



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:08 PM UTC

PDB ID : 5WTJ / pdb_00005wtj
Title : Crystal structure of an endonuclease
Authors : Liu, L.; Wang, Y.
Deposited on : 2016-12-13
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

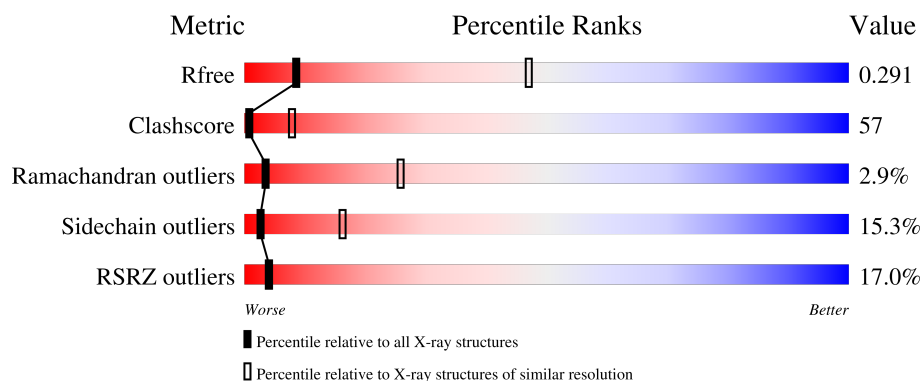
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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

Mol	Chain	Length	Quality of chain
1	A	1397	
1	B	1397	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15952 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 CRISPR-associated endoribonuclease C2c2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1019	Total	C	N	O	S	Se	0	0	0
			8013	5109	1350	1538	5	11			
1	B	1012	Total	C	N	O	S	Se	0	0	0
			7938	5055	1326	1541	6	10			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1390	LEU	-	expression tag	UNP P0DOC6
A	1391	GLU	-	expression tag	UNP P0DOC6
A	1392	HIS	-	expression tag	UNP P0DOC6
A	1393	HIS	-	expression tag	UNP P0DOC6
A	1394	HIS	-	expression tag	UNP P0DOC6
A	1395	HIS	-	expression tag	UNP P0DOC6
A	1396	HIS	-	expression tag	UNP P0DOC6
A	1397	HIS	-	expression tag	UNP P0DOC6
B	1390	LEU	-	expression tag	UNP P0DOC6
B	1391	GLU	-	expression tag	UNP P0DOC6
B	1392	HIS	-	expression tag	UNP P0DOC6
B	1393	HIS	-	expression tag	UNP P0DOC6
B	1394	HIS	-	expression tag	UNP P0DOC6
B	1395	HIS	-	expression tag	UNP P0DOC6
B	1396	HIS	-	expression tag	UNP P0DOC6
B	1397	HIS	-	expression tag	UNP P0DOC6

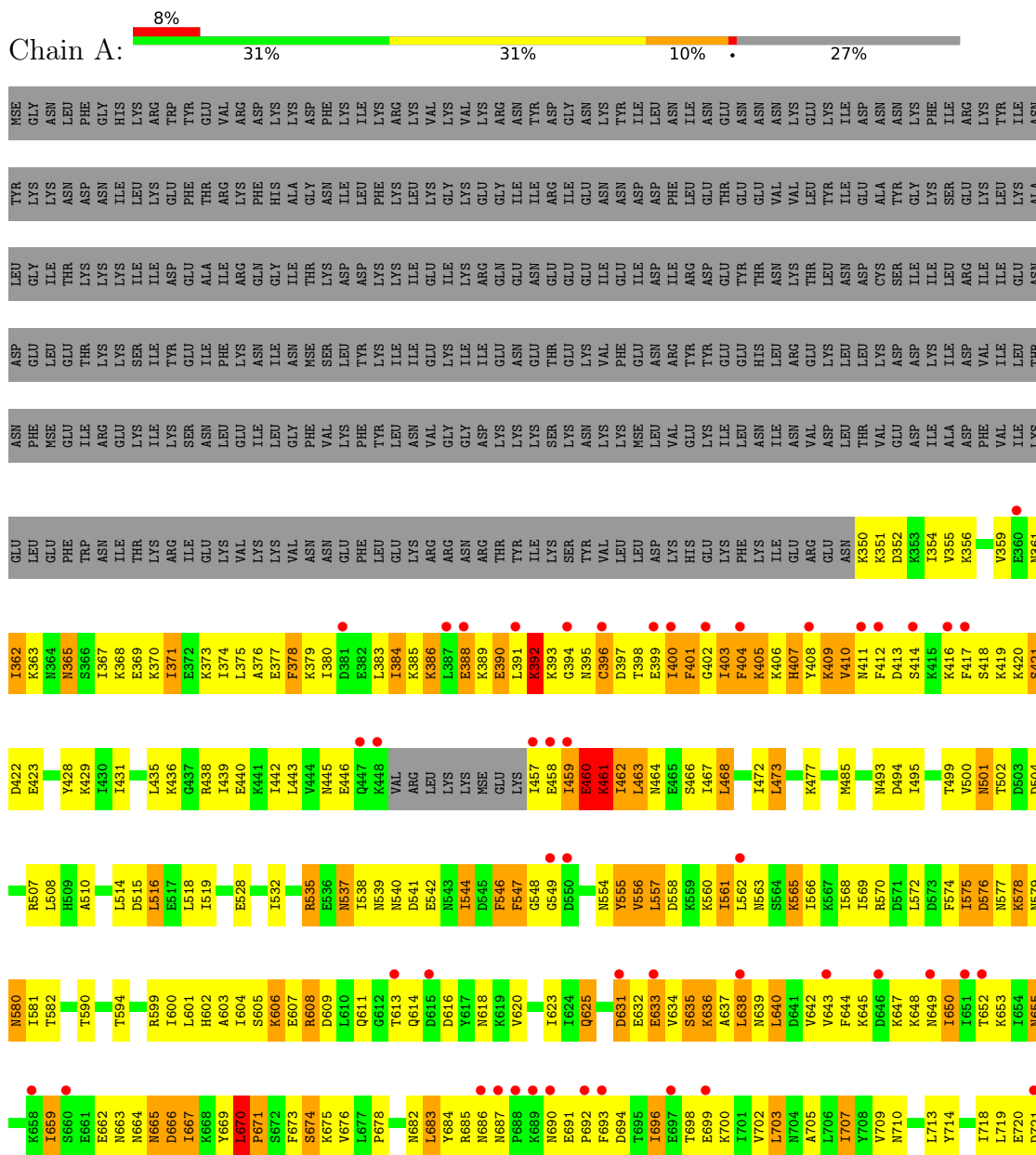
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	O	0	0
			1	1		

3 Residue-property plots

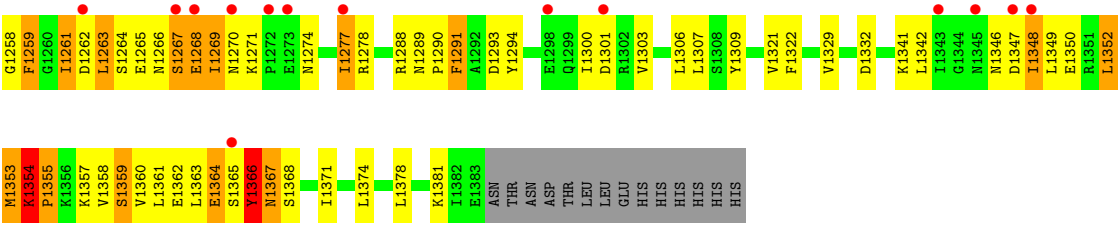
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: CRISPR-associated endoribonuclease C2c2









4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.66Å 94.23Å 338.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.38 – 3.50 48.38 – 3.50	Depositor EDS
% Data completeness (in resolution range)	81.0 (48.38-3.50) 81.0 (48.38-3.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.71 (at 3.48Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.263 , 0.291 0.262 , 0.291	Depositor DCC
R_{free} test set	1546 reflections (4.09%)	wwPDB-VP
Wilson B-factor (Å ²)	18.6	Xtriage
Anisotropy	0.648	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.053 for k,h,-l	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	15952	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.64	10/8117 (0.1%)	0.98	60/10925 (0.5%)
1	B	0.53	4/8038 (0.0%)	0.94	53/10824 (0.5%)
All	All	0.59	14/16155 (0.1%)	0.96	113/21749 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	7
All	All	0	9

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	687	ASN	C-N	7.79	1.40	1.33
1	A	896	TRP	CA-C	-6.25	1.44	1.52
1	B	607	GLU	C-O	-6.03	1.18	1.23
1	A	896	TRP	N-CA	-5.69	1.42	1.46
1	B	1354	LYS	C-N	5.55	1.40	1.33
1	A	670	LEU	C-N	5.41	1.40	1.33
1	A	671	PRO	N-CD	5.31	1.55	1.47
1	A	1272	PRO	N-CD	5.16	1.54	1.47
1	B	671	PRO	N-CD	5.16	1.54	1.47
1	A	1354	LYS	C-N	5.11	1.40	1.33
1	A	1355	PRO	N-CD	5.06	1.54	1.47
1	A	896	TRP	C-O	-5.05	1.19	1.23
1	B	1355	PRO	N-CD	5.02	1.54	1.47
1	A	893	THR	N-CA	-5.00	1.40	1.46

All (113) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	501	ASN	N-CA-C	13.72	125.75	111.07
1	B	634	VAL	CB-CA-C	-12.86	90.21	111.29
1	A	1358	VAL	N-CA-C	12.13	122.99	110.62
1	B	618	ASN	N-CA-C	-10.81	101.13	114.75
1	B	793	PHE	N-CA-C	10.55	122.86	111.36
1	B	1269	ILE	N-CA-C	10.30	121.12	110.72
1	B	635	SER	N-CA-C	-10.29	100.58	113.55
1	A	1356	LYS	CA-C-N	9.66	135.81	122.19
1	A	1356	LYS	C-N-CA	9.66	135.81	122.19
1	B	689	LYS	N-CA-C	9.65	121.80	111.28
1	B	825	THR	N-CA-C	9.56	121.78	111.36
1	A	462	ILE	N-CA-C	8.90	121.80	108.80
1	A	423	GLU	N-CA-C	8.74	120.81	111.28
1	A	602	HIS	N-CA-C	-8.52	99.54	110.53
1	A	578	LYS	N-CA-C	-8.51	100.94	112.94
1	B	809	ILE	CB-CA-C	-8.49	104.50	111.71
1	A	730	ASN	CA-C-N	8.45	132.16	120.49
1	A	730	ASN	C-N-CA	8.45	132.16	120.49
1	A	896	TRP	CB-CA-C	-8.45	104.21	116.54
1	A	868	THR	N-CA-C	8.33	124.00	112.93
1	B	411	ASN	N-CA-C	8.28	120.31	111.28
1	A	1054	ASN	N-CA-C	8.16	121.09	111.71
1	A	997	GLN	CB-CA-C	8.13	124.28	110.86
1	B	403	ILE	CB-CA-C	-7.82	98.46	111.29
1	A	576	ASP	N-CA-C	-7.78	96.05	108.73
1	B	792	LEU	N-CA-C	-7.04	103.60	111.28
1	A	409	LYS	N-CA-C	6.91	118.81	111.28
1	B	641	ASP	N-CA-C	6.89	118.79	111.28
1	A	392	LYS	N-CA-C	6.87	125.43	110.80
1	B	1354	LYS	CA-C-N	-6.86	112.69	119.76
1	B	1354	LYS	C-N-CA	-6.86	112.69	119.76
1	A	600	ILE	N-CA-C	6.79	116.91	110.53
1	A	388	GLU	N-CA-C	6.73	118.62	111.28
1	A	1013	ARG	N-CA-C	-6.68	101.13	110.35
1	B	605	SER	N-CA-C	6.64	119.23	108.41
1	B	551	ARG	N-CA-C	6.53	120.55	111.74
1	A	1354	LYS	CA-C-N	-6.51	113.06	119.76
1	A	1354	LYS	C-N-CA	-6.51	113.06	119.76
1	A	896	TRP	N-CA-C	-6.48	98.82	108.34
1	A	687	ASN	CA-C-N	-6.47	113.06	120.89
1	A	687	ASN	C-N-CA	-6.47	113.06	120.89
1	A	732	PHE	O-C-N	-6.46	114.66	122.22
1	B	644	PHE	N-CA-C	-6.42	104.28	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1357	LYS	N-CA-C	6.38	120.36	111.74
1	A	670	LEU	CA-C-N	-6.35	113.13	119.92
1	A	670	LEU	C-N-CA	-6.35	113.13	119.92
1	B	968	GLU	CA-C-N	6.26	130.71	122.51
1	B	968	GLU	C-N-CA	6.26	130.71	122.51
1	A	803	GLN	N-CA-C	-6.21	104.59	111.36
1	B	630	SER	CA-C-N	6.14	132.75	121.70
1	B	630	SER	C-N-CA	6.14	132.75	121.70
1	B	490	LEU	N-CA-C	-6.13	105.93	113.41
1	A	378	PHE	N-CA-C	6.13	118.04	111.36
1	A	730	ASN	CB-CA-C	6.05	122.47	110.42
1	B	847	ASN	N-CA-C	6.05	118.60	109.41
1	A	461	LYS	N-CA-C	6.03	123.65	110.80
1	B	381	ASP	N-CA-C	6.00	117.49	111.07
1	A	998	TYR	N-CA-C	6.00	121.27	111.37
1	B	460	GLU	N-CA-C	5.96	117.86	111.36
1	A	405	LYS	N-CA-C	-5.95	104.79	111.28
1	B	747	ASP	N-CA-C	5.91	122.08	113.40
1	A	995	VAL	CB-CA-C	-5.88	101.64	111.29
1	B	684	TYR	CA-C-N	5.88	132.29	121.70
1	B	684	TYR	C-N-CA	5.88	132.29	121.70
1	A	1275	GLU	N-CA-C	-5.86	104.97	111.36
1	B	441	LYS	N-CA-C	-5.84	104.92	111.28
1	A	636	LYS	CA-C-N	-5.82	113.53	122.60
1	A	636	LYS	C-N-CA	-5.82	113.53	122.60
1	B	1289	ASN	CA-C-N	-5.74	112.68	119.05
1	B	1289	ASN	C-N-CA	-5.74	112.68	119.05
1	A	1369	ASP	N-CA-C	5.65	117.52	111.36
1	A	696	ILE	N-CA-C	5.64	115.99	107.75
1	A	605	SER	N-CA-C	-5.60	99.39	108.52
1	B	664	ASN	N-CA-C	5.59	118.01	109.62
1	B	1258	GLY	N-CA-C	-5.57	106.04	112.73
1	B	559	LYS	CB-CA-C	-5.56	110.18	116.63
1	A	1153	GLU	N-CA-C	-5.56	105.22	111.28
1	B	846	LEU	N-CA-C	5.55	117.41	111.36
1	B	690	ASN	N-CA-C	5.54	117.84	110.53
1	B	1038	GLU	N-CA-CB	-5.52	101.92	110.04
1	B	393	LYS	N-CA-C	5.46	117.66	111.11
1	A	1272	PRO	CA-N-CD	-5.46	104.36	112.00
1	A	869	SER	N-CA-C	5.42	119.85	113.23
1	A	576	ASP	CB-CA-C	5.38	118.91	110.19
1	B	1096	GLY	N-CA-C	5.34	119.61	112.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	352	ASP	N-CA-C	-5.32	105.48	111.28
1	A	385	LYS	N-CA-C	-5.32	105.48	111.28
1	B	1288	ARG	N-CA-C	5.30	117.14	111.36
1	A	665	ASN	N-CA-C	5.28	118.87	111.74
1	B	676	VAL	N-CA-C	5.28	117.69	111.09
1	A	900	LEU	N-CA-C	5.26	117.48	110.53
1	A	1100	ARG	N-CA-C	5.22	117.05	111.36
1	B	1141	ALA	N-CA-C	5.20	117.62	111.33
1	A	818	TYR	N-CA-C	5.19	116.94	111.28
1	B	664	ASN	CA-C-N	-5.19	116.04	123.20
1	B	664	ASN	C-N-CA	-5.19	116.04	123.20
1	B	795	PHE	N-CA-C	5.19	116.85	108.34
1	A	1091	LEU	N-CA-C	5.18	117.01	111.36
1	A	826	SER	N-CA-C	-5.17	101.69	109.60
1	B	1079	ILE	N-CA-C	5.15	115.92	110.72
1	B	1084	LYS	N-CA-C	5.14	116.97	111.36
1	A	976	LEU	N-CA-C	-5.14	105.70	113.51
1	B	918	LYS	N-CA-C	5.13	115.94	108.14
1	A	913	ASP	N-CA-C	5.12	116.60	108.67
1	A	984	SER	N-CA-C	5.11	116.85	111.28
1	B	834	ASP	N-CA-C	-5.09	103.33	110.50
1	B	1291	PHE	N-CA-C	5.07	119.42	112.88
1	A	1356	LYS	O-C-N	-5.05	116.59	122.96
1	B	1077	GLY	N-CA-C	5.05	118.79	112.73
1	B	1047	TYR	N-CA-C	-5.04	100.07	110.80
1	A	816	LYS	N-CA-C	-5.04	103.40	110.50
1	A	1134	LYS	N-CA-C	5.03	119.41	113.12
1	A	997	GLN	N-CA-C	-5.02	104.76	111.24

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1051	GLU	Peptide
1	A	1356	LYS	Peptide
1	B	1091	LEU	Peptide
1	B	1129	TYR	Peptide
1	B	1268	GLU	Peptide
1	B	412	PHE	Peptide
1	B	605	SER	Peptide
1	B	644	PHE	Peptide
1	B	664	ASN	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8013	0	7662	857	3
1	B	7938	0	7580	910	1
2	A	1	0	0	0	0
All	All	15952	0	15242	1767	4

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 57.

