NZ	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:298:VAL:CA	1:E:331:GLY:O	2.56	0.53
1:E:299:GLY:HA3	1:E:333:ARG:NH2	2.22	0.53
1:A:104:VAL:O	1:A:320:GLN:NE2	2.41	0.53
1:C:110:GLU:O	1:C:118:VAL:HG21	2.08	0.53
1:G:130:LEU:CD2	1:G:131:ALA:CA	2.86	0.53
1:G:44:SER:HB2	1:G:131:ALA:HB1	1.90	0.53
1:D:110:GLU:CG	1:D:113:MET:O	2.57	0.53
1:F:300:THR:HG1	1:F:301:VAL:H	1.52	0.53
1:E:81:ASP:OD2	1:E:81:ASP:N	2.40	0.53
1:E:112:ALA:O	1:E:113:MET:HB2	2.09	0.53
1:B:209:CYS:O	1:B:250:VAL:HG22	2.08	0.53
1:F:25:LEU:O	1:F:28:PHE:CZ	2.61	0.53
1:C:31:VAL:HG12	1:C:32:PHE:N	2.23	0.53
1:B:24:LYS:CE	1:B:25:LEU:CA	2.78	0.53
1:G:92:LYS:HD3	1:G:332:LEU:H	1.74	0.53
1:C:32:PHE:CD1	1:C:33:GLY:N	2.77	0.53
1:E:115:HIS:HE1	1:E:119:ARG:NH2	1.90	0.53
1:D:116:TYR:O	1:D:119:ARG:HB3	2.09	0.53
1:E:192:ARG:C	1:E:195:LEU:HG	2.29	0.53
1:A:66:LEU:HD23	1:A:89:HIS:CE1	2.44	0.53
1:C:32:PHE:HZ	1:C:126:LEU:HD23	1.74	0.53
1:F:211:PRO:HD3	1:F:250:VAL:O	2.08	0.53
1:B:58:GLY:O	1:B:59:LYS:HG2	2.08	0.53
1:F:312:ARG:NH1	1:F:319:ASP:OD2	2.41	0.53
1:C:37:LEU:HD13	1:C:306:LEU:HD21	1.89	0.53
1:B:165:ILE:H	1:B:340:VAL:HG12	1.74	0.53
1:D:242:VAL:HG22	1:D:243:MET:H	1.72	0.53
1:A:207:PHE:CE1	1:A:290:GLY:C	2.83	0.53
1:B:50:HIS:CD2	1:B:51:MET:N	2.77	0.53
1:G:106:ILE:HD11	1:G:107:TYR:C	2.29	0.53
1:F:250:VAL:HG21	1:F:253:LEU:CG	2.39	0.53
1:D:167:THR:O	1:D:168:THR:OG1	2.27	0.53
1:E:298:VAL:HG12	1:E:332:LEU:HD13	1.85	0.53
1:A:73:TYR:CE1	1:F:102:ALA:HB2	2.44	0.53
1:A:115:HIS:HB2	1:A:119:ARG:CG	2.39	0.52
1:D:53:ARG:HH12	1:D:61:ALA:HB1	1.73	0.52
1:D:253:LEU:O	1:D:254:THR:OG1	2.26	0.52
1:G:260:THR:CG2	1:G:269:LYS:NZ	2.73	0.52
1:G:306:LEU:HD13	1:G:325:TYR:CE1	2.44	0.52
1:A:110:GLU:OE1	1:A:118:VAL:CB	2.57	0.52
1:B:151:LYS:HG2	1:B:152:TYR:H	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:84:ARG:O	1:F:84:ARG:HD2	2.08	0.52
1:E:65:VAL:CG1	1:E:333:ARG:HD3	2.37	0.52
1:G:341:VAL:HG22	1:G:342:PHE:H	1.75	0.52
1:A:305:ASP:C	1:A:325:TYR:HE1	2.12	0.52
1:G:149:GLU:OE1	1:G:150:SER:CA	2.57	0.52
1:G:146:CYS:SG	1:G:336:ALA:HB2	2.49	0.52
1:E:24:LYS:C	1:E:24:LYS:HD3	2.28	0.52
1:F:204:ASP:N	1:F:205:ARG:HH21	2.07	0.52
1:C:141:GLU:HG3	1:C:329:HIS:HE1	1.74	0.52
1:C:184:ILE:HD11	1:C:289:ILE:HD13	1.92	0.52
1:D:166:GLU:HA	1:D:341:VAL:HG23	1.91	0.52
1:G:304:ARG:O	1:G:304:ARG:NE	2.39	0.52
1:D:272:PHE:HE1	1:D:285:LYS:HB2	1.74	0.52
1:A:273:PRO:HD2	1:A:284:ALA:HB2	1.92	0.52
1:G:115:HIS:O	1:G:119:ARG:HB2	2.10	0.52
1:F:28:PHE:CE1	1:F:29:LEU:HB2	2.44	0.52
1:B:27:LEU:CD2	1:B:27:LEU:O	2.56	0.52
1:D:272:PHE:CE1	1:D:285:LYS:HB2	2.44	0.52
1:G:100:LEU:O	1:G:325:TYR:N	2.39	0.52
1:C:134:ALA:O	1:C:138:VAL:HG13	2.09	0.52
1:F:241:ASN:N	1:F:241:ASN:OD1	2.43	0.52
1:G:270:HIS:HE2	1:G:329:HIS:CE1	2.27	0.52
1:F:143:ALA:CB	1:F:272:PHE:CE2	2.92	0.52
1:D:142:ILE:CD1	1:D:145:LEU:HG	2.38	0.52
1:C:34:GLY:O	1:C:38:THR:N	2.30	0.52
1:B:24:LYS:HZ3	1:B:25:LEU:H	1.55	0.52
1:A:51:MET:HB2	1:A:299:GLY:HA3	1.92	0.52
1:B:113:MET:CB	1:B:115:HIS:NE2	2.73	0.52
1:B:53:ARG:HH11	1:B:63:PHE:HB3	1.73	0.52
1:A:313:ARG:HH11	1:A:320:GLN:HG2	1.74	0.52
1:C:208:TYR:HB3	1:C:291:LEU:CD2	2.39	0.52
1:E:102:ALA:O	1:F:70:GLN:NE2	2.43	0.52
1:E:36:VAL:HG22	1:E:126:LEU:HD12	1.91	0.52
1:F:31:VAL:HG12	1:F:32:PHE:N	2.24	0.52
1:C:32:PHE:O	1:C:34:GLY:N	2.43	0.52
1:G:46:THR:HG23	1:G:135:ASP:OD1	2.10	0.52
1:B:309:GLU:OE1	1:B:310:ARG:N	2.41	0.52
1:C:299:GLY:O	1:C:300:THR:HB	2.10	0.52
1:G:242:VAL:HG22	1:G:243:MET:H	1.75	0.52
1:B:163:THR:HG23	1:B:164:VAL:HG12	1.92	0.52
1:C:91:GLU:OE1	1:C:91:GLU:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:LYS:NZ	1:B:333:ARG:HH21	2.08	0.52
1:E:181:GLY:N	1:E:183:GLU:OE1	2.43	0.52
1:C:117:ASP:CG	1:D:51:MET:CE	2.73	0.52
1:G:143:ALA:CB	1:G:272:PHE:HB3	2.39	0.52
1:A:62:GLN:OE1	1:A:62:GLN:N	2.43	0.52
1:A:128:GLU:OE2	1:A:129:SER:OG	2.27	0.52
1:E:192:ARG:HA	1:E:195:LEU:CD2	2.40	0.51
1:C:27:LEU:HD22	1:C:28:PHE:N	2.20	0.51
1:F:195:LEU:HD21	1:F:205:ARG:NH1	2.26	0.51
1:F:294:HIS:CG	1:F:295:ARG:N	2.78	0.51
1:A:170:ASN:OD1	1:A:171:LYS:NZ	2.43	0.51
1:C:192:ARG:O	1:C:195:LEU:HB3	2.10	0.51
1:D:46:THR:HG23	1:D:135:ASP:CG	2.25	0.51
1:E:40:PHE:C	1:E:130:LEU:HD21	2.29	0.51
1:B:68:ARG:N	1:B:68:ARG:CD	2.73	0.51
1:C:178:VAL:HG13	1:C:220:ALA:HA	1.92	0.51
1:B:139:LEU:HD21	1:B:255:ALA:HA	1.91	0.51
1:C:32:PHE:HD1	1:C:33:GLY:N	2.08	0.51
1:A:302:LYS:CE	1:A:327:MET:HE2	2.40	0.51
1:C:162:ALA:C	1:C:164:VAL:N	2.63	0.51
1:D:204:ASP:N	1:D:205:ARG:HH21	2.08	0.51
1:G:100:LEU:HD13	1:G:259:GLY:N	2.25	0.51
1:D:62:GLN:HB2	1:D:93:VAL:HG12	1.92	0.51
1:D:130:LEU:HD12	1:D:131:ALA:HA	1.76	0.51
1:F:25:LEU:HB3	1:F:28:PHE:HE2	1.70	0.51
1:A:32:PHE:O	1:A:36:VAL:HG22	2.10	0.51
1:F:254:THR:HA	1:F:270:HIS:NE2	2.25	0.51
1:A:142:ILE:HA	1:A:145:LEU:HD22	1.92	0.51
1:B:135:ASP:O	1:B:138:VAL:HG23	2.11	0.51
1:B:59:LYS:O	1:B:95:THR:OG1	2.27	0.51
1:A:211:PRO:HA	1:A:214:TYR:HB2	1.93	0.51
1:G:181:GLY:HA3	1:G:220:ALA:HB2	1.92	0.51
1:E:333:ARG:CG	1:E:333:ARG:HH11	2.19	0.51
1:C:108:ASP:OD2	1:C:111:ASP:CG	2.48	0.51
1:D:51:MET:HB2	1:D:298:VAL:O	2.10	0.51
1:C:103:ASP:CG	1:C:322:ILE:HA	2.31	0.51
1:G:50:HIS:HD2	1:G:298:VAL:HG23	1.76	0.51
1:A:166:GLU:N	1:A:166:GLU:OE1	2.43	0.51
1:B:64:PRO:HA	1:B:91:GLU:HB3	1.93	0.51
1:G:106:ILE:HG12	1:G:107:TYR:N	2.26	0.51
1:C:162:ALA:HB3	1:C:337:ALA:C	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:295:ARG:HE	1:F:296:SER:N	2.09	0.51
1:B:171:LYS:HG3	1:B:342:PHE:CZ	2.45	0.51
1:C:285:LYS:NZ	1:C:285:LYS:O	2.40	0.51
1:F:306:LEU:HB2	1:F:325:TYR:CZ	2.45	0.51
1:F:64:PRO:N	1:F:91:GLU:HG3	2.25	0.51
1:B:132:MET:HE3	1:B:132:MET:CA	2.36	0.51
1:E:181:GLY:O	1:E:185:ILE:HD11	1.93	0.51
1:B:121:GLU:CD	1:B:121:GLU:C	2.70	0.51
1:F:134:ALA:O	1:F:137:ALA:HB3	2.11	0.51
1:B:294:HIS:CG	1:B:295:ARG:N	2.79	0.51
1:A:135:ASP:OD1	1:A:135:ASP:N	2.43	0.51
1:D:83:LYS:HZ2	1:D:83:LYS:H	1.58	0.51
1:B:132:MET:SD	1:C:199:TYR:HE1	2.32	0.51
1:A:207:PHE:HD1	1:A:291:LEU:O	1.93	0.51
1:B:298:VAL:HG12	1:B:299:GLY:H	1.76	0.51
1:F:270:HIS:N	1:F:272:PHE:O	2.44	0.51
1:F:251:PRO:HD2	1:F:252:HIS:CE1	2.46	0.51
1:B:81:ASP:H	1:B:83:LYS:CE	2.24	0.51
1:G:200:VAL:HG22	1:G:201:PRO:HD2	1.92	0.51
1:B:130:LEU:O	1:B:130:LEU:CD1	2.41	0.51
1:A:26:ALA:C	1:A:29:LEU:HD12	2.24	0.51
1:B:70:GLN:CA	1:B:70:GLN:NE2	2.72	0.51
1:B:312:ARG:NH2	1:B:317:GLN:OE1	2.44	0.51
1:F:103:ASP:CG	1:F:322:ILE:HA	2.31	0.51
1:D:142:ILE:CD1	1:D:145:LEU:CG	2.89	0.50
1:C:192:ARG:HH21	1:C:243:MET:HG3	1.75	0.50
1:C:207:PHE:CE2	1:C:245:PHE:HD2	2.28	0.50
1:B:92:LYS:HZ1	1:B:333:ARG:NH2	2.09	0.50
1:C:36:VAL:HG11	1:C:126:LEU:CD2	2.37	0.50
1:G:106:ILE:CD1	1:G:107:TYR:CA	2.87	0.50
1:D:214:TYR:N	1:D:249:GLU:OE1	2.45	0.50
1:F:63:PHE:C	1:F:91:GLU:HG3	2.31	0.50
1:B:292:PHE:N	1:B:338:GLY:O	2.31	0.50
1:D:305:ASP:N	1:D:305:ASP:OD2	2.44	0.50
1:B:100:LEU:HB3	1:B:326:ALA:HB3	1.92	0.50
1:A:78:GLU:OE1	1:A:79:ASN:N	2.44	0.50
1:D:135:ASP:O	1:D:138:VAL:HG22	2.11	0.50
1:B:332:LEU:HD13	1:B:334:PRO:CD	2.41	0.50
1:D:204:ASP:O	1:D:295:ARG:HB3	2.11	0.50
1:F:138:VAL:HG12	1:F:329:HIS:HE1	1.75	0.50
1:D:310:ARG:HG2	1:D:321:ILE:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:312:ARG:HA	1:F:319:ASP:HA	1.92	0.50
1:G:239:ILE:HB	1:G:247:VAL:HB	1.93	0.50
1:B:112:ALA:C	1:B:113:MET:SD	2.89	0.50
1:B:28:PHE:HZ	1:B:111:ASP:C	2.09	0.50
1:G:110:GLU:CG	1:G:118:VAL:CG2	2.84	0.50
1:E:119:ARG:O	1:E:123:THR:HG23	2.11	0.50
1:F:135:ASP:HB3	1:F:252:HIS:CE1	2.46	0.50
1:G:115:HIS:O	1:G:116:TYR:O	2.30	0.50
1:G:110:GLU:CG	1:G:118:VAL:HG11	2.42	0.50
1:A:114:ASN:O	1:A:114:ASN:OD1	2.30	0.50
1:E:110:GLU:OE2	1:E:110:GLU:O	2.30	0.50
1:A:302:LYS:HE2	1:A:327:MET:HE3	1.90	0.50
1:G:205:ARG:HE	1:G:294:HIS:HB2	1.76	0.50
1:A:226:ALA:HB3	1:C:232:ILE:HB	1.92	0.50
1:B:132:MET:O	1:B:135:ASP:OD2	2.30	0.50
1:A:115:HIS:O	1:A:119:ARG:HG3	2.11	0.50
1:C:108:ASP:O	1:C:108:ASP:OD1	2.30	0.50
