



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:54 PM BST

PDB ID : 3J97
EMDB ID: : EMD-6207
Title : Structure of 20S supercomplex determined by single particle cryoelectron microscopy (State II)
Authors : Zhao, M.; Wu, S.; Cheng, Y.; Brunger, A.T.
Deposited on : 2014-12-05
Resolution : 7.80 Å(reported)
Based on PDB ID : 1QCS, 1NSF, 1N7S

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

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

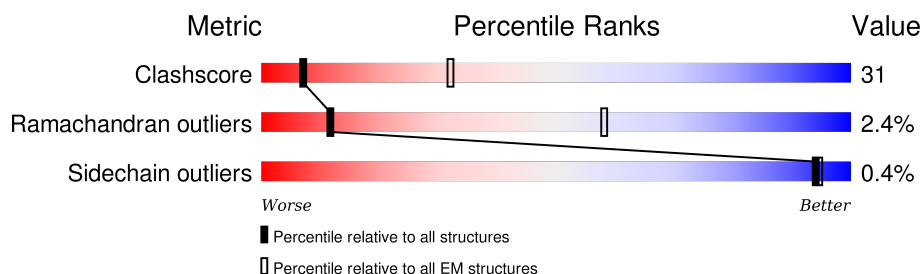
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.80 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	747	45% 44% .. 9%
1	B	747	48% 40% . 10%
1	C	747	46% 42% . 10%
1	D	747	46% 43% . 10%
1	E	747	44% 44% . 10%
1	F	747	46% 40% . 12%
2	G	297	56% 38% . .
2	H	297	52% 42% . .
2	I	297	54% 40% . .

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Mol	Chain	Length	Quality of chain
2	J	297	<div><div></div><div>53%41%</div><div></div><div></div></div>
3	K	63	<div><div></div><div>32%62%</div><div></div><div></div></div>
4	L	67	<div><div></div><div>39%58%</div><div></div><div></div></div>
5	M	198	<div><div></div><div>26%40%</div><div></div><div>34%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 41095 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Vesicle-fusing ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	678	Total	C	N	O	S	0	0
			5044	3201	874	946	23		
1	B	672	Total	C	N	O	S	0	0
			5015	3184	868	939	24		
1	C	676	Total	C	N	O	S	0	0
			5028	3189	869	947	23		
1	D	673	Total	C	N	O	S	0	0
			4986	3169	854	939	24		
1	E	670	Total	C	N	O	S	0	0
			5020	3185	871	940	24		
1	F	654	Total	C	N	O	S	0	0
			4932	3135	852	922	23		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP P18708
A	-1	ALA	-	EXPRESSION TAG	UNP P18708
A	0	HIS	-	EXPRESSION TAG	UNP P18708
B	-2	GLY	-	EXPRESSION TAG	UNP P18708
B	-1	ALA	-	EXPRESSION TAG	UNP P18708
B	0	HIS	-	EXPRESSION TAG	UNP P18708
C	-2	GLY	-	EXPRESSION TAG	UNP P18708
C	-1	ALA	-	EXPRESSION TAG	UNP P18708
C	0	HIS	-	EXPRESSION TAG	UNP P18708
D	-2	GLY	-	EXPRESSION TAG	UNP P18708
D	-1	ALA	-	EXPRESSION TAG	UNP P18708
D	0	HIS	-	EXPRESSION TAG	UNP P18708
E	-2	GLY	-	EXPRESSION TAG	UNP P18708
E	-1	ALA	-	EXPRESSION TAG	UNP P18708
E	0	HIS	-	EXPRESSION TAG	UNP P18708
F	-2	GLY	-	EXPRESSION TAG	UNP P18708
F	-1	ALA	-	EXPRESSION TAG	UNP P18708
F	0	HIS	-	EXPRESSION TAG	UNP P18708

- Molecule 2 is a protein called Alpha-soluble NSF attachment protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		
2	I	286	Total	C	N	O	S	0	0
			2246	1416	373	441	16		
2	J	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		
2	G	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	GLY	-	EXPRESSION TAG	UNP P54921
H	0	SER	-	EXPRESSION TAG	UNP P54921
I	-1	GLY	-	EXPRESSION TAG	UNP P54921
I	0	SER	-	EXPRESSION TAG	UNP P54921
J	-1	GLY	-	EXPRESSION TAG	UNP P54921
J	0	SER	-	EXPRESSION TAG	UNP P54921
G	-1	GLY	-	EXPRESSION TAG	UNP P54921
G	0	SER	-	EXPRESSION TAG	UNP P54921

- Molecule 3 is a protein called Vesicle-associated membrane protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	61	Total	C	N	O	S	0	0
			494	300	94	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	27	GLY	-	EXPRESSION TAG	UNP P63045

- Molecule 4 is a protein called Syntaxin-1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	66	Total	C	N	O	S	0	0
			536	331	91	109	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	190	MET	-	EXPRESSION TAG	UNP P32851

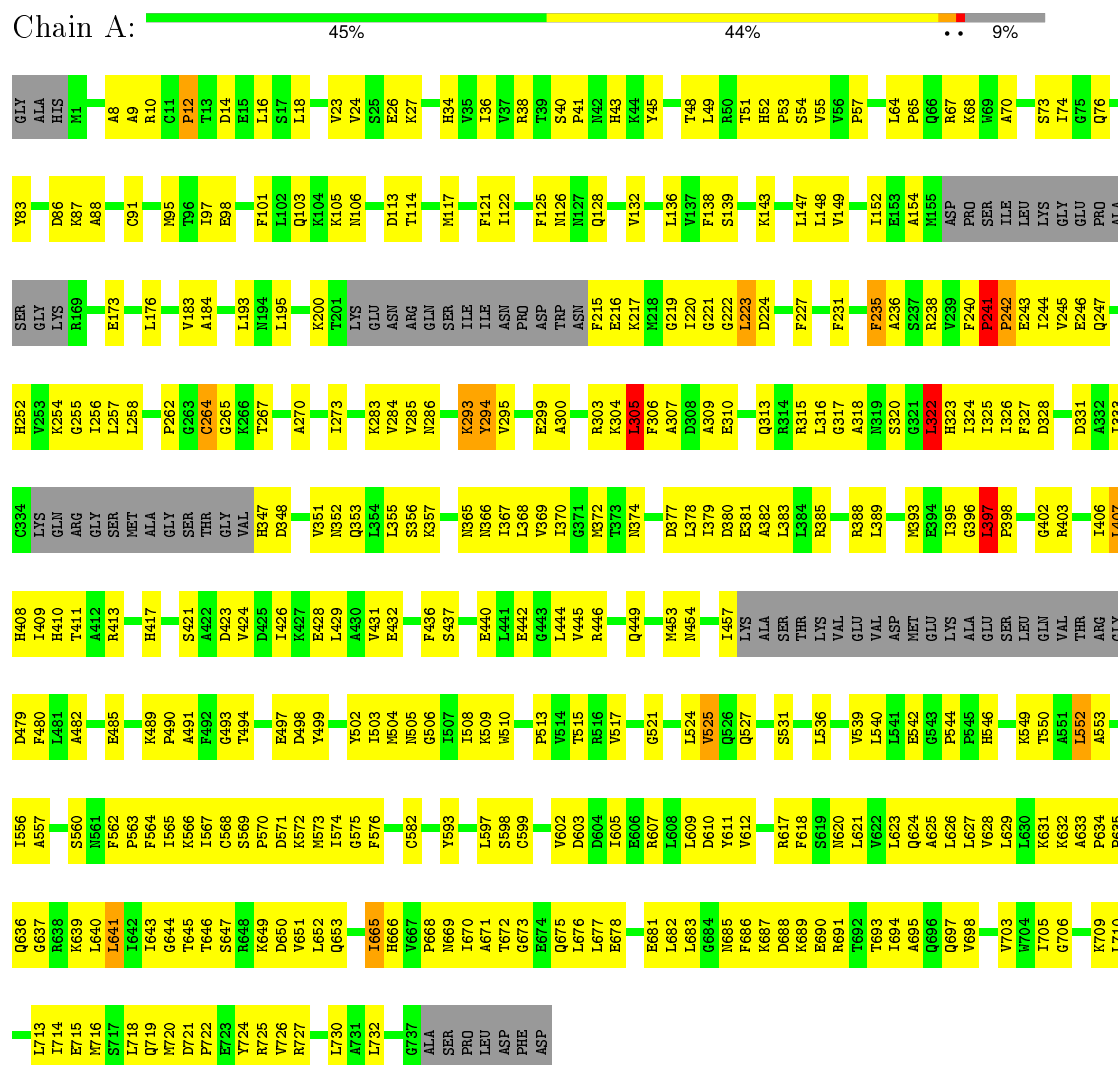
- Molecule 5 is a protein called Synaptosomal-associated protein 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	131	Total	C	N	O	S	0	0
			1029	609	191	220	9		

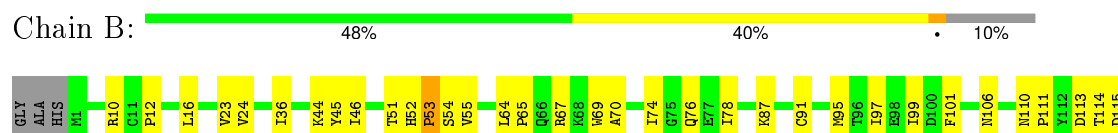
3 Residue-property plots

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

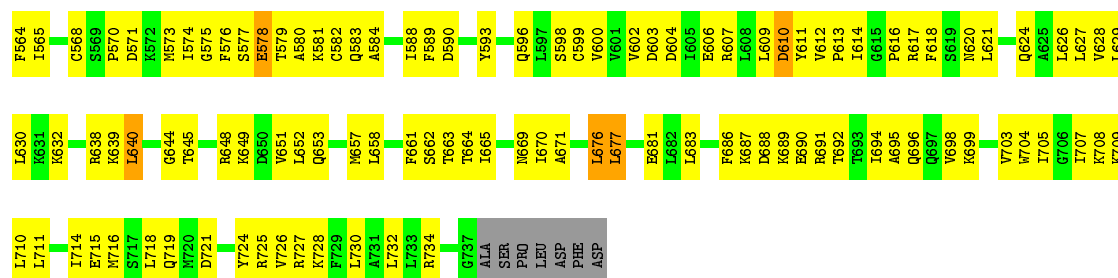
• Molecule 1: Vesicle-fusing ATPase



• Molecule 1: Vesicle-fusing ATPase

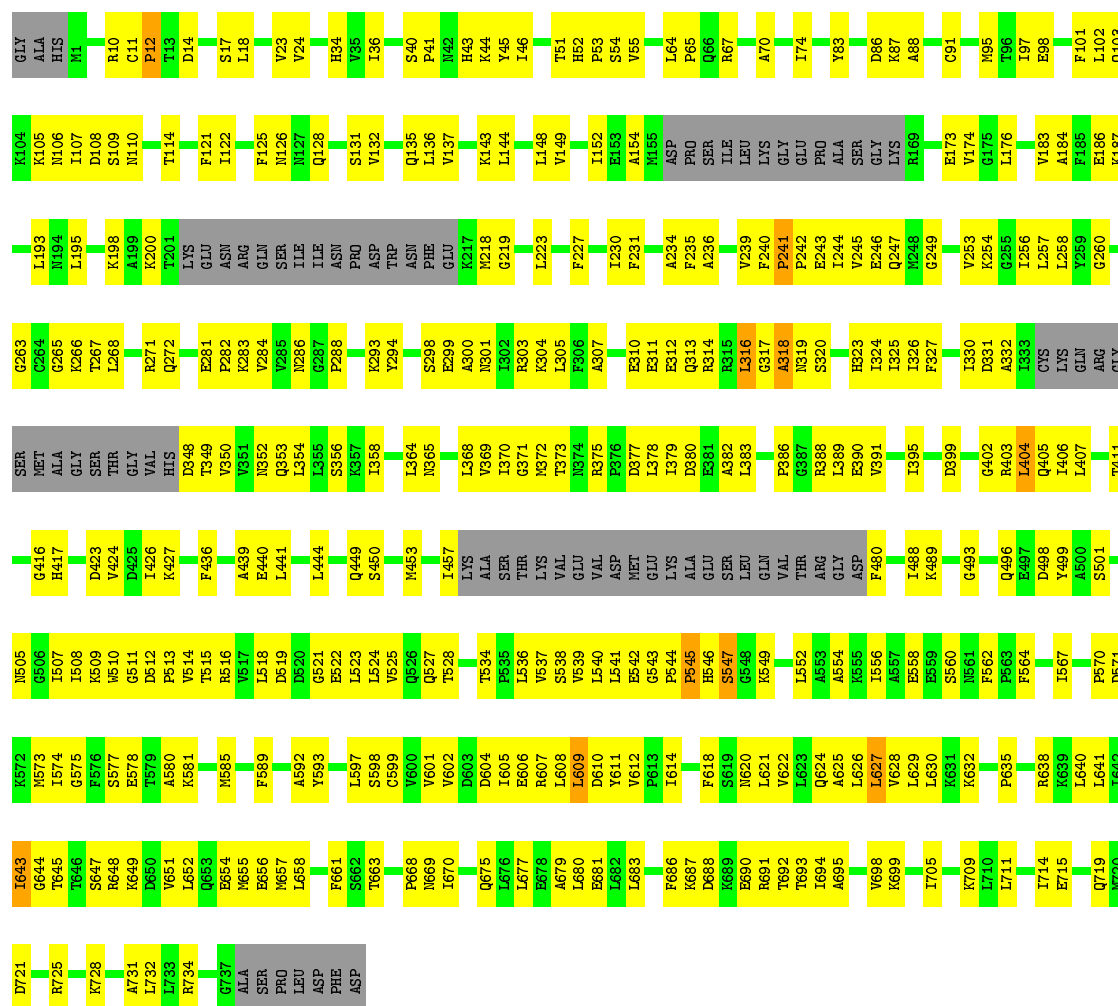






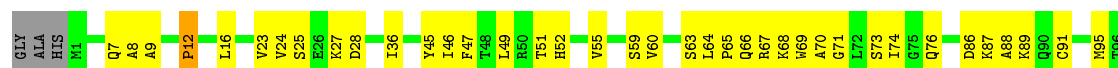
• Molecule 1: Vesicle-fusing ATPase

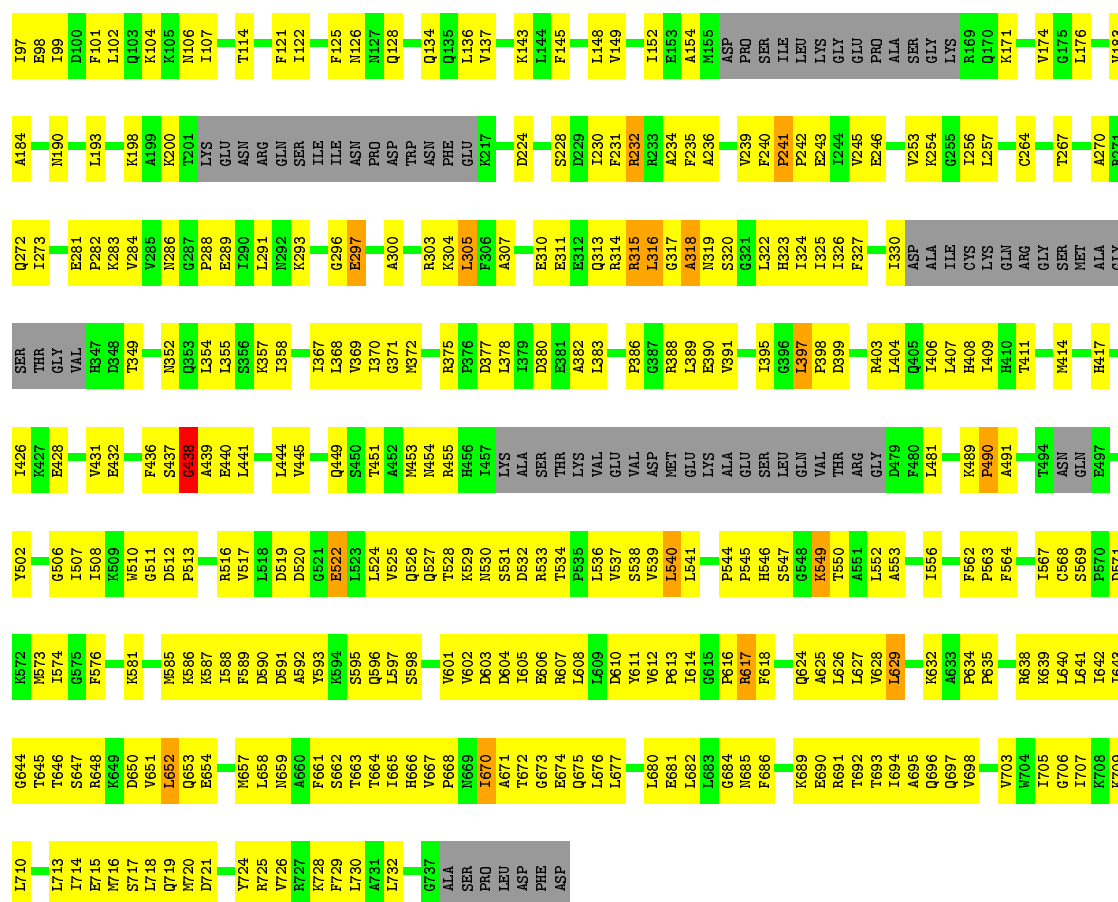
Chain D: 46% 43% • 10%



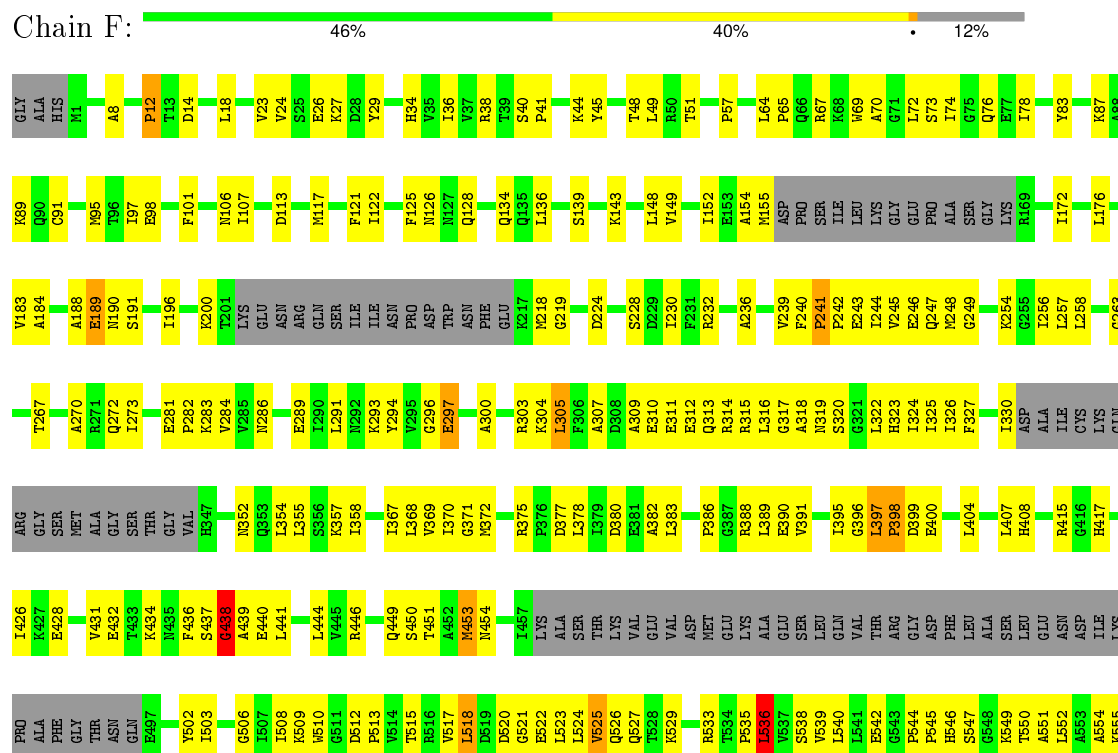
• Molecule 1: Vesicle-fusing ATPase

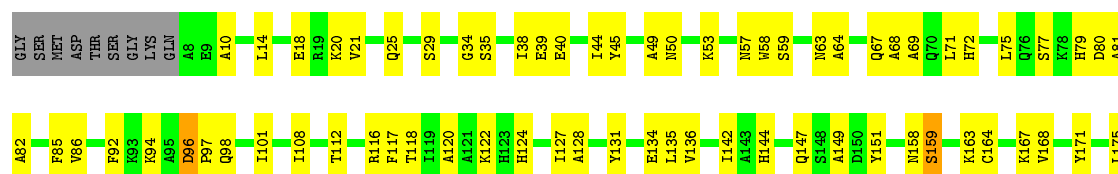
Chain E: 44% 44% • 10%





• Molecule 1: Vesicle-fusing ATPase





4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	21489	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	-1800	Depositor
Maximum defocus (nm)	-2800	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	A	0.46	1/5120 (0.0%)	0.82	10/6930 (0.1%)
1	B	0.41	1/5091 (0.0%)	0.80	12/6887 (0.2%)
1	C	0.38	0/5104	0.72	5/6910 (0.1%)
1	D	0.43	0/5061	0.77	9/6854 (0.1%)
1	E	0.46	1/5095 (0.0%)	0.84	11/6890 (0.2%)
1	F	0.42	0/5007	0.78	10/6767 (0.1%)
2	G	0.33	0/2295	0.59	1/3086 (0.0%)
2	H	0.36	0/2295	0.63	1/3086 (0.0%)
2	I	0.33	0/2285	0.58	0/3074
2	J	0.34	0/2295	0.58	1/3086 (0.0%)
3	K	0.25	0/497	0.41	0/665
4	L	0.24	0/541	0.41	0/723
5	M	0.22	0/1029	0.45	0/1369
All	All	0.40	3/41715 (0.0%)	0.74	60/56327 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	E	0	2
1	F	0	1
2	J	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	232	ARG	CB-CG	-6.33	1.35	1.52
1	B	547	SER	C-O	5.53	1.33	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	235	PHE	CB-CG	-5.23	1.42	1.51