All (1767) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:976:LEU:HD23	1:B:977:GLN:N	1.22	1.45
1:A:696:ILE:CB	1:A:699:GLU:HB3	1.55	1.35
1:B:817:THR:CG2	1:B:818:TYR:HA	1.54	1.35
1:B:914:PHE:HA	1:B:915:ASP:CB	1.47	1.34
1:B:914:PHE:CA	1:B:915:ASP:HB2	1.54	1.32
1:B:900:LEU:HD13	1:B:1056:LEU:CB	1.59	1.30
1:B:582:THR:CB	1:B:583:ASN:OD1	1.82	1.26
1:B:351:LYS:HE2	1:B:483:HIS:CE1	1.70	1.26
1:B:1049:PRO:HD2	1:B:1055:GLU:CB	1.65	1.26
1:A:1329:VAL:HG21	1:A:1353:MSE:CE	1.63	1.26
1:A:933:ILE:HG12	1:A:998:TYR:CD2	1.73	1.24
1:A:1118:LEU:HB3	1:A:1125:TYR:CZ	1.73	1.23
1:B:900:LEU:CD2	1:B:1056:LEU:HD12	1.68	1.22
1:A:732:PHE:HD1	1:A:784:TYR:CD2	1.55	1.22
1:A:1053:LYS:O	1:A:1055:GLU:HB3	1.37	1.22
1:A:560:LYS:O	1:A:561:ILE:HG12	1.36	1.21
1:B:533:PHE:CE1	1:B:557:LEU:HD11	1.74	1.21
1:B:634:VAL:HG21	1:B:891:CYS:SG	1.78	1.21
1:A:1118:LEU:HB3	1:A:1125:TYR:OH	1.40	1.20
1:A:570:ARG:HD3	1:A:577:ASN:OD1	1.40	1.20
1:B:481:LEU:HD23	1:B:1259:PHE:CE2	1.77	1.20
1:B:531:LYS:CB	1:B:562:LEU:HD11	1.73	1.19
1:B:671:PRO:HG3	1:B:774:GLN:NE2	1.54	1.18
1:A:418:SER:HB2	1:A:419:LYS:HA	1.26	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:ALA:HB2	1:A:770:ILE:HG13	1.19	1.17
1:A:501:ASN:O	1:A:502:THR:HG22	1.43	1.17
1:B:976:LEU:CD2	1:B:977:GLN:H	1.57	1.17
1:B:606:LYS:HD3	1:B:1219:THR:CG2	1.76	1.16
1:B:481:LEU:HD23	1:B:1259:PHE:CD2	1.81	1.16
1:A:1366:TYR:CD1	1:A:1367:ASN:HB2	1.81	1.15
1:A:561:ILE:HG22	1:A:562:LEU:HA	1.17	1.14
1:A:738:LYS:HE3	1:A:746:ILE:HD11	1.29	1.14
1:A:1053:LYS:C	1:A:1055:GLU:HB3	1.72	1.14
1:B:1047:TYR:HA	1:B:1057:TYR:HB3	1.20	1.14
1:A:404:PHE:CZ	1:A:439:ILE:HG21	1.81	1.14
1:B:582:THR:HB	1:B:583:ASN:CG	1.70	1.14
1:A:732:PHE:CD1	1:A:784:TYR:CD2	2.35	1.14
1:B:817:THR:HG22	1:B:818:TYR:HA	1.20	1.13
1:A:404:PHE:HE2	1:A:439:ILE:HG13	1.06	1.12
1:B:557:LEU:HD22	1:B:575:ILE:HD11	1.13	1.11
1:B:583:ASN:ND2	1:B:586:ILE:HG13	1.63	1.11
1:A:797:ASP:O	1:A:798:PHE:HB2	1.46	1.11
1:B:490:LEU:HD22	1:B:495:ILE:HG21	1.27	1.11
1:B:900:LEU:HD13	1:B:1056:LEU:HB3	1.12	1.11
1:B:403:ILE:HA	1:B:406:LYS:HG3	1.19	1.11
1:B:531:LYS:HB3	1:B:562:LEU:HD11	1.19	1.11
1:A:375:LEU:HD22	1:A:380:ILE:HD11	1.32	1.11
1:B:533:PHE:CD1	1:B:557:LEU:HD11	1.86	1.11
1:A:1366:TYR:HD1	1:A:1367:ASN:HB2	1.12	1.10
1:B:1253:GLU:CD	1:B:1264:SER:HA	1.76	1.10
1:B:634:VAL:CG2	1:B:891:CYS:SG	2.40	1.10
1:B:976:LEU:CD2	1:B:977:GLN:N	2.11	1.09
1:B:723:LEU:HD23	1:B:727:GLU:HG2	1.34	1.09
1:B:897:ASN:HB2	1:B:1058:ILE:HD11	1.34	1.09
1:B:582:THR:CG2	1:B:583:ASN:OD1	2.00	1.09
1:B:1142:LYS:HG3	1:B:1145:GLN:H	1.10	1.08
1:B:1048:TYR:HD1	1:B:1052:ARG:CB	1.66	1.08
1:B:481:LEU:CD2	1:B:1259:PHE:CD2	2.37	1.08
1:B:606:LYS:HD3	1:B:1219:THR:HG23	1.13	1.08
1:B:648:LYS:HD2	1:B:650:ILE:HD12	1.12	1.08
1:B:1031:LEU:HD12	1:B:1043:PHE:CZ	1.88	1.08
1:B:1267:SER:HB2	1:B:1268:GLU:HA	1.25	1.08
1:B:684:TYR:HB3	1:B:685:ARG:HB2	1.33	1.07
1:A:1111:LEU:HD21	1:A:1363:LEU:CD1	1.84	1.07
1:B:1044:GLN:HA	1:B:1048:TYR:CE2	1.90	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:804:GLU:HA	1:B:807:LYS:HD3	1.11	1.07
1:B:919:ILE:H	1:B:919:ILE:HD12	1.18	1.07
1:A:696:ILE:CB	1:A:699:GLU:CB	2.33	1.07
1:B:1145:GLN:HB3	1:B:1146:ASN:HA	1.36	1.07
1:B:634:VAL:CG2	1:B:634:VAL:O	1.93	1.06
1:A:350:LYS:HA	1:A:352:ASP:H	1.19	1.06
1:B:461:LYS:HG3	1:B:462:ILE:HG23	1.31	1.06
1:B:582:THR:HG22	1:B:583:ASN:OD1	1.55	1.06
1:B:582:THR:CA	1:B:583:ASN:OD1	2.03	1.06
1:A:659:ILE:HG22	1:A:720:GLU:HA	1.37	1.06
1:B:1366:TYR:O	1:B:1367:ASN:ND2	1.87	1.06
1:B:595:ASN:HD21	1:B:610:LEU:CB	1.67	1.05
1:B:1046:ILE:HD13	1:B:1046:ILE:H	1.18	1.05
1:A:464:ASN:HD21	1:A:467:ILE:HG13	1.21	1.05
1:A:394:GLY:HA2	1:A:395:ASN:HB3	1.29	1.05
1:A:375:LEU:HB3	1:A:380:ILE:HD12	1.36	1.05
1:B:557:LEU:HD22	1:B:575:ILE:CD1	1.87	1.05
1:A:1089:LYS:H	1:A:1089:LYS:HD2	1.22	1.05
1:B:897:ASN:CB	1:B:1058:ILE:HD11	1.85	1.05
1:A:404:PHE:CE2	1:A:439:ILE:HG13	1.91	1.04
1:A:547:PHE:HA	1:A:594:THR:HG22	1.40	1.04
1:A:1118:LEU:CB	1:A:1125:TYR:CZ	2.39	1.04
1:B:897:ASN:HB3	1:B:1058:ILE:HD12	1.37	1.04
1:B:583:ASN:HD22	1:B:586:ILE:HG13	0.88	1.03
1:A:367:ILE:O	1:A:371:ILE:HG22	1.57	1.03
1:B:533:PHE:CE1	1:B:557:LEU:CD1	2.41	1.03
1:B:900:LEU:HD22	1:B:1056:LEU:HD12	1.05	1.03
1:A:671:PRO:HG3	1:A:774:GLN:HG2	1.39	1.03
1:B:1048:TYR:HD1	1:B:1052:ARG:CA	1.71	1.03
1:A:384:ILE:HG22	1:A:388:GLU:CB	1.90	1.02
1:A:439:ILE:HD13	1:A:442:ILE:HD12	1.42	1.02
1:A:351:LYS:H	1:A:354:ILE:HD12	1.25	1.02
1:B:582:THR:HA	1:B:583:ASN:OD1	1.59	1.02
1:B:897:ASN:HB3	1:B:1058:ILE:CD1	1.89	1.02
1:B:351:LYS:CE	1:B:483:HIS:CE1	2.43	1.01
1:A:557:LEU:HD22	1:A:558:ASP:H	1.24	1.01
1:A:738:LYS:HE3	1:A:746:ILE:CD1	1.89	1.01
1:B:557:LEU:CD2	1:B:575:ILE:HD11	1.91	1.01
1:A:732:PHE:HA	1:A:784:TYR:CZ	1.94	1.01
1:A:1367:ASN:ND2	1:A:1371:ILE:HD11	1.76	1.01
1:B:439:ILE:O	1:B:442:ILE:HB	1.58	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:634:VAL:O	1:B:634:VAL:HG23	1.19	1.00
1:A:541:ASP:OD1	1:A:1273:GLU:HB2	1.59	1.00
1:A:1264:SER:O	1:A:1265:GLU:HB2	1.54	1.00
1:B:685:ARG:HG2	1:B:685:ARG:HH11	1.20	1.00
1:B:1048:TYR:CD1	1:B:1052:ARG:CB	2.43	1.00
1:B:1142:LYS:HG2	1:B:1143:ASN:HA	1.39	1.00
1:B:461:LYS:HG3	1:B:462:ILE:CG2	1.89	1.00
1:B:817:THR:HG23	1:B:818:TYR:HA	1.37	1.00
1:A:802:ILE:HA	1:A:805:ILE:CB	1.92	1.00
1:A:670:LEU:HD13	1:A:670:LEU:H	1.25	0.99
1:A:683:LEU:HD22	1:A:793:PHE:CE2	1.97	0.99
1:A:1053:LYS:C	1:A:1055:GLU:CB	2.35	0.99
1:A:762:ALA:CB	1:A:770:ILE:HG13	1.91	0.99
1:B:1111:LEU:HD22	1:B:1359:SER:OG	1.61	0.99
1:A:561:ILE:CG2	1:A:562:LEU:HA	1.93	0.99
1:B:892:ILE:HD12	1:B:893:THR:N	1.78	0.99
1:A:669:TYR:HD1	1:A:755:TYR:CD2	1.79	0.99
1:B:1060:LYS:N	1:B:1060:LYS:HE2	1.77	0.99
1:A:1356:LYS:HB3	1:A:1368:SER:OG	1.62	0.98
1:A:1277:ILE:CD1	1:A:1281:ILE:HD13	1.92	0.98
1:B:1048:TYR:N	1:B:1057:TYR:HB2	1.79	0.98
1:B:630:SER:HA	1:B:631:ASP:HB2	1.45	0.98
1:B:533:PHE:CD1	1:B:557:LEU:CD1	2.46	0.98
1:B:1047:TYR:C	1:B:1057:TYR:HB2	1.89	0.98
1:B:381:ASP:O	1:B:384:ILE:HG22	1.63	0.98
1:B:532:ILE:HG22	1:B:562:LEU:CD1	1.94	0.98
1:B:900:LEU:HD23	1:B:901:GLU:N	1.76	0.97
1:B:897:ASN:CB	1:B:1058:ILE:CD1	2.41	0.97
1:A:667:ILE:HG13	1:A:718:ILE:HD12	1.45	0.97
1:A:732:PHE:HD1	1:A:784:TYR:CE2	1.81	0.97
1:A:1096:GLY:HA2	1:A:1099:ILE:HG13	1.46	0.97
1:A:1329:VAL:HG21	1:A:1353:MSE:HE3	1.40	0.97
1:B:532:ILE:N	1:B:562:LEU:HD12	1.79	0.97
1:B:900:LEU:CD1	1:B:1056:LEU:HB3	1.95	0.97
1:B:557:LEU:CD2	1:B:575:ILE:CD1	2.42	0.97
1:B:725:GLU:O	1:B:726:ASN:ND2	1.97	0.97
1:B:817:THR:HG22	1:B:818:TYR:CA	1.95	0.97
1:B:616:ASP:O	1:B:620:VAL:HG13	1.64	0.97
1:A:738:LYS:HE2	1:A:746:ILE:CG1	1.95	0.96
1:B:463:LEU:HD22	1:B:464:ASN:N	1.80	0.96
1:A:683:LEU:CD2	1:A:793:PHE:CD2	2.48	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:LEU:HB3	1:A:380:ILE:CD1	1.96	0.96
1:B:1047:TYR:CA	1:B:1057:TYR:HB3	1.95	0.95
1:B:606:LYS:HB2	1:B:1219:THR:OG1	1.66	0.95
1:B:1141:ALA:HB3	1:B:1142:LYS:C	1.90	0.95
1:B:1142:LYS:HG2	1:B:1143:ASN:CA	1.96	0.95
1:A:665:ASN:HD22	1:A:669:TYR:HE2	1.07	0.95
1:A:361:ASN:HB3	1:A:367:ILE:HG13	1.47	0.95
1:A:738:LYS:CE	1:A:746:ILE:HD11	1.96	0.95
1:B:1329:VAL:HG21	1:B:1353:MSE:HE3	1.49	0.95
1:A:404:PHE:HZ	1:A:439:ILE:HG21	1.13	0.94
1:A:1149:TYR:OH	1:A:1361:LEU:HD22	1.67	0.94
1:A:411:ASN:H	1:A:413:ASP:H	1.15	0.94
1:B:583:ASN:HD22	1:B:586:ILE:CG1	1.80	0.94
1:B:1049:PRO:CD	1:B:1055:GLU:CB	2.44	0.94
1:A:669:TYR:CD1	1:A:755:TYR:HD2	1.84	0.94
1:B:682:ASN:O	1:B:685:ARG:HB3	1.68	0.94
1:B:491:ARG:HE	1:B:1207:ARG:HH21	1.14	0.94
1:A:376:ALA:O	1:A:379:LYS:HG2	1.67	0.93
1:A:439:ILE:CD1	1:A:442:ILE:HD12	1.96	0.93
1:A:669:TYR:HD1	1:A:755:TYR:HD2	0.98	0.93
1:B:461:LYS:CB	1:B:462:ILE:HG13	1.98	0.93
1:B:1048:TYR:HD1	1:B:1052:ARG:HA	1.31	0.93
1:B:674:SER:HB3	1:B:876:ASP:OD1	1.69	0.93
1:A:1350:GLU:HA	1:A:1352:LEU:H	1.28	0.93
1:B:1142:LYS:CG	1:B:1145:GLN:H	1.82	0.93
1:B:749:ASN:ND2	1:B:749:ASN:O	2.00	0.93
1:A:1015:ILE:HG22	1:A:1016:PHE:HD1	1.33	0.93
1:B:804:GLU:CA	1:B:807:LYS:HD3	1.99	0.93
1:B:1044:GLN:HA	1:B:1048:TYR:HE2	1.24	0.93
1:A:805:ILE:O	1:A:807:LYS:N	2.01	0.92
1:B:648:LYS:HD2	1:B:650:ILE:CD1	1.98	0.92
1:B:588:LYS:HD3	1:B:618:ASN:HD21	1.33	0.92
1:B:562:LEU:HD13	1:B:565:LYS:HZ1	1.34	0.92
1:A:807:LYS:O	1:A:808:GLN:C	2.11	0.91
1:A:560:LYS:O	1:A:561:ILE:CG1	2.18	0.91
1:A:792:LEU:HD12	1:A:793:PHE:CD1	2.05	0.91
1:A:613:THR:HG23	1:A:614:GLN:HA	1.50	0.91
1:A:463:LEU:H	1:A:463:LEU:HD12	1.34	0.91
1:A:459:ILE:H	1:A:459:ILE:HD12	1.33	0.91
1:A:638:LEU:HD22	1:A:639:ASN:N	1.85	0.91
1:B:1043:PHE:C	1:B:1046:ILE:HD11	1.96	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:535:ARG:HD3	1:B:540:ASN:O	1.71	0.91
1:A:439:ILE:HD13	1:A:442:ILE:CD1	2.01	0.90
1:B:1048:TYR:H	1:B:1057:TYR:H	1.18	0.90
1:A:792:LEU:HD12	1:A:793:PHE:CE1	2.07	0.90
1:B:1348:ILE:O	1:B:1348:ILE:HG22	1.68	0.90
1:A:801:ASN:HA	1:A:804:GLU:CG	2.01	0.90
1:B:1124:GLU:CB	1:B:1127:GLU:CB	2.49	0.90
1:A:544:ILE:HG21	1:A:555:TYR:CE2	2.06	0.90
1:B:1099:ILE:HA	1:B:1103:LYS:CB	2.02	0.90
1:B:900:LEU:HD23	1:B:901:GLU:H	1.33	0.90
1:B:1360:VAL:C	1:B:1361:LEU:HD23	1.97	0.89
1:A:1015:ILE:HG22	1:A:1016:PHE:CD1	2.07	0.89
1:A:1215:SER:OG	1:A:1242:LYS:HB2	1.71	0.89
1:B:1048:TYR:CD1	1:B:1052:ARG:HA	2.07	0.89
1:A:368:LYS:HG3	1:A:369:GLU:N	1.86	0.89
1:A:1177:ILE:HD11	1:A:1374:LEU:HD11	1.53	0.89
1:B:608:ARG:HA	1:B:609:ASP:C	1.95	0.89
1:A:568:ILE:HD13	1:A:625:GLN:HE22	1.36	0.89
1:A:1055:GLU:N	1:A:1055:GLU:OE2	2.05	0.89
1:B:684:TYR:CB	1:B:685:ARG:HB2	2.01	0.89
1:A:362:ILE:HG12	1:A:367:ILE:HD12	1.52	0.89
1:A:732:PHE:HA	1:A:784:TYR:CE2	2.08	0.89
1:B:434:TYR:CE2	1:B:468:LEU:HD23	2.08	0.89
1:B:616:ASP:O	1:B:620:VAL:HG22	1.71	0.89
1:B:1031:LEU:HD12	1:B:1043:PHE:HZ	1.34	0.89
1:A:519:ILE:HD13	1:A:601:LEU:CD2	2.03	0.88
1:B:434:TYR:CE2	1:B:468:LEU:CD2	2.56	0.88
1:B:1031:LEU:CD1	1:B:1043:PHE:HZ	1.86	0.88
1:B:1357:LYS:HD3	1:B:1362:GLU:OE1	1.73	0.88
1:A:1367:ASN:HD21	1:A:1371:ILE:HD11	1.35	0.88
1:A:638:LEU:HD13	1:A:638:LEU:H	1.37	0.88
1:B:976:LEU:HD23	1:B:977:GLN:CA	2.02	0.88
1:B:897:ASN:HB3	1:B:1059:TYR:CE2	2.08	0.88
1:B:900:LEU:HD13	1:B:1056:LEU:HB2	1.55	0.88
1:A:399:GLU:HG3	1:A:400:ILE:HD13	1.53	0.88
1:A:518:LEU:HD23	1:A:855:ILE:HD11	1.53	0.88
1:A:933:ILE:HG12	1:A:998:TYR:HD2	1.30	0.88
1:B:648:LYS:CD	1:B:650:ILE:HD12	2.01	0.88
1:A:1277:ILE:HD12	1:A:1281:ILE:HD13	1.54	0.88
1:B:1269:ILE:HB	1:B:1270:ASN:HB2	1.55	0.88
1:A:659:ILE:CG2	1:A:720:GLU:HA	2.03	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1360:VAL:O	1:B:1361:LEU:HD23	1.74	0.87
1:B:1367:ASN:O	1:B:1371:ILE:HG22	1.74	0.87
1:B:647:LYS:CB	1:B:648:LYS:HG3	2.03	0.87
1:B:809:ILE:O	1:B:812:ILE:N	2.07	0.87
1:A:462:ILE:HG22	1:A:463:LEU:N	1.88	0.87
1:A:989:LYS:O	1:A:993:LYS:HG2	1.75	0.87
1:A:738:LYS:HE2	1:A:746:ILE:HG13	1.57	0.87
1:A:417:PHE:O	1:A:418:SER:OG	1.91	0.87
1:B:900:LEU:HD22	1:B:1056:LEU:CD1	2.00	0.86
1:A:797:ASP:O	1:A:798:PHE:CB	2.24	0.86
1:A:818:TYR:N	1:A:819:GLU:HA	1.90	0.86
1:A:1096:GLY:HA2	1:A:1099:ILE:CG1	2.05	0.86
1:B:1091:LEU:HA	1:B:1092:PHE:C	1.99	0.86
1:A:371:ILE:CD1	1:A:431:ILE:HD11	2.04	0.86
1:A:1104:ILE:O	1:A:1108:ASP:HB2	1.76	0.86
1:B:969:ILE:CB	1:B:970:ASP:HB3	2.05	0.86
1:B:1145:GLN:CB	1:B:1146:ASN:HA	2.01	0.86
1:A:637:ALA:HB3	1:A:820:ARG:HH12	1.40	0.85
1:A:1367:ASN:ND2	1:A:1371:ILE:CD1	2.40	0.85
1:B:1329:VAL:HG21	1:B:1353:MSE:CE	2.06	0.85
1:B:434:TYR:HE2	1:B:468:LEU:CD2	1.89	0.85
1:A:547:PHE:CA	1:A:594:THR:HG22	2.06	0.85
1:A:738:LYS:CE	1:A:746:ILE:CG1	2.55	0.85
1:B:804:GLU:HA	1:B:807:LYS:CD	2.04	0.85
1:A:351:LYS:N	1:A:354:ILE:HD12	1.90	0.85
1:A:933:ILE:CG1	1:A:998:TYR:CD2	2.59	0.85
1:B:1142:LYS:HG3	1:B:1145:GLN:N	1.90	0.85
1:B:723:LEU:CD2	1:B:727:GLU:HG2	2.07	0.85
1:A:807:LYS:O	1:A:810:LYS:N	2.09	0.85
1:B:457:ILE:HG22	1:B:457:ILE:O	1.76	0.85
1:A:758:ALA:HA	1:A:761:SER:HB2	1.59	0.85
1:B:684:TYR:HB3	1:B:685:ARG:CB	2.06	0.85
1:B:897:ASN:HB3	1:B:1059:TYR:HE2	1.38	0.85
1:A:738:LYS:HB2	1:A:746:ILE:HG12	1.58	0.85
1:B:461:LYS:HB3	1:B:462:ILE:HG13	1.58	0.85
1:B:1058:ILE:HG13	1:B:1059:TYR:CD2	2.12	0.84
1:B:1266:ASN:O	1:B:1267:SER:OG	1.93	0.84
1:A:457:ILE:O	1:A:457:ILE:HG22	1.77	0.84
1:A:1364:GLU:O	1:A:1365:SER:OG	1.96	0.84
1:A:667:ILE:HA	1:A:670:LEU:HD11	1.57	0.84
1:B:576:ASP:OD1	1:B:577:ASN:N	2.09	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:975:ILE:HG22	1:B:976:LEU:HB2	1.60	0.84
1:B:1358:VAL:HG12	1:B:1365:SER:HB3	1.57	0.84
1:B:914:PHE:HA	1:B:915:ASP:HB2	0.84	0.84
1:B:1329:VAL:HG11	1:B:1353:MSE:HE2	1.60	0.84
1:B:1059:TYR:N	1:B:1060:LYS:HB2	1.92	0.84
1:B:398:THR:HA	1:B:401:PHE:CB	2.08	0.83
1:B:673:PHE:CD1	1:B:714:TYR:CD2	2.66	0.83
1:A:368:LYS:HG3	1:A:369:GLU:H	1.41	0.83
1:A:1054:ASN:N	1:A:1055:GLU:HA	1.94	0.83
1:B:1142:LYS:N	1:B:1143:ASN:HA	1.94	0.83
1:A:1348:ILE:HG22	1:A:1348:ILE:O	1.78	0.83
1:A:459:ILE:HD13	1:A:460:GLU:H	1.44	0.83
1:A:946:ASN:HA	1:A:949:ASP:HB3	1.59	0.83
1:B:1364:GLU:O	1:B:1365:SER:OG	1.95	0.83
1:A:350:LYS:HA	1:A:352:ASP:N	1.93	0.83
1:A:696:ILE:CB	1:A:699:GLU:N	2.42	0.83
1:B:532:ILE:HG22	1:B:562:LEU:HD12	1.61	0.83
1:B:1031:LEU:CD1	1:B:1043:PHE:CZ	2.61	0.83
1:A:445:ASN:HD22	1:A:460:GLU:HA	1.42	0.82
1:B:494:ASP:O	1:B:495:ILE:HD13	1.79	0.82