1:A:232:ILE:HB	1:A:240:ARG:HB2	1.93	0.50
1:C:121:GLU:O	1:C:124:SER:OG	2.25	0.50
1:D:253:LEU:O	1:D:285:LYS:NZ	2.44	0.50
1:A:233:ASP:HA	1:A:236:LYS:HZ1	1.76	0.50
1:C:63:PHE:HE1	1:C:94:ILE:HD11	1.76	0.50
1:D:24:LYS:O	1:D:27:LEU:HG	2.11	0.50
1:C:108:ASP:OD2	1:C:111:ASP:OD1	2.30	0.50
1:F:174:LEU:HD13	1:F:180:LEU:HD11	1.94	0.50
1:D:240:ARG:NE	1:D:241:ASN:H	2.10	0.50
1:G:265:THR:C	1:G:266:THR:OG1	2.49	0.50
1:F:41:ALA:O	1:F:44:SER:OG	2.26	0.50
1:D:123:THR:OG1	1:D:124:SER:N	2.45	0.50
1:C:147:ASN:HB3	1:C:281:VAL:HG11	1.93	0.50
1:A:183:GLU:OE1	1:A:184:ILE:N	2.34	0.50
1:C:57:SER:O	1:C:59:LYS:NZ	2.43	0.50
1:G:109:ILE:O	1:G:112:ALA:O	2.30	0.50
1:F:143:ALA:HB3	1:F:272:PHE:CD2	2.47	0.50
1:C:143:ALA:HB3	1:C:271:VAL:HG13	1.94	0.50
1:G:291:LEU:H	1:G:291:LEU:HD12	1.77	0.50
1:D:176:ASP:OD2	1:D:178:VAL:N	2.34	0.50
1:E:110:GLU:HG3	1:E:118:VAL:CG2	2.37	0.50
1:B:170:ASN:O	1:B:171:LYS:NZ	2.36	0.50
1:B:108:ASP:O	1:B:111:ASP:OD2	2.30	0.50
1:B:300:THR:HB	1:B:329:HIS:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:106:ILE:CD1	1:G:107:TYR:C	2.80	0.50
1:G:141:GLU:O	1:G:141:GLU:OE1	2.30	0.50
1:F:253:LEU:O	1:F:270:HIS:NE2	2.42	0.50
1:B:66:LEU:HD21	1:B:200:VAL:HB	1.93	0.50
1:F:129:SER:HA	1:F:132:MET:HB2	1.93	0.50
1:G:295:ARG:CZ	1:G:296:SER:HB2	2.41	0.50
1:A:64:PRO:HG2	1:F:121:GLU:HG2	1.94	0.49
1:F:50:HIS:CD2	1:F:51:MET:H	2.30	0.49
1:G:104:VAL:HG21	1:G:122:TYR:HE1	1.77	0.49
1:G:110:GLU:O	1:G:113:MET:O	2.30	0.49
1:B:332:LEU:HD11	1:B:334:PRO:HG2	1.94	0.49
1:C:35:GLU:O	1:C:38:THR:OG1	2.30	0.49
1:C:166:GLU:HA	1:C:341:VAL:O	2.12	0.49
1:E:212:ASP:C	1:E:214:TYR:H	2.16	0.49
1:F:251:PRO:HB2	1:F:252:HIS:CD2	2.47	0.49
1:A:171:LYS:HE3	1:A:342:PHE:HD2	1.76	0.49
1:C:82:ASP:HA	1:C:85:LYS:HB3	1.93	0.49
1:B:111:ASP:C	1:B:111:ASP:OD1	2.50	0.49
1:B:255:ALA:HB3	1:B:272:PHE:CZ	2.47	0.49
1:G:113:MET:CG	1:G:114:ASN:N	2.74	0.49
1:G:114:ASN:O	1:G:116:TYR:HB2	2.11	0.49
1:A:55:ILE:HG21	1:A:301:VAL:HG23	1.77	0.49
1:B:285:LYS:O	1:B:287:ASN:N	2.45	0.49
1:B:46:THR:C	1:B:48:SER:H	2.14	0.49
1:F:221:LEU:HG	1:F:222:MET:HG3	1.94	0.49
1:B:252:HIS:N	1:C:199:TYR:OH	2.45	0.49
1:A:207:PHE:CE1	1:A:209:CYS:HA	2.47	0.49
1:G:116:TYR:O	1:G:120:SER:OG	2.30	0.49
1:D:45:VAL:N	1:D:135:ASP:OD2	2.45	0.49
1:D:128:GLU:OE2	1:D:128:GLU:O	2.30	0.49
1:C:292:PHE:O	1:C:337:ALA:HB1	2.11	0.49
1:A:236:LYS:HE2	1:A:238:SER:HB2	1.94	0.49
1:D:303:LEU:H	1:D:326:ALA:HB3	1.76	0.49
1:B:119:ARG:O	1:B:123:THR:OG1	2.30	0.49
1:B:131:ALA:O	1:B:135:ASP:OD2	2.30	0.49
1:G:25:LEU:CB	1:G:28:PHE:CE2	2.94	0.49
1:G:137:ALA:HB2	1:G:258:ALA:CB	2.42	0.49
1:A:105:LEU:O	1:A:107:TYR:HE2	1.95	0.49
1:F:301:VAL:HG12	1:F:302:LYS:H	1.76	0.49
1:D:340:VAL:HG22	1:D:341:VAL:H	1.77	0.49
1:D:83:LYS:CE	1:D:83:LYS:H	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:ASP:HB3	1:A:111:ASP:N	2.27	0.49
1:G:45:VAL:HG22	1:G:135:ASP:CG	2.32	0.49
1:F:205:ARG:HE	1:F:205:ARG:N	2.09	0.49
1:E:294:HIS:CG	1:E:295:ARG:N	2.80	0.49
1:B:114:ASN:HB3	1:B:118:VAL:HB	1.93	0.49
1:E:192:ARG:O	1:E:195:LEU:CG	2.60	0.49
1:C:116:TYR:O	1:C:118:VAL:CG1	2.56	0.49
1:B:131:ALA:O	1:B:135:ASP:OD1	2.30	0.49
1:C:195:LEU:HB2	1:C:205:ARG:HH12	1.77	0.49
1:F:27:LEU:CD1	1:F:27:LEU:O	2.32	0.49
1:G:143:ALA:HB1	1:G:272:PHE:HB3	1.94	0.49
1:D:228:TYR:HA	1:D:231:LEU:HB3	1.94	0.49
1:F:62:GLN:HB2	1:F:91:GLU:HB3	1.93	0.49
1:F:83:LYS:O	1:F:83:LYS:NZ	2.34	0.49
1:G:108:ASP:OD2	1:G:109:ILE:N	2.45	0.49
1:C:110:GLU:O	1:C:110:GLU:OE2	2.30	0.49
1:E:32:PHE:C	1:E:32:PHE:HD1	2.16	0.49
1:A:62:GLN:HA	1:A:93:VAL:HA	1.94	0.49
1:B:308:LEU:HA	1:B:323:ALA:HA	1.94	0.49
1:D:327:MET:SD	1:D:328:GLY:N	2.86	0.49
1:C:192:ARG:NH2	1:C:243:MET:HG3	2.28	0.49
1:C:294:HIS:HE1	1:C:335:GLU:HB2	1.74	0.49
1:D:204:ASP:H	1:D:205:ARG:HH21	1.60	0.49
1:A:306:LEU:C	1:A:306:LEU:HD12	2.34	0.49
1:E:240:ARG:HG3	1:E:241:ASN:ND2	2.28	0.49
1:E:101:THR:OG1	1:E:323:ALA:O	2.28	0.49
1:C:165:ILE:CG2	1:C:340:VAL:HB	2.43	0.49
1:F:278:GLU:OE2	1:F:287:ASN:ND2	2.46	0.49
1:E:285:LYS:O	1:E:287:ASN:N	2.46	0.49
1:D:94:ILE:HD13	1:D:94:ILE:H	1.78	0.49
1:C:108:ASP:OD1	1:C:111:ASP:OD1	2.30	0.48
1:G:132:MET:O	1:G:132:MET:SD	2.66	0.48
1:F:209:CYS:O	1:F:250:VAL:HG22	2.13	0.48
1:D:272:PHE:O	1:D:274:ALA:N	2.46	0.48
1:G:204:ASP:O	1:G:205:ARG:NH1	2.36	0.48
1:F:189:THR:OG1	1:F:190:LYS:N	2.45	0.48
1:E:145:LEU:HD21	1:E:334:PRO:HA	1.95	0.48
1:C:108:ASP:O	1:C:111:ASP:OD2	2.30	0.48
1:E:106:ILE:CD1	1:E:108:ASP:HA	2.43	0.48
1:A:33:GLY:HA2	1:A:36:VAL:HG23	1.95	0.48
1:G:53:ARG:O	1:G:301:VAL:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:PRO:HD2	1:A:236:LYS:HE3	1.95	0.48
1:B:140:ALA:HB2	1:B:256:GLY:HA3	1.95	0.48
1:E:65:VAL:HG12	1:E:333:ARG:CD	2.40	0.48
1:C:32:PHE:CD1	1:C:36:VAL:CG2	2.97	0.48
1:C:298:VAL:HB	1:C:330:GLY:HA3	1.94	0.48
1:E:160:GLY:N	1:E:336:ALA:O	2.46	0.48
1:D:241:ASN:ND2	1:D:242:VAL:O	2.46	0.48
1:B:104:VAL:HG23	1:B:321:ILE:HD11	1.94	0.48
1:E:276:LYS:HD2	1:E:279:GLY:HA3	1.95	0.48
1:E:183:GLU:OE1	1:E:183:GLU:N	2.47	0.48
1:C:108:ASP:OD2	1:C:111:ASP:HB2	2.12	0.48
1:G:115:HIS:CG	1:G:119:ARG:HH22	2.25	0.48
1:C:334:PRO:C	1:C:336:ALA:H	2.16	0.48
1:F:28:PHE:CD1	1:F:29:LEU:CA	2.96	0.48
1:B:29:LEU:HD21	1:B:310:ARG:CG	2.35	0.48
1:F:207:PHE:HE2	1:F:209:CYS:HB3	1.77	0.48
1:C:299:GLY:O	1:C:330:GLY:CA	2.59	0.48
1:F:55:ILE:HD13	1:F:301:VAL:HG11	1.95	0.48
1:B:284:ALA:O	1:B:288:VAL:HB	2.12	0.48
1:G:110:GLU:CG	1:G:114:ASN:ND2	2.76	0.48
1:A:29:LEU:HD21	1:A:310:ARG:CD	2.43	0.48
1:G:146:CYS:CB	1:G:336:ALA:HB2	2.25	0.48
1:G:37:LEU:HD12	1:G:40:PHE:HD2	1.78	0.48
1:F:145:LEU:HD21	1:F:334:PRO:CB	2.42	0.48
1:G:201:PRO:HG2	1:G:205:ARG:HH22	1.78	0.48
1:G:265:THR:O	1:G:266:THR:OG1	2.30	0.48
1:C:282:LYS:HE2	1:C:282:LYS:H	1.78	0.48
1:D:319:ASP:OD1	1:D:319:ASP:N	2.47	0.48
1:C:36:VAL:HG13	1:C:126:LEU:CG	2.43	0.48
1:C:32:PHE:CE1	1:C:36:VAL:HG21	2.49	0.48
1:A:29:LEU:CD2	1:A:310:ARG:CD	2.88	0.48
1:G:25:LEU:C	1:G:29:LEU:HG	2.27	0.48
1:A:308:LEU:C	1:A:308:LEU:HD12	2.33	0.48
1:C:240:ARG:HH21	1:C:240:ARG:HG3	1.79	0.48
1:B:121:GLU:OE1	1:B:121:GLU:CA	2.61	0.48
1:D:122:TYR:CE1	1:E:64:PRO:HG3	2.49	0.48
1:D:65:VAL:HG11	1:D:90:THR:HG23	1.95	0.48
1:F:89:HIS:O	1:F:89:HIS:CG	2.67	0.48
1:A:110:GLU:HB2	1:A:114:ASN:HD22	1.78	0.48
1:A:110:GLU:OE2	1:A:110:GLU:O	2.30	0.48
1:A:113:MET:HG2	1:A:114:ASN:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:204:ASP:C	1:F:205:ARG:HE	2.17	0.48
1:E:28:PHE:CE1	1:E:111:ASP:C	2.87	0.48
1:D:53:ARG:HD3	1:D:63:PHE:CZ	2.49	0.48
1:E:68:ARG:HG2	1:E:69:THR:H	1.78	0.48
1:D:106:ILE:HG13	1:D:122:TYR:CZ	2.49	0.48
1:G:215:SER:HA	1:G:218:LEU:HD23	1.96	0.48
1:B:211:PRO:HA	1:B:249:GLU:HB3	1.95	0.48
1:C:207:PHE:CE2	1:C:247:VAL:CG2	2.95	0.48
1:E:191:ALA:C	1:E:195:LEU:HD21	2.34	0.48
1:C:287:ASN:O	1:C:288:VAL:HB	2.14	0.48
1:E:117:ASP:OD1	1:F:52:VAL:O	2.31	0.48
1:E:234:PRO:C	1:E:236:LYS:H	2.17	0.48
1:E:289:ILE:HG22	1:E:290:GLY:H	1.79	0.48
1:E:289:ILE:O	1:E:339:ALA:HB1	2.14	0.48
1:G:260:THR:CG2	1:G:269:LYS:HZ1	2.27	0.48
1:G:122:TYR:O	1:G:125:GLN:HB3	2.13	0.48
1:G:151:LYS:NZ	1:G:160:GLY:O	2.35	0.48
1:C:269:LYS:HD2	1:C:289:ILE:N	2.29	0.48
1:D:287:ASN:HB3	1:D:341:VAL:HG12	1.96	0.48
1:G:49:ARG:O	1:G:50:HIS:ND1	2.47	0.48
1:D:40:PHE:CD1	1:D:131:ALA:HB2	2.49	0.47
1:B:67:GLY:HA3	1:B:68:ARG:CZ	2.44	0.47
1:E:32:PHE:C	1:E:32:PHE:CD1	2.87	0.47
1:C:329:HIS:CG	1:C:330:GLY:N	2.83	0.47
1:E:80:LEU:HD22	1:E:82:ASP:H	1.79	0.47
1:D:128:GLU:CD	1:D:129:SER:CA	2.81	0.47
1:F:25:LEU:O	1:F:28:PHE:CD1	2.67	0.47
1:G:38:THR:OG1	1:G:39:ALA:N	2.47	0.47
1:E:60:SER:HA	1:E:95:THR:CA	2.40	0.47
1:C:100:LEU:HA	1:D:73:TYR:HB3	1.95	0.47
1:E:284:ALA:N	1:E:288:VAL:HG21	2.29	0.47
1:A:73:TYR:HB2	1:F:100:LEU:HD22	1.95	0.47
1:D:106:ILE:HG13	1:D:122:TYR:CE2	2.49	0.47
1:D:84:ARG:NH1	1:D:84:ARG:HB3	2.29	0.47
1:F:27:LEU:HD12	1:F:28:PHE:N	2.28	0.47
1:E:46:THR:C	1:E:48:SER:H	2.17	0.47
