



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2023 – 05:13 AM EDT

PDB ID : 3H7N
Title : Structure of Nup120
Authors : Seo, H.S.; Ma, Y.; Debler, E.W.; Blobel, G.; Hoelz, A.
Deposited on : 2009-04-27
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

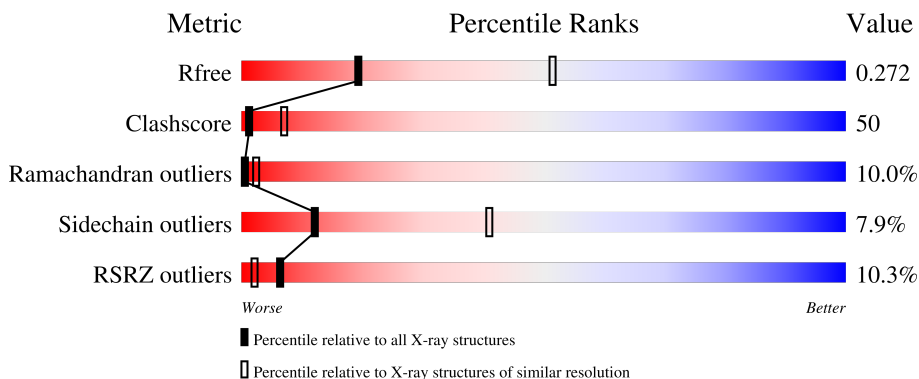
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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

Mol	Chain	Length	Quality of chain
1	A	729	
1	B	729	
1	C	729	
1	D	729	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 22992 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.

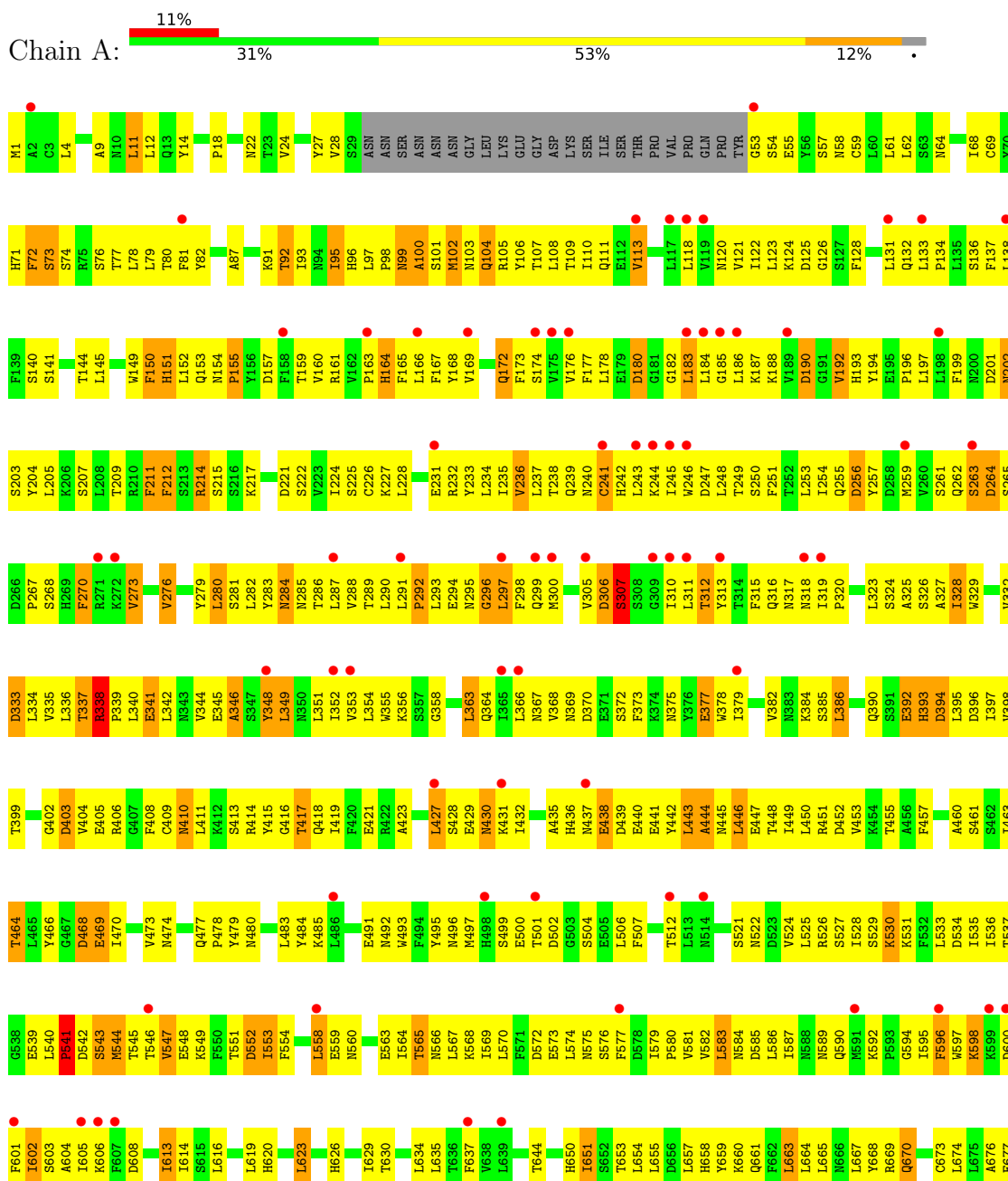
- Molecule 1 is a protein called Nucleoporin NUP120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	706	5748	3718	913	1099	18	0	0	0
1	B	706	5748	3718	913	1099	18	0	0	0
1	C	706	5748	3718	913	1099	18	0	0	0
1	D	706	5748	3718	913	1099	18	0	0	0

3 Residue-property plots i

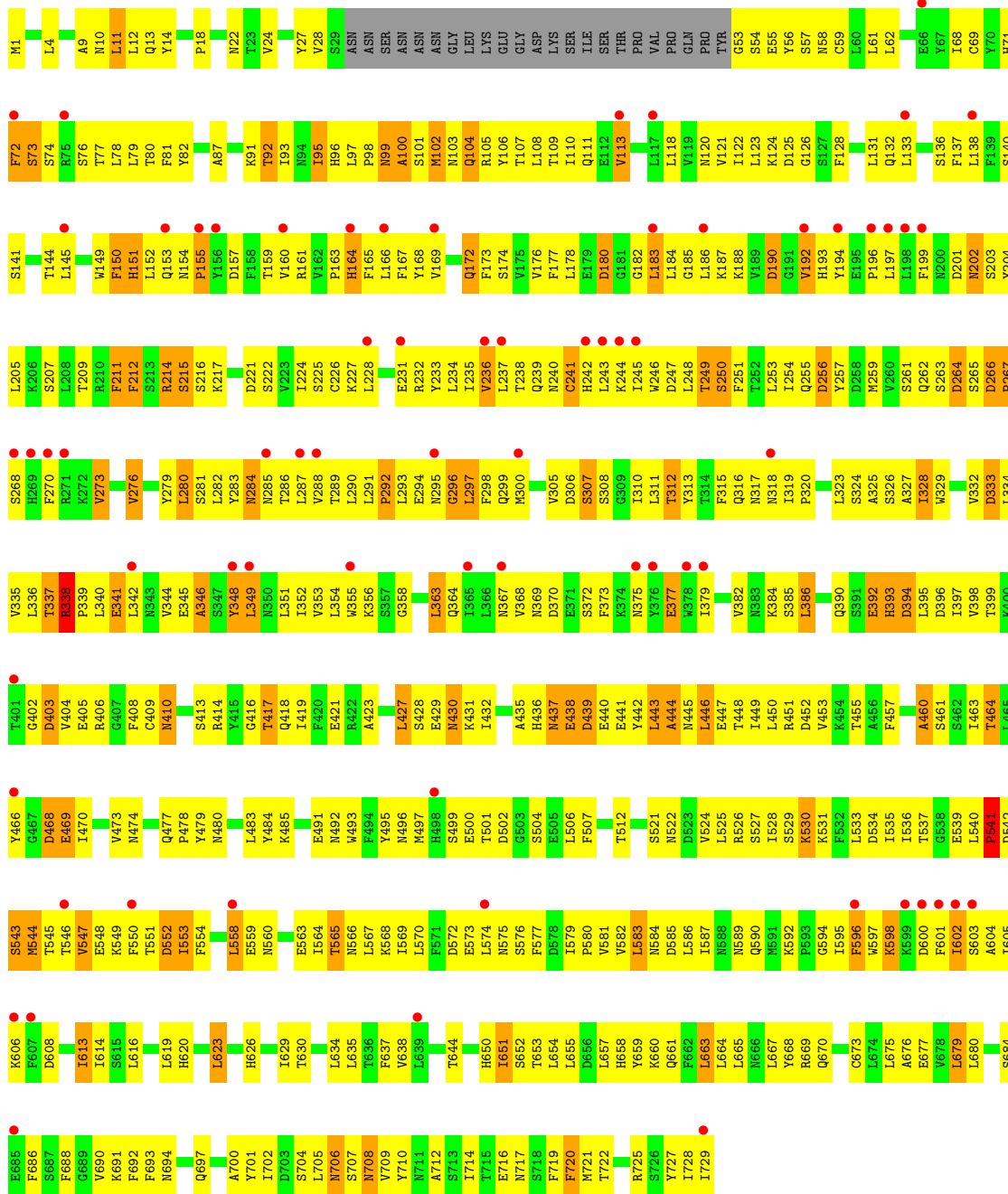
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Nucleoporin NUP120