1:B:673:PHE:HD1	1:B:714:TYR:CD2	1.96	0.82
1:A:468:LEU:O	1:A:472:ILE:HG13	1.79	0.82
1:B:1041:ASN:O	1:B:1042:LYS:O	1.97	0.82
1:A:801:ASN:HA	1:A:804:GLU:HG3	1.61	0.82
1:B:378:PHE:CZ	1:B:435:LEU:CD1	2.63	0.82
1:A:420:LYS:O	1:A:421:SER:OG	1.97	0.82
1:A:461:LYS:HA	1:A:461:LYS:NZ	1.94	0.82
1:A:1366:TYR:CD1	1:A:1367:ASN:CB	2.62	0.82
1:A:696:ILE:CB	1:A:699:GLU:H	1.93	0.82
1:B:461:LYS:HZ2	1:B:461:LYS:HB2	1.44	0.82
1:A:737:LYS:HD2	1:A:750:ILE:HG22	1.62	0.82
1:B:1047:TYR:HA	1:B:1057:TYR:CB	2.08	0.82
1:A:892:ILE:O	1:A:896:TRP:HB3	1.79	0.82
1:B:897:ASN:CB	1:B:1059:TYR:HE2	1.93	0.82
1:B:644:PHE:HE2	1:B:651:ILE:HD11	1.44	0.82
1:B:461:LYS:HB2	1:B:461:LYS:NZ	1.95	0.81
1:B:900:LEU:CD2	1:B:1056:LEU:CD1	2.56	0.81
1:A:395:ASN:OD1	1:A:396:CYS:N	2.14	0.81
1:A:968:GLU:HA	1:A:969:ILE:CB	2.10	0.81
1:B:560:LYS:HE2	1:B:563:ASN:CB	2.10	0.81
1:B:1130:ILE:HG12	1:B:1133:LEU:HD12	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:358:PHE:O	1:B:362:ILE:HG12	1.80	0.81
1:B:1142:LYS:HB3	1:B:1142:LYS:NZ	1.94	0.81
1:A:375:LEU:CD2	1:A:380:ILE:HD11	2.08	0.81
1:A:568:ILE:HD13	1:A:625:GLN:NE2	1.95	0.81
1:A:807:LYS:O	1:A:809:ILE:N	2.13	0.81
1:B:595:ASN:ND2	1:B:610:LEU:CB	2.44	0.80
1:B:888:ARG:NH1	1:B:1011:LEU:HD21	1.96	0.80
1:A:393:LYS:H	1:A:395:ASN:HB3	1.45	0.80
1:B:986:ILE:O	1:B:986:ILE:HD12	1.81	0.80
1:A:351:LYS:H	1:A:354:ILE:CD1	1.94	0.80
1:B:504:ASP:HA	1:B:507:ARG:HD3	1.63	0.80
1:A:514:LEU:HD12	1:A:514:LEU:O	1.81	0.80
1:A:933:ILE:CG1	1:A:998:TYR:CE2	2.65	0.80
1:B:914:PHE:CA	1:B:915:ASP:CB	2.34	0.80
1:A:1106:GLU:O	1:A:1110:ILE:HG13	1.82	0.80
1:B:1130:ILE:O	1:B:1134:LYS:HG3	1.82	0.80
1:A:659:ILE:HG22	1:A:720:GLU:CA	2.12	0.79
1:A:683:LEU:HD23	1:A:684:TYR:N	1.97	0.79
1:A:519:ILE:HD13	1:A:601:LEU:HD23	1.64	0.79
1:A:644:PHE:HB3	1:A:647:LYS:O	1.80	0.79
1:A:1215:SER:OG	1:A:1242:LYS:CB	2.30	0.79
1:A:608:ARG:NH2	1:A:836:PHE:HB2	1.97	0.79
1:A:933:ILE:HG12	1:A:998:TYR:CE2	2.18	0.79
1:B:467:ILE:HD12	1:B:467:ILE:O	1.82	0.79
1:B:1142:LYS:HG2	1:B:1143:ASN:C	2.08	0.79
1:A:896:TRP:CG	1:A:897:ASN:H	1.99	0.79
1:B:588:LYS:HD3	1:B:618:ASN:ND2	1.96	0.79
1:A:738:LYS:CE	1:A:746:ILE:CD1	2.58	0.79
1:B:405:LYS:HA	1:B:408:TYR:CB	2.12	0.79
1:A:738:LYS:CE	1:A:746:ILE:HG13	2.12	0.79
1:A:1045:GLU:HB3	1:A:1091:LEU:HD22	1.65	0.79
1:A:1361:LEU:HD12	1:A:1361:LEU:H	1.48	0.79
1:A:685:ARG:HD2	1:A:685:ARG:O	1.83	0.78
1:B:1357:LYS:CD	1:B:1362:GLU:OE1	2.31	0.78
1:A:391:LEU:O	1:A:392:LYS:CB	2.31	0.78
1:B:434:TYR:HE2	1:B:468:LEU:HD23	1.43	0.78
1:B:427:LEU:H	1:B:427:LEU:HD12	1.46	0.78
1:A:399:GLU:CG	1:A:400:ILE:HD13	2.13	0.78
1:A:464:ASN:ND2	1:A:467:ILE:HG13	1.97	0.78
1:A:1040:GLU:HG2	1:A:1042:LYS:HG2	1.66	0.78
1:B:533:PHE:HE1	1:B:557:LEU:CD1	1.96	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:432:TYR:CE1	1:B:436:LYS:NZ	2.51	0.78
1:A:1111:LEU:HD21	1:A:1363:LEU:HD12	1.65	0.78
1:A:683:LEU:HD21	1:A:793:PHE:CD2	2.18	0.78
1:A:404:PHE:HZ	1:A:439:ILE:CG2	1.92	0.78
1:B:1047:TYR:C	1:B:1057:TYR:CB	2.57	0.78
1:A:683:LEU:CD2	1:A:793:PHE:CE2	2.65	0.77
1:B:465:GLU:O	1:B:466:SER:OG	2.03	0.77
1:B:532:ILE:CG2	1:B:562:LEU:HD12	2.15	0.77
1:B:888:ARG:HH12	1:B:1011:LEU:HD21	1.48	0.77
1:A:557:LEU:CD2	1:A:558:ASP:H	1.97	0.77
1:B:1060:LYS:HE2	1:B:1060:LYS:CA	2.14	0.77
1:A:1090:PHE:CB	1:A:1162:TYR:HE1	1.97	0.77
1:B:461:LYS:CG	1:B:462:ILE:HG13	2.15	0.77
1:B:975:ILE:CG2	1:B:976:LEU:HB2	2.15	0.77
1:B:1091:LEU:CB	1:B:1093:ASN:HB2	2.15	0.77
1:A:1112:LYS:HA	1:A:1115:ASN:HB2	1.66	0.77
1:A:1277:ILE:HD11	1:A:1281:ILE:HD13	1.64	0.77
1:B:357:PHE:HE2	1:B:427:LEU:HD21	1.49	0.77
1:A:913:ASP:HA	1:A:1013:ARG:NH2	2.00	0.77
1:A:350:LYS:CA	1:A:352:ASP:H	1.97	0.77
1:A:1367:ASN:CG	1:A:1371:ILE:CD1	2.57	0.77
1:B:1253:GLU:OE1	1:B:1264:SER:HA	1.83	0.77
1:B:467:ILE:HG23	1:B:468:LEU:CD1	2.15	0.77
1:B:659:ILE:CB	1:B:719:LEU:O	2.32	0.77
1:B:1256:CYS:HB3	1:B:1261:ILE:HG13	1.67	0.77
1:B:1332:ASP:HB2	1:B:1354:LYS:HE3	1.66	0.77
1:B:685:ARG:HG2	1:B:685:ARG:NH1	1.94	0.76
1:B:412:PHE:CB	1:B:413:ASP:HA	2.15	0.76
1:B:1047:TYR:CA	1:B:1057:TYR:CB	2.63	0.76
1:A:1118:LEU:CB	1:A:1125:TYR:CE2	2.68	0.76
1:B:562:LEU:HD13	1:B:565:LYS:NZ	1.99	0.76
1:B:1355:PRO:HB2	1:B:1368:SER:HB2	1.67	0.76
1:A:544:ILE:CG2	1:A:555:TYR:CE2	2.69	0.76
1:A:1119:ASN:HB3	1:A:1120:GLY:HA2	1.68	0.76
1:B:606:LYS:CB	1:B:1219:THR:OG1	2.34	0.76
1:A:643:VAL:O	1:A:644:PHE:C	2.29	0.76
1:A:418:SER:CB	1:A:419:LYS:HA	2.06	0.76
1:B:817:THR:CG2	1:B:818:TYR:CA	2.49	0.76
1:A:1366:TYR:HD1	1:A:1367:ASN:CB	1.95	0.75
1:B:552:GLU:HA	1:B:553:LYS:CB	2.15	0.75
1:A:411:ASN:N	1:A:412:PHE:HA	2.01	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:378:PHE:CZ	1:B:435:LEU:HD13	2.22	0.75
1:A:501:ASN:O	1:A:502:THR:CG2	2.28	0.75
1:B:892:ILE:HD12	1:B:893:THR:CA	2.17	0.75
1:B:1059:TYR:HA	1:B:1060:LYS:C	2.09	0.75
1:A:411:ASN:N	1:A:413:ASP:H	1.85	0.75
1:A:614:GLN:CB	1:A:618:ASN:HB2	2.16	0.75
1:A:643:VAL:O	1:A:645:LYS:CB	2.35	0.75
1:A:703:LEU:O	1:A:707:ILE:HG12	1.87	0.75
1:A:1111:LEU:HD23	1:A:1359:SER:OG	1.86	0.75
1:B:804:GLU:O	1:B:806:LYS:N	2.19	0.75
1:B:464:ASN:O	1:B:467:ILE:HG22	1.86	0.75
1:B:532:ILE:CG2	1:B:562:LEU:CD1	2.64	0.75
1:A:461:LYS:HA	1:A:461:LYS:HZ2	1.49	0.75
1:B:582:THR:CB	1:B:583:ASN:CG	2.41	0.75
1:A:383:LEU:O	1:A:383:LEU:HD23	1.87	0.74
1:A:802:ILE:CA	1:A:805:ILE:CB	2.64	0.74
1:A:806:LYS:O	1:A:809:ILE:HB	1.86	0.74
1:A:398:THR:OG1	1:A:443:LEU:CD1	2.35	0.74
1:A:902:GLU:OE2	1:A:1057:TYR:HD2	1.70	0.74
1:B:374:ILE:HA	1:B:377:GLU:CB	2.17	0.74
1:A:676:VAL:HG12	1:A:778:ILE:HG23	1.70	0.74
1:A:613:THR:CG2	1:A:614:GLN:HA	2.18	0.74
1:A:1358:VAL:CB	1:A:1365:SER:HB3	2.18	0.74
1:B:531:LYS:HB2	1:B:562:LEU:HD11	1.68	0.74
1:B:986:ILE:HD13	1:B:991:LEU:HD12	1.68	0.74
1:B:1141:ALA:N	1:B:1142:LYS:HA	2.02	0.74
1:A:1118:LEU:HB2	1:A:1125:TYR:CE2	2.23	0.74
1:A:1371:ILE:HG22	1:A:1375:ILE:CD1	2.17	0.74
1:B:532:ILE:CA	1:B:562:LEU:HD12	2.17	0.74
1:B:403:ILE:HA	1:B:406:LYS:CG	2.10	0.74
1:B:463:LEU:O	1:B:463:LEU:HD13	1.87	0.74
1:B:582:THR:HB	1:B:583:ASN:ND2	2.01	0.74
1:B:1147:LYS:N	1:B:1148:ASN:HA	2.03	0.74
1:A:399:GLU:CD	1:A:400:ILE:HD13	2.12	0.73
1:A:570:ARG:HD3	1:A:577:ASN:CG	2.12	0.73
1:B:897:ASN:CG	1:B:1059:TYR:HE2	1.96	0.73
1:A:462:ILE:CG2	1:A:463:LEU:N	2.51	0.73
1:A:683:LEU:HD23	1:A:683:LEU:C	2.13	0.73
1:A:1350:GLU:HA	1:A:1352:LEU:N	2.01	0.73
1:B:376:ALA:HA	1:B:379:LYS:CB	2.19	0.73
1:B:616:ASP:O	1:B:620:VAL:CG1	2.35	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1010:ILE:HG23	1:A:1014:ILE:HD12	1.68	0.73
1:B:657:ILE:HD13	1:B:657:ILE:N	2.04	0.73
1:B:749:ASN:HD21	1:B:753:ASN:HD22	1.35	0.73
1:A:515:ASP:O	1:A:519:ILE:HG13	1.88	0.73
1:A:1092:PHE:CB	1:A:1093:ASN:OD1	2.37	0.73
1:A:547:PHE:HA	1:A:594:THR:CG2	2.17	0.73
1:A:667:ILE:HG13	1:A:718:ILE:CD1	2.19	0.73
1:A:1354:LYS:HB2	1:A:1354:LYS:NZ	2.04	0.73
1:B:532:ILE:N	1:B:562:LEU:CD1	2.51	0.73
1:B:919:ILE:H	1:B:919:ILE:CD1	1.94	0.73
1:B:606:LYS:CD	1:B:1219:THR:CG2	2.62	0.73
1:B:1099:ILE:HG23	1:B:1103:LYS:CB	2.19	0.72
1:B:462:ILE:N	1:B:462:ILE:HD12	2.03	0.72
1:A:638:LEU:H	1:A:638:LEU:CD1	2.03	0.72
1:B:532:ILE:HG22	1:B:562:LEU:HD13	1.69	0.72
1:B:1031:LEU:O	1:B:1043:PHE:CE2	2.42	0.72
1:B:1265:GLU:CB	1:B:1266:ASN:HB3	2.20	0.72
1:A:973:SER:HB3	1:A:974:ASN:HA	1.71	0.72
1:B:481:LEU:CD2	1:B:1259:PHE:CE2	2.66	0.72
1:A:608:ARG:HG2	1:A:608:ARG:HH11	1.55	0.72
1:A:802:ILE:O	1:A:805:ILE:CB	2.37	0.72
1:B:640:LEU:HD13	1:B:701:ILE:HG23	1.70	0.72
1:A:1329:VAL:CG2	1:A:1353:MSE:HE3	2.18	0.72
1:B:1079:ILE:HD12	1:B:1079:ILE:N	2.03	0.72
1:A:371:ILE:HD13	1:A:431:ILE:HD11	1.70	0.72
1:B:1048:TYR:N	1:B:1057:TYR:H	1.87	0.72
1:A:557:LEU:HD22	1:A:558:ASP:N	2.02	0.72
1:A:1111:LEU:HD21	1:A:1363:LEU:HD11	1.70	0.72
1:B:720:GLU:OE2	1:B:723:LEU:CD1	2.38	0.72
1:A:1328:ASP:HB3	1:A:1371:ILE:HG21	1.72	0.71
1:B:976:LEU:HD23	1:B:977:GLN:H	0.74	0.71
1:A:666:ASP:O	1:A:667:ILE:HG22	1.91	0.71
1:B:463:LEU:HD22	1:B:463:LEU:C	2.15	0.71
1:B:514:LEU:HG	1:B:862:THR:HG21	1.73	0.71
1:B:903:PHE:CE2	1:B:1021:LEU:HD11	2.25	0.71
1:B:1031:LEU:O	1:B:1043:PHE:HE2	1.73	0.71
1:A:1264:SER:O	1:A:1265:GLU:CB	2.33	0.71
1:B:677:LEU:HD11	1:B:707:ILE:HD12	1.73	0.71
1:B:481:LEU:HD21	1:B:1259:PHE:CD2	2.22	0.71
1:A:703:LEU:HD12	1:A:707:ILE:HD11	1.71	0.71
1:A:775:LYS:HB2	1:A:775:LYS:NZ	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1361:LEU:HD13	1:A:1363:LEU:HD11	1.72	0.71
1:A:400:ILE:HD13	1:A:400:ILE:N	2.05	0.71
1:B:351:LYS:HE2	1:B:483:HIS:HE1	1.50	0.71
1:A:368:LYS:HA	1:A:371:ILE:CG2	2.20	0.71
1:A:1236:THR:HG23	1:A:1242:LYS:HG2	1.72	0.71
1:B:1144:ILE:C	1:B:1145:GLN:HG3	2.15	0.71
1:B:1192:MSE:HE3	1:B:1278:ARG:HG2	1.72	0.71
1:A:638:LEU:HD13	1:A:638:LEU:N	2.05	0.71
1:B:467:ILE:HG23	1:B:468:LEU:HD12	1.72	0.71
1:B:1191:GLN:HE22	1:B:1194:ARG:HH21	1.36	0.70
1:B:1048:TYR:HB2	1:B:1052:ARG:HA	1.72	0.70
1:A:445:ASN:OD1	1:A:446:GLU:N	2.24	0.70
1:B:644:PHE:HE2	1:B:651:ILE:CD1	2.04	0.70
1:A:361:ASN:CB	1:A:367:ILE:HG13	2.21	0.70
1:A:1014:ILE:HG22	1:A:1015:ILE:N	2.04	0.70
1:A:1356:LYS:HD2	1:A:1357:LYS:HB3	1.73	0.70
1:B:489:LYS:HG2	1:B:489:LYS:O	1.91	0.70
1:A:519:ILE:CD1	1:A:601:LEU:HD23	2.22	0.70
1:A:1054:ASN:N	1:A:1055:GLU:CA	2.54	0.70
1:B:438:ARG:NE	1:B:438:ARG:HA	2.06	0.70
1:B:904:ILE:HG12	1:B:1021:LEU:HD13	1.73	0.70
1:B:461:LYS:CG	1:B:462:ILE:HG23	2.16	0.70
1:B:892:ILE:HD12	1:B:892:ILE:C	2.15	0.70
1:A:1346:ASN:HD22	1:A:1349:LEU:HD22	1.56	0.70
1:A:696:ILE:CB	1:A:699:GLU:CA	2.70	0.70
1:B:1263:LEU:HA	1:B:1270:ASN:HD22	1.56	0.70
1:A:792:LEU:C	1:A:792:LEU:HD13	2.17	0.69
1:A:801:ASN:HA	1:A:804:GLU:HG2	1.74	0.69
1:A:1276:SER:OG	1:A:1279:ASN:HB2	1.91	0.69
1:A:1118:LEU:HB3	1:A:1125:TYR:CE2	2.28	0.69
1:B:416:LYS:N	1:B:417:PHE:HA	2.07	0.69
1:B:1171:PHE:HB3	1:B:1174:LEU:HD12	1.74	0.69
1:B:1349:LEU:CD2	1:B:1350:GLU:HG2	2.22	0.69
1:A:371:ILE:HD12	1:A:371:ILE:O	1.92	0.69
1:A:560:LYS:C	1:A:561:ILE:CG1	2.65	0.69
1:A:896:TRP:CG	1:A:897:ASN:N	2.55	0.69
1:B:426:GLU:O	1:B:430:ILE:HG23	1.93	0.69
1:B:436:LYS:NZ	1:B:436:LYS:HB3	2.07	0.69
1:A:933:ILE:HG13	1:A:998:TYR:CE2	2.26	0.69
1:B:533:PHE:HD1	1:B:557:LEU:CD1	2.06	0.69
1:A:560:LYS:C	1:A:561:ILE:HG12	2.18	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:796:SER:N	1:A:797:ASP:HA	2.08	0.69
1:A:1329:VAL:HG21	1:A:1353:MSE:HE2	1.70	0.69
1:B:616:ASP:O	1:B:620:VAL:CG2	2.40	0.69
1:B:634:VAL:O	1:B:638:LEU:CB	2.41	0.69
1:A:670:LEU:H	1:A:670:LEU:CD1	2.02	0.69
1:A:1329:VAL:HG21	1:A:1353:MSE:HE1	1.69	0.69
1:B:914:PHE:CD1	1:B:916:ASP:CB	2.75	0.69
1:B:921:THR:OG1	1:B:924:GLU:CB	2.41	0.69
1:B:1075:ILE:HD11	1:B:1290:PRO:HG2	1.74	0.69
1:A:410:VAL:C	1:A:412:PHE:HA	2.18	0.69
1:B:1267:SER:HA	1:B:1270:ASN:O	1.93	0.68
1:B:1348:ILE:O	1:B:1348:ILE:CG2	2.38	0.68
1:A:1149:TYR:OH	1:A:1361:LEU:CD2	2.41	0.68
1:B:1044:GLN:O	1:B:1046:ILE:HD13	1.93	0.68
1:B:1059:TYR:CA	1:B:1060:LYS:CB	2.72	0.68
1:A:362:ILE:HG12	1:A:367:ILE:CD1	2.23	0.68
1:A:368:LYS:O	1:A:371:ILE:HG23	1.93	0.68
1:A:608:ARG:HG2	1:A:608:ARG:NH1	2.06	0.68
1:B:897:ASN:HB2	1:B:1058:ILE:CD1	2.12	0.68
1:A:516:LEU:HD11	1:A:1197:ARG:HE	1.58	0.68
1:B:1058:ILE:HD12	1:B:1059:TYR:CE2	2.28	0.68
1:A:464:ASN:OD1	1:A:467:ILE:HG12	1.94	0.68
1:A:738:LYS:HB2	1:A:746:ILE:CG1	2.24	0.68
1:A:351:LYS:HA	1:A:354:ILE:HD12	1.76	0.68
1:B:485:MSE:HE2	1:B:1202:ILE:HD11	1.75	0.67
1:B:614:GLN:O	1:B:615:ASP:O	2.12	0.67
1:A:431:ILE:HG12	1:A:472:ILE:HD13	1.75	0.67
1:B:432:TYR:HE1	1:B:436:LYS:NZ	1.91	0.67
1:A:1017:ASN:HB3	1:A:1020:PHE:HB2	1.76	0.67
1:B:1035:MSE:O	1:B:1038:GLU:OE1	2.12	0.67
1:B:1044:GLN:HA	1:B:1048:TYR:CZ	2.29	0.67
1:B:1140:PHE:C	1:B:1142:LYS:HA	2.20	0.67
1:B:1364:GLU:HG2	1:B:1365:SER:N	2.09	0.67
1:A:519:ILE:HD13	1:A:601:LEU:HD21	1.75	0.67
1:B:358:PHE:CZ	1:B:427:LEU:HG	2.28	0.67
1:B:1269:ILE:CB	1:B:1270:ASN:HB2	2.23	0.67
1:A:495:ILE:HD11	1:A:508:LEU:HD22	1.76	0.67
1:B:510:ALA:HB3	1:B:866:LEU:HD21	1.75	0.67
1:B:897:ASN:CG	1:B:1059:TYR:CE2	2.73	0.67
1:B:1056:LEU:O	1:B:1058:ILE:HG22	1.94	0.67
1:A:404:PHE:HD1	1:A:404:PHE:H	1.40	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:ILE:HD12	1:A:459:ILE:N	2.03	0.67
1:B:351:LYS:HE3	1:B:483:HIS:ND1	2.10	0.67
1:B:424:GLU:HA	1:B:427:LEU:HD13	1.76	0.67
1:B:1291:PHE:HZ	1:B:1378:LEU:HD12	1.59	0.66
1:A:518:LEU:CD2	1:A:855:ILE:HD11	2.22	0.66
1:A:900:LEU:HB3	1:A:1056:LEU:HD22	1.76	0.66
1:A:351:LYS:CA	1:A:354:ILE:HD12	2.25	0.66
1:A:493:ASN:OD1	1:A:603:ALA:CB	2.42	0.66
1:A:1322:PHE:HB3	1:A:1331:LEU:HD21	1.77	0.66
1:A:1366:TYR:CE1	1:A:1367:ASN:HB2	2.29	0.66
1:B:351:LYS:CE	1:B:483:HIS:ND1	2.59	0.66
1:A:794:ASP:O	1:A:795:PHE:HD1	1.78	0.66
1:B:358:PHE:CB	1:B:480:THR:HG21	2.25	0.66
1:B:606:LYS:HB2	1:B:1219:THR:CG2	2.25	0.66
1:B:914:PHE:HA	1:B:915:ASP:HB3	1.72	0.66
1:B:1059:TYR:CA	1:B:1060:LYS:HB2	2.26	0.66
1:A:638:LEU:HG	1:A:891:CYS:CB	2.25	0.66
1:B:550:ASP:OD1	1:B:550:ASP:N	2.28	0.66
1:B:606:LYS:HD3	1:B:1219:THR:HG21	1.76	0.66
1:A:637:ALA:CB	1:A:820:ARG:HH12	2.08	0.66
1:B:644:PHE:CE2	1:B:651:ILE:HD11	2.29	0.66
1:A:394:GLY:HA2	1:A:395:ASN:CB	2.12	0.66
1:A:398:THR:OG1	1:A:443:LEU:HD13	1.95	0.66
1:B:1358:VAL:CG1	1:B:1365:SER:HB3	2.26	0.66
1:A:1008:SER:O	1:A:1012:CYS:SG	2.50	0.66
1:A:638:LEU:HD22	1:A:638:LEU:C	2.21	0.66
1:A:1050:LYS:HE2	1:A:1050:LYS:HA	1.76	0.66
