



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:22 AM GMT

PDB ID : 2Q4J
Title : Ensemble refinement of the protein crystal structure of gene product from Arabidopsis thaliana At3g03250, a putative UDP-glucose pyrophosphorylase
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on : 2007-05-31
Resolution : 1.86 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

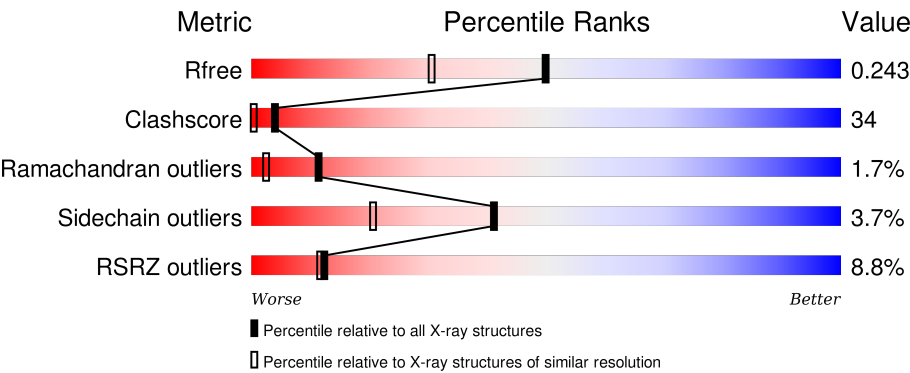
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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}	91344	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	1-A	469	<div><div>12%</div><div>53%</div><div>41%</div><div>• •</div></div>
1	1-B	469	<div><div>5%</div><div>46%</div><div>48%</div><div>• •</div></div>
1	2-A	469	<div><div>12%</div><div>47%</div><div>47%</div><div>• •</div></div>
1	2-B	469	<div><div>5%</div><div>52%</div><div>42%</div><div>• •</div></div>
1	3-A	469	<div><div>12%</div><div>54%</div><div>42%</div><div>• •</div></div>

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Mol	Chain	Length	Quality of chain
1	3-B	469	
1	4-A	469	
1	4-B	469	
1	5-A	469	
1	5-B	469	
1	6-A	469	
1	6-B	469	
1	7-A	469	
1	7-B	469	
1	8-A	469	
1	8-B	469	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 60344 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 Probable UTP-glucose-1-phosphate uridylyltransferase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	2-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	3-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	4-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	5-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	6-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	7-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	8-A	460	Total	C	N	O	S	0	0	0
			3579	2291	591	687	10			
1	1-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			
1	2-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			
1	3-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			
1	4-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			
1	5-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			
1	6-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			
1	7-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			
1	8-B	455	Total	C	N	O	S	0	0	0
			3543	2271	585	677	10			

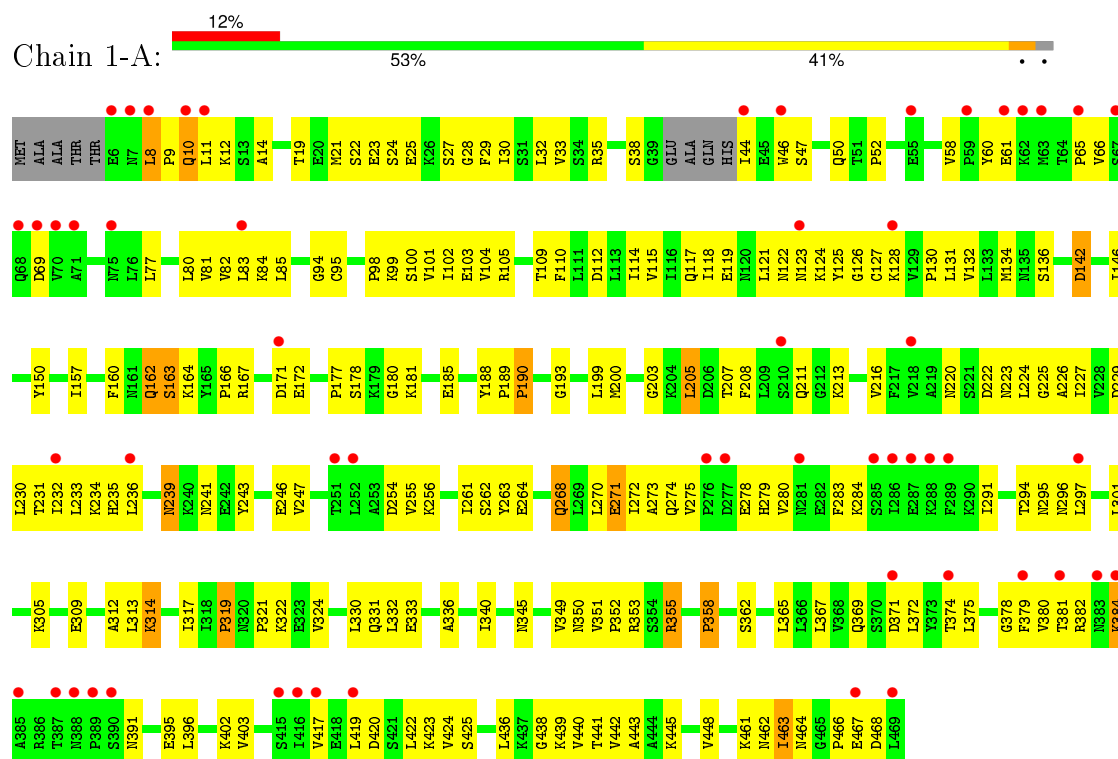
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	1-A	180	Total 180	O 180	0	0
2	2-A	182	Total 182	O 182	0	0
2	3-A	182	Total 182	O 182	0	0
2	4-A	183	Total 183	O 183	0	0
2	5-A	182	Total 182	O 182	0	0
2	6-A	182	Total 182	O 182	0	0
2	7-A	183	Total 183	O 183	0	0
2	8-A	183	Total 183	O 183	0	0
2	1-B	241	Total 241	O 241	0	0
2	2-B	239	Total 239	O 239	0	0
2	3-B	239	Total 239	O 239	0	0
2	4-B	238	Total 238	O 238	0	0
2	5-B	239	Total 239	O 239	0	0
2	6-B	239	Total 239	O 239	0	0
2	7-B	238	Total 238	O 238	0	0
2	8-B	238	Total 238	O 238	0	0

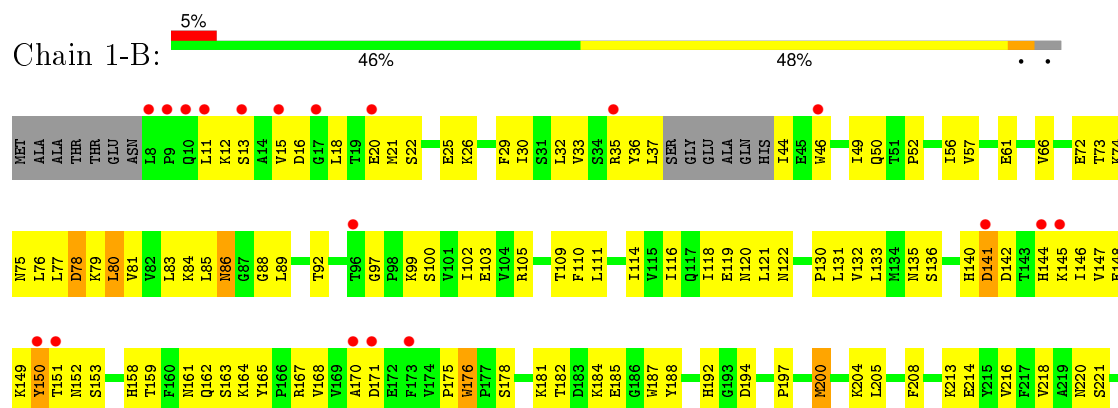
3 Residue-property plots

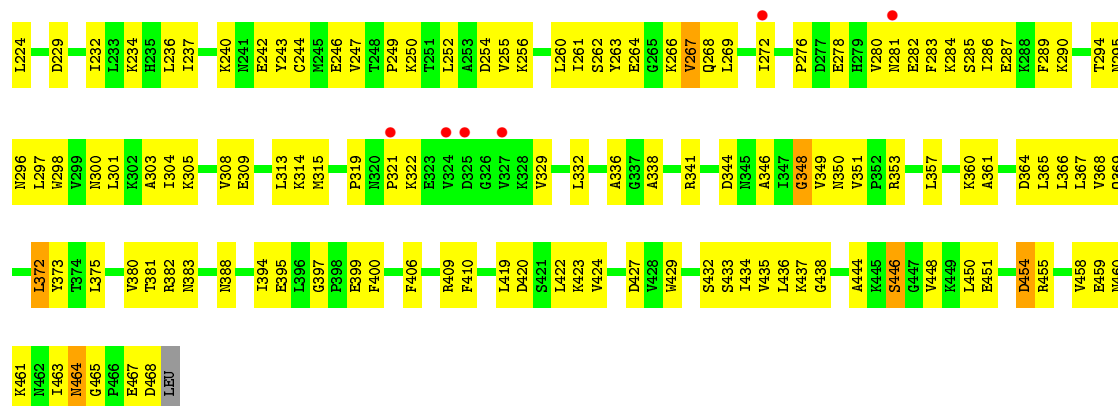
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Probable UTP-glucose-1-phosphate uridylyltransferase 2

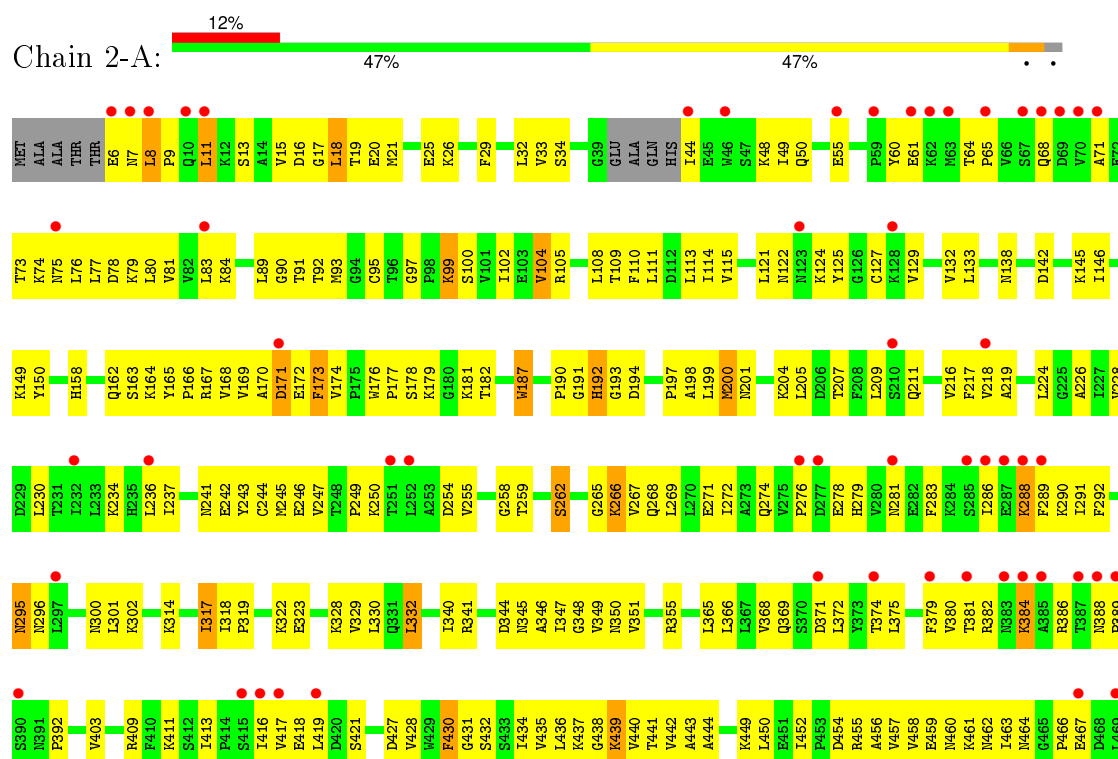


- Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

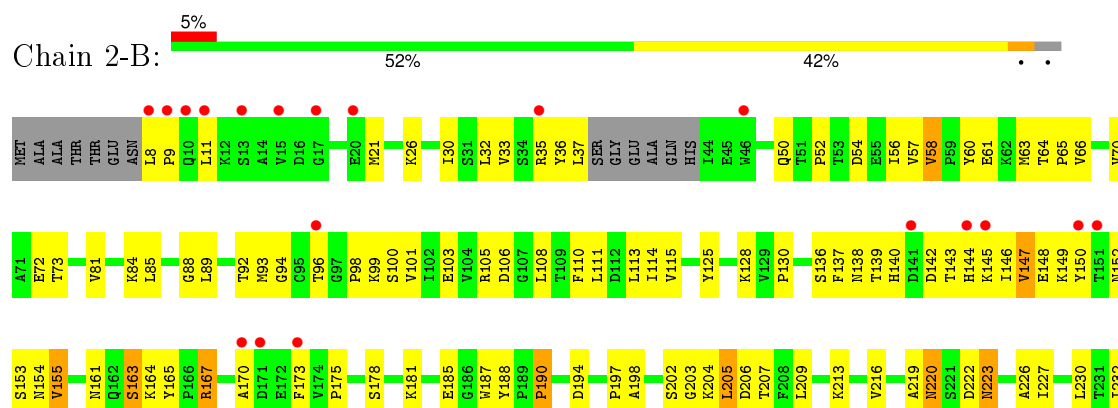


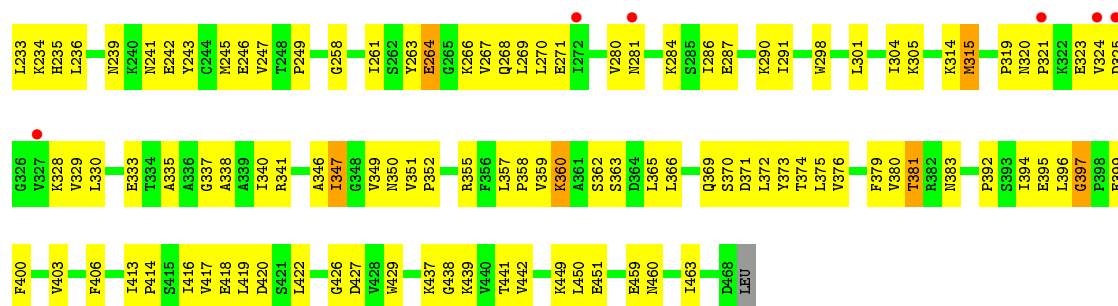


● Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

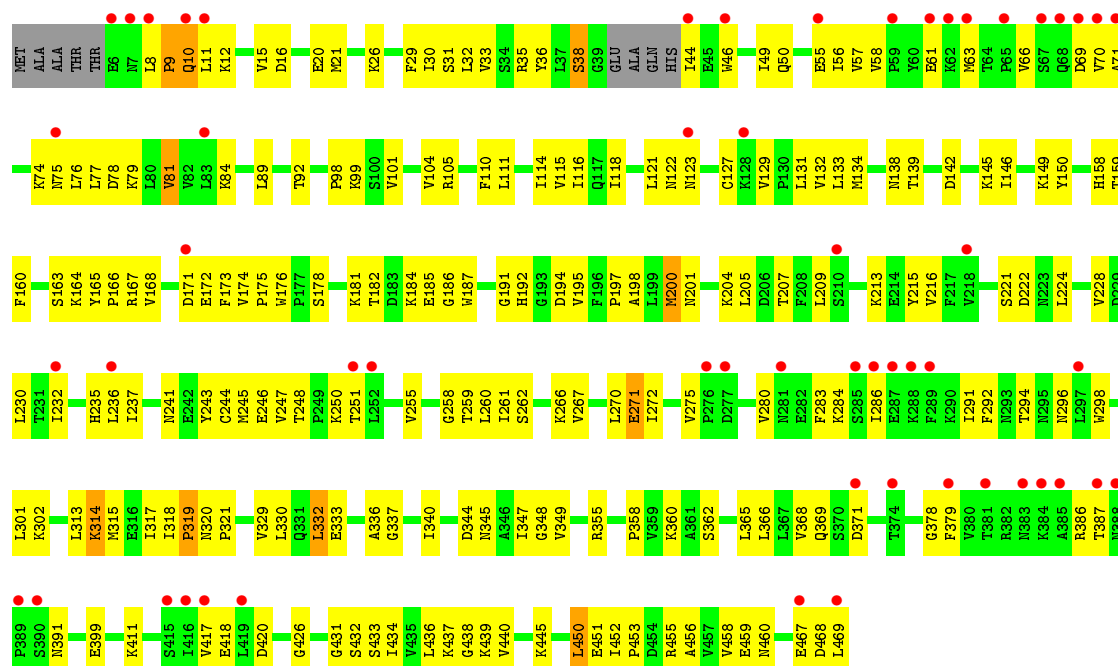


● Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

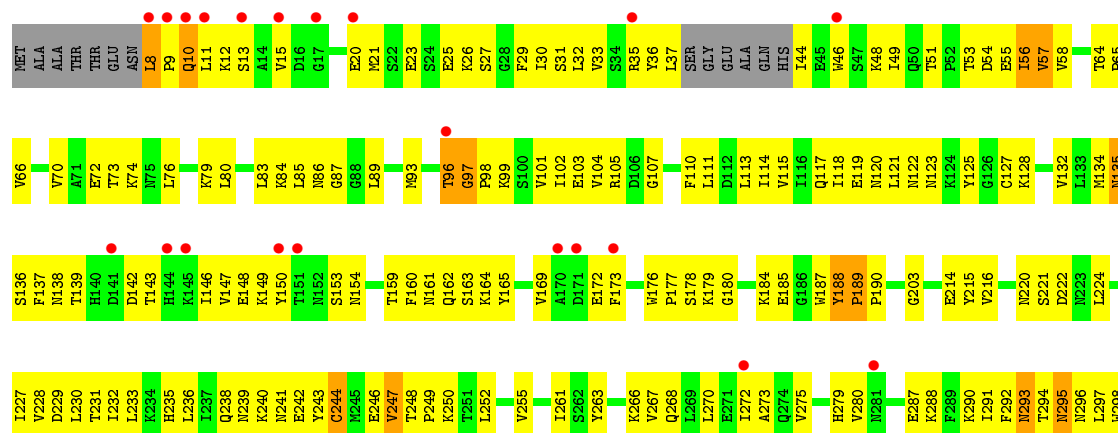


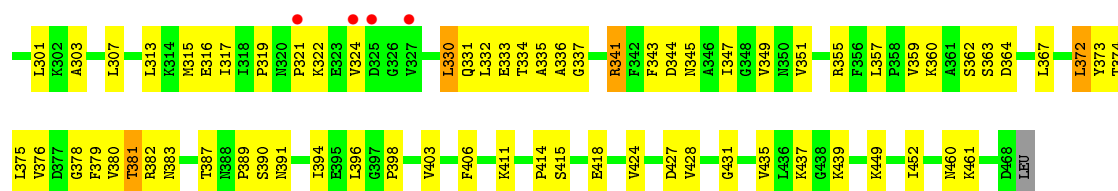


• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

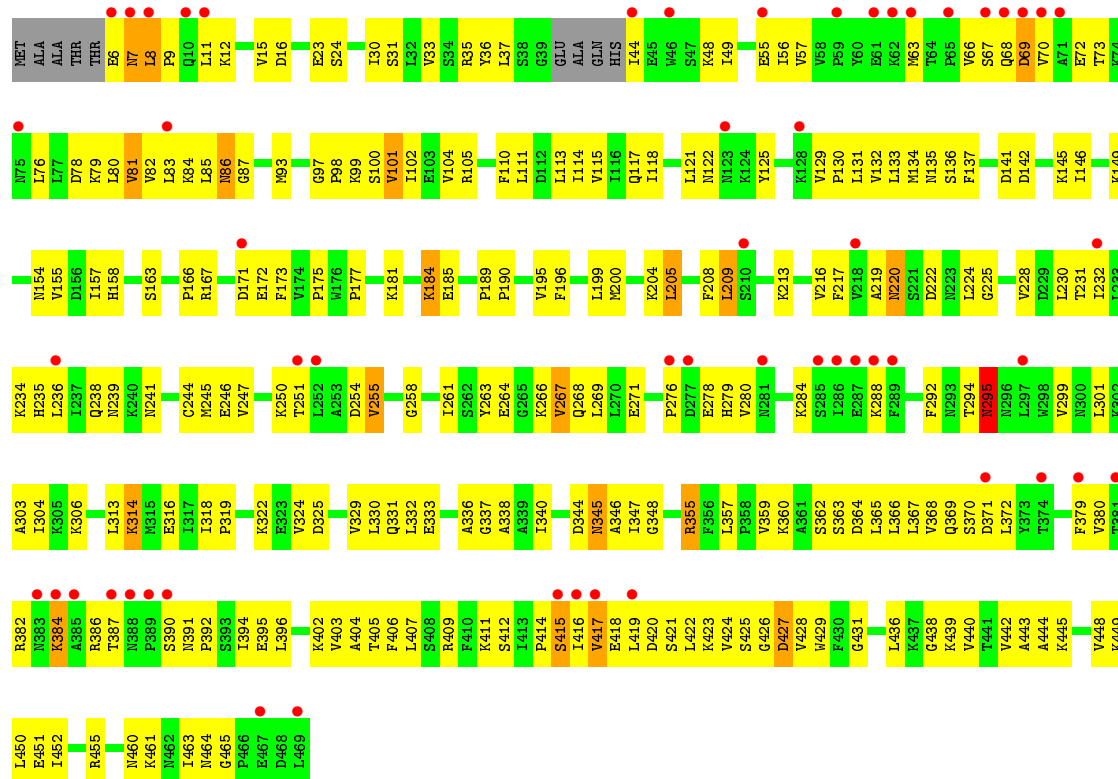


• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

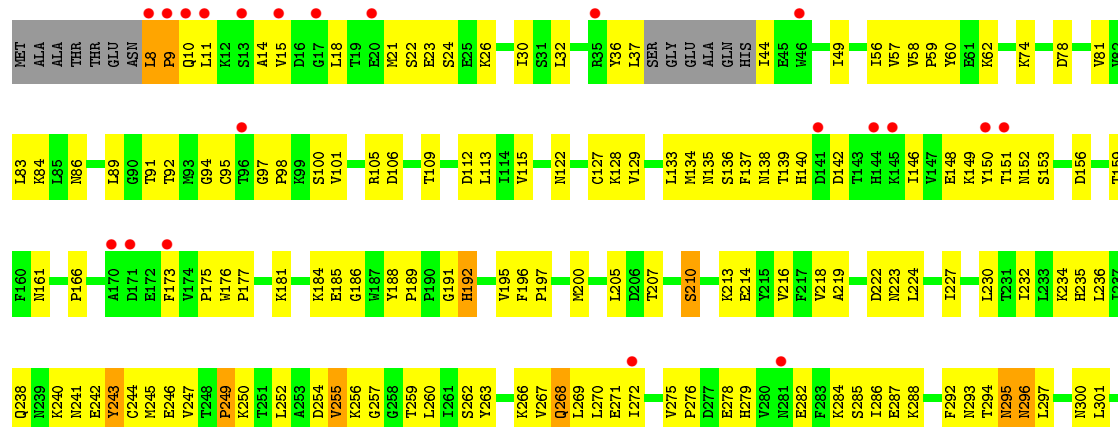


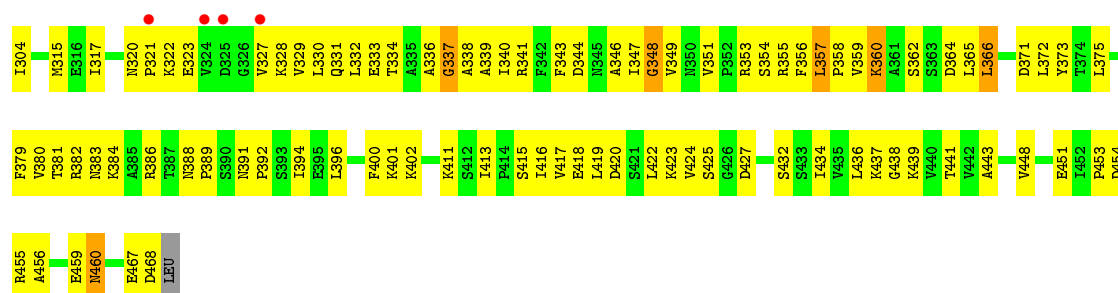


• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

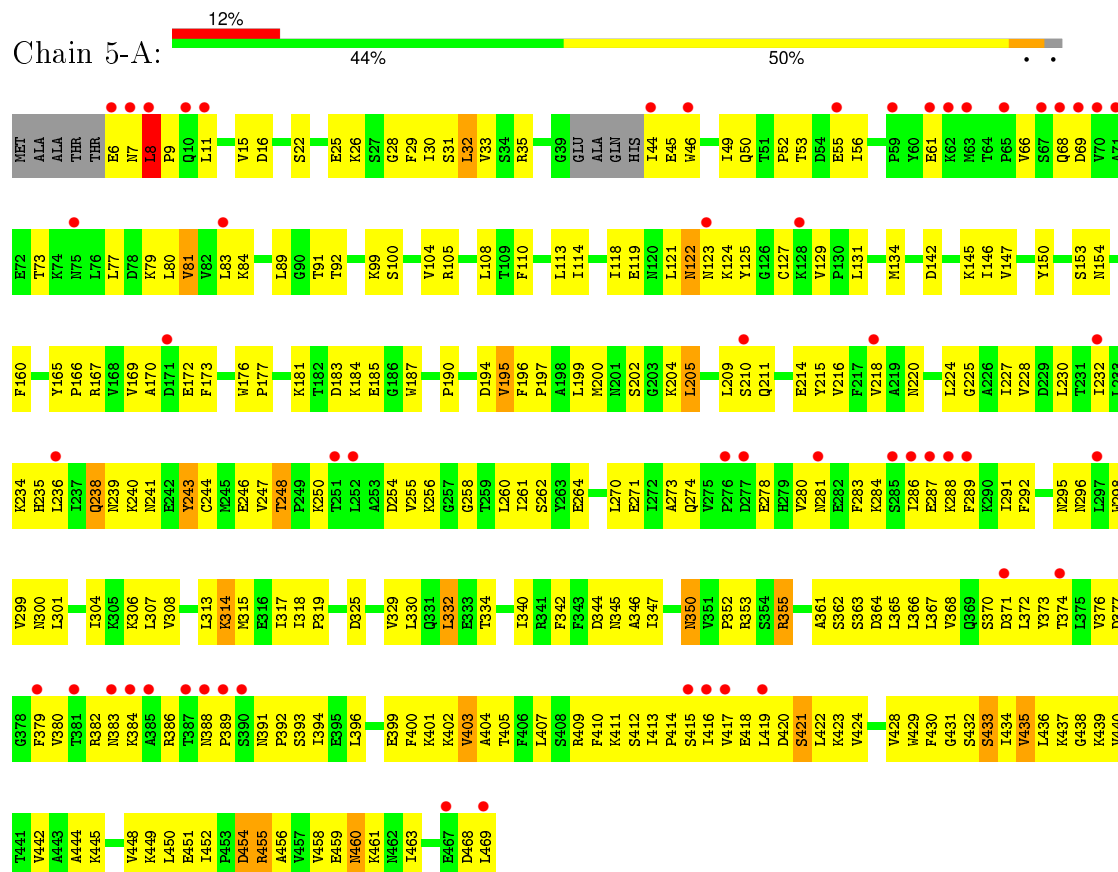


• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

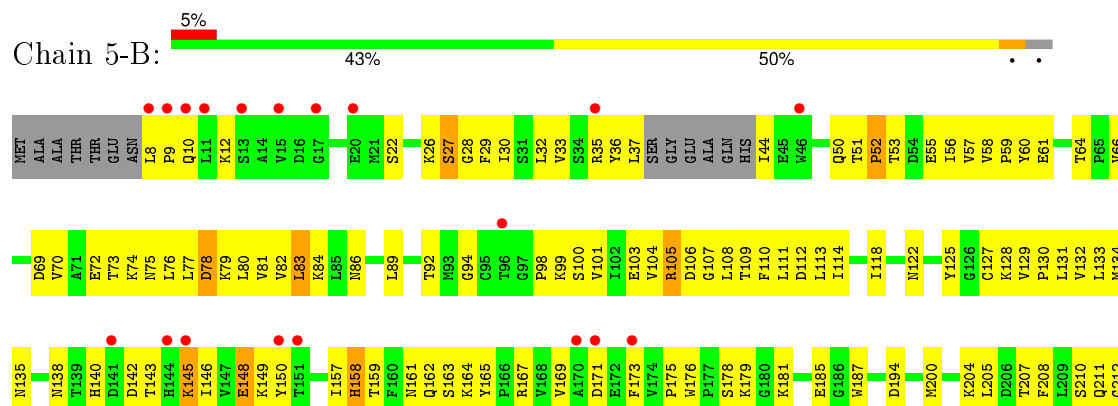


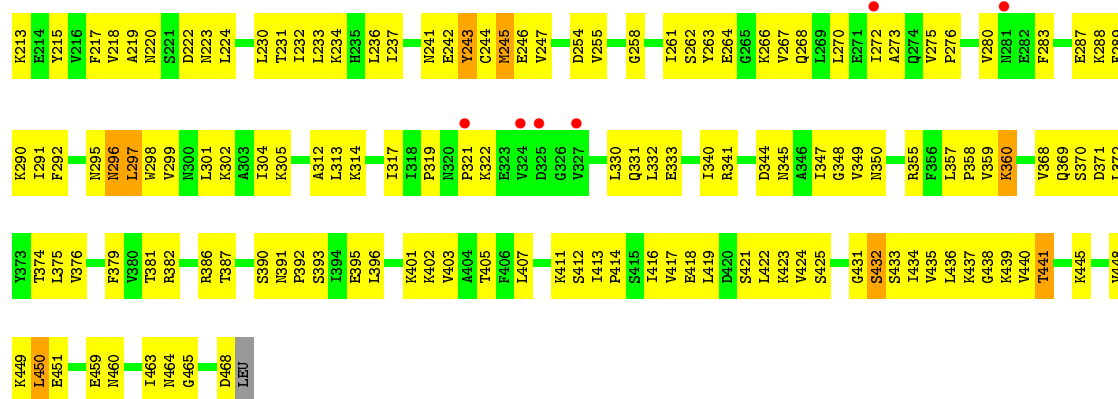


- Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

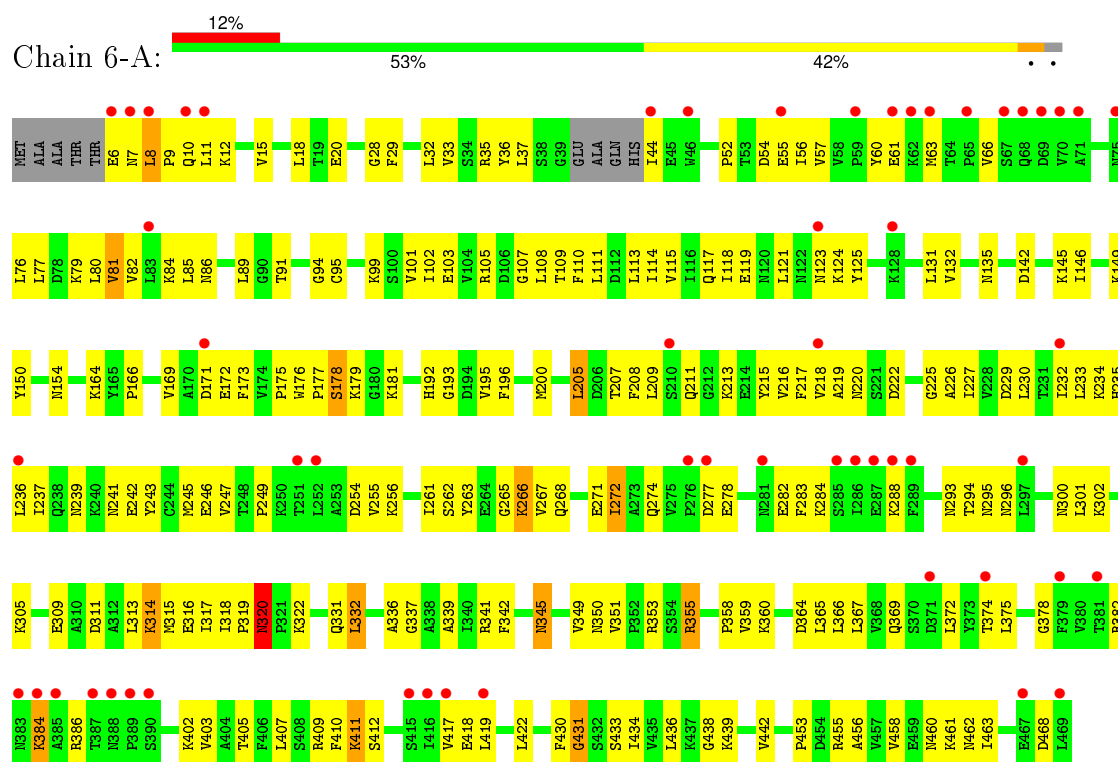


- Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2

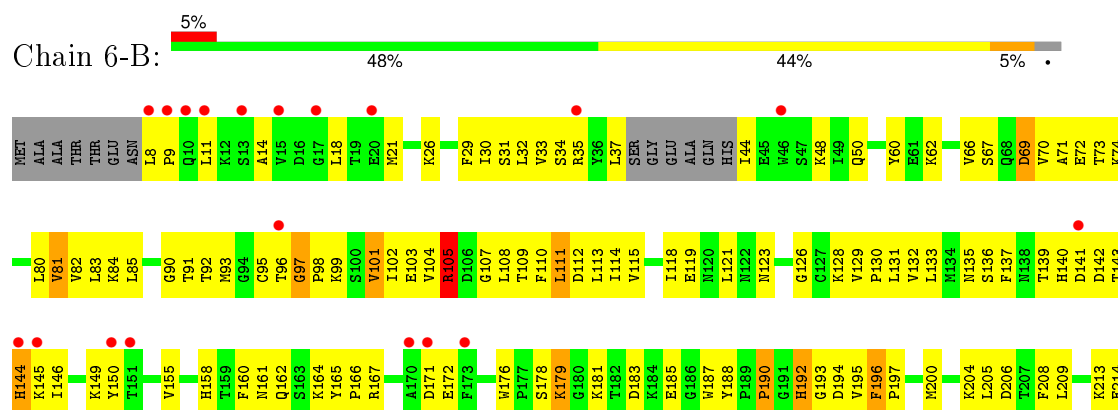


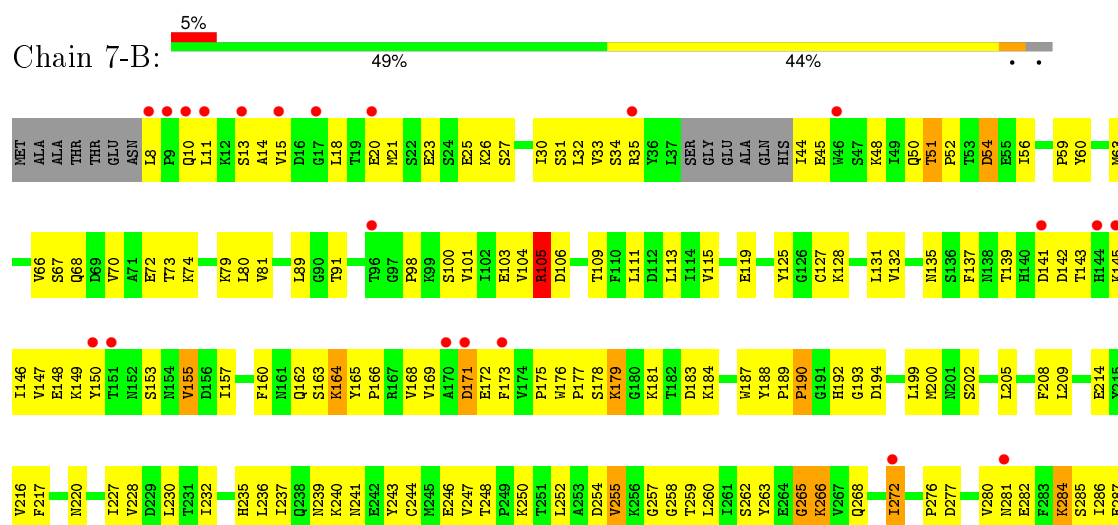


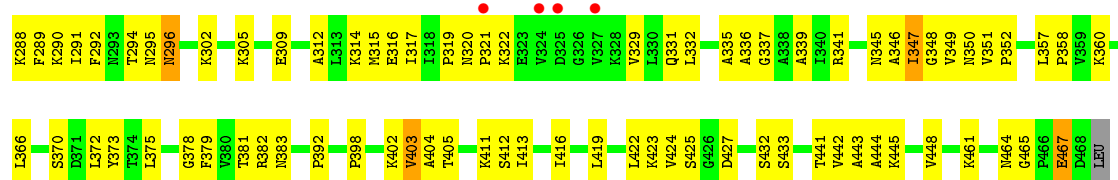
• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2



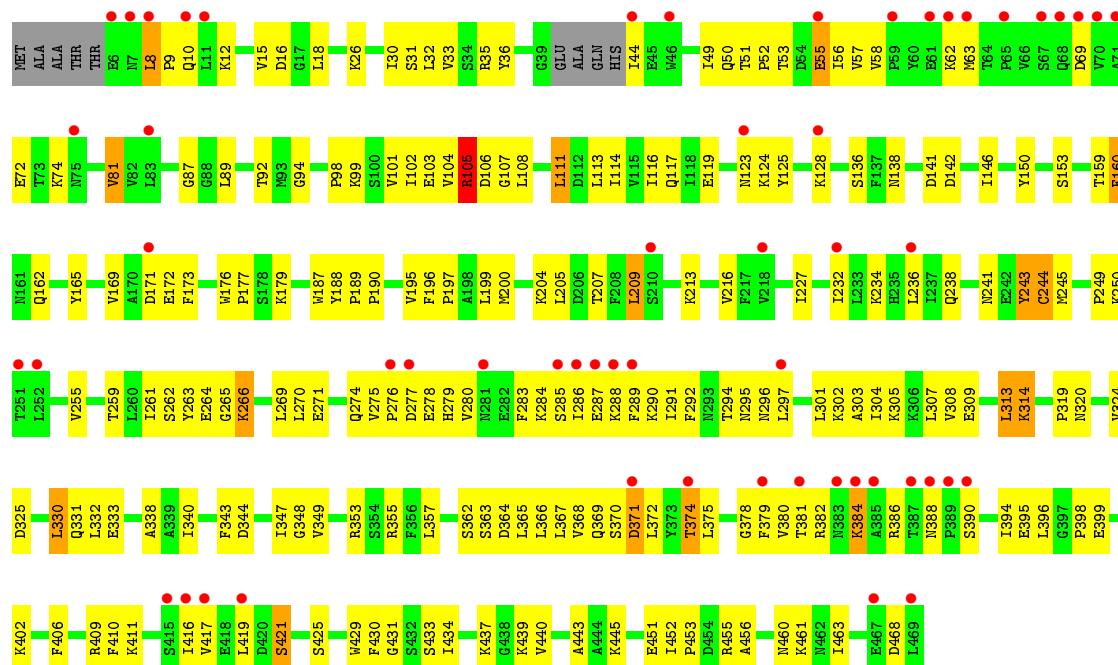
• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2



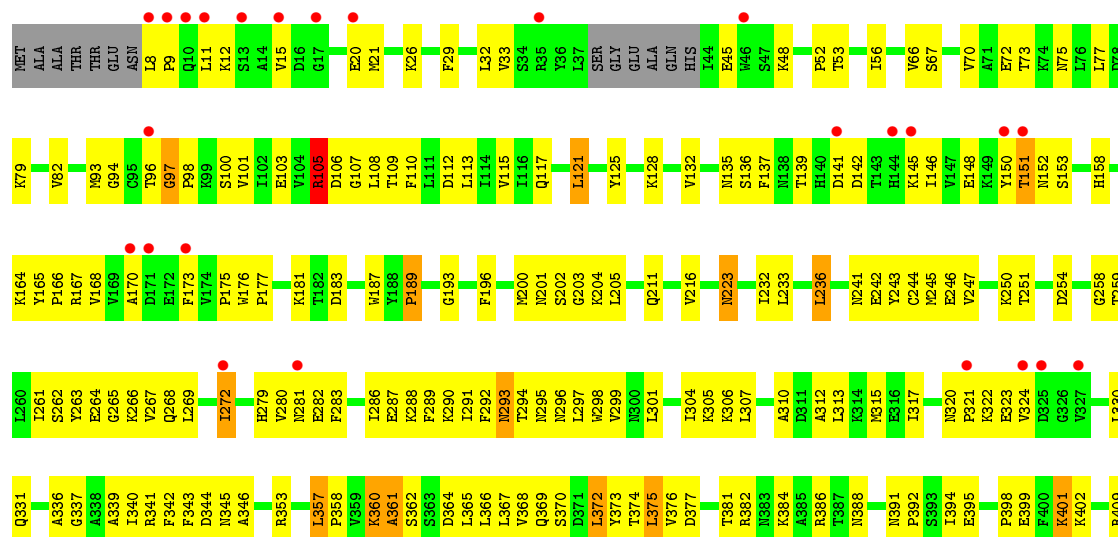




• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2



• Molecule 1: Probable UTP-glucose-1-phosphate uridylyltransferase 2



F410	F411	P414	L419	D420	S421	L422	K423	V424	S425	G426	W429	F430	G431	S432	S433	L434	V435	L436	K437	G438	V439	V440	T452	P453	D454	R455	L456	V457	V458	E459	W460	K461	V462	L463	D468	LEU
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	188.68Å 58.86Å 89.86Å 90.00° 100.40° 90.00°	Depositor
Resolution (Å)	37.37 – 1.86 37.37 – 1.86	Depositor EDS
% Data completeness (in resolution range)	97.6 (37.37-1.86) 97.7 (37.37-1.86)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 1.87Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.171 , 0.231 0.185 , 0.243	Depositor DCC
R_{free} test set	3986 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 66.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 79504 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	60344	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	1-A	0.48	0/3646	0.67	1/4942 (0.0%)
1	1-B	0.56	0/3610	0.73	2/4895 (0.0%)
1	2-A	0.49	0/3646	0.66	0/4942
1	2-B	0.55	1/3610 (0.0%)	0.71	1/4895 (0.0%)
1	3-A	0.47	0/3646	0.66	0/4942
1	3-B	0.55	0/3610	0.71	2/4895 (0.0%)
1	4-A	0.49	0/3646	0.66	0/4942
1	4-B	0.56	0/3610	0.73	2/4895 (0.0%)
1	5-A	0.50	0/3646	0.72	0/4942
1	5-B	0.60	0/3610	0.75	1/4895 (0.0%)
1	6-A	0.50	0/3646	0.68	0/4942
1	6-B	0.60	0/3610	0.76	2/4895 (0.0%)
1	7-A	0.51	0/3646	0.70	0/4942
1	7-B	0.57	0/3610	0.75	3/4895 (0.1%)
1	8-A	0.51	0/3646	0.69	0/4942
1	8-B	0.59	0/3610	0.77	4/4895 (0.1%)
All	All	0.53	1/58048 (0.0%)	0.71	18/78696 (0.0%)

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	3-B	0	1
1	4-B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2-B	242	GLU	CG-CD	5.45	1.60	1.51

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1-B	348	GLY	N-CA-C	-6.06	97.95	113.10
1	4-B	348	GLY	N-CA-C	-5.87	98.43	113.10
1	4-B	296	ASN	N-CA-C	-5.74	95.52	111.00
1	6-B	105	ARG	NE-CZ-NH2	-5.73	117.43	120.30
1	7-B	290	LYS	N-CA-C	5.70	126.39	111.00
1	7-B	105	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	8-B	121	LEU	CA-CB-CG	5.40	127.72	115.30
1	6-B	81	VAL	N-CA-C	-5.37	96.49	111.00
1	8-B	189	PRO	N-CA-C	-5.35	98.19	112.10
1	1-B	388	ASN	N-CA-C	-5.32	96.64	111.00
1	8-B	251	THR	N-CA-C	-5.24	96.85	111.00
1	1-A	85	LEU	N-CA-C	-5.24	96.86	111.00
1	3-B	121	LEU	CA-CB-CG	5.22	127.31	115.30
1	3-B	189	PRO	N-CA-C	-5.21	98.56	112.10
1	7-B	296	ASN	N-CA-C	-5.11	97.20	111.00
1	8-B	105	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	2-B	205	LEU	CA-CB-CG	5.04	126.88	115.30
1	5-B	296	ASN	N-CA-C	-5.03	97.42	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	3-B	125	TYR	Sidechain
1	4-B	243	TYR	Sidechain

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	1-A	3579	0	3652	229	0
1	1-B	3543	0	3621	255	0
1	2-A	3579	0	3652	254	0
1	2-B	3543	0	3621	210	0
1	3-A	3579	0	3652	185	0
1	3-B	3543	0	3621	255	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	4-A	3579	0	3652	293	0
1	4-B	3543	0	3621	256	0
1	5-A	3579	0	3652	320	0
1	5-B	3543	0	3621	273	0
1	6-A	3579	0	3652	229	0
1	6-B	3543	0	3621	253	0
1	7-A	3579	0	3652	233	0
1	7-B	3543	0	3621	239	0
1	8-A	3579	0	3652	222	0
1	8-B	3543	0	3621	230	0
2	1-A	180	0	0	41	0
2	1-B	241	0	0	32	0
2	2-A	182	0	0	23	0
2	2-B	239	0	0	38	0
2	3-A	182	0	0	24	0
2	3-B	239	0	0	41	0
2	4-A	183	0	0	32	0
2	4-B	238	0	0	37	0
2	5-A	182	0	0	43	0
2	5-B	239	0	0	37	0
2	6-A	182	0	0	32	0
2	6-B	239	0	0	33	0
2	7-A	183	0	0	27	0
2	7-B	238	0	0	34	0
2	8-A	183	0	0	24	0
2	8-B	238	0	0	41	0
All	All	60344	0	58184	3934	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 34.