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	316	LEU	CA-CB-CG	11.54	141.84	115.30
1	E	629	LEU	CB-CG-CD1	-9.86	94.24	111.00
1	F	518	LEU	CB-CG-CD1	-9.34	95.12	111.00
1	D	547	SER	C-N-CA	-8.76	103.92	122.30
1	F	629	LEU	CB-CG-CD1	-8.53	96.51	111.00
1	C	677	LEU	CB-CG-CD2	-8.30	96.88	111.00
2	G	197	LEU	CA-CB-CG	8.30	134.39	115.30
1	C	322	LEU	CA-CB-CG	7.96	133.62	115.30
1	A	397	LEU	CA-CB-CG	7.71	133.04	115.30
1	F	305	LEU	CA-CB-CG	7.56	132.69	115.30
1	B	305	LEU	CA-CB-CG	7.52	132.59	115.30
1	E	305	LEU	CA-CB-CG	7.30	132.09	115.30
1	E	316	LEU	CA-CB-CG	7.19	131.85	115.30
1	E	652	LEU	CB-CG-CD2	-7.11	98.91	111.00
1	B	479	ASP	N-CA-C	-7.09	91.86	111.00
1	A	322	LEU	CA-CB-CG	6.76	130.85	115.30
1	F	536	LEU	CA-CB-CG	6.63	130.55	115.30
1	F	518	LEU	CB-CG-CD2	6.60	122.22	111.00
1	A	305	LEU	CA-CB-CG	6.54	130.34	115.30
1	E	232	ARG	CB-CG-CD	-6.37	95.04	111.60
1	B	438	GLY	N-CA-C	6.27	128.78	113.10
1	B	708	LYS	CD-CE-NZ	6.23	126.03	111.70
1	A	641	LEU	CA-CB-CG	6.18	129.51	115.30
1	F	453	MET	CB-CG-SD	6.16	130.88	112.40
1	C	387	GLY	N-CA-C	-6.12	97.79	113.10
1	D	609	LEU	CA-CB-CG	6.10	129.32	115.30
1	F	536	LEU	CB-CG-CD2	-6.07	100.68	111.00
1	B	658	LEU	CB-CG-CD1	-6.02	100.77	111.00
1	B	548	GLY	N-CA-C	-6.00	98.11	113.10
1	B	543	GLY	N-CA-C	-5.99	98.12	113.10
1	B	395	ILE	CG1-CB-CG2	-5.79	98.67	111.40
1	A	525	VAL	CG1-CB-CG2	5.75	120.11	110.90
1	D	627	LEU	CB-CG-CD2	-5.72	101.28	111.00
1	E	438	GLY	N-CA-C	5.69	127.32	113.10
1	D	643	ILE	CB-CA-C	-5.68	100.24	111.60
2	H	119	ILE	CG1-CB-CG2	-5.66	98.95	111.40
1	F	629	LEU	CA-CB-CG	-5.65	102.30	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	617	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	B	455	ARG	CG-CD-NE	-5.61	100.03	111.80
1	D	316	LEU	CB-CA-C	-5.56	99.64	110.20
1	B	610	ASP	CB-CG-OD2	-5.55	113.31	118.30
1	B	455	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	E	522	GLU	CA-CB-CG	5.49	125.48	113.40
1	A	216	GLU	N-CA-C	-5.35	96.56	111.00
1	F	525	VAL	CG1-CB-CG2	5.35	119.45	110.90
1	E	397	LEU	CA-CB-CG	5.33	127.57	115.30
1	A	665	ILE	CG1-CB-CG2	-5.31	99.73	111.40
1	F	396	GLY	N-CA-C	5.30	126.35	113.10
1	A	236	ALA	N-CA-C	-5.28	96.73	111.00
1	D	404	LEU	CA-CB-CG	5.25	127.38	115.30
1	A	552	LEU	CA-CB-CG	5.25	127.38	115.30
1	C	385	ARG	CG-CD-NE	-5.24	100.80	111.80
1	E	670	ILE	CB-CA-C	-5.24	101.13	111.60
1	C	640	LEU	CA-CB-CG	5.17	127.18	115.30
1	D	416	GLY	N-CA-C	-5.16	100.21	113.10
1	E	540	LEU	CB-CG-CD1	-5.07	102.38	111.00
2	J	235	PHE	N-CA-CB	-5.07	101.47	110.60
1	A	407	LEU	CA-CB-CG	5.07	126.96	115.30
1	B	609	LEU	CA-CB-CG	-5.02	103.76	115.30
1	D	643	ILE	CG1-CB-CG2	-5.01	100.38	111.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	PRO	Peptide
1	B	438	GLY	Peptide
1	E	315	ARG	Mainchain
1	E	438	GLY	Peptide
1	F	438	GLY	Peptide
2	J	233	PRO	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	A	5044	0	4963	347	0
1	B	5015	0	4953	300	0
1	C	5028	0	4939	343	0
1	D	4986	0	4905	341	0
1	E	5020	0	4974	390	0
1	F	4932	0	4914	335	0
2	G	2255	0	2199	126	0
2	H	2255	0	2199	138	0
2	I	2246	0	2185	109	0
2	J	2255	0	2199	132	0
3	K	494	0	488	80	0
4	L	536	0	527	73	0
5	M	1029	0	996	143	0
All	All	41095	0	40441	2529	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (2529) 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:F:518:LEU:HD23	1:F:555:LYS:HG2	1.21	1.10
2:H:219:LEU:HB2	2:H:222:LYS:HB3	1.34	1.08
2:I:201:SER:HA	3:K:47:ARG:HH12	1.11	1.08
1:E:593:TYR:O	1:E:638:ARG:NH1	1.90	1.04
1:B:264:CYS:HA	1:B:437:SER:HB2	1.38	1.04
1:B:240:PHE:HD2	1:B:244:ILE:HG21	1.22	1.03
3:K:43:VAL:HA	4:L:212:LEU:HD13	1.36	1.03
2:J:201:SER:HG	2:J:205:TYR:HE1	1.05	1.02
1:C:507:ILE:CD1	1:C:555:LYS:HG2	1.87	1.02
1:B:258:LEU:HB3	1:B:395:ILE:HD11	1.37	1.01
1:E:528:THR:HG21	1:E:641:LEU:HD23	1.41	0.99
5:M:203:LEU:HD23	5:M:204:GLY:H	1.25	0.99
1:A:424:VAL:HG13	1:A:482:ALA:HB2	1.44	0.99
1:A:685:ASN:OD1	1:F:533:ARG:NH1	1.97	0.98
3:K:53:VAL:HG22	4:L:226:GLN:HE22	1.26	0.98
1:C:327:PHE:HB3	1:C:330:ILE:HD11	1.42	0.98
1:C:257:LEU:HB2	1:C:389:LEU:HD13	1.44	0.97
2:J:159:SER:HB2	5:M:169:ASN:HB3	1.46	0.97
1:E:596:GLN:HA	1:E:638:ARG:HG2	1.46	0.97
1:C:507:ILE:HD11	1:C:555:LYS:HB2	1.42	0.96
1:E:540:LEU:HD11	1:E:646:THR:HG22	1.45	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:GLU:HG3	1:F:527:GLN:HE21	1.30	0.96
2:G:219:LEU:HB2	2:G:222:LYS:HB3	1.47	0.95
1:A:331:ASP:HA	1:A:379:ILE:HD11	1.46	0.95
1:E:232:ARG:HH22	1:F:451:THR:HA	1.28	0.95
1:D:628:VAL:HG11	1:E:574:ILE:HG21	1.49	0.95
1:C:507:ILE:CD1	1:C:555:LYS:CG	2.45	0.94
1:E:232:ARG:HE	1:F:454:ASN:HB2	1.29	0.94
1:E:528:THR:HG22	1:E:537:VAL:HG21	1.50	0.94
3:K:83:LYS:HD3	5:M:203:LEU:HD11	1.49	0.94
1:D:509:LYS:HG2	1:D:515:THR:HG23	1.47	0.93
1:C:618:PHE:HE2	1:D:614:ILE:HD11	1.31	0.92
1:D:406:ILE:HG22	1:D:441:LEU:HD22	1.48	0.92
1:F:521:GLY:HA2	1:F:524:LEU:HD12	1.49	0.92
1:A:569:SER:OG	1:A:571:ASP:OD1	1.86	0.92
1:D:256:ILE:HG13	1:D:370:ILE:HG22	1.51	0.92
1:A:264:CYS:SG	1:A:265:GLY:N	2.41	0.91
1:C:240:PHE:HD2	1:C:244:ILE:HG21	1.34	0.91
3:K:36:GLN:HA	4:L:205:LEU:HD13	1.52	0.91
2:J:201:SER:HB2	5:M:165:LEU:HD11	1.53	0.91
1:A:497:GLU:O	1:A:499:TYR:N	2.04	0.91
1:C:490:PRO:HA	1:C:491:ALA:HB3	1.52	0.91
2:G:72:HIS:CE1	2:G:80:ASP:HB2	2.07	0.90
1:B:327:PHE:HB2	1:B:330:ILE:HG22	1.54	0.89
1:D:240:PHE:HD2	1:D:244:ILE:HG21	1.37	0.89
2:J:219:LEU:HB2	2:J:222:LYS:HB3	1.54	0.89
1:A:295:VAL:HB	1:B:294:TYR:HB2	1.55	0.89
5:M:73:GLU:HG3	5:M:77:ASN:HD21	1.36	0.88
2:G:218:MET:HG2	2:G:219:LEU:H	1.36	0.88
2:H:218:MET:HG2	2:H:219:LEU:H	1.35	0.88
1:B:266:LYS:HG2	1:B:395:ILE:HG12	1.52	0.87
1:A:542:GLU:HG2	1:A:649:LYS:HD2	1.56	0.87
1:A:502:TYR:HE2	1:A:567:ILE:HG21	1.40	0.87
1:F:327:PHE:HB2	1:F:330:ILE:HG22	1.55	0.86
1:A:562:PHE:CD2	1:A:597:LEU:HD21	2.09	0.86
1:E:625:ALA:HA	1:F:574:ILE:HD11	1.55	0.86
1:B:566:LYS:HD2	1:B:588:ILE:HG23	1.57	0.86
1:C:507:ILE:HD11	1:C:555:LYS:CB	2.03	0.86
1:D:313:GLN:HE22	1:D:364:LEU:HA	1.40	0.86
1:C:497:GLU:O	1:C:499:TYR:N	2.07	0.86
1:E:256:ILE:HG13	1:E:370:ILE:HG22	1.56	0.86
1:E:327:PHE:HB2	1:E:330:ILE:HG22	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:545:PRO:HA	1:F:547:SER:H	1.39	0.86
1:A:421:SER:HB3	1:A:424:VAL:HG23	1.56	0.86
1:D:606:GLU:HA	1:D:609:LEU:HG	1.57	0.85
5:M:40:LYS:HD3	5:M:156:ILE:HG23	1.58	0.85
1:F:538:SER:HB3	1:F:662:SER:H	1.40	0.85
1:C:386:PRO:HA	1:C:390:GLU:HA	1.57	0.85
3:K:43:VAL:HG22	4:L:212:LEU:HB2	1.59	0.85
1:F:538:SER:HG	1:F:661:PHE:HD1	1.23	0.84
1:E:64:LEU:HA	1:E:67:ARG:HE	1.39	0.84
2:G:38:ILE:HD11	2:G:71:LEU:HB3	1.57	0.84
1:F:539:VAL:HB	1:F:643:ILE:HG12	1.60	0.84
1:E:232:ARG:HH22	1:F:451:THR:CA	1.89	0.84
1:A:305:LEU:HD23	1:A:325:ILE:HG21	1.58	0.84
1:E:490:PRO:HA	1:E:491:ALA:HB3	1.59	0.84
1:E:618:PHE:HZ	1:F:612:VAL:HG11	1.39	0.83
1:D:510:TRP:CD2	1:D:670:ILE:HG22	2.14	0.83
1:F:555:LYS:NZ	1:F:559:GLU:OE2	2.11	0.83
1:F:525:VAL:HG13	1:F:562:PHE:CE1	2.12	0.83
1:E:720:MET:HG3	1:E:728:LYS:HE3	1.60	0.83
1:A:705:ILE:HD13	1:A:710:LEU:HD12	1.60	0.83
1:B:64:LEU:HB2	2:H:293:ASP:O	1.78	0.83
1:B:256:ILE:HG13	1:B:370:ILE:HG22	1.59	0.83
1:D:510:TRP:HE3	1:D:675:GLN:HG2	1.44	0.83
1:E:585:MET:HG3	1:E:589:PHE:CZ	2.13	0.83
1:C:687:LYS:N	1:C:690:GLU:OE2	2.11	0.83
2:J:200:TYR:OH	3:K:41:GLU:O	1.96	0.83
1:F:256:ILE:HG13	1:F:370:ILE:HG22	1.58	0.83
1:E:527:GLN:O	1:E:531:SER:OG	1.95	0.83
2:I:201:SER:CA	3:K:47:ARG:HH12	1.91	0.82
1:C:256:ILE:HG13	1:C:370:ILE:HG22	1.58	0.82
2:J:271:ARG:NH2	2:G:234:ALA:HB2	1.94	0.82
1:A:686:PHE:HE2	1:A:714:ILE:HG12	1.43	0.82
2:I:38:ILE:HG23	2:I:75:LEU:HD12	1.61	0.82
1:F:544:PRO:O	1:F:547:SER:OG	1.96	0.82
1:A:624:GLN:HG3	1:B:610:ASP:OD2	1.80	0.82
2:J:235:PHE:HB3	3:K:38:GLN:HG2	1.62	0.82
2:G:232:PHE:HB2	2:G:233:PRO:HD3	1.59	0.82
1:B:490:PRO:HA	1:B:491:ALA:HB3	1.62	0.82
2:J:228:TYR:OH	2:J:237:ASP:OD1	1.98	0.81
1:A:428:GLU:HG2	1:A:479:ASP:HA	1.62	0.81
1:B:111:PRO:HB2	1:B:196:ILE:HD13	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:232:ARG:NE	1:F:454:ASN:HB2	1.95	0.81
1:F:536:LEU:HD11	1:F:634:PRO:HD3	1.61	0.81
1:C:627:LEU:HD12	1:D:607:ARG:HH12	1.46	0.81
2:I:201:SER:HA	3:K:47:ARG:NH1	1.95	0.81
2:J:218:MET:HG2	2:J:219:LEU:H	1.44	0.81
1:D:518:LEU:HD21	1:D:552:LEU:HD22	1.63	0.81
1:A:285:VAL:HG13	1:A:326:ILE:HD11	1.63	0.80
1:F:386:PRO:HA	1:F:390:GLU:HA	1.63	0.80
3:K:48:VAL:HG12	3:K:52:LYS:HE3	1.61	0.80
1:A:713:LEU:HD21	1:A:732:LEU:HB3	1.63	0.80
1:A:557:ALA:O	1:A:560:SER:OG	1.99	0.80
1:E:549:LYS:HA	1:E:552:LEU:HD12	1.62	0.80
1:F:538:SER:H	1:F:662:SER:HB3	1.45	0.80
2:J:235:PHE:HE2	3:K:37:ALA:HB3	1.42	0.80
1:C:676:LEU:HD12	1:C:705:ILE:HG21	1.64	0.80
1:C:313:GLN:O	1:C:317:GLY:N	2.15	0.80
1:E:586:LYS:NZ	1:F:574:ILE:O	2.14	0.80
1:E:589:PHE:CZ	1:E:629:LEU:HD11	2.16	0.80
1:C:618:PHE:CE2	1:D:614:ILE:HD11	2.16	0.79
1:D:626:LEU:HB3	1:D:657:MET:HE3	1.65	0.79
1:E:386:PRO:HA	1:E:390:GLU:HA	1.63	0.79
1:B:526:GLN:HE21	1:C:719:GLN:HB3	1.47	0.79
1:C:407:LEU:HD11	1:C:426:ILE:HG23	1.64	0.79
1:C:98:GLU:HB3	1:C:148:LEU:HB3	1.65	0.79
1:E:563:PRO:HG2	1:E:595:SER:OG	1.83	0.78
1:E:190:ASN:HD21	1:E:316:LEU:HG	1.49	0.78
1:A:562:PHE:HD2	1:A:597:LEU:HD21	1.46	0.78
2:J:235:PHE:CB	3:K:38:GLN:HG2	2.12	0.78
1:E:686:PHE:HE1	1:E:714:ILE:HG23	1.49	0.78
1:A:490:PRO:HA	1:A:491:ALA:HB3	1.65	0.78
1:E:526:GLN:NE2	1:F:719:GLN:O	2.17	0.78
1:D:654:GLU:HB3	1:E:614:ILE:HD11	1.66	0.78
1:E:587:LYS:O	1:E:587:LYS:NZ	2.15	0.78
1:E:510:TRP:HE1	1:E:707:ILE:HD11	1.48	0.78
2:J:201:SER:HB2	5:M:165:LEU:CD1	2.14	0.78
1:B:111:PRO:HD3	1:B:316:LEU:HG	1.66	0.78
1:D:353:GLN:HE22	1:E:288:PRO:HG2	1.47	0.78
1:A:502:TYR:CE2	1:A:567:ILE:HG21	2.19	0.77
1:C:652:LEU:HD22	1:C:657:MET:HG2	1.66	0.77
1:B:386:PRO:HA	1:B:390:GLU:HA	1.64	0.77
1:A:67:ARG:HD2	2:H:218:MET:HG3	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:39:VAL:HG11	4:L:209:ILE:HD13	1.66	0.77
1:A:525:VAL:HG13	1:A:562:PHE:CZ	2.20	0.77
2:H:289:GLY:O	2:H:293:ASP:HB2	1.84	0.77
1:C:690:GLU:HB2	1:C:726:VAL:HG21	1.66	0.77
1:F:407:LEU:HD11	1:F:426:ILE:HG23	1.66	0.77
1:D:240:PHE:CD2	1:D:244:ILE:HG21	2.19	0.77
1:E:234:ALA:HA	1:F:446:ARG:NH2	1.99	0.77
1:C:540:LEU:HB3	1:C:664:THR:HG22	1.64	0.77
1:C:691:ARG:HA	1:C:694:ILE:HD12	1.67	0.77
1:B:589:PHE:HE1	1:B:600:VAL:HG11	1.49	0.77
1:A:48:THR:HG21	1:A:128:GLN:HG2	1.66	0.77
1:E:653:GLN:HA	1:E:658:LEU:HB2	1.66	0.76
1:C:544:PRO:O	1:C:547:SER:OG	2.01	0.76
1:B:540:LEU:HD23	1:B:661:PHE:CD1	2.21	0.76
1:B:10:ARG:HE	2:H:293:ASP:CG	1.89	0.76
1:B:581:LYS:NZ	1:B:608:LEU:O	2.18	0.76
1:C:40:SER:HB2	1:C:41:PRO:HD2	1.65	0.76
1:A:549:LYS:NZ	1:A:647:SER:OG	2.16	0.76
1:C:496:GLN:O	1:C:498:ASP:N	2.18	0.76
1:C:507:ILE:HD12	1:C:555:LYS:CD	2.16	0.76
1:E:407:LEU:HD11	1:E:426:ILE:HG23	1.66	0.76
1:F:570:PRO:HG2	1:F:604:ASP:HB2	1.68	0.76
1:F:240:PHE:CD2	1:F:244:ILE:HG21	2.20	0.76
5:M:61:GLU:HG2	5:M:65:ASN:HD21	1.50	0.76
1:E:585:MET:HA	1:E:588:ILE:HD12	1.68	0.75
1:F:569:SER:OG	1:F:571:ASP:OD2	2.04	0.75
1:F:564:PHE:O	1:F:598:SER:OG	2.04	0.75
1:D:310:GLU:O	1:D:313:GLN:HG2	1.86	0.75
1:E:311:GLU:OE1	1:E:314:ARG:NE	2.19	0.75
1:A:453:MET:O	1:F:232:ARG:NH2	2.19	0.75
2:G:72:HIS:HE1	2:G:80:ASP:HB2	1.51	0.75
2:G:21:VAL:HG21	2:G:71:LEU:HD22	1.68	0.75
1:D:728:LYS:HE3	1:D:732:LEU:HD11	1.67	0.75
1:B:240:PHE:CD2	1:B:244:ILE:HG21	2.15	0.75
1:E:313:GLN:O	1:E:317:GLY:N	2.20	0.75
4:L:209:ILE:HG21	5:M:32:MET:HG3	1.69	0.75
1:A:677:LEU:HD21	1:A:695:ALA:HA	1.68	0.74
1:C:507:ILE:HD12	1:C:555:LYS:HG2	1.69	0.74
1:F:12:PRO:HG2	1:F:23:VAL:HG11	1.69	0.74
1:A:397:LEU:HB3	1:A:398:PRO:CD	2.17	0.74
1:E:300:ALA:O	1:E:304:LYS:HG2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:ALA:HA	1:A:556:ILE:HD12	1.68	0.74
1:E:349:THR:HA	1:E:352:ASN:HD22	1.52	0.74
1:A:262:PRO:HG2	1:A:374:ASN:OD1	1.87	0.74
1:C:578:GLU:HB3	1:C:621:LEU:HB3	1.67	0.74
5:M:31:ARG:O	5:M:35:LEU:HG	1.88	0.74
1:C:630:LEU:HD11	1:C:661:PHE:CE1	2.23	0.74
1:B:524:LEU:HD21	1:B:663:THR:HG21	1.69	0.74
1:C:724:TYR:HD2	1:C:727:ARG:HH21	1.35	0.74
2:G:228:TYR:OH	2:G:237:ASP:OD1	2.05	0.74
1:E:686:PHE:HB3	1:E:690:GLU:HB2	1.69	0.74
1:F:397:LEU:HD22	1:F:398:PRO:HD3	1.69	0.73
1:D:301:ASN:HA	1:D:304:LYS:HD3	1.70	0.73
1:A:352:ASN:HB3	1:B:288:PRO:HB2	1.68	0.73
1:C:318:ALA:O	1:C:319:ASN:ND2	2.21	0.73
1:C:513:PRO:O	1:C:516:ARG:HG2	1.88	0.73
1:B:300:ALA:O	1:B:304:LYS:HG2	1.88	0.73
1:E:106:ASN:HB3	1:E:143:LYS:NZ	2.03	0.73
1:B:621:LEU:HD11	1:C:575:GLY:HA2	1.70	0.73
1:A:67:ARG:NH1	2:H:217:ASP:O	2.20	0.73
1:F:73:SER:O	1:F:76:GLN:HG2	1.89	0.73
1:F:536:LEU:HD21	1:F:632:LYS:O	1.89	0.73
1:F:634:PRO:HB2	1:F:638:ARG:HG3	1.68	0.73
1:D:399:ASP:O	1:D:403:ARG:N	2.22	0.73
1:E:670:ILE:HG22	1:E:672:THR:H	1.54	0.72
1:F:300:ALA:O	1:F:304:LYS:HG2	1.87	0.72
1:E:553:ALA:HA	1:E:556:ILE:HD12	1.72	0.72
1:D:46:ILE:HD12	1:D:174:VAL:HG21	1.71	0.72
1:B:187:LYS:HB2	1:B:191:SER:HB3	1.70	0.72
1:E:538:SER:OG	1:E:661:PHE:HA	1.90	0.72
1:B:533:ARG:HG3	1:B:534:THR:H	1.54	0.72
2:H:94:LYS:HE3	2:I:153:LYS:HG3	1.70	0.72
1:C:236:ALA:HB1	1:D:453:MET:HB3	1.72	0.72
1:C:596:GLN:HA	1:C:638:ARG:HD3	1.72	0.72
1:B:407:LEU:HD11	1:B:426:ILE:HG23	1.71	0.72
1:B:563:PRO:HD2	1:B:597:LEU:HB2	1.69	0.72
1:A:10:ARG:HB2	2:H:217:ASP:OD2	1.90	0.72
1:E:236:ALA:HB1	1:F:453:MET:HG3	1.72	0.72
1:D:98:GLU:HB3	1:D:148:LEU:HB3	1.72	0.71
1:D:544:PRO:O	1:D:547:SER:HB3	1.90	0.71
1:D:513:PRO:HA	1:D:516:ARG:HG2	1.72	0.71
1:B:496:GLN:O	1:B:498:ASP:N	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:303:ARG:HG3	1:E:357:LYS:HE2	1.72	0.71
1:A:417:HIS:ND1	1:F:246:GLU:O	2.23	0.71
1:A:602:VAL:HG12	1:A:605:ILE:HG12	1.73	0.71
1:E:190:ASN:OD1	1:E:315:ARG:C	2.29	0.71
1:C:507:ILE:HD11	1:C:555:LYS:CG	2.17	0.71
5:M:36:VAL:HG21	5:M:153:VAL:HG13	1.72	0.71
1:F:517:VAL:HG13	1:F:665:ILE:HG21	1.72	0.71
1:A:258:LEU:HA	1:A:393:MET:O	1.90	0.71
1:F:311:GLU:OE1	1:F:314:ARG:NE	2.24	0.71
1:E:9:ALA:HA	1:E:74:ILE:HG23	1.72	0.71
1:E:680:LEU:HD13	1:E:694:ILE:HD13	1.70	0.71
1:B:538:SER:HB3	1:B:661:PHE:HD2	1.55	0.71
1:A:309:ALA:HB1	1:A:367:ILE:HG21	1.73	0.71
1:D:310:GLU:O	1:D:313:GLN:CG	2.39	0.71
1:D:605:ILE:HD11	1:D:644:GLY:HA3	1.72	0.71
2:H:93:LYS:NZ	2:I:156:GLU:OE2	2.21	0.71
1:D:711:LEU:HA	1:D:714:ILE:HD12	1.72	0.71
1:B:627:LEU:HD21	1:B:657:MET:HG3	1.73	0.70
1:B:361:VAL:O	1:C:271:ARG:HD2	1.91	0.70
1:C:564:PHE:O	1:C:598:SER:OG	2.07	0.70
3:K:39:VAL:O	3:K:43:VAL:HG23	1.91	0.70
1:C:611:TYR:CE1	1:C:616:PRO:HB2	2.26	0.70
1:B:624:GLN:NE2	1:C:610:ASP:O	2.24	0.70
1:A:423:ASP:HB3	1:A:480:PHE:CB	2.22	0.70
1:E:527:GLN:HE22	1:F:716:MET:HG2	1.57	0.70
1:C:236:ALA:HB1	1:D:453:MET:CB	2.21	0.70
1:E:190:ASN:OD1	1:E:315:ARG:O	2.09	0.70
1:E:513:PRO:HA	1:E:516:ARG:HG2	1.74	0.70
1:D:620:ASN:O	1:D:624:GLN:HG2	1.91	0.70
2:I:51:MET:HA	2:I:54:MET:HG2	1.74	0.70
1:A:562:PHE:HD2	1:A:597:LEU:CD2	2.05	0.70
1:E:589:PHE:CD2	1:E:629:LEU:HD21	2.26	0.70
2:J:213:HIS:HE1	2:J:221:ALA:HB2	1.55	0.70
1:D:10:ARG:NH2	2:I:293:ASP:OD1	2.24	0.70
1:E:232:ARG:HH21	1:F:454:ASN:HB3	1.56	0.70
2:J:235:PHE:HD1	3:K:34:GLN:NE2	1.89	0.70
1:E:190:ASN:HD21	1:E:316:LEU:CG	2.03	0.70
1:A:503:ILE:O	1:A:505:ASN:N	2.25	0.70
1:F:713:LEU:HD22	1:F:732:LEU:HB3	1.74	0.70
1:F:535:PRO:HA	1:F:639:LYS:HG2	1.74	0.70
1:C:240:PHE:CD2	1:C:244:ILE:HG21	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:PHE:HA	1:A:128:GLN:NE2	2.06	0.70
1:A:353:GLN:HE21	1:A:357:LYS:HG2	1.57	0.70
1:F:125:PHE:HA	1:F:128:GLN:NE2	2.06	0.69
5:M:152:GLN:O	5:M:156:ILE:HG13	1.91	0.69
2:J:235:PHE:CE2	3:K:37:ALA:HB3	2.25	0.69
1:D:353:GLN:HE22	1:E:288:PRO:CG	2.04	0.69
1:C:125:PHE:HA	1:C:128:GLN:NE2	2.07	0.69
1:F:606:GLU:OE1	1:F:606:GLU:N	2.22	0.69
1:E:606:GLU:OE2	1:E:646:THR:OG1	2.09	0.69
1:C:718:LEU:O	1:C:725:ARG:NH1	2.26	0.69
1:A:231:PHE:CD1	1:A:235:PHE:HE2	2.10	0.69
1:E:234:ALA:HA	1:F:446:ARG:HH21	1.57	0.69
1:F:721:ASP:HB2	1:F:724:TYR:HD1	1.57	0.69
1:C:331:ASP:HA	1:C:379:ILE:HD11	1.75	0.69
1:E:232:ARG:NH2	1:F:450:SER:O	2.25	0.69
1:F:545:PRO:HA	1:F:547:SER:N	2.05	0.69
4:L:205:LEU:O	4:L:209:ILE:HG12	1.93	0.69
1:E:592:ALA:HB1	1:E:640:LEU:HD22	1.73	0.69
1:D:230:ILE:HD11	1:D:256:ILE:HD13	1.73	0.69
1:D:386:PRO:HA	1:D:390:GLU:HA	1.74	0.69
1:C:247:GLN:HA	1:D:417:HIS:CD2	2.26	0.69
1:F:670:ILE:HG23	1:F:675:GLN:HB2	1.74	0.69
1:D:245:VAL:O	1:D:249:GLY:N	2.26	0.69
1:B:125:PHE:HA	1:B:128:GLN:NE2	2.08	0.69
2:I:116:ARG:NH2	5:M:183:GLU:OE1	2.25	0.69
1:E:604:ASP:HB3	1:E:607:ARG:HB3	1.74	0.69
1:B:538:SER:HB3	1:B:661:PHE:CD2	2.28	0.69
1:B:303:ARG:HG3	1:B:357:LYS:HE2	1.74	0.68
1:C:507:ILE:HD12	1:C:555:LYS:CG	2.20	0.68
1:F:589:PHE:HD2	1:F:629:LEU:HD13	1.57	0.68
1:B:489:LYS:O	1:B:491:ALA:HB3	1.94	0.68
1:F:303:ARG:HG3	1:F:357:LYS:HE2	1.74	0.68
1:D:125:PHE:HA	1:D:128:GLN:NE2	2.07	0.68
1:E:640:LEU:HD12	1:E:641:LEU:N	2.09	0.68
1:C:358:ILE:CB	1:C:388:ARG:HG3	2.23	0.68
1:D:539:VAL:HG23	1:D:663:THR:HG23	1.75	0.68
2:I:228:TYR:OH	2:I:237:ASP:OD1	2.09	0.68
1:A:564:PHE:CE1	1:A:566:LYS:HB2	2.28	0.68
5:M:73:GLU:HG3	5:M:77:ASN:ND2	2.09	0.68
1:F:358:ILE:HD12	1:F:388:ARG:HB3	1.75	0.68
1:A:521:GLY:O	1:A:525:VAL:HG23	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:685:ASN:HB3	1:E:718:LEU:HD11	1.74	0.68
1:A:351:VAL:O	1:A:355:LEU:HG	1.93	0.68
1:D:543:GLY:H	1:D:549:LYS:HD3	1.59	0.68
3:K:42:VAL:HG13	3:K:45:ILE:HD11	1.76	0.68
1:C:533:ARG:O	1:D:505:ASN:ND2	2.27	0.68
1:B:311:GLU:OE1	1:B:314:ARG:NE	2.26	0.68
1:E:358:ILE:HD12	1:E:388:ARG:HB3	1.75	0.68
1:F:550:THR:HA	1:F:645:THR:HG21	1.76	0.68
1:C:649:LYS:HE2	1:C:658:LEU:HD13	1.75	0.68
2:J:50:ASN:HD21	2:G:115:GLY:CA	2.05	0.67
1:D:527:GLN:NE2	1:E:715:GLU:O	2.27	0.67
1:E:246:GLU:HG3	1:F:417:HIS:HE1	1.59	0.67
1:A:326:ILE:HG22	1:A:370:ILE:HG12	1.74	0.67
5:M:170:GLU:HG3	5:M:174:GLN:NE2	2.09	0.67
3:K:34:GLN:O	3:K:38:GLN:HG3	1.94	0.67
1:E:510:TRP:CZ3	1:E:670:ILE:HG13	2.29	0.67
1:A:612:VAL:HG11	1:F:618:PHE:HZ	1.59	0.67
1:C:64:LEU:HB3	1:C:65:PRO:HD3	1.75	0.67
1:B:358:ILE:HD12	1:B:388:ARG:HB3	1.76	0.67
1:E:525:VAL:O	1:E:528:THR:OG1	2.11	0.67
1:A:683:LEU:HB3	1:A:685:ASN:ND2	2.09	0.67
1:F:518:LEU:HD12	1:F:518:LEU:H	1.59	0.67
1:D:407:LEU:HG	1:D:441:LEU:HD11	1.76	0.67
1:B:240:PHE:CE1	1:C:457:ILE:HD11	2.29	0.67
2:H:35:SER:HB3	2:H:75:LEU:HD12	1.76	0.67
1:A:247:GLN:O	1:B:413:ARG:NH1	2.28	0.67
1:E:232:ARG:HH21	1:F:454:ASN:H	1.41	0.67
1:A:720:MET:O	1:A:725:ARG:NE	2.24	0.67
1:E:540:LEU:HD11	1:E:646:THR:CG2	2.21	0.66
1:C:542:GLU:CB	1:C:649:LYS:HD3	2.25	0.66
1:E:398:PRO:HG3	1:E:436:PHE:O	1.94	0.66
1:B:224:ASP:O	1:B:228:SER:HB2	1.95	0.66
5:M:27:GLU:O	5:M:31:ARG:HG3	1.96	0.66
1:A:563:PRO:HD2	1:A:597:LEU:HD22	1.77	0.66
1:F:538:SER:O	1:F:663:THR:HG22	1.95	0.66
1:E:602:VAL:O	1:E:644:GLY:HA2	1.95	0.66
1:E:232:ARG:NH2	1:F:451:THR:HA	2.07	0.66
1:F:518:LEU:CD2	1:F:555:LYS:HG2	2.13	0.66
1:E:534:THR:HG23	1:F:715:GLU:HG3	1.77	0.66
2:G:149:ALA:HB2	2:G:164:CYS:HB2	1.76	0.66
1:F:695:ALA:HB1	1:F:699:LYS:HE3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:653:GLN:NE2	1:A:653:GLN:O	2.29	0.66
1:B:713:LEU:HD22	1:B:732:LEU:HB3	1.76	0.66
1:D:627:LEU:HD21	1:D:657:MET:HG3	1.77	0.66
1:E:253:VAL:H	1:F:446:ARG:HH12	1.41	0.66
1:B:528:THR:O	1:B:639:LYS:HD2	1.96	0.66
1:A:671:ALA:HA	1:A:703:VAL:O	1.96	0.66
4:L:198:ARG:O	4:L:202:ILE:HG13	1.95	0.66
1:D:319:ASN:HB3	1:D:320:SER:HB2	1.78	0.66
4:L:212:LEU:HA	4:L:215:MET:HE2	1.77	0.66
4:L:255:VAL:HG11	5:M:77:ASN:HB3	1.78	0.66
1:E:625:ALA:O	1:E:629:LEU:HG	1.95	0.66
2:H:230:GLU:HG3	2:H:237:ASP:HB3	1.78	0.66
1:F:224:ASP:O	1:F:228:SER:HB2	1.96	0.66
1:B:67:ARG:NH1	1:B:74:ILE:HD11	2.11	0.66
1:E:544:PRO:O	1:E:547:SER:HB3	1.96	0.66
1:C:533:ARG:HB2	1:D:715:GLU:OE1	1.96	0.66
2:H:72:HIS:HE1	2:H:80:ASP:HB2	1.61	0.66
1:E:603:ASP:OD2	1:E:645:THR:OG1	2.10	0.66
1:B:245:VAL:O	1:B:249:GLY:N	2.28	0.66
2:G:197:LEU:HD23	5:M:162:HIS:NE2	2.10	0.66
1:A:687:LYS:N	1:A:690:GLU:OE1	2.27	0.66
1:E:547:SER:OG	1:E:549:LYS:HD3	1.96	0.65
1:D:510:TRP:CE3	1:D:670:ILE:HG22	2.31	0.65
5:M:26:LEU:HD13	5:M:146:MET:HG3	1.77	0.65
1:A:550:THR:HA	1:A:645:THR:HG21	1.76	0.65
1:D:573:MET:SD	1:D:581:LYS:HD3	2.36	0.65
2:G:112:THR:HG23	2:G:117:PHE:HE1	1.61	0.65
1:B:424:VAL:N	1:B:479:ASP:N	2.44	0.65
2:H:57:ASN:O	2:H:59:SER:N	2.29	0.65
1:B:589:PHE:CE1	1:B:600:VAL:HG11	2.30	0.65
1:D:358:ILE:HD12	1:D:388:ARG:HB3	1.78	0.65
1:E:640:LEU:HD12	1:E:641:LEU:H	1.61	0.65
2:G:175:LEU:HD23	2:G:177:GLN:HE21	1.61	0.65
1:D:234:ALA:HA	1:D:253:VAL:HG11	1.79	0.65
1:E:232:ARG:HH21	1:F:454:ASN:CB	2.09	0.65
1:A:686:PHE:CE2	1:A:714:ILE:HG12	2.31	0.65
1:A:356:SER:CB	1:B:288:PRO:HD3	2.27	0.65
2:G:235:PHE:CD1	5:M:152:GLN:HG2	2.31	0.65
1:F:565:ILE:HG23	1:F:599:CYS:HB3	1.77	0.65
1:A:620:ASN:ND2	1:B:610:ASP:OD1	2.30	0.65
1:B:501:SER:O	1:B:503:ILE:N	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:125:PHE:HA	1:E:128:GLN:NE2	2.11	0.65
1:B:449:GLN:O	1:B:453:MET:HG2	1.97	0.65
1:A:64:LEU:HB3	1:A:65:PRO:HD3	1.77	0.64
1:C:711:LEU:HA	1:C:714:ILE:HD12	1.79	0.64
1:F:240:PHE:HD2	1:F:244:ILE:HG21	1.58	0.64
1:A:527:GLN:HB2	1:B:719:GLN:HG3	1.78	0.64
1:A:670:ILE:HG23	1:A:675:GLN:HB2	1.79	0.64
1:E:536:LEU:HD12	1:E:640:LEU:O	1.97	0.64
1:F:245:VAL:O	1:F:249:GLY:N	2.29	0.64
1:D:286:ASN:HB2	1:D:327:PHE:HD1	1.62	0.64
1:F:513:PRO:O	1:F:517:VAL:HG23	1.97	0.64
1:C:711:LEU:O	1:C:715:GLU:HG2	1.97	0.64
2:G:158:ASN:OD1	2:G:162:ASN:ND2	2.30	0.64
2:H:200:TYR:CE2	5:M:38:GLU:HG3	2.32	0.64
1:F:73:SER:HA	2:G:218:MET:SD	2.38	0.64
1:F:307:ALA:O	1:F:311:GLU:HG2	1.97	0.64
1:E:652:LEU:CD2	1:E:657:MET:HB3	2.28	0.64
1:B:496:GLN:O	1:B:499:TYR:N	2.25	0.64
1:A:408:HIS:HA	1:A:426:ILE:HD12	1.80	0.64
2:J:39:GLU:HB2	2:J:75:LEU:HD13	1.78	0.64
1:D:546:HIS:ND1	1:D:709:LYS:HD3	2.11	0.64
1:F:544:PRO:HD2	1:F:547:SER:OG	1.96	0.64
2:I:232:PHE:HB2	2:I:233:PRO:HD3	1.80	0.64
5:M:188:ASN:O	5:M:192:ILE:HG13	1.98	0.64
1:D:534:THR:OG1	1:E:715:GLU:HG2	1.98	0.64
3:K:56:ARG:HD2	5:M:171:ILE:HG23	1.80	0.64
1:D:695:ALA:HB1	1:D:699:LYS:HE3	1.79	0.64
2:J:128:ALA:HB2	2:J:144:HIS:HB2	1.79	0.64
1:D:284:VAL:HG23	1:D:324:ILE:O	1.97	0.64
3:K:63:LEU:HD22	5:M:178:ILE:HG23	1.79	0.63
1:A:256:ILE:HG13	1:A:370:ILE:HG22	1.79	0.63
1:A:453:MET:C	1:F:232:ARG:HH22	2.01	0.63
2:H:101:ILE:HG21	2:H:135:LEU:HD11	1.80	0.63
1:D:64:LEU:HA	1:D:67:ARG:HE	1.63	0.63
1:C:375:ARG:HH12	1:C:378:LEU:HG	1.64	0.63
1:E:89:LYS:HB3	1:E:89:LYS:HZ3	1.63	0.63
1:D:256:ILE:CG1	1:D:370:ILE:HG22	2.27	0.63
1:B:295:VAL:O	1:C:294:TYR:HB2	1.99	0.63
1:D:404:LEU:HA	1:D:407:LEU:HD12	1.79	0.63
2:I:38:ILE:HD11	2:I:71:LEU:HB3	1.79	0.63
1:F:612:VAL:HG12	1:F:617:ARG:HB2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:72:HIS:CE1	2:J:80:ASP:HB2	2.34	0.63
2:H:216:ILE:HG12	2:H:220:ASN:HB2	1.80	0.63
1:E:232:ARG:NH2	1:F:454:ASN:HB3	2.13	0.63
1:A:710:LEU:O	1:A:714:ILE:HG13	1.98	0.63
1:E:307:ALA:O	1:E:311:GLU:HG2	1.97	0.63
1:F:570:PRO:HA	1:F:573:MET:HE2	1.79	0.63
1:B:307:ALA:O	1:B:311:GLU:HG2	1.98	0.63
5:M:167:MET:O	5:M:171:ILE:HG13	1.99	0.63
5:M:176:ARG:O	5:M:176:ARG:HD3	1.99	0.63
1:B:397:LEU:HB3	1:B:398:PRO:CD	2.29	0.63
1:E:63:SER:O	1:E:67:ARG:HG3	1.99	0.63
1:B:526:GLN:NE2	1:C:719:GLN:HB3	2.11	0.63
1:E:437:SER:O	1:E:440:GLU:HB2	1.98	0.63
2:H:231:LEU:HD13	2:G:271:ARG:HG2	1.80	0.63
2:J:57:ASN:O	2:J:59:SER:N	2.32	0.63
1:E:674:GLU:HA	1:E:677:LEU:HD12	1.81	0.63
2:G:69:ALA:HB1	2:G:85:PHE:CE1	2.33	0.63
1:D:105:LYS:NZ	2:I:291:GLU:HB3	2.13	0.63
4:L:229:MET:HG2	4:L:232:ARG:HH22	1.63	0.63
1:F:635:PRO:O	1:F:638:ARG:HG2	1.98	0.63
1:B:503:ILE:HG12	1:B:551:ALA:HA	1.80	0.63
5:M:34:GLN:HA	5:M:37:GLU:HB2	1.81	0.63
1:B:64:LEU:HB3	1:B:65:PRO:HD3	1.80	0.63
1:E:670:ILE:HD12	1:E:670:ILE:H	1.64	0.63
1:A:449:GLN:NE2	1:F:248:MET:O	2.31	0.63
1:A:313:GLN:NE2	1:A:365:ASN:O	2.30	0.63
1:B:548:GLY:O	1:B:552:LEU:HD23	1.99	0.63
2:J:235:PHE:CD1	3:K:34:GLN:NE2	2.67	0.62
1:B:295:VAL:C	1:C:294:TYR:HB2	2.19	0.62
1:B:101:PHE:CZ	1:B:193:LEU:HD13	2.34	0.62
2:H:232:PHE:HB2	2:H:233:PRO:HD3	1.80	0.62
1:F:64:LEU:HB3	1:F:65:PRO:HD3	1.79	0.62
1:B:380:ASP:OD1	1:B:382:ALA:N	2.32	0.62
1:D:256:ILE:HG22	1:D:391:VAL:HG12	1.80	0.62
1:E:581:LYS:NZ	1:E:610:ASP:OD1	2.31	0.62
1:C:624:GLN:NE2	1:D:610:ASP:HB2	2.14	0.62
2:G:38:ILE:HG23	2:G:75:LEU:HD12	1.81	0.62
1:B:326:ILE:HG22	1:B:370:ILE:HG13	1.82	0.62
1:E:686:PHE:CE1	1:E:714:ILE:HG23	2.34	0.62
1:C:728:LYS:O	1:C:732:LEU:HG	1.99	0.62
1:B:394:GLU:O	1:B:396:GLY:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:326:ILE:HG22	1:F:370:ILE:HG13	1.81	0.62
1:F:404:LEU:O	1:F:408:HIS:HB2	1.99	0.62
1:D:521:GLY:O	1:D:525:VAL:HG23	1.98	0.62
1:B:46:ILE:HD12	1:B:174:VAL:HG21	1.80	0.62
1:D:604:ASP:HB3	1:D:607:ARG:CB	2.29	0.62
1:E:706:GLY:O	1:E:710:LEU:N	2.24	0.62
1:E:380:ASP:OD1	1:E:382:ALA:N	2.33	0.62
2:J:269:ILE:HA	5:M:151:GLU:OE1	1.99	0.62
1:C:383:LEU:O	1:C:389:LEU:HB2	1.98	0.62
1:F:549:LYS:HE2	1:F:645:THR:HB	1.80	0.62
1:D:648:ARG:HG3	1:D:651:VAL:HG23	1.82	0.62
1:D:12:PRO:HG2	1:D:23:VAL:HG11	1.81	0.62
2:H:115:GLY:HA2	2:G:50:ASN:HD21	1.64	0.62
2:J:159:SER:CB	5:M:169:ASN:HB3	2.25	0.62
1:C:624:GLN:O	1:C:628:VAL:HG23	1.99	0.62
1:D:312:GLU:CG	1:D:313:GLN:H	2.12	0.62
1:A:607:ARG:HD3	1:F:624:GLN:NE2	2.13	0.62
1:D:651:VAL:O	1:D:655:MET:HG2	1.99	0.62
1:D:267:THR:HA	1:D:372:MET:SD	2.40	0.62
1:C:490:PRO:HB2	1:C:492:PHE:N	2.15	0.62
1:F:570:PRO:HG2	1:F:604:ASP:CB	2.29	0.62
1:E:349:THR:HG21	1:F:294:TYR:HE1	1.63	0.62
1:F:27:LYS:HD2	1:F:57:PRO:HG3	1.81	0.62
1:C:546:HIS:HA	1:C:708:LYS:HD3	1.82	0.62
2:G:218:MET:HG2	2:G:219:LEU:N	2.11	0.62
1:D:240:PHE:HB3	1:D:244:ILE:HD13	1.80	0.62
1:D:652:LEU:HB3	1:D:658:LEU:HB2	1.82	0.62
1:D:527:GLN:HE22	1:E:715:GLU:C	2.03	0.62
1:A:617:ARG:HH11	1:A:617:ARG:HG3	1.63	0.62
2:G:128:ALA:HB2	2:G:144:HIS:HB2	1.80	0.62
1:A:12:PRO:HG2	1:A:23:VAL:HG11	1.80	0.62
1:C:311:GLU:HA	1:C:314:ARG:HG2	1.81	0.62
5:M:74:ALA:O	5:M:78:LEU:HG	2.00	0.62
5:M:25:SER:O	5:M:29:THR:HG23	1.98	0.61
1:C:285:VAL:HG13	1:C:326:ILE:HD11	1.80	0.61
2:H:93:LYS:HE2	2:H:130:ILE:HD11	1.82	0.61
1:E:624:GLN:HA	1:E:624:GLN:OE1	2.00	0.61
5:M:203:LEU:CD2	5:M:204:GLY:H	2.06	0.61
1:D:512:ASP:O	1:D:515:THR:OG1	2.15	0.61
1:F:524:LEU:HD13	1:F:539:VAL:HG22	1.82	0.61
1:E:64:LEU:HB3	1:E:65:PRO:HD3	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:652:LEU:HD23	1:E:657:MET:HB3	1.82	0.61
2:J:35:SER:HB3	2:J:75:LEU:HD12	1.81	0.61
1:D:545:PRO:HD3	1:D:647:SER:OG	2.00	0.61
1:D:528:THR:OG1	1:D:641:LEU:HD12	2.00	0.61
1:D:36:ILE:HD11	1:D:44:LYS:HB3	1.82	0.61
2:H:218:MET:HG2	2:H:219:LEU:N	2.13	0.61
4:L:216:PHE:HB3	5:M:39:SER:HB2	1.82	0.61
1:D:236:ALA:HB1	1:E:453:MET:HG3	1.82	0.61
1:C:407:LEU:CD1	1:C:426:ILE:HG23	2.30	0.61
1:E:349:THR:HG21	1:F:294:TYR:CE1	2.35	0.61
5:M:177:GLN:HG3	5:M:180:ARG:HH21	1.65	0.61
5:M:174:GLN:O	5:M:178:ILE:HG13	2.01	0.61
1:A:9:ALA:HA	1:A:74:ILE:HG23	1.81	0.61
1:C:334:CYS:HA	1:C:351:VAL:HG22	1.82	0.61
1:F:562:PHE:CD1	1:F:599:CYS:HB2	2.36	0.61
2:G:80:ASP:OD1	4:L:243:TYR:CE1	2.52	0.61
1:E:326:ILE:HG22	1:E:370:ILE:HG13	1.81	0.61
1:E:404:LEU:O	1:E:408:HIS:HB2	2.00	0.61
1:C:511:GLY:HA3	1:C:513:PRO:HD2	1.82	0.61
1:B:383:LEU:O	1:B:389:LEU:HB2	2.01	0.61
1:C:590:ASP:HA	1:C:593:TYR:CD2	2.35	0.61
1:A:598:SER:OG	1:A:640:LEU:HD12	2.00	0.61
1:F:650:ASP:O	1:F:653:GLN:HG3	2.01	0.61
1:E:672:THR:OG1	1:E:675:GLN:HB2	2.00	0.61
1:A:231:PHE:CE1	1:A:235:PHE:HE2	2.19	0.61
1:D:632:LYS:NZ	1:E:571:ASP:HB3	2.16	0.61
1:D:606:GLU:O	1:D:610:ASP:N	2.34	0.61
1:D:239:VAL:HG13	1:D:240:PHE:CD1	2.36	0.61
1:E:710:LEU:O	1:E:714:ILE:HG13	2.00	0.61
1:B:625:ALA:O	1:B:629:LEU:HG	2.01	0.61
1:F:258:LEU:HB3	1:F:395:ILE:HD11	1.82	0.61
1:C:12:PRO:HG2	1:C:23:VAL:HG11	1.82	0.61
1:C:254:LYS:O	1:C:368:LEU:HA	2.01	0.61
1:F:612:VAL:CG1	1:F:617:ARG:HB2	2.31	0.61
1:E:407:LEU:CD1	1:E:426:ILE:HG23	2.31	0.61
1:D:554:ALA:O	1:D:558:GLU:HG2	2.01	0.61
1:C:579:THR:O	1:C:583:GLN:HG2	2.00	0.61
1:E:224:ASP:O	1:E:228:SER:HB2	2.01	0.61
1:B:670:ILE:HG23	1:B:675:GLN:HB2	1.83	0.61
1:E:552:LEU:HD11	1:E:667:VAL:HG11	1.82	0.60
1:E:513:PRO:O	1:E:517:VAL:HG23	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:84:LEU:HD21	5:M:199:ALA:HB1	1.83	0.60
1:D:348:ASP:O	1:D:352:ASN:ND2	2.34	0.60
1:B:437:SER:O	1:B:440:GLU:HB2	2.01	0.60
1:E:64:LEU:O	1:E:68:LYS:HG3	2.01	0.60
1:C:404:LEU:O	1:C:408:HIS:HB2	2.01	0.60
2:H:231:LEU:HD13	2:G:271:ARG:HE	1.65	0.60
1:B:95:MET:HG3	1:B:152:ILE:HG12	1.82	0.60
3:K:83:LYS:HG2	3:K:86:ARG:HH22	1.64	0.60
1:A:610:ASP:HA	1:F:624:GLN:NE2	2.16	0.60
1:D:599:CYS:SG	1:D:641:LEU:HD22	2.42	0.60
2:H:115:GLY:HA2	2:G:50:ASN:ND2	2.17	0.60
2:H:142:ILE:HG23	2:H:168:VAL:HG13	1.83	0.60
1:F:380:ASP:OD1	1:F:382:ALA:N	2.32	0.60
1:A:678:GLU:O	1:A:682:LEU:HD12	2.01	0.60
1:F:525:VAL:HG13	1:F:562:PHE:HE1	1.62	0.60
1:F:521:GLY:O	1:F:525:VAL:HG23	2.01	0.60
2:G:234:ALA:HB3	2:G:237:ASP:HB2	1.84	0.60
1:C:73:SER:O	1:C:76:GLN:HG2	2.00	0.60
1:E:264:CYS:SG	1:E:395:ILE:HG21	2.41	0.60
1:D:436:PHE:HE2	1:D:444:LEU:HD12	1.66	0.60
1:B:404:LEU:O	1:B:408:HIS:HB2	2.02	0.60
