



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:00 PM UTC

PDB ID : 5UJ8 / pdb_00005uj8
Title : Human Origin Recognition Complex subunits 2 and 3
Authors : Tocilj, A.; On, K.F.; Elkayam, E.; Joshua-Tor, L.
Deposited on : 2017-01-17
Resolution : 6.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

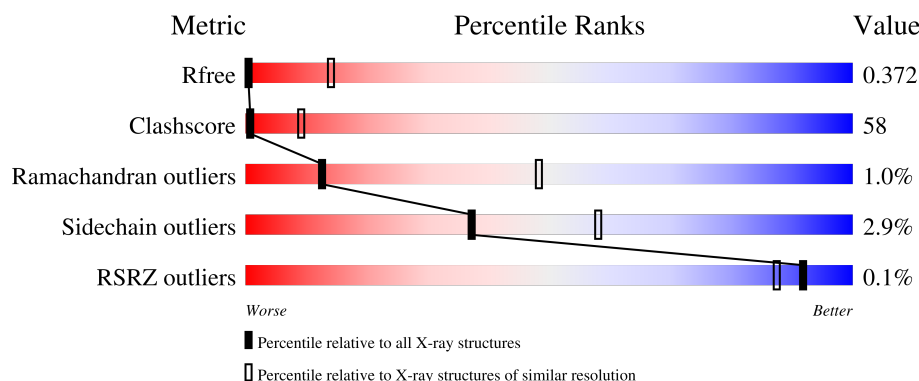
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 6.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1143 (8.00-4.00)
Clashscore	190562	1210 (8.00-4.00)
Ramachandran outliers	187476	1034 (8.00-4.00)
Sidechain outliers	187428	1000 (8.00-4.00)
RSRZ outliers	180081	1136 (8.00-4.00)

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

Mol	Chain	Length	Quality of chain
1	A	712	
1	B	712	
1	C	712	
1	D	712	
2	E	347	

Continued on next page...

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Mol	Chain	Length	Quality of chain
2	F	347	
2	G	347	
2	H	347	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 24144 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Origin recognition complex subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	0	0	0
			4524	2920	767	812	25			
1	B	553	Total	C	N	O	S	0	0	0
			4524	2920	767	812	25			
1	C	553	Total	C	N	O	S	0	0	0
			4524	2920	767	812	25			
1	D	553	Total	C	N	O	S	0	0	0
			4524	2920	767	812	25			

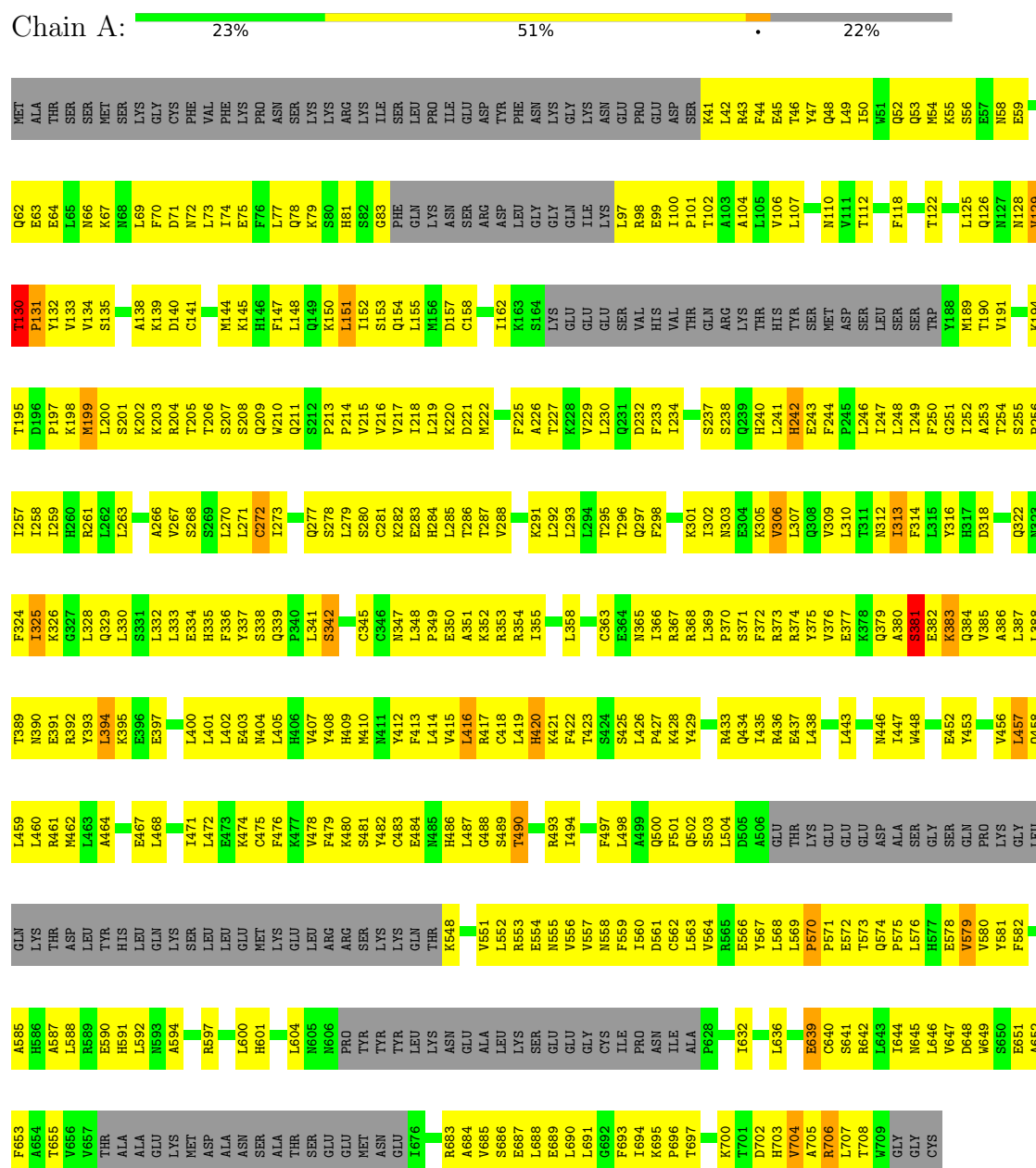
- Molecule 2 is a protein called Origin recognition complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	183	Total	C	N	O	S	0	0	0
			1512	978	249	280	5			
2	F	183	Total	C	N	O	S	0	0	0
			1512	978	249	280	5			
2	G	183	Total	C	N	O	S	0	0	0
			1512	978	249	280	5			
2	H	183	Total	C	N	O	S	0	0	0
			1512	978	249	280	5			

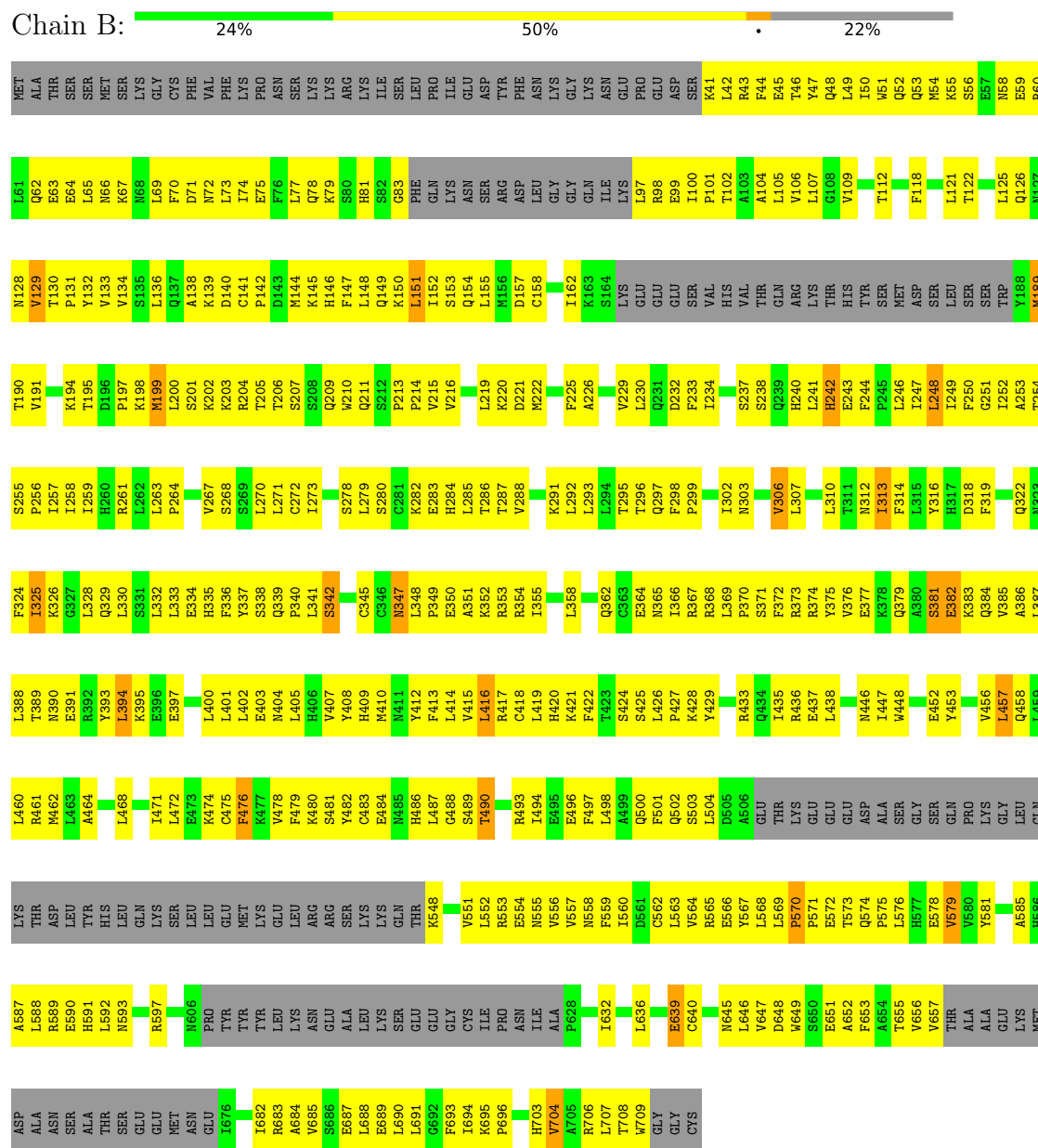
3 Residue-property plots

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

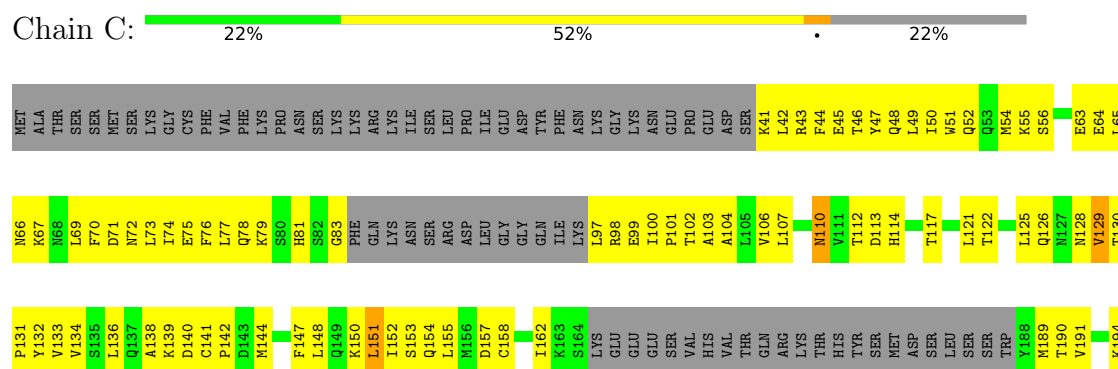
• Molecule 1: Origin recognition complex subunit 3

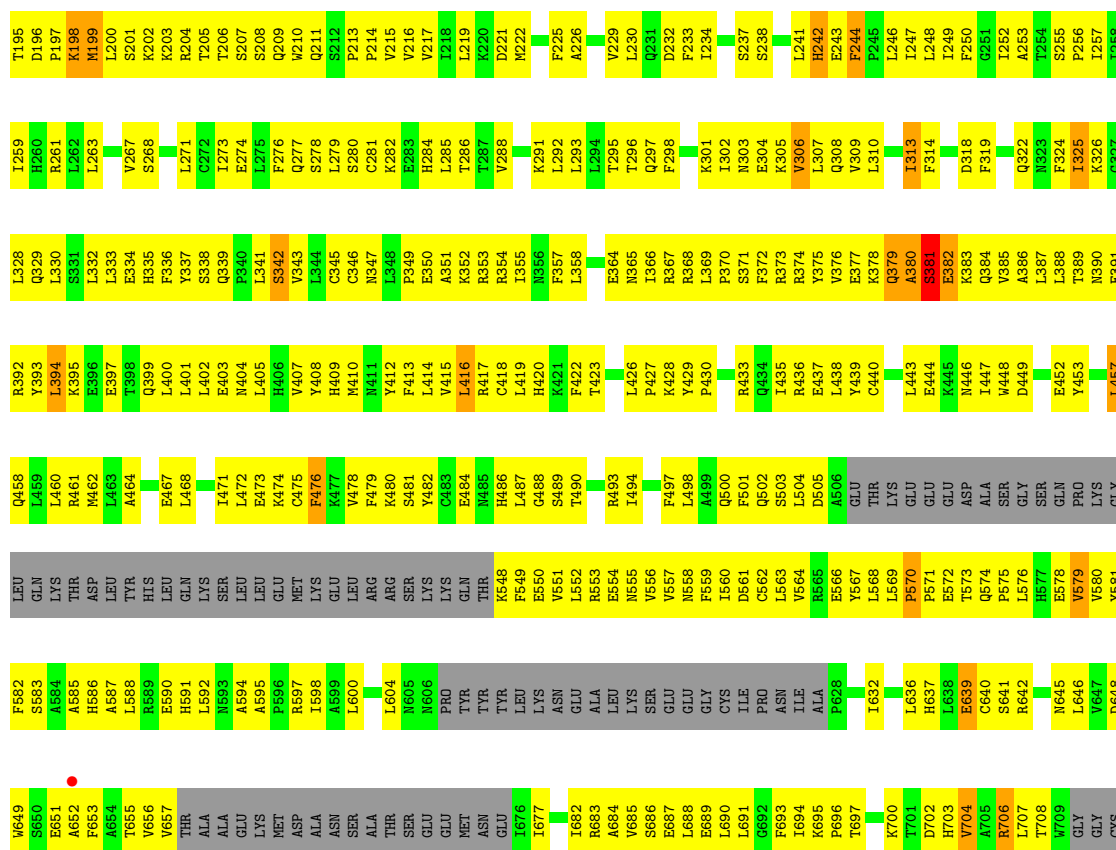


• Molecule 1: Origin recognition complex subunit 3



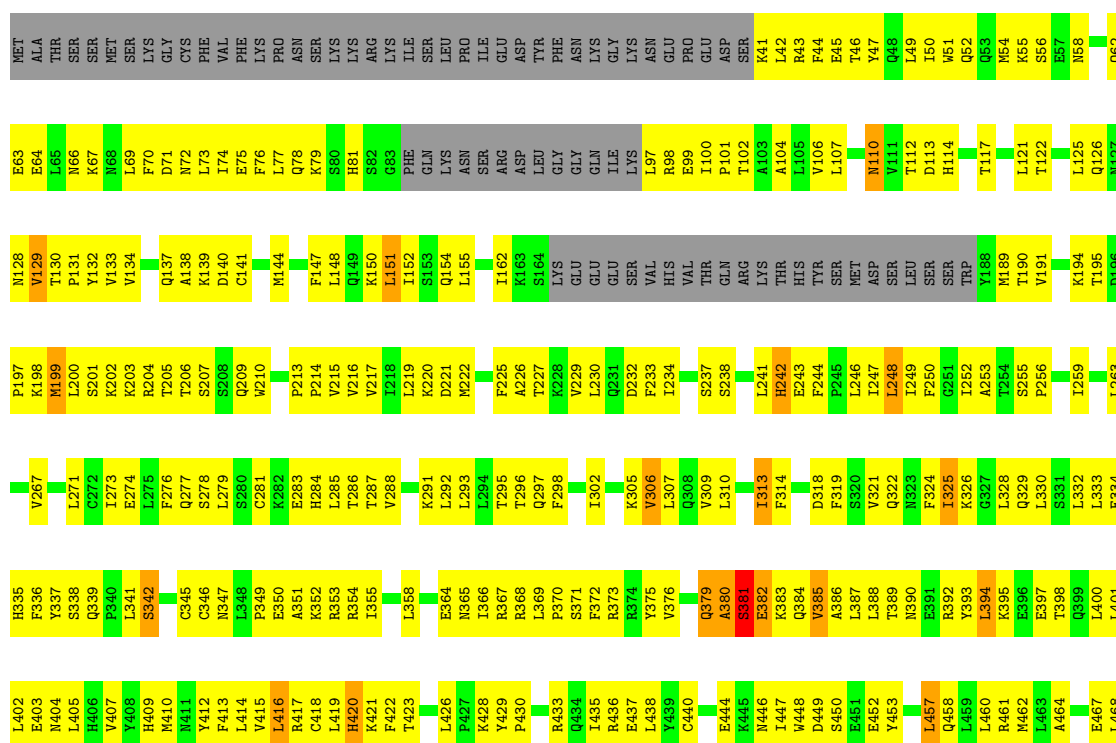
• Molecule 1: Origin recognition complex subunit 3

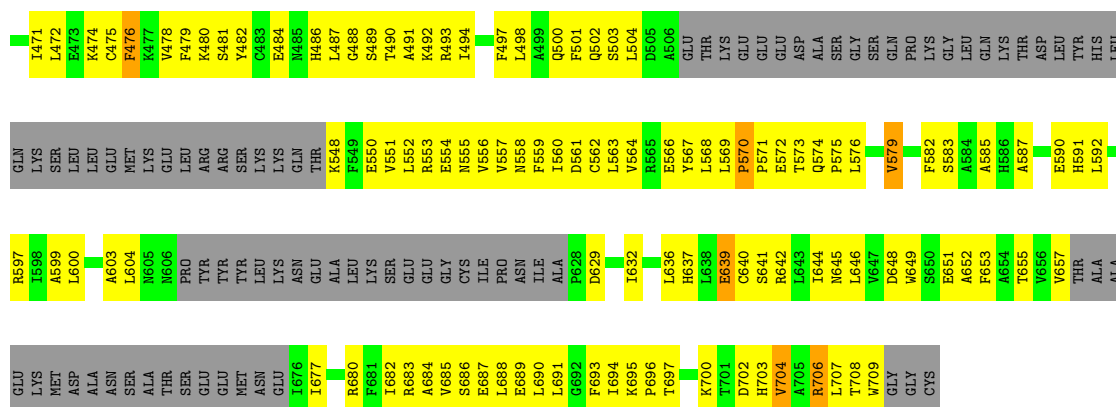




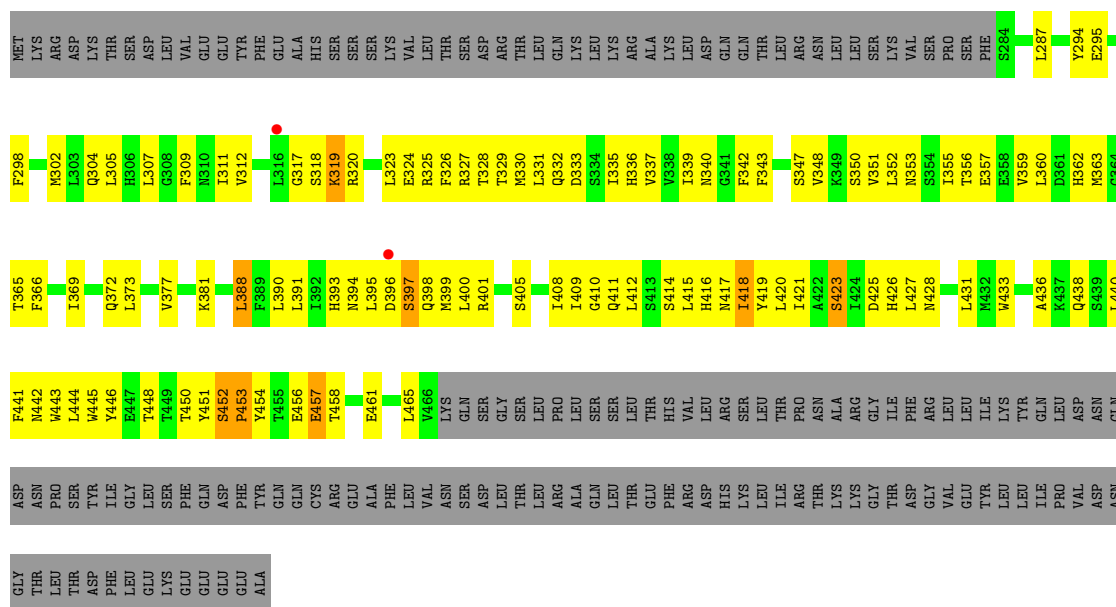
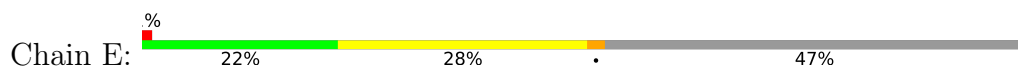
• Molecule 1: Origin recognition complex subunit 3

Chain D: 26% 49% 22%

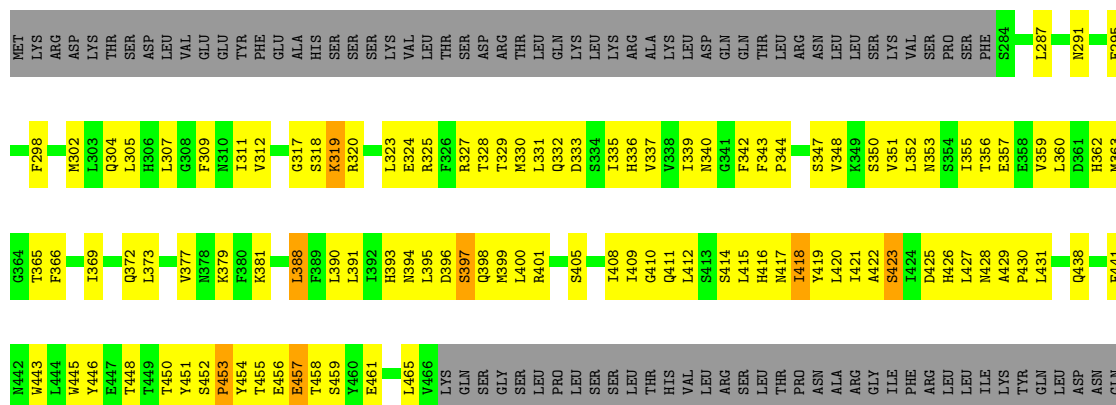




• Molecule 2: Origin recognition complex subunit 2



• Molecule 2: Origin recognition complex subunit 2



[illegible]

- Molecule 2: Origin recognition complex subunit 2

Chain G: 22% 29% . 47%

[illegible]

- Molecule 2: Origin recognition complex subunit 2

Chain H: 21% 30% • 47%

ASP	ASN	GLN	ASN	GLY	THR	LEU	THR	ASP	TYR	ILE	GLY	LEU	GLU	LYS	PHE	GLN	ASP	PHE	TYR	GLN	ALA
Q438	F441	W443	L444	W445	Q446	T447	T448	T449	T450	Y451	S452	P453	Y454	T455	E456	E457	T458	S459	Y460	E461	L465
M863	G364	G365	F366	I369	Q372	L373	V377	F380	K381	E382	D383	L388	F389	L390	L391	L392	H393	N394	L395	D396	L466
R296	L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
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L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
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L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
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L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
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L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	L323
L297	F298	ASP	W301	M302	L303	Q304	L305	H306	L307	G308	F309	N310	I311	V312	G317	S318	K319	R320	D321	L322	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.26Å 114.96Å 316.45Å 90.00° 90.72° 90.00°	Depositor
Resolution (Å)	20.07 – 6.00 20.07 – 6.00	Depositor EDS
% Data completeness (in resolution range)	97.8 (20.07-6.00) 94.2 (20.07-6.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 5.93Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.318 , 0.368 0.336 , 0.372	Depositor DCC
R_{free} test set	753 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	287.3	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 999.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.155 for h,-k,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	24144	wwPDB-VP
Average B, all atoms (Å ²)	303.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.14 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9421e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.42	0/4616	0.74	4/6244 (0.1%)
1	B	0.41	0/4616	0.73	3/6244 (0.0%)
1	C	0.92	8/4616 (0.2%)	0.78	7/6244 (0.1%)
1	D	0.44	0/4616	0.75	6/6244 (0.1%)
2	E	0.37	0/1548	0.68	5/2097 (0.2%)
2	F	0.35	0/1548	0.66	3/2097 (0.1%)
2	G	0.36	0/1548	0.67	4/2097 (0.2%)
2	H	0.39	0/1548	0.68	3/2097 (0.1%)
All	All	0.54	8/24656 (0.0%)	0.73	35/33364 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	5
1	C	0	3
1	D	0	3
All	All	0	16

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	199	MET	CG-SD	40.01	2.80	1.80
1	C	244	PHE	CE1-CZ	17.76	1.92	1.38
1	C	244	PHE	CD2-CE2	17.32	1.90	1.38
1	C	244	PHE	CE2-CZ	16.82	1.89	1.38
1	C	244	PHE	CD1-CE1	16.01	1.86	1.38
1	C	244	PHE	CG-CD2	11.19	1.62	1.38
1	C	244	PHE	CG-CD1	10.04	1.59	1.38
1	C	199	MET	CB-CG	5.41	1.68	1.52

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	199	MET	CG-SD-CE	11.67	126.57	100.90
1	C	381	SER	N-CA-C	8.17	120.81	109.29
1	D	381	SER	N-CA-C	7.69	120.13	109.29
1	C	151	LEU	CA-CB-CG	6.77	140.00	116.30
1	C	199	MET	CB-CG-SD	6.60	132.51	112.70
1	D	151	LEU	CA-CB-CG	6.57	139.29	116.30
1	B	151	LEU	CA-CB-CG	6.41	138.75	116.30
1	A	151	LEU	CA-CB-CG	6.40	138.70	116.30
1	D	476	PHE	CA-CB-CG	-6.13	107.67	113.80
1	A	420	HIS	CA-C-N	-6.05	110.92	120.60
1	A	420	HIS	C-N-CA	-6.05	110.92	120.60
1	D	420	HIS	CA-C-N	-5.90	111.16	120.60
1	D	420	HIS	C-N-CA	-5.90	111.16	120.60
2	F	453	PRO	CA-C-O	-5.76	114.74	121.95
2	G	320	ARG	CG-CD-NE	-5.67	99.52	112.00
1	B	476	PHE	CA-CB-CG	-5.64	108.16	113.80
1	B	151	LEU	N-CA-C	-5.58	102.21	111.37
2	H	453	PRO	CA-C-O	-5.58	114.94	122.08
2	G	453	PRO	CA-C-O	-5.56	115.00	121.95
2	H	397	SER	CA-C-N	5.53	131.66	121.70
2	H	397	SER	C-N-CA	5.53	131.66	121.70
2	E	453	PRO	CA-C-O	-5.52	115.02	122.08
1	C	380	ALA	N-CA-C	5.36	122.21	110.80
2	E	397	SER	CA-C-N	5.33	131.30	121.70
2	E	397	SER	C-N-CA	5.33	131.30	121.70
2	G	397	SER	CA-C-N	5.33	131.30	121.70
2	G	397	SER	C-N-CA	5.33	131.30	121.70
2	E	452	SER	CA-C-N	-5.33	114.76	120.03
2	E	452	SER	C-N-CA	-5.33	114.76	120.03
2	F	397	SER	CA-C-N	5.30	131.24	121.70
2	F	397	SER	C-N-CA	5.30	131.24	121.70
1	A	151	LEU	N-CA-C	-5.26	102.75	111.37
1	C	476	PHE	CA-CB-CG	-5.22	108.58	113.80
1	C	198	LYS	CB-CA-C	-5.21	102.93	110.96
1	D	380	ALA	N-CA-C	5.15	121.77	110.80

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	130	THR	Peptide

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Mol	Chain	Res	Type	Group
1	A	140	ASP	Peptide
1	A	240	HIS	Peptide
1	A	242	HIS	Peptide
1	A	639	GLU	Peptide
1	B	140	ASP	Peptide
1	B	189	MET	Peptide
1	B	240	HIS	Peptide
1	B	242	HIS	Peptide
1	B	639	GLU	Peptide
1	C	140	ASP	Peptide
1	C	242	HIS	Peptide
1	C	639	GLU	Peptide
1	D	140	ASP	Peptide
1	D	242	HIS	Peptide
1	D	639	GLU	Peptide

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	4524	0	4619	575	0
1	B	4524	0	4619	565	0
1	C	4524	0	4619	592	0
1	D	4524	0	4619	562	0
2	E	1512	0	1495	154	0
2	F	1512	0	1495	157	0
2	G	1512	0	1495	163	0
2	H	1512	0	1495	168	0
All	All	24144	0	24456	2826	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 58.