1:F:290:GLY:HA3	1:F:340:VAL:H	1.79	0.47
1:E:222:MET:N	1:E:222:MET:SD	2.87	0.47
1:E:189:THR:HG23	1:E:243:MET:HG3	1.97	0.47
1:E:96:ILE:HD13	1:E:327:MET:O	2.14	0.47
1:A:162:ALA:O	1:A:163:THR:OG1	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:291:LEU:HA	1:F:338:GLY:O	2.14	0.47
1:B:251:PRO:HG2	1:C:199:TYR:HE1	1.61	0.47
1:B:67:GLY:C	1:B:68:ARG:HD2	2.35	0.47
1:B:66:LEU:N	1:B:66:LEU:CD1	2.73	0.47
1:C:165:ILE:HA	1:C:165:ILE:HD12	1.60	0.47
1:D:288:VAL:HG21	1:D:340:VAL:O	2.15	0.47
1:D:55:ILE:HG23	1:D:303:LEU:HD23	1.96	0.47
1:E:53:ARG:HD3	1:E:63:PHE:CE1	2.50	0.47
1:A:309:GLU:O	1:A:322:ILE:CB	2.59	0.47
1:C:32:PHE:O	1:C:33:GLY:C	2.51	0.47
1:A:310:ARG:HA	1:A:321:ILE:HA	1.97	0.47
1:E:101:THR:N	1:F:72:ALA:HB1	2.29	0.47
1:C:251:PRO:O	1:C:252:HIS:ND1	2.48	0.47
1:E:288:VAL:HA	1:E:341:VAL:HG12	1.96	0.47
1:A:65:VAL:HB	1:A:90:THR:HB	1.95	0.47
1:D:103:ASP:CG	1:D:323:ALA:H	2.18	0.47
1:B:251:PRO:CB	1:C:199:TYR:CE2	2.66	0.47
1:C:26:ALA:CA	1:C:29:LEU:HD11	2.25	0.47
1:C:25:LEU:C	1:C:29:LEU:HD11	2.35	0.47
1:C:27:LEU:HA	1:C:30:LYS:HD2	1.96	0.47
1:B:24:LYS:HE2	1:B:25:LEU:CB	2.44	0.47
1:G:188:LEU:HD23	1:G:245:PHE:CD1	2.50	0.47
1:F:129:SER:O	1:F:132:MET:N	2.48	0.47
1:B:207:PHE:HE1	1:B:290:GLY:HA2	1.79	0.47
1:E:204:ASP:OD2	1:E:204:ASP:N	2.48	0.47
1:B:117:ASP:OD1	1:C:53:ARG:CA	2.56	0.47
1:G:113:MET:HE1	1:G:115:HIS:HB3	1.93	0.47
1:A:23:ASP:O	1:A:26:ALA:HB3	2.14	0.47
1:E:110:GLU:HG3	1:E:118:VAL:HG21	1.83	0.47
1:E:325:TYR:HA	1:E:327:MET:CE	2.45	0.47
1:B:70:GLN:HA	1:B:70:GLN:HE21	1.78	0.47
1:B:176:ASP:OD1	1:B:178:VAL:N	2.47	0.47
1:C:141:GLU:HG3	1:C:329:HIS:CE1	2.49	0.47
1:F:136:GLY:HA2	1:F:139:LEU:HB2	1.97	0.47
1:F:128:GLU:OE2	1:F:129:SER:N	2.47	0.47
1:A:289:ILE:CG2	1:A:290:GLY:H	2.28	0.47
1:B:297:ALA:O	1:B:332:LEU:HD13	2.15	0.47
1:D:165:ILE:HA	1:D:165:ILE:HD12	1.77	0.47
1:A:174:LEU:HD13	1:A:183:GLU:HG2	1.97	0.47
1:B:332:LEU:HD13	1:B:333:ARG:H	1.80	0.47
1:A:205:ARG:CZ	1:A:293:MET:HG2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:117:ASP:CG	1:F:53:ARG:HA	2.23	0.47
1:D:218:LEU:HA	1:D:221:LEU:HB3	1.97	0.47
1:E:207:PHE:CZ	1:E:209:CYS:HB2	2.49	0.47
1:G:205:ARG:HD2	1:G:294:HIS:HA	1.97	0.47
1:B:37:LEU:O	1:B:40:PHE:HB3	2.16	0.46
1:A:207:PHE:CD1	1:A:291:LEU:O	2.68	0.46
1:D:25:LEU:O	1:D:28:PHE:HD2	1.98	0.46
1:C:34:GLY:O	1:C:38:THR:OG1	2.30	0.46
1:A:33:GLY:CA	1:A:36:VAL:HG23	2.45	0.46
1:E:35:GLU:H	1:E:35:GLU:HG2	1.39	0.46
1:B:59:LYS:O	1:B:96:ILE:HG12	2.15	0.46
1:D:288:VAL:HG23	1:D:290:GLY:H	1.80	0.46
1:F:65:VAL:HG23	1:F:333:ARG:NH1	2.30	0.46
1:A:136:GLY:HA3	1:A:255:ALA:HB3	1.97	0.46
1:B:212:ASP:C	1:B:214:TYR:H	2.19	0.46
1:G:28:PHE:CD1	1:G:29:LEU:N	2.83	0.46
1:D:314:ALA:HA	1:D:318:ALA:H	1.80	0.46
1:C:177:GLN:HE21	1:C:215:SER:HG	1.57	0.46
1:F:160:GLY:HA2	1:F:198:ASN:HD21	1.80	0.46
1:D:208:TYR:HD1	1:D:293:MET:HE2	1.80	0.46
1:D:27:LEU:CD1	1:D:28:PHE:N	2.74	0.46
1:C:27:LEU:HD23	1:C:28:PHE:HA	1.97	0.46
1:A:115:HIS:HD2	1:A:115:HIS:N	1.93	0.46
1:G:272:PHE:O	1:G:274:ALA:N	2.44	0.46
1:D:294:HIS:CE1	1:D:295:ARG:O	2.68	0.46
1:E:240:ARG:HA	1:E:240:ARG:HH11	1.80	0.46
1:D:214:TYR:OH	1:D:239:ILE:HG12	2.15	0.46
1:G:248:VAL:HG12	1:G:249:GLU:H	1.81	0.46
1:A:142:ILE:O	1:A:145:LEU:HB2	2.15	0.46
1:G:294:HIS:CE1	1:G:297:ALA:HB2	2.50	0.46
1:G:104:VAL:HG21	1:G:122:TYR:CE1	2.50	0.46
1:G:66:LEU:HB2	1:G:67:GLY:H	1.52	0.46
1:G:211:PRO:O	1:G:214:TYR:HB2	2.15	0.46
1:A:136:GLY:HA2	1:A:139:LEU:HB3	1.97	0.46
1:G:109:ILE:CD1	1:G:109:ILE:N	2.30	0.46
1:G:110:GLU:HG2	1:G:118:VAL:HG11	1.95	0.46
1:B:50:HIS:CE1	1:B:298:VAL:HB	2.51	0.46
1:B:62:GLN:OE1	1:B:62:GLN:N	2.48	0.46
1:C:111:ASP:OD2	1:C:112:ALA:N	2.48	0.46
1:D:314:ALA:H	1:D:318:ALA:H	1.62	0.46
1:A:209:CYS:SG	1:A:290:GLY:HA3	2.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:108:ASP:OD2	1:G:109:ILE:HA	2.15	0.46
1:G:141:GLU:CA	1:G:270:HIS:CE1	2.96	0.46
1:E:232:ILE:HG12	1:E:233:ASP:N	2.31	0.46
1:C:136:GLY:O	1:C:139:LEU:HB3	2.15	0.46
1:B:114:ASN:O	1:B:118:VAL:CB	2.61	0.46
1:B:301:VAL:HG22	1:B:302:LYS:H	1.79	0.46
1:F:121:GLU:O	1:F:124:SER:OG	2.26	0.46
1:G:106:ILE:HG12	1:G:107:TYR:H	1.81	0.46
1:C:278:GLU:OE1	1:C:287:ASN:ND2	2.41	0.46
1:B:81:ASP:H	1:B:83:LYS:HE2	1.78	0.46
1:B:165:ILE:HG21	1:B:190:LYS:HD3	1.98	0.46
1:B:132:MET:C	1:B:135:ASP:OD2	2.53	0.46
1:D:46:THR:H	1:D:135:ASP:CG	2.19	0.46
1:E:28:PHE:CE2	1:E:111:ASP:OD2	2.40	0.46
1:F:210:ASP:HA	1:F:250:VAL:HG22	1.98	0.46
1:A:207:PHE:CE2	1:A:247:VAL:CG2	2.88	0.46
1:E:192:ARG:O	1:E:195:LEU:HG	2.15	0.46
1:E:232:ILE:O	1:E:233:ASP:HB2	2.16	0.46
1:G:96:ILE:HG13	1:G:96:ILE:H	1.47	0.46
1:E:298:VAL:HA	1:E:331:GLY:O	2.15	0.46
1:B:141:GLU:CD	1:B:330:GLY:C	2.72	0.46
1:D:109:ILE:HG13	1:D:110:GLU:H	1.80	0.46
1:B:291:LEU:H	1:B:339:ALA:HA	1.81	0.46
1:D:36:VAL:C	1:D:38:THR:N	2.67	0.46
1:C:109:ILE:HD13	1:C:110:GLU:CA	2.46	0.46
1:D:209:CYS:O	1:D:249:GLU:HA	2.15	0.46
1:B:141:GLU:OE1	1:B:329:HIS:C	2.54	0.45
1:C:40:PHE:CE1	1:C:131:ALA:HB2	2.51	0.45
1:A:36:VAL:HG13	1:A:126:LEU:HD11	1.98	0.45
1:F:209:CYS:O	1:F:250:VAL:N	2.28	0.45
1:F:91:GLU:N	1:F:91:GLU:OE1	2.49	0.45
1:B:294:HIS:NE2	1:B:295:ARG:O	2.49	0.45
1:E:176:ASP:OD2	1:E:179:ALA:N	2.47	0.45
1:G:235:GLU:HG2	1:G:237:GLY:H	1.81	0.45
1:D:137:ALA:O	1:D:141:GLU:HG2	2.16	0.45
1:G:285:LYS:HD2	1:G:286:ASP:N	2.31	0.45
1:A:302:LYS:CE	1:A:327:MET:HE3	2.45	0.45
1:E:31:VAL:O	1:E:35:GLU:CD	2.55	0.45
1:E:308:LEU:HB3	1:E:323:ALA:HA	1.97	0.45
1:F:83:LYS:HA	1:F:83:LYS:HD2	1.76	0.45
1:C:105:LEU:HD21	1:D:84:ARG:CZ	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:192:ARG:HB2	1:E:195:LEU:HD11	1.95	0.45
1:D:29:LEU:CD1	1:D:30:LYS:H	2.17	0.45
1:D:250:VAL:HB	1:D:251:PRO:HD3	1.98	0.45
1:D:239:ILE:HB	1:D:247:VAL:HB	1.98	0.45
1:F:66:LEU:HB3	1:F:67:GLY:H	1.49	0.45
1:B:132:MET:CE	1:B:135:ASP:CG	2.84	0.45
1:D:138:VAL:HG23	1:D:139:LEU:N	2.32	0.45
1:G:141:GLU:CB	1:G:270:HIS:HE1	2.27	0.45
1:G:272:PHE:HE1	1:G:285:LYS:HB2	1.81	0.45
1:C:107:TYR:HA	1:C:318:ALA:CB	2.43	0.45
1:B:341:VAL:HG23	1:B:342:PHE:H	1.81	0.45
1:G:53:ARG:NH1	1:G:62:GLN:H	2.14	0.45
1:F:231:LEU:HB3	1:F:233:ASP:OD2	2.17	0.45
1:B:255:ALA:HB3	1:B:272:PHE:CE2	2.51	0.45
1:A:27:LEU:CD1	1:A:28:PHE:HA	2.47	0.45
1:G:32:PHE:HA	1:G:35:GLU:OE2	2.15	0.45
1:D:169:GLN:NE2	1:D:170:ASN:O	2.50	0.45
1:A:231:LEU:HD13	1:A:231:LEU:HA	1.84	0.45
1:B:250:VAL:HG23	1:B:251:PRO:O	2.16	0.45
1:F:25:LEU:HD12	1:F:25:LEU:N	2.31	0.45
1:C:29:LEU:C	1:C:32:PHE:HB3	2.33	0.45
1:E:28:PHE:CD2	1:E:111:ASP:CG	2.49	0.45
1:C:70:GLN:OE1	1:C:71:ALA:N	2.49	0.45
1:F:240:ARG:NE	1:F:241:ASN:OD1	2.46	0.45
1:C:293:MET:SD	1:C:294:HIS:N	2.90	0.45
1:C:35:GLU:C	1:C:38:THR:OG1	2.55	0.45
1:A:113:MET:O	1:A:114:ASN:CB	2.65	0.45
1:A:142:ILE:O	1:A:145:LEU:N	2.50	0.45
1:E:88:LYS:HE3	1:E:88:LYS:HB2	1.75	0.45
1:G:270:HIS:NE2	1:G:329:HIS:HE1	2.15	0.45
1:B:59:LYS:HB3	1:B:59:LYS:HE3	1.82	0.45
1:G:301:VAL:HG12	1:G:302:LYS:H	1.82	0.45
1:G:62:GLN:HB3	1:G:93:VAL:HG13	1.99	0.45
1:E:82:ASP:O	1:E:85:LYS:N	2.43	0.45
1:B:66:LEU:H	1:B:66:LEU:HD13	1.81	0.45
1:C:290:GLY:O	1:C:339:ALA:HA	2.16	0.45
1:G:217:ILE:O	1:G:221:LEU:N	2.26	0.45
1:D:288:VAL:HB	1:D:289:ILE:H	1.61	0.45
1:E:50:HIS:NE2	1:E:298:VAL:O	2.48	0.45
1:D:40:PHE:CE1	1:D:131:ALA:CB	2.99	0.45
1:B:313:ARG:O	1:B:317:GLN:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:HIS:HB2	1:C:253:LEU:H	1.55	0.45
1:B:117:ASP:OD2	1:C:51:MET:SD	2.74	0.45
1:D:126:LEU:O	1:D:129:SER:OG	2.28	0.45
1:E:108:ASP:OD1	1:E:109:ILE:HA	2.17	0.45
1:A:35:GLU:O	1:A:38:THR:OG1	2.32	0.45
1:E:32:PHE:O	1:E:32:PHE:CD1	2.62	0.45
1:A:251:PRO:HB2	1:A:252:HIS:CD2	2.52	0.45
1:C:222:MET:HA	1:C:224:ASN:HD21	1.82	0.45
1:C:62:GLN:HB2	1:C:91:GLU:HB2	1.99	0.44
1:B:257:GLY:N	1:B:272:PHE:HB3	2.32	0.44
1:B:285:LYS:HE3	1:B:286:ASP:H	1.82	0.44
1:F:167:THR:HB	1:F:169:GLN:O	2.17	0.44
1:D:233:ASP:OD1	1:D:240:ARG:N	2.49	0.44