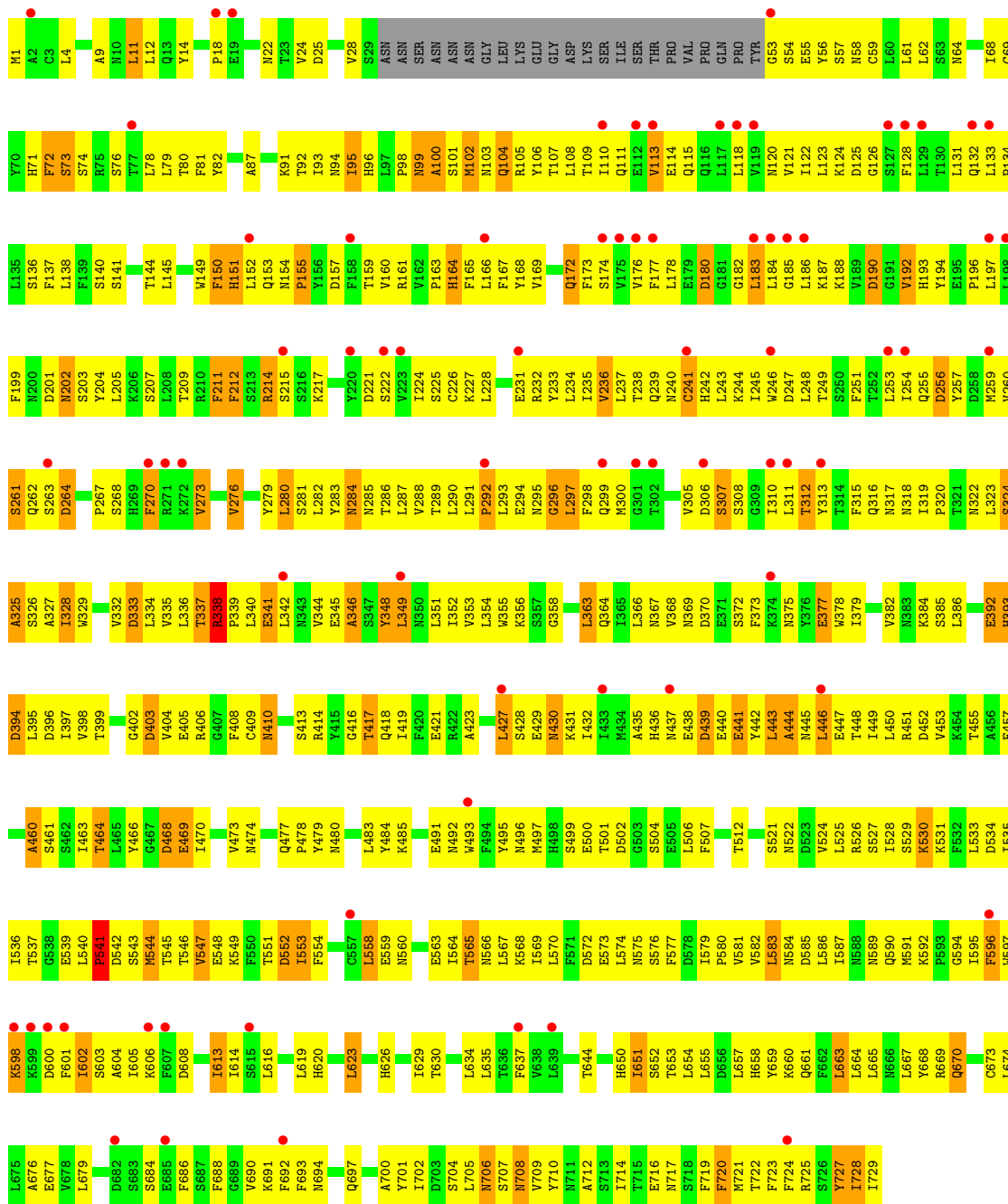


● Molecule 1: Nucleoporin NUP120

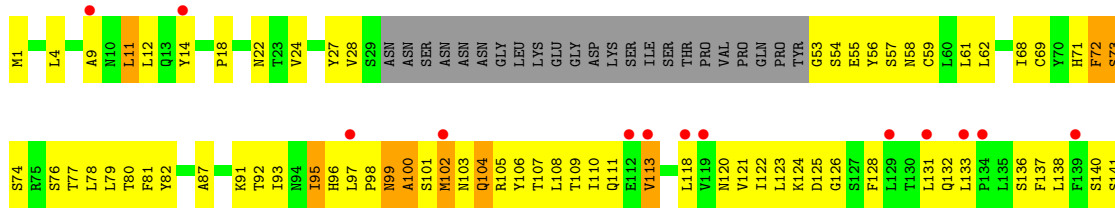


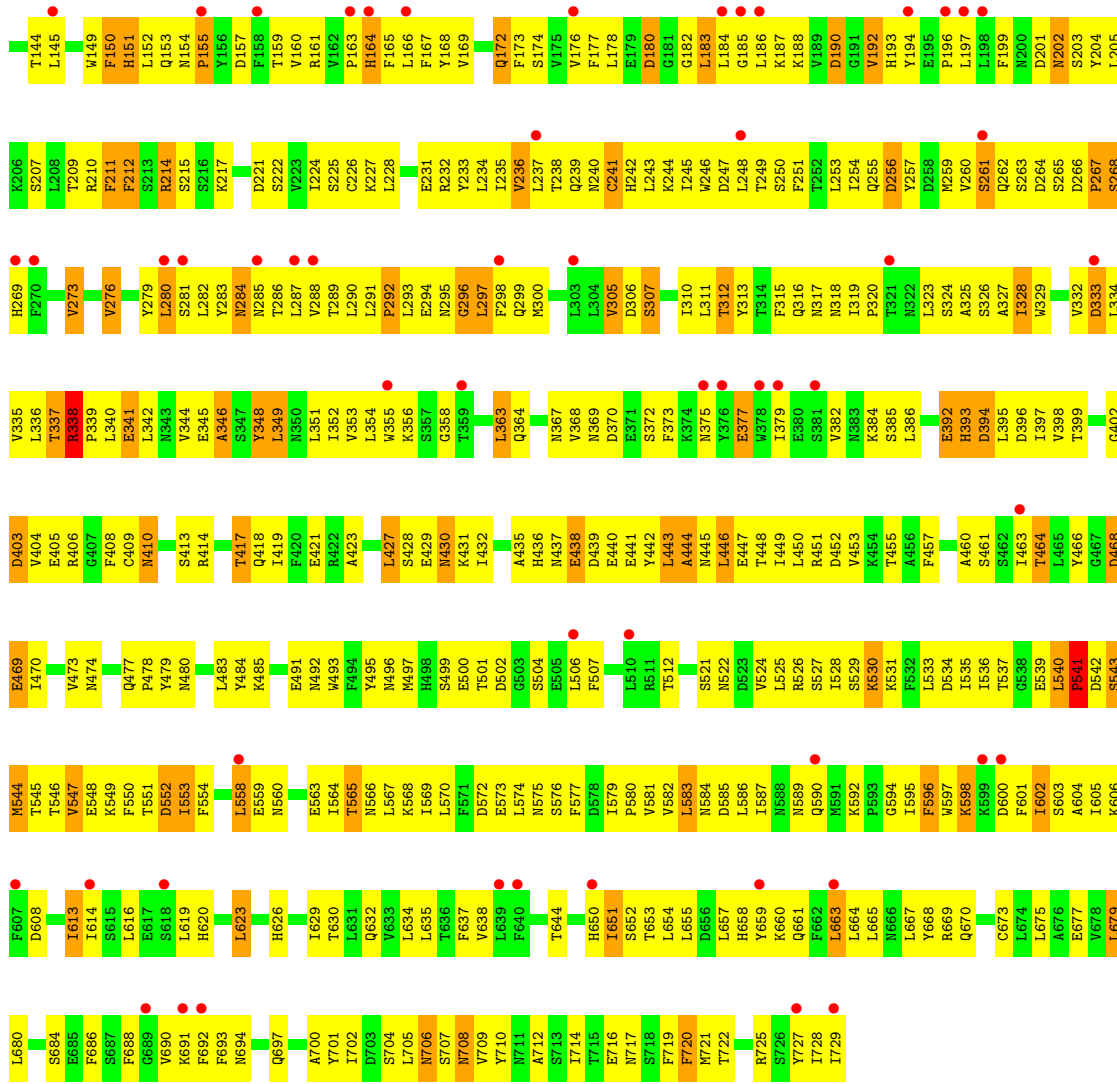
● Molecule 1: Nucleoporin NUP120





● Molecule 1: Nucleoporin NUP120





4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	52.99Å 115.72Å 156.08Å 90.06° 89.96° 90.02°	Depositor
Resolution (Å)	50.00 – 3.00 47.47 – 3.01	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.00) 85.3 (47.47-3.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 3.01Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.255 , 0.274 0.254 , 0.272	Depositor DCC
R_{free} test set	3365 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	93.7	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 67.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.448 for h,-k,-l 0.449 for -h,k,-l 0.447 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	22992	wwPDB-VP
Average B, all atoms (Å ²)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.00% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.48	2/5878 (0.0%)	0.71	3/7981 (0.0%)
1	B	0.46	0/5878	0.71	2/7981 (0.0%)
1	C	0.46	0/5878	0.71	2/7981 (0.0%)
1	D	0.46	0/5878	0.71	3/7981 (0.0%)
All	All	0.47	2/23512 (0.0%)	0.71	10/31924 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	307	SER	C-O	5.94	1.34	1.23
1	A	306	ASP	CB-CG	5.73	1.63	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	358	GLY	N-CA-C	-5.81	98.58	113.10
1	D	358	GLY	N-CA-C	-5.73	98.78	113.10
1	C	358	GLY	N-CA-C	-5.72	98.81	113.10
1	A	307	SER	CB-CA-C	5.71	120.95	110.10
1	A	358	GLY	N-CA-C	-5.66	98.95	113.10
1	C	11	LEU	CA-CB-CG	-5.36	102.98	115.30
1	D	11	LEU	CA-CB-CG	-5.20	103.34	115.30
1	B	11	LEU	CA-CB-CG	-5.19	103.37	115.30
1	A	11	LEU	CA-CB-CG	-5.18	103.39	115.30
1	D	305	VAL	CB-CA-C	-5.02	101.87	111.40

There are no chirality outliers.

There are no planarity outliers.

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	5748	0	5657	593	0
1	B	5748	0	5657	564	0
1	C	5748	0	5657	591	0
1	D	5748	0	5657	567	0
All	All	22992	0	22628	2281	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 50.