All (2826) 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:C:244:PHE:CE1	1:C:244:PHE:CD1	1.86	1.61
1:C:244:PHE:CD2	1:C:244:PHE:CE2	1.90	1.59
1:C:244:PHE:CE1	1:C:244:PHE:CZ	1.91	1.57
1:C:244:PHE:CD2	1:C:246:LEU:HG	1.41	1.48
1:C:202:LYS:NZ	1:C:244:PHE:CE1	1.73	1.40
1:C:244:PHE:CD2	1:C:246:LEU:CG	2.12	1.30
1:C:202:LYS:NZ	1:C:244:PHE:CD1	2.07	1.22
1:C:381:SER:O	1:C:384:GLN:N	1.77	1.16
1:C:379:GLN:HG3	1:C:380:ALA:H	1.03	1.14
1:C:244:PHE:CD2	1:C:246:LEU:CD1	2.33	1.12
1:C:381:SER:O	1:C:383:LYS:N	1.84	1.11
1:D:379:GLN:HG3	1:D:380:ALA:H	1.02	1.11
1:D:381:SER:O	1:D:384:GLN:N	1.84	1.08
1:A:379:GLN:HG3	1:A:380:ALA:H	0.94	1.07
1:D:381:SER:O	1:D:383:LYS:N	1.89	1.03
1:C:244:PHE:CE1	1:C:246:LEU:HD21	1.93	1.03
1:A:394:LEU:O	1:A:397:GLU:N	1.93	1.02
1:D:379:GLN:HG3	1:D:380:ALA:N	1.76	0.99
1:B:394:LEU:O	1:B:397:GLU:N	1.98	0.96
1:C:202:LYS:HZ1	1:C:244:PHE:HE1	1.06	0.96
1:A:379:GLN:HG3	1:A:380:ALA:N	1.77	0.96
1:D:394:LEU:O	1:D:397:GLU:N	1.99	0.96
1:C:394:LEU:O	1:C:397:GLU:N	1.99	0.95
1:A:379:GLN:CG	1:A:380:ALA:H	1.80	0.95
1:B:107:LEU:N	1:B:252:ILE:O	2.01	0.94
1:C:379:GLN:HG3	1:C:380:ALA:N	1.76	0.93
1:D:645:ASN:O	1:D:649:TRP:N	2.03	0.92
1:A:645:ASN:O	1:A:649:TRP:N	2.01	0.92
2:H:317:GLY:N	2:H:450:THR:O	2.03	0.91
2:F:317:GLY:N	2:F:450:THR:O	2.04	0.91
1:C:645:ASN:O	1:C:649:TRP:N	2.03	0.91
2:G:347:SER:O	2:G:351:VAL:N	2.02	0.91
1:B:375:TYR:OH	1:B:397:GLU:OE1	1.88	0.90
1:B:645:ASN:O	1:B:649:TRP:N	2.04	0.90
2:G:317:GLY:N	2:G:450:THR:O	2.04	0.90
1:A:687:GLU:O	1:A:691:LEU:N	2.05	0.89
1:A:375:TYR:OH	1:A:397:GLU:OE1	1.90	0.89
1:A:200:LEU:O	1:A:204:ARG:N	2.06	0.89
1:D:201:SER:O	1:D:205:THR:OG1	1.90	0.88
1:B:43:ARG:NH2	1:B:339:GLN:O	2.07	0.88
1:D:695:LYS:HD2	1:D:707:LEU:HD11	1.54	0.87
2:E:317:GLY:N	2:E:450:THR:O	2.07	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:LEU:N	1:A:252:ILE:O	2.09	0.86
1:B:201:SER:O	1:B:205:THR:OG1	1.92	0.86
1:C:563:LEU:HA	1:C:567:TYR:CD2	2.11	0.86
1:D:77:LEU:O	1:D:81:HIS:ND1	2.08	0.86
1:B:200:LEU:O	1:B:204:ARG:N	2.09	0.86
2:E:347:SER:O	2:E:351:VAL:N	2.08	0.85
1:C:200:LEU:O	1:C:204:ARG:N	2.10	0.85
1:C:372:PHE:O	1:C:376:VAL:N	2.10	0.84
2:F:319:LYS:O	2:F:323:LEU:N	2.11	0.84
1:A:77:LEU:O	1:A:81:HIS:ND1	2.09	0.84
1:A:201:SER:O	1:A:205:THR:OG1	1.95	0.84
2:E:319:LYS:O	2:E:323:LEU:N	2.10	0.83
1:A:112:THR:OG1	1:A:322:GLN:OE1	1.96	0.83
2:H:347:SER:O	2:H:351:VAL:N	2.10	0.83
1:B:77:LEU:O	1:B:81:HIS:ND1	2.11	0.82
2:F:347:SER:O	2:F:351:VAL:N	2.11	0.82
1:C:562:CYS:HB3	1:C:567:TYR:CE2	2.14	0.82
1:C:563:LEU:HA	1:C:567:TYR:HD2	1.42	0.82
2:H:366:PHE:O	2:H:372:GLN:NE2	2.12	0.82
1:D:200:LEU:O	1:D:204:ARG:N	2.12	0.82
1:D:141:CYS:HB3	1:D:147:PHE:CZ	2.15	0.82
1:C:66:ASN:O	1:C:69:LEU:N	2.12	0.81
2:G:319:LYS:O	2:G:323:LEU:N	2.12	0.81
1:C:587:ALA:O	1:C:591:HIS:ND1	2.13	0.81
2:G:320:ARG:NH1	2:G:457:GLU:OE1	2.13	0.81
2:H:319:LYS:O	2:H:323:LEU:N	2.14	0.81
1:A:691:LEU:O	2:G:427:LEU:N	2.12	0.81
1:A:384:GLN:HG2	1:A:388:LEU:HD11	1.63	0.81
1:C:77:LEU:O	1:C:81:HIS:ND1	2.14	0.81
1:A:141:CYS:HB3	1:A:147:PHE:CZ	2.17	0.80
2:F:366:PHE:O	2:F:372:GLN:NE2	2.14	0.80
2:E:318:SER:O	2:E:452:SER:OG	2.00	0.80
2:H:320:ARG:NH1	2:H:457:GLU:OE1	2.15	0.80
1:A:43:ARG:NH2	1:A:339:GLN:O	2.15	0.80
2:G:391:LEU:HD22	2:G:421:ILE:HB	1.64	0.80
1:D:683:ARG:NH1	2:F:458:THR:HA	1.97	0.79
1:C:43:ARG:NH2	1:C:339:GLN:O	2.14	0.79
1:C:201:SER:O	1:C:205:THR:OG1	1.99	0.79
1:A:382:GLU:O	1:A:383:LYS:C	2.25	0.79
1:A:66:ASN:O	1:A:69:LEU:N	2.15	0.79
1:C:202:LYS:CE	1:C:244:PHE:CE1	2.66	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:151:LEU:HD12	1:D:198:LYS:HZ2	1.47	0.78
1:D:107:LEU:N	1:D:252:ILE:O	2.16	0.78
1:D:385:VAL:O	1:D:389:THR:N	2.16	0.78
2:E:391:LEU:HD22	2:E:421:ILE:HB	1.66	0.78
1:A:203:LYS:O	1:A:207:SER:N	2.16	0.78
1:C:375:TYR:CE2	1:C:401:LEU:HD21	2.18	0.78
1:A:591:HIS:HA	2:G:445:TRP:O	1.84	0.77
1:B:151:LEU:HD12	1:B:198:LYS:HZ2	1.48	0.77
1:A:202:LYS:HD2	1:A:244:PHE:CE1	2.19	0.77
2:G:366:PHE:O	2:G:372:GLN:NE2	2.16	0.77
1:B:199:MET:HA	1:B:244:PHE:CZ	2.19	0.77
2:H:328:THR:O	2:H:332:GLN:NE2	2.17	0.77
1:A:385:VAL:O	1:A:389:THR:N	2.18	0.77
2:E:320:ARG:NH1	2:E:457:GLU:OE1	2.18	0.77
1:A:202:LYS:HD2	1:A:244:PHE:HE1	1.49	0.76
1:C:141:CYS:HB3	1:C:147:PHE:CZ	2.20	0.76
1:A:151:LEU:HD12	1:A:198:LYS:HZ2	1.49	0.76
1:C:433:ARG:N	1:C:437:GLU:OE1	2.17	0.76
1:B:302:ILE:CG2	1:B:306:VAL:HG22	2.16	0.76
1:B:687:GLU:O	1:B:691:LEU:N	2.18	0.76
1:C:415:VAL:HG12	1:C:567:TYR:CE1	2.20	0.76
1:C:102:THR:OG1	1:C:273:ILE:HG12	1.85	0.75
1:C:381:SER:O	1:C:383:LYS:CA	2.34	0.75
1:C:381:SER:C	1:C:383:LYS:N	2.40	0.75
1:B:379:GLN:HE22	1:B:387:LEU:CD1	2.00	0.75
1:C:107:LEU:N	1:C:252:ILE:O	2.18	0.75
1:A:302:ILE:CG2	1:A:306:VAL:HG22	2.17	0.75
1:B:141:CYS:HB3	1:B:147:PHE:CE2	2.22	0.75
2:H:391:LEU:HD22	2:H:421:ILE:HB	1.68	0.75
1:B:382:GLU:O	1:B:384:GLN:N	2.17	0.75
1:C:563:LEU:CA	1:C:567:TYR:HD2	1.99	0.75
1:D:43:ARG:NH2	1:D:339:GLN:O	2.20	0.75
2:E:366:PHE:O	2:E:372:GLN:NE2	2.18	0.75
1:A:100:ILE:HG13	1:A:241:LEU:HD11	1.69	0.75
1:B:112:THR:OG1	1:B:322:GLN:OE1	2.03	0.74
1:D:687:GLU:O	1:D:691:LEU:N	2.19	0.74
1:B:347:ASN:OD1	1:D:350:GLU:N	2.20	0.74
1:B:202:LYS:HD2	1:B:244:PHE:CE1	2.22	0.74
1:D:66:ASN:O	1:D:69:LEU:N	2.19	0.74
2:F:391:LEU:HD22	2:F:421:ILE:HB	1.67	0.74
1:A:382:GLU:O	1:A:385:VAL:N	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:587:ALA:O	1:B:591:HIS:ND1	2.21	0.73
1:D:556:VAL:HA	1:D:559:PHE:HB2	1.70	0.73
1:A:199:MET:HA	1:A:244:PHE:CZ	2.23	0.73
1:B:132:TYR:O	1:B:215:VAL:HG22	1.87	0.73
1:B:133:VAL:N	1:B:158:CYS:SG	2.62	0.73
1:B:385:VAL:O	1:B:389:THR:N	2.21	0.73
1:B:452:GLU:OE1	1:B:452:GLU:N	2.21	0.73
1:C:381:SER:O	1:C:383:LYS:C	2.32	0.73
1:B:66:ASN:O	1:B:69:LEU:N	2.20	0.73
1:D:326:LYS:O	1:D:330:LEU:HG	1.87	0.73
1:D:555:ASN:O	1:D:559:PHE:N	2.21	0.73
1:B:372:PHE:O	1:B:376:VAL:N	2.21	0.73
2:G:353:ASN:O	2:G:357:GLU:N	2.22	0.73
1:A:433:ARG:N	1:A:437:GLU:OE1	2.20	0.73
2:F:353:ASN:O	2:F:357:GLU:N	2.20	0.73
1:A:237:SER:O	1:A:241:LEU:HG	1.89	0.72
1:A:452:GLU:OE1	1:A:452:GLU:N	2.22	0.72
1:C:381:SER:O	1:C:382:GLU:C	2.32	0.72
1:A:382:GLU:O	1:A:384:GLN:N	2.22	0.72
1:C:648:ASP:O	1:C:652:ALA:HB2	1.89	0.72
1:D:372:PHE:O	1:D:376:VAL:N	2.22	0.72
1:C:687:GLU:O	1:C:691:LEU:N	2.22	0.72
1:B:100:ILE:HG13	1:B:241:LEU:HD11	1.71	0.72
1:D:189:MET:O	1:D:191:VAL:N	2.23	0.72
1:D:569:LEU:HB3	1:D:571:PRO:HD2	1.71	0.72
1:A:372:PHE:O	1:A:376:VAL:N	2.23	0.71
1:D:302:ILE:CG2	1:D:306:VAL:HG22	2.19	0.71
2:G:318:SER:O	2:G:452:SER:OG	2.08	0.71
1:C:151:LEU:HD12	1:C:198:LYS:NZ	2.04	0.71
1:D:112:THR:OG1	1:D:322:GLN:OE1	2.08	0.71
2:E:353:ASN:O	2:E:357:GLU:N	2.22	0.71
1:C:420:HIS:CD2	1:C:435:ILE:HA	2.25	0.71
2:H:353:ASN:O	2:H:357:GLU:N	2.21	0.71
1:C:244:PHE:CE1	1:C:246:LEU:CD2	2.72	0.71
1:C:385:VAL:O	1:C:389:THR:N	2.22	0.71
1:B:141:CYS:HB3	1:B:147:PHE:CZ	2.26	0.71
1:D:476:PHE:O	1:D:480:LYS:HB2	1.91	0.71
2:E:453:PRO:HA	2:E:454:TYR:HB2	1.73	0.71
1:D:381:SER:C	1:D:383:LYS:N	2.48	0.71
1:D:587:ALA:O	1:D:591:HIS:ND1	2.23	0.71
1:A:556:VAL:HA	1:A:559:PHE:HB2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:ILE:HG13	1:C:241:LEU:HD11	1.72	0.71
1:D:203:LYS:O	1:D:207:SER:N	2.24	0.71
1:D:433:ARG:N	1:D:437:GLU:OE1	2.21	0.71
2:G:356:THR:HA	2:G:360:LEU:HB2	1.73	0.71
1:A:405:LEU:N	1:A:574:GLN:OE1	2.24	0.70
1:B:590:GLU:O	2:E:445:TRP:HB2	1.91	0.70
1:B:482:TYR:O	1:B:486:HIS:N	2.24	0.70
1:D:100:ILE:HG13	1:D:241:LEU:HD11	1.72	0.70
1:D:375:TYR:CE2	1:D:401:LEU:HD21	2.26	0.70
1:A:63:GLU:O	1:A:67:LYS:HG3	1.92	0.70
1:A:556:VAL:HA	1:A:559:PHE:HD2	1.55	0.70
1:C:416:LEU:O	1:C:420:HIS:ND1	2.24	0.70
2:F:453:PRO:HA	2:F:454:TYR:HB2	1.73	0.70
1:B:683:ARG:NH1	2:E:458:THR:HA	2.06	0.70
1:C:302:ILE:CG2	1:C:306:VAL:HG22	2.21	0.70
2:H:453:PRO:HA	2:H:454:TYR:HB2	1.72	0.70
1:B:556:VAL:HA	1:B:559:PHE:HD2	1.56	0.70
1:D:648:ASP:O	1:D:652:ALA:HB2	1.91	0.70
1:A:202:LYS:HE2	1:A:213:PRO:HG2	1.73	0.70
1:B:382:GLU:C	1:B:384:GLN:H	1.99	0.70
1:D:420:HIS:CD2	1:D:435:ILE:HA	2.27	0.70
1:C:476:PHE:O	1:C:480:LYS:HB2	1.92	0.70
1:D:562:CYS:O	1:D:566:GLU:N	2.24	0.70
1:A:291:LYS:O	1:A:295:THR:HG23	1.92	0.69
1:C:556:VAL:HA	1:C:559:PHE:HB2	1.72	0.69
1:D:132:TYR:O	1:D:215:VAL:HG22	1.91	0.69
1:D:291:LYS:O	1:D:295:THR:HG23	1.92	0.69
1:B:556:VAL:HA	1:B:559:PHE:HB2	1.74	0.69
1:C:590:GLU:O	2:H:445:TRP:HB2	1.92	0.69
1:A:335:HIS:NE2	1:A:579:VAL:O	2.25	0.69
1:C:237:SER:O	1:C:241:LEU:HG	1.91	0.69
1:D:416:LEU:O	1:D:420:HIS:ND1	2.24	0.69
1:A:52:GLN:O	1:A:56:SER:OG	2.06	0.69
1:D:202:LYS:HB2	1:D:244:PHE:HE1	1.56	0.69
1:A:125:LEU:O	1:A:131:PRO:HD2	1.93	0.69
1:A:555:ASN:O	1:A:559:PHE:N	2.26	0.69
2:E:298:PHE:HB3	2:E:330:MET:SD	2.32	0.69
1:B:203:LYS:O	1:B:207:SER:N	2.25	0.69
1:B:237:SER:O	1:B:241:LEU:HG	1.92	0.69
1:C:202:LYS:NZ	1:C:244:PHE:HE1	1.69	0.69
1:D:688:LEU:HG	1:D:693:PHE:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:689:GLU:HG3	1:D:694:ILE:HD11	1.74	0.69
2:E:352:LEU:HD23	2:E:372:GLN:OE1	1.93	0.69
2:F:320:ARG:NH1	2:F:457:GLU:OE1	2.25	0.69
2:F:356:THR:HA	2:F:360:LEU:HB2	1.73	0.69
1:A:689:GLU:HG3	1:A:694:ILE:HD11	1.75	0.69
1:C:199:MET:SD	1:C:199:MET:CG	2.80	0.68
1:D:237:SER:O	1:D:241:LEU:HG	1.92	0.68
2:F:318:SER:O	2:F:452:SER:OG	2.11	0.68
1:A:130:THR:OG1	1:A:131:PRO:HD3	1.92	0.68
1:C:147:PHE:HB2	1:C:233:PHE:CZ	2.28	0.68
1:C:209:GLN:N	1:C:210:TRP:HA	2.08	0.68
1:C:405:LEU:N	1:C:574:GLN:OE1	2.26	0.68
2:G:352:LEU:HD23	2:G:372:GLN:OE1	1.92	0.68
1:B:548:LYS:O	1:B:552:LEU:N	2.24	0.68
1:B:405:LEU:N	1:B:574:GLN:OE1	2.27	0.68
1:C:63:GLU:O	1:C:67:LYS:HG3	1.93	0.68
2:G:398:GLN:HB3	2:G:399:MET:HA	1.76	0.68
1:C:291:LYS:O	1:C:295:THR:HG23	1.94	0.68
1:D:151:LEU:HD12	1:D:198:LYS:NZ	2.08	0.68
1:D:457:LEU:HG	1:D:559:PHE:CZ	2.29	0.68
2:G:453:PRO:HA	2:G:454:TYR:HB2	1.75	0.68
1:D:381:SER:O	1:D:382:GLU:C	2.34	0.68
1:B:420:HIS:CD2	1:B:435:ILE:HA	2.29	0.68
1:A:132:TYR:O	1:A:215:VAL:HG22	1.93	0.67
1:B:476:PHE:O	1:B:480:LYS:HB2	1.93	0.67
1:C:562:CYS:O	1:C:566:GLU:N	2.26	0.67
1:A:45:GLU:O	1:A:49:LEU:HG	1.94	0.67
1:C:482:TYR:O	1:C:486:HIS:N	2.28	0.67
1:D:347:ASN:O	1:D:351:ALA:N	2.25	0.67
1:A:415:VAL:HG12	1:A:567:TYR:CZ	2.29	0.67
1:B:151:LEU:HD12	1:B:198:LYS:NZ	2.08	0.67
1:B:453:TYR:OH	1:B:563:LEU:HD13	1.94	0.67
1:C:335:HIS:NE2	1:C:579:VAL:O	2.26	0.67
2:H:398:GLN:HB3	2:H:399:MET:HA	1.77	0.67
1:B:433:ARG:N	1:B:437:GLU:OE1	2.22	0.67
1:B:416:LEU:O	1:B:420:HIS:ND1	2.28	0.67
1:B:648:ASP:O	1:B:652:ALA:HB2	1.93	0.67
2:E:337:VAL:HG22	2:E:359:VAL:HG21	1.76	0.67
2:H:411:GLN:O	2:H:415:LEU:N	2.25	0.67
1:C:125:LEU:O	1:C:131:PRO:CD	2.43	0.67
1:C:347:ASN:O	1:C:351:ALA:N	2.22	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:648:ASP:O	1:A:652:ALA:HB2	1.94	0.67
1:C:47:TYR:OH	1:C:329:GLN:OE1	2.08	0.67
1:C:457:LEU:HG	1:C:559:PHE:CZ	2.29	0.67
1:A:151:LEU:HD12	1:A:198:LYS:NZ	2.09	0.67
1:D:63:GLU:O	1:D:67:LYS:HG3	1.93	0.67
1:D:475:CYS:O	1:D:479:PHE:HB2	1.93	0.67
2:H:428:ASN:O	2:H:431:LEU:HB3	1.95	0.67
1:D:199:MET:HA	1:D:244:PHE:CZ	2.31	0.66
2:E:356:THR:HA	2:E:360:LEU:HB2	1.77	0.66
2:H:352:LEU:HD23	2:H:372:GLN:OE1	1.94	0.66
1:B:63:GLU:O	1:B:67:LYS:HG3	1.94	0.66
1:A:102:THR:OG1	1:A:273:ILE:HG12	1.96	0.66
1:A:151:LEU:HG	1:A:198:LYS:HD2	1.77	0.66
1:A:384:GLN:HG2	1:A:388:LEU:CD1	2.26	0.66
1:B:199:MET:HA	1:B:244:PHE:CE2	2.30	0.66
2:H:356:THR:HA	2:H:360:LEU:HB2	1.77	0.66
1:A:199:MET:HA	1:A:244:PHE:CE2	2.30	0.66
1:B:689:GLU:HG3	1:B:694:ILE:HD11	1.78	0.66
2:E:398:GLN:HB3	2:E:399:MET:HA	1.77	0.66
1:B:570:PRO:O	1:B:573:THR:OG1	2.10	0.66
1:C:429:TYR:HB3	1:C:433:ARG:HG2	1.78	0.66
1:C:569:LEU:HB3	1:C:571:PRO:HD2	1.77	0.66
1:B:688:LEU:HG	1:B:693:PHE:HB2	1.77	0.66
1:C:151:LEU:HG	1:C:198:LYS:HD2	1.76	0.66
1:C:415:VAL:HG12	1:C:567:TYR:CZ	2.30	0.66
1:C:689:GLU:HG3	1:C:694:ILE:HD11	1.77	0.66
1:A:475:CYS:O	1:A:479:PHE:HB2	1.96	0.66
1:D:415:VAL:HG12	1:D:567:TYR:CZ	2.30	0.66
1:D:147:PHE:HB2	1:D:233:PHE:CZ	2.31	0.65
1:B:151:LEU:HG	1:B:198:LYS:HD2	1.77	0.65
1:B:457:LEU:HG	1:B:559:PHE:CZ	2.31	0.65
1:C:683:ARG:HD2	2:H:458:THR:OG1	1.95	0.65
1:B:475:CYS:O	1:B:479:PHE:HB2	1.96	0.65
1:D:379:GLN:CG	1:D:380:ALA:H	1.86	0.65
1:D:381:SER:O	1:D:383:LYS:CA	2.45	0.65
2:H:318:SER:O	2:H:452:SER:OG	2.14	0.65
1:B:691:LEU:O	2:E:427:LEU:N	2.28	0.65
1:C:203:LYS:O	1:C:207:SER:N	2.30	0.65
2:F:352:LEU:HD23	2:F:372:GLN:OE1	1.96	0.65
1:B:555:ASN:O	1:B:559:PHE:N	2.30	0.65
1:C:151:LEU:HD12	1:C:198:LYS:HZ2	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:MET:HA	1:D:244:PHE:CE2	2.31	0.65
2:G:328:THR:O	2:G:332:GLN:NE2	2.25	0.65
1:A:500:GLN:O	1:A:503:SER:OG	2.13	0.65
1:A:397:GLU:HG2	1:A:400:LEU:HD12	1.78	0.65
1:B:415:VAL:HG12	1:B:567:TYR:CZ	2.30	0.65
1:B:500:GLN:O	1:B:503:SER:OG	2.12	0.65
1:D:151:LEU:HG	1:D:198:LYS:HD2	1.79	0.65
2:E:328:THR:O	2:E:332:GLN:NE2	2.22	0.65
2:E:411:GLN:O	2:E:415:LEU:N	2.28	0.65
1:C:189:MET:O	1:C:191:VAL:N	2.30	0.65
1:B:291:LYS:O	1:B:295:THR:HG23	1.96	0.65
1:D:556:VAL:HA	1:D:559:PHE:HD2	1.61	0.65
2:F:398:GLN:HB3	2:F:399:MET:HA	1.79	0.65
2:H:454:TYR:O	2:H:458:THR:OG1	2.14	0.65
1:B:97:LEU:HA	1:B:242:HIS:CD2	2.32	0.64
1:D:330:LEU:HD22	2:F:309:PHE:CE2	2.32	0.64
1:B:379:GLN:HE22	1:B:387:LEU:HD12	1.62	0.64
1:B:562:CYS:O	1:B:566:GLU:N	2.29	0.64
1:B:684:ALA:O	1:B:688:LEU:HD13	1.97	0.64
1:D:556:VAL:HA	1:D:559:PHE:CD2	2.33	0.64
1:A:476:PHE:O	1:A:480:LYS:HB2	1.97	0.64
1:C:325:ILE:O	1:C:328:LEU:N	2.29	0.64
1:D:296:THR:HG22	1:D:413:PHE:CD2	2.33	0.64
2:G:311:ILE:HG13	2:G:421:ILE:HG12	1.78	0.64
2:G:377:VAL:O	2:G:381:LYS:N	2.30	0.64
1:A:47:TYR:OH	1:A:329:GLN:OE1	2.13	0.64
1:C:555:ASN:O	1:C:559:PHE:N	2.31	0.64
2:H:304:GLN:OE1	2:H:446:TYR:OH	2.14	0.64
1:A:684:ALA:O	1:A:688:LEU:HD13	1.97	0.64
1:C:151:LEU:O	1:C:198:LYS:HE3	1.97	0.64
1:D:102:THR:OG1	1:D:273:ILE:HG12	1.98	0.64
1:A:489:SER:HA	1:A:490:THR:HB	1.80	0.64
1:D:222:MET:HG3	1:D:250:PHE:CD1	2.33	0.64
1:A:397:GLU:O	1:A:401:LEU:HG	1.98	0.64
1:A:448:TRP:CZ2	1:A:559:PHE:HB3	2.33	0.64
1:A:457:LEU:HG	1:A:559:PHE:CZ	2.32	0.64
1:A:690:LEU:O	2:G:426:HIS:HA	1.98	0.64
1:B:222:MET:HG3	1:B:250:PHE:CD1	2.33	0.64
1:A:562:CYS:O	1:A:566:GLU:N	2.30	0.63
1:A:694:ILE:HD13	1:A:704:VAL:HG13	1.81	0.63
2:H:373:LEU:HD22	2:H:412:LEU:HD21	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:ILE:O	1:B:54:MET:HG2	1.98	0.63
1:C:648:ASP:O	1:C:652:ALA:CB	2.46	0.63
1:D:379:GLN:CG	1:D:380:ALA:N	2.52	0.63
2:F:394:ASN:ND2	2:F:425:ASP:OD2	2.26	0.63
1:A:597:ARG:NH2	1:A:708:THR:OG1	2.31	0.63
1:B:216:VAL:HA	1:B:247:ILE:O	1.99	0.63
1:D:335:HIS:NE2	1:D:579:VAL:O	2.31	0.63
1:A:234:ILE:O	1:A:238:SER:CB	2.46	0.63
1:B:125:LEU:O	1:B:131:PRO:CD	2.46	0.63
1:B:202:LYS:HE2	1:B:213:PRO:HG2	1.81	0.63
1:C:112:THR:OG1	1:C:322:GLN:OE1	2.17	0.63
1:C:147:PHE:CD2	1:C:233:PHE:CE2	2.86	0.63
1:C:152:ILE:HG23	1:C:198:LYS:N	2.14	0.63
2:G:298:PHE:HB3	2:G:330:MET:SD	2.39	0.63
1:B:488:GLY:O	1:B:490:THR:OG1	2.17	0.63
1:C:556:VAL:HA	1:C:559:PHE:HD2	1.64	0.63
1:B:52:GLN:O	1:B:56:SER:OG	2.10	0.63
1:B:147:PHE:HB2	1:B:233:PHE:CZ	2.34	0.63
1:B:335:HIS:NE2	1:B:579:VAL:O	2.32	0.63
1:C:563:LEU:N	1:C:567:TYR:HD2	1.95	0.63
1:D:209:GLN:N	1:D:210:TRP:HA	2.12	0.63
1:A:353:ARG:NH2	1:C:297:GLN:O	2.31	0.62
1:D:684:ALA:O	1:D:688:LEU:HD13	1.98	0.62
1:A:147:PHE:HB2	1:A:233:PHE:CZ	2.34	0.62
1:B:234:ILE:O	1:B:238:SER:CB	2.47	0.62
1:A:418:CYS:HA	1:A:479:PHE:CZ	2.34	0.62
1:C:216:VAL:HA	1:C:247:ILE:O	1.99	0.62
1:D:97:LEU:HA	1:D:242:HIS:CD2	2.34	0.62
1:B:202:LYS:HD2	1:B:244:PHE:HE1	1.62	0.62
1:B:397:GLU:HG2	1:B:400:LEU:HD12	1.82	0.62
1:C:688:LEU:HG	1:C:693:PHE:HB2	1.80	0.62
1:D:683:ARG:HH12	2:F:461:GLU:HB2	1.63	0.62
2:H:320:ARG:HH22	2:H:457:GLU:N	1.97	0.62
1:A:556:VAL:HA	1:A:559:PHE:CD2	2.34	0.62
1:B:330:LEU:HD13	1:B:592:LEU:HD21	1.81	0.62
1:C:155:LEU:HD11	1:C:215:VAL:HG21	1.80	0.62
1:C:475:CYS:O	1:C:479:PHE:HB3	1.98	0.62
1:D:147:PHE:CD2	1:D:233:PHE:CE2	2.88	0.62
2:G:298:PHE:HB3	2:G:330:MET:HG3	1.80	0.62
1:B:46:THR:O	1:B:50:ILE:HG13	1.99	0.62
1:C:563:LEU:CA	1:C:567:TYR:CD2	2.78	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:151:LEU:O	1:D:198:LYS:HE3	1.99	0.62
2:G:373:LEU:HD22	2:G:412:LEU:HD21	1.81	0.62
1:D:50:ILE:O	1:D:54:MET:HG2	1.99	0.62
1:A:569:LEU:HB3	1:A:571:PRO:HD2	1.81	0.62
1:B:335:HIS:O	1:B:338:SER:N	2.26	0.62
1:B:209:GLN:N	1:B:210:TRP:HA	2.15	0.62
1:D:397:GLU:O	1:D:401:LEU:HG	1.99	0.62
1:A:392:ARG:HD3	1:C:484:GLU:HB3	1.82	0.62
1:A:548:LYS:O	1:A:552:LEU:N	2.29	0.62
1:B:99:GLU:N	1:B:241:LEU:HD12	2.15	0.62
1:C:452:GLU:OE1	1:C:452:GLU:N	2.28	0.62
1:C:152:ILE:HG21	1:C:197:PRO:CG	2.30	0.61
1:D:476:PHE:CE2	1:D:501:PHE:CD1	2.88	0.61
1:C:563:LEU:HG	1:C:567:TYR:CE2	2.35	0.61
1:D:199:MET:CE	1:D:203:LYS:HE3	2.30	0.61
1:D:482:TYR:O	1:D:486:HIS:N	2.33	0.61
1:C:130:THR:OG1	1:C:131:PRO:HD3	2.01	0.61
1:C:132:TYR:O	1:C:215:VAL:HG22	2.00	0.61
1:C:684:ALA:O	1:C:688:LEU:HD13	1.99	0.61
1:D:324:PHE:O	1:D:328:LEU:HG	2.01	0.61
2:H:311:ILE:HG13	2:H:421:ILE:HG12	1.81	0.61
1:A:476:PHE:CE2	1:A:501:PHE:CD1	2.87	0.61
1:C:448:TRP:HZ2	1:C:559:PHE:HB3	1.65	0.61
1:C:480:LYS:NZ	1:C:502:GLN:HG3	2.15	0.61
1:D:314:PHE:HA	1:D:318:ASP:O	2.01	0.61
1:A:475:CYS:O	1:A:479:PHE:CD2	2.53	0.61
1:B:556:VAL:HA	1:B:559:PHE:CD2	2.36	0.61
1:D:429:TYR:HB3	1:D:433:ARG:HG2	1.82	0.61
1:A:272:CYS:O	1:A:272:CYS:SG	2.58	0.61
1:C:591:HIS:HA	2:H:445:TRP:O	1.99	0.61
1:D:152:ILE:HG21	1:D:197:PRO:CB	2.31	0.61
1:D:234:ILE:O	1:D:238:SER:CB	2.48	0.61
1:D:489:SER:HA	1:D:490:THR:HB	1.82	0.61
2:H:340:ASN:HB3	2:H:342:PHE:CE2	2.36	0.61
1:A:64:GLU:O	1:A:67:LYS:N	2.33	0.61
1:A:688:LEU:HG	1:A:693:PHE:HB2	1.82	0.61
1:B:453:TYR:OH	1:B:563:LEU:CD1	2.49	0.61
1:D:199:MET:HG2	1:D:244:PHE:HE2	1.65	0.61
1:A:420:HIS:CD2	1:A:435:ILE:HA	2.35	0.61
1:C:152:ILE:HG12	1:C:198:LYS:H	1.65	0.61
1:C:296:THR:HG22	1:C:413:PHE:CD2	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:489:SER:HA	1:D:490:THR:CB	2.30	0.61
1:A:335:HIS:O	1:A:338:SER:N	2.27	0.61
1:B:155:LEU:CD1	1:B:198:LYS:HE2	2.30	0.61
1:B:353:ARG:NH2	1:D:297:GLN:O	2.34	0.61
1:B:453:TYR:OH	1:B:559:PHE:CE1	2.52	0.61
1:C:234:ILE:O	1:C:238:SER:CB	2.48	0.61
2:E:318:SER:N	2:E:452:SER:O	2.28	0.61
2:E:428:ASN:O	2:E:431:LEU:HB3	1.99	0.61
2:F:311:ILE:HG13	2:F:421:ILE:HG12	1.83	0.61
2:H:287:LEU:HD22	2:H:451:TYR:HB2	1.82	0.61
1:A:104:ALA:HA	1:A:250:PHE:HD2	1.66	0.61
1:B:648:ASP:O	1:B:652:ALA:CB	2.48	0.61
1:C:46:THR:O	1:C:50:ILE:HG13	2.01	0.61
1:D:152:ILE:HG21	1:D:197:PRO:CG	2.31	0.61
1:D:590:GLU:O	2:F:445:TRP:HB2	2.00	0.61
1:A:147:PHE:CD2	1:A:233:PHE:CE2	2.89	0.60
1:B:409:HIS:HA	1:B:412:TYR:HD2	1.66	0.60
1:B:448:TRP:CZ2	1:B:559:PHE:HB3	2.36	0.60
1:C:330:LEU:O	1:C:334:GLU:CB	2.49	0.60
1:C:397:GLU:HG2	1:C:400:LEU:HD12	1.82	0.60
1:C:489:SER:HA	1:C:490:THR:CB	2.31	0.60
2:H:318:SER:N	2:H:452:SER:O	2.29	0.60
1:B:189:MET:O	1:B:191:VAL:N	2.34	0.60
1:B:429:TYR:HB3	1:B:433:ARG:HG2	1.83	0.60
1:A:155:LEU:CD1	1:A:215:VAL:HG21	2.31	0.60
1:A:297:GLN:HA	1:C:353:ARG:CZ	2.31	0.60
1:B:147:PHE:CD2	1:B:233:PHE:CE2	2.89	0.60
1:B:420:HIS:HE2	1:B:438:LEU:HB2	1.66	0.60
1:C:324:PHE:O	1:C:328:LEU:HG	2.02	0.60
1:A:297:GLN:O	1:C:353:ARG:NH1	2.34	0.60
1:B:397:GLU:O	1:B:401:LEU:HG	2.01	0.60
1:B:418:CYS:HA	1:B:479:PHE:CZ	2.36	0.60
1:D:330:LEU:HD22	2:F:309:PHE:HE2	1.66	0.60
1:B:47:TYR:OH	1:B:329:GLN:OE1	2.16	0.60
1:B:569:LEU:HB3	1:B:571:PRO:HD2	1.84	0.60
1:D:47:TYR:OH	1:D:329:GLN:OE1	2.13	0.60
2:F:340:ASN:HB3	2:F:342:PHE:CE2	2.37	0.60
1:A:420:HIS:NE2	1:A:438:LEU:HB2	2.16	0.60
1:A:488:GLY:O	1:A:490:THR:OG1	2.16	0.60
1:B:43:ARG:NH2	1:B:342:SER:OG	2.35	0.60
1:C:226:ALA:O	1:C:230:LEU:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:695:LYS:HD2	1:D:707:LEU:CD1	2.29	0.60
1:D:453:TYR:OH	1:D:563:LEU:HD13	2.02	0.60
1:A:122:THR:HA	1:A:133:VAL:CG2	2.32	0.60
1:B:64:GLU:O	1:B:67:LYS:N	2.35	0.60
1:D:202:LYS:HD2	1:D:244:PHE:CE1	2.36	0.60
1:D:310:LEU:O	1:D:313:ILE:HG22	2.01	0.60
1:D:480:LYS:NZ	1:D:502:GLN:HG3	2.17	0.60
2:E:320:ARG:HH22	2:E:457:GLU:N	1.99	0.60
1:A:155:LEU:CD1	1:A:198:LYS:HE2	2.31	0.60
1:C:152:ILE:HG21	1:C:197:PRO:CD	2.31	0.60
1:C:229:VAL:HG13	1:C:233:PHE:HE2	1.67	0.60
1:D:125:LEU:O	1:D:131:PRO:HD2	2.01	0.60
1:D:381:SER:O	1:D:383:LYS:C	2.44	0.60
2:G:287:LEU:HD22	2:G:451:TYR:HB2	1.82	0.60
2:G:411:GLN:O	2:G:415:LEU:N	2.32	0.60
2:H:390:LEU:HD11	2:H:420:LEU:HD13	1.83	0.60
1:A:97:LEU:HA	1:A:242:HIS:CD2	2.36	0.60
1:A:155:LEU:HD11	1:A:215:VAL:HG21	1.83	0.60
1:D:693:PHE:CZ	2:F:427:LEU:HD21	2.37	0.60
1:C:50:ILE:O	1:C:54:MET:HG2	2.01	0.59
1:C:219:LEU:HB2	1:C:222:MET:HG2	1.84	0.59
2:G:337:VAL:HG22	2:G:359:VAL:HG21	1.83	0.59
1:A:189:MET:O	1:A:191:VAL:N	2.35	0.59
1:A:209:GLN:N	1:A:210:TRP:HA	2.17	0.59
1:B:683:ARG:HH12	2:E:461:GLU:HB2	1.66	0.59
1:D:99:GLU:N	1:D:241:LEU:HD12	2.17	0.59
1:D:695:LYS:HG3	1:D:696:PRO:HD2	1.84	0.59
1:B:480:LYS:O	1:B:484:GLU:CG	2.50	0.59
1:B:484:GLU:HG2	1:D:392:ARG:HD3	1.82	0.59
1:D:421:LYS:HB2	1:D:479:PHE:CE2	2.36	0.59
1:B:489:SER:HA	1:B:490:THR:HB	1.83	0.59
1:C:556:VAL:HA	1:C:559:PHE:CD2	2.37	0.59
1:D:44:PHE:HA	1:D:47:TYR:HB3	1.85	0.59
1:D:155:LEU:CD1	1:D:198:LYS:HE2	2.33	0.59
2:F:320:ARG:HH22	2:F:457:GLU:N	2.01	0.59
2:G:348:VAL:HA	2:G:351:VAL:HB	1.84	0.59
1:B:591:HIS:HA	2:E:445:TRP:O	2.01	0.59
1:B:651:GLU:O	1:B:655:THR:HG23	2.01	0.59
2:E:400:LEU:O	2:E:405:SER:OG	2.20	0.59
2:F:373:LEU:HD22	2:F:412:LEU:HD21	1.83	0.59
1:A:50:ILE:O	1:A:54:MET:HG2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:LEU:O	1:A:198:LYS:HE3	2.02	0.59
1:A:429:TYR:HB3	1:A:433:ARG:HG2	1.83	0.59
1:B:379:GLN:HE22	1:B:387:LEU:HD11	1.66	0.59
1:D:405:LEU:N	1:D:574:GLN:OE1	2.36	0.59
2:G:305:LEU:O	2:G:419:TYR:CE1	2.56	0.59
2:G:397:SER:HB2	2:G:398:GLN:C	2.27	0.59
1:B:230:LEU:HD21	1:B:263:LEU:HD23	1.84	0.59
1:B:297:GLN:O	1:D:353:ARG:NH1	2.36	0.59
1:C:446:ASN:OD1	1:C:569:LEU:HD11	2.02	0.59
1:D:152:ILE:HG21	1:D:197:PRO:CD	2.32	0.59
1:D:397:GLU:HG2	1:D:400:LEU:HD12	1.83	0.59
1:C:476:PHE:CE2	1:C:501:PHE:CD1	2.90	0.59
1:C:651:GLU:O	1:C:655:THR:HG23	2.02	0.59
2:H:331:LEU:HD11	2:H:391:LEU:HD11	1.84	0.59
1:A:99:GLU:N	1:A:241:LEU:HD12	2.18	0.59
1:A:131:PRO:HB3	1:A:214:PRO:O	2.02	0.59
1:C:397:GLU:O	1:C:401:LEU:HG	2.02	0.59
1:D:468:LEU:O	1:D:472:LEU:HG	2.03	0.59
1:A:648:ASP:O	1:A:652:ALA:CB	2.51	0.59
1:C:202:LYS:CE	1:C:244:PHE:HE1	2.10	0.59
1:C:222:MET:HG3	1:C:250:PHE:CD1	2.37	0.59
1:D:130:THR:OG1	1:D:131:PRO:HD3	2.02	0.59
2:E:311:ILE:HG13	2:E:421:ILE:HG12	1.85	0.59
2:H:323:LEU:HD22	2:H:391:LEU:HD13	1.84	0.59
1:A:199:MET:CE	1:A:203:LYS:HE3	2.33	0.58
1:B:147:PHE:O	1:B:151:LEU:HB2	2.02	0.58
1:C:152:ILE:HG12	1:C:198:LYS:CB	2.32	0.58
1:C:155:LEU:HG	1:C:198:LYS:HE2	1.85	0.58
1:D:597:ARG:NH2	1:D:708:THR:OG1	2.35	0.58
1:D:645:ASN:HA	1:D:703:HIS:CE1	2.38	0.58
2:E:323:LEU:HD22	2:E:391:LEU:HD13	1.84	0.58
2:F:328:THR:O	2:F:332:GLN:NE2	2.28	0.58
2:F:412:LEU:HB3	2:F:418:ILE:HD11	1.84	0.58
1:B:476:PHE:CE2	1:B:501:PHE:CD1	2.90	0.58
1:B:489:SER:HA	1:B:490:THR:CB	2.33	0.58
1:C:694:ILE:HA	1:C:706:ARG:HA	1.86	0.58
2:E:340:ASN:HB3	2:E:342:PHE:CE2	2.39	0.58
2:G:365:THR:HB	2:G:372:GLN:CD	2.29	0.58
2:G:366:PHE:N	2:G:372:GLN:HG2	2.18	0.58
1:A:296:THR:HB	1:A:410:MET:SD	2.42	0.58
1:A:489:SER:HA	1:A:490:THR:CB	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:590:GLU:O	2:G:445:TRP:HB2	2.02	0.58
1:B:155:LEU:CD1	1:B:215:VAL:HG21	2.33	0.58
1:C:335:HIS:O	1:C:338:SER:N	2.25	0.58
2:E:394:ASN:ND2	2:E:425:ASP:OD2	2.23	0.58
1:B:98:ARG:HA	1:B:238:SER:O	2.04	0.58
1:B:694:ILE:HD13	1:B:704:VAL:HG13	1.84	0.58
1:D:155:LEU:HD11	1:D:215:VAL:HG21	1.86	0.58
2:E:373:LEU:HD22	2:E:412:LEU:HD21	1.84	0.58
1:B:475:CYS:O	1:B:479:PHE:CD2	2.56	0.58
1:C:489:SER:HA	1:C:490:THR:HB	1.83	0.58
1:D:216:VAL:HA	1:D:247:ILE:O	2.04	0.58
1:D:271:LEU:HD13	1:D:273:ILE:HD11	1.86	0.58
1:D:629:ASP:OD2	1:D:680:ARG:NH1	2.37	0.58
1:B:130:THR:OG1	1:B:131:PRO:HD3	2.03	0.58
1:B:152:ILE:HG21	1:B:197:PRO:CB	2.33	0.58
1:C:125:LEU:O	1:C:131:PRO:HD2	2.02	0.58
1:D:651:GLU:O	1:D:655:THR:HG23	2.03	0.58
1:D:683:ARG:HD2	2:F:458:THR:OG1	2.04	0.58
2:F:390:LEU:HD11	2:F:420:LEU:HD13	1.84	0.58
1:A:99:GLU:C	1:A:241:LEU:CD1	2.77	0.58
1:C:420:HIS:HE2	1:C:438:LEU:HB2	1.67	0.58
1:D:554:GLU:O	1:D:558:ASN:N	2.36	0.58
2:F:318:SER:N	2:F:452:SER:O	2.28	0.58
2:G:298:PHE:HB3	2:G:330:MET:CG	2.34	0.58
1:A:418:CYS:HA	1:A:479:PHE:CE2	2.39	0.58
1:C:152:ILE:HG12	1:C:198:LYS:HB2	1.86	0.58
1:C:314:PHE:HA	1:C:318:ASP:O	2.04	0.58
1:D:125:LEU:HD22	1:D:131:PRO:HG3	1.85	0.58
1:D:288:VAL:O	1:D:292:LEU:N	2.30	0.58
1:D:335:HIS:O	1:D:338:SER:N	2.28	0.58
1:D:420:HIS:CD2	1:D:438:LEU:HD22	2.39	0.58
1:D:648:ASP:O	1:D:652:ALA:CB	2.52	0.58
2:H:337:VAL:HG22	2:H:359:VAL:HG21	1.86	0.58
1:C:148:LEU:HG	1:C:233:PHE:HE1	1.69	0.58
1:C:488:GLY:O	1:C:490:THR:OG1	2.21	0.58
2:F:397:SER:HB2	2:F:398:GLN:C	2.29	0.58
2:H:312:VAL:HB	2:H:445:TRP:HA	1.86	0.58
1:A:155:LEU:HG	1:A:198:LYS:HE2	1.86	0.58
1:B:147:PHE:CE1	1:B:225:PHE:CZ	2.92	0.58
1:B:151:LEU:O	1:B:198:LYS:HE3	2.03	0.58
1:C:147:PHE:CE2	1:C:229:VAL:HG11	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:125:LEU:O	1:D:131:PRO:CD	2.52	0.58
2:E:287:LEU:HD22	2:E:451:TYR:HB2	1.84	0.58
2:F:352:LEU:HA	2:F:355:ILE:HG22	1.86	0.58
2:F:428:ASN:O	2:F:431:LEU:HB3	2.04	0.58
1:B:591:HIS:CD2	2:E:445:TRP:O	2.57	0.57
1:C:468:LEU:O	1:C:472:LEU:HG	2.03	0.57
1:D:267:VAL:HG12	1:D:271:LEU:HD11	1.86	0.57
1:A:302:ILE:HG23	1:A:306:VAL:HG22	1.84	0.57
1:B:152:ILE:HG21	1:B:197:PRO:CG	2.34	0.57
1:B:324:PHE:O	1:B:328:LEU:HG	2.04	0.57
1:C:379:GLN:CG	1:C:380:ALA:N	2.52	0.57
1:C:683:ARG:NH1	2:H:458:THR:HA	2.20	0.57
1:D:453:TYR:HH	1:D:559:PHE:HE1	1.44	0.57
1:A:468:LEU:O	1:A:472:LEU:HG	2.05	0.57
1:B:99:GLU:C	1:B:241:LEU:CD1	2.77	0.57
1:C:480:LYS:O	1:C:484:GLU:CG	2.52	0.57
1:C:500:GLN:O	1:C:503:SER:OG	2.17	0.57
2:E:337:VAL:HG21	2:E:355:ILE:HG13	1.85	0.57
1:A:152:ILE:HG21	1:A:197:PRO:CG	2.34	0.57
1:D:302:ILE:HG23	1:D:306:VAL:HG22	1.87	0.57
2:E:331:LEU:HD11	2:E:391:LEU:HD11	1.85	0.57
2:H:317:GLY:O	2:H:319:LYS:NZ	2.38	0.57
1:A:404:ASN:C	1:A:574:GLN:OE1	2.48	0.57
1:B:310:LEU:O	1:B:313:ILE:HG22	2.04	0.57
1:B:326:LYS:O	1:B:330:LEU:HG	2.05	0.57
1:D:296:THR:HB	1:D:410:MET:SD	2.43	0.57
1:A:152:ILE:HG21	1:A:197:PRO:CB	2.34	0.57
1:B:480:LYS:HE2	1:B:498:LEU:HB3	1.86	0.57
1:B:685:VAL:CG1	1:B:704:VAL:HG21	2.34	0.57
1:C:310:LEU:O	1:C:313:ILE:HG22	2.05	0.57
1:D:226:ALA:O	1:D:230:LEU:N	2.38	0.57
1:D:384:GLN:O	1:D:388:LEU:HG	2.04	0.57
1:D:418:CYS:HA	1:D:479:PHE:CZ	2.39	0.57
2:H:352:LEU:HA	2:H:355:ILE:HG22	1.85	0.57
1:B:297:GLN:O	1:D:353:ARG:CZ	2.53	0.57
1:A:416:LEU:O	1:A:420:HIS:ND1	2.37	0.57
1:A:479:PHE:HA	1:A:482:TYR:HD2	1.70	0.57
1:B:376:VAL:HA	1:B:379:GLN:OE1	2.04	0.57
1:B:447:ILE:HG22	1:B:453:TYR:CG	2.40	0.57
1:B:482:TYR:O	1:B:487:LEU:N	2.33	0.57
1:C:302:ILE:HG23	1:C:306:VAL:HG22	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:98:ARG:HA	1:D:238:SER:O	2.05	0.57
1:D:147:PHE:O	1:D:151:LEU:HB2	2.04	0.57
1:D:230:LEU:HD21	1:D:263:LEU:HD23	1.86	0.57
2:F:323:LEU:HD22	2:F:391:LEU:HD13	1.86	0.57
2:F:337:VAL:HG22	2:F:359:VAL:HG21	1.86	0.57
2:G:331:LEU:HD11	2:G:391:LEU:HD11	1.87	0.57
2:H:365:THR:HB	2:H:372:GLN:CD	2.30	0.57
1:A:310:LEU:O	1:A:313:ILE:HG22	2.05	0.57
1:B:493:ARG:O	1:B:497:PHE:CD2	2.58	0.57
1:D:694:ILE:HB	1:D:704:VAL:HG13	1.86	0.57
1:C:101:PRO:O	1:C:247:ILE:HA	2.05	0.57
1:A:216:VAL:HA	1:A:247:ILE:O	2.05	0.56
1:A:271:LEU:HD13	1:A:273:ILE:HD11	1.87	0.56
2:G:323:LEU:HD22	2:G:391:LEU:HD13	1.87	0.56
1:C:155:LEU:CD1	1:C:215:VAL:HG21	2.35	0.56
1:C:563:LEU:N	1:C:567:TYR:CD2	2.73	0.56
1:A:43:ARG:NH2	1:A:342:SER:OG	2.38	0.56
1:A:134:VAL:HG22	1:A:154:GLN:HB3	1.87	0.56
1:A:280:SER:O	1:A:284:HIS:ND1	2.38	0.56
1:A:560:ILE:HA	1:A:564:VAL:HB	1.88	0.56
1:B:494:ILE:HA	1:B:497:PHE:HD2	1.71	0.56
1:B:548:LYS:O	1:B:551:VAL:N	2.38	0.56
1:B:563:LEU:HA	1:B:567:TYR:HB2	1.86	0.56
1:C:52:GLN:O	1:C:56:SER:OG	2.12	0.56
1:D:234:ILE:O	1:D:238:SER:HB2	2.04	0.56
2:F:331:LEU:HD11	2:F:391:LEU:HD11	1.87	0.56
2:F:365:THR:HB	2:F:372:GLN:CD	2.30	0.56
2:F:416:HIS:O	2:F:419:TYR:CZ	2.59	0.56
2:G:335:ILE:HG22	2:G:388:LEU:HA	1.87	0.56
2:G:352:LEU:HA	2:G:355:ILE:HG22	1.86	0.56
2:G:400:LEU:O	2:G:405:SER:OG	2.23	0.56
2:G:412:LEU:HB3	2:G:418:ILE:HD11	1.87	0.56
1:A:421:LYS:HB2	1:A:479:PHE:CE2	2.40	0.56
1:A:648:ASP:HA	1:A:651:GLU:HB2	1.86	0.56
1:B:296:THR:HB	1:B:410:MET:SD	2.44	0.56
1:B:302:ILE:HG23	1:B:306:VAL:HG22	1.87	0.56
1:D:99:GLU:C	1:D:241:LEU:CD1	2.79	0.56
2:E:397:SER:HB2	2:E:398:GLN:C	2.30	0.56
2:H:366:PHE:N	2:H:372:GLN:HG2	2.20	0.56
2:H:412:LEU:HB3	2:H:418:ILE:HD11	1.88	0.56
1:A:385:VAL:O	1:A:388:LEU:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:694:ILE:HD12	1:A:695:LYS:N	2.19	0.56
1:B:404:ASN:C	1:B:574:GLN:OE1	2.49	0.56
1:C:147:PHE:O	1:C:151:LEU:HB2	2.05	0.56
1:C:271:LEU:HD13	1:C:273:ILE:HD11	1.87	0.56
1:C:480:LYS:HE2	1:C:498:LEU:HB3	1.87	0.56
1:D:64:GLU:O	1:D:67:LYS:N	2.38	0.56
1:D:147:PHE:CE1	1:D:225:PHE:CZ	2.94	0.56
1:D:476:PHE:HB3	1:D:480:LYS:HE3	1.88	0.56
1:D:488:GLY:O	1:D:490:THR:OG1	2.23	0.56
2:E:304:GLN:OE1	2:E:446:TYR:OH	2.22	0.56
2:E:412:LEU:HB3	2:E:418:ILE:HD11	1.88	0.56
2:G:428:ASN:O	2:G:431:LEU:HB3	2.05	0.56
1:A:651:GLU:O	1:A:655:THR:HG23	2.05	0.56
1:C:429:TYR:CB	1:C:433:ARG:HG2	2.35	0.56
2:F:312:VAL:CG2	2:F:443:TRP:CE3	2.89	0.56
1:A:409:HIS:HA	1:A:412:TYR:HD2	1.69	0.56
1:C:296:THR:HB	1:C:410:MET:SD	2.46	0.56
1:C:447:ILE:HG22	1:C:453:TYR:CG	2.41	0.56
1:C:648:ASP:HA	1:C:651:GLU:HB2	1.88	0.56
1:D:104:ALA:HA	1:D:250:PHE:HD2	1.71	0.56
1:D:152:ILE:HG12	1:D:198:LYS:CB	2.35	0.56
1:D:412:TYR:O	1:D:415:VAL:N	2.38	0.56
1:D:446:ASN:HA	1:D:569:LEU:HD21	1.86	0.56
2:H:312:VAL:CG2	2:H:443:TRP:CE3	2.89	0.56
1:A:147:PHE:O	1:A:151:LEU:HB2	2.06	0.56
1:A:202:LYS:CE	1:A:215:VAL:HG23	2.36	0.56
1:A:230:LEU:HD21	1:A:263:LEU:HD23	1.86	0.56
1:B:330:LEU:HD21	2:E:309:PHE:CE2	2.40	0.56
1:D:147:PHE:HE1	1:D:225:PHE:CZ	2.24	0.56
1:A:46:THR:HA	1:A:49:LEU:HD12	1.88	0.56
1:A:482:TYR:O	1:A:486:HIS:N	2.39	0.56
1:B:648:ASP:HA	1:B:651:GLU:HB2	1.88	0.56
1:C:64:GLU:O	1:C:67:LYS:N	2.38	0.56
1:C:285:LEU:O	1:C:288:VAL:HG12	2.06	0.56
1:C:569:LEU:O	1:C:573:THR:CG2	2.54	0.56
2:H:305:LEU:O	2:H:419:TYR:CE1	2.59	0.56
2:H:397:SER:HB2	2:H:398:GLN:C	2.30	0.56
1:A:234:ILE:O	1:A:238:SER:HB2	2.05	0.56
1:B:155:LEU:HD11	1:B:215:VAL:HG21	1.87	0.56
1:B:229:VAL:HG13	1:B:233:PHE:HE2	1.71	0.56
1:B:379:GLN:NE2	1:B:387:LEU:CD1	2.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:GLN:HG2	1:B:388:LEU:HD11	1.88	0.56
1:B:690:LEU:O	2:E:426:HIS:HA	2.06	0.56
1:C:458:GLN:O	1:C:462:MET:HG2	2.05	0.56
1:C:482:TYR:HA	1:C:486:HIS:ND1	2.21	0.56
1:D:148:LEU:HG	1:D:233:PHE:HE1	1.71	0.56
2:H:320:ARG:NH2	2:H:342:PHE:CZ	2.74	0.56
1:A:222:MET:HG3	1:A:250:PHE:CD1	2.41	0.55
1:A:324:PHE:O	1:A:328:LEU:HG	2.05	0.55
1:B:50:ILE:HG12	1:B:298:PHE:CD1	2.41	0.55
1:B:421:LYS:HZ3	1:B:478:VAL:HB	1.70	0.55
1:D:446:ASN:ND2	1:D:449:ASP:OD2	2.39	0.55
1:A:229:VAL:HG13	1:A:233:PHE:HE2	1.71	0.55
1:B:134:VAL:HG22	1:B:154:GLN:HB3	1.88	0.55
1:B:280:SER:O	1:B:284:HIS:ND1	2.39	0.55
1:B:379:GLN:NE2	1:B:387:LEU:HD11	2.21	0.55