All (3934) 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:A:415:SER:HB3	2:A:486:HOH:O	1.18	1.29
1:A:363:SER:HB3	2:A:605:HOH:O	1.42	1.19
1:B:341:ARG:HA	2:B:568:HOH:O	1.47	1.15
1:A:355:ARG:HH11	1:A:355:ARG:HG3	1.12	1.13
1:A:344:ASP:HB3	2:A:570:HOH:O	1.44	1.13
1:B:76:LEU:HD23	1:B:237:ILE:HD12	1.31	1.13
1:A:108:LEU:HD12	1:A:375:LEU:HD23	1.30	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:ILE:HG23	1:B:261:ILE:HD13	1.33	1.09
1:B:351:VAL:HG21	1:B:355:ARG:HD3	1.34	1.09
1:B:132:VAL:HG22	1:B:158:HIS:HB2	1.29	1.07
1:A:355:ARG:HH11	1:A:355:ARG:HG3	1.13	1.07
1:A:355:ARG:HG3	1:A:355:ARG:HH11	1.13	1.06
1:B:453:PRO:HG2	1:B:456:ALA:HB2	1.35	1.06
1:B:32:LEU:HB3	2:B:683:HOH:O	1.53	1.05
1:B:244:CYS:SG	1:B:298:TRP:HB2	1.96	1.05
1:A:268:GLN:HG2	2:A:474:HOH:O	1.55	1.05
1:A:92:THR:HB	2:A:567:HOH:O	1.55	1.05
1:A:8:LEU:HG	1:A:9:PRO:HD3	1.39	1.04
1:A:123:ASN:HB2	2:A:553:HOH:O	1.58	1.03
1:A:319:PRO:HA	1:A:332:LEU:HD12	1.40	1.03
1:B:267:VAL:HG12	2:B:568:HOH:O	1.58	1.02
1:A:428:VAL:HG13	1:A:450:LEU:HB2	1.41	1.02
1:B:100:SER:HB2	1:B:111:LEU:HG	1.37	1.01
1:B:268:GLN:HE21	1:B:341:ARG:HB2	1.20	1.01
1:B:382:ARG:HD3	2:B:704:HOH:O	1.61	1.01
1:A:416:ILE:HG22	1:A:419:LEU:HD13	1.42	1.01
1:B:386:ARG:HB2	1:B:417:VAL:HG23	1.43	1.01
1:A:101:VAL:HG11	1:A:146:ILE:HG13	1.38	1.01
1:B:423:LYS:HB3	1:B:441:THR:HG22	1.39	1.00
1:B:162:GLN:HB2	1:B:194:ASP:OD2	1.62	1.00
1:A:200:MET:HG2	1:A:205:LEU:HD23	1.43	1.00
1:B:382:ARG:HD3	2:B:707:HOH:O	1.60	0.99
1:B:242:GLU:HB2	1:B:343:PHE:HB3	1.43	0.99
1:B:133:LEU:HB2	1:B:159:THR:HG22	1.45	0.99
1:B:382:ARG:HD3	2:B:704:HOH:O	1.64	0.98
1:B:150:TYR:HD2	2:B:652:HOH:O	1.46	0.98
1:B:207:THR:O	1:B:211:GLN:HB2	1.64	0.97
1:A:427:ASP:HB3	1:A:449:LYS:HA	1.43	0.97
1:A:200:MET:HG2	1:A:205:LEU:HD23	1.47	0.97
1:B:92:THR:HG21	1:B:360:LYS:HE2	1.43	0.97
1:B:382:ARG:HD3	2:B:704:HOH:O	1.62	0.97
1:A:441:THR:HB	1:A:462:ASN:HA	1.44	0.96
1:B:268:GLN:NE2	1:B:341:ARG:HB2	1.79	0.96
1:B:358:PRO:HB2	1:B:360:LYS:HD3	1.44	0.96
1:A:94:GLY:HA3	1:A:402:LYS:HG3	1.45	0.96
1:A:366:LEU:HD22	1:A:394:ILE:HD13	1.48	0.95
1:A:168:VAL:HB	1:A:330:LEU:HB2	1.49	0.95
1:A:216:VAL:HB	1:A:301:LEU:HD21	1.50	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:SER:HB2	1:A:435:VAL:HA	1.46	0.94
1:A:200:MET:HG2	1:A:205:LEU:HD23	1.48	0.94
1:A:105:ARG:HD3	1:A:375:LEU:HD13	1.50	0.94
1:A:136:SER:HB3	1:A:162:GLN:HE21	1.30	0.94
1:A:81:VAL:HA	1:A:130:PRO:HG2	1.49	0.94
1:A:81:VAL:HG12	1:A:215:TYR:O	1.66	0.94
1:B:220:ASN:HD21	1:B:295:ASN:HD22	1.13	0.94
1:A:412:SER:HB3	2:A:503:HOH:O	1.65	0.94
1:A:264:GLU:HG3	2:A:604:HOH:O	1.65	0.93
1:A:319:PRO:HB3	1:A:330:LEU:HD22	1.48	0.93
1:B:265:GLY:O	1:B:266:LYS:HB2	1.67	0.93
1:B:358:PRO:HB2	1:B:360:LYS:HD3	1.52	0.92
1:A:6:GLU:HG2	2:A:618:HOH:O	1.67	0.92
1:B:83:LEU:HA	1:B:132:VAL:O	1.67	0.92
1:A:83:LEU:HD22	1:A:218:VAL:HG13	1.51	0.92
1:B:268:GLN:HB3	1:B:341:ARG:HD2	1.49	0.92
1:A:355:ARG:HH11	1:A:355:ARG:HG3	1.32	0.92
1:A:133:LEU:HB2	1:A:159:THR:HG22	1.51	0.92
1:A:295:ASN:O	1:A:297:LEU:HG	1.70	0.92
1:A:249:PRO:HA	1:A:291:ILE:HG22	1.52	0.91
1:A:123:ASN:HB2	2:A:552:HOH:O	1.69	0.91
1:B:105:ARG:HE	1:B:369:GLN:HA	1.34	0.91
1:B:135:ASN:HB2	1:B:139:THR:OG1	1.70	0.91
1:B:386:ARG:NH2	1:B:392:PRO:HD3	1.84	0.91
1:B:56:ILE:O	1:B:58:VAL:HG23	1.70	0.91
1:A:50:GLN:HB2	1:A:262:SER:HB3	1.52	0.91
1:B:81:VAL:HG22	1:B:130:PRO:HG3	1.52	0.91
1:B:111:LEU:HA	1:B:114:ILE:HD12	1.53	0.91
1:A:6:GLU:HG2	1:A:7:ASN:H	1.35	0.90
1:B:382:ARG:HD3	2:B:705:HOH:O	1.72	0.90
1:A:142:ASP:O	1:A:146:ILE:HG12	1.71	0.90
1:A:200:MET:O	2:A:488:HOH:O	1.90	0.90
1:B:246:GLU:HB2	1:B:296:ASN:HB2	1.53	0.90
1:A:85:LEU:HB2	1:A:220:ASN:HA	1.53	0.90
1:A:436:LEU:HD13	1:A:440:VAL:HG11	1.54	0.90
1:B:150:TYR:HD2	2:B:653:HOH:O	1.53	0.90
1:B:375:LEU:HD23	2:B:605:HOH:O	1.72	0.90
1:B:291:ILE:HD12	1:B:291:ILE:O	1.72	0.89
1:A:44:ILE:HG12	2:A:652:HOH:O	1.73	0.89
1:B:319:PRO:O	1:B:321:PRO:HD3	1.72	0.89
1:B:246:GLU:OE2	1:B:296:ASN:HB3	1.73	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:227:ILE:HG13	1:B:355:ARG:HH22	1.34	0.89
1:A:436:LEU:HD22	1:A:458:VAL:HB	1.53	0.89
1:B:382:ARG:HG3	2:B:705:HOH:O	1.71	0.89
1:B:52:PRO:HB3	1:B:56:ILE:HB	1.54	0.88
1:A:302:LYS:HG3	2:A:558:HOH:O	1.73	0.88
1:A:268:GLN:HA	1:A:340:ILE:HG23	1.56	0.88
1:B:111:LEU:HD23	1:B:111:LEU:C	1.93	0.88
1:A:355:ARG:HH11	1:A:355:ARG:CG	1.86	0.88
1:A:455:ARG:HB3	1:A:455:ARG:HH11	1.37	0.88
1:A:55:GLU:HG2	2:A:624:HOH:O	1.73	0.88
1:B:236:LEU:HD22	1:B:244:CYS:SG	2.13	0.88
1:A:247:VAL:HG21	1:A:291:ILE:HD12	1.56	0.88
1:B:245:MET:HB2	1:B:297:LEU:HD22	1.56	0.88
1:B:422:LEU:HD13	1:B:436:LEU:HD13	1.53	0.88
1:A:99:LYS:HG3	1:A:102:ILE:HD12	1.55	0.88
1:B:100:SER:HB2	1:B:111:LEU:HG	1.55	0.88
1:B:158:HIS:HB3	1:B:204:LYS:HE3	1.57	0.87
1:B:281:ASN:HB3	2:B:649:HOH:O	1.74	0.87
1:A:55:GLU:HG2	2:A:624:HOH:O	1.75	0.87
1:A:117:GLN:HG3	1:A:378:GLY:O	1.74	0.87
1:B:179:LYS:HE3	1:B:179:LYS:HA	1.56	0.87
1:A:453:PRO:HG2	1:A:456:ALA:HB2	1.53	0.87
1:B:44:ILE:HG21	1:B:49:ILE:HD11	1.55	0.87
1:A:84:LYS:HB3	1:A:221:SER:HB3	1.57	0.86
1:B:77:LEU:HD21	1:B:230:LEU:HD21	1.57	0.86
1:A:412:SER:OG	2:A:503:HOH:O	1.93	0.86
1:B:61:GLU:OE1	2:B:583:HOH:O	1.91	0.86
1:B:261:ILE:HD13	1:B:270:LEU:HD22	1.57	0.86
1:A:436:LEU:HB3	1:A:440:VAL:HG21	1.58	0.86
1:A:368:VAL:HG23	1:A:369:GLN:HG3	1.57	0.86
1:A:442:VAL:HG11	1:A:452:ILE:HD11	1.58	0.86
1:A:52:PRO:HD3	1:A:261:ILE:HA	1.57	0.86
1:A:364:ASP:O	1:A:368:VAL:HG22	1.75	0.86
1:A:355:ARG:HH11	1:A:355:ARG:CG	1.89	0.86
1:B:147:VAL:HA	2:B:653:HOH:O	1.74	0.86
1:B:266:LYS:HG2	2:B:568:HOH:O	1.74	0.86
1:B:386:ARG:CZ	1:B:392:PRO:HD3	2.05	0.85
1:A:402:LYS:HE3	1:A:404:ALA:HB3	1.57	0.85
1:B:379:PHE:O	1:B:381:THR:HG23	1.76	0.85
1:A:453:PRO:HG2	1:A:456:ALA:HB2	1.55	0.85
1:A:229:ASP:HB3	1:A:232:ILE:HD12	1.57	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ILE:HG12	2:A:649:HOH:O	1.74	0.85
1:B:103:GLU:OE1	1:B:107:GLY:HA2	1.77	0.85
1:B:128:LYS:HD2	2:B:670:HOH:O	1.76	0.85
1:A:55:GLU:HG2	2:A:623:HOH:O	1.76	0.84
1:A:209:LEU:HD11	1:A:301:LEU:HB3	1.59	0.84
1:A:246:GLU:HB2	1:A:296:ASN:HB2	1.58	0.84
1:B:272:ILE:HG22	2:B:510:HOH:O	1.76	0.84
1:A:35:ARG:HG3	1:A:314:LYS:HE2	1.58	0.84
1:A:50:GLN:HB2	1:A:262:SER:HB3	1.58	0.84
1:B:65:PRO:HA	1:B:231:THR:CG2	2.08	0.84
1:A:35:ARG:HG3	1:A:314:LYS:HG3	1.57	0.84
1:B:288:LYS:O	1:B:290:LYS:HG3	1.76	0.84
1:A:6:GLU:HG2	1:A:7:ASN:H	1.40	0.84
1:A:89:LEU:HG	2:A:593:HOH:O	1.77	0.84
1:A:56:ILE:HG22	1:A:57:VAL:HG23	1.59	0.84
1:B:190:PRO:HA	1:B:333:GLU:HG2	1.59	0.84
1:B:266:LYS:HG2	2:B:568:HOH:O	1.76	0.83
1:A:445:LYS:HG3	2:A:563:HOH:O	1.78	0.83
1:B:111:LEU:HD22	2:B:554:HOH:O	1.78	0.83
1:A:344:ASP:HB3	2:A:569:HOH:O	1.77	0.83
1:B:376:VAL:HB	1:B:381:THR:HG21	1.57	0.83
1:A:319:PRO:HA	1:A:332:LEU:HD12	1.61	0.83
1:B:281:ASN:HB2	2:B:649:HOH:O	1.77	0.83
1:A:302:LYS:HG3	2:A:559:HOH:O	1.77	0.83
1:A:8:LEU:HG	1:A:9:PRO:HD3	1.61	0.83
1:A:11:LEU:HD13	1:A:33:VAL:HG11	1.59	0.83
1:B:330:LEU:HD23	1:B:331:GLN:N	1.94	0.83
1:B:77:LEU:CD2	1:B:121:LEU:HD21	2.09	0.83
1:B:146:ILE:HG21	2:B:563:HOH:O	1.77	0.82
1:B:227:ILE:HG13	1:B:355:ARG:HH22	1.44	0.82
1:A:192:HIS:CE1	1:A:336:ALA:H	1.97	0.82
1:A:411:LYS:HB2	1:A:431:GLY:C	2.00	0.82
1:B:272:ILE:HG23	2:B:504:HOH:O	1.78	0.82
1:B:52:PRO:HB3	1:B:56:ILE:HB	1.61	0.82
1:B:99:LYS:NZ	1:B:360:LYS:HA	1.95	0.82
1:A:118:ILE:HD12	1:A:131:LEU:HD22	1.61	0.82
1:B:200:MET:HE1	1:B:305:LYS:HE3	1.61	0.82
1:A:453:PRO:HG2	1:A:456:ALA:HB2	1.61	0.82
1:B:223:ASN:HA	1:B:358:PRO:HA	1.61	0.82
1:A:119:GLU:HG3	1:A:154:ASN:N	1.95	0.82
1:B:81:VAL:HG22	1:B:130:PRO:CG	2.09	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:ARG:HH11	1:B:341:ARG:HB2	1.43	0.81
1:A:432:SER:H	1:A:454:ASP:HA	1.43	0.81
1:A:355:ARG:HG3	1:A:355:ARG:HH11	1.45	0.81
1:B:65:PRO:HA	1:B:231:THR:HG23	1.61	0.81
1:B:330:LEU:HD23	1:B:331:GLN:N	1.95	0.81
1:B:79:LYS:HD3	1:B:214:GLU:OE1	1.80	0.81
1:B:319:PRO:O	1:B:321:PRO:HD3	1.80	0.81
1:B:56:ILE:O	1:B:347:ILE:HB	1.81	0.81
1:A:355:ARG:HG3	1:A:355:ARG:HH11	1.46	0.81
1:B:56:ILE:HG13	1:B:262:SER:OG	1.80	0.81
1:A:394:ILE:HA	1:A:422:LEU:O	1.78	0.81
1:A:11:LEU:HD13	1:A:33:VAL:HG11	1.60	0.81
1:B:23:GLU:HG2	2:B:599:HOH:O	1.81	0.81
1:B:114:ILE:HG23	2:B:529:HOH:O	1.80	0.81
1:B:373:TYR:CD2	1:B:380:VAL:HG12	2.15	0.81
1:B:266:LYS:HB2	2:B:598:HOH:O	1.80	0.81
1:A:455:ARG:HH11	1:A:455:ARG:HB3	1.44	0.81
1:B:205:LEU:HD21	1:B:305:LYS:HB2	1.61	0.81
1:B:398:PRO:O	2:B:499:HOH:O	1.97	0.80
1:B:376:VAL:HB	1:B:381:THR:HG21	1.62	0.80
1:A:195:VAL:HG13	1:A:196:PHE:H	1.45	0.80
1:B:249:PRO:O	2:B:475:HOH:O	1.98	0.80
1:B:11:LEU:HD13	1:B:33:VAL:HG11	1.64	0.80
1:B:372:LEU:HD22	1:B:373:TYR:CE1	2.17	0.80
1:B:256:LYS:HB2	2:B:658:HOH:O	1.81	0.80
1:A:455:ARG:NH1	1:A:455:ARG:HB3	1.96	0.80
1:B:99:LYS:HG3	1:B:102:ILE:HD12	1.62	0.80
1:B:246:GLU:OE1	1:B:355:ARG:NH2	2.15	0.80
1:B:235:HIS:ND1	2:B:506:HOH:O	2.14	0.80
1:A:439:LYS:HE3	1:A:462:ASN:OD1	1.81	0.80
1:A:195:VAL:HG13	1:A:196:PHE:N	1.96	0.80
1:A:44:ILE:HB	2:A:596:HOH:O	1.81	0.80
1:B:143:THR:O	1:B:147:VAL:HG22	1.80	0.80
1:B:121:LEU:HD11	1:B:228:VAL:HG21	1.64	0.80
1:A:455:ARG:NH1	1:A:455:ARG:HB3	1.97	0.80
1:A:371:ASP:OD2	1:A:417:VAL:HB	1.81	0.80
1:B:105:ARG:NE	1:B:369:GLN:HA	1.96	0.80
1:B:164:LYS:HD2	1:B:164:LYS:O	1.82	0.79
1:B:11:LEU:HD13	1:B:33:VAL:HG11	1.65	0.79
1:A:415:SER:HB2	1:A:435:VAL:CA	2.11	0.79
1:A:149:LYS:O	2:A:613:HOH:O	1.99	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:ASP:O	1:B:145:LYS:HG2	1.81	0.79
1:B:132:VAL:HG22	1:B:158:HIS:HB2	1.64	0.79
1:A:207:THR:O	1:A:211:GLN:HG3	1.83	0.79
1:B:236:LEU:HD11	1:B:298:TRP:HB3	1.65	0.79
1:B:331:GLN:O	1:B:333:GLU:HG3	1.82	0.79
1:A:49:ILE:HG23	1:A:261:ILE:HB	1.65	0.79
1:A:114:ILE:HA	1:A:117:GLN:OE1	1.82	0.79
1:A:255:VAL:HG23	1:A:256:LYS:HG3	1.65	0.79
1:A:439:LYS:O	1:A:460:ASN:HA	1.82	0.79
1:B:79:LYS:HD2	1:B:237:ILE:HD13	1.64	0.79
1:B:379:PHE:HB2	1:B:381:THR:HG22	1.64	0.79
1:B:81:VAL:HG22	1:B:130:PRO:HG3	1.65	0.79
1:A:355:ARG:HH11	1:A:355:ARG:CG	1.95	0.79
1:A:246:GLU:CD	1:A:355:ARG:HH12	1.86	0.79
1:B:246:GLU:CD	1:B:296:ASN:HB3	2.04	0.78
1:A:81:VAL:HG13	1:A:216:VAL:HA	1.66	0.78
1:A:35:ARG:HG3	1:A:314:LYS:NZ	1.98	0.78
1:A:330:LEU:HD23	1:A:331:GLN:N	1.98	0.78
1:A:302:LYS:HG3	2:A:558:HOH:O	1.82	0.78
1:A:28:GLY:O	1:A:32:LEU:HD22	1.83	0.78
1:B:266:LYS:HD3	1:B:341:ARG:O	1.84	0.78
1:A:105:ARG:HH21	1:A:374:THR:HA	1.48	0.78
1:A:8:LEU:CG	1:A:9:PRO:HD3	2.14	0.78
1:B:272:ILE:HD11	1:B:280:VAL:HG13	1.66	0.78
1:B:76:LEU:CD2	1:B:237:ILE:HD12	2.12	0.78
1:A:190:PRO:HA	1:A:333:GLU:HG2	1.65	0.78
1:A:44:ILE:HG12	2:A:652:HOH:O	1.82	0.78
1:B:351:VAL:CG2	1:B:355:ARG:HD3	2.13	0.78
1:A:417:VAL:HG12	1:A:418:GLU:HG3	1.65	0.78
1:B:73:THR:HG23	1:B:230:LEU:HD22	1.65	0.78
1:B:376:VAL:HB	1:B:381:THR:CG2	2.13	0.78
1:A:99:LYS:NZ	1:A:102:ILE:HD12	1.98	0.78
1:B:258:GLY:O	1:B:292:PHE:HA	1.85	0.78
1:B:150:TYR:CD2	2:B:652:HOH:O	2.37	0.77
1:A:439:LYS:HD2	1:A:440:VAL:N	1.99	0.77
1:B:30:ILE:C	1:B:32:LEU:H	1.87	0.77
1:B:366:LEU:HD13	1:B:394:ILE:HG21	1.64	0.77
1:B:122:ASN:HA	1:B:127:CYS:SG	2.24	0.77
1:B:150:TYR:HD2	2:B:652:HOH:O	1.67	0.77
1:A:35:ARG:HG3	1:A:314:LYS:CG	2.15	0.77
1:A:83:LEU:HD22	1:A:218:VAL:HG13	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:VAL:HA	1:A:234:LYS:HE2	1.65	0.77
1:A:250:LYS:HG2	1:A:286:ILE:HG22	1.64	0.77
1:A:272:ILE:HG12	2:A:535:HOH:O	1.85	0.77
1:A:99:LYS:HE2	1:A:360:LYS:HD2	1.67	0.77
1:B:419:LEU:HD21	1:B:422:LEU:HB2	1.66	0.77
1:A:84:LYS:HG3	1:A:114:ILE:HD13	1.67	0.77
1:B:14:ALA:HB1	1:B:178:SER:OG	1.85	0.77
1:B:372:LEU:O	1:B:372:LEU:HD23	1.84	0.77
1:A:358:PRO:HB2	1:A:360:LYS:HD3	1.65	0.77
1:B:224:LEU:HD13	1:B:380:VAL:HG21	1.66	0.77
1:A:322:LYS:HG3	1:A:331:GLN:HE22	1.50	0.77
1:B:23:GLU:HG2	2:B:600:HOH:O	1.85	0.77
1:B:273:ALA:HB2	2:B:504:HOH:O	1.83	0.77
1:A:271:GLU:OE1	2:A:535:HOH:O	2.02	0.77
1:A:224:LEU:HD13	1:A:380:VAL:HG21	1.66	0.76
1:A:84:LYS:HG3	1:A:114:ILE:HD13	1.67	0.76
1:A:355:ARG:NH1	1:A:355:ARG:HG3	1.94	0.76
1:A:94:GLY:HA3	1:A:402:LYS:HG3	1.67	0.76
1:B:398:PRO:HD2	2:B:484:HOH:O	1.85	0.76
1:A:55:GLU:HG3	2:A:623:HOH:O	1.85	0.76
1:A:415:SER:CB	1:A:435:VAL:HA	2.15	0.76
1:A:319:PRO:HB3	1:A:330:LEU:CD2	2.13	0.76
1:B:77:LEU:CD2	1:B:230:LEU:HD21	2.15	0.76
1:B:150:TYR:HD2	2:B:653:HOH:O	1.67	0.76
1:B:26:LYS:O	1:B:30:ILE:HG12	1.85	0.76
1:B:370:SER:OG	1:B:416:ILE:HD11	1.86	0.76
1:A:35:ARG:HG3	1:A:314:LYS:HG3	1.67	0.76
1:B:199:LEU:HD23	1:B:205:LEU:HB2	1.67	0.76
1:A:11:LEU:HD11	1:A:173:PHE:HE2	1.50	0.76
1:B:331:GLN:O	1:B:333:GLU:HG3	1.85	0.76
1:A:99:LYS:HE2	2:A:546:HOH:O	1.85	0.76
1:B:236:LEU:HA	1:B:241:ASN:OD1	1.86	0.76
1:A:199:LEU:HD12	1:A:204:LYS:HB2	1.68	0.76
1:B:114:ILE:HD11	1:B:221:SER:HB2	1.65	0.75
1:A:189:PRO:HD2	2:A:621:HOH:O	1.83	0.75
1:B:332:LEU:HD12	2:B:685:HOH:O	1.85	0.75
1:B:425:SER:O	1:B:443:ALA:HA	1.86	0.75
1:A:431:GLY:N	1:A:452:ILE:O	2.19	0.75
1:B:321:PRO:O	1:B:322:LYS:HB2	1.84	0.75
1:B:88:GLY:O	1:B:99:LYS:N	2.19	0.75
1:A:104:VAL:HG21	1:A:224:LEU:HD11	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ASP:HA	1:A:26:LYS:HD3	1.66	0.75
1:A:81:VAL:HA	1:A:130:PRO:CG	2.16	0.75
1:B:233:LEU:HD12	1:B:236:LEU:HD12	1.69	0.75
1:A:77:LEU:HG	1:A:230:LEU:HD11	1.69	0.75
1:B:261:ILE:HD13	1:B:270:LEU:HD22	1.68	0.75
1:B:8:LEU:N	1:B:9:PRO:HD3	2.01	0.75
1:B:312:ALA:O	1:B:314:LYS:HG3	1.85	0.75
1:B:367:LEU:HG	1:B:394:ILE:HD12	1.69	0.75
1:A:117:GLN:HE21	1:A:379:PHE:HA	1.51	0.75
1:A:421:SER:OG	2:A:582:HOH:O	2.04	0.75
1:A:205:LEU:HD11	1:A:301:LEU:HB3	1.67	0.75
1:A:11:LEU:HD13	1:A:33:VAL:HG11	1.68	0.75
1:B:164:LYS:NZ	2:B:658:HOH:O	2.18	0.75
1:B:80:LEU:O	1:B:130:PRO:HD2	1.86	0.75
1:A:12:LYS:HD3	2:A:620:HOH:O	1.87	0.75
1:A:98:PRO:O	1:A:101:VAL:HG22	1.87	0.75
1:A:436:LEU:CD2	1:A:458:VAL:HB	2.17	0.74
1:A:308:VAL:HA	2:A:489:HOH:O	1.85	0.74
1:B:11:LEU:O	1:B:11:LEU:HD23	1.86	0.74
1:B:100:SER:HB2	1:B:111:LEU:CG	2.15	0.74
1:A:112:ASP:OD2	2:A:596:HOH:O	2.05	0.74
1:B:252:LEU:HA	1:B:255:VAL:HG23	1.69	0.74
1:B:35:ARG:O	1:B:317:ILE:HG13	1.87	0.74
1:A:55:GLU:HG2	2:A:623:HOH:O	1.86	0.74
1:B:372:LEU:CD2	1:B:386:ARG:HD3	2.18	0.74
1:B:98:PRO:O	1:B:101:VAL:HG22	1.88	0.74
1:A:132:VAL:HB	1:A:158:HIS:HB2	1.68	0.74
1:B:213:LYS:NZ	2:B:647:HOH:O	2.21	0.74
1:A:442:VAL:CG1	1:A:452:ILE:HD11	2.16	0.74
1:B:199:LEU:CD2	1:B:205:LEU:HB2	2.16	0.74
1:B:77:LEU:HD22	1:B:121:LEU:HD21	1.68	0.74
1:A:200:MET:HG2	1:A:205:LEU:HD23	1.68	0.74
1:A:316:GLU:HG3	2:A:638:HOH:O	1.88	0.74
1:B:98:PRO:O	1:B:101:VAL:HG22	1.87	0.74
1:B:98:PRO:HB2	1:B:101:VAL:HG13	1.70	0.74
1:A:171:ASP:OD2	1:A:172:GLU:HG3	1.88	0.74
1:B:252:LEU:O	1:B:252:LEU:HD23	1.87	0.74
1:B:179:LYS:HE3	1:B:179:LYS:HA	1.66	0.74
1:A:246:GLU:CD	1:A:355:ARG:HH12	1.90	0.74
1:A:307:LEU:HD13	1:A:313:LEU:HD21	1.69	0.74
1:A:461:LYS:HE3	1:A:463:ILE:HG12	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:LYS:HD2	1:B:459:GLU:HB2	1.70	0.74
1:A:111:LEU:HG	1:A:150:TYR:OH	1.88	0.74
1:A:79:LYS:HD2	1:A:237:ILE:HD11	1.70	0.74
1:B:273:ALA:HB2	2:B:504:HOH:O	1.87	0.74
1:A:82:VAL:HG13	2:A:492:HOH:O	1.88	0.74
1:B:246:GLU:HB2	1:B:296:ASN:HB2	1.70	0.73
1:B:105:ARG:HD2	2:B:509:HOH:O	1.87	0.73
1:B:50:GLN:HB2	1:B:262:SER:HB3	1.70	0.73
1:A:246:GLU:HB2	1:A:296:ASN:HB2	1.70	0.73
1:B:81:VAL:HG13	1:B:130:PRO:HG2	1.70	0.73
1:B:358:PRO:HB2	1:B:360:LYS:HD3	1.67	0.73
1:B:272:ILE:HD11	1:B:280:VAL:HG13	1.70	0.73
1:A:268:GLN:HA	1:A:340:ILE:CG2	2.17	0.73
1:A:455:ARG:HB3	1:A:455:ARG:NH1	2.02	0.73
1:B:141:ASP:N	1:B:141:ASP:OD2	2.20	0.73
1:A:35:ARG:HG3	1:A:314:LYS:CE	2.18	0.73
1:A:111:LEU:HD23	2:A:509:HOH:O	1.88	0.73
1:B:94:GLY:HA3	1:B:402:LYS:HG2	1.70	0.73
1:B:103:GLU:OE1	1:B:107:GLY:HA2	1.87	0.73
1:B:53:THR:HB	2:B:572:HOH:O	1.88	0.73
1:B:11:LEU:HD13	1:B:33:VAL:HG11	1.71	0.73
1:B:66:VAL:HG13	1:B:72:GLU:OE1	1.88	0.73
1:A:136:SER:HB3	1:A:162:GLN:NE2	2.04	0.73
1:A:32:LEU:H	1:A:32:LEU:HD12	1.52	0.73
1:B:93:MET:CE	1:B:365:LEU:HD11	2.19	0.73
1:A:442:VAL:HA	1:A:463:ILE:HB	1.71	0.73
1:A:99:LYS:HZ3	1:A:102:ILE:HD12	1.51	0.73
1:A:467:GLU:HB2	2:A:589:HOH:O	1.88	0.73
1:B:90:GLY:HA3	2:B:512:HOH:O	1.89	0.73
1:A:355:ARG:HH11	1:A:355:ARG:HG3	1.53	0.73
1:B:317:ILE:HA	1:B:333:GLU:O	1.89	0.73
1:A:105:ARG:NH2	1:A:374:THR:HA	2.04	0.73
1:A:264:GLU:N	2:A:516:HOH:O	2.20	0.73
1:B:220:ASN:HD21	1:B:295:ASN:ND2	1.87	0.73
1:B:150:TYR:CD2	2:B:652:HOH:O	2.42	0.73
1:B:228:VAL:HG23	2:B:508:HOH:O	1.87	0.73
1:B:79:LYS:HD2	1:B:237:ILE:CD1	2.19	0.73
1:A:166:PRO:HB2	1:A:177:PRO:HD2	1.70	0.73
1:A:191:GLY:O	1:A:194:ASP:HB3	1.89	0.72
1:B:36:TYR:CE1	1:B:319:PRO:HB3	2.24	0.72
1:B:87:GLY:HA2	1:B:136:SER:H	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:467:GLU:HG3	1:B:468:ASP:H	1.54	0.72
1:B:300:ASN:O	1:B:304:ILE:HG13	1.88	0.72
1:A:15:VAL:HG21	1:A:30:ILE:HD11	1.71	0.72
1:B:367:LEU:HG	1:B:394:ILE:HD12	1.69	0.72
1:B:150:TYR:HB2	2:B:653:HOH:O	1.90	0.72
1:B:58:VAL:O	1:B:349:VAL:HA	1.90	0.72
1:B:236:LEU:HD11	1:B:244:CYS:SG	2.29	0.72
1:B:220:ASN:ND2	1:B:295:ASN:HD22	1.88	0.72
1:B:163:SER:HB2	1:B:190:PRO:HG3	1.71	0.72
1:A:128:LYS:HG2	2:A:577:HOH:O	1.89	0.72
1:B:11:LEU:CD1	1:B:33:VAL:HG11	2.20	0.72
1:A:439:LYS:O	1:A:460:ASN:HA	1.88	0.72
1:A:247:VAL:HB	1:A:291:ILE:HD13	1.70	0.72
1:B:412:SER:HB3	1:B:432:SER:HB2	1.70	0.72
1:A:27:SER:O	1:A:30:ILE:HB	1.90	0.72
1:A:6:GLU:HG2	1:A:7:ASN:N	2.05	0.72
1:A:250:LYS:HG2	1:A:286:ILE:HG22	1.72	0.72
1:B:247:VAL:HB	1:B:291:ILE:HB	1.71	0.72
1:B:307:LEU:HD13	1:B:313:LEU:HD21	1.70	0.72
1:A:20:GLU:HB2	2:A:476:HOH:O	1.90	0.72
1:B:246:GLU:HA	1:B:349:VAL:HG12	1.72	0.72
1:B:150:TYR:CD2	2:B:653:HOH:O	2.43	0.72
1:B:81:VAL:HG22	1:B:130:PRO:HG2	1.71	0.72
1:B:427:ASP:HB3	2:B:531:HOH:O	1.88	0.72
1:B:372:LEU:HD22	1:B:373:TYR:CE1	2.24	0.72
1:B:150:TYR:HD2	2:B:652:HOH:O	1.72	0.71
1:B:363:SER:HB3	2:B:545:HOH:O	1.88	0.71
1:A:420:ASP:O	1:A:421:SER:OG	2.07	0.71
1:B:121:LEU:O	1:B:121:LEU:HD23	1.91	0.71
1:B:250:LYS:HE3	1:B:291:ILE:O	1.90	0.71
1:A:83:LEU:HB3	1:A:218:VAL:HG22	1.73	0.71
1:A:314:LYS:HE3	1:A:314:LYS:O	1.90	0.71
1:A:98:PRO:O	1:A:101:VAL:HG22	1.90	0.71
1:B:99:LYS:NZ	1:B:360:LYS:HG3	2.05	0.71
1:A:396:LEU:HD23	1:A:424:VAL:HB	1.72	0.71
1:A:6:GLU:HG2	1:A:7:ASN:H	1.54	0.71
1:B:137:PHE:CG	1:B:164:LYS:HE3	2.26	0.71
1:B:170:ALA:HB2	1:B:328:LYS:C	2.10	0.71
1:A:247:VAL:HB	1:A:291:ILE:HD13	1.72	0.71
1:A:16:ASP:HA	1:A:26:LYS:NZ	2.06	0.71
1:A:49:ILE:HG12	1:A:261:ILE:HD12	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:LYS:HE2	1:B:126:GLY:C	2.11	0.71
1:B:75:ASN:O	1:B:78:ASP:HB2	1.91	0.71
1:B:149:LYS:HG3	1:B:150:TYR:CD2	2.24	0.71
1:A:307:LEU:HD13	1:A:313:LEU:HD21	1.72	0.71
1:A:164:LYS:HB3	2:A:525:HOH:O	1.90	0.71
1:A:271:GLU:OE2	2:A:560:HOH:O	2.08	0.71
1:A:16:ASP:HA	1:A:26:LYS:HD3	1.72	0.71
1:A:461:LYS:NZ	1:A:468:ASP:HB3	2.05	0.71
1:B:368:VAL:HG12	1:B:368:VAL:O	1.90	0.71
1:A:171:ASP:OD1	1:A:172:GLU:HG3	1.89	0.71
1:A:355:ARG:HG3	1:A:355:ARG:NH1	2.05	0.71
1:B:84:LYS:HB3	1:B:221:SER:HB3	1.70	0.71
1:B:285:SER:OG	1:B:287:GLU:HG2	1.91	0.71
1:B:315:MET:HG2	1:B:338:ALA:HB3	1.72	0.71
1:A:81:VAL:HG13	1:A:216:VAL:HA	1.72	0.71
1:A:105:ARG:HD2	1:A:368:VAL:O	1.91	0.71
1:A:250:LYS:HD3	1:A:255:VAL:HA	1.73	0.71
1:A:461:LYS:HE3	1:A:463:ILE:HG12	1.71	0.70
1:A:7:ASN:OD1	1:A:8:LEU:HD23	1.92	0.70
1:A:392:PRO:HB2	1:A:421:SER:HA	1.73	0.70
1:A:370:SER:HB3	1:A:413:ILE:CG2	2.21	0.70
1:A:142:ASP:O	1:A:146:ILE:HG12	1.91	0.70
1:A:224:LEU:HD13	1:A:380:VAL:HG21	1.73	0.70
1:B:256:LYS:HE3	1:B:284:LYS:HE2	1.72	0.70
1:A:455:ARG:HB3	1:A:455:ARG:NH1	2.05	0.70
1:A:421:SER:HB3	1:A:439:LYS:HA	1.73	0.70
1:B:395:GLU:O	1:B:423:LYS:HA	1.91	0.70
1:B:61:GLU:OE1	2:B:656:HOH:O	2.09	0.70
1:A:362:SER:HB2	1:A:406:PHE:CD1	2.27	0.70
1:B:319:PRO:O	1:B:321:PRO:HD3	1.92	0.70
1:B:218:VAL:HB	1:B:297:LEU:HD12	1.72	0.70
1:B:463:ILE:HG23	1:B:468:ASP:HB2	1.72	0.70
1:A:269:LEU:HD21	1:A:271:GLU:OE2	1.92	0.70
1:A:271:GLU:HG3	2:A:560:HOH:O	1.91	0.70
1:A:372:LEU:HD22	1:A:392:PRO:HD2	1.73	0.70
1:A:158:HIS:HB3	1:A:204:LYS:CE	2.21	0.70
1:A:200:MET:CG	1:A:205:LEU:HD23	2.20	0.70
1:B:463:ILE:HG23	1:B:468:ASP:HB3	1.73	0.70
1:B:272:ILE:HD11	1:B:280:VAL:HG13	1.73	0.70
1:B:319:PRO:O	1:B:321:PRO:HD3	1.92	0.70
1:B:282:GLU:HG3	2:B:648:HOH:O	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:ARG:HB2	2:A:580:HOH:O	1.92	0.70
1:A:445:LYS:H	1:A:448:VAL:HB	1.56	0.70
1:A:365:LEU:HB3	1:A:369:GLN:OE1	1.91	0.70
1:A:411:LYS:HD2	1:A:431:GLY:HA2	1.71	0.70
1:A:8:LEU:H	1:A:9:PRO:CD	2.05	0.70
1:B:372:LEU:HD22	1:B:386:ARG:HD3	1.73	0.70
1:A:117:GLN:NE2	1:A:379:PHE:HA	2.06	0.70
1:B:272:ILE:HB	1:B:283:PHE:CE2	2.26	0.70
1:A:256:LYS:HE2	1:A:272:ILE:HD13	1.74	0.70
1:B:366:LEU:O	1:B:366:LEU:HD23	1.91	0.70
1:A:66:VAL:HA	1:A:234:LYS:NZ	2.07	0.70
1:A:123:ASN:HB2	2:A:553:HOH:O	1.90	0.70
1:B:380:VAL:HG23	2:B:516:HOH:O	1.92	0.70
1:B:70:VAL:HG23	2:B:556:HOH:O	1.90	0.70
1:A:77:LEU:HD13	1:A:127:CYS:SG	2.32	0.69
1:B:307:LEU:HD13	1:B:313:LEU:HD21	1.74	0.69
1:B:398:PRO:O	1:B:401:LYS:HG3	1.92	0.69
1:B:66:VAL:HG12	2:B:502:HOH:O	1.90	0.69
1:B:89:LEU:HD21	1:B:138:ASN:O	1.92	0.69
1:A:200:MET:HG2	1:A:205:LEU:HD23	1.73	0.69
1:A:436:LEU:HA	1:A:458:VAL:O	1.93	0.69
1:B:142:ASP:O	1:B:146:ILE:HG13	1.92	0.69
1:A:169:VAL:HG11	1:A:172:GLU:OE1	1.91	0.69
1:A:26:LYS:O	1:A:30:ILE:HG12	1.93	0.69
1:A:433:SER:HB2	1:A:455:ARG:HG2	1.74	0.69
1:B:427:ASP:N	1:B:444:ALA:HB3	2.08	0.69
1:B:411:LYS:HB3	1:B:432:SER:HB3	1.74	0.69
1:A:196:PHE:HD1	1:A:304:ILE:HD13	1.56	0.69
1:A:82:VAL:CG1	1:A:84:LYS:HE2	2.22	0.69
1:B:26:LYS:O	1:B:30:ILE:HG12	1.92	0.69
1:B:267:VAL:HG12	2:B:568:HOH:O	1.92	0.69
1:B:89:LEU:HD23	1:B:139:THR:CG2	2.22	0.69
1:B:89:LEU:HG	2:B:660:HOH:O	1.93	0.69
1:B:438:GLY:HA3	1:B:460:ASN:OD1	1.93	0.69
1:B:266:LYS:HB2	2:B:598:HOH:O	1.93	0.69
1:A:71:ALA:O	1:A:75:ASN:HB2	1.93	0.69
1:A:267:VAL:HG13	1:A:340:ILE:HG12	1.74	0.69
1:A:261:ILE:HD12	1:A:261:ILE:C	2.13	0.69
1:A:8:LEU:H	1:A:9:PRO:CD	2.06	0.69
1:B:137:PHE:CG	1:B:164:LYS:HE3	2.28	0.69
1:B:105:ARG:HD2	2:B:558:HOH:O	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:GLU:HG2	1:B:107:GLY:O	1.91	0.69
1:A:450:LEU:HD23	1:A:451:GLU:N	2.07	0.69
1:B:357:LEU:O	1:B:357:LEU:CD2	2.41	0.69
1:A:111:LEU:HD12	1:A:111:LEU:O	1.93	0.69
1:A:101:VAL:HG11	1:A:146:ILE:CG1	2.17	0.69
1:A:66:VAL:HG12	1:A:234:LYS:HE3	1.74	0.69
1:A:244:CYS:HA	1:A:347:ILE:O	1.93	0.69
1:A:81:VAL:HG21	1:A:208:PHE:CD2	2.27	0.69
1:B:192:HIS:O	1:B:336:ALA:HB2	1.93	0.69
1:A:429:TRP:HB2	1:A:451:GLU:HG2	1.74	0.69
1:A:311:ASP:HA	2:A:489:HOH:O	1.91	0.69
1:B:193:GLY:HA3	1:B:334:THR:OG1	1.93	0.69
1:A:80:LEU:HD22	1:A:233:LEU:HD22	1.75	0.69
1:B:374:THR:HG23	2:B:644:HOH:O	1.93	0.69
1:A:102:ILE:HG22	1:A:103:GLU:N	2.08	0.68
1:B:100:SER:HB2	1:B:111:LEU:HG	1.75	0.68
1:B:263:TYR:HB3	1:B:268:GLN:NE2	2.09	0.68
1:A:461:LYS:HE3	1:A:463:ILE:HD11	1.74	0.68
1:A:48:LYS:HG2	2:A:521:HOH:O	1.92	0.68
1:B:223:ASN:ND2	2:B:637:HOH:O	2.26	0.68
1:A:467:GLU:HB2	2:A:589:HOH:O	1.93	0.68
1:B:382:ARG:NH2	1:B:390:SER:O	2.27	0.68
1:B:60:TYR:HB2	1:B:350:ASN:O	1.93	0.68
1:A:80:LEU:O	1:A:130:PRO:HD2	1.92	0.68
1:B:250:LYS:HE3	1:B:292:PHE:HB3	1.74	0.68
1:B:256:LYS:HE3	1:B:284:LYS:HE2	1.75	0.68
1:B:70:VAL:HG13	1:B:125:TYR:HD1	1.58	0.68
1:A:50:GLN:HB2	1:A:262:SER:HB3	1.74	0.68
1:A:234:LYS:O	1:A:238:GLN:HG3	1.94	0.68
1:A:119:GLU:HG3	1:A:154:ASN:H	1.57	0.68
1:A:271:GLU:HG2	1:A:272:ILE:H	1.57	0.68
1:B:224:LEU:HD13	1:B:380:VAL:HG21	1.73	0.68
1:B:158:HIS:HB3	1:B:204:LYS:HE3	1.76	0.68
1:B:268:GLN:NE2	2:B:598:HOH:O	2.19	0.68
1:A:384:LYS:O	1:A:384:LYS:HE3	1.93	0.68
1:B:386:ARG:HG3	1:B:386:ARG:O	1.93	0.68
1:A:255:VAL:HB	1:A:284:LYS:HB3	1.75	0.68
1:B:392:PRO:HB3	1:B:419:LEU:O	1.92	0.68
1:B:322:LYS:NZ	1:B:324:VAL:HG22	2.08	0.68
1:A:224:LEU:HD13	1:A:380:VAL:HG21	1.74	0.68
1:A:247:VAL:HB	1:A:291:ILE:HD13	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ASP:HA	1:A:26:LYS:HZ2	1.59	0.68
1:A:116:ILE:HG22	1:A:378:GLY:HA3	1.75	0.68
1:A:111:LEU:HD23	2:A:509:HOH:O	1.92	0.68
1:B:340:ILE:HD11	1:B:347:ILE:O	1.93	0.68
1:B:250:LYS:HB3	1:B:286:ILE:HG22	1.74	0.68
1:B:138:ASN:ND2	1:B:184:LYS:HD3	2.09	0.68
1:B:423:LYS:HB3	1:B:441:THR:CG2	2.21	0.68
1:B:411:LYS:HG3	1:B:430:PHE:O	1.93	0.68
1:A:220:ASN:HB3	2:A:626:HOH:O	1.93	0.68
1:B:105:ARG:HD2	1:B:375:LEU:HD13	1.75	0.68
1:A:77:LEU:O	2:A:525:HOH:O	2.10	0.68
1:A:132:VAL:HA	1:A:158:HIS:O	1.94	0.68
1:B:73:THR:HG23	1:B:230:LEU:HD21	1.75	0.68
1:B:245:MET:SD	1:B:293:ASN:HB2	2.34	0.68
1:B:96:THR:O	1:B:97:GLY:O	2.12	0.67
1:A:49:ILE:HD13	1:A:270:LEU:HD22	1.74	0.67
1:A:136:SER:CB	1:A:162:GLN:HE21	2.05	0.67
1:B:203:GLY:HA2	2:B:489:HOH:O	1.93	0.67
1:A:246:GLU:OE1	1:A:355:ARG:NH1	2.28	0.67
1:B:146:ILE:CG2	1:B:149:LYS:HD2	2.24	0.67
1:B:293:ASN:ND2	1:B:295:ASN:H	1.93	0.67
1:B:136:SER:HB3	1:B:162:GLN:HE21	1.57	0.67
1:B:79:LYS:HD3	1:B:214:GLU:OE2	1.95	0.67
1:A:23:GLU:OE2	2:A:545:HOH:O	2.11	0.67
1:B:132:VAL:HG21	1:B:208:PHE:HE2	1.58	0.67
1:A:365:LEU:HB3	1:A:369:GLN:NE2	2.09	0.67
1:B:83:LEU:HD23	1:B:84:LYS:N	2.09	0.67
1:A:382:ARG:NH2	1:A:386:ARG:HG2	2.10	0.67
1:A:268:GLN:NE2	1:A:341:ARG:HE	1.92	0.67
1:B:58:VAL:O	1:B:349:VAL:HG23	1.93	0.67
1:A:370:SER:C	1:A:372:LEU:H	1.98	0.67
1:A:411:LYS:HB2	1:A:431:GLY:C	2.15	0.67
1:B:232:ILE:O	1:B:236:LEU:HG	1.95	0.67
1:A:235:HIS:HD2	2:A:574:HOH:O	1.76	0.67
1:B:374:THR:OG1	2:B:645:HOH:O	2.12	0.67
1:B:114:ILE:HG22	1:B:131:LEU:HD21	1.75	0.67
1:B:132:VAL:HG22	1:B:158:HIS:HB2	1.77	0.67
1:A:355:ARG:NH1	1:A:355:ARG:HG3	2.09	0.67
1:A:442:VAL:HG22	1:A:463:ILE:HD12	1.77	0.67
1:B:14:ALA:HA	2:B:580:HOH:O	1.92	0.67
1:B:103:GLU:OE1	2:B:481:HOH:O	2.13	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:252:LEU:O	1:B:255:VAL:HG13	1.95	0.67
1:B:153:SER:HB2	1:B:155:VAL:HG12	1.77	0.67
1:A:256:LYS:HB3	1:A:272:ILE:HD13	1.77	0.67
1:A:85:LEU:HD11	1:A:295:ASN:ND2	2.09	0.67
1:B:332:LEU:HD12	2:B:683:HOH:O	1.94	0.67
1:B:149:LYS:HG3	1:B:150:TYR:HD2	1.60	0.67
1:A:265:GLY:C	1:A:266:LYS:HD2	2.15	0.67
1:A:355:ARG:HG3	1:A:355:ARG:NH1	1.95	0.67
1:B:111:LEU:HD23	1:B:114:ILE:HD12	1.76	0.67
1:B:355:ARG:HH21	1:B:355:ARG:CB	2.08	0.67
1:B:233:LEU:HA	1:B:236:LEU:CD1	2.25	0.67
1:A:318:ILE:O	1:A:332:LEU:HA	1.95	0.67
1:A:259:THR:O	1:A:269:LEU:HD12	1.95	0.67
1:B:200:MET:SD	1:B:309:GLU:HG3	2.35	0.66
1:B:459:GLU:O	1:B:460:ASN:C	2.34	0.66
1:A:83:LEU:HD22	1:A:218:VAL:CG1	2.23	0.66
1:A:455:ARG:HH11	1:A:455:ARG:HB3	1.57	0.66
1:A:415:SER:CB	1:A:435:VAL:HG13	2.26	0.66
1:A:366:LEU:HD13	1:A:394:ILE:HG21	1.76	0.66
1:A:394:ILE:HG12	1:A:422:LEU:HB3	1.77	0.66
1:A:258:GLY:HA2	1:A:271:GLU:OE2	1.95	0.66
1:B:93:MET:SD	1:B:361:ALA:HA	2.35	0.66
1:B:96:THR:O	2:B:512:HOH:O	2.13	0.66
1:B:320:ASN:N	1:B:321:PRO:HD3	2.09	0.66
1:B:227:ILE:HG13	1:B:355:ARG:NH2	2.10	0.66
1:A:382:ARG:NH2	1:A:386:ARG:HG2	2.10	0.66
1:A:104:VAL:HG13	1:A:105:ARG:N	2.09	0.66
1:B:227:ILE:CG1	1:B:355:ARG:HH22	2.07	0.66
1:B:215:TYR:CD2	1:B:236:LEU:HD13	2.30	0.66
1:A:239:ASN:HD22	1:A:239:ASN:N	1.90	0.66
1:A:82:VAL:O	1:A:132:VAL:HG12	1.95	0.66
1:B:52:PRO:HB3	1:B:56:ILE:CG2	2.24	0.66
1:A:405:THR:HG22	1:A:409:ARG:HD2	1.76	0.66
1:B:165:TYR:OH	2:B:513:HOH:O	2.09	0.66
1:A:266:LYS:HG3	2:A:595:HOH:O	1.96	0.66
1:B:423:LYS:HB3	1:B:441:THR:HG22	1.78	0.66
1:B:12:LYS:HG3	1:B:30:ILE:HD12	1.78	0.66
1:A:123:ASN:CB	2:A:552:HOH:O	2.37	0.66
1:B:294:THR:O	1:B:295:ASN:HB2	1.96	0.66
1:B:227:ILE:HG13	1:B:355:ARG:NH2	2.09	0.66
1:A:411:LYS:HE3	2:A:611:HOH:O	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:ASP:O	1:A:417:VAL:HG23	1.96	0.66
1:A:318:ILE:HB	1:A:333:GLU:HG3	1.78	0.66
1:A:99:LYS:CE	1:A:360:LYS:HD2	2.26	0.66
1:A:355:ARG:HG3	1:A:355:ARG:NH1	1.93	0.66
1:B:383:ASN:HA	2:B:645:HOH:O	1.96	0.66
1:A:302:LYS:HG3	2:A:558:HOH:O	1.95	0.66
1:A:24:SER:OG	2:A:642:HOH:O	2.13	0.66
1:A:332:LEU:N	1:A:332:LEU:HD12	2.11	0.66
1:B:260:LEU:HD23	1:B:269:LEU:HA	1.75	0.66
1:B:411:LYS:HD3	1:B:431:GLY:HA2	1.78	0.66
1:B:247:VAL:O	1:B:350:ASN:HA	1.96	0.66
1:A:44:ILE:HG12	2:A:651:HOH:O	1.96	0.66
1:B:111:LEU:C	1:B:111:LEU:CD2	2.64	0.66
1:A:195:VAL:CG1	1:A:196:PHE:H	2.09	0.66
1:B:146:ILE:O	1:B:146:ILE:HG22	1.94	0.66
1:B:164:LYS:C	1:B:165:TYR:HD1	1.99	0.66
1:B:182:THR:HG23	1:B:187:TRP:HZ2	1.59	0.66
1:A:104:VAL:HG13	1:A:105:ARG:N	2.11	0.66
1:B:358:PRO:HB2	1:B:360:LYS:CD	2.25	0.66
1:B:355:ARG:HB3	1:B:355:ARG:NH2	2.10	0.66
1:B:219:ALA:HA	1:B:295:ASN:O	1.95	0.66
1:A:235:HIS:HD2	2:A:573:HOH:O	1.79	0.66
1:A:106:ASP:HB2	1:A:375:LEU:HD22	1.79	0.66
1:B:315:MET:SD	1:B:339:ALA:HB2	2.36	0.66
1:B:50:GLN:NE2	2:B:487:HOH:O	2.13	0.66
1:B:149:LYS:HG3	1:B:150:TYR:CD2	2.31	0.65
1:A:11:LEU:HD13	1:A:33:VAL:HG11	1.78	0.65
1:A:104:VAL:HG13	1:A:105:ARG:H	1.60	0.65
1:B:79:LYS:HD3	1:B:214:GLU:CD	2.16	0.65
1:B:255:VAL:HG22	1:B:284:LYS:HB3	1.78	0.65
1:B:224:LEU:N	1:B:357:LEU:O	2.29	0.65
1:B:245:MET:HB2	1:B:297:LEU:CD2	2.27	0.65
1:B:140:HIS:HB2	1:B:161:ASN:OD1	1.97	0.65
1:A:274:GLN:HG2	2:A:649:HOH:O	1.95	0.65
1:A:35:ARG:NH2	2:A:648:HOH:O	2.28	0.65
1:A:9:PRO:HB2	2:A:554:HOH:O	1.94	0.65
1:A:276:PRO:HB2	1:A:279:HIS:HD2	1.62	0.65
1:B:436:LEU:HD23	1:B:458:VAL:HB	1.79	0.65
1:B:134:MET:CE	1:B:162:GLN:HE22	2.10	0.65
1:A:353:ARG:HB2	2:A:580:HOH:O	1.95	0.65
1:A:216:VAL:HB	1:A:301:LEU:HD21	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:ARG:NE	1:A:388:ASN:HB3	2.11	0.65
1:B:379:PHE:HB2	1:B:381:THR:HG22	1.79	0.65
1:B:223:ASN:HA	1:B:358:PRO:HA	1.78	0.65
1:B:108:LEU:HD12	1:B:375:LEU:HD21	1.79	0.65
1:B:29:PHE:O	1:B:33:VAL:HG23	1.97	0.65
1:A:117:GLN:HA	1:A:120:ASN:ND2	2.10	0.65
1:B:8:LEU:N	1:B:8:LEU:HD22	2.11	0.65
1:A:63:MET:HG2	1:A:235:HIS:CD2	2.32	0.65
1:B:8:LEU:HD22	1:B:8:LEU:N	2.12	0.65
1:A:291:ILE:HG21	1:A:350:ASN:HD21	1.62	0.65
1:A:171:ASP:OD1	1:A:172:GLU:HG3	1.97	0.65
1:A:81:VAL:HG13	1:A:216:VAL:HA	1.78	0.65
1:B:142:ASP:O	1:B:145:LYS:HG2	1.97	0.65
1:B:242:GLU:OE1	2:B:561:HOH:O	2.14	0.65
1:B:57:VAL:HG11	1:B:291:ILE:HD13	1.78	0.65
1:B:376:VAL:HB	1:B:381:THR:CG2	2.27	0.65
1:A:435:VAL:O	1:A:435:VAL:HG12	1.96	0.65
1:A:411:LYS:HE3	2:A:610:HOH:O	1.96	0.65
1:A:268:GLN:CD	1:A:341:ARG:HE	1.99	0.65
1:A:252:LEU:HD23	1:A:252:LEU:O	1.96	0.65
1:A:146:ILE:O	1:A:149:LYS:HG2	1.96	0.65
1:A:216:VAL:HB	1:A:301:LEU:CD2	2.23	0.65
1:A:142:ASP:O	1:A:146:ILE:HG12	1.96	0.65
1:A:434:ILE:HG23	1:A:456:ALA:O	1.97	0.65
1:A:271:GLU:OE2	2:A:560:HOH:O	2.14	0.65
1:B:150:TYR:HB2	2:B:652:HOH:O	1.96	0.65
1:A:225:GLY:O	1:A:355:ARG:HA	1.96	0.65
1:B:243:TYR:HB2	1:B:343:PHE:CG	2.31	0.65
1:B:181:LYS:HE3	1:B:185:GLU:HB2	1.79	0.65
1:B:218:VAL:HB	1:B:297:LEU:HB2	1.78	0.64
1:A:35:ARG:HG3	1:A:314:LYS:HZ2	1.62	0.64
1:A:81:VAL:HG21	1:A:208:PHE:CE2	2.31	0.64
1:A:370:SER:HB2	1:A:416:ILE:HG12	1.78	0.64
1:A:409:ARG:NH1	1:A:428:VAL:H	1.95	0.64
1:A:57:VAL:HA	1:A:348:GLY:O	1.97	0.64
1:B:422:LEU:HD13	1:B:436:LEU:HD13	1.79	0.64
1:A:280:VAL:HG12	1:A:284:LYS:NZ	2.12	0.64
1:B:236:LEU:HA	1:B:241:ASN:HB2	1.78	0.64
1:A:305:LYS:O	1:A:309:GLU:HG3	1.96	0.64
1:B:96:THR:HG22	1:B:97:GLY:N	2.13	0.64
1:B:167:ARG:HG2	1:B:329:VAL:HG21	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:THR:O	1:B:113:LEU:HG	1.97	0.64
1:A:44:ILE:HD13	1:A:274:GLN:HB3	1.79	0.64
1:B:439:LYS:O	1:B:460:ASN:HA	1.97	0.64
1:B:322:LYS:HB3	1:B:329:VAL:CG2	2.27	0.64
1:B:79:LYS:HD3	1:B:214:GLU:OE2	1.97	0.64
1:A:171:ASP:OD1	1:A:172:GLU:HG3	1.98	0.64
1:A:266:LYS:HG3	2:A:594:HOH:O	1.97	0.64
1:B:11:LEU:CD2	1:B:33:VAL:HG11	2.27	0.64
1:A:79:LYS:HD2	1:A:237:ILE:HD13	1.79	0.64
1:B:140:HIS:ND1	1:B:161:ASN:HB2	2.13	0.64
1:A:77:LEU:O	2:A:526:HOH:O	2.15	0.64
1:A:272:ILE:HG12	2:A:535:HOH:O	1.96	0.64
1:B:26:LYS:O	1:B:30:ILE:HG12	1.98	0.64
1:A:52:PRO:HD3	1:A:261:ILE:HA	1.78	0.64
1:A:416:ILE:HB	1:A:419:LEU:HD22	1.80	0.64
1:B:150:TYR:HE2	2:B:554:HOH:O	1.81	0.64
1:B:287:GLU:HB2	2:B:578:HOH:O	1.98	0.64
1:B:114:ILE:CD1	1:B:221:SER:HB2	2.27	0.64
1:B:32:LEU:HB3	2:B:685:HOH:O	1.97	0.64
1:A:10:GLN:HB3	2:A:495:HOH:O	1.98	0.64
1:B:115:VAL:HG11	1:B:150:TYR:CG	2.32	0.64
1:B:20:GLU:HG2	2:B:563:HOH:O	1.97	0.64
1:A:286:ILE:O	1:A:290:LYS:HG2	1.98	0.64
1:B:349:VAL:HG13	1:B:351:VAL:HG13	1.80	0.64
1:A:134:MET:SD	1:A:195:VAL:HG23	2.38	0.64
1:B:347:ILE:HD13	1:B:347:ILE:C	2.16	0.64
1:A:439:LYS:NZ	1:A:462:ASN:HD21	1.95	0.64
1:A:232:ILE:O	1:A:236:LEU:HG	1.97	0.64
1:B:8:LEU:HD12	2:B:696:HOH:O	1.97	0.64
1:B:80:LEU:O	1:B:129:VAL:HG13	1.98	0.64
1:A:227:ILE:HA	2:A:550:HOH:O	1.98	0.64
1:B:415:SER:HA	2:B:544:HOH:O	1.98	0.64
1:B:266:LYS:HB2	2:B:597:HOH:O	1.97	0.64
1:A:343:PHE:O	2:A:573:HOH:O	2.15	0.64
1:B:320:ASN:OD1	2:B:694:HOH:O	2.15	0.64
1:B:244:CYS:HA	1:B:347:ILE:O	1.98	0.64
1:B:427:ASP:HB3	1:B:448:VAL:O	1.98	0.64
1:B:379:PHE:O	1:B:381:THR:HG23	1.98	0.64
1:A:8:LEU:H	1:A:8:LEU:HD23	1.62	0.64
1:A:355:ARG:HD3	2:A:548:HOH:O	1.98	0.64
1:B:132:VAL:HG22	1:B:158:HIS:CG	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:ALA:O	1:A:365:LEU:HG	1.98	0.64
1:B:296:ASN:O	1:B:297:LEU:HG	1.98	0.64
1:A:256:LYS:HE2	1:A:272:ILE:HD13	1.79	0.64
1:A:428:VAL:HG22	1:A:444:ALA:HB2	1.80	0.64
1:B:132:VAL:HG22	1:B:158:HIS:CB	2.17	0.63
1:B:437:LYS:HB2	1:B:459:GLU:HG3	1.80	0.63
1:A:248:THR:OG1	2:A:579:HOH:O	2.03	0.63
1:A:229:ASP:CB	1:A:232:ILE:HD12	2.27	0.63
1:B:66:VAL:HA	1:B:72:GLU:OE1	1.97	0.63
1:B:116:ILE:HG23	1:B:120:ASN:HD21	1.62	0.63
1:B:168:VAL:HB	1:B:330:LEU:HB3	1.79	0.63
1:A:17:GLY:O	1:A:19:THR:N	2.31	0.63
1:B:379:PHE:O	1:B:381:THR:HG23	1.98	0.63
1:B:77:LEU:HD21	1:B:121:LEU:HD21	1.79	0.63
1:A:99:LYS:O	1:A:99:LYS:HD3	1.99	0.63
1:A:199:LEU:HG	1:A:205:LEU:HB2	1.80	0.63
1:A:99:LYS:CG	1:A:102:ILE:HD12	2.27	0.63
1:B:276:PRO:HD2	1:B:279:HIS:HD2	1.63	0.63
1:B:89:LEU:HD21	1:B:138:ASN:HB3	1.80	0.63
1:B:136:SER:HA	1:B:162:GLN:HG2	1.79	0.63
1:A:392:PRO:CB	1:A:419:LEU:HD23	2.28	0.63
1:B:268:GLN:NE2	1:B:341:ARG:HD2	2.13	0.63
1:A:272:ILE:HG23	2:A:534:HOH:O	1.99	0.63
1:B:12:LYS:HG2	1:B:16:ASP:OD2	1.97	0.63
1:B:420:ASP:HB2	1:B:438:GLY:O	1.97	0.63
1:B:365:LEU:O	1:B:369:GLN:HG3	1.99	0.63
1:A:81:VAL:HG11	1:A:301:LEU:HD11	1.80	0.63
1:B:93:MET:HE1	1:B:365:LEU:HD11	1.80	0.63
1:B:190:PRO:HG2	1:B:194:ASP:HB2	1.78	0.63
1:A:439:LYS:H	1:A:460:ASN:HA	1.61	0.63
1:A:29:PHE:HA	1:A:32:LEU:HD13	1.78	0.63
1:B:50:GLN:HB2	1:B:262:SER:HB3	1.79	0.63
1:B:373:TYR:HA	1:B:381:THR:O	1.98	0.63
1:B:204:LYS:O	1:B:207:THR:HB	1.99	0.63
1:B:99:LYS:HZ2	1:B:360:LYS:HA	1.63	0.63
1:A:76:LEU:HD11	1:A:234:LYS:HB2	1.79	0.63
1:A:8:LEU:HG	1:A:9:PRO:CD	2.24	0.63
1:B:422:LEU:HA	1:B:440:VAL:O	1.98	0.63
1:A:109:THR:OG1	2:A:508:HOH:O	2.08	0.63
1:A:46:TRP:CZ3	1:A:279:HIS:HB3	2.33	0.63
1:B:372:LEU:HD23	1:B:372:LEU:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:330:LEU:HD23	1:B:331:GLN:N	2.14	0.63
1:B:263:TYR:O	1:B:264:GLU:HB2	1.98	0.63
1:A:235:HIS:HD2	2:A:574:HOH:O	1.82	0.63
1:B:98:PRO:HB2	1:B:101:VAL:HG13	1.81	0.63
1:B:359:VAL:C	1:B:360:LYS:HD2	2.18	0.63
1:B:164:LYS:HB3	2:B:572:HOH:O	1.98	0.63
1:B:276:PRO:HB2	1:B:278:GLU:HG2	1.81	0.63
1:A:227:ILE:O	1:A:227:ILE:HG13	1.99	0.63
1:A:205:LEU:O	1:A:209:LEU:HD13	1.99	0.63
1:B:294:THR:OG1	1:B:296:ASN:HB2	1.99	0.63
1:B:99:LYS:HZ1	1:B:360:LYS:HA	1.62	0.63
1:A:56:ILE:O	1:A:347:ILE:HB	1.98	0.63
1:A:306:LYS:NZ	2:A:522:HOH:O	2.31	0.63
1:B:111:LEU:HA	1:B:114:ILE:HD12	1.79	0.63
1:B:332:LEU:HD12	2:B:682:HOH:O	1.99	0.63
1:B:150:TYR:HB2	2:B:652:HOH:O	1.98	0.63
1:A:439:LYS:H	1:A:460:ASN:ND2	1.96	0.63
1:B:145:LYS:HG3	1:B:146:ILE:N	2.13	0.63
1:A:11:LEU:CD1	1:A:33:VAL:HG11	2.29	0.63
1:B:121:LEU:C	1:B:121:LEU:HD23	2.19	0.63
1:A:382:ARG:HH22	1:A:390:SER:C	2.01	0.63
1:A:250:LYS:HE2	1:A:292:PHE:HB3	1.79	0.63
1:A:235:HIS:CE1	1:A:239:ASN:HD22	2.17	0.63
1:A:8:LEU:H	1:A:9:PRO:CD	2.12	0.63
1:B:33:VAL:O	1:B:37:LEU:HG	1.99	0.62
1:A:268:GLN:NE2	1:A:341:ARG:NE	2.46	0.62
1:B:192:HIS:O	1:B:195:VAL:HG12	1.99	0.62
1:B:11:LEU:HD23	1:B:11:LEU:O	1.99	0.62
1:B:132:VAL:HA	1:B:158:HIS:O	1.99	0.62
1:A:275:VAL:HG21	1:A:283:PHE:CD1	2.35	0.62
1:A:8:LEU:CG	1:A:9:PRO:HD3	2.29	0.62
1:A:287:GLU:HA	1:A:290:LYS:HE2	1.81	0.62
1:B:18:LEU:HD13	1:B:187:TRP:CH2	2.34	0.62
1:B:322:LYS:HG3	1:B:323:GLU:H	1.63	0.62
1:B:422:LEU:CD1	1:B:436:LEU:HD13	2.29	0.62
1:A:55:GLU:HA	1:A:55:GLU:OE2	1.99	0.62
1:A:288:LYS:NZ	1:A:288:LYS:HB3	2.15	0.62
1:B:132:VAL:HG22	1:B:158:HIS:CB	2.30	0.62
1:A:423:LYS:HG2	1:A:424:VAL:N	2.14	0.62
1:A:77:LEU:HG	1:A:230:LEU:HD21	1.81	0.62
1:A:358:PRO:HB3	2:A:598:HOH:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:451:GLU:HB3	2:B:651:HOH:O	1.98	0.62
1:B:246:GLU:HA	1:B:349:VAL:HG13	1.81	0.62
1:B:135:ASN:HB2	1:B:139:THR:HG1	1.62	0.62
1:B:316:GLU:OE1	2:B:520:HOH:O	2.16	0.62
1:B:132:VAL:HG21	1:B:208:PHE:CE2	2.34	0.62
1:A:6:GLU:HG2	1:A:7:ASN:N	2.12	0.62
1:B:241:ASN:HD22	1:B:347:ILE:HG21	1.64	0.62
1:B:75:ASN:O	1:B:79:LYS:HE2	2.00	0.62
1:A:435:VAL:HB	1:A:457:VAL:HG22	1.81	0.62
1:B:373:TYR:O	1:B:374:THR:HG23	1.99	0.62
1:B:205:LEU:HD12	1:B:301:LEU:HD22	1.81	0.62
1:B:427:ASP:OD2	1:B:449:LYS:HG3	1.98	0.62
1:B:120:ASN:HA	1:B:123:ASN:HB2	1.81	0.62
1:A:200:MET:CG	1:A:205:LEU:HD23	2.23	0.62
1:B:59:PRO:HG3	2:B:543:HOH:O	2.00	0.62
1:A:243:TYR:OH	1:A:297:LEU:HD13	1.98	0.62
1:B:427:ASP:CB	2:B:531:HOH:O	2.46	0.62
1:B:116:ILE:CG2	1:B:120:ASN:HD21	2.12	0.62
1:B:70:VAL:HG23	2:B:556:HOH:O	1.99	0.62
1:B:85:LEU:O	1:B:221:SER:HB3	2.00	0.62
1:A:108:LEU:HD12	1:A:375:LEU:CD2	2.20	0.62
1:B:376:VAL:HB	1:B:381:THR:HG21	1.82	0.62
1:A:393:SER:HB3	1:A:421:SER:OG	1.99	0.62
1:A:222:ASP:O	1:A:358:PRO:HA	2.00	0.62
1:A:104:VAL:O	1:A:105:ARG:HB2	1.98	0.62
1:A:76:LEU:CD2	1:A:237:ILE:HD12	2.30	0.62
1:A:89:LEU:CB	1:A:91:THR:HG23	2.29	0.62
1:A:171:ASP:OD1	1:A:172:GLU:HG3	2.00	0.62
1:B:151:THR:C	1:B:152:ASN:HD22	2.02	0.62
1:B:396:LEU:HB3	1:B:400:PHE:HB2	1.81	0.62
1:A:142:ASP:O	1:A:146:ILE:HG12	1.99	0.62
1:A:213:LYS:NZ	2:A:526:HOH:O	2.24	0.62
1:B:463:ILE:HG23	1:B:468:ASP:CB	2.29	0.62
1:B:52:PRO:HB3	1:B:56:ILE:CB	2.29	0.62
1:A:83:LEU:HA	1:A:132:VAL:O	2.00	0.62
1:A:171:ASP:OD1	1:A:172:GLU:N	2.29	0.62
1:B:44:ILE:HG13	1:B:263:TYR:CZ	2.34	0.62
1:A:48:LYS:NZ	1:A:264:GLU:HG2	2.14	0.62
1:A:438:GLY:HA3	1:A:460:ASN:OD1	1.99	0.62
1:A:443:ALA:HB3	2:A:542:HOH:O	1.98	0.62
1:A:439:LYS:H	1:A:460:ASN:HD22	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:PRO:HD3	1:B:213:LYS:HE3	1.81	0.62
1:A:258:GLY:HA3	1:A:271:GLU:OE1	1.99	0.62
1:A:165:TYR:O	1:A:187:TRP:HB3	2.00	0.62
1:B:413:ILE:HG12	2:B:638:HOH:O	2.00	0.62
1:A:250:LYS:HE3	1:A:292:PHE:HB3	1.82	0.61
1:A:429:TRP:O	1:A:451:GLU:HA	2.00	0.61
1:A:89:LEU:HB2	1:A:91:THR:HG23	1.82	0.61
1:B:286:ILE:HG13	1:B:286:ILE:O	1.98	0.61
1:B:111:LEU:HD23	1:B:111:LEU:O	2.00	0.61
1:A:119:GLU:OE2	1:A:153:SER:HA	1.99	0.61
1:B:188:TYR:OH	1:B:332:LEU:N	2.32	0.61
1:B:250:LYS:HD2	1:B:289:PHE:O	2.00	0.61
1:A:105:ARG:NH2	1:A:374:THR:HA	2.13	0.61
1:B:105:ARG:HG2	1:B:375:LEU:HD13	1.82	0.61
1:A:7:ASN:HB3	2:A:640:HOH:O	2.00	0.61
1:B:286:ILE:HG12	2:B:657:HOH:O	1.98	0.61
1:B:250:LYS:HD2	1:B:289:PHE:O	1.99	0.61
1:A:6:GLU:O	1:A:7:ASN:HB2	2.00	0.61
1:A:414:PRO:O	1:A:416:ILE:HG23	1.99	0.61
1:A:271:GLU:OE2	2:A:561:HOH:O	2.16	0.61
1:B:66:VAL:HG13	1:B:72:GLU:CD	2.20	0.61
1:A:176:TRP:HH2	1:A:324:VAL:HB	1.65	0.61
1:B:341:ARG:HB2	1:B:341:ARG:NH1	2.15	0.61
1:B:411:LYS:HB3	1:B:431:GLY:C	2.20	0.61
1:B:227:ILE:HG23	1:B:355:ARG:NH2	2.14	0.61
1:B:81:VAL:HG22	1:B:130:PRO:CG	2.30	0.61
1:B:200:MET:SD	1:B:305:LYS:HG3	2.39	0.61
1:B:446:SER:O	1:B:448:VAL:HG23	1.99	0.61
1:A:229:ASP:HB3	1:A:232:ILE:HD12	1.81	0.61
1:B:372:LEU:O	1:B:372:LEU:HD23	2.01	0.61
1:A:372:LEU:HB2	1:A:416:ILE:HG13	1.81	0.61
1:A:81:VAL:O	1:A:216:VAL:HG23	2.00	0.61
1:B:395:GLU:HG2	1:B:423:LYS:HG3	1.81	0.61
1:B:8:LEU:HB3	2:B:697:HOH:O	2.00	0.61
1:A:419:LEU:HG	1:A:420:ASP:N	2.16	0.61
1:B:81:VAL:O	1:B:216:VAL:HA	2.00	0.61
1:B:361:ALA:HB1	2:B:482:HOH:O	2.01	0.61
1:B:20:GLU:HG2	2:B:563:HOH:O	2.01	0.61
1:B:90:GLY:HA2	1:B:99:LYS:HB2	1.83	0.61
1:A:18:LEU:HD21	1:A:178:SER:OG	2.01	0.61
1:A:416:ILE:CG2	1:A:419:LEU:HD13	2.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:ILE:HG12	2:B:624:HOH:O	1.99	0.61
1:A:81:VAL:HG23	1:A:216:VAL:HG23	1.82	0.61
1:A:424:VAL:HG22	1:A:442:VAL:HB	1.82	0.61
1:A:332:LEU:HD12	1:A:332:LEU:N	2.14	0.61
1:A:8:LEU:HD23	1:A:9:PRO:HD3	1.83	0.61
1:A:44:ILE:HG12	2:A:651:HOH:O	2.00	0.61
1:B:291:ILE:O	1:B:291:ILE:HD12	2.01	0.61
1:A:313:LEU:HB3	1:A:315:MET:SD	2.40	0.61
1:B:302:LYS:HG3	2:B:491:HOH:O	2.01	0.61
1:B:236:LEU:HD21	1:B:244:CYS:HB3	1.83	0.61
1:A:219:ALA:HB1	2:A:482:HOH:O	2.00	0.61
1:A:270:LEU:HD12	1:A:274:GLN:HB2	1.80	0.61
1:B:111:LEU:HA	1:B:114:ILE:CD1	2.30	0.61
1:A:384:LYS:HA	1:A:384:LYS:NZ	2.16	0.61
1:A:262:SER:HA	1:A:267:VAL:HA	1.83	0.61
1:B:266:LYS:HB3	2:B:598:HOH:O	2.00	0.61
1:B:355:ARG:CB	1:B:355:ARG:NH2	2.64	0.61
1:A:219:ALA:HA	1:A:295:ASN:O	2.00	0.61
1:A:106:ASP:HB2	1:A:375:LEU:CD2	2.30	0.61
1:B:70:VAL:HG23	2:B:556:HOH:O	1.99	0.61
1:A:136:SER:HB2	1:A:189:PRO:CG	2.31	0.61
1:A:271:GLU:HG3	2:A:560:HOH:O	2.01	0.61
1:B:359:VAL:C	1:B:360:LYS:HD2	2.20	0.61
1:B:29:PHE:O	1:B:33:VAL:HG23	2.00	0.61
1:B:393:SER:HB2	1:B:421:SER:CB	2.31	0.61
1:A:244:CYS:HA	1:A:347:ILE:O	2.01	0.61
1:A:433:SER:HB3	1:A:455:ARG:HG2	1.81	0.61
1:A:11:LEU:HD12	1:A:173:PHE:CE2	2.36	0.61
1:B:382:ARG:NH1	1:B:391:ASN:OD1	2.33	0.61
1:A:209:LEU:HD23	1:A:305:LYS:HD2	1.82	0.61
1:B:29:PHE:O	1:B:33:VAL:HG23	2.01	0.61
1:A:435:VAL:O	1:A:457:VAL:HG13	2.01	0.61
1:A:100:SER:C	1:A:102:ILE:H	2.04	0.60
1:B:57:VAL:HA	1:B:348:GLY:O	2.00	0.60
1:A:33:VAL:O	1:A:36:TYR:HB3	2.01	0.60
1:B:360:LYS:HD2	1:B:360:LYS:N	2.17	0.60
1:B:364:ASP:O	1:B:367:LEU:HB2	2.01	0.60
1:A:122:ASN:HB3	1:A:127:CYS:O	2.01	0.60
1:B:134:MET:SD	1:B:195:VAL:HG23	2.41	0.60
1:A:113:LEU:HD13	1:A:380:VAL:CG2	2.31	0.60
1:A:8:LEU:HG	1:A:9:PRO:HD3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ILE:HG12	2:A:651:HOH:O	2.01	0.60
1:B:360:LYS:HD2	1:B:360:LYS:N	2.16	0.60
1:B:89:LEU:HD11	1:B:138:ASN:HB3	1.83	0.60
1:A:423:LYS:HB3	1:A:441:THR:HG23	1.83	0.60
1:A:200:MET:SD	1:A:205:LEU:HD23	2.41	0.60
1:B:152:ASN:HD22	1:B:152:ASN:N	1.98	0.60
1:B:372:LEU:HD11	1:B:392:PRO:HD2	1.84	0.60
1:B:254:ASP:OD2	1:B:353:ARG:NH1	2.30	0.60
1:B:146:ILE:O	1:B:149:LYS:HG2	2.00	0.60
1:B:44:ILE:HD11	1:B:49:ILE:HD11	1.83	0.60
1:B:52:PRO:HB3	1:B:56:ILE:HG22	1.83	0.60
1:A:52:PRO:HA	1:A:56:ILE:HD12	1.81	0.60
1:B:244:CYS:SG	1:B:298:TRP:CB	2.84	0.60
1:A:167:ARG:HG2	1:A:329:VAL:HG21	1.83	0.60
1:B:232:ILE:O	1:B:236:LEU:HG	2.02	0.60
1:A:374:THR:O	1:A:381:THR:N	2.34	0.60
1:A:104:VAL:HG13	1:A:105:ARG:H	1.66	0.60
1:B:144:HIS:O	1:B:147:VAL:HG22	2.01	0.60
1:A:83:LEU:O	1:A:84:LYS:HD3	2.00	0.60
1:A:421:SER:C	2:A:582:HOH:O	2.40	0.60
1:B:11:LEU:HD12	1:B:173:PHE:CE2	2.36	0.60
1:B:73:THR:HG22	1:B:77:LEU:HD12	1.84	0.60
1:A:243:TYR:OH	1:A:337:GLY:HA2	2.01	0.60
1:B:96:THR:O	1:B:97:GLY:O	2.20	0.60
1:B:134:MET:CE	1:B:162:GLN:NE2	2.65	0.60
1:A:271:GLU:C	1:A:273:ALA:H	2.05	0.60
1:B:296:ASN:C	1:B:297:LEU:HG	2.21	0.60
1:A:275:VAL:HG21	1:A:283:PHE:CD1	2.37	0.60
1:B:244:CYS:HB2	1:B:298:TRP:HB2	1.84	0.60
1:A:26:LYS:O	1:A:30:ILE:HG12	2.02	0.60
1:B:170:ALA:HB2	1:B:328:LYS:CB	2.32	0.60
1:B:200:MET:SD	1:B:205:LEU:HD23	2.41	0.60
1:A:196:PHE:HB2	1:A:197:PRO:CD	2.32	0.60
1:A:370:SER:HB3	1:A:413:ILE:HG22	1.82	0.60
1:A:77:LEU:HG	1:A:230:LEU:HD11	1.82	0.60
1:A:65:PRO:HA	1:A:231:THR:OG1	2.01	0.60
1:A:7:ASN:OD1	1:A:8:LEU:HD23	2.02	0.60
1:B:54:ASP:OD2	1:B:59:PRO:HG2	2.00	0.60
1:B:176:TRP:HB3	1:B:177:PRO:HD3	1.83	0.60
1:A:439:LYS:HD2	1:A:440:VAL:N	2.16	0.60
1:A:79:LYS:HA	1:A:213:LYS:HD3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ASP:CB	1:A:375:LEU:HD22	2.31	0.60
1:B:272:ILE:O	1:B:272:ILE:HG12	2.02	0.60
1:B:11:LEU:HD21	1:B:175:PRO:HG3	1.84	0.60
1:A:62:LYS:HG3	1:A:62:LYS:O	2.01	0.60
1:B:417:VAL:HG13	1:B:418:GLU:HG3	1.83	0.60
1:B:32:LEU:HD11	1:B:317:ILE:HD12	1.84	0.60
1:A:18:LEU:CD1	1:A:177:PRO:HB2	2.31	0.60
1:A:6:GLU:HG2	1:A:7:ASN:N	2.15	0.60
1:B:205:LEU:HD11	1:B:304:ILE:HB	1.83	0.60
1:A:272:ILE:HG12	2:A:535:HOH:O	2.02	0.60
1:A:251:THR:O	1:A:286:ILE:HG21	2.00	0.60
1:B:81:VAL:HG22	1:B:130:PRO:CG	2.31	0.60
1:A:49:ILE:HG12	1:A:261:ILE:HD12	1.84	0.60
1:A:77:LEU:CD2	1:A:230:LEU:HD21	2.32	0.60
1:A:410:PHE:O	1:A:411:LYS:C	2.40	0.59
1:B:208:PHE:HB3	1:B:213:LYS:HB2	1.82	0.59
1:B:150:TYR:HB2	2:B:653:HOH:O	2.01	0.59
1:A:289:PHE:HD1	2:A:531:HOH:O	1.85	0.59
1:B:66:VAL:HG21	1:B:230:LEU:HB3	1.84	0.59
1:A:425:SER:OG	1:A:443:ALA:HA	2.02	0.59
1:A:395:GLU:HB3	1:A:422:LEU:O	2.02	0.59
1:B:272:ILE:HB	1:B:283:PHE:CD2	2.36	0.59
1:B:379:PHE:O	1:B:381:THR:HG23	2.02	0.59
1:A:123:ASN:HB2	2:A:552:HOH:O	2.00	0.59
1:A:459:GLU:O	1:A:460:ASN:C	2.40	0.59
1:A:235:HIS:HA	1:A:238:GLN:HG3	1.82	0.59
1:B:445:LYS:HG3	2:B:564:HOH:O	2.02	0.59
1:A:103:GLU:HA	1:A:109:THR:HA	1.84	0.59
1:B:424:VAL:HG13	1:B:442:VAL:O	2.01	0.59
1:A:250:LYS:CE	1:A:292:PHE:HB3	2.32	0.59
1:B:401:LYS:HB2	2:B:499:HOH:O	2.02	0.59
1:B:32:LEU:HB3	2:B:682:HOH:O	2.02	0.59
1:A:265:GLY:O	1:A:266:LYS:HE2	2.02	0.59
1:A:280:VAL:HG12	1:A:284:LYS:HZ3	1.67	0.59
1:B:287:GLU:OE2	2:B:578:HOH:O	2.17	0.59
1:A:103:GLU:OE1	1:A:107:GLY:HA2	2.03	0.59
1:A:82:VAL:HG11	1:A:118:ILE:HD11	1.84	0.59
1:A:6:GLU:CG	1:A:7:ASN:H	2.15	0.59
1:A:409:ARG:HH12	1:A:428:VAL:H	1.50	0.59
1:B:425:SER:O	1:B:443:ALA:HA	2.02	0.59
1:B:230:LEU:HD12	1:B:230:LEU:N	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:VAL:HB	1:A:30:ILE:HD11	1.84	0.59
1:B:98:PRO:HD2	1:B:101:VAL:HG11	1.83	0.59
1:B:315:MET:CE	1:B:339:ALA:HB2	2.32	0.59
1:A:247:VAL:O	1:A:351:VAL:HG22	2.02	0.59
1:B:420:ASP:HB2	1:B:439:LYS:HG2	1.84	0.59
1:A:268:GLN:HG2	1:A:341:ARG:HB3	1.82	0.59
1:B:96:THR:HG22	1:B:97:GLY:H	1.67	0.59
1:A:181:LYS:HE3	1:A:185:GLU:HB2	1.83	0.59
1:B:109:THR:HG23	1:B:112:ASP:OD2	2.01	0.59
1:A:403:VAL:O	1:A:407:LEU:HG	2.01	0.59
1:A:249:PRO:O	2:A:579:HOH:O	2.17	0.59
1:B:118:ILE:HG12	1:B:131:LEU:HD22	1.84	0.59
1:A:199:LEU:HD12	1:A:204:LYS:HB2	1.84	0.59
1:A:239:ASN:ND2	2:A:625:HOH:O	2.35	0.59
1:A:272:ILE:HG23	1:A:283:PHE:CE2	2.37	0.59
1:A:88:GLY:O	1:A:139:THR:HG21	2.02	0.59
1:B:89:LEU:CG	2:B:660:HOH:O	2.50	0.59
1:B:258:GLY:HA3	1:B:271:GLU:OE2	2.02	0.59
1:A:247:VAL:O	1:A:351:VAL:HG22	2.03	0.59
1:A:424:VAL:HA	1:A:442:VAL:O	2.02	0.59
1:A:11:LEU:HD23	1:A:11:LEU:C	2.22	0.59
1:B:283:PHE:HA	1:B:289:PHE:CD2	2.38	0.59
1:B:366:LEU:HD22	1:B:394:ILE:HD13	1.85	0.59
1:A:271:GLU:OE2	1:A:272:ILE:CG1	2.50	0.59
1:B:142:ASP:O	1:B:145:LYS:HB3	2.02	0.59
1:B:128:LYS:HD2	2:B:669:HOH:O	2.02	0.59
1:B:53:THR:OG1	1:B:55:GLU:HG2	2.03	0.59
1:A:255:VAL:HB	1:A:284:LYS:HB3	1.84	0.59
1:A:225:GLY:O	1:A:355:ARG:HA	2.03	0.59
1:A:197:PRO:HA	1:A:308:VAL:HG11	1.84	0.59
1:B:423:LYS:O	1:B:441:THR:HA	2.03	0.59
1:B:411:LYS:CD	1:B:431:GLY:HA2	2.33	0.59
1:B:243:TYR:OH	1:B:337:GLY:HA2	2.03	0.59
1:A:12:LYS:HG3	1:A:30:ILE:HG13	1.84	0.59
1:B:241:ASN:HD22	1:B:347:ILE:CG2	2.15	0.59
1:A:208:PHE:HA	1:A:211:GLN:OE1	2.02	0.59
1:B:171:ASP:OD1	1:B:172:GLU:HG3	2.03	0.59
1:A:355:ARG:HD3	2:A:549:HOH:O	2.01	0.59
1:B:89:LEU:CB	2:B:660:HOH:O	2.50	0.59
1:A:266:LYS:HA	2:A:594:HOH:O	2.02	0.59
1:A:280:VAL:HG12	1:A:284:LYS:NZ	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:GLN:CD	2:B:592:HOH:O	2.41	0.59
1:B:115:VAL:HG11	1:B:150:TYR:CD1	2.38	0.59
1:B:465:GLY:HA3	1:B:467:GLU:OE2	2.03	0.59
1:B:402:LYS:O	1:B:405:THR:N	2.34	0.59
1:B:122:ASN:ND2	1:B:154:ASN:O	2.32	0.59
1:B:220:ASN:OD1	2:B:637:HOH:O	2.16	0.59
1:B:105:ARG:HD2	2:B:558:HOH:O	2.03	0.59
1:A:77:LEU:HD21	1:A:230:LEU:HD21	1.85	0.59
1:A:140:HIS:CG	1:A:161:ASN:HB2	2.37	0.59
1:A:121:LEU:HD23	1:A:121:LEU:O	2.02	0.59
1:A:219:ALA:HA	1:A:295:ASN:O	2.02	0.59
1:B:330:LEU:HD23	1:B:331:GLN:N	2.18	0.59
1:B:30:ILE:C	1:B:32:LEU:N	2.56	0.59
1:A:124:LYS:HE3	1:A:125:TYR:OH	2.02	0.59
1:A:207:THR:HG22	1:A:211:GLN:OE1	2.02	0.59
1:B:426:GLY:HA3	1:B:444:ALA:HB3	1.85	0.59
1:A:9:PRO:HD2	2:A:553:HOH:O	2.02	0.59
1:B:357:LEU:HD22	1:B:357:LEU:O	2.03	0.59
1:B:235:HIS:O	1:B:239:ASN:ND2	2.35	0.59
1:A:132:VAL:CB	1:A:158:HIS:HB2	2.32	0.59
1:A:366:LEU:O	1:A:366:LEU:HD23	2.02	0.59
1:A:80:LEU:HD11	1:A:217:PHE:HB2	1.85	0.59
1:A:35:ARG:O	1:A:38:SER:HB2	2.03	0.58
1:A:121:LEU:HD23	1:A:121:LEU:C	2.23	0.58
1:A:382:ARG:C	2:A:590:HOH:O	2.40	0.58
1:B:229:ASP:HB3	1:B:232:ILE:HD12	1.84	0.58
1:A:98:PRO:HG3	1:A:139:THR:HB	1.85	0.58
1:A:419:LEU:HG	1:A:420:ASP:H	1.66	0.58
1:A:426:GLY:O	1:A:428:VAL:HG23	2.02	0.58
1:A:11:LEU:HD12	1:A:175:PRO:HD3	1.84	0.58
1:A:439:LYS:H	1:A:460:ASN:ND2	2.01	0.58
1:B:110:PHE:CD1	1:B:222:ASP:HA	2.38	0.58
1:A:272:ILE:HG23	1:A:283:PHE:CE2	2.38	0.58
1:B:267:VAL:O	1:B:341:ARG:HB3	2.03	0.58
1:A:241:ASN:HA	1:A:345:ASN:HD22	1.68	0.58
1:A:208:PHE:O	1:A:213:LYS:HB2	2.03	0.58
1:A:434:ILE:HA	1:A:456:ALA:O	2.02	0.58
1:A:374:THR:HG23	1:A:376:VAL:HG23	1.86	0.58
1:B:369:GLN:O	1:B:413:ILE:HG21	2.03	0.58
1:B:144:HIS:HA	1:B:147:VAL:HG22	1.84	0.58
1:A:110:PHE:O	1:A:114:ILE:HG13	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:MET:SD	1:B:339:ALA:HB2	2.42	0.58
1:A:359:VAL:HA	1:A:364:ASP:CB	2.32	0.58
1:A:246:GLU:OE1	1:A:355:ARG:NH1	2.36	0.58
1:A:56:ILE:HG22	1:A:57:VAL:CG2	2.31	0.58
1:A:9:PRO:HD2	2:A:554:HOH:O	2.02	0.58
1:B:372:LEU:HD22	1:B:373:TYR:CE1	2.38	0.58
1:B:414:PRO:HG3	2:B:495:HOH:O	2.01	0.58
1:A:142:ASP:O	1:A:146:ILE:HG12	2.03	0.58
1:B:242:GLU:CD	1:B:344:ASP:H	2.06	0.58
1:B:332:LEU:HD12	2:B:683:HOH:O	2.02	0.58
1:A:445:LYS:N	1:A:448:VAL:HB	2.18	0.58
1:A:227:ILE:HG21	1:A:379:PHE:CE1	2.38	0.58
1:A:461:LYS:NZ	1:A:468:ASP:HB3	2.18	0.58
1:A:207:THR:O	1:A:211:GLN:HG3	2.03	0.58
1:B:242:GLU:HB3	1:B:343:PHE:HD1	1.68	0.58
1:B:359:VAL:HG13	1:B:364:ASP:HB2	1.85	0.58
1:A:294:THR:O	1:A:295:ASN:HB2	2.02	0.58
1:B:74:LYS:HB3	2:B:706:HOH:O	2.03	0.58
1:A:117:GLN:HG2	2:A:598:HOH:O	2.03	0.58
1:B:366:LEU:HD23	1:B:366:LEU:C	2.24	0.58
1:B:103:GLU:HA	1:B:108:LEU:O	2.04	0.58
1:B:134:MET:HE1	1:B:162:GLN:HE22	1.69	0.58
1:A:77:LEU:HD23	1:A:230:LEU:HD21	1.84	0.58
1:A:232:ILE:O	1:A:236:LEU:HG	2.03	0.58
1:B:35:ARG:NH2	1:B:314:LYS:HD3	2.19	0.58
1:B:405:THR:HG22	2:B:565:HOH:O	2.03	0.58
1:B:105:ARG:HG3	1:B:106:ASP:N	2.18	0.58
1:A:411:LYS:HB3	1:A:432:SER:HB3	1.83	0.58
1:B:103:GLU:OE1	1:B:107:GLY:HA2	2.04	0.58
1:B:69:ASP:HA	2:B:556:HOH:O	2.02	0.58
1:B:420:ASP:OD2	1:B:438:GLY:HA2	2.03	0.58
1:A:76:LEU:CD1	1:A:234:LYS:HB2	2.33	0.58
1:A:196:PHE:CD1	1:A:304:ILE:HD13	2.39	0.58
1:A:44:ILE:N	2:A:595:HOH:O	2.37	0.58
1:A:100:SER:O	1:A:110:PHE:HB2	2.03	0.58
1:A:105:ARG:NH1	1:A:369:GLN:HA	2.19	0.58
1:B:164:LYS:HB3	2:B:571:HOH:O	2.02	0.58
1:A:128:LYS:O	2:A:633:HOH:O	2.16	0.58
1:A:103:GLU:OE1	1:A:107:GLY:HA2	2.03	0.58
1:A:227:ILE:HG13	1:A:227:ILE:O	2.03	0.58
1:A:76:LEU:HD23	1:A:237:ILE:HD12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:HIS:HB3	1:A:204:LYS:HE3	1.85	0.58
1:A:75:ASN:HA	1:A:78:ASP:OD2	2.03	0.58
1:B:150:TYR:HE2	2:B:554:HOH:O	1.86	0.58
1:A:99:LYS:NZ	1:A:360:LYS:HA	2.19	0.58
1:B:169:VAL:HG11	1:B:172:GLU:HG3	1.85	0.58
1:B:66:VAL:HG13	1:B:72:GLU:CD	2.24	0.58
1:A:461:LYS:CE	1:A:463:ILE:HG12	2.33	0.58
1:B:136:SER:CB	1:B:162:GLN:HE21	2.17	0.58
1:B:167:ARG:O	1:B:329:VAL:HB	2.04	0.58
1:B:176:TRP:CE3	1:B:329:VAL:HG11	2.38	0.58
1:B:80:LEU:O	2:B:480:HOH:O	2.16	0.58
1:A:85:LEU:HD12	1:A:220:ASN:OD1	2.04	0.58
1:B:60:TYR:OH	1:B:231:THR:HB	2.03	0.58
1:B:73:THR:HG23	1:B:230:LEU:CD2	2.34	0.58
1:A:219:ALA:HB3	2:A:492:HOH:O	2.02	0.58
1:A:105:ARG:HH11	1:A:105:ARG:HG3	1.69	0.58
1:A:242:GLU:OE1	1:A:344:ASP:HB2	2.04	0.58
1:B:66:VAL:HG22	1:B:234:LYS:HD2	1.85	0.58
1:B:165:TYR:CD2	1:B:190:PRO:HB3	2.39	0.58
1:B:32:LEU:O	1:B:35:ARG:N	2.36	0.58
1:A:367:LEU:HD22	1:A:372:LEU:HD23	1.86	0.58
1:B:432:SER:H	1:B:454:ASP:CG	2.07	0.58
1:B:220:ASN:OD1	2:B:636:HOH:O	2.17	0.58
1:A:200:MET:CG	1:A:205:LEU:HD23	2.31	0.58
1:B:224:LEU:HD13	1:B:380:VAL:HG21	1.86	0.58
1:A:146:ILE:O	1:A:149:LYS:HG2	2.04	0.58
1:A:53:THR:OG1	1:A:55:GLU:HB2	2.04	0.58
1:A:83:LEU:CD2	1:A:218:VAL:HG13	2.30	0.58
1:A:200:MET:C	1:A:200:MET:SD	2.82	0.58
1:A:453:PRO:O	1:A:456:ALA:HB2	2.04	0.57
1:A:81:VAL:HG13	1:A:216:VAL:CA	2.31	0.57
1:B:50:GLN:HB2	1:B:262:SER:HB2	1.86	0.57
1:A:35:ARG:O	1:A:38:SER:N	2.35	0.57
1:B:50:GLN:OE1	2:B:643:HOH:O	2.17	0.57
1:B:135:ASN:O	1:B:161:ASN:HA	2.04	0.57
1:A:8:LEU:HD23	1:A:9:PRO:HD3	1.85	0.57
1:B:132:VAL:CG2	1:B:158:HIS:HB2	2.20	0.57
1:A:124:LYS:HE3	1:A:125:TYR:CZ	2.38	0.57
1:B:276:PRO:HB2	1:B:278:GLU:CG	2.33	0.57
1:A:167:ARG:HG3	1:A:188:TYR:HB3	1.84	0.57
1:A:120:ASN:ND2	1:A:377:ASP:O	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:ARG:HH22	1:A:386:ARG:HG2	1.68	0.57
1:B:359:VAL:HG11	1:B:365:LEU:CD2	2.34	0.57
1:A:8:LEU:H	1:A:9:PRO:HD3	1.69	0.57
1:A:420:ASP:HB2	1:A:438:GLY:C	2.24	0.57
1:A:395:GLU:OE2	1:A:423:LYS:HG3	2.04	0.57
1:B:218:VAL:HB	1:B:297:LEU:HB2	1.86	0.57
1:B:416:ILE:HB	1:B:419:LEU:HD22	1.84	0.57
1:B:399:GLU:HG2	1:B:426:GLY:O	2.03	0.57
1:B:98:PRO:O	1:B:101:VAL:HG22	2.05	0.57
1:A:111:LEU:HA	1:A:114:ILE:HD12	1.87	0.57
1:A:81:VAL:O	1:A:216:VAL:HA	2.03	0.57
1:B:465:GLY:O	1:B:468:ASP:HB2	2.03	0.57
1:B:51:THR:HG23	1:B:52:PRO:HD2	1.85	0.57
1:B:56:ILE:HG13	1:B:262:SER:OG	2.03	0.57
1:A:278:GLU:H	1:A:278:GLU:CD	2.08	0.57
1:B:467:GLU:H	1:B:467:GLU:CD	2.08	0.57
1:A:66:VAL:CA	1:A:234:LYS:HE2	2.34	0.57
1:A:384:LYS:O	1:A:384:LYS:HE3	2.04	0.57
1:A:116:ILE:HG21	1:A:378:GLY:HA3	1.85	0.57
1:B:461:LYS:HG2	1:B:463:ILE:HG13	1.86	0.57
1:A:366:LEU:HD22	1:A:394:ILE:HD13	1.85	0.57
1:B:73:THR:HG23	1:B:230:LEU:HD11	1.84	0.57
1:B:93:MET:SD	1:B:99:LYS:HE3	2.43	0.57
1:A:66:VAL:HA	1:A:234:LYS:HZ1	1.67	0.57
1:B:155:VAL:O	1:B:155:VAL:HG13	2.05	0.57
1:A:425:SER:OG	2:A:578:HOH:O	2.17	0.57
1:B:196:PHE:CD1	1:B:304:ILE:HD13	2.40	0.57
1:A:355:ARG:HH11	1:A:355:ARG:CG	2.00	0.57
1:A:250:LYS:HE3	1:A:292:PHE:HB3	1.86	0.57
1:B:64:THR:N	2:B:506:HOH:O	2.35	0.57
1:B:150:TYR:HD2	2:B:653:HOH:O	1.86	0.57
1:B:324:VAL:O	1:B:325:ASP:HB2	2.04	0.57
1:B:11:LEU:CD1	1:B:33:VAL:HG11	2.34	0.57
1:B:92:THR:O	1:B:92:THR:HG22	2.05	0.57
1:B:268:GLN:NE2	1:B:341:ARG:CB	2.63	0.57
1:A:124:LYS:HE3	1:A:125:TYR:OH	2.04	0.57
1:B:137:PHE:CD1	1:B:184:LYS:HD2	2.39	0.57
1:B:89:LEU:HB2	2:B:660:HOH:O	2.04	0.57
1:B:382:ARG:NH1	1:B:391:ASN:OD1	2.37	0.57
1:B:293:ASN:HD22	1:B:294:THR:H	1.53	0.57
1:B:9:PRO:HA	1:B:12:LYS:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:463:ILE:HG23	1:B:468:ASP:HB2	1.87	0.57
1:A:89:LEU:HD11	1:A:138:ASN:HB3	1.86	0.57
1:B:170:ALA:HB2	1:B:328:LYS:HB2	1.86	0.57
1:A:419:LEU:HD13	1:A:436:LEU:HB3	1.87	0.57
1:B:319:PRO:HA	1:B:331:GLN:O	2.04	0.57
1:A:164:LYS:HE3	2:A:525:HOH:O	2.04	0.57
1:A:200:MET:HG2	1:A:205:LEU:HD13	1.87	0.57
1:B:222:ASP:O	1:B:358:PRO:HA	2.05	0.57
1:B:341:ARG:HH11	1:B:341:ARG:CB	2.14	0.57
1:B:330:LEU:HD21	1:B:332:LEU:HD23	1.87	0.57
1:B:365:LEU:O	1:B:369:GLN:HG3	2.05	0.57
1:A:102:ILE:HG22	1:A:103:GLU:H	1.69	0.57
1:B:242:GLU:OE2	1:B:344:ASP:HB2	2.04	0.57
1:B:319:PRO:O	1:B:321:PRO:HD3	2.05	0.57
1:A:49:ILE:HG12	1:A:261:ILE:HD12	1.85	0.57
1:B:140:HIS:CD2	1:B:161:ASN:HB2	2.40	0.57
1:B:191:GLY:HA3	1:B:334:THR:O	2.04	0.57
1:B:103:GLU:HA	1:B:109:THR:HA	1.86	0.57
1:A:11:LEU:HD11	1:A:173:PHE:CE2	2.36	0.57
1:A:207:THR:HG22	1:A:211:GLN:OE1	2.04	0.57
1:B:336:ALA:C	1:B:338:ALA:H	2.06	0.57
1:B:322:LYS:HZ2	1:B:324:VAL:HG22	1.67	0.57
1:B:106:ASP:OD2	1:B:375:LEU:HD13	2.05	0.57
1:A:291:ILE:HG21	1:A:350:ASN:ND2	2.19	0.57
1:B:103:GLU:OE1	1:B:107:GLY:HA2	2.05	0.56
1:B:106:ASP:HB2	1:B:375:LEU:HD22	1.87	0.56
1:B:140:HIS:CG	1:B:161:ASN:OD1	2.58	0.56
1:A:104:VAL:HG13	1:A:105:ARG:H	1.70	0.56
1:A:232:ILE:O	1:A:236:LEU:HG	2.05	0.56
1:A:439:LYS:HD2	1:A:440:VAL:N	2.20	0.56
1:A:45:GLU:HB3	1:A:48:LYS:HG3	1.86	0.56
1:B:247:VAL:HG21	1:B:291:ILE:HD13	1.87	0.56
1:A:411:LYS:CD	1:A:431:GLY:HA2	2.35	0.56
1:B:272:ILE:HD12	1:B:284:LYS:HE3	1.87	0.56
1:A:117:GLN:NE2	1:A:379:PHE:HD1	2.03	0.56
1:A:8:LEU:HD23	1:A:9:PRO:HD3	1.87	0.56
1:B:420:ASP:HB2	1:B:438:GLY:C	2.25	0.56
1:A:411:LYS:HE3	2:A:610:HOH:O	2.05	0.56
1:B:44:ILE:HG13	1:B:263:TYR:CZ	2.40	0.56
1:A:294:THR:HB	1:A:296:ASN:HD22	1.70	0.56
1:A:171:ASP:OD1	1:A:172:GLU:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:TYR:HB2	1:B:350:ASN:O	2.04	0.56
1:A:121:LEU:HD11	1:A:228:VAL:HG21	1.87	0.56
1:B:14:ALA:HB1	1:B:178:SER:OG	2.06	0.56
1:A:420:ASP:OD2	1:A:438:GLY:HA2	2.04	0.56
1:B:262:SER:HA	1:B:266:LYS:O	2.04	0.56
1:B:21:MET:HG2	2:B:571:HOH:O	2.04	0.56
1:B:9:PRO:HD2	2:B:697:HOH:O	2.05	0.56
1:B:66:VAL:HG11	1:B:73:THR:OG1	2.05	0.56
1:A:15:VAL:HG21	1:A:30:ILE:HD11	1.87	0.56
1:A:246:GLU:OE2	1:A:355:ARG:NH1	2.38	0.56
1:A:362:SER:HB2	2:A:491:HOH:O	2.05	0.56
1:B:30:ILE:O	1:B:32:LEU:N	2.39	0.56
1:A:322:LYS:CG	1:A:331:GLN:HE22	2.16	0.56
1:B:223:ASN:OD1	1:B:357:LEU:N	2.32	0.56
1:B:94:GLY:HA3	1:B:402:LYS:HG2	1.85	0.56
1:B:162:GLN:HB2	1:B:194:ASP:OD2	2.06	0.56
1:B:263:TYR:CE2	1:B:264:GLU:HG3	2.41	0.56
1:A:103:GLU:OE1	1:A:107:GLY:HA2	2.06	0.56
1:B:51:THR:HG22	1:B:52:PRO:HD2	1.87	0.56
1:A:402:LYS:HD3	1:A:405:THR:OG1	2.04	0.56
1:B:223:ASN:OD1	1:B:357:LEU:N	2.37	0.56
1:A:73:THR:HG23	1:A:230:LEU:HD11	1.88	0.56
1:A:255:VAL:O	1:A:284:LYS:HG2	2.05	0.56
1:A:113:LEU:HD13	1:A:380:VAL:HG23	1.87	0.56
1:A:366:LEU:O	1:A:366:LEU:HD23	2.05	0.56
1:B:329:VAL:O	1:B:330:LEU:HD23	2.05	0.56
1:A:8:LEU:CG	1:A:9:PRO:HD3	2.35	0.56
1:A:115:VAL:HG21	1:A:150:TYR:CE1	2.41	0.56
1:A:168:VAL:HG13	1:A:174:VAL:O	2.06	0.56
1:A:255:VAL:O	1:A:284:LYS:HA	2.06	0.56
1:A:396:LEU:HB3	1:A:400:PHE:CD2	2.39	0.56
1:B:242:GLU:OE1	1:B:344:ASP:N	2.28	0.56