All (2281) 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:224:ILE:HG12	1:B:273:VAL:HG11	1.23	1.20
1:D:224:ILE:HG12	1:D:273:VAL:HG11	1.23	1.15
1:A:224:ILE:HG12	1:A:273:VAL:HG11	1.24	1.14
1:C:224:ILE:HG12	1:C:273:VAL:HG11	1.22	1.14
1:D:398:VAL:HB	1:D:669:ARG:NH1	1.62	1.14
1:A:398:VAL:HB	1:A:669:ARG:NH1	1.64	1.12
1:C:398:VAL:HB	1:C:669:ARG:NH1	1.64	1.12
1:B:398:VAL:HB	1:B:669:ARG:NH1	1.65	1.11
1:B:153:GLN:HG2	1:B:155:PRO:HD3	1.39	1.04
1:D:153:GLN:HG2	1:D:155:PRO:HD3	1.39	1.04
1:A:153:GLN:HG2	1:A:155:PRO:HD3	1.39	1.03
1:C:153:GLN:HG2	1:C:155:PRO:HD3	1.39	1.03
1:B:293:LEU:HB2	1:B:297:LEU:HG	1.41	1.02
1:D:293:LEU:HB2	1:D:297:LEU:HG	1.41	1.02
1:A:293:LEU:HB2	1:A:297:LEU:HG	1.41	0.99
1:B:338:ARG:HB2	1:B:339:PRO:HD2	1.43	0.99
1:D:160:VAL:HG23	1:D:161:ARG:H	1.25	0.99
1:C:293:LEU:HB2	1:C:297:LEU:HG	1.41	0.99
1:D:338:ARG:HB2	1:D:339:PRO:HD2	1.43	0.99
1:B:160:VAL:HG23	1:B:161:ARG:H	1.26	0.98
1:C:338:ARG:HB2	1:C:339:PRO:HD2	1.43	0.98
1:A:568:LYS:HD2	1:D:210:ARG:HH12	1.24	0.98
1:A:338:ARG:HB2	1:A:339:PRO:HD2	1.42	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:693:PHE:HB2	1:A:697:GLN:HE22	1.28	0.98
1:C:160:VAL:HG23	1:C:161:ARG:H	1.25	0.97
1:C:693:PHE:HB2	1:C:697:GLN:HE22	1.28	0.97
1:A:160:VAL:HG23	1:A:161:ARG:H	1.25	0.97
1:B:693:PHE:HB2	1:B:697:GLN:HE22	1.26	0.96
1:B:306:ASP:OD1	1:B:307:SER:N	1.99	0.95
1:D:693:PHE:HB2	1:D:697:GLN:HE22	1.29	0.95
1:D:227:LYS:HE3	1:D:281:SER:HA	1.50	0.94
1:A:187:LYS:HD3	1:A:197:LEU:HD11	1.50	0.92
1:B:187:LYS:HD3	1:B:197:LEU:HD11	1.51	0.92
1:D:187:LYS:HD3	1:D:197:LEU:HD11	1.51	0.92
1:D:334:LEU:HD13	1:D:351:LEU:HD11	1.52	0.92
1:A:500:GLU:HG2	1:A:501:THR:H	1.36	0.91
1:C:187:LYS:HD3	1:C:197:LEU:HD11	1.51	0.91
1:A:227:LYS:HE3	1:A:281:SER:HA	1.52	0.91
1:C:500:GLU:HG2	1:C:501:THR:H	1.36	0.91
1:B:102:MET:HB3	1:B:107:THR:HG21	1.51	0.90
1:A:102:MET:HB3	1:A:107:THR:HG21	1.51	0.90
1:A:605:ILE:HG13	1:A:606:LYS:H	1.36	0.90
1:C:340:LEU:HD23	1:C:342:LEU:HD21	1.54	0.90
1:B:227:LYS:HE3	1:B:281:SER:HA	1.53	0.90
1:A:334:LEU:HD13	1:A:351:LEU:HD11	1.53	0.90
1:C:102:MET:HB3	1:C:107:THR:HG21	1.52	0.90
1:D:102:MET:HB3	1:D:107:THR:HG21	1.51	0.90
1:C:227:LYS:HE3	1:C:281:SER:HA	1.53	0.90
1:C:605:ILE:HG13	1:C:606:LYS:H	1.37	0.89
1:B:334:LEU:HD13	1:B:351:LEU:HD11	1.55	0.89
1:D:463:ILE:HG22	1:D:464:THR:N	1.87	0.88
1:A:340:LEU:HD23	1:A:342:LEU:HD21	1.56	0.88
1:B:605:ILE:HG13	1:B:606:LYS:H	1.35	0.88
1:B:340:LEU:HD23	1:B:342:LEU:HD21	1.54	0.88
1:B:500:GLU:HG2	1:B:501:THR:H	1.36	0.88
1:B:463:ILE:HG22	1:B:464:THR:N	1.88	0.88
1:C:334:LEU:HD13	1:C:351:LEU:HD11	1.55	0.88
1:D:500:GLU:HG2	1:D:501:THR:H	1.36	0.88
1:A:463:ILE:HG22	1:A:464:THR:N	1.87	0.88
1:C:463:ILE:HG22	1:C:464:THR:N	1.87	0.87
1:C:398:VAL:HB	1:C:669:ARG:HH12	1.40	0.86
1:D:605:ILE:HG13	1:D:606:LYS:H	1.36	0.86
1:C:259:MET:HE1	1:C:262:GLN:HE22	1.40	0.86
1:C:404:VAL:HG11	1:C:438:GLU:HA	1.57	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:340:LEU:HD23	1:D:342:LEU:HD21	1.56	0.85
1:A:398:VAL:HB	1:A:669:ARG:HH12	1.42	0.85
1:A:323:LEU:HD13	1:A:329:TRP:HB2	1.59	0.85
1:B:323:LEU:HD13	1:B:329:TRP:HB2	1.58	0.85
1:D:398:VAL:HB	1:D:669:ARG:HH12	1.39	0.85
1:D:323:LEU:HD13	1:D:329:TRP:HB2	1.59	0.84
1:D:398:VAL:HB	1:D:669:ARG:HH11	1.42	0.84
1:C:323:LEU:HD13	1:C:329:TRP:HB2	1.60	0.84
1:A:122:ILE:HG13	1:A:166:LEU:HD22	1.60	0.83
1:B:404:VAL:HG11	1:B:438:GLU:HA	1.60	0.83
1:C:239:GLN:HA	1:C:273:VAL:HB	1.59	0.83
1:B:239:GLN:HA	1:B:273:VAL:HB	1.58	0.83
1:A:667:LEU:HD22	1:C:723:PHE:CE2	2.13	0.83
1:C:122:ILE:HG13	1:C:166:LEU:HD22	1.61	0.83
1:D:239:GLN:HA	1:D:273:VAL:HB	1.58	0.83
1:B:122:ILE:HG13	1:B:166:LEU:HD22	1.61	0.83
1:B:122:ILE:HD11	1:B:166:LEU:HD13	1.61	0.83
1:D:122:ILE:HD11	1:D:166:LEU:HD13	1.61	0.83
1:C:122:ILE:HD11	1:C:166:LEU:HD13	1.60	0.82
1:D:122:ILE:HG13	1:D:166:LEU:HD22	1.61	0.82
1:A:239:GLN:HA	1:A:273:VAL:HB	1.60	0.82
1:B:398:VAL:HB	1:B:669:ARG:HH11	1.44	0.82
1:A:122:ILE:HD11	1:A:166:LEU:HD13	1.61	0.82
1:D:291:LEU:O	1:D:297:LEU:HB2	1.80	0.82
1:C:398:VAL:HB	1:C:669:ARG:HH11	1.44	0.82
1:D:176:VAL:HG12	1:D:177:PHE:H	1.44	0.81
1:B:291:LEU:O	1:B:297:LEU:HB2	1.80	0.81
1:B:605:ILE:HG13	1:B:606:LYS:N	1.96	0.81
1:D:623:LEU:HD13	1:D:664:LEU:CD2	2.09	0.81
1:B:398:VAL:HB	1:B:669:ARG:HH12	1.42	0.81
1:A:398:VAL:HB	1:A:669:ARG:HH11	1.43	0.81
1:D:605:ILE:HG13	1:D:606:LYS:N	1.97	0.80
1:A:623:LEU:HD13	1:A:664:LEU:CD2	2.10	0.80
1:D:241:CYS:HB3	1:D:259:MET:HB2	1.63	0.80
1:B:176:VAL:HG12	1:B:177:PHE:H	1.45	0.80
1:A:723:PHE:CE2	1:C:667:LEU:HD22	2.16	0.80
1:B:291:LEU:HD11	1:B:299:GLN:HB2	1.64	0.80
1:C:236:VAL:O	1:C:243:LEU:HD12	1.82	0.80
1:C:176:VAL:HG12	1:C:177:PHE:H	1.44	0.80
1:C:291:LEU:HD11	1:C:299:GLN:HB2	1.63	0.80
1:A:176:VAL:HG12	1:A:177:PHE:H	1.44	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:ASN:H	1:C:107:THR:HG21	1.46	0.80
1:D:291:LEU:HD11	1:D:299:GLN:HB2	1.64	0.80
1:A:568:LYS:HD2	1:D:210:ARG:NH1	1.97	0.80
1:A:605:ILE:HG13	1:A:606:LYS:N	1.96	0.80
1:B:103:ASN:H	1:B:107:THR:HG21	1.46	0.80
1:C:291:LEU:O	1:C:297:LEU:HB2	1.80	0.80
1:C:623:LEU:HD13	1:C:664:LEU:CD2	2.11	0.79
1:C:547:VAL:CG2	1:C:644:THR:HG21	2.11	0.79
1:C:605:ILE:HG13	1:C:606:LYS:N	1.97	0.79
1:A:317:ASN:ND2	1:A:319:ILE:HG13	1.96	0.79
1:C:237:LEU:HD12	1:C:238:THR:H	1.47	0.79
1:D:236:VAL:O	1:D:243:LEU:HD12	1.82	0.79
1:B:237:LEU:HD12	1:B:238:THR:H	1.47	0.79
1:B:547:VAL:CG2	1:B:644:THR:HG21	2.12	0.79
1:A:291:LEU:HD11	1:A:299:GLN:HB2	1.64	0.79
1:C:55:GLU:OE1	1:C:74:SER:HA	1.83	0.79
1:D:103:ASN:H	1:D:107:THR:HG21	1.47	0.79
1:A:404:VAL:HG11	1:A:438:GLU:HA	1.64	0.79
1:B:623:LEU:HD13	1:B:664:LEU:CD2	2.12	0.79
1:D:317:ASN:ND2	1:D:319:ILE:HG13	1.97	0.79
1:A:103:ASN:H	1:A:107:THR:HG21	1.48	0.78
1:A:236:VAL:O	1:A:243:LEU:HD12	1.84	0.78
1:A:237:LEU:HD12	1:A:238:THR:H	1.48	0.78
1:A:291:LEU:O	1:A:297:LEU:HB2	1.81	0.78
1:A:463:ILE:HG22	1:A:464:THR:H	1.47	0.78
1:A:547:VAL:CG2	1:A:644:THR:HG21	2.12	0.78
1:D:55:GLU:OE1	1:D:74:SER:HA	1.82	0.78
1:D:547:VAL:CG2	1:D:644:THR:HG21	2.12	0.78
1:C:177:PHE:HZ	1:C:234:LEU:HD21	1.49	0.78
1:B:58:ASN:HA	1:B:474:ASN:ND2	1.98	0.78
1:B:55:GLU:OE1	1:B:74:SER:HA	1.83	0.78
1:A:177:PHE:HZ	1:A:234:LEU:HD21	1.49	0.78
1:A:292:PRO:O	1:A:293:LEU:HD12	1.84	0.78
1:B:236:VAL:O	1:B:243:LEU:HD12	1.84	0.78
1:B:237:LEU:HD12	1:B:238:THR:N	1.99	0.78
1:B:546:THR:HG22	1:B:546:THR:O	1.85	0.78
1:B:317:ASN:ND2	1:B:319:ILE:HG13	1.98	0.77
1:C:317:ASN:ND2	1:C:319:ILE:HG13	1.98	0.77
1:B:224:ILE:CG1	1:B:273:VAL:HG11	2.11	0.77
1:D:177:PHE:HZ	1:D:234:LEU:HD21	1.48	0.77
1:D:237:LEU:HD12	1:D:238:THR:H	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:237:LEU:HD12	1:C:238:THR:N	1.99	0.77
1:B:177:PHE:HZ	1:B:234:LEU:HD21	1.49	0.77
1:C:463:ILE:HG22	1:C:464:THR:H	1.48	0.77
1:B:522:ASN:O	1:B:526:ARG:HG3	1.84	0.77
1:D:292:PRO:O	1:D:293:LEU:HD12	1.84	0.77
1:A:55:GLU:OE1	1:A:74:SER:HA	1.85	0.77
1:D:224:ILE:CG1	1:D:273:VAL:HG11	2.12	0.77
1:D:546:THR:O	1:D:546:THR:HG22	1.85	0.77
1:D:237:LEU:HD12	1:D:238:THR:N	2.00	0.77
1:A:237:LEU:HD12	1:A:238:THR:N	2.00	0.77
1:C:292:PRO:O	1:C:293:LEU:HD12	1.86	0.76
1:A:463:ILE:CG2	1:A:464:THR:H	1.99	0.76
1:B:292:PRO:O	1:B:293:LEU:HD12	1.85	0.76
1:A:568:LYS:NZ	1:D:210:ARG:HH22	1.82	0.76
1:B:103:ASN:H	1:B:107:THR:CG2	1.98	0.76
1:A:728:ILE:HD12	1:C:724:PHE:CD1	2.21	0.76
1:B:463:ILE:CG2	1:B:464:THR:H	1.99	0.76
1:C:463:ILE:CG2	1:C:464:THR:H	1.99	0.76
1:A:522:ASN:O	1:A:526:ARG:HG3	1.85	0.76
1:D:463:ILE:CG2	1:D:464:THR:H	1.99	0.76
1:D:160:VAL:HG23	1:D:161:ARG:N	2.01	0.75
1:D:522:ASN:O	1:D:526:ARG:HG3	1.85	0.75
1:D:58:ASN:HA	1:D:474:ASN:ND2	2.01	0.75
1:A:608:ASP:HB2	1:A:691:LYS:NZ	2.02	0.75
1:D:103:ASN:H	1:D:107:THR:CG2	1.99	0.75
1:A:58:ASN:HA	1:A:474:ASN:ND2	2.02	0.75
1:B:160:VAL:HG23	1:B:161:ARG:N	2.01	0.75
1:A:724:PHE:CD1	1:C:728:ILE:HD12	2.22	0.75
1:B:224:ILE:HG12	1:B:273:VAL:CG1	2.12	0.75
1:B:153:GLN:HG2	1:B:155:PRO:CD	2.16	0.74
1:D:259:MET:HA	1:D:262:GLN:NE2	2.03	0.74
1:C:160:VAL:HG23	1:C:161:ARG:N	2.01	0.74
1:D:153:GLN:HG2	1:D:155:PRO:CD	2.17	0.74
1:D:224:ILE:HG12	1:D:273:VAL:CG1	2.13	0.74
1:A:288:VAL:HG22	1:A:336:LEU:HD22	1.69	0.74
1:B:296:GLY:O	1:B:320:PRO:HA	1.86	0.74
1:B:608:ASP:HB2	1:B:691:LYS:NZ	2.02	0.74
1:C:608:ASP:HB2	1:C:691:LYS:NZ	2.03	0.74
1:D:247:ASP:HB2	1:D:254:ILE:CG1	2.18	0.74
1:D:608:ASP:HB2	1:D:691:LYS:NZ	2.01	0.74
1:A:103:ASN:H	1:A:107:THR:CG2	1.99	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:VAL:HG23	1:A:161:ARG:N	2.01	0.74
1:D:296:GLY:O	1:D:320:PRO:HA	1.87	0.74
1:C:103:ASN:H	1:C:107:THR:CG2	1.99	0.74
1:C:522:ASN:O	1:C:526:ARG:HG3	1.87	0.74
1:A:247:ASP:HB2	1:A:254:ILE:CG1	2.18	0.74
1:B:247:ASP:HB2	1:B:254:ILE:CG1	2.17	0.74
1:B:463:ILE:HG22	1:B:464:THR:H	1.48	0.74
1:C:553:ILE:HG22	1:C:553:ILE:O	1.87	0.74
1:A:153:GLN:HG2	1:A:155:PRO:CD	2.17	0.74
1:A:342:LEU:HD13	1:A:379:ILE:HD12	1.70	0.74
1:C:153:GLN:HG2	1:C:155:PRO:CD	2.17	0.74
1:C:568:LYS:HG3	1:C:572:ASP:OD2	1.88	0.73
1:D:288:VAL:HG22	1:D:336:LEU:HD22	1.70	0.73
1:D:463:ILE:HG22	1:D:464:THR:H	1.48	0.73
1:D:500:GLU:HG2	1:D:501:THR:N	2.03	0.73
1:A:296:GLY:O	1:A:320:PRO:HA	1.87	0.73
1:A:608:ASP:HB2	1:A:691:LYS:HZ1	1.53	0.73
1:C:296:GLY:O	1:C:320:PRO:HA	1.87	0.73
1:A:546:THR:O	1:A:546:THR:HG22	1.85	0.73
1:B:568:LYS:HG3	1:B:572:ASP:OD2	1.88	0.73
1:A:297:LEU:HD22	1:A:318:ASN:HD21	1.53	0.73
1:C:288:VAL:HG22	1:C:336:LEU:HD22	1.70	0.73
1:D:235:ILE:H	1:D:235:ILE:HD12	1.51	0.73
1:B:500:GLU:HG2	1:B:501:THR:N	2.03	0.73
1:C:705:LEU:H	1:C:705:LEU:HD12	1.53	0.73
1:C:241:CYS:HB3	1:C:259:MET:HB2	1.71	0.73
1:C:286:THR:HG22	1:C:287:LEU:N	2.03	0.73
1:C:463:ILE:CG2	1:C:464:THR:N	2.51	0.73
1:D:568:LYS:HG3	1:D:572:ASP:OD2	1.89	0.73
1:A:694:ASN:ND2	1:A:697:GLN:HE21	1.87	0.73
1:B:305:VAL:HG12	1:B:311:LEU:HD23	1.69	0.73
1:C:224:ILE:CG1	1:C:273:VAL:HG11	2.11	0.73
1:C:305:VAL:HG12	1:C:311:LEU:HD23	1.68	0.73