1:D:645:ASN:OD1	1:D:648:ASP:N	2.37	0.55
1:A:458:GLN:O	1:A:462:MET:HG2	2.05	0.55
1:C:155:LEU:HD12	1:C:198:LYS:CD	2.37	0.55
1:C:379:GLN:CG	1:C:380:ALA:H	1.86	0.55
1:C:464:ALA:HA	1:C:468:LEU:HD12	1.88	0.55
1:D:458:GLN:O	1:D:462:MET:HG2	2.07	0.55
2:E:352:LEU:HA	2:E:355:ILE:HG22	1.88	0.55
1:A:448:TRP:HZ2	1:A:559:PHE:HB3	1.71	0.55
1:A:695:LYS:HD2	1:A:707:LEU:HD11	1.87	0.55
1:B:464:ALA:HA	1:B:468:LEU:HD12	1.89	0.55
1:B:476:PHE:HB3	1:B:480:LYS:HE3	1.87	0.55
1:C:152:ILE:HA	1:C:198:LYS:HG3	1.87	0.55
1:D:81:HIS:CE1	1:D:214:PRO:HG3	2.41	0.55
1:D:369:LEU:HD11	1:D:576:LEU:HD23	1.87	0.55
1:D:479:PHE:HA	1:D:482:TYR:HD2	1.72	0.55
1:D:43:ARG:NH2	1:D:342:SER:OG	2.39	0.55
1:D:480:LYS:HE2	1:D:498:LEU:HB3	1.88	0.55
2:E:366:PHE:O	2:E:372:GLN:CG	2.54	0.55
1:A:147:PHE:HE1	1:A:225:PHE:CZ	2.24	0.55
1:A:687:GLU:O	1:A:690:LEU:N	2.40	0.55
1:B:42:LEU:HD13	1:B:354:ARG:NH1	2.21	0.55
1:B:226:ALA:O	1:B:230:LEU:N	2.38	0.55
1:B:555:ASN:C	1:B:559:PHE:CD2	2.85	0.55
1:B:569:LEU:O	1:B:573:THR:CG2	2.55	0.55
1:B:645:ASN:HA	1:B:703:HIS:CE1	2.42	0.55
2:F:298:PHE:HB3	2:F:330:MET:SD	2.45	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:352:LEU:HD21	2:F:373:LEU:HD21	1.88	0.55
1:A:494:ILE:HA	1:A:497:PHE:HD2	1.72	0.55
1:A:504:LEU:HD11	1:A:554:GLU:CD	2.32	0.55
1:B:152:ILE:HG21	1:B:197:PRO:CD	2.37	0.55
1:B:375:TYR:CZ	1:B:401:LEU:HD21	2.42	0.55
1:B:418:CYS:HA	1:B:479:PHE:CE2	2.42	0.55
1:B:504:LEU:HD11	1:B:554:GLU:CD	2.32	0.55
1:B:560:ILE:HA	1:B:564:VAL:HB	1.88	0.55
1:C:429:TYR:CG	1:C:433:ARG:HG2	2.41	0.55
1:C:645:ASN:OD1	1:C:648:ASP:N	2.35	0.55
1:C:694:ILE:HD13	1:C:704:VAL:HG13	1.89	0.55
1:D:302:ILE:CG2	1:D:307:LEU:HG	2.37	0.55
2:G:295:GLU:O	2:G:298:PHE:HB2	2.07	0.55
2:G:390:LEU:HD11	2:G:420:LEU:HD13	1.89	0.55
2:H:298:PHE:HB3	2:H:330:MET:SD	2.47	0.55
2:H:325:ARG:O	2:H:329:THR:N	2.36	0.55
1:B:404:ASN:CB	1:B:574:GLN:OE1	2.55	0.55
1:C:401:LEU:HD22	1:C:575:PRO:CG	2.37	0.55
1:C:420:HIS:CD2	1:C:438:LEU:HD22	2.42	0.55
1:C:683:ARG:HA	1:C:683:ARG:NE	2.20	0.55
1:D:464:ALA:HA	1:D:468:LEU:HD12	1.87	0.55
1:D:475:CYS:O	1:D:479:PHE:CD2	2.60	0.55
2:E:320:ARG:CZ	2:E:456:GLU:HB2	2.36	0.55
1:A:375:TYR:CZ	1:A:401:LEU:HD21	2.42	0.55
1:B:104:ALA:HA	1:B:250:PHE:HD2	1.72	0.55
1:B:202:LYS:HB2	1:B:244:PHE:CE1	2.42	0.55
1:C:234:ILE:O	1:C:238:SER:HB2	2.06	0.55
1:A:131:PRO:CB	1:A:214:PRO:O	2.55	0.54
1:B:369:LEU:HD11	1:B:576:LEU:HD23	1.89	0.54
1:C:152:ILE:HG21	1:C:197:PRO:CB	2.37	0.54
1:C:367:ARG:CZ	1:C:388:LEU:O	2.55	0.54
2:E:312:VAL:CG2	2:E:443:TRP:CE3	2.91	0.54
2:E:365:THR:HB	2:E:372:GLN:CD	2.31	0.54
2:E:366:PHE:N	2:E:372:GLN:HG2	2.22	0.54
2:G:333:ASP:HB2	2:G:336:HIS:HE2	1.73	0.54
1:A:325:ILE:O	1:A:328:LEU:N	2.40	0.54
1:A:453:TYR:OH	1:A:563:LEU:CD1	2.55	0.54
1:B:199:MET:HE2	1:B:203:LYS:HE3	1.88	0.54
1:C:43:ARG:NH2	1:C:342:SER:H	2.05	0.54
1:C:367:ARG:HA	1:C:372:PHE:CE2	2.42	0.54
1:C:594:ALA:HB2	2:H:445:TRP:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:229:VAL:HG13	1:D:233:PHE:HE2	1.71	0.54
2:F:305:LEU:O	2:F:419:TYR:CE1	2.61	0.54
1:A:478:VAL:O	1:A:481:SER:HB3	2.07	0.54
1:B:63:GLU:O	1:B:66:ASN:HB2	2.07	0.54
1:B:285:LEU:O	1:B:288:VAL:HG12	2.07	0.54
1:B:479:PHE:HA	1:B:482:TYR:HD2	1.73	0.54
1:D:569:LEU:O	1:D:573:THR:CG2	2.56	0.54
2:H:337:VAL:HG21	2:H:355:ILE:HG13	1.88	0.54
1:A:128:ASN:HB2	1:A:130:THR:OG1	2.07	0.54
1:A:152:ILE:HG12	1:A:198:LYS:CB	2.37	0.54
1:A:352:LYS:NZ	1:A:403:GLU:OE2	2.30	0.54
1:A:369:LEU:HD11	1:A:576:LEU:HD23	1.90	0.54
1:A:476:PHE:HB3	1:A:480:LYS:HE3	1.90	0.54
1:B:45:GLU:O	1:B:49:LEU:HG	2.08	0.54
1:B:199:MET:HE1	1:B:243:GLU:OE1	2.07	0.54
1:C:480:LYS:HE2	1:C:498:LEU:CB	2.38	0.54
1:C:562:CYS:C	1:C:567:TYR:HD2	2.15	0.54
1:D:63:GLU:O	1:D:66:ASN:HB2	2.07	0.54
2:E:325:ARG:O	2:E:329:THR:N	2.39	0.54
2:G:366:PHE:O	2:G:372:GLN:CG	2.55	0.54
2:H:320:ARG:CZ	2:H:456:GLU:HB2	2.37	0.54
1:A:387:LEU:HD21	1:A:397:GLU:CD	2.32	0.54
1:B:330:LEU:O	1:B:334:GLU:CB	2.56	0.54
1:C:125:LEU:HD22	1:C:131:PRO:HG3	1.90	0.54
1:C:250:PHE:HB3	1:C:252:ILE:CD1	2.38	0.54
1:C:649:TRP:HZ3	1:C:704:VAL:HB	1.73	0.54
1:D:152:ILE:HG23	1:D:198:LYS:N	2.23	0.54
1:D:202:LYS:CD	1:D:244:PHE:CE1	2.91	0.54
2:E:298:PHE:HB3	2:E:330:MET:HG3	1.90	0.54
2:F:366:PHE:N	2:F:372:GLN:HG2	2.22	0.54
1:A:138:ALA:HB2	1:A:221:ASP:O	2.07	0.54
1:A:330:LEU:O	1:A:334:GLU:HB2	2.07	0.54
1:A:412:TYR:O	1:A:415:VAL:N	2.41	0.54
1:C:267:VAL:HG12	1:C:271:LEU:HD11	1.90	0.54
1:A:152:ILE:HG21	1:A:197:PRO:CD	2.38	0.54
1:A:267:VAL:HG12	1:A:271:LEU:HD11	1.89	0.54
1:A:330:LEU:O	1:A:334:GLU:CB	2.56	0.54
1:B:152:ILE:HG12	1:B:198:LYS:CB	2.38	0.54
1:B:420:HIS:CD2	1:B:438:LEU:HD22	2.43	0.54
1:B:421:LYS:HB2	1:B:479:PHE:CE2	2.43	0.54
1:C:479:PHE:HA	1:C:482:TYR:HD2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:645:ASN:HA	1:C:703:HIS:CE1	2.42	0.54
1:D:417:ARG:O	1:D:479:PHE:CZ	2.60	0.54
1:D:420:HIS:NE2	1:D:438:LEU:HB2	2.21	0.54
1:D:152:ILE:HG12	1:D:198:LYS:H	1.71	0.54
1:A:102:THR:HG1	1:A:273:ILE:HG12	1.72	0.54
1:A:480:LYS:HE2	1:A:498:LEU:HB3	1.90	0.54
1:A:555:ASN:C	1:A:559:PHE:CD2	2.86	0.54
1:B:202:LYS:CE	1:B:215:VAL:HG23	2.38	0.54
1:C:685:VAL:CG1	1:C:704:VAL:HG21	2.38	0.54
2:E:339:ILE:HD13	2:E:351:VAL:HG13	1.90	0.54
2:F:339:ILE:HD13	2:F:351:VAL:HG13	1.90	0.54
1:B:646:LEU:HA	1:B:649:TRP:HB3	1.90	0.54
1:D:199:MET:CE	1:D:244:PHE:CE2	2.91	0.54
2:E:352:LEU:HD21	2:E:373:LEU:HD21	1.90	0.54
2:F:287:LEU:HD22	2:F:451:TYR:HB2	1.90	0.54
1:A:46:THR:O	1:A:50:ILE:HG13	2.09	0.53
1:A:230:LEU:HD11	1:A:263:LEU:HD22	1.89	0.53
1:A:342:SER:O	1:A:345:CYS:N	2.32	0.53
1:A:501:PHE:CE1	1:A:554:GLU:CD	2.86	0.53
1:D:141:CYS:HB3	1:D:147:PHE:CE2	2.43	0.53
1:D:683:ARG:CZ	1:D:686:SER:OG	2.56	0.53
2:H:335:ILE:HG22	2:H:388:LEU:HA	1.89	0.53
1:A:420:HIS:NE2	1:A:435:ILE:HA	2.23	0.53
1:B:125:LEU:O	1:B:131:PRO:HD2	2.09	0.53
1:B:234:ILE:O	1:B:238:SER:HB3	2.08	0.53
1:C:401:LEU:HD22	1:C:575:PRO:HG3	1.89	0.53
2:E:320:ARG:NH2	2:E:342:PHE:CZ	2.75	0.53
2:F:320:ARG:NH2	2:F:342:PHE:CZ	2.76	0.53
2:G:352:LEU:HD21	2:G:373:LEU:HD21	1.89	0.53
2:H:302:MET:HA	2:H:305:LEU:HD12	1.89	0.53
1:D:409:HIS:HA	1:D:412:TYR:HD2	1.73	0.53
1:D:478:VAL:O	1:D:481:SER:HB3	2.08	0.53
2:E:305:LEU:O	2:E:419:TYR:CE1	2.60	0.53
1:B:142:PRO:HD2	1:B:146:HIS:ND1	2.24	0.53
1:B:222:MET:HG3	1:B:250:PHE:CE1	2.43	0.53
1:B:271:LEU:HD13	1:B:273:ILE:HD11	1.90	0.53
1:B:417:ARG:C	1:B:479:PHE:CE1	2.86	0.53
1:C:548:LYS:O	1:C:552:LEU:N	2.39	0.53
1:D:401:LEU:HD22	1:D:575:PRO:CG	2.38	0.53
1:A:591:HIS:CE1	2:G:446:TYR:CD1	2.96	0.53
1:B:685:VAL:HG11	1:B:704:VAL:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:155:LEU:HD12	1:C:198:LYS:HD3	1.90	0.53
1:C:478:VAL:O	1:C:481:SER:HB3	2.07	0.53
1:C:562:CYS:CB	1:C:567:TYR:HE2	2.21	0.53
1:D:604:LEU:CD1	1:D:693:PHE:CZ	2.91	0.53
1:D:694:ILE:HD12	1:D:695:LYS:N	2.24	0.53
2:H:446:TYR:CB	2:H:448:THR:HG23	2.38	0.53
1:A:226:ALA:O	1:A:230:LEU:N	2.40	0.53
1:A:382:GLU:C	1:A:384:GLN:N	2.67	0.53
1:A:493:ARG:O	1:A:497:PHE:CD2	2.62	0.53
1:A:685:VAL:HG11	1:A:704:VAL:HG21	1.90	0.53
1:B:101:PRO:HA	1:B:272:CYS:HB3	1.89	0.53
1:B:694:ILE:HD12	1:B:695:LYS:N	2.23	0.53
1:C:494:ILE:O	1:C:498:LEU:HG	2.08	0.53
1:D:330:LEU:CD1	1:D:592:LEU:HD21	2.39	0.53
1:D:695:LYS:HG3	1:D:696:PRO:CD	2.38	0.53
2:E:298:PHE:HB3	2:E:330:MET:CG	2.38	0.53
2:G:320:ARG:HH22	2:G:457:GLU:N	2.06	0.53
2:G:340:ASN:HB3	2:G:342:PHE:CE2	2.44	0.53
1:A:209:GLN:HE22	1:A:213:PRO:HG3	1.72	0.53
1:A:330:LEU:HD13	1:A:592:LEU:HD21	1.91	0.53
1:B:234:ILE:O	1:B:238:SER:HB2	2.09	0.53
1:C:404:ASN:C	1:C:574:GLN:OE1	2.51	0.53
1:D:155:LEU:HG	1:D:198:LYS:HE2	1.91	0.53
1:D:429:TYR:CB	1:D:433:ARG:HG2	2.39	0.53
1:D:685:VAL:CG1	1:D:704:VAL:HG21	2.39	0.53
2:H:311:ILE:HB	2:H:446:TYR:CE2	2.44	0.53
1:A:347:ASN:CG	1:C:350:GLU:HG3	2.34	0.53
1:B:148:LEU:O	1:B:151:LEU:HB3	2.09	0.53
1:B:155:LEU:HG	1:B:198:LYS:HE2	1.91	0.53
1:B:420:HIS:NE2	1:B:438:LEU:HB2	2.24	0.53
1:C:195:THR:O	1:C:199:MET:HE3	2.08	0.53
1:C:476:PHE:HB3	1:C:480:LYS:HE3	1.91	0.53
1:D:46:THR:O	1:D:50:ILE:HG13	2.08	0.53
1:D:152:ILE:HG12	1:D:198:LYS:HB2	1.91	0.53
1:D:244:PHE:O	1:D:246:LEU:N	2.40	0.53
1:D:452:GLU:OE1	1:D:452:GLU:N	2.31	0.53
1:D:687:GLU:O	1:D:690:LEU:N	2.42	0.53
2:H:416:HIS:O	2:H:419:TYR:CZ	2.61	0.53
1:A:417:ARG:C	1:A:479:PHE:CE1	2.87	0.53
1:A:464:ALA:HA	1:A:468:LEU:HD12	1.91	0.53
1:B:43:ARG:NH2	1:B:342:SER:H	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:385:VAL:O	1:B:388:LEU:N	2.42	0.53
1:B:687:GLU:O	1:B:690:LEU:N	2.42	0.53
1:C:335:HIS:CE1	1:C:579:VAL:HA	2.43	0.53
1:D:219:LEU:HB2	1:D:222:MET:HG2	1.91	0.53
1:D:418:CYS:SG	1:D:422:PHE:HE2	2.32	0.53
1:D:694:ILE:HD13	1:D:704:VAL:HG13	1.91	0.53
2:E:302:MET:HA	2:E:305:LEU:HD12	1.91	0.53
2:G:320:ARG:CZ	2:G:456:GLU:HB2	2.38	0.53
2:H:327:ARG:HA	2:H:331:LEU:HB2	1.91	0.53
1:A:147:PHE:CE2	1:A:229:VAL:HG11	2.43	0.53
1:A:483:CYS:HA	1:A:487:LEU:O	2.09	0.53
1:A:556:VAL:CA	1:A:559:PHE:HD2	2.21	0.53
1:B:268:SER:HA	1:B:271:LEU:HD12	1.91	0.53
1:B:412:TYR:O	1:B:415:VAL:N	2.40	0.53
1:C:330:LEU:O	1:C:334:GLU:HB2	2.09	0.53
1:C:369:LEU:HD11	1:C:576:LEU:HD23	1.90	0.53
1:D:563:LEU:HA	1:D:567:TYR:HB2	1.89	0.53
2:E:377:VAL:O	2:E:381:LYS:N	2.32	0.53
1:A:301:LYS:N	1:A:580:VAL:O	2.39	0.52
1:A:387:LEU:HD22	1:A:394:LEU:HD13	1.90	0.52
1:A:403:GLU:O	1:A:407:VAL:HG23	2.08	0.52
1:B:43:ARG:C	1:B:46:THR:HG1	2.17	0.52
1:B:49:LEU:HD23	1:D:45:GLU:OE2	2.09	0.52
1:B:152:ILE:HG23	1:B:198:LYS:N	2.24	0.52
1:B:429:TYR:CG	1:B:433:ARG:HG2	2.44	0.52
1:C:147:PHE:HE1	1:C:225:PHE:CZ	2.27	0.52
1:C:230:LEU:HD21	1:C:263:LEU:HD23	1.89	0.52
2:G:318:SER:N	2:G:452:SER:O	2.30	0.52
2:G:339:ILE:HD13	2:G:351:VAL:HG22	1.90	0.52
1:A:132:TYR:O	1:A:155:LEU:HD21	2.09	0.52
1:B:403:GLU:O	1:B:407:VAL:HG23	2.08	0.52
1:B:429:TYR:CB	1:B:433:ARG:HG2	2.39	0.52
1:B:478:VAL:O	1:B:481:SER:HB3	2.08	0.52
1:D:417:ARG:C	1:D:479:PHE:CE1	2.87	0.52
1:D:480:LYS:HE2	1:D:498:LEU:CB	2.39	0.52
2:E:348:VAL:HA	2:E:351:VAL:HB	1.90	0.52
1:B:347:ASN:OD1	1:D:350:GLU:HG3	2.09	0.52
1:C:155:LEU:CD1	1:C:198:LYS:HE2	2.39	0.52
1:C:238:SER:HA	1:C:241:LEU:HG	1.92	0.52
1:C:403:GLU:O	1:C:407:VAL:HG23	2.09	0.52
2:G:314:TYR:N	2:G:448:THR:OG1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:PRO:O	1:A:247:ILE:HA	2.10	0.52
1:A:133:VAL:N	1:A:158:CYS:SG	2.83	0.52
1:A:368:ARG:O	1:A:373:ARG:HG3	2.09	0.52
1:A:453:TYR:OH	1:A:559:PHE:CE1	2.60	0.52
1:C:144:MET:SD	1:C:233:PHE:CE2	3.02	0.52
1:C:461:ARG:HG2	1:C:552:LEU:CD2	2.39	0.52
1:D:421:LYS:HZ3	1:D:478:VAL:HB	1.74	0.52
2:E:295:GLU:O	2:E:298:PHE:HB2	2.10	0.52
2:E:373:LEU:O	2:E:377:VAL:HB	2.10	0.52
2:F:454:TYR:O	2:F:458:THR:OG1	2.23	0.52
1:A:296:THR:HG22	1:A:413:PHE:CD2	2.45	0.52
1:A:371:SER:HA	1:A:374:ARG:HB2	1.91	0.52
1:B:97:LEU:HA	1:B:242:HIS:CG	2.45	0.52
1:B:405:LEU:HD23	1:B:574:GLN:HB2	1.92	0.52
1:B:448:TRP:HZ2	1:B:559:PHE:HB3	1.74	0.52
1:C:368:ARG:O	1:C:373:ARG:HG3	2.09	0.52
1:C:412:TYR:O	1:C:415:VAL:N	2.41	0.52
1:C:417:ARG:HD3	1:C:482:TYR:CE1	2.43	0.52
1:C:493:ARG:O	1:C:497:PHE:CD2	2.62	0.52
1:D:155:LEU:CD1	1:D:215:VAL:HG21	2.40	0.52
1:D:448:TRP:CZ2	1:D:559:PHE:HB3	2.44	0.52
2:E:347:SER:N	2:E:350:SER:OG	2.38	0.52
2:E:390:LEU:HD11	2:E:420:LEU:HD13	1.92	0.52
1:A:100:ILE:O	1:A:270:LEU:O	2.28	0.52
1:A:420:HIS:CD2	1:A:438:LEU:HD22	2.43	0.52
1:B:302:ILE:CG2	1:B:307:LEU:HG	2.40	0.52
1:B:468:LEU:O	1:B:472:LEU:HG	2.09	0.52
1:D:649:TRP:HZ3	1:D:704:VAL:HB	1.75	0.52
1:A:199:MET:HE2	1:A:244:PHE:HE2	1.74	0.52
1:C:367:ARG:NE	1:C:388:LEU:O	2.43	0.52
1:D:369:LEU:HD13	1:D:370:PRO:O	2.10	0.52
2:F:302:MET:HA	2:F:305:LEU:HD12	1.92	0.52
2:F:304:GLN:OE1	2:F:446:TYR:OH	2.26	0.52
2:G:416:HIS:O	2:G:419:TYR:CZ	2.62	0.52
2:H:333:ASP:HB2	2:H:336:HIS:HE2	1.74	0.52
1:A:335:HIS:CE1	1:A:579:VAL:HA	2.45	0.52
1:B:202:LYS:HD2	1:B:244:PHE:CD1	2.45	0.52
1:B:342:SER:O	1:B:345:CYS:N	2.33	0.52
1:B:420:HIS:O	1:B:424:SER:N	2.28	0.52
1:C:144:MET:SD	1:C:232:ASP:HB2	2.49	0.52
1:C:446:ASN:HA	1:C:569:LEU:HD21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:131:PRO:CB	1:D:214:PRO:O	2.57	0.52
1:D:330:LEU:O	1:D:334:GLU:HB2	2.10	0.52
1:D:368:ARG:O	1:D:373:ARG:HG3	2.10	0.52
1:D:453:TYR:OH	1:D:559:PHE:CD1	2.60	0.52
2:F:391:LEU:CD2	2:F:421:ILE:HB	2.40	0.52
2:G:337:VAL:HG21	2:G:355:ILE:HG13	1.92	0.52
1:A:417:ARG:O	1:A:479:PHE:CZ	2.62	0.52
1:A:429:TYR:CB	1:A:433:ARG:HG2	2.40	0.52
1:A:548:LYS:O	1:A:551:VAL:N	2.43	0.52
1:B:66:ASN:HB3	1:B:70:PHE:CD2	2.44	0.52
1:B:122:THR:HA	1:B:133:VAL:CG2	2.40	0.52
1:B:367:ARG:HA	1:B:372:PHE:CE2	2.45	0.52
1:C:384:GLN:O	1:C:387:LEU:HB2	2.10	0.52
1:C:387:LEU:HD21	1:C:397:GLU:CD	2.34	0.52
1:C:420:HIS:NE2	1:C:438:LEU:HB2	2.25	0.52
1:D:147:PHE:CE2	1:D:229:VAL:HG11	2.45	0.52
1:D:288:VAL:CG2	1:D:292:LEU:HD12	2.40	0.52
2:E:347:SER:H	2:E:350:SER:HG	1.56	0.52
1:B:497:PHE:HB3	1:B:501:PHE:HE2	1.75	0.52
1:C:694:ILE:HD12	1:C:695:LYS:N	2.24	0.52
1:D:314:PHE:HD2	1:D:324:PHE:HB2	1.74	0.52
1:D:448:TRP:HZ2	1:D:559:PHE:HB3	1.74	0.52
2:H:352:LEU:HD21	2:H:373:LEU:HD21	1.91	0.52
1:A:554:GLU:O	1:A:558:ASN:N	2.38	0.51
1:A:683:ARG:NH1	2:G:458:THR:HA	2.25	0.51
1:B:101:PRO:O	1:B:247:ILE:HA	2.10	0.51
1:B:132:TYR:O	1:B:155:LEU:HD21	2.10	0.51
1:B:337:TYR:OH	2:E:307:LEU:HD11	2.10	0.51
1:B:480:LYS:HE2	1:B:498:LEU:CB	2.41	0.51
1:C:133:VAL:N	1:C:158:CYS:SG	2.82	0.51
1:C:152:ILE:HD12	1:C:194:LYS:O	2.09	0.51
1:C:591:HIS:HA	2:H:445:TRP:H	1.75	0.51
1:D:202:LYS:CD	1:D:244:PHE:HE1	2.23	0.51
1:D:418:CYS:HA	1:D:479:PHE:CE2	2.45	0.51
1:D:691:LEU:O	2:F:427:LEU:N	2.39	0.51
2:F:325:ARG:O	2:F:329:THR:N	2.41	0.51
2:F:337:VAL:HG21	2:F:355:ILE:HG13	1.92	0.51
2:F:366:PHE:O	2:F:372:GLN:CG	2.58	0.51
1:A:63:GLU:O	1:A:66:ASN:HB2	2.11	0.51
1:A:199:MET:HE2	1:A:244:PHE:CE2	2.45	0.51
1:A:685:VAL:CG1	1:A:704:VAL:HG21	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:ILE:HG12	1:B:198:LYS:HG3	1.92	0.51
1:B:330:LEU:O	1:B:334:GLU:HB2	2.10	0.51
1:C:226:ALA:HB3	1:C:229:VAL:HB	1.92	0.51
1:C:342:SER:O	1:C:345:CYS:N	2.35	0.51
1:C:409:HIS:HA	1:C:412:TYR:HD2	1.76	0.51
1:D:101:PRO:O	1:D:247:ILE:HA	2.10	0.51
1:D:152:ILE:CD1	1:D:195:THR:C	2.83	0.51
1:D:325:ILE:O	1:D:328:LEU:N	2.41	0.51
1:D:556:VAL:CA	1:D:559:PHE:HD2	2.23	0.51
2:G:420:LEU:HD12	2:G:421:ILE:N	2.25	0.51
1:A:152:ILE:HG23	1:A:198:LYS:N	2.25	0.51
1:A:288:VAL:O	1:A:292:LEU:N	2.33	0.51
1:A:480:LYS:HE2	1:A:498:LEU:CB	2.40	0.51
1:A:569:LEU:O	1:A:573:THR:CG2	2.59	0.51
1:A:570:PRO:O	1:A:573:THR:OG1	2.26	0.51
1:B:683:ARG:HG3	1:B:687:GLU:OE2	2.11	0.51
1:C:683:ARG:NE	2:H:458:THR:HG23	2.26	0.51
1:D:148:LEU:O	1:D:151:LEU:HB3	2.09	0.51
1:D:385:VAL:O	1:D:388:LEU:N	2.44	0.51
1:D:494:ILE:O	1:D:498:LEU:HG	2.10	0.51
1:D:645:ASN:OD1	1:D:648:ASP:HB2	2.10	0.51
1:A:152:ILE:HA	1:A:198:LYS:HG3	1.93	0.51
1:A:234:ILE:O	1:A:238:SER:HB3	2.10	0.51
1:A:333:LEU:HD13	2:G:307:LEU:HD13	1.92	0.51
1:B:401:LEU:HD22	1:B:575:PRO:HG3	1.92	0.51
1:C:103:ALA:O	1:C:249:ILE:HA	2.11	0.51
1:C:405:LEU:HD23	1:C:574:GLN:HB2	1.93	0.51
1:C:504:LEU:HD11	1:C:554:GLU:CD	2.36	0.51
1:D:421:LYS:NZ	1:D:479:PHE:CD1	2.72	0.51
1:D:461:ARG:HG2	1:D:552:LEU:CD2	2.40	0.51
1:D:482:TYR:O	1:D:487:LEU:N	2.36	0.51
1:A:110:ASN:HB3	1:A:281:CYS:SG	2.51	0.51
1:A:155:LEU:HD12	1:A:198:LYS:CD	2.41	0.51
1:B:645:ASN:OD1	1:B:648:ASP:HB2	2.10	0.51
1:C:244:PHE:CD2	1:C:246:LEU:HD11	2.15	0.51
1:C:453:TYR:OH	1:C:563:LEU:HD13	2.11	0.51
1:C:590:GLU:O	2:H:445:TRP:O	2.28	0.51
1:D:285:LEU:O	1:D:288:VAL:HG12	2.10	0.51
1:D:330:LEU:O	1:D:334:GLU:CB	2.58	0.51
1:D:429:TYR:CG	1:D:433:ARG:HG2	2.45	0.51
2:H:366:PHE:O	2:H:372:GLN:CG	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:267:VAL:O	1:C:271:LEU:HG	2.11	0.51
1:C:387:LEU:HA	1:C:394:LEU:HB2	1.92	0.51
1:C:694:ILE:HB	1:C:704:VAL:HG13	1.92	0.51
1:D:306:VAL:HG12	1:D:585:ALA:HB2	1.91	0.51
1:D:330:LEU:HD13	1:D:592:LEU:HD21	1.93	0.51
1:D:405:LEU:HD23	1:D:574:GLN:HB2	1.93	0.51
2:E:416:HIS:O	2:E:419:TYR:CZ	2.64	0.51
2:H:339:ILE:HD13	2:H:351:VAL:HG13	1.93	0.51
1:A:401:LEU:HD22	1:A:575:PRO:CG	2.41	0.51
1:B:267:VAL:HG12	1:B:271:LEU:HD11	1.92	0.51
1:B:553:ARG:O	1:B:557:VAL:HG23	2.11	0.51
1:C:99:GLU:N	1:C:241:LEU:HD12	2.25	0.51
1:C:134:VAL:HG22	1:C:154:GLN:HB3	1.91	0.51
1:C:497:PHE:CE1	1:C:557:VAL:HG13	2.46	0.51
1:D:555:ASN:C	1:D:559:PHE:CD2	2.89	0.51
1:A:202:LYS:CD	1:A:244:PHE:CE1	2.92	0.51
1:A:694:ILE:HA	1:A:706:ARG:HA	1.93	0.51
1:B:556:VAL:CA	1:B:559:PHE:HD2	2.22	0.51
1:C:268:SER:HA	1:C:271:LEU:HD12	1.92	0.51
1:C:371:SER:O	1:C:575:PRO:HB3	2.10	0.51
1:D:222:MET:SD	1:D:225:PHE:CE2	3.04	0.51
1:D:367:ARG:HA	1:D:372:PHE:CE2	2.46	0.51
1:D:563:LEU:HA	1:D:567:TYR:CD2	2.46	0.51
1:A:152:ILE:HG12	1:A:198:LYS:H	1.76	0.51
1:A:199:MET:CE	1:A:244:PHE:HE2	2.24	0.51
1:A:563:LEU:HA	1:A:567:TYR:HB2	1.92	0.51
1:B:417:ARG:O	1:B:479:PHE:CZ	2.63	0.51
1:B:683:ARG:HD2	2:E:458:THR:OG1	2.11	0.51
1:C:306:VAL:HG12	1:C:585:ALA:HB2	1.93	0.51
1:C:326:LYS:HB3	2:H:442:ASN:HD21	1.76	0.51
1:D:128:ASN:O	1:D:129:VAL:HB	2.11	0.51
1:D:293:LEU:HD21	1:D:328:LEU:HD13	1.92	0.51
1:D:563:LEU:HA	1:D:567:TYR:HD2	1.76	0.51
2:F:373:LEU:O	2:F:377:VAL:HB	2.11	0.51
1:A:98:ARG:HA	1:A:238:SER:O	2.10	0.51
1:A:553:ARG:O	1:A:557:VAL:HG23	2.10	0.51
1:A:689:GLU:CG	1:A:694:ILE:HD11	2.41	0.51
1:C:693:PHE:CZ	2:H:427:LEU:HD21	2.46	0.51
1:D:342:SER:O	1:D:345:CYS:N	2.31	0.51
2:H:446:TYR:HB3	2:H:448:THR:HG23	1.93	0.51
1:A:286:THR:HG22	1:A:436:ARG:HE	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:TYR:O	1:A:487:LEU:N	2.32	0.50
1:A:556:VAL:O	1:A:560:ILE:N	2.42	0.50
1:B:446:ASN:OD1	1:B:569:LEU:HD11	2.12	0.50
1:B:693:PHE:CZ	2:E:427:LEU:HD21	2.46	0.50
1:C:66:ASN:HB3	1:C:70:PHE:CD2	2.46	0.50
1:C:404:ASN:CB	1:C:574:GLN:OE1	2.59	0.50
1:D:252:ILE:HD13	1:D:259:ILE:HD11	1.92	0.50
1:D:281:CYS:HB3	1:D:319:PHE:O	2.10	0.50
1:D:691:LEU:O	2:F:426:HIS:HA	2.11	0.50
1:A:152:ILE:HG12	1:A:198:LYS:HB2	1.93	0.50
1:A:202:LYS:CD	1:A:244:PHE:HE1	2.23	0.50
1:A:367:ARG:HA	1:A:372:PHE:CE2	2.46	0.50
1:A:404:ASN:CB	1:A:574:GLN:OE1	2.59	0.50
1:A:420:HIS:O	1:A:421:LYS:C	2.50	0.50
1:B:132:TYR:O	1:B:155:LEU:CD2	2.59	0.50
1:B:152:ILE:CD1	1:B:195:THR:C	2.84	0.50
1:B:288:VAL:CG2	1:B:292:LEU:HD12	2.42	0.50
1:B:415:VAL:O	1:B:418:CYS:HB3	2.11	0.50
1:C:44:PHE:HA	1:C:47:TYR:HB3	1.93	0.50
1:D:66:ASN:HB3	1:D:70:PHE:CD2	2.45	0.50
1:D:71:ASP:O	1:D:75:GLU:CG	2.59	0.50
1:D:478:VAL:O	1:D:482:TYR:HD2	1.94	0.50
1:D:695:LYS:CG	1:D:696:PRO:HD2	2.41	0.50
2:H:455:THR:CA	2:H:458:THR:HB	2.41	0.50
1:A:155:LEU:CG	1:A:198:LYS:HE2	2.42	0.50
1:A:342:SER:OG	1:A:579:VAL:HG13	2.12	0.50
1:B:369:LEU:HD13	1:B:370:PRO:O	2.11	0.50
1:B:562:CYS:HB3	1:B:567:TYR:CE2	2.46	0.50
1:C:330:LEU:O	1:C:334:GLU:HB3	2.12	0.50
2:E:409:ILE:HG22	2:E:441:PHE:CE1	2.47	0.50
2:H:373:LEU:O	2:H:377:VAL:HB	2.11	0.50
1:A:683:ARG:CZ	2:G:458:THR:HG23	2.42	0.50
1:B:415:VAL:HG12	1:B:567:TYR:CE1	2.46	0.50
1:B:552:LEU:O	1:B:556:VAL:HG23	2.11	0.50
1:C:152:ILE:CD1	1:C:195:THR:C	2.84	0.50
1:C:372:PHE:HA	1:C:375:TYR:HB3	1.92	0.50
1:C:591:HIS:HA	2:H:445:TRP:N	2.26	0.50
1:C:687:GLU:O	1:C:690:LEU:N	2.44	0.50
1:D:230:LEU:HD11	1:D:263:LEU:HD22	1.94	0.50
1:D:555:ASN:HA	1:D:558:ASN:HB2	1.94	0.50
2:F:373:LEU:CD2	2:F:412:LEU:HD21	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:400:LEU:O	2:H:405:SER:OG	2.29	0.50
2:H:412:LEU:HB3	2:H:418:ILE:CD1	2.42	0.50
1:A:43:ARG:NH2	1:A:342:SER:H	2.10	0.50
1:A:66:ASN:HB3	1:A:70:PHE:CD2	2.46	0.50
1:A:429:TYR:CG	1:A:433:ARG:HG2	2.46	0.50
1:A:707:LEU:HD12	1:A:707:LEU:N	2.26	0.50
1:B:148:LEU:HG	1:B:233:PHE:HE1	1.77	0.50
1:B:501:PHE:CE1	1:B:554:GLU:CD	2.90	0.50
1:C:355:ILE:HA	1:C:358:LEU:HG	1.94	0.50
1:D:43:ARG:NH2	1:D:342:SER:H	2.10	0.50
1:D:366:ILE:O	1:D:372:PHE:CD2	2.64	0.50
1:D:371:SER:OG	1:D:576:LEU:N	2.42	0.50
2:F:348:VAL:HA	2:F:351:VAL:HB	1.92	0.50
2:H:331:LEU:HB3	2:H:336:HIS:CG	2.47	0.50
2:H:410:GLY:O	2:H:414:SER:CB	2.59	0.50
1:A:202:LYS:HB2	1:A:244:PHE:CE1	2.47	0.50
1:B:155:LEU:HD12	1:B:198:LYS:CD	2.42	0.50
1:B:364:GLU:HA	1:B:367:ARG:HD2	1.93	0.50
1:B:597:ARG:NH2	1:B:708:THR:OG1	2.45	0.50
1:C:100:ILE:CG1	1:C:241:LEU:HD21	2.42	0.50
1:C:102:THR:HA	1:C:247:ILE:HG23	1.94	0.50
1:D:403:GLU:O	1:D:407:VAL:HG23	2.12	0.50
2:E:311:ILE:HD11	2:E:421:ILE:HG23	1.93	0.50
2:E:420:LEU:HD12	2:E:421:ILE:N	2.26	0.50
2:E:420:LEU:HD21	2:E:443:TRP:CH2	2.47	0.50
2:F:352:LEU:CD2	2:F:369:ILE:HG23	2.42	0.50
2:G:320:ARG:NH2	2:G:457:GLU:N	2.60	0.50
2:H:348:VAL:HA	2:H:351:VAL:HB	1.93	0.50
1:A:645:ASN:OD1	1:A:648:ASP:HB2	2.11	0.50
1:B:102:THR:OG1	1:B:273:ILE:HG12	2.11	0.50
1:B:152:ILE:HG12	1:B:198:LYS:H	1.76	0.50
1:B:306:VAL:O	1:B:310:LEU:HD13	2.11	0.50
1:C:81:HIS:CE1	1:C:214:PRO:HG3	2.46	0.50
1:C:219:LEU:HB2	1:C:222:MET:CG	2.41	0.50
1:C:370:PRO:C	1:C:372:PHE:H	2.20	0.50
1:C:478:VAL:O	1:C:482:TYR:HD2	1.95	0.50
1:C:482:TYR:O	1:C:487:LEU:N	2.34	0.50
1:C:548:LYS:O	1:C:551:VAL:N	2.45	0.50
1:C:562:CYS:C	1:C:567:TYR:CD2	2.90	0.50
1:D:148:LEU:HA	1:D:151:LEU:CD2	2.42	0.50
1:D:155:LEU:HD12	1:D:198:LYS:CD	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:386:ALA:O	1:D:390:ASN:O	2.29	0.50
1:D:553:ARG:O	1:D:557:VAL:HG23	2.11	0.50
1:A:148:LEU:O	1:A:151:LEU:HB3	2.12	0.50
1:A:219:LEU:HB2	1:A:222:MET:HG2	1.93	0.50
1:A:405:LEU:HD23	1:A:574:GLN:HB2	1.94	0.50
1:C:288:VAL:CG2	1:C:292:LEU:HD12	2.42	0.50
1:D:222:MET:HG3	1:D:250:PHE:HD1	1.75	0.50
1:D:329:GLN:O	1:D:332:LEU:N	2.44	0.50
1:D:404:ASN:C	1:D:574:GLN:OE1	2.55	0.50
2:E:355:ILE:O	2:E:360:LEU:HB2	2.12	0.50
2:F:339:ILE:HD13	2:F:351:VAL:HG22	1.93	0.50
1:A:369:LEU:HD13	1:A:370:PRO:O	2.12	0.50
1:A:379:GLN:CG	1:A:380:ALA:N	2.51	0.50
1:A:418:CYS:O	1:A:422:PHE:CD2	2.65	0.50
1:A:446:ASN:HA	1:A:569:LEU:HD21	1.94	0.50
1:A:683:ARG:HD2	2:G:458:THR:OG1	2.12	0.50
1:B:306:VAL:HG12	1:B:585:ALA:HB2	1.93	0.50
1:B:404:ASN:O	1:B:407:VAL:HB	2.12	0.50
1:B:418:CYS:O	1:B:422:PHE:CD2	2.65	0.50
1:B:421:LYS:NZ	1:B:479:PHE:CD1	2.74	0.50
1:C:229:VAL:HG13	1:C:233:PHE:CE2	2.45	0.50
1:C:448:TRP:CZ2	1:C:559:PHE:HB3	2.45	0.50
1:C:604:LEU:CD1	1:C:693:PHE:CZ	2.95	0.50
1:D:493:ARG:O	1:D:497:PHE:CD2	2.64	0.50
2:E:298:PHE:CD2	2:E:330:MET:HG2	2.46	0.50
2:G:325:ARG:O	2:G:329:THR:N	2.39	0.50
2:G:369:ILE:HG12	2:G:372:GLN:OE1	2.12	0.50
2:H:320:ARG:NH2	2:H:457:GLU:N	2.60	0.50
1:A:244:PHE:O	1:A:246:LEU:N	2.41	0.49
1:A:330:LEU:CD1	1:A:592:LEU:HD21	2.42	0.49
1:A:645:ASN:OD1	1:A:648:ASP:N	2.37	0.49
1:B:297:GLN:O	1:D:353:ARG:NH2	2.44	0.49
1:B:418:CYS:SG	1:B:422:PHE:HE2	2.35	0.49
1:B:497:PHE:O	1:B:501:PHE:HD2	1.95	0.49
1:B:588:LEU:O	1:B:592:LEU:N	2.46	0.49
1:C:63:GLU:O	1:C:66:ASN:HB2	2.11	0.49
1:C:330:LEU:CD1	1:C:592:LEU:HD21	2.42	0.49
2:F:355:ILE:O	2:F:360:LEU:HB2	2.12	0.49
2:G:311:ILE:HD11	2:G:421:ILE:HG23	1.94	0.49
2:G:312:VAL:CG2	2:G:443:TRP:CE3	2.95	0.49
2:G:339:ILE:HD13	2:G:351:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:PHE:HA	1:A:375:TYR:HB3	1.94	0.49
1:A:461:ARG:HG2	1:A:552:LEU:CD2	2.42	0.49
1:A:494:ILE:O	1:A:498:LEU:HG	2.12	0.49
1:B:62:GLN:O	1:B:66:ASN:CG	2.56	0.49
1:B:128:ASN:O	1:B:129:VAL:HB	2.12	0.49
1:B:255:SER:HB2	1:B:256:PRO:HD3	1.94	0.49
1:C:562:CYS:CB	1:C:567:TYR:CE2	2.90	0.49
1:C:570:PRO:O	1:C:573:THR:OG1	2.29	0.49
2:E:317:GLY:O	2:E:319:LYS:NZ	2.44	0.49
2:G:302:MET:HA	2:G:305:LEU:HD12	1.94	0.49
1:B:125:LEU:HD22	1:B:131:PRO:HG3	1.94	0.49
1:B:148:LEU:HA	1:B:151:LEU:HD22	1.95	0.49
1:B:252:ILE:HD13	1:B:259:ILE:HD11	1.94	0.49
1:B:267:VAL:O	1:B:271:LEU:HG	2.13	0.49
1:B:314:PHE:HA	1:B:318:ASP:O	2.12	0.49
1:B:419:LEU:HB2	1:B:567:TYR:CE1	2.47	0.49
1:D:134:VAL:HG22	1:D:154:GLN:HB3	1.93	0.49
1:D:482:TYR:HA	1:D:486:HIS:ND1	2.28	0.49
1:D:560:ILE:HA	1:D:564:VAL:HB	1.93	0.49
2:F:311:ILE:HD11	2:F:421:ILE:HG23	1.93	0.49
1:A:71:ASP:O	1:A:75:GLU:CG	2.61	0.49
1:A:417:ARG:HD3	1:A:482:TYR:CE1	2.47	0.49
1:B:152:ILE:HG12	1:B:198:LYS:HB2	1.94	0.49
1:B:302:ILE:HG21	1:B:306:VAL:HG22	1.93	0.49
1:B:347:ASN:O	1:B:351:ALA:N	2.35	0.49
1:C:553:ARG:O	1:C:557:VAL:HG23	2.12	0.49
1:C:591:HIS:O	2:H:444:LEU:HA	2.12	0.49
1:D:117:THR:O	1:D:121:LEU:N	2.45	0.49
1:D:387:LEU:HD21	1:D:397:GLU:CD	2.36	0.49
2:E:333:ASP:HB2	2:E:336:HIS:HE2	1.78	0.49
2:G:410:GLY:HA2	2:G:441:PHE:CE1	2.48	0.49
1:A:457:LEU:CG	1:A:559:PHE:CZ	2.96	0.49
1:B:682:ILE:HD11	2:E:465:LEU:HD12	1.93	0.49
1:C:122:THR:HA	1:C:133:VAL:CG2	2.43	0.49
1:C:132:TYR:O	1:C:155:LEU:HD21	2.12	0.49
1:C:281:CYS:HB3	1:C:319:PHE:O	2.12	0.49
1:C:325:ILE:HG22	1:C:326:LYS:N	2.27	0.49
1:D:139:LYS:C	1:D:141:CYS:H	2.21	0.49
1:D:202:LYS:HB2	1:D:244:PHE:CE1	2.42	0.49
1:D:229:VAL:HG13	1:D:233:PHE:CE2	2.47	0.49
1:D:419:LEU:HB2	1:D:567:TYR:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:480:LYS:O	1:D:484:GLU:CG	2.61	0.49
1:D:501:PHE:CE1	1:D:554:GLU:CD	2.91	0.49
2:E:412:LEU:O	2:E:415:LEU:N	2.46	0.49
2:F:411:GLN:O	2:F:415:LEU:N	2.36	0.49
2:F:455:THR:O	2:F:459:SER:N	2.45	0.49
2:H:311:ILE:HD11	2:H:421:ILE:HG23	1.94	0.49
1:A:152:ILE:HG12	1:A:198:LYS:HG3	1.95	0.49
1:A:252:ILE:HD13	1:A:259:ILE:HD11	1.95	0.49
1:B:100:ILE:O	1:B:270:LEU:O	2.30	0.49
1:C:99:GLU:C	1:C:241:LEU:CD1	2.86	0.49
1:C:430:PRO:HB2	1:C:452:GLU:HB3	1.95	0.49
1:D:476:PHE:CZ	1:D:501:PHE:CG	3.00	0.49
2:F:397:SER:HB2	2:F:400:LEU:H	1.78	0.49
2:G:355:ILE:O	2:G:360:LEU:HB2	2.12	0.49
1:B:401:LEU:HD22	1:B:575:PRO:CG	2.42	0.49
1:C:349:PRO:O	1:C:353:ARG:HG3	2.12	0.49
1:C:372:PHE:CE2	1:C:376:VAL:HG21	2.47	0.49
1:C:418:CYS:SG	1:C:422:PHE:HE2	2.36	0.49
1:C:453:TYR:OH	1:C:559:PHE:HD1	1.94	0.49
1:C:453:TYR:OH	1:C:559:PHE:CD1	2.65	0.49
1:C:695:LYS:HD2	1:C:707:LEU:HD11	1.95	0.49
1:D:132:TYR:O	1:D:155:LEU:HD21	2.12	0.49
1:D:152:ILE:HD12	1:D:194:LYS:O	2.13	0.49
2:F:335:ILE:HG22	2:F:388:LEU:HA	1.93	0.49
1:A:222:MET:SD	1:A:225:PHE:CE2	3.06	0.49
1:A:478:VAL:O	1:A:482:TYR:HD2	1.96	0.49
1:B:683:ARG:NE	1:B:683:ARG:HA	2.28	0.49
1:C:301:LYS:N	1:C:580:VAL:O	2.41	0.49
1:C:560:ILE:HA	1:C:564:VAL:HB	1.95	0.49
1:D:138:ALA:HB2	1:D:221:ASP:O	2.13	0.49
1:D:337:TYR:OH	2:F:307:LEU:HD11	2.13	0.49
1:D:347:ASN:HB3	1:D:349:PRO:HD2	1.94	0.49
1:D:415:VAL:HG12	1:D:567:TYR:CE2	2.48	0.49
1:D:504:LEU:HD21	1:D:550:GLU:HB3	1.94	0.49
1:A:148:LEU:HD23	1:A:151:LEU:HD22	1.93	0.49
1:A:347:ASN:ND2	1:C:350:GLU:OE2	2.45	0.49
1:B:272:CYS:SG	1:B:272:CYS:O	2.71	0.49
1:B:349:PRO:HG2	1:D:347:ASN:CB	2.43	0.49
1:B:554:GLU:O	1:B:558:ASN:N	2.41	0.49
1:C:222:MET:SD	1:C:225:PHE:CE2	3.06	0.49
1:C:447:ILE:HG22	1:C:453:TYR:CD1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:497:PHE:CE1	1:D:557:VAL:CG1	2.96	0.49
1:D:500:GLN:O	1:D:503:SER:OG	2.24	0.49
1:D:683:ARG:NE	1:D:683:ARG:HA	2.27	0.49
2:F:390:LEU:HD23	2:F:418:ILE:HD12	1.93	0.49
2:G:398:GLN:HG3	2:G:401:ARG:HG3	1.95	0.49
1:A:49:LEU:HD11	1:C:49:LEU:HD21	1.95	0.49
1:A:293:LEU:HD21	1:A:328:LEU:HD13	1.95	0.49
1:A:306:VAL:HG12	1:A:585:ALA:HB2	1.94	0.49
1:A:480:LYS:NZ	1:A:502:GLN:HG3	2.28	0.49
1:B:312:ASN:O	1:B:316:TYR:HB2	2.13	0.49
1:C:50:ILE:HG12	1:C:298:PHE:CD1	2.47	0.49
1:C:152:ILE:CG2	1:C:198:LYS:N	2.75	0.49
1:C:198:LYS:O	1:C:201:SER:N	2.46	0.49
1:D:144:MET:SD	1:D:232:ASP:HB2	2.53	0.49
1:D:569:LEU:CB	1:D:571:PRO:HD2	2.43	0.49
2:H:441:PHE:HB3	2:H:443:TRP:CE2	2.48	0.49
1:A:49:LEU:HD22	1:C:45:GLU:HG2	1.94	0.48
1:A:132:TYR:O	1:A:155:LEU:CD2	2.61	0.48
1:A:303:ASN:ND2	1:A:581:TYR:HB3	2.28	0.48
1:A:683:ARG:HH12	2:G:461:GLU:HB2	1.78	0.48
1:B:453:TYR:HH	1:B:559:PHE:HE1	1.52	0.48
1:B:480:LYS:NZ	1:B:502:GLN:HG3	2.28	0.48
1:C:420:HIS:CG	1:C:435:ILE:HG12	2.47	0.48
1:D:202:LYS:HE3	1:D:215:VAL:HG21	1.95	0.48
1:D:355:ILE:HA	1:D:358:LEU:HG	1.95	0.48
1:A:386:ALA:O	1:A:390:ASN:O	2.31	0.48
1:A:387:LEU:HA	1:A:394:LEU:HB2	1.95	0.48
1:A:393:TYR:O	1:A:397:GLU:HG3	2.13	0.48
1:A:446:ASN:OD1	1:A:569:LEU:HD11	2.13	0.48
1:B:368:ARG:O	1:B:373:ARG:HG3	2.12	0.48
1:B:387:LEU:HD22	1:B:394:LEU:HD13	1.96	0.48
1:B:497:PHE:O	1:B:501:PHE:CD2	2.66	0.48
1:C:98:ARG:HA	1:C:238:SER:O	2.12	0.48
1:D:52:GLN:O	1:D:56:SER:OG	2.10	0.48
1:D:151:LEU:CD1	1:D:198:LYS:HZ2	2.23	0.48
1:D:404:ASN:CB	1:D:574:GLN:OE1	2.61	0.48
1:D:504:LEU:HD11	1:D:554:GLU:CD	2.38	0.48
2:E:320:ARG:NH2	2:E:457:GLU:N	2.61	0.48
1:A:100:ILE:HG12	1:A:241:LEU:HD21	1.95	0.48
1:A:341:LEU:HD21	1:A:365:ASN:CB	2.43	0.48
1:A:415:VAL:O	1:A:418:CYS:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:VAL:O	1:A:482:TYR:CD2	2.66	0.48
1:C:501:PHE:CE1	1:C:554:GLU:CD	2.92	0.48
1:D:420:HIS:CG	1:D:435:ILE:HG12	2.47	0.48
1:D:447:ILE:HG22	1:D:453:TYR:CG	2.48	0.48
1:D:494:ILE:HA	1:D:497:PHE:HD2	1.77	0.48
2:G:410:GLY:O	2:G:414:SER:CB	2.61	0.48
2:G:446:TYR:CB	2:G:448:THR:HG23	2.43	0.48
2:H:455:THR:HA	2:H:458:THR:HB	1.96	0.48
1:A:263:LEU:HD13	1:A:271:LEU:HD11	1.96	0.48
1:A:355:ILE:HA	1:A:358:LEU:HG	1.94	0.48
1:A:427:PRO:C	1:A:429:TYR:H	2.22	0.48
1:B:105:LEU:O	1:B:250:PHE:O	2.32	0.48
1:B:494:ILE:O	1:B:498:LEU:HG	2.14	0.48
1:B:683:ARG:NH1	2:E:461:GLU:HB2	2.28	0.48
1:C:234:ILE:O	1:C:238:SER:HB3	2.14	0.48
1:D:152:ILE:HA	1:D:198:LYS:HG3	1.95	0.48
1:D:199:MET:HG2	1:D:244:PHE:CE2	2.48	0.48
1:D:209:GLN:HE22	1:D:213:PRO:HG3	1.78	0.48
2:E:347:SER:N	2:E:350:SER:HG	2.10	0.48
2:E:410:GLY:HA2	2:E:441:PHE:CE1	2.48	0.48
2:E:446:TYR:CB	2:E:448:THR:HG23	2.42	0.48
2:H:355:ILE:O	2:H:360:LEU:HB2	2.13	0.48
1:A:229:VAL:HG13	1:A:233:PHE:CE2	2.49	0.48
1:A:552:LEU:O	1:A:556:VAL:HG23	2.13	0.48
1:B:347:ASN:CG	1:D:350:GLU:HG3	2.37	0.48
1:C:293:LEU:HD21	1:C:328:LEU:HD13	1.94	0.48
1:C:334:GLU:HG3	1:C:582:PHE:CZ	2.48	0.48
1:D:683:ARG:CZ	2:F:458:THR:HG23	2.44	0.48
2:G:332:GLN:O	2:G:336:HIS:CD2	2.66	0.48
1:A:45:GLU:CD	1:C:49:LEU:HD23	2.39	0.48
1:A:325:ILE:HG22	1:A:326:LYS:N	2.29	0.48
1:A:347:ASN:O	1:A:351:ALA:N	2.34	0.48
1:A:475:CYS:O	1:A:479:PHE:CB	2.61	0.48
1:B:387:LEU:HD21	1:B:397:GLU:CD	2.37	0.48
1:B:559:PHE:O	1:B:564:VAL:N	2.32	0.48
1:C:107:LEU:HD23	1:C:278:SER:HB2	1.96	0.48
1:C:244:PHE:CD2	1:C:246:LEU:HD12	2.39	0.48
1:C:252:ILE:HD13	1:C:259:ILE:HD11	1.96	0.48
1:D:126:GLN:HB3	1:D:162:ILE:HD11	1.94	0.48
1:D:478:VAL:O	1:D:482:TYR:CD2	2.66	0.48
1:D:552:LEU:O	1:D:556:VAL:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:397:SER:HB2	2:E:400:LEU:H	1.79	0.48
2:G:369:ILE:HA	2:G:372:GLN:CD	2.38	0.48
1:A:285:LEU:O	1:A:288:VAL:HG12	2.13	0.48
1:A:402:LEU:HA	1:A:405:LEU:HD12	1.96	0.48
1:A:480:LYS:O	1:A:484:GLU:CG	2.61	0.48
1:B:152:ILE:HA	1:B:198:LYS:HG3	1.96	0.48
1:B:226:ALA:HB3	1:B:229:VAL:HB	1.96	0.48
1:B:372:PHE:HA	1:B:375:TYR:HB3	1.95	0.48
1:B:482:TYR:HA	1:B:486:HIS:ND1	2.28	0.48
1:C:42:LEU:HD13	1:C:354:ARG:NH1	2.28	0.48
1:C:369:LEU:HD13	1:C:370:PRO:O	2.13	0.48
1:C:497:PHE:HE1	1:C:557:VAL:HG13	1.79	0.48
2:E:295:GLU:HG2	2:E:298:PHE:CE2	2.49	0.48
2:F:318:SER:HA	2:F:319:LYS:HZ1	1.79	0.48
2:F:320:ARG:NH2	2:F:457:GLU:N	2.61	0.48
2:F:400:LEU:HD22	2:F:409:ILE:CD1	2.44	0.48
2:H:291:ASN:O	2:H:295:GLU:HG3	2.13	0.48
1:A:139:LYS:C	1:A:141:CYS:H	2.21	0.48
1:A:255:SER:HB2	1:A:256:PRO:HD3	1.95	0.48
1:A:302:ILE:CG2	1:A:307:LEU:HG	2.44	0.48
1:A:418:CYS:SG	1:A:422:PHE:HE2	2.37	0.48
1:A:590:GLU:O	2:G:445:TRP:O	2.32	0.48
1:B:100:ILE:HG12	1:B:241:LEU:HD21	1.95	0.48
1:B:461:ARG:HG2	1:B:552:LEU:CD2	2.44	0.48
1:B:483:CYS:HA	1:B:487:LEU:O	2.14	0.48
1:C:79:LYS:O	1:C:83:GLY:N	2.36	0.48
1:C:117:THR:O	1:C:121:LEU:N	2.47	0.48