1:B:247:VAL:O	1:B:351:VAL:N	2.32	0.56
1:A:14:ALA:O	2:A:494:HOH:O	2.18	0.56
1:B:11:LEU:HG	1:B:175:PRO:HD3	1.87	0.56
1:B:66:VAL:CG1	2:B:502:HOH:O	2.52	0.56
1:B:170:ALA:HB2	1:B:328:LYS:O	2.05	0.56
1:A:236:LEU:HA	1:A:241:ASN:HB2	1.86	0.56
1:A:99:LYS:NZ	2:A:546:HOH:O	2.38	0.56
1:B:162:GLN:NE2	1:B:189:PRO:HB2	2.20	0.56
1:B:51:THR:CG2	1:B:288:LYS:HE3	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:LEU:HD23	1:B:114:ILE:HD12	1.87	0.56
1:B:152:ASN:HD22	1:B:152:ASN:N	2.01	0.56
1:A:18:LEU:HD13	1:A:177:PRO:HB2	1.86	0.56
1:A:111:LEU:CD2	1:A:146:ILE:HG21	2.35	0.56
1:B:20:GLU:HG2	2:B:563:HOH:O	2.04	0.56
1:B:330:LEU:HD23	1:B:331:GLN:H	1.71	0.56
1:B:363:SER:HB3	1:B:396:LEU:HG	1.87	0.56
1:B:244:CYS:SG	1:B:347:ILE:HG13	2.45	0.56
1:B:246:GLU:HG2	1:B:349:VAL:HG13	1.88	0.56
1:A:255:VAL:HB	1:A:284:LYS:CD	2.35	0.56
1:A:255:VAL:HB	1:A:284:LYS:HD2	1.86	0.56
1:A:442:VAL:HG11	1:A:452:ILE:HD11	1.86	0.56
1:A:295:ASN:OD1	1:A:297:LEU:HD11	2.06	0.56
1:B:335:ALA:O	1:B:338:ALA:HB3	2.06	0.56
1:B:145:LYS:HG3	1:B:146:ILE:H	1.69	0.56
1:A:322:LYS:HG3	1:A:331:GLN:NE2	2.21	0.56
1:A:89:LEU:HB3	1:A:91:THR:HG23	1.87	0.56
1:B:259:THR:OG1	1:B:291:ILE:HD12	2.06	0.56
1:A:98:PRO:HB2	1:A:101:VAL:HG13	1.86	0.56
1:A:271:GLU:HG2	1:A:272:ILE:N	2.20	0.56
1:A:85:LEU:O	1:A:221:SER:HB3	2.06	0.56
1:B:461:LYS:HG3	2:B:625:HOH:O	2.05	0.56
1:B:267:VAL:HG13	2:B:568:HOH:O	2.05	0.56
1:A:190:PRO:HA	1:A:333:GLU:HG2	1.88	0.56
1:B:100:SER:O	1:B:110:PHE:HB2	2.05	0.56
1:B:227:ILE:CG1	1:B:355:ARG:NH2	2.68	0.56
1:A:318:ILE:HD12	1:A:318:ILE:N	2.21	0.56
1:A:77:LEU:HD23	1:A:230:LEU:HD21	1.88	0.56
1:A:79:LYS:HD2	1:A:237:ILE:CD1	2.34	0.56
1:A:318:ILE:N	1:A:318:ILE:HD12	2.21	0.56
1:B:370:SER:HB2	1:B:416:ILE:HG12	1.88	0.56
1:B:164:LYS:O	1:B:165:TYR:HD1	1.88	0.56
1:A:10:GLN:HB2	2:A:552:HOH:O	2.05	0.56
1:A:127:CYS:HB2	2:A:644:HOH:O	2.05	0.56
1:B:133:LEU:O	1:B:135:ASN:ND2	2.39	0.56
1:B:103:GLU:HA	1:B:109:THR:HA	1.87	0.56
1:A:99:LYS:NZ	1:A:110:PHE:CE2	2.74	0.56
1:A:81:VAL:CG1	1:A:301:LEU:HD11	2.36	0.56
1:A:149:LYS:HE2	2:A:613:HOH:O	2.06	0.56
1:B:185:GLU:OE1	1:B:324:VAL:HG11	2.05	0.56
1:B:369:GLN:HB3	1:B:413:ILE:HG13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:LEU:N	1:B:9:PRO:CD	2.69	0.56
1:B:243:TYR:OH	1:B:336:ALA:O	2.23	0.56
1:B:177:PRO:O	1:B:180:GLY:N	2.33	0.56
1:B:347:ILE:HD13	1:B:347:ILE:O	2.04	0.56
1:A:247:VAL:CB	1:A:291:ILE:HD13	2.34	0.56
1:B:119:GLU:CD	1:B:153:SER:HB3	2.26	0.56
1:A:105:ARG:HH11	1:A:369:GLN:HA	1.70	0.56
1:A:364:ASP:O	1:A:367:LEU:HB2	2.06	0.56
1:A:44:ILE:N	1:A:44:ILE:HD12	2.21	0.56
1:A:8:LEU:CD2	1:A:9:PRO:HD3	2.35	0.55
1:A:58:VAL:O	1:A:349:VAL:HG23	2.06	0.55
1:A:272:ILE:HG12	2:A:535:HOH:O	2.06	0.55
1:B:98:PRO:O	1:B:101:VAL:HG13	2.05	0.55
1:A:119:GLU:HG3	1:A:154:ASN:HB3	1.87	0.55
1:B:425:SER:HA	2:B:476:HOH:O	2.06	0.55
1:B:116:ILE:CG2	1:B:120:ASN:ND2	2.69	0.55
1:A:44:ILE:N	1:A:44:ILE:HD12	2.21	0.55
1:B:162:GLN:HB2	1:B:194:ASP:OD2	2.06	0.55
1:A:117:GLN:HE21	1:A:379:PHE:CA	2.19	0.55
1:A:83:LEU:O	1:A:218:VAL:HA	2.06	0.55
1:B:170:ALA:CB	1:B:328:LYS:HB2	2.36	0.55
1:A:236:LEU:HD22	1:A:241:ASN:HB2	1.88	0.55
1:B:285:SER:OG	1:B:287:GLU:HB3	2.06	0.55
1:A:436:LEU:HD23	1:A:458:VAL:HB	1.87	0.55
1:A:246:GLU:OE1	1:A:355:ARG:NH1	2.39	0.55
1:A:436:LEU:HD13	1:A:440:VAL:CG1	2.30	0.55
1:B:374:THR:N	1:B:381:THR:O	2.33	0.55
1:A:402:LYS:O	1:A:405:THR:N	2.32	0.55
1:B:56:ILE:HG13	2:B:612:HOH:O	2.06	0.55
1:A:271:GLU:OE2	1:A:272:ILE:HG13	2.06	0.55
1:A:422:LEU:HD11	1:A:424:VAL:HG23	1.88	0.55
1:B:279:HIS:HA	1:B:282:GLU:OE1	2.05	0.55
1:B:322:LYS:HD3	1:B:323:GLU:N	2.21	0.55
1:A:433:SER:O	1:A:455:ARG:HA	2.05	0.55
1:A:90:GLY:N	1:A:97:GLY:O	2.37	0.55
1:B:224:LEU:HD13	1:B:380:VAL:CG2	2.36	0.55
1:A:261:ILE:O	1:A:267:VAL:HA	2.06	0.55
1:A:83:LEU:CD2	1:A:218:VAL:HG13	2.36	0.55
1:B:150:TYR:HE2	2:B:554:HOH:O	1.89	0.55
1:B:402:LYS:O	1:B:404:ALA:N	2.38	0.55
1:A:77:LEU:HD13	1:A:121:LEU:HD21	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:LEU:HB3	1:B:400:PHE:CB	2.37	0.55
1:A:384:LYS:HA	1:A:384:LYS:CE	2.36	0.55
1:B:103:GLU:HG2	1:B:107:GLY:C	2.27	0.55
1:B:98:PRO:O	1:B:101:VAL:HG22	2.06	0.55
1:B:358:PRO:HB2	1:B:360:LYS:CD	2.31	0.55
1:A:308:VAL:HG22	1:A:313:LEU:HD12	1.87	0.55
1:A:205:LEU:O	1:A:205:LEU:HD12	2.06	0.55
1:B:450:LEU:HD22	1:B:465:GLY:HA2	1.87	0.55
1:B:289:PHE:HB3	2:B:588:HOH:O	2.06	0.55
1:B:200:MET:SD	1:B:205:LEU:HD23	2.46	0.55
1:B:223:ASN:HA	1:B:358:PRO:CA	2.34	0.55
1:B:101:VAL:HG12	1:B:111:LEU:HD12	1.88	0.55
1:B:81:VAL:HA	1:B:130:PRO:HG2	1.88	0.55
1:A:291:ILE:HD12	1:A:291:ILE:C	2.26	0.55
1:B:200:MET:SD	1:B:205:LEU:HD23	2.46	0.55
1:A:8:LEU:HD23	1:A:9:PRO:HD3	1.89	0.55
1:A:239:ASN:ND2	1:A:239:ASN:N	2.54	0.55
1:B:301:LEU:HA	1:B:304:ILE:HD12	1.88	0.55
1:A:6:GLU:CG	1:A:7:ASN:N	2.70	0.55
1:A:244:CYS:HA	1:A:347:ILE:O	2.07	0.55
1:B:366:LEU:O	1:B:366:LEU:HD23	2.07	0.55
1:A:81:VAL:HG12	1:A:215:TYR:O	2.07	0.55
1:B:72:GLU:O	1:B:76:LEU:HG	2.07	0.55
1:A:282:GLU:HB3	1:A:288:LYS:HD3	1.88	0.55
1:B:222:ASP:O	1:B:358:PRO:HA	2.06	0.55
1:B:77:LEU:HD11	1:B:230:LEU:HD11	1.89	0.55
1:A:235:HIS:O	1:A:238:GLN:N	2.38	0.55
1:A:11:LEU:O	1:A:11:LEU:HD23	2.06	0.55
1:A:416:ILE:HB	1:A:419:LEU:CB	2.36	0.55
1:A:11:LEU:CD1	1:A:175:PRO:HD3	2.37	0.55
1:A:136:SER:HA	1:A:162:GLN:HG2	1.88	0.55
1:B:87:GLY:HA2	1:B:136:SER:N	2.21	0.55
1:B:137:PHE:HD1	1:B:184:LYS:HE3	1.71	0.55
1:B:82:VAL:HG23	1:B:129:VAL:HG11	1.89	0.55
1:B:176:TRP:N	1:B:177:PRO:CD	2.70	0.55
1:A:83:LEU:O	1:A:218:VAL:HA	2.06	0.55
1:A:134:MET:SD	1:A:195:VAL:HG23	2.47	0.55
1:B:58:VAL:O	1:B:349:VAL:CG2	2.54	0.55
1:B:181:LYS:O	1:B:186:GLY:HA3	2.06	0.55
1:B:149:LYS:HG3	1:B:150:TYR:CD2	2.42	0.55
1:A:168:VAL:HG13	1:A:174:VAL:C	2.27	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:ASN:HB2	2:A:552:HOH:O	2.05	0.55
1:B:169:VAL:HG21	1:B:179:LYS:HD3	1.88	0.55
1:B:396:LEU:HA	1:B:424:VAL:O	2.07	0.55
1:A:280:VAL:HG12	1:A:284:LYS:HZ2	1.72	0.55
1:A:81:VAL:CG1	1:A:216:VAL:HA	2.37	0.55
1:B:10:GLN:O	1:B:13:SER:HB3	2.06	0.55
1:A:258:GLY:O	1:A:292:PHE:HA	2.07	0.55
1:B:207:THR:O	1:B:210:SER:HB2	2.07	0.55
1:A:188:TYR:CE1	1:A:331:GLN:HB3	2.42	0.55
1:A:158:HIS:CD2	1:A:204:LYS:HE3	2.42	0.55
1:B:243:TYR:OH	1:B:297:LEU:HD13	2.07	0.55
1:B:89:LEU:HD23	1:B:139:THR:HG23	1.89	0.55
1:B:64:THR:O	1:B:231:THR:HG23	2.07	0.55
1:A:74:LYS:HD3	1:A:78:ASP:OD1	2.07	0.55
1:A:53:THR:H	1:A:56:ILE:HD12	1.72	0.55
1:A:448:VAL:HG13	2:A:566:HOH:O	2.07	0.55
1:A:117:GLN:HA	1:A:120:ASN:HD22	1.71	0.55
1:A:173:PHE:CE1	1:A:330:LEU:HD12	2.42	0.55
1:A:236:LEU:HA	1:A:241:ASN:HB2	1.89	0.55
1:A:67:SER:HB2	1:A:68:GLN:NE2	2.22	0.55
1:B:268:GLN:HG3	1:B:341:ARG:HB3	1.88	0.55
1:B:26:LYS:O	1:B:30:ILE:HG12	2.06	0.55
1:A:455:ARG:HH11	1:A:455:ARG:HB3	1.72	0.55
1:A:32:LEU:HD22	1:A:165:TYR:HE2	1.71	0.55
1:A:131:LEU:HD21	1:A:133:LEU:HD21	1.89	0.55
1:B:227:ILE:O	1:B:228:VAL:C	2.45	0.55
1:A:265:GLY:O	1:A:266:LYS:HE2	2.07	0.55
1:A:365:LEU:O	1:A:369:GLN:HG3	2.07	0.55
1:A:305:LYS:O	1:A:309:GLU:HG3	2.07	0.55
1:B:115:VAL:HG11	1:B:150:TYR:CD1	2.42	0.55
1:B:105:ARG:NH2	1:B:370:SER:O	2.40	0.55
1:A:263:TYR:CE2	1:A:264:GLU:HG3	2.42	0.55
1:A:20:GLU:HG3	1:A:164:LYS:NZ	2.22	0.55
1:A:371:ASP:CG	1:A:417:VAL:HG23	2.27	0.55
1:B:145:LYS:NZ	1:B:146:ILE:HG13	2.21	0.54
1:B:252:LEU:O	1:B:255:VAL:HG13	2.07	0.54
1:A:102:ILE:HG12	2:A:514:HOH:O	2.06	0.54
1:A:99:LYS:HE3	1:A:222:ASP:OD2	2.08	0.54
1:A:169:VAL:CG1	1:A:172:GLU:HB2	2.36	0.54
1:B:434:ILE:HB	2:B:495:HOH:O	2.06	0.54
1:A:349:VAL:O	1:A:349:VAL:HG13	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:TYR:HE2	2:B:554:HOH:O	1.90	0.54
1:B:63:MET:O	1:B:65:PRO:HD3	2.06	0.54
1:A:288:LYS:HG2	1:B:287:GLU:OE1	2.07	0.54
1:B:293:ASN:ND2	1:B:295:ASN:H	2.05	0.54
1:B:143:THR:O	1:B:147:VAL:HG13	2.07	0.54
1:B:243:TYR:HB3	1:B:346:ALA:HB1	1.88	0.54
1:A:461:LYS:HZ3	1:A:468:ASP:HB3	1.69	0.54
1:B:322:LYS:O	1:B:329:VAL:HG22	2.07	0.54
1:A:124:LYS:HE3	1:A:125:TYR:CZ	2.42	0.54
1:A:36:TYR:CE1	1:A:319:PRO:HG3	2.41	0.54
1:A:384:LYS:HA	1:A:384:LYS:HE3	1.89	0.54
1:B:122:ASN:HB3	1:B:127:CYS:O	2.08	0.54
1:A:330:LEU:HD22	1:A:331:GLN:N	2.22	0.54
1:B:414:PRO:HG3	2:B:495:HOH:O	2.06	0.54
1:A:235:HIS:CD2	2:A:574:HOH:O	2.60	0.54
1:B:48:LYS:HZ1	1:B:264:GLU:HG2	1.71	0.54
1:B:92:THR:O	1:B:401:LYS:HE3	2.06	0.54
1:A:241:ASN:ND2	1:A:347:ILE:HG23	2.21	0.54
1:A:445:LYS:HB2	1:A:448:VAL:HG21	1.89	0.54
1:A:123:ASN:CG	2:A:551:HOH:O	2.45	0.54
1:B:205:LEU:HD11	1:B:209:LEU:CD1	2.37	0.54
1:B:267:VAL:HG13	1:B:340:ILE:HG12	1.89	0.54
1:A:290:LYS:HB2	2:A:505:HOH:O	2.07	0.54
1:B:77:LEU:HD22	1:B:121:LEU:HD13	1.89	0.54
1:B:235:HIS:O	1:B:238:GLN:N	2.40	0.54
1:A:345:ASN:HD22	1:A:345:ASN:N	2.04	0.54
1:A:118:ILE:HD13	1:A:131:LEU:HB2	1.88	0.54
1:A:370:SER:HB3	1:A:413:ILE:HG21	1.88	0.54
1:A:445:LYS:CD	2:A:588:HOH:O	2.56	0.54
1:B:294:THR:O	1:B:295:ASN:HB2	2.06	0.54
1:B:164:LYS:HE2	1:B:187:TRP:CG	2.43	0.54
1:A:18:LEU:HD13	1:A:187:TRP:CH2	2.42	0.54
1:A:169:VAL:HG21	1:A:179:LYS:HD3	1.89	0.54
1:A:104:VAL:O	1:A:369:GLN:HG3	2.07	0.54
1:B:137:PHE:HZ	1:B:187:TRP:O	1.90	0.54
1:B:279:HIS:HA	2:B:649:HOH:O	2.06	0.54
1:B:229:ASP:HB3	1:B:232:ILE:HD12	1.89	0.54
1:B:104:VAL:O	1:B:105:ARG:HB3	2.06	0.54
1:B:26:LYS:O	1:B:30:ILE:HG12	2.07	0.54
1:A:83:LEU:HG	1:A:132:VAL:HG13	1.89	0.54
1:B:132:VAL:HG21	1:B:208:PHE:CE2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ILE:CG1	2:A:592:HOH:O	2.55	0.54
1:A:84:LYS:HA	1:A:219:ALA:O	2.08	0.54
1:A:48:LYS:HZ1	1:A:264:GLU:HG2	1.72	0.54
1:B:399:GLU:HG2	1:B:426:GLY:C	2.28	0.54
1:B:110:PHE:CE1	1:B:222:ASP:HA	2.42	0.54
1:A:439:LYS:O	1:A:460:ASN:HA	2.08	0.54
1:A:77:LEU:HD21	1:A:228:VAL:HG11	1.90	0.54
1:B:248:THR:HG23	1:B:292:PHE:CE2	2.43	0.54
1:B:330:LEU:HD23	1:B:331:GLN:H	1.70	0.54
1:B:214:GLU:O	1:B:300:ASN:HA	2.08	0.54
1:A:367:LEU:HD21	1:A:392:PRO:HG2	1.88	0.54
1:A:205:LEU:HD13	1:A:301:LEU:HD22	1.89	0.54
1:B:247:VAL:HG22	1:B:349:VAL:O	2.08	0.54
1:A:15:VAL:CB	1:A:30:ILE:HD11	2.38	0.54
1:A:74:LYS:HD2	1:A:125:TYR:O	2.08	0.54
1:A:131:LEU:HD21	1:A:133:LEU:HD21	1.89	0.54
1:B:9:PRO:C	1:B:11:LEU:H	2.11	0.54
1:A:142:ASP:HA	1:A:145:LYS:HE3	1.89	0.54
1:A:44:ILE:HD12	1:A:44:ILE:N	2.23	0.54
1:B:386:ARG:HB2	1:B:417:VAL:CG2	2.25	0.54
1:A:438:GLY:HA3	1:A:460:ASN:ND2	2.23	0.54
1:A:410:PHE:O	1:A:412:SER:N	2.41	0.54
1:A:242:GLU:HA	1:A:300:ASN:HB2	1.90	0.54
1:A:240:LYS:O	1:A:345:ASN:HB2	2.07	0.54
1:A:255:VAL:HG23	1:A:256:LYS:N	2.22	0.54
1:A:420:ASP:OD2	1:A:438:GLY:HA2	2.08	0.54
1:A:8:LEU:HG	1:A:9:PRO:CD	2.33	0.54
1:A:58:VAL:O	1:A:349:VAL:HG23	2.08	0.54
1:A:267:VAL:HG11	1:A:346:ALA:O	2.07	0.54
1:B:60:TYR:HB2	1:B:351:VAL:HG12	1.89	0.54
1:A:105:ARG:HH22	1:A:371:ASP:HA	1.72	0.54
1:A:440:VAL:HG13	1:A:461:LYS:O	2.07	0.54
1:B:8:LEU:HD12	2:B:697:HOH:O	2.07	0.54
1:A:56:ILE:HD11	2:A:585:HOH:O	2.07	0.54
1:A:450:LEU:C	1:A:450:LEU:HD23	2.28	0.54
1:A:44:ILE:HD13	2:A:595:HOH:O	2.07	0.54
1:A:200:MET:SD	1:A:205:LEU:HD23	2.47	0.54
1:B:79:LYS:HB3	1:B:214:GLU:HB2	1.89	0.54
1:A:255:VAL:HG23	1:A:256:LYS:H	1.72	0.54
1:A:256:LYS:HG2	1:A:284:LYS:HZ3	1.73	0.54
1:A:411:LYS:HB2	1:A:431:GLY:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:VAL:O	1:B:329:VAL:HG13	2.07	0.54
1:A:82:VAL:HG13	1:A:217:PHE:HD2	1.72	0.54
1:B:92:THR:O	1:B:401:LYS:HE2	2.07	0.54
1:A:249:PRO:CA	1:A:291:ILE:HG22	2.31	0.54
1:A:35:ARG:HG3	1:A:314:LYS:HE2	1.89	0.54
1:B:434:ILE:HA	1:B:456:ALA:O	2.07	0.54
1:A:439:LYS:HD2	1:A:440:VAL:H	1.71	0.54
1:A:250:LYS:CG	1:A:286:ILE:HG22	2.36	0.54
1:B:8:LEU:HD12	2:B:697:HOH:O	2.07	0.54
1:A:134:MET:HG3	1:A:160:PHE:CE1	2.43	0.54
1:A:131:LEU:HD23	1:A:157:ILE:HG12	1.90	0.54
1:A:83:LEU:HB3	1:A:218:VAL:HG22	1.89	0.54
1:A:431:GLY:N	1:A:452:ILE:O	2.41	0.54
1:B:285:SER:OG	1:B:287:GLU:HB3	2.08	0.54
1:A:136:SER:HB2	1:A:189:PRO:HG2	1.90	0.54
1:B:142:ASP:O	1:B:146:ILE:HG13	2.08	0.54
1:B:100:SER:HB2	1:B:111:LEU:CG	2.32	0.54
1:A:442:VAL:HG22	1:A:463:ILE:HB	1.90	0.54
1:A:418:GLU:HB2	1:A:437:LYS:HG2	1.90	0.54
1:B:392:PRO:HA	1:B:420:ASP:O	2.07	0.54
1:B:196:PHE:O	1:B:197:PRO:C	2.44	0.54
1:A:226:ALA:HB3	2:A:478:HOH:O	2.08	0.54
1:A:386:ARG:NH1	1:A:419:LEU:O	2.40	0.54
1:A:256:LYS:HE2	1:A:272:ILE:CD1	2.37	0.54
1:A:85:LEU:HD12	1:A:220:ASN:OD1	2.07	0.54
1:B:8:LEU:HD12	2:B:696:HOH:O	2.06	0.54
1:B:143:THR:O	1:B:147:VAL:HG13	2.08	0.54
1:A:8:LEU:H	1:A:9:PRO:HD2	1.73	0.54
1:A:355:ARG:HH11	1:A:355:ARG:CG	2.17	0.54
1:A:458:VAL:HG13	1:A:461:LYS:HB3	1.89	0.54
1:A:149:LYS:HE2	2:A:613:HOH:O	2.07	0.54
1:B:21:MET:O	1:B:26:LYS:HE3	2.07	0.54
1:A:437:LYS:O	1:A:459:GLU:HA	2.08	0.53
1:A:261:ILE:O	1:A:267:VAL:HG23	2.07	0.53
1:B:270:LEU:HD23	1:B:283:PHE:CE1	2.43	0.53
1:B:317:ILE:HG12	2:B:623:HOH:O	2.07	0.53
1:A:353:ARG:CB	2:A:580:HOH:O	2.51	0.53
1:B:137:PHE:CD2	1:B:164:LYS:HE3	2.43	0.53
1:A:69:ASP:OD2	1:A:71:ALA:HB3	2.09	0.53
1:B:105:ARG:CG	1:B:375:LEU:HD22	2.38	0.53
1:A:109:THR:H	1:A:112:ASP:HB2	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:PHE:HD1	2:A:597:HOH:O	1.90	0.53
1:A:60:TYR:HB2	1:A:351:VAL:HG12	1.89	0.53
1:A:134:MET:HG3	1:A:160:PHE:CE1	2.43	0.53
1:A:384:LYS:NZ	2:A:560:HOH:O	2.41	0.53
1:A:411:LYS:HD2	1:A:431:GLY:CA	2.39	0.53
1:A:36:TYR:HE1	1:A:319:PRO:HG3	1.73	0.53
1:A:461:LYS:HE3	1:A:463:ILE:HG12	1.90	0.53
1:B:241:ASN:ND2	1:B:345:ASN:O	2.30	0.53
1:B:382:ARG:HG3	1:B:382:ARG:HH11	1.73	0.53
1:B:33:VAL:HA	1:B:332:LEU:CD1	2.39	0.53
1:A:355:ARG:HD3	2:A:547:HOH:O	2.08	0.53
1:B:280:VAL:CG1	1:B:284:LYS:HE3	2.38	0.53
1:B:330:LEU:C	1:B:330:LEU:HD23	2.29	0.53
1:A:280:VAL:HG12	1:A:284:LYS:NZ	2.23	0.53
1:A:98:PRO:O	1:A:101:VAL:HG22	2.08	0.53
1:A:99:LYS:HG2	1:A:102:ILE:HD12	1.89	0.53
1:B:66:VAL:HG11	2:B:502:HOH:O	2.08	0.53
1:A:227:ILE:HG21	1:A:379:PHE:CE1	2.43	0.53
1:B:379:PHE:HB2	1:B:381:THR:CG2	2.38	0.53
1:B:358:PRO:HB2	1:B:360:LYS:HD3	1.90	0.53
1:A:84:LYS:HG3	1:A:114:ILE:HD13	1.89	0.53
1:A:68:GLN:H	1:A:68:GLN:CD	2.12	0.53
1:A:99:LYS:HE2	1:A:360:LYS:CD	2.37	0.53
1:B:317:ILE:CG2	1:B:332:LEU:HD22	2.39	0.53
1:A:89:LEU:HB2	1:A:91:THR:HG23	1.90	0.53
1:B:118:ILE:CG1	1:B:131:LEU:HD22	2.38	0.53
1:A:83:LEU:HD12	1:A:199:LEU:HD13	1.90	0.53
1:B:372:LEU:O	1:B:383:ASN:HB2	2.09	0.53
1:A:271:GLU:OE2	2:A:561:HOH:O	2.17	0.53
1:A:247:VAL:HG23	1:A:247:VAL:O	2.09	0.53
1:A:105:ARG:HG3	1:A:369:GLN:HA	1.89	0.53
1:A:370:SER:CB	1:A:416:ILE:HG12	2.39	0.53
1:A:372:LEU:HA	1:A:417:VAL:HG22	1.89	0.53
1:B:419:LEU:HG	1:B:420:ASP:N	2.23	0.53
1:B:140:HIS:O	1:B:143:THR:N	2.41	0.53
1:A:108:LEU:HD12	1:A:375:LEU:HD21	1.90	0.53
1:A:439:LYS:NZ	2:A:527:HOH:O	2.41	0.53
1:B:244:CYS:SG	1:B:347:ILE:HD11	2.48	0.53
1:B:9:PRO:HD2	2:B:697:HOH:O	2.09	0.53
1:B:92:THR:HG23	1:B:401:LYS:HE3	1.90	0.53
1:A:384:LYS:HA	1:A:384:LYS:CE	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:GLY:N	1:A:434:ILE:HD11	2.24	0.53
1:B:93:MET:CE	1:B:365:LEU:CD1	2.86	0.53
1:A:291:ILE:C	1:A:291:ILE:HD12	2.28	0.53
1:A:109:THR:O	1:A:113:LEU:HG	2.09	0.53
1:A:25:GLU:OE2	1:A:163:SER:HA	2.09	0.53
1:A:15:VAL:O	1:A:18:LEU:HG	2.08	0.53
1:B:229:ASP:HB2	1:B:355:ARG:NH1	2.23	0.53
1:A:322:LYS:HE3	2:A:630:HOH:O	2.09	0.53
1:B:171:ASP:OD1	1:B:172:GLU:N	2.35	0.53
1:A:382:ARG:NH2	1:A:386:ARG:HG2	2.23	0.53
1:A:318:ILE:HD12	1:A:318:ILE:N	2.24	0.53
1:B:445:LYS:HB2	1:B:448:VAL:HG21	1.91	0.53
1:B:383:ASN:HA	2:B:644:HOH:O	2.07	0.53
1:B:67:SER:N	1:B:72:GLU:OE2	2.41	0.53
1:A:81:VAL:CG1	1:A:301:LEU:HD11	2.38	0.53
1:B:271:GLU:HB3	2:B:504:HOH:O	2.09	0.53
1:A:12:LYS:HD2	1:A:30:ILE:HG21	1.91	0.53
1:A:411:LYS:HB2	1:A:431:GLY:C	2.28	0.53
1:B:32:LEU:HB3	2:B:683:HOH:O	2.07	0.53
1:B:150:TYR:HB2	2:B:653:HOH:O	2.09	0.53
1:B:227:ILE:HG12	1:B:228:VAL:N	2.23	0.53
1:B:101:VAL:HG11	1:B:146:ILE:HD13	1.91	0.53
1:B:108:LEU:HD13	1:B:113:LEU:CD2	2.39	0.53
1:A:358:PRO:CB	2:A:598:HOH:O	2.56	0.53
1:B:118:ILE:O	1:B:122:ASN:ND2	2.40	0.53
1:B:233:LEU:HA	1:B:236:LEU:HG	1.90	0.53
1:B:98:PRO:O	1:B:101:VAL:HG22	2.09	0.53
1:B:268:GLN:CD	1:B:341:ARG:HD3	2.28	0.53
1:A:63:MET:SD	1:A:232:ILE:HA	2.49	0.53
1:B:317:ILE:HG12	2:B:623:HOH:O	2.07	0.53
1:B:337:GLY:HA3	2:B:474:HOH:O	2.09	0.53
1:B:60:TYR:CD1	1:B:351:VAL:HG12	2.44	0.53
1:A:456:ALA:O	1:A:457:VAL:HG23	2.09	0.53
1:A:236:LEU:HA	1:A:241:ASN:OD1	2.09	0.53
1:B:177:PRO:O	1:B:179:LYS:N	2.42	0.53
1:B:163:SER:HB3	1:B:165:TYR:CE1	2.44	0.53
1:B:80:LEU:HD12	1:B:215:TYR:O	2.09	0.53
1:A:44:ILE:HD12	1:A:44:ILE:N	2.24	0.53
1:B:128:LYS:HB3	2:B:670:HOH:O	2.08	0.53
1:A:419:LEU:HD11	1:A:422:LEU:HB2	1.89	0.53
1:B:162:GLN:HB2	1:B:194:ASP:OD2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:445:LYS:CG	2:A:588:HOH:O	2.56	0.53
1:B:266:LYS:HD3	1:B:341:ARG:O	2.08	0.53
1:A:243:TYR:CD1	1:A:340:ILE:HA	2.44	0.53
1:B:453:PRO:HG2	1:B:456:ALA:CB	2.24	0.53
1:A:417:VAL:CG1	1:A:418:GLU:HG3	2.37	0.53
1:A:76:LEU:HD12	1:A:230:LEU:HD22	1.90	0.53
1:B:232:ILE:O	1:B:236:LEU:HG	2.09	0.53
1:B:52:PRO:HD3	1:B:261:ILE:HA	1.90	0.53
1:B:293:ASN:HD22	1:B:294:THR:N	2.05	0.53
1:B:436:LEU:HA	1:B:458:VAL:O	2.08	0.53
1:A:171:ASP:OD1	1:A:172:GLU:N	2.33	0.53
1:B:113:LEU:O	1:B:117:GLN:HG3	2.09	0.53
1:B:29:PHE:HD1	1:B:165:TYR:CD2	2.26	0.53
1:A:93:MET:SD	1:A:99:LYS:HE2	2.49	0.53
1:A:395:GLU:O	1:A:396:LEU:HD23	2.07	0.53
1:B:275:VAL:CG1	1:B:279:HIS:HB2	2.38	0.53
1:B:138:ASN:HD21	1:B:184:LYS:HD3	1.72	0.53
1:A:358:PRO:HB2	1:A:360:LYS:HD3	1.91	0.53
1:A:250:LYS:HG2	1:A:286:ILE:CG2	2.36	0.53
1:A:402:LYS:HB3	1:A:405:THR:OG1	2.08	0.53
1:B:450:LEU:CD2	1:B:465:GLY:HA2	2.39	0.53
1:B:244:CYS:HA	1:B:347:ILE:O	2.09	0.53
1:A:428:VAL:HA	1:A:450:LEU:O	2.08	0.53
1:A:117:GLN:HE22	1:A:379:PHE:HD1	1.57	0.53
1:B:21:MET:O	1:B:26:LYS:HE3	2.09	0.53
1:A:176:TRP:CH2	1:A:324:VAL:HB	2.43	0.53
1:B:11:LEU:HD13	1:B:33:VAL:HG11	1.90	0.53
1:A:272:ILE:HG23	1:A:283:PHE:CE2	2.45	0.52
1:A:422:LEU:HA	1:A:440:VAL:O	2.09	0.52
1:A:255:VAL:HB	1:A:284:LYS:CB	2.39	0.52
1:B:243:TYR:O	1:B:347:ILE:HD13	2.08	0.52
1:A:358:PRO:HB2	1:A:360:LYS:CD	2.39	0.52
1:B:247:VAL:HA	1:B:292:PHE:O	2.08	0.52
1:B:423:LYS:O	1:B:441:THR:HA	2.07	0.52
1:A:247:VAL:CB	1:A:291:ILE:HD13	2.37	0.52
1:B:439:LYS:O	1:B:460:ASN:HA	2.10	0.52
1:A:415:SER:HB2	1:A:435:VAL:HG13	1.90	0.52
1:B:50:GLN:O	1:B:261:ILE:HB	2.10	0.52
1:B:110:PHE:O	1:B:114:ILE:HG13	2.09	0.52
1:A:84:LYS:HG3	1:A:114:ILE:HD13	1.90	0.52
1:A:294:THR:O	1:A:295:ASN:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:LEU:CD2	1:A:305:LYS:HD2	2.39	0.52
1:B:422:LEU:HG	1:B:423:LYS:N	2.23	0.52
1:A:265:GLY:O	1:A:266:LYS:HE2	2.09	0.52
1:A:176:TRP:CD2	1:A:181:LYS:HG2	2.45	0.52
1:B:359:VAL:HA	1:B:364:ASP:CB	2.40	0.52
1:A:438:GLY:HA3	1:A:460:ASN:ND2	2.24	0.52
1:A:429:TRP:HB2	1:A:451:GLU:HG2	1.91	0.52
1:B:255:VAL:N	2:B:659:HOH:O	2.42	0.52
1:B:81:VAL:HG22	1:B:130:PRO:HG2	1.89	0.52
1:A:271:GLU:OE2	1:A:272:ILE:HG12	2.10	0.52
1:A:15:VAL:O	1:A:26:LYS:HE2	2.10	0.52
1:A:110:PHE:O	1:A:114:ILE:HG13	2.09	0.52
1:A:105:ARG:HD2	1:A:368:VAL:O	2.10	0.52
1:B:56:ILE:HG21	1:B:262:SER:OG	2.09	0.52
1:B:113:LEU:CD2	1:B:375:LEU:HD21	2.39	0.52
1:B:250:LYS:N	1:B:290:LYS:O	2.42	0.52
1:B:329:VAL:C	1:B:330:LEU:HD23	2.30	0.52
1:A:174:VAL:CG2	1:A:179:LYS:HD2	2.39	0.52
1:B:224:LEU:CD1	1:B:380:VAL:HG21	2.39	0.52
1:B:357:LEU:O	1:B:357:LEU:CD2	2.57	0.52
1:A:243:TYR:HA	1:A:298:TRP:O	2.08	0.52
1:A:461:LYS:HE3	1:A:463:ILE:HG12	1.90	0.52
1:B:52:PRO:HD3	1:B:261:ILE:HA	1.91	0.52
1:B:461:LYS:HE3	1:B:463:ILE:HG12	1.91	0.52
1:A:197:PRO:O	1:A:198:ALA:C	2.48	0.52
1:A:68:GLN:H	1:A:68:GLN:CD	2.12	0.52
1:B:242:GLU:HB2	1:B:343:PHE:HB3	1.91	0.52
1:B:52:PRO:HA	2:B:611:HOH:O	2.09	0.52
1:B:250:LYS:HE2	1:B:292:PHE:HB3	1.92	0.52
1:B:83:LEU:HD23	1:B:83:LEU:C	2.29	0.52
1:A:411:LYS:HB2	1:A:431:GLY:O	2.09	0.52
1:A:123:ASN:HB2	2:A:551:HOH:O	2.09	0.52
1:A:271:GLU:HG3	2:A:561:HOH:O	2.08	0.52
1:A:365:LEU:O	1:A:368:VAL:HG22	2.09	0.52
1:B:98:PRO:HB2	1:B:101:VAL:HG13	1.92	0.52
1:B:149:LYS:HG3	1:B:150:TYR:CD2	2.45	0.52
1:B:287:GLU:OE2	2:B:578:HOH:O	2.19	0.52
1:B:347:ILE:N	1:B:347:ILE:HD13	2.25	0.52
1:B:224:LEU:HD13	1:B:380:VAL:CB	2.40	0.52
1:B:419:LEU:HD21	1:B:422:LEU:CB	2.36	0.52
1:B:355:ARG:HH21	1:B:355:ARG:HB2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:TRP:NE1	1:A:449:LYS:HG3	2.25	0.52
1:A:129:VAL:HG22	2:A:526:HOH:O	2.09	0.52
1:A:77:LEU:CG	1:A:230:LEU:HD11	2.39	0.52
1:A:68:GLN:NE2	1:A:69:ASP:H	2.08	0.52
1:A:291:ILE:HD12	1:A:291:ILE:C	2.30	0.52
1:B:167:ARG:NH1	1:B:185:GLU:O	2.42	0.52
1:A:176:TRP:C	1:A:178:SER:H	2.13	0.52
1:A:86:ASN:OD1	1:A:100:SER:HB3	2.09	0.52
1:A:124:LYS:NZ	2:A:642:HOH:O	2.42	0.52
1:A:314:LYS:CD	2:A:564:HOH:O	2.57	0.52
1:A:411:LYS:HB3	1:A:432:SER:HB3	1.91	0.52
1:B:437:LYS:HB2	1:B:459:GLU:HG3	1.90	0.52
1:A:44:ILE:CD1	1:A:274:GLN:HE21	2.23	0.52
1:A:398:PRO:HD2	2:A:507:HOH:O	2.09	0.52
1:B:268:GLN:HG3	2:B:598:HOH:O	2.08	0.52
1:B:397:GLY:HA3	2:B:476:HOH:O	2.09	0.52
1:A:267:VAL:HG13	1:A:340:ILE:HG12	1.91	0.52
1:A:196:PHE:HB3	1:A:304:ILE:HG23	1.90	0.52
1:A:220:ASN:HB3	2:A:626:HOH:O	2.10	0.52
1:B:175:PRO:O	1:B:178:SER:HB2	2.10	0.52
1:B:176:TRP:CD2	1:B:181:LYS:HG2	2.45	0.52
1:A:439:LYS:HE3	1:A:462:ASN:OD1	2.09	0.52
1:B:433:SER:O	1:B:455:ARG:HA	2.09	0.52
1:B:181:LYS:CE	1:B:185:GLU:HB2	2.39	0.52
1:A:244:CYS:HA	1:A:347:ILE:O	2.10	0.52
1:B:18:LEU:HD13	1:B:187:TRP:CH2	2.44	0.52
1:A:60:TYR:HB2	1:A:350:ASN:O	2.10	0.52
1:B:135:ASN:HD21	1:B:159:THR:HB	1.75	0.52
1:B:438:GLY:HA3	1:B:460:ASN:OD1	2.10	0.52
1:A:319:PRO:O	1:A:331:GLN:O	2.28	0.52
1:A:25:GLU:OE2	1:A:163:SER:HA	2.10	0.52
1:B:355:ARG:HD2	2:B:635:HOH:O	2.08	0.52
1:B:243:TYR:HB3	1:B:346:ALA:CB	2.39	0.52
1:B:48:LYS:NZ	1:B:48:LYS:HB3	2.25	0.52
1:A:372:LEU:HD21	1:A:391:ASN:OD1	2.10	0.52
1:A:200:MET:SD	1:A:205:LEU:HD23	2.50	0.52
1:B:345:ASN:O	1:B:347:ILE:HG23	2.10	0.52
1:A:288:LYS:HG2	1:B:287:GLU:OE1	2.10	0.52
1:B:155:VAL:O	1:B:157:ILE:HG13	2.09	0.52
1:B:422:LEU:HD22	1:B:436:LEU:CD1	2.40	0.52
1:A:29:PHE:O	1:A:33:VAL:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:VAL:HG23	1:A:284:LYS:HD2	1.92	0.52
1:A:259:THR:HG22	1:A:270:LEU:HB3	1.92	0.52
1:B:203:GLY:HA2	2:B:489:HOH:O	2.09	0.52
1:A:313:LEU:HB3	1:A:315:MET:SD	2.50	0.52
1:A:94:GLY:HA3	1:A:402:LYS:HG2	1.92	0.52
1:A:419:LEU:HD21	1:A:422:LEU:HB2	1.92	0.52
1:A:319:PRO:CB	1:A:330:LEU:HD22	2.32	0.52
1:A:444:ALA:HB2	1:A:450:LEU:HB3	1.92	0.52
1:B:175:PRO:O	1:B:178:SER:HB2	2.10	0.52
1:A:317:ILE:HD13	1:A:334:THR:HG22	1.91	0.52
1:B:99:LYS:HG2	1:B:99:LYS:O	2.10	0.52
1:B:83:LEU:HD23	1:B:84:LYS:N	2.24	0.52
1:A:111:LEU:HD23	1:A:146:ILE:HG21	1.91	0.52
1:B:341:ARG:HA	2:B:568:HOH:O	2.10	0.52
1:B:268:GLN:HA	2:B:472:HOH:O	2.10	0.51
1:B:243:TYR:OH	1:B:337:GLY:HA2	2.10	0.51
1:A:76:LEU:CD2	1:A:237:ILE:HD12	2.40	0.51
1:A:57:VAL:HA	1:A:348:GLY:O	2.09	0.51
1:A:320:ASN:HB2	1:A:331:GLN:O	2.10	0.51
1:B:280:VAL:CG1	1:B:284:LYS:HE3	2.40	0.51
1:B:44:ILE:HG22	1:B:276:PRO:HD3	1.92	0.51
1:B:93:MET:O	1:B:403:VAL:HG23	2.10	0.51
1:A:10:GLN:HB3	2:A:495:HOH:O	2.08	0.51
1:B:347:ILE:HD13	1:B:347:ILE:N	2.25	0.51
1:A:242:GLU:HG3	1:A:344:ASP:HB2	1.91	0.51
1:B:452:ILE:N	1:B:452:ILE:HD13	2.24	0.51
1:A:36:TYR:CE1	1:A:319:PRO:HG3	2.45	0.51
1:B:301:LEU:O	1:B:302:LYS:C	2.47	0.51
1:A:167:ARG:CG	1:A:188:TYR:HB3	2.41	0.51
1:A:188:TYR:CD1	1:A:331:GLN:HB3	2.45	0.51
1:B:427:ASP:H	1:B:444:ALA:HB3	1.75	0.51
1:A:318:ILE:HB	1:A:333:GLU:O	2.10	0.51
1:B:232:ILE:O	1:B:236:LEU:HG	2.11	0.51
1:A:322:LYS:NZ	2:A:631:HOH:O	2.43	0.51
1:B:422:LEU:HG	1:B:424:VAL:HG23	1.91	0.51
1:B:382:ARG:HH11	1:B:382:ARG:HG3	1.76	0.51
1:A:77:LEU:CG	1:A:230:LEU:HD11	2.38	0.51
1:B:203:GLY:HA2	2:B:489:HOH:O	2.10	0.51
1:A:13:SER:HA	1:A:16:ASP:HB2	1.91	0.51
1:B:107:GLY:HA2	2:B:481:HOH:O	2.09	0.51
1:B:81:VAL:HG13	1:B:130:PRO:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:PHE:HA	1:B:289:PHE:CE2	2.45	0.51
1:B:259:THR:HG21	1:B:289:PHE:HB3	1.92	0.51
1:A:274:GLN:CD	1:A:316:GLU:HG2	2.30	0.51
1:A:445:LYS:HD2	2:A:588:HOH:O	2.10	0.51
1:A:8:LEU:HG	1:A:9:PRO:HD3	1.91	0.51
1:B:308:VAL:HG22	1:B:313:LEU:CD1	2.40	0.51
1:B:312:ALA:O	1:B:314:LYS:HG3	2.10	0.51
1:A:332:LEU:HD12	1:A:332:LEU:H	1.75	0.51
1:A:303:ALA:O	1:A:304:ILE:C	2.49	0.51
1:A:285:SER:HB3	1:A:288:LYS:HB2	1.90	0.51
1:A:294:THR:OG1	1:A:296:ASN:HB2	2.10	0.51
1:B:144:HIS:HA	1:B:147:VAL:CG2	2.40	0.51
1:A:101:VAL:CG1	1:A:146:ILE:HG21	2.41	0.51
1:B:164:LYS:HE2	1:B:187:TRP:CD2	2.45	0.51
1:B:82:VAL:O	1:B:217:PHE:O	2.28	0.51
1:B:263:TYR:CE2	1:B:264:GLU:HG3	2.45	0.51
1:B:301:LEU:HD23	1:B:304:ILE:HD12	1.90	0.51
1:A:468:ASP:O	1:A:469:LEU:O	2.29	0.51
1:B:213:LYS:NZ	2:B:480:HOH:O	2.38	0.51
1:A:365:LEU:O	1:A:369:GLN:N	2.42	0.51
1:A:224:LEU:HD13	1:A:380:VAL:HG21	1.91	0.51
1:B:243:TYR:OH	1:B:337:GLY:HA2	2.10	0.51
1:B:439:LYS:O	1:B:460:ASN:HA	2.10	0.51
1:A:269:LEU:HD22	1:A:337:GLY:C	2.31	0.51
1:A:200:MET:HG2	1:A:205:LEU:CD2	2.32	0.51
1:B:246:GLU:CB	1:B:296:ASN:HB2	2.36	0.51
1:A:244:CYS:SG	1:A:244:CYS:O	2.68	0.51
1:A:116:ILE:CG2	1:A:378:GLY:HA3	2.40	0.51
1:A:77:LEU:CD2	1:A:230:LEU:HD21	2.40	0.51
1:B:317:ILE:HD11	2:B:532:HOH:O	2.09	0.51
1:A:222:ASP:O	1:A:358:PRO:HA	2.10	0.51
1:A:101:VAL:HG12	1:A:146:ILE:HG21	1.92	0.51
1:B:164:LYS:HE2	1:B:187:TRP:CG	2.45	0.51
1:A:261:ILE:CD1	1:A:261:ILE:C	2.79	0.51
1:B:57:VAL:HG21	1:B:291:ILE:CD1	2.41	0.51
1:A:53:THR:N	1:A:56:ILE:HD12	2.25	0.51
1:B:244:CYS:HB2	1:B:347:ILE:HD11	1.92	0.51
1:B:131:LEU:HD12	1:B:132:VAL:H	1.75	0.51
1:A:455:ARG:CB	1:A:455:ARG:HH11	2.21	0.51
1:A:15:VAL:CG2	1:A:30:ILE:HD11	2.38	0.51
1:B:434:ILE:HG12	1:B:456:ALA:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:VAL:HG12	1:A:171:ASP:OD1	2.10	0.51
1:A:267:VAL:CG1	1:A:340:ILE:HG12	2.41	0.51
1:B:258:GLY:HA3	1:B:271:GLU:CD	2.30	0.51
1:B:187:TRP:O	1:B:188:TYR:HB3	2.09	0.51
1:B:317:ILE:HG21	1:B:332:LEU:HD22	1.93	0.51
1:A:431:GLY:N	1:A:452:ILE:O	2.44	0.51
1:B:208:PHE:O	1:B:213:LYS:N	2.30	0.51
1:A:281:ASN:HA	1:A:284:LYS:HZ3	1.75	0.51
1:B:448:VAL:HG11	2:B:565:HOH:O	2.11	0.51
1:A:317:ILE:O	1:A:319:PRO:HD3	2.10	0.51
1:B:260:LEU:HD23	1:B:269:LEU:HA	1.91	0.51
1:B:57:VAL:HA	1:B:348:GLY:O	2.10	0.51
1:A:95:CYS:SG	1:A:403:VAL:HB	2.50	0.51
1:B:105:ARG:NH2	1:B:373:TYR:O	2.44	0.51
1:B:175:PRO:C	1:B:177:PRO:HD2	2.31	0.51
1:A:149:LYS:HE2	2:A:614:HOH:O	2.10	0.51
1:B:461:LYS:HG3	2:B:625:HOH:O	2.10	0.51
1:B:135:ASN:HB3	1:B:139:THR:OG1	2.10	0.51
1:A:247:VAL:O	1:A:351:VAL:HG22	2.11	0.51
1:B:254:ASP:O	1:B:256:LYS:N	2.43	0.51
1:A:371:ASP:CG	1:A:417:VAL:HB	2.31	0.51
1:A:319:PRO:O	1:A:331:GLN:O	2.29	0.51
1:B:236:LEU:O	1:B:241:ASN:N	2.43	0.51
1:B:137:PHE:CD2	1:B:164:LYS:HE3	2.45	0.51
1:B:96:THR:CG2	1:B:97:GLY:N	2.73	0.51
1:A:124:LYS:HE3	1:A:125:TYR:OH	2.10	0.51
1:A:99:LYS:CD	1:A:102:ILE:HD12	2.41	0.51
1:B:81:VAL:HG13	1:B:130:PRO:HG2	1.92	0.51
1:A:134:MET:SD	1:A:195:VAL:HA	2.51	0.51
1:A:110:PHE:O	1:A:114:ILE:HG13	2.10	0.51
1:A:11:LEU:HD23	1:A:11:LEU:O	2.11	0.51
1:B:281:ASN:HB2	2:B:649:HOH:O	2.10	0.51
1:A:6:GLU:CG	1:A:7:ASN:H	2.15	0.51
1:A:372:LEU:HD23	1:A:373:TYR:HE2	1.75	0.51
1:A:392:PRO:HB3	1:A:419:LEU:HD23	1.92	0.51
1:B:236:LEU:CD1	1:B:244:CYS:SG	2.99	0.51
1:A:214:GLU:O	1:A:300:ASN:HA	2.11	0.51
1:B:268:GLN:CD	2:B:599:HOH:O	2.48	0.51
1:B:136:SER:O	1:B:140:HIS:HB2	2.10	0.51
1:A:433:SER:O	1:A:455:ARG:HA	2.11	0.51
1:B:48:LYS:NZ	1:B:263:TYR:CZ	2.78	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:423:LYS:HB3	1:B:441:THR:HG22	1.91	0.51
1:A:52:PRO:HG3	2:A:505:HOH:O	2.11	0.51
1:A:171:ASP:OD1	2:A:569:HOH:O	2.19	0.51
1:A:271:GLU:HG3	2:A:561:HOH:O	2.11	0.51
1:B:21:MET:HG2	2:B:571:HOH:O	2.11	0.51
1:A:81:VAL:HG13	1:A:216:VAL:HA	1.92	0.51
1:A:230:LEU:HG	2:A:636:HOH:O	2.11	0.51
1:B:115:VAL:HG11	1:B:150:TYR:CD1	2.46	0.51
1:B:150:TYR:CD2	2:B:653:HOH:O	2.50	0.51
1:B:64:THR:HB	1:B:234:LYS:HE2	1.93	0.51
1:B:56:ILE:CG2	1:B:267:VAL:HB	2.41	0.51
1:A:44:ILE:HD12	1:A:44:ILE:N	2.26	0.51
1:B:119:GLU:HB2	1:B:155:VAL:HB	1.92	0.51
1:B:317:ILE:O	1:B:319:PRO:HD3	2.10	0.51
1:B:44:ILE:HD13	2:B:634:HOH:O	2.11	0.51
1:B:223:ASN:HA	1:B:358:PRO:HA	1.93	0.51
1:A:367:LEU:HG	1:A:394:ILE:HD12	1.91	0.51
1:B:188:TYR:HD1	1:B:189:PRO:O	1.94	0.51
1:A:395:GLU:O	1:A:396:LEU:HD23	2.11	0.51
1:A:119:GLU:OE2	1:A:153:SER:HB3	2.11	0.51
1:A:435:VAL:HB	1:A:457:VAL:CG2	2.41	0.51
1:A:190:PRO:HG2	1:A:194:ASP:HB2	1.92	0.51
1:B:136:SER:HA	1:B:161:ASN:OD1	2.09	0.51
1:B:243:TYR:HH	1:B:336:ALA:C	2.14	0.51
1:A:200:MET:SD	1:A:200:MET:O	2.69	0.51
1:A:439:LYS:C	1:A:439:LYS:HD2	2.31	0.51
1:B:165:TYR:OH	2:B:513:HOH:O	2.18	0.51
1:A:132:VAL:HG23	1:A:158:HIS:HB2	1.92	0.51
1:A:165:TYR:OH	2:A:501:HOH:O	2.20	0.51
1:A:89:LEU:C	1:A:91:THR:H	2.14	0.51
1:B:206:ASP:HA	1:B:209:LEU:HB2	1.93	0.51
1:B:448:VAL:CG1	1:B:450:LEU:HD13	2.41	0.51
1:B:419:LEU:HD12	1:B:438:GLY:O	2.11	0.51
1:B:121:LEU:CD2	1:B:121:LEU:C	2.79	0.51
1:A:35:ARG:CZ	2:A:648:HOH:O	2.59	0.51
1:B:412:SER:O	1:B:413:ILE:C	2.48	0.51
1:B:339:ALA:O	1:B:343:PHE:CD2	2.64	0.51
1:B:304:ILE:HG12	1:B:343:PHE:HE1	1.76	0.51
1:A:432:SER:O	1:A:454:ASP:HA	2.11	0.51
1:B:362:SER:OG	2:B:500:HOH:O	2.19	0.51
1:B:142:ASP:O	1:B:146:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:LEU:HD13	1:B:394:ILE:HD13	1.93	0.51
1:B:394:ILE:HG12	1:B:422:LEU:HB3	1.93	0.51
1:B:435:VAL:O	1:B:436:LEU:HD23	2.11	0.51
1:A:271:GLU:HG3	2:A:560:HOH:O	2.11	0.51
1:A:243:TYR:C	1:A:243:TYR:HD2	2.15	0.51
1:B:368:VAL:CG1	1:B:368:VAL:O	2.59	0.51
1:A:11:LEU:CD1	1:A:33:VAL:HG11	2.36	0.51
1:B:160:PHE:HB2	1:B:202:SER:HB3	1.93	0.51
1:B:320:ASN:N	1:B:321:PRO:HD3	2.26	0.51
1:A:213:LYS:NZ	2:A:526:HOH:O	2.31	0.51
1:B:263:TYR:O	1:B:265:GLY:N	2.43	0.51
1:A:455:ARG:HH11	1:A:455:ARG:CB	2.22	0.51
1:B:84:LYS:HA	1:B:219:ALA:O	2.11	0.51
1:A:224:LEU:HD12	1:A:368:VAL:HG11	1.93	0.50
1:A:439:LYS:HD2	1:A:439:LYS:C	2.31	0.50
1:A:272:ILE:HG23	1:A:283:PHE:CD2	2.46	0.50
1:A:294:THR:OG1	1:A:296:ASN:HB2	2.11	0.50
1:B:129:VAL:HA	2:B:480:HOH:O	2.12	0.50
1:A:291:ILE:HG21	1:A:350:ASN:ND2	2.25	0.50
1:B:234:LYS:HG2	2:B:479:HOH:O	2.11	0.50
1:A:382:ARG:NH2	1:A:391:ASN:OD1	2.43	0.50
1:B:402:LYS:O	1:B:403:VAL:C	2.50	0.50
1:A:330:LEU:HD23	1:A:330:LEU:C	2.31	0.50
1:B:138:ASN:ND2	1:B:184:LYS:HD3	2.26	0.50
1:A:12:LYS:HG2	1:A:16:ASP:OD2	2.11	0.50
1:A:355:ARG:NH1	1:A:355:ARG:CG	2.67	0.50
1:A:113:LEU:HD21	1:A:375:LEU:HD11	1.92	0.50
1:A:382:ARG:HH22	1:A:386:ARG:HG2	1.76	0.50
1:B:236:LEU:HD21	1:B:244:CYS:HB2	1.92	0.50
1:A:278:GLU:H	1:A:278:GLU:CD	2.15	0.50
1:B:73:THR:HG23	1:B:230:LEU:CD1	2.41	0.50
1:B:98:PRO:HD2	1:B:101:VAL:CG2	2.41	0.50
1:A:61:GLU:CD	1:A:61:GLU:H	2.14	0.50
1:A:189:PRO:HD3	2:A:609:HOH:O	2.11	0.50
1:A:229:ASP:OD2	1:A:232:ILE:HG13	2.11	0.50
1:A:226:ALA:HB3	2:A:478:HOH:O	2.12	0.50
1:B:243:TYR:OH	1:B:337:GLY:HA2	2.11	0.50
1:A:243:TYR:HD2	1:A:244:CYS:N	2.09	0.50
1:B:35:ARG:HH21	1:B:314:LYS:NZ	2.09	0.50
1:B:195:VAL:HG13	1:B:196:PHE:N	2.26	0.50
1:B:366:LEU:HD23	1:B:413:ILE:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:VAL:HG12	1:A:171:ASP:CG	2.32	0.50
1:A:255:VAL:HG12	1:A:286:ILE:HG23	1.92	0.50
1:A:104:VAL:HG23	1:A:368:VAL:HG21	1.93	0.50
1:A:438:GLY:HA3	1:A:460:ASN:CG	2.31	0.50
1:A:411:LYS:CB	1:A:432:SER:HB3	2.40	0.50
1:A:440:VAL:HG22	1:A:458:VAL:HG12	1.93	0.50
1:A:349:VAL:HG13	1:A:349:VAL:O	2.11	0.50
1:B:84:LYS:HG3	1:B:114:ILE:HG21	1.93	0.50
1:A:361:ALA:HB1	2:A:500:HOH:O	2.11	0.50
1:B:242:GLU:CD	1:B:344:ASP:HB2	2.30	0.50
1:B:182:THR:HG22	1:B:182:THR:O	2.11	0.50
1:A:255:VAL:HB	1:A:284:LYS:HB3	1.93	0.50
1:B:59:PRO:HB2	1:B:62:LYS:HG2	1.93	0.50
1:A:105:ARG:CG	1:A:369:GLN:HA	2.40	0.50
1:B:357:LEU:N	1:B:358:PRO:CD	2.74	0.50
1:B:11:LEU:CD2	1:B:15:VAL:HG23	2.41	0.50
1:A:107:GLY:HA2	2:A:516:HOH:O	2.10	0.50
1:B:100:SER:HA	1:B:110:PHE:CD2	2.47	0.50
1:A:432:SER:HA	2:A:503:HOH:O	2.10	0.50
1:A:99:LYS:HD2	1:A:102:ILE:HD12	1.92	0.50
1:B:11:LEU:O	1:B:11:LEU:HD23	2.12	0.50
1:B:162:GLN:CD	1:B:189:PRO:HB2	2.31	0.50
1:B:319:PRO:O	1:B:320:ASN:C	2.50	0.50
1:A:432:SER:HA	2:A:503:HOH:O	2.11	0.50
1:A:432:SER:O	1:A:434:ILE:N	2.44	0.50
1:B:104:VAL:HG22	1:B:110:PHE:CZ	2.46	0.50
1:B:444:ALA:HB2	1:B:450:LEU:HB2	1.92	0.50
1:A:114:ILE:HG13	2:A:592:HOH:O	2.12	0.50
1:B:14:ALA:HB3	1:B:175:PRO:HG2	1.94	0.50
1:B:322:LYS:HG3	1:B:323:GLU:N	2.27	0.50
1:B:84:LYS:HA	1:B:219:ALA:O	2.11	0.50
1:A:444:ALA:HB2	1:A:450:LEU:HD12	1.94	0.50
1:A:44:ILE:HD11	1:A:274:GLN:HE21	1.76	0.50
1:A:8:LEU:CD2	1:A:9:PRO:HD3	2.41	0.50
1:A:174:VAL:HG21	1:A:179:LYS:HD2	1.93	0.50
1:B:355:ARG:NH2	2:B:636:HOH:O	2.45	0.50
1:A:382:ARG:O	2:A:590:HOH:O	2.18	0.50
1:A:205:LEU:CD1	1:A:301:LEU:HB3	2.42	0.50
1:A:307:LEU:HD11	1:A:342:PHE:O	2.12	0.50
1:B:53:THR:C	1:B:55:GLU:H	2.15	0.50
1:A:399:GLU:HB3	1:A:409:ARG:CZ	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:272:ILE:HB	1:B:283:PHE:CE2	2.47	0.50
1:B:197:PRO:HA	1:B:308:VAL:HG11	1.93	0.50
1:A:220:ASN:HB3	2:A:625:HOH:O	2.11	0.50
1:A:256:LYS:HG2	1:A:284:LYS:NZ	2.26	0.50
1:A:86:ASN:C	1:A:88:GLY:H	2.15	0.50
1:B:259:THR:HG21	1:B:289:PHE:CD1	2.46	0.50
1:A:44:ILE:HD13	1:A:274:GLN:HG2	1.92	0.50
1:A:80:LEU:HD11	1:A:217:PHE:CB	2.41	0.50
1:B:261:ILE:HD13	1:B:270:LEU:HB2	1.93	0.50
1:A:459:GLU:O	1:A:460:ASN:C	2.49	0.50
1:B:70:VAL:HG12	1:B:70:VAL:O	2.11	0.50
1:A:318:ILE:HB	1:A:333:GLU:HG3	1.94	0.50
1:B:145:LYS:HZ2	1:B:146:ILE:HG13	1.75	0.50
1:A:272:ILE:HG23	1:A:283:PHE:CE2	2.46	0.50
1:A:79:LYS:HD2	1:A:237:ILE:CD1	2.40	0.50
1:B:21:MET:O	1:B:26:LYS:HE3	2.11	0.50
1:A:244:CYS:HA	1:A:347:ILE:O	2.10	0.50
1:B:315:MET:HG2	1:B:338:ALA:HB3	1.94	0.50
1:B:105:ARG:O	1:B:106:ASP:HB2	2.11	0.50
1:B:286:ILE:HG12	2:B:656:HOH:O	2.11	0.50
1:A:245:MET:HE1	1:A:269:LEU:HD13	1.93	0.50
1:B:382:ARG:HG3	1:B:382:ARG:HH11	1.77	0.50
1:B:105:ARG:HG3	1:B:106:ASP:N	2.27	0.50
1:A:384:LYS:C	1:A:386:ARG:H	2.14	0.50
1:A:247:VAL:HA	1:A:292:PHE:O	2.12	0.50
1:A:443:ALA:HB3	1:A:464:ASN:ND2	2.27	0.50
1:B:425:SER:HA	2:B:476:HOH:O	2.10	0.50
1:A:382:ARG:CZ	1:A:386:ARG:HG2	2.41	0.50
1:A:111:LEU:HD11	1:A:133:LEU:HD11	1.94	0.50
1:A:434:ILE:HD13	1:A:452:ILE:HG22	1.94	0.50
1:B:105:ARG:HG3	1:B:375:LEU:HD22	1.93	0.50
1:B:167:ARG:HD2	1:B:187:TRP:O	2.12	0.50
1:B:246:GLU:HA	1:B:349:VAL:HG13	1.93	0.50
1:B:153:SER:CB	1:B:155:VAL:HG12	2.40	0.50
1:B:263:TYR:O	2:B:597:HOH:O	2.20	0.50
1:A:299:VAL:HB	1:A:304:ILE:HD11	1.94	0.50
1:B:410:PHE:O	1:B:411:LYS:C	2.49	0.50
1:A:61:GLU:CD	1:A:61:GLU:H	2.14	0.50
1:A:427:ASP:O	1:A:449:LYS:HA	2.12	0.50
1:A:365:LEU:O	1:A:369:GLN:HB2	2.11	0.50
1:B:427:ASP:HB3	1:B:449:LYS:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:GLU:N	2:A:612:HOH:O	2.45	0.50
1:B:176:TRP:CD2	1:B:181:LYS:HG2	2.46	0.50
1:B:247:VAL:HA	1:B:293:ASN:HA	1.94	0.50
1:B:270:LEU:HG	1:B:283:PHE:HE1	1.77	0.50
1:A:109:THR:N	1:A:112:ASP:HB2	2.27	0.50
1:B:399:GLU:HB3	1:B:409:ARG:NE	2.27	0.50
1:A:384:LYS:HA	1:A:384:LYS:HE3	1.93	0.50
1:B:395:GLU:O	1:B:423:LYS:HA	2.12	0.50
1:B:222:ASP:OD1	1:B:360:LYS:HE3	2.12	0.50
1:B:249:PRO:CD	1:B:351:VAL:O	2.59	0.50
1:A:285:SER:C	1:A:287:GLU:H	2.14	0.50
1:B:32:LEU:HD11	1:B:317:ILE:HD12	1.94	0.50
1:B:79:LYS:HD3	1:B:214:GLU:CD	2.31	0.50
1:B:103:GLU:CD	1:B:107:GLY:HA2	2.32	0.50
1:B:83:LEU:HD12	1:B:132:VAL:O	2.11	0.50
1:B:332:LEU:HD12	2:B:683:HOH:O	2.11	0.50
1:A:241:ASN:ND2	1:A:347:ILE:CG2	2.75	0.50
1:B:145:LYS:O	1:B:148:GLU:HB2	2.12	0.50
1:B:305:LYS:O	1:B:309:GLU:HB2	2.12	0.50
1:B:148:GLU:HA	1:B:151:THR:HG23	1.92	0.50
1:B:153:SER:O	1:B:155:VAL:N	2.45	0.50
1:B:317:ILE:HD11	2:B:532:HOH:O	2.12	0.50
1:A:340:ILE:O	1:A:340:ILE:HG12	2.12	0.50
1:A:111:LEU:O	1:A:115:VAL:HG23	2.12	0.50
1:B:392:PRO:HB3	1:B:419:LEU:O	2.11	0.50
1:A:57:VAL:HA	1:A:348:GLY:O	2.12	0.50
1:B:150:TYR:C	1:B:152:ASN:H	2.15	0.50
1:B:267:VAL:HG11	1:B:346:ALA:HB3	1.94	0.50
1:B:152:ASN:HD22	1:B:152:ASN:N	2.09	0.50
1:A:167:ARG:HB3	1:A:329:VAL:HB	1.93	0.50
1:B:111:LEU:O	1:B:115:VAL:HG23	2.12	0.49
1:B:239:ASN:O	1:B:240:LYS:HB2	2.11	0.49
1:B:244:CYS:HB3	1:B:347:ILE:HG13	1.94	0.49
1:A:255:VAL:O	1:A:284:LYS:HA	2.12	0.49
1:A:8:LEU:CD2	1:A:9:PRO:HD3	2.42	0.49
1:B:459:GLU:O	1:B:460:ASN:C	2.50	0.49
1:B:300:ASN:O	1:B:304:ILE:HG13	2.11	0.49
1:B:176:TRP:HB3	1:B:177:PRO:HD3	1.94	0.49
1:A:121:LEU:HD11	1:A:228:VAL:HB	1.94	0.49
1:A:247:VAL:HA	1:A:292:PHE:O	2.11	0.49
1:A:244:CYS:SG	1:A:347:ILE:HG13	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:PRO:O	1:A:201:ASN:HB2	2.12	0.49
1:B:143:THR:HA	1:B:146:ILE:HD12	1.94	0.49
1:B:215:TYR:HA	1:B:299:VAL:O	2.11	0.49
1:A:287:GLU:OE2	1:A:287:GLU:HA	2.12	0.49
1:A:44:ILE:HG22	1:A:49:ILE:HD11	1.93	0.49
1:B:176:TRP:N	1:B:177:PRO:HD2	2.27	0.49
1:B:398:PRO:HD2	2:B:484:HOH:O	2.11	0.49
1:A:370:SER:C	1:A:372:LEU:N	2.62	0.49
1:B:73:THR:HG21	1:B:125:TYR:CZ	2.47	0.49
1:A:77:LEU:CD2	1:A:228:VAL:HG11	2.41	0.49
1:A:243:TYR:O	1:A:346:ALA:HA	2.11	0.49
1:B:36:TYR:O	1:B:37:LEU:HD23	2.12	0.49
1:A:86:ASN:O	1:A:135:ASN:HA	2.11	0.49
1:B:246:GLU:HG2	1:B:349:VAL:CG1	2.43	0.49
1:B:56:ILE:HG12	2:B:611:HOH:O	2.13	0.49
1:A:92:THR:O	1:A:401:LYS:NZ	2.42	0.49
1:B:351:VAL:HB	1:B:352:PRO:HD2	1.93	0.49
1:B:360:LYS:N	1:B:360:LYS:HD2	2.27	0.49
1:B:286:ILE:HG12	2:B:656:HOH:O	2.11	0.49
1:A:8:LEU:CD2	1:A:9:PRO:HD3	2.42	0.49
1:B:375:LEU:N	1:B:375:LEU:HD12	2.27	0.49
1:A:171:ASP:CG	1:A:172:GLU:H	2.15	0.49
1:B:194:ASP:OD1	1:B:197:PRO:HG2	2.12	0.49
1:B:286:ILE:O	1:B:290:LYS:HG2	2.12	0.49
1:A:364:ASP:O	1:A:367:LEU:HB2	2.13	0.49
1:B:459:GLU:O	1:B:460:ASN:C	2.51	0.49
1:B:305:LYS:O	1:B:309:GLU:HB2	2.13	0.49
1:B:77:LEU:CD1	1:B:230:LEU:HD11	2.42	0.49
1:A:169:VAL:HG11	1:A:172:GLU:HB2	1.94	0.49
1:A:167:ARG:HD3	1:A:329:VAL:HG21	1.94	0.49
1:A:147:VAL:HA	1:A:150:TYR:CD2	2.47	0.49
1:B:242:GLU:HA	1:B:300:ASN:HB2	1.94	0.49
1:A:439:LYS:C	1:A:439:LYS:HD2	2.32	0.49
1:A:372:LEU:HA	1:A:417:VAL:HG22	1.94	0.49
1:A:259:THR:N	1:A:270:LEU:O	2.43	0.49
1:A:459:GLU:O	1:A:460:ASN:C	2.49	0.49
1:A:266:LYS:HA	1:A:266:LYS:HE2	1.94	0.49
1:A:317:ILE:HG22	1:A:318:ILE:N	2.28	0.49
1:B:89:LEU:HB3	1:B:91:THR:HG23	1.94	0.49
1:A:113:LEU:O	1:A:117:GLN:HG3	2.12	0.49
1:A:137:PHE:HE1	1:A:184:LYS:HB2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:LEU:C	1:A:121:LEU:HD23	2.32	0.49
1:A:219:ALA:HB2	1:A:296:ASN:HA	1.94	0.49
1:A:430:PHE:HB3	1:A:434:ILE:HD12	1.93	0.49
1:B:390:SER:OG	2:B:605:HOH:O	2.20	0.49
1:B:76:LEU:HD23	1:B:237:ILE:CD1	2.21	0.49
1:A:278:GLU:CD	1:A:278:GLU:H	2.16	0.49
1:A:113:LEU:HD21	1:A:375:LEU:HD11	1.95	0.49
1:B:109:THR:O	1:B:112:ASP:N	2.44	0.49
1:B:351:VAL:HB	1:B:352:PRO:CD	2.43	0.49
1:A:200:MET:HA	1:A:205:LEU:HB2	1.93	0.49
1:B:87:GLY:HA2	1:B:135:ASN:HA	1.94	0.49
1:A:36:TYR:HE1	1:A:319:PRO:HG3	1.78	0.49
1:B:81:VAL:HA	1:B:130:PRO:HD2	1.95	0.49
1:A:246:GLU:HB2	1:A:296:ASN:HB2	1.94	0.49
1:A:314:LYS:HD2	1:A:315:MET:O	2.13	0.49
1:A:22:SER:O	1:A:26:LYS:HG3	2.13	0.49
1:A:32:LEU:HG	1:A:317:ILE:HD11	1.93	0.49
1:B:103:GLU:HB2	2:B:542:HOH:O	2.12	0.49
1:B:21:MET:HA	1:B:25:GLU:OE1	2.13	0.49
1:B:316:GLU:OE1	2:B:520:HOH:O	2.20	0.49
1:B:196:PHE:O	1:B:197:PRO:C	2.51	0.49
1:B:113:LEU:HD22	1:B:375:LEU:HD21	1.95	0.49
1:B:150:TYR:HE2	2:B:554:HOH:O	1.96	0.49
1:A:8:LEU:HG	1:A:9:PRO:HD3	1.92	0.49
1:B:193:GLY:HA2	1:B:336:ALA:HA	1.95	0.49
1:B:358:PRO:HB2	1:B:360:LYS:CD	2.42	0.49
1:B:142:ASP:HA	1:B:145:LYS:HE3	1.95	0.49
1:B:104:VAL:HG22	1:B:110:PHE:CZ	2.47	0.49
1:B:48:LYS:HZ2	1:B:48:LYS:HB3	1.77	0.49
1:A:437:LYS:HB2	1:A:459:GLU:HG3	1.93	0.49
1:A:8:LEU:CG	1:A:9:PRO:HD3	2.42	0.49
1:B:346:ALA:C	1:B:347:ILE:HG23	2.33	0.49
1:B:247:VAL:CB	1:B:291:ILE:HD13	2.42	0.49
1:B:14:ALA:CA	2:B:580:HOH:O	2.57	0.49
1:B:243:TYR:CD2	1:B:340:ILE:HD12	2.48	0.49
1:A:245:MET:O	1:A:348:GLY:HA2	2.12	0.49
1:A:269:LEU:CD2	1:A:271:GLU:OE2	2.60	0.49
1:A:386:ARG:CZ	1:A:388:ASN:HB3	2.42	0.49
1:A:433:SER:CB	1:A:455:ARG:HG2	2.43	0.49
1:B:73:THR:HG21	1:B:125:TYR:CE1	2.48	0.49
1:B:211:GLN:OE1	2:B:630:HOH:O	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:GLY:O	1:B:207:THR:OG1	2.19	0.49
1:B:248:THR:O	1:B:291:ILE:HA	2.12	0.49
1:B:242:GLU:CG	1:B:344:ASP:H	2.26	0.49
1:A:118:ILE:CD1	1:A:131:LEU:HB2	2.43	0.49
1:A:469:LEU:HD11	2:A:627:HOH:O	2.13	0.49
1:B:115:VAL:CG1	1:B:150:TYR:CD1	2.96	0.49
1:B:142:ASP:HA	1:B:145:LYS:HE3	1.93	0.49
1:B:259:THR:HG1	1:B:291:ILE:HD12	1.77	0.49
1:A:434:ILE:N	2:A:503:HOH:O	2.44	0.49
1:B:403:VAL:HG12	1:B:404:ALA:N	2.27	0.49
1:B:98:PRO:HD2	1:B:101:VAL:HG22	1.95	0.49
1:A:384:LYS:HB3	1:A:384:LYS:NZ	2.27	0.49
1:A:142:ASP:O	1:A:145:LYS:HG2	2.13	0.49
1:A:246:GLU:OE1	1:A:355:ARG:NH1	2.46	0.49
1:B:354:SER:HB3	2:B:609:HOH:O	2.13	0.49
1:A:37:LEU:HD21	1:A:173:PHE:HE2	1.78	0.49
1:B:86:ASN:HB3	1:B:135:ASN:HB3	1.95	0.49
1:B:115:VAL:CG1	1:B:155:VAL:HG11	2.43	0.49
1:A:461:LYS:NZ	1:A:468:ASP:HB3	2.28	0.49
1:A:261:ILE:HD12	1:A:261:ILE:O	2.13	0.49
1:B:216:VAL:HG13	1:B:299:VAL:HG22	1.94	0.49
1:B:229:ASP:OD1	1:B:232:ILE:HG13	2.13	0.49
1:B:247:VAL:HG23	1:B:350:ASN:HA	1.95	0.49
1:A:123:ASN:CB	2:A:551:HOH:O	2.61	0.49
1:B:373:TYR:CD2	1:B:380:VAL:HG12	2.48	0.49
1:B:322:LYS:NZ	2:B:693:HOH:O	2.41	0.49
1:A:108:LEU:HA	1:A:112:ASP:OD2	2.12	0.49
1:B:247:VAL:O	1:B:351:VAL:HG22	2.12	0.49
1:A:414:PRO:HB2	1:A:436:LEU:CD1	2.43	0.49
1:A:181:LYS:HE3	1:A:185:GLU:CB	2.41	0.49
1:B:357:LEU:HD23	1:B:357:LEU:C	2.34	0.49
1:A:366:LEU:O	1:A:366:LEU:HD23	2.13	0.49
1:A:10:GLN:HB2	2:A:553:HOH:O	2.13	0.49
1:A:118:ILE:CD1	1:A:131:LEU:HB2	2.43	0.49
1:B:255:VAL:HB	1:B:284:LYS:O	2.12	0.49
1:A:89:LEU:C	1:A:91:THR:N	2.66	0.49
1:A:225:GLY:O	1:A:227:ILE:N	2.46	0.49
1:A:243:TYR:OH	1:A:337:GLY:HA2	2.12	0.49
1:B:8:LEU:N	1:B:8:LEU:HD22	2.27	0.49
1:A:104:VAL:HG13	1:A:105:ARG:N	2.27	0.49
1:B:242:GLU:HG3	1:B:344:ASP:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:ILE:O	1:B:267:VAL:HA	2.12	0.49
1:B:73:THR:HA	1:B:76:LEU:HD12	1.93	0.49
1:A:58:VAL:O	1:A:349:VAL:HG23	2.13	0.49
1:A:11:LEU:HD23	1:A:11:LEU:C	2.33	0.49
1:B:192:HIS:CE1	1:B:336:ALA:H	2.29	0.49
1:A:80:LEU:O	1:A:129:VAL:HG13	2.13	0.49
1:B:359:VAL:HG13	1:B:364:ASP:HB2	1.95	0.49
1:B:181:LYS:CE	1:B:185:GLU:HB2	2.41	0.49
1:A:99:LYS:HZ2	1:A:102:ILE:HD12	1.78	0.49
1:B:343:PHE:N	1:B:343:PHE:CD2	2.80	0.49
1:A:363:SER:HB3	1:A:396:LEU:HG	1.95	0.49
1:B:150:TYR:HE2	2:B:554:HOH:O	1.95	0.49
1:B:246:GLU:HA	1:B:349:VAL:CG1	2.43	0.48
1:B:48:LYS:NZ	1:B:263:TYR:CZ	2.81	0.48
1:A:200:MET:CG	1:A:205:LEU:HD23	2.42	0.48
1:A:122:ASN:OD1	1:A:129:VAL:N	2.45	0.48
1:B:305:LYS:O	1:B:309:GLU:CB	2.61	0.48
1:B:116:ILE:HG23	1:B:120:ASN:ND2	2.28	0.48
1:B:372:LEU:CD2	1:B:372:LEU:O	2.61	0.48
1:B:132:VAL:HG13	1:B:158:HIS:HB2	1.94	0.48
1:A:425:SER:OG	1:A:443:ALA:HA	2.12	0.48
1:B:111:LEU:O	1:B:114:ILE:HB	2.13	0.48
1:A:171:ASP:CG	1:A:172:GLU:N	2.66	0.48
1:B:417:VAL:HG12	2:B:496:HOH:O	2.12	0.48
1:B:206:ASP:CG	1:B:305:LYS:HZ2	2.16	0.48
1:B:108:LEU:HD22	1:B:112:ASP:HB3	1.95	0.48
1:B:176:TRP:CD2	1:B:181:LYS:HG2	2.47	0.48
1:B:224:LEU:HB2	1:B:357:LEU:HD12	1.95	0.48
1:B:163:SER:HB3	1:B:165:TYR:CE1	2.49	0.48
1:A:113:LEU:HD13	1:A:380:VAL:HG23	1.94	0.48
1:B:137:PHE:CE1	1:B:184:LYS:HD2	2.49	0.48
1:A:124:LYS:HE3	1:A:125:TYR:OH	2.12	0.48
1:A:429:TRP:HB2	1:A:451:GLU:CD	2.33	0.48
1:A:57:VAL:HA	1:A:348:GLY:O	2.12	0.48
1:A:204:LYS:O	1:A:208:PHE:CD2	2.66	0.48
1:B:249:PRO:HB2	2:B:533:HOH:O	2.12	0.48
1:B:250:LYS:CE	1:B:292:PHE:HB3	2.42	0.48
1:A:409:ARG:NH1	1:A:428:VAL:O	2.43	0.48
1:A:8:LEU:H	1:A:9:PRO:HD2	1.75	0.48
1:A:411:LYS:HB2	1:A:431:GLY:C	2.34	0.48
1:B:280:VAL:HG12	1:B:281:ASN:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:GLU:H	1:A:278:GLU:CD	2.16	0.48
1:B:122:ASN:HA	1:B:127:CYS:O	2.13	0.48
1:B:83:LEU:O	1:B:83:LEU:HD23	2.13	0.48
1:B:110:PHE:CD1	1:B:222:ASP:HA	2.48	0.48
1:B:21:MET:HA	1:B:25:GLU:OE1	2.13	0.48
1:B:382:ARG:NH1	1:B:389:PRO:HA	2.28	0.48
1:B:382:ARG:NH2	1:B:391:ASN:OD1	2.38	0.48
1:A:119:GLU:CG	1:A:154:ASN:H	2.22	0.48
1:B:22:SER:O	1:B:26:LYS:HG3	2.13	0.48
1:B:322:LYS:NZ	2:B:694:HOH:O	2.43	0.48
1:A:27:SER:O	1:A:30:ILE:CB	2.59	0.48
1:A:247:VAL:CB	1:A:291:ILE:HD13	2.42	0.48
1:A:117:GLN:HG2	1:A:378:GLY:O	2.13	0.48
1:B:346:ALA:O	1:B:347:ILE:CG2	2.61	0.48
1:B:176:TRP:O	1:B:179:LYS:N	2.35	0.48
1:A:89:LEU:HA	1:A:98:PRO:HA	1.94	0.48
1:B:305:LYS:HE2	1:B:309:GLU:OE1	2.12	0.48
1:B:140:HIS:CG	1:B:161:ASN:HB2	2.48	0.48
1:A:12:LYS:HG2	1:A:16:ASP:OD2	2.12	0.48
1:A:359:VAL:O	1:A:360:LYS:HD2	2.13	0.48
1:A:379:PHE:HB2	2:A:598:HOH:O	2.12	0.48
1:A:364:ASP:O	1:A:367:LEU:HB2	2.14	0.48
1:B:242:GLU:OE1	1:B:343:PHE:HA	2.14	0.48
1:B:96:THR:HG22	1:B:97:GLY:N	2.27	0.48
1:A:436:LEU:HD23	1:A:458:VAL:HB	1.94	0.48
1:B:296:ASN:C	1:B:297:LEU:HG	2.33	0.48
1:B:305:LYS:HG2	1:B:305:LYS:O	2.13	0.48
1:B:268:GLN:HE22	1:B:341:ARG:HD2	1.78	0.48
1:B:436:LEU:HD23	1:B:458:VAL:HB	1.94	0.48
1:A:102:ILE:HB	1:A:110:PHE:HE2	1.78	0.48
1:B:116:ILE:HG22	1:B:120:ASN:ND2	2.29	0.48
1:B:15:VAL:HB	1:B:30:ILE:HD11	1.96	0.48
1:A:116:ILE:CG2	1:A:378:GLY:HA3	2.42	0.48
1:A:429:TRP:HB2	1:A:451:GLU:HG2	1.96	0.48
1:B:105:ARG:NH2	1:B:373:TYR:O	2.46	0.48
1:B:176:TRP:CD2	1:B:181:LYS:HG2	2.48	0.48
1:A:322:LYS:O	1:A:329:VAL:HG22	2.14	0.48
1:B:66:VAL:HG22	1:B:234:LYS:CD	2.44	0.48
1:A:108:LEU:HD12	1:A:375:LEU:CD2	2.43	0.48
1:B:267:VAL:O	1:B:341:ARG:CA	2.61	0.48
1:B:49:ILE:HD13	1:B:270:LEU:HD22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:LEU:HD11	1:A:228:VAL:HG21	1.95	0.48
1:A:29:PHE:O	1:A:32:LEU:N	2.38	0.48
1:A:20:GLU:HA	1:A:20:GLU:OE2	2.13	0.48
1:A:209:LEU:C	1:A:211:GLN:H	2.16	0.48
1:A:239:ASN:O	1:A:345:ASN:ND2	2.47	0.48
1:B:184:LYS:O	1:B:185:GLU:OE2	2.31	0.48
1:B:66:VAL:HG13	1:B:72:GLU:CD	2.33	0.48
1:B:175:PRO:O	1:B:176:TRP:C	2.50	0.48
1:A:87:GLY:HA2	1:A:135:ASN:HA	1.95	0.48
1:A:167:ARG:NH2	1:A:331:GLN:OE1	2.42	0.48
1:A:267:VAL:HG13	1:A:346:ALA:HB3	1.94	0.48
1:A:31:SER:O	1:A:35:ARG:HG2	2.14	0.48
1:A:371:ASP:OD1	1:A:417:VAL:N	2.46	0.48
1:B:218:VAL:O	1:B:297:LEU:N	2.42	0.48
1:B:411:LYS:HB3	1:B:432:SER:HB3	1.96	0.48
1:A:455:ARG:HB3	1:A:455:ARG:CZ	2.43	0.48
1:A:291:ILE:O	1:A:291:ILE:HD12	2.12	0.48
1:B:21:MET:HG2	2:B:571:HOH:O	2.14	0.48
1:A:122:ASN:OD1	1:A:129:VAL:N	2.40	0.48
1:B:252:LEU:C	1:B:252:LEU:HD23	2.33	0.48
1:A:415:SER:OG	1:A:435:VAL:HG22	2.14	0.48
1:A:366:LEU:HD11	1:A:422:LEU:HD23	1.94	0.48
1:A:393:SER:O	2:A:635:HOH:O	2.20	0.48
1:B:241:ASN:ND2	1:B:347:ILE:HG21	2.28	0.48
1:B:412:SER:OG	1:B:433:SER:N	2.43	0.48
1:A:461:LYS:NZ	1:A:468:ASP:HB3	2.28	0.48
1:B:391:ASN:HB3	1:B:392:PRO:HD2	1.96	0.48
1:B:322:LYS:HB3	1:B:329:VAL:HG23	1.94	0.48
1:B:131:LEU:HD12	1:B:132:VAL:N	2.28	0.48
1:A:12:LYS:HA	1:A:30:ILE:HD11	1.96	0.48
1:A:87:GLY:HA2	1:A:136:SER:N	2.28	0.48
1:B:22:SER:OG	1:B:24:SER:HB2	2.13	0.48
1:A:90:GLY:O	1:A:95:CYS:HB2	2.13	0.48
1:B:175:PRO:O	1:B:178:SER:HB2	2.13	0.48
1:B:359:VAL:HG13	1:B:364:ASP:CB	2.43	0.48
1:B:334:THR:HA	2:B:492:HOH:O	2.14	0.48
1:A:81:VAL:HG22	1:A:216:VAL:HG23	1.96	0.48
1:A:315:MET:SD	1:A:339:ALA:HB2	2.54	0.48
1:A:73:THR:HG23	1:A:230:LEU:HD12	1.94	0.48
1:B:411:LYS:HB3	1:B:431:GLY:C	2.34	0.48
1:A:165:TYR:O	1:A:187:TRP:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:ILE:HD12	1:B:262:SER:O	2.13	0.48
1:B:136:SER:HA	1:B:161:ASN:OD1	2.14	0.48
1:A:207:THR:HG22	1:A:211:GLN:CD	2.33	0.48
1:B:300:ASN:HB3	1:B:303:ALA:HB3	1.95	0.48
1:B:66:VAL:HG22	1:B:234:LYS:HD2	1.95	0.48
1:B:80:LEU:HD11	1:B:217:PHE:HB2	1.94	0.48
1:A:104:VAL:HG11	1:A:113:LEU:HD12	1.94	0.48
1:A:403:VAL:O	1:A:407:LEU:HG	2.13	0.48
1:B:128:LYS:HD2	2:B:669:HOH:O	2.12	0.48
1:B:110:PHE:CE1	1:B:359:VAL:HG21	2.48	0.48
1:B:56:ILE:O	1:B:347:ILE:HB	2.13	0.48
1:B:92:THR:C	1:B:94:GLY:H	2.16	0.48
1:A:121:LEU:HD23	1:A:121:LEU:O	2.14	0.48
1:B:282:GLU:HB3	1:B:288:LYS:HG3	1.96	0.48
1:A:195:VAL:CG1	1:A:196:PHE:N	2.64	0.48
1:B:70:VAL:HG13	1:B:125:TYR:CD1	2.45	0.48
1:A:243:TYR:C	1:A:243:TYR:CD2	2.86	0.48
1:A:28:GLY:O	1:A:32:LEU:HD22	2.14	0.48
1:B:76:LEU:HD23	1:B:237:ILE:HD12	1.96	0.48
1:A:384:LYS:O	1:A:384:LYS:HE3	2.12	0.48
1:B:346:ALA:C	1:B:347:ILE:CG2	2.82	0.48
1:B:322:LYS:HB3	1:B:329:VAL:CG2	2.44	0.48
1:A:135:ASN:HD21	1:A:143:THR:HG21	1.78	0.48
1:A:99:LYS:O	1:A:102:ILE:N	2.46	0.48
1:A:363:SER:HB2	1:A:394:ILE:HG22	1.95	0.48
1:B:315:MET:HG3	1:B:338:ALA:O	2.13	0.48
1:A:110:PHE:O	1:A:114:ILE:HG13	2.14	0.48
1:A:232:ILE:O	1:A:236:LEU:HG	2.14	0.48
1:B:310:ALA:O	1:B:311:ASP:O	2.31	0.48
1:A:391:ASN:HB3	1:A:392:PRO:HD2	1.94	0.48
1:B:418:GLU:HB2	1:B:437:LYS:HG2	1.96	0.48
1:A:271:GLU:C	1:A:273:ALA:N	2.66	0.48
1:A:100:SER:C	1:A:102:ILE:N	2.66	0.48
1:A:366:LEU:HB2	1:A:406:PHE:HZ	1.79	0.48
1:A:444:ALA:HB1	1:A:448:VAL:O	2.13	0.48
1:B:267:VAL:CG1	1:B:346:ALA:HB3	2.43	0.48
1:B:93:MET:HE1	1:B:365:LEU:CD1	2.42	0.48
1:B:9:PRO:O	1:B:11:LEU:N	2.47	0.48
1:B:188:TYR:HB2	1:B:189:PRO:HD2	1.96	0.48
1:B:107:GLY:HA2	2:B:481:HOH:O	2.14	0.48
1:A:405:THR:CG2	1:A:409:ARG:HE	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:VAL:O	1:B:73:THR:HB	2.14	0.48
1:B:137:PHE:N	2:B:507:HOH:O	2.47	0.48
1:B:379:PHE:HZ	2:B:522:HOH:O	1.97	0.48
1:B:192:HIS:CE1	1:B:336:ALA:H	2.30	0.48
1:B:372:LEU:HD22	1:B:373:TYR:CD1	2.49	0.48
1:A:173:PHE:HE1	1:A:330:LEU:HD12	1.77	0.48
1:B:11:LEU:HD21	1:B:175:PRO:HG3	1.96	0.48
1:A:363:SER:HB3	2:A:606:HOH:O	2.14	0.48
1:A:181:LYS:HE3	1:A:185:GLU:HB2	1.94	0.48
1:B:150:TYR:HD1	1:B:153:SER:OG	1.97	0.48
1:A:141:ASP:HB2	2:A:483:HOH:O	2.14	0.48
1:A:259:THR:HG22	1:A:283:PHE:CE1	2.49	0.48
1:A:411:LYS:CD	1:A:431:GLY:HA2	2.44	0.48
1:B:372:LEU:O	1:B:383:ASN:N	2.40	0.48
1:A:453:PRO:CG	1:A:456:ALA:HB2	2.40	0.47
1:A:412:SER:HB3	1:A:433:SER:H	1.79	0.47
1:B:108:LEU:HD22	1:B:112:ASP:CB	2.44	0.47
1:B:445:LYS:NZ	1:B:464:ASN:O	2.46	0.47
1:A:429:TRP:HB2	1:A:451:GLU:OE1	2.13	0.47
1:B:230:LEU:N	1:B:230:LEU:CD1	2.77	0.47
1:A:73:THR:HG21	1:A:125:TYR:CD1	2.49	0.47
1:A:69:ASP:O	1:A:72:GLU:HB3	2.14	0.47
1:A:324:VAL:HG12	1:A:325:ASP:OD2	2.13	0.47
1:A:386:ARG:HE	1:A:388:ASN:HB3	1.77	0.47
1:B:409:ARG:HA	1:B:429:TRP:CE3	2.48	0.47
1:A:365:LEU:O	1:A:369:GLN:HB2	2.13	0.47
1:B:73:THR:HG21	1:B:125:TYR:CZ	2.49	0.47
1:A:420:ASP:OD2	1:A:438:GLY:HA2	2.13	0.47
1:B:283:PHE:HA	1:B:289:PHE:CD2	2.49	0.47
1:A:8:LEU:N	1:A:8:LEU:HD23	2.29	0.47
1:B:217:PHE:HA	1:B:297:LEU:O	2.14	0.47
1:A:32:LEU:HG	1:A:317:ILE:CD1	2.44	0.47
1:B:287:GLU:OE2	2:B:579:HOH:O	2.20	0.47
1:B:15:VAL:HG13	1:B:18:LEU:HD12	1.96	0.47
1:B:434:ILE:HG22	1:B:435:VAL:N	2.29	0.47
1:B:11:LEU:HD12	1:B:173:PHE:CD2	2.49	0.47
1:A:132:VAL:O	1:A:132:VAL:HG13	2.14	0.47
1:A:176:TRP:CD2	1:A:181:LYS:HG2	2.50	0.47
1:A:45:GLU:OE1	1:A:45:GLU:HA	2.14	0.47
1:A:415:SER:HB3	1:A:435:VAL:HA	1.95	0.47
1:A:330:LEU:HD22	1:A:332:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:LEU:CD1	1:A:386:ARG:HD3	2.44	0.47
1:B:461:LYS:HE3	1:B:463:ILE:HG12	1.96	0.47
1:B:227:ILE:HD13	2:B:535:HOH:O	2.14	0.47
1:A:411:LYS:HD2	1:A:431:GLY:HA2	1.95	0.47
1:A:384:LYS:NZ	2:A:559:HOH:O	2.38	0.47
1:B:370:SER:C	1:B:372:LEU:H	2.18	0.47
1:A:411:LYS:HB3	1:A:432:SER:HB3	1.95	0.47
1:A:164:LYS:HE2	2:A:541:HOH:O	2.14	0.47
1:A:114:ILE:HG22	1:A:131:LEU:HD22	1.96	0.47
1:B:14:ALA:HA	2:B:581:HOH:O	2.13	0.47
1:B:66:VAL:HG13	1:B:72:GLU:CG	2.45	0.47
1:A:372:LEU:HD23	1:A:373:TYR:CE2	2.49	0.47
1:A:176:TRP:N	1:A:177:PRO:CD	2.77	0.47
1:A:127:CYS:HB2	2:A:646:HOH:O	2.14	0.47
1:A:190:PRO:HG2	1:A:194:ASP:CB	2.44	0.47
1:A:246:GLU:HB2	1:A:294:THR:OG1	2.15	0.47
1:A:330:LEU:HD22	1:A:332:LEU:CD1	2.44	0.47
1:A:465:GLY:HA3	2:A:590:HOH:O	2.14	0.47
1:B:437:LYS:CB	1:B:459:GLU:HG3	2.44	0.47
1:B:193:GLY:HA2	1:B:336:ALA:CA	2.44	0.47
1:A:66:VAL:HG11	1:A:230:LEU:HB3	1.97	0.47
1:B:37:LEU:HD21	1:B:173:PHE:CZ	2.48	0.47
1:A:28:GLY:C	1:A:30:ILE:N	2.67	0.47
1:A:255:VAL:HG23	1:A:256:LYS:H	1.80	0.47
1:B:259:THR:HG21	1:B:289:PHE:CD1	2.50	0.47
1:A:224:LEU:HB2	1:A:357:LEU:HB3	1.95	0.47
1:A:455:ARG:NH1	1:A:455:ARG:HB3	2.29	0.47
1:A:76:LEU:HD11	1:A:234:LYS:HB2	1.96	0.47
1:A:190:PRO:HB2	2:A:475:HOH:O	2.14	0.47
1:A:46:TRP:HA	1:A:49:ILE:CD1	2.44	0.47
1:A:391:ASN:HB2	2:A:556:HOH:O	2.14	0.47
1:A:85:LEU:HB2	1:A:220:ASN:HA	1.97	0.47
1:A:8:LEU:H	1:A:9:PRO:CD	2.26	0.47
1:A:434:ILE:HG22	1:A:435:VAL:N	2.29	0.47
1:A:402:LYS:O	1:A:404:ALA:N	2.47	0.47
1:A:142:ASP:O	1:A:146:ILE:HG12	2.15	0.47
1:B:159:THR:HG22	2:B:483:HOH:O	2.14	0.47
1:B:136:SER:O	1:B:140:HIS:HB2	2.15	0.47
1:B:396:LEU:HB3	1:B:400:PHE:CD2	2.49	0.47
1:B:164:LYS:O	1:B:165:TYR:HD1	1.98	0.47
1:B:453:PRO:HG2	1:B:456:ALA:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:ARG:O	1:A:430:PHE:HB2	2.14	0.47
1:A:319:PRO:HA	1:A:332:LEU:CD1	2.27	0.47
1:B:150:TYR:CD2	2:B:653:HOH:O	2.41	0.47
1:B:96:THR:CG2	1:B:97:GLY:H	2.25	0.47
1:A:121:LEU:HD23	1:A:121:LEU:O	2.14	0.47
1:A:61:GLU:H	1:A:61:GLU:CD	2.17	0.47
1:B:28:GLY:O	1:B:32:LEU:HB2	2.13	0.47
1:B:243:TYR:CE2	1:B:340:ILE:HB	2.50	0.47
1:A:445:LYS:N	2:A:563:HOH:O	2.47	0.47
1:B:163:SER:HB3	1:B:165:TYR:CE1	2.49	0.47
1:A:367:LEU:HD22	1:A:372:LEU:HD23	1.97	0.47
1:A:256:LYS:HG3	1:A:284:LYS:HD3	1.96	0.47
1:B:165:TYR:CE2	1:B:190:PRO:HG3	2.49	0.47
1:A:353:ARG:CB	2:A:580:HOH:O	2.57	0.47
1:B:35:ARG:NH2	1:B:314:LYS:NZ	2.62	0.47
1:A:119:GLU:HG3	1:A:154:ASN:HB3	1.95	0.47
1:B:382:ARG:NH1	1:B:382:ARG:HG3	2.29	0.47
1:B:115:VAL:HG11	1:B:150:TYR:CD1	2.49	0.47
1:B:152:ASN:ND2	1:B:152:ASN:N	2.62	0.47
1:B:467:GLU:HG3	1:B:468:ASP:N	2.27	0.47
1:B:371:ASP:OD1	1:B:415:SER:HA	2.14	0.47
1:A:79:LYS:HA	1:A:213:LYS:HA	1.97	0.47
1:B:48:LYS:NZ	1:B:263:TYR:CZ	2.82	0.47
1:B:246:GLU:HA	1:B:349:VAL:CG1	2.44	0.47
1:B:63:MET:HE3	1:B:349:VAL:HG23	1.97	0.47
1:A:258:GLY:CA	1:A:271:GLU:OE1	2.62	0.47
1:A:456:ALA:O	1:A:457:VAL:CG2	2.63	0.47
1:B:394:ILE:HG23	1:B:422:LEU:HD23	1.96	0.47
1:B:293:ASN:HB3	2:B:691:HOH:O	2.14	0.47
1:B:315:MET:HB2	1:B:334:THR:HB	1.96	0.47
1:A:21:MET:SD	1:A:166:PRO:HD3	2.55	0.47
1:A:142:ASP:O	1:A:145:LYS:HG2	2.14	0.47
1:A:11:LEU:CD1	1:A:33:VAL:HG11	2.38	0.47
1:A:365:LEU:HB3	1:A:369:GLN:HE22	1.80	0.47
1:A:247:VAL:HG12	1:A:293:ASN:HA	1.96	0.47
1:B:137:PHE:HE2	1:B:188:TYR:C	2.18	0.47
1:A:418:GLU:O	1:A:438:GLY:N	2.48	0.47
1:B:131:LEU:O	1:B:157:ILE:HA	2.14	0.47
1:A:33:VAL:HG22	1:A:332:LEU:CD2	2.45	0.47
1:A:124:LYS:HE3	1:A:125:TYR:OH	2.15	0.47
1:A:461:LYS:HE3	1:A:463:ILE:CG1	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:PRO:HB3	1:A:177:PRO:HG2	1.97	0.47
1:A:355:ARG:NH1	1:A:355:ARG:CG	2.60	0.47
1:A:278:GLU:CD	1:A:278:GLU:N	2.68	0.47
1:A:181:LYS:HE3	1:A:185:GLU:HB2	1.96	0.47
1:B:105:ARG:NH2	1:B:370:SER:O	2.46	0.47
1:B:165:TYR:HB3	1:B:166:PRO:HD2	1.95	0.47
1:A:100:SER:O	1:A:102:ILE:N	2.47	0.47
1:B:366:LEU:HD13	1:B:394:ILE:HD13	1.97	0.47
1:A:78:ASP:HA	2:A:647:HOH:O	2.14	0.47
1:B:246:GLU:HB2	1:B:296:ASN:HB2	1.97	0.47
1:A:105:ARG:O	1:A:106:ASP:HB2	2.15	0.47
1:B:268:GLN:HG3	2:B:472:HOH:O	2.15	0.47
1:A:280:VAL:HG12	1:A:284:LYS:NZ	2.29	0.47
1:B:351:VAL:HB	1:B:352:PRO:HD2	1.96	0.47
1:A:122:ASN:HA	1:A:127:CYS:SG	2.54	0.47
1:B:213:LYS:NZ	2:B:480:HOH:O	2.33	0.47
1:B:322:LYS:NZ	2:B:694:HOH:O	2.46	0.47
1:A:314:LYS:CD	1:A:317:ILE:HD11	2.44	0.47
1:A:84:LYS:HG2	1:A:131:LEU:HD11	1.96	0.47
1:B:182:THR:HG23	1:B:187:TRP:CZ2	2.44	0.47
1:B:397:GLY:N	1:B:424:VAL:O	2.48	0.47
1:B:445:LYS:HG3	2:B:564:HOH:O	2.15	0.47
1:B:247:VAL:HA	1:B:292:PHE:O	2.15	0.47
1:B:336:ALA:O	1:B:338:ALA:N	2.47	0.47
1:A:372:LEU:CD2	1:A:392:PRO:HD2	2.41	0.47
1:A:241:ASN:ND2	1:A:345:ASN:HD22	2.12	0.47
1:B:176:TRP:HB3	1:B:177:PRO:HD3	1.97	0.47
1:A:51:THR:HG23	1:A:52:PRO:HD2	1.97	0.47
1:B:366:LEU:HD23	1:B:366:LEU:O	2.15	0.47
1:B:135:ASN:HD22	1:B:135:ASN:C	2.18	0.47
1:B:227:ILE:HB	2:B:508:HOH:O	2.14	0.47
1:A:319:PRO:HA	1:A:332:LEU:HD12	1.97	0.47
1:B:128:LYS:HD2	2:B:670:HOH:O	2.15	0.47
1:B:249:PRO:HA	1:B:290:LYS:O	2.15	0.47
1:A:15:VAL:HA	1:A:18:LEU:HG	1.96	0.47
1:A:268:GLN:NE2	1:A:341:ARG:CD	2.78	0.47
1:A:363:SER:N	2:A:491:HOH:O	2.46	0.47
1:B:59:PRO:HA	1:B:350:ASN:CB	2.45	0.47
1:A:371:ASP:OD2	1:A:417:VAL:HG23	2.15	0.47
1:A:46:TRP:CD1	2:A:649:HOH:O	2.65	0.47
1:B:403:VAL:O	1:B:407:LEU:HG	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:LYS:CE	1:A:468:ASP:HB3	2.45	0.47
1:B:255:VAL:HG13	1:B:284:LYS:O	2.15	0.47
1:B:463:ILE:HG22	1:B:465:GLY:H	1.80	0.47
1:A:19:THR:HG23	2:A:630:HOH:O	2.14	0.47
1:B:89:LEU:CB	1:B:91:THR:HG23	2.45	0.47
1:A:250:LYS:HD2	1:A:289:PHE:O	2.15	0.47
1:B:459:GLU:O	1:B:460:ASN:O	2.33	0.47
1:A:195:VAL:HG13	1:A:196:PHE:N	2.30	0.47
1:A:445:LYS:HD2	2:A:588:HOH:O	2.14	0.47
1:A:115:VAL:HG22	1:A:157:ILE:HD11	1.97	0.47
1:A:270:LEU:HG	1:A:283:PHE:HE1	1.78	0.47
1:A:439:LYS:C	1:A:439:LYS:HD2	2.35	0.47
1:B:100:SER:CB	1:B:111:LEU:HG	2.45	0.47
1:A:314:LYS:HD2	1:A:314:LYS:HA	1.68	0.47
1:B:74:LYS:HG2	1:B:125:TYR:HB3	1.97	0.47
1:A:417:VAL:HG12	1:A:418:GLU:HG3	1.96	0.47
1:A:424:VAL:HG22	1:A:442:VAL:O	2.15	0.47
1:B:356:PHE:CZ	1:B:358:PRO:HG3	2.50	0.47
1:A:56:ILE:HD11	2:A:586:HOH:O	2.15	0.47
1:B:439:LYS:O	1:B:460:ASN:HA	2.15	0.47
1:A:142:ASP:OD1	1:A:145:LYS:HE3	2.14	0.47
1:B:154:ASN:CG	1:B:154:ASN:O	2.51	0.47
1:B:66:VAL:CG1	2:B:502:HOH:O	2.59	0.46
1:A:266:LYS:N	1:A:266:LYS:HD2	2.30	0.46
1:B:263:TYR:CD2	1:B:264:GLU:HG3	2.50	0.46
1:B:260:LEU:HD22	1:B:267:VAL:CG2	2.45	0.46
1:B:312:ALA:O	1:B:314:LYS:N	2.48	0.46
1:A:429:TRP:CD1	1:A:449:LYS:HG3	2.50	0.46
1:B:56:ILE:HG23	1:B:267:VAL:HB	1.97	0.46
1:B:89:LEU:HG	2:B:661:HOH:O	2.15	0.46
1:B:346:ALA:O	1:B:347:ILE:HG22	2.15	0.46
1:B:175:PRO:O	1:B:178:SER:N	2.48	0.46
1:B:160:PHE:HB2	1:B:202:SER:CB	2.45	0.46
1:A:226:ALA:HA	1:A:296:ASN:HD21	1.80	0.46
1:B:255:VAL:HG22	1:B:286:ILE:HG23	1.97	0.46
1:A:83:LEU:HA	1:A:132:VAL:HG13	1.96	0.46
1:A:439:LYS:HD2	1:A:439:LYS:C	2.35	0.46
1:A:49:ILE:HG12	1:A:261:ILE:CD1	2.42	0.46
1:A:370:SER:OG	1:A:372:LEU:HB3	2.15	0.46
1:B:360:LYS:HB2	1:B:364:ASP:OD2	2.15	0.46