1:A:463:ILE:CG2	1:A:464:THR:N	2.51	0.73
1:A:568:LYS:HG3	1:A:572:ASP:OD2	1.89	0.73
1:C:235:ILE:HD12	1:C:235:ILE:H	1.51	0.73
1:C:694:ASN:ND2	1:C:697:GLN:HE21	1.86	0.73
1:A:553:ILE:HG22	1:A:553:ILE:O	1.88	0.73
1:B:293:LEU:HD22	1:B:297:LEU:HD11	1.71	0.73
1:C:58:ASN:HA	1:C:474:ASN:ND2	2.04	0.73
1:C:546:THR:O	1:C:546:THR:HG22	1.85	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:553:ILE:O	1:D:553:ILE:HG22	1.89	0.73
1:A:305:VAL:HG12	1:A:311:LEU:HD23	1.69	0.72
1:B:288:VAL:HG22	1:B:336:LEU:HD22	1.71	0.72
1:B:463:ILE:CG2	1:B:464:THR:N	2.51	0.72
1:C:342:LEU:HD13	1:C:379:ILE:HD12	1.71	0.72
1:A:286:THR:HG22	1:A:287:LEU:N	2.04	0.72
1:B:235:ILE:H	1:B:235:ILE:HD12	1.52	0.72
1:D:463:ILE:CG2	1:D:464:THR:N	2.51	0.72
1:D:342:LEU:CD1	1:D:379:ILE:HD12	2.19	0.72
1:A:235:ILE:H	1:A:235:ILE:HD12	1.52	0.72
1:D:247:ASP:OD1	1:D:249:THR:HB	1.89	0.72
1:D:293:LEU:HD22	1:D:297:LEU:HD11	1.71	0.72
1:A:317:ASN:HD21	1:A:319:ILE:HG13	1.54	0.72
1:D:342:LEU:HD13	1:D:379:ILE:HD12	1.70	0.72
1:A:558:LEU:HD11	1:A:635:LEU:HD11	1.72	0.72
1:C:297:LEU:HD22	1:C:318:ASN:HD21	1.54	0.72
1:B:553:ILE:O	1:B:553:ILE:HG22	1.89	0.72
1:A:254:ILE:HG21	1:A:311:LEU:HB2	1.72	0.72
1:B:342:LEU:CD1	1:B:379:ILE:HD12	2.20	0.72
1:D:558:LEU:HD11	1:D:635:LEU:HD11	1.71	0.71
1:A:224:ILE:CG1	1:A:273:VAL:HG11	2.12	0.71
1:A:500:GLU:HG2	1:A:501:THR:N	2.03	0.71
1:A:705:LEU:HD12	1:A:705:LEU:H	1.55	0.71
1:B:694:ASN:ND2	1:B:697:GLN:HE21	1.88	0.71
1:C:558:LEU:HD11	1:C:635:LEU:HD11	1.72	0.71
1:B:297:LEU:HD22	1:B:318:ASN:HD21	1.53	0.71
1:D:286:THR:HG22	1:D:287:LEU:N	2.04	0.71
1:B:108:LEU:HD23	1:B:109:THR:N	2.05	0.71
1:B:442:TYR:O	1:B:445:ASN:HB2	1.90	0.71
1:C:293:LEU:HD22	1:C:297:LEU:HD11	1.72	0.71
1:C:500:GLU:HG2	1:C:501:THR:N	2.04	0.71
1:D:694:ASN:ND2	1:D:697:GLN:HE21	1.89	0.71
1:A:293:LEU:HD22	1:A:297:LEU:HD11	1.72	0.71
1:A:342:LEU:CD1	1:A:379:ILE:HD12	2.20	0.71
1:C:224:ILE:HG12	1:C:273:VAL:CG1	2.12	0.71
1:C:342:LEU:CD1	1:C:379:ILE:HD12	2.20	0.71
1:B:342:LEU:HD13	1:B:379:ILE:HD12	1.71	0.71
1:D:108:LEU:HD23	1:D:109:THR:N	2.06	0.71
1:A:442:TYR:O	1:A:445:ASN:HB2	1.90	0.71
1:B:286:THR:HG22	1:B:287:LEU:N	2.05	0.70
1:B:608:ASP:HB2	1:B:691:LYS:HZ1	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:LEU:HD23	1:C:109:THR:N	2.06	0.70
1:D:442:TYR:O	1:D:445:ASN:HB2	1.91	0.70
1:B:705:LEU:H	1:B:705:LEU:HD12	1.56	0.70
1:D:297:LEU:HD22	1:D:318:ASN:HD21	1.54	0.70
1:B:558:LEU:HD11	1:B:635:LEU:HD11	1.72	0.70
1:D:705:LEU:HD12	1:D:705:LEU:H	1.55	0.70
1:C:201:ASP:OD1	1:C:205:LEU:HG	1.91	0.70
1:C:247:ASP:HB2	1:C:254:ILE:CG1	2.22	0.70
1:C:442:TYR:O	1:C:445:ASN:HB2	1.91	0.70
1:A:259:MET:HE1	1:A:262:GLN:HE22	1.57	0.70
1:B:259:MET:HE1	1:B:262:GLN:HE22	1.55	0.70
1:C:254:ILE:HG21	1:C:311:LEU:HB2	1.74	0.70
1:C:521:SER:OG	1:C:524:VAL:HG23	1.92	0.70
1:D:714:ILE:O	1:D:714:ILE:HG13	1.92	0.70
1:A:201:ASP:OD1	1:A:205:LEU:HG	1.91	0.70
1:A:241:CYS:HB3	1:A:259:MET:HB2	1.74	0.70
1:A:693:PHE:CB	1:A:697:GLN:HE22	2.04	0.70
1:A:108:LEU:HD23	1:A:109:THR:N	2.07	0.70
1:A:224:ILE:HG12	1:A:273:VAL:CG1	2.13	0.70
1:B:201:ASP:OD1	1:B:205:LEU:HG	1.91	0.70
1:B:521:SER:OG	1:B:524:VAL:HG23	1.92	0.70
1:D:521:SER:OG	1:D:524:VAL:HG23	1.92	0.69
1:B:693:PHE:CB	1:B:697:GLN:HE22	2.03	0.69
1:C:68:ILE:HD12	1:C:138:LEU:HD13	1.74	0.69
1:D:201:ASP:OD1	1:D:205:LEU:HG	1.91	0.69
1:A:521:SER:OG	1:A:524:VAL:HG23	1.92	0.69
1:B:714:ILE:O	1:B:714:ILE:HG13	1.92	0.69
1:C:317:ASN:HD21	1:C:319:ILE:HG13	1.56	0.69
1:A:701:TYR:O	1:A:705:LEU:HD12	1.93	0.69
1:B:226:CYS:SG	1:B:227:LYS:N	2.66	0.69
1:B:306:ASP:O	1:B:307:SER:OG	2.11	0.69
1:C:693:PHE:CB	1:C:697:GLN:HE22	2.05	0.69
1:C:701:TYR:O	1:C:704:SER:HB3	1.91	0.69
1:D:154:ASN:N	1:D:155:PRO:HD3	2.07	0.69
1:B:154:ASN:N	1:B:155:PRO:HD3	2.07	0.69
1:B:344:VAL:HG12	1:B:345:GLU:N	2.08	0.69
1:A:603:SER:HA	1:A:686:PHE:HD1	1.58	0.69
1:B:136:SER:O	1:B:140:SER:HB3	1.92	0.69
1:B:506:LEU:HD11	1:B:586:LEU:HB2	1.75	0.69
1:C:154:ASN:N	1:C:155:PRO:HD3	2.07	0.69
1:C:608:ASP:HB2	1:C:691:LYS:HZ1	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:VAL:HG12	1:D:177:PHE:N	2.08	0.69
1:D:317:ASN:HD21	1:D:319:ILE:HG13	1.56	0.69
1:A:154:ASN:N	1:A:155:PRO:HD3	2.07	0.68
1:C:310:ILE:O	1:C:310:ILE:HG22	1.92	0.68
1:A:226:CYS:SG	1:A:227:LYS:N	2.65	0.68
1:D:344:VAL:HG12	1:D:345:GLU:N	2.09	0.68
1:C:603:SER:HA	1:C:686:PHE:HD1	1.59	0.68
1:D:160:VAL:CG2	1:D:161:ARG:H	2.05	0.68
1:A:136:SER:O	1:A:140:SER:HB3	1.93	0.68
1:A:349:LEU:H	1:A:368:VAL:HG22	1.58	0.68
1:C:176:VAL:HG12	1:C:177:PHE:N	2.08	0.68
1:C:349:LEU:H	1:C:368:VAL:HG22	1.58	0.68
1:D:238:THR:OG1	1:D:242:HIS:HB2	1.94	0.68
1:A:68:ILE:HD12	1:A:138:LEU:HD13	1.75	0.68
1:B:603:SER:HA	1:B:686:PHE:HD1	1.59	0.68
1:B:701:TYR:O	1:B:705:LEU:HD12	1.94	0.68
1:C:78:LEU:HD12	1:C:79:LEU:H	1.58	0.68
1:C:136:SER:O	1:C:140:SER:HB3	1.92	0.68
1:C:547:VAL:HG21	1:C:644:THR:HG21	1.74	0.68
1:D:78:LEU:HD12	1:D:79:LEU:H	1.57	0.68
1:D:136:SER:O	1:D:140:SER:HB3	1.93	0.68
1:B:160:VAL:CG2	1:B:161:ARG:H	2.05	0.68
1:B:176:VAL:HG12	1:B:177:PHE:N	2.09	0.68
1:B:238:THR:OG1	1:B:242:HIS:HB2	1.94	0.68
1:B:317:ASN:HD21	1:B:319:ILE:HG13	1.57	0.68
1:B:349:LEU:H	1:B:368:VAL:HG22	1.58	0.68
1:A:176:VAL:HG12	1:A:177:PHE:N	2.08	0.68
1:D:226:CYS:SG	1:D:227:LYS:N	2.67	0.68
1:D:349:LEU:H	1:D:368:VAL:HG22	1.58	0.68
1:D:506:LEU:HD11	1:D:586:LEU:HB2	1.76	0.68
1:D:603:SER:HA	1:D:686:PHE:HD1	1.59	0.68
1:B:630:THR:O	1:B:634:LEU:HD12	1.94	0.68
1:A:185:GLY:O	1:A:186:LEU:HD12	1.94	0.68
1:C:226:CYS:SG	1:C:227:LYS:N	2.66	0.68
1:C:404:VAL:HG23	1:C:443:LEU:CD1	2.24	0.67
1:A:238:THR:OG1	1:A:242:HIS:HB2	1.94	0.67
1:C:185:GLY:O	1:C:186:LEU:HD12	1.94	0.67
1:D:368:VAL:O	1:D:368:VAL:HG23	1.94	0.67
1:D:608:ASP:HB2	1:D:691:LYS:HZ1	1.58	0.67
1:D:701:TYR:O	1:D:705:LEU:HD12	1.94	0.67
1:A:338:ARG:HB2	1:A:339:PRO:CD	2.22	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:630:THR:O	1:A:634:LEU:HD12	1.95	0.67
1:B:368:VAL:HG23	1:B:368:VAL:O	1.94	0.67
1:C:244:LYS:HB3	1:C:253:LEU:HD11	1.76	0.67
1:C:604:ALA:HB1	1:C:691:LYS:HE2	1.75	0.67
1:D:68:ILE:HD12	1:D:138:LEU:HD13	1.74	0.67
1:D:604:ALA:HB1	1:D:691:LYS:HE2	1.75	0.67
1:D:693:PHE:CB	1:D:697:GLN:HE22	2.05	0.67
1:D:701:TYR:O	1:D:704:SER:HB3	1.94	0.67
1:B:78:LEU:HD12	1:B:79:LEU:H	1.58	0.67
1:C:338:ARG:HB2	1:C:339:PRO:CD	2.22	0.67
1:C:344:VAL:HG12	1:C:345:GLU:N	2.09	0.67
1:D:232:ARG:HD3	1:D:247:ASP:OD1	1.95	0.67
1:A:344:VAL:HG12	1:A:345:GLU:N	2.09	0.67
1:A:604:ALA:HB1	1:A:691:LYS:HE2	1.75	0.67
1:A:674:LEU:HD23	1:C:723:PHE:CD1	2.29	0.67
1:B:68:ILE:HD12	1:B:138:LEU:HD13	1.75	0.67
1:C:238:THR:OG1	1:C:242:HIS:HB2	1.94	0.67
1:D:626:HIS:HB3	1:D:661:GLN:HE21	1.60	0.67
1:A:626:HIS:HB3	1:A:661:GLN:HE21	1.60	0.67
1:B:604:ALA:HB1	1:B:691:LYS:HE2	1.75	0.67
1:B:626:HIS:HB3	1:B:661:GLN:NE2	2.10	0.67
1:B:701:TYR:O	1:B:704:SER:HB3	1.94	0.67
1:C:701:TYR:O	1:C:705:LEU:HD12	1.95	0.67
1:D:404:VAL:HG11	1:D:438:GLU:HA	1.75	0.67
1:A:506:LEU:HD11	1:A:586:LEU:HB2	1.76	0.67
1:D:241:CYS:O	1:D:259:MET:HG2	1.94	0.67
1:A:701:TYR:O	1:A:704:SER:HB3	1.94	0.67
1:B:232:ARG:HD3	1:B:247:ASP:OD1	1.96	0.67
1:C:232:ARG:HD3	1:C:247:ASP:OD1	1.95	0.67
1:B:547:VAL:HG21	1:B:644:THR:HG21	1.77	0.66
1:A:547:VAL:HG21	1:A:644:THR:HG21	1.76	0.66
1:C:506:LEU:HD11	1:C:586:LEU:HB2	1.76	0.66
1:B:449:ILE:O	1:B:453:VAL:HG23	1.94	0.66
1:A:78:LEU:HD12	1:A:79:LEU:H	1.60	0.66
1:A:449:ILE:O	1:A:453:VAL:HG23	1.94	0.66
1:C:541:PRO:HB2	1:C:544:MET:HE2	1.77	0.66
1:A:73:SER:HB3	1:A:78:LEU:H	1.60	0.66
1:C:368:VAL:HG23	1:C:368:VAL:O	1.94	0.66
1:D:185:GLY:O	1:D:186:LEU:HD12	1.94	0.66
1:A:232:ARG:HD3	1:A:247:ASP:OD1	1.95	0.66
1:A:714:ILE:HG13	1:A:714:ILE:O	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:GLY:O	1:B:186:LEU:HD12	1.94	0.66
1:D:404:VAL:HG23	1:D:443:LEU:CD1	2.25	0.66
1:D:547:VAL:HG21	1:D:644:THR:HG21	1.77	0.66
1:B:626:HIS:HB3	1:B:661:GLN:HE21	1.61	0.66
1:C:626:HIS:HB3	1:C:661:GLN:HE21	1.61	0.66
1:C:160:VAL:CG2	1:C:161:ARG:H	2.05	0.66
1:A:368:VAL:O	1:A:368:VAL:HG23	1.94	0.66
1:B:547:VAL:HG22	1:B:644:THR:HG21	1.77	0.66
1:C:449:ILE:O	1:C:453:VAL:HG23	1.95	0.66
1:D:259:MET:HA	1:D:262:GLN:HE21	1.61	0.66
1:A:317:ASN:HD21	1:A:319:ILE:CG1	2.08	0.65
1:C:630:THR:O	1:C:634:LEU:HD12	1.97	0.65
1:A:160:VAL:CG2	1:A:161:ARG:H	2.05	0.65
1:B:338:ARG:HB2	1:B:339:PRO:CD	2.22	0.65
1:D:317:ASN:HD21	1:D:319:ILE:CG1	2.09	0.65
1:C:291:LEU:HB2	1:C:297:LEU:HB3	1.78	0.65
1:C:714:ILE:HG13	1:C:714:ILE:O	1.95	0.65
1:D:626:HIS:HB3	1:D:661:GLN:NE2	2.11	0.65
1:A:291:LEU:HB2	1:A:297:LEU:HB3	1.79	0.65
1:A:547:VAL:HG22	1:A:644:THR:HG21	1.78	0.65
1:B:254:ILE:HG21	1:B:311:LEU:HB2	1.79	0.65
1:B:291:LEU:HB2	1:B:297:LEU:HB3	1.79	0.65
1:C:725:ARG:O	1:C:729:ILE:HG22	1.95	0.65
1:D:547:VAL:HG22	1:D:644:THR:HG21	1.77	0.65
1:A:404:VAL:HG23	1:A:443:LEU:CD1	2.27	0.65
1:C:73:SER:HB3	1:C:78:LEU:H	1.61	0.65
1:C:95:ILE:HD11	1:C:133:LEU:HD11	1.79	0.65
1:D:73:SER:HB3	1:D:78:LEU:H	1.61	0.65
1:B:446:LEU:HD22	1:B:450:LEU:CD1	2.26	0.65
1:D:244:LYS:HB3	1:D:253:LEU:HD11	1.78	0.65
1:B:404:VAL:HG23	1:B:443:LEU:CD1	2.25	0.65
1:B:317:ASN:HD21	1:B:319:ILE:CG1	2.10	0.65
1:C:626:HIS:HB3	1:C:661:GLN:NE2	2.11	0.65
1:B:310:ILE:HG22	1:B:310:ILE:O	1.97	0.65
1:B:725:ARG:O	1:B:729:ILE:HG22	1.97	0.64
1:D:291:LEU:HB2	1:D:297:LEU:HB3	1.79	0.64
1:D:449:ILE:O	1:D:453:VAL:HG23	1.96	0.64
1:A:257:TYR:CE2	1:A:313:TYR:HB3	2.32	0.64
1:A:626:HIS:HB3	1:A:661:GLN:NE2	2.11	0.64
1:B:73:SER:HB3	1:B:78:LEU:H	1.62	0.64
1:C:547:VAL:HG22	1:C:644:THR:HG21	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:338:ARG:HB2	1:D:339:PRO:CD	2.23	0.64
1:D:341:GLU:C	1:D:342:LEU:HD23	2.18	0.64
1:A:95:ILE:HD11	1:A:133:LEU:HD11	1.80	0.64
1:A:168:TYR:HA	1:A:174:SER:HB2	1.80	0.64
1:A:721:MET:HE1	1:C:721:MET:HB3	1.79	0.64
1:B:430:ASN:HD22	1:B:430:ASN:N	1.95	0.64
1:C:317:ASN:HD21	1:C:319:ILE:CG1	2.10	0.64
1:A:446:LEU:HD22	1:A:450:LEU:CD1	2.27	0.64