1:F:45:VAL:HG23	1:F:46:THR:HG22	1.97	0.44
1:A:227:ASN:N	1:A:227:ASN:OD1	2.48	0.44
1:E:305:ASP:OD2	1:E:306:LEU:N	2.44	0.44
1:B:27:LEU:O	1:B:30:LYS:N	2.49	0.44
1:F:294:HIS:NE2	1:F:295:ARG:O	2.50	0.44
1:E:103:ASP:CG	1:E:323:ALA:H	2.17	0.44
1:B:199:TYR:O	1:B:200:VAL:HG22	2.18	0.44
1:B:56:SER:OG	1:B:304:ARG:NH2	2.49	0.44
1:D:196:THR:O	1:D:198:ASN:N	2.51	0.44
1:B:86:ASP:O	1:B:155:ASN:ND2	2.48	0.44
1:D:40:PHE:CE1	1:D:131:ALA:HB2	2.52	0.44
1:C:117:ASP:OD1	1:C:117:ASP:O	2.36	0.44
1:C:110:GLU:CG	1:C:122:TYR:HE2	2.29	0.44
1:E:31:VAL:O	1:E:35:GLU:OE2	2.36	0.44
1:G:60:SER:OG	1:G:61:ALA:N	2.51	0.44
1:C:306:LEU:HB3	1:C:325:TYR:CZ	2.52	0.44
1:G:151:LYS:HG2	1:G:152:TYR:H	1.82	0.44
1:E:119:ARG:CB	1:E:119:ARG:CZ	2.95	0.44
1:A:36:VAL:HG11	1:A:126:LEU:HD11	1.98	0.44
1:G:170:ASN:OD1	1:G:171:LYS:N	2.51	0.44
1:G:241:ASN:ND2	1:G:244:GLY:O	2.47	0.44
1:B:44:SER:OG	1:B:46:THR:N	2.36	0.44
1:F:128:GLU:O	1:F:132:MET:HB2	2.17	0.44
1:F:84:ARG:HH11	1:F:84:ARG:C	2.20	0.44
1:C:231:LEU:HB2	1:C:234:PRO:CG	2.47	0.44
1:E:198:ASN:ND2	1:E:198:ASN:O	2.51	0.44
1:C:288:VAL:N	1:C:341:VAL:HG12	2.33	0.44
1:G:49:ARG:NH2	1:G:248:VAL:HG21	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:207:PHE:HB2	1:E:292:PHE:HB3	1.99	0.44
1:B:305:ASP:OD2	1:B:305:ASP:N	2.49	0.44
1:E:84:ARG:HB3	1:E:84:ARG:NH1	2.33	0.44
1:C:24:LYS:HE3	1:C:24:LYS:HB2	1.46	0.44
1:G:274:ALA:HA	1:G:284:ALA:HB1	2.00	0.44
1:E:108:ASP:O	1:E:108:ASP:OD1	2.35	0.44
1:D:46:THR:OG1	1:D:46:THR:O	2.35	0.44
1:D:25:LEU:O	1:D:28:PHE:CD2	2.70	0.44
1:A:102:ALA:HB2	1:B:71:ALA:CA	2.46	0.44
1:B:95:THR:OG1	1:B:96:ILE:N	2.51	0.44
1:C:251:PRO:C	1:C:252:HIS:CG	2.91	0.44
1:A:66:LEU:HD22	1:F:125:GLN:HG2	2.00	0.44
1:F:136:GLY:HA3	1:F:255:ALA:HB3	1.99	0.44
1:B:171:LYS:HE3	1:B:171:LYS:HB3	1.79	0.44
1:A:160:GLY:N	1:A:334:PRO:HG2	2.33	0.44
1:E:100:LEU:HD21	1:F:73:TYR:CE1	2.53	0.44
1:C:120:SER:O	1:C:124:SER:HB3	2.18	0.44
1:G:265:THR:O	1:G:266:THR:HG23	2.18	0.44
1:B:188:LEU:HG	1:B:188:LEU:H	1.38	0.44
1:G:110:GLU:CA	1:G:114:ASN:HB2	2.44	0.44
1:G:116:TYR:HB3	1:G:117:ASP:H	1.29	0.44
1:G:132:MET:CG	1:G:133:ALA:N	2.81	0.44
1:B:176:ASP:OD2	1:B:179:ALA:HB2	2.18	0.44
1:E:239:ILE:HG22	1:E:240:ARG:N	2.33	0.44
1:F:31:VAL:O	1:F:32:PHE:C	2.55	0.43
1:D:239:ILE:HD13	1:D:239:ILE:HA	1.85	0.43
1:A:45:VAL:HG12	1:A:46:THR:HG23	2.00	0.43
1:F:101:THR:OG1	1:F:325:TYR:N	2.38	0.43
1:B:145:LEU:HA	1:B:145:LEU:HD13	1.76	0.43
1:A:67:GLY:O	1:F:125:GLN:NE2	2.51	0.43
1:D:25:LEU:O	1:D:25:LEU:CD1	2.49	0.43
1:C:110:GLU:HB2	1:C:118:VAL:CG2	2.49	0.43
1:C:115:HIS:HD2	1:C:115:HIS:O	2.00	0.43
1:C:68:ARG:H	1:C:68:ARG:HG3	1.65	0.43
1:C:125:GLN:HE22	1:D:68:ARG:HG3	1.82	0.43
1:D:290:GLY:CA	1:D:340:VAL:HG12	2.47	0.43
1:G:47:THR:OG1	1:G:48:SER:N	2.51	0.43
1:C:113:MET:C	1:C:113:MET:SD	2.95	0.43
1:C:119:ARG:CZ	1:C:119:ARG:HB2	2.49	0.43
1:C:40:PHE:CD1	1:C:131:ALA:HB2	2.52	0.43
1:B:24:LYS:HE2	1:B:25:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:240:ARG:HA	1:F:240:ARG:NH1	2.33	0.43
1:A:193:ALA:O	1:A:196:THR:OG1	2.30	0.43
1:F:142:ILE:HD12	1:F:142:ILE:HA	1.73	0.43
1:C:202:ALA:HB1	1:C:205:ARG:CZ	2.46	0.43
1:B:50:HIS:CG	1:B:51:MET:N	2.86	0.43
1:C:119:ARG:CZ	1:C:119:ARG:CB	2.96	0.43
1:C:162:ALA:CB	1:C:337:ALA:C	2.86	0.43
1:A:245:PHE:HB2	1:A:246:GLU:H	1.52	0.43
1:E:329:HIS:HE1	1:F:73:TYR:OH	2.01	0.43
1:A:167:THR:HG21	1:A:183:GLU:HB3	2.01	0.43
1:D:122:TYR:HE1	1:E:64:PRO:HG3	1.84	0.43
1:E:181:GLY:H	1:E:184:ILE:HG12	1.83	0.43
1:D:63:PHE:HA	1:D:64:PRO:HD2	1.76	0.43
1:E:212:ASP:O	1:E:214:TYR:N	2.50	0.43
1:A:160:GLY:HA2	1:A:336:ALA:HA	2.01	0.43
1:F:132:MET:HA	1:F:135:ASP:OD1	2.19	0.43
1:B:153:ASN:N	1:B:153:ASN:OD1	2.51	0.43
1:B:183:GLU:CD	1:B:183:GLU:H	2.21	0.43
1:B:130:LEU:HD12	1:B:131:ALA:CA	2.48	0.43
1:G:110:GLU:HG2	1:G:118:VAL:CG1	2.48	0.43
1:C:206:VAL:HG21	1:C:248:VAL:CG2	2.21	0.43
1:F:28:PHE:CG	1:F:29:LEU:N	2.84	0.43
1:F:143:ALA:HB3	1:F:272:PHE:CE2	2.52	0.43
1:G:167:THR:C	1:G:169:GLN:N	2.71	0.43
1:E:31:VAL:O	1:E:35:GLU:HG2	2.18	0.43
1:C:297:ALA:O	1:C:298:VAL:CG1	2.66	0.43
1:C:135:ASP:OD1	1:C:136:GLY:N	2.50	0.43
1:A:276:LYS:NZ	1:A:278:GLU:H	2.16	0.43
1:F:179:ALA:HA	1:F:182:LYS:HZ1	1.83	0.43
1:D:325:TYR:HA	1:D:325:TYR:HD1	1.69	0.43
1:B:335:GLU:O	1:B:336:ALA:C	2.57	0.43
1:F:32:PHE:HB3	1:F:33:GLY:H	1.69	0.43
1:G:270:HIS:O	1:G:271:VAL:C	2.48	0.43
1:A:302:LYS:CG	1:A:327:MET:CB	2.76	0.43
1:A:107:TYR:HA	1:A:318:ALA:HB1	2.01	0.43
1:B:57:SER:O	1:B:57:SER:OG	2.35	0.43
1:D:241:ASN:HB2	1:D:244:GLY:O	2.19	0.43
1:C:313:ARG:O	1:C:317:GLN:HB3	2.18	0.43
1:B:40:PHE:HB2	1:B:130:LEU:HD23	1.63	0.43
1:E:301:VAL:HG22	1:E:302:LYS:H	1.84	0.43
1:C:28:PHE:HD2	1:C:29:LEU:CA	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:250:VAL:HG22	1:G:252:HIS:O	2.18	0.43
1:A:185:ILE:O	1:A:188:LEU:N	2.51	0.43
1:C:329:HIS:CG	1:C:330:GLY:H	2.36	0.43
1:C:321:ILE:HG13	1:C:321:ILE:H	1.59	0.43
1:D:104:VAL:H	1:D:321:ILE:HD12	1.83	0.43
1:E:192:ARG:CA	1:E:195:LEU:HG	2.47	0.43
1:F:28:PHE:HD1	1:F:28:PHE:C	2.16	0.43
1:G:252:HIS:CE1	1:G:255:ALA:HB3	2.54	0.43
1:A:55:ILE:CG2	1:A:301:VAL:HG21	2.31	0.43
1:F:211:PRO:HA	1:F:214:TYR:HB3	2.00	0.43
1:C:288:VAL:H	1:C:341:VAL:HG12	1.84	0.43
1:D:185:ILE:O	1:D:188:LEU:N	2.51	0.43
1:G:132:MET:HE2	1:G:132:MET:CA	2.49	0.43
1:C:107:TYR:H	1:C:107:TYR:HD2	1.58	0.43
1:F:298:VAL:HG12	1:F:331:GLY:HA2	2.01	0.43
1:E:253:LEU:O	1:E:285:LYS:NZ	2.41	0.43
1:B:110:GLU:HG2	1:C:53:ARG:HH22	1.84	0.42
1:E:145:LEU:HB3	1:E:332:LEU:CD2	2.40	0.42
1:G:23:ASP:HB3	1:G:26:ALA:HB3	2.01	0.42
1:B:176:ASP:OD1	1:B:177:GLN:N	2.52	0.42
1:A:305:ASP:C	1:A:325:TYR:CE1	2.91	0.42
1:F:62:GLN:HB3	1:F:93:VAL:HG12	2.01	0.42
1:G:195:LEU:HD11	1:G:205:ARG:HG3	2.01	0.42
1:G:185:ILE:O	1:G:189:THR:HG23	2.18	0.42
1:C:227:ASN:OD1	1:C:227:ASN:N	2.46	0.42
1:E:192:ARG:HA	1:E:195:LEU:HD21	2.01	0.42
1:F:183:GLU:OE1	1:F:184:ILE:HG13	2.19	0.42
1:D:83:LYS:NZ	1:D:83:LYS:H	2.17	0.42
1:G:207:PHE:CE2	1:G:247:VAL:HG22	2.54	0.42
1:G:115:HIS:HA	1:G:119:ARG:HH12	1.85	0.42
1:B:334:PRO:HB3	1:B:335:GLU:O	2.19	0.42
1:G:270:HIS:NE2	1:G:329:HIS:CE1	2.87	0.42
1:F:55:ILE:HA	1:F:55:ILE:HD12	1.77	0.42
1:E:126:LEU:O	1:E:129:SER:OG	2.31	0.42
1:G:294:HIS:NE2	1:G:297:ALA:HB2	2.34	0.42
1:B:80:LEU:H	1:B:80:LEU:HD12	1.84	0.42
1:B:114:ASN:HB2	1:B:118:VAL:HB	1.99	0.42
1:E:166:GLU:HA	1:E:340:VAL:HG23	2.02	0.42
1:A:115:HIS:HB2	1:A:119:ARG:HG3	2.01	0.42
1:A:101:THR:HG21	1:A:323:ALA:O	2.20	0.42
1:G:147:ASN:ND2	1:G:273:PRO:CG	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:LYS:HD2	1:A:92:LYS:HA	1.68	0.42
1:E:239:ILE:HG22	1:E:240:ARG:H	1.83	0.42
1:E:103:ASP:CB	1:E:322:ILE:HA	2.48	0.42
1:E:207:PHE:HA	1:E:292:PHE:HA	2.00	0.42
1:E:163:THR:HB	1:E:338:GLY:HA2	2.01	0.42
1:A:287:ASN:CG	1:A:288:VAL:H	2.08	0.42
1:C:27:LEU:CD2	1:C:28:PHE:CA	2.92	0.42
1:E:320:GLN:HE21	1:E:322:ILE:HG23	1.83	0.42
1:G:217:ILE:HA	1:G:220:ALA:HB3	2.02	0.42
1:F:233:ASP:N	1:F:234:PRO:HD3	2.34	0.42
1:G:186:ALA:O	1:G:189:THR:OG1	2.33	0.42
1:B:202:ALA:HB1	1:B:205:ARG:CZ	2.49	0.42
1:F:94:ILE:HA	1:F:94:ILE:HD12	1.67	0.42
1:A:274:ALA:CB	1:A:285:LYS:HD2	2.49	0.42
1:C:29:LEU:O	1:C:32:PHE:CA	2.67	0.42
1:G:130:LEU:HD23	1:G:131:ALA:HA	2.01	0.42
1:A:106:ILE:HG22	1:A:122:TYR:HE2	1.73	0.42
1:B:218:LEU:HD23	1:B:228:TYR:CD1	2.54	0.42
1:C:167:THR:OG1	1:C:168:THR:N	2.52	0.42
1:D:166:GLU:HB3	1:D:167:THR:HG22	2.01	0.42
1:C:332:LEU:HB3	1:C:333:ARG:H	1.42	0.42
1:B:222:MET:H	1:B:222:MET:HG3	1.76	0.42
1:B:139:LEU:CA	1:B:142:ILE:HG23	2.49	0.42
1:D:27:LEU:HD12	1:D:28:PHE:CA	2.49	0.42
1:C:32:PHE:CZ	1:C:126:LEU:CD2	3.02	0.42
1:G:130:LEU:CD2	1:G:131:ALA:HA	2.50	0.42
1:E:58:GLY:C	1:E:59:LYS:HD2	2.40	0.42
1:E:202:ALA:HB1	1:E:205:ARG:NH1	2.34	0.42
1:D:43:THR:HG21	1:D:128:GLU:HA	2.02	0.42
1:F:29:LEU:O	1:F:32:PHE:CB	2.67	0.42
1:C:299:GLY:C	1:C:330:GLY:HA2	2.40	0.42
1:E:48:SER:OG	1:E:49:ARG:N	2.52	0.42