1:A:176:TRP:HB3	1:A:177:PRO:HD3	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:GLN:HG2	1:A:341:ARG:CB	2.45	0.46
1:B:227:ILE:O	1:B:355:ARG:NH1	2.47	0.46
1:A:432:SER:C	1:A:434:ILE:N	2.68	0.46
1:A:432:SER:O	1:A:433:SER:C	2.54	0.46
1:A:205:LEU:HD11	1:A:301:LEU:HB3	1.96	0.46
1:B:134:MET:HE3	1:B:162:GLN:NE2	2.30	0.46
1:A:422:LEU:HG	1:A:424:VAL:HG23	1.96	0.46
1:A:379:PHE:HB2	2:A:598:HOH:O	2.14	0.46
1:B:424:VAL:HA	1:B:442:VAL:O	2.14	0.46
1:A:363:SER:HB2	1:A:394:ILE:HG22	1.98	0.46
1:B:32:LEU:CB	2:B:682:HOH:O	2.62	0.46
1:A:169:VAL:O	1:A:173:PHE:HA	2.15	0.46
1:A:355:ARG:HH11	1:A:355:ARG:CG	2.20	0.46
1:B:383:ASN:HA	2:B:645:HOH:O	2.14	0.46
1:A:167:ARG:HB2	1:A:186:GLY:O	2.16	0.46
1:B:246:GLU:HB2	1:B:296:ASN:HB2	1.97	0.46
1:A:366:LEU:HD11	1:A:422:LEU:CD2	2.45	0.46
1:B:80:LEU:HD11	1:B:298:TRP:CZ3	2.51	0.46
1:B:272:ILE:HD11	1:B:280:VAL:CG1	2.42	0.46
1:A:66:VAL:HA	1:A:234:LYS:HE2	1.96	0.46
1:B:146:ILE:HG22	1:B:149:LYS:HD2	1.94	0.46
1:B:135:ASN:ND2	1:B:159:THR:HB	2.30	0.46
1:A:365:LEU:HA	1:A:368:VAL:HG22	1.96	0.46
1:B:359:VAL:HG11	1:B:365:LEU:HD21	1.98	0.46
1:A:366:LEU:HD22	1:A:394:ILE:CD1	2.45	0.46
1:A:338:ALA:O	2:A:474:HOH:O	2.21	0.46
1:B:235:HIS:CE1	1:B:239:ASN:ND2	2.84	0.46
1:A:419:LEU:HA	1:A:437:LYS:HA	1.97	0.46
1:B:296:ASN:O	1:B:297:LEU:HD23	2.15	0.46
1:A:105:ARG:HE	1:A:375:LEU:HB2	1.80	0.46
1:B:29:PHE:CD1	1:B:166:PRO:HD2	2.50	0.46
1:A:455:ARG:CZ	1:A:455:ARG:HB3	2.45	0.46
1:A:254:ASP:OD2	1:A:353:ARG:NH1	2.48	0.46
1:B:382:ARG:CD	2:B:705:HOH:O	2.46	0.46
1:A:442:VAL:HG21	1:A:452:ILE:HD11	1.97	0.46
1:B:56:ILE:CG1	2:B:611:HOH:O	2.63	0.46
1:A:241:ASN:HD22	1:A:347:ILE:HG23	1.79	0.46
1:B:81:VAL:HG21	1:B:208:PHE:CG	2.50	0.46
1:B:144:HIS:CA	1:B:147:VAL:HG22	2.46	0.46
1:A:467:GLU:HB2	2:A:589:HOH:O	2.15	0.46
1:B:169:VAL:HG12	1:B:171:ASP:CG	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:TYR:CE2	1:B:340:ILE:HB	2.51	0.46
1:A:280:VAL:HG12	1:A:284:LYS:HZ2	1.79	0.46
1:B:110:PHE:O	1:B:114:ILE:HG13	2.15	0.46
1:A:158:HIS:HB3	1:A:204:LYS:HE2	1.96	0.46
1:A:236:LEU:HB3	1:A:241:ASN:HB2	1.97	0.46
1:A:314:LYS:HD2	1:A:314:LYS:HA	1.80	0.46
1:A:115:VAL:HG21	1:A:150:TYR:CZ	2.51	0.46
1:A:256:LYS:HE2	1:A:272:ILE:CD1	2.43	0.46
1:A:165:TYR:HB3	1:A:166:PRO:HD2	1.98	0.46
1:A:423:LYS:HD3	1:A:441:THR:HG23	1.97	0.46
1:B:250:LYS:NZ	2:B:590:HOH:O	2.35	0.46
1:B:454:ASP:O	1:B:455:ARG:HB2	2.15	0.46
1:B:131:LEU:HG	1:B:133:LEU:HD21	1.98	0.46
1:B:85:LEU:HD13	1:B:192:HIS:HB2	1.98	0.46
1:A:105:ARG:NH1	1:A:368:VAL:O	2.42	0.46
1:A:370:SER:O	1:A:372:LEU:N	2.48	0.46
1:A:32:LEU:O	1:A:33:VAL:C	2.53	0.46
1:A:74:LYS:HD3	1:A:125:TYR:O	2.15	0.46
1:B:450:LEU:HD21	1:B:463:ILE:HG22	1.97	0.46
1:B:44:ILE:CD1	1:B:49:ILE:HD11	2.45	0.46
1:A:255:VAL:HG12	1:A:286:ILE:CG2	2.44	0.46
1:B:379:PHE:HZ	2:B:522:HOH:O	1.99	0.46
1:B:270:LEU:HD21	1:B:275:VAL:HG22	1.97	0.46
1:A:431:GLY:H	1:A:434:ILE:HD11	1.80	0.46
1:A:299:VAL:HG11	1:A:304:ILE:HD11	1.97	0.46
1:B:150:TYR:CD2	2:B:652:HOH:O	2.35	0.46
1:A:35:ARG:HG3	1:A:314:LYS:NZ	2.30	0.46
1:A:44:ILE:N	1:A:44:ILE:HD12	2.31	0.46
1:A:384:LYS:HE3	1:A:384:LYS:CA	2.45	0.46
1:A:15:VAL:CG2	1:A:30:ILE:HD11	2.46	0.46
1:B:105:ARG:HG3	1:B:375:LEU:HD22	1.97	0.46
1:B:384:LYS:O	2:B:583:HOH:O	2.21	0.46
1:A:69:ASP:O	1:A:72:GLU:HB3	2.15	0.46
1:A:21:MET:HB2	1:A:26:LYS:HG3	1.98	0.46
1:A:134:MET:HG3	1:A:160:PHE:CZ	2.50	0.46
1:B:240:LYS:HG2	2:B:546:HOH:O	2.16	0.46
1:A:399:GLU:OE2	1:A:426:GLY:HA2	2.15	0.46
1:B:144:HIS:HA	1:B:147:VAL:CG2	2.46	0.46
1:B:135:ASN:HB3	1:B:139:THR:OG1	2.16	0.46
1:A:267:VAL:HG22	1:A:340:ILE:CD1	2.46	0.46
1:B:254:ASP:OD2	1:B:353:ARG:NH1	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:MET:CG	1:B:338:ALA:HB3	2.44	0.46
1:A:276:PRO:HB2	1:A:279:HIS:CD2	2.46	0.46
1:B:388:ASN:OD1	1:B:389:PRO:HD2	2.15	0.46
1:B:86:ASN:OD1	1:B:100:SER:HB3	2.16	0.46
1:B:320:ASN:N	1:B:321:PRO:CD	2.78	0.46
1:A:200:MET:HG2	1:A:205:LEU:HD23	1.96	0.46
1:A:25:GLU:HG2	1:A:163:SER:HB3	1.98	0.46
1:A:322:LYS:O	1:A:328:LYS:HA	2.16	0.46
1:A:99:LYS:HZ3	1:A:360:LYS:HA	1.80	0.46
1:B:330:LEU:HD22	1:B:332:LEU:HG	1.98	0.46
1:A:9:PRO:O	1:A:12:LYS:HB3	2.15	0.46
1:A:428:VAL:HG22	1:A:444:ALA:HB2	1.98	0.46
1:B:74:LYS:HG2	1:B:125:TYR:HB3	1.97	0.46
1:B:393:SER:HB2	1:B:421:SER:HB2	1.98	0.46
1:B:111:LEU:HD23	1:B:111:LEU:HA	1.79	0.46
1:A:136:SER:CB	1:A:162:GLN:NE2	2.73	0.46
1:B:146:ILE:HG23	1:B:149:LYS:HD2	1.97	0.46
1:A:104:VAL:CG1	1:A:105:ARG:H	2.28	0.46
1:A:384:LYS:HA	1:A:384:LYS:CE	2.46	0.46
1:B:412:SER:HG	1:B:433:SER:H	1.61	0.46
1:A:97:GLY:HA2	2:A:556:HOH:O	2.16	0.46
1:B:250:LYS:HE2	1:B:254:ASP:O	2.16	0.46
1:A:81:VAL:CA	1:A:130:PRO:HG2	2.33	0.46
1:B:359:VAL:C	1:B:360:LYS:HD2	2.36	0.46
1:B:250:LYS:CG	1:B:292:PHE:HD2	2.29	0.46
1:B:150:TYR:C	1:B:152:ASN:H	2.18	0.46
1:B:320:ASN:HD22	1:B:333:GLU:CD	2.18	0.46
1:A:421:SER:OG	1:A:439:LYS:HG2	2.16	0.46
1:A:32:LEU:HD22	1:A:165:TYR:HE2	1.81	0.46
1:A:8:LEU:N	1:A:8:LEU:HD23	2.31	0.46
1:A:160:PHE:CE1	1:A:198:ALA:HB1	2.50	0.46
1:B:113:LEU:HD22	1:B:378:GLY:O	2.16	0.46
1:B:117:GLN:NE2	1:B:378:GLY:O	2.42	0.46
1:A:80:LEU:HA	1:A:215:TYR:O	2.15	0.46
1:B:48:LYS:HZ1	1:B:264:GLU:CG	2.28	0.46
1:B:84:LYS:HG3	1:B:114:ILE:HG21	1.98	0.46
1:B:80:LEU:HD13	1:B:233:LEU:HD22	1.98	0.46
1:B:371:ASP:OD1	1:B:416:ILE:N	2.46	0.46
1:A:300:ASN:ND2	2:A:558:HOH:O	2.48	0.46
1:A:45:GLU:HA	1:A:45:GLU:OE1	2.16	0.46
1:A:99:LYS:C	1:A:99:LYS:HD3	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:PRO:HG2	1:A:198:ALA:H	1.80	0.46
1:A:113:LEU:HD13	1:A:380:VAL:CG2	2.46	0.46
1:B:216:VAL:HG22	1:B:217:PHE:N	2.31	0.46
1:A:166:PRO:HB2	1:A:177:PRO:CD	2.41	0.46
1:A:166:PRO:HB3	1:A:177:PRO:HG2	1.96	0.46
1:B:236:LEU:CD2	1:B:244:CYS:HB2	2.46	0.46
1:B:21:MET:SD	1:B:166:PRO:HD3	2.56	0.46
1:B:78:ASP:O	1:B:213:LYS:HD3	2.15	0.46
1:A:200:MET:CB	1:A:308:VAL:HG11	2.46	0.46
1:B:360:LYS:O	1:B:361:ALA:HB2	2.16	0.46
1:A:73:THR:O	1:A:230:LEU:HD13	2.15	0.46
1:B:115:VAL:HG22	1:B:131:LEU:CD2	2.46	0.46
1:B:80:LEU:HG	1:B:81:VAL:O	2.16	0.46
1:B:14:ALA:HB1	1:B:178:SER:CB	2.46	0.46
1:B:45:GLU:N	1:B:263:TYR:OH	2.49	0.46
1:A:359:VAL:HA	1:A:364:ASP:HB2	1.97	0.46
1:A:235:HIS:CE1	1:A:239:ASN:ND2	2.83	0.46
1:A:142:ASP:O	1:A:145:LYS:HG3	2.16	0.46
1:B:233:LEU:CA	1:B:236:LEU:HG	2.46	0.46
1:A:15:VAL:HG21	1:A:30:ILE:HD11	1.98	0.46
1:B:272:ILE:O	1:B:272:ILE:CG1	2.63	0.46
1:A:89:LEU:CD1	1:A:138:ASN:HB3	2.46	0.46
1:B:82:VAL:HG13	2:B:473:HOH:O	2.14	0.46
1:B:317:ILE:O	1:B:319:PRO:HD3	2.15	0.45
1:B:32:LEU:HB3	2:B:683:HOH:O	2.15	0.45
1:A:200:MET:C	1:A:200:MET:SD	2.95	0.45
1:A:294:THR:CB	1:A:296:ASN:HD22	2.28	0.45
1:B:176:TRP:N	1:B:177:PRO:CD	2.79	0.45
1:B:35:ARG:HE	1:B:314:LYS:HD3	1.81	0.45
1:B:81:VAL:CG1	1:B:130:PRO:HG2	2.43	0.45
1:B:227:ILE:CG1	1:B:228:VAL:N	2.79	0.45
1:B:236:LEU:CD2	1:B:244:CYS:HB2	2.47	0.45
1:A:245:MET:SD	1:A:293:ASN:HB2	2.56	0.45
1:B:362:SER:HB2	1:B:406:PHE:CD1	2.51	0.45
1:B:266:LYS:HB2	2:B:599:HOH:O	2.17	0.45
1:A:102:ILE:CG2	1:A:103:GLU:N	2.77	0.45
1:A:115:VAL:HG21	1:A:150:TYR:CD2	2.51	0.45
1:B:308:VAL:HG22	1:B:313:LEU:HD12	1.97	0.45
1:B:56:ILE:HG13	2:B:610:HOH:O	2.16	0.45
1:B:83:LEU:HD23	1:B:83:LEU:C	2.36	0.45
1:A:461:LYS:HE3	1:A:463:ILE:HG12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:374:THR:HG23	1:A:381:THR:HB	1.97	0.45
1:A:49:ILE:HG23	1:A:261:ILE:CB	2.41	0.45
1:B:29:PHE:CD1	1:B:165:TYR:HB3	2.50	0.45
1:B:368:VAL:O	1:B:368:VAL:HG12	2.16	0.45
1:A:439:LYS:HD2	1:A:440:VAL:N	2.30	0.45
1:A:321:PRO:HA	1:A:329:VAL:O	2.16	0.45
1:A:10:GLN:HB2	2:A:553:HOH:O	2.15	0.45
1:B:245:MET:SD	1:B:293:ASN:HB3	2.57	0.45
1:A:115:VAL:HG21	1:A:150:TYR:CD2	2.51	0.45
1:A:442:VAL:HG11	1:A:452:ILE:CD1	2.40	0.45
1:B:301:LEU:O	1:B:304:ILE:N	2.49	0.45
1:A:124:LYS:HE3	1:A:125:TYR:CE1	2.52	0.45
1:B:243:TYR:HB3	1:B:346:ALA:HB1	1.98	0.45
1:B:18:LEU:HD13	1:B:187:TRP:HH2	1.79	0.45
1:B:133:LEU:HD12	1:B:159:THR:CG2	2.46	0.45
1:A:269:LEU:HB2	1:A:337:GLY:O	2.16	0.45
1:A:63:MET:SD	1:A:231:THR:HG22	2.56	0.45
1:B:307:LEU:CD2	1:B:312:ALA:HB3	2.46	0.45
1:A:87:GLY:HA2	1:A:136:SER:N	2.31	0.45
1:A:98:PRO:O	1:A:101:VAL:HG22	2.16	0.45
1:A:357:LEU:HD12	2:A:574:HOH:O	2.17	0.45
1:B:267:VAL:O	1:B:341:ARG:HA	2.16	0.45
1:A:35:ARG:CB	1:A:314:LYS:NZ	2.79	0.45
1:A:80:LEU:HD12	1:A:215:TYR:O	2.17	0.45
1:A:384:LYS:CE	1:A:384:LYS:HA	2.45	0.45
1:B:222:ASP:OD1	1:B:360:LYS:HE3	2.16	0.45
1:B:224:LEU:HB2	1:B:357:LEU:HD22	1.97	0.45
1:B:44:ILE:HG23	1:B:44:ILE:O	2.17	0.45
1:A:445:LYS:HB2	2:A:588:HOH:O	2.17	0.45
1:B:176:TRP:CZ3	1:B:329:VAL:HG11	2.52	0.45
1:A:114:ILE:O	1:A:114:ILE:HG22	2.16	0.45
1:B:9:PRO:C	1:B:11:LEU:H	2.19	0.45
1:A:416:ILE:CG2	1:A:419:LEU:HD22	2.46	0.45
1:A:416:ILE:HB	1:A:419:LEU:HB3	1.97	0.45
1:B:454:ASP:O	1:B:455:ARG:HB2	2.16	0.45
1:B:259:THR:OG1	1:B:291:ILE:HG13	2.16	0.45
1:A:255:VAL:HG12	1:A:286:ILE:CG2	2.46	0.45
1:A:160:PHE:C	1:A:160:PHE:CD1	2.89	0.45
1:B:135:ASN:HB2	1:B:161:ASN:HA	1.98	0.45
1:B:322:LYS:HD2	2:B:694:HOH:O	2.15	0.45
1:B:405:THR:HG22	2:B:565:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:ILE:O	1:A:120:ASN:ND2	2.50	0.45
1:A:35:ARG:CG	1:A:314:LYS:HE2	2.38	0.45
1:B:74:LYS:HD3	1:B:74:LYS:C	2.37	0.45
1:B:74:LYS:O	1:B:74:LYS:HD3	2.16	0.45
1:B:142:ASP:O	1:B:146:ILE:HG13	2.16	0.45
1:B:165:TYR:HB2	1:B:188:TYR:CE2	2.51	0.45
1:A:192:HIS:C	1:A:194:ASP:N	2.67	0.45
1:B:359:VAL:HA	1:B:364:ASP:HB3	1.97	0.45
1:B:382:ARG:NH1	1:B:382:ARG:HG3	2.31	0.45
1:B:332:LEU:CD1	2:B:683:HOH:O	2.62	0.45
1:B:366:LEU:CD1	1:B:394:ILE:HG21	2.41	0.45
1:A:55:GLU:OE2	1:A:55:GLU:CA	2.65	0.45
1:A:442:VAL:CG2	1:A:452:ILE:HD11	2.46	0.45
1:B:128:LYS:HD3	2:B:552:HOH:O	2.16	0.45
1:B:247:VAL:HG21	1:B:291:ILE:HD12	1.98	0.45
1:A:44:ILE:HG23	1:A:263:TYR:CE1	2.51	0.45
1:A:433:SER:CB	1:A:455:ARG:HG2	2.46	0.45
1:B:184:LYS:NZ	2:B:657:HOH:O	2.28	0.45
1:B:383:ASN:O	1:B:386:ARG:HB3	2.16	0.45
1:B:336:ALA:C	1:B:338:ALA:N	2.70	0.45
1:B:232:ILE:O	1:B:236:LEU:HG	2.16	0.45
1:B:299:VAL:HB	1:B:304:ILE:HD11	1.99	0.45
1:A:314:LYS:HD2	1:A:314:LYS:HA	1.66	0.45
1:B:403:VAL:O	1:B:406:PHE:HB3	2.16	0.45
1:A:245:MET:O	1:A:348:GLY:HA2	2.15	0.45
1:A:371:ASP:CG	1:A:417:VAL:HG23	2.37	0.45
1:A:175:PRO:O	1:A:178:SER:N	2.50	0.45
1:B:69:ASP:OD2	1:B:71:ALA:HB3	2.16	0.45
1:B:60:TYR:HE1	1:B:232:ILE:HG13	1.80	0.45
1:A:353:ARG:HB3	2:A:621:HOH:O	2.16	0.45
1:B:268:GLN:NE2	2:B:599:HOH:O	2.50	0.45
1:B:420:ASP:OD2	1:B:438:GLY:HA2	2.16	0.45
1:B:437:LYS:HB2	1:B:459:GLU:HG3	1.99	0.45
1:A:80:LEU:HD12	1:A:81:VAL:H	1.80	0.45
1:A:197:PRO:O	1:A:200:MET:N	2.50	0.45
1:A:444:ALA:HA	1:A:450:LEU:CD1	2.47	0.45
1:A:84:LYS:HB2	1:A:133:LEU:CD2	2.46	0.45
1:B:101:VAL:HG22	2:B:512:HOH:O	2.16	0.45
1:A:409:ARG:HH12	1:A:428:VAL:N	2.15	0.45
1:A:236:LEU:HA	1:A:241:ASN:OD1	2.16	0.45
1:B:259:THR:O	1:B:269:LEU:HD12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:LEU:HD12	1:B:375:LEU:CD2	2.47	0.45
1:A:74:LYS:NZ	1:A:78:ASP:OD2	2.44	0.45
1:B:335:ALA:N	2:B:492:HOH:O	2.50	0.45
1:A:195:VAL:HG13	1:A:196:PHE:N	2.32	0.45
1:B:217:PHE:HD1	1:B:297:LEU:O	1.99	0.45
1:B:109:THR:O	1:B:113:LEU:HG	2.17	0.45
1:A:165:TYR:CE2	1:A:190:PRO:HG3	2.51	0.45
1:B:32:LEU:CB	2:B:685:HOH:O	2.61	0.45
1:A:241:ASN:ND2	1:A:345:ASN:ND2	2.65	0.45
1:A:255:VAL:HG22	2:A:607:HOH:O	2.15	0.45
1:A:340:ILE:HG12	1:A:346:ALA:HB1	1.97	0.45
1:A:444:ALA:HA	1:A:450:LEU:HD12	1.98	0.45
1:A:366:LEU:O	1:A:370:SER:HB3	2.16	0.45
1:A:415:SER:OG	2:A:486:HOH:O	2.21	0.45
1:B:66:VAL:HG12	1:B:67:SER:N	2.31	0.45
1:B:365:LEU:O	1:B:369:GLN:HG3	2.17	0.45
1:A:200:MET:HA	1:A:205:LEU:CB	2.46	0.45
1:B:379:PHE:O	1:B:381:THR:N	2.50	0.45
1:B:417:VAL:HG22	2:B:609:HOH:O	2.16	0.45
1:A:418:GLU:HB2	1:A:437:LYS:HG2	1.98	0.45
1:A:246:GLU:HB2	1:A:296:ASN:HB2	1.99	0.45
1:A:74:LYS:O	1:A:78:ASP:OD1	2.35	0.45
1:B:80:LEU:HD22	1:B:233:LEU:HD22	1.98	0.45
1:B:32:LEU:HD11	1:B:317:ILE:CD1	2.46	0.45
1:A:194:ASP:O	1:A:195:VAL:C	2.54	0.45
1:B:99:LYS:HD2	1:B:99:LYS:O	2.17	0.45
1:A:164:LYS:HB3	2:A:524:HOH:O	2.17	0.45
1:B:358:PRO:HB2	1:B:360:LYS:CD	2.30	0.45
1:B:164:LYS:CD	1:B:164:LYS:O	2.59	0.45
1:B:357:LEU:HD23	1:B:357:LEU:O	2.14	0.45
1:B:109:THR:O	1:B:113:LEU:HG	2.17	0.45
1:B:358:PRO:HB2	1:B:360:LYS:HD3	1.98	0.45
1:B:270:LEU:HA	2:B:493:HOH:O	2.17	0.45
1:B:398:PRO:HA	1:B:401:LYS:HG3	1.99	0.45
1:A:136:SER:HB2	1:A:189:PRO:HG2	1.98	0.45
1:A:33:VAL:O	1:A:36:TYR:HB3	2.16	0.45
1:B:293:ASN:HD22	1:B:294:THR:N	2.14	0.45
1:B:9:PRO:C	1:B:11:LEU:N	2.70	0.45
1:B:321:PRO:O	1:B:322:LYS:CB	2.58	0.45
1:A:455:ARG:NH1	1:A:455:ARG:HB3	2.32	0.45
1:B:132:VAL:HG22	1:B:158:HIS:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:ASN:ND2	2:A:541:HOH:O	2.49	0.45
1:A:203:GLY:HA2	2:A:488:HOH:O	2.17	0.45
1:B:153:SER:HB2	1:B:155:VAL:CG1	2.46	0.45
1:A:7:ASN:HB3	2:A:554:HOH:O	2.16	0.45
1:B:282:GLU:O	1:B:285:SER:HB3	2.16	0.45
1:B:135:ASN:HD21	1:B:159:THR:HB	1.82	0.45
1:B:340:ILE:HG13	1:B:346:ALA:HB1	1.97	0.45
1:A:136:SER:HB2	1:A:189:PRO:CG	2.46	0.45
1:B:267:VAL:CG1	2:B:568:HOH:O	2.62	0.45
1:B:209:LEU:HD21	1:B:301:LEU:HB2	1.99	0.45
1:A:146:ILE:O	1:A:149:LYS:HG2	2.17	0.45
1:B:242:GLU:HG3	1:B:344:ASP:O	2.17	0.45
1:B:36:TYR:HB2	1:B:332:LEU:HD13	1.99	0.45
1:B:162:GLN:OE1	1:B:194:ASP:HB3	2.17	0.45
1:B:140:HIS:O	1:B:144:HIS:HB2	2.17	0.45
1:A:124:LYS:NZ	2:A:641:HOH:O	2.48	0.45
1:A:295:ASN:HB2	2:A:482:HOH:O	2.16	0.45
1:B:146:ILE:O	1:B:146:ILE:CG2	2.64	0.45
1:A:50:GLN:HB2	1:A:262:SER:O	2.17	0.45
1:A:109:THR:H	1:A:112:ASP:CG	2.20	0.45
1:B:247:VAL:CG2	1:B:291:ILE:HD13	2.46	0.45
1:B:371:ASP:OD2	1:B:417:VAL:HB	2.17	0.45
1:A:234:LYS:NZ	1:A:238:GLN:NE2	2.65	0.45
1:A:275:VAL:HA	1:A:276:PRO:HD3	1.87	0.45
1:A:232:ILE:O	1:A:236:LEU:HG	2.17	0.44
1:B:128:LYS:HD3	2:B:552:HOH:O	2.17	0.44
1:B:196:PHE:HB2	1:B:197:PRO:CD	2.47	0.44
1:A:215:TYR:HA	1:A:299:VAL:O	2.18	0.44
1:A:44:ILE:HB	2:A:595:HOH:O	2.17	0.44
1:B:200:MET:HE1	1:B:309:GLU:OE1	2.16	0.44
1:A:104:VAL:CG1	1:A:105:ARG:N	2.77	0.44
1:A:384:LYS:C	1:A:386:ARG:N	2.70	0.44
1:A:131:LEU:O	1:A:157:ILE:HA	2.18	0.44
1:B:306:LYS:O	1:B:310:ALA:N	2.50	0.44
1:B:349:VAL:HG13	1:B:349:VAL:O	2.17	0.44
1:A:464:ASN:ND2	2:A:542:HOH:O	2.49	0.44
1:A:104:VAL:CG1	1:A:105:ARG:N	2.79	0.44
1:B:415:SER:HB3	1:B:435:VAL:HG13	1.99	0.44
1:B:330:LEU:HD23	1:B:331:GLN:H	1.75	0.44
1:B:357:LEU:CD2	1:B:357:LEU:O	2.65	0.44
1:B:132:VAL:HG13	1:B:158:HIS:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:LYS:HB3	1:A:306:LYS:HE2	1.78	0.44
1:B:57:VAL:HG21	1:B:291:ILE:HD11	1.99	0.44
1:B:414:PRO:HB3	1:B:436:LEU:HG	1.99	0.44
1:A:410:PHE:CD1	1:A:414:PRO:HD3	2.52	0.44
1:A:23:GLU:HG2	2:A:543:HOH:O	2.17	0.44
1:B:320:ASN:ND2	1:B:333:GLU:OE1	2.46	0.44
1:A:332:LEU:N	1:A:332:LEU:CD1	2.79	0.44
1:A:439:LYS:HD2	2:A:581:HOH:O	2.18	0.44
1:A:64:THR:CG2	1:A:65:PRO:HD2	2.48	0.44
1:B:357:LEU:HD23	1:B:357:LEU:O	2.18	0.44
1:A:77:LEU:HD22	1:A:121:LEU:HD21	1.98	0.44
1:B:46:TRP:CZ3	1:B:275:VAL:HG13	2.52	0.44
1:A:455:ARG:HD2	2:A:628:HOH:O	2.17	0.44
1:B:236:LEU:HD11	1:B:244:CYS:SG	2.57	0.44
1:B:291:ILE:CG2	1:B:350:ASN:HD21	2.31	0.44
1:B:181:LYS:HE3	1:B:185:GLU:HB2	2.00	0.44
1:B:249:PRO:HD2	1:B:351:VAL:O	2.17	0.44
1:B:151:THR:O	1:B:151:THR:HG22	2.17	0.44
1:B:382:ARG:NH2	1:B:388:ASN:O	2.49	0.44
1:A:12:LYS:HG3	1:A:30:ILE:HG13	1.99	0.44
1:B:33:VAL:HG13	1:B:173:PHE:HZ	1.83	0.44
1:B:167:ARG:NE	1:B:331:GLN:OE1	2.45	0.44
1:B:36:TYR:O	1:B:37:LEU:HD23	2.17	0.44
1:A:36:TYR:C	1:A:38:SER:N	2.69	0.44
1:A:204:LYS:O	1:A:207:THR:HB	2.17	0.44
1:A:169:VAL:O	1:A:173:PHE:HA	2.16	0.44
1:A:274:GLN:NE2	1:A:316:GLU:HG2	2.32	0.44
1:B:181:LYS:HE3	1:B:185:GLU:HB2	2.00	0.44
1:B:91:THR:HA	1:B:95:CYS:O	2.17	0.44
1:A:362:SER:HA	1:A:365:LEU:HB2	1.98	0.44
1:A:104:VAL:HG11	1:A:113:LEU:CD1	2.46	0.44
1:B:76:LEU:CD2	1:B:237:ILE:HD12	2.47	0.44
1:B:77:LEU:HD22	1:B:121:LEU:CD2	2.44	0.44
1:B:168:VAL:HG11	1:B:173:PHE:CZ	2.52	0.44
1:B:32:LEU:HB3	2:B:682:HOH:O	2.18	0.44
1:A:136:SER:C	1:A:161:ASN:OD1	2.56	0.44
1:A:220:ASN:HB3	2:A:627:HOH:O	2.17	0.44
1:B:270:LEU:HD21	1:B:275:VAL:HG22	1.98	0.44
1:B:32:LEU:HB3	2:B:682:HOH:O	2.18	0.44
1:B:233:LEU:HA	1:B:236:LEU:CG	2.48	0.44
1:B:250:LYS:NZ	2:B:588:HOH:O	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:VAL:O	1:A:349:VAL:HG13	2.17	0.44
2:A:539:HOH:O	1:B:287:GLU:HB2	2.16	0.44
1:A:349:VAL:O	1:A:349:VAL:HG13	2.18	0.44
1:B:115:VAL:HG13	1:B:155:VAL:HG11	1.99	0.44
1:B:134:MET:HG3	1:B:160:PHE:CE1	2.53	0.44
1:A:453:PRO:O	1:A:456:ALA:CB	2.64	0.44
1:A:256:LYS:HG2	1:A:284:LYS:HD3	1.99	0.44
1:A:235:HIS:CE1	1:A:239:ASN:HD22	2.35	0.44
1:A:8:LEU:N	1:A:9:PRO:CD	2.81	0.44
1:A:392:PRO:CB	1:A:419:LEU:CD2	2.96	0.44
1:B:158:HIS:N	1:B:158:HIS:CD2	2.85	0.44
1:A:80:LEU:HD12	1:A:215:TYR:O	2.18	0.44
1:A:29:PHE:O	1:A:33:VAL:HG23	2.18	0.44
1:A:243:TYR:HD2	1:A:244:CYS:N	2.16	0.44
1:B:176:TRP:CE3	1:B:181:LYS:HG2	2.52	0.44
1:B:80:LEU:HG	1:B:81:VAL:N	2.33	0.44
1:B:461:LYS:NZ	1:B:468:ASP:HB3	2.33	0.44
1:A:371:ASP:OD1	1:A:417:VAL:HG23	2.17	0.44
1:B:20:GLU:HG2	2:B:564:HOH:O	2.16	0.44
1:A:305:LYS:HZ2	1:A:309:GLU:CD	2.20	0.44
1:B:150:TYR:HE1	2:B:664:HOH:O	1.99	0.44
1:A:245:MET:HB3	1:A:260:LEU:HD11	2.00	0.44
1:A:246:GLU:OE2	1:A:355:ARG:NH1	2.43	0.44
1:B:382:ARG:NH1	1:B:382:ARG:HG3	2.32	0.44
1:B:242:GLU:HG3	1:B:344:ASP:O	2.18	0.44
1:B:246:GLU:OE1	1:B:355:ARG:NH1	2.47	0.44
1:A:249:PRO:HD3	1:A:350:ASN:OD1	2.16	0.44
1:A:283:PHE:HA	1:A:289:PHE:CE2	2.53	0.44
1:B:442:VAL:HG13	1:B:463:ILE:HB	1.99	0.44
1:A:133:LEU:O	1:A:159:THR:HA	2.17	0.44
1:A:163:SER:OG	1:A:194:ASP:OD1	2.34	0.44
1:A:437:LYS:HB2	1:A:459:GLU:HB2	1.99	0.44
1:A:314:LYS:HD2	1:A:317:ILE:HD11	2.00	0.44
1:B:279:HIS:HA	2:B:649:HOH:O	2.17	0.44
1:A:384:LYS:HA	1:A:384:LYS:NZ	2.30	0.44
1:A:294:THR:OG1	1:A:296:ASN:HB2	2.17	0.44
1:B:77:LEU:C	1:B:79:LYS:H	2.20	0.44
1:B:74:LYS:NZ	1:B:78:ASP:OD1	2.47	0.44
1:A:22:SER:OG	1:A:25:GLU:HG3	2.17	0.44
1:B:102:ILE:O	1:B:109:THR:HB	2.18	0.44
1:A:255:VAL:HG23	1:A:256:LYS:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:LEU:HD11	1:B:317:ILE:HD12	1.99	0.44
1:A:431:GLY:HA3	1:A:454:ASP:OD1	2.17	0.44
1:B:255:VAL:HG13	1:B:284:LYS:O	2.17	0.44
1:B:250:LYS:HG3	1:B:292:PHE:HB3	2.00	0.44
1:A:149:LYS:O	2:A:614:HOH:O	2.21	0.44
1:B:422:LEU:HA	1:B:440:VAL:O	2.18	0.44
1:A:87:GLY:HA2	1:A:136:SER:H	1.82	0.44
1:A:107:GLY:CA	2:A:516:HOH:O	2.65	0.44
1:A:363:SER:CB	1:A:394:ILE:HG22	2.48	0.44
1:A:399:GLU:HB3	1:A:409:ARG:CZ	2.47	0.44
1:A:462:ASN:O	1:A:463:ILE:HG13	2.18	0.44
1:B:233:LEU:HB2	1:B:298:TRP:CZ3	2.53	0.44
1:B:375:LEU:HD12	1:B:380:VAL:HA	2.00	0.44
1:A:445:LYS:HD2	2:A:588:HOH:O	2.17	0.44
1:B:10:GLN:HE21	1:B:13:SER:CB	2.31	0.44
1:B:104:VAL:HG22	1:B:110:PHE:CZ	2.53	0.44
1:A:177:PRO:O	1:A:179:LYS:N	2.51	0.44
1:A:104:VAL:HG12	1:A:108:LEU:O	2.18	0.44
1:B:167:ARG:HD2	1:B:185:GLU:O	2.17	0.44
1:B:210:SER:C	1:B:212:GLY:N	2.71	0.44
1:B:81:VAL:HA	1:B:130:PRO:HG2	1.98	0.44
1:A:8:LEU:H	1:A:9:PRO:CD	2.31	0.44
1:A:256:LYS:HE2	1:A:284:LYS:HD3	1.98	0.44
1:A:255:VAL:HG23	1:A:256:LYS:HG3	2.00	0.44
1:A:165:TYR:HB2	1:A:188:TYR:CZ	2.53	0.44
1:A:63:MET:HG2	1:A:235:HIS:CD2	2.53	0.44
1:A:8:LEU:C	1:A:8:LEU:HD12	2.38	0.44
1:A:196:PHE:HB2	1:A:197:PRO:CD	2.48	0.44
1:A:382:ARG:HH22	1:A:390:SER:C	2.21	0.44
1:A:411:LYS:HD2	1:A:431:GLY:CA	2.48	0.44
1:A:77:LEU:HG	1:A:230:LEU:CD1	2.44	0.44
1:A:236:LEU:CB	1:A:241:ASN:HB2	2.48	0.44
1:A:213:LYS:NZ	2:A:526:HOH:O	2.50	0.44
1:A:365:LEU:HA	1:A:365:LEU:HD23	1.75	0.44
1:B:53:THR:C	1:B:55:GLU:N	2.71	0.44
1:B:68:GLN:NE2	2:B:687:HOH:O	2.41	0.44
1:B:8:LEU:HA	2:B:696:HOH:O	2.18	0.44
1:B:427:ASP:HB3	1:B:448:VAL:O	2.18	0.44
1:B:94:GLY:HA3	1:B:402:LYS:HG2	1.99	0.44
1:A:107:GLY:N	2:A:516:HOH:O	2.47	0.44
1:A:158:HIS:HD2	1:A:204:LYS:HE3	1.79	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:PHE:CE1	1:B:138:ASN:ND2	2.86	0.44
1:B:181:LYS:HE2	1:B:185:GLU:HB2	2.00	0.44
1:B:54:ASP:OD2	2:B:572:HOH:O	2.21	0.44
1:B:57:VAL:HG11	1:B:291:ILE:CD1	2.44	0.44
1:B:227:ILE:O	1:B:228:VAL:C	2.56	0.44
1:B:227:ILE:HD13	1:B:379:PHE:CE1	2.53	0.44
1:A:71:ALA:O	1:A:75:ASN:ND2	2.51	0.44
1:A:77:LEU:HD13	1:A:127:CYS:SG	2.58	0.44
1:B:176:TRP:CE3	1:B:181:LYS:HG2	2.53	0.44
1:B:33:VAL:N	2:B:683:HOH:O	2.49	0.44
1:A:119:GLU:HG3	1:A:154:ASN:CA	2.48	0.44
1:B:58:VAL:HB	1:B:348:GLY:O	2.18	0.44
1:B:236:LEU:CD2	1:B:244:CYS:SG	3.06	0.44
1:B:270:LEU:HG	1:B:283:PHE:CE1	2.53	0.44
1:A:79:LYS:HD3	1:A:214:GLU:OE1	2.18	0.44
1:B:268:GLN:CG	2:B:599:HOH:O	2.66	0.44
1:B:286:ILE:O	1:B:290:LYS:HG2	2.18	0.44
1:A:172:GLU:HB2	1:A:174:VAL:HG13	2.00	0.44
1:A:84:LYS:HE3	1:A:114:ILE:HG23	2.00	0.44
1:B:382:ARG:CZ	1:B:386:ARG:HG2	2.48	0.44
1:B:233:LEU:O	1:B:236:LEU:HG	2.17	0.44
1:B:110:PHE:CZ	1:B:359:VAL:HG21	2.52	0.44
1:B:242:GLU:CB	1:B:343:PHE:HD1	2.30	0.43
1:A:6:GLU:O	1:A:7:ASN:HB2	2.18	0.43
1:B:81:VAL:CG2	1:B:130:PRO:HG2	2.44	0.43
1:A:31:SER:O	1:A:35:ARG:HG2	2.18	0.43
1:A:243:TYR:CD2	1:A:340:ILE:HG13	2.53	0.43
1:B:252:LEU:HA	1:B:255:VAL:HG23	2.00	0.43
1:B:347:ILE:HD13	1:B:347:ILE:H	1.83	0.43
1:A:244:CYS:SG	1:A:349:VAL:HG12	2.58	0.43
1:A:330:LEU:C	1:A:330:LEU:CD2	2.86	0.43
1:B:301:LEU:O	1:B:304:ILE:HB	2.17	0.43
1:A:366:LEU:HD23	1:A:366:LEU:C	2.38	0.43
1:B:438:GLY:HA3	1:B:460:ASN:OD1	2.18	0.43
1:B:278:GLU:HG3	1:B:279:HIS:CE1	2.53	0.43
1:A:303:ALA:O	1:A:306:LYS:N	2.51	0.43
1:A:86:ASN:N	1:A:134:MET:O	2.51	0.43
1:B:128:LYS:HD2	2:B:669:HOH:O	2.16	0.43
1:A:461:LYS:HZ2	1:A:468:ASP:HB3	1.83	0.43
1:A:384:LYS:HA	1:A:384:LYS:HE3	1.98	0.43
1:A:50:GLN:HB2	1:A:262:SER:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:PRO:C	1:B:179:LYS:N	2.72	0.43
1:A:122:ASN:HB3	1:A:127:CYS:O	2.18	0.43
1:A:139:THR:HA	2:A:483:HOH:O	2.17	0.43
1:A:439:LYS:HE2	2:A:527:HOH:O	2.17	0.43
1:B:214:GLU:O	1:B:300:ASN:ND2	2.51	0.43
1:B:364:ASP:O	1:B:368:VAL:HB	2.18	0.43
1:B:299:VAL:HB	1:B:304:ILE:HD11	2.01	0.43
1:A:28:GLY:C	1:A:30:ILE:H	2.21	0.43
1:B:365:LEU:HB3	1:B:369:GLN:CD	2.39	0.43
1:B:434:ILE:CG2	1:B:435:VAL:N	2.81	0.43
1:B:284:LYS:HB2	1:B:284:LYS:HE3	1.63	0.43
1:B:351:VAL:HB	1:B:352:PRO:CD	2.47	0.43
1:B:372:LEU:O	1:B:383:ASN:N	2.51	0.43
1:B:339:ALA:O	1:B:343:PHE:HD2	2.00	0.43
1:B:22:SER:HB2	2:B:599:HOH:O	2.17	0.43
1:B:437:LYS:HB2	1:B:459:GLU:CG	2.47	0.43
1:B:94:GLY:HA3	1:B:402:LYS:CG	2.46	0.43
1:B:353:ARG:HB2	2:B:475:HOH:O	2.18	0.43
1:B:105:ARG:HG3	1:B:106:ASP:CG	2.39	0.43
1:B:291:ILE:HD12	1:B:291:ILE:C	2.36	0.43
1:A:8:LEU:H	1:A:8:LEU:HD23	1.83	0.43
1:A:11:LEU:CD1	1:A:173:PHE:HD2	2.31	0.43
1:A:382:ARG:HH12	1:A:389:PRO:HA	1.83	0.43
1:A:366:LEU:HD23	1:A:366:LEU:O	2.18	0.43
1:A:255:VAL:CG2	1:A:284:LYS:HD2	2.47	0.43
1:B:372:LEU:O	1:B:372:LEU:HD22	2.17	0.43
1:B:439:LYS:O	1:B:460:ASN:HA	2.19	0.43
1:B:372:LEU:CD2	1:B:386:ARG:HD3	2.48	0.43
1:A:417:VAL:HG12	1:A:418:GLU:HG3	2.00	0.43
1:A:308:VAL:CG2	1:A:313:LEU:HD12	2.49	0.43
1:B:252:LEU:HD23	1:B:252:LEU:HA	1.87	0.43
1:B:242:GLU:OE1	2:B:562:HOH:O	2.21	0.43
1:B:133:LEU:HD23	1:B:133:LEU:N	2.33	0.43
1:A:375:LEU:HD12	1:A:375:LEU:HA	1.89	0.43
1:A:200:MET:CG	1:A:205:LEU:HD13	2.48	0.43
1:A:384:LYS:HA	1:A:384:LYS:HE3	2.00	0.43
1:A:168:VAL:HG13	1:A:174:VAL:N	2.33	0.43
1:B:276:PRO:O	1:B:277:ASP:C	2.56	0.43
1:A:423:LYS:O	1:A:441:THR:HA	2.18	0.43
1:B:249:PRO:HD3	1:B:351:VAL:O	2.18	0.43
1:A:171:ASP:OD1	1:A:171:ASP:C	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:372:LEU:HD21	1:A:391:ASN:OD1	2.17	0.43
1:B:307:LEU:HD13	1:B:313:LEU:CD2	2.46	0.43
1:A:169:VAL:HG12	1:A:171:ASP:OD1	2.17	0.43
1:A:124:LYS:HE2	1:A:125:TYR:OH	2.18	0.43
1:B:375:LEU:N	1:B:375:LEU:CD1	2.81	0.43
1:A:249:PRO:HA	1:A:290:LYS:O	2.18	0.43
1:A:198:ALA:O	1:A:199:LEU:C	2.56	0.43
1:A:459:GLU:HG2	2:A:617:HOH:O	2.18	0.43
1:A:275:VAL:HG21	1:A:283:PHE:CD1	2.54	0.43
1:B:165:TYR:CD2	1:B:190:PRO:HG2	2.53	0.43
1:B:216:VAL:HB	1:B:301:LEU:HD21	1.99	0.43
1:B:363:SER:HB3	2:B:545:HOH:O	2.19	0.43
1:A:263:TYR:N	1:A:266:LYS:O	2.50	0.43
1:B:291:ILE:C	1:B:291:ILE:HD12	2.39	0.43
1:A:54:ASP:HA	1:A:57:VAL:O	2.19	0.43
1:B:104:VAL:CG1	1:B:368:VAL:HG11	2.49	0.43
1:B:77:LEU:O	1:B:79:LYS:N	2.51	0.43
1:B:46:TRP:HZ2	1:B:282:GLU:HB3	1.83	0.43
1:A:322:LYS:NZ	2:A:629:HOH:O	2.50	0.43
1:B:11:LEU:HD12	1:B:173:PHE:HD2	1.83	0.43
1:A:105:ARG:HD2	1:A:375:LEU:HD11	2.00	0.43
1:A:266:LYS:HE2	1:A:266:LYS:HA	2.00	0.43
1:B:181:LYS:HE3	1:B:183:ASP:OD1	2.18	0.43
1:A:6:GLU:O	1:A:7:ASN:HB2	2.18	0.43
1:A:115:VAL:HG21	1:A:150:TYR:CE1	2.53	0.43
1:B:416:ILE:O	1:B:416:ILE:HG13	2.18	0.43
1:B:382:ARG:HA	1:B:382:ARG:HD2	1.83	0.43
1:A:115:VAL:HG11	1:A:150:TYR:HB3	2.01	0.43
1:B:382:ARG:CZ	1:B:386:ARG:HG2	2.49	0.43
1:B:140:HIS:CB	1:B:161:ASN:OD1	2.63	0.43
1:B:146:ILE:O	1:B:149:LYS:HG2	2.18	0.43
1:B:105:ARG:HD3	1:B:375:LEU:HB2	2.00	0.43
1:B:209:LEU:HD21	1:B:302:LYS:N	2.34	0.43
1:B:357:LEU:HD23	1:B:357:LEU:C	2.39	0.43
1:B:434:ILE:HB	2:B:495:HOH:O	2.18	0.43
1:B:29:PHE:CE2	1:B:166:PRO:HG2	2.53	0.43
1:B:322:LYS:HZ3	1:B:324:VAL:HG22	1.83	0.43
1:B:295:ASN:ND2	1:B:297:LEU:HD11	2.33	0.43
1:A:331:GLN:HA	2:A:533:HOH:O	2.17	0.43
1:A:165:TYR:CD2	1:A:190:PRO:HG3	2.54	0.43
1:A:445:LYS:HD2	2:A:589:HOH:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:ASN:HB3	1:B:226:ALA:CB	2.48	0.43
1:A:35:ARG:HG3	1:A:314:LYS:HZ3	1.84	0.43
1:A:415:SER:HB2	1:A:435:VAL:CG1	2.49	0.43
1:A:205:LEU:O	1:A:209:LEU:HB2	2.19	0.43
1:B:236:LEU:HD23	1:B:236:LEU:N	2.34	0.43
1:B:135:ASN:HD22	1:B:135:ASN:N	2.17	0.43
1:B:250:LYS:HE2	1:B:257:GLY:H	1.83	0.43
1:B:63:MET:HE1	1:B:349:VAL:HG21	2.00	0.43
1:B:63:MET:CE	1:B:349:VAL:HG21	2.49	0.43
1:A:355:ARG:NH1	1:A:355:ARG:CG	2.64	0.43
1:A:422:LEU:N	2:A:582:HOH:O	2.51	0.43
1:B:9:PRO:C	1:B:11:LEU:N	2.71	0.43
1:A:336:ALA:C	1:A:338:ALA:N	2.72	0.43
1:B:293:ASN:ND2	1:B:294:THR:N	2.67	0.43
1:A:195:VAL:O	1:A:199:LEU:HB2	2.18	0.43
1:A:236:LEU:HA	1:A:241:ASN:OD1	2.18	0.43
1:A:197:PRO:O	1:A:201:ASN:N	2.41	0.43
1:A:250:LYS:HG3	1:A:254:ASP:HB2	2.01	0.43
1:A:418:GLU:CD	1:A:437:LYS:HE2	2.39	0.43
1:B:81:VAL:O	1:B:216:VAL:HA	2.18	0.43
1:B:83:LEU:HA	1:B:132:VAL:O	2.19	0.43
1:B:386:ARG:HD2	1:B:417:VAL:O	2.17	0.43
1:A:105:ARG:CZ	1:A:374:THR:HA	2.49	0.43
1:A:268:GLN:NE2	1:A:341:ARG:HD2	2.34	0.43
1:A:419:LEU:HA	1:A:438:GLY:O	2.19	0.43
1:B:132:VAL:HG12	1:B:133:LEU:N	2.33	0.43
1:A:44:ILE:CD1	2:A:595:HOH:O	2.65	0.43
1:B:459:GLU:O	1:B:460:ASN:C	2.56	0.43
1:A:52:PRO:HD3	1:A:260:LEU:O	2.19	0.43
1:B:164:LYS:HE2	1:B:187:TRP:CG	2.52	0.43
1:B:44:ILE:HD13	1:B:49:ILE:HD11	2.00	0.43
1:A:270:LEU:HD12	1:A:274:GLN:HB2	2.00	0.43
1:A:9:PRO:HA	1:A:12:LYS:HB3	2.00	0.43
1:A:130:PRO:HD3	1:A:213:LYS:NZ	2.33	0.43
1:B:199:LEU:HD21	1:B:205:LEU:HA	2.00	0.43
1:B:179:LYS:HE3	1:B:179:LYS:CA	2.39	0.43
1:A:459:GLU:O	1:A:461:LYS:N	2.52	0.43
1:A:84:LYS:HA	1:A:219:ALA:O	2.19	0.43
1:A:176:TRP:C	1:A:178:SER:N	2.72	0.43
1:A:444:ALA:CA	1:A:450:LEU:HD12	2.49	0.43
1:A:23:GLU:HG2	2:A:545:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:LYS:HB2	1:A:149:LYS:HE3	1.85	0.43
1:A:461:LYS:HZ1	1:A:468:ASP:HB3	1.83	0.43
1:B:282:GLU:HG3	2:B:648:HOH:O	2.19	0.43
1:A:200:MET:SD	1:A:201:ASN:OD1	2.77	0.43
1:B:173:PHE:HE1	1:B:330:LEU:HD12	1.83	0.43
1:A:32:LEU:HD22	1:A:165:TYR:HE2	1.83	0.43
1:B:66:VAL:HG13	1:B:72:GLU:CD	2.39	0.43
1:B:83:LEU:HG	1:B:132:VAL:HB	2.01	0.43
1:A:379:PHE:HB2	2:A:597:HOH:O	2.17	0.43
1:B:190:PRO:HG2	1:B:194:ASP:CB	2.45	0.43
1:B:194:ASP:O	1:B:195:VAL:C	2.57	0.43
1:A:6:GLU:HB2	1:A:37:LEU:HD13	2.00	0.43
1:A:63:MET:SD	1:A:349:VAL:HG23	2.59	0.43
1:A:8:LEU:O	1:A:12:LYS:HB2	2.18	0.43
1:A:299:VAL:CG1	1:A:304:ILE:HD11	2.49	0.43
1:A:255:VAL:HG23	1:A:256:LYS:HG3	2.00	0.43
1:B:448:VAL:HG12	1:B:450:LEU:HD13	1.99	0.43
1:B:83:LEU:HD22	1:B:218:VAL:HG22	1.99	0.43
1:A:312:ALA:O	1:A:313:LEU:C	2.57	0.43
1:A:225:GLY:O	1:A:227:ILE:N	2.52	0.43
1:B:411:LYS:HB3	1:B:432:SER:CB	2.45	0.43
1:A:108:LEU:HD12	1:A:375:LEU:HD21	2.01	0.43
1:A:165:TYR:HB2	1:A:188:TYR:CE2	2.53	0.43
1:B:81:VAL:O	1:B:216:VAL:HA	2.19	0.43
1:B:307:LEU:HD12	1:B:343:PHE:CE1	2.54	0.43
1:B:201:ASN:C	1:B:203:GLY:H	2.22	0.43
1:A:243:TYR:HD2	1:A:244:CYS:N	2.17	0.43
1:A:116:ILE:HG21	1:A:378:GLY:CA	2.49	0.43
1:B:135:ASN:HB3	1:B:139:THR:OG1	2.19	0.43
1:A:355:ARG:NH1	1:A:355:ARG:CG	2.82	0.43
1:B:376:VAL:HG23	1:B:381:THR:OG1	2.19	0.43
1:A:169:VAL:O	1:A:173:PHE:N	2.52	0.43
1:A:246:GLU:HA	1:A:349:VAL:CG1	2.48	0.43
1:B:350:ASN:HB3	2:B:583:HOH:O	2.19	0.43
1:A:383:ASN:C	2:A:590:HOH:O	2.56	0.43
1:A:458:VAL:HA	2:A:624:HOH:O	2.17	0.43
1:A:81:VAL:HG13	1:A:216:VAL:CB	2.49	0.43
1:A:177:PRO:HA	1:A:181:LYS:O	2.19	0.43
1:A:243:TYR:HE1	1:A:339:ALA:HB3	1.84	0.43
1:A:190:PRO:HG2	1:A:194:ASP:HB2	1.99	0.43
1:B:243:TYR:HE2	1:B:245:MET:HB2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:416:ILE:HB	1:B:419:LEU:CD2	2.49	0.43
1:B:242:GLU:CD	1:B:344:ASP:HB2	2.39	0.43
1:B:243:TYR:CD1	1:B:299:VAL:HG13	2.53	0.43
1:B:436:LEU:CD2	1:B:458:VAL:HB	2.48	0.43
1:A:18:LEU:HD13	1:A:187:TRP:CZ3	2.54	0.43
1:A:234:LYS:HZ1	1:A:238:GLN:NE2	2.17	0.43
1:A:60:TYR:HB2	1:A:350:ASN:O	2.19	0.43
1:B:29:PHE:O	1:B:30:ILE:C	2.57	0.43
1:A:36:TYR:O	1:A:38:SER:N	2.52	0.43
1:B:373:TYR:OH	1:B:391:ASN:ND2	2.48	0.43
1:B:114:ILE:O	1:B:118:ILE:HG12	2.18	0.43
1:B:111:LEU:O	1:B:112:ASP:C	2.58	0.43
1:B:319:PRO:HA	1:B:330:LEU:HD21	2.01	0.43
1:A:366:LEU:HD23	1:A:366:LEU:O	2.19	0.43
1:A:29:PHE:CZ	1:A:166:PRO:HG2	2.54	0.43
1:A:422:LEU:HD13	1:A:436:LEU:CD1	2.49	0.43
1:A:195:VAL:O	1:A:199:LEU:N	2.38	0.43
1:A:11:LEU:HD12	1:A:173:PHE:CZ	2.54	0.43
1:A:89:LEU:CB	1:A:91:THR:HG23	2.48	0.43
1:B:258:GLY:O	1:B:292:PHE:HA	2.18	0.43
1:A:353:ARG:C	1:A:355:ARG:H	2.21	0.43
1:A:29:PHE:CE2	1:A:166:PRO:HG2	2.54	0.43
1:B:357:LEU:HD13	1:B:357:LEU:O	2.18	0.43
1:B:22:SER:OG	1:B:25:GLU:HG3	2.19	0.43
1:B:375:LEU:HD21	1:B:378:GLY:HA2	2.01	0.43
1:A:61:GLU:CD	1:A:61:GLU:H	2.22	0.43
1:A:205:LEU:HD12	1:A:205:LEU:O	2.18	0.43
1:A:429:TRP:O	1:A:451:GLU:HA	2.19	0.43
1:B:283:PHE:HA	1:B:289:PHE:CD2	2.54	0.43
1:B:164:LYS:HE2	1:B:187:TRP:CB	2.49	0.43
1:B:399:GLU:CD	1:B:399:GLU:N	2.72	0.43
1:B:93:MET:O	1:B:403:VAL:HG23	2.19	0.43
1:B:459:GLU:O	1:B:460:ASN:C	2.57	0.43
1:B:113:LEU:HD13	1:B:380:VAL:HG23	2.01	0.43
1:A:89:LEU:HD21	1:A:138:ASN:O	2.18	0.43
1:B:419:LEU:HD12	1:B:438:GLY:O	2.18	0.43
1:B:54:ASP:O	1:B:58:VAL:HG22	2.19	0.42
1:B:330:LEU:HD22	1:B:332:LEU:HG	2.00	0.42
1:A:121:LEU:C	1:A:123:ASN:H	2.22	0.42
1:A:250:LYS:HG3	1:A:254:ASP:HB2	2.01	0.42
1:B:445:LYS:NZ	1:B:464:ASN:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:LEU:HD21	1:B:422:LEU:HB2	1.99	0.42
1:A:115:VAL:HG21	1:A:150:TYR:CG	2.54	0.42
1:A:119:GLU:O	1:A:123:ASN:HB2	2.19	0.42
1:A:395:GLU:HG2	1:A:395:GLU:O	2.18	0.42
1:A:425:SER:O	1:A:443:ALA:HA	2.19	0.42
1:B:104:VAL:HG21	1:B:113:LEU:HD12	2.01	0.42
1:A:163:SER:O	1:A:189:PRO:HA	2.18	0.42
1:B:375:LEU:HD12	1:B:379:PHE:O	2.19	0.42
1:B:395:GLU:O	1:B:423:LYS:HA	2.18	0.42
1:B:73:THR:HG22	1:B:77:LEU:HD12	2.01	0.42
1:A:35:ARG:HG3	1:A:314:LYS:CE	2.48	0.42
1:A:462:ASN:C	1:A:463:ILE:HG13	2.39	0.42
1:A:371:ASP:OD1	1:A:417:VAL:HG23	2.19	0.42
1:B:267:VAL:O	1:B:341:ARG:CB	2.67	0.42
1:B:56:ILE:HG22	1:B:57:VAL:N	2.33	0.42
1:A:192:HIS:O	1:A:195:VAL:HG12	2.19	0.42
1:B:322:LYS:HD2	2:B:694:HOH:O	2.19	0.42
1:A:245:MET:SD	1:A:260:LEU:HD21	2.59	0.42
1:A:314:LYS:NZ	2:A:603:HOH:O	2.52	0.42
1:A:288:LYS:HZ3	1:A:288:LYS:HB3	1.82	0.42
1:B:8:LEU:C	2:B:697:HOH:O	2.57	0.42
1:B:247:VAL:CG2	1:B:350:ASN:HA	2.49	0.42
1:B:294:THR:O	1:B:295:ASN:CB	2.67	0.42
1:A:452:ILE:HD12	1:A:452:ILE:N	2.34	0.42
1:A:84:LYS:HE3	1:A:114:ILE:CG2	2.49	0.42
1:A:8:LEU:HG	1:A:9:PRO:HD3	1.99	0.42
1:B:320:ASN:N	1:B:331:GLN:O	2.49	0.42
1:A:374:THR:C	1:A:375:LEU:HD12	2.39	0.42
1:B:9:PRO:HD2	2:B:696:HOH:O	2.19	0.42
1:A:259:THR:HG21	1:A:289:PHE:CG	2.55	0.42
1:B:145:LYS:O	1:B:148:GLU:HB2	2.19	0.42
1:A:244:CYS:HB3	1:A:298:TRP:HB2	2.01	0.42
1:B:111:LEU:O	1:B:115:VAL:HG23	2.19	0.42
1:B:163:SER:HB3	1:B:165:TYR:CE1	2.55	0.42
1:A:21:MET:SD	1:A:166:PRO:HD3	2.59	0.42
1:A:28:GLY:O	1:A:30:ILE:N	2.51	0.42
1:A:8:LEU:HD23	1:A:8:LEU:N	2.34	0.42
1:A:177:PRO:HA	1:A:181:LYS:C	2.39	0.42
1:A:419:LEU:HD13	1:A:436:LEU:HB3	2.02	0.42
1:B:79:LYS:HD2	1:B:237:ILE:HD11	2.00	0.42
1:A:176:TRP:CH2	1:A:181:LYS:HE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:TRP:O	1:A:178:SER:N	2.53	0.42
1:B:193:GLY:HA2	1:B:336:ALA:HA	2.01	0.42
1:A:294:THR:OG1	1:A:296:ASN:HB2	2.19	0.42
1:B:332:LEU:HD13	2:B:682:HOH:O	2.18	0.42
1:A:86:ASN:HB3	1:A:135:ASN:OD1	2.19	0.42
1:B:108:LEU:HB3	1:B:112:ASP:HB3	2.01	0.42
1:B:254:ASP:CG	1:B:353:ARG:HH12	2.20	0.42
1:B:11:LEU:HD11	1:B:33:VAL:HG11	2.00	0.42
1:B:245:MET:HB2	1:B:245:MET:HE3	1.93	0.42
1:A:226:ALA:HB3	2:A:478:HOH:O	2.19	0.42
1:B:340:ILE:CG1	1:B:346:ALA:HB1	2.49	0.42
1:B:150:TYR:HB3	1:B:153:SER:OG	2.20	0.42
1:B:363:SER:HA	1:B:396:LEU:HD11	2.01	0.42
1:B:452:ILE:N	1:B:452:ILE:HD13	2.34	0.42
1:B:229:ASP:HB2	1:B:355:ARG:HH12	1.83	0.42
1:B:105:ARG:HG2	1:B:375:LEU:HD22	2.01	0.42
1:A:341:ARG:CZ	1:A:342:PHE:CE1	3.02	0.42
1:B:12:LYS:HE3	1:B:30:ILE:HG21	2.01	0.42
1:B:46:TRP:HA	1:B:49:ILE:HD12	2.01	0.42
1:A:193:GLY:HA2	1:A:336:ALA:HA	2.01	0.42
1:A:109:THR:N	1:A:112:ASP:OD2	2.45	0.42
1:B:422:LEU:HD11	1:B:424:VAL:CG2	2.49	0.42
1:B:188:TYR:HA	1:B:189:PRO:HD3	1.79	0.42
1:A:315:MET:HG2	1:A:338:ALA:HB3	2.01	0.42
1:A:277:ASP:C	1:A:279:HIS:H	2.22	0.42
1:A:319:PRO:O	1:A:320:ASN:C	2.58	0.42
1:B:399:GLU:OE2	1:B:426:GLY:C	2.58	0.42
1:B:137:PHE:CD1	1:B:184:LYS:HE3	2.52	0.42
1:B:49:ILE:HG12	1:B:263:TYR:CD1	2.54	0.42
1:B:119:GLU:O	1:B:123:ASN:N	2.52	0.42
1:B:259:THR:OG1	1:B:291:ILE:O	2.37	0.42
1:A:193:GLY:HA2	1:A:336:ALA:HA	2.01	0.42
1:B:192:HIS:CE1	2:B:478:HOH:O	2.72	0.42
1:A:29:PHE:O	1:A:33:VAL:HG23	2.20	0.42
1:B:83:LEU:C	1:B:83:LEU:HD23	2.39	0.42
1:B:416:ILE:CG2	1:B:419:LEU:HD22	2.50	0.42
1:A:176:TRP:N	1:A:177:PRO:CD	2.81	0.42
1:A:108:LEU:HB3	1:A:112:ASP:HB2	2.02	0.42
1:B:258:GLY:O	1:B:292:PHE:HA	2.19	0.42
1:B:74:LYS:HD3	1:B:127:CYS:HB3	2.00	0.42
1:B:14:ALA:O	1:B:18:LEU:HG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:TYR:HA	1:B:189:PRO:HD3	1.82	0.42
1:B:32:LEU:HG	2:B:682:HOH:O	2.19	0.42
1:A:314:LYS:NZ	1:A:317:ILE:HD11	2.34	0.42
1:A:8:LEU:N	1:A:9:PRO:CD	2.78	0.42
1:A:372:LEU:HD21	1:A:392:PRO:HD2	2.01	0.42
1:A:192:HIS:O	1:A:193:GLY:C	2.57	0.42
1:A:278:GLU:CD	1:A:278:GLU:H	2.22	0.42
1:B:57:VAL:HG12	1:B:57:VAL:O	2.20	0.42
1:A:200:MET:HA	1:A:205:LEU:CB	2.49	0.42
1:A:450:LEU:HD23	1:A:451:GLU:N	2.34	0.42
1:B:80:LEU:O	1:B:129:VAL:HG13	2.19	0.42
1:B:357:LEU:HD22	1:B:357:LEU:O	2.20	0.42
1:B:8:LEU:O	1:B:10:GLN:N	2.52	0.42
1:B:29:PHE:O	1:B:33:VAL:HG23	2.19	0.42
1:A:371:ASP:CG	1:A:417:VAL:HG23	2.40	0.42
1:A:345:ASN:O	1:A:347:ILE:HG23	2.19	0.42
1:A:83:LEU:HD23	1:A:84:LYS:N	2.35	0.42
1:B:288:LYS:HA	1:B:288:LYS:HD3	1.74	0.42
1:A:219:ALA:CB	2:A:492:HOH:O	2.62	0.42
1:A:171:ASP:OD1	1:A:172:GLU:N	2.53	0.42
1:A:445:LYS:HD2	2:A:589:HOH:O	2.19	0.42
1:A:439:LYS:O	1:A:460:ASN:HA	2.20	0.42
1:B:151:THR:HG22	1:B:151:THR:O	2.19	0.42
1:A:266:LYS:HA	1:A:266:LYS:HE2	2.02	0.42
1:A:11:LEU:O	1:A:15:VAL:HG23	2.19	0.42
1:A:18:LEU:HD21	1:A:178:SER:OG	2.19	0.42
1:A:379:PHE:HB2	2:A:597:HOH:O	2.20	0.42
1:B:316:GLU:CD	1:B:316:GLU:H	2.23	0.42
1:A:84:LYS:HA	1:A:219:ALA:O	2.18	0.42
1:A:176:TRP:CE3	1:A:181:LYS:HG2	2.54	0.42
1:B:223:ASN:HA	1:B:358:PRO:HA	2.01	0.42
1:A:442:VAL:HG21	1:A:452:ILE:CD1	2.49	0.42
1:B:376:VAL:HB	1:B:381:THR:HG21	2.01	0.42
1:B:382:ARG:HG3	1:B:382:ARG:HH11	1.85	0.42
1:A:28:GLY:O	1:A:32:LEU:HD12	2.20	0.42
1:B:432:SER:O	1:B:454:ASP:HA	2.20	0.42
1:B:464:ASN:HB2	1:B:467:GLU:CD	2.40	0.42
1:A:134:MET:HG3	1:A:160:PHE:CZ	2.55	0.42
1:B:35:ARG:HH21	1:B:314:LYS:HZ2	1.67	0.42
1:A:205:LEU:O	1:A:209:LEU:HD13	2.20	0.42
1:A:453:PRO:O	1:A:456:ALA:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:VAL:HB	1:B:301:LEU:HD21	2.01	0.42
1:A:303:ALA:O	1:A:304:ILE:C	2.58	0.42
1:A:409:ARG:NH1	1:A:428:VAL:O	2.53	0.42
1:A:205:LEU:CD1	1:A:301:LEU:HD22	2.50	0.42
1:A:32:LEU:HG	1:A:317:ILE:HD12	2.02	0.42
1:A:46:TRP:HA	1:A:49:ILE:HD11	2.02	0.42
1:B:34:SER:O	1:B:37:LEU:HG	2.20	0.42
1:A:225:GLY:HA2	1:A:379:PHE:HE1	1.84	0.42
1:A:366:LEU:HD23	1:A:366:LEU:C	2.40	0.42
1:A:420:ASP:O	1:A:421:SER:CB	2.67	0.42
1:A:250:LYS:CG	1:A:286:ILE:HG22	2.42	0.42
1:B:143:THR:O	1:B:146:ILE:N	2.53	0.42
1:A:255:VAL:CG2	1:A:284:LYS:HD2	2.49	0.42
1:A:49:ILE:CD1	1:A:270:LEU:HD22	2.46	0.42
1:A:235:HIS:O	1:A:238:GLN:HB2	2.19	0.42
1:A:238:GLN:C	1:A:240:LYS:H	2.23	0.42
1:A:273:ALA:HB3	1:A:274:GLN:NE2	2.35	0.42
1:B:135:ASN:ND2	1:B:159:THR:HB	2.34	0.42
1:A:181:LYS:NZ	1:A:325:ASP:OD2	2.53	0.42
1:B:249:PRO:HA	1:B:290:LYS:O	2.20	0.42
1:A:223:ASN:HA	1:A:358:PRO:HA	2.02	0.42
1:B:247:VAL:O	1:B:351:VAL:HG22	2.20	0.42
1:B:21:MET:O	1:B:26:LYS:HE3	2.19	0.42
1:B:216:VAL:HB	1:B:301:LEU:HD21	2.01	0.42
1:A:205:LEU:HD21	1:A:305:LYS:HB2	2.01	0.42
1:B:260:LEU:CD1	1:B:348:GLY:HA3	2.50	0.42
1:A:422:LEU:HA	2:A:582:HOH:O	2.20	0.42
1:A:11:LEU:CD2	1:A:33:VAL:HG11	2.50	0.42
1:A:209:LEU:HD12	1:A:209:LEU:HA	1.85	0.42
1:A:122:ASN:O	1:A:154:ASN:ND2	2.53	0.42
1:B:254:ASP:OD1	1:B:353:ARG:NH2	2.34	0.42
1:A:314:LYS:HD2	1:A:314:LYS:HA	1.82	0.42
1:A:29:PHE:CD1	1:A:166:PRO:HD2	2.54	0.42
1:B:88:GLY:O	1:B:139:THR:HG21	2.19	0.42
1:B:235:HIS:O	1:B:236:LEU:C	2.58	0.42
1:B:66:VAL:HG12	2:B:502:HOH:O	2.19	0.42
1:A:241:ASN:HA	1:A:345:ASN:ND2	2.34	0.42
1:A:89:LEU:HB2	1:A:91:THR:CG2	2.49	0.42
1:B:61:GLU:CD	1:B:61:GLU:H	2.22	0.42
1:A:428:VAL:CG2	1:A:444:ALA:HB2	2.50	0.42
1:A:49:ILE:HG23	1:A:261:ILE:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ASN:HA	1:A:127:CYS:SG	2.59	0.42
1:B:52:PRO:HB3	1:B:56:ILE:CG2	2.50	0.42
1:A:9:PRO:O	1:A:13:SER:N	2.51	0.42
1:A:256:LYS:CG	1:A:284:LYS:HD3	2.50	0.42
1:B:15:VAL:HG11	1:B:30:ILE:HD11	2.02	0.42
1:B:366:LEU:CD2	1:B:366:LEU:C	2.89	0.42
1:A:70:VAL:C	1:A:72:GLU:N	2.73	0.42
1:B:196:PHE:HD1	1:B:304:ILE:HD13	1.85	0.42
1:B:279:HIS:O	1:B:282:GLU:HB2	2.20	0.42
1:A:111:LEU:CD1	1:A:133:LEU:HD11	2.49	0.42
1:A:349:VAL:O	1:A:349:VAL:HG13	2.20	0.42
1:B:167:ARG:HD2	1:B:185:GLU:O	2.20	0.42
1:A:341:ARG:CZ	1:A:342:PHE:CZ	3.03	0.42
1:B:35:ARG:HD3	1:B:35:ARG:HA	1.90	0.42
1:A:248:THR:HG23	2:A:579:HOH:O	2.19	0.42
1:B:83:LEU:HA	1:B:132:VAL:O	2.20	0.42
1:A:124:LYS:HG2	1:A:125:TYR:CE1	2.55	0.42
1:B:86:ASN:ND2	2:B:517:HOH:O	2.52	0.42
1:B:181:LYS:HA	1:B:181:LYS:HD2	1.90	0.42
1:B:247:VAL:O	1:B:351:VAL:HG22	2.19	0.42
1:A:194:ASP:CG	1:A:194:ASP:O	2.58	0.42
1:A:99:LYS:HG3	1:A:102:ILE:CD1	2.37	0.42
1:A:314:LYS:HA	1:A:314:LYS:HD2	1.76	0.42
1:A:395:GLU:C	1:A:396:LEU:HG	2.40	0.42
1:A:372:LEU:HD22	1:A:392:PRO:CD	2.47	0.42
1:B:366:LEU:HD23	1:B:413:ILE:CG2	2.50	0.42
1:B:36:TYR:O	1:B:37:LEU:HD23	2.19	0.42
1:A:200:MET:HB2	1:A:308:VAL:HG11	2.01	0.42
1:B:52:PRO:HB3	1:B:56:ILE:CB	2.41	0.42
1:B:437:LYS:HB2	1:B:459:GLU:HA	2.01	0.42
1:B:96:THR:CG2	1:B:97:GLY:H	2.33	0.42
1:A:58:VAL:O	1:A:349:VAL:HG23	2.19	0.42
1:B:247:VAL:CG2	1:B:350:ASN:HA	2.50	0.42
1:B:198:ALA:O	1:B:202:SER:HB3	2.19	0.42
1:B:268:GLN:CA	2:B:472:HOH:O	2.68	0.41
1:B:84:LYS:HG3	1:B:114:ILE:HD13	2.01	0.41
1:B:383:ASN:CA	2:B:645:HOH:O	2.63	0.41
1:A:177:PRO:C	1:A:179:LYS:N	2.73	0.41
1:A:418:GLU:O	1:A:438:GLY:HA2	2.19	0.41
1:B:449:LYS:HE2	1:B:451:GLU:OE2	2.20	0.41
1:A:340:ILE:HG12	1:A:346:ALA:HB1	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:TRP:CZ2	1:B:282:GLU:HB3	2.55	0.41
1:B:254:ASP:OD2	1:B:353:ARG:NH1	2.48	0.41
1:A:215:TYR:CA	1:A:301:LEU:HG	2.50	0.41
1:B:179:LYS:CE	1:B:179:LYS:HA	2.44	0.41
1:A:249:PRO:HA	1:A:290:LYS:O	2.20	0.41
1:A:384:LYS:HA	1:A:384:LYS:NZ	2.34	0.41
1:B:72:GLU:HB3	2:B:502:HOH:O	2.20	0.41
1:A:242:GLU:HB2	1:A:343:PHE:HB3	2.02	0.41
1:A:71:ALA:O	1:A:75:ASN:ND2	2.52	0.41
1:B:250:LYS:HG3	1:B:292:PHE:HD2	1.85	0.41
1:A:142:ASP:O	1:A:146:ILE:HG12	2.20	0.41
1:B:200:MET:SD	1:B:305:LYS:HD2	2.60	0.41
1:B:205:LEU:HD11	1:B:301:LEU:HB3	2.02	0.41
1:B:232:ILE:HG12	1:B:349:VAL:HG21	2.02	0.41
1:A:323:GLU:HA	1:A:328:LYS:HA	2.02	0.41
1:B:35:ARG:HE	1:B:314:LYS:HD3	1.85	0.41
1:B:137:PHE:CD2	1:B:164:LYS:HD2	2.55	0.41
1:A:99:LYS:HZ1	1:A:360:LYS:HA	1.85	0.41
1:A:8:LEU:N	1:A:9:PRO:CD	2.83	0.41
1:B:357:LEU:N	1:B:358:PRO:CD	2.83	0.41
1:A:382:ARG:CZ	1:A:386:ARG:HG2	2.50	0.41
1:A:367:LEU:HD22	1:A:372:LEU:CD2	2.49	0.41
1:B:8:LEU:HA	1:B:9:PRO:HD3	1.92	0.41
1:B:62:LYS:HA	1:B:62:LYS:HD2	1.89	0.41
1:B:119:GLU:CG	1:B:123:ASN:ND2	2.83	0.41
1:B:224:LEU:HD12	1:B:357:LEU:HD22	2.01	0.41
1:A:110:PHE:O	1:A:114:ILE:HG13	2.19	0.41
1:A:15:VAL:HG21	1:A:30:ILE:CD1	2.50	0.41
1:B:59:PRO:HA	1:B:350:ASN:HB3	2.02	0.41
1:A:25:GLU:HA	2:A:501:HOH:O	2.20	0.41
1:A:280:VAL:HG12	1:A:284:LYS:HZ3	1.81	0.41
1:B:204:LYS:HD3	2:B:667:HOH:O	2.19	0.41
1:B:11:LEU:O	1:B:15:VAL:HG23	2.20	0.41
1:B:169:VAL:CG2	1:B:176:TRP:HA	2.50	0.41
1:B:150:TYR:HD1	1:B:153:SER:OG	2.02	0.41
1:B:417:VAL:HG13	1:B:418:GLU:HG3	2.02	0.41
1:B:418:GLU:OE1	1:B:437:LYS:HE2	2.20	0.41
1:B:235:HIS:CD2	1:B:241:ASN:OD1	2.73	0.41
1:A:336:ALA:O	1:A:338:ALA:N	2.53	0.41
1:B:200:MET:HE3	2:B:489:HOH:O	2.20	0.41
1:B:245:MET:HG2	1:B:247:VAL:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:PRO:HD3	1:B:350:ASN:OD1	2.20	0.41
1:B:167:ARG:NH1	1:B:185:GLU:OE1	2.54	0.41
1:A:242:GLU:HA	1:A:300:ASN:HB2	2.01	0.41
1:B:132:VAL:CG1	1:B:160:PHE:HE2	2.34	0.41
1:A:79:LYS:HD2	1:A:237:ILE:HD11	2.03	0.41
1:B:367:LEU:HG	1:B:394:ILE:HD12	2.02	0.41
1:A:182:THR:C	1:A:187:TRP:HE1	2.22	0.41
1:A:116:ILE:CG2	1:A:378:GLY:HA3	2.51	0.41
1:A:61:GLU:H	1:A:61:GLU:CD	2.23	0.41
1:B:424:VAL:HG13	1:B:428:VAL:HG21	2.01	0.41
1:B:133:LEU:HD12	1:B:143:THR:HG21	2.01	0.41
1:A:121:LEU:O	1:A:123:ASN:N	2.54	0.41
1:B:296:ASN:O	1:B:297:LEU:HD23	2.20	0.41
1:B:66:VAL:HG11	1:B:73:THR:OG1	2.20	0.41
1:A:314:LYS:O	1:A:314:LYS:HE3	2.21	0.41
1:A:255:VAL:HG21	1:A:284:LYS:HD2	2.02	0.41
1:B:104:VAL:HG13	1:B:368:VAL:HG11	2.02	0.41
1:A:165:TYR:CD2	1:A:190:PRO:HG3	2.54	0.41
1:A:344:ASP:CG	2:A:569:HOH:O	2.57	0.41
1:B:11:LEU:CD1	1:B:33:VAL:HG11	2.43	0.41
1:A:247:VAL:O	1:A:350:ASN:HA	2.20	0.41
1:B:15:VAL:HA	1:B:18:LEU:HG	2.02	0.41
1:A:351:VAL:HB	1:A:352:PRO:CD	2.51	0.41
1:B:85:LEU:HD12	1:B:220:ASN:ND2	2.34	0.41
1:B:168:VAL:HG11	1:B:173:PHE:CE2	2.55	0.41
1:B:320:ASN:HA	1:B:321:PRO:HD3	1.88	0.41
1:A:364:ASP:O	1:A:367:LEU:HB2	2.20	0.41
1:A:173:PHE:O	1:A:173:PHE:CD2	2.73	0.41
1:A:168:VAL:HG13	1:A:174:VAL:C	2.41	0.41
1:A:8:LEU:CG	1:A:9:PRO:HD3	2.49	0.41
1:A:8:LEU:N	2:A:495:HOH:O	2.52	0.41
1:A:118:ILE:HD12	1:A:131:LEU:HD22	2.02	0.41
1:B:411:LYS:NZ	1:B:411:LYS:HB3	2.35	0.41
1:A:89:LEU:CG	1:A:138:ASN:HB3	2.51	0.41
1:A:410:PHE:HA	1:A:430:PHE:HB2	2.02	0.41
1:A:410:PHE:O	1:A:411:LYS:C	2.57	0.41
1:A:317:ILE:HG22	1:A:332:LEU:HB3	2.02	0.41
1:A:392:PRO:HB3	1:A:419:LEU:O	2.21	0.41
1:B:269:LEU:CD2	1:B:337:GLY:C	2.89	0.41
1:B:366:LEU:HD23	1:B:366:LEU:O	2.19	0.41
1:B:227:ILE:O	1:B:227:ILE:HG13	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:ILE:CG2	1:B:332:LEU:HB3	2.50	0.41
1:B:31:SER:O	1:B:35:ARG:HG2	2.20	0.41
1:B:102:ILE:O	1:B:109:THR:HA	2.21	0.41
1:B:82:VAL:HG21	1:B:118:ILE:HD12	2.02	0.41
1:B:139:THR:HA	1:B:142:ASP:HB2	2.02	0.41
1:B:160:PHE:CG	1:B:160:PHE:O	2.72	0.41
1:B:89:LEU:CD1	1:B:138:ASN:HB3	2.48	0.41
1:B:164:LYS:HB2	1:B:164:LYS:HE3	1.96	0.41
1:B:152:ASN:ND2	1:B:152:ASN:N	2.68	0.41
1:B:36:TYR:O	1:B:37:LEU:HD23	2.21	0.41
1:B:240:LYS:HG2	1:B:240:LYS:O	2.21	0.41
1:B:252:LEU:O	1:B:255:VAL:HB	2.21	0.41
1:A:93:MET:O	1:A:403:VAL:HG23	2.20	0.41
1:B:8:LEU:O	1:B:10:GLN:N	2.53	0.41
1:B:214:GLU:C	1:B:301:LEU:HG	2.41	0.41
1:A:416:ILE:HB	1:A:419:LEU:HB2	2.02	0.41
1:A:8:LEU:HD23	1:A:8:LEU:N	2.34	0.41
1:B:236:LEU:HD21	1:B:244:CYS:HB2	2.02	0.41
1:B:240:LYS:HZ1	1:B:344:ASP:HB3	1.84	0.41
1:B:146:ILE:C	1:B:148:GLU:H	2.24	0.41
1:B:136:SER:HB2	1:B:189:PRO:HB3	2.01	0.41
1:B:236:LEU:HA	1:B:241:ASN:HB2	2.01	0.41
1:A:44:ILE:CG2	1:A:49:ILE:HD11	2.50	0.41
1:B:269:LEU:HD22	1:B:337:GLY:HA3	2.01	0.41
1:A:162:GLN:HB2	1:A:194:ASP:OD2	2.19	0.41
1:B:164:LYS:NZ	2:B:658:HOH:O	2.46	0.41
1:B:93:MET:O	1:B:403:VAL:HG23	2.21	0.41
1:B:85:LEU:HD12	1:B:220:ASN:HD22	1.85	0.41
1:B:461:LYS:HG3	2:B:626:HOH:O	2.21	0.41
1:B:103:GLU:CG	1:B:107:GLY:O	2.65	0.41
1:A:384:LYS:HE3	1:A:384:LYS:HA	2.01	0.41
1:A:436:LEU:CD1	1:A:440:VAL:HG11	2.38	0.41
1:A:258:GLY:O	1:A:292:PHE:HA	2.21	0.41
1:A:15:VAL:HG21	1:A:30:ILE:HD11	2.01	0.41
1:A:403:VAL:O	1:A:407:LEU:HG	2.20	0.41
1:B:12:LYS:HA	1:B:30:ILE:HD11	2.02	0.41
1:A:160:PHE:HB2	1:A:202:SER:HB2	2.03	0.41
1:B:118:ILE:HG22	1:B:122:ASN:HD21	1.86	0.41
1:B:142:ASP:O	1:B:146:ILE:HG13	2.21	0.41
1:B:235:HIS:O	1:B:239:ASN:HB2	2.20	0.41
1:A:160:PHE:C	1:A:160:PHE:CD1	2.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ILE:HD11	2:A:586:HOH:O	2.21	0.41
1:A:250:LYS:HG2	1:A:292:PHE:CD2	2.56	0.41
1:A:97:GLY:HA2	2:A:556:HOH:O	2.19	0.41
1:A:105:ARG:NH1	1:A:368:VAL:O	2.53	0.41
1:A:57:VAL:HG13	1:A:348:GLY:C	2.40	0.41
1:B:8:LEU:HA	1:B:9:PRO:HD3	1.90	0.41
1:A:439:LYS:CD	1:A:440:VAL:N	2.76	0.41
1:B:315:MET:HG2	1:B:338:ALA:HB3	2.01	0.41
1:B:128:LYS:HD2	2:B:670:HOH:O	2.19	0.41
1:B:293:ASN:HB3	2:B:488:HOH:O	2.21	0.41
1:B:248:THR:HG22	1:B:294:THR:HG22	2.03	0.41
1:B:119:GLU:HG3	1:B:154:ASN:HB3	2.03	0.41
1:A:175:PRO:O	1:A:178:SER:HB2	2.21	0.41
1:A:110:PHE:CZ	1:A:359:VAL:HG21	2.56	0.41
1:B:233:LEU:O	1:B:233:LEU:HD12	2.21	0.41
1:A:134:MET:HG3	1:A:160:PHE:CE1	2.56	0.41
1:A:365:LEU:O	1:A:369:GLN:HB2	2.20	0.41
1:B:176:TRP:CD2	1:B:181:LYS:HG2	2.55	0.41
1:B:366:LEU:HD23	1:B:366:LEU:O	2.21	0.41
1:B:340:ILE:CD1	1:B:347:ILE:O	2.66	0.41
1:B:56:ILE:HG13	2:B:610:HOH:O	2.20	0.41
1:A:83:LEU:HA	1:A:132:VAL:O	2.21	0.41
1:A:435:VAL:H	1:A:457:VAL:HG22	1.86	0.41
1:B:181:LYS:HE3	1:B:185:GLU:HB2	2.03	0.41
1:B:394:ILE:HG22	1:B:395:GLU:N	2.34	0.41
1:A:430:PHE:CD2	1:A:430:PHE:N	2.89	0.41
1:B:441:THR:O	1:B:441:THR:OG1	2.38	0.41
1:A:93:MET:O	1:A:403:VAL:HG23	2.19	0.41
1:B:56:ILE:O	1:B:58:VAL:N	2.54	0.41
1:B:32:LEU:HB3	2:B:683:HOH:O	2.20	0.41
1:B:422:LEU:HG	1:B:423:LYS:N	2.35	0.41
1:A:430:PHE:CZ	1:A:442:VAL:HG21	2.56	0.41
1:A:68:GLN:N	1:A:68:GLN:CD	2.73	0.41
1:B:403:VAL:HG12	1:B:407:LEU:CD1	2.51	0.41
1:B:266:LYS:O	1:B:268:GLN:HG3	2.21	0.41
1:B:361:ALA:N	1:B:364:ASP:OD2	2.39	0.41
1:B:260:LEU:HD12	1:B:348:GLY:HA3	2.02	0.41
1:A:193:GLY:HA2	1:A:336:ALA:N	2.35	0.41
1:B:115:VAL:HG21	1:B:150:TYR:CD2	2.55	0.41
1:A:461:LYS:HD2	2:A:625:HOH:O	2.21	0.41
1:B:44:ILE:HG13	1:B:263:TYR:OH	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:THR:HG23	1:B:292:PHE:CE2	2.55	0.41
1:A:467:GLU:HB2	2:A:590:HOH:O	2.19	0.41
1:A:365:LEU:HD23	1:A:365:LEU:HA	1.87	0.41
1:A:422:LEU:HD12	1:A:423:LYS:H	1.85	0.41
1:B:250:LYS:HE2	1:B:257:GLY:H	1.85	0.41
1:A:386:ARG:HD2	1:A:387:THR:H	1.86	0.41
1:B:234:LYS:O	1:B:238:GLN:HG3	2.21	0.41
1:B:66:VAL:CG1	1:B:67:SER:N	2.83	0.41
1:B:399:GLU:H	1:B:399:GLU:CD	2.22	0.41
1:B:376:VAL:O	1:B:377:ASP:C	2.59	0.41
1:B:268:GLN:HG2	1:B:341:ARG:HB3	2.01	0.41
1:B:246:GLU:HG2	1:B:349:VAL:CG1	2.50	0.41
1:B:8:LEU:CD2	1:B:8:LEU:N	2.83	0.41
1:A:79:LYS:HD2	1:A:237:ILE:CD1	2.51	0.41
1:B:363:SER:HB2	1:B:394:ILE:O	2.19	0.41
1:B:370:SER:HB3	1:B:413:ILE:HG21	2.02	0.41
1:B:85:LEU:O	1:B:221:SER:CB	2.68	0.41
1:A:217:PHE:CD1	1:A:218:VAL:N	2.88	0.41
1:A:439:LYS:H	1:A:460:ASN:ND2	2.19	0.41
1:B:52:PRO:HB3	1:B:56:ILE:HB	2.02	0.41
1:B:371:ASP:OD2	1:B:417:VAL:HB	2.21	0.41
1:A:183:ASP:OD1	1:A:185:GLU:HB2	2.21	0.41
1:B:74:LYS:NZ	1:B:78:ASP:OD2	2.54	0.41
1:B:89:LEU:CG	2:B:661:HOH:O	2.69	0.41
1:B:424:VAL:HG13	1:B:442:VAL:HB	2.03	0.41
1:A:15:VAL:HG21	1:A:30:ILE:CD1	2.45	0.41
1:A:111:LEU:C	1:A:111:LEU:HD12	2.41	0.41
1:B:63:MET:O	1:B:65:PRO:CD	2.68	0.41
1:B:111:LEU:HD23	1:B:114:ILE:CD1	2.47	0.41
1:A:15:VAL:HA	1:A:18:LEU:HG	2.02	0.41
1:A:276:PRO:HB2	1:A:279:HIS:HD2	1.85	0.41
1:B:429:TRP:HB2	1:B:451:GLU:HG2	2.02	0.41
1:B:48:LYS:NZ	1:B:48:LYS:CB	2.83	0.41
1:A:98:PRO:HB2	1:A:101:VAL:HG13	2.03	0.41
1:A:200:MET:CB	1:A:205:LEU:HD23	2.50	0.41
1:B:15:VAL:O	1:B:26:LYS:HE2	2.21	0.41
1:B:122:ASN:O	1:B:154:ASN:ND2	2.54	0.41
1:A:433:SER:O	1:A:455:ARG:HA	2.21	0.41
1:B:362:SER:HB2	1:B:406:PHE:CD1	2.56	0.41
1:B:82:VAL:CG1	1:B:84:LYS:HE2	2.50	0.41
1:A:439:LYS:CE	2:A:527:HOH:O	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:VAL:CG1	1:A:234:LYS:HE3	2.51	0.41
1:A:216:VAL:HB	1:A:301:LEU:HD21	2.03	0.41
1:A:410:PHE:C	1:A:412:SER:N	2.74	0.41
1:A:411:LYS:HG3	2:A:512:HOH:O	2.21	0.41
1:B:315:MET:HG2	1:B:338:ALA:HB3	2.01	0.41
1:B:295:ASN:HA	1:B:295:ASN:HD22	1.56	0.41
1:A:355:ARG:NH1	1:A:355:ARG:CG	2.58	0.41
1:B:66:VAL:HG12	2:B:502:HOH:O	2.21	0.41
1:B:94:GLY:HA3	1:B:402:LYS:CG	2.51	0.41
1:B:434:ILE:HG22	1:B:435:VAL:N	2.36	0.41
1:B:86:ASN:OD1	1:B:100:SER:HB3	2.20	0.41
1:A:131:LEU:O	1:A:157:ILE:HA	2.21	0.41
1:B:432:SER:O	1:B:455:ARG:N	2.51	0.41
1:B:433:SER:O	1:B:455:ARG:HA	2.20	0.41
1:B:429:TRP:O	1:B:451:GLU:HA	2.21	0.41
1:A:178:SER:C	1:A:180:GLY:H	2.23	0.41
1:A:374:THR:HG23	1:A:381:THR:HB	2.03	0.41
1:A:321:PRO:HB3	1:A:330:LEU:HD23	2.03	0.41
1:B:115:VAL:HG13	1:B:155:VAL:HG11	2.02	0.41
1:B:11:LEU:HD11	1:B:33:VAL:HG11	2.00	0.41
1:A:243:TYR:C	1:A:243:TYR:HD2	2.23	0.41
1:A:83:LEU:CB	1:A:132:VAL:HG13	2.51	0.41
1:B:239:ASN:HB2	1:B:241:ASN:OD1	2.20	0.41
1:B:35:ARG:NH2	1:B:314:LYS:HZ2	2.19	0.41
1:B:412:SER:O	2:B:495:HOH:O	2.22	0.41
1:A:245:MET:CE	1:A:269:LEU:HD13	2.51	0.41
1:A:30:ILE:HA	1:A:30:ILE:HD13	1.91	0.41
1:A:95:CYS:SG	1:A:403:VAL:HB	2.61	0.41
1:A:440:VAL:HG13	1:A:458:VAL:HG11	2.02	0.41
1:A:84:LYS:HB2	1:A:133:LEU:HD23	2.03	0.41
1:B:384:LYS:C	1:B:386:ARG:N	2.73	0.41
1:B:150:TYR:C	1:B:152:ASN:N	2.74	0.41
1:B:23:GLU:OE1	1:B:26:LYS:HD2	2.21	0.41
1:B:322:LYS:HB3	1:B:329:VAL:HG23	2.02	0.41
1:A:336:ALA:C	1:A:338:ALA:H	2.25	0.41
1:B:91:THR:HA	1:B:95:CYS:O	2.21	0.41
1:A:437:LYS:O	1:A:440:VAL:HG23	2.21	0.41
1:A:369:GLN:HB3	1:A:413:ILE:HG13	2.03	0.41
1:B:263:TYR:O	1:B:264:GLU:CB	2.66	0.41
1:B:437:LYS:O	1:B:459:GLU:HA	2.21	0.41
1:A:241:ASN:HD22	1:A:345:ASN:HB3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:SER:O	1:A:110:PHE:HB2	2.20	0.41
1:B:280:VAL:CG1	1:B:284:LYS:HE3	2.51	0.41
1:A:177:PRO:HB3	1:A:182:THR:HG22	2.03	0.41
1:B:159:THR:O	1:B:160:PHE:HB3	2.20	0.41
1:A:145:LYS:HG3	1:A:146:ILE:N	2.36	0.41
1:B:298:TRP:C	1:B:299:VAL:CG1	2.90	0.41
1:B:448:VAL:HG12	1:B:449:LYS:N	2.35	0.41
1:B:52:PRO:HB3	1:B:56:ILE:CB	2.50	0.41
1:A:402:LYS:O	1:A:403:VAL:C	2.58	0.41
1:B:261:ILE:O	1:B:267:VAL:HA	2.21	0.41
1:B:366:LEU:HD11	1:B:410:PHE:CZ	2.57	0.41
1:A:205:LEU:C	1:A:205:LEU:HD12	2.41	0.41
1:A:100:SER:CA	1:A:110:PHE:HB2	2.51	0.41
1:B:375:LEU:HD12	1:B:375:LEU:HA	1.90	0.41
1:A:80:LEU:HD22	1:A:233:LEU:HD22	2.02	0.41
1:B:59:PRO:HA	1:B:350:ASN:HB3	2.02	0.41
1:A:169:VAL:O	1:A:173:PHE:N	2.54	0.41
1:A:429:TRP:HB2	1:A:451:GLU:CG	2.51	0.41
1:A:336:ALA:O	1:A:338:ALA:N	2.54	0.41
1:B:254:ASP:O	1:B:255:VAL:C	2.58	0.41
1:B:11:LEU:HD12	1:B:173:PHE:CE2	2.56	0.41
1:B:188:TYR:CD1	1:B:189:PRO:O	2.74	0.41
1:A:12:LYS:O	1:A:16:ASP:CG	2.58	0.41
1:B:109:THR:N	1:B:112:ASP:HB2	2.36	0.41
1:A:324:VAL:HG12	1:A:325:ASP:OD2	2.20	0.41
1:A:331:GLN:C	1:A:332:LEU:HD12	2.41	0.41
1:B:113:LEU:HA	1:B:113:LEU:HD23	1.82	0.41
1:B:202:SER:OG	1:B:204:LYS:HG2	2.21	0.41
1:B:241:ASN:HA	1:B:345:ASN:ND2	2.35	0.41
1:B:340:ILE:C	1:B:342:PHE:H	2.23	0.41
1:B:223:ASN:HB3	1:B:226:ALA:HB2	2.02	0.41
1:A:91:THR:HA	1:A:95:CYS:O	2.20	0.41
1:A:29:PHE:CZ	1:A:166:PRO:HG2	2.56	0.41
1:B:54:ASP:O	1:B:58:VAL:HG13	2.20	0.41
1:B:239:ASN:O	1:B:240:LYS:CB	2.69	0.40
1:A:175:PRO:O	1:A:176:TRP:C	2.59	0.40
1:A:208:PHE:C	1:A:213:LYS:HB2	2.41	0.40
1:B:181:LYS:HD2	1:B:183:ASP:OD2	2.21	0.40
1:B:275:VAL:O	1:B:276:PRO:C	2.59	0.40
1:A:271:GLU:CG	1:A:272:ILE:N	2.84	0.40
1:B:322:LYS:HD2	2:B:695:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:ILE:HD13	1:B:56:ILE:HA	1.86	0.40
1:A:136:SER:HB2	1:A:189:PRO:HG3	2.04	0.40
1:A:74:LYS:HG2	1:A:125:TYR:O	2.21	0.40
1:A:190:PRO:HG2	1:A:194:ASP:CG	2.40	0.40
1:A:73:THR:HG21	1:A:125:TYR:CE1	2.56	0.40
1:A:251:THR:N	1:A:254:ASP:OD2	2.54	0.40
1:A:245:MET:O	1:A:348:GLY:HA2	2.21	0.40
1:A:307:LEU:HB3	1:A:313:LEU:HG	2.03	0.40
1:B:368:VAL:O	1:B:368:VAL:CG1	2.69	0.40
1:A:195:VAL:HG13	1:A:196:PHE:N	2.36	0.40
1:B:93:MET:SD	1:B:99:LYS:HE3	2.61	0.40
1:B:266:LYS:CB	2:B:598:HOH:O	2.60	0.40
1:B:261:ILE:CD1	1:B:270:LEU:HB2	2.51	0.40
1:A:200:MET:HA	1:A:205:LEU:HB3	2.02	0.40
1:B:313:LEU:HB2	2:B:560:HOH:O	2.22	0.40
1:B:418:GLU:HB2	1:B:437:LYS:HG2	2.03	0.40
1:B:358:PRO:HB2	1:B:360:LYS:CE	2.51	0.40
1:A:95:CYS:SG	1:A:403:VAL:HB	2.61	0.40
1:A:119:GLU:HA	1:A:154:ASN:O	2.21	0.40
1:A:208:PHE:O	1:A:213:LYS:HB2	2.22	0.40
1:A:104:VAL:O	1:A:369:GLN:HG2	2.21	0.40
1:B:60:TYR:N	1:B:350:ASN:O	2.54	0.40
1:B:247:VAL:HB	1:B:291:ILE:HD13	2.03	0.40
1:B:289:PHE:CB	2:B:588:HOH:O	2.68	0.40
1:A:366:LEU:HB2	1:A:406:PHE:HZ	1.86	0.40
1:B:48:LYS:CB	1:B:48:LYS:NZ	2.85	0.40
1:A:204:LYS:O	1:A:207:THR:HB	2.22	0.40
1:A:314:LYS:CD	2:A:563:HOH:O	2.68	0.40
1:A:441:THR:HB	1:A:462:ASN:OD1	2.21	0.40
1:B:32:LEU:CG	2:B:683:HOH:O	2.69	0.40
1:A:16:ASP:HA	1:A:26:LYS:CD	2.47	0.40
1:A:258:GLY:HA2	1:A:271:GLU:HA	2.03	0.40
1:A:35:ARG:HE	1:A:314:LYS:HE2	1.87	0.40
1:B:85:LEU:O	1:B:221:SER:HB3	2.21	0.40
1:B:84:LYS:CE	2:B:471:HOH:O	2.69	0.40
1:B:362:SER:HB2	1:B:406:PHE:CG	2.56	0.40
1:A:108:LEU:HD12	1:A:375:LEU:CD2	2.52	0.40
1:B:115:VAL:HB	1:B:150:TYR:CE1	2.56	0.40
1:A:177:PRO:C	1:A:179:LYS:H	2.25	0.40
1:B:306:LYS:CE	2:B:561:HOH:O	2.69	0.40
1:A:415:SER:H	1:A:435:VAL:HA	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:263:TYR:HB3	1:B:268:GLN:CD	2.41	0.40
1:A:280:VAL:O	1:A:283:PHE:HB3	2.21	0.40
1:B:243:TYR:HE2	1:B:297:LEU:HD22	1.86	0.40
1:B:320:ASN:N	1:B:331:GLN:O	2.54	0.40
1:B:239:ASN:O	1:B:240:LYS:O	2.39	0.40
1:B:31:SER:O	1:B:34:SER:HB2	2.21	0.40
1:A:224:LEU:HD12	1:A:368:VAL:HG11	2.04	0.40
1:B:254:ASP:CG	1:B:353:ARG:HH12	2.23	0.40
1:A:263:TYR:CE2	1:A:264:GLU:HG3	2.56	0.40
1:B:122:ASN:OD1	1:B:129:VAL:N	2.45	0.40
1:A:86:ASN:OD1	2:A:477:HOH:O	2.22	0.40
1:A:105:ARG:NH1	1:A:105:ARG:HG3	2.33	0.40
1:B:337:GLY:CA	2:B:474:HOH:O	2.67	0.40
1:A:10:GLN:O	1:A:10:GLN:HG3	2.20	0.40
1:B:75:ASN:O	1:B:79:LYS:HG3	2.21	0.40
1:B:227:ILE:CD1	2:B:535:HOH:O	2.68	0.40
1:B:150:TYR:HB3	1:B:153:SER:HB2	2.03	0.40
1:B:85:LEU:HB2	1:B:220:ASN:HA	2.03	0.40
1:A:259:THR:HG23	1:A:261:ILE:HG23	2.03	0.40
1:A:468:ASP:O	1:A:469:LEU:O	2.40	0.40
1:B:374:THR:OG1	2:B:645:HOH:O	2.22	0.40
1:B:355:ARG:HG2	1:B:355:ARG:HH21	1.86	0.40
1:A:261:ILE:O	1:A:267:VAL:CG2	2.69	0.40
1:A:169:VAL:HG12	1:A:171:ASP:OD1	2.21	0.40
1:A:109:THR:O	1:A:110:PHE:C	2.60	0.40
1:B:396:LEU:HD23	1:B:424:VAL:HB	2.02	0.40
1:A:209:LEU:HA	1:A:209:LEU:HD12	1.95	0.40
1:A:100:SER:HA	1:A:110:PHE:CD2	2.56	0.40
1:B:146:ILE:O	1:B:149:LYS:HG2	2.21	0.40
1:B:56:ILE:HD13	1:B:56:ILE:HA	1.77	0.40
1:A:35:ARG:HG3	1:A:314:LYS:CE	2.51	0.40
1:A:466:PRO:C	1:A:468:ASP:H	2.24	0.40
1:A:118:ILE:HA	1:A:121:LEU:HD12	2.02	0.40
1:A:122:ASN:O	1:A:126:GLY:N	2.52	0.40
1:A:316:GLU:CD	1:A:316:GLU:H	2.24	0.40
1:A:439:LYS:HE3	1:A:462:ASN:CG	2.41	0.40
1:A:35:ARG:O	1:A:38:SER:N	2.55	0.40
1:A:260:LEU:HD23	1:A:269:LEU:HA	2.03	0.40
1:B:192:HIS:CE1	1:B:335:ALA:HA	2.57	0.40
1:B:277:ASP:HA	1:B:280:VAL:HG23	2.04	0.40
1:B:259:THR:O	1:B:269:LEU:HD12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:ASN:ND2	1:A:345:ASN:ND2	2.69	0.40
1:B:105:ARG:O	1:B:106:ASP:HB2	2.22	0.40
1:B:227:ILE:HD11	2:B:636:HOH:O	2.20	0.40
1:B:63:MET:HE3	1:B:349:VAL:CG2	2.51	0.40
1:A:450:LEU:CD2	1:A:466:PRO:HD3	2.51	0.40
1:A:104:VAL:HG21	1:A:224:LEU:HD11	2.02	0.40
1:A:20:GLU:HG3	1:A:164:LYS:HZ3	1.86	0.40
1:A:388:ASN:HA	1:A:389:PRO:HD3	1.91	0.40
1:B:93:MET:HB3	1:B:403:VAL:HG23	2.03	0.40
1:A:104:VAL:CG1	1:A:105:ARG:H	2.32	0.40
1:A:337:GLY:O	1:A:340:ILE:HG22	2.21	0.40
1:B:189:PRO:HG2	1:B:189:PRO:O	2.21	0.40
1:B:315:MET:CB	1:B:334:THR:HB	2.51	0.40
1:B:303:ALA:O	1:B:307:LEU:HG	2.21	0.40
1:B:351:VAL:HB	1:B:352:PRO:HD2	2.02	0.40
1:A:388:ASN:HA	1:A:389:PRO:HD3	1.92	0.40
1:B:287:GLU:O	1:B:290:LYS:NZ	2.37	0.40
1:B:151:THR:C	1:B:152:ASN:HD22	2.24	0.40
1:B:400:PHE:O	1:B:406:PHE:HB2	2.22	0.40
1:B:227:ILE:CG1	1:B:355:ARG:NH2	2.82	0.40
1:B:250:LYS:HE2	1:B:254:ASP:O	2.22	0.40
1:B:101:VAL:CG2	2:B:512:HOH:O	2.68	0.40
1:A:439:LYS:O	1:A:460:ASN:HA	2.22	0.40
1:B:419:LEU:HD13	1:B:436:LEU:HB2	2.03	0.40
1:B:200:MET:HA	1:B:205:LEU:HB2	2.04	0.40
1:B:137:PHE:CE1	1:B:138:ASN:OD1	2.75	0.40
1:A:200:MET:CG	1:A:205:LEU:HD23	2.34	0.40
1:B:66:VAL:HG13	1:B:72:GLU:CG	2.51	0.40
1:A:452:ILE:HD12	1:A:452:ILE:N	2.36	0.40
1:A:159:THR:O	1:A:160:PHE:HB3	2.21	0.40
1:A:245:MET:HE1	1:A:269:LEU:HD22	2.02	0.40
1:B:413:ILE:HA	1:B:414:PRO:HD3	1.91	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	1-A	456/469 (97%)	399 (88%)	48 (10%)	9 (2%)	9	2
1	1-B	451/469 (96%)	408 (90%)	38 (8%)	5 (1%)	17	5
1	2-A	456/469 (97%)	407 (89%)	44 (10%)	5 (1%)	17	5
1	2-B	451/469 (96%)	405 (90%)	38 (8%)	8 (2%)	11	2
1	3-A	456/469 (97%)	415 (91%)	33 (7%)	8 (2%)	11	2
1	3-B	451/469 (96%)	410 (91%)	34 (8%)	7 (2%)	12	3
1	4-A	456/469 (97%)	403 (88%)	42 (9%)	11 (2%)	7	1
1	4-B	451/469 (96%)	411 (91%)	33 (7%)	7 (2%)	12	3
1	5-A	456/469 (97%)	406 (89%)	37 (8%)	13 (3%)	6	0
1	5-B	451/469 (96%)	406 (90%)	41 (9%)	4 (1%)	21	7
1	6-A	456/469 (97%)	402 (88%)	48 (10%)	6 (1%)	15	3
1	6-B	451/469 (96%)	399 (88%)	40 (9%)	12 (3%)	6	1
1	7-A	456/469 (97%)	415 (91%)	34 (8%)	7 (2%)	13	3
1	7-B	451/469 (96%)	407 (90%)	38 (8%)	6 (1%)	15	3
1	8-A	456/469 (97%)	403 (88%)	46 (10%)	7 (2%)	13	3
1	8-B	451/469 (96%)	409 (91%)	34 (8%)	8 (2%)	11	2
All	All	7256/7504 (97%)	6505 (90%)	628 (9%)	123 (2%)	11	2