1:B:341:GLU:C	1:B:342:LEU:HD23	2.18	0.64
1:D:630:THR:O	1:D:634:LEU:HD12	1.98	0.64
1:B:257:TYR:CE2	1:B:313:TYR:HB3	2.33	0.64
1:C:168:TYR:HA	1:C:174:SER:HB2	1.80	0.64
1:D:725:ARG:O	1:D:729:ILE:HG22	1.98	0.64
1:A:723:PHE:CD1	1:C:674:LEU:HD23	2.32	0.64
1:D:430:ASN:N	1:D:430:ASN:HD22	1.96	0.64
1:A:99:ASN:O	1:A:123:LEU:HD22	1.97	0.63
1:D:95:ILE:HD11	1:D:133:LEU:HD11	1.80	0.63
1:D:99:ASN:O	1:D:123:LEU:HD22	1.97	0.63
1:D:446:LEU:HD22	1:D:450:LEU:CD1	2.28	0.63
1:A:101:SER:HA	1:A:123:LEU:HA	1.80	0.63
1:A:725:ARG:O	1:A:729:ILE:HG22	1.97	0.63
1:B:101:SER:HA	1:B:123:LEU:HA	1.80	0.63
1:A:341:GLU:C	1:A:342:LEU:HD23	2.19	0.63
1:C:430:ASN:HD22	1:C:430:ASN:N	1.95	0.63
1:D:101:SER:HA	1:D:123:LEU:HA	1.81	0.63
1:B:168:TYR:HA	1:B:174:SER:HB2	1.80	0.63
1:D:351:LEU:HG	1:D:353:VAL:HG22	1.79	0.63
1:A:601:PHE:O	1:A:690:VAL:HG13	1.99	0.63
1:C:341:GLU:C	1:C:342:LEU:HD23	2.19	0.63
1:B:397:ILE:HG23	1:B:526:ARG:HG2	1.81	0.63
1:B:247:ASP:HB2	1:B:254:ILE:HG12	1.80	0.62
1:A:244:LYS:HB3	1:A:253:LEU:HD11	1.80	0.62
1:A:430:ASN:HD22	1:A:430:ASN:N	1.96	0.62
1:B:297:LEU:HD22	1:B:318:ASN:ND2	2.14	0.62
1:B:95:ILE:HD11	1:B:133:LEU:HD11	1.81	0.62
1:C:169:VAL:HG23	1:C:174:SER:HA	1.81	0.62
1:D:168:TYR:HA	1:D:174:SER:HB2	1.80	0.62
1:C:132:GLN:NE2	1:C:151:HIS:NE2	2.48	0.62
1:B:99:ASN:O	1:B:123:LEU:HD22	1.98	0.62
1:D:169:VAL:HG23	1:D:174:SER:HA	1.80	0.62
1:D:297:LEU:HD22	1:D:318:ASN:ND2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:541:PRO:HB2	1:A:544:MET:HE2	1.81	0.62
1:B:417:THR:HG22	1:B:418:GLN:N	2.15	0.62
1:D:575:ASN:O	1:D:577:PHE:N	2.30	0.62
1:A:169:VAL:HG23	1:A:174:SER:HA	1.81	0.62
1:A:581:VAL:O	1:A:584:ASN:N	2.31	0.62
1:D:132:GLN:NE2	1:D:151:HIS:NE2	2.48	0.62
1:C:291:LEU:HB2	1:C:297:LEU:CB	2.30	0.62
1:C:601:PHE:O	1:C:690:VAL:HG13	2.00	0.62
1:A:397:ILE:HG23	1:A:526:ARG:HG2	1.82	0.62
1:A:436:HIS:CD2	1:A:438:GLU:HB2	2.35	0.62
1:B:601:PHE:O	1:B:690:VAL:HG13	2.00	0.62
1:A:190:ASP:OD1	1:A:193:HIS:HB2	2.00	0.62
1:A:297:LEU:HD22	1:A:318:ASN:ND2	2.14	0.62
1:B:132:GLN:NE2	1:B:151:HIS:NE2	2.48	0.62
1:C:351:LEU:HG	1:C:353:VAL:HG22	1.80	0.62
1:C:446:LEU:HD22	1:C:450:LEU:CD1	2.30	0.62
1:A:637:PHE:HD2	1:A:651:ILE:HD11	1.65	0.61
1:C:581:VAL:O	1:C:584:ASN:N	2.31	0.61
1:D:190:ASP:OD1	1:D:193:HIS:HB2	2.00	0.61
1:A:132:GLN:NE2	1:A:151:HIS:NE2	2.49	0.61
1:A:545:THR:C	1:A:547:VAL:H	2.02	0.61
1:C:99:ASN:O	1:C:123:LEU:HD22	1.99	0.61
1:A:291:LEU:HB2	1:A:297:LEU:CB	2.31	0.61
1:A:579:ILE:HB	1:A:580:PRO:HD3	1.82	0.61
1:B:579:ILE:HB	1:B:580:PRO:HD3	1.82	0.61
1:C:690:VAL:HG12	1:C:691:LYS:N	2.15	0.61
1:D:601:PHE:O	1:D:690:VAL:HG13	2.00	0.61
1:B:545:THR:C	1:B:547:VAL:H	2.03	0.61
1:C:101:SER:HA	1:C:123:LEU:HA	1.82	0.61
1:C:297:LEU:HD22	1:C:318:ASN:ND2	2.15	0.61
1:D:305:VAL:HG23	1:D:306:ASP:N	2.14	0.61
1:A:721:MET:HB3	1:C:721:MET:HE1	1.81	0.61
1:B:101:SER:HB2	1:B:107:THR:OG1	2.00	0.61
1:B:217:LYS:HG3	1:B:217:LYS:O	2.00	0.61
1:B:351:LEU:HG	1:B:353:VAL:HG22	1.81	0.61
1:D:101:SER:HB2	1:D:107:THR:OG1	2.00	0.61
1:D:217:LYS:HG3	1:D:217:LYS:O	2.00	0.61
1:A:101:SER:HB2	1:A:107:THR:OG1	2.01	0.61
1:A:351:LEU:HG	1:A:353:VAL:HG22	1.81	0.61
1:A:427:LEU:HD12	1:A:442:TYR:CE2	2.35	0.61
1:C:545:THR:OG1	1:C:548:GLU:HG3	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:417:THR:HG22	1:D:418:GLN:N	2.16	0.61
1:D:545:THR:C	1:D:547:VAL:H	2.03	0.61
1:C:101:SER:HB2	1:C:107:THR:OG1	2.01	0.61
1:D:579:ILE:HB	1:D:580:PRO:HD3	1.83	0.61
1:B:190:ASP:OD1	1:B:193:HIS:HB2	2.01	0.61
1:D:398:VAL:CB	1:D:669:ARG:HH12	2.13	0.61
1:B:690:VAL:HG12	1:B:691:LYS:N	2.15	0.61
1:A:217:LYS:O	1:A:217:LYS:HG3	2.00	0.60
1:B:169:VAL:HG23	1:B:174:SER:HA	1.82	0.60
1:B:293:LEU:HD22	1:B:297:LEU:HD21	1.83	0.60
1:C:291:LEU:HD11	1:C:299:GLN:CB	2.31	0.60
1:A:690:VAL:HG12	1:A:691:LYS:N	2.16	0.60
1:B:334:LEU:HD12	1:B:335:VAL:N	2.17	0.60
1:C:217:LYS:HG3	1:C:217:LYS:O	2.00	0.60
1:D:397:ILE:HG23	1:D:526:ARG:HG2	1.83	0.60
1:D:545:THR:OG1	1:D:548:GLU:HG3	2.01	0.60
1:B:291:LEU:HB2	1:B:297:LEU:CB	2.31	0.60
1:C:190:ASP:OD1	1:C:193:HIS:HB2	2.01	0.60
1:D:293:LEU:HD22	1:D:297:LEU:HD21	1.83	0.60
1:D:690:VAL:HG12	1:D:691:LYS:N	2.15	0.60
1:C:545:THR:C	1:C:547:VAL:H	2.03	0.60
1:A:545:THR:OG1	1:A:548:GLU:HG3	2.02	0.60
1:B:539:GLU:O	1:B:541:PRO:HD3	2.01	0.60
1:C:530:LYS:HE2	1:C:530:LYS:HA	1.84	0.60
1:D:241:CYS:O	1:D:259:MET:CG	2.49	0.60
1:B:581:VAL:O	1:B:584:ASN:N	2.30	0.60
1:C:167:PHE:CD2	1:C:168:TYR:N	2.69	0.60
1:C:579:ILE:HB	1:C:580:PRO:HD3	1.84	0.60
1:C:332:VAL:HB	1:C:354:LEU:HD23	1.84	0.60
1:D:291:LEU:HB2	1:D:297:LEU:CB	2.31	0.60
1:D:427:LEU:HD12	1:D:442:TYR:CE2	2.36	0.60
1:A:167:PHE:CD2	1:A:168:TYR:N	2.69	0.60
1:B:332:VAL:HB	1:B:354:LEU:HD23	1.84	0.60
1:B:637:PHE:HD2	1:B:651:ILE:HD11	1.67	0.60
1:C:293:LEU:HD22	1:C:297:LEU:HD21	1.83	0.60
1:C:570:LEU:O	1:C:574:LEU:HB2	2.02	0.60
1:D:310:ILE:HG22	1:D:310:ILE:O	2.00	0.60
1:D:719:PHE:O	1:D:721:MET:N	2.35	0.60
1:A:539:GLU:O	1:A:541:PRO:HD3	2.01	0.59
1:C:443:LEU:O	1:C:445:ASN:N	2.35	0.59
1:C:539:GLU:O	1:C:541:PRO:HD3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:165:PHE:HD2	1:D:177:PHE:CD2	2.20	0.59
1:A:530:LYS:HA	1:A:530:LYS:HE2	1.85	0.59
1:A:719:PHE:O	1:A:721:MET:N	2.35	0.59
1:A:721:MET:HB3	1:C:721:MET:CE	2.32	0.59
1:B:165:PHE:HD2	1:B:177:PHE:CD2	2.20	0.59
1:C:693:PHE:H	1:C:697:GLN:NE2	2.00	0.59
1:D:539:GLU:O	1:D:541:PRO:HD3	2.02	0.59
1:D:581:VAL:O	1:D:584:ASN:N	2.31	0.59
1:A:291:LEU:HD11	1:A:299:GLN:CB	2.32	0.59
1:A:443:LEU:O	1:A:445:ASN:N	2.35	0.59
1:B:241:CYS:HB3	1:B:259:MET:HB2	1.85	0.59
1:B:545:THR:OG1	1:B:548:GLU:HG3	2.02	0.59
1:B:693:PHE:H	1:B:697:GLN:NE2	2.00	0.59
1:C:165:PHE:HD2	1:C:177:PHE:CD2	2.19	0.59
1:C:404:VAL:HG23	1:C:443:LEU:HD12	1.84	0.59
1:D:183:LEU:HD21	1:D:246:TRP:CZ2	2.38	0.59
1:D:291:LEU:HD11	1:D:299:GLN:CB	2.31	0.59
1:B:575:ASN:O	1:B:577:PHE:N	2.32	0.59
1:C:533:LEU:HD13	1:C:729:ILE:HD11	1.84	0.59
1:D:257:TYR:CE2	1:D:313:TYR:HB3	2.37	0.59
1:D:332:VAL:HB	1:D:354:LEU:HD23	1.85	0.59
1:D:443:LEU:O	1:D:445:ASN:N	2.35	0.59
1:A:293:LEU:HD22	1:A:297:LEU:HD21	1.84	0.59
1:D:512:THR:HG22	1:D:573:GLU:OE2	2.03	0.59
1:D:637:PHE:HD2	1:D:651:ILE:HD11	1.68	0.59
1:B:244:LYS:HB3	1:B:253:LEU:HD11	1.85	0.59
1:B:291:LEU:CD1	1:B:299:GLN:HB2	2.33	0.59
1:C:398:VAL:CB	1:C:669:ARG:HH12	2.14	0.59
1:C:492:ASN:O	1:C:496:ASN:HB2	2.02	0.59
1:D:297:LEU:HD13	1:D:318:ASN:HD21	1.68	0.59
1:D:492:ASN:O	1:D:496:ASN:HB2	2.02	0.59
1:B:443:LEU:O	1:B:445:ASN:N	2.36	0.59
1:D:291:LEU:CD1	1:D:299:GLN:HB2	2.33	0.59
1:D:293:LEU:CB	1:D:297:LEU:HG	2.27	0.59
1:D:693:PHE:H	1:D:697:GLN:NE2	2.00	0.59
1:A:332:VAL:HB	1:A:354:LEU:HD23	1.85	0.59
1:A:533:LEU:HD13	1:A:729:ILE:HD11	1.85	0.59
1:A:568:LYS:HZ2	1:D:210:ARG:HH22	1.51	0.59
1:B:291:LEU:HD11	1:B:299:GLN:CB	2.31	0.59
1:C:244:LYS:HE2	1:C:256:ASP:OD1	2.02	0.59
1:C:247:ASP:HB2	1:C:254:ILE:HG12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:332:VAL:O	1:C:333:ASP:HB2	2.03	0.59
1:A:165:PHE:HD2	1:A:177:PHE:CD2	2.20	0.59
1:B:108:LEU:HD23	1:B:108:LEU:C	2.24	0.59
1:C:154:ASN:H	1:C:155:PRO:HD3	1.68	0.59
1:C:244:LYS:HB3	1:C:253:LEU:CD1	2.33	0.59
1:C:427:LEU:HD12	1:C:442:TYR:CE2	2.38	0.59
1:C:719:PHE:O	1:C:721:MET:N	2.36	0.59
1:B:183:LEU:HD21	1:B:246:TRP:CZ2	2.38	0.58
1:B:224:ILE:HA	1:B:276:VAL:HG13	1.85	0.58
1:B:719:PHE:O	1:B:721:MET:N	2.36	0.58
1:C:457:PHE:CD1	1:C:477:GLN:HG2	2.38	0.58
1:B:530:LYS:HE2	1:B:530:LYS:HA	1.84	0.58
1:D:167:PHE:CD2	1:D:168:TYR:N	2.69	0.58
1:D:397:ILE:O	1:D:397:ILE:HG22	2.04	0.58
1:C:596:PHE:C	1:C:598:LYS:H	2.07	0.58
1:D:247:ASP:HB2	1:D:254:ILE:HG13	1.85	0.58
1:A:154:ASN:H	1:A:155:PRO:HD3	1.69	0.58
1:A:332:VAL:O	1:A:333:ASP:HB2	2.04	0.58
1:B:167:PHE:CD2	1:B:168:TYR:N	2.69	0.58
1:D:332:VAL:O	1:D:333:ASP:HB2	2.03	0.58
1:D:334:LEU:HD12	1:D:335:VAL:N	2.19	0.58
1:A:693:PHE:H	1:A:697:GLN:NE2	2.01	0.58
1:A:694:ASN:ND2	1:A:697:GLN:NE2	2.50	0.58
1:B:297:LEU:HD13	1:B:318:ASN:HD21	1.69	0.58
1:B:570:LEU:O	1:B:574:LEU:HB2	2.03	0.58
1:D:292:PRO:C	1:D:293:LEU:HD12	2.23	0.58
1:A:241:CYS:O	1:A:259:MET:HG2	2.02	0.58
1:A:247:ASP:HB2	1:A:254:ILE:HG12	1.85	0.58
1:A:596:PHE:C	1:A:598:LYS:H	2.07	0.58
1:B:427:LEU:HD12	1:B:442:TYR:CE2	2.38	0.58
1:B:501:THR:O	1:B:502:ASP:HB2	2.03	0.58
1:C:180:ASP:OD2	1:C:180:ASP:N	2.34	0.58
1:C:293:LEU:HD13	1:C:297:LEU:CD1	2.34	0.58
1:D:211:PHE:CD1	1:D:212:PHE:N	2.72	0.58
1:D:232:ARG:HG2	1:D:248:LEU:H	1.69	0.58
1:D:255:GLN:O	1:D:256:ASP:HB2	2.03	0.58
1:D:404:VAL:HG23	1:D:443:LEU:HD12	1.84	0.58
1:A:492:ASN:O	1:A:496:ASN:HB2	2.04	0.58
1:B:492:ASN:O	1:B:496:ASN:HB2	2.03	0.58
1:C:417:THR:HG22	1:C:418:GLN:N	2.17	0.58
1:D:694:ASN:ND2	1:D:697:GLN:NE2	2.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:LEU:O	1:A:153:GLN:HB2	2.04	0.58
1:A:180:ASP:OD2	1:A:180:ASP:N	2.35	0.58
1:B:332:VAL:O	1:B:333:ASP:HB2	2.03	0.58
1:B:397:ILE:O	1:B:397:ILE:HG22	2.04	0.58
1:B:694:ASN:ND2	1:B:697:GLN:NE2	2.52	0.58
1:C:152:LEU:O	1:C:153:GLN:HB2	2.04	0.58
1:C:241:CYS:O	1:C:259:MET:HG2	2.03	0.58
1:D:254:ILE:HG21	1:D:311:LEU:HB2	1.85	0.58
1:D:530:LYS:HE2	1:D:530:LYS:HA	1.84	0.58
1:B:292:PRO:C	1:B:293:LEU:HD12	2.23	0.58
1:C:694:ASN:ND2	1:C:697:GLN:NE2	2.50	0.58
1:D:533:LEU:HD13	1:D:729:ILE:HD11	1.85	0.58
1:B:398:VAL:CB	1:B:669:ARG:HH12	2.16	0.57
1:C:297:LEU:HD13	1:C:318:ASN:HD21	1.68	0.57
1:C:637:PHE:HD2	1:C:651:ILE:HD11	1.69	0.57
1:D:501:THR:O	1:D:502:ASP:HB2	2.04	0.57
1:A:334:LEU:HD12	1:A:335:VAL:N	2.19	0.57
1:A:398:VAL:CB	1:A:669:ARG:HH12	2.15	0.57
1:A:417:THR:HG22	1:A:418:GLN:N	2.18	0.57
1:A:446:LEU:HD22	1:A:450:LEU:HD11	1.85	0.57
1:B:541:PRO:HB2	1:B:544:MET:HE2	1.86	0.57
1:C:183:LEU:HD21	1:C:246:TRP:CZ2	2.39	0.57
1:C:183:LEU:HD12	1:C:199:PHE:CE1	2.39	0.57
1:D:180:ASP:OD2	1:D:180:ASP:N	2.34	0.57
1:D:457:PHE:CD1	1:D:477:GLN:HG2	2.40	0.57
1:A:403:ASP:OD2	1:A:404:VAL:N	2.34	0.57
1:B:512:THR:HG22	1:B:573:GLU:OE2	2.04	0.57
1:B:596:PHE:C	1:B:598:LYS:H	2.07	0.57