1:C:280:ASN:O	1:C:280:ASN:ND2	2.52	0.42
1:F:275:ASN:OD1	1:F:275:ASN:N	2.52	0.42
1:F:80:LEU:HG	1:F:80:LEU:H	1.46	0.42
1:E:298:VAL:HG12	1:E:332:LEU:CB	2.50	0.42
1:E:53:ARG:HD3	1:E:63:PHE:HD1	1.83	0.42
1:D:46:THR:OG1	1:D:135:ASP:OD1	2.36	0.42
1:C:115:HIS:O	1:C:118:VAL:HG12	2.20	0.42
1:A:206:VAL:HG12	1:A:246:GLU:HB3	2.02	0.42
1:A:161:THR:N	1:A:336:ALA:HA	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:LYS:H	1:C:171:LYS:CE	2.31	0.42
1:D:285:LYS:HD3	1:D:286:ASP:H	1.85	0.42
1:D:171:LYS:HE3	1:D:171:LYS:HB2	1.90	0.42
1:E:298:VAL:C	1:E:333:ARG:NH2	2.72	0.42
1:D:142:ILE:HG22	1:D:143:ALA:N	2.35	0.42
1:C:37:LEU:HA	1:C:37:LEU:HD12	1.77	0.42
1:G:106:ILE:CD1	1:G:107:TYR:O	2.67	0.42
1:G:32:PHE:CE1	1:G:36:VAL:HG21	2.55	0.42
1:G:313:ARG:N	1:G:318:ALA:O	2.42	0.42
1:D:95:THR:OG1	1:D:96:ILE:HG12	2.20	0.42
1:F:276:LYS:NZ	1:F:278:GLU:H	2.17	0.42
1:C:49:ARG:O	1:C:50:HIS:HB3	2.20	0.41
1:D:135:ASP:C	1:D:139:LEU:CD2	2.86	0.41
1:E:168:THR:HG22	1:E:183:GLU:HB2	2.02	0.41
1:B:125:GLN:HG2	1:C:66:LEU:HB2	1.56	0.41
1:F:233:ASP:OD2	1:F:233:ASP:N	2.49	0.41
1:F:257:GLY:HA3	1:F:271:VAL:HB	2.01	0.41
1:A:272:PHE:O	1:A:274:ALA:N	2.53	0.41
1:D:142:ILE:HD13	1:D:145:LEU:HD23	1.71	0.41
1:F:123:THR:OG1	1:F:124:SER:N	2.53	0.41
1:A:122:TYR:HA	1:A:122:TYR:HD1	1.65	0.41
1:E:292:PHE:O	1:E:337:ALA:N	2.53	0.41
1:F:240:ARG:NE	1:F:241:ASN:H	2.19	0.41
1:C:177:GLN:NE2	1:C:215:SER:OG	2.27	0.41
1:F:82:ASP:HA	1:F:85:LYS:HB2	2.01	0.41
1:D:282:LYS:H	1:D:282:LYS:NZ	2.18	0.41
1:F:81:ASP:OD2	1:F:81:ASP:N	2.51	0.41
1:C:161:THR:OG1	1:C:161:THR:O	2.37	0.41
1:D:128:GLU:OE2	1:D:129:SER:N	2.52	0.41
1:B:161:THR:CG2	1:B:335:GLU:H	2.32	0.41
1:A:108:ASP:HB3	1:A:111:ASP:H	1.85	0.41
1:F:205:ARG:CG	1:F:245:PHE:HA	2.47	0.41
1:B:125:GLN:OE1	1:B:125:GLN:HA	2.20	0.41
1:G:188:LEU:HB3	1:G:245:PHE:CE1	2.55	0.41
1:G:51:MET:N	1:G:299:GLY:HA3	2.36	0.41
1:F:287:ASN:HB3	1:F:288:VAL:HG22	2.01	0.41
1:D:175:THR:OG1	1:D:176:ASP:N	2.52	0.41
1:F:182:LYS:O	1:F:185:ILE:N	2.53	0.41
1:D:188:LEU:HA	1:D:191:ALA:HB3	2.02	0.41
1:D:105:LEU:HA	1:D:320:GLN:CB	2.50	0.41
1:F:88:LYS:HG3	1:F:90:THR:H	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:SER:OG	1:A:218:LEU:HD13	2.20	0.41
1:A:218:LEU:HD12	1:A:221:LEU:HD12	2.02	0.41
1:A:42:ARG:HB3	1:A:42:ARG:NH2	2.35	0.41
1:G:115:HIS:CG	1:G:119:ARG:NH2	2.86	0.41
1:C:242:VAL:HG23	1:C:243:MET:O	2.21	0.41
1:C:33:GLY:O	1:C:36:VAL:CG2	2.64	0.41
1:B:228:TYR:O	1:B:232:ILE:HG12	2.19	0.41
1:A:63:PHE:N	1:A:92:LYS:O	2.49	0.41
1:D:53:ARG:HD3	1:D:63:PHE:HZ	1.84	0.41
1:F:128:GLU:OE2	1:F:128:GLU:N	2.53	0.41
1:C:60:SER:OG	1:C:94:ILE:O	2.27	0.41
1:F:273:PRO:HG3	1:F:281:VAL:HG21	2.01	0.41
1:C:308:LEU:HD23	1:C:308:LEU:H	1.85	0.41
1:E:301:VAL:HG22	1:E:302:LYS:N	2.36	0.41
1:A:207:PHE:HD1	1:A:291:LEU:N	2.18	0.41
1:C:209:CYS:HB3	1:C:249:GLU:HB3	2.01	0.41
1:B:92:LYS:HZ1	1:B:333:ARG:CZ	2.33	0.41
1:A:126:LEU:O	1:A:130:LEU:HG	2.20	0.41
1:A:36:VAL:O	1:A:38:THR:N	2.54	0.41
1:C:104:VAL:H	1:C:321:ILE:HD11	1.86	0.41
1:B:181:GLY:O	1:B:185:ILE:N	2.48	0.41
1:G:265:THR:O	1:G:266:THR:CB	2.69	0.41
1:B:28:PHE:CE2	1:B:111:ASP:OD1	2.73	0.41
1:B:130:LEU:CD1	1:B:131:ALA:N	2.75	0.41
1:B:130:LEU:CG	1:B:131:ALA:N	2.81	0.41
1:E:53:ARG:NH1	1:E:62:GLN:H	2.09	0.41
1:G:110:GLU:HG2	1:G:114:ASN:ND2	2.35	0.41
1:B:141:GLU:OE1	1:B:330:GLY:N	2.41	0.41
1:G:137:ALA:CB	1:G:258:ALA:HB3	2.50	0.41
1:E:110:GLU:CG	1:E:118:VAL:CB	2.96	0.41
1:F:117:ASP:O	1:F:118:VAL:HG12	2.21	0.41
1:G:312:ARG:HD3	1:G:319:ASP:OD1	2.20	0.41
1:A:239:ILE:HB	1:A:247:VAL:O	2.21	0.41
1:D:29:LEU:C	1:D:29:LEU:CD2	2.85	0.41
1:A:115:HIS:O	1:A:119:ARG:CG	2.69	0.41
1:F:143:ALA:HB1	1:F:272:PHE:CD2	2.56	0.41
1:B:178:VAL:O	1:B:182:LYS:HB2	2.20	0.41
1:D:231:LEU:O	1:D:234:PRO:HD3	2.21	0.41
1:A:41:ALA:C	1:A:43:THR:N	2.72	0.41
1:F:310:ARG:HB3	1:F:321:ILE:HA	2.02	0.41
1:D:286:ASP:OD2	1:D:286:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:63:PHE:HA	1:F:64:PRO:HD2	1.85	0.41
1:C:95:THR:OG1	1:C:96:ILE:N	2.53	0.41
1:A:30:LYS:HB3	1:A:30:LYS:HE3	1.84	0.41
1:D:236:LYS:HD3	1:D:236:LYS:HA	1.96	0.41
1:A:207:PHE:CD1	1:A:290:GLY:C	2.93	0.41
1:E:199:TYR:HB3	1:E:200:VAL:H	1.37	0.41
1:A:232:ILE:HB	1:A:240:ARG:CB	2.51	0.41
1:G:101:THR:HG23	1:G:323:ALA:O	2.21	0.41
1:G:298:VAL:HB	1:G:299:GLY:H	1.71	0.41
1:B:205:ARG:O	1:B:245:PHE:HA	2.20	0.41
1:A:215:SER:O	1:A:216:ALA:HB3	2.21	0.41
1:G:113:MET:CE	1:G:114:ASN:N	2.65	0.41
1:E:195:LEU:HG	1:E:195:LEU:H	1.42	0.41
1:B:145:LEU:HD12	1:B:145:LEU:C	2.32	0.41
1:F:25:LEU:O	1:F:28:PHE:CE1	2.74	0.41
1:C:325:TYR:HD1	1:C:325:TYR:HA	1.75	0.41
1:A:110:GLU:OE2	1:A:111:ASP:HA	2.19	0.41
1:G:37:LEU:HD12	1:G:40:PHE:CD2	2.56	0.41
1:D:113:MET:SD	1:D:114:ASN:N	2.94	0.41
1:G:39:ALA:O	1:G:43:THR:OG1	2.38	0.41
1:E:100:LEU:HG	1:F:72:ALA:O	2.21	0.41
1:D:73:TYR:N	1:D:73:TYR:CD2	2.88	0.41
1:D:164:VAL:HG12	1:D:339:ALA:N	2.36	0.41
1:A:163:THR:O	1:A:164:VAL:HG13	2.21	0.41
1:B:227:ASN:O	1:B:229:ALA:N	2.54	0.41
1:C:236:LYS:HB2	1:C:236:LYS:NZ	2.36	0.41
1:E:288:VAL:HG22	1:E:341:VAL:CG1	2.50	0.41
1:A:217:ILE:O	1:A:219:ALA:N	2.54	0.41
1:G:69:THR:H	1:G:70:GLN:NE2	2.19	0.41
1:E:315:ASN:ND2	1:E:315:ASN:H	2.19	0.41
1:B:75:ALA:C	1:B:77:GLY:H	2.24	0.41
1:E:23:ASP:O	1:E:26:ALA:HB3	2.20	0.41
1:C:146:CYS:SG	1:C:161:THR:N	2.87	0.41
1:A:29:LEU:H	1:A:29:LEU:HG	1.72	0.41
1:G:285:LYS:HD2	1:G:286:ASP:H	1.86	0.41
1:C:43:THR:HG21	1:C:128:GLU:OE2	2.21	0.41
1:C:141:GLU:N	1:C:141:GLU:OE1	2.53	0.41
1:C:299:GLY:N	1:C:330:GLY:O	2.44	0.41
1:F:54:SER:OG	1:F:302:LYS:NZ	2.54	0.41
1:D:303:LEU:HB3	1:D:304:ARG:HD3	2.03	0.41
1:F:178:VAL:O	1:F:182:LYS:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:73:TYR:O	1:E:74:LEU:HD23	2.21	0.41
1:C:196:THR:C	1:C:198:ASN:H	2.24	0.41
1:C:40:PHE:CE1	1:C:131:ALA:CB	3.04	0.40
1:G:210:ASP:OD1	1:G:253:LEU:HD11	2.21	0.40
1:B:27:LEU:CD2	1:B:27:LEU:C	2.90	0.40
1:D:209:CYS:CB	1:D:249:GLU:HG2	2.48	0.40
1:A:287:ASN:HD21	1:A:341:VAL:HG11	1.83	0.40
1:G:150:SER:C	1:G:151:LYS:O	2.59	0.40
1:B:24:LYS:CE	1:B:24:LYS:C	2.74	0.40
1:G:252:HIS:O	1:G:253:LEU:HD23	2.21	0.40
1:E:68:ARG:HE	1:E:70:GLN:NE2	2.09	0.40
1:A:233:ASP:O	1:A:235:GLU:N	2.55	0.40
1:E:126:LEU:HA	1:E:126:LEU:HD23	1.92	0.40
1:G:205:ARG:HA	1:G:205:ARG:HD3	1.89	0.40
1:G:110:GLU:CG	1:G:118:VAL:HG21	2.30	0.40
1:E:166:GLU:CD	1:E:167:THR:H	2.25	0.40
1:A:114:ASN:H	1:A:115:HIS:HD2	1.54	0.40
1:G:271:VAL:HG13	1:G:271:VAL:O	2.21	0.40
1:B:68:ARG:C	1:B:69:THR:OG1	2.56	0.40
1:C:292:PHE:N	1:C:338:GLY:O	2.48	0.40
1:E:126:LEU:HA	1:E:129:SER:OG	2.22	0.40
1:C:315:ASN:CG	1:C:316:PHE:H	2.23	0.40
1:F:75:ALA:HA	1:F:76:PRO:HD3	1.95	0.40
1:E:192:ARG:C	1:E:195:LEU:CG	2.89	0.40
1:C:141:GLU:OE2	1:C:142:ILE:HG12	2.20	0.40
1:D:226:ALA:HA	1:D:228:TYR:CD2	2.57	0.40
1:C:84:ARG:HH12	1:C:89:HIS:CE1	2.40	0.40
1:A:251:PRO:O	1:A:252:HIS:ND1	2.54	0.40
1:E:61:ALA:O	1:E:94:ILE:N	2.45	0.40
1:C:231:LEU:HD22	1:C:231:LEU:HA	1.90	0.40
1:E:25:LEU:HD12	1:E:26:ALA:CA	2.51	0.40
1:C:112:ALA:O	1:C:115:HIS:NE2	2.55	0.40
1:A:295:ARG:NE	1:A:296:SER:H	2.20	0.40
1:B:67:GLY:C	1:B:68:ARG:CD	2.90	0.40
1:E:233:ASP:OD2	1:E:236:LYS:HG3	2.22	0.40
1:D:70:GLN:HB2	1:D:71:ALA:H	1.70	0.40
1:F:303:LEU:H	1:F:326:ALA:HB3	1.87	0.40
1:A:78:GLU:HB2	1:A:79:ASN:H	1.61	0.40
1:F:60:SER:HB3	1:F:94:ILE:O	2.22	0.40
1:A:169:GLN:HE22	1:A:173:ALA:HB3	1.87	0.40
1:C:276:LYS:HD3	1:C:279:GLY:HA3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	294/345 (85%)	224 (76%)	61 (21%)	9 (3%)	5	44
1	B	305/345 (88%)	229 (75%)	67 (22%)	9 (3%)	5	44
1	C	290/345 (84%)	206 (71%)	65 (22%)	19 (7%)	1	25
1	D	292/345 (85%)	213 (73%)	70 (24%)	9 (3%)	5	44
1	E	287/345 (83%)	214 (75%)	65 (23%)	8 (3%)	6	46
1	F	293/345 (85%)	225 (77%)	61 (21%)	7 (2%)	7	49
1	G	313/345 (91%)	240 (77%)	60 (19%)	13 (4%)	3	35
All	All	2074/2415 (86%)	1551 (75%)	449 (22%)	74 (4%)	7	40