All (123) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	8	LEU
1	1-B	170	ALA
1	3-A	38	SER
1	3-A	319	PRO
1	3-B	96	THR
1	3-B	97	GLY
1	4-A	8	LEU
1	4-A	220	ASN
1	4-B	255	VAL
1	4-B	295	ASN
1	4-B	460	ASN
1	5-A	403	VAL

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Mol	Chain	Res	Type
1	5-A	433	SER
1	6-B	67	SER
1	6-B	311	ASP
1	6-B	321	PRO
1	6-B	322	LYS
1	7-A	38	SER
1	7-B	266	LYS
1	8-A	8	LEU
1	8-B	170	ALA
1	8-B	264	GLU
1	1-B	78	ASP
1	2-A	170	ALA
1	2-B	96	THR
1	2-B	264	GLU
1	2-B	323	GLU
1	3-A	387	THR
1	3-B	178	SER
1	4-A	313	LEU
1	5-A	460	ASN
1	5-B	9	PRO
1	5-B	27	SER
1	5-B	313	LEU
1	6-A	277	ASP
1	6-A	431	GLY
1	6-B	31	SER
1	6-B	97	GLY
1	6-B	403	VAL
1	7-A	8	LEU
1	7-A	202	SER
1	7-A	445	LYS
1	7-A	460	ASN
1	7-B	155	VAL
1	7-B	403	VAL
1	8-A	340	ILE
1	1-A	47	SER
1	1-A	69	ASP
1	1-B	150	TYR
1	2-A	8	LEU
1	2-A	18	LEU
1	2-A	171	ASP
1	3-B	10	GLN
1	4-A	86	ASN