1:B:565:LYS:HA	1:B:568:ILE:HD12	1.77	0.66
1:B:1358:VAL:HG22	1:B:1359:SER:H	1.60	0.66
1:B:1355:PRO:CB	1:B:1368:SER:HB2	2.24	0.66
1:A:544:ILE:HD13	1:A:555:TYR:CD2	2.30	0.65
1:A:570:ARG:CD	1:A:577:ASN:OD1	2.33	0.65
1:B:1142:LYS:HG2	1:B:1144:ILE:N	2.11	0.65
1:B:1192:MSE:CE	1:B:1278:ARG:HG2	2.26	0.65
1:B:1357:LYS:HA	1:B:1363:LEU:O	1.96	0.65
1:A:439:ILE:CD1	1:A:442:ILE:CD1	2.66	0.65
1:B:439:ILE:C	1:B:442:ILE:HB	2.21	0.65
1:A:1371:ILE:CG2	1:A:1375:ILE:HD11	2.25	0.65
1:B:809:ILE:O	1:B:810:LYS:C	2.37	0.65
1:A:792:LEU:HD13	1:A:792:LEU:O	1.95	0.65
1:A:666:ASP:N	1:A:666:ASP:OD1	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1356:LYS:HB3	1:A:1368:SER:HG	1.61	0.65
1:B:503:ASP:N	1:B:503:ASP:OD1	2.29	0.65
1:A:806:LYS:N	1:A:809:ILE:CD1	2.59	0.65
1:A:1102:ASN:O	1:A:1106:GLU:HB2	1.96	0.65
1:B:615:ASP:OD2	1:B:615:ASP:N	2.24	0.65
1:A:738:LYS:HB2	1:A:746:ILE:CD1	2.26	0.65
1:B:489:LYS:HD3	1:B:508:LEU:HD13	1.79	0.65
1:A:705:ALA:O	1:A:709:VAL:HG23	1.97	0.65
1:B:421:SER:HB3	1:B:424:GLU:OE1	1.97	0.65
1:B:380:ILE:O	1:B:384:ILE:HB	1.97	0.65
1:A:462:ILE:HG22	1:A:464:ASN:N	2.12	0.65
1:B:557:LEU:HD21	1:B:575:ILE:CD1	2.26	0.65
1:B:917:PHE:O	1:B:918:LYS:HG3	1.95	0.65
1:B:1048:TYR:N	1:B:1057:TYR:CB	2.58	0.65
1:B:1329:VAL:HG11	1:B:1353:MSE:CE	2.27	0.65
1:A:463:LEU:O	1:A:463:LEU:HD13	1.97	0.64
1:A:892:ILE:O	1:A:896:TRP:CB	2.44	0.64
1:B:913:ASP:O	1:B:915:ASP:HB2	1.96	0.64
1:B:946:ASN:HA	1:B:949:ASP:HB3	1.79	0.64
1:B:1099:ILE:CA	1:B:1103:LYS:CB	2.75	0.64
1:B:1358:VAL:O	1:B:1359:SER:HB2	1.97	0.64
1:B:492:HIS:CE1	1:B:1200:HIS:CD2	2.84	0.64
1:A:459:ILE:CD1	1:A:460:GLU:H	2.11	0.64
1:A:518:LEU:HD23	1:A:855:ILE:CD1	2.27	0.64
1:B:987:ASN:HB3	1:B:990:ASP:HB2	1.79	0.64
1:B:1045:GLU:O	1:B:1057:TYR:CD2	2.50	0.64
1:A:576:ASP:O	1:A:578:LYS:N	2.31	0.64
1:A:535:ARG:CG	1:A:535:ARG:HH11	2.11	0.64
1:A:732:PHE:CD1	1:A:784:TYR:CE2	2.72	0.64
1:A:806:LYS:N	1:A:809:ILE:HD12	2.12	0.64
1:B:490:LEU:HA	1:B:495:ILE:HG13	1.79	0.64
1:B:842:ILE:O	1:B:846:LEU:CD1	2.46	0.64
1:B:914:PHE:N	1:B:915:ASP:HB2	2.12	0.64
1:A:987:ASN:HD21	1:A:990:ASP:HB2	1.62	0.64
1:A:1298:GLU:HA	1:A:1343:ILE:CB	2.28	0.64
1:B:1277:ILE:HG22	1:B:1294:TYR:HE1	1.62	0.64
1:B:666:ASP:C	1:B:667:ILE:HG22	2.23	0.64
1:B:666:ASP:O	1:B:667:ILE:C	2.39	0.64
1:B:1023:LYS:HA	1:B:1026:LYS:HB3	1.79	0.64
1:B:1071:ASN:HD22	1:B:1075:ILE:HG13	1.63	0.64
1:B:463:LEU:HD23	1:B:468:LEU:HD13	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:665:ASN:O	1:B:666:ASP:OD1	2.16	0.63
1:B:852:ILE:HG22	1:B:882:MSE:HE2	1.81	0.63
1:B:975:ILE:CG2	1:B:976:LEU:CB	2.76	0.63
1:A:732:PHE:CE1	1:A:784:TYR:CD2	2.86	0.63
1:A:888:ARG:HG2	1:A:888:ARG:O	1.98	0.63
1:B:492:HIS:HE1	1:B:1200:HIS:CD2	2.16	0.63
1:B:1059:TYR:HA	1:B:1060:LYS:CB	2.29	0.63
1:A:821:ILE:HG22	1:A:822:THR:N	2.13	0.63
1:B:900:LEU:CD2	1:B:901:GLU:H	2.09	0.63
1:A:670:LEU:HD13	1:A:670:LEU:N	2.08	0.63
1:A:868:THR:HG23	1:A:869:SER:N	2.13	0.63
1:B:400:ILE:O	1:B:403:ILE:CB	2.46	0.63
1:B:1358:VAL:HG22	1:B:1359:SER:N	2.13	0.63
1:A:473:LEU:HD22	1:A:477:LYS:HE3	1.81	0.63
1:A:738:LYS:HE2	1:A:746:ILE:HG12	1.80	0.63
1:A:1048:TYR:HD1	1:A:1049:PRO:O	1.81	0.63
1:A:1348:ILE:O	1:A:1348:ILE:CG2	2.46	0.63
1:A:399:GLU:HG3	1:A:400:ILE:CD1	2.28	0.63
1:A:399:GLU:CD	1:A:400:ILE:CD1	2.72	0.63
1:A:913:ASP:HA	1:A:1013:ARG:HH22	1.60	0.63
1:B:490:LEU:HD22	1:B:495:ILE:CG2	2.17	0.63
1:B:684:TYR:N	1:B:685:ARG:HB2	2.13	0.63
1:A:463:LEU:HD12	1:A:463:LEU:N	2.06	0.63
1:A:554:ASN:N	1:A:555:TYR:HA	2.14	0.63
1:A:608:ARG:HH11	1:A:608:ARG:CG	2.12	0.63
1:A:659:ILE:HG22	1:A:719:LEU:O	1.99	0.63
1:A:685:ARG:HG2	1:A:685:ARG:HH11	1.64	0.63
1:A:732:PHE:HA	1:A:784:TYR:OH	1.98	0.63
1:A:735:GLU:O	1:A:739:THR:HG23	1.99	0.63
1:A:896:TRP:CD1	1:A:897:ASN:H	2.16	0.63
1:A:439:ILE:HD12	1:A:442:ILE:HD12	1.81	0.62
1:A:1026:LYS:HB2	1:A:1026:LYS:NZ	2.13	0.62
1:A:1346:ASN:HB3	1:A:1349:LEU:HB2	1.81	0.62
1:B:1099:ILE:O	1:B:1103:LYS:N	2.32	0.62
1:B:364:ASN:ND2	1:B:364:ASN:H	1.96	0.62
1:A:756:LYS:HA	1:A:759:GLN:HG2	1.82	0.62
1:A:1354:LYS:HB2	1:A:1354:LYS:HZ2	1.63	0.62
1:A:1367:ASN:CG	1:A:1371:ILE:HD12	2.23	0.62
1:A:1367:ASN:O	1:A:1371:ILE:HD12	1.98	0.62
1:B:643:VAL:HG12	1:B:643:VAL:O	2.00	0.62
1:B:842:ILE:O	1:B:846:LEU:HD12	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:LYS:HA	1:A:351:LYS:HB3	1.81	0.62
1:A:1371:ILE:HG22	1:A:1375:ILE:HD12	1.80	0.62
1:B:378:PHE:CE2	1:B:435:LEU:HD13	2.34	0.62
1:A:1359:SER:HB3	1:A:1363:LEU:HD12	1.82	0.62
1:A:1371:ILE:CG2	1:A:1375:ILE:CD1	2.76	0.62
1:B:913:ASP:O	1:B:915:ASP:CB	2.47	0.62
1:A:1285:TYR:HA	1:A:1288:ARG:HG2	1.81	0.62
1:B:1191:GLN:NE2	1:B:1194:ARG:HH21	1.98	0.62
1:B:892:ILE:HD12	1:B:893:THR:HA	1.81	0.62
1:B:907:MSE:O	1:B:911:GLU:HG2	1.99	0.62
1:A:623:ILE:HG23	1:A:830:ILE:HB	1.82	0.61
1:A:659:ILE:CG2	1:A:719:LEU:C	2.73	0.61
1:B:892:ILE:CD1	1:B:893:THR:N	2.58	0.61
1:A:775:LYS:HB2	1:A:775:LYS:HZ3	1.64	0.61
1:A:599:ARG:NH2	1:A:606:LYS:O	2.34	0.61
1:A:1060:LYS:NZ	1:A:1170:GLU:OE2	2.33	0.61
1:B:684:TYR:CA	1:B:685:ARG:HB2	2.30	0.61
1:B:900:LEU:HD13	1:B:1056:LEU:CD1	2.30	0.61
1:B:1144:ILE:O	1:B:1144:ILE:HG22	2.01	0.61
1:B:936:ASN:O	1:B:940:GLU:HG3	1.99	0.61
1:B:1048:TYR:CD1	1:B:1052:ARG:CA	2.63	0.61
1:A:384:ILE:HD11	1:A:463:LEU:CD1	2.31	0.61
1:A:401:PHE:HA	1:A:403:ILE:HD13	1.82	0.61
1:A:632:GLU:O	1:A:634:VAL:N	2.34	0.61
1:A:1090:PHE:CB	1:A:1162:TYR:CE1	2.82	0.61
1:B:1045:GLU:O	1:B:1057:TYR:HD2	1.83	0.61
1:A:638:LEU:HG	1:A:891:CYS:HA	1.82	0.61
1:B:519:ILE:HD11	1:B:600:ILE:HB	1.81	0.61
1:B:900:LEU:CD1	1:B:1056:LEU:CD1	2.78	0.61
1:A:655:ASN:OD1	1:A:655:ASN:N	2.33	0.61
1:B:748:GLU:O	1:B:749:ASN:HB3	2.01	0.61
1:B:697:GLU:O	1:B:701:ILE:HG12	2.01	0.61
1:A:384:ILE:CD1	1:A:463:LEU:CD1	2.79	0.61
1:A:1148:ASN:ND2	1:A:1151:SER:HB3	2.16	0.61
1:B:674:SER:HB3	1:B:876:ASP:CG	2.25	0.61
1:B:1364:GLU:C	1:B:1365:SER:HG	2.03	0.61
1:A:1050:LYS:HA	1:A:1050:LYS:CE	2.29	0.61
1:A:1277:ILE:HD12	1:A:1277:ILE:O	2.01	0.61
1:B:1058:ILE:HB	1:B:1059:TYR:CE1	2.35	0.61
1:B:1048:TYR:CE1	1:B:1052:ARG:CB	2.84	0.60
1:B:809:ILE:O	1:B:811:ASP:N	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1046:ILE:HD13	1:B:1046:ILE:N	2.02	0.60
1:A:1207:ARG:HD3	1:A:1214:LEU:HD22	1.82	0.60
1:A:1349:LEU:O	1:A:1351:ARG:HB3	2.01	0.60
1:B:1360:VAL:O	1:B:1360:VAL:HG12	2.00	0.60
1:B:1041:ASN:C	1:B:1042:LYS:O	2.44	0.60
1:B:1358:VAL:CG2	1:B:1359:SER:H	2.14	0.60
1:A:914:PHE:H	1:A:1013:ARG:HH22	1.48	0.60
1:B:667:ILE:HG12	1:B:667:ILE:O	2.00	0.60
1:A:713:LEU:HD21	1:A:785:LEU:HD21	1.83	0.60
1:A:933:ILE:HG13	1:A:998:TYR:HE2	1.66	0.60
1:B:1291:PHE:CD1	1:B:1381:LYS:HB3	2.36	0.60
1:A:580:ASN:O	1:A:581:ILE:C	2.44	0.60
1:A:957:LYS:O	1:A:958:ILE:HD12	2.01	0.60
1:B:1274:ASN:O	1:B:1277:ILE:HG12	2.02	0.60
1:A:389:LYS:O	1:A:390:GLU:CB	2.50	0.60
1:A:561:ILE:HG22	1:A:562:LEU:CA	2.11	0.60
1:B:723:LEU:HD23	1:B:727:GLU:CG	2.23	0.60
1:B:983:LEU:O	1:B:986:ILE:HG13	2.01	0.60
1:B:1091:LEU:O	1:B:1162:TYR:HE1	1.85	0.60
1:A:920:GLN:NE2	1:A:1006:ILE:CD1	2.65	0.60
1:A:1013:ARG:O	1:A:1014:ILE:HB	2.01	0.60
1:A:1063:LEU:HD12	1:A:1171:PHE:CZ	2.37	0.60
1:B:434:TYR:HE2	1:B:468:LEU:CG	2.15	0.60
1:B:467:ILE:HG23	1:B:468:LEU:HD13	1.83	0.60
1:B:533:PHE:HE1	1:B:557:LEU:HD13	1.64	0.60
1:B:917:PHE:HD1	1:B:917:PHE:H	1.50	0.60
1:B:1058:ILE:CD1	1:B:1059:TYR:CE2	2.85	0.60
1:B:1191:GLN:HG3	1:B:1307:LEU:HD21	1.84	0.60
1:A:1357:LYS:HD2	1:A:1357:LYS:C	2.26	0.59
1:B:583:ASN:HB2	1:B:586:ILE:HB	1.82	0.59
1:B:1079:ILE:HD12	1:B:1079:ILE:H	1.67	0.59
1:A:667:ILE:HG23	1:A:667:ILE:O	2.01	0.59
1:A:683:LEU:HD22	1:A:793:PHE:HE2	1.63	0.59
1:A:733:LEU:HD12	1:A:751:ILE:CD1	2.32	0.59
1:A:493:ASN:O	1:A:494:ASP:HB3	2.01	0.59
1:B:975:ILE:HG23	1:B:976:LEU:CB	2.32	0.59
1:A:738:LYS:CB	1:A:746:ILE:HG12	2.29	0.59
1:B:381:ASP:O	1:B:384:ILE:CG2	2.45	0.59
1:B:400:ILE:HD13	1:B:400:ILE:N	2.16	0.59
1:B:1277:ILE:HG22	1:B:1294:TYR:CE1	2.37	0.59
1:B:424:GLU:O	1:B:427:LEU:HD13	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:986:ILE:HD12	1:B:986:ILE:C	2.27	0.59
1:B:1075:ILE:CD1	1:B:1290:PRO:HG2	2.32	0.59
1:B:1141:ALA:HB3	1:B:1142:LYS:O	2.02	0.59
1:B:659:ILE:CB	1:B:719:LEU:C	2.75	0.59
1:B:463:LEU:HD13	1:B:463:LEU:C	2.27	0.59
1:B:1060:LYS:HE2	1:B:1060:LYS:H	1.62	0.59
1:B:1212:ILE:HG12	1:B:1252:PHE:HB2	1.84	0.59
1:A:393:LYS:H	1:A:394:GLY:HA2	1.68	0.59
1:A:958:ILE:HG22	1:A:958:ILE:O	2.02	0.59
1:B:405:LYS:O	1:B:409:LYS:N	2.36	0.59
1:B:630:SER:CA	1:B:631:ASP:HB2	2.28	0.59
1:A:793:PHE:N	1:A:793:PHE:HD1	2.00	0.59
1:B:606:LYS:O	1:B:606:LYS:HG2	2.03	0.59
1:A:404:PHE:O	1:A:408:TYR:N	2.33	0.58
1:A:459:ILE:O	1:A:460:GLU:HB3	2.03	0.58
1:A:632:GLU:C	1:A:634:VAL:H	2.11	0.58
1:A:683:LEU:HD22	1:A:793:PHE:CD2	2.28	0.58
1:A:1152:PHE:HA	1:A:1155:ASP:HB2	1.85	0.58
1:B:461:LYS:HG3	1:B:462:ILE:CG1	2.32	0.58
1:B:568:ILE:HA	1:B:625:GLN:HE22	1.68	0.58
1:A:394:GLY:CA	1:A:395:ASN:HB3	2.18	0.58
1:A:548:GLY:N	1:A:549:GLY:HA2	2.18	0.58
1:A:696:ILE:HA	1:A:698:THR:N	2.18	0.58
1:A:555:TYR:O	1:A:581:ILE:HD12	2.02	0.58
1:A:727:GLU:CB	1:A:728:SER:HA	2.33	0.58
1:A:1266:ASN:OD1	1:A:1266:ASN:N	2.35	0.58
1:B:1147:LYS:CB	1:B:1148:ASN:HA	2.32	0.58
1:A:368:LYS:O	1:A:371:ILE:CG2	2.52	0.58
1:A:436:LYS:O	1:A:440:GLU:N	2.30	0.58
1:A:457:ILE:O	1:A:457:ILE:CG2	2.51	0.58
1:A:667:ILE:CG1	1:A:718:ILE:HD12	2.24	0.58
1:A:1152:PHE:O	1:A:1156:TYR:N	2.35	0.58
1:A:401:PHE:HB3	1:A:404:PHE:HE1	1.68	0.58
1:B:491:ARG:HE	1:B:1207:ARG:NH2	1.95	0.58
1:B:913:ASP:C	1:B:915:ASP:HB2	2.28	0.58
1:A:411:ASN:CB	1:A:414:SER:H	2.17	0.58
1:A:535:ARG:HH11	1:A:535:ARG:HB2	1.68	0.58
1:B:524:SER:O	1:B:527:MSE:HG3	2.04	0.58
1:A:659:ILE:CG2	1:A:720:GLU:CA	2.79	0.58
1:B:671:PRO:CB	1:B:675:LYS:HZ2	2.16	0.58
1:B:748:GLU:OE1	1:B:749:ASN:OD1	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:LYS:C	1:A:461:LYS:HZ1	2.11	0.58
1:A:678:PRO:O	1:A:682:ASN:N	2.35	0.58
1:A:848:SER:HB2	1:A:851:VAL:HG23	1.86	0.58
1:B:432:TYR:HA	1:B:435:LEU:HD12	1.86	0.58
1:B:439:ILE:O	1:B:442:ILE:CB	2.41	0.58
1:B:630:SER:HA	1:B:631:ASP:CB	2.29	0.58
1:A:673:PHE:HD1	1:A:714:TYR:CD2	2.22	0.58
1:B:532:ILE:CG2	1:B:562:LEU:HD13	2.32	0.58
1:B:609:ASP:C	1:B:611:GLN:H	2.12	0.58
1:B:1271:LYS:O	1:B:1274:ASN:N	2.37	0.58
1:A:1118:LEU:N	1:A:1125:TYR:CE1	2.72	0.57
1:A:1271:LYS:HB3	1:A:1275:GLU:HB3	1.85	0.57
1:B:373:LYS:O	1:B:377:GLU:N	2.37	0.57
1:B:1058:ILE:HG13	1:B:1059:TYR:CE2	2.38	0.57
1:B:1141:ALA:CB	1:B:1142:LYS:C	2.73	0.57
1:A:590:THR:O	1:A:594:THR:HG23	2.05	0.57
1:A:649:ASN:O	1:A:652:THR:N	2.37	0.57
1:A:979:GLU:CG	1:A:982:LYS:CB	2.82	0.57
1:A:1015:ILE:CG2	1:A:1016:PHE:CD1	2.86	0.57
1:A:1119:ASN:CB	1:A:1120:GLY:HA2	2.29	0.57
1:A:1383:GLU:OE2	1:A:1383:GLU:HA	2.04	0.57
1:B:562:LEU:CD1	1:B:565:LYS:HZ1	2.13	0.57
1:A:638:LEU:HG	1:A:891:CYS:CA	2.34	0.57
1:A:673:PHE:O	1:A:675:LYS:N	2.37	0.57
1:A:973:SER:HB3	1:A:975:ILE:H	1.68	0.57
1:A:932:ASP:N	1:A:932:ASP:OD1	2.34	0.57
1:A:1322:PHE:HE2	1:A:1352:LEU:HD12	1.69	0.57
1:B:897:ASN:CB	1:B:1059:TYR:CE2	2.77	0.57
1:B:1051:GLU:HB3	1:B:1054:ASN:HB2	1.86	0.57
1:B:574:PHE:HB3	1:B:586:ILE:HG12	1.85	0.57
1:B:671:PRO:HG3	1:B:774:GLN:CD	2.27	0.57
1:B:929:TYR:CE2	1:B:1006:ILE:HD11	2.40	0.57
1:B:1269:ILE:CA	1:B:1270:ASN:HB2	2.34	0.57
1:A:568:ILE:CD1	1:A:625:GLN:NE2	2.67	0.57
1:A:637:ALA:HB3	1:A:820:ARG:NH1	2.16	0.57
1:A:720:GLU:HG2	1:A:721:ASP:O	2.03	0.57
1:A:749:ASN:O	1:A:749:ASN:OD1	2.22	0.57
1:A:461:LYS:HA	1:A:461:LYS:CE	2.32	0.57
1:A:631:ASP:N	1:A:631:ASP:OD1	2.37	0.57
1:A:937:ILE:HG21	1:A:953:LYS:HZ1	1.69	0.57
1:B:528:GLU:O	1:B:565:LYS:NZ	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:886:THR:O	1:B:890:GLU:HB2	2.03	0.57
1:B:975:ILE:HG23	1:B:976:LEU:CA	2.34	0.57
1:B:1079:ILE:O	1:B:1083:ILE:HG13	2.04	0.57
1:A:804:GLU:O	1:A:805:ILE:O	2.22	0.57
1:A:1102:ASN:N	1:A:1102:ASN:OD1	2.36	0.57
1:B:533:PHE:HD1	1:B:557:LEU:HD12	1.68	0.57
1:B:606:LYS:HB2	1:B:1219:THR:HG21	1.86	0.57
1:B:753:ASN:O	1:B:757:ASN:N	2.36	0.57
1:B:1262:ASP:C	1:B:1263:LEU:HD12	2.30	0.57
1:B:478:GLN:O	1:B:478:GLN:HG2	2.04	0.57
1:B:774:GLN:O	1:B:778:ILE:HG12	2.05	0.57
1:B:1059:TYR:N	1:B:1059:TYR:CD1	2.73	0.57
1:B:1156:TYR:OH	1:B:1365:SER:HA	2.05	0.57
1:B:1263:LEU:HA	1:B:1270:ASN:ND2	2.19	0.57
1:A:659:ILE:HG22	1:A:719:LEU:C	2.30	0.57
1:A:729:LYS:O	1:A:730:ASN:HB2	2.05	0.57
1:A:1060:LYS:NZ	1:A:1170:GLU:CD	2.63	0.57
1:A:1315:ASN:ND2	1:A:1336:LEU:O	2.38	0.57
1:B:384:ILE:HG23	1:B:385:LYS:N	2.19	0.57
1:B:537:ASN:O	1:B:538:ILE:HG22	2.04	0.57
1:B:606:LYS:HB2	1:B:1219:THR:CB	2.34	0.57
1:B:673:PHE:O	1:B:674:SER:C	2.47	0.57
1:A:685:ARG:HG2	1:A:685:ARG:NH1	2.20	0.56
1:A:917:PHE:N	1:A:917:PHE:CD1	2.73	0.56
1:B:588:LYS:HZ2	1:B:614:GLN:CB	2.17	0.56
1:B:605:SER:HB3	1:B:1219:THR:OG1	2.04	0.56
1:A:541:ASP:OD1	1:A:1273:GLU:CB	2.43	0.56
1:A:793:PHE:CD1	1:A:793:PHE:N	2.73	0.56
1:A:921:THR:OG1	1:A:924:GLU:CB	2.53	0.56
1:A:1099:ILE:O	1:A:1103:LYS:HB2	2.05	0.56
1:B:666:ASP:C	1:B:667:ILE:CG2	2.78	0.56
1:B:1044:GLN:C	1:B:1046:ILE:HD13	2.30	0.56
1:B:1091:LEU:HA	1:B:1093:ASN:N	2.20	0.56
1:A:401:PHE:HB3	1:A:402:GLY:HA2	1.86	0.56
1:A:412:PHE:O	1:A:413:ASP:HB3	2.06	0.56
1:A:632:GLU:C	1:A:634:VAL:N	2.59	0.56