1:C:122:ILE:CD1	1:C:166:LEU:HD13	2.32	0.57
1:C:211:PHE:CD1	1:C:212:PHE:N	2.72	0.57
1:C:501:THR:O	1:C:502:ASP:HB2	2.04	0.57
1:D:58:ASN:OD1	1:D:59:CYS:N	2.37	0.57
1:D:473:VAL:HG21	1:D:484:TYR:HE2	1.68	0.57
1:A:211:PHE:CD1	1:A:212:PHE:N	2.73	0.57
1:A:244:LYS:HB3	1:A:253:LEU:CD1	2.34	0.57
1:A:704:SER:O	1:A:707:SER:HB2	2.04	0.57
1:B:211:PHE:CD1	1:B:212:PHE:N	2.73	0.57
1:B:446:LEU:HD22	1:B:450:LEU:HD11	1.85	0.57
1:B:533:LEU:HD13	1:B:729:ILE:HD11	1.85	0.57
1:C:403:ASP:OD2	1:C:404:VAL:N	2.34	0.57
1:D:446:LEU:HD22	1:D:450:LEU:HD11	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:596:PHE:C	1:D:598:LYS:H	2.07	0.57
1:A:183:LEU:HD21	1:A:246:TRP:CZ2	2.39	0.57
1:A:188:LYS:HA	1:A:193:HIS:O	2.05	0.57
1:A:404:VAL:HG23	1:A:443:LEU:HD12	1.86	0.57
1:A:501:THR:O	1:A:502:ASP:HB2	2.04	0.57
1:B:180:ASP:OD2	1:B:180:ASP:N	2.34	0.57
1:B:255:GLN:O	1:B:256:ASP:HB2	2.04	0.57
1:B:344:VAL:HG12	1:B:345:GLU:H	1.69	0.57
1:C:334:LEU:HD12	1:C:335:VAL:N	2.19	0.57
1:A:293:LEU:HD13	1:A:297:LEU:CD1	2.35	0.57
1:B:152:LEU:O	1:B:153:GLN:HB2	2.03	0.57
1:C:397:ILE:HG23	1:C:526:ARG:HG2	1.87	0.57
1:D:78:LEU:HD12	1:D:79:LEU:N	2.20	0.57
1:D:108:LEU:HD23	1:D:108:LEU:C	2.25	0.57
1:D:224:ILE:HA	1:D:276:VAL:HG13	1.86	0.57
1:A:183:LEU:HD12	1:A:199:PHE:CE1	2.40	0.57
1:A:545:THR:O	1:A:547:VAL:N	2.33	0.57
1:A:570:LEU:O	1:A:574:LEU:HB2	2.05	0.57
1:B:293:LEU:HD13	1:B:297:LEU:CD1	2.35	0.57
1:C:384:LYS:NZ	1:C:392:GLU:OE2	2.36	0.57
1:D:403:ASP:CG	1:D:404:VAL:H	2.08	0.57
1:D:545:THR:O	1:D:547:VAL:N	2.33	0.57
1:D:658:HIS:HA	1:D:661:GLN:OE1	2.05	0.57
1:A:721:MET:CE	1:C:721:MET:HB3	2.34	0.57
1:B:58:ASN:OD1	1:B:59:CYS:N	2.37	0.57
1:B:163:PRO:HA	1:B:178:LEU:HA	1.87	0.57
1:B:188:LYS:HA	1:B:193:HIS:O	2.05	0.57
1:B:545:THR:O	1:B:547:VAL:N	2.33	0.57
1:C:257:TYR:CE2	1:C:313:TYR:HB3	2.40	0.57
1:D:211:PHE:CG	1:D:212:PHE:N	2.72	0.57
1:D:317:ASN:OD1	1:D:318:ASN:N	2.38	0.57
1:A:122:ILE:CD1	1:A:166:LEU:HD13	2.33	0.57
1:C:188:LYS:HA	1:C:193:HIS:O	2.05	0.57
1:C:292:PRO:C	1:C:293:LEU:HD12	2.24	0.57
1:C:716:GLU:HG2	1:C:722:THR:HA	1.87	0.57
1:A:255:GLN:O	1:A:256:ASP:HB2	2.03	0.57
1:B:211:PHE:CG	1:B:212:PHE:N	2.72	0.57
1:B:404:VAL:HG23	1:B:443:LEU:HD12	1.86	0.57
1:C:446:LEU:HD22	1:C:450:LEU:HD11	1.87	0.57
1:C:658:HIS:HA	1:C:661:GLN:OE1	2.04	0.57
1:A:292:PRO:C	1:A:293:LEU:HD12	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:LEU:HD13	1:A:318:ASN:HD21	1.70	0.56
1:B:457:PHE:CD1	1:B:477:GLN:HG2	2.41	0.56
1:C:291:LEU:CD1	1:C:299:GLN:HB2	2.33	0.56
1:C:473:VAL:HG21	1:C:484:TYR:HE2	1.70	0.56
1:C:704:SER:O	1:C:707:SER:HB2	2.05	0.56
1:D:293:LEU:HD13	1:D:297:LEU:CD1	2.35	0.56
1:D:558:LEU:HD11	1:D:635:LEU:CD1	2.35	0.56
1:A:291:LEU:CD1	1:A:299:GLN:HB2	2.33	0.56
1:A:473:VAL:HG21	1:A:484:TYR:HE2	1.70	0.56
1:A:658:HIS:HA	1:A:661:GLN:OE1	2.05	0.56
1:A:716:GLU:HG2	1:A:722:THR:HA	1.87	0.56
1:B:716:GLU:HG2	1:B:722:THR:HA	1.87	0.56
1:C:545:THR:O	1:C:547:VAL:N	2.33	0.56
1:D:152:LEU:O	1:D:153:GLN:HB2	2.04	0.56
1:D:188:LYS:HA	1:D:193:HIS:O	2.06	0.56
1:D:704:SER:O	1:D:707:SER:HB2	2.05	0.56
1:A:344:VAL:HG12	1:A:345:GLU:H	1.70	0.56
1:B:78:LEU:HD12	1:B:79:LEU:N	2.20	0.56
1:B:183:LEU:HD12	1:B:199:PHE:CE1	2.39	0.56
1:B:473:VAL:HG21	1:B:484:TYR:HE2	1.69	0.56
1:B:558:LEU:HD11	1:B:635:LEU:CD1	2.36	0.56
1:C:58:ASN:OD1	1:C:59:CYS:N	2.38	0.56
1:C:211:PHE:CG	1:C:212:PHE:N	2.72	0.56
1:C:224:ILE:HA	1:C:276:VAL:HG13	1.86	0.56
1:C:255:GLN:O	1:C:256:ASP:HB2	2.03	0.56
1:C:286:THR:HG22	1:C:287:LEU:H	1.70	0.56
1:D:163:PRO:HA	1:D:178:LEU:HA	1.87	0.56
1:D:183:LEU:HD12	1:D:199:PHE:CE1	2.39	0.56
1:D:344:VAL:HG12	1:D:345:GLU:H	1.70	0.56
1:A:393:HIS:O	1:A:395:LEU:HG	2.04	0.56
1:B:658:HIS:HA	1:B:661:GLN:OE1	2.06	0.56
1:C:344:VAL:HG12	1:C:345:GLU:H	1.70	0.56
1:D:570:LEU:O	1:D:574:LEU:HB2	2.04	0.56
1:A:211:PHE:CG	1:A:212:PHE:N	2.72	0.56
1:A:457:PHE:CD1	1:A:477:GLN:HG2	2.40	0.56
1:A:634:LEU:CD2	1:A:655:LEU:HD23	2.36	0.56
1:D:716:GLU:HG2	1:D:722:THR:HA	1.88	0.56
1:C:108:LEU:HD23	1:C:108:LEU:C	2.25	0.56
1:A:286:THR:HG22	1:A:287:LEU:H	1.70	0.56
1:A:512:THR:HG22	1:A:573:GLU:OE2	2.04	0.56
1:A:575:ASN:O	1:A:577:PHE:N	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:LYS:NZ	1:B:392:GLU:OE2	2.37	0.56
1:B:650:HIS:O	1:B:653:THR:N	2.34	0.56
1:C:512:THR:HG22	1:C:573:GLU:OE2	2.04	0.56
1:B:18:PRO:HG3	1:B:421:GLU:OE1	2.06	0.56
1:B:405:GLU:OE2	1:B:437:ASN:ND2	2.39	0.56
1:C:575:ASN:O	1:C:577:PHE:N	2.31	0.56
1:B:289:THR:O	1:B:298:PHE:HA	2.06	0.56
1:A:397:ILE:HG22	1:A:397:ILE:O	2.05	0.56
1:A:405:GLU:OE2	1:A:437:ASN:ND2	2.39	0.56
1:B:101:SER:HB2	1:B:107:THR:HG1	1.71	0.56
1:B:332:VAL:HG22	1:B:356:LYS:HB2	1.88	0.56
1:D:244:LYS:HB3	1:D:253:LEU:CD1	2.36	0.56
1:B:403:ASP:CG	1:B:404:VAL:H	2.09	0.55
1:C:332:VAL:HG22	1:C:356:LYS:HB2	1.87	0.55
1:C:634:LEU:CD2	1:C:655:LEU:HD23	2.37	0.55
1:D:384:LYS:NZ	1:D:392:GLU:OE2	2.38	0.55
1:D:541:PRO:HB2	1:D:544:MET:HE2	1.88	0.55
1:B:704:SER:O	1:B:707:SER:HB2	2.06	0.55
1:D:650:HIS:O	1:D:653:THR:N	2.35	0.55
1:B:11:LEU:HB3	1:B:87:ALA:CB	2.37	0.55
1:B:149:TRP:CE3	1:B:150:PHE:HB3	2.41	0.55
1:D:332:VAL:HG22	1:D:356:LYS:HB2	1.89	0.55
1:D:552:ASP:C	1:D:554:PHE:H	2.10	0.55
1:C:113:VAL:HG23	1:C:118:LEU:HB2	1.87	0.55
1:C:397:ILE:HG22	1:C:397:ILE:O	2.05	0.55
1:A:558:LEU:HD11	1:A:635:LEU:CD1	2.36	0.55
1:C:558:LEU:HD11	1:C:635:LEU:CD1	2.36	0.55
1:D:419:ILE:HG12	1:D:457:PHE:CD2	2.41	0.55
1:A:108:LEU:HD23	1:A:108:LEU:C	2.26	0.55
1:A:149:TRP:CE3	1:A:150:PHE:HB3	2.42	0.55
1:A:403:ASP:CG	1:A:404:VAL:H	2.09	0.55
1:A:724:PHE:HE1	1:C:667:LEU:HD21	1.70	0.55
1:B:293:LEU:CB	1:B:297:LEU:HG	2.27	0.55
1:C:11:LEU:HB3	1:C:87:ALA:CB	2.37	0.55
1:C:149:TRP:CE3	1:C:150:PHE:HB3	2.42	0.55
1:C:289:THR:O	1:C:298:PHE:HA	2.06	0.55
1:D:149:TRP:CE3	1:D:150:PHE:HB3	2.42	0.55
1:D:634:LEU:CD2	1:D:655:LEU:HD23	2.36	0.55
1:A:73:SER:HB2	1:A:78:LEU:HB3	1.89	0.55
1:A:293:LEU:CB	1:A:297:LEU:HG	2.27	0.55
1:B:113:VAL:HG23	1:B:118:LEU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:552:ASP:C	1:B:554:PHE:H	2.10	0.55
1:C:450:LEU:O	1:C:451:ARG:C	2.44	0.55
1:D:393:HIS:O	1:D:395:LEU:HG	2.06	0.55
1:D:403:ASP:OD2	1:D:404:VAL:N	2.33	0.55
1:A:163:PRO:HA	1:A:178:LEU:HA	1.87	0.55
1:A:224:ILE:HA	1:A:276:VAL:HG13	1.88	0.55
1:B:403:ASP:HB3	1:B:406:ARG:HB3	1.89	0.55
1:C:428:SER:O	1:C:431:LYS:N	2.39	0.55
1:D:239:GLN:O	1:D:273:VAL:HG23	2.07	0.55
1:A:674:LEU:HD23	1:C:723:PHE:CE1	2.42	0.55
1:B:286:THR:HG22	1:B:287:LEU:H	1.71	0.55
1:C:404:VAL:HG23	1:C:443:LEU:HD11	1.87	0.55
1:D:154:ASN:H	1:D:155:PRO:HD3	1.69	0.55
1:A:289:THR:O	1:A:298:PHE:HA	2.07	0.55
1:C:163:PRO:HA	1:C:178:LEU:HA	1.87	0.55
1:A:241:CYS:O	1:A:259:MET:CG	2.55	0.54
1:A:332:VAL:HG22	1:A:356:LYS:HB2	1.88	0.54
1:A:545:THR:C	1:A:547:VAL:N	2.60	0.54
1:B:71:HIS:CE1	1:B:478:PRO:CA	2.90	0.54
1:C:11:LEU:HD12	1:C:479:TYR:HA	1.89	0.54
1:C:71:HIS:CE1	1:C:478:PRO:CA	2.90	0.54
1:C:293:LEU:CB	1:C:297:LEU:HG	2.27	0.54
1:A:58:ASN:OD1	1:A:59:CYS:N	2.40	0.54
1:A:113:VAL:HG23	1:A:118:LEU:HB2	1.88	0.54
1:A:243:LEU:HB3	1:A:259:MET:HE3	1.88	0.54
1:B:122:ILE:CD1	1:B:166:LEU:HD13	2.33	0.54
1:D:113:VAL:HG23	1:D:118:LEU:HB2	1.88	0.54
1:D:122:ILE:CD1	1:D:166:LEU:HD13	2.33	0.54
1:D:404:VAL:HG13	1:D:405:GLU:N	2.23	0.54
1:B:154:ASN:H	1:B:155:PRO:HD3	1.69	0.54
1:B:546:THR:O	1:B:546:THR:CG2	2.54	0.54
1:D:247:ASP:HB2	1:D:254:ILE:HG12	1.90	0.54
1:A:403:ASP:HB3	1:A:406:ARG:HB3	1.89	0.54
1:B:634:LEU:CD2	1:B:655:LEU:HD23	2.36	0.54
1:C:73:SER:HB2	1:C:78:LEU:HB3	1.89	0.54
1:C:78:LEU:HD12	1:C:79:LEU:N	2.20	0.54
1:C:286:THR:CG2	1:C:287:LEU:N	2.71	0.54
1:C:393:HIS:O	1:C:395:LEU:HG	2.06	0.54
1:C:403:ASP:CG	1:C:404:VAL:H	2.09	0.54
1:C:457:PHE:CE1	1:C:477:GLN:HG2	2.43	0.54
1:D:211:PHE:CE1	1:D:212:PHE:HB2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:SER:O	1:A:431:LYS:N	2.40	0.54
1:B:404:VAL:HG13	1:B:405:GLU:N	2.23	0.54
1:C:28:VAL:HB	1:C:98:PRO:HD3	1.90	0.54
1:D:11:LEU:HB3	1:D:87:ALA:CB	2.38	0.54
1:D:719:PHE:C	1:D:721:MET:N	2.60	0.54
1:A:404:VAL:HG13	1:A:405:GLU:N	2.23	0.54
1:A:723:PHE:CE1	1:C:674:LEU:HD23	2.42	0.54
1:B:527:SER:O	1:B:530:LYS:HB3	2.08	0.54
1:C:54:SER:HB2	1:C:74:SER:OG	2.08	0.54
1:C:404:VAL:HG13	1:C:405:GLU:N	2.23	0.54
1:C:545:THR:C	1:C:547:VAL:N	2.61	0.54
1:C:551:THR:O	1:C:554:PHE:HB3	2.08	0.54
1:D:224:ILE:HG22	1:D:276:VAL:HA	1.89	0.54
1:D:286:THR:HG22	1:D:287:LEU:H	1.70	0.54
1:A:54:SER:HB2	1:A:74:SER:OG	2.08	0.54
1:A:384:LYS:NZ	1:A:392:GLU:OE2	2.39	0.54
1:B:403:ASP:OD2	1:B:404:VAL:N	2.34	0.54
1:B:551:THR:O	1:B:554:PHE:HB3	2.08	0.54
1:D:73:SER:HB2	1:D:78:LEU:HB3	1.89	0.54
1:D:257:TYR:CZ	1:D:313:TYR:HB3	2.43	0.54
1:D:286:THR:CG2	1:D:287:LEU:N	2.71	0.54
1:D:289:THR:O	1:D:298:PHE:HA	2.08	0.54
1:B:404:VAL:HG23	1:B:443:LEU:HD11	1.88	0.54
1:B:604:ALA:HB2	1:B:691:LYS:HG2	1.90	0.54
1:C:521:SER:O	1:C:524:VAL:HB	2.08	0.54
1:C:527:SER:O	1:C:530:LYS:HB3	2.08	0.54
1:A:211:PHE:CE1	1:A:212:PHE:HB2	2.43	0.54
1:A:286:THR:CG2	1:A:287:LEU:N	2.71	0.54
1:A:551:THR:O	1:A:554:PHE:HB3	2.08	0.54
1:B:28:VAL:HB	1:B:98:PRO:HD3	1.90	0.54
1:C:211:PHE:CE1	1:C:212:PHE:HB2	2.43	0.54
1:D:71:HIS:CE1	1:D:478:PRO:CA	2.91	0.54
1:D:546:THR:O	1:D:546:THR:CG2	2.54	0.54
1:B:719:PHE:C	1:B:721:MET:N	2.61	0.54
1:C:224:ILE:HG22	1:C:276:VAL:HA	1.90	0.54
1:D:403:ASP:HB3	1:D:406:ARG:HB3	1.90	0.54
1:D:604:ALA:HB2	1:D:691:LYS:HG2	1.90	0.54
1:A:419:ILE:HG12	1:A:457:PHE:CD2	2.43	0.53
1:B:393:HIS:O	1:B:395:LEU:HG	2.07	0.53
1:D:28:VAL:HB	1:D:98:PRO:HD3	1.90	0.53
1:A:552:ASP:C	1:A:554:PHE:H	2.10	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:286:THR:HG22	1:C:287:LEU:O	2.08	0.53
1:C:604:ALA:HB2	1:C:691:LYS:HG2	1.89	0.53
1:C:601:PHE:O	1:C:602:ILE:HB	2.09	0.53
1:A:78:LEU:HD12	1:A:79:LEU:N	2.21	0.53
1:A:172:GLN:CD	1:A:172:GLN:H	2.11	0.53
1:A:427:LEU:HD12	1:A:442:TYR:HE2	1.74	0.53
1:A:500:GLU:CG	1:A:501:THR:H	2.15	0.53
1:A:604:ALA:HB2	1:A:691:LYS:HG2	1.90	0.53