1:D:585:MET:O	1:D:589:PHE:HD2	1.84	0.60
1:E:383:LEU:O	1:E:389:LEU:HB2	2.02	0.60
1:A:413:ARG:NH1	1:F:249:GLY:O	2.27	0.60
1:F:655:MET:O	1:F:656:GLU:HG2	2.01	0.60
3:K:79:THR:HG22	3:K:83:LYS:HE3	1.84	0.60
5:M:203:LEU:HD23	5:M:204:GLY:N	2.07	0.60
1:D:256:ILE:O	1:D:370:ILE:HA	2.01	0.60
1:A:597:LEU:C	1:A:597:LEU:HD23	2.22	0.60
1:E:705:ILE:HD13	1:E:710:LEU:HD13	1.84	0.60
1:F:407:LEU:CD1	1:F:426:ILE:HG23	2.32	0.60
1:D:547:SER:OG	1:D:549:LYS:HG3	2.02	0.60
1:D:527:GLN:NE2	1:E:716:MET:HA	2.16	0.60
1:A:582:CYS:SG	1:A:621:LEU:HG	2.42	0.60
2:I:128:ALA:HB2	2:I:144:HIS:HB2	1.84	0.60
1:D:513:PRO:HB3	1:D:516:ARG:HE	1.66	0.60
1:C:695:ALA:HB1	1:C:699:LYS:HE3	1.83	0.60
1:D:64:LEU:HB3	1:D:65:PRO:HD3	1.82	0.60
1:A:508:ILE:HB	1:A:682:LEU:HD22	1.83	0.60
1:E:289:GLU:O	1:E:291:LEU:N	2.24	0.60
2:H:128:ALA:HB2	2:H:144:HIS:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:513:PRO:O	1:D:516:ARG:HG2	2.02	0.60
1:E:671:ALA:HA	1:E:703:VAL:O	2.02	0.60
1:B:533:ARG:HG3	1:B:534:THR:HG23	1.84	0.60
1:A:270:ALA:O	1:A:273:ILE:HG22	2.02	0.60
1:B:36:ILE:HD11	1:B:44:LYS:HB3	1.84	0.60
1:B:240:PHE:HB3	1:B:244:ILE:HB	1.84	0.59
1:C:383:LEU:HD22	1:C:388:ARG:HD2	1.84	0.59
1:A:687:LYS:HB2	1:A:690:GLU:HG3	1.83	0.59
1:A:628:VAL:HG11	1:B:571:ASP:HA	1.83	0.59
2:I:57:ASN:O	2:I:59:SER:N	2.35	0.59
2:I:21:VAL:HG21	2:I:71:LEU:HD22	1.82	0.59
2:J:233:PRO:HA	2:J:235:PHE:CE1	2.37	0.59
1:B:407:LEU:CD1	1:B:426:ILE:HG23	2.31	0.59
2:I:287:ILE:O	2:I:291:GLU:HG3	2.02	0.59
2:I:101:ILE:HG21	2:I:135:LEU:HD11	1.84	0.59
1:E:284:VAL:HG23	1:E:324:ILE:O	2.02	0.59
1:A:676:LEU:CD1	1:A:710:LEU:HD11	2.33	0.59
1:B:284:VAL:HG23	1:B:324:ILE:O	2.02	0.59
3:K:56:ARG:HH11	5:M:171:ILE:HG23	1.67	0.59
1:A:627:LEU:HD13	1:B:607:ARG:HH12	1.66	0.59
1:C:507:ILE:HD13	1:C:555:LYS:HG2	1.77	0.59
5:M:40:LYS:O	5:M:44:ILE:HG13	2.03	0.59
1:D:618:PHE:CE2	1:E:614:ILE:HD12	2.37	0.59
1:E:532:ASP:OD2	1:E:533:ARG:N	2.35	0.59
1:C:606:GLU:HG2	1:C:607:ARG:N	2.18	0.59
1:C:542:GLU:HB3	1:C:649:LYS:HD3	1.82	0.59
1:C:540:LEU:HB2	1:C:661:PHE:CD2	2.37	0.59
1:B:589:PHE:HE2	1:B:629:LEU:HB3	1.67	0.59
1:B:540:LEU:HA	1:B:644:GLY:O	2.02	0.59
1:A:694:ILE:O	1:A:698:VAL:HG13	2.02	0.59
2:I:69:ALA:HB1	2:I:85:PHE:CE1	2.36	0.59
5:M:17:ARG:O	5:M:21:LEU:HG	2.02	0.59
2:H:235:PHE:CD2	5:M:31:ARG:HA	2.37	0.59
1:D:310:GLU:O	1:D:313:GLN:NE2	2.36	0.59
1:E:713:LEU:HD22	1:E:732:LEU:HD13	1.85	0.59
2:H:200:TYR:CE2	5:M:42:ALA:HB2	2.38	0.59
1:F:236:ALA:HA	1:F:239:VAL:HG12	1.83	0.59
1:D:18:LEU:HA	1:D:137:VAL:CG2	2.32	0.59
1:B:121:PHE:CD2	1:B:183:VAL:HG21	2.37	0.59
2:H:289:GLY:O	2:H:293:ASP:CB	2.51	0.59
1:C:540:LEU:HD12	1:C:644:GLY:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:18:GLU:HA	2:H:21:VAL:HG12	1.85	0.59
1:F:437:SER:O	1:F:440:GLU:HB2	2.02	0.59
1:E:586:LYS:HA	1:E:589:PHE:CD2	2.37	0.59
1:E:510:TRP:NE1	1:E:707:ILE:HD11	2.18	0.59
1:A:449:GLN:O	1:A:453:MET:HG2	2.03	0.59
4:L:199:HIS:CE1	5:M:21:LEU:HD22	2.38	0.59
1:E:502:TYR:OH	1:E:569:SER:OG	2.19	0.59
1:D:312:GLU:HG2	1:D:313:GLN:H	1.68	0.59
1:B:571:ASP:OD2	1:B:571:ASP:N	2.35	0.59
2:G:101:ILE:HG21	2:G:135:LEU:HD11	1.85	0.59
1:F:589:PHE:CD2	1:F:629:LEU:HD22	2.37	0.59
1:B:67:ARG:NH2	2:H:293:ASP:O	2.36	0.59
1:B:421:SER:HG	1:B:479:ASP:N	2.01	0.59
1:D:383:LEU:O	1:D:389:LEU:HB2	2.03	0.59
1:C:577:SER:O	1:C:580:ALA:N	2.34	0.59
5:M:148:GLU:O	5:M:152:GLN:HG3	2.03	0.58
1:A:716:MET:HG2	1:A:732:LEU:HD11	1.85	0.58
1:E:190:ASN:ND2	1:E:316:LEU:HA	2.18	0.58
1:A:397:LEU:HB3	1:A:398:PRO:HD3	1.84	0.58
1:A:238:ARG:HA	1:A:252:HIS:CE1	2.37	0.58
1:A:307:ALA:O	1:A:310:GLU:HG3	2.02	0.58
1:E:506:GLY:O	1:E:508:ILE:N	2.36	0.58
2:G:235:PHE:CZ	5:M:151:GLU:HG2	2.38	0.58
1:A:503:ILE:HG23	1:A:506:GLY:HA2	1.83	0.58
1:F:383:LEU:O	1:F:389:LEU:HB2	2.02	0.58
1:A:411:THR:OG1	1:A:426:ILE:HD11	2.03	0.58
1:D:11:CYS:SG	1:D:17:SER:HB2	2.43	0.58
1:C:527:GLN:HB2	1:D:719:GLN:HG3	1.85	0.58
2:H:218:MET:CG	2:H:219:LEU:H	2.06	0.58
2:J:167:LYS:HE2	2:J:171:TYR:HE2	1.67	0.58
1:B:596:GLN:HA	1:B:638:ARG:HG2	1.86	0.58
5:M:49:MET:HG2	5:M:53:GLN:HE21	1.68	0.58
1:D:527:GLN:HE21	1:E:715:GLU:HG3	1.68	0.58
1:A:382:ALA:O	1:A:385:ARG:HG2	2.02	0.58
3:K:35:THR:HA	3:K:38:GLN:OE1	2.03	0.58
1:E:310:GLU:OE2	1:E:357:LYS:NZ	2.36	0.58
5:M:34:GLN:O	5:M:38:GLU:N	2.35	0.58
1:C:377:ASP:OD2	1:C:377:ASP:N	2.36	0.58
1:B:578:GLU:HG3	1:B:619:SER:HB2	1.85	0.58
2:J:18:GLU:HA	2:J:21:VAL:HG12	1.85	0.58
5:M:191:ARG:HG3	5:M:191:ARG:HH11	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:628:VAL:O	1:E:632:LYS:N	2.35	0.58
1:B:605:ILE:HD11	1:B:644:GLY:HA3	1.85	0.58
2:H:231:LEU:HD13	2:G:271:ARG:NE	2.18	0.58
2:G:218:MET:CG	2:G:219:LEU:H	2.05	0.58
1:D:312:GLU:OE1	1:D:323:HIS:ND1	2.33	0.58
1:E:587:LYS:HZ3	1:E:587:LYS:C	2.06	0.58
1:C:621:LEU:HD11	1:D:575:GLY:HA2	1.85	0.58
1:E:289:GLU:C	1:E:291:LEU:H	2.05	0.58
1:D:242:PRO:HD2	1:D:243:GLU:H	1.69	0.58
1:F:284:VAL:HG23	1:F:324:ILE:O	2.03	0.58
1:A:353:GLN:HA	1:B:288:PRO:CG	2.34	0.58
1:B:631:LYS:NZ	1:C:604:ASP:OD2	2.36	0.58
2:H:21:VAL:HG21	2:H:71:LEU:HD22	1.84	0.58
1:B:236:ALA:HA	1:B:239:VAL:HG12	1.86	0.58
2:I:108:ILE:HD12	2:I:127:ILE:HD12	1.85	0.58
1:E:296:GLY:H	1:E:297:GLU:CB	2.17	0.58
1:A:257:LEU:HG	1:A:389:LEU:HD12	1.86	0.58
1:C:289:GLU:O	1:C:291:LEU:N	2.31	0.58
1:C:490:PRO:HA	1:C:491:ALA:CB	2.28	0.58
1:D:313:GLN:O	1:D:317:GLY:N	2.36	0.58
1:B:64:LEU:HA	1:B:67:ARG:HE	1.69	0.58
1:F:715:GLU:O	1:F:719:GLN:HG2	2.04	0.58
1:E:270:ALA:O	1:E:273:ILE:HG22	2.04	0.58
1:F:566:LYS:HD2	1:F:567:ILE:N	2.19	0.58
1:C:507:ILE:CD1	1:C:555:LYS:CD	2.79	0.57
1:A:571:ASP:HA	1:A:574:ILE:HG23	1.86	0.57
1:A:428:GLU:HG2	1:A:479:ASP:CA	2.31	0.57
2:H:94:LYS:CE	2:I:153:LYS:HG3	2.34	0.57
1:D:687:LYS:O	1:D:691:ARG:HG3	2.05	0.57
5:M:170:GLU:HG3	5:M:174:GLN:HE21	1.68	0.57
1:A:726:VAL:O	1:A:730:LEU:HG	2.04	0.57
1:D:18:LEU:HA	1:D:137:VAL:HG23	1.85	0.57
1:A:18:LEU:HD13	1:A:139:SER:HB2	1.84	0.57
2:J:201:SER:OG	2:J:205:TYR:HE1	1.81	0.57
1:C:614:ILE:C	1:C:616:PRO:HA	2.24	0.57
1:A:549:LYS:HE3	1:A:646:THR:C	2.24	0.57
1:C:658:LEU:HD11	1:C:664:THR:HG21	1.86	0.57
1:F:604:ASP:HB3	1:F:607:ARG:HB2	1.85	0.57
1:B:423:ASP:HB2	1:B:479:ASP:N	2.19	0.57
1:B:695:ALA:HB1	1:B:699:LYS:HE3	1.85	0.57
1:F:106:ASN:HB3	1:F:143:LYS:NZ	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:218:ASP:O	4:L:222:LEU:HG	2.03	0.57
1:E:171:LYS:HB3	1:E:171:LYS:NZ	2.20	0.57
1:C:688:ASP:OD1	1:C:691:ARG:NH2	2.26	0.57
1:F:606:GLU:OE2	1:F:647:SER:HB2	2.04	0.57
2:H:271:ARG:HH22	2:I:231:LEU:HB2	1.69	0.57
1:C:510:TRP:CE3	1:C:670:ILE:HG12	2.39	0.57
2:G:235:PHE:CD2	5:M:152:GLN:HA	2.40	0.57
2:I:235:PHE:CB	4:L:207:ASN:HB3	2.35	0.57
1:A:542:GLU:OE2	1:A:666:HIS:NE2	2.37	0.57
1:C:256:ILE:HG22	1:C:391:VAL:HG11	1.84	0.57
1:A:299:GLU:HG2	1:A:353:GLN:HG2	1.86	0.57
2:H:149:ALA:HB2	2:H:164:CYS:HB2	1.86	0.57
1:E:267:THR:HA	1:E:372:MET:SD	2.44	0.57
1:D:380:ASP:OD1	1:D:382:ALA:N	2.36	0.57
1:E:697:GLN:HG3	1:E:730:LEU:HD11	1.84	0.57
1:A:536:LEU:HD23	1:A:633:ALA:HA	1.86	0.57
1:A:445:VAL:O	1:A:449:GLN:HG2	2.04	0.57
1:B:289:GLU:O	1:B:291:LEU:N	2.28	0.57
1:E:721:ASP:O	1:E:725:ARG:HG3	2.05	0.57
1:A:560:SER:HB2	1:A:562:PHE:CE1	2.40	0.57
1:D:604:ASP:HB3	1:D:607:ARG:HB3	1.86	0.57
1:E:550:THR:HA	1:E:645:THR:HG21	1.85	0.57
1:B:589:PHE:CE2	1:B:629:LEU:HB3	2.39	0.57
1:A:678:GLU:O	1:A:681:GLU:HG2	2.04	0.57
1:D:628:VAL:HG13	1:E:571:ASP:OD1	2.02	0.57
1:D:404:LEU:HD11	1:D:427:LYS:HE3	1.85	0.57
1:F:653:GLN:HB3	1:F:658:LEU:HD23	1.86	0.57
1:D:528:THR:OG1	1:D:537:VAL:HG21	2.05	0.57
4:L:199:HIS:CD2	5:M:21:LEU:HD13	2.39	0.57
1:F:242:PRO:HD2	1:F:243:GLU:H	1.69	0.57
1:D:223:LEU:HD12	1:D:395:ILE:HG23	1.87	0.57
2:G:256:VAL:HG11	2:G:288:GLN:HG2	1.87	0.57
2:H:116:ARG:NH2	3:K:68:ASP:HB3	2.20	0.57
1:B:110:ASN:HB3	1:B:111:PRO:HD2	1.85	0.57
1:C:540:LEU:HD23	1:C:649:LYS:HE3	1.86	0.57
1:A:352:ASN:HA	1:A:355:LEU:HD12	1.87	0.57
1:D:625:ALA:O	1:D:629:LEU:HG	2.04	0.57
1:E:27:LYS:N	1:E:27:LYS:HD2	2.20	0.57
1:F:562:PHE:HE2	1:F:597:LEU:HD12	1.69	0.57
1:C:677:LEU:HD11	1:C:698:VAL:HG21	1.87	0.57
1:F:296:GLY:H	1:F:297:GLU:CB	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:397:LEU:HD22	1:E:398:PRO:HD2	1.86	0.57
2:J:96:ASP:H	2:J:97:PRO:HD2	1.70	0.57
1:A:267:THR:OG1	1:A:328:ASP:OD2	2.23	0.57
2:J:231:LEU:O	2:J:234:ALA:N	2.19	0.57
1:E:673:GLY:HA3	1:E:698:VAL:HB	1.87	0.57
1:C:436:PHE:HB3	1:C:440:GLU:OE1	2.05	0.57
1:B:542:GLU:O	1:B:542:GLU:HG3	2.05	0.57
1:F:562:PHE:HB2	1:F:565:ILE:HG12	1.86	0.56
1:E:190:ASN:ND2	1:E:316:LEU:HG	2.17	0.56
1:A:489:LYS:N	1:A:490:PRO:HD2	2.19	0.56
1:B:296:GLY:H	1:B:297:GLU:CB	2.18	0.56
1:A:295:VAL:HB	1:B:294:TYR:CB	2.34	0.56
1:A:568:CYS:O	1:A:603:ASP:HB3	2.04	0.56
1:D:300:ALA:O	1:D:303:ARG:HB3	2.05	0.56
1:B:404:LEU:HG	1:B:426:ILE:HG22	1.87	0.56
1:D:686:PHE:HB2	1:D:691:ARG:HG2	1.87	0.56
1:B:654:GLU:O	1:C:613:PRO:HG3	2.04	0.56
1:A:513:PRO:O	1:A:517:VAL:HG23	2.05	0.56
1:C:555:LYS:HA	1:C:558:GLU:OE1	2.05	0.56
1:F:632:LYS:HD2	1:F:633:ALA:H	1.71	0.56
1:D:312:GLU:CG	1:D:313:GLN:N	2.67	0.56
1:D:313:GLN:HG3	1:D:314:ARG:N	2.20	0.56
3:K:63:LEU:HD13	5:M:182:MET:HG2	1.87	0.56
1:A:690:GLU:O	1:A:694:ILE:HG13	2.04	0.56
1:C:375:ARG:NH2	1:C:377:ASP:OD1	2.38	0.56
1:D:656:GLU:OE1	1:E:613:PRO:HB3	2.05	0.56
4:L:199:HIS:CG	5:M:21:LEU:HD13	2.40	0.56
1:E:693:THR:O	1:E:697:GLN:NE2	2.20	0.56
1:A:544:PRO:HB2	1:A:669:ASN:ND2	2.21	0.56
1:D:493:GLY:HA2	1:D:496:GLN:CB	2.36	0.56
1:A:565:ILE:HG13	1:A:599:CYS:HB3	1.88	0.56
1:B:559:GLU:O	1:B:561:ASN:ND2	2.38	0.56
2:H:230:GLU:HG2	2:H:231:LEU:N	2.20	0.56
4:L:202:ILE:O	4:L:205:LEU:HB3	2.05	0.56
1:E:598:SER:OG	1:E:639:LYS:O	2.20	0.56
2:J:266:TYR:CZ	2:J:270:SER:HB2	2.40	0.56
1:D:284:VAL:HB	1:D:325:ILE:HA	1.87	0.56
1:A:64:LEU:HA	1:A:67:ARG:HE	1.71	0.56
1:F:542:GLU:HB2	1:F:666:HIS:HA	1.87	0.56
1:C:694:ILE:O	1:C:698:VAL:HG22	2.05	0.56
1:E:352:ASN:HA	1:E:355:LEU:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:53:LYS:HE3	2:G:117:PHE:CE2	2.40	0.56
1:D:299:GLU:OE1	1:D:350:VAL:HG13	2.06	0.56
1:A:539:VAL:HG13	1:A:643:ILE:HA	1.87	0.56
1:B:242:PRO:HD2	1:B:243:GLU:H	1.71	0.56
1:B:327:PHE:HB2	1:B:330:ILE:CG2	2.33	0.56
1:E:502:TYR:CZ	1:E:567:ILE:HG21	2.40	0.56
1:E:648:ARG:NE	1:E:650:ASP:OD1	2.32	0.56
1:C:503:ILE:HG22	1:C:506:GLY:HA2	1.86	0.56
1:C:245:VAL:O	1:C:249:GLY:N	2.36	0.56
1:B:545:PRO:O	1:B:546:HIS:HB2	2.05	0.56
1:E:98:GLU:HB3	1:E:148:LEU:HB3	1.87	0.56
1:A:73:SER:O	1:A:76:GLN:HG2	2.06	0.56
1:C:330:ILE:HG22	1:C:379:ILE:CD1	2.36	0.56
1:E:490:PRO:HA	1:E:491:ALA:CB	2.33	0.56
1:C:653:GLN:HG3	1:C:658:LEU:HD23	1.86	0.56
2:I:200:TYR:CE2	4:L:211:GLU:HG3	2.41	0.56
5:M:26:LEU:HD22	5:M:146:MET:HE3	1.88	0.56
1:A:223:LEU:CD1	1:A:227:PHE:HB2	2.36	0.56
1:D:40:SER:OG	1:D:41:PRO:HD2	2.06	0.56
1:F:267:THR:HA	1:F:372:MET:SD	2.45	0.56
2:H:256:VAL:HG21	2:H:288:GLN:HG3	1.88	0.56
1:A:540:LEU:HD11	1:A:646:THR:HG22	1.86	0.56
1:A:525:VAL:HG13	1:A:562:PHE:CE1	2.40	0.56
2:H:271:ARG:HH22	2:I:231:LEU:CB	2.17	0.56
1:C:375:ARG:NH1	1:C:378:LEU:HG	2.20	0.56
2:I:127:ILE:HG23	2:I:131:TYR:CE1	2.41	0.56
2:H:179:GLN:HB3	2:H:214:PHE:HB3	1.88	0.56
1:F:559:GLU:OE1	1:F:559:GLU:HA	2.06	0.56
1:F:602:VAL:N	1:F:643:ILE:O	2.23	0.56
2:I:67:GLN:O	2:I:71:LEU:HG	2.06	0.56
1:D:627:LEU:HD13	1:E:607:ARG:HH12	1.70	0.56
1:C:40:SER:OG	1:C:43:HIS:HB2	2.05	0.56
5:M:42:ALA:HA	5:M:45:ARG:CZ	2.36	0.56
2:J:69:ALA:HB1	2:J:85:PHE:CE1	2.41	0.56
1:F:270:ALA:O	1:F:273:ILE:HG22	2.06	0.56
2:J:218:MET:CG	2:J:219:LEU:H	2.14	0.55
1:B:10:ARG:NE	2:H:293:ASP:OD2	2.34	0.55
1:E:681:GLU:HA	1:E:691:ARG:HE	1.71	0.55
1:C:688:ASP:O	1:C:692:THR:HG23	2.07	0.55
1:E:354:LEU:O	1:E:358:ILE:HG12	2.06	0.55
1:A:536:LEU:HD23	1:A:634:PRO:HD3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:ARG:HD2	2:H:218:MET:CG	2.35	0.55
1:B:398:PRO:HG3	1:B:436:PHE:O	2.06	0.55
1:E:528:THR:HG21	1:E:641:LEU:CD2	2.27	0.55
4:L:233:ILE:O	4:L:237:VAL:HG23	2.06	0.55
2:J:243:LEU:HD22	2:J:266:TYR:CG	2.41	0.55
1:E:705:ILE:HG13	1:E:709:LYS:HG3	1.88	0.55
5:M:50:LEU:HD12	5:M:167:MET:HG2	1.88	0.55
2:G:57:ASN:O	2:G:59:SER:N	2.39	0.55
1:C:106:ASN:HB3	1:C:143:LYS:NZ	2.21	0.55
1:A:549:LYS:HG3	1:A:550:THR:N	2.21	0.55
1:E:242:PRO:HD2	1:E:243:GLU:H	1.70	0.55
1:E:573:MET:SD	1:E:581:LYS:HG2	2.46	0.55
1:A:709:LYS:HA	1:A:709:LYS:HE2	1.89	0.55
1:F:69:TRP:NE1	1:F:134:GLN:HA	2.21	0.55
1:B:198:LYS:N	1:B:198:LYS:HD2	2.21	0.55
5:M:56:GLN:O	5:M:60:VAL:HG23	2.05	0.55
1:E:232:ARG:NH2	1:F:454:ASN:H	2.03	0.55
1:F:554:ALA:O	1:F:558:GLU:HG3	2.06	0.55
2:H:119:ILE:HD13	3:K:65:ASP:OD1	2.06	0.55
1:A:531:SER:O	1:A:639:LYS:HE2	2.07	0.55
1:B:270:ALA:O	1:B:273:ILE:HG22	2.06	0.55
1:A:383:LEU:O	1:A:389:LEU:HB2	2.07	0.55
1:C:128:GLN:O	1:C:176:LEU:HD12	2.07	0.55
1:F:91:CYS:O	1:F:154:ALA:HA	2.07	0.55
1:A:724:TYR:HD1	1:A:727:ARG:HH12	1.54	0.55
2:J:182:ILE:O	2:J:186:GLU:HG2	2.07	0.55
2:J:175:LEU:HD23	2:J:177:GLN:HE21	1.70	0.55
1:C:507:ILE:HD12	1:C:555:LYS:HD3	1.89	0.55
1:D:510:TRP:CE3	1:D:675:GLN:HG2	2.34	0.55
1:C:256:ILE:HA	1:C:391:VAL:HG13	1.87	0.55
1:A:355:LEU:HB3	1:A:388:ARG:NH1	2.21	0.55
1:B:289:GLU:C	1:B:291:LEU:H	2.09	0.55
3:K:70:LEU:HD13	5:M:185:ALA:O	2.07	0.55
1:C:95:MET:HG3	1:C:152:ILE:HG12	1.87	0.55
2:I:175:LEU:HD23	2:I:177:GLN:HE21	1.72	0.55
1:C:327:PHE:CB	1:C:330:ILE:HD11	2.28	0.55
4:L:211:GLU:HA	4:L:214:ASP:OD2	2.07	0.55
1:F:354:LEU:O	1:F:358:ILE:HG12	2.07	0.55
1:B:354:LEU:O	1:B:358:ILE:HG12	2.05	0.55
2:H:72:HIS:CE1	2:H:80:ASP:HB2	2.42	0.55
1:B:552:LEU:O	1:B:556:ILE:HG13	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:213:HIS:CD2	5:M:35:LEU:HB3	2.42	0.55
1:A:705:ILE:HD13	1:A:710:LEU:CD1	2.34	0.55
1:D:681:GLU:HG2	1:D:691:ARG:NH1	2.21	0.55
2:H:182:ILE:O	2:H:186:GLU:HG2	2.06	0.55
1:C:284:VAL:HG11	1:C:305:LEU:HD11	1.88	0.55
1:A:688:ASP:OD1	1:A:689:LYS:N	2.40	0.55
1:E:449:GLN:O	1:E:453:MET:HG2	2.05	0.55
3:K:37:ALA:HA	3:K:40:ASP:OD2	2.06	0.55
1:E:604:ASP:O	1:E:608:LEU:N	2.38	0.55
1:A:485:GLU:O	1:A:489:LYS:CB	2.54	0.55
1:A:40:SER:OG	1:A:41:PRO:HD2	2.07	0.55
5:M:149:ASN:O	5:M:153:VAL:HG23	2.07	0.55
1:F:617:ARG:HG3	1:F:617:ARG:HH11	1.72	0.55
5:M:26:LEU:HB2	5:M:146:MET:HE2	1.88	0.55
1:B:421:SER:HB3	1:B:424:VAL:HG23	1.87	0.55
1:D:40:SER:HB3	1:D:43:HIS:HB2	1.88	0.55
2:J:101:ILE:HG21	2:J:135:LEU:HD11	1.89	0.55
1:A:286:ASN:HB2	1:A:327:PHE:CB	2.37	0.55
1:A:562:PHE:CD2	1:A:597:LEU:CD2	2.83	0.54
3:K:52:LYS:NZ	3:K:52:LYS:HB2	2.23	0.54
1:A:406:ILE:O	1:A:409:ILE:HG22	2.06	0.54
1:B:267:THR:HA	1:B:372:MET:SD	2.47	0.54
4:L:202:ILE:CG2	5:M:25:SER:HB3	2.37	0.54
1:F:538:SER:OG	1:F:661:PHE:HD1	1.88	0.54
1:A:398:PRO:HG3	1:A:437:SER:HA	1.90	0.54
1:D:690:GLU:O	1:D:693:THR:OG1	2.21	0.54
1:A:315:ARG:HG2	1:A:316:LEU:CD1	2.37	0.54
1:A:293:LYS:O	1:A:294:TYR:CG	2.60	0.54
1:A:563:PRO:HG2	1:A:597:LEU:O	2.06	0.54
1:C:355:LEU:O	1:C:388:ARG:NH2	2.34	0.54
1:B:570:PRO:HG3	1:B:608:LEU:HD23	1.88	0.54
1:D:686:PHE:CE1	1:D:714:ILE:HG23	2.42	0.54
1:F:721:ASP:HB2	1:F:724:TYR:CD1	2.41	0.54
2:I:231:LEU:O	2:I:234:ALA:N	2.40	0.54
1:C:577:SER:O	1:C:579:THR:N	2.40	0.54
1:E:508:ILE:HB	1:E:682:LEU:HD13	1.89	0.54
1:F:89:LYS:O	1:F:172:ILE:HG21	2.07	0.54
1:D:423:ASP:HB2	1:D:480:PHE:CB	2.37	0.54
1:A:677:LEU:HG	1:A:695:ALA:HB2	1.88	0.54
1:B:64:LEU:HB2	2:H:293:ASP:C	2.28	0.54
2:J:243:LEU:HD13	2:J:266:TYR:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:570:PRO:HD3	1:B:603:ASP:HB3	1.90	0.54
1:D:651:VAL:HG13	1:D:655:MET:HE3	1.88	0.54
5:M:78:LEU:CD1	5:M:195:ALA:HB1	2.37	0.54
1:B:571:ASP:O	1:B:574:ILE:HG13	2.08	0.54
1:A:625:ALA:O	1:A:629:LEU:HG	2.08	0.54
1:A:570:PRO:HD3	1:A:603:ASP:OD2	2.08	0.54
1:D:353:GLN:NE2	1:E:288:PRO:HG2	2.21	0.54
1:A:457:ILE:HG13	1:F:240:PHE:HE1	1.73	0.54
1:C:281:GLU:CB	1:C:324:ILE:HD13	2.38	0.54
1:B:527:GLN:NE2	1:C:716:MET:SD	2.69	0.54
1:E:590:ASP:O	1:E:593:TYR:HB2	2.08	0.54
1:D:657:MET:HG2	1:D:661:PHE:CE2	2.42	0.54
1:C:570:PRO:HG2	1:C:604:ASP:HB2	1.90	0.54
1:F:686:PHE:HE1	1:F:714:ILE:HG23	1.73	0.54
1:C:589:PHE:CD2	1:C:629:LEU:HD13	2.42	0.54
2:J:112:THR:HG23	2:J:117:PHE:HE1	1.73	0.54
1:A:686:PHE:CE2	1:A:714:ILE:HG23	2.43	0.54
2:G:142:ILE:HG23	2:G:168:VAL:HG13	1.89	0.54
1:A:672:THR:OG1	1:A:675:GLN:OE1	2.14	0.54
1:A:565:ILE:HA	1:A:599:CYS:O	2.08	0.54
2:H:124:HIS:HE1	2:H:147:GLN:HB3	1.73	0.54
2:I:124:HIS:HE1	2:I:147:GLN:HB3	1.72	0.54
1:E:8:ALA:HB3	1:E:73:SER:O	2.08	0.54
5:M:156:ILE:HG22	5:M:160:LEU:HG	1.89	0.54
1:C:388:ARG:NH1	1:C:388:ARG:HB2	2.23	0.54
1:C:690:GLU:CB	1:C:726:VAL:HG21	2.36	0.54
1:D:356:SER:HB2	1:E:288:PRO:HG3	1.90	0.54
1:E:516:ARG:O	1:E:519:ASP:OD1	2.25	0.54
1:A:286:ASN:HB2	1:A:327:PHE:HB3	1.90	0.54
4:L:229:MET:O	4:L:233:ILE:HG13	2.08	0.54
1:E:236:ALA:O	1:E:239:VAL:HG12	2.08	0.54
1:A:610:ASP:OD1	1:F:624:GLN:HG3	2.06	0.54
1:A:407:LEU:HD12	1:A:426:ILE:HG23	1.90	0.54
1:D:260:GLY:N	1:D:266:LYS:HD3	2.23	0.54
1:C:63:SER:O	1:C:67:ARG:HG3	2.08	0.54
1:C:34:HIS:HB2	1:C:83:TYR:O	2.08	0.54
1:C:399:ASP:O	1:C:402:GLY:N	2.41	0.54
1:F:40:SER:HB2	1:F:41:PRO:HD2	1.90	0.54
5:M:61:GLU:HG2	5:M:65:ASN:ND2	2.19	0.53
1:B:539:VAL:HG21	1:B:665:ILE:HD12	1.88	0.53
1:F:113:ASP:O	1:F:117:MET:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:ILE:HD12	1:C:174:VAL:HG21	1.89	0.53
5:M:29:THR:HB	5:M:150:LEU:HD21	1.89	0.53
2:J:201:SER:HA	5:M:161:ARG:HD2	1.90	0.53
1:F:535:PRO:HB2	1:F:536:LEU:HD13	1.90	0.53
1:C:242:PRO:HD2	1:C:243:GLU:H	1.73	0.53
1:E:585:MET:HG3	1:E:589:PHE:HZ	1.70	0.53
5:M:143:GLU:HA	5:M:146:MET:HB3	1.89	0.53
2:J:179:GLN:HB3	2:J:214:PHE:CG	2.43	0.53
1:F:522:GLU:OE2	1:F:526:GLN:HG2	2.09	0.53
1:B:452:ALA:HA	1:B:455:ARG:NH2	2.23	0.53
1:A:122:ILE:O	1:A:126:ASN:HB3	2.08	0.53
1:E:149:VAL:HG11	1:E:152:ILE:HD11	1.89	0.53
1:D:593:TYR:O	1:D:638:ARG:HG2	2.08	0.53
1:A:521:GLY:HA2	1:A:524:LEU:HD12	1.89	0.53
2:H:20:LYS:HE2	2:H:37:LYS:HA	1.89	0.53
1:C:347:HIS:O	1:C:350:VAL:HG22	2.08	0.53
1:F:555:LYS:HA	1:F:555:LYS:HE2	1.90	0.53
2:J:218:MET:HG2	2:J:219:LEU:N	2.19	0.53
1:E:313:GLN:HE21	1:E:317:GLY:HA3	1.72	0.53
1:C:612:VAL:HG12	1:C:617:ARG:HB3	1.90	0.53
1:B:101:PHE:HZ	1:B:193:LEU:HD13	1.72	0.53
2:I:120:ALA:O	2:I:124:HIS:HB2	2.08	0.53
1:C:536:LEU:HD12	1:C:640:LEU:HB3	1.89	0.53
2:H:95:ALA:HB1	2:H:97:PRO:HD2	1.91	0.53
2:I:232:PHE:C	2:I:234:ALA:H	2.12	0.53
3:K:68:ASP:O	3:K:71:GLN:HG3	2.09	0.53
1:F:503:ILE:HG22	1:F:506:GLY:H	1.73	0.53
1:F:710:LEU:O	1:F:714:ILE:HG13	2.09	0.53
1:F:26:GLU:HG2	1:F:51:THR:HB	1.91	0.53
1:F:184:ALA:HB1	1:F:200:LYS:O	2.09	0.53
5:M:67:ILE:O	5:M:71:MET:HG2	2.08	0.53
1:F:525:VAL:HG11	1:F:560:SER:CB	2.38	0.53
1:D:510:TRP:HB3	1:D:679:ALA:HB2	1.90	0.53
1:B:576:PHE:HB2	1:B:581:LYS:HG3	1.90	0.53
2:I:254:GLN:HB2	2:I:291:GLU:HG2	1.89	0.53
1:D:731:ALA:HA	1:D:734:ARG:NH1	2.23	0.53
2:I:179:GLN:O	2:I:182:ILE:HG12	2.08	0.53
1:D:136:LEU:H	1:D:136:LEU:HD23	1.73	0.53
1:B:184:ALA:HB1	1:B:200:LYS:O	2.07	0.53
1:F:525:VAL:HG11	1:F:560:SER:HB2	1.91	0.53
1:D:522:GLU:OE2	1:D:556:ILE:HA	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:569:SER:HA	1:B:603:ASP:HB3	1.91	0.53
1:D:686:PHE:HB3	1:D:690:GLU:HG3	1.91	0.53
1:D:14:ASP:O	1:D:18:LEU:HG	2.08	0.53
1:B:546:HIS:O	1:B:549:LYS:HE3	2.09	0.53
1:D:263:GLY:O	1:D:439:ALA:N	2.38	0.53
1:E:664:THR:C	1:E:665:ILE:HD13	2.29	0.53
1:A:421:SER:HB3	1:A:424:VAL:CG2	2.33	0.53
5:M:33:LEU:HA	5:M:153:VAL:HG22	1.90	0.53
1:E:307:ALA:HA	1:E:310:GLU:HG2	1.91	0.53
1:A:306:PHE:CD1	1:A:357:LYS:HB3	2.44	0.53
1:B:310:GLU:OE2	1:B:357:LYS:NZ	2.41	0.53
1:E:89:LYS:NZ	1:E:89:LYS:HB3	2.23	0.53
1:C:38:ARG:HB3	1:C:79:GLU:HB2	1.91	0.53
1:A:347:HIS:N	1:A:348:ASP:HA	2.23	0.53
1:A:300:ALA:HA	1:A:303:ARG:HG2	1.91	0.53
1:F:34:HIS:HB2	1:F:83:TYR:O	2.08	0.53
1:F:605:ILE:HD11	1:F:644:GLY:HA3	1.89	0.53
1:D:303:ARG:HD3	1:D:353:GLN:CD	2.28	0.53
1:A:255:GLY:HA3	1:A:389:LEU:HD13	1.90	0.53
1:C:606:GLU:HB2	1:C:648:ARG:HD2	1.90	0.53
1:D:101:PHE:CD2	1:D:107:ILE:HA	2.44	0.53
1:F:635:PRO:HD2	1:F:638:ARG:HD2	1.90	0.52
1:A:550:THR:HG23	1:A:603:ASP:OD1	2.08	0.52
1:D:67:ARG:NH1	1:D:74:ILE:HD11	2.24	0.52
1:D:528:THR:HG22	1:D:597:LEU:HD11	1.90	0.52
2:I:219:LEU:HA	2:I:222:LYS:HB3	1.91	0.52
2:G:179:GLN:O	2:G:182:ILE:HG12	2.09	0.52
2:H:235:PHE:HB3	5:M:31:ARG:HB3	1.91	0.52
1:E:540:LEU:HD12	1:E:541:LEU:N	2.24	0.52
1:F:517:VAL:HG13	1:F:665:ILE:CG2	2.38	0.52
2:J:225:VAL:HG23	2:J:241:CYS:HB2	1.91	0.52
1:F:612:VAL:HG13	1:F:614:ILE:O	2.10	0.52
1:D:680:LEU:HB2	1:D:691:ARG:HH21	1.73	0.52
1:D:527:GLN:HE22	1:E:716:MET:HA	1.73	0.52
3:K:73:GLY:HA3	5:M:189:LYS:HE2	1.91	0.52
1:A:68:LYS:HD2	2:H:219:LEU:CD2	2.39	0.52
4:L:210:ARG:HG2	4:L:210:ARG:HH11	1.75	0.52
1:D:604:ASP:HB3	1:D:607:ARG:HB2	1.91	0.52
1:A:437:SER:OG	1:A:440:GLU:HG2	2.09	0.52
5:M:177:GLN:O	5:M:181:ILE:HG13	2.09	0.52
1:F:720:MET:HB3	1:F:724:TYR:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:127:ILE:HG23	2:H:131:TYR:CE1	2.44	0.52
1:B:656:GLU:OE1	1:C:648:ARG:NH2	2.42	0.52
1:B:402:GLY:O	1:B:406:ILE:HD12	2.10	0.52
1:C:308:ASP:OD1	1:C:309:ALA:N	2.42	0.52
1:A:611:TYR:CE2	1:A:651:VAL:HG11	2.44	0.52
1:F:515:THR:HA	1:F:518:LEU:CD1	2.39	0.52
2:I:39:GLU:HB2	2:I:75:LEU:CD1	2.39	0.52
1:C:677:LEU:HD21	1:C:695:ALA:CB	2.40	0.52
2:J:127:ILE:HG23	2:J:131:TYR:CE1	2.43	0.52
2:H:69:ALA:HB1	2:H:85:PHE:CE1	2.44	0.52
2:I:159:SER:OG	3:K:55:GLU:HG2	2.09	0.52
1:C:45:TYR:CE2	1:C:70:ALA:HA	2.44	0.52
2:I:149:ALA:HB2	2:I:164:CYS:HB2	1.92	0.52
5:M:68:ASN:O	5:M:72:LYS:HG3	2.10	0.52
1:F:315:ARG:HG3	1:F:316:LEU:HD12	1.90	0.52
3:K:83:LYS:HB3	5:M:203:LEU:HD21	1.92	0.52
1:F:310:GLU:OE2	1:F:357:LYS:NZ	2.42	0.52
2:G:267:ASP:CG	2:G:271:ARG:HH11	2.13	0.52
2:H:126:SER:O	2:H:130:ILE:HG13	2.09	0.52
1:B:503:ILE:HD11	1:B:554:ALA:HB3	1.90	0.52
1:E:128:GLN:O	1:E:176:LEU:HD12	2.10	0.52
2:G:127:ILE:HG23	2:G:131:TYR:CE1	2.44	0.52
1:E:696:GLN:HB3	1:E:697:GLN:NE2	2.25	0.52
1:A:64:LEU:O	1:A:68:LYS:HG2	2.10	0.52
1:E:536:LEU:HD22	1:E:634:PRO:HD3	1.92	0.52
4:L:216:PHE:CE2	5:M:160:LEU:HD22	2.45	0.52
1:D:326:ILE:HG22	1:D:370:ILE:HG13	1.92	0.52
2:G:40:GLU:O	2:G:44:ILE:HG12	2.09	0.52
1:A:454:ASN:HA	1:F:232:ARG:CZ	2.39	0.52
1:B:728:LYS:HE3	1:B:732:LEU:HD21	1.90	0.52
5:M:26:LEU:O	5:M:30:ARG:HG3	2.10	0.52
2:G:243:LEU:HD13	2:G:266:TYR:HB2	1.92	0.52
1:D:136:LEU:N	1:D:136:LEU:HD23	2.25	0.52
2:H:244:MET:O	2:H:248:LEU:HG	2.10	0.52
1:C:227:PHE:O	1:C:231:PHE:HB2	2.09	0.52
1:C:231:PHE:O	1:C:235:PHE:HB2	2.10	0.52
1:A:73:SER:HA	2:H:218:MET:SD	2.49	0.52
1:C:611:TYR:HE1	1:C:616:PRO:HB2	1.75	0.52
1:C:686:PHE:CE1	1:C:714:ILE:HG23	2.45	0.52
1:A:356:SER:HB2	1:B:288:PRO:HD3	1.91	0.52
1:B:533:ARG:HG3	1:B:534:THR:N	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:596:GLN:HA	1:C:638:ARG:CD	2.38	0.52
1:E:612:VAL:HG11	1:E:617:ARG:HH21	1.74	0.52
1:A:223:LEU:HD12	1:A:227:PHE:HB2	1.91	0.52
1:D:187:LYS:NZ	1:D:316:LEU:HD11	2.25	0.52
1:D:512:ASP:N	1:D:513:PRO:CD	2.73	0.52
2:H:179:GLN:O	2:H:182:ILE:HG12	2.10	0.52
1:B:122:ILE:O	1:B:126:ASN:HB3	2.09	0.52
1:E:618:PHE:CZ	1:F:612:VAL:HG11	2.31	0.51
1:A:258:LEU:O	1:A:372:MET:HA	2.09	0.51
1:A:227:PHE:CE1	1:A:273:ILE:HD13	2.45	0.51
1:D:18:LEU:HD13	1:D:144:LEU:HD21	1.90	0.51
2:G:244:MET:O	2:G:248:LEU:HG	2.10	0.51
1:D:24:VAL:O	1:D:51:THR:HA	2.10	0.51
1:D:184:ALA:HB1	1:D:200:LYS:O	2.10	0.51
1:A:136:LEU:HD23	1:A:136:LEU:N	2.25	0.51
3:K:49:ASN:HB3	4:L:219:MET:CE	2.39	0.51
1:C:285:VAL:HA	1:C:326:ILE:HG13	1.92	0.51
2:I:40:GLU:O	2:I:44:ILE:HG12	2.11	0.51
1:D:539:VAL:HG23	1:D:663:THR:CG2	2.41	0.51
1:C:64:LEU:O	1:C:68:LYS:HG3	2.10	0.51
3:K:84:LEU:HD13	5:M:78:LEU:HD22	1.91	0.51
1:E:45:TYR:CE2	1:E:70:ALA:HA	2.45	0.51
2:G:78:LYS:HB3	2:G:110:ILE:HG23	1.92	0.51
2:J:149:ALA:HB2	2:J:164:CYS:HB2	1.91	0.51
5:M:156:ILE:O	5:M:160:LEU:HG	2.09	0.51
1:C:616:PRO:HG2	1:D:614:ILE:HD13	1.92	0.51
1:F:327:PHE:HB2	1:F:330:ILE:CG2	2.33	0.51
1:D:657:MET:HG2	1:D:661:PHE:HE2	1.75	0.51
1:A:489:LYS:H	1:A:490:PRO:HD2	1.75	0.51
1:E:106:ASN:HB3	1:E:143:LYS:HZ1	1.73	0.51
3:K:88:TYR:HB2	5:M:81:LEU:HD11	1.91	0.51
1:B:626:LEU:O	1:B:630:LEU:HG	2.10	0.51
3:K:83:LYS:CD	5:M:203:LEU:HD11	2.33	0.51
1:C:686:PHE:HE1	1:C:714:ILE:HG23	1.75	0.51
1:E:627:LEU:HG	1:E:657:MET:HE1	1.92	0.51
1:D:528:THR:CB	1:D:641:LEU:HD12	2.40	0.51
1:C:612:VAL:CG1	1:C:617:ARG:HB3	2.40	0.51
1:C:399:ASP:O	1:C:403:ARG:N	2.39	0.51
1:E:666:HIS:CD2	1:E:668:PRO:HD3	2.45	0.51
1:E:136:LEU:N	1:E:136:LEU:HD23	2.25	0.51
2:H:235:PHE:CD1	5:M:31:ARG:HG2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:521:GLY:HA3	1:C:556:ILE:HD13	1.91	0.51
1:E:540:LEU:HD12	1:E:541:LEU:H	1.76	0.51
2:J:50:ASN:HD21	2:G:115:GLY:HA2	1.75	0.51
1:A:607:ARG:NH1	1:F:624:GLN:OE1	2.44	0.51
1:D:325:ILE:O	1:D:369:VAL:HA	2.10	0.51
1:C:728:LYS:HE3	1:C:732:LEU:HD21	1.91	0.51
1:A:184:ALA:HB1	1:A:200:LYS:O	2.10	0.51
1:C:270:ALA:O	1:C:273:ILE:HG22	2.10	0.51
1:C:121:PHE:CD2	1:C:183:VAL:HG21	2.46	0.51
1:D:254:LYS:O	1:D:368:LEU:HA	2.11	0.51
1:B:395:ILE:HD12	1:B:395:ILE:H	1.75	0.51
1:B:327:PHE:CZ	1:B:369:VAL:HG21	2.46	0.51
1:B:249:GLY:HA3	1:C:414:MET:CE	2.40	0.51
1:E:510:TRP:CE3	1:E:511:GLY:HA3	2.45	0.51
2:G:267:ASP:OD2	2:G:271:ARG:NH1	2.42	0.51
1:E:674:GLU:O	1:E:677:LEU:HB2	2.11	0.51
1:B:236:ALA:O	1:B:239:VAL:HG12	2.10	0.51
1:A:106:ASN:HB3	1:A:143:LYS:NZ	2.24	0.51
2:I:208:LYS:HG2	2:I:275:TRP:CZ3	2.45	0.51
1:E:121:PHE:HD2	1:E:183:VAL:HG21	1.75	0.51
1:F:122:ILE:O	1:F:126:ASN:HB3	2.10	0.51
4:L:225:SER:O	4:L:229:MET:HE2	2.10	0.51
1:E:327:PHE:CZ	1:E:369:VAL:HG21	2.46	0.51
2:J:233:PRO:HA	2:J:235:PHE:CZ	2.45	0.51
1:C:411:THR:O	1:C:414:MET:HB2	2.10	0.51
1:B:397:LEU:HD11	1:B:638:ARG:HH21	1.76	0.51
1:E:545:PRO:O	1:E:546:HIS:HB2	2.10	0.51
2:G:21:VAL:HG23	2:G:38:ILE:HD13	1.92	0.51
1:C:689:LYS:O	1:C:692:THR:OG1	2.19	0.51
1:D:602:VAL:O	1:D:644:GLY:HA2	2.11	0.51
1:D:524:LEU:HD13	1:D:663:THR:HG21	1.93	0.51
1:C:322:LEU:HD12	1:C:324:ILE:HD11	1.93	0.51
1:A:222:GLY:O	1:A:224:ASP:N	2.44	0.51
2:I:119:ILE:HD12	2:I:122:LYS:HB2	1.93	0.51
1:B:313:GLN:O	1:B:317:GLY:N	2.43	0.51
1:C:356:SER:HB3	1:D:288:PRO:HG3	1.92	0.51
1:F:512:ASP:OD1	1:F:513:PRO:HD3	2.10	0.51
1:F:542:GLU:O	1:F:666:HIS:ND1	2.44	0.51
1:F:658:LEU:HA	1:F:661:PHE:HD2	1.76	0.51
2:I:39:GLU:HB2	2:I:75:LEU:HD11	1.92	0.51
1:C:691:ARG:HB2	1:C:691:ARG:HH11	1.77	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:652:LEU:HD22	1:E:658:LEU:HD13	1.91	0.51
1:D:330:ILE:HD12	1:D:331:ASP:N	2.25	0.51
1:D:560:SER:HB2	1:D:562:PHE:CD1	2.45	0.51
1:F:609:LEU:HD13	1:F:655:MET:CE	2.41	0.51
1:A:270:ALA:HA	1:A:273:ILE:HG22	1.92	0.51
1:E:666:HIS:HD2	1:E:668:PRO:HD3	1.76	0.51
1:D:508:ILE:HG12	1:D:683:LEU:HD21	1.92	0.51
1:C:136:LEU:N	1:C:136:LEU:HD23	2.26	0.51
1:D:313:GLN:OE1	1:D:365:ASN:O	2.29	0.50
1:A:489:LYS:N	1:A:490:PRO:CD	2.74	0.50
1:C:542:GLU:HB2	1:C:649:LYS:HD3	1.93	0.50
1:D:677:LEU:O	1:D:691:ARG:NH2	2.44	0.50
1:D:589:PHE:CE2	1:D:629:LEU:HD13	2.46	0.50
1:D:257:LEU:HG	1:D:371:GLY:O	2.11	0.50
1:E:24:VAL:O	1:E:51:THR:HA	2.11	0.50
1:D:108:ASP:OD2	1:D:143:LYS:HE2	2.10	0.50
1:F:136:LEU:N	1:F:136:LEU:HD23	2.26	0.50
3:K:39:VAL:HG21	4:L:209:ILE:CD1	2.39	0.50
1:C:560:SER:HB2	1:C:562:PHE:CE1	2.46	0.50
2:G:235:PHE:CG	5:M:152:GLN:HG2	2.46	0.50
1:E:327:PHE:HB2	1:E:330:ILE:CG2	2.33	0.50
1:D:511:GLY:HA3	1:D:675:GLN:HE21	1.76	0.50
1:C:688:ASP:HA	1:C:691:ARG:NH1	2.26	0.50
1:D:128:GLN:O	1:D:176:LEU:HD12	2.12	0.50
1:A:300:ALA:O	1:A:304:LYS:HG3	2.10	0.50
1:C:121:PHE:HD2	1:C:183:VAL:HG21	1.76	0.50
1:A:16:LEU:HD11	1:A:52:HIS:HD2	1.75	0.50
2:H:185:TYR:HA	2:H:188:VAL:HG12	1.93	0.50
1:E:232:ARG:CZ	1:F:450:SER:O	2.58	0.50
1:C:614:ILE:O	1:C:616:PRO:HA	2.11	0.50
1:C:611:TYR:CZ	1:C:651:VAL:HG11	2.46	0.50
1:D:356:SER:OG	1:E:288:PRO:HB3	2.12	0.50
1:D:686:PHE:HE1	1:D:714:ILE:HG23	1.76	0.50
5:M:64:MET:HE3	5:M:181:ILE:O	2.11	0.50
1:A:242:PRO:HD2	1:A:243:GLU:CD	2.32	0.50
2:J:40:GLU:O	2:J:44:ILE:HG12	2.11	0.50
1:E:563:PRO:HD2	1:E:597:LEU:O	2.12	0.50
1:A:326:ILE:HG22	1:A:370:ILE:CG1	2.40	0.50
1:E:549:LYS:HG2	1:E:550:THR:N	2.26	0.50
1:D:540:LEU:HD12	1:D:661:PHE:CE1	2.46	0.50
2:I:116:ARG:HH22	5:M:183:GLU:HA	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:576:PHE:HB2	1:C:581:LYS:HE3	1.94	0.50
3:K:68:ASP:OD2	4:L:236:ASN:ND2	2.45	0.50
1:E:232:ARG:NH2	1:F:454:ASN:CB	2.74	0.50
1:D:593:TYR:OH	1:D:632:LYS:HD2	2.12	0.50
2:J:223:LEU:O	2:J:227:LYS:HG3	2.11	0.50
1:F:327:PHE:CZ	1:F:369:VAL:HG21	2.46	0.50
2:I:18:GLU:HA	2:I:21:VAL:HG12	1.93	0.50
1:C:404:LEU:HG	1:C:426:ILE:HG22	1.94	0.50
1:D:298:SER:O	1:D:301:ASN:HB3	2.11	0.50
1:B:576:PHE:HB3	1:B:580:ALA:HB3	1.92	0.50
2:J:72:HIS:CE1	2:J:77:SER:HB2	2.46	0.50
1:A:18:LEU:HD13	1:A:139:SER:CB	2.41	0.50
1:C:730:LEU:O	1:C:734:ARG:HG3	2.12	0.50
1:F:289:GLU:O	1:F:291:LEU:N	2.33	0.50
1:D:198:LYS:O	1:D:198:LYS:HD3	2.12	0.50
1:E:596:GLN:O	1:E:638:ARG:HA	2.12	0.50
5:M:36:VAL:HG23	5:M:156:ILE:HD12	1.94	0.50
1:E:232:ARG:HH21	1:F:454:ASN:N	2.07	0.50
1:F:529:LYS:HG3	1:F:597:LEU:HD11	1.93	0.50
2:J:53:LYS:HE3	2:G:117:PHE:CD2	2.47	0.50