1:A:640:LEU:N	1:A:640:LEU:HD23	2.20	0.56
1:A:733:LEU:HD12	1:A:751:ILE:HD11	1.88	0.56
1:A:900:LEU:CG	1:A:1056:LEU:HD22	2.35	0.56
1:A:902:GLU:HG3	1:A:1057:TYR:CD2	2.40	0.56
1:A:946:ASN:O	1:A:950:VAL:N	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1105:SER:O	1:A:1109:ALA:N	2.37	0.56
1:B:606:LYS:CD	1:B:1219:THR:HG21	2.34	0.56
1:B:666:ASP:O	1:B:667:ILE:CG2	2.53	0.56
1:B:669:TYR:HB3	1:B:755:TYR:OH	2.06	0.56
1:B:683:LEU:O	1:B:684:TYR:C	2.47	0.56
1:B:900:LEU:CD2	1:B:901:GLU:N	2.62	0.56
1:B:975:ILE:CG2	1:B:976:LEU:CA	2.83	0.56
1:B:1059:TYR:H	1:B:1060:LYS:HB2	1.67	0.56
1:A:648:LYS:CB	1:A:650:ILE:CD1	2.84	0.56
1:B:560:LYS:CE	1:B:563:ASN:CB	2.84	0.56
1:B:975:ILE:HG23	1:B:976:LEU:HA	1.86	0.56
1:A:648:LYS:CB	1:A:650:ILE:HG13	2.35	0.56
1:A:772:LYS:O	1:A:776:LYS:HG3	2.06	0.56
1:A:1079:ILE:HD11	1:A:1177:ILE:HD12	1.86	0.56
1:B:930:TYR:OH	1:B:953:LYS:HB3	2.06	0.56
1:A:435:LEU:O	1:A:439:ILE:HG12	2.06	0.56
1:A:649:ASN:O	1:A:652:THR:HB	2.06	0.56
1:A:820:ARG:HB3	1:A:820:ARG:CZ	2.35	0.56
1:A:1192:MSE:HE2	1:A:1278:ARG:HB2	1.86	0.56
1:B:609:ASP:O	1:B:611:GLN:N	2.31	0.56
1:A:729:LYS:O	1:A:729:LYS:HD3	2.06	0.56
1:A:1367:ASN:CG	1:A:1371:ILE:HD11	2.24	0.56
1:B:358:PHE:HB3	1:B:480:THR:HG21	1.87	0.56
1:B:682:ASN:C	1:B:685:ARG:HB3	2.31	0.56
1:B:1259:PHE:N	1:B:1259:PHE:CD1	2.73	0.56
1:A:1049:PRO:HD2	1:A:1056:LEU:O	2.05	0.56
1:B:659:ILE:CB	1:B:719:LEU:HB3	2.36	0.56
1:B:1141:ALA:HB3	1:B:1143:ASN:N	2.20	0.56
1:B:1267:SER:CB	1:B:1268:GLU:HA	2.07	0.56
1:A:404:PHE:CZ	1:A:439:ILE:CG2	2.71	0.55
1:A:807:LYS:C	1:A:809:ILE:N	2.59	0.55
1:B:823:VAL:HG12	1:B:824:LYS:H	1.71	0.55
1:A:1123:LYS:O	1:A:1127:GLU:CB	2.54	0.55
1:B:481:LEU:HD21	1:B:1259:PHE:HD2	1.69	0.55
1:B:531:LYS:C	1:B:562:LEU:CD1	2.80	0.55
1:B:535:ARG:CD	1:B:540:ASN:O	2.50	0.55
1:A:507:ARG:HG2	1:A:866:LEU:HD22	1.88	0.55
1:A:547:PHE:N	1:A:547:PHE:CD1	2.72	0.55
1:A:732:PHE:CD1	1:A:784:TYR:CG	2.93	0.55
1:B:981:ARG:HG3	1:B:982:LYS:N	2.21	0.55
1:B:1366:TYR:CD1	1:B:1366:TYR:C	2.85	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:LEU:HD23	1:A:383:LEU:C	2.31	0.55
1:A:576:ASP:C	1:A:578:LYS:H	2.15	0.55
1:A:902:GLU:OE2	1:A:1057:TYR:CD2	2.58	0.55
1:B:892:ILE:HD11	1:B:1015:ILE:HD12	1.89	0.55
1:B:1047:TYR:N	1:B:1047:TYR:CD1	2.73	0.55
1:A:662:GLU:CD	1:A:663:ASN:H	2.15	0.55
1:A:729:LYS:HD2	1:A:788:ASN:OD1	2.07	0.55
1:B:461:LYS:HG3	1:B:462:ILE:HG13	1.88	0.55
1:B:1350:GLU:HA	1:B:1352:LEU:HD13	1.89	0.55
1:A:798:PHE:CD1	1:A:799:LYS:N	2.73	0.55
1:A:806:LYS:H	1:A:809:ILE:CD1	2.18	0.55
1:A:1147:LYS:O	1:A:1148:ASN:C	2.50	0.55
1:A:1228:ARG:HD2	1:A:1265:GLU:HG3	1.89	0.55
1:B:398:THR:O	1:B:402:GLY:N	2.32	0.55
1:B:552:GLU:CA	1:B:553:LYS:CB	2.85	0.55
1:B:657:ILE:HD13	1:B:657:ILE:H	1.72	0.55
1:B:1115:ASN:OD1	1:B:1360:VAL:HG23	2.06	0.55
1:B:1322:PHE:HZ	1:B:1342:LEU:HD21	1.71	0.55
1:A:404:PHE:CD1	1:A:404:PHE:N	2.73	0.55
1:A:673:PHE:HD1	1:A:714:TYR:HD2	1.53	0.55
1:A:738:LYS:HE3	1:A:746:ILE:CG1	2.30	0.55
1:A:1356:LYS:CB	1:A:1368:SER:OG	2.45	0.55
1:A:401:PHE:N	1:A:401:PHE:CD1	2.73	0.55
1:A:735:GLU:HB3	1:A:784:TYR:HE2	1.72	0.55
1:A:1188:LEU:HD22	1:A:1303:VAL:HG21	1.89	0.55
1:A:1277:ILE:CD1	1:A:1281:ILE:CD1	2.77	0.55
1:B:667:ILE:O	1:B:667:ILE:HG23	2.06	0.55
1:B:917:PHE:N	1:B:917:PHE:CD1	2.73	0.55
1:A:464:ASN:HD21	1:A:467:ILE:CG1	2.07	0.54
1:A:1024:TYR:CD1	1:A:1024:TYR:C	2.85	0.54
1:B:493:ASN:N	1:B:493:ASN:OD1	2.40	0.54
1:B:631:ASP:OD2	1:B:888:ARG:HA	2.07	0.54
1:B:1188:LEU:HD22	1:B:1303:VAL:HG21	1.88	0.54
1:A:738:LYS:NZ	1:A:743:ILE:HA	2.22	0.54
1:A:786:ARG:O	1:A:790:GLU:HB2	2.06	0.54
1:A:792:LEU:CD1	1:A:793:PHE:CD1	2.85	0.54
1:A:1044:GLN:HA	1:A:1048:TYR:CE1	2.42	0.54
1:B:1130:ILE:O	1:B:1130:ILE:HG22	2.05	0.54
1:A:461:LYS:CE	1:A:461:LYS:CA	2.85	0.54
1:A:647:LYS:CB	1:A:648:LYS:CB	2.86	0.54
1:A:1096:GLY:HA2	1:A:1099:ILE:HG12	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:671:PRO:HB3	1:B:675:LYS:NZ	2.22	0.54
1:B:1366:TYR:CE1	1:B:1367:ASN:CG	2.85	0.54
1:A:544:ILE:CG2	1:A:555:TYR:HE2	2.21	0.54
1:A:694:ASP:CB	1:A:800:MSE:HG2	2.38	0.54
1:A:941:PHE:O	1:A:946:ASN:ND2	2.41	0.54
1:B:538:ILE:HG23	1:B:538:ILE:O	2.08	0.54
1:B:608:ARG:HA	1:B:609:ASP:O	2.08	0.54
1:B:1136:ASN:OD1	1:B:1149:TYR:CE1	2.61	0.54
1:A:637:ALA:CB	1:A:820:ARG:NH1	2.69	0.54
1:A:1032:ILE:HD13	1:A:1048:TYR:HD2	1.72	0.54
1:B:427:LEU:O	1:B:431:ILE:HG12	2.07	0.54
1:B:1036:GLU:CB	1:B:1038:GLU:OE1	2.56	0.54
1:B:1256:CYS:O	1:B:1261:ILE:HG13	2.08	0.54
1:A:409:LYS:CA	1:A:410:VAL:CB	2.85	0.54
1:A:774:GLN:O	1:A:778:ILE:HG12	2.07	0.54
1:B:835:ASP:O	1:B:838:TYR:HB3	2.08	0.54
1:B:1044:GLN:HA	1:B:1048:TYR:OH	2.08	0.54
1:B:1046:ILE:C	1:B:1047:TYR:CD1	2.85	0.54
1:A:355:VAL:O	1:A:359:VAL:HG23	2.08	0.54
1:A:368:LYS:CA	1:A:371:ILE:HG22	2.38	0.54
1:A:375:LEU:HB3	1:A:380:ILE:HD11	1.86	0.54
1:A:568:ILE:CD1	1:A:625:GLN:HE22	2.16	0.54
1:A:733:LEU:O	1:A:737:LYS:HG3	2.08	0.54
1:A:1093:ASN:O	1:A:1094:ILE:HB	2.07	0.54
1:A:1128:LYS:O	1:A:1132:LYS:NZ	2.41	0.54
1:B:614:GLN:C	1:B:615:ASP:O	2.49	0.54
1:A:409:LYS:CB	1:A:410:VAL:CB	2.85	0.53
1:A:1366:TYR:CD1	1:A:1366:TYR:C	2.85	0.53
1:B:671:PRO:CG	1:B:774:GLN:NE2	2.49	0.53
1:B:830:ILE:HG21	1:B:877:ILE:HG12	1.90	0.53
1:B:980:GLN:O	1:B:980:GLN:HG2	2.06	0.53
1:A:375:LEU:HD22	1:A:380:ILE:CD1	2.22	0.53
1:A:393:LYS:N	1:A:394:GLY:HA2	2.22	0.53
1:A:987:ASN:OD1	1:A:988:LYS:N	2.42	0.53
1:B:710:ASN:HA	1:B:713:LEU:HB3	1.90	0.53
1:B:1265:GLU:CB	1:B:1266:ASN:CB	2.87	0.53
1:A:378:PHE:CE2	1:A:435:LEU:HD12	2.43	0.53
1:A:383:LEU:O	1:A:386:LYS:HB2	2.09	0.53
1:A:1048:TYR:CD1	1:A:1048:TYR:C	2.86	0.53
1:B:1111:LEU:CD2	1:B:1359:SER:OG	2.46	0.53
1:A:662:GLU:HG3	1:A:663:ASN:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:673:PHE:CD1	1:A:714:TYR:HD2	2.26	0.53
1:A:1089:LYS:HD2	1:A:1089:LYS:N	1.94	0.53
1:B:393:LYS:N	1:B:394:GLY:HA2	2.24	0.53
1:B:684:TYR:N	1:B:685:ARG:CB	2.72	0.53
1:A:535:ARG:NH1	1:A:535:ARG:HG2	2.23	0.53
1:A:801:ASN:O	1:A:803:GLN:N	2.38	0.53
1:A:1177:ILE:HG23	1:A:1378:LEU:HD21	1.91	0.53
1:A:1299:GLN:HE22	1:A:1302:ARG:HH11	1.55	0.53
1:B:354:ILE:HG22	1:B:358:PHE:CE2	2.44	0.53
1:B:784:TYR:HE1	1:B:788:ASN:OD1	1.91	0.53
1:A:665:ASN:ND2	1:A:669:TYR:HE2	1.91	0.53
1:A:1291:PHE:O	1:A:1383:GLU:N	2.40	0.53
1:A:1359:SER:OG	1:A:1360:VAL:N	2.37	0.53
1:B:884:LEU:O	1:B:888:ARG:N	2.41	0.53
1:A:613:THR:CG2	1:A:614:GLN:CA	2.85	0.53
1:B:1048:TYR:H	1:B:1057:TYR:N	1.98	0.53
1:A:900:LEU:CB	1:A:1056:LEU:HD22	2.38	0.53
1:A:973:SER:HB3	1:A:974:ASN:CA	2.38	0.53
1:B:654:ILE:O	1:B:657:ILE:HG12	2.09	0.53
1:B:1332:ASP:OD2	1:B:1354:LYS:HE2	2.09	0.53
1:A:636:LYS:HA	1:A:638:LEU:CD1	2.39	0.52
1:A:1192:MSE:HE2	1:A:1278:ARG:CB	2.39	0.52
1:B:873:ASN:C	1:B:873:ASN:HD22	2.17	0.52
1:A:738:LYS:HA	1:A:746:ILE:HG12	1.90	0.52
1:A:1032:ILE:HD13	1:A:1048:TYR:CD2	2.45	0.52
1:B:631:ASP:O	1:B:635:SER:HB3	2.09	0.52
1:B:1367:ASN:C	1:B:1367:ASN:HD22	2.18	0.52
1:A:411:ASN:N	1:A:412:PHE:CA	2.72	0.52
1:B:491:ARG:NH1	1:B:1208:GLU:OE1	2.43	0.52
1:B:807:LYS:H	1:B:807:LYS:HD2	1.73	0.52
1:B:1366:TYR:CD1	1:B:1367:ASN:CG	2.87	0.52
1:A:371:ILE:HD11	1:A:472:ILE:HG21	1.91	0.52
1:A:631:ASP:HB2	1:A:635:SER:HB3	1.91	0.52
1:A:1049:PRO:CD	1:A:1056:LEU:O	2.57	0.52
1:B:1149:TYR:HA	1:B:1152:PHE:HB3	1.90	0.52
1:A:409:LYS:N	1:A:410:VAL:CB	2.73	0.52
1:A:637:ALA:O	1:A:640:LEU:N	2.37	0.52
1:A:663:ASN:OD1	1:A:664:ASN:HB2	2.09	0.52
1:A:673:PHE:O	1:A:674:SER:C	2.53	0.52
1:A:1111:LEU:O	1:A:1115:ASN:N	2.40	0.52
1:B:493:ASN:O	1:B:495:ILE:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:668:LYS:O	1:B:670:LEU:N	2.42	0.52
1:A:368:LYS:HA	1:A:371:ILE:HG22	1.92	0.52
1:A:669:TYR:CD1	1:A:755:TYR:CD2	2.71	0.52
1:A:1052:ARG:HH12	1:A:1054:ASN:CB	2.22	0.52
1:B:748:GLU:O	1:B:749:ASN:CB	2.57	0.52
1:B:1062:ASN:ND2	1:B:1175:ASN:OD1	2.42	0.52
1:B:1141:ALA:N	1:B:1142:LYS:CA	2.71	0.52
1:B:1357:LYS:CG	1:B:1362:GLU:OE1	2.57	0.52
1:A:407:HIS:O	1:A:411:ASN:HA	2.10	0.52
1:A:664:ASN:HB3	1:A:665:ASN:OD1	2.10	0.52
1:A:802:ILE:C	1:A:805:ILE:CB	2.82	0.52
1:B:388:GLU:CB	1:B:389:LYS:HA	2.38	0.52
1:B:408:TYR:O	1:B:411:ASN:N	2.43	0.52
1:B:436:LYS:NZ	1:B:436:LYS:CB	2.73	0.52
1:B:634:VAL:HG21	1:B:891:CYS:HG	1.69	0.52
1:B:900:LEU:O	1:B:902:GLU:N	2.42	0.52
1:A:439:ILE:HD13	1:A:442:ILE:HD11	1.90	0.52
1:A:461:LYS:NZ	1:A:461:LYS:O	2.35	0.52
1:A:1007:LYS:O	1:A:1010:ILE:HB	2.09	0.52
1:A:1052:ARG:NH1	1:A:1054:ASN:CB	2.73	0.52
1:A:1367:ASN:OD1	1:A:1371:ILE:HD12	2.09	0.52
1:B:531:LYS:CB	1:B:562:LEU:CD1	2.67	0.52
1:B:975:ILE:HG22	1:B:976:LEU:CB	2.37	0.52
1:B:1142:LYS:HB3	1:B:1142:LYS:HZ1	1.75	0.52
1:B:1358:VAL:CG2	1:B:1359:SER:N	2.73	0.52
1:A:821:ILE:CG2	1:A:822:THR:N	2.73	0.52
1:B:427:LEU:HD12	1:B:427:LEU:N	2.21	0.52
1:B:582:THR:CA	1:B:583:ASN:CG	2.78	0.52
1:B:807:LYS:HD2	1:B:807:LYS:N	2.24	0.52
1:B:1269:ILE:N	1:B:1270:ASN:CB	2.73	0.52
1:A:418:SER:CB	1:A:419:LYS:CA	2.85	0.52
1:A:546:PHE:CD2	1:A:546:PHE:N	2.73	0.52
1:A:662:GLU:CG	1:A:663:ASN:N	2.73	0.52
1:B:427:LEU:O	1:B:430:ILE:HG13	2.09	0.52
1:B:434:TYR:HE2	1:B:468:LEU:HG	1.75	0.52
1:B:1051:GLU:HB2	1:B:1055:GLU:H	1.74	0.52
1:B:1069:ASN:HB3	1:B:1071:ASN:OD1	2.10	0.52
1:B:1079:ILE:N	1:B:1079:ILE:CD1	2.73	0.52
1:B:492:HIS:HE1	1:B:1200:HIS:HD2	1.56	0.51
1:B:1357:LYS:NZ	1:B:1362:GLU:OE1	2.33	0.51
1:B:434:TYR:CE2	1:B:468:LEU:HG	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:684:TYR:C	1:B:684:TYR:CD1	2.85	0.51
1:B:746:ILE:HB	1:B:747:ASP:OD1	2.10	0.51
1:A:532:ILE:O	1:A:557:LEU:HD23	2.11	0.51
1:A:643:VAL:C	1:A:645:LYS:N	2.63	0.51
1:A:888:ARG:HB2	1:A:888:ARG:HH11	1.75	0.51
1:A:994:LYS:O	1:A:994:LYS:HE3	2.11	0.51
1:A:1010:ILE:O	1:A:1014:ILE:HB	2.10	0.51
1:B:378:PHE:N	1:B:379:LYS:HA	2.25	0.51
1:B:1047:TYR:O	1:B:1048:TYR:HD2	1.93	0.51
1:A:537:ASN:C	1:A:537:ASN:HD22	2.15	0.51
1:B:1059:TYR:N	1:B:1060:LYS:CB	2.72	0.51
1:B:1142:LYS:N	1:B:1143:ASN:CA	2.72	0.51
1:A:671:PRO:HG3	1:A:774:GLN:CG	2.26	0.51
1:A:802:ILE:C	1:A:805:ILE:H	2.19	0.51
1:A:1024:TYR:CE1	1:A:1028:ILE:HD12	2.46	0.51
1:A:1329:VAL:CG2	1:A:1353:MSE:CE	2.59	0.51
1:B:416:LYS:N	1:B:417:PHE:CA	2.74	0.51
1:B:837:GLU:HG2	1:B:874:ILE:HG12	1.93	0.51
1:B:1142:LYS:HB3	1:B:1142:LYS:HZ2	1.73	0.51
1:A:638:LEU:CD2	1:A:639:ASN:ND2	2.73	0.51
1:B:438:ARG:NE	1:B:438:ARG:CA	2.73	0.51
1:B:640:LEU:HD22	1:B:701:ILE:CG2	2.41	0.51
1:B:1046:ILE:H	1:B:1046:ILE:CD1	1.97	0.51
1:B:1156:TYR:HH	1:B:1365:SER:HA	1.75	0.51
1:B:1263:LEU:N	1:B:1263:LEU:CD1	2.73	0.51
1:A:399:GLU:OE2	1:A:400:ILE:CD1	2.59	0.51
1:A:548:GLY:N	1:A:549:GLY:CA	2.73	0.51
1:B:1048:TYR:O	1:B:1049:PRO:C	2.53	0.51
1:B:1078:LEU:HD23	1:B:1374:LEU:HD12	1.93	0.51
1:B:1291:PHE:CZ	1:B:1378:LEU:HD12	2.41	0.51
1:A:350:LYS:CA	1:A:351:LYS:HB3	2.41	0.51
1:A:384:ILE:CD1	1:A:463:LEU:HD11	2.41	0.51
1:A:643:VAL:O	1:A:645:LYS:N	2.44	0.51
1:A:979:GLU:HG2	1:A:982:LYS:CB	2.41	0.51
1:B:489:LYS:HD3	1:B:508:LEU:CD1	2.41	0.51
1:B:642:VAL:O	1:B:642:VAL:HG22	2.10	0.51
1:B:1349:LEU:HD21	1:B:1350:GLU:HG2	1.91	0.51
1:A:461:LYS:NZ	1:A:461:LYS:CA	2.73	0.51
1:A:576:ASP:O	1:A:579:ASN:N	2.44	0.51
1:B:439:ILE:N	1:B:439:ILE:CD1	2.73	0.51
1:B:560:LYS:HD3	1:B:563:ASN:CB	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1075:ILE:HG23	1:B:1177:ILE:HG21	1.92	0.51
1:A:375:LEU:CB	1:A:380:ILE:CD1	2.82	0.50
1:A:535:ARG:HG3	1:A:537:ASN:O	2.11	0.50
1:A:638:LEU:HD22	1:A:639:ASN:ND2	2.25	0.50
1:A:871:TYR:O	1:A:875:ILE:HG13	2.11	0.50
1:B:531:LYS:C	1:B:562:LEU:HD12	2.35	0.50
1:B:976:LEU:CG	1:B:977:GLN:H	2.20	0.50
1:B:461:LYS:CG	1:B:462:ILE:CG1	2.86	0.50
1:B:569:ILE:HG22	1:B:575:ILE:HB	1.92	0.50
1:B:832:ILE:HD11	1:B:838:TYR:HA	1.93	0.50
1:B:1042:LYS:O	1:B:1044:GLN:N	2.44	0.50
1:A:393:LYS:H	1:A:395:ASN:CB	2.21	0.50
1:A:403:ILE:N	1:A:403:ILE:CD1	2.73	0.50
1:A:714:TYR:HE1	1:A:718:ILE:HD11	1.75	0.50
1:A:535:ARG:HH11	1:A:535:ARG:HG2	1.76	0.50
1:A:937:ILE:HD11	1:A:995:VAL:HG22	1.91	0.50
1:A:1024:TYR:HB2	1:A:1067:ILE:CD1	2.41	0.50
1:B:767:ASN:OD1	1:B:767:ASN:N	2.44	0.50
1:B:778:ILE:O	1:B:782:ILE:HG12	2.12	0.50
1:B:1291:PHE:CE1	1:B:1381:LYS:HB3	2.47	0.50
1:A:973:SER:HB3	1:A:975:ILE:N	2.26	0.50
1:B:987:ASN:O	1:B:991:LEU:N	2.31	0.50
1:B:1203:VAL:HG11	1:B:1241:TYR:CD2	2.46	0.50
1:B:616:ASP:HA	1:B:619:LYS:HB2	1.94	0.50
1:B:1027:GLU:HG2	1:B:1076:TYR:HE2	1.76	0.50
1:A:683:LEU:CD2	1:A:793:PHE:HD2	2.21	0.50
1:B:467:ILE:HD12	1:B:467:ILE:C	2.35	0.50
1:B:616:ASP:O	1:B:620:VAL:CB	2.60	0.50
1:B:1265:GLU:CB	1:B:1266:ASN:C	2.84	0.50
1:A:886:THR:O	1:A:890:GLU:HB2	2.10	0.50
1:A:1054:ASN:N	1:A:1055:GLU:CB	2.75	0.50
1:B:1058:ILE:CG1	1:B:1059:TYR:CE2	2.94	0.50
1:B:1265:GLU:CA	1:B:1266:ASN:CB	2.90	0.50
1:A:662:GLU:CG	1:A:663:ASN:H	2.25	0.50
1:B:436:LYS:HB3	1:B:436:LYS:HZ3	1.76	0.50
1:B:425:LYS:O	1:B:428:TYR:N	2.45	0.49
1:B:491:ARG:NE	1:B:1207:ARG:HH21	1.96	0.49
1:A:389:LYS:O	1:A:390:GLU:HB2	2.11	0.49
1:A:493:ASN:OD1	1:A:603:ALA:HB1	2.12	0.49
1:A:535:ARG:HH11	1:A:535:ARG:CB	2.24	0.49
1:A:670:LEU:HD22	1:A:670:LEU:C	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:403:ILE:O	1:B:407:HIS:N	2.41	0.49
1:B:897:ASN:N	1:B:897:ASN:ND2	2.60	0.49
1:A:383:LEU:C	1:A:383:LEU:CD2	2.86	0.49
1:A:493:ASN:OD1	1:A:603:ALA:HB2	2.11	0.49
1:A:920:GLN:NE2	1:A:1006:ILE:HD13	2.27	0.49
