



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:31 PM UTC

PDB ID : 1G4B / pdb_00001g4b
Title : CRYSTAL STRUCTURES OF THE HSLVU PEPTIDASE-ATPASE COMPLEX REVEAL AN ATP-DEPENDENT PROTEOLYSIS MECHANISM
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Deposited on : 2000-10-26
Resolution : 7.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

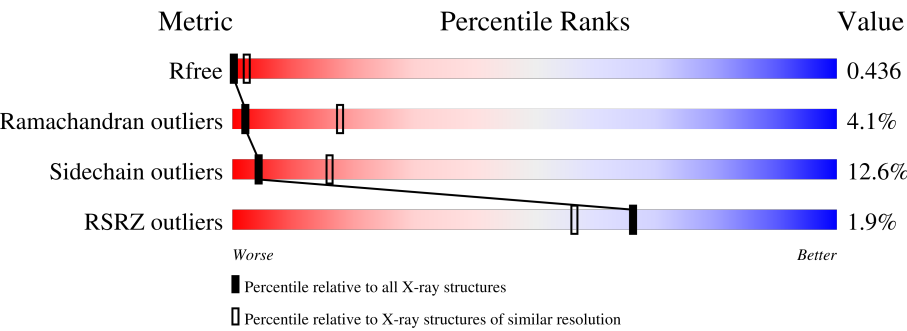
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 7.00 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)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1167 (10.00-4.00)
Ramachandran outliers	187476	1054 (10.00-4.00)
Sidechain outliers	187428	1017 (10.00-4.00)
RSRZ outliers	180081	1161 (10.00-4.00)

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

Mol	Chain	Length	Quality of chain
1	E	443	
1	F	443	
1	K	443	
1	L	443	
2	M	175	
2	N	175	
2	O	175	

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Mol	Chain	Length	Quality of chain
2	P	175	2% 33% 57% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 17660 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUB-UNIT HSLU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	393	Total	C	N	O	S	0	0	0
			3096	1935	551	600	10			
1	F	393	Total	C	N	O	S	0	0	0
			3096	1935	551	600	10			
1	K	393	Total	C	N	O	S	0	0	0
			3096	1935	551	600	10			
1	L	393	Total	C	N	O	S	0	0	0
			3096	1935	551	600	10			

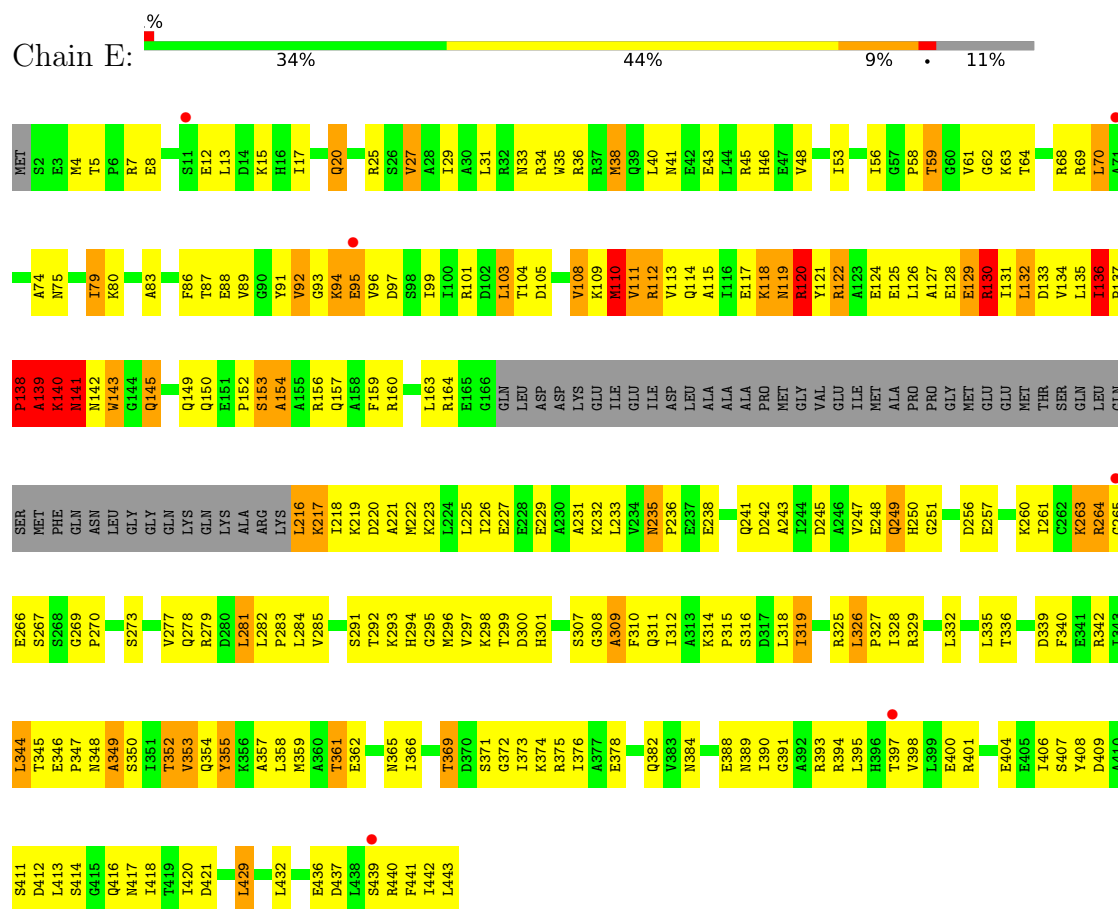
- Molecule 2 is a protein called ATP-DEPENDENT PROTEASE HSLV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	173	Total	C	N	O	S	0	0	0
			1319	828	235	252	4			
2	N	173	Total	C	N	O	S	0	0	0
			1319	828	235	252	4			
2	O	173	Total	C	N	O	S	0	0	0
			1319	828	235	252	4			
2	P	173	Total	C	N	O	S	0	0	0
			1319	828	235	252	4			

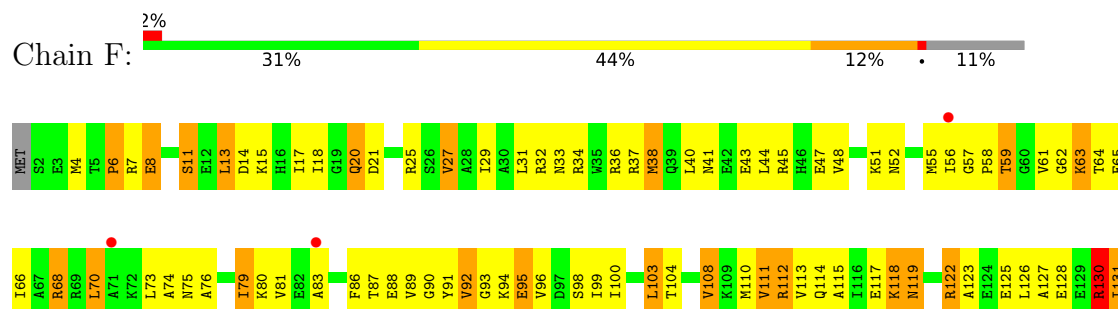
3 Residue-property plots

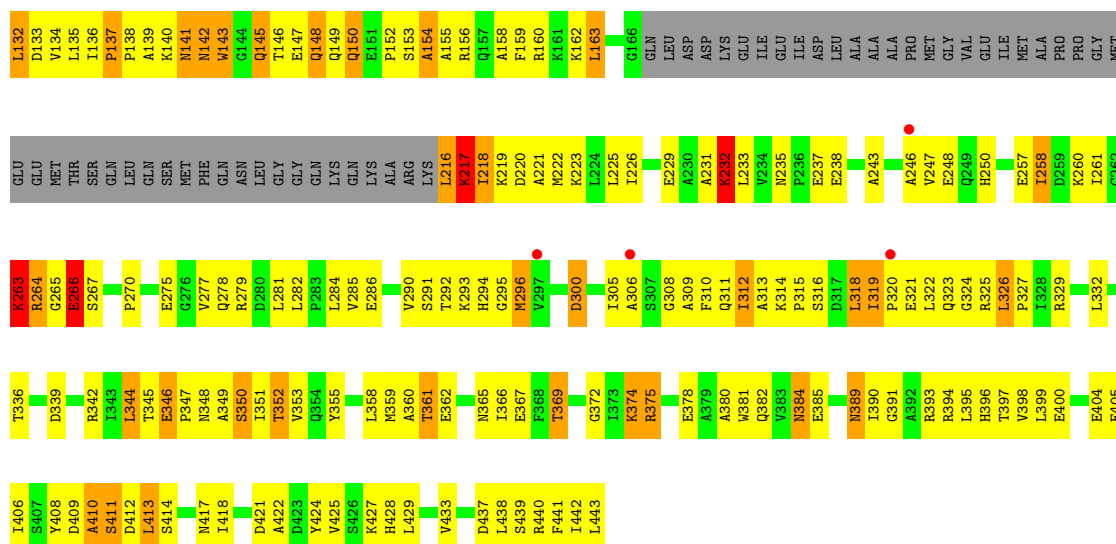
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU

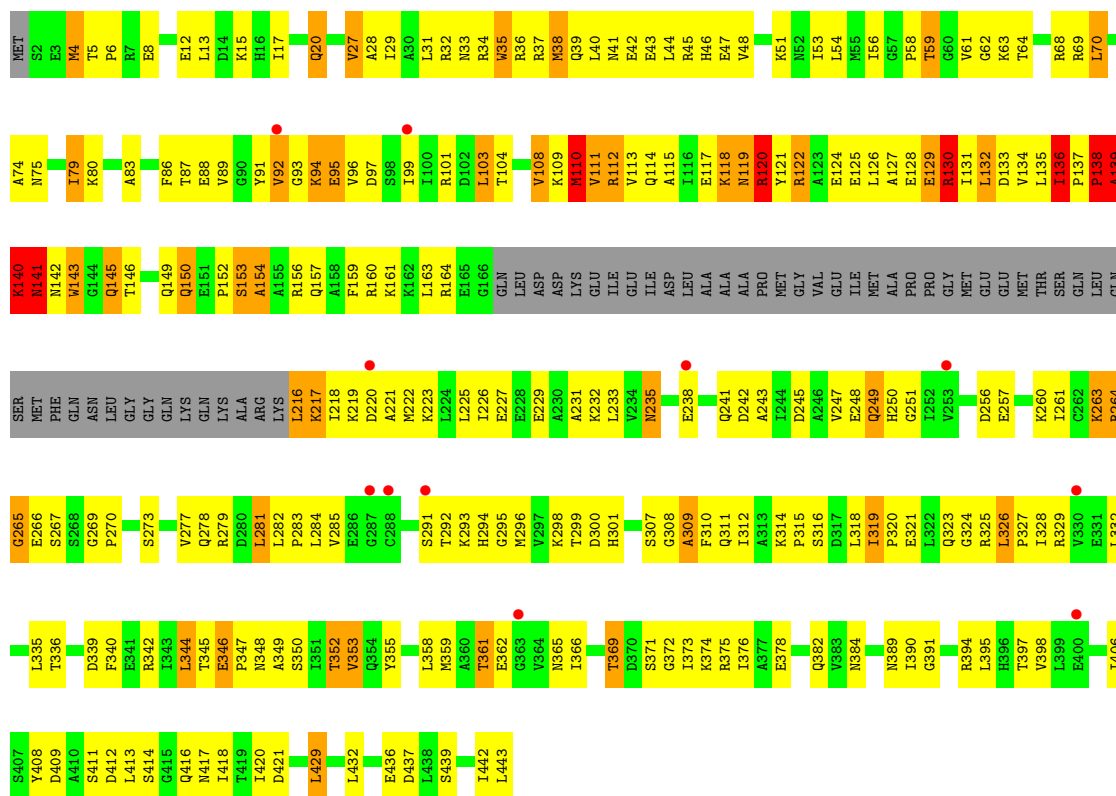


• Molecule 1: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU



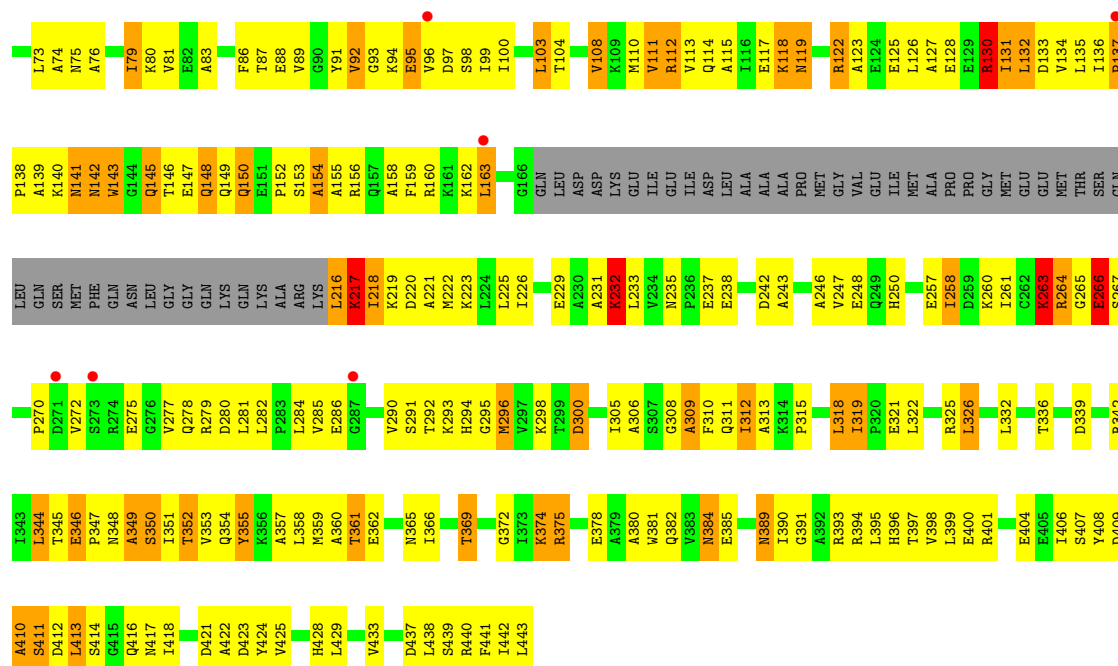


• Molecule 1: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU

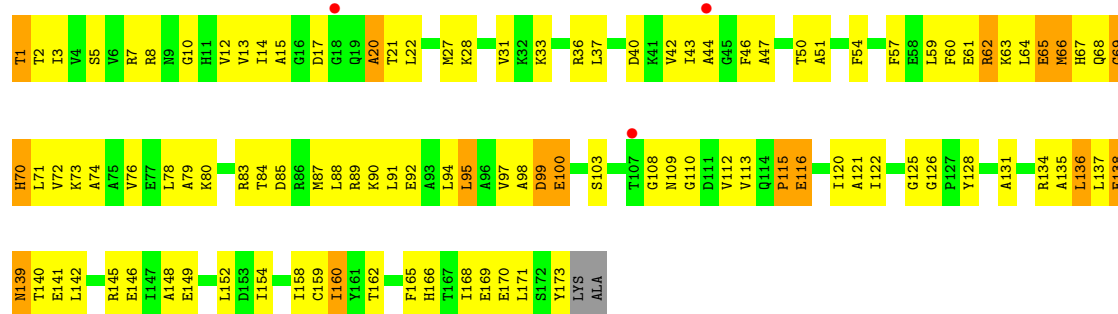


• Molecule 1: ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT HSLU

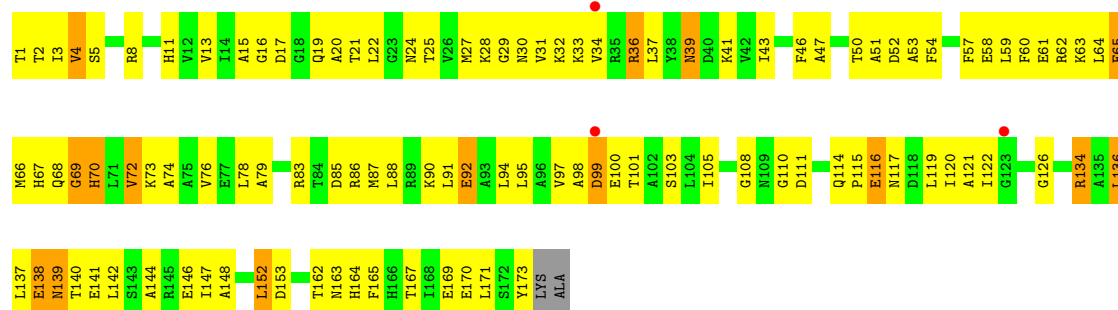




• Molecule 2: ATP-DEPENDENT PROTEASE HSLV

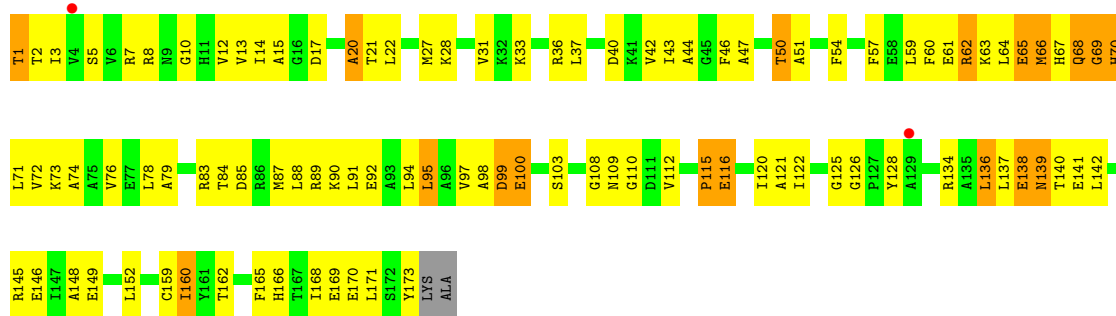


• Molecule 2: ATP-DEPENDENT PROTEASE HSLV



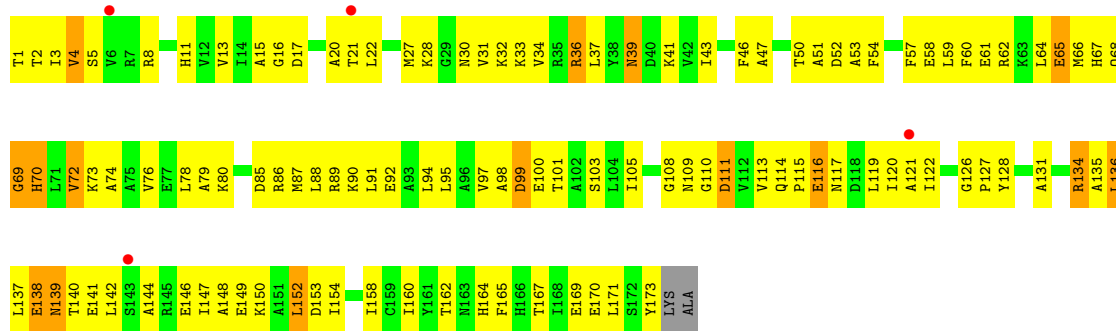
• Molecule 2: ATP-DEPENDENT PROTEASE HSLV

Chain O:  41% 47% 10%



• Molecule 2: ATP-DEPENDENT PROTEASE HSLV

Chain P:  33% 57% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	173.38Å 173.38Å 254.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 7.00 10.00 – 7.00	Depositor EDS
% Data completeness (in resolution range)	66.0 (10.00-7.00) 80.2 (10.00-7.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 6.72Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.401 , 0.432 0.449 , 0.436	Depositor DCC
R_{free} test set	607 reflections (9.48%)	wwPDB-VP
Wilson B-factor (Å ²)	101.1	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.350 for -h,-k,l	Xtriage
F_o, F_c correlation	0.49	EDS
Total number of atoms	17660	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.82% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	E	0.82	4/3135 (0.1%)	1.29	34/4228 (0.8%)
1	F	0.58	2/3135 (0.1%)	1.04	16/4228 (0.4%)
1	K	0.82	4/3135 (0.1%)	1.29	35/4228 (0.8%)
1	L	0.58	1/3135 (0.0%)	1.05	16/4228 (0.4%)
2	M	0.45	0/1336	0.93	2/1806 (0.1%)
2	N	0.42	0/1336	0.98	2/1806 (0.1%)
2	O	0.45	0/1336	0.93	2/1806 (0.1%)
2	P	0.42	0/1336	0.98	2/1806 (0.1%)
All	All	0.64	11/17884 (0.1%)	1.11	109/24136 (0.5%)

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	E	0	2
1	K	0	2
All	All	0	4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	139	ALA	C-N	-29.05	0.93	1.33
1	K	139	ALA	C-N	-29.05	0.93	1.33
1	E	122	ARG	CB-CG	9.32	1.80	1.52
1	K	122	ARG	CB-CG	9.28	1.80	1.52
1	E	145	GLN	CA-CB	-8.03	1.40	1.53
1	K	145	GLN	CA-CB	-8.02	1.40	1.53
1	E	145	GLN	CG-CD	7.65	1.71	1.52
1	K	145	GLN	CG-CD	7.63	1.71	1.52
1	L	145	GLN	CA-CB	-7.30	1.42	1.53
1	F	145	GLN	CA-CB	-7.30	1.42	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	145	GLN	CG-CD	5.01	1.64	1.52

All (109) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	122	ARG	CA-CB-CG	-20.16	73.78	114.10
1	K	122	ARG	CA-CB-CG	-20.15	73.80	114.10
1	K	140	LYS	CG-CD-CE	15.09	146.01	111.30
1	E	140	LYS	CG-CD-CE	15.08	145.98	111.30
1	E	138	PRO	CA-C-N	13.76	147.83	121.54
1	E	138	PRO	C-N-CA	13.76	147.83	121.54
1	K	138	PRO	CA-C-N	13.71	147.73	121.54
1	K	138	PRO	C-N-CA	13.71	147.73	121.54
1	K	145	GLN	CA-CB-CG	-13.65	86.80	114.10
1	E	145	GLN	CA-CB-CG	-13.65	86.81	114.10
1	E	141	ASN	O-C-N	13.43	139.39	122.87
1	K	141	ASN	O-C-N	13.42	139.38	122.87
1	E	139	ALA	O-C-N	-13.33	104.86	122.59
1	K	139	ALA	O-C-N	-13.31	104.89	122.59
1	K	139	ALA	CA-C-N	12.42	145.26	121.54
1	K	139	ALA	C-N-CA	12.42	145.26	121.54
1	E	139	ALA	CA-C-N	12.41	145.25	121.54
1	E	139	ALA	C-N-CA	12.41	145.25	121.54
1	E	122	ARG	CB-CG-CD	-11.86	84.01	111.30
1	K	122	ARG	CB-CG-CD	-11.85	84.05	111.30
1	F	145	GLN	CA-CB-CG	-10.42	93.26	114.10
1	L	145	GLN	CA-CB-CG	-10.42	93.26	114.10
1	K	249	GLN	CB-CG-CD	9.61	128.93	112.60
1	E	249	GLN	CB-CG-CD	9.55	128.84	112.60
1	K	249	GLN	CA-CB-CG	9.30	132.70	114.10
1	E	249	GLN	CA-CB-CG	9.29	132.68	114.10
1	E	137	PRO	N-CA-C	-9.02	99.69	110.70
1	K	137	PRO	N-CA-C	-9.01	99.71	110.70
1	E	137	PRO	CA-N-CD	7.28	122.20	112.00
1	K	137	PRO	CA-N-CD	7.25	122.15	112.00
1	K	62	GLY	N-CA-C	6.96	122.77	114.48
1	E	62	GLY	N-CA-C	6.90	122.69	114.48
1	E	429	LEU	N-CA-C	6.89	121.74	113.12
1	K	429	LEU	N-CA-C	6.88	121.71	113.12
1	F	137	PRO	N-CA-C	6.82	119.02	110.70
1	L	137	PRO	N-CA-C	6.77	118.96	110.70
1	K	309	ALA	O-C-N	6.74	129.01	122.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	309	ALA	O-C-N	6.66	128.93	122.07
1	L	345	THR	N-CA-C	6.53	121.08	112.72
1	K	349	ALA	N-CA-C	-6.52	103.48	112.03
1	F	345	THR	N-CA-C	6.51	121.06	112.72
1	E	349	ALA	N-CA-C	-6.47	103.56	112.03
1	L	309	ALA	O-C-N	6.25	128.84	122.09
1	K	136	ILE	O-C-N	-6.19	114.04	121.10
1	E	136	ILE	O-C-N	-6.17	114.07	121.10
1	F	309	ALA	O-C-N	6.13	128.71	122.09
1	L	57	GLY	CA-C-N	6.09	126.05	120.21
1	L	57	GLY	C-N-CA	6.09	126.05	120.21
1	E	136	ILE	CA-C-N	-6.08	114.11	120.38
1	E	136	ILE	C-N-CA	-6.08	114.11	120.38
1	F	57	GLY	CA-C-N	6.06	126.03	120.21
1	F	57	GLY	C-N-CA	6.06	126.03	120.21
1	K	136	ILE	CA-C-N	-6.02	114.18	120.38
1	K	136	ILE	C-N-CA	-6.02	114.18	120.38
1	E	319	ILE	CA-C-N	5.95	127.27	119.84
1	E	319	ILE	C-N-CA	5.95	127.27	119.84
1	K	319	ILE	CA-C-N	5.88	127.19	119.84
1	K	319	ILE	C-N-CA	5.88	127.19	119.84
1	L	326	LEU	CA-C-N	5.77	127.05	119.84
1	L	326	LEU	C-N-CA	5.77	127.05	119.84
1	F	428	HIS	N-CA-C	5.72	118.73	111.69
1	L	428	HIS	N-CA-C	5.71	118.72	111.69
1	F	326	LEU	CA-C-N	5.67	126.93	119.84
1	F	326	LEU	C-N-CA	5.67	126.93	119.84
2	M	20	ALA	N-CA-C	-5.60	99.29	108.76
2	O	20	ALA	N-CA-C	-5.59	99.32	108.76
1	E	353	VAL	N-CA-C	-5.53	105.13	110.72
1	K	353	VAL	N-CA-C	-5.51	105.15	110.72
1	E	35	TRP	N-CA-C	-5.49	104.94	111.03
2	P	52	ASP	N-CA-C	-5.46	105.33	111.28
1	E	326	LEU	CA-C-N	5.42	125.76	119.47
1	E	326	LEU	C-N-CA	5.42	125.76	119.47
2	N	52	ASP	N-CA-C	-5.41	105.39	111.28
1	K	35	TRP	N-CA-C	-5.40	105.04	111.03
1	K	326	LEU	CA-C-N	5.34	125.67	119.47
1	K	326	LEU	C-N-CA	5.34	125.67	119.47
1	L	130	ARG	N-CA-C	-5.31	106.94	113.41
1	K	120	ARG	CA-CB-CG	-5.27	103.56	114.10
1	F	130	ARG	N-CA-C	-5.25	107.00	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	346	GLU	N-CA-C	5.25	120.07	113.25
1	E	120	ARG	CA-CB-CG	-5.25	103.61	114.10
2	O	62	ARG	N-CA-C	-5.22	106.06	112.90
2	M	62	ARG	N-CA-C	-5.22	106.06	112.90
1	F	346	GLU	N-CA-C	5.19	120.00	113.25
1	E	129	GLU	CA-C-N	-5.15	110.67	121.80
1	E	129	GLU	C-N-CA	-5.15	110.67	121.80
1	K	129	GLU	CA-C-N	-5.14	110.69	121.80
1	K	129	GLU	C-N-CA	-5.14	110.69	121.80
2	P	72	VAL	N-CA-C	5.13	115.57	110.23
1	F	300	ASP	N-CA-C	5.11	121.67	110.80
1	K	309	ALA	CA-C-N	5.11	129.80	122.40
1	K	309	ALA	C-N-CA	5.11	129.80	122.40
1	F	309	ALA	CA-C-N	5.10	129.80	122.40
1	F	309	ALA	C-N-CA	5.10	129.80	122.40
1	E	309	ALA	CA-C-N	5.09	129.79	122.40
1	E	309	ALA	C-N-CA	5.09	129.79	122.40
1	F	248	GLU	N-CA-C	5.09	117.57	111.71
1	L	300	ASP	N-CA-C	5.08	121.63	110.80
2	N	72	VAL	N-CA-C	5.08	115.52	110.23
1	E	136	ILE	N-CA-CB	-5.07	104.11	111.21
1	L	309	ALA	CA-C-N	5.06	129.73	122.40
1	L	309	ALA	C-N-CA	5.06	129.73	122.40
1	K	136	ILE	N-CA-CB	-5.05	104.14	111.21
1	L	248	GLU	N-CA-C	5.04	117.51	111.71
1	E	130	ARG	NE-CZ-NH2	5.04	123.73	119.20
1	K	346	GLU	N-CA-C	5.03	119.08	112.35
1	L	349	ALA	N-CA-C	-5.02	104.63	111.56
1	K	130	ARG	NE-CZ-NH2	5.02	123.72	119.20
1	F	349	ALA	N-CA-C	-5.01	104.64	111.56

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	139	ALA	Mainchain
1	E	141	ASN	Mainchain
1	K	139	ALA	Mainchain
1	K	141	ASN	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3096	0	3151	589	49
1	F	3096	0	3155	609	54
1	K	3096	0	3150	333	220
1	L	3096	0	3152	405	225
2	M	1319	0	1335	175	12
2	N	1319	0	1335	148	15
2	O	1319	0	1330	203	14
2	P	1319	0	1327	181	19
All	All	17660	0	17935	2121	305

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

All (2121) 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:E:441:PHE:CD1	1:F:56:ILE:HD13	1.27	1.66
1:K:122:ARG:CB	1:K:122:ARG:CG	1.80	1.59
1:L:309:ALA:HB1	2:O:66:MET:CE	1.28	1.58
1:E:442:ILE:HA	1:F:329:ARG:CB	1.12	1.58
1:E:122:ARG:CG	1:E:122:ARG:CB	1.80	1.56
1:E:139:ALA:HB2	1:E:152:PRO:CG	1.36	1.53
1:L:264:ARG:NH2	2:O:59:LEU:CD2	1.69	1.53
1:E:407:SER:CA	1:F:36:ARG:HH12	1.11	1.50
1:K:408:TYR:CE2	1:L:7:ARG:NH2	1.79	1.50
1:K:139:ALA:HB2	1:K:152:PRO:CG	1.36	1.50
2:M:135:ALA:HB2	2:P:154:ILE:CD1	1.36	1.50
1:E:354:GLN:NE2	1:F:47:GLU:HB3	1.30	1.44
1:E:357:ALA:HB2	1:F:44:LEU:CD1	1.46	1.43
1:E:311:GLN:CB	2:N:66:MET:O	1.68	1.41
1:E:92:VAL:CG1	1:F:92:VAL:HA	1.47	1.41
1:F:145:GLN:CD	1:F:145:GLN:H	1.29	1.40
1:E:139:ALA:HB2	1:E:152:PRO:CB	1.52	1.40
1:K:145:GLN:CB	1:K:149:GLN:HB2	1.52	1.39
1:E:145:GLN:CB	1:E:149:GLN:HB2	1.52	1.38