2:G:243:LEU:HD22	2:G:266:TYR:CD2	2.47	0.50
2:I:72:HIS:CE1	2:I:80:ASP:HB2	2.47	0.50
1:D:375:ARG:NH2	1:D:377:ASP:OD2	2.42	0.50
1:F:188:ALA:O	1:F:191:SER:HB2	2.12	0.50
1:C:703:VAL:O	1:C:704:TRP:HD1	1.95	0.50
2:G:118:THR:O	2:G:122:LYS:HG2	2.12	0.50
4:L:209:ILE:HG21	5:M:32:MET:CG	2.40	0.50
1:E:256:ILE:O	1:E:370:ILE:HA	2.12	0.50
1:C:721:ASP:O	1:C:725:ARG:HG3	2.11	0.50
1:E:538:SER:OG	1:E:662:SER:N	2.40	0.50
3:K:56:ARG:HD2	5:M:171:ILE:HG12	1.94	0.50
1:A:612:VAL:HG12	1:A:617:ARG:HB2	1.93	0.50
2:G:180:LYS:O	2:G:184:ILE:HG13	2.12	0.50
2:H:79:HIS:CE1	3:K:72:ALA:HB1	2.46	0.50
1:B:428:GLU:O	1:B:432:GLU:HG2	2.12	0.50
2:I:244:MET:O	2:I:248:LEU:HG	2.12	0.50
1:C:428:GLU:O	1:C:432:GLU:HG2	2.12	0.50
1:C:445:VAL:HG12	1:C:449:GLN:HE22	1.76	0.50
1:B:23:VAL:HG12	1:B:55:VAL:HG21	1.93	0.50
1:C:568:CYS:HB2	1:C:602:VAL:HA	1.93	0.50
1:C:618:PHE:HE1	1:C:620:ASN:OD1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:GLN:O	1:A:176:LEU:HD12	2.12	0.50
2:I:53:LYS:HE3	2:J:117:PHE:CE2	2.46	0.50
1:A:149:VAL:HG11	1:A:152:ILE:HD11	1.94	0.50
1:D:402:GLY:HA2	1:D:405:GLN:OE1	2.12	0.50
1:D:91:CYS:O	1:D:154:ALA:HA	2.11	0.50
1:C:525:VAL:HG13	1:C:562:PHE:CZ	2.47	0.50
1:C:507:ILE:CD1	1:C:555:LYS:HD3	2.42	0.50
1:B:395:ILE:N	1:B:395:ILE:HD12	2.27	0.50
1:B:490:PRO:HA	1:B:491:ALA:CB	2.31	0.50
1:A:353:GLN:HA	1:B:288:PRO:HG3	1.94	0.50
1:F:303:ARG:CG	1:F:357:LYS:HE2	2.40	0.50
1:D:539:VAL:HG13	1:D:643:ILE:HG13	1.93	0.50
1:D:331:ASP:HA	1:D:379:ILE:HD11	1.92	0.50
1:A:14:ASP:O	1:A:18:LEU:HG	2.12	0.50
3:K:70:LEU:HD22	5:M:185:ALA:HA	1.94	0.50
2:I:179:GLN:HB3	2:I:214:PHE:HB3	1.93	0.50
1:B:106:ASN:HB3	1:B:143:LYS:NZ	2.26	0.50
2:H:266:TYR:CZ	2:H:270:SER:HB2	2.47	0.50
1:E:47:PHE:HE2	1:E:66:GLN:HB3	1.76	0.50
4:L:223:VAL:O	5:M:49:MET:HE3	2.12	0.49
2:G:67:GLN:O	2:G:71:LEU:HG	2.11	0.49
1:A:454:ASN:HA	1:F:232:ARG:NH2	2.27	0.49
2:H:233:PRO:CG	2:G:268:SER:HA	2.42	0.49
1:A:598:SER:O	1:A:640:LEU:HA	2.11	0.49
1:F:428:GLU:O	1:F:432:GLU:HG2	2.12	0.49
1:B:516:ARG:O	1:B:519:ASP:OD1	2.29	0.49
1:E:428:GLU:O	1:E:432:GLU:HG2	2.12	0.49
1:E:236:ALA:HA	1:E:239:VAL:HG12	1.94	0.49
1:F:450:SER:O	1:F:453:MET:HB2	2.12	0.49
1:D:628:VAL:O	1:D:632:LYS:N	2.45	0.49
1:B:256:ILE:O	1:B:370:ILE:HA	2.12	0.49
1:C:677:LEU:HD11	1:C:698:VAL:CG2	2.41	0.49
1:C:361:VAL:HA	1:D:267:THR:CG2	2.43	0.49
1:E:524:LEU:HD11	1:E:663:THR:HG21	1.93	0.49
2:I:167:LYS:HE2	2:I:171:TYR:HE2	1.77	0.49
1:D:95:MET:HG3	1:D:152:ILE:HG12	1.94	0.49
1:D:609:LEU:CD1	1:D:611:TYR:HB2	2.42	0.49
1:C:533:ARG:HD2	1:D:505:ASN:OD1	2.12	0.49
3:K:88:TYR:CB	5:M:81:LEU:HD11	2.41	0.49
2:J:118:THR:O	2:J:122:LYS:HG2	2.13	0.49
1:B:45:TYR:CE2	1:B:70:ALA:HA	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:256:ILE:O	1:C:370:ILE:HA	2.13	0.49
2:J:233:PRO:O	2:J:235:PHE:CE2	2.66	0.49
1:D:694:ILE:O	1:D:698:VAL:HG22	2.12	0.49
1:A:687:LYS:NZ	1:A:722:PRO:HB3	2.27	0.49
1:D:105:LYS:HZ3	2:I:291:GLU:HB3	1.75	0.49
1:C:149:VAL:HG11	1:C:152:ILE:HD11	1.93	0.49
2:I:95:ALA:HB1	2:I:97:PRO:HD2	1.93	0.49
2:J:142:ILE:HG23	2:J:168:VAL:HG13	1.94	0.49
1:B:136:LEU:N	1:B:136:LEU:HD23	2.26	0.49
1:A:540:LEU:HD12	1:A:644:GLY:O	2.12	0.49
1:B:499:TYR:HA	1:B:502:TYR:CE2	2.48	0.49
1:F:311:GLU:O	1:F:314:ARG:HG2	2.13	0.49
5:M:34:GLN:O	5:M:37:GLU:HB2	2.13	0.49
1:B:578:GLU:CG	1:B:619:SER:HB2	2.42	0.49
1:C:589:PHE:CE1	1:C:600:VAL:HG11	2.46	0.49
1:F:536:LEU:HD11	1:F:633:ALA:HA	1.94	0.49
1:D:312:GLU:HG3	1:D:313:GLN:N	2.28	0.49
1:E:303:ARG:CG	1:E:357:LYS:HE2	2.39	0.49
2:H:94:LYS:HG3	2:H:94:LYS:O	2.12	0.49
1:B:303:ARG:CG	1:B:357:LYS:HE2	2.41	0.49
1:A:610:ASP:OD1	1:F:620:ASN:ND2	2.45	0.49
1:B:479:ASP:O	1:B:482:ALA:N	2.45	0.49
1:C:593:TYR:CE2	1:C:632:LYS:NZ	2.80	0.49
1:B:406:ILE:HB	1:B:441:LEU:HD13	1.94	0.49
1:B:113:ASP:OD1	1:B:115:ASP:HB2	2.12	0.49
3:K:44:ASP:O	3:K:47:ARG:HB3	2.13	0.49
1:E:562:PHE:CD1	1:E:597:LEU:HG	2.48	0.49
1:E:540:LEU:HD12	1:E:644:GLY:O	2.12	0.49
1:A:571:ASP:OD1	1:A:572:LYS:N	2.46	0.49
2:G:18:GLU:HA	2:G:21:VAL:HG12	1.95	0.49
1:C:311:GLU:O	1:C:314:ARG:HG2	2.13	0.49
2:G:182:ILE:O	2:G:186:GLU:HG2	2.13	0.49
2:H:98:GLN:CD	2:H:98:GLN:H	2.15	0.49
1:E:101:PHE:HE1	1:E:193:LEU:HB2	1.78	0.49
1:B:710:LEU:O	1:B:714:ILE:HG13	2.13	0.49
1:A:113:ASP:O	1:A:117:MET:HG3	2.11	0.49
1:B:606:GLU:N	1:B:606:GLU:OE1	2.45	0.49
4:L:247:ALA:O	4:L:251:THR:HG23	2.13	0.49
1:C:512:ASP:N	1:C:513:PRO:CD	2.76	0.49
1:A:231:PHE:CE2	1:A:235:PHE:HD2	2.31	0.49
1:A:617:ARG:NH1	1:A:617:ARG:HG3	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:GLN:OE1	1:A:317:GLY:HA2	2.13	0.49
1:B:95:MET:CE	1:B:97:ILE:HD11	2.43	0.49
1:A:517:VAL:HG13	1:A:665:ILE:HG21	1.94	0.49
1:A:283:LYS:HA	1:A:324:ILE:O	2.13	0.49
1:B:653:GLN:OE1	1:B:658:LEU:HD22	2.12	0.49
1:E:232:ARG:HH22	1:F:451:THR:C	2.16	0.49
1:E:64:LEU:HB2	1:E:67:ARG:HH21	1.77	0.49
2:J:266:TYR:C	2:J:268:SER:H	2.15	0.49
2:J:116:ARG:HH22	5:M:65:ASN:CG	2.16	0.49
2:G:175:LEU:HD23	2:G:177:GLN:NE2	2.26	0.49
1:F:236:ALA:O	1:F:239:VAL:HG12	2.12	0.49
1:B:121:PHE:HD2	1:B:183:VAL:HG21	1.77	0.49
3:K:70:LEU:HA	5:M:189:LYS:HD3	1.94	0.49
1:D:114:THR:HG21	1:D:200:LYS:HG2	1.95	0.49
2:H:162:ASN:O	2:H:166:LEU:HG	2.13	0.49
2:J:94:LYS:HE3	2:G:153:LYS:HG3	1.94	0.49
1:A:67:ARG:CD	2:H:218:MET:HG3	2.38	0.49
1:D:511:GLY:CA	1:D:675:GLN:HE21	2.26	0.49
1:B:128:GLN:O	1:B:176:LEU:HD12	2.13	0.49
1:B:193:LEU:HG	1:B:195:LEU:HG	1.94	0.49
1:A:95:MET:HG3	1:A:152:ILE:HG12	1.95	0.49
1:E:46:ILE:HD12	1:E:174:VAL:HG21	1.93	0.49
1:A:636:GLN:HA	1:A:637:GLY:HA2	1.49	0.49
2:G:72:HIS:HE1	2:G:80:ASP:CB	2.23	0.48
1:E:254:LYS:O	1:E:368:LEU:HA	2.13	0.48
1:B:523:LEU:HA	1:B:526:GLN:HG2	1.95	0.48
1:E:684:GLY:HA2	1:E:691:ARG:HH21	1.78	0.48
1:D:681:GLU:HG2	1:D:691:ARG:CZ	2.42	0.48
2:J:287:ILE:O	2:J:291:GLU:HG3	2.13	0.48
1:D:86:ASP:C	1:D:88:ALA:H	2.16	0.48
1:C:16:LEU:HD11	1:C:52:HIS:HD2	1.78	0.48
1:B:258:LEU:HB3	1:B:395:ILE:CD1	2.27	0.48
2:G:218:MET:CG	2:G:219:LEU:N	2.75	0.48
1:F:395:ILE:HD12	1:F:395:ILE:N	2.29	0.48
2:G:101:ILE:HD13	2:G:135:LEU:HD11	1.95	0.48
1:E:95:MET:HG3	1:E:152:ILE:HG12	1.94	0.48
1:E:281:GLU:N	1:E:282:PRO:HA	2.28	0.48
1:C:18:LEU:HD13	1:C:139:SER:OG	2.12	0.48
1:E:411:THR:O	1:E:414:MET:HB2	2.13	0.48
4:L:198:ARG:HG2	4:L:202:ILE:HD11	1.95	0.48
5:M:33:LEU:HD12	5:M:149:ASN:CB	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:330:ILE:HB	1:C:373:THR:HB	1.94	0.48
1:D:670:ILE:HD11	1:D:705:ILE:HG23	1.95	0.48
1:D:552:LEU:O	1:D:556:ILE:HG13	2.12	0.48
1:E:670:ILE:HG22	1:E:672:THR:N	2.25	0.48
2:H:72:HIS:O	2:H:75:LEU:HB3	2.13	0.48
2:J:67:GLN:O	2:J:71:LEU:HG	2.13	0.48
1:D:592:ALA:HB1	1:D:640:LEU:HD13	1.93	0.48
1:C:584:ALA:O	1:C:588:ILE:HG13	2.12	0.48
1:F:319:ASN:HB3	1:F:320:SER:HB2	1.95	0.48
1:E:689:LYS:O	1:E:692:THR:OG1	2.26	0.48
1:A:45:TYR:CE2	1:A:70:ALA:HA	2.49	0.48
1:C:299:GLU:OE2	1:C:349:THR:OG1	2.26	0.48
2:H:180:LYS:O	2:H:184:ILE:HG13	2.13	0.48
1:F:313:GLN:O	1:F:317:GLY:N	2.46	0.48
1:C:681:GLU:HG3	1:C:691:ARG:HD2	1.96	0.48
1:E:404:LEU:HG	1:E:426:ILE:HG22	1.94	0.48
1:E:243:GLU:O	1:E:246:GLU:HG2	2.13	0.48
2:H:207:PHE:HB2	2:H:240:GLU:HG2	1.96	0.48
1:B:193:LEU:HD21	1:B:195:LEU:HD21	1.95	0.48
1:A:627:LEU:O	1:A:631:LYS:NZ	2.46	0.48
1:F:36:ILE:HD11	1:F:44:LYS:HD2	1.95	0.48
1:B:281:GLU:N	1:B:282:PRO:HA	2.28	0.48
1:E:16:LEU:HD11	1:E:52:HIS:HD2	1.79	0.48
1:D:326:ILE:HG22	1:D:370:ILE:CG1	2.44	0.48
1:C:386:PRO:HD2	1:D:440:GLU:OE1	2.13	0.48
1:E:526:GLN:HA	1:E:529:LYS:HG2	1.95	0.48
2:J:271:ARG:HD2	2:G:231:LEU:HD12	1.96	0.48
2:G:59:SER:OG	2:G:97:PRO:HD3	2.13	0.48
1:C:325:ILE:HG13	1:C:369:VAL:HG23	1.95	0.48
3:K:51:ASP:O	3:K:55:GLU:HG3	2.14	0.48
2:J:49:ALA:HB2	2:J:64:ALA:HB3	1.95	0.48
2:I:178:TYR:OH	2:I:282:ARG:HG2	2.14	0.48
1:C:89:LYS:O	1:C:89:LYS:HG2	2.12	0.48
1:F:256:ILE:O	1:F:370:ILE:HA	2.13	0.48
1:C:540:LEU:HD22	1:C:661:PHE:CD2	2.49	0.48
1:A:353:GLN:HA	1:B:288:PRO:HG2	1.95	0.48
1:C:609:LEU:O	1:C:610:ASP:HB2	2.13	0.48
1:D:257:LEU:HB2	1:D:389:LEU:HD13	1.95	0.48
1:F:230:ILE:HD11	1:F:391:VAL:HG11	1.95	0.48
1:A:193:LEU:HD21	1:A:195:LEU:HD21	1.96	0.48
1:B:609:LEU:HA	1:B:609:LEU:HD23	1.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ALA:HB3	1:A:73:SER:O	2.13	0.48
3:K:39:VAL:HA	3:K:42:VAL:HG23	1.96	0.48
5:M:53:GLN:HA	5:M:56:GLN:HG2	1.96	0.48
1:D:635:PRO:O	1:D:638:ARG:HB2	2.14	0.48
1:F:635:PRO:HB2	1:F:638:ARG:NH1	2.29	0.48
2:I:38:ILE:CD1	2:I:71:LEU:HB3	2.43	0.48
2:J:235:PHE:CG	3:K:38:GLN:HG2	2.48	0.48
1:E:658:LEU:HA	1:E:658:LEU:HD12	1.64	0.48
1:D:581:LYS:O	1:D:585:MET:HG2	2.13	0.48
1:A:240:PHE:HE2	1:B:453:MET:SD	2.37	0.48
1:D:286:ASN:HB2	1:D:327:PHE:CD1	2.46	0.48
1:C:613:PRO:HD3	1:C:648:ARG:NH2	2.29	0.48
3:K:83:LYS:HG2	3:K:86:ARG:NH2	2.29	0.48
1:F:601:VAL:HG22	1:F:643:ILE:HD12	1.95	0.48
1:D:536:LEU:HD21	1:D:630:LEU:O	2.14	0.48
1:E:440:GLU:O	1:E:444:LEU:HG	2.14	0.48
1:A:407:LEU:CD1	1:A:426:ILE:HG23	2.44	0.48
2:H:233:PRO:HB3	2:G:268:SER:O	2.14	0.48
1:E:184:ALA:HB1	1:E:200:LYS:O	2.14	0.48
1:C:380:ASP:OD1	1:C:382:ALA:N	2.43	0.48
2:J:185:TYR:HA	2:J:188:VAL:HG12	1.96	0.48
1:F:517:VAL:HG21	1:F:667:VAL:HG22	1.95	0.48
1:A:562:PHE:CE1	1:A:641:LEU:HD21	2.49	0.48
1:E:314:ARG:HG3	1:E:315:ARG:N	2.29	0.48
1:B:589:PHE:HD2	1:B:629:LEU:HD22	1.78	0.48
1:E:653:GLN:OE1	1:E:658:LEU:HD23	2.13	0.48
1:C:64:LEU:HG	1:C:68:LYS:HD2	1.96	0.48
1:C:322:LEU:HD22	1:C:366:ASN:O	2.14	0.48
1:F:113:ASP:HA	1:F:196:ILE:HG13	1.96	0.48
2:H:81:ALA:O	2:H:85:PHE:HD1	1.97	0.48
1:D:564:PHE:HB3	1:D:598:SER:HB3	1.95	0.48
1:C:538:SER:OG	1:C:662:SER:N	2.40	0.48
1:E:445:VAL:O	1:E:449:GLN:HG2	2.14	0.48
1:F:286:ASN:OD1	1:F:327:PHE:HD1	1.97	0.48
5:M:191:ARG:NH1	5:M:191:ARG:HG3	2.29	0.48
2:G:79:HIS:CG	4:L:242:ASP:OD2	2.67	0.48
1:D:721:ASP:O	1:D:725:ARG:HG3	2.13	0.48
2:H:40:GLU:O	2:H:44:ILE:HG12	2.14	0.48
2:J:276:LEU:O	2:J:280:LEU:HG	2.14	0.48
2:J:222:LYS:HA	2:J:225:VAL:HG12	1.96	0.47
1:F:327:PHE:CE2	1:F:369:VAL:HG21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:527:GLN:HA	1:F:719:GLN:CD	2.34	0.47
1:A:388:ARG:O	1:A:389:LEU:HD22	2.14	0.47
1:F:236:ALA:HA	1:F:239:VAL:CG1	2.44	0.47
1:F:436:PHE:HB3	1:F:440:GLU:CB	2.44	0.47
1:F:428:GLU:O	1:F:431:VAL:HG12	2.14	0.47
1:F:14:ASP:O	1:F:18:LEU:HG	2.13	0.47
1:B:640:LEU:CD2	1:B:642:ILE:HG13	2.44	0.47
1:C:618:PHE:HZ	1:D:612:VAL:HG11	1.79	0.47
1:D:242:PRO:HD2	1:D:243:GLU:N	2.28	0.47
1:F:653:GLN:HA	1:F:658:LEU:HB3	1.95	0.47
1:A:673:GLY:O	1:A:677:LEU:HD22	2.12	0.47
2:I:17:ALA:O	2:I:21:VAL:HG12	2.13	0.47
1:E:257:LEU:HG	1:E:371:GLY:O	2.14	0.47
1:E:436:PHE:HB3	1:E:440:GLU:CB	2.44	0.47
1:D:281:GLU:N	1:D:282:PRO:HA	2.30	0.47
1:A:719:GLN:HG2	1:F:523:LEU:HG	1.96	0.47
2:I:281:LEU:O	2:I:285:LYS:HG3	2.14	0.47
1:C:331:ASP:HA	1:C:379:ILE:CD1	2.41	0.47
1:C:355:LEU:HA	1:C:388:ARG:NE	2.30	0.47
1:A:331:ASP:CA	1:A:379:ILE:HD11	2.32	0.47
1:D:407:LEU:O	1:D:411:THR:HG23	2.14	0.47
1:F:557:ALA:HB2	1:F:601:VAL:HG21	1.97	0.47
2:J:268:SER:HA	2:G:233:PRO:HB2	1.97	0.47
1:B:257:LEU:HB2	1:B:389:LEU:HD13	1.95	0.47
1:B:76:GLN:HE21	1:B:78:ILE:CG2	2.26	0.47
1:B:436:PHE:CD2	1:B:444:LEU:HD11	2.49	0.47
1:F:307:ALA:HA	1:F:310:GLU:HG2	1.96	0.47
1:E:428:GLU:O	1:E:431:VAL:HG12	2.14	0.47
1:D:149:VAL:HG11	1:D:152:ILE:HD11	1.95	0.47
1:E:23:VAL:HG12	1:E:55:VAL:CG2	2.44	0.47
1:C:36:ILE:HG23	1:C:36:ILE:O	2.15	0.47
1:B:436:PHE:N	1:B:436:PHE:CD1	2.82	0.47
1:B:307:ALA:HA	1:B:310:GLU:HG2	1.96	0.47
1:A:609:LEU:O	1:A:610:ASP:HB3	2.13	0.47
1:B:479:ASP:O	1:B:480:PHE:C	2.51	0.47
1:A:242:PRO:O	1:A:246:GLU:OE1	2.33	0.47
1:A:411:THR:HG21	1:A:426:ILE:HD11	1.96	0.47
1:D:284:VAL:HG21	1:D:325:ILE:HG22	1.95	0.47
1:E:573:MET:O	1:E:576:PHE:HB2	2.15	0.47
2:J:163:LYS:O	2:J:167:LYS:HG2	2.15	0.47
1:F:87:LYS:HA	1:F:91:CYS:SG	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:186:GLU:O	2:J:190:THR:HG23	2.14	0.47
1:C:193:LEU:HD21	1:C:195:LEU:HD21	1.96	0.47
2:J:219:LEU:HD12	2:J:223:LEU:HB2	1.97	0.47
1:C:582:CYS:SG	1:C:621:LEU:HG	2.55	0.47
1:D:318:ALA:O	1:D:319:ASN:ND2	2.47	0.47
2:J:45:TYR:HB2	2:J:68:ALA:HB2	1.96	0.47
2:J:124:HIS:HE1	2:J:147:GLN:HB3	1.79	0.47
1:F:281:GLU:N	1:F:282:PRO:HA	2.29	0.47
1:F:149:VAL:HG11	1:F:152:ILE:HD11	1.95	0.47
1:D:567:ILE:HG23	1:D:601:VAL:HB	1.96	0.47
2:I:188:VAL:HG13	2:I:205:TYR:HD2	1.80	0.47
1:A:429:LEU:HG	1:A:482:ALA:HB1	1.96	0.47
1:A:683:LEU:HB3	1:A:685:ASN:HD22	1.76	0.47
4:L:237:VAL:HG11	5:M:60:VAL:HG13	1.96	0.47
1:D:609:LEU:O	1:D:610:ASP:OD1	2.32	0.47
1:E:67:ARG:HB3	2:J:217:ASP:OD2	2.14	0.47
1:D:652:LEU:HD13	1:D:657:MET:HB3	1.95	0.47
1:F:404:LEU:HG	1:F:426:ILE:HG22	1.96	0.47
1:E:241:PRO:HA	1:E:242:PRO:HA	1.54	0.47
1:F:415:ARG:O	1:F:417:HIS:O	2.33	0.47
1:D:570:PRO:HA	1:D:573:MET:HB3	1.97	0.47
1:A:240:PHE:CE2	1:B:453:MET:SD	3.08	0.47
1:B:295:VAL:HB	1:C:294:TYR:CG	2.50	0.47
1:F:64:LEU:HA	1:F:67:ARG:HE	1.79	0.47
1:A:23:VAL:HG12	1:A:55:VAL:HG21	1.95	0.47
1:C:510:TRP:CZ3	1:C:670:ILE:HG12	2.50	0.47
4:L:240:ALA:O	4:L:244:VAL:HG23	2.14	0.47
1:B:428:GLU:O	1:B:431:VAL:HG12	2.14	0.47
2:H:243:LEU:HD22	2:H:266:TYR:CG	2.50	0.47
2:I:58:TRP:HB3	2:I:95:ALA:HB2	1.96	0.47
1:D:246:GLU:HG2	1:D:247:GLN:N	2.29	0.47
1:E:23:VAL:HG12	1:E:55:VAL:HG21	1.95	0.47
1:A:98:GLU:HB3	1:A:148:LEU:HB3	1.97	0.47
2:J:92:PHE:HB3	2:J:98:GLN:O	2.15	0.47
1:A:650:ASP:OD1	1:A:650:ASP:N	2.46	0.47
1:A:34:HIS:HB2	1:A:83:TYR:O	2.14	0.47
1:D:122:ILE:O	1:D:126:ASN:HB3	2.14	0.47
1:C:122:ILE:O	1:C:126:ASN:HB3	2.14	0.47
1:F:508:ILE:C	1:F:509:LYS:HD3	2.34	0.47
1:D:688:ASP:O	1:D:692:THR:HG23	2.14	0.47
1:B:246:GLU:HG3	1:C:417:HIS:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:407:LEU:O	1:C:411:THR:OG1	2.27	0.47
1:F:570:PRO:CG	1:F:604:ASP:HB2	2.41	0.47
1:F:257:LEU:HG	1:F:371:GLY:O	2.14	0.47
1:A:247:GLN:C	1:B:413:ARG:HH12	2.18	0.47
2:G:267:ASP:OD1	2:G:271:ARG:NH1	2.48	0.47
2:G:81:ALA:O	2:G:85:PHE:HD1	1.98	0.47
2:J:21:VAL:HG21	2:J:71:LEU:HD22	1.96	0.47
1:C:106:ASN:HB3	1:C:143:LYS:HZ1	1.80	0.47
1:F:188:ALA:O	1:F:189:GLU:C	2.53	0.47
1:E:318:ALA:O	1:E:319:ASN:ND2	2.48	0.47
1:C:539:VAL:HG23	1:C:663:THR:HG23	1.95	0.47
1:D:519:ASP:O	1:D:523:LEU:HG	2.15	0.47
1:B:272:GLN:OE1	1:B:272:GLN:HA	2.15	0.47
1:C:499:TYR:HB3	1:C:558:GLU:OE2	2.15	0.47
1:B:327:PHE:CE2	1:B:369:VAL:HG21	2.50	0.47
1:B:568:CYS:SG	1:B:588:ILE:HD12	2.55	0.47
1:B:247:GLN:O	1:C:414:MET:SD	2.73	0.47
1:E:627:LEU:HG	1:E:657:MET:CE	2.45	0.47
1:B:627:LEU:CD2	1:B:657:MET:HG3	2.42	0.47
1:D:527:GLN:HA	1:E:719:GLN:HG3	1.97	0.47
2:I:200:TYR:HD1	2:I:200:TYR:H	1.63	0.47
2:I:228:TYR:CE2	2:I:230:GLU:HB2	2.49	0.47
1:F:613:PRO:HD3	1:F:648:ARG:HH12	1.80	0.47
1:B:614:ILE:O	1:B:616:PRO:HA	2.15	0.47
1:C:233:ARG:CZ	1:C:233:ARG:HB2	2.44	0.47
5:M:23:ASP:O	5:M:27:GLU:N	2.44	0.47
1:D:407:LEU:HA	1:D:441:LEU:HD21	1.96	0.47
1:E:627:LEU:HD13	1:F:607:ARG:NE	2.30	0.47
1:C:511:GLY:CA	1:C:513:PRO:HD2	2.45	0.47
2:H:39:GLU:HB2	2:H:75:LEU:HD13	1.97	0.47
1:E:436:PHE:N	1:E:436:PHE:CD1	2.83	0.47
1:E:612:VAL:HG22	1:E:613:PRO:HD2	1.97	0.47
1:C:632:LYS:HG3	1:D:571:ASP:CG	2.36	0.47
2:H:219:LEU:HD12	2:H:223:LEU:HB2	1.97	0.46
1:E:628:VAL:HB	1:F:574:ILE:CD1	2.44	0.46
1:C:513:PRO:HA	1:C:516:ARG:HG2	1.97	0.46
1:E:106:ASN:HB3	1:E:143:LYS:HZ2	1.79	0.46
1:A:690:GLU:HB3	1:A:726:VAL:HG22	1.97	0.46
1:A:517:VAL:HG13	1:A:665:ILE:CG2	2.45	0.46
1:B:319:ASN:HB3	1:B:320:SER:HB2	1.97	0.46
1:B:353:GLN:HA	1:C:288:PRO:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:VAL:O	1:A:51:THR:HA	2.16	0.46
2:J:244:MET:O	2:J:248:LEU:HG	2.14	0.46
2:H:195:SER:C	2:H:197:LEU:H	2.18	0.46
1:A:36:ILE:O	1:A:36:ILE:HG23	2.15	0.46
2:G:219:LEU:HB2	2:G:222:LYS:CB	2.33	0.46
1:C:240:PHE:HB3	1:C:244:ILE:HB	1.97	0.46
2:G:108:ILE:HD12	2:G:127:ILE:HD12	1.96	0.46
2:H:186:GLU:O	2:H:190:THR:HG23	2.15	0.46
2:J:179:GLN:O	2:J:182:ILE:HG12	2.15	0.46
2:J:112:THR:HG23	2:J:117:PHE:CE1	2.50	0.46
1:A:611:TYR:HD1	1:A:618:PHE:HB3	1.81	0.46
1:E:122:ILE:O	1:E:126:ASN:HB3	2.14	0.46
1:C:428:GLU:O	1:C:431:VAL:HG12	2.14	0.46
2:H:243:LEU:HD22	2:H:266:TYR:CD2	2.51	0.46
1:C:555:LYS:O	1:C:559:GLU:HG2	2.15	0.46
3:K:79:THR:O	3:K:83:LYS:HG3	2.15	0.46
4:L:216:PHE:HE2	5:M:160:LEU:HD22	1.81	0.46
2:I:21:VAL:HG23	2:I:38:ILE:CD1	2.44	0.46
1:A:428:GLU:O	1:A:431:VAL:HG12	2.15	0.46
1:D:627:LEU:CD2	1:D:657:MET:HG3	2.44	0.46
1:B:311:GLU:O	1:B:314:ARG:HG2	2.15	0.46
1:D:36:ILE:HG23	1:D:36:ILE:O	2.15	0.46
1:C:573:MET:HB3	1:C:576:PHE:CD2	2.49	0.46
2:H:45:TYR:HB2	2:H:68:ALA:HB2	1.96	0.46
2:J:45:TYR:HE2	2:J:71:LEU:HD11	1.79	0.46
1:E:73:SER:HB2	1:E:76:GLN:HG2	1.96	0.46
1:C:385:ARG:NH2	1:D:263:GLY:HA3	2.30	0.46
1:F:189:GLU:O	1:F:190:ASN:HB2	2.15	0.46
1:C:16:LEU:HD11	1:C:52:HIS:CD2	2.51	0.46
2:G:246:LYS:HZ1	2:G:258:SER:HB3	1.80	0.46
1:B:230:ILE:HD11	1:B:391:VAL:HG11	1.97	0.46
1:A:593:TYR:HB3	1:A:635:PRO:HD3	1.97	0.46
1:B:385:ARG:NH1	1:C:263:GLY:HA2	2.29	0.46
3:K:46:MET:CE	4:L:216:PHE:HA	2.45	0.46
1:E:327:PHE:CE2	1:E:369:VAL:HG21	2.50	0.46
1:C:657:MET:HE3	1:C:661:PHE:CZ	2.51	0.46
1:B:540:LEU:O	1:B:540:LEU:HD12	2.16	0.46
1:C:511:GLY:C	1:C:513:PRO:HD2	2.35	0.46
1:E:246:GLU:CG	1:F:417:HIS:HE1	2.27	0.46
1:D:436:PHE:CE2	1:D:444:LEU:HD12	2.48	0.46
1:C:612:VAL:CG2	1:C:613:PRO:HD2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:ALA:HA	1:B:239:VAL:CG1	2.45	0.46
1:E:73:SER:HB2	1:E:76:GLN:CG	2.46	0.46
2:G:167:LYS:HE2	2:G:171:TYR:HE2	1.80	0.46
1:A:121:PHE:HD2	1:A:183:VAL:HG21	1.81	0.46
2:H:276:LEU:O	2:H:280:LEU:HG	2.16	0.46
1:A:493:GLY:HA2	1:A:494:THR:CB	2.45	0.46
1:F:272:GLN:OE1	1:F:272:GLN:HA	2.15	0.46
3:K:39:VAL:HG21	4:L:209:ILE:HD11	1.97	0.46
1:F:552:LEU:O	1:F:556:ILE:HG13	2.15	0.46
1:C:326:ILE:HB	1:C:370:ILE:HD11	1.96	0.46
1:C:48:THR:HG21	1:C:128:GLN:HG2	1.97	0.46
3:K:56:ARG:HD2	5:M:171:ILE:CG2	2.45	0.46
1:E:677:LEU:HD11	1:E:695:ALA:HA	1.96	0.46
1:D:18:LEU:HD23	1:D:137:VAL:HG21	1.98	0.46
1:E:721:ASP:HB2	1:E:724:TYR:CD2	2.51	0.46
1:B:99:ILE:HD11	1:B:145:PHE:CD2	2.50	0.46
1:C:86:ASP:C	1:C:88:ALA:H	2.18	0.46
1:E:272:GLN:HA	1:E:272:GLN:OE1	2.15	0.46
5:M:32:MET:HA	5:M:35:LEU:HD12	1.97	0.46
1:F:325:ILE:HG13	1:F:369:VAL:HB	1.98	0.46
1:F:128:GLN:O	1:F:176:LEU:HD12	2.15	0.46
5:M:57:LEU:HD12	5:M:174:GLN:OE1	2.16	0.46
1:D:589:PHE:CD2	1:D:629:LEU:HD13	2.50	0.46
2:H:200:TYR:CZ	5:M:42:ALA:HB2	2.51	0.46
5:M:42:ALA:HA	5:M:45:ARG:NH2	2.31	0.46
4:L:199:HIS:ND1	5:M:21:LEU:HB3	2.31	0.46
1:F:106:ASN:HB3	1:F:143:LYS:HZ1	1.81	0.46
2:J:263:VAL:HG23	2:J:280:LEU:HD13	1.97	0.46
1:E:36:ILE:O	1:E:36:ILE:HG23	2.16	0.46
1:E:198:LYS:HG2	1:E:198:LYS:O	2.16	0.46
2:H:219:LEU:CD1	2:H:223:LEU:HB2	2.45	0.46
3:K:43:VAL:HA	4:L:212:LEU:CD1	2.25	0.46
1:E:232:ARG:HE	1:F:454:ASN:CB	2.15	0.46
1:E:628:VAL:HB	1:F:574:ILE:HD12	1.98	0.46
1:C:690:GLU:HB2	1:C:726:VAL:CG2	2.42	0.46
1:E:527:GLN:NE2	1:F:716:MET:HG2	2.27	0.46
1:E:527:GLN:HG3	1:F:719:GLN:HG3	1.98	0.46
1:E:314:ARG:CG	1:E:315:ARG:N	2.78	0.46
1:F:246:GLU:HG2	1:F:247:GLN:N	2.31	0.46
1:D:524:LEU:O	1:D:527:GLN:HB3	2.15	0.46
2:I:230:GLU:HG2	2:I:231:LEU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:240:PHE:HA	1:E:241:PRO:HD3	1.69	0.46
1:A:315:ARG:O	1:A:316:LEU:HD12	2.15	0.46
2:J:147:GLN:HG2	2:J:151:TYR:CE2	2.51	0.46
1:C:536:LEU:CD1	1:C:640:LEU:HB3	2.45	0.46
1:D:132:VAL:HG23	1:D:173:GLU:HA	1.97	0.46
1:F:579:THR:O	1:F:583:GLN:HG2	2.15	0.46
4:L:219:MET:O	4:L:223:VAL:HG23	2.16	0.46
1:F:540:LEU:O	1:F:665:ILE:HB	2.16	0.46
1:C:236:ALA:HB1	1:D:453:MET:HB2	1.98	0.46
1:A:215:PHE:N	1:A:231:PHE:CE2	2.84	0.46
1:F:686:PHE:CE1	1:F:714:ILE:HG23	2.50	0.46
1:B:536:LEU:HD12	1:B:640:LEU:O	2.16	0.46
1:D:268:LEU:HA	1:D:271:ARG:HD2	1.97	0.46
1:F:352:ASN:HA	1:F:355:LEU:HD12	1.98	0.46
1:B:352:ASN:HA	1:B:355:LEU:HD12	1.98	0.46
2:H:51:MET:O	2:H:54:MET:HB3	2.16	0.46
1:A:64:LEU:HA	1:A:67:ARG:HH21	1.81	0.46
1:B:240:PHE:HA	1:B:241:PRO:HD3	1.73	0.46
1:E:595:SER:HB3	1:E:598:SER:HB3	1.96	0.46
1:F:8:ALA:HB3	1:F:73:SER:O	2.16	0.46
1:E:654:GLU:CD	1:F:614:ILE:HD11	2.36	0.46
1:B:539:VAL:HA	1:B:663:THR:O	2.16	0.46
1:D:711:LEU:O	1:D:715:GLU:HG2	2.15	0.46
2:G:162:ASN:OD1	2:G:188:VAL:HG23	2.16	0.46
2:J:72:HIS:O	2:J:75:LEU:HB3	2.16	0.46
2:J:80:ASP:OD1	5:M:66:HIS:CD2	2.69	0.46
1:D:571:ASP:O	1:D:574:ILE:HG13	2.15	0.46
1:F:436:PHE:N	1:F:436:PHE:CD1	2.83	0.46
1:F:241:PRO:HA	1:F:242:PRO:HA	1.60	0.46
4:L:236:ASN:O	4:L:240:ALA:HB2	2.16	0.46
2:H:256:VAL:HG21	2:H:288:GLN:CG	2.44	0.46
2:I:185:TYR:HA	2:I:188:VAL:HG12	1.97	0.46
1:D:578:GLU:OE1	1:D:621:LEU:HD13	2.15	0.46
1:B:91:CYS:O	1:B:154:ALA:HA	2.16	0.46
1:A:103:GLN:C	1:A:105:LYS:H	2.19	0.46
2:G:45:TYR:HB2	2:G:68:ALA:HB2	1.97	0.46
1:C:705:ILE:HD11	1:C:710:LEU:HA	1.97	0.46
1:E:24:VAL:HG11	1:E:49:LEU:HD22	1.96	0.46
1:A:322:LEU:HD12	1:A:323:HIS:H	1.81	0.46
2:G:10:ALA:O	2:G:14:LEU:HG	2.16	0.46
1:A:410:HIS:NE2	1:A:442:GLU:HG2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:218:MET:HA	1:D:219:GLY:HA2	1.72	0.46
1:E:611:TYR:CE1	1:E:616:PRO:HB2	2.51	0.46
1:F:121:PHE:HD2	1:F:183:VAL:HG21	1.81	0.46
1:A:542:GLU:OE2	1:A:666:HIS:CD2	2.68	0.45
2:J:266:TYR:HD2	2:J:272:LEU:HD21	1.80	0.45
1:D:135:GLN:HG2	1:D:148:LEU:HD13	1.97	0.45
1:A:240:PHE:HA	1:A:241:PRO:HD3	1.81	0.45
2:H:233:PRO:HB3	2:G:268:SER:HA	1.98	0.45
3:K:54:LEU:HD21	4:L:222:LEU:HD22	1.98	0.45
1:D:40:SER:HB3	1:D:43:HIS:CG	2.50	0.45
1:F:95:MET:HG3	1:F:152:ILE:HG12	1.97	0.45
1:C:104:LYS:HA	1:C:107:ILE:HG13	1.98	0.45
1:E:104:LYS:HA	1:E:107:ILE:HD11	1.97	0.45
1:C:507:ILE:HD12	1:C:555:LYS:HE2	1.98	0.45
1:E:286:ASN:OD1	1:E:327:PHE:HD1	1.99	0.45
1:E:714:ILE:O	1:E:718:LEU:HG	2.15	0.45
1:A:356:SER:OG	1:B:288:PRO:HD3	2.16	0.45
2:I:142:ILE:HG23	2:I:168:VAL:HG13	1.99	0.45
1:C:349:THR:O	1:C:352:ASN:HB3	2.15	0.45
1:B:254:LYS:O	1:B:368:LEU:HA	2.16	0.45
1:D:542:GLU:OE2	1:D:649:LYS:HD2	2.16	0.45
1:D:669:ASN:OD1	1:D:669:ASN:N	2.44	0.45
1:E:438:GLY:O	1:E:441:LEU:N	2.39	0.45
1:D:303:ARG:HD2	1:D:353:GLN:NE2	2.32	0.45
5:M:17:ARG:CB	5:M:20:GLN:HB3	2.46	0.45
2:H:38:ILE:HD11	2:H:71:LEU:HB3	1.98	0.45
1:B:669:ASN:CG	1:B:706:GLY:HA2	2.36	0.45
3:K:85:LYS:O	3:K:89:TRP:HB3	2.15	0.45
1:E:593:TYR:CD2	1:E:635:PRO:HD3	2.50	0.45
2:J:243:LEU:O	2:J:247:LEU:HG	2.17	0.45
1:E:519:ASP:O	1:E:522:GLU:HB2	2.17	0.45
1:A:721:ASP:O	1:A:725:ARG:HG3	2.17	0.45
1:B:528:THR:HG21	1:B:641:LEU:HD13	1.98	0.45
1:B:531:SER:HA	1:B:639:LYS:HD3	1.98	0.45
1:C:221:GLY:HA3	1:C:406:ILE:HG13	1.97	0.45
1:C:671:ALA:HA	1:C:703:VAL:O	2.17	0.45
1:E:399:ASP:O	1:E:403:ARG:N	2.42	0.45
5:M:36:VAL:O	5:M:40:LYS:HB2	2.16	0.45
1:F:602:VAL:O	1:F:644:GLY:HA2	2.17	0.45
1:F:307:ALA:O	1:F:310:GLU:HG2	2.16	0.45
1:B:307:ALA:O	1:B:310:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:246:GLU:HG3	1:F:417:HIS:CE1	2.46	0.45
1:D:193:LEU:HD21	1:D:195:LEU:HD21	1.97	0.45
2:I:223:LEU:O	2:I:227:LYS:HG3	2.16	0.45
5:M:33:LEU:HD12	5:M:149:ASN:HB3	1.99	0.45
4:L:223:VAL:HG12	5:M:49:MET:CE	2.46	0.45
1:C:327:PHE:HB3	1:C:330:ILE:CD1	2.31	0.45
1:E:325:ILE:HG13	1:E:369:VAL:HB	1.98	0.45
1:C:707:ILE:O	1:C:711:LEU:HG	2.16	0.45
1:E:143:LYS:HB3	1:E:145:PHE:HE1	1.81	0.45
1:A:242:PRO:HD2	1:A:243:GLU:OE1	2.17	0.45
2:H:200:TYR:HD2	4:L:217:MET:SD	2.40	0.45
1:E:289:GLU:C	1:E:291:LEU:N	2.69	0.45
1:C:143:LYS:HB3	1:C:145:PHE:HE1	1.81	0.45
1:A:546:HIS:CE1	1:A:709:LYS:HE3	2.52	0.45
1:A:402:GLY:O	1:A:406:ILE:HD12	2.15	0.45
1:D:424:VAL:HG22	1:D:480:PHE:N	2.32	0.45
1:E:16:LEU:HD11	1:E:52:HIS:CD2	2.52	0.45
2:H:53:LYS:HE3	2:I:117:PHE:CE2	2.52	0.45
2:I:125:ILE:HD12	2:I:126:SER:N	2.32	0.45
1:D:109:SER:O	1:D:110:ASN:C	2.54	0.45
1:A:27:LYS:HD2	1:A:57:PRO:HG2	1.99	0.45
1:A:575:GLY:HA3	1:F:586:LYS:CE	2.45	0.45
2:G:204:ASP:OD2	2:G:208:LYS:HE2	2.17	0.45
1:A:421:SER:CB	1:A:424:VAL:HG23	2.39	0.45
1:C:388:ARG:O	1:C:389:LEU:HD23	2.17	0.45
1:C:677:LEU:O	1:C:681:GLU:OE1	2.35	0.45
1:A:446:ARG:HA	1:A:449:GLN:HG3	1.98	0.45
2:J:50:ASN:HD21	2:G:115:GLY:HA3	1.82	0.45
5:M:50:LEU:HD13	5:M:167:MET:HB3	1.99	0.45
1:E:397:LEU:HD13	1:E:398:PRO:HD2	1.99	0.45
1:B:531:SER:CB	1:B:639:LYS:HD3	2.47	0.45
1:B:36:ILE:HG23	1:B:36:ILE:O	2.16	0.45
2:J:231:LEU:O	2:J:232:PHE:C	2.55	0.45
2:J:175:LEU:HD23	2:J:177:GLN:NE2	2.32	0.45
2:I:216:ILE:HG12	2:I:217:ASP:N	2.31	0.45
2:I:182:ILE:CG2	2:I:212:CYS:HB2	2.47	0.45
2:I:182:ILE:O	2:I:186:GLU:HG2	2.17	0.45
2:I:276:LEU:O	2:I:280:LEU:HG	2.17	0.45
1:B:508:ILE:HD13	1:B:683:LEU:HD21	1.99	0.45
2:J:134:GLU:O	2:J:136:VAL:HG23	2.17	0.45
1:B:507:ILE:CG1	1:B:555:LYS:HD3	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:406:ILE:CG2	1:D:441:LEU:HD22	2.34	0.45
1:E:64:LEU:CA	1:E:67:ARG:HE	2.20	0.45
1:B:249:GLY:HA3	1:C:414:MET:HE1	1.98	0.45
2:G:263:VAL:O	2:G:267:ASP:HB2	2.16	0.45
1:D:286:ASN:CB	1:D:327:PHE:HD1	2.29	0.45
1:A:403:ARG:O	1:A:407:LEU:HG	2.16	0.45
1:A:219:GLY:O	1:A:220:ILE:HG13	2.16	0.45
1:F:242:PRO:CD	1:F:243:GLU:H	2.30	0.45
2:I:214:PHE:HD1	2:I:214:PHE:H	1.62	0.45
2:I:118:THR:O	2:I:122:LYS:HG2	2.16	0.45
1:C:441:LEU:O	1:C:444:LEU:HG	2.17	0.45
2:J:176:GLU:O	2:J:178:TYR:N	2.49	0.45
1:F:694:ILE:O	1:F:698:VAL:HG22	2.17	0.45
1:E:641:LEU:HD12	1:E:641:LEU:O	2.16	0.45
1:B:246:GLU:HB2	1:C:413:ARG:HH22	1.80	0.45
1:A:607:ARG:NH2	1:F:627:LEU:HD22	2.31	0.45
1:E:612:VAL:CG2	1:E:613:PRO:HD2	2.47	0.45
1:D:223:LEU:HD23	1:D:223:LEU:O	2.17	0.45
1:C:324:ILE:HD12	1:C:324:ILE:N	2.32	0.45
2:I:219:LEU:O	2:I:221:ALA:N	2.46	0.45
3:K:43:VAL:HG22	4:L:212:LEU:HD22	1.98	0.45
4:L:216:PHE:CB	5:M:39:SER:HB2	2.45	0.45
1:C:330:ILE:HD13	1:C:330:ILE:HA	1.60	0.45
1:F:525:VAL:CG1	1:F:560:SER:HB2	2.46	0.45
1:B:284:VAL:O	1:B:326:ILE:HG12	2.17	0.45
1:E:527:GLN:HA	1:F:719:GLN:HG3	1.99	0.45
1:D:626:LEU:HA	1:D:626:LEU:HD23	1.72	0.45
1:D:626:LEU:O	1:D:630:LEU:HG	2.17	0.45
1:E:605:ILE:HA	1:E:608:LEU:HB3	1.99	0.45
1:A:355:LEU:HD22	1:A:388:ARG:NH1	2.32	0.45
1:A:357:LYS:HE3	1:A:357:LYS:HA	1.97	0.45
1:D:453:MET:O	1:D:457:ILE:HG13	2.17	0.45
5:M:142:ARG:HG2	5:M:143:GLU:N	2.32	0.45
2:G:243:LEU:HD22	2:G:266:TYR:CG	2.52	0.45
2:G:101:ILE:HB	2:G:131:TYR:CZ	2.51	0.45
3:K:51:ASP:OD2	3:K:55:GLU:OE2	2.35	0.45
1:E:114:THR:HG21	1:E:200:LYS:HG2	1.99	0.45
1:E:319:ASN:HB3	1:E:320:SER:HB2	1.99	0.45
1:E:25:SER:HB3	1:E:28:ASP:OD2	2.17	0.45
1:C:24:VAL:HG11	1:C:49:LEU:HD22	1.99	0.45
2:G:82:ALA:O	2:G:86:VAL:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:596:GLN:HA	1:E:638:ARG:CG	2.32	0.44
5:M:33:LEU:HA	5:M:153:VAL:CG2	2.47	0.44
1:D:510:TRP:HZ2	1:D:668:PRO:O	2.00	0.44
1:C:715:GLU:HA	1:C:715:GLU:OE1	2.16	0.44
1:B:523:LEU:O	1:B:526:GLN:HG2	2.16	0.44
1:D:300:ALA:O	1:D:304:LYS:HG3	2.17	0.44
1:C:677:LEU:CD1	1:C:698:VAL:HG21	2.47	0.44
2:G:185:TYR:HA	2:G:188:VAL:HG12	1.98	0.44
1:D:105:LYS:HZ1	2:I:291:GLU:CB	2.29	0.44
2:J:21:VAL:HG23	2:J:38:ILE:HD12	2.00	0.44
1:E:696:GLN:OE1	1:E:696:GLN:HA	2.17	0.44
1:E:596:GLN:CA	1:E:638:ARG:HG2	2.31	0.44
2:J:180:LYS:O	2:J:184:ILE:HG13	2.18	0.44
1:C:562:PHE:O	1:C:565:ILE:HD11	2.16	0.44
1:F:552:LEU:HD12	1:F:667:VAL:HG21	1.98	0.44
2:G:72:HIS:NE2	2:G:77:SER:HB2	2.32	0.44
2:G:40:GLU:O	2:G:43:GLU:HG3	2.17	0.44
1:E:717:SER:OG	1:E:729:PHE:HB2	2.17	0.44
2:H:237:ASP:C	2:H:239:ARG:H	2.20	0.44
1:B:424:VAL:H	1:B:479:ASP:N	2.15	0.44
1:F:707:ILE:O	1:F:710:LEU:HB3	2.17	0.44
1:B:626:LEU:HA	1:B:626:LEU:HD23	1.52	0.44
1:F:36:ILE:HG23	1:F:36:ILE:O	2.16	0.44
1:D:564:PHE:HD2	1:D:598:SER:HB2	1.83	0.44
1:F:375:ARG:NH2	1:F:377:ASP:OD2	2.50	0.44
1:B:260:GLY:CA	1:B:395:ILE:HB	2.48	0.44
4:L:223:VAL:HG12	5:M:49:MET:HE3	2.00	0.44
2:G:17:ALA:O	2:G:21:VAL:HG12	2.16	0.44
1:F:284:VAL:O	1:F:326:ILE:HG12	2.17	0.44
1:B:523:LEU:HD22	1:B:526:GLN:NE2	2.32	0.44
1:E:510:TRP:CE3	1:E:670:ILE:HG13	2.51	0.44
1:D:304:LYS:HA	1:D:307:ALA:HB3	1.99	0.44
1:C:540:LEU:HD22	1:C:661:PHE:CE2	2.53	0.44
2:H:203:LYS:HB3	2:H:240:GLU:HG3	1.99	0.44
2:H:95:ALA:CB	2:H:97:PRO:HD2	2.47	0.44
1:A:106:ASN:HB3	1:A:143:LYS:HZ1	1.83	0.44
1:C:113:ASP:O	1:C:117:MET:HG3	2.17	0.44
1:C:114:THR:OG1	1:C:199:ALA:HB3	2.17	0.44
2:H:161:ALA:O	2:H:165:LEU:HG	2.17	0.44
1:B:114:THR:OG1	1:B:199:ALA:HB3	2.17	0.44
1:F:449:GLN:O	1:F:453:MET:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:ILE:HG13	1:B:369:VAL:HB	1.98	0.44
1:D:510:TRP:NE1	1:D:514:VAL:HG21	2.33	0.44
4:L:211:GLU:O	4:L:214:ASP:HB2	2.18	0.44
2:G:266:TYR:C	2:G:268:SER:H	2.21	0.44
1:D:18:LEU:HD13	1:D:144:LEU:CD2	2.48	0.44
2:J:38:ILE:HD11	2:J:71:LEU:HB3	1.98	0.44
1:E:697:GLN:HG3	1:E:730:LEU:CD1	2.45	0.44
1:F:242:PRO:HD2	1:F:243:GLU:N	2.33	0.44
1:E:27:LYS:H	1:E:27:LYS:HD2	1.82	0.44
1:F:95:MET:CE	1:F:97:ILE:HD11	2.47	0.44
1:C:295:VAL:O	1:D:294:TYR:HB2	2.17	0.44
1:C:518:LEU:HD23	1:C:518:LEU:HA	1.84	0.44
3:K:43:VAL:CG2	4:L:212:LEU:HD22	2.48	0.44
1:B:258:LEU:CB	1:B:395:ILE:HD11	2.27	0.44
5:M:63:GLY:O	5:M:67:ILE:HG13	2.16	0.44
1:A:295:VAL:HG12	1:B:293:LYS:N	2.32	0.44
1:E:585:MET:HG3	1:E:589:PHE:CE2	2.51	0.44
1:E:676:LEU:O	1:E:680:LEU:HG	2.17	0.44
1:C:721:ASP:HB2	1:C:724:TYR:CD1	2.52	0.44
1:B:95:MET:HE2	1:B:97:ILE:HD11	2.00	0.44
2:H:164:CYS:O	2:H:168:VAL:HG23	2.17	0.44
1:E:726:VAL:O	1:E:730:LEU:HG	2.17	0.44