1:B:431:ILE:HG23	1:B:472:ILE:HD12	1.94	0.49
1:B:505:PHE:O	1:B:508:LEU:N	2.46	0.49
1:B:516:LEU:HD11	1:B:1194:ARG:HD3	1.93	0.49
1:A:369:GLU:HG3	1:A:373:LYS:HE3	1.92	0.49
1:A:714:TYR:CE1	1:A:718:ILE:HD11	2.48	0.49
1:A:760:ILE:O	1:A:764:LYS:HG2	2.12	0.49
1:B:684:TYR:HB3	1:B:685:ARG:CA	2.42	0.49
1:B:794:ASP:C	1:B:795:PHE:CD1	2.90	0.49
1:B:1200:HIS:CE1	1:B:1224:ALA:HB2	2.48	0.49
1:A:400:ILE:N	1:A:400:ILE:CD1	2.73	0.49
1:A:514:LEU:HD12	1:A:514:LEU:C	2.34	0.49
1:A:1024:TYR:HB2	1:A:1067:ILE:HD11	1.94	0.49
1:A:1105:SER:O	1:A:1109:ALA:HB2	2.12	0.49
1:A:1226:PRO:HD2	1:A:1249:TYR:HE1	1.78	0.49
1:A:1277:ILE:HD11	1:A:1281:ILE:CD1	2.37	0.49
1:B:433:ARG:O	1:B:436:LYS:HG2	2.13	0.49
1:B:616:ASP:HB3	1:B:620:VAL:HG13	1.94	0.49
1:B:666:ASP:O	1:B:667:ILE:HG23	2.13	0.49
1:B:792:LEU:C	1:B:792:LEU:CD2	2.85	0.49
1:B:1041:ASN:O	1:B:1042:LYS:C	2.56	0.49
1:B:1079:ILE:HG22	1:B:1083:ILE:CD1	2.43	0.49
1:B:1163:LYS:HE2	1:B:1366:TYR:CE2	2.47	0.49
1:B:1208:GLU:OE2	1:B:1208:GLU:HA	2.13	0.49
1:A:546:PHE:C	1:A:547:PHE:CD1	2.90	0.49
1:B:439:ILE:HA	1:B:442:ILE:HB	1.93	0.49
1:B:851:VAL:HA	1:B:854:LYS:HG3	1.95	0.49
1:B:1058:ILE:HD12	1:B:1059:TYR:CZ	2.47	0.49
1:A:792:LEU:C	1:A:792:LEU:CD1	2.85	0.49
1:A:1177:ILE:HD11	1:A:1374:LEU:CD1	2.35	0.49
1:A:1269:ILE:O	1:A:1278:ARG:NH2	2.46	0.49
1:B:1049:PRO:O	1:B:1050:LYS:HB2	2.13	0.49
1:A:825:THR:C	1:A:826:SER:O	2.48	0.49
1:A:1148:ASN:ND2	1:A:1151:SER:CB	2.75	0.49
1:B:412:PHE:CB	1:B:413:ASP:CA	2.87	0.49
1:B:434:TYR:CE2	1:B:468:LEU:HD21	2.47	0.49
1:B:823:VAL:HG12	1:B:824:LYS:N	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1251:LYS:O	1:B:1255:ILE:HG12	2.13	0.49
1:A:735:GLU:HB3	1:A:784:TYR:CE2	2.48	0.49
1:B:1249:TYR:CE1	1:B:1253:GLU:HB2	2.48	0.49
1:A:395:ASN:CG	1:A:396:CYS:H	2.13	0.49
1:A:403:ILE:O	1:A:406:LYS:CB	2.61	0.49
1:A:608:ARG:HH21	1:A:836:PHE:HB2	1.75	0.49
1:A:1382:ILE:O	1:A:1382:ILE:HG23	2.12	0.49
1:B:570:ARG:HA	1:B:575:ILE:HG22	1.94	0.49
1:B:900:LEU:HD13	1:B:1056:LEU:CG	2.37	0.49
1:B:1265:GLU:HA	1:B:1266:ASN:HB2	1.94	0.49
1:A:638:LEU:C	1:A:638:LEU:CD2	2.85	0.48
1:A:1105:SER:O	1:A:1109:ALA:CB	2.61	0.48
1:B:608:ARG:CA	1:B:609:ASP:C	2.78	0.48
1:B:1099:ILE:HG22	1:B:1104:ILE:HG13	1.94	0.48
1:A:973:SER:N	1:A:974:ASN:HA	2.29	0.48
1:B:431:ILE:HG22	1:B:435:LEU:HD11	1.94	0.48
1:B:669:TYR:CB	1:B:755:TYR:OH	2.62	0.48
1:A:416:LYS:O	1:A:417:PHE:C	2.56	0.48
1:A:767:ASN:HB2	1:A:867:ASN:CG	2.37	0.48
1:B:1043:PHE:O	1:B:1046:ILE:HD11	2.13	0.48
1:B:1051:GLU:HB2	1:B:1055:GLU:N	2.28	0.48
1:A:418:SER:HB2	1:A:419:LYS:CA	2.18	0.48
1:A:1055:GLU:HG3	1:A:1057:TYR:CZ	2.49	0.48
1:B:624:ILE:O	1:B:628:LYS:HG2	2.14	0.48
1:B:711:LYS:O	1:B:715:LYS:HG3	2.13	0.48
1:B:1069:ASN:ND2	1:B:1178:GLU:OE2	2.46	0.48
1:A:462:ILE:HG22	1:A:463:LEU:C	2.37	0.48
1:B:457:ILE:O	1:B:457:ILE:CG2	2.49	0.48
1:B:1044:GLN:CA	1:B:1048:TYR:HE2	2.11	0.48
1:A:417:PHE:C	1:A:418:SER:HG	2.10	0.48
1:A:462:ILE:CG2	1:A:463:LEU:H	2.24	0.48
1:A:659:ILE:CG2	1:A:719:LEU:O	2.61	0.48
1:A:899:ASN:OD1	1:A:1059:TYR:HD1	1.95	0.48
1:A:997:GLN:O	1:A:1000:LYS:HB2	2.13	0.48
1:A:1118:LEU:HB2	1:A:1125:TYR:CZ	2.32	0.48
1:B:490:LEU:O	1:B:493:ASN:O	2.32	0.48
1:B:568:ILE:HD13	1:B:845:LEU:O	2.14	0.48
1:B:899:ASN:HA	1:B:900:LEU:HA	1.58	0.48
1:A:659:ILE:HG21	1:A:719:LEU:C	2.39	0.48
1:A:758:ALA:O	1:A:762:ALA:N	2.37	0.48
1:A:979:GLU:CD	1:A:982:LYS:CB	2.87	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1349:LEU:O	1:A:1349:LEU:HD12	2.14	0.48
1:B:647:LYS:CB	1:B:648:LYS:CG	2.85	0.48
1:B:792:LEU:O	1:B:792:LEU:HD23	2.13	0.48
1:B:893:THR:O	1:B:897:ASN:ND2	2.47	0.48
1:A:356:LYS:HG2	1:A:1211:ILE:HD11	1.96	0.48
1:A:538:ILE:HG13	1:A:538:ILE:O	2.13	0.48
1:A:613:THR:HG23	1:A:614:GLN:CA	2.31	0.48
1:A:614:GLN:CB	1:A:618:ASN:CB	2.90	0.48
1:B:486:TYR:O	1:B:490:LEU:HG	2.14	0.48
1:B:671:PRO:HB2	1:B:675:LYS:HD3	1.96	0.48
1:A:473:LEU:CD2	1:A:477:LYS:HE3	2.44	0.48
1:A:1134:LYS:HG3	1:A:1135:GLU:HG2	1.94	0.48
1:B:746:ILE:O	1:B:747:ASP:HB2	2.14	0.48
1:B:920:GLN:O	1:B:925:ILE:CD1	2.62	0.48
1:B:1262:ASP:O	1:B:1263:LEU:HD12	2.14	0.48
1:A:374:ILE:HG23	1:A:428:TYR:CE2	2.49	0.48
1:A:501:ASN:HB3	1:A:504:ASP:H	1.79	0.48
1:A:738:LYS:CA	1:A:746:ILE:HG12	2.44	0.48
1:A:1227:LYS:HG3	1:A:1270:ASN:ND2	2.29	0.48
1:B:507:ARG:O	1:B:866:LEU:HD21	2.14	0.48
1:B:1164:LYS:HD3	1:B:1367:ASN:H	1.79	0.48
1:A:398:THR:O	1:A:399:GLU:C	2.57	0.47
1:A:1026:LYS:HG3	1:A:1027:GLU:N	2.29	0.47
1:A:1330:ASN:HD22	1:A:1357:LYS:HG2	1.79	0.47
1:B:1046:ILE:C	1:B:1047:TYR:HD1	2.21	0.47
1:B:1142:LYS:CG	1:B:1144:ILE:N	2.77	0.47
1:B:461:LYS:HG3	1:B:462:ILE:CB	2.45	0.47
1:B:809:ILE:C	1:B:811:ASP:N	2.72	0.47
1:B:1063:LEU:HD12	1:B:1171:PHE:CE1	2.49	0.47
1:B:1072:PHE:HA	1:B:1075:ILE:HB	1.96	0.47
1:B:1084:LYS:NZ	1:B:1084:LYS:HB3	2.30	0.47
1:B:1352:LEU:HD13	1:B:1352:LEU:H	1.78	0.47
1:A:806:LYS:HA	1:A:809:ILE:HD13	1.97	0.47
1:A:1111:LEU:CD2	1:A:1359:SER:OG	2.61	0.47
1:B:641:ASP:C	1:B:643:VAL:H	2.21	0.47
1:B:907:MSE:O	1:B:911:GLU:CG	2.62	0.47
1:B:1223:ARG:HB3	1:B:1223:ARG:NH1	2.29	0.47
1:A:802:ILE:O	1:A:805:ILE:CA	2.63	0.47
1:B:1130:ILE:O	1:B:1130:ILE:CG2	2.63	0.47
1:A:368:LYS:CA	1:A:371:ILE:CG2	2.90	0.47
1:A:408:TYR:C	1:A:411:ASN:N	2.73	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1133:LEU:CD2	1:A:1149:TYR:CE2	2.98	0.47
1:A:1199:MSE:O	1:A:1203:VAL:HG23	2.14	0.47
1:A:1346:ASN:ND2	1:A:1349:LEU:HD22	2.25	0.47
1:B:376:ALA:CA	1:B:379:LYS:CB	2.92	0.47
1:B:385:LYS:O	1:B:388:GLU:N	2.45	0.47
1:B:609:ASP:O	1:B:610:LEU:CB	2.59	0.47
1:B:620:VAL:HA	1:B:623:ILE:HD12	1.96	0.47
1:B:627:LEU:HD21	1:B:829:THR:HA	1.95	0.47
1:B:656:ASP:OD1	1:B:656:ASP:N	2.47	0.47
1:B:807:LYS:HE3	1:B:807:LYS:HB3	1.62	0.47
1:B:842:ILE:O	1:B:846:LEU:HD13	2.14	0.47
1:A:431:ILE:O	1:A:435:LEU:HG	2.15	0.47
1:A:461:LYS:NZ	1:A:461:LYS:C	2.73	0.47
1:A:684:TYR:OH	1:A:693:PHE:CE2	2.68	0.47
1:A:1215:SER:OG	1:A:1242:LYS:HB3	2.10	0.47
1:B:614:GLN:O	1:B:615:ASP:C	2.56	0.47
1:A:500:VAL:O	1:A:500:VAL:HG13	2.14	0.47
1:A:755:TYR:C	1:A:755:TYR:CD1	2.89	0.47
1:B:900:LEU:CD1	1:B:1056:LEU:HD13	2.44	0.47
1:B:1177:ILE:HD11	1:B:1374:LEU:HD21	1.96	0.47
1:A:995:VAL:O	1:A:996:ASP:C	2.58	0.47
1:A:1047:TYR:HE1	1:A:1171:PHE:HE2	1.61	0.47
1:A:1089:LYS:C	1:A:1089:LYS:CD	2.85	0.47
1:B:398:THR:O	1:B:398:THR:HG22	2.15	0.46
1:B:439:ILE:CA	1:B:442:ILE:HB	2.45	0.46
1:B:772:LYS:O	1:B:776:LYS:HG3	2.15	0.46
1:B:920:GLN:O	1:B:925:ILE:HD11	2.16	0.46
1:B:925:ILE:HD13	1:B:1003:ASP:OD1	2.14	0.46
1:B:1055:GLU:O	1:B:1056:LEU:C	2.58	0.46
1:A:485:MSE:HE1	1:A:1309:TYR:CE1	2.50	0.46
1:A:578:LYS:O	1:A:579:ASN:HB2	2.15	0.46
1:A:702:VAL:HG11	1:A:795:PHE:HE2	1.81	0.46
1:A:986:ILE:O	1:A:987:ASN:ND2	2.48	0.46
1:A:1096:GLY:O	1:A:1099:ILE:N	2.48	0.46
1:A:1277:ILE:HG23	1:A:1278:ARG:N	2.30	0.46
1:A:1375:ILE:O	1:A:1379:LEU:HG	2.15	0.46
1:A:368:LYS:HA	1:A:371:ILE:HG21	1.95	0.46
1:A:1046:ILE:HG21	1:A:1169:VAL:HG11	1.97	0.46
1:A:1322:PHE:CE2	1:A:1352:LEU:HD12	2.50	0.46
1:B:665:ASN:HD22	1:B:665:ASN:N	2.13	0.46
1:B:713:LEU:HG	1:B:717:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:930:TYR:CE2	1:B:954:LYS:HG2	2.50	0.46
1:A:464:ASN:ND2	1:A:467:ILE:CG1	2.73	0.46
1:A:566:ILE:HA	1:A:569:ILE:HG22	1.96	0.46
1:B:462:ILE:HD13	1:B:464:ASN:ND2	2.31	0.46
1:B:613:THR:HA	1:B:614:GLN:HA	1.72	0.46
1:B:671:PRO:HG3	1:B:774:GLN:HE21	1.64	0.46
1:B:880:GLU:O	1:B:884:LEU:HG	2.14	0.46
1:A:575:ILE:C	1:A:582:THR:HG23	2.40	0.46
1:A:748:GLU:HG3	1:A:749:ASN:N	2.30	0.46
1:A:756:LYS:O	1:A:759:GLN:HG2	2.16	0.46
1:B:531:LYS:C	1:B:562:LEU:HD11	2.40	0.46
1:B:615:ASP:C	1:B:617:TYR:H	2.23	0.46
1:B:671:PRO:CB	1:B:675:LYS:NZ	2.78	0.46
1:B:1028:ILE:O	1:B:1032:ILE:HG12	2.16	0.46
1:B:756:LYS:O	1:B:759:GLN:HG2	2.16	0.46
1:B:1262:ASP:C	1:B:1263:LEU:CD1	2.89	0.46
1:A:528:GLU:OE1	1:A:565:LYS:HD3	2.15	0.46
1:A:569:ILE:O	1:A:574:PHE:HB2	2.16	0.46
1:A:901:GLU:H	1:A:1056:LEU:HD23	1.79	0.46
1:A:946:ASN:O	1:A:950:VAL:HG23	2.16	0.46
1:B:350:LYS:O	1:B:351:LYS:HB3	2.16	0.46
1:B:485:MSE:HG3	1:B:1202:ILE:HD11	1.97	0.46
1:B:539:ASN:ND2	1:B:551:ARG:HH12	2.14	0.46
1:B:578:LYS:O	1:B:579:ASN:CB	2.63	0.46
1:A:405:LYS:O	1:A:409:LYS:N	2.40	0.46
1:A:718:ILE:HA	1:A:733:LEU:HD21	1.98	0.46
1:A:994:LYS:HA	1:A:994:LYS:HD2	1.82	0.46
1:B:562:LEU:HD13	1:B:565:LYS:CE	2.45	0.46
1:B:675:LYS:O	1:B:678:PRO:HD2	2.15	0.46
1:A:397:ASP:O	1:A:400:ILE:HG12	2.16	0.46
1:A:547:PHE:N	1:A:547:PHE:HD1	2.14	0.46
1:A:608:ARG:HD3	1:A:608:ARG:HA	1.70	0.46
1:A:900:LEU:HG	1:A:1056:LEU:HD22	1.97	0.46
1:B:685:ARG:HB3	1:B:686:ASN:H	1.59	0.46
1:B:1119:ASN:HA	1:B:1120:GLY:HA2	1.69	0.46
1:A:370:LYS:HE3	1:A:370:LYS:HB2	1.76	0.46
1:A:576:ASP:OD2	1:A:580:ASN:O	2.34	0.46
1:A:759:GLN:O	1:A:763:SER:N	2.46	0.46
1:A:1055:GLU:N	1:A:1055:GLU:CD	2.73	0.46
1:A:1072:PHE:CD2	1:A:1076:TYR:HB2	2.51	0.46
1:B:439:ILE:HA	1:B:442:ILE:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:539:ASN:HD21	1:B:551:ARG:HH12	1.63	0.46
1:B:900:LEU:CD1	1:B:1056:LEU:CB	2.55	0.46
1:A:1096:GLY:O	1:A:1099:ILE:HB	2.16	0.45
1:B:644:PHE:HE2	1:B:651:ILE:CG1	2.29	0.45
1:B:804:GLU:O	1:B:807:LYS:HG2	2.16	0.45
1:B:969:ILE:CB	1:B:970:ASP:CB	2.88	0.45
1:B:1035:MSE:O	1:B:1038:GLU:CD	2.60	0.45
1:B:1367:ASN:ND2	1:B:1367:ASN:C	2.72	0.45
1:B:1048:TYR:O	1:B:1048:TYR:CD2	2.70	0.45
1:A:696:ILE:CB	1:A:700:LYS:H	2.30	0.45
1:A:806:LYS:N	1:A:809:ILE:HD13	2.32	0.45
1:A:930:TYR:OH	1:A:954:LYS:HG2	2.15	0.45
1:A:1215:SER:HG	1:A:1242:LYS:CB	2.29	0.45
1:B:434:TYR:CE2	1:B:468:LEU:CG	2.96	0.45
1:B:735:GLU:O	1:B:739:THR:HG23	2.17	0.45
1:B:1048:TYR:O	1:B:1048:TYR:CG	2.69	0.45
1:A:762:ALA:CB	1:A:770:ILE:CG1	2.80	0.45
1:A:766:ASN:OD1	1:A:769:ALA:HB2	2.16	0.45
1:B:559:LYS:HB3	1:B:560:LYS:H	1.47	0.45
1:B:609:ASP:C	1:B:611:GLN:N	2.74	0.45
1:B:631:ASP:OD2	1:B:888:ARG:HG2	2.16	0.45
1:B:1084:LYS:HB3	1:B:1084:LYS:HZ3	1.80	0.45
1:A:930:TYR:OH	1:A:954:LYS:N	2.49	0.45
1:B:355:VAL:O	1:B:359:VAL:HG23	2.16	0.45
1:B:732:PHE:HB2	1:B:784:TYR:CE2	2.51	0.45
1:B:1269:ILE:CA	1:B:1270:ASN:CB	2.95	0.45
1:A:1078:LEU:HD12	1:A:1177:ILE:HD13	1.99	0.45
1:B:675:LYS:NZ	1:B:774:GLN:OE1	2.50	0.45
1:B:900:LEU:CG	1:B:1056:LEU:HD12	2.42	0.45
1:B:900:LEU:HD21	1:B:1056:LEU:HD12	1.84	0.45
1:B:1062:ASN:HB2	1:B:1170:GLU:O	2.17	0.45
1:A:554:ASN:H	1:A:555:TYR:HA	1.82	0.45
1:A:791:GLU:O	1:A:792:LEU:C	2.60	0.45
1:B:515:ASP:O	1:B:519:ILE:HG12	2.17	0.45
1:B:521:PHE:CD2	1:B:855:ILE:HD12	2.52	0.45
1:B:771:LYS:NZ	1:B:869:SER:HB2	2.32	0.45
1:B:833:ASN:OD1	1:B:834:ASP:N	2.46	0.45
1:A:682:ASN:O	1:A:686:ASN:N	2.44	0.45
1:A:1006:ILE:O	1:A:1006:ILE:HG22	2.16	0.45
1:B:531:LYS:HB3	1:B:562:LEU:CD1	2.14	0.45
1:B:626:ASN:O	1:B:629:ILE:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:695:THR:OG1	1:B:698:THR:HG23	2.17	0.45
1:A:934:LYS:O	1:A:938:LEU:HG	2.17	0.45
1:A:1112:LYS:O	1:A:1115:ASN:N	2.49	0.45
1:A:1152:PHE:O	1:A:1155:ASP:N	2.50	0.45
1:B:753:ASN:O	1:B:757:ASN:OD1	2.34	0.45
1:A:411:ASN:CB	1:A:414:SER:N	2.79	0.45
1:A:1229:ASN:HB3	1:A:1238:THR:HG21	1.99	0.45
1:A:1244:PHE:CD2	1:A:1245:ASP:OD2	2.70	0.45
1:B:461:LYS:HA	1:B:462:ILE:HA	1.77	0.45
1:B:464:ASN:H	1:B:467:ILE:HG21	1.82	0.45
1:B:500:VAL:O	1:B:505:PHE:CE1	2.70	0.45
1:B:749:ASN:ND2	1:B:749:ASN:C	2.73	0.45
1:A:868:THR:CG2	1:A:869:SER:N	2.79	0.44
1:A:973:SER:CB	1:A:974:ASN:HA	2.37	0.44
1:A:980:GLN:O	1:A:984:SER:N	2.50	0.44
1:A:1048:TYR:CD1	1:A:1048:TYR:O	2.70	0.44
1:A:1053:LYS:O	1:A:1055:GLU:CB	2.31	0.44
1:A:1094:ILE:O	1:A:1094:ILE:HG22	2.18	0.44
1:B:494:ASP:O	1:B:495:ILE:CD1	2.58	0.44
1:B:575:ILE:HG12	1:B:579:ASN:HA	1.98	0.44
1:B:917:PHE:O	1:B:917:PHE:CD1	2.70	0.44
1:B:1113:ASN:O	1:B:1117:LYS:N	2.47	0.44
1:B:1357:LYS:HD3	1:B:1362:GLU:CD	2.40	0.44
1:A:755:TYR:CD1	1:A:755:TYR:O	2.70	0.44
1:A:1017:ASN:HD22	1:A:1020:PHE:HD1	1.65	0.44
1:A:1027:GLU:HA	1:A:1027:GLU:OE2	2.17	0.44
1:A:1048:TYR:CD1	1:A:1049:PRO:O	2.66	0.44
1:A:1075:ILE:HD11	1:A:1181:LEU:HD11	1.99	0.44
1:B:531:LYS:HB2	1:B:562:LEU:CD1	2.44	0.44
1:B:856:ARG:CD	1:B:875:ILE:HG23	2.48	0.44
1:A:499:THR:O	1:A:499:THR:OG1	2.34	0.44
1:B:512:GLU:CD	1:B:1197:ARG:HH21	2.26	0.44
1:B:793:PHE:O	1:B:795:PHE:CD1	2.70	0.44
1:B:1046:ILE:O	1:B:1047:TYR:HD1	2.00	0.44
1:A:375:LEU:CB	1:A:380:ILE:HD11	2.46	0.44
1:A:557:LEU:HD11	1:A:566:ILE:HD11	2.00	0.44
1:A:738:LYS:CD	1:A:746:ILE:HD11	2.47	0.44
1:A:799:LYS:O	1:A:804:GLU:HB3	2.17	0.44
1:A:899:ASN:HD22	1:A:899:ASN:HA	1.60	0.44
1:A:1148:ASN:HD21	1:A:1151:SER:HB3	1.82	0.44
1:A:1278:ARG:HE	1:A:1278:ARG:HB3	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:354:ILE:CG2	1:B:358:PHE:HE2	2.30	0.44
1:B:1265:GLU:HA	1:B:1266:ASN:CB	2.47	0.44
1:B:1365:SER:O	1:B:1366:TYR:CD2	2.70	0.44
1:A:979:GLU:OE2	1:A:982:LYS:CB	2.66	0.44
1:B:1366:TYR:CE1	1:B:1367:ASN:OD1	2.71	0.44
1:A:920:GLN:NE2	1:A:1006:ILE:HD12	2.31	0.44
1:A:1209:LEU:HB2	1:A:1211:ILE:HG13	2.00	0.44
1:A:1230:GLY:HA2	1:A:1231:SER:HA	1.52	0.44
1:B:355:VAL:HG21	1:B:483:HIS:CD2	2.51	0.44
1:B:358:PHE:CE1	1:B:427:LEU:HG	2.52	0.44
1:B:576:ASP:CG	1:B:577:ASN:N	2.74	0.44
1:B:605:SER:CB	1:B:1219:THR:OG1	2.65	0.44
1:B:644:PHE:HD1	1:B:644:PHE:HA	1.71	0.44
1:B:1097:LYS:O	1:B:1098:ASN:C	2.61	0.44
1:B:1293:ASP:O	1:B:1294:TYR:CD2	2.70	0.44
1:A:384:ILE:HD13	1:A:463:LEU:HD12	2.00	0.44