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:357:ALA:CB	1:F:44:LEU:HD13	1.53	1.38
1:K:139:ALA:HB2	1:K:152:PRO:CB	1.52	1.38
1:K:122:ARG:CG	1:K:122:ARG:CA	2.01	1.37
1:E:314:LYS:NZ	2:N:65:GLU:CG	1.70	1.36
1:E:122:ARG:CG	1:E:122:ARG:CA	2.01	1.36
1:E:91:TYR:CG	1:F:90:GLY:O	1.80	1.34
1:L:264:ARG:HD3	2:O:62:ARG:CD	1.57	1.34
2:M:135:ALA:CB	2:P:154:ILE:CD1	2.06	1.34
1:F:264:ARG:HH22	2:M:62:ARG:CB	1.40	1.33
1:E:442:ILE:CA	1:F:329:ARG:CB	2.07	1.32
1:K:311:GLN:HG2	2:P:66:MET:CE	1.60	1.31
1:L:145:GLN:H	1:L:145:GLN:CD	1.29	1.31
1:F:264:ARG:CZ	2:M:62:ARG:HD2	1.61	1.30
1:K:293:LYS:HE3	1:L:296:MET:CE	1.60	1.30
1:L:145:GLN:CG	1:L:150:GLN:N	1.93	1.30
1:L:264:ARG:HG2	2:O:62:ARG:NH2	1.41	1.30
1:F:145:GLN:CG	1:F:150:GLN:N	1.93	1.29
1:K:311:GLN:HG3	2:P:66:MET:SD	1.69	1.27
1:E:408:TYR:OH	1:F:7:ARG:CA	1.82	1.27
1:E:441:PHE:HD1	1:F:56:ILE:CD1	1.48	1.27
1:E:357:ALA:O	1:F:40:LEU:CD2	1.82	1.26
2:O:28:LYS:CG	2:P:113:VAL:HG11	1.58	1.26
1:E:357:ALA:C	1:F:40:LEU:CD2	2.07	1.26
1:E:440:ARG:O	1:F:315:PRO:CB	1.82	1.26
1:E:92:VAL:HG11	1:F:92:VAL:CA	1.63	1.25
1:E:442:ILE:CA	1:F:329:ARG:HB2	1.67	1.25
1:E:311:GLN:CD	2:N:66:MET:O	1.71	1.25
1:L:145:GLN:HG3	1:L:150:GLN:N	1.49	1.24
1:F:311:GLN:HG3	2:M:66:MET:CE	1.68	1.24
2:M:135:ALA:CB	2:P:154:ILE:HD13	1.66	1.24
1:F:145:GLN:HG3	1:F:150:GLN:N	1.49	1.24
1:E:442:ILE:C	1:F:329:ARG:HG3	1.62	1.23
1:F:264:ARG:NH2	2:M:62:ARG:HD2	1.53	1.23
1:K:311:GLN:CG	2:P:66:MET:HE2	1.68	1.22
1:K:139:ALA:CB	1:K:152:PRO:HG3	1.68	1.22
1:E:139:ALA:CB	1:E:152:PRO:HG3	1.68	1.21
1:F:264:ARG:HH12	2:M:62:ARG:CB	1.53	1.21
1:L:145:GLN:CD	1:L:145:GLN:N	1.87	1.21
1:E:408:TYR:OH	1:F:7:ARG:N	1.70	1.21
1:F:264:ARG:NH2	2:M:62:ARG:HB2	1.52	1.21
1:F:145:GLN:CB	1:F:149:GLN:HB2	1.71	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:264:ARG:CG	2:O:62:ARG:NH2	2.04	1.20
2:M:154:ILE:CG2	2:P:131:ALA:HB1	1.71	1.20
1:L:145:GLN:CB	1:L:149:GLN:HB2	1.71	1.20
1:E:441:PHE:CD1	1:F:56:ILE:CD1	2.22	1.20
1:F:145:GLN:CD	1:F:145:GLN:N	1.87	1.20
1:E:311:GLN:CG	2:N:66:MET:O	1.91	1.19
1:E:354:GLN:NE2	1:F:47:GLU:CB	2.06	1.18
1:K:264:ARG:HG3	2:P:62:ARG:NH2	1.55	1.18
1:L:309:ALA:CA	2:O:66:MET:SD	2.32	1.18
1:F:264:ARG:NH2	2:M:62:ARG:CD	2.07	1.18
1:F:264:ARG:CZ	2:M:62:ARG:HB2	1.74	1.17
1:E:91:TYR:CD2	1:F:90:GLY:O	1.96	1.17
1:E:138:PRO:HB2	1:E:152:PRO:HB2	1.25	1.17
1:E:442:ILE:C	1:F:329:ARG:CG	2.17	1.17
1:F:312:ILE:HD11	2:M:62:ARG:HA	1.21	1.17
1:E:145:GLN:CG	1:E:149:GLN:HB2	1.73	1.17
1:F:264:ARG:NH2	2:M:62:ARG:CB	2.01	1.17
1:E:354:GLN:OE1	1:F:48:VAL:HA	1.46	1.16
1:K:145:GLN:CG	1:K:149:GLN:HB2	1.74	1.16
1:K:145:GLN:HG3	1:K:149:GLN:CG	1.76	1.16
1:F:311:GLN:CG	2:M:66:MET:HE1	1.74	1.16
1:L:264:ARG:CG	2:O:62:ARG:HH21	1.58	1.16
1:K:122:ARG:CB	1:K:122:ARG:CD	2.24	1.15
1:E:145:GLN:HG3	1:E:149:GLN:CG	1.76	1.15
1:E:407:SER:HA	1:F:36:ARG:NH1	1.38	1.15
1:E:442:ILE:HA	1:F:329:ARG:HB3	1.23	1.15
1:K:122:ARG:CG	1:K:122:ARG:HA	1.73	1.15
1:E:145:GLN:HB2	1:E:149:GLN:CB	1.76	1.15
1:E:440:ARG:O	1:F:315:PRO:HB2	0.98	1.15
1:K:145:GLN:HB2	1:K:149:GLN:CB	1.75	1.15
1:E:441:PHE:HB3	1:F:56:ILE:HD12	1.29	1.14
1:E:122:ARG:CB	1:E:122:ARG:CD	2.24	1.14
1:F:145:GLN:NE2	1:F:150:GLN:HA	1.63	1.13
1:L:145:GLN:HB3	1:L:149:GLN:HB2	1.15	1.13
1:L:264:ARG:NH2	2:O:59:LEU:CB	2.10	1.13
1:E:122:ARG:CG	1:E:122:ARG:HA	1.73	1.13
1:L:264:ARG:CD	2:O:62:ARG:HH21	1.60	1.13
1:F:145:GLN:HB3	1:F:149:GLN:HB2	1.15	1.12
1:E:139:ALA:HB2	1:E:152:PRO:HG3	1.13	1.12
1:E:442:ILE:HA	1:F:329:ARG:CG	1.79	1.12
1:L:145:GLN:NE2	1:L:150:GLN:HA	1.64	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:264:ARG:NH1	2:M:62:ARG:HB2	1.64	1.12
1:E:311:GLN:NE2	2:N:67:HIS:HA	1.30	1.12
1:F:264:ARG:NH1	2:M:62:ARG:CB	2.11	1.12
1:K:264:ARG:HG3	2:P:62:ARG:HH22	1.04	1.12
1:E:408:TYR:OH	1:F:7:ARG:HA	1.36	1.12
1:K:139:ALA:HB2	1:K:152:PRO:HG3	1.12	1.12
1:F:264:ARG:CZ	2:M:62:ARG:CD	2.27	1.11
1:L:86:PHE:O	1:L:89:VAL:HG22	1.51	1.11
1:F:86:PHE:O	1:F:89:VAL:HG22	1.51	1.11
1:F:264:ARG:NH1	2:M:62:ARG:CG	2.12	1.11
1:E:139:ALA:CB	1:E:152:PRO:CG	2.26	1.11
1:K:138:PRO:HB2	1:K:152:PRO:HB2	1.25	1.11
1:L:264:ARG:NH1	2:O:62:ARG:HB3	1.66	1.11
1:E:357:ALA:C	1:F:40:LEU:HD21	1.71	1.10
1:E:358:LEU:HD11	1:F:48:VAL:CG1	1.81	1.10
1:E:310:PHE:O	2:N:66:MET:HB2	1.29	1.10
1:E:311:GLN:HE22	2:N:67:HIS:CA	1.64	1.10
2:M:135:ALA:HA	2:P:154:ILE:HD11	1.32	1.10
1:E:441:PHE:O	1:F:329:ARG:HD2	1.50	1.10
1:L:264:ARG:NH2	2:O:59:LEU:HG	1.57	1.10
1:E:311:GLN:NE2	2:N:67:HIS:CA	2.16	1.09
1:E:311:GLN:HB3	2:N:66:MET:O	1.25	1.09
1:E:400:GLU:CD	1:F:51:LYS:HG2	1.75	1.09
1:F:145:GLN:HG3	1:F:149:GLN:C	1.76	1.09
1:E:357:ALA:CB	1:F:44:LEU:CD1	2.15	1.09
1:L:145:GLN:HG3	1:L:149:GLN:C	1.76	1.09
1:E:441:PHE:HA	1:F:315:PRO:HG2	1.28	1.08
1:F:264:ARG:CZ	2:M:62:ARG:CG	2.31	1.08
2:O:28:LYS:HG3	2:P:113:VAL:CG1	1.84	1.08
1:E:400:GLU:CD	1:F:51:LYS:CG	2.26	1.08
1:E:442:ILE:CA	1:F:329:ARG:CG	2.32	1.08
1:L:266:GLU:O	2:O:87:MET:SD	2.11	1.08
1:F:264:ARG:NH1	2:M:62:ARG:HG3	1.65	1.08
1:K:264:ARG:CG	2:P:62:ARG:NH2	2.16	1.08
1:F:292:THR:HG22	1:F:294:HIS:H	1.19	1.08
1:E:145:GLN:HB2	1:E:149:GLN:HB2	1.11	1.07
1:E:408:TYR:CZ	1:F:7:ARG:N	2.21	1.07
1:E:349:ALA:CB	1:F:47:GLU:HG3	1.84	1.07
1:E:357:ALA:C	1:F:40:LEU:HD22	1.75	1.07
1:K:292:THR:HG22	1:K:294:HIS:H	1.20	1.07
1:E:393:ARG:HB3	1:F:324:GLY:HA3	1.37	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:145:GLN:HB2	1:K:149:GLN:HB2	1.11	1.06
2:M:154:ILE:HG21	2:P:131:ALA:HB1	1.08	1.06
1:L:312:ILE:HA	2:O:62:ARG:HA	1.07	1.06
1:L:292:THR:HG22	1:L:294:HIS:H	1.19	1.06
1:E:354:GLN:OE1	1:F:48:VAL:CA	2.03	1.06
1:F:145:GLN:HG3	1:F:149:GLN:CA	1.86	1.06
1:L:312:ILE:C	2:O:65:GLU:HG3	1.59	1.06
1:E:139:ALA:HB2	1:E:152:PRO:HB3	1.35	1.05
1:E:354:GLN:CD	1:F:47:GLU:C	2.24	1.05
1:L:145:GLN:HG3	1:L:149:GLN:CA	1.86	1.05
1:E:354:GLN:NE2	1:F:47:GLU:C	2.14	1.05
1:L:344:LEU:HD13	1:L:395:LEU:HD13	1.39	1.05
1:E:408:TYR:CZ	1:F:6:PRO:C	2.34	1.05
1:E:349:ALA:HB1	1:F:47:GLU:CG	1.87	1.04
1:L:132:LEU:HD13	1:L:156:ARG:HG2	1.38	1.04
1:E:441:PHE:HB3	1:F:56:ILE:CD1	1.87	1.04
1:F:344:LEU:HD13	1:F:395:LEU:HD13	1.39	1.04
2:M:135:ALA:CA	2:P:154:ILE:HD11	1.85	1.04
1:K:139:ALA:CB	1:K:152:PRO:CG	2.26	1.04
1:K:408:TYR:HE2	1:L:7:ARG:NH2	1.28	1.04
1:E:358:LEU:HD11	1:F:48:VAL:HG11	1.08	1.03
1:E:442:ILE:CA	1:F:329:ARG:HG3	1.87	1.03
1:K:139:ALA:HB2	1:K:152:PRO:HB3	1.35	1.03
1:K:265:GLY:O	2:P:87:MET:HE3	1.58	1.03
1:L:264:ARG:CD	2:O:62:ARG:HD2	1.87	1.03
1:E:400:GLU:OE2	1:F:51:LYS:CE	2.06	1.02
1:L:309:ALA:CB	2:O:66:MET:SD	0.96	1.02
1:L:312:ILE:HA	2:O:62:ARG:CA	1.71	1.02
1:E:92:VAL:HG11	1:F:92:VAL:CB	1.89	1.02
1:E:314:LYS:NZ	2:N:65:GLU:HG3	1.12	1.02
1:F:145:GLN:CD	1:F:149:GLN:C	2.28	1.02
1:F:369:THR:HG22	1:F:372:GLY:H	1.22	1.02
1:L:145:GLN:CD	1:L:149:GLN:C	2.27	1.02
1:E:292:THR:HG22	1:E:294:HIS:H	1.20	1.01
1:K:293:LYS:HE3	1:L:296:MET:HE3	1.03	1.01
1:L:309:ALA:HB1	2:O:66:MET:SD	0.66	1.01
1:E:393:ARG:NE	1:F:321:GLU:HA	1.74	1.01
1:K:311:GLN:CG	2:P:66:MET:SD	2.44	1.01
1:K:408:TYR:CE2	1:L:7:ARG:CZ	2.37	1.01
1:L:313:ALA:O	2:O:65:GLU:OE2	1.79	1.01
1:E:357:ALA:HB3	1:F:44:LEU:HD13	1.39	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:369:THR:HG22	1:L:372:GLY:H	1.22	1.01
1:E:163:LEU:HD11	1:E:218:ILE:HG21	1.39	1.01
1:E:139:ALA:CB	1:E:152:PRO:CB	2.38	1.00
1:E:400:GLU:OE2	1:F:51:LYS:NZ	1.94	1.00
1:K:163:LEU:HD11	1:K:218:ILE:HG21	1.39	1.00
1:E:400:GLU:OE1	1:F:51:LYS:HG2	1.57	1.00
1:K:139:ALA:CB	1:K:152:PRO:CB	2.39	1.00
1:F:145:GLN:CG	1:F:149:GLN:HB2	1.90	1.00
1:L:311:GLN:HE22	2:O:68:GLN:C	1.69	1.00
1:L:264:ARG:NH2	2:O:59:LEU:CG	0.85	1.00
1:E:357:ALA:O	1:F:40:LEU:HD21	1.54	1.00
1:F:132:LEU:HD13	1:F:156:ARG:HG2	1.38	1.00
1:L:264:ARG:HD3	2:O:62:ARG:HD2	1.02	1.00
1:K:293:LYS:CE	1:L:296:MET:HE3	1.91	1.00
1:K:88:GLU:OE2	1:L:280:ASP:OD2	1.79	0.99
1:L:145:GLN:CG	1:L:149:GLN:HB2	1.90	0.99
1:E:139:ALA:CB	1:E:152:PRO:HB3	1.91	0.99
1:K:139:ALA:CB	1:K:152:PRO:HB3	1.91	0.99
1:K:265:GLY:O	2:P:87:MET:CE	2.11	0.99
1:L:132:LEU:HD11	1:L:160:ARG:HB3	1.42	0.99
1:L:312:ILE:CA	2:O:62:ARG:HA	1.90	0.99
1:K:145:GLN:HG3	1:K:149:GLN:CB	1.92	0.99
1:E:145:GLN:HG3	1:E:149:GLN:CB	1.92	0.98
1:E:113:VAL:O	1:E:117:GLU:HG3	1.64	0.98
1:L:130:ARG:HD2	1:L:130:ARG:O	1.64	0.98
1:E:407:SER:CA	1:F:36:ARG:NH1	1.96	0.98
1:E:441:PHE:CG	1:F:56:ILE:HD13	1.97	0.98
1:F:264:ARG:HH22	2:M:62:ARG:HB2	1.12	0.98
1:E:408:TYR:OH	1:F:6:PRO:C	2.06	0.98
1:E:361:THR:HG21	1:F:36:ARG:HA	1.43	0.98
1:E:358:LEU:CD2	1:F:37:ARG:HA	1.94	0.98
1:E:393:ARG:CD	1:F:321:GLU:HA	1.94	0.97
1:E:354:GLN:HB3	1:F:48:VAL:HG22	1.46	0.97
1:F:130:ARG:O	1:F:130:ARG:HD2	1.64	0.97
1:E:92:VAL:HG11	1:F:92:VAL:HA	0.99	0.97
1:L:309:ALA:HB2	2:O:66:MET:SD	1.59	0.97
1:E:131:ILE:O	1:E:134:VAL:HG12	1.64	0.97
1:E:441:PHE:CD1	1:F:56:ILE:HG21	2.00	0.97
1:K:131:ILE:O	1:K:134:VAL:HG12	1.64	0.97
2:O:2:THR:OG1	2:O:162:THR:HG21	1.64	0.96
1:E:145:GLN:CB	1:E:149:GLN:CB	2.39	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:264:ARG:HH22	2:M:62:ARG:HB3	1.28	0.96
1:L:145:GLN:CG	1:L:149:GLN:C	2.35	0.96
2:M:154:ILE:CG2	2:P:131:ALA:CB	2.43	0.96
1:F:132:LEU:HD11	1:F:160:ARG:HB3	1.42	0.96
2:M:2:THR:OG1	2:M:162:THR:HG21	1.64	0.96
1:K:113:VAL:O	1:K:117:GLU:HG3	1.64	0.96
1:E:264:ARG:HH12	2:N:63:LYS:HZ3	1.12	0.96
1:E:92:VAL:CG1	1:F:92:VAL:CA	2.30	0.95
1:E:357:ALA:HB2	1:F:44:LEU:HD12	1.48	0.95
1:F:145:GLN:CG	1:F:149:GLN:C	2.35	0.95
1:K:145:GLN:CB	1:K:149:GLN:CB	2.39	0.95
1:E:442:ILE:HA	1:F:329:ARG:HB2	0.97	0.95
1:K:264:ARG:CG	2:P:62:ARG:HH22	1.74	0.95
1:E:139:ALA:CA	1:E:152:PRO:HB3	1.97	0.94
1:E:141:ASN:H	1:E:141:ASN:HD22	1.14	0.94
1:E:355:TYR:HE2	1:F:51:LYS:HZ3	0.96	0.94
1:E:400:GLU:OE2	1:F:51:LYS:HE2	1.65	0.94
1:L:145:GLN:HG3	1:L:150:GLN:H	1.24	0.94
1:E:59:THR:HG23	1:F:321:GLU:OE1	1.67	0.94
1:E:91:TYR:CG	1:F:90:GLY:C	2.44	0.94
1:K:139:ALA:CA	1:K:152:PRO:HB3	1.97	0.94
2:O:28:LYS:CG	2:P:113:VAL:CG1	2.41	0.94
1:E:355:TYR:HE2	1:F:51:LYS:NZ	1.64	0.94
1:E:441:PHE:O	1:F:329:ARG:CD	2.15	0.94
1:E:354:GLN:HA	1:F:44:LEU:HD22	1.46	0.93
1:L:264:ARG:HG2	2:O:62:ARG:HH22	1.29	0.93
1:E:358:LEU:HG	1:F:40:LEU:HD11	1.47	0.93
2:M:135:ALA:CB	2:P:154:ILE:HD11	1.96	0.93
1:K:311:GLN:CG	2:P:66:MET:CE	2.32	0.93
1:E:91:TYR:CD1	1:F:90:GLY:O	2.22	0.93
1:K:141:ASN:HD22	1:K:141:ASN:H	1.14	0.92
1:L:145:GLN:HB3	1:L:149:GLN:CB	1.99	0.92
1:L:309:ALA:CB	2:O:66:MET:CG	2.47	0.92
1:E:440:ARG:NE	1:F:316:SER:OG	2.02	0.92
1:E:354:GLN:NE2	1:F:47:GLU:O	2.02	0.92
1:E:354:GLN:OE1	1:F:47:GLU:C	2.13	0.92
1:F:145:GLN:HB3	1:F:149:GLN:CB	1.99	0.92
1:F:344:LEU:HD12	1:F:351:ILE:HD11	1.50	0.92
2:M:135:ALA:CA	2:P:154:ILE:CD1	2.45	0.92
1:L:344:LEU:HD12	1:L:351:ILE:HD11	1.50	0.92
1:L:145:GLN:CG	1:L:150:GLN:H	1.75	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:92:VAL:HG13	1:F:91:TYR:O	1.70	0.91
1:E:354:GLN:OE1	1:F:48:VAL:N	2.03	0.91
1:E:358:LEU:CA	1:F:40:LEU:HD21	1.99	0.91
1:E:91:TYR:HB3	1:F:91:TYR:CA	2.00	0.91
1:E:122:ARG:CB	1:E:122:ARG:HD2	2.00	0.91
1:E:235:ASN:H	1:E:235:ASN:ND2	1.67	0.91
1:K:122:ARG:CB	1:K:122:ARG:HD2	2.00	0.91
1:E:122:ARG:HA	1:E:122:ARG:HG3	1.53	0.91
2:M:37:LEU:HD21	2:M:57:PHE:HB3	1.52	0.91
1:K:27:VAL:HG13	1:K:70:LEU:HG	1.53	0.90
1:K:264:ARG:CD	2:P:62:ARG:HH21	1.84	0.90
1:E:92:VAL:HG21	1:F:92:VAL:O	1.72	0.90
1:E:235:ASN:HD22	1:E:235:ASN:N	1.65	0.90
1:E:145:GLN:CG	1:E:149:GLN:CB	2.50	0.90
1:E:349:ALA:HB1	1:F:47:GLU:HG3	0.94	0.90
1:F:145:GLN:NE2	1:F:145:GLN:O	2.05	0.90
1:K:145:GLN:HB2	1:K:149:GLN:CA	2.01	0.90
1:E:145:GLN:HB2	1:E:149:GLN:CA	2.01	0.90
1:K:122:ARG:HA	1:K:122:ARG:HG3	1.53	0.90
2:O:37:LEU:HD21	2:O:57:PHE:HB3	1.52	0.90
1:E:27:VAL:HG13	1:E:70:LEU:HG	1.53	0.89
1:E:357:ALA:HB1	1:F:40:LEU:HD22	1.55	0.89
1:E:358:LEU:HA	1:F:40:LEU:HD21	1.52	0.89
1:K:145:GLN:CG	1:K:149:GLN:CB	2.50	0.89
1:K:235:ASN:H	1:K:235:ASN:ND2	1.67	0.89
2:M:140:THR:HG22	2:M:142:LEU:H	1.37	0.89
2:O:140:THR:HG22	2:O:142:LEU:H	1.37	0.89
1:K:264:ARG:HD2	2:P:62:ARG:HH21	1.38	0.88
1:E:441:PHE:CB	1:F:56:ILE:CD1	2.51	0.88
1:K:293:LYS:HE3	1:L:296:MET:SD	2.13	0.88
1:L:145:GLN:NE2	1:L:145:GLN:O	2.05	0.88
1:L:311:GLN:NE2	2:O:68:GLN:O	2.05	0.88
1:K:369:THR:HG22	1:K:372:GLY:H	1.39	0.88
1:L:264:ARG:HH11	2:O:62:ARG:CB	1.87	0.88
2:O:28:LYS:HG3	2:P:113:VAL:HG11	0.88	0.88
2:P:2:THR:OG1	2:P:162:THR:HG21	1.74	0.88
1:E:442:ILE:O	1:F:329:ARG:HG2	1.73	0.88
2:P:140:THR:HG21	2:P:142:LEU:HG	1.54	0.88
1:F:312:ILE:CD1	2:M:62:ARG:HA	2.04	0.87
1:L:264:ARG:NH1	2:O:62:ARG:HD3	1.89	0.87
1:F:17:ILE:HD13	1:F:66:ILE:HG12	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:2:THR:OG1	2:N:162:THR:HG21	1.73	0.87
2:N:140:THR:HG21	2:N:142:LEU:HG	1.54	0.87
1:E:358:LEU:CD1	1:F:48:VAL:HG11	2.01	0.87
1:E:393:ARG:NH2	1:F:321:GLU:HG3	1.88	0.87
1:F:145:GLN:CD	1:F:150:GLN:N	2.33	0.87
1:F:145:GLN:HE21	1:F:150:GLN:HA	1.39	0.87
1:E:145:GLN:HG3	1:E:149:GLN:HG3	1.57	0.87
2:M:154:ILE:HG21	2:P:131:ALA:CB	1.98	0.87
1:E:130:ARG:NE	1:E:225:LEU:HD11	1.90	0.87
1:E:400:GLU:HG2	1:F:51:LYS:HG3	1.55	0.87
1:F:145:GLN:HG3	1:F:150:GLN:H	1.23	0.86
1:E:358:LEU:HD23	1:F:37:ARG:HA	1.54	0.86
1:L:264:ARG:HH11	2:O:62:ARG:HB3	1.38	0.86
2:N:72:VAL:O	2:N:76:VAL:HG23	1.76	0.86
1:L:145:GLN:HE21	1:L:150:GLN:HA	1.39	0.86
1:E:141:ASN:H	1:E:141:ASN:ND2	1.72	0.86
1:E:369:THR:HG22	1:E:372:GLY:H	1.38	0.86
1:L:264:ARG:NH1	2:O:59:LEU:HA	1.90	0.86
1:E:407:SER:CB	1:F:36:ARG:HH12	1.89	0.85
1:E:441:PHE:O	1:F:329:ARG:CG	2.24	0.85
1:F:130:ARG:HG3	1:F:225:LEU:CD1	2.06	0.85
1:F:264:ARG:NH2	2:M:62:ARG:CG	2.37	0.85
1:L:17:ILE:HD13	1:L:66:ILE:HG12	1.57	0.85
1:K:130:ARG:NE	1:K:225:LEU:HD11	1.90	0.85
1:L:145:GLN:CD	1:L:150:GLN:N	2.33	0.85
1:K:145:GLN:HG3	1:K:149:GLN:HG3	1.57	0.85
1:E:130:ARG:HD3	1:E:225:LEU:CD1	2.07	0.85
1:E:264:ARG:HH12	2:N:63:LYS:NZ	1.75	0.85
1:E:235:ASN:H	1:E:235:ASN:HD22	0.87	0.85
1:E:357:ALA:CB	1:F:40:LEU:HD22	2.07	0.85
2:P:140:THR:HG22	2:P:142:LEU:H	1.42	0.85
1:E:358:LEU:N	1:F:40:LEU:HD21	1.91	0.85
1:K:141:ASN:H	1:K:141:ASN:ND2	1.72	0.85
1:K:235:ASN:H	1:K:235:ASN:HD22	0.87	0.84
1:K:130:ARG:HD3	1:K:225:LEU:CD1	2.07	0.84
2:P:72:VAL:O	2:P:76:VAL:HG23	1.76	0.84
1:L:264:ARG:HH11	2:O:62:ARG:CD	1.91	0.84
2:P:36:ARG:HB3	2:P:36:ARG:HH11	1.43	0.84
1:K:130:ARG:HD3	1:K:225:LEU:HD12	1.60	0.84
1:K:235:ASN:HD22	1:K:235:ASN:N	1.65	0.84
1:L:130:ARG:HG3	1:L:225:LEU:CD1	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:312:ILE:HD12	2:N:67:HIS:CE1	2.13	0.83
1:E:145:GLN:HG3	1:E:149:GLN:HB2	1.51	0.83
1:F:145:GLN:HG3	1:F:149:GLN:N	1.92	0.83
2:N:134:ARG:HB3	2:N:134:ARG:HH11	1.43	0.83
1:L:145:GLN:HG3	1:L:149:GLN:N	1.93	0.83
2:N:140:THR:HG22	2:N:142:LEU:H	1.42	0.83
1:E:130:ARG:CD	1:E:225:LEU:CD1	2.57	0.83
1:E:400:GLU:CD	1:F:51:LYS:HG3	2.02	0.83
2:P:134:ARG:HB3	2:P:134:ARG:HH11	1.43	0.83
1:K:109:LYS:HG3	1:L:298:LYS:HD2	1.59	0.83
1:L:264:ARG:HG2	2:O:62:ARG:HH21	1.23	0.82
1:E:442:ILE:O	1:F:329:ARG:CG	2.25	0.82
1:K:130:ARG:CD	1:K:225:LEU:CD1	2.57	0.82
1:E:408:TYR:HA	1:F:6:PRO:HG2	1.59	0.82
1:F:145:GLN:CG	1:F:150:GLN:H	1.75	0.82
1:E:355:TYR:CE2	1:F:51:LYS:NZ	2.46	0.82
1:F:132:LEU:CD1	1:F:160:ARG:HB3	2.09	0.82
1:L:264:ARG:CD	2:O:62:ARG:CD	2.51	0.82
1:E:354:GLN:NE2	1:F:47:GLU:CA	2.41	0.82
1:E:407:SER:HA	1:F:36:ARG:HH12	0.65	0.82
2:N:36:ARG:HB3	2:N:36:ARG:HH11	1.43	0.82
1:E:441:PHE:O	1:F:329:ARG:HB3	1.80	0.82
2:P:139:ASN:HD22	2:P:139:ASN:N	1.78	0.82
1:E:354:GLN:CD	1:F:47:GLU:HB3	2.05	0.82
1:L:311:GLN:NE2	2:O:68:GLN:C	2.37	0.82
1:E:389:ASN:HD22	1:E:389:ASN:C	1.88	0.81
1:K:293:LYS:CE	1:L:296:MET:CE	2.53	0.81
1:K:408:TYR:CZ	1:L:7:ARG:NH2	2.42	0.81
1:L:132:LEU:CD1	1:L:160:ARG:HB3	2.09	0.81
2:O:51:ALA:HB2	2:P:110:GLY:HA3	1.61	0.81
1:E:130:ARG:HD3	1:E:225:LEU:HD12	1.60	0.81
1:E:384:ASN:ND2	1:E:394:ARG:HD2	1.95	0.81
1:E:400:GLU:CG	1:F:51:LYS:HG3	2.10	0.81
1:L:264:ARG:HD3	2:O:62:ARG:HH21	1.44	0.81
2:M:36:ARG:HD3	2:M:40:ASP:OD1	1.80	0.81
2:O:36:ARG:HD3	2:O:40:ASP:OD1	1.80	0.81
1:E:354:GLN:HE21	1:F:47:GLU:HB3	0.91	0.81
1:F:59:THR:HG22	1:F:393:ARG:HH12	1.43	0.81
2:M:135:ALA:HB2	2:P:154:ILE:HD12	1.60	0.81
2:P:67:HIS:HD2	2:P:73:LYS:HE3	1.44	0.81
2:M:135:ALA:HB2	2:P:154:ILE:HD13	0.83	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:67:HIS:HD2	2:N:73:LYS:HE3	1.44	0.81
1:E:92:VAL:CG1	1:F:92:VAL:HG12	2.12	0.80
2:N:139:ASN:N	2:N:139:ASN:HD22	1.78	0.80
1:E:357:ALA:CB	1:F:44:LEU:HD12	2.07	0.80
1:K:384:ASN:ND2	1:K:394:ARG:HD2	1.95	0.80
1:F:136:ILE:HG22	1:F:138:PRO:HD3	1.64	0.80
1:K:389:ASN:C	1:K:389:ASN:HD22	1.88	0.80
2:N:140:THR:CG2	2:N:142:LEU:HG	2.12	0.80
1:E:358:LEU:CD2	1:F:37:ARG:CA	2.60	0.80
1:L:59:THR:HG22	1:L:393:ARG:HH12	1.43	0.80
1:L:136:ILE:HG22	1:L:138:PRO:HD3	1.64	0.80
1:L:141:ASN:HD22	1:L:141:ASN:H	1.30	0.80
1:E:358:LEU:CG	1:F:40:LEU:HD11	2.11	0.80
1:E:357:ALA:HB2	1:F:44:LEU:HD13	1.15	0.79
1:E:83:ALA:HB1	1:E:261:ILE:HD12	1.64	0.79
2:M:131:ALA:O	2:P:154:ILE:HG21	1.83	0.79
1:F:312:ILE:HD11	2:M:62:ARG:CA	2.09	0.79
2:P:140:THR:CG2	2:P:142:LEU:HG	2.12	0.79
1:K:138:PRO:HG3	1:K:156:ARG:HD3	1.63	0.79
1:F:145:GLN:CG	1:F:149:GLN:CB	2.61	0.79
2:M:160:ILE:HD13	2:O:160:ILE:HG23	1.64	0.79
2:M:1:THR:HB	2:M:33:LYS:HZ3	1.48	0.79
2:M:139:ASN:OD1	2:P:150:LYS:HD3	1.82	0.79
1:L:145:GLN:CG	1:L:149:GLN:CB	2.61	0.78
1:E:138:PRO:HG3	1:E:156:ARG:HD3	1.63	0.78
1:K:120:ARG:NH1	1:K:124:GLU:OE2	2.16	0.78
1:E:120:ARG:C	1:E:120:ARG:CD	2.56	0.78
1:K:83:ALA:HB1	1:K:261:ILE:HD12	1.64	0.78
1:F:141:ASN:HD22	1:F:141:ASN:H	1.30	0.78
1:F:217:LYS:HB3	1:F:220:ASP:HB3	1.66	0.78
1:E:408:TYR:HH	1:F:7:ARG:HA	1.46	0.78
1:L:89:VAL:CG1	1:L:94:LYS:O	2.32	0.78
1:E:120:ARG:NH1	1:E:124:GLU:OE2	2.16	0.78
1:F:369:THR:HG22	1:F:372:GLY:N	1.98	0.78
1:L:264:ARG:HD3	2:O:62:ARG:HD3	1.62	0.78
1:F:89:VAL:CG1	1:F:94:LYS:O	2.32	0.78
1:L:369:THR:HG22	1:L:372:GLY:N	1.98	0.78
1:E:400:GLU:CD	1:F:51:LYS:NZ	2.41	0.77
1:L:217:LYS:HB3	1:L:220:ASP:HB3	1.66	0.77
1:E:130:ARG:CD	1:E:225:LEU:HD11	2.15	0.77
1:K:130:ARG:CD	1:K:225:LEU:HD11	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:89:VAL:HG12	1:E:94:LYS:H	1.48	0.77
1:F:264:ARG:HH12	2:M:62:ARG:CA	1.96	0.77
1:E:354:GLN:CD	1:F:47:GLU:CB	2.57	0.77
1:E:407:SER:CB	1:F:36:ARG:NH1	2.47	0.77
1:E:441:PHE:HA	1:F:315:PRO:CG	2.13	0.77
1:K:120:ARG:C	1:K:120:ARG:CD	2.56	0.77
1:E:397:THR:HG21	1:E:443:LEU:O	1.84	0.77
1:K:5:THR:OG1	1:K:8:GLU:HG3	1.85	0.77
1:K:91:TYR:CE1	1:L:272:VAL:HG11	2.20	0.77
2:N:36:ARG:C	2:N:37:LEU:HD12	2.10	0.77
1:K:89:VAL:HG12	1:K:94:LYS:H	1.48	0.77
1:E:5:THR:OG1	1:E:8:GLU:HG3	1.85	0.77
1:E:94:LYS:HD2	1:E:95:GLU:H	1.50	0.77
2:P:36:ARG:C	2:P:37:LEU:HD12	2.10	0.77
1:E:92:VAL:CB	1:F:92:VAL:HA	2.15	0.76
1:F:160:ARG:O	1:F:163:LEU:HG	1.85	0.76
1:F:27:VAL:HG13	1:F:70:LEU:HG	1.67	0.76
1:L:130:ARG:HG3	1:L:225:LEU:HD11	1.66	0.76
1:L:145:GLN:HG2	1:L:150:GLN:N	1.99	0.76
2:O:1:THR:HB	2:O:33:LYS:HZ3	1.48	0.76
1:E:361:THR:HG21	1:F:36:ARG:CA	2.14	0.76
1:K:94:LYS:HD2	1:K:95:GLU:H	1.50	0.76
1:L:311:GLN:HE21	2:O:67:HIS:H	1.33	0.76
2:N:32:LYS:HG2	2:N:167:THR:HG21	1.67	0.76
1:F:311:GLN:HG3	2:M:66:MET:HE1	0.83	0.76
1:L:27:VAL:HG13	1:L:70:LEU:HG	1.67	0.76
1:E:257:GLU:OE1	1:F:279:ARG:HG3	1.83	0.76
1:L:145:GLN:CG	1:L:149:GLN:CA	2.64	0.76
1:L:311:GLN:CG	2:O:66:MET:HE3	2.15	0.76
2:M:138:GLU:C	2:M:139:ASN:HD22	1.94	0.76
1:E:92:VAL:CG2	1:F:92:VAL:HA	2.15	0.76
1:E:264:ARG:NH1	2:N:63:LYS:HZ3	1.83	0.76
1:L:160:ARG:O	1:L:163:LEU:HG	1.85	0.76
1:K:397:THR:HG21	1:K:443:LEU:O	1.84	0.76
2:N:138:GLU:C	2:N:139:ASN:HD22	1.94	0.76
1:E:92:VAL:HG13	1:F:92:VAL:HA	1.63	0.76
1:K:91:TYR:CE1	1:L:272:VAL:CG1	2.68	0.76
2:P:138:GLU:C	2:P:139:ASN:HD22	1.94	0.76
1:E:397:THR:HG23	1:F:327:PRO:O	1.86	0.75
1:E:359:MET:HE1	1:F:36:ARG:HD3	1.68	0.75
1:E:91:TYR:HB3	1:F:91:TYR:C	2.11	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:264:ARG:C	1:L:266:GLU:H	1.94	0.75
2:P:105:ILE:HD11	2:P:120:ILE:HG23	1.69	0.75
1:E:141:ASN:HD22	1:E:141:ASN:N	1.79	0.75
1:F:145:GLN:NE2	1:F:150:GLN:CA	2.49	0.75
1:L:145:GLN:NE2	1:L:150:GLN:CA	2.49	0.75
1:E:358:LEU:O	1:E:361:THR:HG22	1.87	0.75
1:F:20:GLN:HG2	1:F:332:LEU:HD23	1.68	0.75
1:K:389:ASN:ND2	1:K:391:GLY:H	1.85	0.75
1:K:92:VAL:HG23	1:K:93:GLY:N	2.02	0.75
2:O:138:GLU:C	2:O:139:ASN:HD22	1.94	0.75
1:E:389:ASN:ND2	1:E:391:GLY:H	1.85	0.74
1:K:261:ILE:HG22	1:K:261:ILE:O	1.86	0.74
1:L:20:GLN:HG2	1:L:332:LEU:HD23	1.68	0.74
1:F:132:LEU:HD13	1:F:156:ARG:CG	2.17	0.74
2:P:32:LYS:HG2	2:P:167:THR:HG21	1.68	0.74
1:L:264:ARG:HH12	2:O:62:ARG:HB3	1.50	0.74
1:F:130:ARG:HG3	1:F:225:LEU:HD11	1.66	0.74
1:F:264:ARG:HH12	2:M:62:ARG:HB2	1.28	0.74
1:K:358:LEU:O	1:K:361:THR:HG22	1.87	0.74
1:L:311:GLN:CA	2:O:65:GLU:OE1	2.31	0.74
1:E:163:LEU:CD1	1:E:218:ILE:HG21	2.18	0.74
2:N:105:ILE:HD11	2:N:120:ILE:HG23	1.69	0.74
1:E:92:VAL:HG23	1:E:93:GLY:N	2.02	0.74
1:E:311:GLN:CB	2:N:66:MET:C	2.57	0.74
1:L:145:GLN:OE1	1:L:149:GLN:CB	2.36	0.74
1:E:441:PHE:CE1	1:F:310:PHE:HB2	2.23	0.74
1:E:118:LYS:HA	1:E:118:LYS:NZ	2.03	0.73
1:E:266:GLU:HA	2:N:85:ASP:OD1	1.88	0.73
1:F:132:LEU:CD1	1:F:156:ARG:HG2	2.17	0.73
1:F:344:LEU:CD1	1:F:395:LEU:HD13	2.17	0.73
1:E:59:THR:HG21	1:F:320:PRO:HB2	1.70	0.73
1:E:261:ILE:O	1:E:261:ILE:HG22	1.86	0.73
1:F:258:ILE:HG13	1:F:306:ALA:HB1	1.70	0.73
1:L:264:ARG:CD	2:O:62:ARG:NH2	2.42	0.73
1:L:344:LEU:CD1	1:L:395:LEU:HD13	2.17	0.73
1:E:358:LEU:HD21	1:F:37:ARG:HA	1.69	0.73
1:E:393:ARG:HH21	1:F:321:GLU:HG3	1.51	0.73
1:F:145:GLN:OE1	1:F:149:GLN:CB	2.36	0.73
1:E:357:ALA:O	1:F:40:LEU:HD23	1.83	0.73
1:L:132:LEU:CD1	1:L:156:ARG:HG2	2.17	0.73
1:L:309:ALA:HB3	2:O:66:MET:SD	1.12	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:264:ARG:HH11	2:O:62:ARG:HD3	1.50	0.73
1:L:258:ILE:HG13	1:L:306:ALA:HB1	1.70	0.73
1:E:235:ASN:HB2	1:E:238:GLU:OE2	1.89	0.73
1:E:442:ILE:HD13	1:F:329:ARG:HB3	1.71	0.73
1:K:163:LEU:CD1	1:K:218:ILE:HG21	2.18	0.73
1:L:309:ALA:CB	2:O:66:MET:CE	2.16	0.73
2:O:50:THR:HG21	2:P:111:ASP:OD1	1.89	0.73
1:E:88:GLU:HG2	1:F:89:VAL:O	1.89	0.73
1:E:411:SER:HB3	1:F:32:ARG:NH2	2.03	0.73
1:E:135:LEU:HD13	1:E:159:PHE:CE1	2.24	0.72
1:E:374:LYS:HE2	1:E:378:GLU:OE2	1.89	0.72
1:K:141:ASN:HD22	1:K:141:ASN:N	1.79	0.72
1:E:409:ASP:O	1:E:413:LEU:HD13	1.89	0.72
1:F:264:ARG:NE	2:M:62:ARG:HD2	2.02	0.72
1:K:374:LYS:HE2	1:K:378:GLU:OE2	1.89	0.72
1:E:312:ILE:HD12	2:N:67:HIS:HE1	1.50	0.72
1:E:408:TYR:CA	1:F:6:PRO:HG2	2.19	0.72
1:K:235:ASN:HB2	1:K:238:GLU:OE2	1.89	0.72
1:K:409:ASP:O	1:K:413:LEU:HD13	1.90	0.72
1:E:441:PHE:O	1:F:329:ARG:CB	2.37	0.72
1:F:145:GLN:CG	1:F:149:GLN:CA	2.64	0.72
1:L:132:LEU:HD13	1:L:156:ARG:CG	2.17	0.72
1:E:139:ALA:HB2	1:E:152:PRO:CD	2.19	0.72
1:E:311:GLN:CG	2:N:66:MET:C	2.42	0.72
1:L:264:ARG:NH2	2:O:59:LEU:HD21	1.98	0.72
1:E:353:VAL:HG12	1:F:44:LEU:HD21	1.70	0.72
1:F:33:ASN:ND2	1:F:36:ARG:HD2	2.05	0.72
1:F:264:ARG:C	1:F:266:GLU:H	1.94	0.72
1:L:264:ARG:NH1	2:O:59:LEU:CA	2.52	0.72
2:P:134:ARG:O	2:P:138:GLU:HB2	1.90	0.72
1:F:381:TRP:CH2	1:F:385:GLU:OE2	2.43	0.72
1:K:118:LYS:HA	1:K:118:LYS:NZ	2.03	0.72
1:K:130:ARG:CD	1:K:225:LEU:HD12	2.19	0.72
1:K:311:GLN:HG2	2:P:66:MET:HE2	0.78	0.72
1:L:358:LEU:O	1:L:361:THR:HB	1.90	0.72
2:N:3:ILE:HB	2:N:122:ILE:CG1	2.20	0.72
1:E:130:ARG:CD	1:E:225:LEU:HD12	2.20	0.72
1:K:88:GLU:OE2	1:L:280:ASP:CG	2.33	0.72
1:K:135:LEU:HD13	1:K:159:PHE:CE1	2.24	0.72
1:K:245:ASP:O	1:K:249:GLN:HG3	1.89	0.72
1:L:381:TRP:CH2	1:L:385:GLU:OE2	2.43	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:245:ASP:O	1:E:249:GLN:HG3	1.89	0.71
1:L:264:ARG:CZ	2:O:59:LEU:CB	2.42	0.71
1:E:142:ASN:O	1:E:143:TRP:HB2	1.89	0.71
1:F:358:LEU:O	1:F:361:THR:HB	1.90	0.71
1:E:292:THR:HB	1:E:295:GLY:O	1.90	0.71
1:E:397:THR:HA	1:F:327:PRO:CB	2.19	0.71
1:L:389:ASN:C	1:L:389:ASN:HD22	1.98	0.71
1:E:279:ARG:HH11	1:E:319:ILE:HD12	1.55	0.71
1:K:142:ASN:O	1:K:143:TRP:HB2	1.89	0.71
2:M:140:THR:CG2	2:M:142:LEU:H	2.03	0.71
2:O:54:PHE:HE2	2:P:80:LYS:CD	2.03	0.71
1:F:145:GLN:OE1	1:F:149:GLN:HB3	1.90	0.71
1:L:130:ARG:HD2	1:L:130:ARG:C	2.15	0.71
1:L:142:ASN:O	1:L:143:TRP:HB2	1.90	0.71
1:L:384:ASN:ND2	1:L:394:ARG:HD2	2.06	0.71
1:E:357:ALA:CA	1:F:40:LEU:HD22	2.21	0.71
1:K:120:ARG:C	1:K:120:ARG:HD2	2.16	0.71
1:K:292:THR:HB	1:K:295:GLY:O	1.91	0.71
2:M:1:THR:HB	2:M:33:LYS:NZ	2.05	0.71
2:P:5:SER:HB3	2:P:120:ILE:HB	1.72	0.71
1:F:130:ARG:HD2	1:F:130:ARG:C	2.15	0.71
1:L:344:LEU:O	1:L:352:THR:HB	1.91	0.71
1:E:139:ALA:HB3	1:E:152:PRO:HG3	1.70	0.71
1:F:145:GLN:HG2	1:F:150:GLN:N	1.99	0.71
1:F:389:ASN:ND2	1:F:391:GLY:H	1.88	0.71
1:K:139:ALA:HB2	1:K:152:PRO:CD	2.19	0.71
1:K:279:ARG:HH11	1:K:319:ILE:HD12	1.55	0.71
1:L:264:ARG:CZ	2:O:59:LEU:CA	2.69	0.70
2:P:3:ILE:HB	2:P:122:ILE:CG1	2.20	0.70
1:E:407:SER:OG	1:F:36:ARG:NH1	2.24	0.70
1:F:389:ASN:C	1:F:389:ASN:HD22	1.98	0.70
1:L:33:ASN:ND2	1:L:36:ARG:HD2	2.05	0.70
1:F:384:ASN:ND2	1:F:394:ARG:HD2	2.06	0.70
1:K:264:ARG:CD	2:P:62:ARG:NH2	2.50	0.70
1:F:429:LEU:O	1:F:433:VAL:HG23	1.92	0.70
2:M:22:LEU:HB2	2:M:27:MET:HE2	1.74	0.70
2:M:140:THR:CG2	2:M:142:LEU:HG	2.21	0.70
2:N:5:SER:HB3	2:N:120:ILE:HB	1.72	0.70
2:O:140:THR:CG2	2:O:142:LEU:H	2.03	0.70
1:L:389:ASN:ND2	1:L:391:GLY:H	1.88	0.70
2:O:1:THR:HB	2:O:33:LYS:NZ	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:22:LEU:HB2	2:O:27:MET:HE2	1.74	0.70
2:O:140:THR:CG2	2:O:142:LEU:HG	2.21	0.70
2:N:134:ARG:O	2:N:138:GLU:HB2	1.90	0.70
1:E:411:SER:CB	1:F:32:ARG:NH2	2.54	0.70
1:E:441:PHE:CE1	1:F:56:ILE:HG21	2.27	0.70
1:F:344:LEU:O	1:F:352:THR:HB	1.91	0.70
1:F:261:ILE:HG22	1:F:278:GLN:HG3	1.74	0.70
1:L:145:GLN:OE1	1:L:149:GLN:HB3	1.90	0.70
1:E:282:LEU:HD11	1:E:319:ILE:HD11	1.74	0.70
1:F:55:MET:HE3	1:F:305:ILE:HG21	1.72	0.70
1:F:141:ASN:H	1:F:141:ASN:ND2	1.88	0.70
1:F:263:LYS:O	1:F:264:ARG:HB3	1.92	0.70
1:K:126:LEU:HD23	1:K:229:GLU:CD	2.17	0.70
1:K:261:ILE:HD13	1:K:277:VAL:HB	1.74	0.70
2:N:67:HIS:CD2	2:N:73:LYS:HE3	2.27	0.70
1:E:33:ASN:ND2	1:E:36:ARG:HD2	2.07	0.70
1:E:120:ARG:C	1:E:120:ARG:HD2	2.16	0.70
1:E:411:SER:OG	1:F:32:ARG:NH2	2.25	0.70
1:K:282:LEU:HD11	1:K:319:ILE:HD11	1.74	0.70
1:L:55:MET:HE3	1:L:305:ILE:HG21	1.72	0.70
1:L:264:ARG:CZ	2:O:59:LEU:HA	2.22	0.70
1:E:92:VAL:CG2	1:E:93:GLY:N	2.55	0.69
1:K:92:VAL:CG2	1:K:93:GLY:N	2.55	0.69
1:L:141:ASN:H	1:L:141:ASN:ND2	1.88	0.69
1:E:139:ALA:HA	1:E:152:PRO:HB3	1.74	0.69
1:E:139:ALA:O	1:E:140:LYS:CB	2.38	0.69
2:M:160:ILE:HD11	2:O:160:ILE:O	1.92	0.69
1:E:222:MET:O	1:E:226:ILE:HG13	1.93	0.69
1:E:440:ARG:CD	1:F:316:SER:OG	2.39	0.69
1:E:126:LEU:HD23	1:E:229:GLU:CD	2.17	0.69
1:F:142:ASN:O	1:F:143:TRP:HB2	1.90	0.69
1:K:222:MET:O	1:K:226:ILE:HG13	1.93	0.69
1:L:92:VAL:HG23	1:L:93:GLY:N	2.08	0.69
2:N:85:ASP:HB2	2:N:88:LEU:HD23	1.73	0.69
2:O:54:PHE:HE2	2:P:80:LYS:HG3	1.57	0.69
2:O:79:ALA:HB1	2:O:110:GLY:HA2	1.74	0.69
2:M:79:ALA:HB1	2:M:110:GLY:HA2	1.74	0.69
2:P:33:LYS:HA	2:P:46:PHE:CE1	2.27	0.69
1:K:92:VAL:CG1	1:L:89:VAL:O	2.40	0.69
1:E:122:ARG:CG	1:E:122:ARG:C	2.66	0.69
1:E:354:GLN:HE22	1:F:47:GLU:C	1.87	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:432:LEU:H	1:E:432:LEU:HD12	1.56	0.69
1:K:122:ARG:CG	1:K:122:ARG:C	2.66	0.69
1:K:139:ALA:HB3	1:K:152:PRO:HG3	1.70	0.68
1:K:389:ASN:HD22	1:K:390:ILE:N	1.91	0.68
1:K:432:LEU:HD12	1:K:432:LEU:H	1.56	0.68
2:N:33:LYS:HA	2:N:46:PHE:CE1	2.27	0.68
2:O:20:ALA:HB2	2:O:31:VAL:HG21	1.75	0.68
1:E:27:VAL:CG1	1:E:70:LEU:HG	2.23	0.68
1:F:89:VAL:HG11	1:F:94:LYS:O	1.92	0.68
2:M:160:ILE:CG2	2:O:160:ILE:CD1	2.71	0.68
2:N:3:ILE:HD12	2:N:122:ILE:HD11	1.76	0.68
2:P:85:ASP:HB2	2:P:88:LEU:HD23	1.73	0.68
1:K:104:THR:HG21	1:K:292:THR:HG21	1.75	0.68
1:L:261:ILE:HG22	1:L:278:GLN:HG3	1.74	0.68
2:P:67:HIS:CD2	2:P:73:LYS:HE3	2.27	0.68
1:E:267:SER:HB3	1:E:270:PRO:HG3	1.75	0.68
1:F:142:ASN:O	1:F:143:TRP:CB	2.42	0.68
1:L:429:LEU:O	1:L:433:VAL:HG23	1.92	0.68
1:K:33:ASN:HD22	1:K:36:ARG:HD2	1.58	0.68
1:K:33:ASN:ND2	1:K:36:ARG:HD2	2.07	0.68
2:M:20:ALA:HB2	2:M:31:VAL:HG21	1.75	0.68
2:M:160:ILE:HG23	2:O:160:ILE:HD11	1.75	0.68
1:E:163:LEU:HD11	1:E:218:ILE:CG2	2.21	0.68
1:E:261:ILE:HD13	1:E:277:VAL:HB	1.74	0.68
1:K:27:VAL:CG1	1:K:70:LEU:HG	2.23	0.68
1:E:104:THR:HG21	1:E:292:THR:HG21	1.75	0.68
1:F:27:VAL:HG22	1:F:70:LEU:HD12	1.76	0.68
1:L:89:VAL:HG11	1:L:94:LYS:O	1.92	0.68
1:E:389:ASN:HD22	1:E:390:ILE:N	1.91	0.68
1:E:441:PHE:CA	1:F:315:PRO:HG2	2.17	0.68
1:F:229:GLU:HA	1:F:232:LYS:HG2	1.76	0.68
2:M:160:ILE:HG23	2:O:160:ILE:CD1	2.23	0.68
2:P:3:ILE:HD12	2:P:122:ILE:HD11	1.76	0.68
1:F:292:THR:HG22	1:F:294:HIS:N	2.03	0.68
1:L:292:THR:HG22	1:L:294:HIS:N	2.03	0.68
1:K:139:ALA:HA	1:K:152:PRO:HB3	1.74	0.67
1:F:336:THR:O	1:F:339:ASP:HB2	1.95	0.67
1:K:267:SER:HB3	1:K:270:PRO:HG3	1.75	0.67
1:L:130:ARG:C	1:L:130:ARG:HH11	2.01	0.67
1:F:130:ARG:C	1:F:130:ARG:HH11	2.01	0.67
1:L:229:GLU:HA	1:L:232:LYS:HG2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:311:GLN:HE21	2:O:68:GLN:N	1.92	0.67
1:E:132:LEU:HD12	1:E:156:ARG:HG2	1.76	0.67
1:L:27:VAL:HG22	1:L:70:LEU:HD12	1.76	0.67
1:L:263:LYS:O	1:L:264:ARG:HB3	1.92	0.67
1:L:311:GLN:HG2	2:O:66:MET:HE3	1.75	0.67
2:M:160:ILE:HG21	2:O:160:ILE:HD13	1.77	0.67
1:E:33:ASN:HD22	1:E:36:ARG:HD2	1.58	0.67
1:E:311:GLN:NE2	2:N:66:MET:O	2.26	0.67
1:L:59:THR:HG22	1:L:393:ARG:NH1	2.10	0.67
2:N:134:ARG:HH11	2:N:134:ARG:CB	2.07	0.67
2:P:134:ARG:HH11	2:P:134:ARG:CB	2.07	0.67
1:F:92:VAL:HG23	1:F:93:GLY:N	2.08	0.67
1:F:130:ARG:HG3	1:F:225:LEU:HD12	1.77	0.67
1:F:222:MET:HE3	1:F:226:ILE:HD11	1.75	0.67
1:F:319:ILE:HG22	1:F:322:LEU:HB2	1.77	0.67
1:K:163:LEU:HD11	1:K:218:ILE:CG2	2.21	0.67
1:E:400:GLU:CG	1:F:51:LYS:CG	2.72	0.67
1:F:125:GLU:O	1:F:128:GLU:HG2	1.95	0.67
1:L:264:ARG:NH2	2:O:59:LEU:HD22	2.00	0.67
1:L:264:ARG:NH1	2:O:62:ARG:CB	2.45	0.67
1:L:336:THR:O	1:L:339:ASP:HB2	1.95	0.67
2:O:72:VAL:O	2:O:76:VAL:HG23	1.95	0.67
2:P:94:LEU:HD13	2:P:122:ILE:HB	1.77	0.67
1:E:397:THR:OG1	1:F:327:PRO:HA	1.95	0.67
1:E:404:GLU:HG2	1:F:29:ILE:HD12	1.76	0.67
1:L:141:ASN:HD22	1:L:141:ASN:N	1.92	0.67
2:M:131:ALA:O	2:P:154:ILE:CG2	2.43	0.67
2:N:100:GLU:HG2	2:N:173:TYR:CD2	2.30	0.67
1:L:222:MET:HE3	1:L:226:ILE:HD11	1.75	0.66
2:P:17:ASP:HA	2:P:165:PHE:O	1.95	0.66
1:E:314:LYS:HZ1	2:N:65:GLU:CG	2.03	0.66
1:E:440:ARG:O	1:F:315:PRO:CG	2.42	0.66
1:L:163:LEU:C	1:L:163:LEU:HD12	2.20	0.66
1:L:312:ILE:C	2:O:62:ARG:HA	2.20	0.66
1:E:88:GLU:CG	1:F:89:VAL:O	2.44	0.66
1:E:397:THR:HA	1:F:327:PRO:CA	2.25	0.66
2:M:152:LEU:HD22	2:M:166:HIS:CE1	2.31	0.66
1:E:91:TYR:CE2	1:F:90:GLY:O	2.47	0.66
1:L:125:GLU:O	1:L:128:GLU:HG2	1.95	0.66