All (74) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	VAL
1	A	288	VAL
1	B	70	GLN
1	B	114	ASN
1	B	232	ILE
1	B	334	PRO
1	C	42	ARG
1	C	43	THR
1	C	117	ASP
1	C	163	THR
1	C	178	VAL
1	C	300	THR
1	D	37	LEU
1	D	96	ILE
1	D	118	VAL
1	D	145	LEU

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Mol	Chain	Res	Type
1	E	115	HIS
1	E	335	GLU
1	F	32	PHE
1	F	118	VAL
1	G	116	TYR
1	G	150	SER
1	G	151	LYS
1	G	271	VAL
1	B	245	PHE
1	B	286	ASP
1	C	32	PHE
1	C	289	ILE
1	D	341	VAL
1	F	87	ILE
1	F	298	VAL
1	G	85	LYS
1	G	166	GLU
1	G	266	THR
1	B	69	THR
1	C	115	HIS
1	C	162	ALA
1	C	201	PRO
1	E	286	ASP
1	G	115	HIS
1	G	149	GLU
1	G	232	ILE
1	C	116	TYR
1	D	71	ALA
1	E	30	LYS
1	A	36	VAL
1	A	245	PHE
1	C	52	VAL
1	C	288	VAL
1	E	226	ALA
1	E	235	GLU
1	A	298	VAL
1	B	226	ALA
1	C	33	GLY
1	C	169	GLN
1	E	251	PRO
1	F	33	GLY
1	G	55	ILE