1:C:427:PRO:C	1:C:429:TYR:H	2.22	0.48
2:G:373:LEU:O	2:G:377:VAL:HB	2.14	0.48
2:G:382:GLU:O	2:H:383:ASP:OD1	2.32	0.48
2:H:339:ILE:HD13	2:H:351:VAL:HG22	1.95	0.48
1:A:126:GLN:HB3	1:A:162:ILE:HD11	1.95	0.48
1:B:230:LEU:HD11	1:B:263:LEU:HD22	1.94	0.48
1:B:297:GLN:HA	1:D:353:ARG:CZ	2.43	0.48
1:C:43:ARG:C	1:C:46:THR:HG1	2.21	0.48
1:C:50:ILE:HG12	1:C:298:PHE:CE1	2.49	0.48
1:C:128:ASN:O	1:C:129:VAL:HB	2.14	0.48
1:C:138:ALA:HB2	1:C:221:ASP:O	2.14	0.48
1:C:206:THR:HB	1:C:209:GLN:HG2	1.96	0.48
1:C:241:LEU:C	1:C:243:GLU:H	2.21	0.48
1:C:381:SER:C	1:C:383:LYS:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:386:ALA:O	1:C:390:ASN:O	2.31	0.48
1:C:414:LEU:HD13	1:C:494:ILE:HD11	1.94	0.48
1:D:151:LEU:CD1	1:D:198:LYS:HD2	2.43	0.48
1:D:341:LEU:HD21	1:D:365:ASN:CB	2.44	0.48
1:D:342:SER:OG	1:D:579:VAL:HG13	2.14	0.48
2:F:353:ASN:OD1	2:F:365:THR:N	2.45	0.48
2:F:369:ILE:HG21	2:F:408:ILE:CD1	2.43	0.48
2:F:420:LEU:HD21	2:F:443:TRP:CH2	2.49	0.48
2:H:297:LEU:HB3	2:H:301:TRP:NE1	2.28	0.48
2:H:339:ILE:CD1	2:H:351:VAL:HG13	2.44	0.48
2:H:352:LEU:CD2	2:H:369:ILE:HG23	2.44	0.48
1:A:151:LEU:CD1	1:A:198:LYS:HD2	2.44	0.48
1:A:226:ALA:HB3	1:A:229:VAL:HB	1.96	0.48
1:B:286:THR:HG22	1:B:436:ARG:HE	1.79	0.48
1:B:370:PRO:C	1:B:372:PHE:H	2.21	0.48
1:B:555:ASN:O	1:B:559:PHE:CD2	2.67	0.48
1:C:420:HIS:NE2	1:C:435:ILE:HA	2.28	0.48
1:C:552:LEU:O	1:C:556:VAL:HG23	2.14	0.48
1:C:683:ARG:CZ	1:C:686:SER:OG	2.62	0.48
1:D:370:PRO:C	1:D:372:PHE:H	2.22	0.48
1:D:476:PHE:O	1:D:480:LYS:CB	2.61	0.48
2:E:369:ILE:HG12	2:E:372:GLN:OE1	2.13	0.48
2:F:412:LEU:HB3	2:F:418:ILE:CD1	2.43	0.48
2:G:352:LEU:CD2	2:G:369:ILE:HG23	2.43	0.48
1:A:497:PHE:O	1:A:501:PHE:HD2	1.97	0.47
1:B:229:VAL:HG13	1:B:233:PHE:CE2	2.49	0.47
1:B:326:LYS:HA	1:B:329:GLN:HE21	1.78	0.47
1:B:349:PRO:O	1:B:353:ARG:HG3	2.14	0.47
1:B:371:SER:O	1:B:575:PRO:HB3	2.14	0.47
1:B:384:GLN:O	1:B:387:LEU:HB2	2.13	0.47
1:C:255:SER:HB2	1:C:256:PRO:HD3	1.96	0.47
1:C:420:HIS:CE1	1:C:435:ILE:HG23	2.49	0.47
1:C:632:ILE:O	1:C:636:LEU:HG	2.14	0.47
1:D:476:PHE:HB3	1:D:480:LYS:CE	2.44	0.47
2:F:317:GLY:O	2:F:319:LYS:NZ	2.47	0.47
2:H:298:PHE:HB3	2:H:330:MET:HG3	1.96	0.47
2:H:410:GLY:HA2	2:H:441:PHE:CE1	2.49	0.47
1:A:326:LYS:HA	1:A:329:GLN:HE21	1.79	0.47
1:A:588:LEU:O	1:A:592:LEU:N	2.48	0.47
1:A:690:LEU:O	2:G:426:HIS:CA	2.62	0.47
1:B:341:LEU:HD21	1:B:365:ASN:CB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:352:LYS:HG2	1:B:355:ILE:HD12	1.95	0.47
1:B:355:ILE:HA	1:B:358:LEU:HG	1.95	0.47
1:B:478:VAL:O	1:B:482:TYR:HD2	1.96	0.47
1:C:440:CYS:O	1:C:444:GLU:HG3	2.15	0.47
1:C:478:VAL:O	1:C:482:TYR:CD2	2.67	0.47
1:C:555:ASN:C	1:C:559:PHE:CD2	2.92	0.47
1:D:371:SER:O	1:D:575:PRO:HA	2.14	0.47
2:E:369:ILE:HA	2:E:372:GLN:CD	2.39	0.47
2:F:420:LEU:HD12	2:F:421:ILE:N	2.29	0.47
2:H:369:ILE:HA	2:H:372:GLN:CD	2.39	0.47
1:A:404:ASN:O	1:A:407:VAL:HB	2.14	0.47
1:A:646:LEU:HA	1:A:649:TRP:HB3	1.94	0.47
1:A:691:LEU:O	2:G:427:LEU:HG	2.14	0.47
1:A:695:LYS:HG3	1:A:696:PRO:HD2	1.95	0.47
1:B:349:PRO:HG2	1:D:347:ASN:HB3	1.95	0.47
1:B:694:ILE:HD13	1:B:704:VAL:HG22	1.96	0.47
1:C:139:LYS:C	1:C:141:CYS:H	2.23	0.47
2:G:298:PHE:CD2	2:G:330:MET:HG2	2.49	0.47
2:G:320:ARG:HH22	2:G:457:GLU:CA	2.27	0.47
2:H:320:ARG:NH1	2:H:457:GLU:CD	2.72	0.47
2:H:353:ASN:OD1	2:H:365:THR:N	2.47	0.47
1:A:288:VAL:CG2	1:A:292:LEU:HD12	2.43	0.47
1:B:340:PRO:HB2	1:B:362:GLN:HE21	1.79	0.47
1:B:350:GLU:CD	1:D:350:GLU:OE2	2.57	0.47
1:B:386:ALA:O	1:B:390:ASN:O	2.33	0.47
1:B:478:VAL:O	1:B:482:TYR:CD2	2.68	0.47
1:C:337:TYR:OH	2:H:307:LEU:HD11	2.14	0.47
1:C:422:PHE:HE1	1:C:472:LEU:HD22	1.78	0.47
2:E:320:ARG:NH1	2:E:457:GLU:CD	2.72	0.47
2:F:327:ARG:HA	2:F:331:LEU:HB2	1.95	0.47
2:F:395:LEU:HD12	2:F:400:LEU:HD13	1.95	0.47
2:G:362:HIS:O	2:G:363:MET:HG2	2.15	0.47
2:G:409:ILE:HG22	2:G:441:PHE:CE1	2.49	0.47
2:G:425:ASP:OD1	2:G:454:TYR:OH	2.32	0.47
2:H:428:ASN:O	2:H:431:LEU:CB	2.61	0.47
1:A:102:THR:HA	1:A:247:ILE:HG23	1.97	0.47
1:A:199:MET:HG2	1:A:244:PHE:CE2	2.50	0.47
1:A:370:PRO:C	1:A:372:PHE:H	2.22	0.47
1:B:81:HIS:NE2	1:B:214:PRO:HB3	2.30	0.47
1:B:329:GLN:O	1:B:332:LEU:N	2.47	0.47
1:B:387:LEU:HA	1:B:394:LEU:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:649:TRP:HZ3	1:B:704:VAL:HB	1.79	0.47
1:C:41:LYS:HD2	1:C:44:PHE:HE2	1.80	0.47
1:C:70:PHE:HA	1:C:73:LEU:HB2	1.96	0.47
1:C:152:ILE:CG1	1:C:198:LYS:H	2.26	0.47
1:D:71:ASP:O	1:D:75:GLU:HB2	2.14	0.47
1:D:267:VAL:O	1:D:271:LEU:HG	2.14	0.47
1:D:422:PHE:HE1	1:D:472:LEU:HD22	1.79	0.47
1:D:570:PRO:O	1:D:573:THR:OG1	2.28	0.47
2:F:410:GLY:HA2	2:F:441:PHE:CE1	2.49	0.47
1:A:100:ILE:O	1:A:271:LEU:HA	2.14	0.47
1:B:148:LEU:HD23	1:B:151:LEU:HD22	1.94	0.47
1:C:219:LEU:CB	1:C:222:MET:HG2	2.44	0.47
1:C:306:VAL:O	1:C:310:LEU:HB2	2.14	0.47
1:C:554:GLU:O	1:C:558:ASN:N	2.42	0.47
1:D:423:THR:CG2	1:D:438:LEU:HD21	2.45	0.47
1:D:472:LEU:O	1:D:476:PHE:CD2	2.67	0.47
1:D:497:PHE:O	1:D:501:PHE:HD2	1.97	0.47
2:H:409:ILE:HG22	2:H:441:PHE:CE1	2.49	0.47
1:A:43:ARG:HH11	1:A:336:PHE:C	2.23	0.47
1:A:49:LEU:CD2	1:C:45:GLU:HG2	2.44	0.47
1:A:252:ILE:CD1	1:A:259:ILE:HD11	2.44	0.47
1:A:363:CYS:SG	1:A:391:GLU:CD	2.98	0.47
1:A:419:LEU:HD23	1:A:438:LEU:HD23	1.97	0.47
1:A:457:LEU:HG	1:A:559:PHE:HZ	1.77	0.47
1:A:555:ASN:HA	1:A:558:ASN:HB2	1.97	0.47
1:B:144:MET:SD	1:B:232:ASP:HB2	2.55	0.47
1:B:148:LEU:HB2	1:B:195:THR:HG22	1.97	0.47
1:B:202:LYS:CD	1:B:244:PHE:CE1	2.96	0.47
1:B:310:LEU:O	1:B:313:ILE:N	2.47	0.47
1:B:386:ALA:HB1	1:B:393:TYR:CB	2.45	0.47
1:B:688:LEU:HB3	1:B:694:ILE:HG13	1.97	0.47
1:C:341:LEU:HD21	1:C:365:ASN:CB	2.45	0.47
1:C:422:PHE:CE1	1:C:472:LEU:HD22	2.50	0.47
1:C:497:PHE:O	1:C:501:PHE:HD2	1.98	0.47
1:C:497:PHE:CD1	1:C:557:VAL:CG1	2.97	0.47
1:D:51:TRP:CH2	1:D:55:LYS:HE3	2.50	0.47
1:D:152:ILE:HG12	1:D:198:LYS:HG3	1.96	0.47
1:D:404:ASN:O	1:D:407:VAL:HB	2.13	0.47
1:D:461:ARG:HG2	1:D:552:LEU:HD21	1.96	0.47
1:D:472:LEU:O	1:D:475:CYS:N	2.46	0.47
2:G:327:ARG:HA	2:G:331:LEU:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:318:SER:HA	2:H:319:LYS:HZ1	1.79	0.47
2:H:340:ASN:HB3	2:H:342:PHE:CZ	2.49	0.47
2:H:369:ILE:HG21	2:H:408:ILE:CD1	2.45	0.47
1:A:405:LEU:HD21	1:A:575:PRO:O	2.15	0.47
1:B:381:SER:O	1:B:384:GLN:HB3	2.15	0.47
1:B:421:LYS:NZ	1:B:479:PHE:CE1	2.81	0.47
1:B:563:LEU:HA	1:B:567:TYR:HD2	1.80	0.47
1:B:563:LEU:HA	1:B:567:TYR:CD2	2.49	0.47
1:C:250:PHE:HB3	1:C:252:ILE:HD11	1.97	0.47
1:C:355:ILE:O	1:C:395:LYS:HE3	2.15	0.47
1:C:366:ILE:O	1:C:372:PHE:CD2	2.68	0.47
1:C:404:ASN:O	1:C:407:VAL:HB	2.14	0.47
1:D:100:ILE:HG12	1:D:241:LEU:HD21	1.97	0.47
1:D:420:HIS:CE1	1:D:435:ILE:HG23	2.49	0.47
2:G:412:LEU:O	2:G:415:LEU:N	2.47	0.47
1:A:148:LEU:HA	1:A:151:LEU:CD2	2.45	0.47
1:A:645:ASN:HA	1:A:703:HIS:CE1	2.49	0.47
1:B:306:VAL:O	1:B:310:LEU:HB2	2.15	0.47
1:B:409:HIS:HA	1:B:412:TYR:CD2	2.50	0.47
1:C:148:LEU:HA	1:C:151:LEU:CD2	2.45	0.47
1:C:326:LYS:HA	1:C:329:GLN:HE21	1.80	0.47
1:D:226:ALA:HB3	1:D:229:VAL:HB	1.96	0.47
1:D:352:LYS:NZ	1:D:403:GLU:OE2	2.26	0.47
1:D:646:LEU:HA	1:D:649:TRP:HB3	1.97	0.47
2:H:342:PHE:CE1	2:H:343:PHE:CE1	3.02	0.47
1:A:44:PHE:HA	1:A:47:TYR:HB3	1.96	0.47
1:A:422:PHE:CE1	1:A:472:LEU:HD22	2.50	0.47
1:A:555:ASN:O	1:A:559:PHE:CD2	2.67	0.47
1:B:257:ILE:HG22	1:B:261:ARG:NE	2.30	0.47
1:B:282:LYS:O	1:B:286:THR:HG23	2.15	0.47
1:B:555:ASN:O	1:B:558:ASN:N	2.48	0.47
1:C:474:LYS:O	1:C:478:VAL:HG23	2.15	0.47
1:C:555:ASN:HA	1:C:558:ASN:HB2	1.97	0.47
1:D:202:LYS:CE	1:D:215:VAL:HG23	2.45	0.47
1:D:417:ARG:HD3	1:D:482:TYR:CE1	2.49	0.47
1:D:646:LEU:HD12	1:D:702:ASP:HB3	1.97	0.47
2:F:327:ARG:HE	2:F:391:LEU:HD12	1.79	0.47
2:F:377:VAL:O	2:F:381:LYS:N	2.41	0.47
2:F:441:PHE:HB3	2:F:443:TRP:CE2	2.50	0.47
2:G:331:LEU:HD11	2:G:391:LEU:CD1	2.45	0.47
2:H:362:HIS:O	2:H:363:MET:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ILE:HG21	1:A:267:VAL:HG13	1.96	0.46
1:A:267:VAL:O	1:A:271:LEU:HG	2.15	0.46
1:A:401:LEU:HD22	1:A:575:PRO:HG3	1.97	0.46
1:A:695:LYS:HD2	1:A:707:LEU:CD1	2.45	0.46
1:B:148:LEU:HA	1:B:151:LEU:CD2	2.44	0.46
1:B:254:THR:CB	1:B:258:ILE:HD12	2.44	0.46
1:C:54:MET:HE1	1:C:292:LEU:HB3	1.96	0.46
1:C:67:LYS:O	1:C:71:ASP:HB2	2.16	0.46
1:C:148:LEU:HD23	1:C:151:LEU:HD22	1.97	0.46
1:D:421:LYS:NZ	1:D:479:PHE:CE1	2.79	0.46
1:D:648:ASP:HA	1:D:651:GLU:HB2	1.97	0.46
2:E:332:GLN:O	2:E:336:HIS:CD2	2.68	0.46
2:F:332:GLN:O	2:F:336:HIS:CD2	2.68	0.46
2:H:373:LEU:CD2	2:H:412:LEU:HD21	2.43	0.46
2:H:443:TRP:HB2	2:H:445:TRP:NE1	2.30	0.46
1:A:297:GLN:O	1:C:353:ARG:CZ	2.63	0.46
1:A:306:VAL:O	1:A:310:LEU:HD13	2.15	0.46
1:B:694:ILE:HB	1:B:704:VAL:HG13	1.97	0.46
1:C:81:HIS:NE2	1:C:214:PRO:HB3	2.30	0.46
1:C:148:LEU:O	1:C:151:LEU:HB3	2.14	0.46
1:C:244:PHE:CG	1:C:246:LEU:HG	2.37	0.46
1:C:324:PHE:CE2	1:C:328:LEU:HD11	2.49	0.46
1:C:364:GLU:HA	1:C:367:ARG:HD2	1.97	0.46
1:C:476:PHE:O	1:C:480:LYS:CB	2.63	0.46
1:C:645:ASN:OD1	1:C:648:ASP:HB2	2.15	0.46
1:D:54:MET:HE1	1:D:292:LEU:HB3	1.96	0.46
1:D:72:ASN:HA	1:D:75:GLU:HB2	1.97	0.46
1:D:77:LEU:CD2	1:D:247:ILE:HG21	2.46	0.46
1:D:155:LEU:CG	1:D:198:LYS:HE2	2.45	0.46
1:D:222:MET:HG3	1:D:250:PHE:CE1	2.50	0.46
2:F:333:ASP:HB2	2:F:336:HIS:HE2	1.79	0.46
2:F:339:ILE:CD1	2:F:351:VAL:HG13	2.45	0.46
2:F:340:ASN:O	2:F:343:PHE:HB2	2.15	0.46
2:G:325:ARG:HA	2:G:328:THR:OG1	2.15	0.46
2:H:331:LEU:HD11	2:H:391:LEU:CD1	2.44	0.46
1:A:50:ILE:HG12	1:A:298:PHE:CE1	2.50	0.46
1:A:101:PRO:HB3	1:A:272:CYS:SG	2.55	0.46
1:A:125:LEU:HB3	1:A:133:VAL:HG11	1.97	0.46
1:A:222:MET:HG3	1:A:250:PHE:CE1	2.50	0.46
1:B:131:PRO:CB	1:B:214:PRO:O	2.64	0.46
1:B:151:LEU:CD1	1:B:198:LYS:HD2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:ILE:HG22	1:B:326:LYS:N	2.29	0.46
1:B:497:PHE:HE1	1:B:557:VAL:HG13	1.80	0.46
1:C:152:ILE:HG21	1:C:197:PRO:HD2	1.98	0.46
1:C:155:LEU:CG	1:C:198:LYS:HE2	2.44	0.46
1:C:342:SER:OG	1:C:579:VAL:HG13	2.15	0.46
1:D:74:ILE:HD13	1:D:128:ASN:OD1	2.14	0.46
1:D:335:HIS:CE1	1:D:579:VAL:HA	2.50	0.46
2:E:311:ILE:HB	2:E:446:TYR:CE2	2.51	0.46
2:E:327:ARG:HA	2:E:331:LEU:HB2	1.97	0.46
2:E:331:LEU:HD11	2:E:391:LEU:CD1	2.45	0.46
2:E:453:PRO:CA	2:E:454:TYR:HB2	2.45	0.46
2:F:332:GLN:O	2:F:333:ASP:C	2.59	0.46
2:G:441:PHE:HB3	2:G:443:TRP:CE2	2.50	0.46
1:A:145:LYS:HZ1	1:A:194:LYS:HE2	1.81	0.46
1:A:152:ILE:CD1	1:A:195:THR:C	2.88	0.46
1:A:366:ILE:O	1:A:372:PHE:CD2	2.68	0.46
1:A:420:HIS:CG	1:A:435:ILE:HG12	2.51	0.46
1:A:421:LYS:HZ3	1:A:478:VAL:HB	1.80	0.46
1:B:71:ASP:O	1:B:75:GLU:CG	2.63	0.46
1:B:234:ILE:HG21	1:B:267:VAL:HG13	1.96	0.46
1:B:422:PHE:HE1	1:B:472:LEU:HD22	1.80	0.46
1:D:306:VAL:O	1:D:310:LEU:HD13	2.16	0.46
1:D:420:HIS:NE2	1:D:435:ILE:HA	2.30	0.46
2:E:396:ASP:O	2:E:401:ARG:NE	2.48	0.46
2:G:336:HIS:ND1	2:G:389:PHE:HB2	2.30	0.46
1:A:62:GLN:O	1:A:66:ASN:CG	2.58	0.46
1:A:202:LYS:HE3	1:A:215:VAL:CG2	2.46	0.46
1:A:422:PHE:HE1	1:A:472:LEU:HD22	1.80	0.46
1:B:70:PHE:HA	1:B:73:LEU:HB2	1.98	0.46
1:B:151:LEU:HG	1:B:198:LYS:CD	2.45	0.46
1:C:147:PHE:HB2	1:C:233:PHE:CE1	2.51	0.46
1:C:147:PHE:CE1	1:C:225:PHE:CE1	3.04	0.46
1:C:150:LYS:O	1:C:151:LEU:C	2.59	0.46
1:C:371:SER:O	1:C:375:TYR:HB2	2.16	0.46
1:C:413:PHE:O	1:C:414:LEU:C	2.59	0.46
1:D:50:ILE:HG12	1:D:298:PHE:CE1	2.50	0.46
1:D:100:ILE:CG1	1:D:241:LEU:HD21	2.46	0.46
1:D:371:SER:O	1:D:575:PRO:HB3	2.16	0.46
1:D:401:LEU:HD22	1:D:575:PRO:HG3	1.96	0.46
2:E:410:GLY:O	2:E:414:SER:CB	2.64	0.46
2:F:416:HIS:O	2:F:417:ASN:C	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:317:GLY:O	2:G:319:LYS:NZ	2.49	0.46
1:A:497:PHE:HE1	1:A:557:VAL:HG13	1.80	0.46
1:B:42:LEU:O	1:B:46:THR:HG23	2.16	0.46
1:B:81:HIS:CE1	1:B:214:PRO:HG3	2.50	0.46
1:B:155:LEU:CG	1:B:198:LYS:HE2	2.45	0.46
1:B:254:THR:HB	1:B:258:ILE:HD12	1.96	0.46
1:B:420:HIS:CE1	1:B:435:ILE:HG23	2.50	0.46
1:B:422:PHE:CE1	1:B:472:LEU:HD22	2.49	0.46
1:B:569:LEU:O	1:B:573:THR:HG23	2.14	0.46
1:C:141:CYS:HB3	1:C:147:PHE:CE2	2.49	0.46
1:C:152:ILE:HG12	1:C:198:LYS:N	2.31	0.46
1:C:572:GLU:O	1:C:573:THR:HG23	2.16	0.46
1:C:695:LYS:HG3	1:C:696:PRO:CD	2.46	0.46
1:D:548:LYS:O	1:D:551:VAL:N	2.48	0.46
1:D:569:LEU:O	1:D:573:THR:HG23	2.16	0.46
1:D:682:ILE:HD11	2:F:465:LEU:HD12	1.97	0.46
2:F:398:GLN:HG3	2:F:401:ARG:HG3	1.97	0.46
2:F:400:LEU:O	2:F:405:SER:OG	2.34	0.46
2:F:438:GLN:O	2:F:441:PHE:O	2.33	0.46
2:H:324:GLU:O	2:H:328:THR:HG23	2.16	0.46
2:H:390:LEU:HD23	2:H:418:ILE:HD12	1.98	0.46
1:A:49:LEU:CD2	1:C:45:GLU:CG	2.94	0.46
1:A:130:THR:O	1:A:131:PRO:O	2.33	0.46
1:A:144:MET:SD	1:A:232:ASP:HB2	2.56	0.46
1:A:153:SER:O	1:A:157:ASP:CG	2.59	0.46
1:B:44:PHE:HA	1:B:47:TYR:HB3	1.98	0.46
1:B:325:ILE:O	1:B:328:LEU:N	2.49	0.46
1:B:342:SER:OG	1:B:579:VAL:HG13	2.16	0.46
1:B:371:SER:HA	1:B:374:ARG:HB2	1.97	0.46
1:C:43:ARG:NH2	1:C:342:SER:OG	2.48	0.46
1:C:71:ASP:O	1:C:75:GLU:CG	2.64	0.46
1:C:414:LEU:O	1:C:479:PHE:HE1	1.98	0.46
1:C:480:LYS:O	1:C:484:GLU:CB	2.64	0.46
1:C:497:PHE:CE1	1:C:557:VAL:CG1	2.99	0.46
1:C:646:LEU:HD12	1:C:702:ASP:HB3	1.97	0.46
1:D:202:LYS:CE	1:D:215:VAL:CG2	2.94	0.46
1:D:296:THR:CB	1:D:410:MET:SD	3.03	0.46
1:D:384:GLN:HG2	1:D:388:LEU:HD11	1.97	0.46
2:F:369:ILE:HG12	2:F:372:GLN:OE1	2.16	0.46
2:G:324:GLU:O	2:G:328:THR:HG23	2.16	0.46
2:G:331:LEU:HB3	2:G:336:HIS:CG	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:SER:O	1:A:575:PRO:HB3	2.15	0.46
1:A:416:LEU:HD12	1:A:567:TYR:HD1	1.80	0.46
1:A:569:LEU:O	1:A:573:THR:HG23	2.16	0.46
1:B:46:THR:HA	1:B:49:LEU:HD12	1.97	0.46
1:B:104:ALA:HA	1:B:250:PHE:CD2	2.50	0.46
1:B:415:VAL:HG12	1:B:567:TYR:CE2	2.50	0.46
1:C:122:THR:HA	1:C:133:VAL:HG21	1.98	0.46
1:C:335:HIS:HB2	1:C:582:PHE:CG	2.51	0.46
1:C:480:LYS:O	1:C:484:GLU:HB2	2.16	0.46
1:D:216:VAL:HG11	1:D:249:ILE:CD1	2.46	0.46
1:D:414:LEU:HG	1:D:487:LEU:HD13	1.98	0.46
1:D:450:SER:OG	1:D:452:GLU:OE1	2.31	0.46
2:G:340:ASN:O	2:G:343:PHE:HB2	2.15	0.46
2:H:377:VAL:O	2:H:381:LYS:N	2.41	0.46
1:A:43:ARG:C	1:A:46:THR:HG1	2.22	0.46
1:A:202:LYS:C	1:A:206:THR:O	2.58	0.46
1:A:302:ILE:HG22	1:A:307:LEU:HG	1.98	0.46
1:A:497:PHE:CE1	1:A:557:VAL:CG1	2.98	0.46
1:B:106:VAL:O	1:B:278:SER:HB2	2.16	0.46
1:B:366:ILE:O	1:B:372:PHE:CD2	2.69	0.46
1:B:427:PRO:C	1:B:429:TYR:H	2.23	0.46
1:C:72:ASN:HA	1:C:75:GLU:HB2	1.98	0.46
1:C:501:PHE:CD1	1:C:554:GLU:CD	2.94	0.46
1:C:687:GLU:OE2	2:H:454:TYR:HB3	2.15	0.46
1:D:199:MET:HE2	1:D:244:PHE:CE2	2.50	0.46
2:F:298:PHE:HB3	2:F:330:MET:HG3	1.98	0.46
2:F:446:TYR:CB	2:F:448:THR:HG23	2.46	0.46
2:H:311:ILE:CG1	2:H:421:ILE:HG12	2.46	0.46
2:H:438:GLN:O	2:H:441:PHE:O	2.34	0.46
1:A:347:ASN:HB2	1:C:347:ASN:OD1	2.15	0.46
1:A:421:LYS:NZ	1:A:479:PHE:CD1	2.71	0.46
1:A:572:GLU:O	1:A:573:THR:HG23	2.16	0.46
1:A:695:LYS:CD	1:A:707:LEU:HD11	2.46	0.46
1:B:202:LYS:C	1:B:206:THR:O	2.59	0.46
1:B:417:ARG:HD3	1:B:482:TYR:CE1	2.51	0.46
1:B:504:LEU:CD1	1:B:554:GLU:CD	2.89	0.46
1:B:695:LYS:CG	1:B:696:PRO:HD2	2.46	0.46
1:D:341:LEU:HD21	1:D:365:ASN:HB2	1.98	0.46
1:D:457:LEU:CG	1:D:559:PHE:CZ	2.98	0.46
2:E:337:VAL:CG2	2:E:359:VAL:HG21	2.46	0.46
2:E:395:LEU:HD12	2:E:400:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:444:LEU:O	2:E:446:TYR:CE2	2.69	0.46
2:F:340:ASN:HB2	2:F:343:PHE:CG	2.51	0.46
2:G:320:ARG:HH22	2:G:457:GLU:HG3	1.81	0.46
2:G:400:LEU:HD22	2:G:409:ILE:HD11	1.98	0.46
1:A:150:LYS:O	1:A:151:LEU:C	2.59	0.45
1:A:447:ILE:HG22	1:A:453:TYR:CG	2.50	0.45
1:B:50:ILE:O	1:B:53:GLN:HB2	2.16	0.45
1:B:476:PHE:HB3	1:B:480:LYS:CE	2.46	0.45
1:B:497:PHE:CE1	1:B:557:VAL:HG13	2.51	0.45
1:B:647:VAL:O	1:B:651:GLU:HB2	2.16	0.45
1:C:504:LEU:HD21	1:C:550:GLU:HB3	1.98	0.45
1:D:683:ARG:NE	1:D:686:SER:OG	2.48	0.45
1:D:685:VAL:O	1:D:689:GLU:HG3	2.16	0.45
2:E:355:ILE:HG23	2:E:356:THR:N	2.31	0.45
2:F:295:GLU:O	2:F:298:PHE:HB2	2.16	0.45
2:F:331:LEU:HB3	2:F:336:HIS:CG	2.51	0.45
2:H:320:ARG:HH12	2:H:457:GLU:H	1.63	0.45
1:A:559:PHE:O	1:A:564:VAL:N	2.33	0.45
1:B:43:ARG:HH11	1:B:336:PHE:C	2.25	0.45
1:B:144:MET:SD	1:B:229:VAL:HA	2.56	0.45
1:B:222:MET:SD	1:B:225:PHE:CE2	3.09	0.45
1:B:402:LEU:HA	1:B:405:LEU:HD12	1.98	0.45
1:B:480:LYS:O	1:B:484:GLU:CB	2.63	0.45
1:C:695:LYS:CG	1:C:696:PRO:HD2	2.46	0.45
1:D:70:PHE:HA	1:D:73:LEU:HB2	1.97	0.45
1:D:162:ILE:O	1:D:162:ILE:HG22	2.17	0.45
1:D:199:MET:CE	1:D:243:GLU:OE1	2.64	0.45
1:D:302:ILE:HG22	1:D:307:LEU:HG	1.99	0.45
1:D:313:ILE:HG12	1:D:318:ASP:OD1	2.16	0.45
1:D:414:LEU:HD13	1:D:494:ILE:HD11	1.97	0.45
2:E:324:GLU:O	2:E:328:THR:HG23	2.16	0.45
2:G:295:GLU:HG2	2:G:298:PHE:CE2	2.51	0.45
1:A:151:LEU:CD1	1:A:198:LYS:HZ2	2.25	0.45
1:A:330:LEU:HD11	2:G:309:PHE:CE2	2.51	0.45
1:A:419:LEU:HB2	1:A:567:TYR:CE1	2.50	0.45
1:A:695:LYS:CG	1:A:696:PRO:HD2	2.45	0.45
1:B:153:SER:O	1:B:157:ASP:CG	2.60	0.45
1:B:283:GLU:O	1:B:287:THR:HG23	2.16	0.45
1:B:332:LEU:HD23	1:B:336:PHE:CD2	2.51	0.45
1:B:414:LEU:HD13	1:B:494:ILE:HD11	1.97	0.45
1:C:691:LEU:O	2:H:426:HIS:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:106:VAL:HG13	1:D:253:ALA:O	2.16	0.45
1:D:497:PHE:CE1	1:D:557:VAL:HG13	2.52	0.45
2:E:318:SER:HA	2:E:319:LYS:HZ1	1.82	0.45
2:F:342:PHE:CE1	2:F:343:PHE:CE1	3.05	0.45
2:G:397:SER:HB2	2:G:400:LEU:H	1.80	0.45
1:B:139:LYS:C	1:B:141:CYS:H	2.24	0.45
1:B:457:LEU:CG	1:B:559:PHE:CZ	2.97	0.45
1:B:475:CYS:O	1:B:479:PHE:HD2	1.98	0.45
1:B:548:LYS:O	1:B:552:LEU:HG	2.16	0.45
1:D:302:ILE:HG21	1:D:306:VAL:HG22	1.98	0.45
1:D:306:VAL:O	1:D:310:LEU:HB2	2.16	0.45
1:D:325:ILE:HG22	1:D:326:LYS:N	2.31	0.45
1:D:394:LEU:O	1:D:395:LYS:C	2.60	0.45
2:E:335:ILE:HG22	2:E:335:ILE:O	2.17	0.45
2:E:339:ILE:HD13	2:E:351:VAL:HG22	1.99	0.45
2:F:455:THR:HA	2:F:458:THR:HB	1.99	0.45
2:H:301:TRP:NE1	2:H:446:TYR:CE1	2.84	0.45
2:H:336:HIS:ND1	2:H:389:PHE:HB2	2.32	0.45
2:H:340:ASN:O	2:H:343:PHE:HB2	2.16	0.45
1:A:128:ASN:O	1:A:129:VAL:HB	2.17	0.45
1:A:394:LEU:O	1:A:395:LYS:C	2.60	0.45
1:B:248:LEU:CD1	1:B:250:PHE:CZ	2.99	0.45
1:B:263:LEU:CD1	1:B:271:LEU:HD11	2.47	0.45
1:B:400:LEU:O	1:B:404:ASN:ND2	2.49	0.45
1:B:636:LEU:HD13	1:B:653:PHE:HD1	1.82	0.45
1:C:155:LEU:HB2	1:C:198:LYS:HG2	1.99	0.45
1:C:302:ILE:HG22	1:C:307:LEU:HG	1.97	0.45
1:C:350:GLU:O	1:C:354:ARG:HG2	2.16	0.45
1:C:554:GLU:HA	1:C:557:VAL:HB	1.98	0.45
1:D:137:GLN:NE2	1:D:220:LYS:HD2	2.32	0.45
1:D:355:ILE:O	1:D:395:LYS:HE3	2.16	0.45
1:D:415:VAL:O	1:D:418:CYS:HB3	2.16	0.45
1:D:476:PHE:CZ	1:D:501:PHE:CD1	3.04	0.45
1:A:348:LEU:CD2	1:A:403:GLU:HA	2.46	0.45
1:A:421:LYS:NZ	1:A:479:PHE:CE1	2.79	0.45
1:A:636:LEU:O	1:A:639:GLU:N	2.49	0.45
1:B:244:PHE:O	1:B:246:LEU:N	2.45	0.45
1:C:689:GLU:CG	1:C:694:ILE:HD11	2.46	0.45
1:D:148:LEU:HB2	1:D:195:THR:HG22	1.98	0.45
1:D:387:LEU:HD22	1:D:394:LEU:HD13	1.99	0.45
2:G:311:ILE:CG1	2:G:421:ILE:HG12	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:348:VAL:HG22	2:G:400:LEU:HD23	1.99	0.45
2:H:412:LEU:O	2:H:415:LEU:N	2.49	0.45
1:A:341:LEU:HD21	1:A:365:ASN:HB3	1.99	0.45
1:B:51:TRP:CH2	1:B:55:LYS:HE3	2.52	0.45
1:B:293:LEU:HD21	1:B:328:LEU:HD13	1.99	0.45
1:B:302:ILE:HG22	1:B:307:LEU:HG	1.99	0.45
1:B:458:GLN:O	1:B:462:MET:HG2	2.16	0.45
1:C:69:LEU:HD22	1:C:277:GLN:O	2.16	0.45
1:C:209:GLN:HE22	1:C:213:PRO:HG3	1.82	0.45
1:C:332:LEU:HD23	1:C:336:PHE:CD2	2.52	0.45
1:C:694:ILE:HD13	1:C:704:VAL:HG22	1.99	0.45
1:D:100:ILE:O	1:D:271:LEU:HA	2.17	0.45
1:D:255:SER:HB2	1:D:256:PRO:HD3	1.97	0.45
2:F:425:ASP:OD1	2:F:454:TYR:OH	2.34	0.45
2:G:339:ILE:HG21	2:G:351:VAL:HG22	1.99	0.45
2:H:332:GLN:O	2:H:333:ASP:C	2.59	0.45
2:H:340:ASN:HB2	2:H:343:PHE:CG	2.52	0.45
2:H:397:SER:HB2	2:H:400:LEU:H	1.82	0.45
1:A:44:PHE:HZ	1:A:337:TYR:CE1	2.35	0.45
1:A:104:ALA:HA	1:A:250:PHE:CD2	2.50	0.45
1:A:349:PRO:HG2	1:C:347:ASN:CG	2.42	0.45
1:A:597:ARG:CZ	1:A:708:THR:OG1	2.65	0.45
1:B:286:THR:HG22	1:B:436:ARG:NE	2.32	0.45
1:B:416:LEU:HD12	1:B:567:TYR:HD1	1.81	0.45
1:C:288:VAL:O	1:C:292:LEU:N	2.35	0.45
1:C:314:PHE:HD2	1:C:324:PHE:HB2	1.81	0.45
1:C:405:LEU:HD11	1:C:576:LEU:HB2	1.98	0.45
1:C:646:LEU:HA	1:C:649:TRP:HB3	1.98	0.45
1:C:708:THR:HB	2:H:427:LEU:HD12	1.98	0.45
1:D:74:ILE:O	1:D:78:GLN:HB2	2.17	0.45
1:D:271:LEU:CB	1:D:273:ILE:HG13	2.46	0.45
1:D:421:LYS:HB2	1:D:479:PHE:CZ	2.52	0.45
2:E:332:GLN:O	2:E:333:ASP:C	2.60	0.45
2:E:441:PHE:HB3	2:E:443:TRP:CE2	2.52	0.45
2:F:369:ILE:HA	2:F:372:GLN:CD	2.42	0.45
2:G:332:GLN:O	2:G:333:ASP:C	2.60	0.45
2:G:412:LEU:HB3	2:G:418:ILE:CD1	2.46	0.45
2:H:369:ILE:HG12	2:H:372:GLN:OE1	2.17	0.45
2:H:455:THR:O	2:H:459:SER:N	2.50	0.45
1:A:50:ILE:HG12	1:A:298:PHE:CD1	2.52	0.45
1:A:70:PHE:HA	1:A:73:LEU:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:LEU:HA	1:A:151:LEU:HD22	1.99	0.45
1:A:151:LEU:HG	1:A:198:LYS:CD	2.46	0.45
1:A:202:LYS:HD2	1:A:244:PHE:CD1	2.52	0.45
1:A:443:LEU:HA	1:A:570:PRO:HD3	1.99	0.45
1:A:683:ARG:NE	1:A:683:ARG:HA	2.32	0.45
1:B:426:LEU:HD21	1:B:460:LEU:HG	1.99	0.45
1:B:472:LEU:O	1:B:475:CYS:N	2.49	0.45
1:C:563:LEU:HG	1:C:567:TYR:CD2	2.52	0.45
1:D:81:HIS:NE2	1:D:214:PRO:HB3	2.32	0.45
1:D:107:LEU:HD23	1:D:278:SER:HB2	1.99	0.45
1:D:217:VAL:HG12	1:D:219:LEU:HD21	1.99	0.45
1:D:695:LYS:CG	1:D:696:PRO:CD	2.94	0.45
2:E:339:ILE:CD1	2:E:351:VAL:HG13	2.47	0.45
2:E:352:LEU:CD2	2:E:369:ILE:HG23	2.46	0.45
2:F:325:ARG:HA	2:F:328:THR:OG1	2.17	0.45
2:G:355:ILE:HG23	2:G:356:THR:N	2.31	0.45
2:G:442:ASN:HD22	2:G:442:ASN:HA	1.68	0.45
2:H:325:ARG:HA	2:H:328:THR:OG1	2.17	0.45
1:A:148:LEU:HG	1:A:233:PHE:HE1	1.82	0.45
1:B:72:ASN:HA	1:B:75:GLU:HB2	1.99	0.45
1:B:74:ILE:O	1:B:78:GLN:HB2	2.16	0.45
1:B:147:PHE:HE2	1:B:229:VAL:HG11	1.82	0.45
1:B:151:LEU:CD1	1:B:198:LYS:HZ2	2.24	0.45
1:B:209:GLN:HE22	1:B:213:PRO:HG3	1.81	0.45
1:C:151:LEU:CD1	1:C:198:LYS:HD2	2.47	0.45
1:C:371:SER:HA	1:C:374:ARG:HB2	1.99	0.45
1:C:414:LEU:HG	1:C:487:LEU:HD13	1.98	0.45
1:C:415:VAL:O	1:C:418:CYS:HB3	2.17	0.45
1:C:641:SER:OG	1:C:642:ARG:N	2.49	0.45
1:D:42:LEU:HD13	1:D:354:ARG:NH1	2.32	0.45
1:D:263:LEU:HD13	1:D:271:LEU:HD11	1.98	0.45
1:D:335:HIS:HB2	1:D:582:PHE:CG	2.52	0.45
1:D:591:HIS:CD2	2:F:445:TRP:O	2.70	0.45
1:D:686:SER:O	1:D:689:GLU:HB2	2.16	0.45
2:E:347:SER:HA	2:E:399:MET:HG3	1.99	0.45
1:A:122:THR:HA	1:A:133:VAL:HG23	1.98	0.44
1:A:384:GLN:O	1:A:387:LEU:HB2	2.16	0.44
1:B:63:GLU:C	1:B:66:ASN:HB2	2.42	0.44
1:B:152:ILE:CG2	1:B:198:LYS:N	2.80	0.44
1:B:420:HIS:NE2	1:B:435:ILE:HA	2.31	0.44
1:B:480:LYS:O	1:B:484:GLU:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:208:SER:HB2	1:C:210:TRP:CE2	2.52	0.44
1:C:209:GLN:OE1	1:C:211:GLN:O	2.35	0.44
1:C:238:SER:HA	1:C:241:LEU:CD1	2.47	0.44
1:C:252:ILE:CD1	1:C:259:ILE:HD11	2.47	0.44
1:D:144:MET:SD	1:D:233:PHE:CE2	3.10	0.44
1:D:148:LEU:HA	1:D:151:LEU:HD22	1.97	0.44
1:D:189:MET:C	1:D:191:VAL:H	2.26	0.44
1:D:548:LYS:O	1:D:552:LEU:N	2.42	0.44
2:G:340:ASN:HB2	2:G:343:PHE:CG	2.52	0.44
2:G:369:ILE:HA	2:G:372:GLN:CG	2.47	0.44
2:H:326:PHE:O	2:H:331:LEU:N	2.46	0.44
1:A:104:ALA:CA	1:A:250:PHE:HD2	2.29	0.44
1:A:138:ALA:O	1:A:141:CYS:HB2	2.17	0.44
1:A:423:THR:HG21	1:A:438:LEU:HD21	2.00	0.44
1:B:199:MET:HE2	1:B:244:PHE:HE2	1.82	0.44
1:C:153:SER:O	1:C:157:ASP:CG	2.60	0.44
1:C:305:LYS:O	1:C:309:VAL:HG23	2.17	0.44
1:C:472:LEU:O	1:C:475:CYS:N	2.50	0.44
1:C:683:ARG:HH11	2:H:458:THR:HA	1.81	0.44
1:D:446:ASN:OD1	1:D:569:LEU:HD11	2.17	0.44
2:F:298:PHE:CD2	2:F:330:MET:HG2	2.53	0.44
2:H:425:ASP:OD1	2:H:454:TYR:OH	2.35	0.44
1:A:415:VAL:HG12	1:A:567:TYR:CE1	2.52	0.44
1:A:425:SER:OG	1:A:471:ILE:HD13	2.18	0.44
1:A:497:PHE:HB3	1:A:501:PHE:HE2	1.83	0.44
1:B:150:LYS:O	1:B:151:LEU:C	2.58	0.44
1:B:296:THR:HG22	1:B:413:PHE:CD2	2.53	0.44
1:B:310:LEU:HB3	1:B:324:PHE:HE1	1.82	0.44
1:B:393:TYR:O	1:B:397:GLU:HG3	2.18	0.44
1:C:65:LEU:HB3	1:C:279:LEU:HD12	1.98	0.44
1:C:147:PHE:CE2	1:C:229:VAL:CG1	3.00	0.44
1:C:341:LEU:HD21	1:C:365:ASN:HB2	2.00	0.44
1:C:387:LEU:HD22	1:C:394:LEU:HD13	2.00	0.44
1:D:106:VAL:O	1:D:278:SER:HB2	2.17	0.44
1:D:152:ILE:CG2	1:D:198:LYS:N	2.80	0.44
1:D:284:HIS:HA	1:D:287:THR:OG1	2.18	0.44
1:D:476:PHE:CE2	1:D:501:PHE:CG	3.05	0.44
2:F:319:LYS:HE3	2:F:423:SER:HB2	2.00	0.44
1:A:268:SER:HA	1:A:271:LEU:HD12	1.99	0.44
1:A:373:ARG:O	1:A:377:GLU:HG3	2.18	0.44
1:A:497:PHE:CE1	1:A:557:VAL:HG13	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:ASN:O	1:B:62:GLN:HG3	2.17	0.44
1:B:191:VAL:O	1:B:191:VAL:HG12	2.18	0.44
1:B:348:LEU:O	1:B:352:LYS:HG3	2.17	0.44
1:B:419:LEU:HB2	1:B:567:TYR:CZ	2.53	0.44
1:B:649:TRP:O	1:B:653:PHE:HB3	2.17	0.44
1:C:683:ARG:HD3	1:C:686:SER:OG	2.17	0.44
1:D:75:GLU:O	1:D:79:LYS:HG3	2.18	0.44
1:D:421:LYS:HE3	1:D:479:PHE:CE1	2.53	0.44
1:D:475:CYS:O	1:D:479:PHE:CB	2.62	0.44
1:D:475:CYS:O	1:D:479:PHE:HD2	2.01	0.44
2:F:356:THR:HG22	2:F:363:MET:O	2.18	0.44
2:G:335:ILE:CG2	2:G:388:LEU:HB2	2.47	0.44
2:G:396:ASP:O	2:G:401:ARG:NE	2.51	0.44
1:A:81:HIS:CE1	1:A:214:PRO:HG3	2.53	0.44
1:A:152:ILE:CG2	1:A:198:LYS:N	2.81	0.44
1:A:216:VAL:HG11	1:A:249:ILE:CD1	2.47	0.44
1:A:414:LEU:HD13	1:A:494:ILE:HD11	1.99	0.44
1:A:415:VAL:HG12	1:A:567:TYR:CE2	2.53	0.44
1:B:79:LYS:O	1:B:83:GLY:N	2.39	0.44
1:B:382:GLU:C	1:B:384:GLN:N	2.63	0.44
1:C:42:LEU:O	1:C:46:THR:HG23	2.17	0.44
1:C:144:MET:SD	1:C:232:ASP:CB	3.06	0.44
1:C:405:LEU:HD21	1:C:575:PRO:O	2.18	0.44
1:C:683:ARG:CZ	2:H:458:THR:HG23	2.47	0.44
1:C:691:LEU:HA	2:H:425:ASP:HB3	1.99	0.44
1:D:150:LYS:O	1:D:151:LEU:C	2.59	0.44
1:D:384:GLN:O	1:D:387:LEU:HB2	2.17	0.44
1:D:480:LYS:HG2	1:D:498:LEU:HD22	2.00	0.44
1:D:582:PHE:CE1	1:D:583:SER:O	2.70	0.44
2:E:319:LYS:HE3	2:E:423:SER:HB2	2.00	0.44
2:F:312:VAL:HB	2:F:445:TRP:HA	2.00	0.44
2:H:332:GLN:O	2:H:336:HIS:CD2	2.71	0.44
2:H:416:HIS:O	2:H:417:ASN:C	2.59	0.44
1:A:134:VAL:HG13	1:A:154:GLN:CB	2.48	0.44
1:A:144:MET:SD	1:A:233:PHE:CE2	3.11	0.44
1:A:405:LEU:HD11	1:A:576:LEU:HB2	2.00	0.44
1:B:65:LEU:HB3	1:B:279:LEU:HD12	1.99	0.44
1:B:284:HIS:HA	1:B:287:THR:OG1	2.18	0.44
1:B:303:ASN:ND2	1:B:581:TYR:HB3	2.33	0.44
1:B:372:PHE:CE2	1:B:376:VAL:HG21	2.52	0.44
1:C:259:ILE:CG2	1:C:263:LEU:HD12	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:386:ALA:HB1	1:C:393:TYR:CB	2.48	0.44
1:C:683:ARG:HH12	2:H:461:GLU:HB2	1.82	0.44
1:D:42:LEU:O	1:D:46:THR:HG23	2.18	0.44
1:D:69:LEU:HD13	1:D:278:SER:HA	2.00	0.44
1:D:222:MET:SD	1:D:225:PHE:CD2	3.11	0.44
1:D:688:LEU:HB3	1:D:694:ILE:HG13	2.00	0.44
2:E:320:ARG:O	2:E:324:GLU:HB2	2.17	0.44
2:E:373:LEU:CD2	2:E:412:LEU:HD21	2.48	0.44
2:F:323:LEU:HD12	2:F:393:HIS:CE1	2.53	0.44
2:F:398:GLN:CG	2:F:401:ARG:HG3	2.47	0.44
2:F:410:GLY:O	2:F:414:SER:CB	2.66	0.44
2:H:331:LEU:C	2:H:336:HIS:NE2	2.76	0.44
1:A:67:LYS:O	1:A:71:ASP:HB2	2.18	0.44
1:A:428:LYS:O	1:A:429:TYR:C	2.60	0.44
1:A:647:VAL:O	1:A:651:GLU:HB2	2.18	0.44
1:B:216:VAL:HG11	1:B:249:ILE:HG13	2.00	0.44
1:B:384:GLN:O	1:B:388:LEU:HG	2.18	0.44
1:C:100:ILE:HG12	1:C:241:LEU:HD21	2.00	0.44
1:C:196:ASP:O	1:C:199:MET:HG2	2.18	0.44
1:C:202:LYS:HE3	1:C:244:PHE:HE1	1.82	0.44
1:C:333:LEU:HD13	2:H:307:LEU:HD13	1.99	0.44
1:C:557:VAL:O	1:C:561:ASP:HB2	2.18	0.44
1:C:636:LEU:HD13	1:C:653:PHE:HD1	1.83	0.44
1:C:685:VAL:O	1:C:689:GLU:HG3	2.18	0.44
1:D:234:ILE:O	1:D:238:SER:HB3	2.15	0.44
2:H:309:PHE:N	2:H:309:PHE:CD1	2.86	0.44
2:H:347:SER:CB	2:H:399:MET:HG3	2.48	0.44
1:A:100:ILE:HD11	1:A:237:SER:CB	2.48	0.44
1:A:416:LEU:HD12	1:A:567:TYR:CD1	2.53	0.44
1:A:587:ALA:O	1:A:591:HIS:CD2	2.71	0.44
1:B:100:ILE:HD11	1:B:237:SER:CB	2.48	0.44
1:B:105:LEU:HB2	1:B:250:PHE:O	2.18	0.44
1:B:138:ALA:HB2	1:B:221:ASP:O	2.18	0.44
1:B:367:ARG:NE	1:B:388:LEU:O	2.50	0.44
1:B:428:LYS:O	1:B:429:TYR:C	2.60	0.44
1:C:97:LEU:HA	1:C:242:HIS:CD2	2.53	0.44
1:C:134:VAL:HG21	1:C:155:LEU:HG	2.00	0.44
1:C:302:ILE:CG2	1:C:307:LEU:HG	2.48	0.44
1:C:303:ASN:ND2	1:C:581:TYR:HB3	2.33	0.44
1:D:148:LEU:HD23	1:D:151:LEU:HD22	1.98	0.44
1:D:250:PHE:HB3	1:D:252:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:286:THR:HG22	1:D:436:ARG:NE	2.33	0.44
1:D:402:LEU:HD21	1:D:576:LEU:HD13	1.99	0.44
1:D:453:TYR:OH	1:D:563:LEU:CD1	2.64	0.44
2:E:311:ILE:CG1	2:E:421:ILE:HG12	2.47	0.44
2:G:398:GLN:C	2:G:399:MET:HE2	2.43	0.44
2:H:287:LEU:CD2	2:H:451:TYR:HB2	2.47	0.44
1:A:72:ASN:HA	1:A:75:GLU:HB2	1.99	0.44
1:A:563:LEU:HA	1:A:567:TYR:HD2	1.83	0.44
1:B:405:LEU:HD21	1:B:575:PRO:O	2.17	0.44
1:B:632:ILE:O	1:B:636:LEU:HG	2.17	0.44
1:C:104:ALA:HA	1:C:250:PHE:HB2	1.99	0.44
1:C:286:THR:HG22	1:C:436:ARG:HE	1.83	0.44
1:C:354:ARG:HA	1:C:357:PHE:HD2	1.82	0.44
1:C:482:TYR:CD1	1:C:486:HIS:CG	3.06	0.44
1:C:504:LEU:CD1	1:C:554:GLU:CD	2.91	0.44
1:C:556:VAL:CA	1:C:559:PHE:HD2	2.30	0.44
1:D:216:VAL:HG11	1:D:249:ILE:HG13	1.99	0.44
1:D:564:VAL:O	1:D:568:LEU:HD21	2.17	0.44
1:D:700:LYS:HD3	1:D:703:HIS:NE2	2.32	0.44
2:E:335:ILE:CG2	2:E:388:LEU:HB2	2.48	0.44
2:E:342:PHE:CE1	2:E:343:PHE:CE1	3.06	0.44
2:G:355:ILE:HD11	2:G:388:LEU:HD21	1.98	0.44
2:G:379:LYS:O	2:G:383:ASP:HB2	2.18	0.44
2:G:433:TRP:HB3	2:G:438:GLN:HG3	1.99	0.44
2:H:348:VAL:HG22	2:H:400:LEU:HD23	1.98	0.44
1:A:50:ILE:O	1:A:53:GLN:HB2	2.17	0.43
1:A:125:LEU:HB3	1:A:131:PRO:HG2	2.00	0.43
1:A:147:PHE:CE1	1:A:225:PHE:CE1	3.06	0.43
1:B:355:ILE:O	1:B:395:LYS:HE3	2.18	0.43
1:B:636:LEU:CD2	1:B:656:VAL:HG11	2.48	0.43
1:C:44:PHE:HZ	1:C:337:TYR:CZ	2.36	0.43
1:C:385:VAL:O	1:C:388:LEU:N	2.51	0.43
1:D:387:LEU:HA	1:D:394:LEU:HB2	2.00	0.43
1:D:413:PHE:O	1:D:414:LEU:C	2.60	0.43
1:D:557:VAL:O	1:D:561:ASP:HB2	2.17	0.43
1:D:636:LEU:HD13	1:D:653:PHE:HD1	1.83	0.43
1:D:695:LYS:HB3	1:D:697:THR:CG2	2.48	0.43
2:G:320:ARG:NH2	2:G:342:PHE:CZ	2.85	0.43
2:G:323:LEU:HD12	2:G:393:HIS:CE1	2.53	0.43
2:H:391:LEU:CD2	2:H:421:ILE:HB	2.44	0.43
2:H:420:LEU:HD21	2:H:443:TRP:CH2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:MET:CE	1:A:244:PHE:CE2	3.01	0.43
1:A:279:LEU:HD22	1:A:283:GLU:OE1	2.18	0.43
1:A:557:VAL:HG22	1:A:561:ASP:OD2	2.17	0.43
1:A:697:THR:HG21	1:A:705:ALA:HB3	2.00	0.43
1:B:51:TRP:CH2	1:B:329:GLN:NE2	2.86	0.43
1:B:151:LEU:CG	1:B:198:LYS:HD2	2.48	0.43
1:B:367:ARG:NH2	1:B:391:GLU:HG2	2.33	0.43
1:B:636:LEU:O	1:B:639:GLU:N	2.50	0.43
1:C:106:VAL:O	1:C:278:SER:HB2	2.18	0.43
1:C:280:SER:O	1:C:284:HIS:ND1	2.51	0.43
1:C:473:GLU:HG2	1:C:505:ASP:CG	2.44	0.43
1:C:685:VAL:HG13	1:C:704:VAL:HG21	2.00	0.43
1:C:688:LEU:HB3	1:C:694:ILE:HG13	2.00	0.43
1:D:69:LEU:HD22	1:D:277:GLN:O	2.18	0.43
1:D:221:ASP:OD1	1:D:221:ASP:N	2.47	0.43
1:D:332:LEU:HD23	1:D:336:PHE:CD2	2.53	0.43
1:D:422:PHE:CE1	1:D:472:LEU:HD22	2.53	0.43
2:E:295:GLU:HA	2:E:298:PHE:CD2	2.53	0.43
2:E:331:LEU:HD11	2:E:391:LEU:CG	2.49	0.43
2:E:398:GLN:HG3	2:E:401:ARG:HG3	2.00	0.43
2:F:355:ILE:HG23	2:F:356:THR:N	2.32	0.43
1:A:42:LEU:HD13	1:A:354:ARG:NH1	2.32	0.43
1:A:418:CYS:O	1:A:422:PHE:HD2	2.01	0.43
1:B:371:SER:OG	1:B:576:LEU:N	2.49	0.43
1:B:572:GLU:O	1:B:573:THR:HG23	2.19	0.43
1:B:707:LEU:N	1:B:707:LEU:HD12	2.33	0.43
1:C:370:PRO:C	1:C:372:PHE:N	2.76	0.43
1:D:334:GLU:HG3	1:D:582:PHE:CZ	2.54	0.43
2:E:411:GLN:O	2:E:415:LEU:HG	2.18	0.43
2:E:420:LEU:HD21	2:E:443:TRP:HH2	1.82	0.43
2:G:304:GLN:OE1	2:G:446:TYR:OH	2.30	0.43
2:H:309:PHE:CE2	2:H:442:ASN:ND2	2.86	0.43
1:A:128:ASN:C	1:A:130:THR:H	2.25	0.43
1:A:250:PHE:HB3	1:A:252:ILE:CD1	2.48	0.43
1:A:312:ASN:O	1:A:316:TYR:HB2	2.18	0.43
1:A:354:ARG:O	1:A:358:LEU:HG	2.19	0.43
1:A:632:ILE:O	1:A:636:LEU:HG	2.18	0.43
1:B:144:MET:SD	1:B:233:PHE:CE2	3.11	0.43