2:N:17:ASP:HA	2:N:165:PHE:O	1.95	0.66
1:F:4:MET:HE1	1:F:73:LEU:HD11	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:139:ALA:O	1:K:140:LYS:CB	2.38	0.66
1:L:319:ILE:HG22	1:L:322:LEU:HB2	1.77	0.66
1:K:132:LEU:HD12	1:K:156:ARG:HG2	1.76	0.66
1:L:142:ASN:O	1:L:143:TRP:CB	2.42	0.66
2:O:140:THR:HG21	2:O:142:LEU:HG	1.78	0.66
1:F:163:LEU:HD12	1:F:163:LEU:C	2.20	0.66
1:L:130:ARG:HG3	1:L:225:LEU:HD12	1.78	0.66
2:P:100:GLU:HG2	2:P:173:TYR:CD2	2.30	0.66
1:E:441:PHE:CD1	1:F:56:ILE:CG2	2.77	0.66
2:N:61:GLU:O	2:N:65:GLU:HG2	1.95	0.66
2:P:61:GLU:O	2:P:65:GLU:HG2	1.95	0.66
1:F:145:GLN:N	1:F:145:GLN:OE1	2.12	0.65
1:K:96:VAL:HG13	1:K:99:ILE:HD12	1.78	0.65
1:L:92:VAL:CG2	1:L:93:GLY:N	2.59	0.65
1:L:311:GLN:HG2	2:O:66:MET:CE	2.26	0.65
2:P:58:GLU:O	2:P:62:ARG:HG3	1.96	0.65
1:E:20:GLN:HG3	1:E:332:LEU:HD23	1.78	0.65
1:F:362:GLU:HG3	1:F:411:SER:HA	1.78	0.65
1:L:4:MET:HE1	1:L:73:LEU:HD11	1.78	0.65
1:L:311:GLN:HA	2:O:65:GLU:OE1	1.96	0.65
1:K:20:GLN:HG3	1:K:332:LEU:HD23	1.78	0.65
1:K:293:LYS:CE	1:L:296:MET:SD	2.83	0.65
2:N:58:GLU:O	2:N:62:ARG:HG3	1.96	0.65
1:E:59:THR:CG2	1:F:321:GLU:OE1	2.43	0.65
1:E:393:ARG:HD3	1:F:321:GLU:HA	1.79	0.65
1:L:362:GLU:HG3	1:L:411:SER:HA	1.78	0.65
2:O:152:LEU:HD22	2:O:166:HIS:CE1	2.31	0.65
1:F:96:VAL:HG13	1:F:99:ILE:HD12	1.78	0.65
1:F:92:VAL:CG2	1:F:93:GLY:N	2.59	0.65
1:K:138:PRO:CG	1:K:156:ARG:HD3	2.26	0.65
1:L:96:VAL:HG13	1:L:99:ILE:HD12	1.77	0.65
2:M:72:VAL:O	2:M:76:VAL:HG23	1.96	0.65
2:N:94:LEU:HD13	2:N:122:ILE:HB	1.77	0.65
1:E:79:ILE:HD13	1:E:80:LYS:N	2.12	0.65
1:F:59:THR:HG22	1:F:393:ARG:NH1	2.10	0.65
1:E:96:VAL:HG13	1:E:99:ILE:HD12	1.78	0.65
1:E:264:ARG:C	1:E:266:GLU:H	2.05	0.65
1:K:264:ARG:C	1:K:266:GLU:H	2.05	0.65
2:M:140:THR:HG21	2:M:142:LEU:HG	1.78	0.65
1:K:79:ILE:HD13	1:K:80:LYS:N	2.12	0.65
2:M:14:ILE:HD12	2:M:43:ILE:HG13	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:28:LYS:HE2	2:N:30:ASN:OD1	1.97	0.64
1:E:138:PRO:CG	1:E:156:ARG:HD3	2.26	0.64
1:E:354:GLN:HB3	1:F:48:VAL:CG2	2.24	0.64
1:L:145:GLN:CB	1:L:149:GLN:CB	2.62	0.64
1:K:92:VAL:HG11	1:L:89:VAL:HB	1.80	0.64
2:O:14:ILE:HD12	2:O:43:ILE:HG13	1.78	0.64
1:F:292:THR:HB	1:F:295:GLY:O	1.98	0.64
1:L:311:GLN:HG3	2:O:66:MET:HE3	1.79	0.64
1:E:63:LYS:HG2	1:E:332:LEU:HD22	1.80	0.64
1:L:381:TRP:CZ3	1:L:385:GLU:OE2	2.50	0.64
1:E:91:TYR:HB3	1:F:91:TYR:N	2.11	0.64
1:K:86:PHE:O	1:K:89:VAL:HG13	1.98	0.64
1:E:91:TYR:CB	1:F:90:GLY:C	2.71	0.64
1:K:243:ALA:O	1:K:247:VAL:HG23	1.97	0.64
1:L:344:LEU:CD1	1:L:351:ILE:HD11	2.25	0.64
2:P:90:LYS:HD2	2:P:90:LYS:C	2.23	0.64
1:E:401:ARG:NH2	1:F:329:ARG:H	1.95	0.64
1:F:381:TRP:CZ3	1:F:385:GLU:OE2	2.50	0.64
2:N:138:GLU:HB3	2:N:139:ASN:ND2	2.12	0.64
1:E:311:GLN:HG2	2:N:66:MET:SD	2.21	0.63
1:E:359:MET:HG3	1:E:366:ILE:HG13	1.80	0.63
1:K:436:GLU:O	1:K:439:SER:HB2	1.98	0.63
1:L:145:GLN:N	1:L:145:GLN:OE1	2.12	0.63
2:P:138:GLU:HB3	2:P:139:ASN:ND2	2.12	0.63
1:K:63:LYS:HG2	1:K:332:LEU:HD22	1.80	0.63
1:E:243:ALA:O	1:E:247:VAL:HG23	1.97	0.63
1:E:358:LEU:CD2	1:F:40:LEU:HD11	2.29	0.63
1:E:359:MET:HE1	1:F:36:ARG:HH11	1.64	0.63
1:E:442:ILE:CB	1:F:329:ARG:HB2	2.29	0.63
1:K:359:MET:HG3	1:K:366:ILE:HG13	1.80	0.63
1:L:313:ALA:N	2:O:65:GLU:HG3	2.13	0.63
1:E:145:GLN:H	1:E:149:GLN:HB2	1.63	0.63
1:F:108:VAL:HG21	1:F:294:HIS:ND1	2.13	0.63
1:F:163:LEU:HD13	1:F:218:ILE:HG21	1.80	0.63
1:E:308:GLY:HA3	1:E:310:PHE:CE2	2.33	0.63
1:L:108:VAL:HG21	1:L:294:HIS:ND1	2.13	0.63
1:E:83:ALA:HB1	1:E:261:ILE:CD1	2.29	0.63
1:E:390:ILE:HA	1:F:320:PRO:HB3	1.79	0.63
1:F:145:GLN:CB	1:F:149:GLN:CB	2.62	0.63
1:K:83:ALA:HB1	1:K:261:ILE:CD1	2.29	0.63
1:K:145:GLN:CG	1:K:149:GLN:CG	2.67	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:309:ALA:C	2:P:66:MET:HE3	2.22	0.63
1:K:432:LEU:H	1:K:432:LEU:CD1	2.12	0.63
1:E:91:TYR:CE2	1:F:91:TYR:CE2	2.87	0.63
1:E:221:ALA:O	1:E:225:LEU:HD23	1.99	0.63
1:E:264:ARG:NH2	2:N:63:LYS:HZ1	1.97	0.63
1:F:261:ILE:HG22	1:F:261:ILE:O	1.99	0.63
1:E:432:LEU:H	1:E:432:LEU:CD1	2.12	0.63
1:E:436:GLU:O	1:E:439:SER:HB2	1.98	0.63
1:F:344:LEU:CD1	1:F:351:ILE:HD11	2.25	0.63
2:M:2:THR:HG1	2:M:162:THR:HG21	1.61	0.63
2:M:85:ASP:HB2	2:M:88:LEU:HD23	1.81	0.63
1:E:96:VAL:HG12	1:E:284:LEU:HD11	1.81	0.63
1:E:354:GLN:OE1	1:F:47:GLU:O	2.17	0.63
2:M:28:LYS:HD3	2:M:31:VAL:HG22	1.81	0.63
2:O:28:LYS:HD3	2:O:31:VAL:HG22	1.81	0.63
1:E:86:PHE:O	1:E:89:VAL:HG13	1.98	0.62
1:E:393:ARG:HB3	1:F:324:GLY:CA	2.23	0.62
1:E:441:PHE:HE1	1:F:310:PHE:HB2	1.64	0.62
1:F:89:VAL:HG12	1:F:94:LYS:H	1.64	0.62
1:K:221:ALA:O	1:K:225:LEU:HD23	1.99	0.62
2:N:90:LYS:HD2	2:N:90:LYS:C	2.23	0.62
1:E:389:ASN:C	1:E:389:ASN:ND2	2.57	0.62
1:E:397:THR:CB	1:F:327:PRO:HA	2.29	0.62
1:L:292:THR:HB	1:L:295:GLY:O	1.98	0.62
1:E:311:GLN:HE22	2:N:67:HIS:HA	0.69	0.62
1:F:141:ASN:O	1:F:142:ASN:HB2	1.98	0.62
1:L:163:LEU:HD13	1:L:218:ILE:HG21	1.80	0.62
2:M:139:ASN:HD22	2:M:139:ASN:N	1.98	0.62
2:O:70:HIS:HD2	2:O:73:LYS:HB2	1.65	0.62
1:F:91:TYR:C	1:F:92:VAL:HG13	2.24	0.62
2:M:70:HIS:HD2	2:M:73:LYS:HB2	1.65	0.62
1:E:108:VAL:HG21	1:E:294:HIS:ND1	2.15	0.62
1:E:91:TYR:CD2	1:F:91:TYR:CD2	2.88	0.62
1:K:129:GLU:O	1:K:133:ASP:HB2	1.99	0.62
1:K:309:ALA:O	2:P:66:MET:HE3	1.99	0.62
1:L:91:TYR:C	1:L:92:VAL:HG13	2.24	0.62
1:L:264:ARG:HD3	2:O:62:ARG:NH2	2.12	0.62
1:F:384:ASN:ND2	1:F:394:ARG:HH11	1.98	0.62
1:K:308:GLY:HA3	1:K:310:PHE:CE2	2.34	0.62
1:L:261:ILE:HG22	1:L:261:ILE:O	1.99	0.62
1:L:311:GLN:NE2	2:O:68:GLN:N	2.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:109:LYS:HG2	1:F:296:MET:CB	2.30	0.62
1:E:264:ARG:NH1	2:N:63:LYS:NZ	2.46	0.62
1:E:393:ARG:CZ	1:F:321:GLU:HG3	2.30	0.62
1:E:354:GLN:CD	1:F:47:GLU:O	2.38	0.62
1:K:96:VAL:HG12	1:K:284:LEU:HD11	1.81	0.62
1:K:108:VAL:HG21	1:K:294:HIS:ND1	2.15	0.62
1:L:141:ASN:O	1:L:142:ASN:HB2	1.98	0.62
1:L:145:GLN:HG3	1:L:149:GLN:CB	2.30	0.62
1:F:291:SER:HA	1:F:296:MET:HE2	1.81	0.61
1:L:311:GLN:NE2	2:O:64:LEU:O	2.33	0.61
2:M:17:ASP:O	2:M:33:LYS:HD3	2.00	0.61
1:F:389:ASN:HD22	1:F:391:GLY:H	1.48	0.61
1:K:432:LEU:HD12	1:K:432:LEU:N	2.15	0.61
2:O:54:PHE:HE2	2:P:80:LYS:CG	2.12	0.61
2:O:85:ASP:HB2	2:O:88:LEU:HD23	1.81	0.61
1:E:92:VAL:CG1	1:F:92:VAL:CG1	2.77	0.61
1:E:411:SER:CB	1:F:32:ARG:HH21	2.11	0.61
1:F:223:LYS:HA	1:F:226:ILE:HD12	1.81	0.61
1:F:285:VAL:HG12	1:F:325:ARG:HG2	1.83	0.61
1:L:221:ALA:O	1:L:225:LEU:HD23	2.00	0.61
1:L:384:ASN:ND2	1:L:394:ARG:HH11	1.98	0.61
2:N:86:ARG:CG	2:N:87:MET:N	2.64	0.61
2:N:86:ARG:HG2	2:N:87:MET:N	2.16	0.61
2:P:28:LYS:HE2	2:P:30:ASN:OD1	1.97	0.61
1:E:141:ASN:ND2	1:E:141:ASN:N	2.42	0.61
1:E:344:LEU:O	1:E:352:THR:HB	2.01	0.61
1:L:309:ALA:C	2:O:66:MET:SD	2.84	0.61
2:O:17:ASP:O	2:O:33:LYS:HD3	2.00	0.61
1:E:92:VAL:HG11	1:F:92:VAL:CG1	2.30	0.61
1:F:311:GLN:HB2	2:M:66:MET:SD	2.40	0.61
1:E:92:VAL:CG2	1:E:93:GLY:H	2.14	0.61
1:F:158:ALA:O	1:F:162:LYS:HB2	2.00	0.61
2:N:11:HIS:HA	2:N:171:LEU:O	2.01	0.61
2:N:47:ALA:HB3	2:N:94:LEU:HB2	1.83	0.61
2:O:139:ASN:HD22	2:O:139:ASN:N	1.98	0.61
1:E:145:GLN:HB2	1:E:149:GLN:N	2.15	0.61
1:E:129:GLU:O	1:E:133:ASP:HB2	1.99	0.61
1:F:91:TYR:O	1:F:92:VAL:CG1	2.49	0.61
1:E:145:GLN:N	1:E:149:GLN:HB2	2.16	0.61
1:E:401:ARG:NH2	1:F:329:ARG:O	2.30	0.61
1:F:141:ASN:HD22	1:F:141:ASN:N	1.92	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:158:ALA:O	1:L:162:LYS:HB2	2.00	0.61
1:L:223:LYS:HA	1:L:226:ILE:HD12	1.81	0.61
2:N:20:ALA:HB2	2:N:31:VAL:HG21	1.82	0.61
1:E:136:ILE:O	1:E:138:PRO:HD3	2.00	0.60
1:F:126:LEU:HD23	1:F:229:GLU:CD	2.26	0.60
1:K:145:GLN:N	1:K:149:GLN:HB2	2.16	0.60
1:F:286:GLU:HG2	1:F:325:ARG:NH1	2.16	0.60
1:K:145:GLN:H	1:K:149:GLN:HB2	1.63	0.60
1:L:122:ARG:HG2	1:L:122:ARG:HH21	1.66	0.60
1:E:400:GLU:HG2	1:F:51:LYS:CG	2.30	0.60
1:E:432:LEU:HD12	1:E:432:LEU:N	2.15	0.60
2:P:20:ALA:HB2	2:P:31:VAL:HG21	1.82	0.60
2:P:86:ARG:HG2	2:P:87:MET:N	2.16	0.60
1:F:122:ARG:HG2	1:F:122:ARG:HH21	1.66	0.60
1:K:145:GLN:HB2	1:K:149:GLN:N	2.15	0.60
1:K:222:MET:HE3	1:K:226:ILE:HD11	1.83	0.60
1:L:285:VAL:HG12	1:L:325:ARG:HG2	1.83	0.60
1:L:291:SER:HA	1:L:296:MET:HE2	1.81	0.60
1:F:222:MET:O	1:F:226:ILE:HG13	2.01	0.60
1:K:153:SER:O	1:K:154:ALA:C	2.45	0.60
1:L:126:LEU:HD23	1:L:229:GLU:CD	2.26	0.60
1:L:312:ILE:O	2:O:62:ARG:HA	2.02	0.60
2:P:47:ALA:HB3	2:P:94:LEU:HB2	1.83	0.60
1:F:221:ALA:O	1:F:225:LEU:HD23	2.00	0.60
1:K:136:ILE:O	1:K:138:PRO:HD3	2.01	0.60
1:L:89:VAL:HG12	1:L:94:LYS:H	1.64	0.60
1:K:92:VAL:CG2	1:K:93:GLY:H	2.14	0.60
1:K:344:LEU:O	1:K:352:THR:HB	2.01	0.60
2:P:11:HIS:HA	2:P:171:LEU:O	2.01	0.60
1:E:384:ASN:HD22	1:E:394:ARG:HH11	1.48	0.60
1:L:389:ASN:HD22	1:L:391:GLY:H	1.48	0.60
2:N:13:VAL:HG12	2:N:170:GLU:HG3	1.84	0.60
2:P:86:ARG:CG	2:P:87:MET:N	2.64	0.60
1:F:86:PHE:HB2	1:F:277:VAL:HG13	1.84	0.60
1:K:20:GLN:CG	1:K:332:LEU:HD23	2.31	0.60
1:K:86:PHE:O	1:K:89:VAL:HG22	2.02	0.60
1:L:286:GLU:HG2	1:L:325:ARG:NH1	2.16	0.60
2:N:60:PHE:CE2	2:N:97:VAL:HG21	2.37	0.60
2:N:88:LEU:HD22	2:N:88:LEU:H	1.67	0.60
1:F:103:LEU:HD13	1:F:247:VAL:HG13	1.84	0.60
1:F:160:ARG:HA	1:F:163:LEU:HD23	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:60:PHE:HB2	2:O:78:LEU:HD22	1.84	0.60
1:E:223:LYS:HA	1:E:226:ILE:HD12	1.84	0.59
1:E:390:ILE:HD13	1:F:323:GLN:CB	2.32	0.59
1:E:441:PHE:C	1:F:329:ARG:HB3	2.27	0.59
1:F:384:ASN:ND2	1:F:390:ILE:H	2.00	0.59
1:K:384:ASN:HD22	1:K:394:ARG:HH11	1.49	0.59
1:L:91:TYR:O	1:L:92:VAL:CG1	2.49	0.59
2:P:88:LEU:H	2:P:88:LEU:HD22	1.67	0.59
1:E:20:GLN:CG	1:E:332:LEU:HD23	2.31	0.59
1:E:109:LYS:CG	1:F:296:MET:CB	2.80	0.59
1:E:310:PHE:O	2:N:66:MET:CB	2.11	0.59
1:L:86:PHE:O	1:L:89:VAL:CG2	2.41	0.59
2:M:60:PHE:HB2	2:M:78:LEU:HD22	1.84	0.59
1:E:34:ARG:CZ	1:E:250:HIS:HA	2.32	0.59
1:E:261:ILE:HG22	1:E:278:GLN:HG3	1.85	0.59
1:E:390:ILE:HD13	1:F:323:GLN:HB2	1.83	0.59
1:F:264:ARG:HH12	2:M:62:ARG:HA	1.68	0.59
1:L:384:ASN:ND2	1:L:390:ILE:H	2.00	0.59
1:E:92:VAL:CG1	1:F:92:VAL:CB	2.75	0.59
1:E:361:THR:CG2	1:F:36:ARG:HA	2.27	0.59
2:N:3:ILE:HB	2:N:122:ILE:HG12	1.85	0.59
2:P:60:PHE:CE2	2:P:97:VAL:HG21	2.37	0.59
1:E:153:SER:O	1:E:154:ALA:C	2.45	0.59
1:K:34:ARG:CZ	1:K:250:HIS:HA	2.32	0.59
1:L:222:MET:O	1:L:226:ILE:HG13	2.01	0.59
1:E:92:VAL:HG13	1:F:92:VAL:CA	2.28	0.59
1:E:109:LYS:HG2	1:F:296:MET:HB2	1.84	0.59
1:E:263:LYS:O	1:E:264:ARG:HB3	2.02	0.59
1:F:130:ARG:NH2	1:F:225:LEU:HD21	2.18	0.59
1:K:122:ARG:CA	1:K:122:ARG:HG2	2.26	0.59
1:L:86:PHE:HB2	1:L:277:VAL:HG13	1.84	0.59
1:L:264:ARG:CB	2:O:62:ARG:NH2	2.64	0.59
1:F:145:GLN:HG3	1:F:149:GLN:CB	2.30	0.59
2:P:3:ILE:HB	2:P:122:ILE:HG12	1.85	0.59
1:E:59:THR:O	1:E:61:VAL:HG13	2.03	0.59
1:F:128:GLU:O	1:F:132:LEU:HB2	2.03	0.59
1:E:222:MET:HE3	1:E:226:ILE:HD11	1.83	0.58
1:L:384:ASN:HD21	1:L:390:ILE:HG12	1.68	0.58
2:O:59:LEU:O	2:O:62:ARG:HB3	2.03	0.58
1:K:261:ILE:HG22	1:K:278:GLN:HG3	1.85	0.58
1:K:263:LYS:O	1:K:264:ARG:HB3	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:13:VAL:HG12	2:P:170:GLU:HG3	1.84	0.58
1:F:384:ASN:HD21	1:F:390:ILE:HG12	1.68	0.58
1:L:130:ARG:NH2	1:L:225:LEU:HD21	2.18	0.58
1:L:128:GLU:O	1:L:132:LEU:HB2	2.03	0.58
1:L:160:ARG:HA	1:L:163:LEU:HD23	1.84	0.58
1:E:92:VAL:HG21	1:F:92:VAL:HA	1.84	0.58
1:E:397:THR:HA	1:F:327:PRO:HA	1.85	0.58
2:P:85:ASP:CB	2:P:88:LEU:HD23	2.34	0.58
1:E:86:PHE:O	1:E:89:VAL:HG22	2.02	0.58
1:K:59:THR:O	1:K:61:VAL:HG13	2.03	0.58
1:K:223:LYS:HA	1:K:226:ILE:HD12	1.84	0.58
2:M:47:ALA:HB3	2:M:94:LEU:HB2	1.85	0.58
1:E:92:VAL:HG13	1:F:91:TYR:C	2.28	0.58
1:L:145:GLN:OE1	1:L:149:GLN:C	2.46	0.58
1:E:145:GLN:HG3	1:E:149:GLN:HG2	1.78	0.58
1:E:261:ILE:O	1:E:261:ILE:CG2	2.52	0.58
1:F:63:LYS:HG2	1:F:332:LEU:HD22	1.85	0.58
1:F:264:ARG:C	1:F:266:GLU:N	2.62	0.58
1:K:261:ILE:O	1:K:261:ILE:CG2	2.52	0.58
1:L:103:LEU:HD13	1:L:247:VAL:HG13	1.84	0.58
2:O:139:ASN:N	2:O:139:ASN:ND2	2.52	0.58
1:F:59:THR:O	1:F:61:VAL:HG13	2.04	0.58
1:F:41:ASN:ND2	1:F:43:GLU:HB3	2.19	0.58
1:F:145:GLN:OE1	1:F:149:GLN:C	2.46	0.58
2:O:47:ALA:HB3	2:O:94:LEU:HB2	1.85	0.58
2:N:85:ASP:CB	2:N:88:LEU:HD23	2.34	0.57
1:E:408:TYR:O	1:F:6:PRO:HG2	2.03	0.57
1:K:91:TYR:C	1:K:92:VAL:HG13	2.30	0.57
1:K:267:SER:HB3	1:K:270:PRO:CG	2.34	0.57
1:K:285:VAL:CG1	1:K:325:ARG:HB3	2.34	0.57
1:E:91:TYR:C	1:E:92:VAL:HG13	2.30	0.57
1:E:109:LYS:HG3	1:F:296:MET:HB3	1.86	0.57
1:E:285:VAL:CG1	1:E:325:ARG:HB3	2.34	0.57
1:L:41:ASN:ND2	1:L:43:GLU:HB3	2.19	0.57
1:L:397:THR:HG21	1:L:443:LEU:C	2.29	0.57
2:M:131:ALA:HA	2:P:158:ILE:CD1	2.34	0.57
2:O:54:PHE:CE2	2:P:80:LYS:CD	2.85	0.57
2:P:86:ARG:HG2	2:P:87:MET:H	1.69	0.57
1:K:264:ARG:CB	2:P:62:ARG:HH22	2.17	0.57
1:K:389:ASN:C	1:K:389:ASN:ND2	2.57	0.57
2:M:59:LEU:O	2:M:62:ARG:HB3	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:1:THR:HA	2:O:162:THR:HG22	1.87	0.57
1:E:92:VAL:HG21	1:F:92:VAL:C	2.29	0.57
1:E:358:LEU:N	1:F:40:LEU:CD2	2.59	0.57
1:L:59:THR:O	1:L:61:VAL:HG13	2.04	0.57
1:E:128:GLU:O	1:E:131:ILE:HG22	2.04	0.57
1:K:128:GLU:O	1:K:131:ILE:HG22	2.04	0.57
1:E:92:VAL:CG1	1:F:91:TYR:O	2.50	0.57
1:L:63:LYS:HG2	1:L:332:LEU:HD22	1.85	0.57
2:P:79:ALA:HB1	2:P:110:GLY:HA2	1.86	0.57
1:E:267:SER:HB3	1:E:270:PRO:CG	2.34	0.57
1:F:397:THR:HG21	1:F:443:LEU:C	2.29	0.57
2:M:13:VAL:HG12	2:M:170:GLU:HG3	1.86	0.57
2:O:37:LEU:HD21	2:O:57:PHE:CB	2.32	0.57
1:E:41:ASN:ND2	1:E:43:GLU:HB3	2.20	0.57
1:E:408:TYR:HE2	1:F:7:ARG:HG3	1.70	0.57
1:F:4:MET:HB3	1:F:8:GLU:HB3	1.86	0.57
1:F:264:ARG:NH2	2:M:59:LEU:HA	2.20	0.57
1:L:145:GLN:CD	1:L:150:GLN:CA	2.78	0.57
2:M:1:THR:HA	2:M:162:THR:HG22	1.86	0.57
2:O:3:ILE:HD11	2:O:46:PHE:O	2.05	0.57
2:O:13:VAL:HG12	2:O:170:GLU:HG3	1.86	0.57
1:E:38:MET:HE3	1:E:38:MET:HA	1.87	0.57
1:F:94:LYS:HD2	1:F:95:GLU:H	1.70	0.57
1:L:4:MET:HB3	1:L:8:GLU:HB3	1.86	0.57
2:O:54:PHE:CE2	2:P:80:LYS:HG3	2.39	0.57
1:F:145:GLN:N	1:F:145:GLN:NE2	2.51	0.56
1:K:92:VAL:HG11	1:L:89:VAL:O	2.05	0.56
1:F:104:THR:HG21	1:F:292:THR:HG21	1.87	0.56
1:F:235:ASN:HB2	1:F:238:GLU:OE2	2.05	0.56
1:F:366:ILE:HD13	1:F:418:ILE:HB	1.87	0.56
1:K:41:ASN:ND2	1:K:43:GLU:HB3	2.20	0.56
1:K:89:VAL:CG1	1:K:94:LYS:O	2.53	0.56
1:K:142:ASN:O	1:K:143:TRP:CB	2.53	0.56
1:L:117:GLU:C	1:L:119:ASN:H	2.13	0.56
2:M:139:ASN:N	2:M:139:ASN:ND2	2.52	0.56
1:K:38:MET:HA	1:K:38:MET:HE3	1.87	0.56
1:L:145:GLN:N	1:L:145:GLN:NE2	2.51	0.56
1:L:235:ASN:HB2	1:L:238:GLU:OE2	2.05	0.56
2:N:86:ARG:HG2	2:N:87:MET:H	1.69	0.56
1:E:411:SER:OG	1:F:32:ARG:CZ	2.54	0.56
1:F:145:GLN:HG2	1:F:150:GLN:H	1.64	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:17:ILE:HD11	1:K:69:ARG:HG3	1.86	0.56
1:L:96:VAL:HG12	1:L:284:LEU:HD11	1.86	0.56
1:L:308:GLY:HA3	1:L:310:PHE:CE2	2.40	0.56
2:N:3:ILE:HD11	2:N:46:PHE:O	2.05	0.56
1:E:358:LEU:HD23	1:F:37:ARG:CA	2.29	0.56
1:E:358:LEU:HD21	1:F:37:ARG:CA	2.29	0.56
1:F:96:VAL:HG12	1:F:284:LEU:HD11	1.86	0.56
1:F:308:GLY:HA3	1:F:310:PHE:CE2	2.40	0.56
1:L:104:THR:HG21	1:L:292:THR:HG21	1.88	0.56
2:N:79:ALA:HB1	2:N:110:GLY:HA2	1.86	0.56
1:F:145:GLN:CD	1:F:150:GLN:HA	2.29	0.56
2:N:1:THR:HB	2:N:33:LYS:NZ	2.20	0.56
2:O:57:PHE:CE1	2:O:95:LEU:HD21	2.41	0.56
2:P:3:ILE:HD11	2:P:46:PHE:O	2.05	0.56
1:E:122:ARG:C	1:E:122:ARG:HG2	2.30	0.56
1:E:362:GLU:OE1	1:F:36:ARG:HG2	2.06	0.56
1:E:441:PHE:CE1	1:F:56:ILE:CG2	2.89	0.56
1:F:86:PHE:O	1:F:89:VAL:CG2	2.41	0.56
1:K:91:TYR:HE1	1:L:272:VAL:HG11	1.69	0.56
1:L:145:GLN:CD	1:L:149:GLN:HB2	2.30	0.56
2:M:3:ILE:HD11	2:M:46:PHE:O	2.05	0.56
2:M:135:ALA:CA	2:P:154:ILE:HD13	2.25	0.56
2:N:21:THR:HG22	2:N:22:LEU:N	2.21	0.56
1:F:145:GLN:CD	1:F:150:GLN:CA	2.78	0.56
1:K:103:LEU:HD13	1:K:247:VAL:HG13	1.88	0.56
1:E:145:GLN:CG	1:E:149:GLN:CG	2.67	0.56
1:F:33:ASN:HD22	1:F:36:ARG:HD2	1.71	0.56
1:K:145:GLN:CA	1:K:149:GLN:HB2	2.29	0.56
1:L:89:VAL:HG12	1:L:94:LYS:N	2.21	0.56
1:L:155:ALA:O	1:L:159:PHE:HB2	2.06	0.56
2:M:108:GLY:C	2:M:110:GLY:H	2.14	0.56
1:E:17:ILE:HD11	1:E:69:ARG:HG3	1.86	0.56
1:E:118:LYS:HA	1:E:118:LYS:CE	2.36	0.56
1:F:58:PRO:HG2	1:F:61:VAL:HG11	1.88	0.56
1:K:122:ARG:C	1:K:122:ARG:HG2	2.30	0.56
1:L:33:ASN:HD22	1:L:36:ARG:HD2	1.71	0.56
1:L:313:ALA:C	2:O:65:GLU:OE2	2.49	0.56
1:E:91:TYR:HB3	1:F:91:TYR:HA	1.85	0.55
1:E:400:GLU:OE1	1:F:51:LYS:NZ	2.36	0.55
1:F:27:VAL:CG1	1:F:70:LEU:HG	2.35	0.55
1:F:89:VAL:HG12	1:F:94:LYS:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:366:ILE:HD13	1:L:418:ILE:HB	1.88	0.55
2:O:108:GLY:C	2:O:110:GLY:H	2.14	0.55
2:P:1:THR:HB	2:P:33:LYS:NZ	2.20	0.55
1:E:89:VAL:CG1	1:E:94:LYS:O	2.53	0.55
1:E:92:VAL:HG11	1:F:92:VAL:HB	1.81	0.55
1:F:155:ALA:O	1:F:159:PHE:HB2	2.06	0.55
1:L:94:LYS:HD2	1:L:95:GLU:H	1.70	0.55
1:L:111:VAL:HG21	1:L:243:ALA:HB2	1.88	0.55
1:L:128:GLU:O	1:L:131:ILE:HG22	2.06	0.55
2:M:136:LEU:HD11	2:P:135:ALA:HB1	1.88	0.55
2:P:21:THR:HG22	2:P:22:LEU:N	2.21	0.55
1:E:15:LYS:HB3	1:E:348:ASN:ND2	2.21	0.55
1:E:257:GLU:HG2	1:E:260:LYS:HG3	1.88	0.55
1:K:366:ILE:HD13	1:K:418:ILE:HB	1.88	0.55
1:F:117:GLU:C	1:F:119:ASN:H	2.13	0.55
1:F:91:TYR:O	1:F:92:VAL:HG13	2.07	0.55
1:K:64:THR:HG22	1:K:68:ARG:HD2	1.88	0.55
1:K:118:LYS:HA	1:K:118:LYS:CE	2.36	0.55
1:L:374:LYS:NZ	1:L:378:GLU:OE2	2.29	0.55
2:O:54:PHE:CE2	2:P:80:LYS:HD2	2.42	0.55
1:E:103:LEU:HD13	1:E:247:VAL:HG13	1.88	0.55
1:E:408:TYR:HB2	1:F:29:ILE:HG12	1.87	0.55
1:F:128:GLU:O	1:F:131:ILE:HG22	2.06	0.55
2:M:57:PHE:CE1	2:M:95:LEU:HD21	2.41	0.55
2:M:62:ARG:O	2:M:65:GLU:HB2	2.07	0.55
2:M:160:ILE:CG2	2:O:160:ILE:HD13	2.36	0.55
2:N:17:ASP:O	2:N:33:LYS:HD2	2.07	0.55
1:E:64:THR:HG22	1:E:68:ARG:HD2	1.88	0.55
1:E:362:GLU:OE2	1:F:32:ARG:NH2	2.40	0.55
1:E:440:ARG:HD3	1:F:314:LYS:HB3	1.89	0.55
1:L:58:PRO:HG2	1:L:61:VAL:HG11	1.88	0.55
2:P:70:HIS:HD2	2:P:73:LYS:HB2	1.72	0.55
1:E:139:ALA:O	1:E:140:LYS:CG	2.55	0.55
1:E:292:THR:HG22	1:E:294:HIS:N	2.05	0.55
1:E:400:GLU:CD	1:F:51:LYS:CE	2.80	0.55
1:E:442:ILE:CG2	1:F:329:ARG:HB2	2.37	0.55
1:F:108:VAL:HA	1:F:111:VAL:HG22	1.89	0.55
1:F:145:GLN:CD	1:F:149:GLN:HB2	2.30	0.55
1:F:397:THR:HG21	1:F:443:LEU:O	2.07	0.55
2:M:85:ASP:CB	2:M:88:LEU:HD23	2.36	0.55
2:O:85:ASP:CB	2:O:88:LEU:HD23	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:442:ILE:HD13	1:F:329:ARG:CB	2.35	0.55
2:N:139:ASN:N	2:N:139:ASN:ND2	2.48	0.55
2:P:17:ASP:O	2:P:33:LYS:HD2	2.07	0.55
1:F:264:ARG:O	1:F:266:GLU:N	2.40	0.54
1:K:309:ALA:HB1	2:P:66:MET:HG2	1.88	0.54
1:L:108:VAL:HA	1:L:111:VAL:HG22	1.89	0.54
1:E:222:MET:HE2	1:E:223:LYS:HZ2	1.73	0.54
1:K:15:LYS:HB3	1:K:348:ASN:ND2	2.21	0.54
2:O:62:ARG:O	2:O:65:GLU:HB2	2.07	0.54
1:K:122:ARG:HG2	1:K:122:ARG:O	2.06	0.54
1:K:264:ARG:CB	2:P:62:ARG:NH2	2.69	0.54
1:L:264:ARG:C	1:L:266:GLU:N	2.62	0.54
1:E:132:LEU:HD12	1:E:156:ARG:CG	2.38	0.54
2:P:139:ASN:N	2:P:139:ASN:ND2	2.48	0.54
1:E:145:GLN:CA	1:E:149:GLN:HB2	2.29	0.54
1:F:111:VAL:HG21	1:F:243:ALA:HB2	1.88	0.54
1:F:264:ARG:HH21	2:M:62:ARG:HD2	1.65	0.54
1:K:257:GLU:HG2	1:K:260:LYS:HG3	1.88	0.54
2:M:128:TYR:CD1	2:P:128:TYR:CE1	2.95	0.54
1:E:366:ILE:HD13	1:E:418:ILE:HB	1.88	0.54
1:E:394:ARG:NH2	1:F:323:GLN:OE1	2.40	0.54
1:K:91:TYR:CE1	1:L:272:VAL:HG12	2.40	0.54
1:K:132:LEU:HD12	1:K:156:ARG:CG	2.38	0.54
1:L:285:VAL:CG1	1:L:325:ARG:HB3	2.38	0.54
2:M:158:ILE:HG21	2:P:127:PRO:HB3	1.90	0.54
2:N:70:HIS:HD2	2:N:73:LYS:HB2	1.72	0.54
1:E:122:ARG:HG2	1:E:122:ARG:O	2.06	0.54
1:E:397:THR:HG23	1:F:327:PRO:C	2.32	0.54
1:F:285:VAL:CG1	1:F:325:ARG:HB3	2.38	0.54
1:K:312:ILE:HD12	2:P:62:ARG:O	2.07	0.54
1:L:264:ARG:O	1:L:266:GLU:N	2.40	0.54
2:M:131:ALA:HA	2:P:158:ILE:HD11	1.88	0.54
1:E:142:ASN:O	1:E:143:TRP:CB	2.53	0.54
2:N:60:PHE:HB2	2:N:78:LEU:HD22	1.90	0.54
2:P:60:PHE:HB2	2:P:78:LEU:HD22	1.90	0.54
1:E:41:ASN:HD22	1:E:43:GLU:HB3	1.73	0.54
1:F:131:ILE:O	1:F:134:VAL:HG12	2.08	0.54
1:F:131:ILE:C	1:F:133:ASP:H	2.15	0.54
1:K:139:ALA:O	1:K:140:LYS:CG	2.55	0.54
1:L:397:THR:HG21	1:L:443:LEU:O	2.07	0.54
1:K:41:ASN:HD22	1:K:43:GLU:HB3	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:91:TYR:O	1:L:92:VAL:HG13	2.07	0.53
1:L:131:ILE:C	1:L:133:ASP:H	2.15	0.53
1:E:91:TYR:CD2	1:F:91:TYR:HA	2.43	0.53
1:K:131:ILE:HD12	1:K:134:VAL:CG1	2.39	0.53
2:N:67:HIS:O	2:N:69:GLY:N	2.41	0.53
2:O:98:ALA:CB	2:O:103:SER:HB3	2.38	0.53
2:P:140:THR:HG22	2:P:141:GLU:N	2.23	0.53
1:K:374:LYS:O	1:K:378:GLU:HG3	2.07	0.53
1:L:20:GLN:CG	1:L:332:LEU:HD23	2.36	0.53
2:P:67:HIS:O	2:P:69:GLY:N	2.41	0.53
1:K:111:VAL:HG21	1:K:243:ALA:HB2	1.90	0.53
1:L:145:GLN:CD	1:L:149:GLN:CB	2.81	0.53
1:L:285:VAL:HG12	1:L:325:ARG:CG	2.38	0.53
2:M:140:THR:HG21	2:M:142:LEU:CG	2.38	0.53
2:N:140:THR:HG22	2:N:141:GLU:N	2.23	0.53
1:E:442:ILE:HG23	1:F:329:ARG:HB2	1.90	0.53
1:K:145:GLN:H	1:K:149:GLN:CB	2.22	0.53
2:M:98:ALA:CB	2:M:103:SER:HB3	2.38	0.53
1:E:111:VAL:HG21	1:E:243:ALA:HB2	1.90	0.53
1:E:374:LYS:O	1:E:378:GLU:HG3	2.07	0.53
1:E:390:ILE:CD1	1:F:323:GLN:HB2	2.39	0.53
1:E:411:SER:OG	1:F:32:ARG:NE	2.40	0.53
1:F:374:LYS:NZ	1:F:378:GLU:OE2	2.29	0.53
1:K:257:GLU:OE1	1:L:279:ARG:NH2	2.42	0.53
2:O:98:ALA:HB2	2:O:103:SER:HB3	1.91	0.53
1:E:145:GLN:H	1:E:149:GLN:CB	2.22	0.53
1:E:358:LEU:HG	1:F:40:LEU:CD1	2.30	0.53
1:K:108:VAL:C	1:K:110:MET:N	2.66	0.53
1:E:312:ILE:CD1	2:N:67:HIS:CE1	2.91	0.53
1:E:354:GLN:CD	1:F:48:VAL:N	2.60	0.53
1:F:219:LYS:O	1:F:223:LYS:HD3	2.09	0.53
2:P:59:LEU:O	2:P:62:ARG:HB2	2.09	0.53
1:E:358:LEU:CD2	1:F:37:ARG:N	2.71	0.53
1:F:285:VAL:HG12	1:F:325:ARG:CG	2.38	0.53
1:K:382:GLN:OE1	1:K:382:GLN:HA	2.09	0.53
1:L:217:LYS:HB3	1:L:220:ASP:CB	2.38	0.53
2:O:7:ARG:HB2	2:O:12:VAL:HG23	1.91	0.53
2:O:66:MET:O	2:O:67:HIS:ND1	2.42	0.53
1:F:145:GLN:CD	1:F:149:GLN:CB	2.81	0.53
1:F:217:LYS:HB3	1:F:220:ASP:CB	2.38	0.53
2:M:85:ASP:O	2:M:89:ARG:HB3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:98:ALA:HB2	2:M:103:SER:HB3	1.90	0.53
2:M:140:THR:HG22	2:M:142:LEU:N	2.17	0.53
2:O:85:ASP:O	2:O:89:ARG:HB3	2.09	0.53
2:O:90:LYS:HZ1	2:P:89:ARG:HD2	1.74	0.53
1:K:282:LEU:CD1	1:K:319:ILE:HD11	2.39	0.52
1:L:219:LYS:O	1:L:223:LYS:HD3	2.09	0.52
2:O:140:THR:HG21	2:O:142:LEU:CG	2.38	0.52
1:E:108:VAL:C	1:E:110:MET:N	2.66	0.52
1:F:20:GLN:CG	1:F:332:LEU:HD23	2.36	0.52
1:F:92:VAL:CG2	1:F:93:GLY:H	2.21	0.52
1:K:117:GLU:C	1:K:119:ASN:H	2.16	0.52
1:K:292:THR:HG22	1:K:294:HIS:N	2.05	0.52
1:L:27:VAL:CG1	1:L:70:LEU:HG	2.35	0.52
1:L:131:ILE:O	1:L:134:VAL:HG12	2.08	0.52
1:L:145:GLN:CD	1:L:150:GLN:HA	2.30	0.52
1:K:91:TYR:O	1:K:92:VAL:CG1	2.58	0.52
1:E:92:VAL:HG21	1:F:92:VAL:CA	2.39	0.52
1:E:131:ILE:HD12	1:E:134:VAL:CG1	2.39	0.52
1:K:145:GLN:HG3	1:K:149:GLN:HG2	1.78	0.52
2:M:66:MET:O	2:M:67:HIS:ND1	2.42	0.52
1:E:443:LEU:N	1:F:329:ARG:HG3	2.21	0.52
1:F:18:ILE:HD13	1:F:347:PRO:HG3	1.92	0.52
1:F:231:ALA:C	1:F:233:LEU:H	2.17	0.52
1:K:118:LYS:HA	1:K:118:LYS:HZ3	1.72	0.52
1:L:231:ALA:C	1:L:233:LEU:H	2.17	0.52
2:N:64:LEU:HD23	2:N:74:ALA:CB	2.40	0.52
2:O:2:THR:HG1	2:O:162:THR:HG21	1.74	0.52
1:L:17:ILE:HD13	1:L:66:ILE:CG1	2.36	0.52
1:L:92:VAL:CG2	1:L:93:GLY:H	2.22	0.52
1:L:312:ILE:C	2:O:62:ARG:HG3	2.33	0.52
2:N:59:LEU:O	2:N:62:ARG:HB2	2.09	0.52
1:F:362:GLU:HG2	1:F:411:SER:N	2.24	0.52
1:K:216:LEU:O	1:K:220:ASP:HB3	2.10	0.52
1:L:146:THR:C	1:L:150:GLN:HB2	2.35	0.52
1:E:117:GLU:C	1:E:119:ASN:H	2.16	0.52
2:P:64:LEU:HD23	2:P:74:ALA:CB	2.40	0.52
1:E:91:TYR:CD1	1:F:90:GLY:C	2.83	0.52
1:E:92:VAL:HG12	1:F:92:VAL:HG12	1.90	0.52
1:F:263:LYS:HE2	1:F:275:GLU:OE1	2.10	0.52
1:F:15:LYS:HB3	1:F:348:ASN:ND2	2.25	0.51
1:L:18:ILE:HD13	1:L:347:PRO:HG3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:362:GLU:HG2	1:L:411:SER:N	2.24	0.51
2:O:149:GLU:HG3	2:O:166:HIS:HD2	1.74	0.51
2:M:7:ARG:HB2	2:M:12:VAL:HG23	1.91	0.51
2:M:149:GLU:HG3	2:M:166:HIS:HD2	1.74	0.51
1:F:141:ASN:C	1:F:142:ASN:HD22	2.18	0.51
1:L:263:LYS:HE2	1:L:275:GLU:OE1	2.10	0.51
1:E:145:GLN:HB2	1:E:149:GLN:H	1.74	0.51
1:E:382:GLN:OE1	1:E:382:GLN:HA	2.09	0.51
1:K:362:GLU:HG3	1:K:411:SER:HA	1.93	0.51
2:M:37:LEU:HD21	2:M:57:PHE:CB	2.32	0.51
2:O:88:LEU:HD22	2:O:88:LEU:H	1.76	0.51
1:E:91:TYR:O	1:E:92:VAL:CG1	2.58	0.51
1:E:216:LEU:O	1:E:220:ASP:HB3	2.10	0.51
1:F:263:LYS:O	1:F:264:ARG:CB	2.59	0.51
1:K:96:VAL:CG1	1:K:99:ILE:HD12	2.40	0.51
1:K:145:GLN:HB2	1:K:149:GLN:H	1.74	0.51
1:L:264:ARG:NH1	2:O:59:LEU:O	2.39	0.51
2:N:3:ILE:HB	2:N:122:ILE:HG13	1.93	0.51
2:N:98:ALA:HA	2:N:103:SER:HA	1.93	0.51
2:P:3:ILE:HB	2:P:122:ILE:HG13	1.93	0.51
1:E:440:ARG:O	1:F:315:PRO:CD	2.58	0.51
1:K:91:TYR:HE1	1:L:272:VAL:CG1	2.23	0.51
1:L:122:ARG:HH21	1:L:122:ARG:CG	2.24	0.51
1:L:153:SER:O	1:L:154:ALA:C	2.53	0.51
2:N:8:ARG:NH1	2:N:142:LEU:O	2.43	0.51
1:E:442:ILE:C	1:F:329:ARG:HB2	2.34	0.51
1:L:311:GLN:NE2	2:O:68:GLN:CA	2.73	0.51
2:M:88:LEU:H	2:M:88:LEU:HD22	1.76	0.51
2:O:22:LEU:HB2	2:O:27:MET:HG3	1.93	0.51
1:E:139:ALA:O	1:E:140:LYS:HB2	2.11	0.51
1:E:282:LEU:CD1	1:E:319:ILE:HD11	2.39	0.51
1:F:235:ASN:OD1	1:F:238:GLU:OE2	2.29	0.51
1:K:139:ALA:O	1:K:140:LYS:HB2	2.11	0.51
1:L:91:TYR:C	1:L:92:VAL:CG1	2.83	0.51
2:M:22:LEU:HB2	2:M:27:MET:HG3	1.93	0.51
2:P:8:ARG:NH1	2:P:142:LEU:O	2.43	0.51
1:E:34:ARG:NH1	1:E:250:HIS:HA	2.25	0.51
1:E:263:LYS:O	1:E:264:ARG:CB	2.58	0.51
1:E:278:GLN:OE1	1:E:319:ILE:HG23	2.10	0.51
1:F:146:THR:C	1:F:150:GLN:HB2	2.35	0.51
1:F:285:VAL:HG11	1:F:325:ARG:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:369:THR:O	1:K:373:ILE:HG12	2.11	0.51
1:E:96:VAL:CG1	1:E:99:ILE:HD12	2.40	0.51
1:E:131:ILE:HG23	1:E:132:LEU:N	2.26	0.51
1:F:264:ARG:HH12	2:M:62:ARG:CG	1.94	0.51
1:K:34:ARG:NH1	1:K:250:HIS:HA	2.25	0.51
1:K:350:SER:OG	1:K:353:VAL:HG23	2.11	0.51
1:E:109:LYS:CG	1:F:296:MET:HB2	2.41	0.50
1:F:91:TYR:C	1:F:92:VAL:CG1	2.83	0.50
1:F:153:SER:O	1:F:154:ALA:C	2.53	0.50
1:L:94:LYS:NZ	1:L:95:GLU:OE2	2.37	0.50
2:N:59:LEU:HA	2:N:62:ARG:HD2	1.93	0.50
2:P:98:ALA:HA	2:P:103:SER:HA	1.93	0.50
1:E:145:GLN:CB	1:E:149:GLN:H	2.25	0.50
1:F:389:ASN:HD22	1:F:390:ILE:N	2.09	0.50
1:L:15:LYS:HB3	1:L:348:ASN:ND2	2.25	0.50
2:O:15:ALA:CB	2:O:152:LEU:HD12	2.41	0.50
1:E:120:ARG:HG3	1:E:121:TYR:N	2.25	0.50
1:E:359:MET:CE	1:F:36:ARG:HD3	2.40	0.50
1:K:20:GLN:HG3	1:K:332:LEU:CD2	2.42	0.50
1:L:76:ALA:HB1	1:L:250:HIS:O	2.11	0.50
1:L:235:ASN:OD1	1:L:238:GLU:OE2	2.29	0.50
1:L:264:ARG:CZ	2:O:62:ARG:HD3	2.39	0.50
2:N:90:LYS:HD2	2:N:91:LEU:N	2.27	0.50
2:P:99:ASP:C	2:P:99:ASP:OD1	2.55	0.50
1:E:86:PHE:HB2	1:E:277:VAL:HG13	1.92	0.50
1:E:440:ARG:CD	1:F:314:LYS:HD2	2.41	0.50
1:K:329:ARG:HH11	1:K:329:ARG:HG3	1.77	0.50
1:L:141:ASN:C	1:L:142:ASN:HD22	2.18	0.50
2:M:21:THR:HG22	2:M:22:LEU:N	2.26	0.50
1:E:350:SER:OG	1:E:353:VAL:HG23	2.11	0.50
1:K:128:GLU:HA	1:K:131:ILE:HG22	1.92	0.50
1:K:131:ILE:HG23	1:K:132:LEU:N	2.26	0.50
1:L:389:ASN:HD22	1:L:390:ILE:N	2.09	0.50
2:P:90:LYS:HD2	2:P:91:LEU:N	2.27	0.50
1:E:136:ILE:O	1:E:136:ILE:CG2	2.60	0.50
1:F:135:LEU:O	1:F:136:ILE:HG12	2.10	0.50
1:K:278:GLN:OE1	1:K:319:ILE:HG23	2.11	0.50
1:L:135:LEU:O	1:L:136:ILE:HG12	2.11	0.50
2:M:15:ALA:CB	2:M:152:LEU:HD12	2.41	0.50
2:M:37:LEU:CD2	2:M:57:PHE:HB3	2.35	0.50
2:M:51:ALA:O	2:M:54:PHE:HB3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:140:THR:HG21	2:N:142:LEU:CG	2.35	0.50
2:O:51:ALA:O	2:O:54:PHE:HB3	2.11	0.50
1:E:20:GLN:HG3	1:E:332:LEU:CD2	2.42	0.50
1:E:362:GLU:HG3	1:E:411:SER:HA	1.93	0.50
1:E:397:THR:CA	1:F:327:PRO:HA	2.42	0.50
1:K:86:PHE:HB2	1:K:277:VAL:HG13	1.92	0.50
2:M:100:GLU:HG2	2:M:173:TYR:CD2	2.47	0.50
2:O:70:HIS:CD2	2:O:73:LYS:H	2.30	0.50
1:F:76:ALA:HB1	1:F:250:HIS:O	2.11	0.50
1:F:232:LYS:HB2	1:F:232:LYS:NZ	2.27	0.50
1:K:263:LYS:O	1:K:264:ARG:CB	2.58	0.50
1:L:369:THR:HB	1:L:421:ASP:HA	1.94	0.50
2:N:99:ASP:C	2:N:99:ASP:OD1	2.55	0.50
2:O:37:LEU:CD2	2:O:57:PHE:HB3	2.35	0.50
2:O:140:THR:HG22	2:O:142:LEU:N	2.17	0.50
2:P:59:LEU:HA	2:P:62:ARG:HD2	1.93	0.50
1:E:440:ARG:HD2	1:F:314:LYS:HD2	1.94	0.50
1:F:369:THR:HB	1:F:421:ASP:HA	1.94	0.50
1:K:120:ARG:HG3	1:K:121:TYR:N	2.25	0.50
2:M:138:GLU:HB3	2:M:139:ASN:ND2	2.26	0.50
2:O:66:MET:HE3	2:O:66:MET:HA	1.93	0.50
1:E:329:ARG:HG3	1:E:329:ARG:HH11	1.77	0.49
1:F:130:ARG:HH11	1:F:131:ILE:N	2.10	0.49
2:M:36:ARG:C	2:M:37:LEU:HD12	2.37	0.49
2:O:21:THR:HG22	2:O:22:LEU:N	2.26	0.49
2:O:138:GLU:HB3	2:O:139:ASN:ND2	2.26	0.49
2:P:39:ASN:HD22	2:P:39:ASN:N	2.09	0.49
1:F:122:ARG:HH21	1:F:122:ARG:CG	2.24	0.49
1:E:369:THR:O	1:E:373:ILE:HG12	2.11	0.49
1:F:94:LYS:NZ	1:F:95:GLU:OE2	2.36	0.49
1:F:264:ARG:NH1	1:F:312:ILE:HD12	2.27	0.49
1:K:141:ASN:ND2	1:K:141:ASN:N	2.42	0.49
2:O:100:GLU:HG2	2:O:173:TYR:CD2	2.47	0.49
1:E:128:GLU:HA	1:E:131:ILE:HG22	1.92	0.49
1:F:286:GLU:HG2	1:F:325:ARG:HH12	1.77	0.49
1:L:342:ARG:HE	1:L:346:GLU:CD	2.21	0.49
2:M:70:HIS:CD2	2:M:73:LYS:H	2.30	0.49
1:E:441:PHE:CG	1:F:56:ILE:CD1	2.69	0.49
1:F:409:ASP:O	1:F:413:LEU:HD22	2.12	0.49
1:E:79:ILE:HD13	1:E:80:LYS:H	1.78	0.49
1:E:357:ALA:HB2	1:F:44:LEU:HD11	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:397:THR:HG21	1:E:443:LEU:HA	1.94	0.49
1:F:89:VAL:CG1	1:F:94:LYS:H	2.26	0.49
1:F:130:ARG:NH1	1:F:131:ILE:HA	2.28	0.49
1:K:217:LYS:HB2	1:K:220:ASP:HB3	1.95	0.49
1:L:264:ARG:HH11	2:O:62:ARG:CG	2.25	0.49
1:L:413:LEU:HD13	1:L:413:LEU:N	2.28	0.49
2:M:159:CYS:HB3	2:M:162:THR:OG1	2.13	0.49
2:N:53:ALA:HB1	2:N:57:PHE:CE2	2.48	0.49
1:E:91:TYR:CD2	1:F:91:TYR:HD2	2.31	0.49
1:K:108:VAL:HA	1:K:111:VAL:HG22	1.95	0.49
2:M:66:MET:HA	2:M:66:MET:HE3	1.93	0.49
2:P:51:ALA:O	2:P:54:PHE:HB3	2.12	0.49
2:P:140:THR:HG21	2:P:142:LEU:CG	2.35	0.49
1:E:388:GLU:OE2	1:F:318:LEU:O	2.30	0.49
1:K:384:ASN:ND2	1:K:390:ILE:H	2.10	0.49
1:L:130:ARG:NH1	1:L:131:ILE:HA	2.28	0.49
1:L:285:VAL:HG11	1:L:325:ARG:HB3	1.93	0.49
1:E:217:LYS:HB2	1:E:220:ASP:HB3	1.95	0.49
1:E:384:ASN:ND2	1:E:390:ILE:H	2.10	0.49
1:F:123:ALA:O	1:F:127:ALA:HB2	2.13	0.49
1:F:342:ARG:HE	1:F:346:GLU:CD	2.21	0.49
1:K:89:VAL:HG12	1:K:94:LYS:N	2.25	0.49
1:K:136:ILE:O	1:K:136:ILE:CG2	2.60	0.49
1:K:145:GLN:CB	1:K:149:GLN:H	2.25	0.49
1:L:409:ASP:O	1:L:413:LEU:HD22	2.12	0.49
2:N:39:ASN:HD22	2:N:39:ASN:N	2.09	0.49
1:F:79:ILE:HD13	1:F:80:LYS:O	2.13	0.49
1:K:389:ASN:HD22	1:K:391:GLY:H	1.56	0.49
1:L:79:ILE:HD13	1:L:80:LYS:O	2.13	0.49
2:O:61:GLU:O	2:O:65:GLU:HG2	2.13	0.49
1:E:108:VAL:HA	1:E:111:VAL:HG22	1.95	0.48
1:E:441:PHE:CE1	1:F:310:PHE:CB	2.95	0.48
1:F:94:LYS:NZ	1:F:98:SER:HB3	2.28	0.48
1:K:145:GLN:HB2	1:K:149:GLN:C	2.38	0.48
1:L:286:GLU:HG2	1:L:325:ARG:HH12	1.77	0.48
2:N:108:GLY:C	2:N:110:GLY:H	2.21	0.48
2:O:5:SER:HB2	2:O:14:ILE:HG12	1.95	0.48
2:O:36:ARG:C	2:O:37:LEU:HD12	2.37	0.48
1:E:109:LYS:HG3	1:F:296:MET:CB	2.43	0.48
1:E:145:GLN:HB2	1:E:149:GLN:C	2.38	0.48
2:N:88:LEU:HD22	2:N:88:LEU:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:100:GLU:HG2	2:N:173:TYR:HB3	1.96	0.48
2:O:66:MET:C	2:O:67:HIS:ND1	2.71	0.48