1:A:638:LEU:C	1:A:640:LEU:HD23	2.43	0.44
1:A:665:ASN:ND2	1:A:669:TYR:CE2	2.72	0.44
1:A:740:LEU:HD13	1:A:754:TYR:CD2	2.53	0.44
1:A:378:PHE:N	1:A:379:LYS:HA	2.32	0.44
1:A:673:PHE:C	1:A:675:LYS:N	2.75	0.44
1:A:804:GLU:CD	1:A:804:GLU:C	2.85	0.44
1:A:1291:PHE:N	1:A:1291:PHE:CD1	2.85	0.44
1:B:424:GLU:CA	1:B:427:LEU:HD13	2.44	0.44
1:A:1366:TYR:C	1:A:1368:SER:H	2.25	0.44
1:A:1370:TYR:CD1	1:A:1370:TYR:C	2.95	0.44
1:B:569:ILE:CG2	1:B:575:ILE:HB	2.47	0.44
1:B:1365:SER:O	1:B:1366:TYR:CG	2.70	0.44
1:A:377:GLU:HG2	1:A:377:GLU:O	2.17	0.43
1:A:968:GLU:CA	1:A:969:ILE:CB	2.85	0.43
1:B:432:TYR:HD1	1:B:432:TYR:O	2.01	0.43
1:B:636:LYS:O	1:B:641:ASP:HB2	2.17	0.43
1:B:681:LEU:O	1:B:685:ARG:NH1	2.50	0.43
1:A:405:LYS:HE3	1:A:405:LYS:HB3	1.66	0.43
1:A:1367:ASN:OD1	1:A:1371:ILE:CD1	2.64	0.43
1:B:424:GLU:C	1:B:427:LEU:HD13	2.42	0.43
1:B:601:LEU:O	1:B:602:HIS:HB2	2.17	0.43
1:A:546:PHE:O	1:A:547:PHE:CG	2.72	0.43
1:A:775:LYS:NZ	1:A:775:LYS:CB	2.73	0.43
1:B:614:GLN:CB	1:B:618:ASN:CB	2.96	0.43
1:B:629:ILE:HB	1:B:888:ARG:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:830:ILE:HG21	1:B:877:ILE:CD1	2.49	0.43
1:B:946:ASN:O	1:B:950:VAL:HG23	2.18	0.43
1:B:1147:LYS:N	1:B:1148:ASN:CA	2.76	0.43
1:B:1366:TYR:HE1	1:B:1367:ASN:OD1	2.00	0.43
1:A:599:ARG:HG3	1:A:604:ILE:HB	2.00	0.43
1:A:707:ILE:HG12	1:A:707:ILE:H	1.66	0.43
1:A:1133:LEU:HD22	1:A:1149:TYR:CE2	2.53	0.43
1:A:1154:LYS:C	1:A:1154:LYS:CD	2.91	0.43
1:B:711:LYS:HB3	1:B:711:LYS:HE3	1.84	0.43
1:A:401:PHE:HB3	1:A:404:PHE:CE1	2.51	0.43
1:A:510:ALA:HB2	1:A:865:TRP:CD2	2.54	0.43
1:A:557:LEU:CD2	1:A:558:ASP:N	2.73	0.43
1:A:684:TYR:HB2	1:A:793:PHE:CD2	2.53	0.43
1:A:738:LYS:CG	1:A:746:ILE:HD11	2.48	0.43
1:A:900:LEU:HD23	1:A:1056:LEU:HD13	2.01	0.43
1:A:1024:TYR:C	1:A:1024:TYR:HD1	2.27	0.43
1:A:1049:PRO:HG2	1:A:1056:LEU:HB2	2.01	0.43
1:A:1262:ASP:OD1	1:A:1262:ASP:N	2.48	0.43
1:A:1325:PHE:HB3	1:A:1375:ILE:HD13	2.00	0.43
1:A:1354:LYS:NZ	1:A:1354:LYS:CB	2.73	0.43
1:B:380:ILE:O	1:B:384:ILE:N	2.51	0.43
1:B:511:LYS:HG2	1:B:866:LEU:HD11	2.00	0.43
1:B:1029:ASP:OD1	1:B:1056:LEU:HD21	2.18	0.43
1:A:778:ILE:O	1:A:782:ILE:HG12	2.19	0.43
1:A:1156:TYR:O	1:A:1159:VAL:HG12	2.18	0.43
1:B:430:ILE:HD11	1:B:431:ILE:HD13	2.01	0.43
1:B:569:ILE:HG22	1:B:575:ILE:H	1.83	0.43
1:B:794:ASP:C	1:B:795:PHE:HD1	2.26	0.43
1:B:1047:TYR:O	1:B:1048:TYR:CD2	2.70	0.43
1:B:1102:ASN:O	1:B:1106:GLU:N	2.49	0.43
1:A:411:ASN:N	1:A:413:ASP:N	2.60	0.43
1:A:920:GLN:HE22	1:A:1006:ILE:CD1	2.30	0.43
1:A:1111:LEU:CD2	1:A:1359:SER:CB	2.97	0.43
1:A:1354:LYS:HB2	1:A:1354:LYS:HZ3	1.82	0.43
1:B:467:ILE:HG13	1:B:468:LEU:HD12	2.00	0.43
1:B:856:ARG:HB3	1:B:882:MSE:HE1	2.01	0.43
1:A:468:LEU:HD12	1:A:468:LEU:HA	1.80	0.43
1:A:554:ASN:HB2	1:A:555:TYR:C	2.44	0.43
1:A:575:ILE:HG22	1:A:577:ASN:OD1	2.18	0.43
1:A:696:ILE:HA	1:A:698:THR:H	1.82	0.43
1:B:394:GLY:HA2	1:B:395:ASN:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:533:PHE:CD1	1:B:555:TYR:CB	3.01	0.43
1:B:677:LEU:O	1:B:678:PRO:C	2.60	0.43
1:B:746:ILE:HG22	1:B:747:ASP:OD1	2.18	0.43
1:B:899:ASN:HD22	1:B:1058:ILE:HG23	1.83	0.43
1:B:1079:ILE:H	1:B:1079:ILE:CD1	2.28	0.43
1:B:1161:GLU:O	1:B:1165:ILE:HG12	2.19	0.43
1:A:549:GLY:HA2	1:A:594:THR:CG2	2.49	0.43
1:A:791:GLU:O	1:A:794:ASP:HB3	2.18	0.43
1:A:943:ASP:C	1:A:945:ILE:H	2.27	0.43
1:B:1347:ASP:O	1:B:1348:ILE:HB	2.19	0.43
1:A:1111:LEU:CD2	1:A:1363:LEU:HD12	2.43	0.43
1:A:1118:LEU:N	1:A:1125:TYR:CZ	2.87	0.43
1:A:1235:TYR:HD1	1:A:1236:THR:HG1	1.65	0.43
1:B:495:ILE:HG22	1:B:496:ASP:N	2.33	0.43
1:B:561:ILE:HG22	1:B:562:LEU:HG	2.01	0.43
1:B:1048:TYR:CB	1:B:1052:ARG:HA	2.43	0.43
1:B:1099:ILE:CG2	1:B:1103:LYS:CB	2.94	0.43
1:B:1267:SER:HA	1:B:1270:ASN:C	2.43	0.43
1:A:501:ASN:C	1:A:502:THR:HG22	2.32	0.42
1:B:538:ILE:O	1:B:538:ILE:HG12	2.19	0.42
1:B:578:LYS:O	1:B:579:ASN:HB3	2.19	0.42
1:B:659:ILE:CB	1:B:719:LEU:CB	2.96	0.42
1:A:401:PHE:CB	1:A:402:GLY:HA2	2.47	0.42
1:A:575:ILE:CA	1:A:582:THR:HG23	2.49	0.42
1:A:806:LYS:CA	1:A:809:ILE:HD13	2.49	0.42
1:A:1191:GLN:HB3	1:A:1307:LEU:HD11	2.00	0.42
1:B:427:LEU:H	1:B:427:LEU:CD1	2.23	0.42
1:B:930:TYR:OH	1:B:954:LYS:N	2.52	0.42
1:B:930:TYR:CZ	1:B:954:LYS:HG2	2.54	0.42
1:B:934:LYS:O	1:B:938:LEU:HG	2.19	0.42
1:B:1031:LEU:HD13	1:B:1084:LYS:HD3	2.00	0.42
1:B:1049:PRO:O	1:B:1050:LYS:HE2	2.19	0.42
1:B:1050:LYS:HD3	1:B:1050:LYS:HA	1.84	0.42
1:B:1195:PHE:CG	1:B:1306:LEU:HD21	2.53	0.42
1:A:691:GLU:CB	1:A:692:PRO:HD2	2.49	0.42
1:A:780:CYS:O	1:A:784:TYR:N	2.42	0.42
1:B:505:PHE:O	1:B:506:SER:C	2.61	0.42
1:B:557:LEU:CD2	1:B:575:ILE:HD13	2.43	0.42
1:B:1142:LYS:CG	1:B:1143:ASN:C	2.85	0.42
1:A:404:PHE:O	1:A:407:HIS:N	2.53	0.42
1:A:983:LEU:O	1:A:986:ILE:HD12	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1111:LEU:CD2	1:A:1363:LEU:CD1	2.77	0.42
1:B:634:VAL:HG23	1:B:891:CYS:SG	2.49	0.42
1:B:657:ILE:N	1:B:657:ILE:CD1	2.73	0.42
1:B:900:LEU:CD1	1:B:1056:LEU:HD12	2.48	0.42
1:B:942:LYS:HB2	1:B:942:LYS:HE3	1.82	0.42
1:B:1058:ILE:C	1:B:1059:TYR:CG	2.96	0.42
1:B:1249:TYR:OH	1:B:1253:GLU:OE1	2.30	0.42
1:A:463:LEU:N	1:A:463:LEU:CD1	2.76	0.42
1:A:1032:ILE:CD1	1:A:1048:TYR:HD2	2.32	0.42
1:A:1060:LYS:HZ1	1:A:1170:GLU:CD	2.27	0.42
1:A:1063:LEU:HD12	1:A:1171:PHE:CE2	2.55	0.42
1:B:589:PHE:CE1	1:B:842:ILE:HG21	2.54	0.42
1:B:591:LYS:HA	1:B:591:LYS:HD3	1.76	0.42
1:B:930:TYR:OH	1:B:954:LYS:HG2	2.20	0.42
1:B:1352:LEU:N	1:B:1352:LEU:CD1	2.82	0.42
1:A:643:VAL:O	1:A:643:VAL:HG12	2.18	0.42
1:A:1063:LEU:O	1:A:1067:ILE:HG13	2.19	0.42
1:B:384:ILE:CG2	1:B:385:LYS:N	2.82	0.42
1:B:568:ILE:HG23	1:B:625:GLN:NE2	2.34	0.42
1:A:371:ILE:HD12	1:A:371:ILE:C	2.42	0.42
1:A:997:GLN:O	1:A:1000:LYS:N	2.52	0.42
1:A:1240:TYR:HD2	1:A:1241:TYR:CE1	2.38	0.42
1:B:588:LYS:O	1:B:592:ILE:HG13	2.20	0.42
1:B:670:LEU:HD12	1:B:670:LEU:HA	1.76	0.42
1:B:716:LYS:HE2	1:B:716:LYS:HA	2.01	0.42
1:B:733:LEU:O	1:B:737:LYS:HG3	2.19	0.42
1:B:1034:ASP:OD1	1:B:1040:GLU:HB2	2.18	0.42
1:A:384:ILE:CD1	1:A:463:LEU:HD12	2.48	0.42
1:A:1046:ILE:CG2	1:A:1169:VAL:HG11	2.49	0.42
1:A:1148:ASN:ND2	1:A:1151:SER:OG	2.53	0.42
1:B:641:ASP:C	1:B:643:VAL:N	2.78	0.42
1:B:1133:LEU:HA	1:B:1136:ASN:HB2	2.02	0.42
1:A:368:LYS:C	1:A:371:ILE:HG22	2.45	0.42
1:A:775:LYS:HB2	1:A:775:LYS:HZ2	1.82	0.42
1:A:893:THR:HB	1:A:1059:TYR:OH	2.20	0.42
1:A:995:VAL:C	1:A:997:GLN:N	2.77	0.42
1:A:1118:LEU:HB3	1:A:1125:TYR:HH	1.69	0.42
1:B:616:ASP:O	1:B:620:VAL:N	2.43	0.42
1:B:670:LEU:HG	1:B:671:PRO:HD2	2.02	0.42
1:B:713:LEU:O	1:B:716:LYS:N	2.51	0.42
1:B:1202:ILE:HG22	1:B:1202:ILE:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1230:GLY:HA2	1:B:1231:SER:C	2.45	0.42
1:B:1357:LYS:CB	1:B:1362:GLU:OE1	2.68	0.42
1:A:409:LYS:O	1:A:413:ASP:HB2	2.20	0.42
1:A:710:ASN:HA	1:A:713:LEU:HB3	2.01	0.42
1:A:1117:LYS:HD3	1:A:1117:LYS:HA	1.81	0.42
1:A:1340:PHE:CD1	1:A:1349:LEU:HD21	2.55	0.42
1:B:366:SER:O	1:B:367:ILE:C	2.61	0.42
1:B:478:GLN:HA	1:B:481:LEU:HB3	2.02	0.42
1:B:639:ASN:HA	1:B:640:LEU:HA	1.71	0.42
1:B:1043:PHE:CA	1:B:1046:ILE:HD11	2.49	0.42
1:B:1091:LEU:O	1:B:1162:TYR:CE1	2.69	0.42
1:B:1366:TYR:C	1:B:1367:ASN:HD22	2.15	0.42
1:B:354:ILE:HG22	1:B:358:PHE:HE2	1.83	0.41
1:B:378:PHE:CZ	1:B:435:LEU:HD11	2.54	0.41
1:B:533:PHE:CE1	1:B:557:LEU:HD13	2.39	0.41
1:B:1011:LEU:HA	1:B:1011:LEU:HD23	1.66	0.41
1:A:392:LYS:CB	1:A:395:ASN:ND2	2.83	0.41
1:A:632:GLU:O	1:A:633:GLU:C	2.63	0.41
1:A:659:ILE:CG2	1:A:720:GLU:N	2.83	0.41
1:A:830:ILE:HG22	1:A:831:VAL:N	2.35	0.41
1:A:979:GLU:HG3	1:A:982:LYS:H	1.86	0.41
1:A:1321:VAL:HG12	1:A:1322:PHE:HD1	1.86	0.41
1:B:681:LEU:O	1:B:685:ARG:HG2	2.19	0.41
1:B:793:PHE:O	1:B:795:PHE:HD1	2.03	0.41
1:B:930:TYR:CD1	1:B:930:TYR:C	2.98	0.41
1:B:1152:PHE:HA	1:B:1155:ASP:HB2	2.02	0.41
1:B:1277:ILE:CG1	1:B:1278:ARG:N	2.82	0.41
1:B:1300:ILE:HD13	1:B:1321:VAL:HG11	2.02	0.41
1:A:840:ILE:HG22	1:A:878:LEU:HD11	2.01	0.41
1:A:1091:LEU:N	1:A:1091:LEU:HD12	2.34	0.41
1:A:1094:ILE:O	1:A:1094:ILE:CG2	2.69	0.41
1:B:473:LEU:O	1:B:476:VAL:N	2.53	0.41
1:B:485:MSE:HG3	1:B:1202:ILE:CD1	2.50	0.41
1:B:637:ALA:HB1	1:B:821:ILE:HG21	2.02	0.41
1:B:697:GLU:O	1:B:701:ILE:CG1	2.67	0.41
1:B:844:ALA:O	1:B:852:ILE:HD11	2.19	0.41
1:B:892:ILE:C	1:B:892:ILE:CD1	2.85	0.41
1:A:367:ILE:C	1:A:371:ILE:HG22	2.40	0.41
1:A:1059:TYR:HE2	1:A:1061:LYS:HE3	1.85	0.41
1:A:1100:ARG:HA	1:A:1104:ILE:HG23	2.02	0.41
1:A:1118:LEU:HD12	1:A:1121:TYR:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:LYS:C	1:B:417:PHE:HA	2.44	0.41
1:B:821:ILE:HG22	1:B:822:THR:N	2.35	0.41
1:A:801:ASN:O	1:A:802:ILE:HB	2.20	0.41
1:A:1048:TYR:HA	1:A:1049:PRO:HD3	1.86	0.41
1:B:364:ASN:H	1:B:364:ASN:HD22	1.67	0.41
1:B:431:ILE:O	1:B:432:TYR:C	2.63	0.41
1:B:432:TYR:CD1	1:B:436:LYS:NZ	2.87	0.41
1:B:1102:ASN:O	1:B:1106:GLU:HB2	2.21	0.41
1:A:554:ASN:HB3	1:A:555:TYR:O	2.20	0.41
1:A:664:ASN:O	1:A:666:ASP:OD1	2.39	0.41
1:A:733:LEU:O	1:A:737:LYS:CG	2.68	0.41
1:A:796:SER:CB	1:A:797:ASP:C	2.93	0.41
1:A:906:LYS:O	1:A:910:ILE:HG13	2.21	0.41
1:A:1048:TYR:HD1	1:A:1048:TYR:C	2.28	0.41
1:B:465:GLU:C	1:B:466:SER:HG	2.13	0.41
1:B:476:VAL:O	1:B:479:TYR:N	2.53	0.41
1:B:665:ASN:N	1:B:665:ASN:ND2	2.67	0.41
1:B:882:MSE:O	1:B:886:THR:HG23	2.21	0.41
1:B:888:ARG:HH11	1:B:1011:LEU:HD11	1.85	0.41
1:B:943:ASP:O	1:B:946:ASN:ND2	2.53	0.41
1:B:1198:ASP:OD2	1:B:1309:TYR:OH	2.30	0.41
1:B:1301:ASP:OD2	1:B:1341:LYS:HB2	2.20	0.41
1:B:1332:ASP:HB2	1:B:1354:LYS:CE	2.42	0.41
1:A:616:ASP:O	1:A:620:VAL:HG23	2.20	0.41
1:A:806:LYS:H	1:A:809:ILE:HD13	1.86	0.41
1:A:992:LYS:O	1:A:992:LYS:HG2	2.20	0.41
1:A:1268:GLU:HG2	1:A:1268:GLU:O	2.21	0.41
1:B:491:ARG:HG2	1:B:1204:ASN:HD22	1.84	0.41
1:B:747:ASP:OD1	1:B:747:ASP:N	2.53	0.41
1:B:1067:ILE:HD13	1:B:1072:PHE:CZ	2.55	0.41
1:B:1166:ARG:O	1:B:1170:GLU:HB2	2.21	0.41
1:A:556:VAL:HG22	1:A:557:LEU:H	1.86	0.41
1:A:817:THR:C	1:A:819:GLU:HA	2.45	0.41
1:B:505:PHE:C	1:B:507:ARG:N	2.77	0.41
1:B:532:ILE:HG22	1:B:562:LEU:CB	2.50	0.41
1:B:671:PRO:C	1:B:672:SER:HG	2.28	0.41
1:A:379:LYS:O	1:A:407:HIS:NE2	2.53	0.41
1:A:409:LYS:O	1:A:413:ASP:HA	2.21	0.41
1:A:438:ARG:O	1:A:442:ILE:HG13	2.21	0.41
1:A:574:PHE:O	1:A:575:ILE:HG13	2.21	0.41
1:A:607:GLU:O	1:A:609:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:670:LEU:HD22	1:A:670:LEU:O	2.20	0.41
1:A:747:ASP:O	1:A:748:GLU:HG2	2.21	0.41
1:A:798:PHE:CG	1:A:799:LYS:N	2.89	0.41
1:A:1212:ILE:HD13	1:A:1252:PHE:HB2	2.02	0.41
1:B:537:ASN:C	1:B:538:ILE:HG22	2.44	0.41
1:B:595:ASN:OD1	1:B:607:GLU:HG3	2.20	0.41
1:B:673:PHE:O	1:B:676:VAL:N	2.53	0.41
1:B:675:LYS:HZ2	1:B:774:GLN:HE22	1.69	0.41
1:B:713:LEU:O	1:B:717:LEU:HD12	2.21	0.41
1:B:720:GLU:OE2	1:B:723:LEU:HD13	2.18	0.41
1:B:812:ILE:O	1:B:816:LYS:N	2.54	0.41
1:B:900:LEU:HD11	1:B:1056:LEU:HD13	2.03	0.41
1:B:995:VAL:O	1:B:999:ILE:HG13	2.21	0.41
1:B:1031:LEU:HD13	1:B:1043:PHE:HZ	1.79	0.41
1:B:1043:PHE:O	1:B:1048:TYR:CE2	2.74	0.41
1:A:384:ILE:HD13	1:A:463:LEU:CD1	2.50	0.41
1:A:796:SER:OG	1:A:797:ASP:O	2.33	0.41
1:B:483:HIS:O	1:B:487:LEU:HD12	2.21	0.41
1:B:644:PHE:CE2	1:B:651:ILE:HG13	2.56	0.41
1:B:899:ASN:OD1	1:B:899:ASN:N	2.54	0.41
1:B:1097:LYS:C	1:B:1099:ILE:N	2.78	0.41
1:A:684:TYR:OH	1:A:693:PHE:CZ	2.74	0.40
1:A:690:ASN:ND2	1:A:693:PHE:CZ	2.89	0.40
1:A:837:GLU:OE1	1:A:873:ASN:ND2	2.54	0.40
1:A:896:TRP:HA	1:A:896:TRP:CE3	2.56	0.40
1:A:1112:LYS:CA	1:A:1115:ASN:HB2	2.43	0.40
1:A:1380:THR:O	1:A:1381:LYS:C	2.61	0.40
1:B:512:GLU:OE1	1:B:1197:ARG:NH2	2.54	0.40
1:B:900:LEU:HD21	1:B:1056:LEU:CD1	2.46	0.40
1:B:1250:LYS:HB2	1:B:1250:LYS:HE3	1.93	0.40
1:A:670:LEU:C	1:A:670:LEU:CD2	2.95	0.40
1:A:781:TYR:O	1:A:785:LEU:N	2.54	0.40
1:A:1053:LYS:O	1:A:1053:LYS:CG	2.70	0.40
1:B:376:ALA:C	1:B:379:LYS:CB	2.95	0.40
1:B:383:LEU:O	1:B:383:LEU:HG	2.21	0.40
1:B:421:SER:O	1:B:422:ASP:HB2	2.20	0.40
1:B:623:ILE:H	1:B:623:ILE:HG13	1.62	0.40
1:B:641:ASP:OD1	1:B:705:ALA:HB1	2.21	0.40
1:B:899:ASN:CB	1:B:900:LEU:HB2	2.51	0.40
1:A:365:ASN:O	1:A:368:LYS:HE2	2.20	0.40
1:B:614:GLN:CB	1:B:618:ASN:HB2	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:LYS:HE3	1:A:429:LYS:HB2	1.74	0.40
1:A:554:ASN:CB	1:A:555:TYR:C	2.94	0.40
1:A:685:ARG:HD2	1:A:685:ARG:C	2.46	0.40
1:A:802:ILE:C	1:A:805:ILE:N	2.79	0.40
1:A:1277:ILE:HD12	1:A:1277:ILE:C	2.46	0.40
1:B:423:GLU:H	1:B:423:GLU:HG3	1.65	0.40
1:B:486:TYR:CD1	1:B:486:TYR:C	2.99	0.40
1:B:640:LEU:HD22	1:B:701:ILE:HG21	2.02	0.40
1:B:908:LYS:HA	1:B:908:LYS:HD2	1.79	0.40
1:B:908:LYS:HA	1:B:911:GLU:HG3	2.04	0.40
1:B:1093:ASN:HB3	1:B:1096:GLY:H	1.86	0.40
1:B:1155:ASP:O	1:B:1159:VAL:HG23	2.21	0.40
1:A:546:PHE:O	1:A:547:PHE:CB	2.69	0.40
1:A:1038:GLU:H	1:A:1038:GLU:HG3	1.56	0.40
1:A:1146:ASN:O	1:A:1147:LYS:CB	2.70	0.40
1:A:1194:ARG:HG3	1:A:1197:ARG:NH2	2.37	0.40
1:A:1299:GLN:O	1:A:1303:VAL:HG23	2.22	0.40
1:B:504:ASP:HA	1:B:507:ARG:CD	2.43	0.40
1:B:549:GLY:HA2	1:B:594:THR:HG21	2.03	0.40
1:B:1036:GLU:O	1:B:1037:SER:CB	2.69	0.40
1:B:1352:LEU:H	1:B:1352:LEU:CD1	2.34	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:426:GLU:OE1	1:B:1037:SER:OG[4_446]	1.51	0.69
1:A:776:LYS:CB	1:A:1348:ILE:CD1[3_655]	1.91	0.29
1:A:398:THR:CB	1:A:907:MSE:CE[3_655]	2.08	0.12
1:A:776:LYS:CD	1:A:1348:ILE:CD1[3_655]	2.10	0.10