1:B:199:MET:CE	1:B:244:PHE:HE2	2.31	0.43
1:B:420:HIS:CG	1:B:435:ILE:HG12	2.53	0.43
1:B:474:LYS:O	1:B:478:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:475:CYS:O	1:B:479:PHE:CB	2.63	0.43
1:B:496:GLU:O	1:B:500:GLN:HG3	2.18	0.43
1:C:47:TYR:O	1:C:48:GLN:C	2.62	0.43
1:C:271:LEU:CB	1:C:273:ILE:HG13	2.49	0.43
1:C:428:LYS:O	1:C:429:TYR:C	2.62	0.43
1:D:250:PHE:HB3	1:D:252:ILE:CD1	2.47	0.43
1:D:401:LEU:HD12	1:D:576:LEU:HD11	1.99	0.43
1:D:497:PHE:CD1	1:D:557:VAL:CG1	3.01	0.43
1:D:644:ILE:HB	1:D:649:TRP:CE3	2.52	0.43
2:E:323:LEU:HD12	2:E:393:HIS:CE1	2.53	0.43
2:E:325:ARG:HA	2:E:328:THR:OG1	2.17	0.43
2:E:425:ASP:OD1	2:E:454:TYR:OH	2.35	0.43
2:F:362:HIS:HB3	2:F:379:LYS:HZ3	1.83	0.43
2:G:327:ARG:HA	2:G:331:LEU:HD12	2.01	0.43
2:H:411:GLN:O	2:H:415:LEU:HG	2.18	0.43
1:A:150:LYS:O	1:A:154:GLN:CG	2.66	0.43
1:A:254:THR:HB	1:A:258:ILE:HD12	2.00	0.43
1:A:335:HIS:HB2	1:A:582:PHE:CG	2.53	0.43
1:B:49:LEU:CD2	1:D:45:GLU:OE2	2.65	0.43
1:B:145:LYS:HZ1	1:B:194:LYS:HE2	1.83	0.43
1:B:234:ILE:HD13	1:B:267:VAL:HG13	1.99	0.43
1:B:564:VAL:O	1:B:568:LEU:HD21	2.18	0.43
1:C:71:ASP:O	1:C:75:GLU:HB2	2.19	0.43
1:C:136:LEU:HB2	1:C:219:LEU:HD22	2.00	0.43
1:C:306:VAL:O	1:C:310:LEU:HD13	2.19	0.43
1:C:461:ARG:HG2	1:C:552:LEU:HD22	1.99	0.43
1:D:259:ILE:CG2	1:D:263:LEU:HD12	2.47	0.43
1:D:412:TYR:HE1	1:D:568:LEU:O	2.02	0.43
1:D:636:LEU:O	1:D:639:GLU:N	2.50	0.43
2:E:412:LEU:HB3	2:E:418:ILE:CD1	2.49	0.43
1:A:310:LEU:O	1:A:313:ILE:N	2.52	0.43
1:A:476:PHE:CD1	1:A:480:LYS:HE3	2.53	0.43
1:A:557:VAL:O	1:A:561:ASP:HB2	2.18	0.43
1:A:694:ILE:HD13	1:A:704:VAL:HG22	2.00	0.43
1:B:476:PHE:CD1	1:B:480:LYS:HE3	2.53	0.43
1:B:556:VAL:O	1:B:560:ILE:N	2.42	0.43
1:B:564:VAL:O	1:B:568:LEU:HD11	2.18	0.43
1:C:69:LEU:HD13	1:C:278:SER:HA	2.00	0.43
1:C:202:LYS:C	1:C:206:THR:O	2.62	0.43
1:C:371:SER:OG	1:C:576:LEU:N	2.50	0.43
1:C:423:THR:CG2	1:C:438:LEU:HD21	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:457:LEU:CG	1:C:559:PHE:CZ	3.01	0.43
1:C:494:ILE:HA	1:C:497:PHE:HD2	1.82	0.43
1:C:569:LEU:O	1:C:573:THR:HG23	2.18	0.43
1:C:682:ILE:HD11	2:H:465:LEU:HD12	2.00	0.43
1:C:685:VAL:HG11	1:C:704:VAL:HG21	2.00	0.43
1:D:152:ILE:CG1	1:D:198:LYS:H	2.31	0.43
1:D:419:LEU:HD22	1:D:567:TYR:CE1	2.54	0.43
1:D:476:PHE:CD1	1:D:480:LYS:HE3	2.54	0.43
1:A:134:VAL:O	1:A:218:ILE:HD12	2.18	0.43
1:A:413:PHE:O	1:A:414:LEU:C	2.60	0.43
1:A:461:ARG:HG2	1:A:552:LEU:HD21	2.01	0.43
1:A:478:VAL:HA	1:A:481:SER:HB3	2.01	0.43
1:A:564:VAL:O	1:A:568:LEU:HD21	2.18	0.43
1:B:408:TYR:HB3	1:B:412:TYR:HE2	1.83	0.43
1:D:58:ASN:ND2	1:D:325:ILE:HD11	2.34	0.43
1:D:152:ILE:HG21	1:D:197:PRO:CA	2.49	0.43
1:D:199:MET:HE3	1:D:244:PHE:CE2	2.53	0.43
1:D:335:HIS:HB2	1:D:582:PHE:CD1	2.53	0.43
1:D:428:LYS:O	1:D:429:TYR:C	2.62	0.43
1:D:430:PRO:HB2	1:D:452:GLU:HB3	1.99	0.43
1:D:564:VAL:O	1:D:568:LEU:HD11	2.18	0.43
2:G:295:GLU:HA	2:G:298:PHE:CD2	2.54	0.43
2:H:388:LEU:O	2:H:418:ILE:HA	2.19	0.43
1:A:453:TYR:OH	1:A:563:LEU:HD13	2.19	0.43
1:A:504:LEU:CD1	1:A:554:GLU:CD	2.92	0.43
1:B:59:GLU:O	1:B:63:GLU:HG3	2.18	0.43
1:B:136:LEU:HD13	1:B:147:PHE:HD1	1.84	0.43
1:B:338:SER:O	1:B:339:GLN:HG3	2.19	0.43
1:B:560:ILE:O	1:B:565:ARG:HG3	2.19	0.43
1:B:645:ASN:OD1	1:B:648:ASP:N	2.41	0.43
1:C:110:ASN:HB3	1:C:281:CYS:SG	2.59	0.43
1:C:555:ASN:O	1:C:559:PHE:CD2	2.72	0.43
1:C:695:LYS:CG	1:C:696:PRO:CD	2.96	0.43
1:D:102:THR:HA	1:D:247:ILE:HG23	2.00	0.43
1:D:110:ASN:HB3	1:D:281:CYS:SG	2.58	0.43
1:D:326:LYS:HA	1:D:329:GLN:HE21	1.83	0.43
1:D:562:CYS:HB3	1:D:567:TYR:CE2	2.53	0.43
1:D:641:SER:OG	1:D:642:ARG:N	2.51	0.43
2:E:294:TYR:CZ	2:E:448:THR:HA	2.54	0.43
2:E:335:ILE:HG22	2:E:388:LEU:HA	2.01	0.43
2:E:400:LEU:HD22	2:E:409:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:291:ASN:O	2:F:295:GLU:HG3	2.19	0.43
2:F:327:ARG:HA	2:F:331:LEU:HD12	2.01	0.43
2:F:352:LEU:C	2:F:355:ILE:HG22	2.43	0.43
2:F:429:ALA:N	2:F:430:PRO:HD2	2.34	0.43
2:G:331:LEU:O	2:G:336:HIS:NE2	2.52	0.43
1:A:107:LEU:HD23	1:A:278:SER:HB2	2.00	0.43
1:A:219:LEU:HD13	1:A:222:MET:SD	2.59	0.43
1:A:286:THR:HG21	1:A:434:GLN:NE2	2.33	0.43
1:A:355:ILE:O	1:A:395:LYS:HE3	2.19	0.43
1:A:563:LEU:HA	1:A:567:TYR:CD2	2.54	0.43
1:A:693:PHE:CZ	2:G:427:LEU:HD21	2.53	0.43
1:B:77:LEU:CD2	1:B:247:ILE:HG21	2.47	0.43
1:B:125:LEU:O	1:B:131:PRO:CG	2.67	0.43
1:B:148:LEU:HD13	1:B:195:THR:HB	2.01	0.43
1:B:263:LEU:HD13	1:B:271:LEU:HD11	1.99	0.43
1:B:497:PHE:CE1	1:B:557:VAL:CG1	3.01	0.43
1:B:558:ASN:O	1:B:563:LEU:HD12	2.19	0.43
1:C:51:TRP:CH2	1:C:55:LYS:HE3	2.54	0.43
1:C:241:LEU:C	1:C:243:GLU:N	2.77	0.43
1:C:352:LYS:HG2	1:C:399:GLN:HG2	2.00	0.43
1:C:446:ASN:OD1	1:C:569:LEU:CD1	2.64	0.43
1:C:504:LEU:CD2	1:C:550:GLU:HB3	2.48	0.43
1:C:597:ARG:NH2	1:C:708:THR:OG1	2.51	0.43
1:D:371:SER:O	1:D:375:TYR:HB2	2.18	0.43
2:G:398:GLN:CG	2:G:401:ARG:HG3	2.49	0.43
2:G:400:LEU:HD22	2:G:409:ILE:CD1	2.47	0.43
2:H:400:LEU:HD22	2:H:409:ILE:HD11	2.00	0.43
1:A:71:ASP:O	1:A:75:GLU:HB2	2.18	0.43
1:A:372:PHE:CE2	1:A:376:VAL:HG21	2.54	0.43
1:A:448:TRP:CH2	1:A:559:PHE:HB3	2.54	0.43
1:A:476:PHE:HB3	1:A:480:LYS:CE	2.49	0.43
1:B:333:LEU:HB3	1:B:337:TYR:HE2	1.83	0.43
1:C:144:MET:O	1:C:233:PHE:HZ	2.02	0.43
1:C:150:LYS:O	1:C:154:GLN:CG	2.67	0.43
1:C:230:LEU:HD21	1:C:263:LEU:CD2	2.49	0.43
1:C:313:ILE:HG12	1:C:318:ASP:OD1	2.19	0.43
1:C:372:PHE:CE2	1:C:376:VAL:CG2	3.02	0.43
1:C:429:TYR:HB2	1:C:433:ARG:HE	1.83	0.43
1:C:549:PHE:HA	1:C:552:LEU:HB2	2.00	0.43
1:C:578:GLU:O	1:C:579:VAL:HB	2.19	0.43
1:D:99:GLU:C	1:D:241:LEU:HD13	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:286:THR:HG22	1:D:436:ARG:HE	1.84	0.43
1:D:419:LEU:HD23	1:D:438:LEU:HD23	2.01	0.43
1:D:501:PHE:CD1	1:D:554:GLU:OE2	2.71	0.43
1:D:689:GLU:CG	1:D:694:ILE:HD11	2.45	0.43
2:E:436:ALA:O	2:E:440:LEU:HG	2.19	0.43
2:F:340:ASN:HB3	2:F:342:PHE:CZ	2.54	0.43
2:G:377:VAL:HG13	2:G:381:LYS:HG3	2.01	0.43
2:H:433:TRP:HB3	2:H:438:GLN:HG3	2.00	0.43
1:A:74:ILE:O	1:A:78:GLN:HB2	2.18	0.42
1:A:421:LYS:HE3	1:A:479:PHE:CE1	2.54	0.42
1:A:467:GLU:HG2	1:A:471:ILE:HD12	2.00	0.42
1:A:646:LEU:HD12	1:A:702:ASP:HB3	2.00	0.42
1:A:693:PHE:CE2	2:G:427:LEU:HD21	2.54	0.42
1:B:152:ILE:HD13	1:B:197:PRO:HD2	2.01	0.42
1:B:155:LEU:HD21	1:B:215:VAL:CG1	2.49	0.42
1:B:202:LYS:HE3	1:B:215:VAL:CG2	2.49	0.42
1:B:457:LEU:HG	1:B:559:PHE:HZ	1.81	0.42
1:C:367:ARG:NH2	1:C:391:GLU:HG2	2.34	0.42
1:C:402:LEU:HA	1:C:405:LEU:HD12	2.01	0.42
1:C:552:LEU:O	1:C:556:VAL:CG2	2.67	0.42
1:C:657:VAL:HG12	1:C:677:ILE:HD11	2.01	0.42
1:D:333:LEU:HB3	1:D:337:TYR:HE2	1.83	0.42
2:F:330:MET:O	2:F:331:LEU:C	2.62	0.42
2:F:355:ILE:HD11	2:F:388:LEU:HD21	2.01	0.42
2:F:397:SER:CB	2:F:400:LEU:H	2.31	0.42
2:H:295:GLU:O	2:H:298:PHE:HB2	2.19	0.42
1:A:49:LEU:HD22	1:C:45:GLU:CG	2.49	0.42
1:A:234:ILE:HD13	1:A:267:VAL:HG13	2.00	0.42
1:A:371:SER:O	1:A:575:PRO:HA	2.18	0.42
1:A:419:LEU:HD22	1:A:567:TYR:CE1	2.53	0.42
1:B:241:LEU:C	1:B:243:GLU:H	2.27	0.42
1:B:494:ILE:HA	1:B:497:PHE:CD2	2.52	0.42
1:B:563:LEU:HG	1:B:567:TYR:CD2	2.55	0.42
1:C:335:HIS:HB2	1:C:582:PHE:CD1	2.53	0.42
1:C:476:PHE:CE2	1:C:501:PHE:CG	3.07	0.42
1:C:636:LEU:CD2	1:C:656:VAL:HG11	2.50	0.42
1:D:107:LEU:HD22	1:D:114:HIS:NE2	2.34	0.42
1:D:352:LYS:O	1:D:355:ILE:HB	2.20	0.42
1:D:474:LYS:O	1:D:478:VAL:HG23	2.19	0.42
2:G:339:ILE:CD1	2:G:351:VAL:HG13	2.49	0.42
2:H:298:PHE:CD2	2:H:330:MET:HG2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:355:ILE:HG23	2:H:356:THR:N	2.33	0.42
1:A:44:PHE:HZ	1:A:337:TYR:CZ	2.37	0.42
1:A:152:ILE:HD12	1:A:194:LYS:O	2.20	0.42
1:A:202:LYS:HE3	1:A:215:VAL:HG21	2.02	0.42
1:A:238:SER:HA	1:A:241:LEU:CD1	2.50	0.42
1:A:367:ARG:CZ	1:A:388:LEU:O	2.68	0.42
1:A:409:HIS:HA	1:A:412:TYR:CD2	2.53	0.42
1:A:484:GLU:HG2	1:C:392:ARG:HD3	2.01	0.42
1:A:649:TRP:O	1:A:653:PHE:HB3	2.18	0.42
1:B:476:PHE:CZ	1:B:501:PHE:CG	3.06	0.42
1:C:113:ASP:OD2	1:C:322:GLN:HG3	2.18	0.42
1:C:142:PRO:O	1:C:229:VAL:HG21	2.20	0.42
1:C:152:ILE:HD12	1:C:195:THR:HA	2.01	0.42
1:C:414:LEU:O	1:C:479:PHE:CE1	2.71	0.42
1:D:54:MET:CE	1:D:292:LEU:HB3	2.49	0.42
1:D:71:ASP:O	1:D:75:GLU:CB	2.67	0.42
1:D:97:LEU:HA	1:D:242:HIS:CG	2.54	0.42
1:D:402:LEU:HA	1:D:405:LEU:HD12	2.00	0.42
1:D:552:LEU:O	1:D:556:VAL:CG2	2.67	0.42
2:F:311:ILE:CG1	2:F:421:ILE:HG12	2.49	0.42
2:F:335:ILE:HG22	2:F:335:ILE:O	2.19	0.42
2:F:420:LEU:HD11	2:F:422:ALA:HB2	2.01	0.42
2:G:318:SER:HB2	2:G:457:GLU:OE1	2.19	0.42
2:G:373:LEU:CD2	2:G:412:LEU:HD21	2.47	0.42
1:A:100:ILE:HD11	1:A:237:SER:HB2	2.01	0.42
1:A:234:ILE:HD13	1:A:267:VAL:CG1	2.50	0.42
1:A:251:GLY:C	1:A:252:ILE:HG13	2.44	0.42
1:A:475:CYS:O	1:A:479:PHE:HD2	1.97	0.42
1:A:562:CYS:HB3	1:A:567:TYR:CE2	2.54	0.42
1:A:641:SER:OG	1:A:642:ARG:N	2.51	0.42
1:A:649:TRP:HZ3	1:A:704:VAL:HB	1.85	0.42
1:B:71:ASP:O	1:B:75:GLU:HB2	2.19	0.42
1:B:100:ILE:HD11	1:B:237:SER:HB2	2.02	0.42
1:C:76:PHE:CG	1:C:276:PHE:CZ	3.07	0.42
1:C:582:PHE:CE1	1:C:583:SER:O	2.72	0.42
1:D:227:THR:HA	1:D:230:LEU:HB3	2.02	0.42
1:D:556:VAL:O	1:D:560:ILE:N	2.50	0.42
1:D:649:TRP:CZ3	1:D:704:VAL:HB	2.53	0.42
2:F:324:GLU:O	2:F:328:THR:HG23	2.19	0.42
2:G:319:LYS:HE3	2:G:423:SER:HB2	2.00	0.42
2:G:362:HIS:HB3	2:G:379:LYS:NZ	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:330:MET:O	2:H:331:LEU:C	2.61	0.42
1:B:563:LEU:N	1:B:567:TYR:HD2	2.18	0.42
1:C:209:GLN:H	1:C:210:TRP:HA	1.82	0.42
1:C:252:ILE:HG22	1:C:253:ALA:N	2.34	0.42
1:C:563:LEU:HD23	1:C:567:TYR:CG	2.54	0.42
1:C:564:VAL:O	1:C:568:LEU:HD21	2.19	0.42
1:D:202:LYS:C	1:D:206:THR:O	2.62	0.42
2:E:416:HIS:O	2:E:417:ASN:C	2.63	0.42
2:F:356:THR:OG1	2:F:365:THR:CG2	2.68	0.42
2:F:412:LEU:O	2:F:415:LEU:N	2.53	0.42
2:G:397:SER:CB	2:G:400:LEU:H	2.32	0.42
2:G:397:SER:HB3	2:G:400:LEU:HD12	2.02	0.42
2:H:331:LEU:O	2:H:336:HIS:NE2	2.52	0.42
2:H:410:GLY:O	2:H:414:SER:HB3	2.19	0.42
1:A:118:PHE:HB3	1:A:220:LYS:HE2	2.02	0.42
1:A:342:SER:O	1:A:345:CYS:CB	2.68	0.42
1:A:416:LEU:HA	1:A:567:TYR:HE1	1.84	0.42
1:B:75:GLU:O	1:B:79:LYS:HG3	2.19	0.42
1:B:341:LEU:HD21	1:B:365:ASN:HB2	2.00	0.42
1:B:446:ASN:HA	1:B:569:LEU:HD21	2.02	0.42
1:C:636:LEU:O	1:C:639:GLU:N	2.50	0.42
1:D:314:PHE:CD2	1:D:324:PHE:HB2	2.54	0.42
1:D:372:PHE:HA	1:D:375:TYR:HB3	2.01	0.42
1:D:398:THR:O	1:D:402:LEU:HG	2.19	0.42
1:D:591:HIS:HA	2:F:445:TRP:H	1.85	0.42
1:D:632:ILE:O	1:D:636:LEU:HG	2.20	0.42
2:E:398:GLN:CG	2:E:401:ARG:HG3	2.50	0.42
2:F:347:SER:N	2:F:350:SER:OG	2.45	0.42
1:A:305:LYS:O	1:A:309:VAL:HG23	2.20	0.42
1:A:367:ARG:NE	1:A:388:LEU:O	2.52	0.42
1:A:381:SER:HB3	1:A:382:GLU:H	1.52	0.42
1:A:387:LEU:HD23	1:A:394:LEU:HA	2.02	0.42
1:A:408:TYR:HB3	1:A:412:TYR:HE2	1.84	0.42
1:A:694:ILE:CG1	1:A:704:VAL:HG13	2.49	0.42
1:B:152:ILE:HD12	1:B:194:LYS:O	2.20	0.42
1:B:152:ILE:CG1	1:B:198:LYS:HG3	2.50	0.42
1:B:421:LYS:HZ1	1:B:482:TYR:HE2	1.67	0.42
1:C:162:ILE:O	1:C:162:ILE:HG22	2.19	0.42
1:C:286:THR:HG22	1:C:436:ARG:NE	2.34	0.42
1:C:402:LEU:HD21	1:C:576:LEU:HD13	2.02	0.42
1:D:104:ALA:CA	1:D:250:PHE:HD2	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:147:PHE:CE1	1:D:225:PHE:CE1	3.08	0.42
1:D:216:VAL:CG1	1:D:249:ILE:HG13	2.49	0.42
2:E:309:PHE:N	2:E:309:PHE:CD1	2.86	0.42
2:F:320:ARG:CZ	2:F:456:GLU:HB2	2.50	0.42
2:G:318:SER:HA	2:G:319:LYS:HZ1	1.85	0.42
2:H:298:PHE:HB3	2:H:330:MET:CG	2.49	0.42
1:A:106:VAL:O	1:A:278:SER:HB2	2.20	0.42
1:A:191:VAL:O	1:A:191:VAL:HG12	2.19	0.42
1:A:217:VAL:HG12	1:A:219:LEU:HD21	2.00	0.42
1:B:394:LEU:O	1:B:395:LYS:C	2.63	0.42
1:B:404:ASN:HB2	1:B:574:GLN:OE1	2.20	0.42
1:B:421:LYS:HB2	1:B:479:PHE:CZ	2.55	0.42
1:C:136:LEU:HB2	1:C:219:LEU:CD2	2.50	0.42
1:C:263:LEU:CD1	1:C:271:LEU:HD11	2.50	0.42
1:C:273:ILE:HG22	1:C:274:GLU:N	2.34	0.42
1:C:302:ILE:HG21	1:C:306:VAL:HG22	1.98	0.42
1:C:330:LEU:HD21	2:H:309:PHE:CE2	2.54	0.42
1:C:552:LEU:O	1:C:556:VAL:HB	2.19	0.42
1:C:695:LYS:O	1:C:697:THR:HG23	2.20	0.42
1:D:113:ASP:OD2	1:D:322:GLN:HG3	2.20	0.42
1:D:426:LEU:HD21	1:D:460:LEU:HG	2.01	0.42
1:D:685:VAL:HG13	1:D:704:VAL:HG21	2.01	0.42
2:F:453:PRO:CA	2:F:454:TYR:HB2	2.46	0.42
2:H:394:ASN:ND2	2:H:425:ASP:OD2	2.32	0.42
1:A:79:LYS:O	1:A:83:GLY:N	2.38	0.42
1:A:147:PHE:CE1	1:A:225:PHE:CZ	3.07	0.42
1:A:152:ILE:HD13	1:A:197:PRO:HD2	2.02	0.42
1:A:386:ALA:HB1	1:A:393:TYR:CB	2.50	0.42
1:A:569:LEU:CB	1:A:571:PRO:HD2	2.48	0.42
1:B:216:VAL:HG11	1:B:249:ILE:CD1	2.50	0.42
1:B:416:LEU:HA	1:B:567:TYR:HE1	1.84	0.42
1:B:555:ASN:HB3	1:B:559:PHE:CE2	2.55	0.42
1:C:131:PRO:CB	1:C:214:PRO:O	2.68	0.42
1:C:132:TYR:O	1:C:155:LEU:CD2	2.68	0.42
1:C:257:ILE:O	1:C:261:ARG:HG3	2.20	0.42
1:C:330:LEU:HD21	2:H:309:PHE:CD2	2.55	0.42
1:C:330:LEU:HD13	1:C:592:LEU:HD21	2.00	0.42
1:C:400:LEU:O	1:C:404:ASN:ND2	2.53	0.42
1:C:590:GLU:C	2:H:445:TRP:O	2.63	0.42
1:C:686:SER:O	1:C:689:GLU:HB2	2.19	0.42
1:D:41:LYS:HD2	1:D:44:PHE:HE2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:67:LYS:O	1:D:71:ASP:HB2	2.19	0.42
1:D:563:LEU:CA	1:D:567:TYR:HD2	2.33	0.42
2:F:309:PHE:N	2:F:309:PHE:CD1	2.87	0.42
2:H:320:ARG:HH22	2:H:457:GLU:CA	2.33	0.42
1:A:41:LYS:HD2	1:A:44:PHE:HE2	1.85	0.42
1:A:47:TYR:O	1:A:48:GLN:C	2.63	0.42
1:A:332:LEU:HD23	1:A:336:PHE:CD2	2.54	0.42
1:A:594:ALA:HB2	2:G:445:TRP:CE2	2.55	0.42
1:B:126:GLN:HB3	1:B:162:ILE:HD11	2.01	0.42
1:B:234:ILE:HD13	1:B:267:VAL:CG1	2.50	0.42
1:B:480:LYS:O	1:B:484:GLU:HG3	2.19	0.42
1:B:552:LEU:O	1:B:556:VAL:CG2	2.68	0.42
1:C:75:GLU:O	1:C:79:LYS:HG3	2.20	0.42
1:C:202:LYS:HE3	1:C:215:VAL:HG21	2.02	0.42
1:C:222:MET:SD	1:C:225:PHE:CD2	3.13	0.42
1:C:310:LEU:HB3	1:C:324:PHE:HE1	1.84	0.42
1:C:352:LYS:O	1:C:355:ILE:HB	2.20	0.42
1:C:591:HIS:CD2	2:H:445:TRP:O	2.73	0.42
1:C:687:GLU:OE2	2:H:454:TYR:CB	2.68	0.42
2:F:331:LEU:C	2:F:336:HIS:NE2	2.78	0.42
2:G:332:GLN:O	2:G:336:HIS:HD2	2.03	0.42
1:A:81:HIS:NE2	1:A:214:PRO:HB3	2.35	0.41
1:A:474:LYS:O	1:A:478:VAL:HG23	2.20	0.41
1:A:569:LEU:HB3	1:A:570:PRO:HD2	2.01	0.41
1:A:694:ILE:CD1	1:A:704:VAL:HG13	2.48	0.41
1:B:41:LYS:HD2	1:B:44:PHE:HE2	1.84	0.41
1:B:426:LEU:CD2	1:B:456:VAL:HG13	2.50	0.41
1:B:476:PHE:O	1:B:480:LYS:CB	2.63	0.41
1:C:376:VAL:HG13	1:C:384:GLN:NE2	2.35	0.41
1:C:426:LEU:HD21	1:C:460:LEU:HG	2.02	0.41
1:C:461:ARG:HG2	1:C:552:LEU:HD21	2.02	0.41
1:C:636:LEU:HD11	1:C:657:VAL:HG21	2.02	0.41
1:C:637:HIS:CD2	1:C:694:ILE:CG2	3.03	0.41
1:C:649:TRP:CZ3	1:C:704:VAL:HB	2.52	0.41
1:D:101:PRO:HA	1:D:271:LEU:O	2.20	0.41
1:D:199:MET:CE	1:D:243:GLU:HB3	2.50	0.41
1:D:419:LEU:HB2	1:D:567:TYR:CZ	2.55	0.41
1:D:552:LEU:O	1:D:556:VAL:HB	2.20	0.41
2:E:348:VAL:HG23	2:E:399:MET:HB2	2.03	0.41
2:F:362:HIS:O	2:F:363:MET:HG2	2.19	0.41
2:G:453:PRO:HB2	2:G:454:TYR:C	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:400:LEU:HD22	2:H:409:ILE:CD1	2.50	0.41
1:A:75:GLU:O	1:A:79:LYS:HG3	2.21	0.41
1:B:338:SER:O	1:B:339:GLN:CG	2.69	0.41
1:B:476:PHE:CE2	1:B:501:PHE:CG	3.08	0.41
1:B:480:LYS:O	1:B:484:GLU:CD	2.64	0.41
1:B:653:PHE:O	1:B:657:VAL:HB	2.20	0.41
1:C:152:ILE:HA	1:C:198:LYS:CG	2.50	0.41
1:C:255:SER:CB	1:C:256:PRO:CD	2.98	0.41
1:C:263:LEU:HD13	1:C:271:LEU:HD11	2.02	0.41
1:C:373:ARG:O	1:C:377:GLU:HG3	2.20	0.41
1:C:446:ASN:HB2	1:C:449:ASP:HB2	2.03	0.41
1:D:104:ALA:HA	1:D:250:PHE:CD2	2.52	0.41
1:D:255:SER:CB	1:D:256:PRO:CD	2.98	0.41
1:D:324:PHE:CE2	1:D:328:LEU:HD11	2.54	0.41
1:D:694:ILE:HD13	1:D:704:VAL:HG22	2.02	0.41
2:E:320:ARG:HH12	2:E:457:GLU:H	1.68	0.41
2:E:348:VAL:HG22	2:E:400:LEU:HD23	2.02	0.41
2:E:369:ILE:HG21	2:E:408:ILE:CD1	2.50	0.41
2:G:318:SER:HB2	2:G:454:TYR:H	1.86	0.41
2:G:320:ARG:NH2	2:G:457:GLU:HG3	2.35	0.41
2:G:388:LEU:HB3	2:G:418:ILE:HG22	2.02	0.41
2:G:390:LEU:CD2	2:G:418:ILE:HD12	2.50	0.41
2:G:395:LEU:HD12	2:G:400:LEU:HD13	2.02	0.41
2:H:321:ASP:O	2:H:325:ARG:HG3	2.20	0.41
2:H:453:PRO:CA	2:H:454:TYR:HB2	2.45	0.41
1:A:122:THR:HA	1:A:133:VAL:HG21	2.02	0.41
1:A:202:LYS:CE	1:A:215:VAL:CG2	2.98	0.41
1:A:255:SER:CB	1:A:256:PRO:CD	2.99	0.41
1:A:420:HIS:CE1	1:A:435:ILE:HG23	2.55	0.41
1:A:604:LEU:CD1	1:A:693:PHE:CZ	3.03	0.41
1:A:695:LYS:O	1:A:697:THR:HG23	2.21	0.41
1:B:58:ASN:ND2	1:B:325:ILE:HD11	2.35	0.41
1:B:141:CYS:CB	1:B:147:PHE:CZ	3.01	0.41
1:B:333:LEU:O	1:B:336:PHE:N	2.52	0.41
1:B:371:SER:O	1:B:575:PRO:HA	2.20	0.41
1:B:413:PHE:O	1:B:414:LEU:C	2.63	0.41
1:B:482:TYR:HA	1:B:486:HIS:HB2	2.01	0.41
1:C:370:PRO:HA	1:C:373:ARG:HB2	2.02	0.41
1:C:439:TYR:O	1:C:443:LEU:HD13	2.20	0.41
1:C:595:ALA:HB1	1:C:598:ILE:HD12	2.03	0.41
1:C:700:LYS:HB3	1:C:703:HIS:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:416:LEU:C	1:D:420:HIS:HD1	2.28	0.41
1:D:482:TYR:CD1	1:D:486:HIS:CG	3.08	0.41
1:D:570:PRO:CD	1:D:571:PRO:HD3	2.50	0.41
2:E:298:PHE:CD2	2:E:330:MET:CG	3.03	0.41
2:E:330:MET:O	2:E:331:LEU:C	2.62	0.41
2:E:356:THR:OG1	2:E:365:THR:CG2	2.68	0.41
2:F:342:PHE:O	2:F:344:PRO:HD3	2.20	0.41
2:F:396:ASP:O	2:F:401:ARG:NE	2.53	0.41
2:F:409:ILE:HG22	2:F:441:PHE:CE1	2.56	0.41
1:A:134:VAL:HG13	1:A:154:GLN:CD	2.46	0.41
1:A:199:MET:HG2	1:A:244:PHE:HE2	1.85	0.41
1:A:238:SER:HA	1:A:241:LEU:HG	2.02	0.41
1:A:263:LEU:CD1	1:A:271:LEU:HD11	2.50	0.41
1:A:283:GLU:O	1:A:287:THR:HG23	2.20	0.41
1:A:352:LYS:HG2	1:A:355:ILE:HD12	2.02	0.41
1:A:401:LEU:HD12	1:A:576:LEU:HD11	2.03	0.41
1:A:426:LEU:HD21	1:A:460:LEU:HG	2.02	0.41
1:A:548:LYS:O	1:A:552:LEU:HG	2.20	0.41
1:B:147:PHE:HE1	1:B:225:PHE:CZ	2.37	0.41
1:B:350:GLU:HG3	1:D:347:ASN:OD1	2.20	0.41
1:C:43:ARG:O	1:C:46:THR:OG1	2.36	0.41
1:C:152:ILE:HG23	1:C:197:PRO:C	2.44	0.41
1:C:394:LEU:O	1:C:395:LYS:C	2.61	0.41
1:C:476:PHE:CZ	1:C:501:PHE:CG	3.08	0.41
1:D:199:MET:HE1	1:D:203:LYS:HE3	2.01	0.41
1:D:405:LEU:HD21	1:D:575:PRO:O	2.21	0.41
1:D:453:TYR:OH	1:D:559:PHE:HD1	2.02	0.41
1:D:467:GLU:HG2	1:D:471:ILE:HD12	2.02	0.41
1:D:504:LEU:CD2	1:D:550:GLU:HB3	2.51	0.41
1:D:694:ILE:CB	1:D:704:VAL:HG13	2.49	0.41
2:E:362:HIS:O	2:E:363:MET:HG2	2.19	0.41
2:E:393:HIS:HA	2:E:423:SER:OG	2.21	0.41
2:E:454:TYR:O	2:E:458:THR:OG1	2.29	0.41
2:F:298:PHE:HB3	2:F:330:MET:CG	2.51	0.41
2:F:320:ARG:HH22	2:F:457:GLU:CA	2.34	0.41
2:F:335:ILE:CG2	2:F:388:LEU:HB2	2.51	0.41
2:F:352:LEU:O	2:F:355:ILE:HG22	2.20	0.41
2:G:326:PHE:CE2	2:G:421:ILE:CD1	3.04	0.41
1:A:97:LEU:HA	1:A:242:HIS:CG	2.55	0.41
1:A:337:TYR:CD1	2:G:300:LYS:HE3	2.56	0.41
1:B:107:LEU:HD23	1:B:278:SER:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:ILE:O	1:B:162:ILE:HG22	2.20	0.41
1:B:248:LEU:CD1	1:B:250:PHE:CE1	3.03	0.41
1:B:255:SER:CB	1:B:256:PRO:CD	2.98	0.41
1:B:314:PHE:O	1:B:319:PHE:HD1	2.03	0.41
1:C:70:PHE:CZ	1:C:117:THR:HB	2.55	0.41
1:C:304:GLU:O	1:C:308:GLN:HG3	2.21	0.41
1:C:467:GLU:HG2	1:C:471:ILE:HD12	2.01	0.41
1:C:637:HIS:CD2	1:C:694:ILE:HG22	2.55	0.41
1:D:144:MET:SD	1:D:232:ASP:CB	3.09	0.41
1:D:241:LEU:C	1:D:243:GLU:H	2.28	0.41
1:D:423:THR:HG21	1:D:438:LEU:HD21	2.02	0.41
1:D:555:ASN:HB3	1:D:559:PHE:CE2	2.55	0.41
1:D:597:ARG:CZ	1:D:708:THR:OG1	2.69	0.41
1:D:685:VAL:HG11	1:D:704:VAL:HG21	2.01	0.41
2:E:295:GLU:HA	2:E:298:PHE:CG	2.56	0.41
2:E:335:ILE:HG22	2:E:388:LEU:HD13	2.03	0.41
2:E:369:ILE:HA	2:E:372:GLN:CG	2.51	0.41
2:E:433:TRP:HB3	2:E:438:GLN:HG3	2.02	0.41
2:F:304:GLN:HA	2:F:307:LEU:HD12	2.03	0.41
2:F:320:ARG:O	2:F:324:GLU:HB2	2.21	0.41
2:F:352:LEU:CA	2:F:355:ILE:HG22	2.50	0.41
2:G:416:HIS:O	2:G:417:ASN:C	2.64	0.41
1:A:69:LEU:HD22	1:A:277:GLN:O	2.20	0.41
1:A:241:LEU:C	1:A:243:GLU:H	2.28	0.41
1:A:342:SER:CB	1:A:579:VAL:CG1	2.98	0.41
1:A:370:PRO:HA	1:A:373:ARG:HB2	2.02	0.41
1:A:419:LEU:HB2	1:A:567:TYR:OH	2.21	0.41
1:A:686:SER:O	1:A:690:LEU:HG	2.20	0.41
1:B:67:LYS:O	1:B:71:ASP:HB2	2.21	0.41
1:B:209:GLN:OE1	1:B:211:GLN:O	2.38	0.41
1:B:250:PHE:HB3	1:B:252:ILE:HD11	2.01	0.41
1:B:288:VAL:O	1:B:292:LEU:N	2.43	0.41
1:B:484:GLU:HB3	1:D:392:ARG:NE	2.35	0.41
1:B:497:PHE:O	1:B:500:GLN:HB2	2.21	0.41
1:B:554:GLU:HA	1:B:557:VAL:HB	2.02	0.41
1:C:74:ILE:O	1:C:78:GLN:HB2	2.20	0.41
1:D:44:PHE:HZ	1:D:337:TYR:CZ	2.39	0.41
1:D:305:LYS:O	1:D:309:VAL:HG23	2.21	0.41
1:D:342:SER:CB	1:D:579:VAL:CG1	2.98	0.41
1:D:707:LEU:HD12	1:D:707:LEU:N	2.35	0.41
2:G:295:GLU:HA	2:G:298:PHE:CG	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:380:PHE:O	2:H:383:ASP:O	2.39	0.41
1:A:59:GLU:O	1:A:63:GLU:HG3	2.20	0.41
1:A:147:PHE:CE2	1:A:229:VAL:CG1	3.03	0.41
1:A:209:GLN:OE1	1:A:211:GLN:O	2.39	0.41
1:A:266:ALA:O	1:A:270:LEU:HG	2.21	0.41
1:A:314:PHE:HD2	1:A:324:PHE:HB2	1.85	0.41
1:A:402:LEU:HD21	1:A:576:LEU:HD13	2.02	0.41
1:A:695:LYS:HG3	1:A:696:PRO:CD	2.50	0.41
1:B:121:LEU:HD21	1:B:125:LEU:HD12	2.03	0.41
1:B:370:PRO:C	1:B:372:PHE:N	2.78	0.41
1:B:416:LEU:HD12	1:B:567:TYR:CD1	2.56	0.41
1:C:125:LEU:O	1:C:131:PRO:CG	2.67	0.41
1:C:196:ASP:HB2	1:C:197:PRO:HD3	2.03	0.41
1:C:408:TYR:CE2	1:C:574:GLN:HG3	2.56	0.41
1:C:476:PHE:HB3	1:C:480:LYS:CE	2.51	0.41
1:C:497:PHE:O	1:C:500:GLN:N	2.54	0.41
1:C:586:HIS:O	1:C:590:GLU:HG3	2.20	0.41
1:C:588:LEU:O	1:C:591:HIS:N	2.52	0.41
1:D:147:PHE:HB2	1:D:233:PHE:CE1	2.56	0.41
1:D:152:ILE:CG2	1:D:197:PRO:HB2	2.50	0.41
1:D:350:GLU:O	1:D:354:ARG:HG2	2.20	0.41
1:D:393:TYR:O	1:D:397:GLU:HG3	2.21	0.41
1:D:453:TYR:CZ	1:D:563:LEU:HD13	2.56	0.41
1:D:476:PHE:CZ	1:D:501:PHE:CD2	3.09	0.41
1:D:563:LEU:HD23	1:D:567:TYR:CG	2.56	0.41
2:F:355:ILE:O	2:F:359:VAL:HG23	2.21	0.41
2:H:335:ILE:CG2	2:H:388:LEU:HB2	2.50	0.41
1:A:367:ARG:NH2	1:A:391:GLU:HG2	2.36	0.41
1:A:421:LYS:HB2	1:A:479:PHE:CZ	2.56	0.41
1:A:497:PHE:O	1:A:500:GLN:HB2	2.21	0.41
1:A:501:PHE:CD1	1:A:554:GLU:OE2	2.73	0.41
1:A:578:GLU:O	1:A:579:VAL:HB	2.21	0.41
1:B:482:TYR:CD1	1:B:486:HIS:CG	3.09	0.41
1:B:709:TRP:N	1:B:709:TRP:CD1	2.87	0.41
1:C:282:LYS:O	1:C:286:THR:HG23	2.21	0.41
1:C:418:CYS:O	1:C:422:PHE:CD2	2.74	0.41
1:C:419:LEU:HD23	1:C:438:LEU:HD23	2.02	0.41
1:C:600:LEU:HB3	1:C:693:PHE:HZ	1.86	0.41
1:D:694:ILE:HA	1:D:706:ARG:HA	2.03	0.41
2:F:320:ARG:NH1	2:F:457:GLU:CD	2.79	0.41
2:F:342:PHE:CE1	2:F:343:PHE:CD1	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:355:ILE:O	2:G:359:VAL:HG23	2.20	0.41
2:H:445:TRP:N	2:H:445:TRP:CD1	2.88	0.41
1:A:139:LYS:C	1:A:141:CYS:N	2.79	0.41
1:A:162:ILE:O	1:A:162:ILE:HG22	2.21	0.41
1:A:282:LYS:O	1:A:285:LEU:HB3	2.21	0.41
1:A:314:PHE:HA	1:A:318:ASP:O	2.21	0.41
1:A:335:HIS:HB2	1:A:582:PHE:CD1	2.56	0.41
1:A:369:LEU:C	1:A:369:LEU:HD12	2.46	0.41
1:A:423:THR:CG2	1:A:438:LEU:HD21	2.51	0.41
1:A:456:VAL:HA	1:A:459:LEU:HD12	2.02	0.41
1:A:476:PHE:CE2	1:A:501:PHE:CG	3.09	0.41
1:A:482:TYR:CD1	1:A:486:HIS:CG	3.09	0.41
1:A:700:LYS:HB3	1:A:703:HIS:CE1	2.56	0.41
1:B:47:TYR:O	1:B:48:GLN:C	2.64	0.41
1:B:50:ILE:HG12	1:B:298:PHE:CE1	2.55	0.41
1:B:131:PRO:HB3	1:B:214:PRO:O	2.21	0.41
1:B:132:TYR:C	1:B:158:CYS:SG	3.03	0.41
1:B:142:PRO:HD2	1:B:146:HIS:HD1	1.86	0.41
1:B:145:LYS:HG2	1:B:149:GLN:CD	2.46	0.41
1:B:221:ASP:OD1	1:B:221:ASP:N	2.52	0.41
1:B:251:GLY:C	1:B:252:ILE:HG13	2.46	0.41
1:B:282:LYS:HE3	1:B:319:PHE:CE2	2.56	0.41
1:B:299:PRO:HB2	1:B:345:CYS:SG	2.61	0.41
1:B:370:PRO:HA	1:B:373:ARG:HB2	2.02	0.41
1:B:373:ARG:O	1:B:377:GLU:HG3	2.21	0.41
1:B:425:SER:OG	1:B:471:ILE:HD13	2.20	0.41
1:B:570:PRO:CD	1:B:571:PRO:HD3	2.51	0.41
1:C:97:LEU:HD22	1:C:242:HIS:CB	2.51	0.41
1:C:217:VAL:N	1:C:247:ILE:O	2.46	0.41
1:C:217:VAL:HG12	1:C:219:LEU:HD21	2.02	0.41
1:C:244:PHE:O	1:C:246:LEU:N	2.51	0.41
1:C:375:TYR:CZ	1:C:401:LEU:HD21	2.54	0.41
1:C:404:ASN:O	1:C:408:TYR:HD2	2.04	0.41
1:C:482:TYR:HA	1:C:486:HIS:HB2	2.03	0.41
1:D:122:THR:HA	1:D:133:VAL:HG23	2.03	0.41
1:D:152:ILE:HG12	1:D:198:LYS:N	2.34	0.41
1:D:238:SER:HA	1:D:241:LEU:CD1	2.51	0.41
1:D:248:LEU:CD1	1:D:250:PHE:CE1	3.04	0.41
1:D:252:ILE:HG22	1:D:253:ALA:N	2.35	0.41
1:D:370:PRO:C	1:D:372:PHE:N	2.79	0.41
1:D:554:GLU:HA	1:D:557:VAL:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:572:GLU:O	1:D:573:THR:HG23	2.20	0.41
1:D:688:LEU:HD12	1:D:691:LEU:HD12	2.03	0.41
2:E:327:ARG:HA	2:E:331:LEU:HD12	2.03	0.41
2:E:355:ILE:HD11	2:E:388:LEU:HD21	2.03	0.41
2:E:446:TYR:HB2	2:E:448:THR:HG23	2.03	0.41
2:F:329:THR:O	2:F:332:GLN:CD	2.64	0.41
2:F:331:LEU:HD11	2:F:391:LEU:CD1	2.49	0.41
2:G:309:PHE:HB2	2:G:444:LEU:HD11	2.03	0.41
2:G:318:SER:HA	2:G:319:LYS:NZ	2.36	0.41
2:G:320:ARG:NE	2:G:456:GLU:HB2	2.36	0.41
2:G:330:MET:O	2:G:331:LEU:C	2.62	0.41
2:H:398:GLN:C	2:H:399:MET:HE2	2.45	0.41
1:A:54:MET:HE3	1:A:292:LEU:HD13	2.03	0.41
1:A:126:GLN:HB3	1:A:162:ILE:CD1	2.51	0.41
1:A:282:LYS:O	1:A:286:THR:HG23	2.21	0.41
1:A:306:VAL:O	1:A:310:LEU:HB2	2.21	0.41
1:A:332:LEU:HD23	1:A:336:PHE:HD2	1.86	0.41
1:B:118:PHE:HB3	1:B:220:LYS:HE2	2.03	0.41
1:B:238:SER:HA	1:B:241:LEU:CD1	2.51	0.41
1:B:252:ILE:CD1	1:B:259:ILE:HD11	2.51	0.41
1:B:563:LEU:CA	1:B:567:TYR:HD2	2.34	0.41
1:C:103:ALA:O	1:C:250:PHE:HD2	2.04	0.41
1:C:151:LEU:CG	1:C:198:LYS:HD2	2.47	0.41
1:D:50:ILE:HG12	1:D:298:PHE:CD1	2.56	0.41
1:D:273:ILE:HG22	1:D:274:GLU:N	2.35	0.41
1:D:476:PHE:CD2	1:D:476:PHE:N	2.89	0.41
1:D:504:LEU:CD1	1:D:554:GLU:CD	2.95	0.41
2:G:356:THR:OG1	2:G:365:THR:CG2	2.68	0.41
2:H:377:VAL:HG22	2:H:415:LEU:HD13	2.03	0.41
1:A:209:GLN:NE2	1:A:213:PRO:HG3	2.36	0.40
1:A:219:LEU:CB	1:A:222:MET:HG2	2.51	0.40
1:A:222:MET:HG3	1:A:250:PHE:HD1	1.83	0.40
1:A:252:ILE:HG22	1:A:253:ALA:N	2.36	0.40
1:A:350:GLU:HG3	1:C:347:ASN:OD1	2.21	0.40
1:A:555:ASN:O	1:A:558:ASN:N	2.54	0.40
1:B:60:ARG:O	1:B:63:GLU:HB2	2.21	0.40
1:B:264:PRO:HG2	1:B:267:VAL:HG23	2.03	0.40
1:B:387:LEU:HD23	1:B:394:LEU:HA	2.03	0.40
1:B:589:ARG:HG3	1:B:593:ASN:OD1	2.22	0.40
1:B:689:GLU:CG	1:B:694:ILE:HD11	2.47	0.40
1:C:107:LEU:HD22	1:C:114:HIS:NE2	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:219:LEU:CD1	1:C:222:MET:SD	3.09	0.40
1:C:448:TRP:CZ2	1:C:559:PHE:CD1	3.09	0.40
1:C:480:LYS:O	1:C:484:GLU:HG3	2.19	0.40
1:C:683:ARG:HG3	1:C:687:GLU:OE2	2.22	0.40
1:C:688:LEU:O	1:C:693:PHE:N	2.55	0.40
1:C:694:ILE:CB	1:C:704:VAL:HG13	2.51	0.40
1:D:76:PHE:CG	1:D:276:PHE:CZ	3.09	0.40
1:D:279:LEU:HD22	1:D:283:GLU:OE1	2.20	0.40
1:D:321:VAL:O	1:D:325:ILE:HB	2.21	0.40
1:D:440:CYS:O	1:D:444:GLU:HG3	2.21	0.40
1:D:491:ALA:O	1:D:492:LYS:HB2	2.21	0.40
1:D:555:ASN:O	1:D:558:ASN:N	2.54	0.40
2:E:309:PHE:CE2	2:E:442:ASN:ND2	2.89	0.40
2:F:287:LEU:CD2	2:F:451:TYR:HB2	2.51	0.40
2:G:336:HIS:HA	2:G:389:PHE:O	2.21	0.40
2:H:340:ASN:HB2	2:H:343:PHE:CD2	2.57	0.40
2:H:352:LEU:O	2:H:365:THR:CG2	2.69	0.40
2:H:390:LEU:HG	2:H:419:TYR:O	2.21	0.40
1:A:97:LEU:HD23	1:A:242:HIS:CG	2.56	0.40
1:A:296:THR:CB	1:A:410:MET:SD	3.09	0.40
1:A:341:LEU:HD21	1:A:365:ASN:HB2	2.03	0.40
1:A:564:VAL:O	1:A:568:LEU:HD11	2.21	0.40
1:A:600:LEU:O	1:A:601:HIS:C	2.64	0.40
1:B:252:ILE:HG22	1:B:253:ALA:N	2.35	0.40
1:B:257:ILE:O	1:B:261:ARG:HG3	2.21	0.40
1:B:497:PHE:CD1	1:B:557:VAL:CG1	3.03	0.40
1:B:578:GLU:O	1:B:579:VAL:HB	2.20	0.40
1:C:144:MET:SD	1:C:229:VAL:HA	2.61	0.40
1:C:238:SER:HA	1:C:241:LEU:CG	2.51	0.40
1:C:343:VAL:HG13	1:C:354:ARG:HH11	1.87	0.40
1:D:310:LEU:HB3	1:D:324:PHE:HE1	1.86	0.40
1:D:421:LYS:HZ1	1:D:482:TYR:HE2	1.68	0.40
1:D:472:LEU:O	1:D:476:PHE:HD2	2.03	0.40
1:D:599:ALA:O	1:D:603:ALA:HB2	2.21	0.40
1:D:600:LEU:HB3	1:D:693:PHE:HZ	1.86	0.40
2:E:318:SER:HB2	2:E:454:TYR:H	1.86	0.40
2:E:331:LEU:HB3	2:E:336:HIS:CE1	2.57	0.40
2:E:340:ASN:O	2:E:343:PHE:HB2	2.21	0.40
2:E:347:SER:O	2:E:350:SER:N	2.55	0.40
2:F:352:LEU:HA	2:F:355:ILE:CG2	2.50	0.40
2:G:319:LYS:HE3	2:G:423:SER:CB	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:433:TRP:HB3	2:G:438:GLN:CG	2.51	0.40
2:G:446:TYR:O	2:G:447:GLU:C	2.64	0.40
2:H:341:GLY:N	2:H:393:HIS:O	2.45	0.40
2:H:396:ASP:O	2:H:401:ARG:NE	2.55	0.40
1:A:221:ASP:OD1	1:A:221:ASP:N	2.51	0.40
1:A:552:LEU:O	1:A:556:VAL:CG2	2.69	0.40
1:A:685:VAL:O	1:A:689:GLU:HG3	2.21	0.40
1:B:109:VAL:O	1:B:109:VAL:HG22	2.21	0.40
1:B:369:LEU:C	1:B:369:LEU:HD12	2.46	0.40
1:B:386:ALA:CB	1:B:393:TYR:HB3	2.51	0.40
1:B:419:LEU:HB2	1:B:567:TYR:OH	2.21	0.40
1:B:420:HIS:CD2	1:B:435:ILE:HG12	2.56	0.40
1:C:126:GLN:HB3	1:C:162:ILE:HD11	2.03	0.40
1:C:504:LEU:CD1	1:C:554:GLU:OE1	2.69	0.40
1:C:645:ASN:HA	1:C:703:HIS:NE2	2.36	0.40
1:C:700:LYS:HD3	1:C:703:HIS:NE2	2.35	0.40
1:D:152:ILE:HG21	1:D:197:PRO:HD2	2.03	0.40
1:D:241:LEU:HB3	1:D:242:HIS:CD2	2.57	0.40
1:D:364:GLU:O	1:D:368:ARG:HG3	2.21	0.40
1:D:415:VAL:O	1:D:567:TYR:CE1	2.75	0.40
1:D:472:LEU:O	1:D:475:CYS:HB2	2.21	0.40
1:D:591:HIS:C	2:F:445:TRP:HD1	2.29	0.40
1:D:709:TRP:CD1	1:D:709:TRP:N	2.89	0.40
2:E:326:PHE:CE2	2:E:421:ILE:CD1	3.05	0.40
2:E:397:SER:CB	2:E:400:LEU:H	2.34	0.40
2:F:369:ILE:HG21	2:F:408:ILE:HG12	2.02	0.40
2:F:373:LEU:O	2:F:377:VAL:HG23	2.21	0.40
2:F:455:THR:CA	2:F:458:THR:HB	2.52	0.40
2:G:320:ARG:NH1	2:G:457:GLU:CD	2.77	0.40
2:G:393:HIS:HA	2:G:423:SER:OG	2.21	0.40
2:G:445:TRP:CD1	2:G:445:TRP:N	2.89	0.40
2:H:356:THR:OG1	2:H:365:THR:CG2	2.70	0.40
1:A:55:LYS:HA	1:A:58:ASN:HB2	2.03	0.40
1:A:199:MET:CE	1:A:243:GLU:OE1	2.69	0.40
1:A:208:SER:HB2	1:A:210:TRP:CE2	2.57	0.40
1:B:45:GLU:CD	1:D:49:LEU:HD23	2.46	0.40
1:B:144:MET:HE2	1:B:232:ASP:HB3	2.03	0.40
1:B:219:LEU:HD13	1:B:222:MET:SD	2.62	0.40
1:B:404:ASN:HB2	1:B:574:GLN:NE2	2.36	0.40
1:C:41:LYS:O	1:C:42:LEU:C	2.64	0.40
1:C:74:ILE:HD13	1:C:128:ASN:OD1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:62:GLN:O	1:D:66:ASN:CG	2.64	0.40
1:D:369:LEU:C	1:D:369:LEU:HD12	2.46	0.40
2:E:400:LEU:HD22	2:E:409:ILE:CD1	2.52	0.40
2:E:438:GLN:O	2:E:441:PHE:O	2.39	0.40
2:F:397:SER:CB	2:F:398:GLN:CA	2.99	0.40
2:F:446:TYR:HB2	2:F:448:THR:HG23	2.04	0.40
2:G:309:PHE:CE2	2:G:442:ASN:OD1	2.75	0.40
2:G:420:LEU:HD21	2:G:443:TRP:HH2	1.86	0.40
2:H:331:LEU:HD11	2:H:391:LEU:CG	2.51	0.40
1:A:106:VAL:HG13	1:A:253:ALA:O	2.20	0.40
1:A:135:SER:HB2	1:A:220:LYS:HE3	2.02	0.40
1:A:227:THR:HA	1:A:230:LEU:HB3	2.04	0.40
1:A:257:ILE:HG22	1:A:261:ARG:NE	2.36	0.40
1:A:284:HIS:HA	1:A:287:THR:OG1	2.22	0.40
1:A:306:VAL:HG12	1:A:585:ALA:CB	2.52	0.40
1:A:480:LYS:HG2	1:A:498:LEU:HD22	2.03	0.40
1:B:102:THR:HA	1:B:247:ILE:HG23	2.04	0.40
1:B:333:LEU:O	1:B:334:GLU:C	2.65	0.40
1:B:342:SER:O	1:B:345:CYS:CB	2.70	0.40
1:B:347:ASN:HD21	1:D:353:ARG:NH2	2.19	0.40
1:B:421:LYS:HE3	1:B:479:PHE:CE1	2.56	0.40
1:B:476:PHE:CZ	1:B:501:PHE:CD1	3.09	0.40
1:B:591:HIS:O	2:E:445:TRP:HD1	2.05	0.40
1:C:306:VAL:HG12	1:C:585:ALA:CB	2.52	0.40
1:C:378:LYS:O	1:C:379:GLN:HB2	2.21	0.40
1:C:479:PHE:HA	1:C:482:TYR:CD2	2.56	0.40
1:C:501:PHE:CE1	1:C:554:GLU:HB3	2.57	0.40
1:D:139:LYS:C	1:D:141:CYS:N	2.80	0.40
1:D:248:LEU:CD1	1:D:250:PHE:CZ	3.05	0.40
1:D:263:LEU:CD1	1:D:271:LEU:HD11	2.52	0.40
1:D:636:LEU:HD11	1:D:657:VAL:HG21	2.04	0.40
1:D:657:VAL:HG12	1:D:677:ILE:HD11	2.02	0.40
2:E:318:SER:HA	2:E:319:LYS:NZ	2.37	0.40
2:G:310:ASN:HB3	2:G:420:LEU:O	2.22	0.40
2:G:331:LEU:HD11	2:G:391:LEU:CG	2.51	0.40
2:G:350:SER:HA	2:G:353:ASN:HB2	2.04	0.40
2:G:388:LEU:O	2:G:418:ILE:HA	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	541/712 (76%)	460 (85%)	72 (13%)	9 (2%)	7	36
1	B	541/712 (76%)	463 (86%)	72 (13%)	6 (1%)	11	46
1	C	541/712 (76%)	462 (85%)	72 (13%)	7 (1%)	9	42
1	D	541/712 (76%)	464 (86%)	70 (13%)	7 (1%)	9	42
2	E	181/347 (52%)	161 (89%)	20 (11%)	0	100	100
2	F	181/347 (52%)	161 (89%)	20 (11%)	0	100	100
2	G	181/347 (52%)	161 (89%)	20 (11%)	0	100	100
2	H	181/347 (52%)	163 (90%)	18 (10%)	0	100	100
All	All	2888/4236 (68%)	2495 (86%)	364 (13%)	29 (1%)	12	48