2:J:108:ILE:HD12	2:J:127:ILE:HD12	1.99	0.44
1:E:520:ASP:OD2	1:E:665:ILE:HD12	2.18	0.44
1:A:101:PHE:CE1	1:A:193:LEU:HD13	2.53	0.44
1:A:132:VAL:HG23	1:A:173:GLU:O	2.18	0.44
1:B:628:VAL:HG13	1:C:571:ASP:OD1	2.16	0.44
1:E:69:TRP:CE2	1:E:134:GLN:HA	2.52	0.44
2:J:245:LYS:O	2:J:249:GLU:HG3	2.16	0.44
1:E:91:CYS:O	1:E:154:ALA:HA	2.17	0.44
1:F:218:MET:HA	1:F:219:GLY:HA2	1.78	0.44
1:F:399:ASP:N	1:F:399:ASP:OD1	2.49	0.44
4:L:206:GLU:O	4:L:209:ILE:HB	2.18	0.44
1:E:589:PHE:CE2	1:E:629:LEU:HD21	2.52	0.44
1:D:670:ILE:HG12	1:D:705:ILE:O	2.18	0.44
1:A:624:GLN:HA	1:A:624:GLN:OE1	2.17	0.44
1:D:686:PHE:HB2	1:D:691:ARG:CG	2.47	0.44
1:E:8:ALA:HA	1:E:60:VAL:O	2.18	0.44
1:D:95:MET:CE	1:D:97:ILE:HD11	2.48	0.44
1:D:564:PHE:HB3	1:D:598:SER:CB	2.47	0.44
1:B:507:ILE:HG13	1:B:555:LYS:HD3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:513:PRO:O	1:B:517:VAL:HG23	2.17	0.44
1:F:45:TYR:CE2	1:F:70:ALA:HA	2.53	0.44
4:L:200:SER:O	4:L:204:LYS:HG3	2.17	0.44
1:A:380:ASP:OD1	1:A:381:GLU:N	2.51	0.44
4:L:209:ILE:HG13	5:M:32:MET:CE	2.46	0.44
1:B:246:GLU:O	1:C:414:MET:HE1	2.17	0.44
1:B:576:PHE:HB2	1:B:581:LYS:CG	2.48	0.44
1:B:541:LEU:HA	1:B:665:ILE:O	2.18	0.44
1:B:297:GLU:O	1:B:300:ALA:HB3	2.18	0.44
3:K:77:PHE:HB2	5:M:192:ILE:CG2	2.47	0.44
1:D:23:VAL:HG12	1:D:55:VAL:CG2	2.48	0.44
1:A:315:ARG:C	1:A:316:LEU:HD12	2.38	0.44
2:J:120:ALA:O	2:J:124:HIS:HB2	2.18	0.44
1:E:24:VAL:CG1	1:E:49:LEU:HD22	2.48	0.44
1:A:95:MET:CE	1:A:97:ILE:HD11	2.47	0.44
1:D:268:LEU:HA	1:D:271:ARG:CD	2.48	0.44
1:C:24:VAL:O	1:C:51:THR:HA	2.18	0.44
5:M:29:THR:O	5:M:32:MET:HB3	2.17	0.44
1:E:190:ASN:HD21	1:E:316:LEU:CB	2.30	0.44
2:G:263:VAL:HG23	2:G:280:LEU:HD13	2.00	0.44
5:M:142:ARG:HG2	5:M:143:GLU:H	1.82	0.44
1:B:450:SER:O	1:B:453:MET:HB2	2.16	0.44
1:E:95:MET:CE	1:E:97:ILE:HD11	2.48	0.44
2:G:182:ILE:CG2	2:G:212:CYS:HB2	2.47	0.44
2:G:182:ILE:HG22	2:G:212:CYS:HB2	1.99	0.44
2:J:20:LYS:NZ	2:J:40:GLU:HG2	2.33	0.44
1:A:121:PHE:CD2	1:A:183:VAL:HG21	2.52	0.44
1:B:669:ASN:OD1	1:B:706:GLY:HA2	2.17	0.44
1:E:102:LEU:HD22	1:E:137:VAL:HG12	2.00	0.44
1:C:237:SER:OG	1:C:252:HIS:ND1	2.49	0.44
1:A:573:MET:HA	1:A:576:PHE:CD2	2.53	0.44
2:H:223:LEU:O	2:H:227:LYS:HG3	2.18	0.44
1:B:260:GLY:HA3	1:B:266:LYS:HD3	2.00	0.44
1:F:562:PHE:CE2	1:F:597:LEU:HD12	2.51	0.44
1:C:686:PHE:HB3	1:C:690:GLU:OE2	2.18	0.44
2:I:45:TYR:HE2	2:I:71:LEU:HD11	1.83	0.44
2:J:243:LEU:HD22	2:J:266:TYR:CD2	2.53	0.44
1:D:651:VAL:CG1	1:D:655:MET:HE3	2.47	0.44
1:C:590:ASP:HA	1:C:593:TYR:HD2	1.81	0.44
1:C:613:PRO:HD3	1:C:648:ARG:HH22	1.83	0.44
2:H:256:VAL:HG11	2:H:288:GLN:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:582:CYS:SG	1:C:574:ILE:HG22	2.58	0.44
2:H:134:GLU:O	2:H:136:VAL:HG23	2.18	0.44
1:F:48:THR:HG22	1:F:49:LEU:N	2.33	0.44
1:C:603:ASP:HA	1:C:645:THR:OG1	2.18	0.44
1:D:231:PHE:HA	1:D:235:PHE:CD2	2.52	0.44
1:D:303:ARG:HD3	1:D:353:GLN:CG	2.48	0.43
1:A:240:PHE:HB3	1:A:244:ILE:HD11	1.99	0.43
2:I:81:ALA:O	2:I:85:PHE:HD1	2.01	0.43
1:A:632:LYS:HE3	1:A:633:ALA:O	2.18	0.43
2:H:182:ILE:CG2	2:H:212:CYS:HB2	2.48	0.43
2:H:119:ILE:HD11	2:H:123:HIS:CE1	2.53	0.43
2:H:92:PHE:HB3	2:H:98:GLN:O	2.17	0.43
1:E:12:PRO:HG2	1:E:23:VAL:HG11	1.98	0.43
1:D:121:PHE:HD2	1:D:183:VAL:HG21	1.83	0.43
1:A:575:GLY:HA3	1:F:586:LYS:HZ1	1.83	0.43
1:C:132:VAL:HG23	1:C:173:GLU:O	2.18	0.43
2:G:119:ILE:HD11	2:G:123:HIS:HE1	1.82	0.43
1:C:507:ILE:HD12	1:C:555:LYS:CE	2.47	0.43
1:F:589:PHE:O	1:F:593:TYR:CD1	2.71	0.43
1:D:310:GLU:O	1:D:313:GLN:CD	2.55	0.43
1:F:657:MET:SD	1:F:661:PHE:CE2	3.10	0.43
1:F:712:MET:O	1:F:716:MET:HG3	2.18	0.43
1:E:713:LEU:CD2	1:E:732:LEU:HD13	2.47	0.43
1:E:512:ASP:N	1:E:513:PRO:CD	2.81	0.43
2:G:195:SER:C	2:G:197:LEU:H	2.21	0.43
1:D:103:GLN:C	1:D:105:LYS:H	2.20	0.43
2:I:182:ILE:HG22	2:I:212:CYS:HB2	2.01	0.43
1:A:300:ALA:O	1:A:303:ARG:HG2	2.19	0.43
2:G:179:GLN:HG3	2:G:180:LYS:N	2.33	0.43
2:G:124:HIS:HE1	2:G:147:GLN:HB3	1.83	0.43
1:E:7:GLN:O	1:E:59:SER:HB2	2.18	0.43
1:D:354:LEU:HA	1:D:354:LEU:HD23	1.77	0.43
2:H:222:LYS:HA	2:H:225:VAL:HG12	2.00	0.43
1:B:241:PRO:HA	1:B:242:PRO:HA	1.55	0.43
3:K:50:VAL:O	3:K:53:VAL:HG12	2.19	0.43
1:D:632:LYS:HZ3	1:E:571:ASP:HB3	1.82	0.43
1:C:688:ASP:HA	1:C:691:ARG:CZ	2.48	0.43
1:A:262:PRO:CG	1:A:374:ASN:OD1	2.64	0.43
2:G:112:THR:HG23	2:G:117:PHE:CE1	2.47	0.43
1:C:402:GLY:O	1:C:406:ILE:HD12	2.18	0.43
1:B:221:GLY:HA3	1:B:406:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:188:VAL:HG13	2:H:205:TYR:HD2	1.83	0.43
1:B:677:LEU:O	1:B:681:GLU:HG3	2.18	0.43
2:H:118:THR:O	2:H:122:LYS:HG2	2.18	0.43
1:E:375:ARG:NH2	1:E:377:ASP:OD2	2.51	0.43
1:B:69:TRP:NE1	1:B:134:GLN:HA	2.33	0.43
1:A:67:ARG:HD2	2:H:218:MET:SD	2.58	0.43
1:A:68:LYS:HD2	2:H:219:LEU:HD23	2.00	0.43
1:B:440:GLU:O	1:B:444:LEU:HG	2.18	0.43
1:D:241:PRO:HA	1:D:242:PRO:HA	1.68	0.43
1:A:502:TYR:N	1:A:502:TYR:HD1	2.17	0.43
2:J:203:LYS:HE3	2:J:203:LYS:HB2	1.85	0.43
1:A:258:LEU:HD12	1:A:258:LEU:O	2.18	0.43
2:H:230:GLU:HG2	2:H:231:LEU:H	1.83	0.43
2:H:203:LYS:NZ	2:H:239:ARG:HH21	2.15	0.43
1:A:242:PRO:HD2	1:A:243:GLU:H	1.82	0.43
1:F:101:PHE:CD2	1:F:107:ILE:HA	2.53	0.43
2:I:162:ASN:O	2:I:166:LEU:HG	2.18	0.43
1:F:74:ILE:HB	2:G:216:ILE:CD1	2.48	0.43
1:E:231:PHE:O	1:E:235:PHE:CD2	2.71	0.43
1:A:395:ILE:N	1:A:395:ILE:HD12	2.32	0.43
1:A:395:ILE:HG22	1:A:396:GLY:N	2.33	0.43
4:L:209:ILE:CG2	5:M:32:MET:HG3	2.45	0.43
1:F:72:LEU:O	2:G:218:MET:SD	2.77	0.43
1:D:632:LYS:HZ1	1:E:571:ASP:HB3	1.82	0.43
2:J:235:PHE:HD1	3:K:34:GLN:HE21	1.62	0.43
1:A:457:ILE:HD12	1:F:232:ARG:HH21	1.83	0.43
1:A:718:LEU:O	1:A:725:ARG:NE	2.51	0.43
1:A:510:TRP:CE3	1:A:675:GLN:HG2	2.54	0.43
2:J:167:LYS:HE2	2:J:171:TYR:CE2	2.49	0.43
2:J:230:GLU:HG2	2:J:231:LEU:N	2.34	0.43
1:B:455:ARG:NH2	1:B:481:LEU:CB	2.81	0.43
1:D:498:ASP:O	1:D:501:SER:HB3	2.19	0.43
1:D:34:HIS:HB2	1:D:83:TYR:O	2.18	0.43
1:F:555:LYS:HD3	1:F:559:GLU:HG2	2.00	0.43
4:L:210:ARG:HG2	4:L:210:ARG:NH1	2.32	0.43
5:M:49:MET:O	5:M:53:GLN:HG3	2.19	0.43
1:F:629:LEU:O	1:F:632:LYS:HB3	2.18	0.43
1:C:241:PRO:HA	1:C:242:PRO:HA	1.66	0.43
1:A:646:THR:HG21	1:A:652:LEU:HD22	1.99	0.43
1:E:531:SER:HB3	1:E:534:THR:O	2.18	0.43
1:A:256:ILE:CG1	1:A:370:ILE:HG22	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:676:LEU:HD22	1:E:703:VAL:HG11	2.01	0.43
1:E:732:LEU:HA	1:E:732:LEU:HD23	1.73	0.43
2:H:130:ILE:C	2:H:132:GLU:H	2.21	0.43
1:A:612:VAL:CG1	1:A:617:ARG:HB2	2.49	0.43
2:H:231:LEU:HD13	2:G:271:ARG:CG	2.48	0.43
1:B:715:GLU:O	1:B:719:GLN:HG2	2.18	0.43
1:D:331:ASP:CA	1:D:379:ILE:HD11	2.48	0.43
1:D:102:LEU:HD22	1:D:137:VAL:CG1	2.48	0.43
2:J:21:VAL:HG23	2:J:38:ILE:CD1	2.48	0.43
1:B:549:LYS:NZ	1:B:647:SER:HA	2.34	0.43
1:C:265:GLY:O	1:C:268:LEU:HG	2.18	0.43
3:K:46:MET:O	3:K:50:VAL:HG23	2.19	0.43
1:F:597:LEU:HA	1:F:639:LYS:O	2.18	0.43
1:C:508:ILE:HD13	1:C:683:LEU:HD21	2.01	0.43
2:J:197:LEU:CD2	3:K:48:VAL:HG11	2.48	0.43
1:E:684:GLY:HA2	1:E:691:ARG:NH2	2.33	0.43
1:C:544:PRO:HG2	1:C:669:ASN:CG	2.39	0.43
1:A:457:ILE:HD12	1:F:232:ARG:NH2	2.33	0.43
1:A:564:PHE:CZ	1:A:566:LYS:HB2	2.53	0.43
1:D:655:MET:O	1:D:656:GLU:HB2	2.18	0.43
2:G:96:ASP:N	2:G:97:PRO:HD2	2.34	0.43
4:L:248:VAL:HB	5:M:70:ASP:HB3	1.99	0.43
1:A:436:PHE:CD2	1:A:444:LEU:HD11	2.54	0.43
1:A:377:ASP:OD2	1:A:378:LEU:HD23	2.19	0.43
1:C:526:GLN:OE1	1:C:530:ASN:ND2	2.52	0.43
2:H:82:ALA:HB2	2:H:110:ILE:HG21	2.00	0.43
1:E:530:ASN:O	1:E:639:LYS:HE3	2.19	0.43
1:F:76:GLN:HE21	1:F:78:ILE:CG2	2.32	0.43
1:E:625:ALA:HA	1:F:574:ILE:CD1	2.39	0.43
1:F:571:ASP:HA	1:F:574:ILE:HB	2.00	0.43
2:G:45:TYR:HE2	2:G:71:LEU:HD11	1.83	0.43
1:B:485:GLU:O	1:B:489:LYS:CB	2.67	0.43
1:A:713:LEU:CD2	1:A:732:LEU:HB3	2.40	0.43
1:B:541:LEU:O	1:B:541:LEU:HD12	2.19	0.43
1:E:242:PRO:CD	1:E:243:GLU:H	2.32	0.43
1:B:388:ARG:O	1:B:389:LEU:HD23	2.19	0.43
1:D:105:LYS:O	1:D:106:ASN:ND2	2.51	0.43
1:C:12:PRO:HB3	1:C:54:SER:OG	2.18	0.43
2:I:72:HIS:ND1	2:I:81:ALA:HB2	2.34	0.43
1:B:547:SER:HA	1:B:707:ILE:HG22	2.00	0.43
1:F:91:CYS:HB3	1:F:155:MET:CE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:101:ILE:HB	2:J:131:TYR:OH	2.18	0.43
1:A:114:THR:HG21	1:A:200:LYS:HG2	2.00	0.43
2:G:147:GLN:HG2	2:G:151:TYR:CE2	2.53	0.43
4:L:248:VAL:O	4:L:252:LYS:HG3	2.18	0.43
1:F:677:LEU:O	1:F:681:GLU:HG3	2.18	0.43
2:J:10:ALA:O	2:J:14:LEU:HG	2.19	0.43
1:C:709:LYS:HD2	1:C:709:LYS:HA	1.84	0.43
1:F:524:LEU:HD13	1:F:539:VAL:CG2	2.49	0.43
1:F:560:SER:HB2	1:F:562:PHE:CD1	2.54	0.43
1:D:227:PHE:O	1:D:230:ILE:HG22	2.18	0.43
2:G:35:SER:HA	2:G:38:ILE:HG22	2.01	0.43
1:F:254:LYS:O	1:F:368:LEU:HA	2.18	0.43
1:F:408:HIS:O	1:F:408:HIS:ND1	2.45	0.43
2:I:200:TYR:O	2:I:203:LYS:NZ	2.45	0.43
1:A:247:GLN:CA	1:B:413:ARG:HH12	2.32	0.43
2:H:231:LEU:HB2	2:H:234:ALA:CB	2.49	0.43
1:D:327:PHE:HB2	1:D:330:ILE:CG2	2.48	0.43
1:F:263:GLY:HA3	1:F:437:SER:HB2	2.01	0.43
2:J:21:VAL:HG13	2:J:21:VAL:O	2.19	0.43
2:J:63:ASN:O	2:J:67:GLN:HG3	2.19	0.43
1:F:106:ASN:HB3	1:F:143:LYS:HZ2	1.83	0.43
1:B:549:LYS:HZ3	1:B:647:SER:HA	1.84	0.43
2:I:147:GLN:HG2	2:I:151:TYR:CE2	2.53	0.43
2:G:179:GLN:HB3	2:G:214:PHE:HB3	2.00	0.43
1:D:247:GLN:O	1:E:414:MET:SD	2.77	0.43
1:C:24:VAL:HG12	1:C:60:VAL:HG13	1.99	0.43
1:B:218:MET:HA	1:B:219:GLY:HA2	1.70	0.43
1:F:24:VAL:HG21	1:F:29:TYR:HB2	2.00	0.43
2:I:12:ALA:O	2:I:16:GLU:HG3	2.19	0.43
4:L:225:SER:C	4:L:229:MET:HE2	2.39	0.43
1:D:406:ILE:HG23	1:D:406:ILE:HD12	1.70	0.43
1:E:586:LYS:O	1:E:589:PHE:HB2	2.19	0.43
2:J:271:ARG:CZ	2:G:234:ALA:HB2	2.48	0.43
2:I:45:TYR:CE2	2:I:71:LEU:HD11	2.54	0.43
3:K:48:VAL:HG12	3:K:52:LYS:CE	2.40	0.43
3:K:48:VAL:O	3:K:52:LYS:HG3	2.18	0.43
1:B:288:PRO:HG2	1:B:289:GLU:H	1.83	0.43
1:A:231:PHE:CE1	1:A:235:PHE:CE2	3.04	0.43
1:D:105:LYS:HZ1	2:I:291:GLU:HB3	1.84	0.43
1:A:313:GLN:NE2	1:A:365:ASN:OD1	2.52	0.43
2:H:67:GLN:O	2:H:71:LEU:HG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:167:LYS:HE2	2:I:171:TYR:CE2	2.53	0.43
2:H:169:ALA:HB2	2:H:184:ILE:HB	2.01	0.43
2:G:167:LYS:HE2	2:G:171:TYR:CE2	2.54	0.43
2:I:263:VAL:HG21	2:I:280:LEU:HD13	2.01	0.43
1:B:492:PHE:C	1:B:494:THR:H	2.19	0.43
1:B:375:ARG:NH2	1:B:377:ASP:OD2	2.51	0.43
1:F:518:LEU:HD23	1:F:555:LYS:CG	2.16	0.42
1:E:564:PHE:HB3	1:E:595:SER:HB2	2.01	0.42
2:J:269:ILE:HG22	5:M:151:GLU:OE1	2.19	0.42
1:C:620:ASN:O	1:C:624:GLN:HG2	2.20	0.42
1:B:286:ASN:OD1	1:B:327:PHE:HD1	2.02	0.42
1:E:67:ARG:HH11	1:E:74:ILE:HD11	1.84	0.42
2:I:17:ALA:HB2	2:I:44:ILE:HG21	2.01	0.42
1:E:587:LYS:HZ1	1:E:591:ASP:CG	2.22	0.42
1:E:242:PRO:HD2	1:E:243:GLU:N	2.34	0.42
5:M:167:MET:HA	5:M:170:GLU:HB3	2.00	0.42
2:G:95:ALA:HB1	2:G:97:PRO:HD2	2.00	0.42
2:I:161:ALA:O	2:I:165:LEU:HG	2.18	0.42
2:H:218:MET:CG	2:H:219:LEU:N	2.77	0.42
1:D:236:ALA:HA	1:D:239:VAL:HG12	2.00	0.42
2:I:17:ALA:HB2	2:I:44:ILE:CG2	2.50	0.42
1:E:608:LEU:HD23	1:E:626:LEU:HD11	2.01	0.42
1:A:453:MET:HA	1:F:240:PHE:CE2	2.54	0.42
1:E:297:GLU:O	1:E:300:ALA:HB3	2.19	0.42
1:D:690:GLU:O	1:D:694:ILE:HG13	2.19	0.42
1:A:407:LEU:O	1:A:411:THR:HG23	2.19	0.42
2:G:266:TYR:CZ	2:G:270:SER:HB2	2.55	0.42
1:A:12:PRO:HB3	1:A:54:SER:OG	2.19	0.42
1:F:440:GLU:O	1:F:444:LEU:HG	2.18	0.42
1:E:73:SER:O	1:E:76:GLN:HG2	2.19	0.42
2:H:58:TRP:HB3	2:H:95:ALA:HB2	2.00	0.42
2:I:267:ASP:OD2	2:I:271:ARG:NH2	2.52	0.42
1:B:671:ALA:HA	1:B:703:VAL:O	2.19	0.42
1:A:73:SER:HB2	1:A:76:GLN:OE1	2.18	0.42
3:K:67:ALA:HB1	4:L:237:VAL:HG22	2.01	0.42
1:D:518:LEU:HD23	1:D:518:LEU:HA	1.86	0.42
1:E:705:ILE:CD1	1:E:713:LEU:HD12	2.49	0.42
1:C:533:ARG:C	1:D:505:ASN:HD21	2.22	0.42
1:A:235:PHE:N	1:A:235:PHE:CD1	2.81	0.42
1:F:721:ASP:O	1:F:725:ARG:HG3	2.20	0.42
3:K:60:LEU:HD23	5:M:178:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:75:LEU:O	2:H:76:GLN:HB2	2.19	0.42
3:K:77:PHE:HB2	5:M:192:ILE:HG23	2.02	0.42
1:F:436:PHE:CD2	1:F:444:LEU:HD11	2.55	0.42
1:F:503:ILE:HD11	1:F:554:ALA:HB3	2.02	0.42
1:B:612:VAL:HG13	1:B:614:ILE:O	2.19	0.42
1:D:131:SER:HA	1:D:173:GLU:O	2.20	0.42
1:E:86:ASP:C	1:E:88:ALA:H	2.21	0.42
2:G:134:GLU:O	2:G:136:VAL:HG23	2.19	0.42
1:B:436:PHE:CE2	1:B:444:LEU:HD11	2.54	0.42
2:J:188:VAL:HG13	2:J:205:TYR:CD2	2.55	0.42
2:G:235:PHE:CG	5:M:152:GLN:HA	2.53	0.42
1:C:490:PRO:HB2	1:C:492:PHE:H	1.83	0.42
1:F:653:GLN:CB	1:F:658:LEU:HD23	2.49	0.42
1:C:386:PRO:HA	1:C:390:GLU:CA	2.39	0.42
1:D:510:TRP:CB	1:D:679:ALA:HB2	2.50	0.42
2:J:200:TYR:O	2:J:203:LYS:HG3	2.19	0.42
2:G:232:PHE:CB	2:G:233:PRO:HD3	2.40	0.42
1:E:691:ARG:HA	1:E:694:ILE:HD12	2.01	0.42
1:C:691:ARG:HB2	1:C:691:ARG:NH1	2.35	0.42
1:D:543:GLY:N	1:D:549:LYS:HD3	2.30	0.42
1:E:388:ARG:O	1:E:389:LEU:HD23	2.20	0.42
1:F:618:PHE:HE1	1:F:620:ASN:HA	1.85	0.42
1:D:388:ARG:O	1:D:389:LEU:HD23	2.19	0.42
2:H:179:GLN:HB3	2:H:214:PHE:CB	2.50	0.42
1:C:629:LEU:HD23	1:C:629:LEU:HA	1.74	0.42
1:A:611:TYR:HA	1:A:618:PHE:HB3	2.00	0.42
2:J:260:THR:HA	2:J:263:VAL:HG12	2.01	0.42
1:D:52:HIS:C	1:D:54:SER:H	2.23	0.42
2:G:166:LEU:HD21	2:G:205:TYR:CE2	2.54	0.42
1:C:517:VAL:HG13	1:C:665:ILE:HG21	2.02	0.42
1:B:24:VAL:O	1:B:51:THR:HA	2.19	0.42
2:J:184:ILE:O	2:J:188:VAL:HG12	2.20	0.42
1:C:499:TYR:OH	1:C:565:ILE:HB	2.20	0.42
1:C:560:SER:HB2	1:C:562:PHE:CZ	2.54	0.42
1:D:407:LEU:HB2	1:D:426:ILE:HG23	2.02	0.42
1:A:502:TYR:N	1:A:502:TYR:CD1	2.86	0.42
1:D:538:SER:OG	1:D:661:PHE:HA	2.19	0.42
1:C:318:ALA:C	1:C:319:ASN:HD22	2.21	0.42
1:A:231:PHE:CE2	1:A:235:PHE:CD2	3.08	0.42
1:E:245:VAL:HG13	1:E:246:GLU:N	2.34	0.42
1:A:687:LYS:HZ3	1:A:722:PRO:HB3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:331:ASP:O	1:D:332:ALA:HB3	2.19	0.42
2:H:101:ILE:HB	2:H:131:TYR:OH	2.20	0.42
1:B:232:ARG:O	1:B:236:ALA:HB3	2.19	0.42
1:B:23:VAL:HG12	1:B:55:VAL:CG2	2.50	0.42
2:I:277:THR:O	2:I:281:LEU:HD13	2.20	0.42
1:A:322:LEU:HD13	1:A:366:ASN:O	2.20	0.42
1:C:220:ILE:HD11	1:C:272:GLN:HG3	2.01	0.42
2:H:163:LYS:O	2:H:167:LYS:HG2	2.19	0.42
1:C:519:ASP:O	1:C:523:LEU:HG	2.20	0.42
1:F:38:ARG:HG2	1:F:38:ARG:HH11	1.84	0.42
1:B:242:PRO:HD2	1:B:243:GLU:N	2.34	0.42
5:M:28:SER:O	5:M:32:MET:N	2.53	0.42
1:F:524:LEU:HD11	1:F:665:ILE:HD11	2.01	0.42
1:B:64:LEU:HA	1:B:67:ARG:HH21	1.84	0.42
1:D:549:LYS:HB3	1:D:645:THR:HB	2.01	0.42
1:F:388:ARG:O	1:F:389:LEU:HD23	2.20	0.42
1:A:220:ILE:HG22	1:A:221:GLY:N	2.34	0.42
1:E:648:ARG:NE	1:E:651:VAL:HG13	2.33	0.42
1:E:122:ILE:HD11	1:E:183:VAL:CG2	2.50	0.42
2:I:118:THR:HG22	2:I:155:GLU:HG3	2.02	0.42
2:H:266:TYR:HD2	2:H:272:LEU:HD21	1.85	0.42
2:H:118:THR:HG22	2:H:155:GLU:HG3	2.00	0.42
1:E:406:ILE:O	1:E:409:ILE:HG22	2.19	0.42
1:D:499:TYR:N	1:D:499:TYR:CD1	2.86	0.42
2:H:219:LEU:O	2:H:219:LEU:HD12	2.19	0.42
1:E:643:ILE:N	1:E:643:ILE:HD12	2.35	0.42
5:M:49:MET:HG2	5:M:53:GLN:NE2	2.33	0.42
1:F:589:PHE:N	1:F:589:PHE:CD1	2.84	0.42
1:F:632:LYS:NZ	1:F:633:ALA:O	2.36	0.42
1:D:240:PHE:HA	1:D:241:PRO:HD3	1.89	0.42
1:E:313:GLN:HE21	1:E:317:GLY:CA	2.32	0.42
1:A:552:LEU:HD22	1:A:556:ILE:HD11	2.00	0.42
1:D:709:LYS:HA	1:D:709:LYS:HD2	1.85	0.42
1:C:576:PHE:HB3	1:C:580:ALA:HB3	2.01	0.42
1:A:315:ARG:HG2	1:A:316:LEU:HD12	2.00	0.42
2:I:216:ILE:HG12	2:I:217:ASP:H	1.85	0.42
2:I:49:ALA:HB2	2:I:64:ALA:HB3	2.02	0.42
1:A:86:ASP:C	1:A:88:ALA:H	2.22	0.42
5:M:23:ASP:O	5:M:27:GLU:HB2	2.20	0.42
1:C:521:GLY:O	1:C:525:VAL:HG23	2.20	0.42
1:E:284:VAL:O	1:E:326:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:670:ILE:HG21	1:D:670:ILE:HD13	1.75	0.42
1:A:706:GLY:O	1:A:710:LEU:N	2.53	0.42
1:A:676:LEU:HD12	1:A:710:LEU:HD11	2.01	0.42
2:J:203:LYS:HD3	2:J:236:SER:HB3	2.02	0.42
2:J:265:GLU:O	2:J:268:SER:HB2	2.20	0.42
1:E:307:ALA:O	1:E:310:GLU:HG2	2.20	0.42
1:E:714:ILE:HG12	1:E:729:PHE:HE1	1.84	0.42
1:F:12:PRO:HD2	1:F:23:VAL:HG21	2.01	0.42
2:H:45:TYR:HE2	2:H:71:LEU:HD11	1.84	0.42
1:B:546:HIS:O	1:B:547:SER:OG	2.27	0.42
2:J:81:ALA:O	2:J:85:PHE:HD1	2.02	0.42
2:I:163:LYS:O	2:I:167:LYS:HG2	2.20	0.42
1:D:268:LEU:O	1:D:271:ARG:HG2	2.19	0.42
1:C:24:VAL:CG1	1:C:49:LEU:HD22	2.49	0.42
1:C:26:GLU:HG2	1:C:51:THR:HB	2.01	0.42
1:E:377:ASP:OD1	1:E:378:LEU:N	2.53	0.42
1:F:74:ILE:HB	2:G:216:ILE:HD11	2.01	0.42
1:D:186:GLU:HG3	1:D:186:GLU:O	2.19	0.42
2:J:25:GLN:N	2:J:29:SER:HB2	2.35	0.42
1:A:542:GLU:HA	1:A:646:THR:O	2.19	0.42
1:F:545:PRO:HB3	1:F:546:HIS:HA	2.01	0.42
1:E:534:THR:HG21	1:F:712:MET:HA	2.01	0.42
1:D:627:LEU:HA	1:D:627:LEU:HD23	1.65	0.42
1:A:247:GLN:HA	1:B:413:ARG:HH12	1.85	0.42
1:D:545:PRO:CD	1:D:647:SER:OG	2.68	0.42
1:A:16:LEU:HD11	1:A:52:HIS:CD2	2.54	0.42
1:F:289:GLU:C	1:F:291:LEU:H	2.16	0.42
2:I:95:ALA:CB	2:I:97:PRO:HD2	2.50	0.42
1:B:579:THR:O	1:B:583:GLN:HG2	2.20	0.42
1:A:38:ARG:HH11	1:A:38:ARG:HG2	1.85	0.42
1:C:562:PHE:HD2	1:C:599:CYS:CB	2.33	0.42
2:G:75:LEU:O	2:G:76:GLN:HB3	2.19	0.42
1:C:508:ILE:HD11	1:C:707:ILE:HD11	2.02	0.42
1:B:520:ASP:OD2	1:B:665:ILE:HG12	2.20	0.42
2:G:164:CYS:O	2:G:168:VAL:HG23	2.20	0.42
1:D:573:MET:SD	1:D:608:LEU:HD22	2.59	0.42
1:A:240:PHE:CG	1:A:244:ILE:HD11	2.55	0.42
2:G:92:PHE:HD1	2:G:97:PRO:HG2	1.84	0.42
1:C:284:VAL:HB	1:C:325:ILE:HA	2.01	0.42
1:B:452:ALA:HA	1:B:455:ARG:CZ	2.50	0.42
1:E:545:PRO:HG3	1:E:647:SER:OG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:195:ILE:HG21	5:M:18:ALA:HB1	2.02	0.42
2:I:250:ALA:HB1	2:I:259:TYR:HB2	2.02	0.42
1:E:568:CYS:HB3	1:E:601:VAL:O	2.20	0.42
4:L:241:VAL:HG21	5:M:63:GLY:HA3	2.01	0.41
5:M:36:VAL:HA	5:M:39:SER:OG	2.20	0.41
2:J:247:LEU:HD22	2:J:259:TYR:CE1	2.55	0.41
1:E:670:ILE:HG21	1:E:675:GLN:HB3	2.02	0.41
1:B:539:VAL:CG2	1:B:665:ILE:HD12	2.50	0.41
1:B:295:VAL:HB	1:C:294:TYR:CB	2.50	0.41
2:J:117:PHE:HA	2:J:120:ALA:HB3	2.01	0.41
1:F:438:GLY:O	1:F:441:LEU:N	2.45	0.41
1:C:218:MET:HA	1:C:219:GLY:HA2	1.76	0.41
2:J:82:ALA:O	2:J:86:VAL:HG23	2.20	0.41
2:H:208:LYS:HG2	2:H:275:TRP:CZ3	2.55	0.41
1:A:10:ARG:HD2	2:H:217:ASP:HB2	2.02	0.41
4:L:202:ILE:HG22	5:M:25:SER:HB3	2.01	0.41
5:M:36:VAL:CG2	5:M:156:ILE:HD12	2.51	0.41
1:C:624:GLN:OE1	1:C:624:GLN:HA	2.20	0.41
1:F:542:GLU:N	1:F:665:ILE:O	2.52	0.41
1:A:686:PHE:O	1:A:691:ARG:NH2	2.52	0.41
3:K:35:THR:O	3:K:35:THR:HG22	2.20	0.41
2:J:195:SER:C	2:J:197:LEU:H	2.23	0.41
1:E:190:ASN:HB2	1:E:315:ARG:HH12	1.85	0.41
1:E:99:ILE:HD11	1:E:145:PHE:CD2	2.55	0.41
1:A:235:PHE:HD1	1:A:235:PHE:HA	1.58	0.41
1:F:549:LYS:HE3	1:F:646:THR:C	2.40	0.41
1:D:570:PRO:O	1:D:573:MET:HB3	2.20	0.41
1:D:349:THR:HA	1:D:352:ASN:HD22	1.84	0.41
1:A:220:ILE:HD11	1:A:227:PHE:CZ	2.54	0.41
1:D:377:ASP:OD1	1:D:378:LEU:N	2.53	0.41
1:A:97:ILE:HG21	1:A:147:LEU:HD22	2.03	0.41
1:F:18:LEU:HD13	1:F:139:SER:OG	2.21	0.41
1:D:122:ILE:HD11	1:D:183:VAL:CG2	2.50	0.41
1:F:377:ASP:OD1	1:F:378:LEU:N	2.53	0.41
1:C:113:ASP:HA	1:C:196:ILE:HG13	2.01	0.41
1:B:377:ASP:OD1	1:B:378:LEU:N	2.53	0.41
1:A:509:LYS:HG2	1:A:515:THR:OG1	2.20	0.41
2:I:236:SER:HA	2:I:239:ARG:NH1	2.35	0.41
1:F:400:GLU:OE2	1:F:434:LYS:HA	2.21	0.41
1:E:539:VAL:HG13	1:E:643:ILE:HA	2.02	0.41
1:F:324:ILE:HG12	1:F:368:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:271:ARG:NH2	2:G:231:LEU:HB2	2.35	0.41
1:E:670:ILE:CG2	1:E:672:THR:H	2.29	0.41
1:C:232:ARG:O	1:C:236:ALA:HB3	2.21	0.41
1:C:125:PHE:CD2	1:C:130:PHE:HZ	2.39	0.41
1:E:242:PRO:O	1:E:245:VAL:HG12	2.20	0.41
1:F:624:GLN:O	1:F:628:VAL:HG23	2.21	0.41
2:H:21:VAL:HG23	2:H:38:ILE:CD1	2.50	0.41
1:F:263:GLY:HA3	1:F:437:SER:CB	2.50	0.41
3:K:54:LEU:HD21	4:L:222:LEU:HD13	2.02	0.41
2:H:256:VAL:O	2:H:256:VAL:HG22	2.19	0.41
2:I:219:LEU:O	2:I:220:ASN:HB3	2.21	0.41
1:B:536:LEU:HD22	1:B:632:LYS:O	2.19	0.41
1:C:233:ARG:HA	1:D:450:SER:HB2	2.02	0.41
1:D:541:LEU:HD12	1:D:541:LEU:O	2.21	0.41
2:J:188:VAL:HG13	2:J:205:TYR:HD2	1.86	0.41
5:M:33:LEU:C	5:M:33:LEU:HD23	2.40	0.41
1:D:256:ILE:HG22	1:D:391:VAL:CG1	2.48	0.41
2:G:39:GLU:HB2	2:G:75:LEU:HD11	2.01	0.41
2:I:203:LYS:HD2	2:I:237:ASP:HA	2.03	0.41
1:B:479:ASP:C	1:B:483:SER:H	2.23	0.41
1:D:331:ASP:HA	1:D:379:ILE:CD1	2.51	0.41
2:J:232:PHE:CZ	2:J:242:LYS:HD3	2.55	0.41
1:C:67:ARG:CZ	2:I:217:ASP:OD1	2.69	0.41
1:A:138:PHE:HB2	1:A:147:LEU:HD11	2.01	0.41
1:C:538:SER:O	1:C:662:SER:OG	2.27	0.41
1:A:24:VAL:HG11	1:A:49:LEU:HD22	2.02	0.41
1:A:254:LYS:O	1:A:368:LEU:HA	2.20	0.41
1:F:520:ASP:O	1:F:524:LEU:HG	2.20	0.41
1:E:586:LYS:NZ	1:F:574:ILE:HG23	2.35	0.41
1:A:242:PRO:O	1:A:245:VAL:HG12	2.20	0.41
1:A:510:TRP:CE3	1:A:675:GLN:HB3	2.56	0.41
1:D:11:CYS:HA	1:D:12:PRO:HD3	1.92	0.41
1:C:436:PHE:N	1:C:436:PHE:CD1	2.84	0.41
1:C:38:ARG:HH11	1:C:38:ARG:HG2	1.85	0.41
2:G:118:THR:HG22	2:G:155:GLU:HG3	2.03	0.41
2:G:116:ARG:HB3	2:G:119:ILE:HG22	2.02	0.41
1:B:69:TRP:CE2	1:B:134:GLN:HA	2.56	0.41
1:F:101:PHE:H	1:F:101:PHE:HD1	1.67	0.41
1:D:45:TYR:CE2	1:D:70:ALA:HA	2.56	0.41
1:E:230:ILE:HD11	1:E:391:VAL:HG11	2.02	0.41
1:C:528:THR:O	1:C:639:LYS:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:9:GLU:O	2:H:13:LEU:HG	2.20	0.41
1:B:52:HIS:C	1:B:54:SER:H	2.23	0.41
1:D:272:GLN:HA	1:D:272:GLN:OE1	2.21	0.41
1:E:441:LEU:O	1:E:445:VAL:HG23	2.21	0.41
2:J:219:LEU:O	2:J:223:LEU:N	2.52	0.41
1:D:604:ASP:O	1:D:607:ARG:N	2.54	0.41
1:D:627:LEU:CD1	1:E:607:ARG:HH12	2.32	0.41
1:F:670:ILE:O	1:F:704:TRP:HA	2.20	0.41
1:A:693:THR:O	1:A:697:GLN:OE1	2.38	0.41
3:K:84:LEU:HD21	5:M:199:ALA:CB	2.50	0.41
1:B:631:LYS:HB2	1:B:631:LYS:HE3	1.67	0.41
1:E:721:ASP:HB2	1:E:724:TYR:HD2	1.85	0.41
2:G:179:GLN:HG3	2:G:180:LYS:H	1.85	0.41
2:I:164:CYS:O	2:I:168:VAL:HG23	2.20	0.41
1:B:143:LYS:HB3	1:B:145:PHE:HE1	1.84	0.41
1:D:247:GLN:HA	1:E:417:HIS:ND1	2.35	0.41
1:B:512:ASP:N	1:B:513:PRO:CD	2.83	0.41
1:F:323:HIS:HB2	1:F:367:ILE:HG22	2.01	0.41
2:I:180:LYS:O	2:I:184:ILE:HG13	2.20	0.41
1:C:552:LEU:HA	1:C:552:LEU:HD23	1.78	0.41
1:B:414:MET:HE2	1:B:414:MET:HA	2.03	0.41
1:C:320:SER:O	1:C:320:SER:OG	2.31	0.41
2:H:217:ASP:OD1	2:H:217:ASP:N	2.50	0.41
1:E:562:PHE:HE2	1:E:641:LEU:CD2	2.34	0.41
1:E:640:LEU:HG	1:E:642:ILE:CD1	2.50	0.41
1:D:509:LYS:HE2	1:D:515:THR:HG22	2.03	0.41
1:E:659:ASN:HD21	1:F:545:PRO:HB2	1.86	0.41
3:K:52:LYS:CB	3:K:52:LYS:NZ	2.84	0.41
1:C:414:MET:HE2	1:C:414:MET:HA	2.02	0.41
1:E:709:LYS:O	1:E:709:LYS:HD3	2.20	0.41
1:B:407:LEU:O	1:B:411:THR:OG1	2.27	0.41
1:F:709:LYS:HG3	1:F:713:LEU:HG	2.02	0.41
1:F:510:TRP:HZ3	1:F:675:GLN:NE2	2.18	0.41
1:A:241:PRO:HA	1:A:242:PRO:HA	1.62	0.41
1:C:604:ASP:HB3	1:C:607:ARG:HB3	2.02	0.41
1:D:258:LEU:HB2	1:D:395:ILE:HD11	2.02	0.41
1:B:143:LYS:HB3	1:B:145:PHE:CE1	2.56	0.41
1:D:265:GLY:O	1:D:268:LEU:HG	2.20	0.41
1:C:272:GLN:HA	1:C:272:GLN:OE1	2.20	0.41
1:C:297:GLU:O	1:C:301:ASN:N	2.32	0.41
2:H:175:LEU:HD23	2:H:177:GLN:HE21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:112:THR:HG23	2:H:117:PHE:CE1	2.56	0.41
1:C:626:LEU:HA	1:C:626:LEU:HD23	1.87	0.41
4:L:237:VAL:O	4:L:241:VAL:HG23	2.21	0.41
1:C:240:PHE:HA	1:C:241:PRO:HD3	1.94	0.41
1:A:673:GLY:O	1:A:676:LEU:HB3	2.21	0.41
1:C:649:LYS:HE2	1:C:658:LEU:CD1	2.45	0.41
1:A:215:PHE:N	1:A:231:PHE:CZ	2.89	0.41
1:D:527:GLN:HE22	1:E:716:MET:CA	2.33	0.41
1:B:257:LEU:HG	1:B:371:GLY:O	2.21	0.41
1:D:562:PHE:CD2	1:D:597:LEU:HG	2.55	0.41
1:E:395:ILE:HD12	1:E:395:ILE:H	1.86	0.41
2:G:95:ALA:CB	2:G:97:PRO:HD2	2.51	0.41
2:I:124:HIS:CE1	2:I:147:GLN:HB3	2.55	0.41
1:D:198:LYS:C	1:D:198:LYS:HD3	2.41	0.41
1:E:451:THR:O	1:E:454:ASN:HB3	2.21	0.41
2:G:200:TYR:O	2:G:203:LYS:HE2	2.21	0.41
3:K:39:VAL:CG1	4:L:209:ILE:HD13	2.46	0.41
1:E:598:SER:O	1:E:640:LEU:HA	2.21	0.41
1:C:257:LEU:HG	1:C:371:GLY:O	2.21	0.41
1:F:658:LEU:HD12	1:F:658:LEU:O	2.20	0.41
1:E:604:ASP:HB3	1:E:607:ARG:CB	2.49	0.41
1:C:653:GLN:HA	1:C:658:LEU:HB3	2.02	0.41
1:A:457:ILE:HB	1:F:232:ARG:HH21	1.86	0.41
1:D:449:GLN:O	1:D:453:MET:HG2	2.21	0.41
2:J:213:HIS:CE1	2:J:221:ALA:HB2	2.44	0.41
1:F:709:LYS:HE2	1:F:709:LYS:HB2	1.82	0.41
5:M:174:GLN:O	5:M:177:GLN:HB3	2.21	0.41
1:D:608:LEU:O	1:D:622:VAL:HG11	2.20	0.41
1:D:330:ILE:CD1	1:D:373:THR:HB	2.50	0.41
1:D:560:SER:HB2	1:D:562:PHE:CE1	2.55	0.41
1:D:40:SER:HB3	1:D:43:HIS:CB	2.51	0.41
1:F:503:ILE:HD11	1:F:551:ALA:HA	2.02	0.41
1:A:40:SER:HB3	1:A:43:HIS:ND1	2.36	0.41
1:B:406:ILE:O	1:B:409:ILE:HG22	2.20	0.41
1:F:230:ILE:HD13	1:F:391:VAL:HG21	2.03	0.41
1:A:26:GLU:HG2	1:A:51:THR:HB	2.03	0.41
1:F:121:PHE:CD2	1:F:183:VAL:HG21	2.56	0.41
1:A:27:LYS:HD2	1:A:57:PRO:CG	2.51	0.41
2:H:167:LYS:HE2	2:H:171:TYR:HE2	1.85	0.41
1:B:16:LEU:HD11	1:B:52:HIS:HD2	1.86	0.41
1:E:455:ARG:HH21	1:E:481:LEU:H	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:CYS:O	1:A:154:ALA:HA	2.21	0.41
1:F:98:GLU:HB3	1:F:148:LEU:HB3	2.02	0.41
1:F:705:ILE:HG12	1:F:706:GLY:O	2.20	0.41
2:G:178:TYR:OH	2:G:282:ARG:HG2	2.20	0.41
2:H:260:THR:HG21	2:H:284:LYS:HE3	2.02	0.41
1:E:553:ALA:HB1	1:E:643:ILE:HG21	2.03	0.41
4:L:226:GLN:O	4:L:230:ILE:HG13	2.20	0.41
1:C:379:ILE:HA	1:C:379:ILE:HD13	1.74	0.41
1:D:507:ILE:HG21	1:D:509:LYS:NZ	2.36	0.41
1:D:609:LEU:HD12	1:D:611:TYR:H	1.86	0.41
1:F:297:GLU:O	1:F:300:ALA:HB3	2.21	0.41
1:F:257:LEU:HB2	1:F:389:LEU:HD13	2.03	0.41
1:A:243:GLU:O	1:A:246:GLU:HG2	2.21	0.41
2:G:101:ILE:O	2:G:105:MET:HG3	2.20	0.41
1:C:402:GLY:O	1:C:405:GLN:HB2	2.22	0.41
2:I:236:SER:HA	2:I:239:ARG:HH12	1.86	0.41
1:D:577:SER:O	1:D:580:ALA:N	2.54	0.41
1:B:178:VAL:HG22	1:B:181:SER:OG	2.20	0.41
1:B:633:ALA:HA	1:B:634:PRO:HD3	1.94	0.41
1:F:309:ALA:HA	1:F:312:GLU:OE1	2.21	0.41
1:C:696:GLN:NE2	1:C:696:GLN:O	2.54	0.41
2:H:221:ALA:O	2:H:225:VAL:N	2.53	0.40
5:M:165:LEU:O	5:M:169:ASN:ND2	2.48	0.40
1:A:429:LEU:CD2	1:A:482:ALA:HB1	2.51	0.40
1:E:324:ILE:HG12	1:E:368:LEU:HD11	2.03	0.40
1:B:67:ARG:HH12	1:B:74:ILE:HD11	1.84	0.40
1:E:190:ASN:HB2	1:E:315:ARG:NH1	2.36	0.40
1:A:352:ASN:CB	1:B:288:PRO:HB2	2.44	0.40
1:C:449:GLN:O	1:C:453:MET:HG2	2.21	0.40
1:B:309:ALA:HA	1:B:312:GLU:OE1	2.22	0.40
1:A:623:LEU:O	1:A:626:LEU:HB3	2.22	0.40
2:G:279:MET:O	2:G:283:ILE:HG13	2.21	0.40
1:E:323:HIS:HB2	1:E:367:ILE:HG22	2.03	0.40
4:L:223:VAL:C	5:M:49:MET:HE3	2.42	0.40
1:C:331:ASP:CA	1:C:379:ILE:HD11	2.46	0.40
1:A:428:GLU:O	1:A:432:GLU:HG2	2.21	0.40
1:F:437:SER:OG	1:F:440:GLU:HG2	2.20	0.40
2:H:116:ARG:HG3	2:H:116:ARG:NH1	2.37	0.40
1:E:414:MET:HA	1:E:414:MET:HE2	2.02	0.40
4:L:209:ILE:HG21	5:M:32:MET:HE2	2.03	0.40
3:K:53:VAL:HB	4:L:219:MET:HE1	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:236:ALA:HA	1:E:239:VAL:CG1	2.50	0.40
2:G:17:ALA:HB2	2:G:44:ILE:HG21	2.04	0.40
1:E:618:PHE:CD1	1:E:618:PHE:C	2.95	0.40
2:J:235:PHE:CG	3:K:38:GLN:CG	3.04	0.40
1:C:98:GLU:HG2	1:C:188:ALA:HB2	2.04	0.40
1:C:98:GLU:O	1:C:147:LEU:HA	2.21	0.40
1:C:630:LEU:HA	1:C:630:LEU:HD23	1.94	0.40
1:A:255:GLY:HA2	1:A:369:VAL:O	2.22	0.40
1:A:231:PHE:CD2	1:A:235:PHE:HD2	2.38	0.40
1:C:65:PRO:HG2	1:C:137:VAL:HG13	2.03	0.40
1:F:502:TYR:HD2	1:F:503:ILE:HG13	1.86	0.40
2:H:266:TYR:C	2:H:268:SER:H	2.25	0.40
1:B:113:ASP:O	1:B:117:MET:HG3	2.21	0.40
1:C:36:ILE:HD11	1:C:44:LYS:HB3	2.03	0.40
2:I:10:ALA:O	2:I:14:LEU:HG	2.20	0.40
1:B:721:ASP:HB2	1:B:724:TYR:CD1	2.57	0.40
1:F:678:GLU:O	1:F:682:LEU:HG	2.22	0.40
1:E:641:LEU:CD1	1:E:643:ILE:HD11	2.51	0.40
1:A:624:GLN:HG3	1:B:610:ASP:CG	2.39	0.40
1:A:284:VAL:O	1:A:326:ILE:HG13	2.21	0.40
1:B:403:ARG:O	1:B:407:LEU:HG	2.22	0.40
1:E:242:PRO:CD	1:E:243:GLU:N	2.85	0.40
2:J:59:SER:OG	2:J:97:PRO:HD3	2.21	0.40
1:F:652:LEU:O	1:F:655:MET:HB2	2.22	0.40
1:D:18:LEU:HD21	1:D:144:LEU:HD13	2.02	0.40
2:J:45:TYR:CE2	2:J:71:LEU:HD11	2.56	0.40
1:F:242:PRO:CD	1:F:243:GLU:N	2.84	0.40
1:C:99:ILE:HD11	1:C:145:PHE:CD2	2.57	0.40
1:B:221:GLY:HA3	1:B:406:ILE:CD1	2.52	0.40
1:B:52:HIS:HA	1:B:53:PRO:HD3	1.91	0.40
2:G:126:SER:O	2:G:130:ILE:HG13	2.22	0.40
1:B:323:HIS:HB2	1:B:367:ILE:HG22	2.02	0.40
2:I:256:VAL:HG22	2:I:256:VAL:O	2.21	0.40
4:L:209:ILE:HG22	4:L:210:ARG:N	2.35	0.40
1:E:64:LEU:HA	1:E:67:ARG:NE	2.21	0.40
2:J:261:GLU:O	2:J:265:GLU:HG3	2.21	0.40
1:E:544:PRO:O	1:E:547:SER:CB	2.68	0.40
1:E:190:ASN:ND2	1:E:316:LEU:CA	2.85	0.40
1:E:686:PHE:O	1:E:691:ARG:NH1	2.54	0.40
1:E:253:VAL:H	1:F:446:ARG:NH1	2.15	0.40
1:A:215:PHE:C	1:A:217:LYS:N	2.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:246:GLU:HG2	1:C:247:GLN:N	2.37	0.40
2:I:232:PHE:O	2:I:234:ALA:N	2.54	0.40
1:E:257:LEU:HB2	1:E:389:LEU:HD13	2.02	0.40
1:A:694:ILE:HA	1:A:697:GLN:OE1	2.22	0.40
1:D:379:ILE:HA	1:D:379:ILE:HD13	1.74	0.40
2:H:216:ILE:HG21	2:H:220:ASN:HB3	2.03	0.40
2:I:175:LEU:HD23	2:I:177:GLN:NE2	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	668/747 (89%)	613 (92%)	39 (6%)	16 (2%)	7	47
1	B	662/747 (89%)	589 (89%)	54 (8%)	19 (3%)	6	43
1	C	666/747 (89%)	616 (92%)	37 (6%)	13 (2%)	9	51
1	D	663/747 (89%)	601 (91%)	52 (8%)	10 (2%)	13	57
1	E	658/747 (88%)	603 (92%)	42 (6%)	13 (2%)	9	51
1	F	644/747 (86%)	585 (91%)	46 (7%)	13 (2%)	9	51
2	G	284/297 (96%)	227 (80%)	47 (16%)	10 (4%)	4	39
2	H	284/297 (96%)	230 (81%)	44 (16%)	10 (4%)	4	39
2	I	284/297 (96%)	229 (81%)	41 (14%)	14 (5%)	3	31
2	J	284/297 (96%)	229 (81%)	45 (16%)	10 (4%)	4	39
3	K	59/63 (94%)	56 (95%)	2 (3%)	1 (2%)	11	55
4	L	64/67 (96%)	58 (91%)	5 (8%)	1 (2%)	12	56
5	M	127/198 (64%)	119 (94%)	7 (6%)	1 (1%)	24	69
All	All	5347/5998 (89%)	4755 (89%)	461 (9%)	131 (2%)	12	47