2:P:53:ALA:HB1	2:P:57:PHE:CE2	2.48	0.48
2:P:108:GLY:C	2:P:110:GLY:H	2.21	0.48
1:E:92:VAL:CG2	1:F:92:VAL:CA	2.91	0.48
1:K:79:ILE:HD13	1:K:80:LYS:H	1.78	0.48
1:K:89:VAL:HG12	1:K:94:LYS:O	2.14	0.48
1:K:96:VAL:HG13	1:K:99:ILE:CD1	2.43	0.48
2:O:51:ALA:CB	2:P:109:ASN:O	2.61	0.48
2:O:70:HIS:HD2	2:O:73:LYS:CB	2.25	0.48
1:L:89:VAL:CG1	1:L:94:LYS:H	2.26	0.48
1:L:118:LYS:CE	1:L:118:LYS:HA	2.44	0.48
2:O:5:SER:HB3	2:O:120:ILE:HB	1.95	0.48
2:O:43:ILE:HG23	2:O:171:LEU:HD13	1.95	0.48
2:P:39:ASN:N	2:P:39:ASN:ND2	2.62	0.48
1:E:89:VAL:HG12	1:E:94:LYS:O	2.14	0.48
1:E:442:ILE:N	1:F:329:ARG:HG3	2.29	0.48
1:L:130:ARG:HH11	1:L:131:ILE:N	2.10	0.48
2:P:88:LEU:HD22	2:P:88:LEU:N	2.28	0.48
1:E:441:PHE:HD1	1:F:56:ILE:CG1	2.20	0.48
1:F:217:LYS:O	1:F:221:ALA:N	2.44	0.48
1:L:94:LYS:HZ2	1:L:98:SER:HB3	1.77	0.48
1:L:232:LYS:HB2	1:L:232:LYS:NZ	2.27	0.48
2:M:8:ARG:HH21	2:M:137:LEU:HA	1.78	0.48
2:P:16:GLY:CA	2:P:152:LEU:HD11	2.44	0.48
2:M:61:GLU:O	2:M:65:GLU:HG2	2.14	0.48
2:M:70:HIS:HD2	2:M:73:LYS:CB	2.25	0.48
1:F:145:GLN:CD	1:F:145:GLN:O	2.57	0.48
1:F:374:LYS:O	1:F:378:GLU:HG3	2.13	0.48
1:K:264:ARG:C	1:K:266:GLU:N	2.72	0.48
1:L:123:ALA:O	1:L:127:ALA:HB2	2.13	0.48
1:L:263:LYS:O	1:L:264:ARG:CB	2.59	0.48
2:M:17:ASP:HA	2:M:165:PHE:O	2.13	0.48
2:M:66:MET:C	2:M:67:HIS:ND1	2.71	0.48
2:M:134:ARG:O	2:M:138:GLU:HB2	2.14	0.48
2:N:51:ALA:O	2:N:54:PHE:HB3	2.13	0.48
2:O:17:ASP:HA	2:O:165:PHE:O	2.13	0.48
2:O:134:ARG:O	2:O:138:GLU:HB2	2.14	0.48
2:P:28:LYS:HD3	2:P:31:VAL:HG22	1.96	0.48
1:E:389:ASN:HD22	1:E:391:GLY:H	1.56	0.48
1:F:135:LEU:HD13	1:F:159:PHE:CE1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:135:LEU:HD13	1:L:159:PHE:CE1	2.49	0.48
2:M:83:ARG:HG3	2:M:108:GLY:O	2.14	0.48
2:M:128:TYR:CE1	2:P:128:TYR:CE1	3.01	0.48
2:N:28:LYS:HD3	2:N:31:VAL:HG22	1.96	0.48
2:O:15:ALA:HB1	2:O:152:LEU:HD12	1.96	0.48
2:O:83:ARG:HG3	2:O:108:GLY:O	2.14	0.48
2:P:32:LYS:HD3	2:P:34:VAL:O	2.14	0.48
1:E:358:LEU:O	1:E:361:THR:CG2	2.60	0.48
1:E:359:MET:HE1	1:F:36:ARG:NH1	2.27	0.48
1:E:369:THR:HB	1:E:421:ASP:HA	1.96	0.48
1:K:278:GLN:CD	1:K:319:ILE:HG23	2.39	0.48
1:L:309:ALA:HB3	2:O:66:MET:CG	2.28	0.48
2:N:58:GLU:HG3	2:N:62:ARG:HE	1.78	0.48
2:N:116:GLU:H	2:N:116:GLU:HG2	1.42	0.48
2:O:8:ARG:HH21	2:O:137:LEU:HA	1.78	0.48
2:O:159:CYS:HB3	2:O:162:THR:OG1	2.13	0.48
1:E:344:LEU:HD13	1:E:395:LEU:HD13	1.96	0.47
1:F:131:ILE:CG2	1:F:132:LEU:N	2.77	0.47
1:L:94:LYS:NZ	1:L:98:SER:HB3	2.29	0.47
2:N:3:ILE:HD11	2:N:46:PHE:C	2.39	0.47
2:P:58:GLU:HG3	2:P:62:ARG:HE	1.78	0.47
2:P:100:GLU:HG2	2:P:173:TYR:HB3	1.96	0.47
1:F:17:ILE:HD13	1:F:66:ILE:CG1	2.35	0.47
1:L:374:LYS:O	1:L:378:GLU:HG3	2.13	0.47
2:M:3:ILE:HB	2:M:122:ILE:CG1	2.44	0.47
2:N:16:GLY:CA	2:N:152:LEU:HD11	2.44	0.47
2:N:39:ASN:N	2:N:39:ASN:ND2	2.62	0.47
2:O:51:ALA:HB2	2:P:109:ASN:O	2.14	0.47
1:E:440:ARG:C	1:F:315:PRO:HD2	2.38	0.47
1:F:311:GLN:CG	2:M:66:MET:CE	2.59	0.47
1:F:312:ILE:HG12	2:M:65:GLU:HB3	0.83	0.47
1:F:413:LEU:HD13	1:F:413:LEU:N	2.28	0.47
1:K:397:THR:HG21	1:K:443:LEU:HA	1.94	0.47
2:M:5:SER:HB3	2:M:120:ILE:HB	1.95	0.47
2:N:32:LYS:HD3	2:N:34:VAL:O	2.14	0.47
1:K:63:LYS:HE2	1:K:307:SER:OG	2.15	0.47
1:K:235:ASN:ND2	1:K:235:ASN:N	2.37	0.47
1:L:216:LEU:O	1:L:220:ASP:HB3	2.14	0.47
1:E:91:TYR:C	1:E:92:VAL:CG1	2.88	0.47
1:E:354:GLN:HG2	1:F:47:GLU:HB2	1.95	0.47
1:F:257:GLU:HG2	1:F:260:LYS:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:278:GLN:OE1	1:F:319:ILE:HB	2.15	0.47
1:K:91:TYR:C	1:K:92:VAL:CG1	2.87	0.47
1:K:369:THR:HB	1:K:421:ASP:HA	1.96	0.47
2:M:15:ALA:HB1	2:M:152:LEU:HD12	1.96	0.47
1:F:4:MET:HE1	1:F:73:LEU:CD1	2.44	0.47
1:F:55:MET:HE3	1:F:305:ILE:CG2	2.43	0.47
1:F:118:LYS:HA	1:F:118:LYS:CE	2.44	0.47
1:K:264:ARG:HD2	2:P:62:ARG:NH2	2.16	0.47
1:L:292:THR:C	1:L:294:HIS:N	2.73	0.47
2:M:5:SER:HB2	2:M:14:ILE:HG12	1.95	0.47
1:E:63:LYS:HE2	1:E:307:SER:OG	2.15	0.47
1:E:96:VAL:HG11	1:E:281:LEU:CD1	2.44	0.47
1:F:132:LEU:CG	1:F:160:ARG:HB3	2.44	0.47
1:K:96:VAL:HG11	1:K:281:LEU:CD1	2.44	0.47
2:M:63:LYS:CB	2:M:74:ALA:HB1	2.45	0.47
2:N:88:LEU:H	2:N:88:LEU:CD2	2.28	0.47
2:O:115:PRO:HG2	2:O:120:ILE:HG12	1.95	0.47
2:O:145:ARG:NE	2:O:170:GLU:OE1	2.47	0.47
2:P:3:ILE:HD11	2:P:46:PHE:C	2.39	0.47
1:E:96:VAL:HG13	1:E:99:ILE:CD1	2.43	0.47
1:E:118:LYS:HA	1:E:118:LYS:HZ3	1.76	0.47
1:E:278:GLN:CD	1:E:319:ILE:HG23	2.39	0.47
1:E:406:ILE:CD1	1:E:420:ILE:HD11	2.45	0.47
1:F:110:MET:O	1:F:112:ARG:N	2.48	0.47
1:K:344:LEU:HD13	1:K:395:LEU:HD13	1.96	0.47
1:K:369:THR:HG22	1:K:371:SER:N	2.30	0.47
1:L:55:MET:HE3	1:L:305:ILE:CG2	2.43	0.47
1:L:141:ASN:ND2	1:L:141:ASN:N	2.53	0.47
1:L:257:GLU:HG2	1:L:260:LYS:HG3	1.96	0.47
2:M:10:GLY:HA2	2:M:173:TYR:CE1	2.50	0.47
2:M:43:ILE:HG23	2:M:171:LEU:HD13	1.95	0.47
2:N:3:ILE:O	2:N:121:ALA:HA	2.15	0.47
2:O:63:LYS:HB3	2:O:74:ALA:HB1	1.97	0.47
1:E:87:THR:HG23	1:E:273:SER:HB2	1.97	0.47
1:F:261:ILE:CG2	1:F:278:GLN:HG3	2.44	0.47
1:F:365:ASN:HB3	1:F:417:ASN:HD22	1.79	0.47
1:K:222:MET:HE2	1:K:223:LYS:NZ	2.29	0.47
1:L:131:ILE:CG2	1:L:132:LEU:N	2.77	0.47
1:L:147:GLU:HG2	1:L:148:GLN:N	2.29	0.47
1:L:238:GLU:CD	1:L:238:GLU:H	2.22	0.47
2:M:99:ASP:O	2:M:100:GLU:C	2.58	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:115:PRO:HG2	2:M:120:ILE:HG12	1.95	0.47
2:M:138:GLU:C	2:M:139:ASN:ND2	2.70	0.47
2:O:3:ILE:HB	2:O:122:ILE:CG1	2.44	0.47
1:E:109:LYS:HG2	1:F:296:MET:CG	2.45	0.47
1:E:110:MET:O	1:E:112:ARG:N	2.49	0.47
1:F:216:LEU:O	1:F:220:ASP:HB3	2.15	0.47
1:K:257:GLU:OE1	1:L:279:ARG:NH1	2.49	0.47
1:L:110:MET:O	1:L:112:ARG:N	2.48	0.47
1:L:132:LEU:CG	1:L:160:ARG:HB3	2.44	0.47
2:M:154:ILE:HD11	2:P:135:ALA:HB2	1.97	0.47
2:P:3:ILE:O	2:P:121:ALA:HA	2.15	0.47
2:P:138:GLU:HB3	2:P:139:ASN:HD22	1.80	0.47
1:E:124:GLU:O	1:E:127:ALA:HB3	2.15	0.46
1:E:441:PHE:C	1:F:329:ARG:HG3	2.40	0.46
1:F:147:GLU:HG2	1:F:148:GLN:N	2.30	0.46
1:K:87:THR:HG23	1:K:273:SER:HB2	1.97	0.46
1:K:406:ILE:CD1	1:K:420:ILE:HD11	2.45	0.46
1:K:408:TYR:HE2	1:L:7:ARG:HH22	0.58	0.46
1:L:312:ILE:HD11	2:O:59:LEU:O	2.15	0.46
2:M:168:ILE:HG22	2:M:169:GLU:N	2.30	0.46
2:O:99:ASP:O	2:O:100:GLU:C	2.58	0.46
1:E:88:GLU:CD	1:F:89:VAL:O	2.58	0.46
1:E:89:VAL:HG11	1:E:94:LYS:O	2.16	0.46
1:F:375:ARG:HB3	1:F:425:VAL:HG11	1.97	0.46
2:N:87:MET:O	2:N:90:LYS:HB3	2.16	0.46
1:K:110:MET:O	1:K:112:ARG:N	2.49	0.46
1:L:267:SER:O	1:L:270:PRO:HG2	2.16	0.46
1:L:312:ILE:CA	2:O:62:ARG:CA	2.55	0.46
1:L:375:ARG:HB3	1:L:425:VAL:HG11	1.97	0.46
2:O:50:THR:HG21	2:P:111:ASP:CG	2.39	0.46
2:O:168:ILE:HG22	2:O:169:GLU:N	2.30	0.46
1:E:408:TYR:C	1:F:6:PRO:HG2	2.39	0.46
1:L:145:GLN:HG2	1:L:150:GLN:H	1.64	0.46
2:O:10:GLY:HA2	2:O:173:TYR:CE1	2.50	0.46
2:P:1:THR:HB	2:P:33:LYS:HZ2	1.80	0.46
1:E:222:MET:HE2	1:E:223:LYS:NZ	2.29	0.46
1:E:354:GLN:CG	1:F:47:GLU:CB	2.93	0.46
1:K:124:GLU:O	1:K:127:ALA:HB3	2.15	0.46
1:K:408:TYR:OH	1:L:7:ARG:CG	2.63	0.46
1:L:278:GLN:OE1	1:L:319:ILE:HB	2.15	0.46
2:M:160:ILE:CD1	2:O:160:ILE:HG23	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:5:SER:O	2:N:119:LEU:HD12	2.15	0.46
1:E:361:THR:HG21	1:F:36:ARG:O	2.15	0.46
1:F:350:SER:OG	1:F:353:VAL:HG23	2.16	0.46
1:F:389:ASN:ND2	1:F:389:ASN:C	2.69	0.46
1:K:89:VAL:HG11	1:K:94:LYS:O	2.16	0.46
1:L:145:GLN:CD	1:L:145:GLN:O	2.57	0.46
1:L:350:SER:OG	1:L:353:VAL:HG23	2.16	0.46
1:L:384:ASN:HD22	1:L:394:ARG:HH11	1.63	0.46
2:M:63:LYS:HB3	2:M:74:ALA:HB1	1.97	0.46
1:E:384:ASN:ND2	1:E:394:ARG:HH11	2.13	0.46
1:E:440:ARG:HG2	1:F:316:SER:HB3	1.97	0.46
1:F:384:ASN:HD22	1:F:394:ARG:HH11	1.63	0.46
1:K:139:ALA:CA	1:K:152:PRO:CB	2.79	0.46
1:K:299:THR:O	1:K:301:HIS:N	2.49	0.46
2:N:17:ASP:OD1	2:N:33:LYS:NZ	2.49	0.46
2:O:134:ARG:HG3	2:O:134:ARG:HH11	1.81	0.46
2:O:63:LYS:CB	2:O:74:ALA:HB1	2.45	0.46
1:E:299:THR:O	1:E:301:HIS:N	2.49	0.46
1:E:369:THR:HG22	1:E:371:SER:N	2.30	0.46
1:E:401:ARG:HH21	1:F:329:ARG:H	1.63	0.46
1:F:112:ARG:HH11	1:F:112:ARG:HG3	1.81	0.46
1:K:342:ARG:HE	1:K:346:GLU:CD	2.23	0.46
1:K:432:LEU:CD1	1:K:432:LEU:N	2.78	0.46
1:L:108:VAL:HA	1:L:111:VAL:CG2	2.46	0.46
1:L:293:LYS:HG2	1:L:294:HIS:HD2	1.81	0.46
1:L:319:ILE:HD12	1:L:319:ILE:HA	1.79	0.46
2:M:135:ALA:CB	2:P:154:ILE:HD12	2.30	0.46
2:N:99:ASP:O	2:N:100:GLU:C	2.58	0.46
1:E:309:ALA:O	2:N:66:MET:SD	2.74	0.46
1:E:358:LEU:HD21	1:F:37:ARG:CB	2.46	0.46
1:E:372:GLY:O	1:E:376:ILE:HG13	2.16	0.46
1:E:441:PHE:C	1:F:329:ARG:CG	2.89	0.46
1:F:11:SER:O	1:F:14:ASP:HB2	2.15	0.46
1:L:11:SER:O	1:L:14:ASP:HB2	2.15	0.46
2:M:67:HIS:O	2:M:69:GLY:N	2.49	0.46
2:P:91:LEU:HD12	2:P:91:LEU:O	2.16	0.46
2:P:99:ASP:O	2:P:100:GLU:C	2.58	0.46
1:E:400:GLU:CD	1:F:51:LYS:HZ2	2.10	0.45
1:F:108:VAL:HA	1:F:111:VAL:CG2	2.46	0.45
1:K:110:MET:O	1:K:111:VAL:C	2.59	0.45
1:K:122:ARG:HD2	1:K:122:ARG:HB2	1.92	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:89:VAL:HG12	1:L:94:LYS:O	2.15	0.45
1:L:362:GLU:CG	1:L:411:SER:HA	2.45	0.45
1:L:365:ASN:HB3	1:L:417:ASN:HD22	1.80	0.45
2:M:145:ARG:NE	2:M:170:GLU:OE1	2.47	0.45
2:P:5:SER:O	2:P:119:LEU:HD12	2.15	0.45
1:E:122:ARG:HD2	1:E:122:ARG:HB2	1.92	0.45
1:E:291:SER:HA	1:E:296:MET:HE2	1.98	0.45
1:E:441:PHE:HD1	1:F:56:ILE:CG2	2.24	0.45
1:F:406:ILE:HG13	1:F:424:TYR:OH	2.16	0.45
1:K:231:ALA:C	1:K:233:LEU:H	2.24	0.45
1:K:293:LYS:HG2	1:K:294:HIS:CD2	2.51	0.45
1:L:384:ASN:CG	1:L:394:ARG:HD2	2.41	0.45
2:M:134:ARG:HH11	2:M:134:ARG:HG3	1.81	0.45
2:P:36:ARG:HH11	2:P:36:ARG:CB	2.21	0.45
1:E:235:ASN:ND2	1:E:235:ASN:N	2.37	0.45
1:E:358:LEU:HD23	1:F:36:ARG:C	2.41	0.45
1:K:64:THR:HG21	1:K:68:ARG:NH1	2.32	0.45
1:L:38:MET:HA	1:L:38:MET:HE3	1.98	0.45
2:P:87:MET:O	2:P:90:LYS:HB3	2.16	0.45
1:F:134:VAL:O	1:F:135:LEU:HD23	2.16	0.45
1:F:267:SER:O	1:F:270:PRO:HG2	2.16	0.45
1:K:384:ASN:ND2	1:K:394:ARG:HH11	2.14	0.45
2:M:99:ASP:HA	2:M:171:LEU:HD22	1.99	0.45
1:E:293:LYS:HG2	1:E:294:HIS:CD2	2.51	0.45
1:E:397:THR:HG23	1:F:327:PRO:HA	1.98	0.45
1:F:38:MET:HA	1:F:38:MET:HE3	1.99	0.45
1:F:238:GLU:H	1:F:238:GLU:CD	2.22	0.45
1:K:442:ILE:O	1:K:442:ILE:HG22	2.17	0.45
1:L:79:ILE:HD13	1:L:80:LYS:N	2.32	0.45
2:N:138:GLU:HB3	2:N:139:ASN:HD22	1.80	0.45
1:E:64:THR:HG21	1:E:68:ARG:NH1	2.32	0.45
1:E:92:VAL:HG11	1:F:92:VAL:HG12	1.93	0.45
1:E:110:MET:O	1:E:111:VAL:C	2.59	0.45
1:E:269:GLY:N	1:E:270:PRO:HD2	2.32	0.45
1:E:413:LEU:O	1:E:416:GLN:HG3	2.17	0.45
1:F:25:ARG:O	1:F:29:ILE:HG13	2.17	0.45
2:M:3:ILE:HD11	2:M:46:PHE:C	2.42	0.45
2:N:1:THR:HB	2:N:33:LYS:HZ2	1.80	0.45
2:O:3:ILE:HD11	2:O:46:PHE:C	2.42	0.45
2:P:17:ASP:OD1	2:P:33:LYS:NZ	2.49	0.45
2:P:116:GLU:H	2:P:116:GLU:HG2	1.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:231:ALA:C	1:E:233:LEU:H	2.24	0.45
1:K:372:GLY:O	1:K:376:ILE:HG13	2.16	0.45
1:L:315:PRO:O	1:L:318:LEU:HB2	2.17	0.45
2:O:67:HIS:O	2:O:69:GLY:N	2.49	0.45
2:P:8:ARG:HB2	2:P:144:ALA:HB2	1.98	0.45
2:P:22:LEU:HB2	2:P:27:MET:HE2	1.98	0.45
1:E:97:ASP:HB2	1:E:101:ARG:NH2	2.32	0.45
1:E:125:GLU:O	1:E:128:GLU:HB2	2.17	0.45
1:E:358:LEU:HD23	1:F:40:LEU:HD11	1.98	0.45
1:E:408:TYR:CE2	1:F:7:ARG:HG3	2.51	0.45
1:F:365:ASN:HB3	1:F:417:ASN:ND2	2.32	0.45
1:L:4:MET:HE1	1:L:73:LEU:CD1	2.44	0.45
1:E:58:PRO:HG2	1:E:61:VAL:HG11	1.99	0.45
1:E:390:ILE:HD13	1:F:323:GLN:HB3	1.99	0.45
1:E:442:ILE:C	1:F:329:ARG:CB	2.69	0.45
1:F:79:ILE:HD13	1:F:80:LYS:N	2.31	0.45
1:K:248:GLU:OE1	1:K:298:LYS:N	2.46	0.45
1:K:398:VAL:HG13	1:K:429:LEU:HD13	1.99	0.45
1:L:346:GLU:O	1:L:347:PRO:C	2.58	0.45
2:N:22:LEU:HB2	2:N:27:MET:HE2	1.98	0.45
2:O:60:PHE:CE2	2:O:97:VAL:HG21	2.52	0.45
2:P:105:ILE:CD1	2:P:120:ILE:HG23	2.44	0.45
1:E:342:ARG:HE	1:E:346:GLU:CD	2.23	0.45
1:F:119:ASN:HD22	1:F:119:ASN:HA	1.57	0.45
1:F:315:PRO:O	1:F:318:LEU:HB2	2.17	0.45
1:K:91:TYR:CZ	1:L:272:VAL:HG11	2.52	0.45
1:K:97:ASP:HB2	1:K:101:ARG:NH2	2.31	0.45
1:K:346:GLU:O	1:K:347:PRO:C	2.59	0.45
1:L:365:ASN:HB3	1:L:417:ASN:ND2	2.32	0.45
2:N:91:LEU:O	2:N:91:LEU:HD12	2.16	0.45
1:E:250:HIS:O	1:E:251:GLY:C	2.60	0.44
1:E:390:ILE:CG2	1:F:320:PRO:HA	2.46	0.44
1:F:34:ARG:NH2	1:F:250:HIS:HA	2.32	0.44
1:K:125:GLU:O	1:K:128:GLU:HB2	2.17	0.44
1:L:112:ARG:HG3	1:L:112:ARG:HH11	1.81	0.44
2:M:60:PHE:CE2	2:M:97:VAL:HG21	2.52	0.44
2:P:148:ALA:O	2:P:152:LEU:HB2	2.17	0.44
1:E:346:GLU:O	1:E:347:PRO:C	2.59	0.44
1:E:365:ASN:HB3	1:E:417:ASN:HD22	1.81	0.44
1:K:413:LEU:O	1:K:416:GLN:HG3	2.17	0.44
1:L:134:VAL:O	1:L:135:LEU:HD23	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:145:GLN:HB3	1:L:149:GLN:CG	2.47	0.44
2:N:8:ARG:HB2	2:N:144:ALA:HB2	1.98	0.44
1:E:86:PHE:HB2	1:E:277:VAL:CG1	2.48	0.44
1:E:132:LEU:HD22	1:E:132:LEU:HA	1.83	0.44
1:F:110:MET:O	1:F:111:VAL:C	2.60	0.44
1:F:406:ILE:O	1:F:410:ALA:N	2.48	0.44
1:K:358:LEU:O	1:K:361:THR:CG2	2.60	0.44
1:L:217:LYS:O	1:L:221:ALA:N	2.44	0.44
1:L:406:ILE:O	1:L:410:ALA:N	2.48	0.44
1:L:406:ILE:HG13	1:L:424:TYR:OH	2.16	0.44
2:M:92:GLU:HG3	2:M:92:GLU:O	2.16	0.44
2:N:5:SER:HB3	2:N:120:ILE:CB	2.44	0.44
2:N:90:LYS:C	2:N:90:LYS:CD	2.91	0.44
2:N:98:ALA:CB	2:N:103:SER:HB3	2.47	0.44
2:O:99:ASP:HA	2:O:171:LEU:HD22	1.98	0.44
1:E:256:ASP:O	1:E:257:GLU:HB2	2.17	0.44
1:E:398:VAL:HG13	1:E:429:LEU:HD13	1.99	0.44
1:F:141:ASN:O	1:F:142:ASN:CB	2.62	0.44
1:K:264:ARG:O	1:K:266:GLU:N	2.50	0.44
1:L:25:ARG:O	1:L:29:ILE:HG13	2.17	0.44
1:L:34:ARG:NH2	1:L:250:HIS:HA	2.32	0.44
1:E:105:ASP:HB3	1:F:296:MET:HE1	1.99	0.44
1:E:293:LYS:HG2	1:E:294:HIS:HD2	1.83	0.44
1:E:442:ILE:O	1:E:442:ILE:HG22	2.17	0.44
1:F:384:ASN:CG	1:F:394:ARG:HD2	2.42	0.44
1:K:86:PHE:HB2	1:K:277:VAL:CG1	2.48	0.44
1:K:291:SER:HA	1:K:296:MET:HE2	1.98	0.44
1:K:293:LYS:HG2	1:K:294:HIS:HD2	1.83	0.44
1:K:365:ASN:HB3	1:K:417:ASN:HD22	1.81	0.44
1:L:83:ALA:HB1	1:L:261:ILE:HG13	2.00	0.44
1:L:145:GLN:CG	1:L:150:GLN:CA	2.87	0.44
2:N:60:PHE:HE2	2:N:97:VAL:HG21	1.79	0.44
1:F:117:GLU:C	1:F:119:ASN:N	2.75	0.44
2:M:43:ILE:HG13	2:M:43:ILE:O	2.17	0.44
2:P:86:ARG:O	2:P:87:MET:C	2.61	0.44
2:P:98:ALA:CB	2:P:103:SER:HB3	2.47	0.44
1:E:135:LEU:HD13	1:E:159:PHE:CD1	2.52	0.44
1:E:264:ARG:O	1:E:266:GLU:N	2.50	0.44
1:F:62:GLY:O	1:F:66:ILE:HG13	2.18	0.44
1:F:145:GLN:CG	1:F:150:GLN:CA	2.87	0.44
1:F:293:LYS:HG2	1:F:294:HIS:HD2	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:393:ARG:HA	1:F:396:HIS:CD2	2.53	0.44
1:K:269:GLY:N	1:K:270:PRO:HD2	2.32	0.44
1:L:100:ILE:HG13	1:L:290:VAL:HG21	1.99	0.44
1:L:264:ARG:CD	2:O:62:ARG:HD3	2.38	0.44
2:N:46:PHE:HB3	2:N:57:PHE:CZ	2.53	0.44
2:N:148:ALA:O	2:N:152:LEU:HB2	2.17	0.44
2:P:88:LEU:H	2:P:88:LEU:CD2	2.28	0.44
1:E:128:GLU:C	1:E:130:ARG:N	2.75	0.44
1:F:64:THR:HG22	1:F:68:ARG:HD2	2.00	0.44
1:F:131:ILE:HD13	1:F:134:VAL:HG12	2.00	0.44
1:F:346:GLU:O	1:F:347:PRO:C	2.58	0.44
1:K:58:PRO:HG2	1:K:61:VAL:HG11	1.99	0.44
1:L:62:GLY:O	1:L:66:ILE:HG13	2.18	0.44
1:L:282:LEU:HD21	1:L:321:GLU:HG2	2.00	0.44
2:M:44:ALA:HB2	2:M:97:VAL:HG23	2.00	0.44
2:N:21:THR:HG22	2:N:22:LEU:H	1.81	0.44
2:O:36:ARG:NH1	2:O:40:ASP:HB3	2.33	0.44
2:P:62:ARG:O	2:P:65:GLU:HB2	2.17	0.44
2:P:117:ASN:C	2:P:119:LEU:N	2.76	0.44
1:E:354:GLN:CG	1:F:47:GLU:HB2	2.48	0.44
1:K:135:LEU:HD13	1:K:159:PHE:CD1	2.52	0.44
1:L:131:ILE:HD13	1:L:134:VAL:HG12	2.00	0.44
1:L:380:ALA:HA	1:L:394:ARG:HG2	2.00	0.44
2:N:36:ARG:HH11	2:N:36:ARG:CB	2.21	0.44
2:P:5:SER:HB3	2:P:120:ILE:CB	2.45	0.44
1:E:443:LEU:C	1:F:329:ARG:NH1	2.76	0.43
1:F:237:GLU:HA	1:F:237:GLU:OE2	2.18	0.43
1:F:359:MET:HE2	1:F:359:MET:HA	1.99	0.43
1:F:362:GLU:CG	1:F:411:SER:HA	2.46	0.43
1:F:380:ALA:HA	1:F:394:ARG:HG2	2.00	0.43
1:K:94:LYS:HA	1:K:94:LYS:HD3	1.74	0.43
1:L:21:ASP:OD2	1:L:25:ARG:HD2	2.18	0.43
1:L:113:VAL:O	1:L:117:GLU:HG3	2.18	0.43
2:M:21:THR:CG2	2:M:22:LEU:N	2.81	0.43
2:M:131:ALA:HB1	2:P:154:ILE:HG22	1.99	0.43
2:P:60:PHE:HE2	2:P:97:VAL:HG21	1.79	0.43
1:K:119:ASN:HD22	1:K:119:ASN:HA	1.56	0.43
1:L:118:LYS:HA	1:L:118:LYS:HE2	2.00	0.43
1:L:263:LYS:HB3	1:L:264:ARG:H	1.36	0.43
2:M:160:ILE:CG2	2:O:160:ILE:HD11	2.40	0.43
2:N:39:ASN:O	2:N:41:LYS:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:117:ASN:C	2:N:119:LEU:N	2.76	0.43
2:O:43:ILE:HG13	2:O:43:ILE:O	2.17	0.43
1:E:56:ILE:HA	1:E:308:GLY:O	2.18	0.43
1:F:34:ARG:CZ	1:F:250:HIS:HA	2.47	0.43
1:F:83:ALA:HB1	1:F:261:ILE:HG13	2.00	0.43
1:F:292:THR:C	1:F:294:HIS:N	2.73	0.43
1:K:40:LEU:O	1:K:45:ARG:NH1	2.52	0.43
1:K:120:ARG:HD2	1:K:121:TYR:N	2.33	0.43
1:K:250:HIS:O	1:K:251:GLY:C	2.60	0.43
1:K:336:THR:O	1:K:339:ASP:HB2	2.19	0.43
1:L:359:MET:HE2	1:L:359:MET:HA	1.99	0.43
2:O:92:GLU:HG3	2:O:92:GLU:O	2.16	0.43
2:P:46:PHE:HB3	2:P:57:PHE:CZ	2.53	0.43
1:E:89:VAL:HG12	1:E:94:LYS:N	2.25	0.43
1:E:436:GLU:O	1:E:437:ASP:C	2.61	0.43
1:F:21:ASP:OD2	1:F:25:ARG:HD2	2.18	0.43
1:F:89:VAL:HG12	1:F:94:LYS:O	2.15	0.43
1:F:100:ILE:HG13	1:F:290:VAL:HG21	1.99	0.43
1:F:110:MET:C	1:F:112:ARG:N	2.76	0.43
1:K:256:ASP:O	1:K:257:GLU:HB2	2.17	0.43
1:L:131:ILE:O	1:L:135:LEU:HG	2.19	0.43
1:L:238:GLU:O	1:L:242:ASP:N	2.49	0.43
2:M:36:ARG:NH1	2:M:40:ASP:HB3	2.33	0.43
1:E:59:THR:CG2	1:F:321:GLU:CD	2.92	0.43
1:E:112:ARG:O	1:E:115:ALA:N	2.51	0.43
1:K:56:ILE:HA	1:K:308:GLY:O	2.18	0.43
1:K:128:GLU:C	1:K:130:ARG:N	2.75	0.43
2:N:62:ARG:O	2:N:65:GLU:HB2	2.18	0.43
2:N:86:ARG:O	2:N:87:MET:C	2.61	0.43
2:O:21:THR:CG2	2:O:22:LEU:N	2.81	0.43
2:O:44:ALA:HB2	2:O:97:VAL:HG23	2.00	0.43
1:E:119:ASN:HD22	1:E:119:ASN:HA	1.56	0.43
1:E:241:GLN:HG2	1:E:241:GLN:O	2.18	0.43
1:E:442:ILE:CD1	1:F:329:ARG:CB	2.97	0.43
1:F:113:VAL:O	1:F:117:GLU:HG3	2.19	0.43
1:F:360:ALA:O	1:F:361:THR:C	2.62	0.43
1:K:222:MET:HE2	1:K:223:LYS:HZ2	1.83	0.43
1:L:86:PHE:HB2	1:L:277:VAL:CG1	2.47	0.43
1:L:110:MET:C	1:L:112:ARG:N	2.75	0.43
1:L:237:GLU:OE2	1:L:237:GLU:HA	2.18	0.43
1:E:89:VAL:C	1:E:91:TYR:H	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:145:GLN:HB3	1:F:149:GLN:CG	2.47	0.43
1:F:275:GLU:O	1:F:278:GLN:HB2	2.19	0.43
1:L:275:GLU:O	1:L:278:GLN:HB2	2.19	0.43
1:L:360:ALA:O	1:L:361:THR:C	2.62	0.43
2:M:98:ALA:HA	2:M:103:SER:HA	2.00	0.43
2:N:15:ALA:HB1	2:N:152:LEU:HD12	2.01	0.43
2:P:39:ASN:O	2:P:41:LYS:HG3	2.18	0.43
1:E:139:ALA:N	1:E:152:PRO:HB3	2.32	0.43
1:E:349:ALA:CB	1:F:47:GLU:CG	2.69	0.43
1:F:86:PHE:HB2	1:F:277:VAL:CG1	2.47	0.43
2:N:114:GLN:HA	2:N:115:PRO:HD2	1.84	0.43
1:E:92:VAL:HG22	1:E:93:GLY:H	1.84	0.43
1:E:336:THR:O	1:E:339:ASP:HB2	2.19	0.43
1:F:282:LEU:HD21	1:F:321:GLU:HG2	2.00	0.43
1:L:110:MET:O	1:L:111:VAL:C	2.60	0.43
1:L:409:ASP:O	1:L:410:ALA:C	2.62	0.43
2:M:87:MET:O	2:M:90:LYS:HB3	2.19	0.43
2:M:125:GLY:HA2	2:M:128:TYR:CD2	2.53	0.43
2:N:4:VAL:CG2	2:N:152:LEU:HG	2.49	0.43
2:P:21:THR:HG22	2:P:22:LEU:H	1.82	0.43
1:E:132:LEU:HD21	1:E:160:ARG:HA	2.01	0.43
1:E:264:ARG:C	1:E:266:GLU:N	2.72	0.43
1:F:293:LYS:HG2	1:F:294:HIS:CD2	2.54	0.43
1:K:89:VAL:C	1:K:91:TYR:H	2.25	0.43
1:K:131:ILE:HD12	1:K:134:VAL:HG11	2.01	0.43
1:L:117:GLU:C	1:L:119:ASN:N	2.75	0.43
1:L:136:ILE:HG22	1:L:138:PRO:CD	2.42	0.43
1:L:293:LYS:HG2	1:L:294:HIS:CD2	2.54	0.43
1:L:393:ARG:HA	1:L:396:HIS:CD2	2.53	0.43
2:M:42:VAL:HG21	2:M:64:LEU:HD13	2.01	0.43
2:M:76:VAL:HA	2:M:112:VAL:HG21	2.00	0.43
1:E:40:LEU:O	1:E:45:ARG:NH1	2.51	0.42
1:E:109:LYS:HG2	1:F:296:MET:HG3	2.01	0.42
1:E:120:ARG:HD2	1:E:121:TYR:N	2.33	0.42
1:E:354:GLN:CG	1:F:47:GLU:HB3	2.49	0.42
1:E:417:ASN:HD22	1:E:417:ASN:HA	1.65	0.42
1:F:118:LYS:HA	1:F:118:LYS:HE2	2.00	0.42
1:K:139:ALA:N	1:K:152:PRO:HB3	2.32	0.42
1:L:34:ARG:CZ	1:L:250:HIS:HA	2.47	0.42
2:N:136:LEU:O	2:N:137:LEU:C	2.62	0.42
2:N:153:ASP:OD1	2:N:164:HIS:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:13:VAL:CG1	2:O:170:GLU:HG3	2.49	0.42
2:O:98:ALA:HA	2:O:103:SER:HA	2.00	0.42
2:O:125:GLY:HA2	2:O:128:TYR:CD2	2.53	0.42
1:E:340:PHE:CD2	1:E:395:LEU:HD21	2.54	0.42
1:K:241:GLN:HG2	1:K:241:GLN:O	2.18	0.42
2:O:136:LEU:O	2:O:137:LEU:C	2.63	0.42
1:E:335:LEU:HD22	1:E:339:ASP:HB3	2.01	0.42
1:E:384:ASN:HD22	1:E:394:ARG:NH1	2.16	0.42
1:E:413:LEU:O	1:E:414:SER:C	2.63	0.42
1:F:131:ILE:O	1:F:135:LEU:HG	2.19	0.42
1:F:145:GLN:CD	1:F:149:GLN:O	2.61	0.42
1:F:257:GLU:OE1	1:F:260:LYS:NZ	2.53	0.42
1:F:375:ARG:CZ	1:F:422:ALA:HB1	2.50	0.42
1:L:18:ILE:CD1	1:L:347:PRO:HG3	2.49	0.42
1:L:384:ASN:HD22	1:L:384:ASN:HA	1.64	0.42
2:M:98:ALA:O	2:M:99:ASP:HB3	2.19	0.42
2:P:134:ARG:HH11	2:P:134:ARG:CG	2.33	0.42
1:F:112:ARG:O	1:F:115:ALA:N	2.53	0.42
1:F:310:PHE:HB3	1:F:313:ALA:O	2.19	0.42
1:K:132:LEU:HD21	1:K:160:ARG:HA	2.01	0.42
1:L:397:THR:HG21	1:L:443:LEU:HA	2.00	0.42
2:N:58:GLU:HG3	2:N:62:ARG:NE	2.34	0.42
2:N:134:ARG:HH11	2:N:134:ARG:CG	2.33	0.42
2:O:84:THR:O	2:O:85:ASP:C	2.62	0.42
2:O:87:MET:O	2:O:90:LYS:HB3	2.19	0.42
2:P:153:ASP:OD1	2:P:164:HIS:HD2	2.02	0.42
1:E:248:GLU:OE1	1:E:298:LYS:N	2.46	0.42
1:F:131:ILE:O	1:F:131:ILE:HD13	2.20	0.42
1:F:397:THR:HG21	1:F:443:LEU:HA	2.00	0.42
1:F:442:ILE:O	1:F:443:LEU:HD23	2.20	0.42
1:K:91:TYR:O	1:K:92:VAL:HG13	2.19	0.42
1:K:112:ARG:O	1:K:115:ALA:N	2.51	0.42
1:K:264:ARG:HA	2:P:62:ARG:HH22	1.84	0.42
1:K:345:THR:HG22	1:K:352:THR:HG21	2.01	0.42
2:P:4:VAL:CG2	2:P:152:LEU:HG	2.49	0.42
1:E:440:ARG:HE	1:F:316:SER:HG	1.61	0.42
1:F:130:ARG:NH1	1:F:131:ILE:CA	2.82	0.42
1:L:52:ASN:HB2	1:L:325:ARG:O	2.19	0.42
1:L:375:ARG:CZ	1:L:422:ALA:HB1	2.50	0.42
1:E:91:TYR:CE2	1:F:91:TYR:CD2	3.08	0.42
1:E:139:ALA:CA	1:E:152:PRO:CB	2.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:217:LYS:O	1:E:218:ILE:C	2.63	0.42
1:E:398:VAL:HG13	1:E:429:LEU:CD1	2.50	0.42
1:F:4:MET:HB3	1:F:8:GLU:CB	2.50	0.42
1:F:94:LYS:HZ2	1:F:98:SER:HB3	1.83	0.42
1:K:74:ALA:O	1:K:75:ASN:HB3	2.20	0.42
1:L:64:THR:HG22	1:L:68:ARG:HD2	2.00	0.42
1:E:111:VAL:CG2	1:E:243:ALA:HB2	2.49	0.42
1:E:354:GLN:OE1	1:F:48:VAL:CG2	2.67	0.42
1:F:89:VAL:C	1:F:91:TYR:H	2.27	0.42
1:F:136:ILE:O	1:F:138:PRO:HD2	2.20	0.42
1:K:111:VAL:CG2	1:K:243:ALA:HB2	2.49	0.42
1:K:340:PHE:CD2	1:K:395:LEU:HD21	2.54	0.42
1:L:89:VAL:C	1:L:91:TYR:H	2.27	0.42
1:L:246:ALA:O	1:L:247:VAL:C	2.63	0.42
1:L:398:VAL:HG13	1:L:429:LEU:HD13	2.00	0.42
1:L:442:ILE:O	1:L:443:LEU:HD23	2.20	0.42
2:N:37:LEU:HD12	2:N:37:LEU:N	2.34	0.42
2:N:169:GLU:HA	2:N:169:GLU:OE2	2.20	0.42
2:O:138:GLU:C	2:O:139:ASN:ND2	2.70	0.42
1:E:5:THR:HG1	1:E:8:GLU:HG3	1.82	0.42
1:E:329:ARG:HG3	1:E:329:ARG:NH1	2.35	0.42
1:E:345:THR:HG22	1:E:352:THR:HG21	2.01	0.42
1:F:18:ILE:CD1	1:F:347:PRO:HG3	2.49	0.42
1:L:15:LYS:HB3	1:L:348:ASN:HD21	1.85	0.42
1:L:136:ILE:O	1:L:138:PRO:HD2	2.20	0.42
1:L:257:GLU:OE1	1:L:260:LYS:NZ	2.53	0.42
2:O:42:VAL:HG21	2:O:64:LEU:HD13	2.02	0.42
2:O:140:THR:CG2	2:O:141:GLU:N	2.83	0.42
2:P:58:GLU:HG3	2:P:62:ARG:NE	2.34	0.42
2:P:136:LEU:O	2:P:137:LEU:C	2.62	0.42
1:E:131:ILE:HD12	1:E:134:VAL:HG11	2.01	0.42
1:E:411:SER:HB3	1:F:32:ARG:HH21	1.75	0.42
1:F:263:LYS:HB3	1:F:264:ARG:H	1.36	0.42
1:F:351:ILE:HG13	1:F:399:LEU:HD22	2.02	0.42
1:K:227:GLU:O	1:K:227:GLU:HG2	2.20	0.42
1:L:112:ARG:O	1:L:115:ALA:N	2.53	0.42
1:L:261:ILE:CG2	1:L:278:GLN:HG3	2.44	0.42
1:L:310:PHE:HB3	1:L:313:ALA:O	2.19	0.42
2:M:84:THR:O	2:M:85:ASP:C	2.62	0.42
2:O:76:VAL:HA	2:O:112:VAL:HG21	2.00	0.42
1:E:74:ALA:O	1:E:75:ASN:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:441:PHE:O	1:F:329:ARG:HG3	2.15	0.41
1:K:329:ARG:HG3	1:K:329:ARG:NH1	2.35	0.41
1:K:398:VAL:HG13	1:K:429:LEU:CD1	2.50	0.41
2:M:1:THR:CA	2:M:162:THR:HG22	2.50	0.41
2:M:13:VAL:CG1	2:M:170:GLU:HG3	2.49	0.41
2:O:121:ALA:O	2:O:126:GLY:HA3	2.20	0.41
1:F:15:LYS:HB3	1:F:348:ASN:HD21	1.85	0.41
1:F:229:GLU:O	1:F:232:LYS:HG2	2.20	0.41
1:F:264:ARG:HH11	1:F:312:ILE:HD12	1.85	0.41
1:L:74:ALA:O	1:L:75:ASN:HB3	2.20	0.41
1:L:91:TYR:O	1:L:92:VAL:HG12	2.20	0.41
1:L:397:THR:CG2	1:L:443:LEU:HA	2.50	0.41
2:M:148:ALA:O	2:M:152:LEU:HB2	2.19	0.41
2:N:98:ALA:HB2	2:N:103:SER:HB3	2.03	0.41
2:O:148:ALA:O	2:O:152:LEU:HB2	2.19	0.41
2:P:37:LEU:HD12	2:P:37:LEU:N	2.34	0.41
2:P:66:MET:O	2:P:67:HIS:ND1	2.53	0.41
1:E:139:ALA:CB	1:E:152:PRO:CD	2.92	0.41
1:E:310:PHE:HB2	2:N:66:MET:HE3	2.03	0.41
1:E:440:ARG:O	1:F:315:PRO:HD2	2.20	0.41
1:F:52:ASN:HB2	1:F:325:ARG:O	2.19	0.41
1:F:409:ASP:O	1:F:410:ALA:C	2.62	0.41
1:K:335:LEU:HD22	1:K:339:ASP:HB3	2.01	0.41
1:L:130:ARG:NH1	1:L:131:ILE:CA	2.83	0.41
1:L:229:GLU:O	1:L:232:LYS:HG2	2.20	0.41
2:P:15:ALA:HB1	2:P:152:LEU:HD12	2.01	0.41
2:P:22:LEU:HD12	2:P:27:MET:HE2	2.03	0.41
1:E:94:LYS:HD3	1:E:94:LYS:HA	1.74	0.41
1:E:160:ARG:O	1:E:163:LEU:HB3	2.20	0.41
1:E:257:GLU:OE1	1:F:279:ARG:CG	2.63	0.41
1:F:398:VAL:HG13	1:F:429:LEU:HD13	2.01	0.41
1:F:404:GLU:O	1:F:405:GLU:C	2.63	0.41
1:K:108:VAL:O	1:K:110:MET:N	2.54	0.41
1:K:219:LYS:CG	1:K:220:ASP:N	2.84	0.41
1:L:389:ASN:C	1:L:389:ASN:ND2	2.69	0.41
2:M:99:ASP:HA	2:M:171:LEU:CD2	2.51	0.41
2:N:121:ALA:HB1	2:N:126:GLY:O	2.20	0.41
1:E:108:VAL:O	1:E:110:MET:N	2.54	0.41
1:E:131:ILE:HD12	1:E:134:VAL:HG12	2.03	0.41
1:F:74:ALA:O	1:F:75:ASN:HB3	2.20	0.41
1:F:397:THR:CG2	1:F:443:LEU:HA	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:91:TYR:HD2	1:L:91:TYR:HA	1.76	0.41
1:L:119:ASN:HD22	1:L:119:ASN:HA	1.57	0.41
1:L:442:ILE:O	1:L:442:ILE:HG22	2.20	0.41
2:M:136:LEU:O	2:M:137:LEU:C	2.62	0.41
2:N:136:LEU:HB3	2:N:147:ILE:HG12	2.02	0.41
2:O:99:ASP:HA	2:O:171:LEU:CD2	2.50	0.41
1:E:152:PRO:O	1:E:153:SER:C	2.63	0.41
1:E:222:MET:O	1:E:226:ILE:N	2.53	0.41
1:E:282:LEU:N	1:E:283:PRO:HD2	2.35	0.41
1:F:87:THR:HG23	1:F:277:VAL:HG21	2.02	0.41
1:F:246:ALA:O	1:F:247:VAL:C	2.63	0.41
1:K:92:VAL:HG22	1:K:93:GLY:H	1.84	0.41
1:K:97:ASP:OD1	1:K:97:ASP:N	2.52	0.41
1:K:152:PRO:O	1:K:153:SER:C	2.63	0.41
1:K:160:ARG:O	1:K:163:LEU:HB3	2.20	0.41
1:L:87:THR:HG23	1:L:277:VAL:HG21	2.02	0.41
1:L:232:LYS:HB3	1:L:232:LYS:HE2	1.76	0.41
1:L:264:ARG:NH1	2:O:59:LEU:C	2.79	0.41
1:L:374:LYS:HG2	1:L:375:ARG:N	2.35	0.41
1:L:384:ASN:HD21	1:L:390:ILE:H	1.69	0.41
2:M:121:ALA:HB1	2:M:126:GLY:O	2.19	0.41
2:N:66:MET:O	2:N:67:HIS:ND1	2.53	0.41
2:N:99:ASP:HA	2:N:171:LEU:CD2	2.51	0.41
2:P:43:ILE:O	2:P:43:ILE:HG13	2.20	0.41
2:P:98:ALA:HB2	2:P:103:SER:HB3	2.03	0.41
2:P:121:ALA:HB1	2:P:126:GLY:O	2.20	0.41
2:P:169:GLU:OE2	2:P:169:GLU:HA	2.20	0.41
1:F:13:LEU:HD12	1:F:13:LEU:HA	1.93	0.41
1:F:359:MET:HG3	1:F:366:ILE:HG13	2.03	0.41
1:F:412:ASP:C	1:F:414:SER:H	2.27	0.41
1:K:417:ASN:HD22	1:K:417:ASN:HA	1.65	0.41
1:K:436:GLU:O	1:K:437:ASP:C	2.61	0.41
1:L:163:LEU:C	1:L:163:LEU:CD1	2.90	0.41
1:L:382:GLN:OE1	1:L:382:GLN:HA	2.20	0.41
2:M:121:ALA:O	2:M:126:GLY:HA3	2.20	0.41
2:N:19:GLN:HB2	2:N:163:ASN:ND2	2.36	0.41
1:K:281:LEU:HD12	1:K:281:LEU:HA	1.83	0.41
1:L:131:ILE:O	1:L:131:ILE:HD13	2.20	0.41
1:L:150:GLN:O	1:L:152:PRO:HD3	2.21	0.41
1:L:351:ILE:HG13	1:L:399:LEU:HD22	2.02	0.41
1:L:412:ASP:C	1:L:414:SER:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:98:ALA:O	2:M:99:ASP:CB	2.68	0.41
2:O:88:LEU:H	2:O:88:LEU:CD2	2.34	0.41
2:O:121:ALA:HB1	2:O:126:GLY:O	2.20	0.41
2:P:114:GLN:O	2:P:114:GLN:HG3	2.20	0.41
2:P:136:LEU:HB3	2:P:147:ILE:HG12	2.02	0.41
1:E:108:VAL:O	1:E:109:LYS:C	2.63	0.41
1:E:117:GLU:C	1:E:119:ASN:N	2.79	0.41
1:E:358:LEU:HD21	1:F:37:ARG:HB2	2.01	0.41
1:E:369:THR:HG22	1:E:372:GLY:N	2.20	0.41
1:E:388:GLU:OE2	1:F:323:GLN:NE2	2.53	0.41
1:E:404:GLU:O	1:F:29:ILE:HD13	2.20	0.41
1:F:64:THR:O	1:F:65:GLU:C	2.61	0.41
1:F:150:GLN:O	1:F:152:PRO:HD3	2.20	0.41
1:K:41:ASN:O	1:K:42:GLU:C	2.64	0.41
1:L:4:MET:HB3	1:L:8:GLU:CB	2.50	0.41
1:L:13:LEU:HD12	1:L:13:LEU:HA	1.93	0.41
1:L:42:GLU:HA	1:L:45:ARG:NH2	2.36	0.41
1:L:217:LYS:O	1:L:218:ILE:C	2.63	0.41
1:L:232:LYS:HG3	1:L:232:LYS:O	2.21	0.41
2:M:51:ALA:HB1	2:N:83:ARG:NH2	2.35	0.41
2:M:91:LEU:HD12	2:M:91:LEU:O	2.21	0.41
2:M:140:THR:CG2	2:M:141:GLU:N	2.83	0.41
2:M:154:ILE:HG23	2:P:131:ALA:CB	2.45	0.41
2:N:39:ASN:HB2	2:N:41:LYS:HE3	2.03	0.41
2:O:98:ALA:O	2:O:99:ASP:CB	2.68	0.41
2:O:98:ALA:O	2:O:99:ASP:HB3	2.19	0.41
2:P:114:GLN:HA	2:P:115:PRO:HD2	1.84	0.41
1:E:342:ARG:NH2	1:E:346:GLU:OE2	2.50	0.41
1:F:232:LYS:HG3	1:F:232:LYS:O	2.21	0.41
1:F:292:THR:C	1:F:294:HIS:H	2.28	0.41
1:K:146:THR:C	1:K:150:GLN:HB2	2.46	0.41
1:K:157:GLN:O	1:K:160:ARG:HB3	2.21	0.41
1:K:261:ILE:HD13	1:K:277:VAL:CB	2.49	0.41
1:K:282:LEU:N	1:K:283:PRO:HD2	2.35	0.41
2:N:108:GLY:C	2:N:110:GLY:N	2.79	0.41
1:E:12:GLU:O	1:E:15:LYS:HB2	2.20	0.40
1:E:97:ASP:OD1	1:E:97:ASP:N	2.52	0.40
1:E:227:GLU:HG2	1:E:227:GLU:O	2.20	0.40
1:F:40:LEU:O	1:F:45:ARG:NH1	2.54	0.40
1:F:131:ILE:C	1:F:133:ASP:N	2.79	0.40
1:F:136:ILE:HG22	1:F:138:PRO:CD	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:384:ASN:HD22	1:K:394:ARG:NH1	2.17	0.40
1:L:64:THR:O	1:L:65:GLU:C	2.61	0.40
1:L:122:ARG:CG	1:L:122:ARG:NH2	2.82	0.40
2:N:100:GLU:HG2	2:N:173:TYR:CG	2.56	0.40
1:E:75:ASN:ND2	1:E:75:ASN:O	2.54	0.40
1:E:157:GLN:O	1:E:160:ARG:HB3	2.21	0.40
1:E:248:GLU:HG3	1:E:297:VAL:HG13	2.04	0.40
1:E:393:ARG:CZ	1:F:321:GLU:HA	2.46	0.40
1:K:75:ASN:O	1:K:75:ASN:ND2	2.54	0.40
1:K:139:ALA:N	1:K:152:PRO:CB	2.85	0.40
1:K:161:LYS:C	1:K:163:LEU:N	2.79	0.40
1:K:217:LYS:O	1:K:218:ILE:C	2.63	0.40
1:L:309:ALA:CA	2:O:66:MET:CE	2.94	0.40
1:E:53:ILE:HG12	1:E:328:ILE:CG2	2.51	0.40
1:E:130:ARG:O	1:E:133:ASP:HB3	2.22	0.40
1:E:219:LYS:CG	1:E:220:ASP:N	2.84	0.40
1:K:4:MET:HB2	1:K:8:GLU:HB2	2.03	0.40
1:K:12:GLU:O	1:K:15:LYS:HB2	2.20	0.40
1:K:130:ARG:O	1:K:133:ASP:HB3	2.22	0.40
1:K:413:LEU:O	1:K:414:SER:C	2.63	0.40
1:L:292:THR:C	1:L:294:HIS:H	2.28	0.40
2:N:22:LEU:HD12	2:N:27:MET:HE2	2.03	0.40
2:N:43:ILE:O	2:N:43:ILE:HG13	2.21	0.40
2:N:62:ARG:HA	2:N:65:GLU:HG3	2.03	0.40
2:N:105:ILE:CD1	2:N:120:ILE:HG23	2.44	0.40
1:F:264:ARG:CZ	2:M:62:ARG:HG3	2.20	0.40
1:F:382:GLN:OE1	1:F:382:GLN:HA	2.20	0.40
1:F:406:ILE:HD13	1:F:418:ILE:HG21	2.02	0.40
1:K:53:ILE:HG12	1:K:328:ILE:CG2	2.51	0.40
1:K:222:MET:O	1:K:226:ILE:N	2.53	0.40
1:L:97:ASP:OD1	1:L:97:ASP:N	2.54	0.40
1:L:359:MET:HG3	1:L:366:ILE:HG13	2.02	0.40
2:M:88:LEU:H	2:M:88:LEU:CD2	2.33	0.40
2:M:154:ILE:HD13	2:P:131:ALA:O	2.21	0.40
2:N:121:ALA:O	2:N:126:GLY:HA3	2.21	0.40
2:P:121:ALA:O	2:P:126:GLY:HA3	2.21	0.40
1:E:235:ASN:HA	1:E:236:PRO:HD2	1.88	0.40
1:F:217:LYS:O	1:F:218:ILE:C	2.63	0.40
1:F:374:LYS:HG2	1:F:375:ARG:N	2.35	0.40
1:F:442:ILE:O	1:F:442:ILE:HG22	2.20	0.40
1:K:108:VAL:O	1:K:109:LYS:C	2.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:117:GLU:C	1:K:119:ASN:N	2.79	0.40
1:K:131:ILE:HD12	1:K:134:VAL:HG12	2.02	0.40
1:K:217:LYS:CB	1:K:220:ASP:HB3	2.52	0.40
1:L:38:MET:HE3	1:L:45:ARG:HD2	2.04	0.40
1:L:266:GLU:HB3	1:L:267:SER:H	1.75	0.40
1:L:421:ASP:OD2	1:L:423:ASP:HB2	2.21	0.40
2:M:88:LEU:HD22	2:M:88:LEU:N	2.36	0.40
2:N:114:GLN:O	2:N:114:GLN:HG3	2.19	0.40
2:O:91:LEU:HD12	2:O:91:LEU:O	2.21	0.40
2:P:62:ARG:HA	2:P:65:GLU:HG3	2.03	0.40
2:P:140:THR:HG22	2:P:142:LEU:HG	2.00	0.40