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Mol	Chain	Res	Type
1	G	87	ILE
1	A	217	ILE
1	C	232	ILE
1	C	242	VAL
1	D	288	VAL
1	D	298	VAL
1	F	281	VAL
1	A	232	ILE
1	B	55	ILE
1	C	165	ILE
1	D	242	VAL
1	E	341	VAL
1	F	164	VAL
1	A	164	VAL
1	A	165	ILE
1	G	281	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	230/261 (88%)	168 (73%)	62 (27%)	0	5
1	B	238/261 (91%)	157 (66%)	81 (34%)	0	2
1	C	230/261 (88%)	151 (66%)	79 (34%)	0	2
1	D	230/261 (88%)	160 (70%)	70 (30%)	0	3
1	E	227/261 (87%)	157 (69%)	70 (31%)	0	3
1	F	230/261 (88%)	167 (73%)	63 (27%)	0	5
1	G	242/261 (93%)	163 (67%)	79 (33%)	0	3
All	All	1627/1827 (89%)	1123 (69%)	504 (31%)	2	3

All (504) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASP

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Mol	Chain	Res	Type
1	A	24	LYS
1	A	25	LEU
1	A	27	LEU
1	A	28	PHE
1	A	29	LEU
1	A	36	VAL
1	A	42	ARG
1	A	50	HIS
1	A	53	ARG
1	A	66	LEU
1	A	70	GLN
1	A	82	ASP
1	A	84	ARG
1	A	87	ILE
1	A	88	LYS
1	A	101	THR
1	A	104	VAL
1	A	105	LEU
1	A	107	TYR
1	A	109	ILE
1	A	110	GLU
1	A	113	MET
1	A	114	ASN
1	A	115	HIS
1	A	119	ARG
1	A	122	TYR
1	A	128	GLU
1	A	141	GLU
1	A	145	LEU
1	A	163	THR
1	A	164	VAL
1	A	169	GLN
1	A	171	LYS
1	A	174	LEU
1	A	176	ASP
1	A	177	GLN
1	A	180	LEU
1	A	183	GLU
1	A	190	LYS
1	A	205	ARG
1	A	207	PHE
1	A	212	ASP

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Mol	Chain	Res	Type
1	A	232	ILE
1	A	236	LYS
1	A	245	PHE
1	A	249	GLU
1	A	253	LEU
1	A	272	PHE
1	A	280	ASN
1	A	282	LYS
1	A	283	VAL
1	A	285	LYS
1	A	287	ASN
1	A	288	VAL
1	A	298	VAL
1	A	315	ASN
1	A	317	GLN
1	A	325	TYR
1	A	327	MET
1	A	332	LEU
1	A	335	GLU
1	B	24	LYS
1	B	25	LEU
1	B	27	LEU
1	B	30	LYS
1	B	31	VAL
1	B	32	PHE
1	B	35	GLU
1	B	37	LEU
1	B	51	MET
1	B	52	VAL
1	B	59	LYS
1	B	66	LEU
1	B	68	ARG
1	B	70	GLN
1	B	74	LEU
1	B	80	LEU
1	B	83	LYS
1	B	84	ARG
1	B	85	LYS
1	B	92	LYS
1	B	104	VAL
1	B	105	LEU
1	B	107	TYR