All (131) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	LEU
1	A	293	LYS
1	A	294	TYR
1	A	318	ALA
1	A	320	SER
1	A	333	ILE
1	A	498	ASP
1	A	504	MET
1	B	283	LYS
1	B	297	GLU
1	B	318	ALA
1	B	395	ILE
1	B	439	ALA
1	B	497	GLU
1	B	502	TYR
1	C	297	GLU
1	C	318	ALA
1	C	497	GLU
1	C	498	ASP
1	C	578	GLU
1	D	283	LYS
1	D	318	ALA
1	D	489	LYS
1	E	283	LYS
1	E	297	GLU
1	E	318	ALA
1	E	439	ALA
1	E	489	LYS
1	F	12	PRO
1	F	283	LYS
1	F	297	GLU
1	F	318	ALA
1	F	439	ALA
2	H	58	TRP
2	H	76	GLN
2	I	58	TRP
2	I	77	SER
2	I	219	LEU
2	J	58	TRP
2	J	218	MET
2	J	235	PHE
2	G	58	TRP

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Mol	Chain	Res	Type
1	A	397	LEU
1	B	12	PRO
1	B	188	ALA
1	C	12	PRO
1	C	89	LYS
1	C	293	LYS
1	C	610	ASP
1	D	12	PRO
1	E	507	ILE
1	F	189	GLU
2	H	33	GLY
2	H	79	HIS
2	I	136	VAL
2	I	218	MET
2	I	254	GLN
2	I	256	VAL
2	G	76	GLN
3	K	30	ARG
4	L	209	ILE
1	A	12	PRO
1	A	241	PRO
1	A	264	CYS
1	B	241	PRO
1	B	293	LYS
1	B	546	HIS
1	C	87	LYS
1	C	241	PRO
1	D	87	LYS
1	D	293	LYS
1	E	87	LYS
1	E	241	PRO
1	E	293	LYS
1	F	241	PRO
1	F	293	LYS
2	H	159	SER
2	H	240	GLU
2	H	256	VAL
2	I	78	LYS
2	J	158	ASN
2	J	159	SER
2	G	79	HIS
2	G	156	GLU