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Mol	Chain	Res	Type
1	4-B	97	GLY
1	5-A	8	LEU
1	5-A	122	ASN
1	5-A	170	ALA
1	5-A	184	LYS
1	5-A	238	GLN
1	5-A	435	VAL
1	6-A	178	SER
1	6-A	411	LYS
1	8-A	371	ASP
1	8-A	419	LEU
1	8-B	361	ALA
1	8-B	401	LYS
1	1-A	61	GLU
1	1-A	463	ILE
1	2-B	371	ASP
1	3-A	386	ARG
1	4-A	7	ASN
1	4-A	101	VAL
1	4-A	184	LYS
1	4-B	328	LYS
1	5-A	210	SER
1	5-B	83	LEU
1	6-A	320	ASN
1	6-B	144	HIS
1	6-B	190	PRO
1	6-B	312	ALA
1	6-B	320	ASN
1	7-A	399	GLU
1	7-B	255	VAL
1	8-A	105	ARG
1	8-B	97	GLY
1	1-A	10	GLN
1	1-A	319	PRO
1	1-B	97	GLY
1	1-B	168	VAL
1	2-A	191	GLY
1	2-B	61	GLU
1	2-B	163	SER
1	3-A	184	LYS
1	3-B	390	SER
1	4-A	295	ASN