All (305) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:51:LYS:CG	1:L:400:GLU:OE1[3_665]	0.41	1.79
1:K:35:TRP:CE3	1:L:362:GLU:OE2[3_665]	0.55	1.65
1:K:47:GLU:O	1:L:354:GLN:OE1[3_665]	0.59	1.61
1:E:316:SER:CB	1:F:440:ARG:O[2_655]	0.62	1.58
1:K:315:PRO:CA	1:L:440:ARG:O[3_665]	0.66	1.54
1:K:32:ARG:NE	1:L:411:SER:OG[3_665]	0.69	1.51
1:K:33:ASN:OD1	1:L:407:SER:OG[3_665]	0.73	1.47
1:K:36:ARG:NE	1:L:410:ALA:CB[3_665]	0.74	1.46
1:K:35:TRP:CE3	1:L:362:GLU:CD[3_665]	0.75	1.45
1:E:36:ARG:NE	1:F:362:GLU:OE1[2_655]	0.76	1.44
1:E:314:LYS:CG	1:F:441:PHE:CZ[2_655]	0.78	1.42
1:K:32:ARG:CZ	1:L:411:SER:CB[3_665]	0.80	1.40
1:K:51:LYS:NZ	1:L:355:TYR:CZ[3_665]	0.81	1.39
1:K:48:VAL:CG1	1:L:358:LEU:CD1[3_665]	0.82	1.38
1:K:36:ARG:NH2	1:L:410:ALA:N[3_665]	0.85	1.35
1:K:316:SER:OG	1:L:440:ARG:CG[3_665]	0.88	1.32
1:E:314:LYS:CD	1:F:441:PHE:CE2[2_655]	0.89	1.31
2:O:83:ARG:NE	2:P:90:LYS:CD[2_655]	0.93	1.27
1:F:427:LYS:NZ	1:L:149:GLN:OE1[4_545]	0.97	1.23
1:K:329:ARG:NH1	1:L:443:LEU:N[3_665]	0.97	1.23
1:K:323:GLN:OE1	1:L:394:ARG:NH2[3_665]	0.99	1.21
1:K:40:LEU:CD2	1:L:357:ALA:O[3_665]	1.00	1.20
1:K:32:ARG:NH2	1:L:411:SER:CB[3_665]	1.02	1.18
1:K:47:GLU:C	1:L:354:GLN:OE1[3_665]	1.02	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:28:ALA:CB	1:L:408:TYR:CE1[3_665]	1.04	1.16
1:K:315:PRO:CG	1:L:441:PHE:CA[3_665]	1.09	1.11
1:K:329:ARG:N	1:L:401:ARG:NH2[3_665]	1.09	1.11
1:K:35:TRP:CD2	1:L:362:GLU:OE2[3_665]	1.10	1.10
1:K:315:PRO:C	1:L:440:ARG:O[3_665]	1.11	1.09
1:F:149:GLN:OE1	1:F:367:GLU:OE1[5_556]	1.12	1.08
1:E:314:LYS:CG	1:F:441:PHE:CE2[2_655]	1.13	1.07
1:K:51:LYS:NZ	1:L:355:TYR:CE2[3_665]	1.15	1.05
1:E:316:SER:CB	1:F:440:ARG:C[2_655]	1.17	1.03
1:K:310:PHE:CG	1:L:441:PHE:CE1[3_665]	1.18	1.02
1:K:40:LEU:CG	1:L:357:ALA:O[3_665]	1.19	1.01
1:K:320:PRO:CB	1:L:390:ILE:CB[3_665]	1.19	1.01
1:K:320:PRO:CB	1:L:390:ILE:CG2[3_665]	1.19	1.01
1:K:37:ARG:CG	1:L:358:LEU:CD2[3_665]	1.20	1.00
1:K:47:GLU:O	1:L:354:GLN:CD[3_665]	1.21	0.99
1:K:47:GLU:OE1	1:L:349:ALA:O[3_665]	1.22	0.98
1:K:6:PRO:CG	1:L:408:TYR:O[3_665]	1.23	0.97
1:K:310:PHE:CB	1:L:441:PHE:CE1[3_665]	1.24	0.96
1:K:328:ILE:CG2	1:L:404:GLU:OE1[3_665]	1.24	0.96
1:E:316:SER:CA	1:F:440:ARG:O[2_655]	1.26	0.94
1:K:36:ARG:CZ	1:L:410:ALA:CB[3_665]	1.26	0.94
1:K:323:GLN:O	1:L:397:THR:OG1[3_665]	1.27	0.93
1:K:315:PRO:CB	1:L:441:PHE:CA[3_665]	1.28	0.92
1:K:39:GLN:CB	1:L:361:THR:O[3_665]	1.30	0.90
1:K:310:PHE:CB	1:L:441:PHE:CZ[3_665]	1.30	0.90
2:O:83:ARG:CD	2:P:90:LYS:NZ[2_655]	1.30	0.90
1:K:32:ARG:NE	1:L:411:SER:CB[3_665]	1.31	0.89
1:K:51:LYS:CB	1:L:400:GLU:OE1[3_665]	1.31	0.89
1:K:316:SER:OG	1:L:440:ARG:CD[3_665]	1.32	0.88
1:F:427:LYS:CE	1:L:149:GLN:OE1[4_545]	1.34	0.86
1:K:47:GLU:CB	1:L:354:GLN:CG[3_665]	1.34	0.86
1:K:39:GLN:CB	1:L:361:THR:C[3_665]	1.36	0.84
1:K:329:ARG:NH1	1:L:442:ILE:C[3_665]	1.36	0.84
1:K:35:TRP:CZ3	1:L:362:GLU:OE2[3_665]	1.37	0.83
1:K:36:ARG:O	1:L:361:THR:CB[3_665]	1.37	0.83
1:K:51:LYS:CG	1:L:400:GLU:CD[3_665]	1.37	0.83
1:K:40:LEU:CD1	1:L:357:ALA:C[3_665]	1.38	0.82
1:E:29:ILE:CD1	1:F:408:TYR:CA[2_655]	1.39	0.81
1:K:44:LEU:CB	1:L:357:ALA:CB[3_665]	1.40	0.80
1:E:316:SER:OG	1:F:440:ARG:O[2_655]	1.41	0.79
1:K:51:LYS:NZ	1:L:355:TYR:OH[3_665]	1.42	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:329:ARG:CB	1:L:442:ILE:CG2[3_665]	1.42	0.78
2:M:116:GLU:OE1	2:N:29:GLY:N[3_665]	1.42	0.78
1:K:32:ARG:CZ	1:L:411:SER:OG[3_665]	1.43	0.77
1:K:329:ARG:O	1:L:401:ARG:NH1[3_665]	1.43	0.77
1:E:314:LYS:CB	1:F:441:PHE:CZ[2_655]	1.44	0.76
1:K:48:VAL:CG2	1:L:354:GLN:O[3_665]	1.44	0.76
1:K:320:PRO:CG	1:L:390:ILE:CG2[3_665]	1.44	0.76
2:M:116:GLU:OE1	2:N:28:LYS:CA[3_665]	1.44	0.76
1:K:40:LEU:CD1	1:L:358:LEU:N[3_665]	1.45	0.75
1:E:36:ARG:NE	1:F:362:GLU:CD[2_655]	1.46	0.74
1:K:315:PRO:CG	1:L:441:PHE:CB[3_665]	1.47	0.73
2:M:116:GLU:OE1	2:N:28:LYS:C[3_665]	1.47	0.73
1:K:47:GLU:C	1:L:354:GLN:CD[3_665]	1.48	0.72
2:O:83:ARG:CZ	2:P:90:LYS:CD[2_655]	1.48	0.72
1:K:33:ASN:CG	1:L:407:SER:OG[3_665]	1.49	0.71
1:K:329:ARG:CG	1:L:442:ILE:O[3_665]	1.52	0.68
1:E:36:ARG:CZ	1:F:362:GLU:OE1[2_655]	1.54	0.66
1:K:320:PRO:CA	1:L:390:ILE:CG2[3_665]	1.54	0.66
2:O:83:ARG:CD	2:P:90:LYS:CE[2_655]	1.54	0.66
1:K:35:TRP:CZ3	1:L:362:GLU:CG[3_665]	1.55	0.65
1:K:39:GLN:CG	1:L:361:THR:O[3_665]	1.55	0.65
1:K:48:VAL:CG1	1:L:358:LEU:CG[3_665]	1.55	0.65
1:K:51:LYS:CE	1:L:355:TYR:CE2[3_665]	1.55	0.65
1:K:315:PRO:CB	1:L:441:PHE:N[3_665]	1.55	0.65
1:E:314:LYS:CA	1:F:441:PHE:CE1[2_655]	1.56	0.64
1:K:35:TRP:CZ3	1:L:362:GLU:CD[3_665]	1.56	0.64
2:O:116:GLU:OE1	2:P:28:LYS:CE[2_655]	1.57	0.63
1:K:6:PRO:O	1:L:408:TYR:OH[3_665]	1.58	0.62
1:K:36:ARG:NH2	1:L:410:ALA:CA[3_665]	1.58	0.62
1:K:316:SER:N	1:L:440:ARG:CA[3_665]	1.58	0.62
1:K:328:ILE:CB	1:L:404:GLU:OE1[3_665]	1.58	0.62
1:E:7:ARG:NE	1:F:412:ASP:OD2[2_655]	1.59	0.61
1:K:40:LEU:CD1	1:L:357:ALA:O[3_665]	1.60	0.60
1:K:314:LYS:CD	1:L:437:ASP:OD2[3_665]	1.60	0.60
1:K:315:PRO:CB	1:L:440:ARG:O[3_665]	1.60	0.60
1:K:327:PRO:CB	1:L:400:GLU:CB[3_665]	1.60	0.60
1:K:29:ILE:CG1	1:L:408:TYR:CB[3_665]	1.62	0.58
1:K:39:GLN:CB	1:L:361:THR:CA[3_665]	1.62	0.58
1:K:320:PRO:O	1:L:390:ILE:CD1[3_665]	1.62	0.58
1:E:25:ARG:CB	1:F:408:TYR:CZ[2_655]	1.63	0.57
1:F:149:GLN:CD	1:F:367:GLU:OE1[5_556]	1.64	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:321:GLU:CG	1:L:393:ARG:NH1[3_665]	1.65	0.55
1:K:328:ILE:CG1	1:L:404:GLU:OE1[3_665]	1.66	0.54
1:E:315:PRO:CD	1:F:441:PHE:CD1[2_655]	1.67	0.53
1:K:5:THR:CG2	1:L:412:ASP:OD1[3_665]	1.67	0.53
1:K:316:SER:CB	1:L:440:ARG:CG[3_665]	1.67	0.53
1:K:329:ARG:CG	1:L:442:ILE:CA[3_665]	1.67	0.53
1:E:25:ARG:CA	1:F:408:TYR:CE1[2_655]	1.68	0.52
1:K:36:ARG:O	1:L:358:LEU:O[3_665]	1.69	0.51
1:K:39:GLN:N	1:L:361:THR:OG1[3_665]	1.69	0.51
1:K:315:PRO:N	1:L:440:ARG:O[3_665]	1.69	0.51
1:E:25:ARG:C	1:F:408:TYR:CE1[2_655]	1.70	0.50
1:K:315:PRO:CD	1:L:441:PHE:CD2[3_665]	1.71	0.49
1:K:315:PRO:CB	1:L:440:ARG:C[3_665]	1.71	0.49
1:L:416:GLN:NE2	2:P:149:GLU:OE1[4_655]	1.71	0.49
1:K:35:TRP:CE3	1:L:362:GLU:OE1[3_665]	1.72	0.48
1:K:315:PRO:CG	1:L:441:PHE:CG[3_665]	1.72	0.48
1:E:29:ILE:CD1	1:F:408:TYR:CB[2_655]	1.73	0.47
1:K:32:ARG:CD	1:L:411:SER:OG[3_665]	1.74	0.46
1:K:315:PRO:CA	1:L:440:ARG:C[3_665]	1.74	0.46
1:K:316:SER:OG	1:L:440:ARG:CB[3_665]	1.74	0.46
1:E:36:ARG:CB	1:F:361:THR:CG2[2_655]	1.75	0.45
1:E:316:SER:OG	1:F:440:ARG:C[2_655]	1.75	0.45
1:K:32:ARG:NH2	1:L:411:SER:CA[3_665]	1.75	0.45
2:O:83:ARG:CD	2:P:90:LYS:CD[2_655]	1.75	0.45
1:E:314:LYS:CB	1:F:441:PHE:CE1[2_655]	1.76	0.44
1:K:329:ARG:CG	1:L:442:ILE:C[3_665]	1.76	0.44
1:E:25:ARG:O	1:F:408:TYR:CE1[2_655]	1.77	0.43
1:K:321:GLU:CG	1:L:393:ARG:CZ[3_665]	1.78	0.42
1:K:329:ARG:NH2	1:L:443:LEU:C[3_665]	1.78	0.42
1:K:329:ARG:CA	1:L:401:ARG:NH2[3_665]	1.78	0.42
1:K:36:ARG:O	1:L:361:THR:CG2[3_665]	1.79	0.41
1:K:47:GLU:CA	1:L:354:GLN:CD[3_665]	1.79	0.41
1:K:323:GLN:OE1	1:L:394:ARG:CZ[3_665]	1.79	0.41
1:E:314:LYS:CB	1:F:441:PHE:CE2[2_655]	1.80	0.40
1:K:316:SER:N	1:L:440:ARG:CB[3_665]	1.80	0.40
1:K:328:ILE:CD1	1:L:404:GLU:CG[3_665]	1.80	0.40
1:K:328:ILE:CD1	1:L:404:GLU:OE1[3_665]	1.80	0.40
2:M:116:GLU:CD	2:N:29:GLY:N[3_665]	1.80	0.40
1:K:44:LEU:CD2	1:L:353:VAL:O[3_665]	1.81	0.39
1:K:47:GLU:OE2	1:L:349:ALA:CB[3_665]	1.81	0.39
1:E:7:ARG:CZ	1:F:412:ASP:OD2[2_655]	1.82	0.38