1:B:73:SER:HB2	1:B:78:LEU:HB3	1.90	0.53
1:B:109:THR:HG23	1:B:120:ASN:HD22	1.74	0.53
1:B:211:PHE:CE1	1:B:212:PHE:HB2	2.43	0.53
1:B:286:THR:CG2	1:B:287:LEU:N	2.72	0.53
1:C:419:ILE:HG12	1:C:457:PHE:CD2	2.43	0.53
1:D:414:ARG:O	1:D:414:ARG:HG2	2.07	0.53
1:D:527:SER:O	1:D:530:LYS:HB3	2.09	0.53
1:A:286:THR:HG22	1:A:287:LEU:O	2.08	0.53
1:A:670:GLN:HG3	1:C:727:TYR:OH	2.07	0.53
1:B:239:GLN:O	1:B:273:VAL:HG23	2.09	0.53
1:A:173:PHE:HD1	1:A:186:LEU:O	1.92	0.53
1:A:349:LEU:H	1:A:368:VAL:CG2	2.20	0.53
1:A:601:PHE:N	1:A:601:PHE:CD1	2.77	0.53
1:B:54:SER:HB2	1:B:74:SER:OG	2.08	0.53
1:B:419:ILE:HG12	1:B:457:PHE:CD2	2.44	0.53
1:D:109:THR:HG23	1:D:120:ASN:HD22	1.74	0.53
1:D:450:LEU:O	1:D:451:ARG:C	2.44	0.53
1:D:551:THR:O	1:D:554:PHE:HB3	2.09	0.53
1:D:707:SER:O	1:D:709:VAL:N	2.41	0.53
1:A:28:VAL:HB	1:A:98:PRO:HD3	1.91	0.53
1:A:71:HIS:CE1	1:A:478:PRO:CA	2.91	0.53
1:A:297:LEU:CD2	1:A:318:ASN:HD21	2.21	0.53
1:C:552:ASP:C	1:C:554:PHE:H	2.11	0.53
1:D:286:THR:HG22	1:D:287:LEU:O	2.08	0.53
1:A:188:LYS:HB2	1:A:194:TYR:CE1	2.44	0.53
1:A:457:PHE:CE1	1:A:477:GLN:HG2	2.44	0.53
1:A:521:SER:O	1:A:524:VAL:HB	2.09	0.53
1:A:546:THR:O	1:A:546:THR:CG2	2.54	0.53
1:B:545:THR:C	1:B:547:VAL:N	2.60	0.53
1:B:663:LEU:O	1:B:667:LEU:HG	2.09	0.53
1:C:241:CYS:O	1:C:259:MET:CG	2.56	0.53
1:C:403:ASP:HB3	1:C:406:ARG:HB3	1.91	0.53
1:D:259:MET:HE1	1:D:262:GLN:HE22	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:LEU:HB3	1:A:87:ALA:CB	2.39	0.53
1:A:254:ILE:CG2	1:A:311:LEU:HB2	2.39	0.53
1:A:450:LEU:O	1:A:451:ARG:C	2.46	0.53
1:C:72:PHE:O	1:C:73:SER:C	2.46	0.53
1:B:111:GLN:HG3	1:B:168:TYR:CD2	2.44	0.53
1:B:232:ARG:HG2	1:B:248:LEU:H	1.75	0.53
1:C:546:THR:O	1:C:546:THR:CG2	2.55	0.53
1:C:601:PHE:N	1:C:601:PHE:CD1	2.77	0.53
1:C:707:SER:O	1:C:709:VAL:N	2.42	0.53
1:D:349:LEU:H	1:D:368:VAL:CG2	2.20	0.53
1:D:483:LEU:HD13	1:D:614:ILE:HD12	1.91	0.53
1:D:601:PHE:O	1:D:602:ILE:HB	2.09	0.53
1:A:239:GLN:O	1:A:273:VAL:HG23	2.09	0.52
1:A:293:LEU:HB2	1:A:297:LEU:CG	2.27	0.52
1:A:601:PHE:O	1:A:602:ILE:HB	2.09	0.52
1:A:707:SER:O	1:A:709:VAL:N	2.42	0.52
1:B:11:LEU:HD12	1:B:479:TYR:HA	1.90	0.52
1:B:92:THR:HG21	1:B:479:TYR:OH	2.09	0.52
1:C:101:SER:HB2	1:C:107:THR:HG1	1.73	0.52
1:C:414:ARG:O	1:C:414:ARG:HG2	2.08	0.52
1:D:111:GLN:HG3	1:D:168:TYR:CD2	2.44	0.52
1:D:404:VAL:HG23	1:D:443:LEU:HD11	1.89	0.52
1:B:14:TYR:HB3	1:B:673:CYS:HB2	1.90	0.52
1:B:297:LEU:CD2	1:B:318:ASN:HD21	2.22	0.52
1:B:450:LEU:O	1:B:451:ARG:C	2.44	0.52
1:B:601:PHE:O	1:B:602:ILE:HB	2.09	0.52
1:C:293:LEU:HB2	1:C:297:LEU:CG	2.28	0.52
1:D:172:GLN:CD	1:D:172:GLN:H	2.12	0.52
1:D:184:LEU:HG	1:D:185:GLY:H	1.73	0.52
1:A:14:TYR:HB3	1:A:673:CYS:HB2	1.91	0.52
1:A:224:ILE:HG22	1:A:276:VAL:HA	1.92	0.52
1:A:404:VAL:HG23	1:A:443:LEU:HD11	1.90	0.52
1:A:634:LEU:HD21	1:A:655:LEU:HD23	1.92	0.52
1:B:349:LEU:H	1:B:368:VAL:CG2	2.20	0.52
1:C:239:GLN:O	1:C:273:VAL:HG23	2.09	0.52
1:C:500:GLU:CG	1:C:501:THR:H	2.16	0.52
1:D:72:PHE:O	1:D:73:SER:C	2.45	0.52
1:B:73:SER:N	1:B:78:LEU:O	2.42	0.52
1:B:184:LEU:HG	1:B:185:GLY:H	1.74	0.52
1:B:286:THR:HG22	1:B:287:LEU:O	2.09	0.52
1:C:317:ASN:OD1	1:C:318:ASN:N	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:427:LEU:HD12	1:D:442:TYR:HE2	1.74	0.52
1:D:428:SER:O	1:D:431:LYS:N	2.38	0.52
1:D:545:THR:C	1:D:547:VAL:N	2.61	0.52
1:A:72:PHE:O	1:A:73:SER:C	2.46	0.52
1:A:201:ASP:O	1:A:203:SER:N	2.42	0.52
1:A:536:ILE:HD11	1:A:655:LEU:HB3	1.90	0.52
1:A:623:LEU:HD13	1:A:664:LEU:HD22	1.91	0.52
1:B:224:ILE:HG22	1:B:276:VAL:HA	1.90	0.52
1:B:317:ASN:OD1	1:B:318:ASN:N	2.38	0.52
1:B:457:PHE:CE1	1:B:477:GLN:HG2	2.44	0.52
1:B:601:PHE:N	1:B:601:PHE:CD1	2.77	0.52
1:C:173:PHE:HD1	1:C:186:LEU:O	1.93	0.52
1:C:201:ASP:O	1:C:203:SER:N	2.42	0.52
1:C:663:LEU:CD1	1:C:729:ILE:HD12	2.40	0.52
1:D:54:SER:HB2	1:D:74:SER:OG	2.09	0.52
1:D:237:LEU:HD11	1:D:241:CYS:HA	1.91	0.52
1:A:104:GLN:O	1:A:106:TYR:N	2.43	0.52
1:A:317:ASN:OD1	1:A:318:ASN:N	2.38	0.52
1:A:650:HIS:O	1:A:653:THR:N	2.35	0.52
1:B:541:PRO:HB2	1:B:544:MET:CE	2.40	0.52
1:C:259:MET:HE1	1:C:262:GLN:NE2	2.17	0.52
1:C:623:LEU:HD13	1:C:664:LEU:HD22	1.91	0.52
1:D:457:PHE:CE1	1:D:477:GLN:HG2	2.44	0.52
1:A:172:GLN:NE2	1:A:172:GLN:N	2.58	0.52
1:A:257:TYR:CZ	1:A:313:TYR:HB3	2.45	0.52
1:B:72:PHE:O	1:B:73:SER:C	2.46	0.52
1:B:506:LEU:HA	1:B:582:VAL:CG1	2.40	0.52
1:C:349:LEU:H	1:C:368:VAL:CG2	2.21	0.52
1:C:536:ILE:HD12	1:C:659:TYR:HB2	1.91	0.52
1:D:73:SER:N	1:D:78:LEU:O	2.42	0.52
1:D:201:ASP:O	1:D:203:SER:N	2.42	0.52
1:B:521:SER:O	1:B:524:VAL:HB	2.09	0.52
1:C:650:HIS:O	1:C:653:THR:N	2.35	0.52
1:D:225:SER:OG	1:D:279:TYR:HB2	2.10	0.52
1:D:297:LEU:CD2	1:D:318:ASN:HD21	2.22	0.52
1:B:368:VAL:O	1:B:368:VAL:CG2	2.57	0.52
1:C:14:TYR:HB3	1:C:673:CYS:HB2	1.91	0.52
1:C:317:ASN:HB3	1:C:373:PHE:HB3	1.92	0.52
1:C:716:GLU:HG2	1:C:722:THR:N	2.25	0.52
1:D:173:PHE:HD1	1:D:186:LEU:O	1.92	0.52
1:D:368:VAL:O	1:D:368:VAL:CG2	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:405:GLU:OE2	1:D:437:ASN:ND2	2.42	0.52
1:D:601:PHE:N	1:D:601:PHE:CD1	2.77	0.52
1:A:104:GLN:C	1:A:106:TYR:H	2.13	0.52
1:B:104:GLN:C	1:B:106:TYR:H	2.13	0.52
1:B:201:ASP:O	1:B:203:SER:N	2.43	0.52
1:B:237:LEU:HD11	1:B:241:CYS:HA	1.92	0.52
1:C:410:ASN:O	1:C:413:SER:N	2.42	0.52
1:C:663:LEU:O	1:C:667:LEU:HG	2.09	0.52
1:D:393:HIS:O	1:D:394:ASP:C	2.48	0.52
1:D:708:ASN:O	1:D:712:ALA:HB2	2.09	0.52
1:B:172:GLN:H	1:B:172:GLN:CD	2.13	0.51
1:B:650:HIS:O	1:B:651:ILE:C	2.48	0.51
1:C:111:GLN:HG3	1:C:168:TYR:CD2	2.45	0.51
1:C:297:LEU:CD2	1:C:318:ASN:HD21	2.23	0.51
1:D:11:LEU:HD12	1:D:479:TYR:HA	1.91	0.51
1:D:332:VAL:CG2	1:D:356:LYS:HB2	2.40	0.51
1:A:564:ILE:HG21	1:D:203:SER:HB2	1.93	0.51
1:B:634:LEU:HD21	1:B:655:LEU:HD23	1.92	0.51
1:C:237:LEU:HD11	1:C:241:CYS:HA	1.91	0.51
1:C:283:TYR:CG	1:C:284:ASN:N	2.78	0.51
1:A:11:LEU:HD12	1:A:479:TYR:HA	1.92	0.51
1:A:184:LEU:HG	1:A:185:GLY:H	1.74	0.51
1:B:188:LYS:HB2	1:B:194:TYR:CE1	2.45	0.51
1:B:483:LEU:HD13	1:B:614:ILE:HD12	1.92	0.51
1:B:663:LEU:CD1	1:B:729:ILE:HD12	2.40	0.51
1:C:92:THR:HG21	1:C:479:TYR:OH	2.11	0.51
1:D:214:ARG:O	1:D:214:ARG:HG2	2.11	0.51
1:D:536:ILE:HD11	1:D:655:LEU:HB3	1.91	0.51
1:A:663:LEU:CD1	1:A:729:ILE:HD12	2.40	0.51
1:B:214:ARG:HG2	1:B:214:ARG:O	2.11	0.51
1:B:414:ARG:HG2	1:B:414:ARG:O	2.10	0.51
1:C:184:LEU:HG	1:C:185:GLY:H	1.74	0.51
1:C:188:LYS:HB2	1:C:194:TYR:CE1	2.46	0.51
1:D:104:GLN:C	1:D:106:TYR:H	2.14	0.51
1:A:111:GLN:HG3	1:A:168:TYR:CD2	2.45	0.51
1:A:568:LYS:CD	1:D:210:ARG:HH22	2.23	0.51
1:B:690:VAL:CG1	1:B:691:LYS:N	2.74	0.51
1:C:104:GLN:O	1:C:106:TYR:N	2.44	0.51
1:C:214:ARG:O	1:C:214:ARG:HG2	2.10	0.51
1:D:18:PRO:HG3	1:D:421:GLU:OE1	2.11	0.51
1:D:188:LYS:HB2	1:D:194:TYR:CE1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:506:LEU:HA	1:D:582:VAL:CG1	2.41	0.51
1:A:1:MET:O	1:A:1:MET:HG2	2.10	0.51
1:A:317:ASN:HB3	1:A:373:PHE:HB3	1.93	0.51
1:A:719:PHE:C	1:A:721:MET:N	2.60	0.51
1:B:707:SER:O	1:B:709:VAL:N	2.43	0.51
1:C:172:GLN:H	1:C:172:GLN:CD	2.14	0.51
1:C:232:ARG:NH1	1:C:233:TYR:OH	2.44	0.51
1:C:368:VAL:O	1:C:368:VAL:CG2	2.57	0.51
1:D:232:ARG:NH1	1:D:233:TYR:OH	2.44	0.51
1:D:634:LEU:HD21	1:D:655:LEU:HD23	1.92	0.51
1:A:237:LEU:HD11	1:A:241:CYS:HA	1.92	0.51
1:A:410:ASN:O	1:A:413:SER:N	2.43	0.51
1:A:667:LEU:HD21	1:C:724:PHE:HE1	1.74	0.51
1:B:173:PHE:HD1	1:B:186:LEU:O	1.93	0.51
1:B:244:LYS:HB3	1:B:253:LEU:CD1	2.41	0.51
1:B:257:TYR:CZ	1:B:313:TYR:HB3	2.46	0.51
1:B:290:LEU:O	1:B:291:LEU:HD23	2.10	0.51
1:A:214:ARG:O	1:A:214:ARG:HG2	2.11	0.51
1:A:483:LEU:HD13	1:A:614:ILE:HD12	1.91	0.51
1:A:527:SER:O	1:A:530:LYS:HB3	2.11	0.51
1:B:104:GLN:O	1:B:106:TYR:N	2.43	0.51
1:B:393:HIS:O	1:B:394:ASP:C	2.49	0.51
1:B:708:ASN:O	1:B:712:ALA:HB2	2.10	0.51
1:D:1:MET:HG2	1:D:1:MET:O	2.11	0.51
1:D:69:CYS:HB2	1:D:82:TYR:CE1	2.46	0.51
1:D:104:GLN:O	1:D:106:TYR:N	2.43	0.51
1:D:247:ASP:HB3	1:D:250:SER:HB2	1.92	0.51
1:D:650:HIS:O	1:D:651:ILE:C	2.49	0.51
1:D:690:VAL:CG1	1:D:691:LYS:N	2.74	0.51
1:A:283:TYR:CG	1:A:284:ASN:N	2.79	0.51
1:A:311:LEU:O	1:A:312:THR:HG23	2.11	0.51
1:A:443:LEU:C	1:A:445:ASN:N	2.64	0.51
1:B:232:ARG:NH1	1:B:233:TYR:OH	2.44	0.51
1:B:716:GLU:HG2	1:B:722:THR:N	2.26	0.51
1:C:332:VAL:CG2	1:C:356:LYS:HB2	2.40	0.51
1:C:399:THR:O	1:C:526:ARG:NH2	2.44	0.51
1:D:9:ALA:CB	1:D:613:ILE:HD11	2.41	0.51
1:D:317:ASN:HB3	1:D:373:PHE:HB3	1.92	0.51
1:D:536:ILE:HD11	1:D:655:LEU:C	2.32	0.51
1:D:663:LEU:O	1:D:667:LEU:HG	2.11	0.51
1:A:232:ARG:NH1	1:A:233:TYR:OH	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:VAL:O	1:A:368:VAL:CG2	2.58	0.51
1:A:506:LEU:HA	1:A:582:VAL:CG1	2.40	0.51
1:C:443:LEU:C	1:C:445:ASN:N	2.64	0.51
1:C:553:ILE:O	1:C:553:ILE:CG2	2.59	0.51
1:D:317:ASN:ND2	1:D:319:ILE:CG1	2.70	0.51
1:D:521:SER:O	1:D:524:VAL:HB	2.11	0.51
1:D:541:PRO:HB2	1:D:544:MET:CE	2.41	0.51
1:A:620:HIS:CD2	1:A:668:TYR:CD2	2.99	0.50
1:B:280:LEU:O	1:B:280:LEU:HD12	2.12	0.50
1:B:311:LEU:O	1:B:312:THR:HG23	2.11	0.50
1:B:317:ASN:HB3	1:B:373:PHE:HB3	1.92	0.50
1:C:290:LEU:O	1:C:291:LEU:HD23	2.11	0.50
1:D:9:ALA:HB1	1:D:613:ILE:HD11	1.92	0.50
1:D:92:THR:HG21	1:D:479:TYR:OH	2.11	0.50
1:D:604:ALA:O	1:D:688:PHE:HB2	2.11	0.50
1:A:109:THR:HG23	1:A:120:ASN:HD22	1.75	0.50
1:A:249:THR:HG22	1:A:249:THR:O	2.11	0.50
1:A:332:VAL:CG2	1:A:356:LYS:HB2	2.41	0.50
1:A:724:PHE:HB3	1:C:724:PHE:HB3	1.92	0.50
1:A:727:TYR:OH	1:C:670:GLN:HG3	2.09	0.50
1:B:335:VAL:CG1	1:B:352:ILE:HB	2.42	0.50
1:C:104:GLN:C	1:C:106:TYR:H	2.14	0.50
1:C:690:VAL:CG1	1:C:691:LYS:N	2.74	0.50
1:C:708:ASN:O	1:C:712:ALA:HB2	2.10	0.50
1:C:719:PHE:C	1:C:721:MET:N	2.61	0.50
1:D:623:LEU:HD13	1:D:664:LEU:HD22	1.91	0.50
1:A:708:ASN:O	1:A:712:ALA:HB2	2.10	0.50
1:B:287:LEU:HG	1:B:288:VAL:N	2.26	0.50
1:B:536:ILE:HD11	1:B:655:LEU:HB3	1.92	0.50
1:D:500:GLU:CG	1:D:501:THR:H	2.15	0.50
1:D:575:ASN:C	1:D:577:PHE:H	2.14	0.50
1:D:663:LEU:CD1	1:D:729:ILE:HD12	2.41	0.50
1:D:707:SER:O	1:D:708:ASN:C	2.50	0.50