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Mol	Chain	Res	Type
1	5-A	421	SER
1	8-A	160	PHE
1	8-B	151	THR
1	8-B	272	ILE
1	8-B	460	ASN
1	1-A	162	GLN
1	2-B	190	PRO
1	2-B	397	GLY
1	4-A	345	ASN
1	4-B	337	GLY
1	6-B	196	PHE
1	7-B	265	GLY
1	8-A	313	LEU
1	3-A	9	PRO
1	3-B	56	ILE
1	4-B	9	PRO
1	6-A	8	LEU
1	7-B	190	PRO
1	1-A	190	PRO
1	4-A	190	PRO
1	3-A	70	VAL
1	3-A	320	ASN
1	3-B	57	VAL
1	4-A	255	VAL
1	5-A	352	PRO
1	5-A	195	VAL
1	7-A	197	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	1-A	408/414 (99%)	394 (97%)	14 (3%)	44	24
1	1-B	404/414 (98%)	390 (96%)	14 (4%)	43	23
1	2-A	408/414 (99%)	389 (95%)	19 (5%)	32	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2-B	404/414 (98%)	392 (97%)	12 (3%)	48	29
1	3-A	408/414 (99%)	396 (97%)	12 (3%)	50	31
1	3-B	404/414 (98%)	389 (96%)	15 (4%)	41	20
1	4-A	408/414 (99%)	388 (95%)	20 (5%)	31	12
1	4-B	404/414 (98%)	392 (97%)	12 (3%)	48	29
1	5-A	408/414 (99%)	392 (96%)	16 (4%)	39	19
1	5-B	404/414 (98%)	385 (95%)	19 (5%)	32	13
1	6-A	408/414 (99%)	395 (97%)	13 (3%)	46	27
1	6-B	404/414 (98%)	389 (96%)	15 (4%)	41	20
1	7-A	408/414 (99%)	395 (97%)	13 (3%)	46	27
1	7-B	404/414 (98%)	385 (95%)	19 (5%)	32	13
1	8-A	408/414 (99%)	392 (96%)	16 (4%)	39	19
1	8-B	404/414 (98%)	391 (97%)	13 (3%)	46	27
All	All	6496/6624 (98%)	6254 (96%)	242 (4%)	41	20