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	VAL
1	A	130	THR
1	A	383	LYS
1	B	129	VAL
1	B	383	LYS
1	C	129	VAL
1	C	382	GLU
1	D	129	VAL
1	D	382	GLU
1	D	579	VAL
1	A	190	THR
1	A	381	SER
1	A	579	VAL
1	A	640	CYS
1	B	190	THR
1	B	579	VAL
1	B	640	CYS

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Mol	Chain	Res	Type
1	C	190	THR
1	C	579	VAL
1	C	640	CYS
1	D	190	THR
1	A	131	PRO
1	C	379	GLN
1	D	640	CYS
1	D	379	GLN
1	C	570	PRO
1	D	570	PRO
1	A	570	PRO
1	B	570	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	517/659 (78%)	502 (97%)	15 (3%)	37	58
1	B	517/659 (78%)	502 (97%)	15 (3%)	37	58
1	C	517/659 (78%)	504 (98%)	13 (2%)	42	62
1	D	517/659 (78%)	501 (97%)	16 (3%)	35	56
2	E	171/323 (53%)	166 (97%)	5 (3%)	37	58
2	F	171/323 (53%)	166 (97%)	5 (3%)	37	58
2	G	171/323 (53%)	165 (96%)	6 (4%)	32	53
2	H	171/323 (53%)	166 (97%)	5 (3%)	37	58
All	All	2752/3928 (70%)	2672 (97%)	80 (3%)	37	58