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:33:ASN:OD1	1:L:407:SER:CB[3_665]	1.83	0.37
1:K:329:ARG:CG	1:L:442:ILE:CG2[3_665]	1.83	0.37
2:M:80:LYS:CE	2:N:87:MET:CE[3_665]	1.83	0.37
2:M:116:GLU:OE2	2:N:29:GLY:N[3_665]	1.83	0.37
1:E:36:ARG:O	1:F:361:THR:OG1[2_655]	1.84	0.36
1:E:316:SER:N	1:F:440:ARG:O[2_655]	1.84	0.36
1:K:6:PRO:CB	1:L:408:TYR:CD2[3_665]	1.84	0.36
1:K:37:ARG:CB	1:L:358:LEU:CD2[3_665]	1.84	0.36
1:K:40:LEU:CD1	1:L:358:LEU:CA[3_665]	1.84	0.36
1:K:28:ALA:C	1:L:408:TYR:CD1[3_665]	1.85	0.35
1:K:329:ARG:NH2	1:L:443:LEU:OXT[3_665]	1.85	0.35
1:K:37:ARG:O	1:L:361:THR:OG1[3_665]	1.86	0.34
1:K:51:LYS:CD	1:L:400:GLU:OE1[3_665]	1.86	0.34
1:K:329:ARG:C	1:L:401:ARG:NH2[3_665]	1.86	0.34
1:K:51:LYS:CD	1:L:400:GLU:OE2[3_665]	1.87	0.33
1:E:25:ARG:CG	1:F:408:TYR:OH[2_655]	1.88	0.32
1:K:5:THR:CB	1:L:412:ASP:OD1[3_665]	1.88	0.32
1:K:51:LYS:CE	1:L:400:GLU:OE2[3_665]	1.88	0.32
1:K:315:PRO:CG	1:L:441:PHE:N[3_665]	1.88	0.32
1:K:316:SER:OG	1:L:440:ARG:NE[3_665]	1.88	0.32
1:K:321:GLU:CA	1:L:393:ARG:CD[3_665]	1.88	0.32
1:K:329:ARG:N	1:L:401:ARG:CZ[3_665]	1.88	0.32
1:K:329:ARG:CB	1:L:442:ILE:CB[3_665]	1.88	0.32
2:M:80:LYS:CE	2:N:87:MET:SD[3_665]	1.88	0.32
1:K:47:GLU:CA	1:L:354:GLN:CG[3_665]	1.89	0.31
1:K:47:GLU:CD	1:L:349:ALA:CB[3_665]	1.89	0.31
1:K:316:SER:N	1:L:440:ARG:O[3_665]	1.89	0.31
2:O:83:ARG:NE	2:P:90:LYS:CE[2_655]	1.89	0.31
1:K:40:LEU:N	1:L:361:THR:OG1[3_665]	1.90	0.30
1:K:47:GLU:C	1:L:354:GLN:CG[3_665]	1.90	0.30
1:K:315:PRO:C	1:L:440:ARG:C[3_665]	1.90	0.30
1:K:328:ILE:CG1	1:L:404:GLU:CD[3_665]	1.90	0.30
1:K:329:ARG:O	1:L:401:ARG:CZ[3_665]	1.90	0.30
1:E:314:LYS:CD	1:F:441:PHE:CD2[2_655]	1.92	0.28
1:K:36:ARG:NH1	1:L:406:ILE:O[3_665]	1.92	0.28
1:K:321:GLU:CB	1:L:393:ARG:CD[3_665]	1.92	0.28
1:K:323:GLN:CD	1:L:394:ARG:NH2[3_665]	1.92	0.28
2:M:83:ARG:NH1	2:N:92:GLU:OE2[3_665]	1.92	0.28
1:K:29:ILE:N	1:L:408:TYR:CD1[3_665]	1.93	0.27
1:K:44:LEU:CG	1:L:357:ALA:CB[3_665]	1.93	0.27
1:K:329:ARG:CZ	1:L:442:ILE:C[3_665]	1.93	0.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:84:THR:CG2	2:P:86:ARG:NH1[2_655]	1.93	0.27
1:E:7:ARG:NH2	1:F:412:ASP:OD2[2_655]	1.94	0.26
1:K:35:TRP:CE2	1:L:362:GLU:OE2[3_665]	1.94	0.26
1:K:329:ARG:O	1:L:401:ARG:NH2[3_665]	1.94	0.26
1:K:329:ARG:NE	1:L:442:ILE:O[3_665]	1.94	0.26
2:N:24:ASN:CA	2:P:160:ILE:CD1[2_655]	1.94	0.26
1:E:25:ARG:CB	1:F:408:TYR:CE1[2_655]	1.95	0.25
1:E:316:SER:CB	1:F:440:ARG:CA[2_655]	1.95	0.25
1:K:320:PRO:CA	1:L:390:ILE:CB[3_665]	1.95	0.25
1:E:25:ARG:CA	1:F:408:TYR:OH[2_655]	1.96	0.24
1:E:25:ARG:CA	1:F:408:TYR:CZ[2_655]	1.96	0.24
1:K:36:ARG:NH2	1:L:410:ALA:CB[3_665]	1.96	0.24
1:K:315:PRO:CD	1:L:441:PHE:CG[3_665]	1.96	0.24
1:K:316:SER:N	1:L:440:ARG:C[3_665]	1.96	0.24
1:K:327:PRO:O	1:L:401:ARG:CB[3_665]	1.96	0.24
2:O:83:ARG:NH2	2:P:90:LYS:CE[2_655]	1.96	0.24
2:O:116:GLU:OE2	2:P:30:ASN:ND2[2_655]	1.96	0.24
1:K:36:ARG:C	1:L:361:THR:CG2[3_665]	1.97	0.23
1:K:36:ARG:CZ	1:L:410:ALA:CA[3_665]	1.97	0.23
1:K:323:GLN:C	1:L:397:THR:OG1[3_665]	1.97	0.23
2:N:25:THR:CG2	2:P:158:ILE:O[2_655]	1.97	0.23
1:K:6:PRO:CG	1:L:408:TYR:C[3_665]	1.98	0.22
1:K:28:ALA:CB	1:L:408:TYR:CZ[3_665]	1.98	0.22
2:O:84:THR:CG2	2:P:86:ARG:NE[2_655]	1.98	0.22
1:K:327:PRO:CG	1:L:400:GLU:CG[3_665]	1.99	0.21
1:K:6:PRO:CB	1:L:408:TYR:CE2[3_665]	2.00	0.20
1:K:44:LEU:CD1	1:L:357:ALA:CB[3_665]	2.00	0.20
1:K:328:ILE:C	1:L:401:ARG:NH2[3_665]	2.00	0.20
1:K:329:ARG:NH1	1:L:443:LEU:CA[3_665]	2.00	0.20
1:E:36:ARG:CD	1:F:362:GLU:OE1[2_655]	2.01	0.19
1:K:35:TRP:CE3	1:L:362:GLU:CG[3_665]	2.01	0.19
1:K:329:ARG:CZ	1:L:443:LEU:N[3_665]	2.01	0.19
1:E:314:LYS:CD	1:F:441:PHE:CZ[2_655]	2.02	0.18
1:K:28:ALA:CA	1:L:408:TYR:CE1[3_665]	2.02	0.18
1:K:28:ALA:CB	1:L:408:TYR:CD1[3_665]	2.02	0.18
1:K:36:ARG:CD	1:L:410:ALA:CB[3_665]	2.02	0.18
1:K:310:PHE:CD2	1:L:441:PHE:CE1[3_665]	2.02	0.18
1:E:314:LYS:CE	1:F:437:ASP:OD2[2_655]	2.03	0.17
1:K:29:ILE:CD1	1:L:404:GLU:O[3_665]	2.03	0.17
1:K:39:GLN:C	1:L:361:THR:CA[3_665]	2.03	0.17
1:K:321:GLU:CG	1:L:393:ARG:NE[3_665]	2.03	0.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:427:LYS:NZ	1:L:149:GLN:CD[4_545]	2.04	0.16
1:K:320:PRO:CB	1:L:390:ILE:CA[3_665]	2.04	0.16
1:K:321:GLU:CB	1:L:393:ARG:NE[3_665]	2.04	0.16
1:K:327:PRO:CG	1:L:400:GLU:CB[3_665]	2.04	0.16
1:L:416:GLN:OE1	2:P:149:GLU:OE2[4_655]	2.04	0.16
1:K:40:LEU:CG	1:L:357:ALA:C[3_665]	2.05	0.15
1:K:47:GLU:CA	1:L:354:GLN:OE1[3_665]	2.05	0.15
1:K:47:GLU:CD	1:L:349:ALA:O[3_665]	2.05	0.15
1:K:51:LYS:CD	1:L:400:GLU:CD[3_665]	2.05	0.15
1:K:54:LEU:CD2	1:L:441:PHE:O[3_665]	2.05	0.15
1:K:328:ILE:CD1	1:L:404:GLU:CD[3_665]	2.05	0.15
1:E:25:ARG:CB	1:F:408:TYR:OH[2_655]	2.06	0.14
2:M:83:ARG:NH1	2:N:92:GLU:CD[3_665]	2.06	0.14
2:M:113:VAL:CG1	2:N:27:MET:SD[3_665]	2.06	0.14
1:E:327:PRO:CB	1:F:400:GLU:CG[2_655]	2.07	0.13
1:K:329:ARG:CB	1:L:442:ILE:CD1[3_665]	2.07	0.13
1:K:329:ARG:CD	1:L:442:ILE:O[3_665]	2.07	0.13
1:K:36:ARG:NH2	1:L:406:ILE:O[3_665]	2.08	0.12
1:K:51:LYS:NZ	1:L:355:TYR:CE1[3_665]	2.08	0.12
1:K:315:PRO:N	1:L:440:ARG:C[3_665]	2.08	0.12
1:K:35:TRP:CD2	1:L:362:GLU:CD[3_665]	2.09	0.11
1:K:48:VAL:CB	1:L:358:LEU:CG[3_665]	2.09	0.11
1:K:310:PHE:CG	1:L:441:PHE:CZ[3_665]	2.09	0.11
1:K:329:ARG:CZ	1:L:442:ILE:O[3_665]	2.09	0.11
1:K:329:ARG:CG	1:L:442:ILE:CB[3_665]	2.09	0.11
1:K:36:ARG:C	1:L:358:LEU:O[3_665]	2.10	0.10
2:M:116:GLU:CD	2:N:28:LYS:C[3_665]	2.10	0.10
1:E:36:ARG:CA	1:F:361:THR:CG2[2_655]	2.11	0.09
1:K:35:TRP:O	1:L:361:THR:CG2[3_665]	2.11	0.09
1:K:36:ARG:NH1	1:L:407:SER:CA[3_665]	2.11	0.09
1:K:36:ARG:CZ	1:L:410:ALA:N[3_665]	2.11	0.09
1:K:36:ARG:NH2	1:L:409:ASP:C[3_665]	2.11	0.09
1:K:47:GLU:OE1	1:L:349:ALA:C[3_665]	2.11	0.09
1:K:51:LYS:CG	1:L:400:GLU:OE2[3_665]	2.11	0.09
2:O:83:ARG:CZ	2:P:90:LYS:CE[2_655]	2.11	0.09
1:K:32:ARG:NH1	1:L:411:SER:CB[3_665]	2.12	0.08
1:K:35:TRP:CH2	1:L:362:GLU:OE2[3_665]	2.12	0.08
1:K:40:LEU:CD2	1:L:357:ALA:C[3_665]	2.12	0.08
1:K:314:LYS:CG	1:L:437:ASP:OD2[3_665]	2.12	0.08
1:K:315:PRO:CD	1:L:441:PHE:N[3_665]	2.12	0.08
1:E:25:ARG:O	1:F:408:TYR:CD1[2_655]	2.13	0.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:314:LYS:CG	1:F:441:PHE:CE1[2_655]	2.13	0.07
1:E:314:LYS:CA	1:F:441:PHE:CZ[2_655]	2.13	0.07
1:K:39:GLN:CA	1:L:361:THR:CA[3_665]	2.13	0.07
1:K:324:GLY:CA	1:L:397:THR:OG1[3_665]	2.13	0.07
1:K:329:ARG:CD	1:L:442:ILE:CA[3_665]	2.13	0.07
2:M:83:ARG:NH1	2:N:92:GLU:CG[3_665]	2.13	0.07
2:N:24:ASN:CA	2:P:160:ILE:CG1[2_655]	2.13	0.07
2:O:83:ARG:CG	2:P:90:LYS:NZ[2_655]	2.13	0.07
1:E:36:ARG:NH2	1:F:362:GLU:OE1[2_655]	2.14	0.06
1:K:310:PHE:CD1	1:L:441:PHE:CE1[3_665]	2.14	0.06
1:K:328:ILE:CG2	1:L:404:GLU:CD[3_665]	2.14	0.06
1:K:310:PHE:CG	1:L:441:PHE:CD1[3_665]	2.15	0.05
1:E:25:ARG:CG	1:F:408:TYR:CZ[2_655]	2.16	0.04
1:E:36:ARG:CZ	1:F:362:GLU:CD[2_655]	2.16	0.04
1:K:44:LEU:CD1	1:L:357:ALA:CA[3_665]	2.16	0.04
1:K:48:VAL:CG2	1:L:354:GLN:C[3_665]	2.16	0.04
1:K:48:VAL:N	1:L:354:GLN:OE1[3_665]	2.16	0.04
1:K:316:SER:CB	1:L:440:ARG:CB[3_665]	2.16	0.04
1:K:39:GLN:CG	1:L:361:THR:C[3_665]	2.17	0.03
1:K:39:GLN:CD	1:L:361:THR:O[3_665]	2.17	0.03
1:K:39:GLN:N	1:L:361:THR:CG2[3_665]	2.17	0.03
1:K:39:GLN:C	1:L:361:THR:OG1[3_665]	2.17	0.03
1:K:39:GLN:O	1:L:361:THR:CA[3_665]	2.17	0.03
1:K:315:PRO:O	1:L:440:ARG:O[3_665]	2.17	0.03
1:K:323:GLN:OE1	1:L:394:ARG:NH1[3_665]	2.17	0.03
2:O:83:ARG:NE	2:P:90:LYS:CG[2_655]	2.17	0.03
1:E:29:ILE:CD1	1:F:408:TYR:N[2_655]	2.18	0.02
1:K:6:PRO:CD	1:L:408:TYR:O[3_665]	2.18	0.02
1:K:33:ASN:ND2	1:L:359:MET:CE[3_665]	2.18	0.02
1:K:328:ILE:CG1	1:L:404:GLU:CG[3_665]	2.18	0.02
1:E:36:ARG:NE	1:F:362:GLU:CG[2_655]	2.19	0.01
1:E:48:VAL:CG1	1:F:358:LEU:CD2[2_655]	2.19	0.01
1:K:32:ARG:NH2	1:L:411:SER:C[3_665]	2.19	0.01
1:K:39:GLN:CA	1:L:361:THR:OG1[3_665]	2.19	0.01
1:K:39:GLN:N	1:L:361:THR:CB[3_665]	2.19	0.01