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Mol	Chain	Res	Type
2	G	232	PHE
2	G	240	GLU
5	M	165	LEU
1	A	87	LYS
1	A	242	PRO
1	E	71	GLY
2	H	267	ASP
2	I	30	GLY
2	I	76	GLN
2	I	79	HIS
2	I	240	GLU
2	J	79	HIS
2	J	177	GLN
2	J	256	VAL
2	G	218	MET
1	A	668	PRO
1	B	87	LYS
1	B	397	LEU
1	B	547	SER
1	D	53	PRO
1	D	241	PRO
1	E	438	GLY
1	F	398	PRO
2	H	26	SER
2	I	232	PHE
2	I	233	PRO
2	J	96	ASP
2	G	97	PRO
2	G	256	VAL
1	B	53	PRO
1	B	438	GLY
1	B	490	PRO
1	E	490	PRO
1	F	397	LEU
1	F	668	PRO
1	B	398	PRO
1	D	488	ILE
1	F	438	GLY
1	F	684	GLY
2	G	30	GLY
1	C	490	PRO
1	D	545	PRO

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Mol	Chain	Res	Type
1	E	12	PRO
2	H	34	GLY
1	A	53	PRO
2	J	34	GLY
1	C	3	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	514/638 (81%)	512 (100%)	2 (0%)	93	96
1	B	514/638 (81%)	510 (99%)	4 (1%)	86	94
1	C	513/638 (80%)	511 (100%)	2 (0%)	93	96
1	D	509/638 (80%)	507 (100%)	2 (0%)	93	96
1	E	518/638 (81%)	515 (99%)	3 (1%)	90	95
1	F	513/638 (80%)	510 (99%)	3 (1%)	90	95
2	G	235/244 (96%)	235 (100%)	0	100	100
2	H	235/244 (96%)	234 (100%)	1 (0%)	93	96
2	I	233/244 (96%)	233 (100%)	0	100	100
2	J	235/244 (96%)	235 (100%)	0	100	100
3	K	52/54 (96%)	50 (96%)	2 (4%)	40	73
4	L	60/61 (98%)	60 (100%)	0	100	100
5	M	111/171 (65%)	111 (100%)	0	100	100
All	All	4242/5090 (83%)	4223 (100%)	19 (0%)	94	96