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

The Analysed column shows the number of residues for which the backbone conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1013/1397 (72%)	908 (90%)	79 (8%)	26 (3%)	4	27
1	B	1004/1397 (72%)	888 (88%)	84 (8%)	32 (3%)	3	24
All	All	2017/2794 (72%)	1796 (89%)	163 (8%)	58 (3%)	3	26

All (58) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	392	LYS
1	A	410	VAL
1	A	458	GLU
1	A	460	GLU
1	A	461	LYS
1	A	798	PHE
1	A	805	ILE
1	A	806	LYS
1	A	894	GLU
1	A	914	PHE
1	A	969	ILE
1	A	1094	ILE
1	A	1272	PRO
1	B	390	GLU
1	B	615	ASP
1	B	645	LYS
1	B	669	TYR
1	B	685	ARG
1	B	706	LEU
1	B	749	ASN
1	B	805	ILE
1	B	806	LYS
1	B	1042	LYS
1	A	633	GLU
1	A	674	SER
1	A	1014	ILE
1	B	416	LYS
1	B	616	ASP
1	B	810	LYS
1	B	1043	PHE
1	A	730	ASN
1	B	672	SER
1	B	1036	GLU
1	B	1037	SER

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Mol	Chain	Res	Type
1	B	1050	LYS
1	B	1052	ARG
1	B	1267	SER
1	A	421	SER
1	A	747	ASP
1	A	915	ASP
1	A	987	ASN
1	A	996	ASP
1	B	391	LEU
1	B	608	ARG
1	B	766	ASN
1	B	1059	TYR
1	A	390	GLU
1	A	807	LYS
1	A	808	GLN
1	B	611	GLN
1	B	668	LYS
1	B	1144	ILE
1	B	1366	TYR
1	B	667	ILE
1	B	1138	ASP
1	B	832	ILE
1	B	1348	ILE
1	A	1070	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	824/1316 (63%)	689 (84%)	135 (16%)	2	14
1	B	822/1316 (62%)	705 (86%)	117 (14%)	3	18
All	All	1646/2632 (62%)	1394 (85%)	252 (15%)	3	16

All (252) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	362	ILE
1	A	363	LYS
1	A	365	ASN
1	A	371	ILE
1	A	384	ILE
1	A	386	LYS
1	A	396	CYS
1	A	400	ILE
1	A	401	PHE
1	A	403	ILE
1	A	404	PHE
1	A	407	HIS
1	A	422	ASP
1	A	459	ILE
1	A	460	GLU
1	A	461	LYS
1	A	463	LEU
1	A	466	SER
1	A	468	LEU
1	A	473	LEU
1	A	516	LEU
1	A	535	ARG
1	A	537	ASN
1	A	539	ASN
1	A	540	ASN
1	A	542	GLU
1	A	544	ILE
1	A	546	PHE
1	A	547	PHE
1	A	555	TYR
1	A	556	VAL
1	A	557	LEU
1	A	561	ILE
1	A	563	ASN
1	A	565	LYS
1	A	572	LEU
1	A	575	ILE
1	A	580	ASN
1	A	606	LYS
1	A	608	ARG
1	A	611	GLN
1	A	625	GLN
1	A	631	ASP

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Mol	Chain	Res	Type
1	A	635	SER
1	A	638	LEU
1	A	640	LEU
1	A	642	VAL
1	A	650	ILE
1	A	653	LYS
1	A	655	ASN
1	A	659	ILE
1	A	666	ASP
1	A	667	ILE
1	A	670	LEU
1	A	683	LEU
1	A	703	LEU
1	A	707	ILE
1	A	729	LYS
1	A	731	ILE
1	A	752	GLU
1	A	761	SER
1	A	775	LYS
1	A	792	LEU
1	A	793	PHE
1	A	796	SER
1	A	800	MSE
1	A	804	GLU
1	A	817	THR
1	A	820	ARG
1	A	826	SER
1	A	869	SER
1	A	870	GLU
1	A	888	ARG
1	A	890	GLU
1	A	899	ASN
1	A	909	GLU
1	A	916	ASP
1	A	917	PHE
1	A	932	ASP
1	A	958	ILE
1	A	970	ASP
1	A	979	GLU
1	A	986	ILE
1	A	987	ASN
1	A	988	LYS

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Mol	Chain	Res	Type
1	A	989	LYS
1	A	994	LYS
1	A	1015	ILE
1	A	1021	LEU
1	A	1025	LYS
1	A	1026	LYS
1	A	1035	MSE
1	A	1038	GLU
1	A	1045	GLU
1	A	1050	LYS
1	A	1053	LYS
1	A	1055	GLU
1	A	1089	LYS
1	A	1095	ASP
1	A	1102	ASN
1	A	1104	ILE
1	A	1106	GLU
1	A	1108	ASP
1	A	1111	LEU
1	A	1112	LYS
1	A	1115	ASN
1	A	1116	ASP
1	A	1117	LYS
1	A	1118	LEU
1	A	1134	LYS
1	A	1135	GLU
1	A	1149	TYR
1	A	1154	LYS
1	A	1219	THR
1	A	1243	PHE
1	A	1254	LYS
1	A	1264	SER
1	A	1265	GLU
1	A	1266	ASN
1	A	1273	GLU
1	A	1275	GLU
1	A	1276	SER
1	A	1277	ILE
1	A	1293	ASP
1	A	1353	MSE
1	A	1354	LYS
1	A	1357	LYS

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Mol	Chain	Res	Type
1	A	1360	VAL
1	A	1361	LEU
1	A	1368	SER
1	A	1371	ILE
1	A	1372	LYS
1	A	1374	LEU
1	A	1378	LEU
1	A	1382	ILE
1	B	363	LYS
1	B	364	ASN
1	B	366	SER
1	B	382	GLU
1	B	389	LYS
1	B	390	GLU
1	B	400	ILE
1	B	406	LYS
1	B	410	VAL
1	B	418	SER
1	B	424	GLU
1	B	436	LYS
1	B	439	ILE
1	B	461	LYS
1	B	462	ILE
1	B	463	LEU
1	B	467	ILE
1	B	489	LYS
1	B	492	HIS
1	B	493	ASN
1	B	494	ASP
1	B	499	THR
1	B	502	THR
1	B	503	ASP
1	B	506	SER
1	B	532	ILE
1	B	535	ARG
1	B	538	ILE
1	B	550	ASP
1	B	551	ARG
1	B	559	LYS
1	B	575	ILE
1	B	601	LEU
1	B	605	SER

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Mol	Chain	Res	Type
1	B	613	THR
1	B	617	TYR
1	B	640	LEU
1	B	641	ASP
1	B	644	PHE
1	B	657	ILE
1	B	662	GLU
1	B	663	ASN
1	B	665	ASN
1	B	667	ILE
1	B	670	LEU
1	B	672	SER
1	B	675	LYS
1	B	676	VAL
1	B	685	ARG
1	B	695	THR
1	B	698	THR
1	B	699	GLU
1	B	701	ILE
1	B	723	LEU
1	B	725	GLU
1	B	726	ASN
1	B	733	LEU
1	B	746	ILE
1	B	748	GLU
1	B	749	ASN
1	B	792	LEU
1	B	794	ASP
1	B	807	LYS
1	B	809	ILE
1	B	823	VAL
1	B	825	THR
1	B	828	LYS
1	B	834	ASP
1	B	848	SER
1	B	849	ASN
1	B	888	ARG
1	B	890	GLU
1	B	896	TRP
1	B	897	ASN
1	B	898	LEU
1	B	911	GLU

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Mol	Chain	Res	Type
1	B	912	LYS
1	B	913	ASP
1	B	915	ASP
1	B	917	PHE
1	B	918	LYS
1	B	919	ILE
1	B	931	GLU
1	B	970	ASP
1	B	980	GLN
1	B	981	ARG
1	B	985	ASN
1	B	1007	LYS
1	B	1035	MSE
1	B	1043	PHE
1	B	1046	ILE
1	B	1047	TYR
1	B	1048	TYR
1	B	1050	LYS
1	B	1058	ILE
1	B	1059	TYR
1	B	1060	LYS
1	B	1079	ILE
1	B	1084	LYS
1	B	1089	LYS
1	B	1095	ASP
1	B	1122	SER
1	B	1142	LYS
1	B	1191	GLN
1	B	1214	LEU
1	B	1259	PHE
1	B	1261	ILE
1	B	1263	LEU
1	B	1277	ILE
1	B	1346	ASN
1	B	1352	LEU
1	B	1353	MSE
1	B	1354	LYS
1	B	1359	SER
1	B	1364	GLU
1	B	1366	TYR
1	B	1367	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	365	ASN
1	A	537	ASN
1	A	554	ASN
1	A	579	ASN
1	A	618	ASN
1	A	639	ASN
1	A	664	ASN
1	A	710	ASN
1	A	899	ASN
1	A	905	GLN
1	A	920	GLN
1	A	1039	ASN
1	A	1115	ASN
1	A	1148	ASN
1	A	1157	ASN
1	A	1175	ASN
1	A	1270	ASN
1	A	1346	ASN
1	B	361	ASN
1	B	364	ASN
1	B	464	ASN
1	B	483	HIS
1	B	492	HIS
1	B	539	ASN
1	B	618	ASN
1	B	625	GLN
1	B	665	ASN
1	B	753	ASN
1	B	788	ASN
1	B	936	ASN
1	B	946	ASN
1	B	980	GLN
1	B	1017	ASN
1	B	1041	ASN
1	B	1062	ASN
1	B	1119	ASN
1	B	1191	GLN
1	B	1200	HIS
1	B	1204	ASN
1	B	1279	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	A	1008/1397 (72%)	0.79	116 (11%) 9 6	2, 42, 106, 153	0
1	B	1002/1397 (71%)	1.33	226 (22%) 2 2	12, 67, 134, 199	0
All	All	2010/2794 (71%)	1.06	342 (17%) 4 4	2, 55, 128, 199	0

All (342) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	500	VAL	7.1
1	B	407	HIS	6.7
1	B	396	CYS	6.5
1	B	1345	ASN	6.1
1	B	726	ASN	5.9
1	B	404	PHE	5.3
1	A	687	ASN	5.2
1	B	770	ILE	5.2
1	B	400	ILE	5.1
1	A	891	CYS	5.1
1	B	744	ASP	4.8
1	B	743	ILE	4.7
1	B	1273	GLU	4.6
1	A	1012	CYS	4.5
1	B	1138	ASP	4.5
1	A	743	ILE	4.5
1	A	458	GLU	4.5
1	B	499	THR	4.2
1	A	1267	SER	4.2
1	B	583	ASN	4.2
1	B	694	ASP	4.1
1	B	391	LEU	4.1
1	B	1136	ASN	4.1
1	B	670	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	727	GLU	4.0
1	B	956	GLU	4.0
1	A	381	ASP	4.0
1	B	948	CYS	4.0
1	B	1087	ASP	4.0
1	A	742	ASN	4.0
1	A	792	LEU	4.0
1	B	410	VAL	3.9
1	B	447	GLN	3.9
1	B	552	GLU	3.9
1	B	797	ASP	3.9
1	B	461	LYS	3.9
1	A	744	ASP	3.8
1	B	399	GLU	3.8
1	A	692	PRO	3.8
1	B	498	THR	3.8
1	A	412	PHE	3.8
1	B	412	PHE	3.7
1	A	1138	ASP	3.6
1	B	761	SER	3.6
1	B	1108	ASP	3.6
1	A	726	ASN	3.6
1	B	395	ASN	3.6
1	B	457	ILE	3.6
1	A	447	GLN	3.5
1	B	803	GLN	3.5
1	B	728	SER	3.5
1	A	615	ASP	3.5
1	A	1093	ASN	3.5
1	B	1301	ASP	3.5
1	A	747	ASP	3.5
1	B	958	ILE	3.5
1	B	505	PHE	3.5
1	B	804	GLU	3.4
1	B	666	ASP	3.4
1	B	790	GLU	3.4
1	B	1036	GLU	3.4
1	B	667	ILE	3.4
1	B	459	ILE	3.4
1	A	943	ASP	3.4
1	B	944	ASP	3.4
1	B	671	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	1204	ASN	3.4
1	B	1122	SER	3.4
1	A	1121	TYR	3.4
1	B	444	VAL	3.3
1	B	579	ASN	3.3
1	B	443	LEU	3.3
1	A	722	ASP	3.3
1	B	408	TYR	3.3
1	B	718	ILE	3.3
1	A	411	ASN	3.3
1	A	399	GLU	3.3
1	B	458	GLU	3.3
1	A	750	ILE	3.3
1	A	457	ILE	3.2
1	B	372	GLU	3.2
1	B	759	GLN	3.2
1	B	537	ASN	3.2
1	A	1008	SER	3.2
1	B	750	ILE	3.2
1	B	742	ASN	3.2
1	B	397	ASP	3.2
1	B	388	GLU	3.2
1	B	657	ILE	3.1
1	A	417	PHE	3.1
1	A	1347	ASP	3.1
1	B	442	ILE	3.1
1	B	561	ILE	3.1
1	B	562	LEU	3.1
1	B	661	GLU	3.1
1	B	465	GLU	3.1
1	B	725	GLU	3.1
1	B	952	GLU	3.1
1	A	1301	ASP	3.1
1	B	1120	GLY	3.1
1	B	760	ILE	3.0
1	B	757	ASN	3.0
1	B	821	ILE	3.0
1	B	1148	ASN	3.0
1	B	1034	ASP	3.0
1	B	1205	GLY	3.0
1	B	350	LYS	3.0
1	B	1105	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	1145	GLN	3.0
1	A	766	ASN	3.0
1	B	1135	GLU	3.0
1	B	1268	GLU	3.0
1	B	1347	ASP	3.0
1	A	1125	TYR	2.9
1	B	1039	ASN	2.9
1	B	440	GLU	2.9
1	A	1348	ILE	2.9
1	A	1056	LEU	2.9
1	B	996	ASP	2.9
1	B	762	ALA	2.9
1	B	636	LYS	2.9
1	B	942	LYS	2.9
1	B	751	ILE	2.9
1	B	1127	GLU	2.9
1	B	729	LYS	2.9
1	B	1037	SER	2.9
1	B	1042	LYS	2.9
1	B	746	ILE	2.8
1	B	1088	ALA	2.8
1	B	1114	LEU	2.8
1	B	401	PHE	2.8
1	A	785	LEU	2.8
1	B	735	GLU	2.8
1	B	949	ASP	2.8
1	B	371	ILE	2.8
1	B	764	LYS	2.8
1	A	562	LEU	2.8
1	B	955	LEU	2.8
1	B	582	THR	2.8
1	B	698	THR	2.8
1	B	740	LEU	2.7
1	A	408	TYR	2.7
1	B	432	TYR	2.7
1	B	632	GLU	2.7
1	B	1208	GLU	2.7
1	B	413	ASP	2.7
1	B	1116	ASP	2.7
1	B	448	LYS	2.7
1	A	725	GLU	2.7
1	B	1113	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	919	ILE	2.7
1	A	729	LYS	2.7
1	B	554	ASN	2.7
1	B	1150	LYS	2.7
1	B	414	SER	2.7
1	B	1272	PRO	2.7
1	B	549	GLY	2.7
1	B	637	ALA	2.7
1	B	986	ILE	2.7
1	B	769	ALA	2.6
1	A	899	ASN	2.6
1	B	978	ASP	2.6
1	A	902	GLU	2.6
1	A	1069	ASN	2.6
1	B	767	ASN	2.6
1	A	652	THR	2.6
1	B	773	TYR	2.6
1	A	404	PHE	2.6
1	A	1146	ASN	2.6
1	B	674	SER	2.6
1	B	1041	ASN	2.6
1	B	771	LYS	2.6
1	B	398	THR	2.6
1	B	1139	PHE	2.6
1	A	550	ASP	2.6
1	B	460	GLU	2.6
1	B	1117	LYS	2.6
1	B	723	LEU	2.6
1	B	765	GLY	2.6
1	B	555	TYR	2.6
1	B	1040	GLU	2.6
1	A	1123	LYS	2.6
1	B	1141	ALA	2.6
1	A	754	TYR	2.5
1	A	658	LYS	2.5
1	B	716	LYS	2.5
1	A	633	GLU	2.5
1	B	1161	GLU	2.5
1	A	688	PRO	2.5
1	A	388	GLU	2.5
1	A	1266	ASN	2.5
1	B	1109	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1094	ILE	2.5
1	A	901	GLU	2.5
1	B	968	GLU	2.5
1	B	539	ASN	2.5
1	B	1092	PHE	2.5
1	A	768	LYS	2.5
1	A	916	ASP	2.5
1	A	990	ASP	2.5
1	B	433	ARG	2.5
1	B	755	TYR	2.5
1	B	975	ILE	2.5
1	B	1223	ARG	2.5
1	B	684	TYR	2.5
1	B	693	PHE	2.4
1	B	722	ASP	2.4
1	A	1359	SER	2.4
1	A	689	LYS	2.4
1	B	1343	ILE	2.4
1	B	352	ASP	2.4
1	B	752	GLU	2.4
1	B	976	LEU	2.4
1	B	543	ASN	2.4
1	A	1070	PRO	2.4
1	B	406	LYS	2.4
1	B	1365	SER	2.4
1	A	789	TYR	2.4
1	A	948	CYS	2.4
1	A	1141	ALA	2.4
1	A	394	GLY	2.4
1	B	731	ILE	2.4
1	A	697	GLU	2.4
1	A	402	GLY	2.4
1	B	1230	GLY	2.4
1	B	777	VAL	2.4
1	B	662	GLU	2.4
1	B	445	ASN	2.3
1	B	753	ASN	2.3
1	A	459	ILE	2.3
1	B	439	ILE	2.3
1	B	747	ASP	2.3
1	B	357	PHE	2.3
1	A	765	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1119	ASN	2.3
1	B	1270	ASN	2.3
1	B	1348	ILE	2.3
1	B	580	ASN	2.3
1	B	664	ASN	2.3
1	B	702	VAL	2.3
1	A	1140	PHE	2.3
1	A	724	GLU	2.3
1	A	727	GLU	2.3
1	A	804	GLU	2.3
1	B	940	GLU	2.3
1	B	783	GLY	2.3
1	B	540	ASN	2.3
1	B	737	LYS	2.3
1	A	396	CYS	2.3
1	A	693	PHE	2.3
1	B	758	ALA	2.3
1	B	1121	TYR	2.3
1	B	707	ILE	2.3
1	A	631	ASP	2.3
1	B	893	THR	2.2
1	B	733	LEU	2.2
1	B	866	LEU	2.2
1	A	414	SER	2.2
1	B	418	SER	2.2
1	B	390	GLU	2.2
1	B	894	GLU	2.2
1	A	978	ASP	2.2
1	B	558	ASP	2.2
1	B	631	ASP	2.2
1	A	1265	GLU	2.2
1	A	638	LEU	2.2
1	A	649	ASN	2.2
1	A	686	ASN	2.2
1	A	1113	ASN	2.2
1	B	625	GLN	2.2
1	A	819	GLU	2.2
1	A	651	ILE	2.2
1	B	695	THR	2.2
1	A	646	ASP	2.2
1	B	422	ASP	2.2
1	A	643	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	549	GLY	2.2
1	A	741	GLY	2.2
1	A	400	ILE	2.2
1	A	613	THR	2.2
1	B	1152	PHE	2.2
1	B	1098	ASN	2.2
1	A	721	ASP	2.2
1	B	979	GLU	2.2
1	B	419	LYS	2.2
1	A	1367	ASN	2.2
1	B	1078	LEU	2.2
1	A	1358	VAL	2.1
1	B	818	TYR	2.1
1	B	703	LEU	2.1
1	B	1267	SER	2.1
1	A	811	ASP	2.1
1	A	817	THR	2.1
1	B	730	ASN	2.1
1	B	1130	ILE	2.1
1	A	416	LYS	2.1
1	A	798	PHE	2.1
1	B	409	LYS	2.1
1	B	642	VAL	2.1
1	B	738	LYS	2.1
1	B	1134	LYS	2.1
1	B	1140	PHE	2.1
1	B	669	TYR	2.1
1	A	769	ALA	2.1
1	A	892	ILE	2.1
1	B	368	LYS	2.1
1	B	1089	LYS	2.1
1	B	1227	LYS	2.1
1	B	496	ASP	2.1
1	B	778	ILE	2.1
1	A	767	ASN	2.1
1	A	815	ASN	2.1
1	B	611	GLN	2.1
1	A	391	LEU	2.1
1	A	794	ASP	2.1
1	A	814	ASP	2.1
1	B	1262	ASP	2.1
1	B	369	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	446	GLU	2.1
1	B	1038	GLU	2.1
1	A	1142	LYS	2.1
1	A	801	ASN	2.1
1	B	501	ASN	2.1
1	B	721	ASP	2.0
1	B	865	TRP	2.0
1	A	360	GLU	2.0
1	A	448	LYS	2.0
1	B	353	LYS	2.0
1	B	830	ILE	2.0
1	B	1056	LEU	2.0
1	A	690	ASN	2.0
1	B	685	ARG	2.0
1	A	728	SER	2.0
1	B	1222	SER	2.0
1	A	1270	ASN	2.0
1	B	1277	ILE	2.0
1	A	387	LEU	2.0
1	A	699	GLU	2.0
1	B	732	PHE	2.0
1	B	900	LEU	2.0
1	B	1298	GLU	2.0
1	A	660	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.