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	E	389/443 (88%)	335 (86%)	40 (10%)	14 (4%)	2	20
1	F	389/443 (88%)	329 (85%)	41 (10%)	19 (5%)	1	16
1	K	389/443 (88%)	335 (86%)	40 (10%)	14 (4%)	2	20
1	L	389/443 (88%)	329 (85%)	41 (10%)	19 (5%)	1	16
2	M	171/175 (98%)	145 (85%)	18 (10%)	8 (5%)	2	16
2	N	171/175 (98%)	143 (84%)	23 (14%)	5 (3%)	3	23
2	O	154/175 (88%)	132 (86%)	14 (9%)	8 (5%)	1	15
2	P	171/175 (98%)	143 (84%)	23 (14%)	5 (3%)	3	23
All	All	2223/2472 (90%)	1891 (85%)	240 (11%)	92 (4%)	2	18

All (92) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	92	VAL
1	E	140	LYS
1	E	154	ALA
1	E	300	ASP
1	F	92	VAL
1	F	139	ALA
1	F	142	ASN
1	F	154	ALA
1	F	263	LYS
1	F	266	GLU
1	K	92	VAL
1	K	140	LYS
1	K	154	ALA
1	K	300	ASP
1	L	92	VAL
1	L	139	ALA
1	L	142	ASN