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	199	MET
1	A	248	LEU
1	A	272	CYS

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Mol	Chain	Res	Type
1	A	306	VAL
1	A	313	ILE
1	A	325	ILE
1	A	342	SER
1	A	381	SER
1	A	394	LEU
1	A	416	LEU
1	A	457	LEU
1	A	490	THR
1	A	644	ILE
1	A	704	VAL
1	A	706	ARG
1	B	199	MET
1	B	248	LEU
1	B	306	VAL
1	B	313	ILE
1	B	325	ILE
1	B	342	SER
1	B	347	ASN
1	B	381	SER
1	B	382	GLU
1	B	394	LEU
1	B	416	LEU
1	B	457	LEU
1	B	490	THR
1	B	704	VAL
1	B	706	ARG
1	C	110	ASN
1	C	248	LEU
1	C	306	VAL
1	C	313	ILE
1	C	325	ILE
1	C	342	SER
1	C	346	CYS
1	C	381	SER
1	C	394	LEU
1	C	416	LEU
1	C	457	LEU
1	C	704	VAL
1	C	706	ARG
1	D	110	ASN
1	D	199	MET

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Mol	Chain	Res	Type
1	D	248	LEU
1	D	306	VAL
1	D	313	ILE
1	D	325	ILE
1	D	342	SER
1	D	346	CYS
1	D	381	SER
1	D	385	VAL
1	D	394	LEU
1	D	416	LEU
1	D	457	LEU
1	D	637	HIS
1	D	704	VAL
1	D	706	ARG
2	E	319	LYS
2	E	388	LEU
2	E	418	ILE
2	E	423	SER
2	E	457	GLU
2	F	319	LYS
2	F	388	LEU
2	F	418	ILE
2	F	423	SER
2	F	457	GLU
2	G	319	LYS
2	G	388	LEU
2	G	418	ILE
2	G	423	SER
2	G	442	ASN
2	G	457	GLU
2	H	319	LYS
2	H	388	LEU
2	H	418	ILE
2	H	423	SER
2	H	457	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	347	ASN
1	A	384	GLN