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	LEU
1	A	322	LEU
1	B	240	PHE

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Mol	Chain	Res	Type
1	B	305	LEU
1	B	322	LEU
1	B	327	PHE
1	C	305	LEU
1	C	676	LEU
1	D	305	LEU
1	D	311	GLU
1	E	305	LEU
1	E	322	LEU
1	E	549	LYS
1	F	305	LEU
1	F	322	LEU
1	F	536	LEU
2	H	251	HIS
3	K	45	ILE
3	K	68	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	353	GLN
1	B	128	GLN
1	B	526	GLN
1	B	561	ASN
1	B	624	GLN
1	C	319	ASN
1	D	20	ASN
1	D	313	GLN
1	D	319	ASN
1	D	352	ASN
1	D	353	GLN
1	D	527	GLN
1	D	675	GLN
1	E	170	GLN
1	E	313	GLN
1	E	319	ASN
1	E	352	ASN
1	E	527	GLN
1	E	659	ASN
1	E	666	HIS
1	F	456	HIS
1	F	527	GLN

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Mol	Chain	Res	Type
2	H	72	HIS
2	H	124	HIS
2	H	147	GLN
2	H	162	ASN
2	J	50	ASN
2	J	124	HIS
2	J	147	GLN
2	J	213	HIS
2	G	50	ASN
2	G	72	HIS
3	K	34	GLN
4	L	199	HIS
4	L	213	HIS
4	L	226	GLN
5	M	53	GLN
5	M	65	ASN
5	M	77	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.