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Mol	Chain	Res	Type
1	B	108	ASP
1	B	109	ILE
1	B	110	GLU
1	B	111	ASP
1	B	113	MET
1	B	116	TYR
1	B	118	VAL
1	B	121	GLU
1	B	122	TYR
1	B	123	THR
1	B	124	SER
1	B	126	LEU
1	B	128	GLU
1	B	129	SER
1	B	130	LEU
1	B	132	MET
1	B	135	ASP
1	B	138	VAL
1	B	142	ILE
1	B	145	LEU
1	B	146	CYS
1	B	163	THR
1	B	168	THR
1	B	169	GLN
1	B	171	LYS
1	B	174	LEU
1	B	176	ASP
1	B	188	LEU
1	B	192	ARG
1	B	197	LYS
1	B	200	VAL
1	B	205	ARG
1	B	210	ASP
1	B	217	ILE
1	B	222	MET
1	B	227	ASN
1	B	231	LEU
1	B	232	ILE
1	B	233	ASP
1	B	239	ILE
1	B	243	MET
1	B	247	VAL

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Mol	Chain	Res	Type
1	B	283	VAL
1	B	285	LYS
1	B	286	ASP
1	B	289	ILE
1	B	294	HIS
1	B	298	VAL
1	B	302	LYS
1	B	304	ARG
1	B	305	ASP
1	B	306	LEU
1	B	310	ARG
1	B	313	ARG
1	B	327	MET
1	B	332	LEU
1	B	333	ARG
1	B	343	LYS
1	C	24	LYS
1	C	25	LEU
1	C	27	LEU
1	C	28	PHE
1	C	29	LEU
1	C	31	VAL
1	C	35	GLU
1	C	36	VAL
1	C	38	THR
1	C	42	ARG
1	C	51	MET
1	C	52	VAL
1	C	59	LYS
1	C	62	GLN
1	C	65	VAL
1	C	69	THR
1	C	70	GLN
1	C	73	TYR
1	C	78	GLU
1	C	80	LEU
1	C	84	ARG
1	C	87	ILE
1	C	89	HIS
1	C	90	THR
1	C	91	GLU
1	C	104	VAL

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Mol	Chain	Res	Type
1	C	105	LEU
1	C	107	TYR
1	C	109	ILE
1	C	110	GLU
1	C	113	MET
1	C	114	ASN
1	C	116	TYR
1	C	119	ARG
1	C	120	SER
1	C	126	LEU
1	C	146	CYS
1	C	165	ILE
1	C	167	THR
1	C	169	GLN
1	C	170	ASN
1	C	171	LYS
1	C	176	ASP
1	C	183	GLU
1	C	184	ILE
1	C	190	LYS
1	C	199	TYR
1	C	212	ASP
1	C	214	TYR
1	C	221	LEU
1	C	222	MET
1	C	224	ASN
1	C	231	LEU
1	C	235	GLU
1	C	249	GLU
1	C	250	VAL
1	C	252	HIS
1	C	253	LEU
1	C	271	VAL
1	C	272	PHE
1	C	276	LYS
1	C	282	LYS
1	C	285	LYS
1	C	288	VAL
1	C	289	ILE
1	C	293	MET
1	C	295	ARG
1	C	305	ASP

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Mol	Chain	Res	Type
1	C	306	LEU
1	C	309	GLU
1	C	310	ARG
1	C	316	PHE
1	C	317	GLN
1	C	322	ILE
1	C	325	TYR
1	C	333	ARG
1	C	335	GLU
1	C	340	VAL
1	C	342	PHE
1	D	25	LEU
1	D	27	LEU
1	D	28	PHE
1	D	29	LEU
1	D	30	LYS
1	D	32	PHE
1	D	35	GLU
1	D	36	VAL
1	D	43	THR
1	D	44	SER
1	D	46	THR
1	D	47	THR
1	D	51	MET
1	D	52	VAL
1	D	55	ILE
1	D	59	LYS
1	D	73	TYR
1	D	74	LEU
1	D	81	ASP
1	D	83	LYS
1	D	84	ARG
1	D	85	LYS
1	D	88	LYS
1	D	91	GLU
1	D	92	LYS
1	D	94	ILE
1	D	95	THR
1	D	104	VAL
1	D	105	LEU
1	D	106	ILE
1	D	109	ILE

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Mol	Chain	Res	Type
1	D	110	GLU
1	D	118	VAL
1	D	128	GLU
1	D	130	LEU
1	D	135	ASP
1	D	139	LEU
1	D	142	ILE
1	D	145	LEU
1	D	167	THR
1	D	169	GLN
1	D	176	ASP
1	D	182	LYS
1	D	183	GLU
1	D	200	VAL
1	D	205	ARG
1	D	210	ASP
1	D	218	LEU
1	D	236	LYS
1	D	252	HIS
1	D	253	LEU
1	D	275	ASN
1	D	282	LYS
1	D	285	LYS
1	D	291	LEU
1	D	293	MET
1	D	294	HIS
1	D	300	THR
1	D	304	ARG
1	D	305	ASP
1	D	308	LEU
1	D	309	GLU
1	D	310	ARG
1	D	319	ASP
1	D	320	GLN
1	D	325	TYR
1	D	327	MET
1	D	332	LEU
1	D	335	GLU
1	D	341	VAL
1	E	24	LYS
1	E	25	LEU
1	E	27	LEU

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Mol	Chain	Res	Type
1	E	29	LEU
1	E	32	PHE
1	E	35	GLU
1	E	51	MET
1	E	53	ARG
1	E	59	LYS
1	E	63	PHE
1	E	70	GLN
1	E	78	GLU
1	E	80	LEU
1	E	81	ASP
1	E	82	ASP
1	E	84	ARG
1	E	85	LYS
1	E	89	HIS
1	E	90	THR
1	E	91	GLU
1	E	101	THR
1	E	108	ASP
1	E	109	ILE
1	E	110	GLU
1	E	111	ASP
1	E	118	VAL
1	E	119	ARG
1	E	120	SER
1	E	123	THR
1	E	129	SER
1	E	130	LEU
1	E	132	MET
1	E	135	ASP
1	E	138	VAL
1	E	142	ILE
1	E	147	ASN
1	E	149	GLU
1	E	163	THR
1	E	165	ILE
1	E	166	GLU
1	E	170	ASN
1	E	171	LYS
1	E	174	LEU
1	E	176	ASP
1	E	183	GLU

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Mol	Chain	Res	Type
1	E	188	LEU
1	E	190	LYS
1	E	192	ARG
1	E	195	LEU
1	E	199	TYR
1	E	200	VAL
1	E	205	ARG
1	E	210	ASP
1	E	217	ILE
1	E	222	MET
1	E	235	GLU
1	E	243	MET
1	E	249	GLU
1	E	275	ASN
1	E	276	LYS
1	E	294	HIS
1	E	300	THR
1	E	308	LEU
1	E	310	ARG
1	E	312	ARG
1	E	317	GLN
1	E	327	MET
1	E	335	GLU
1	E	340	VAL
1	E	341	VAL
1	F	24	LYS
1	F	25	LEU
1	F	27	LEU
1	F	28	PHE
1	F	29	LEU
1	F	31	VAL
1	F	32	PHE
1	F	65	VAL
1	F	68	ARG
1	F	73	TYR
1	F	80	LEU
1	F	84	ARG
1	F	87	ILE
1	F	88	LYS
1	F	89	HIS
1	F	100	LEU
1	F	101	THR

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Mol	Chain	Res	Type
1	F	104	VAL
1	F	105	LEU
1	F	108	ASP
1	F	110	GLU
1	F	118	VAL
1	F	121	GLU
1	F	128	GLU
1	F	130	LEU
1	F	139	LEU
1	F	142	ILE
1	F	145	LEU
1	F	147	ASN
1	F	176	ASP
1	F	180	LEU
1	F	183	GLU
1	F	188	LEU
1	F	192	ARG
1	F	200	VAL
1	F	204	ASP
1	F	205	ARG
1	F	210	ASP
1	F	212	ASP
1	F	231	LEU
1	F	240	ARG
1	F	252	HIS
1	F	282	LYS
1	F	283	VAL
1	F	285	LYS
1	F	288	VAL
1	F	291	LEU
1	F	292	PHE
1	F	295	ARG
1	F	298	VAL
1	F	300	THR
1	F	304	ARG
1	F	309	GLU
1	F	310	ARG
1	F	316	PHE
1	F	319	ASP
1	F	320	GLN
1	F	322	ILE
1	F	325	TYR

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Mol	Chain	Res	Type
1	F	332	LEU
1	F	333	ARG
1	F	335	GLU
1	F	341	VAL
1	G	25	LEU
1	G	27	LEU
1	G	28	PHE
1	G	49	ARG
1	G	55	ILE
1	G	59	LYS
1	G	63	PHE
1	G	66	LEU
1	G	68	ARG
1	G	70	GLN
1	G	73	TYR
1	G	74	LEU
1	G	78	GLU
1	G	79	ASN
1	G	83	LYS
1	G	85	LYS
1	G	86	ASP
1	G	96	ILE
1	G	103	ASP
1	G	106	ILE
1	G	107	TYR
1	G	108	ASP
1	G	109	ILE
1	G	113	MET
1	G	116	TYR
1	G	118	VAL
1	G	119	ARG
1	G	120	SER
1	G	122	TYR
1	G	129	SER
1	G	130	LEU
1	G	132	MET
1	G	138	VAL
1	G	139	LEU
1	G	141	GLU
1	G	145	LEU
1	G	149	GLU
1	G	157	GLU

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Mol	Chain	Res	Type
1	G	165	ILE
1	G	169	GLN
1	G	171	LYS
1	G	175	THR
1	G	178	VAL
1	G	183	GLU
1	G	199	TYR
1	G	200	VAL
1	G	207	PHE
1	G	209	CYS
1	G	214	TYR
1	G	224	ASN
1	G	231	LEU
1	G	249	GLU
1	G	262	ARG
1	G	263	GLU
1	G	265	THR
1	G	266	THR
1	G	268	GLN
1	G	269	LYS
1	G	275	ASN
1	G	278	GLU
1	G	285	LYS
1	G	293	MET
1	G	298	VAL
1	G	301	VAL
1	G	303	LEU
1	G	304	ARG
1	G	308	LEU
1	G	309	GLU
1	G	310	ARG
1	G	313	ARG
1	G	320	GLN
1	G	322	ILE
1	G	324	LYS
1	G	325	TYR
1	G	327	MET
1	G	329	HIS
1	G	333	ARG
1	G	340	VAL
1	G	341	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	89	HIS
1	A	169	GLN
1	A	287	ASN
1	B	70	GLN
1	B	115	HIS
1	B	287	ASN
1	B	315	ASN
1	C	115	HIS
1	C	169	GLN
1	C	170	ASN
1	C	280	ASN
1	C	329	HIS
1	D	125	GLN
1	D	252	HIS
1	D	294	HIS
1	D	320	GLN
1	E	70	GLN
1	E	115	HIS
1	E	177	GLN
1	E	315	ASN
1	E	320	GLN
1	E	329	HIS
1	F	79	ASN
1	F	169	GLN
1	F	198	ASN
1	F	224	ASN
1	F	317	GLN
1	G	70	GLN
1	G	79	ASN
1	G	114	ASN
1	G	115	HIS
1	G	241	ASN
1	G	329	HIS

5.3.3 RNA ⓘ

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 carbohydrates 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.