All (242) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-A	142	ASP
1	1-A	163	SER
1	1-A	205	LEU
1	1-A	239	ASN
1	1-A	254	ASP
1	1-A	268	GLN
1	1-A	271	GLU
1	1-A	314	LYS
1	1-A	324	VAL
1	1-A	332	LEU
1	1-A	355	ARG
1	1-A	358	PRO
1	1-A	362	SER
1	1-A	384	LYS
1	1-B	13	SER
1	1-B	80	LEU
1	1-B	86	ASN
1	1-B	141	ASP
1	1-B	150	TYR

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Mol	Chain	Res	Type
1	1-B	171	ASP
1	1-B	176	TRP
1	1-B	200	MET
1	1-B	267	VAL
1	1-B	372	LEU
1	1-B	381	THR
1	1-B	446	SER
1	1-B	454	ASP
1	1-B	464	ASN
1	2-A	11	LEU
1	2-A	34	SER
1	2-A	81	VAL
1	2-A	99	LYS
1	2-A	104	VAL
1	2-A	173	PHE
1	2-A	187	TRP
1	2-A	192	HIS
1	2-A	200	MET
1	2-A	262	SER
1	2-A	266	LYS
1	2-A	281	ASN
1	2-A	288	LYS
1	2-A	295	ASN
1	2-A	317	ILE
1	2-A	332	LEU
1	2-A	384	LYS
1	2-A	430	PHE
1	2-A	439	LYS
1	2-B	58	VAL
1	2-B	147	VAL
1	2-B	148	GLU
1	2-B	155	VAL
1	2-B	167	ARG
1	2-B	220	ASN
1	2-B	223	ASN
1	2-B	315	MET
1	2-B	347	ILE
1	2-B	357	LEU
1	2-B	360	LYS
1	2-B	381	THR
1	3-A	10	GLN
1	3-A	31	SER

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Mol	Chain	Res	Type
1	3-A	81	VAL
1	3-A	92	THR
1	3-A	138	ASN
1	3-A	200	MET
1	3-A	209	LEU
1	3-A	271	GLU
1	3-A	314	LYS
1	3-A	330	LEU
1	3-A	332	LEU
1	3-A	450	LEU
1	3-B	8	LEU
1	3-B	27	SER
1	3-B	74	LYS
1	3-B	135	ASN
1	3-B	148	GLU
1	3-B	188	TYR
1	3-B	244	CYS
1	3-B	247	VAL
1	3-B	293	ASN
1	3-B	295	ASN
1	3-B	330	LEU
1	3-B	341	ARG
1	3-B	372	LEU
1	3-B	381	THR
1	3-B	387	THR
1	4-A	24	SER
1	4-A	69	ASP
1	4-A	81	VAL
1	4-A	141	ASP
1	4-A	155	VAL
1	4-A	205	LEU
1	4-A	209	LEU
1	4-A	222	ASP
1	4-A	267	VAL
1	4-A	278	GLU
1	4-A	288	LYS
1	4-A	295	ASN
1	4-A	314	LYS
1	4-A	316	GLU
1	4-A	344	ASP
1	4-A	355	ARG
1	4-A	384	LYS

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Mol	Chain	Res	Type
1	4-A	415	SER
1	4-A	417	VAL
1	4-A	427	ASP
1	4-B	8	LEU
1	4-B	148	GLU
1	4-B	156	ASP
1	4-B	192	HIS
1	4-B	210	SER
1	4-B	249	PRO
1	4-B	268	GLN
1	4-B	288	LYS
1	4-B	357	LEU
1	4-B	360	LYS
1	4-B	362	SER
1	4-B	366	LEU
1	5-A	8	LEU
1	5-A	16	ASP
1	5-A	32	LEU
1	5-A	55	GLU
1	5-A	81	VAL
1	5-A	205	LEU
1	5-A	243	TYR
1	5-A	248	THR
1	5-A	295	ASN
1	5-A	314	LYS
1	5-A	332	LEU
1	5-A	350	ASN
1	5-A	355	ARG
1	5-A	377	ASP
1	5-A	454	ASP
1	5-A	455	ARG
1	5-B	27	SER
1	5-B	52	PRO
1	5-B	78	ASP
1	5-B	79	LYS
1	5-B	105	ARG
1	5-B	145	LYS
1	5-B	148	GLU
1	5-B	158	HIS
1	5-B	171	ASP
1	5-B	220	ASN
1	5-B	243	TYR

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Mol	Chain	Res	Type
1	5-B	245	MET
1	5-B	254	ASP
1	5-B	297	LEU
1	5-B	360	LYS
1	5-B	387	THR
1	5-B	432	SER
1	5-B	441	THR
1	5-B	450	LEU
1	6-A	81	VAL
1	6-A	111	LEU
1	6-A	192	HIS
1	6-A	205	LEU
1	6-A	209	LEU
1	6-A	266	LYS
1	6-A	272	ILE
1	6-A	314	LYS
1	6-A	320	ASN
1	6-A	332	LEU
1	6-A	345	ASN
1	6-A	355	ARG
1	6-A	384	LYS
1	6-B	69	ASP
1	6-B	101	VAL
1	6-B	105	ARG
1	6-B	111	LEU
1	6-B	179	LYS
1	6-B	192	HIS
1	6-B	227	ILE
1	6-B	295	ASN
1	6-B	299	VAL
1	6-B	347	ILE
1	6-B	357	LEU
1	6-B	360	LYS
1	6-B	365	LEU
1	6-B	382	ARG
1	6-B	408	SER
1	7-A	45	GLU
1	7-A	92	THR
1	7-A	155	VAL
1	7-A	174	VAL
1	7-A	200	MET
1	7-A	243	TYR

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Mol	Chain	Res	Type
1	7-A	266	LYS
1	7-A	330	LEU
1	7-A	332	LEU
1	7-A	375	LEU
1	7-A	384	LYS
1	7-A	420	ASP
1	7-A	455	ARG
1	7-B	27	SER
1	7-B	51	THR
1	7-B	54	ASP
1	7-B	105	ARG
1	7-B	141	ASP
1	7-B	148	GLU
1	7-B	164	LYS
1	7-B	171	ASP
1	7-B	179	LYS
1	7-B	183	ASP
1	7-B	200	MET
1	7-B	268	GLN
1	7-B	272	ILE
1	7-B	281	ASN
1	7-B	284	LYS
1	7-B	287	GLU
1	7-B	345	ASN
1	7-B	347	ILE
1	7-B	467	GLU
1	8-A	31	SER
1	8-A	55	GLU
1	8-A	81	VAL
1	8-A	92	THR
1	8-A	105	ARG
1	8-A	111	LEU
1	8-A	209	LEU
1	8-A	243	TYR
1	8-A	244	CYS
1	8-A	266	LYS
1	8-A	314	LYS
1	8-A	330	LEU
1	8-A	362	SER
1	8-A	374	THR
1	8-A	384	LYS
1	8-A	421	SER

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Mol	Chain	Res	Type
1	8-B	45	GLU
1	8-B	105	ARG
1	8-B	141	ASP
1	8-B	223	ASN
1	8-B	236	LEU
1	8-B	288	LYS
1	8-B	293	ASN
1	8-B	357	LEU
1	8-B	360	LYS
1	8-B	362	SER
1	8-B	372	LEU
1	8-B	375	LEU
1	8-B	381	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (126) such sidechains are listed below:

Mol	Chain	Res	Type
1	1-A	75	ASN
1	1-A	138	ASN
1	1-A	162	GLN
1	1-A	239	ASN
1	1-A	345	ASN
1	1-A	464	ASN
1	1-B	75	ASN
1	1-B	86	ASN
1	1-B	120	ASN
1	1-B	135	ASN
1	1-B	138	ASN
1	1-B	152	ASN
1	1-B	162	GLN
1	1-B	220	ASN
1	1-B	268	GLN
1	1-B	464	ASN
1	2-A	50	GLN
1	2-A	138	ASN
1	2-A	158	HIS
1	2-A	238	GLN
1	2-A	241	ASN
1	2-A	268	GLN
1	2-A	279	HIS
1	2-B	50	GLN
1	2-B	138	ASN

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Mol	Chain	Res	Type
1	2-B	152	ASN
1	2-B	154	ASN
1	2-B	162	GLN
1	2-B	220	ASN
1	2-B	235	HIS
1	2-B	239	ASN
1	2-B	279	HIS
1	2-B	296	ASN
1	2-B	345	ASN
1	3-A	10	GLN
1	3-A	50	GLN
1	3-A	68	GLN
1	3-A	75	ASN
1	3-A	138	ASN
1	3-A	158	HIS
1	3-A	268	GLN
1	3-A	296	ASN
1	3-A	345	ASN
1	3-A	460	ASN
1	3-B	10	GLN
1	3-B	50	GLN
1	3-B	75	ASN
1	3-B	120	ASN
1	3-B	138	ASN
1	3-B	152	ASN
1	3-B	162	GLN
1	3-B	220	ASN
1	3-B	268	GLN
1	3-B	293	ASN
1	3-B	295	ASN
1	4-A	68	GLN
1	4-A	75	ASN
1	4-A	117	GLN
1	4-A	120	ASN
1	4-A	138	ASN
1	4-A	158	HIS
1	4-A	239	ASN
1	4-A	268	GLN
1	4-A	279	HIS
1	4-A	320	ASN
1	4-A	345	ASN
1	4-A	460	ASN

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Mol	Chain	Res	Type
1	4-B	10	GLN
1	4-B	50	GLN
1	4-B	75	ASN
1	4-B	138	ASN
1	4-B	140	HIS
1	4-B	152	ASN
1	4-B	235	HIS
1	4-B	268	GLN
1	4-B	279	HIS
1	5-A	50	GLN
1	5-A	68	GLN
1	5-A	75	ASN
1	5-A	158	HIS
1	5-A	238	GLN
1	5-A	295	ASN
1	5-B	50	GLN
1	5-B	68	GLN
1	5-B	152	ASN
1	5-B	162	GLN
1	5-B	220	ASN
1	5-B	350	ASN
1	6-A	50	GLN
1	6-A	162	GLN
1	6-A	239	ASN
1	6-A	268	GLN
1	6-A	331	GLN
1	6-A	345	ASN
1	6-A	369	GLN
1	6-A	460	ASN
1	6-B	50	GLN
1	6-B	75	ASN
1	6-B	138	ASN
1	6-B	152	ASN
1	6-B	235	HIS
1	6-B	295	ASN
1	7-A	50	GLN
1	7-A	68	GLN
1	7-A	75	ASN
1	7-A	120	ASN
1	7-A	162	GLN
1	7-A	268	GLN
1	7-A	462	ASN

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Mol	Chain	Res	Type
1	7-B	75	ASN
1	7-B	152	ASN
1	7-B	220	ASN
1	7-B	268	GLN
1	8-A	138	ASN
1	8-A	158	HIS
1	8-A	162	GLN
1	8-A	238	GLN
1	8-A	320	ASN
1	8-A	460	ASN
1	8-B	50	GLN
1	8-B	138	ASN
1	8-B	152	ASN
1	8-B	162	GLN
1	8-B	220	ASN
1	8-B	293	ASN
1	8-B	295	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	1-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
1	2-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	2-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
1	3-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	3-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
1	4-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	4-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
1	5-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	5-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
1	6-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	6-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
1	7-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	7-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
1	8-A	460/469 (98%)	0.66	55 (11%) 6 6	9, 24, 48, 69	460 (100%)
1	8-B	455/469 (97%)	0.14	25 (5%) 29 27	3, 17, 39, 55	455 (100%)
All	All	7320/7504 (97%)	0.40	640 (8%) 12 12	3, 21, 47, 69	7320 (100%)

All (640) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	387	THR	7.6
1	2-A	387	THR	7.6
1	3-A	387	THR	7.6
1	4-A	387	THR	7.6
1	5-A	387	THR	7.6

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Mol	Chain	Res	Type	RSRZ
1	6-A	387	THR	7.6
1	7-A	387	THR	7.6
1	8-A	387	THR	7.6
1	1-A	8	LEU	7.6
1	2-A	8	LEU	7.6
1	3-A	8	LEU	7.6
1	4-A	8	LEU	7.6
1	5-A	8	LEU	7.6
1	6-A	8	LEU	7.6
1	7-A	8	LEU	7.6
1	8-A	8	LEU	7.6
1	1-A	7	ASN	7.1
1	2-A	7	ASN	7.1
1	3-A	7	ASN	7.1
1	4-A	7	ASN	7.1
1	5-A	7	ASN	7.1
1	6-A	7	ASN	7.1
1	7-A	7	ASN	7.1
1	8-A	7	ASN	7.1
1	1-A	68	GLN	6.7
1	2-A	68	GLN	6.7
1	3-A	68	GLN	6.7
1	4-A	68	GLN	6.7
1	5-A	68	GLN	6.7
1	6-A	68	GLN	6.7
1	7-A	68	GLN	6.7
1	8-A	68	GLN	6.7
1	1-A	44	ILE	6.7
1	2-A	44	ILE	6.7
1	3-A	44	ILE	6.7
1	4-A	44	ILE	6.7
1	5-A	44	ILE	6.7
1	6-A	44	ILE	6.7
1	7-A	44	ILE	6.7
1	8-A	44	ILE	6.7
1	1-A	384	LYS	6.3
1	2-A	384	LYS	6.3
1	3-A	384	LYS	6.3
1	4-A	384	LYS	6.3
1	5-A	384	LYS	6.3
1	6-A	384	LYS	6.3
1	7-A	384	LYS	6.3

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Mol	Chain	Res	Type	RSRZ
1	8-A	384	LYS	6.3
1	1-A	287	GLU	6.3
1	2-A	287	GLU	6.3
1	3-A	287	GLU	6.3
1	4-A	287	GLU	6.3
1	5-A	287	GLU	6.3
1	6-A	287	GLU	6.3
1	7-A	287	GLU	6.3
1	8-A	287	GLU	6.3
1	1-A	385	ALA	6.1
1	2-A	385	ALA	6.1
1	3-A	385	ALA	6.1
1	4-A	385	ALA	6.1
1	5-A	385	ALA	6.1
1	6-A	385	ALA	6.1
1	7-A	385	ALA	6.1
1	8-A	385	ALA	6.1
1	1-A	388	ASN	5.9
1	2-A	388	ASN	5.9
1	3-A	388	ASN	5.9
1	4-A	388	ASN	5.9
1	5-A	388	ASN	5.9
1	6-A	388	ASN	5.9
1	7-A	388	ASN	5.9
1	8-A	388	ASN	5.9
1	1-A	55	GLU	5.7
1	2-A	55	GLU	5.7
1	3-A	55	GLU	5.7
1	4-A	55	GLU	5.7
1	5-A	55	GLU	5.7
1	6-A	55	GLU	5.7
1	7-A	55	GLU	5.7
1	8-A	55	GLU	5.7
1	1-A	371	ASP	5.3
1	2-A	371	ASP	5.3
1	3-A	371	ASP	5.3
1	4-A	371	ASP	5.3
1	5-A	371	ASP	5.3
1	6-A	371	ASP	5.3
1	7-A	371	ASP	5.3
1	8-A	371	ASP	5.3
1	1-A	389	PRO	4.9

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Mol	Chain	Res	Type	RSRZ
1	2-A	389	PRO	4.9
1	3-A	389	PRO	4.9
1	4-A	389	PRO	4.9
1	5-A	389	PRO	4.9
1	6-A	389	PRO	4.9
1	7-A	389	PRO	4.9
1	8-A	389	PRO	4.9
1	1-A	288	LYS	4.9
1	2-A	288	LYS	4.9
1	3-A	288	LYS	4.9
1	4-A	288	LYS	4.9
1	5-A	288	LYS	4.9
1	6-A	288	LYS	4.9
1	7-A	288	LYS	4.9
1	8-A	288	LYS	4.9
1	1-A	70	VAL	4.4
1	2-A	70	VAL	4.4
1	3-A	70	VAL	4.4
1	4-A	70	VAL	4.4
1	5-A	70	VAL	4.4
1	6-A	70	VAL	4.4
1	7-A	70	VAL	4.4
1	8-A	70	VAL	4.4
1	1-B	9	PRO	4.4
1	2-B	9	PRO	4.4
1	3-B	9	PRO	4.4
1	4-B	9	PRO	4.4
1	5-B	9	PRO	4.4
1	6-B	9	PRO	4.4
1	7-B	9	PRO	4.4
1	8-B	9	PRO	4.4
1	1-A	285	SER	4.2
1	2-A	285	SER	4.2
1	3-A	285	SER	4.2
1	4-A	285	SER	4.2
1	5-A	285	SER	4.2
1	6-A	285	SER	4.2
1	7-A	285	SER	4.2
1	8-A	285	SER	4.2
1	1-B	151	THR	4.0
1	2-B	151	THR	4.0
1	3-B	151	THR	4.0

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Mol	Chain	Res	Type	RSRZ
1	4-B	151	THR	4.0
1	5-B	151	THR	4.0
1	6-B	151	THR	4.0
1	7-B	151	THR	4.0
1	8-B	151	THR	4.0
1	1-A	123	ASN	3.9
1	2-A	123	ASN	3.9
1	3-A	123	ASN	3.9
1	4-A	123	ASN	3.9
1	5-A	123	ASN	3.9
1	6-A	123	ASN	3.9
1	7-A	123	ASN	3.9
1	8-A	123	ASN	3.9
1	1-A	69	ASP	3.9
1	2-A	69	ASP	3.9
1	3-A	69	ASP	3.9
1	4-A	69	ASP	3.9
1	5-A	69	ASP	3.9
1	6-A	69	ASP	3.9
1	7-A	69	ASP	3.9
1	8-A	69	ASP	3.9
1	1-B	325	ASP	3.8
1	2-B	325	ASP	3.8
1	3-B	325	ASP	3.8
1	4-B	325	ASP	3.8
1	5-B	325	ASP	3.8
1	6-B	325	ASP	3.8
1	7-B	325	ASP	3.8
1	8-B	325	ASP	3.8
1	1-A	277	ASP	3.7
1	1-B	141	ASP	3.7
1	2-A	277	ASP	3.7
1	2-B	141	ASP	3.7
1	3-A	277	ASP	3.7
1	3-B	141	ASP	3.7
1	4-A	277	ASP	3.7
1	4-B	141	ASP	3.7
1	5-A	277	ASP	3.7
1	5-B	141	ASP	3.7
1	6-A	277	ASP	3.7
1	6-B	141	ASP	3.7
1	7-A	277	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	7-B	141	ASP	3.7
1	8-A	277	ASP	3.7
1	8-B	141	ASP	3.7
1	1-B	321	PRO	3.6
1	2-B	321	PRO	3.6
1	3-B	321	PRO	3.6
1	4-B	321	PRO	3.6
1	5-B	321	PRO	3.6
1	6-B	321	PRO	3.6
1	7-B	321	PRO	3.6
1	8-B	321	PRO	3.6
1	1-A	210	SER	3.5
1	2-A	210	SER	3.5
1	3-A	210	SER	3.5
1	4-A	210	SER	3.5
1	5-A	210	SER	3.5
1	6-A	210	SER	3.5
1	7-A	210	SER	3.5
1	8-A	210	SER	3.5
1	1-B	327	VAL	3.5
1	2-B	327	VAL	3.5
1	3-B	327	VAL	3.5
1	4-B	327	VAL	3.5
1	5-B	327	VAL	3.5
1	6-B	327	VAL	3.5
1	7-B	327	VAL	3.5
1	8-B	327	VAL	3.5
1	1-A	417	VAL	3.5
1	2-A	417	VAL	3.5
1	3-A	417	VAL	3.5
1	4-A	417	VAL	3.5
1	5-A	417	VAL	3.5
1	6-A	417	VAL	3.5
1	7-A	417	VAL	3.5
1	8-A	417	VAL	3.5
1	1-B	324	VAL	3.4
1	2-B	324	VAL	3.4
1	3-B	324	VAL	3.4
1	4-B	324	VAL	3.4
1	5-B	324	VAL	3.4
1	6-B	324	VAL	3.4
1	7-B	324	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
1	8-B	324	VAL	3.4
1	1-A	67	SER	3.4
1	2-A	67	SER	3.4
1	3-A	67	SER	3.4
1	4-A	67	SER	3.4
1	5-A	67	SER	3.4
1	6-A	67	SER	3.4
1	7-A	67	SER	3.4
1	8-A	67	SER	3.4
1	1-A	379	PHE	3.3
1	2-A	379	PHE	3.3
1	3-A	379	PHE	3.3
1	4-A	379	PHE	3.3
1	5-A	379	PHE	3.3
1	6-A	379	PHE	3.3
1	7-A	379	PHE	3.3
1	8-A	379	PHE	3.3
1	1-B	150	TYR	3.3
1	2-B	150	TYR	3.3
1	3-B	150	TYR	3.3
1	4-B	150	TYR	3.3
1	5-B	150	TYR	3.3
1	6-B	150	TYR	3.3
1	7-B	150	TYR	3.3
1	8-B	150	TYR	3.3
1	1-A	65	PRO	3.2
1	2-A	65	PRO	3.2
1	3-A	65	PRO	3.2
1	4-A	65	PRO	3.2
1	5-A	65	PRO	3.2
1	6-A	65	PRO	3.2
1	7-A	65	PRO	3.2
1	8-A	65	PRO	3.2
1	1-A	252	LEU	3.2
1	2-A	252	LEU	3.2
1	3-A	252	LEU	3.2
1	4-A	252	LEU	3.2
1	5-A	252	LEU	3.2
1	6-A	252	LEU	3.2
1	7-A	252	LEU	3.2
1	8-A	252	LEU	3.2
1	1-B	15	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	2-B	15	VAL	3.1
1	3-B	15	VAL	3.1
1	4-B	15	VAL	3.1
1	5-B	15	VAL	3.1
1	6-B	15	VAL	3.1
1	7-B	15	VAL	3.1
1	8-B	15	VAL	3.1
1	1-A	232	ILE	3.1
1	2-A	232	ILE	3.1
1	3-A	232	ILE	3.1
1	4-A	232	ILE	3.1
1	5-A	232	ILE	3.1
1	6-A	232	ILE	3.1
1	7-A	232	ILE	3.1
1	8-A	232	ILE	3.1
1	1-B	281	ASN	3.1
1	2-B	281	ASN	3.1
1	3-B	281	ASN	3.1
1	4-B	281	ASN	3.1
1	5-B	281	ASN	3.1
1	6-B	281	ASN	3.1
1	7-B	281	ASN	3.1
1	8-B	281	ASN	3.1
1	1-B	145	LYS	3.0
1	2-B	145	LYS	3.0
1	3-B	145	LYS	3.0
1	4-B	145	LYS	3.0
1	5-B	145	LYS	3.0
1	6-B	145	LYS	3.0
1	7-B	145	LYS	3.0
1	8-B	145	LYS	3.0
1	1-A	75	ASN	3.0
1	2-A	75	ASN	3.0
1	3-A	75	ASN	3.0
1	4-A	75	ASN	3.0
1	5-A	75	ASN	3.0
1	6-A	75	ASN	3.0
1	7-A	75	ASN	3.0
1	8-A	75	ASN	3.0
1	1-A	286	ILE	2.9
1	2-A	286	ILE	2.9
1	3-A	286	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	4-A	286	ILE	2.9
1	5-A	286	ILE	2.9
1	6-A	286	ILE	2.9
1	7-A	286	ILE	2.9
1	8-A	286	ILE	2.9
1	1-A	467	GLU	2.9
1	2-A	467	GLU	2.9
1	3-A	467	GLU	2.9
1	4-A	467	GLU	2.9
1	5-A	467	GLU	2.9
1	6-A	467	GLU	2.9
1	7-A	467	GLU	2.9
1	8-A	467	GLU	2.9
1	1-B	96	THR	2.9
1	2-B	96	THR	2.9
1	3-B	96	THR	2.9
1	4-B	96	THR	2.9
1	5-B	96	THR	2.9
1	6-B	96	THR	2.9
1	7-B	96	THR	2.9
1	8-B	96	THR	2.9
1	1-A	218	VAL	2.9
1	2-A	218	VAL	2.9
1	3-A	218	VAL	2.9
1	4-A	218	VAL	2.9
1	5-A	218	VAL	2.9
1	6-A	218	VAL	2.9
1	7-A	218	VAL	2.9
1	8-A	218	VAL	2.9
1	1-A	289	PHE	2.8
1	2-A	289	PHE	2.8
1	3-A	289	PHE	2.8
1	4-A	289	PHE	2.8
1	5-A	289	PHE	2.8
1	6-A	289	PHE	2.8
1	7-A	289	PHE	2.8
1	8-A	289	PHE	2.8
1	1-A	251	THR	2.8
1	2-A	251	THR	2.8
1	3-A	251	THR	2.8
1	4-A	251	THR	2.8
1	5-A	251	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	6-A	251	THR	2.8
1	7-A	251	THR	2.8
1	8-A	251	THR	2.8
1	1-B	17	GLY	2.8
1	2-B	17	GLY	2.8
1	3-B	17	GLY	2.8
1	4-B	17	GLY	2.8
1	5-B	17	GLY	2.8
1	6-B	17	GLY	2.8
1	7-B	17	GLY	2.8
1	8-B	17	GLY	2.8
1	1-A	390	SER	2.8
1	2-A	390	SER	2.8
1	3-A	390	SER	2.8
1	4-A	390	SER	2.8
1	5-A	390	SER	2.8
1	6-A	390	SER	2.8
1	7-A	390	SER	2.8
1	8-A	390	SER	2.8
1	1-A	6	GLU	2.7
1	2-A	6	GLU	2.7
1	3-A	6	GLU	2.7
1	4-A	6	GLU	2.7
1	5-A	6	GLU	2.7
1	6-A	6	GLU	2.7
1	7-A	6	GLU	2.7
1	8-A	6	GLU	2.7
1	1-B	173	PHE	2.7
1	2-B	173	PHE	2.7
1	3-B	173	PHE	2.7
1	4-B	173	PHE	2.7
1	5-B	173	PHE	2.7
1	6-B	173	PHE	2.7
1	7-B	173	PHE	2.7
1	8-B	173	PHE	2.7
1	1-A	61	GLU	2.6
1	2-A	61	GLU	2.6
1	3-A	61	GLU	2.6
1	4-A	61	GLU	2.6
1	5-A	61	GLU	2.6
1	6-A	61	GLU	2.6
1	7-A	61	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	8-A	61	GLU	2.6
1	1-B	171	ASP	2.6
1	2-B	171	ASP	2.6
1	3-B	171	ASP	2.6
1	4-B	171	ASP	2.6
1	5-B	171	ASP	2.6
1	6-B	171	ASP	2.6
1	7-B	171	ASP	2.6
1	8-B	171	ASP	2.6
1	1-A	416	ILE	2.6
1	2-A	416	ILE	2.6
1	3-A	416	ILE	2.6
1	4-A	416	ILE	2.6
1	5-A	416	ILE	2.6
1	6-A	416	ILE	2.6
1	7-A	416	ILE	2.6
1	8-A	416	ILE	2.6
1	1-B	13	SER	2.5
1	2-B	13	SER	2.5
1	3-B	13	SER	2.5
1	4-B	13	SER	2.5
1	5-B	13	SER	2.5
1	6-B	13	SER	2.5
1	7-B	13	SER	2.5
1	8-B	13	SER	2.5
1	1-A	59	PRO	2.5
1	2-A	59	PRO	2.5
1	3-A	59	PRO	2.5
1	4-A	59	PRO	2.5
1	5-A	59	PRO	2.5
1	6-A	59	PRO	2.5
1	7-A	59	PRO	2.5
1	8-A	59	PRO	2.5
1	1-A	374	THR	2.5
1	2-A	374	THR	2.5
1	3-A	374	THR	2.5
1	4-A	374	THR	2.5
1	5-A	374	THR	2.5
1	6-A	374	THR	2.5
1	7-A	374	THR	2.5
1	8-A	374	THR	2.5
1	1-A	83	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	2-A	83	LEU	2.5
1	3-A	83	LEU	2.5
1	4-A	83	LEU	2.5
1	5-A	83	LEU	2.5
1	6-A	83	LEU	2.5
1	7-A	83	LEU	2.5
1	8-A	83	LEU	2.5
1	1-B	170	ALA	2.4
1	2-B	170	ALA	2.4
1	3-B	170	ALA	2.4
1	4-B	170	ALA	2.4
1	5-B	170	ALA	2.4
1	6-B	170	ALA	2.4
1	7-B	170	ALA	2.4
1	8-B	170	ALA	2.4
1	1-A	62	LYS	2.4
1	2-A	62	LYS	2.4
1	3-A	62	LYS	2.4
1	4-A	62	LYS	2.4
1	5-A	62	LYS	2.4
1	6-A	62	LYS	2.4
1	7-A	62	LYS	2.4
1	8-A	62	LYS	2.4
1	1-B	8	LEU	2.4
1	2-B	8	LEU	2.4
1	3-B	8	LEU	2.4
1	4-B	8	LEU	2.4
1	5-B	8	LEU	2.4
1	6-B	8	LEU	2.4
1	7-B	8	LEU	2.4
1	8-B	8	LEU	2.4
1	1-A	415	SER	2.4
1	2-A	415	SER	2.4
1	3-A	415	SER	2.4
1	4-A	415	SER	2.4
1	5-A	415	SER	2.4
1	6-A	415	SER	2.4
1	7-A	415	SER	2.4
1	8-A	415	SER	2.4
1	1-A	11	LEU	2.3
1	2-A	11	LEU	2.3
1	3-A	11	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	4-A	11	LEU	2.3
1	5-A	11	LEU	2.3
1	6-A	11	LEU	2.3
1	7-A	11	LEU	2.3
1	8-A	11	LEU	2.3
1	1-A	381	THR	2.3
1	2-A	381	THR	2.3
1	3-A	381	THR	2.3
1	4-A	381	THR	2.3
1	5-A	381	THR	2.3
1	6-A	381	THR	2.3
1	7-A	381	THR	2.3
1	8-A	381	THR	2.3
1	1-A	281	ASN	2.3
1	2-A	281	ASN	2.3
1	3-A	281	ASN	2.3
1	4-A	281	ASN	2.3
1	5-A	281	ASN	2.3
1	6-A	281	ASN	2.3
1	7-A	281	ASN	2.3
1	8-A	281	ASN	2.3
1	1-A	63	MET	2.3
1	2-A	63	MET	2.3
1	3-A	63	MET	2.3
1	4-A	63	MET	2.3
1	5-A	63	MET	2.3
1	6-A	63	MET	2.3
1	7-A	63	MET	2.3
1	8-A	63	MET	2.3
1	1-A	297	LEU	2.3
1	2-A	297	LEU	2.3
1	3-A	297	LEU	2.3
1	4-A	297	LEU	2.3
1	5-A	297	LEU	2.3
1	6-A	297	LEU	2.3
1	7-A	297	LEU	2.3
1	8-A	297	LEU	2.3
1	1-A	71	ALA	2.3
1	2-A	71	ALA	2.3
1	3-A	71	ALA	2.3
1	4-A	71	ALA	2.3
1	5-A	71	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	6-A	71	ALA	2.3
1	7-A	71	ALA	2.3
1	8-A	71	ALA	2.3
1	1-A	419	LEU	2.3
1	2-A	419	LEU	2.3
1	3-A	419	LEU	2.3
1	4-A	419	LEU	2.3
1	5-A	419	LEU	2.3
1	6-A	419	LEU	2.3
1	7-A	419	LEU	2.3
1	8-A	419	LEU	2.3
1	1-A	383	ASN	2.3
1	2-A	383	ASN	2.3
1	3-A	383	ASN	2.3
1	4-A	383	ASN	2.3
1	5-A	383	ASN	2.3
1	6-A	383	ASN	2.3
1	7-A	383	ASN	2.3
1	8-A	383	ASN	2.3
1	1-A	10	GLN	2.2
1	2-A	10	GLN	2.2
1	3-A	10	GLN	2.2
1	4-A	10	GLN	2.2
1	5-A	10	GLN	2.2
1	6-A	10	GLN	2.2
1	7-A	10	GLN	2.2
1	8-A	10	GLN	2.2
1	1-A	469	LEU	2.2
1	1-B	11	LEU	2.2
1	2-A	469	LEU	2.2
1	2-B	11	LEU	2.2
1	3-A	469	LEU	2.2
1	3-B	11	LEU	2.2
1	4-A	469	LEU	2.2
1	4-B	11	LEU	2.2
1	5-A	469	LEU	2.2
1	5-B	11	LEU	2.2
1	6-A	469	LEU	2.2
1	6-B	11	LEU	2.2
1	7-A	469	LEU	2.2
1	7-B	11	LEU	2.2
1	8-A	469	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	8-B	11	LEU	2.2
1	1-B	144	HIS	2.2
1	2-B	144	HIS	2.2
1	3-B	144	HIS	2.2
1	4-B	144	HIS	2.2
1	5-B	144	HIS	2.2
1	6-B	144	HIS	2.2
1	7-B	144	HIS	2.2
1	8-B	144	HIS	2.2
1	1-A	276	PRO	2.2
1	2-A	276	PRO	2.2
1	3-A	276	PRO	2.2
1	4-A	276	PRO	2.2
1	5-A	276	PRO	2.2
1	6-A	276	PRO	2.2
1	7-A	276	PRO	2.2
1	8-A	276	PRO	2.2
1	1-A	171	ASP	2.2
1	2-A	171	ASP	2.2
1	3-A	171	ASP	2.2
1	4-A	171	ASP	2.2
1	5-A	171	ASP	2.2
1	6-A	171	ASP	2.2
1	7-A	171	ASP	2.2
1	8-A	171	ASP	2.2
1	1-B	35	ARG	2.2
1	2-B	35	ARG	2.2
1	3-B	35	ARG	2.2
1	4-B	35	ARG	2.2
1	5-B	35	ARG	2.2
1	6-B	35	ARG	2.2
1	7-B	35	ARG	2.2
1	8-B	35	ARG	2.2
1	1-B	20	GLU	2.1
1	2-B	20	GLU	2.1
1	3-B	20	GLU	2.1
1	4-B	20	GLU	2.1
1	5-B	20	GLU	2.1
1	6-B	20	GLU	2.1
1	7-B	20	GLU	2.1
1	8-B	20	GLU	2.1
1	1-B	272	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	2-B	272	ILE	2.1
1	3-B	272	ILE	2.1
1	4-B	272	ILE	2.1
1	5-B	272	ILE	2.1
1	6-B	272	ILE	2.1
1	7-B	272	ILE	2.1
1	8-B	272	ILE	2.1
1	1-A	128	LYS	2.1
1	2-A	128	LYS	2.1
1	3-A	128	LYS	2.1
1	4-A	128	LYS	2.1
1	5-A	128	LYS	2.1
1	6-A	128	LYS	2.1
1	7-A	128	LYS	2.1
1	8-A	128	LYS	2.1
1	1-A	46	TRP	2.1
1	1-B	46	TRP	2.1
1	2-A	46	TRP	2.1
1	2-B	46	TRP	2.1
1	3-A	46	TRP	2.1
1	3-B	46	TRP	2.1
1	4-A	46	TRP	2.1
1	4-B	46	TRP	2.1
1	5-A	46	TRP	2.1
1	5-B	46	TRP	2.1
1	6-A	46	TRP	2.1
1	6-B	46	TRP	2.1
1	7-A	46	TRP	2.1
1	7-B	46	TRP	2.1
1	8-A	46	TRP	2.1
1	8-B	46	TRP	2.1
1	1-A	236	LEU	2.0
1	2-A	236	LEU	2.0
1	3-A	236	LEU	2.0
1	4-A	236	LEU	2.0
1	5-A	236	LEU	2.0
1	6-A	236	LEU	2.0
1	7-A	236	LEU	2.0
1	8-A	236	LEU	2.0
1	1-B	10	GLN	2.0
1	2-B	10	GLN	2.0
1	3-B	10	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	4-B	10	GLN	2.0
1	5-B	10	GLN	2.0
1	6-B	10	GLN	2.0
1	7-B	10	GLN	2.0
1	8-B	10	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.