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Mol	Chain	Res	Type
1	A	601	HIS
1	A	605	ASN
1	A	606	ASN
1	B	209	GLN
1	B	242	HIS
1	B	362	GLN
1	B	384	GLN
1	B	605	ASN
1	B	606	ASN
1	C	110	ASN
1	C	146	HIS
1	C	277	GLN
1	C	356	ASN
1	C	362	GLN
1	C	384	GLN
1	C	606	ASN
1	D	110	ASN
1	D	242	HIS
1	D	277	GLN
1	D	384	GLN
1	D	404	ASN
1	D	406	HIS
1	D	601	HIS
1	D	605	ASN
1	D	606	ASN
1	D	678	HIS
2	E	299	HIS
2	E	340	ASN
2	F	299	HIS
2	F	435	HIS
2	H	299	HIS
2	H	442	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	553/712 (77%)	-0.61	0 100 100	214, 295, 363, 401	0
1	B	553/712 (77%)	-0.61	0 100 100	208, 300, 363, 410	0
1	C	553/712 (77%)	-0.60	1 (0%) 91 84	219, 302, 365, 407	0
1	D	553/712 (77%)	-0.64	0 100 100	227, 299, 363, 406	0
2	E	183/347 (52%)	-0.53	2 (1%) 78 66	256, 307, 348, 381	0
2	F	183/347 (52%)	-0.68	0 100 100	254, 310, 353, 374	0
2	G	183/347 (52%)	-0.60	0 100 100	250, 306, 352, 375	0
2	H	183/347 (52%)	-0.60	0 100 100	248, 310, 349, 376	0
All	All	2944/4236 (69%)	-0.61	3 (0%) 92 87	208, 303, 360, 410	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	652	ALA	3.1
2	E	316	LEU	2.9
2	E	396	ASP	2.9

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.