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Mol	Chain	Res	Type
1	L	154	ALA
1	L	263	LYS
1	L	266	GLU
2	M	116	GLU
2	O	116	GLU
1	E	143	TRP
1	F	143	TRP
1	F	265	GLY
1	F	350	SER
1	K	143	TRP
1	L	143	TRP
1	L	265	GLY
1	L	350	SER
1	E	111	VAL
1	E	264	ARG
1	F	217	LYS
1	F	264	ARG
1	F	300	ASP
1	F	410	ALA
1	K	111	VAL
1	K	264	ARG
1	L	217	LYS
1	L	264	ARG
1	L	300	ASP
1	L	410	ALA
2	M	65	GLU
2	M	68	GLN
2	M	69	GLY
2	M	100	GLU
2	M	109	ASN
2	N	65	GLU
2	N	68	GLN
2	N	69	GLY
2	O	65	GLU
2	O	68	GLN
2	O	69	GLY
2	O	100	GLU
2	O	109	ASN
2	P	65	GLU
2	P	68	GLN
2	P	69	GLY
1	E	110	MET

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Mol	Chain	Res	Type
1	K	110	MET
2	M	70	HIS
2	N	101	THR
2	O	70	HIS
2	P	101	THR
1	E	138	PRO
1	E	153	SER
1	E	217	LYS
1	E	263	LYS
1	F	111	VAL
1	F	112	ARG
1	F	218	ILE
1	F	232	LYS
1	K	138	PRO
1	K	153	SER
1	K	217	LYS
1	K	263	LYS
1	L	111	VAL
1	L	112	ARG
1	L	218	ILE
1	L	232	LYS
2	M	115	PRO
2	N	70	HIS
2	O	115	PRO
2	P	70	HIS
1	E	112	ARG
1	F	63	LYS
1	K	112	ARG
1	L	63	LYS
1	E	265	GLY
1	K	265	GLY
1	L	137	PRO
1	F	137	PRO

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 X-ray entries followed by that with respect to entries of similar resolution.

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	E	336/377 (89%)	297 (88%)	39 (12%)	5	18
1	F	336/377 (89%)	282 (84%)	54 (16%)	2	11
1	K	336/377 (89%)	297 (88%)	39 (12%)	5	18
1	L	336/377 (89%)	282 (84%)	54 (16%)	2	11
2	M	135/136 (99%)	124 (92%)	11 (8%)	11	31
2	N	135/136 (99%)	120 (89%)	15 (11%)	6	19
2	O	135/136 (99%)	124 (92%)	11 (8%)	11	31
2	P	135/136 (99%)	120 (89%)	15 (11%)	6	19
All	All	1884/2052 (92%)	1646 (87%)	238 (13%)	4	16

All (238) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	4	MET
1	E	13	LEU
1	E	20	GLN
1	E	27	VAL
1	E	31	LEU
1	E	38	MET
1	E	46	HIS
1	E	59	THR
1	E	70	LEU
1	E	79	ILE
1	E	94	LYS
1	E	95	GLU
1	E	103	LEU
1	E	108	VAL
1	E	110	MET
1	E	114	GLN
1	E	118	LYS
1	E	119	ASN
1	E	120	ARG
1	E	130	ARG
1	E	132	LEU
1	E	136	ILE
1	E	141	ASN
1	E	150	GLN
1	E	164	ARG
1	E	216	LEU
1	E	232	LYS

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Mol	Chain	Res	Type
1	E	235	ASN
1	E	242	ASP
1	E	281	LEU
1	E	318	LEU
1	E	326	LEU
1	E	344	LEU
1	E	352	THR
1	E	355	TYR
1	E	361	THR
1	E	369	THR
1	E	375	ARG
1	E	412	ASP
1	F	6	PRO
1	F	8	GLU
1	F	11	SER
1	F	13	LEU
1	F	20	GLN
1	F	27	VAL
1	F	31	LEU
1	F	38	MET
1	F	59	THR
1	F	68	ARG
1	F	70	LEU
1	F	79	ILE
1	F	81	VAL
1	F	88	GLU
1	F	95	GLU
1	F	103	LEU
1	F	108	VAL
1	F	114	GLN
1	F	118	LYS
1	F	119	ASN
1	F	122	ARG
1	F	130	ARG
1	F	131	ILE
1	F	132	LEU
1	F	140	LYS
1	F	141	ASN
1	F	148	GLN
1	F	150	GLN
1	F	163	LEU
1	F	216	LEU

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Mol	Chain	Res	Type
1	F	217	LYS
1	F	232	LYS
1	F	258	ILE
1	F	263	LYS
1	F	266	GLU
1	F	281	LEU
1	F	296	MET
1	F	312	ILE
1	F	318	LEU
1	F	319	ILE
1	F	326	LEU
1	F	344	LEU
1	F	352	THR
1	F	355	TYR
1	F	361	THR
1	F	369	THR
1	F	374	LYS
1	F	375	ARG
1	F	384	ASN
1	F	389	ASN
1	F	411	SER
1	F	413	LEU
1	F	438	LEU
1	F	439	SER
1	K	4	MET
1	K	13	LEU
1	K	20	GLN
1	K	27	VAL
1	K	31	LEU
1	K	38	MET
1	K	46	HIS
1	K	59	THR
1	K	70	LEU
1	K	79	ILE
1	K	94	LYS
1	K	95	GLU
1	K	103	LEU
1	K	108	VAL
1	K	110	MET
1	K	114	GLN
1	K	118	LYS
1	K	119	ASN

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Mol	Chain	Res	Type
1	K	120	ARG
1	K	130	ARG
1	K	132	LEU
1	K	136	ILE
1	K	141	ASN
1	K	150	GLN
1	K	164	ARG
1	K	216	LEU
1	K	232	LYS
1	K	235	ASN
1	K	242	ASP
1	K	281	LEU
1	K	318	LEU
1	K	326	LEU
1	K	344	LEU
1	K	352	THR
1	K	355	TYR
1	K	361	THR
1	K	369	THR
1	K	375	ARG
1	K	412	ASP
1	L	6	PRO
1	L	8	GLU
1	L	11	SER
1	L	13	LEU
1	L	20	GLN
1	L	27	VAL
1	L	31	LEU
1	L	38	MET
1	L	59	THR
1	L	68	ARG
1	L	70	LEU
1	L	79	ILE
1	L	81	VAL
1	L	88	GLU
1	L	95	GLU
1	L	103	LEU
1	L	108	VAL
1	L	114	GLN
1	L	118	LYS
1	L	119	ASN
1	L	122	ARG

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Mol	Chain	Res	Type
1	L	130	ARG
1	L	131	ILE
1	L	132	LEU
1	L	140	LYS
1	L	141	ASN
1	L	148	GLN
1	L	150	GLN
1	L	163	LEU
1	L	216	LEU
1	L	217	LYS
1	L	232	LYS
1	L	258	ILE
1	L	263	LYS
1	L	266	GLU
1	L	281	LEU
1	L	296	MET
1	L	312	ILE
1	L	318	LEU
1	L	319	ILE
1	L	326	LEU
1	L	344	LEU
1	L	352	THR
1	L	355	TYR
1	L	361	THR
1	L	369	THR
1	L	374	LYS
1	L	375	ARG
1	L	384	ASN
1	L	389	ASN
1	L	411	SER
1	L	413	LEU
1	L	438	LEU
1	L	439	SER
2	M	1	THR
2	M	50	THR
2	M	66	MET
2	M	71	LEU
2	M	95	LEU
2	M	99	ASP
2	M	136	LEU
2	M	138	GLU
2	M	139	ASN

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Mol	Chain	Res	Type
2	M	146	GLU
2	M	160	ILE
2	N	4	VAL
2	N	36	ARG
2	N	39	ASN
2	N	50	THR
2	N	92	GLU
2	N	95	LEU
2	N	99	ASP
2	N	111	ASP
2	N	116	GLU
2	N	134	ARG
2	N	136	LEU
2	N	138	GLU
2	N	139	ASN
2	N	146	GLU
2	N	152	LEU
2	O	1	THR
2	O	50	THR
2	O	66	MET
2	O	71	LEU
2	O	95	LEU
2	O	99	ASP
2	O	136	LEU
2	O	138	GLU
2	O	139	ASN
2	O	146	GLU
2	O	160	ILE
2	P	4	VAL
2	P	36	ARG
2	P	39	ASN
2	P	50	THR
2	P	92	GLU
2	P	95	LEU
2	P	99	ASP
2	P	111	ASP
2	P	116	GLU
2	P	134	ARG
2	P	136	LEU
2	P	138	GLU
2	P	139	ASN
2	P	146	GLU

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Mol	Chain	Res	Type
2	P	152	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	22	ASN
1	E	33	ASN
1	E	75	ASN
1	E	141	ASN
1	E	145	GLN
1	E	148	GLN
1	E	157	GLN
1	E	235	ASN
1	E	241	GLN
1	E	294	HIS
1	E	333	GLN
1	E	384	ASN
1	E	389	ASN
1	E	416	GLN
1	E	417	ASN
1	F	16	HIS
1	F	22	ASN
1	F	33	ASN
1	F	75	ASN
1	F	119	ASN
1	F	141	ASN
1	F	142	ASN
1	F	148	GLN
1	F	150	GLN
1	F	157	GLN
1	F	235	ASN
1	F	241	GLN
1	F	348	ASN
1	F	384	ASN
1	F	389	ASN
1	F	396	HIS
1	F	416	GLN
1	F	417	ASN
1	K	22	ASN
1	K	33	ASN
1	K	75	ASN
1	K	141	ASN

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Mol	Chain	Res	Type
1	K	145	GLN
1	K	148	GLN
1	K	157	GLN
1	K	235	ASN
1	K	241	GLN
1	K	294	HIS
1	K	333	GLN
1	K	384	ASN
1	K	389	ASN
1	K	396	HIS
1	K	416	GLN
1	K	417	ASN
1	L	16	HIS
1	L	22	ASN
1	L	33	ASN
1	L	75	ASN
1	L	119	ASN
1	L	141	ASN
1	L	142	ASN
1	L	148	GLN
1	L	150	GLN
1	L	157	GLN
1	L	235	ASN
1	L	241	GLN
1	L	311	GLN
1	L	348	ASN
1	L	384	ASN
1	L	389	ASN
1	L	396	HIS
1	L	416	GLN
1	L	417	ASN
2	M	9	ASN
2	M	24	ASN
2	M	70	HIS
2	M	114	GLN
2	M	139	ASN
2	M	166	HIS
2	N	19	GLN
2	N	39	ASN
2	N	70	HIS
2	N	114	GLN
2	N	139	ASN

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Mol	Chain	Res	Type
2	N	164	HIS
2	O	9	ASN
2	O	24	ASN
2	O	70	HIS
2	O	114	GLN
2	O	139	ASN
2	O	166	HIS
2	P	19	GLN
2	P	39	ASN
2	P	70	HIS
2	P	164	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	E	1

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Mol	Chain	Number of breaks
1	K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	139:ALA	C	140:LYS	N	0.93
1	K	139:ALA	C	140:LYS	N	0.93

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	E	393/443 (88%)	-0.04	6 (1%) 72 60	60, 60, 60, 60	0
1	F	393/443 (88%)	-0.00	7 (1%) 67 58	60, 60, 60, 60	0
1	K	393/443 (88%)	0.07	11 (2%) 55 48	60, 60, 60, 60	0
1	L	393/443 (88%)	0.00	6 (1%) 72 60	60, 60, 60, 60	0
2	M	173/175 (98%)	-0.07	3 (1%) 69 59	60, 60, 60, 60	0
2	N	173/175 (98%)	0.09	3 (1%) 69 59	60, 60, 60, 60	0
2	O	173/175 (98%)	0.14	2 (1%) 76 65	60, 60, 60, 60	0
2	P	173/175 (98%)	0.03	4 (2%) 61 53	60, 60, 60, 60	0
All	All	2264/2472 (91%)	0.02	42 (1%) 66 56	60, 60, 60, 60	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	363	GLY	5.7
2	M	107	THR	5.1
2	P	121	ALA	4.7
2	M	44	ALA	4.7
1	F	83	ALA	4.3
1	K	288	CYS	4.1
1	E	71	ALA	4.1
1	K	238	GLU	3.7
2	N	34	VAL	3.7
2	O	4	VAL	3.5
1	L	271	ASP	3.2
1	F	246	ALA	3.2
2	P	6	VAL	3.2
2	O	129	ALA	3.0
1	F	297	VAL	2.9
1	K	400	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	L	163	LEU	2.8
1	E	439	SER	2.7
1	L	273	SER	2.7
1	L	287	GLY	2.7
2	P	143	SER	2.7
1	E	397	THR	2.6
1	E	95	GLU	2.6
1	F	306	ALA	2.6
1	F	56	ILE	2.5
1	K	330	VAL	2.5
1	K	253	VAL	2.4
2	P	21	THR	2.4
1	K	99	ILE	2.4
2	N	99	ASP	2.3
1	E	265	GLY	2.3
1	E	11	SER	2.3
1	K	291	SER	2.3
1	L	96	VAL	2.3
1	L	137	PRO	2.3
2	N	123	GLY	2.3
1	F	71	ALA	2.2
1	F	320	PRO	2.2
1	K	92	VAL	2.1
2	M	18	GLY	2.1
1	K	287	GLY	2.0
1	K	220	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.