1:B:370:ASP:OD1	1:B:372:SER:HB3	2.11	0.50
1:A:69:CYS:HB2	1:A:82:TYR:CE1	2.47	0.50
1:A:541:PRO:HB2	1:A:544:MET:CE	2.40	0.50
1:B:55:GLU:OE1	1:B:74:SER:CA	2.59	0.50
1:B:192:VAL:O	1:B:192:VAL:HG12	2.11	0.50
1:B:221:ASP:O	1:B:238:THR:HB	2.12	0.50
1:B:239:GLN:HG2	1:B:273:VAL:O	2.11	0.50
1:B:332:VAL:CG2	1:B:356:LYS:HB2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:719:PHE:O	1:C:720:PHE:C	2.50	0.50
1:D:172:GLN:NE2	1:D:172:GLN:N	2.60	0.50
1:D:370:ASP:OD1	1:D:372:SER:HB3	2.11	0.50
1:A:528:ILE:O	1:A:529:SER:C	2.50	0.50
1:B:225:SER:OG	1:B:279:TYR:HB2	2.12	0.50
1:B:317:ASN:ND2	1:B:319:ILE:CG1	2.71	0.50
1:B:342:LEU:HD12	1:B:379:ILE:HD12	1.94	0.50
1:B:428:SER:O	1:B:431:LYS:N	2.40	0.50
1:B:604:ALA:O	1:B:688:PHE:HB2	2.12	0.50
1:C:109:THR:HG23	1:C:120:ASN:HD22	1.76	0.50
1:C:284:ASN:HB3	1:C:285:ASN:OD1	2.11	0.50
1:C:306:ASP:OD1	1:C:307:SER:N	2.44	0.50
1:A:393:HIS:O	1:A:394:ASP:C	2.49	0.50
1:B:349:LEU:N	1:B:368:VAL:HG22	2.26	0.50
1:B:493:TRP:CD1	1:B:507:PHE:HD1	2.29	0.50
1:B:500:GLU:CG	1:B:501:THR:H	2.15	0.50
1:C:311:LEU:O	1:C:312:THR:HG23	2.12	0.50
1:C:427:LEU:HD12	1:C:442:TYR:HE2	1.77	0.50
1:C:634:LEU:HD21	1:C:655:LEU:HD23	1.94	0.50
1:D:224:ILE:CG2	1:D:276:VAL:HA	2.41	0.50
1:D:657:LEU:O	1:D:658:HIS:C	2.50	0.50
1:A:247:ASP:HB2	1:A:254:ILE:HG13	1.94	0.50
1:A:323:LEU:HD11	1:A:355:TRP:CD2	2.47	0.50
1:A:414:ARG:O	1:A:414:ARG:HG2	2.11	0.50
1:A:536:ILE:HD11	1:A:655:LEU:C	2.32	0.50
1:A:663:LEU:O	1:A:667:LEU:HG	2.11	0.50
1:B:410:ASN:O	1:B:413:SER:N	2.43	0.50
1:B:536:ILE:HD11	1:B:655:LEU:C	2.32	0.50
1:C:18:PRO:HG3	1:C:421:GLU:OE1	2.12	0.50
1:C:225:SER:OG	1:C:279:TYR:HB2	2.12	0.50
1:C:344:VAL:CG1	1:C:345:GLU:N	2.74	0.50
1:C:528:ILE:O	1:C:529:SER:C	2.50	0.50
1:D:95:ILE:HD13	1:D:131:LEU:HD13	1.93	0.50
1:D:221:ASP:O	1:D:238:THR:HB	2.12	0.50
1:D:290:LEU:O	1:D:291:LEU:HD23	2.11	0.50
1:D:349:LEU:N	1:D:368:VAL:HG22	2.26	0.50
1:A:225:SER:OG	1:A:279:TYR:HB2	2.12	0.50
1:A:396:ASP:C	1:A:396:ASP:OD1	2.50	0.50
1:A:553:ILE:O	1:A:553:ILE:CG2	2.60	0.50
1:A:604:ALA:O	1:A:688:PHE:HB2	2.12	0.50
1:B:11:LEU:HB3	1:B:87:ALA:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MET:O	1:C:1:MET:HG2	2.12	0.50
1:C:57:SER:HB2	1:C:71:HIS:CD2	2.47	0.50
1:C:396:ASP:C	1:C:396:ASP:OD1	2.50	0.50
1:C:506:LEU:HA	1:C:582:VAL:CG1	2.41	0.50
1:C:575:ASN:C	1:C:577:PHE:H	2.14	0.50
1:D:404:VAL:O	1:D:408:PHE:HB2	2.12	0.50
1:D:525:LEU:O	1:D:526:ARG:C	2.49	0.50
1:A:290:LEU:O	1:A:291:LEU:HD23	2.12	0.49
1:B:575:ASN:C	1:B:577:PHE:H	2.14	0.49
1:D:11:LEU:HB3	1:D:87:ALA:HB3	1.94	0.49
1:D:176:VAL:CG1	1:D:177:PHE:H	2.21	0.49
1:A:287:LEU:HG	1:A:288:VAL:N	2.27	0.49
1:A:575:ASN:C	1:A:577:PHE:H	2.14	0.49
1:B:69:CYS:HB2	1:B:82:TYR:CE1	2.47	0.49
1:B:140:SER:OG	1:B:141:SER:N	2.43	0.49
1:C:69:CYS:HB2	1:C:82:TYR:CE1	2.47	0.49
1:C:95:ILE:CD1	1:C:133:LEU:HD11	2.41	0.49
1:C:287:LEU:HG	1:C:288:VAL:N	2.26	0.49
1:D:236:VAL:HG23	1:D:244:LYS:HB2	1.95	0.49
1:D:262:GLN:OE1	1:D:315:PHE:HB2	2.12	0.49
1:A:73:SER:N	1:A:78:LEU:O	2.41	0.49
1:C:172:GLN:N	1:C:172:GLN:NE2	2.61	0.49
1:C:707:SER:O	1:C:708:ASN:C	2.50	0.49
1:D:192:VAL:O	1:D:192:VAL:HG12	2.12	0.49
1:D:280:LEU:HD12	1:D:280:LEU:O	2.13	0.49
1:D:716:GLU:HG2	1:D:722:THR:N	2.28	0.49
1:A:207:SER:C	1:A:209:THR:H	2.15	0.49
1:A:568:LYS:NZ	1:D:210:ARG:NH2	2.57	0.49
1:B:58:ASN:HA	1:B:474:ASN:HD22	1.75	0.49
1:B:95:ILE:HD13	1:B:131:LEU:HD13	1.93	0.49
1:B:224:ILE:CG2	1:B:276:VAL:HA	2.43	0.49
1:B:399:THR:O	1:B:526:ARG:NH2	2.45	0.49
1:B:404:VAL:O	1:B:408:PHE:HB2	2.13	0.49
1:C:9:ALA:CB	1:C:613:ILE:HD11	2.42	0.49
1:D:287:LEU:HG	1:D:288:VAL:N	2.27	0.49
1:D:719:PHE:O	1:D:720:PHE:C	2.50	0.49
1:A:344:VAL:CG1	1:A:345:GLU:N	2.75	0.49
1:B:71:HIS:O	1:B:79:LEU:HD12	2.12	0.49
1:B:344:VAL:CG1	1:B:345:GLU:N	2.73	0.49
1:C:14:TYR:CE2	1:C:613:ILE:HG22	2.47	0.49
1:C:176:VAL:CG1	1:C:177:PHE:H	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:ASP:O	1:C:238:THR:HB	2.12	0.49
1:C:393:HIS:O	1:C:394:ASP:C	2.50	0.49
1:C:404:VAL:O	1:C:408:PHE:HB2	2.12	0.49
1:C:536:ILE:HD11	1:C:655:LEU:HB3	1.93	0.49
1:D:396:ASP:C	1:D:396:ASP:OD1	2.50	0.49
1:A:80:THR:HG22	1:A:81:PHE:N	2.27	0.49
1:A:335:VAL:CG1	1:A:352:ILE:HB	2.43	0.49
1:A:716:GLU:HG2	1:A:722:THR:N	2.27	0.49
1:B:57:SER:HB2	1:B:71:HIS:CD2	2.47	0.49
1:B:207:SER:C	1:B:209:THR:H	2.15	0.49
1:C:4:LEU:HA	1:C:485:LYS:O	2.12	0.49
1:C:236:VAL:HG23	1:C:244:LYS:HB2	1.94	0.49
1:C:335:VAL:CG1	1:C:352:ILE:HB	2.43	0.49
1:D:283:TYR:CG	1:D:284:ASN:N	2.79	0.49
1:A:95:ILE:HD13	1:A:131:LEU:HD13	1.93	0.49
1:A:176:VAL:CG1	1:A:177:PHE:H	2.21	0.49
1:B:172:GLN:N	1:B:172:GLN:NE2	2.61	0.49
1:B:187:LYS:HD3	1:B:197:LEU:CD1	2.34	0.49
1:C:95:ILE:HD13	1:C:131:LEU:HD13	1.93	0.49
1:C:192:VAL:O	1:C:192:VAL:HG12	2.12	0.49
1:D:311:LEU:O	1:D:312:THR:HG23	2.12	0.49
1:D:335:VAL:CG1	1:D:352:ILE:HB	2.43	0.49
1:D:410:ASN:O	1:D:413:SER:N	2.43	0.49
1:A:221:ASP:O	1:A:238:THR:HB	2.12	0.49
1:A:284:ASN:HB3	1:A:285:ASN:OD1	2.12	0.49
1:A:707:SER:O	1:A:708:ASN:C	2.51	0.49
1:A:719:PHE:O	1:A:720:PHE:C	2.51	0.49
1:B:1:MET:HG2	1:B:1:MET:O	2.12	0.49
1:C:9:ALA:HB1	1:C:613:ILE:HD11	1.93	0.49
1:C:207:SER:C	1:C:209:THR:H	2.16	0.49
1:C:604:ALA:O	1:C:688:PHE:HB2	2.13	0.49
1:C:693:PHE:N	1:C:697:GLN:NE2	2.60	0.49
1:D:57:SER:HB2	1:D:71:HIS:CD2	2.47	0.49
1:A:18:PRO:HG3	1:A:421:GLU:OE1	2.13	0.49
1:A:236:VAL:HG23	1:A:244:LYS:HB2	1.95	0.49
1:A:404:VAL:O	1:A:408:PHE:HB2	2.12	0.49
1:B:176:VAL:CG1	1:B:177:PHE:H	2.22	0.49
1:B:283:TYR:CG	1:B:284:ASN:N	2.79	0.49
1:B:693:PHE:N	1:B:697:GLN:NE2	2.60	0.49
1:C:140:SER:OG	1:C:141:SER:N	2.43	0.49
1:C:541:PRO:HB2	1:C:544:MET:CE	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:587:ILE:O	1:C:592:LYS:HB2	2.13	0.49
1:D:71:HIS:O	1:D:79:LEU:HD12	2.12	0.49
1:A:4:LEU:HA	1:A:485:LYS:O	2.12	0.49
1:A:71:HIS:O	1:A:79:LEU:HD12	2.12	0.49
1:A:95:ILE:CD1	1:A:133:LEU:HD11	2.43	0.49
1:A:690:VAL:CG1	1:A:691:LYS:N	2.75	0.49
1:B:80:THR:HG22	1:B:81:PHE:N	2.27	0.49
1:B:587:ILE:O	1:B:592:LYS:HB2	2.12	0.49
1:C:201:ASP:O	1:C:204:TYR:N	2.46	0.49
1:C:536:ILE:HD11	1:C:655:LEU:C	2.33	0.49
1:C:650:HIS:O	1:C:651:ILE:C	2.50	0.49
1:C:716:GLU:HG2	1:C:722:THR:CA	2.43	0.49
1:D:14:TYR:HB3	1:D:673:CYS:HB2	1.94	0.49
1:D:344:VAL:CG1	1:D:345:GLU:N	2.74	0.49
1:A:57:SER:HB2	1:A:71:HIS:CD2	2.48	0.48
1:A:140:SER:OG	1:A:141:SER:N	2.44	0.48
1:A:192:VAL:O	1:A:192:VAL:HG12	2.12	0.48
1:A:657:LEU:O	1:A:658:HIS:C	2.52	0.48
1:B:236:VAL:HG23	1:B:244:LYS:HB2	1.95	0.48
1:B:427:LEU:HD12	1:B:442:TYR:HE2	1.77	0.48
1:B:525:LEU:O	1:B:526:ARG:C	2.50	0.48
1:B:536:ILE:HD12	1:B:659:TYR:HB2	1.93	0.48
1:B:707:SER:O	1:B:708:ASN:C	2.51	0.48
1:C:335:VAL:HG22	1:C:337:THR:HG22	1.95	0.48
1:C:363:LEU:HG	1:C:364:GLN:N	2.28	0.48
1:D:18:PRO:HB3	1:D:417:THR:CG2	2.43	0.48
1:D:336:LEU:C	1:D:337:THR:HG22	2.33	0.48
1:D:566:ASN:HA	1:D:569:ILE:HD12	1.94	0.48
1:D:587:ILE:O	1:D:592:LYS:HB2	2.12	0.48
1:A:92:THR:HG21	1:A:479:TYR:OH	2.13	0.48
1:A:335:VAL:HG22	1:A:337:THR:HG22	1.96	0.48
1:B:382:VAL:HG21	1:B:495:TYR:CD1	2.48	0.48
1:C:224:ILE:CG2	1:C:276:VAL:HA	2.42	0.48
1:C:493:TRP:CD1	1:C:507:PHE:HD1	2.31	0.48
1:C:566:ASN:HA	1:C:569:ILE:HD12	1.95	0.48
1:D:187:LYS:HD3	1:D:197:LEU:CD1	2.34	0.48
1:D:493:TRP:CD1	1:D:507:PHE:HD1	2.31	0.48
1:A:370:ASP:OD1	1:A:372:SER:HB3	2.12	0.48
1:A:448:THR:O	1:A:452:ASP:OD2	2.31	0.48
1:B:180:ASP:C	1:B:182:GLY:H	2.17	0.48
1:B:247:ASP:HB2	1:B:254:ILE:HG13	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:LEU:HD11	1:B:355:TRP:CD2	2.48	0.48
1:C:71:HIS:O	1:C:79:LEU:HD12	2.12	0.48
1:C:405:GLU:OE2	1:C:437:ASN:ND2	2.47	0.48
1:D:201:ASP:O	1:D:204:TYR:N	2.46	0.48
1:A:101:SER:HB3	1:A:121:VAL:CG1	2.44	0.48
1:A:101:SER:HB3	1:A:121:VAL:HG13	1.94	0.48
1:A:566:ASN:HA	1:A:569:ILE:HD12	1.95	0.48
1:A:650:HIS:O	1:A:651:ILE:C	2.50	0.48
1:B:101:SER:HB3	1:B:121:VAL:HG13	1.94	0.48
1:B:201:ASP:O	1:B:204:TYR:N	2.46	0.48
1:B:403:ASP:HB3	1:B:406:ARG:CB	2.43	0.48
1:C:71:HIS:HE1	1:C:478:PRO:N	2.11	0.48
1:C:657:LEU:O	1:C:658:HIS:C	2.52	0.48
1:A:201:ASP:O	1:A:204:TYR:N	2.46	0.48
1:C:80:THR:HG22	1:C:81:PHE:N	2.28	0.48
1:C:263:SER:O	1:C:264:ASP:C	2.51	0.48
1:C:533:LEU:HD13	1:C:729:ILE:CD1	2.44	0.48
1:D:101:SER:HB3	1:D:121:VAL:HG13	1.94	0.48
1:D:207:SER:C	1:D:209:THR:H	2.16	0.48
1:A:263:SER:O	1:A:264:ASP:C	2.51	0.48
1:A:363:LEU:HG	1:A:364:GLN:N	2.29	0.48
1:A:533:LEU:HD13	1:A:729:ILE:CD1	2.44	0.48
1:A:587:ILE:O	1:A:592:LYS:HB2	2.13	0.48
1:B:101:SER:HB3	1:B:121:VAL:CG1	2.44	0.48
1:B:254:ILE:CG2	1:B:311:LEU:HB2	2.44	0.48
1:C:483:LEU:HD13	1:C:614:ILE:HD12	1.94	0.48
1:D:101:SER:HB3	1:D:121:VAL:CG1	2.44	0.48
1:D:533:LEU:HD13	1:D:729:ILE:CD1	2.44	0.48
1:B:232:ARG:HD2	1:B:233:TYR:CE1	2.49	0.48
1:B:263:SER:O	1:B:264:ASP:C	2.51	0.48
1:B:293:LEU:HB2	1:B:297:LEU:CG	2.27	0.48
1:B:506:LEU:HA	1:B:582:VAL:HG13	1.94	0.48
1:B:623:LEU:HD13	1:B:664:LEU:HD22	1.93	0.48
1:B:657:LEU:O	1:B:658:HIS:C	2.52	0.48
1:C:11:LEU:HB3	1:C:87:ALA:HB3	1.94	0.48
1:C:101:SER:HB3	1:C:121:VAL:CG1	2.44	0.48
1:D:80:THR:HG22	1:D:81:PHE:N	2.27	0.48
1:A:536:ILE:HD12	1:A:659:TYR:HB2	1.95	0.48
1:A:693:PHE:N	1:A:697:GLN:NE2	2.61	0.48
1:B:249:THR:O	1:B:249:THR:HG22	2.14	0.48
1:B:335:VAL:HG22	1:B:337:THR:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:370:ASP:OD1	1:C:372:SER:HB3	2.13	0.48
1:D:283:TYR:O	1:D:284:ASN:O	2.32	0.48
1:A:317:ASN:CG	1:A:318:ASN:N	2.67	0.48
1:A:493:TRP:CD1	1:A:507:PHE:HD1	2.31	0.48
1:C:28:VAL:HG23	1:C:96:HIS:O	2.14	0.48
1:D:232:ARG:HD2	1:D:233:TYR:CE1	2.49	0.48
1:D:335:VAL:HG22	1:D:337:THR:HG22	1.96	0.48
1:D:693:PHE:N	1:D:697:GLN:NE2	2.60	0.48
1:B:71:HIS:HE1	1:B:478:PRO:N	2.11	0.48
1:B:336:LEU:C	1:B:337:THR:HG22	2.34	0.48
1:C:253:LEU:HG	1:C:255:GLN:O	2.14	0.48
1:D:239:GLN:HG2	1:D:273:VAL:O	2.13	0.48
1:D:585:ASP:OD1	1:D:589:ASN:HB2	2.14	0.48
1:D:619:LEU:HD11	1:D:623:LEU:HD11	1.96	0.48
1:A:9:ALA:CB	1:A:613:ILE:HD11	2.43	0.47
1:B:585:ASP:OD1	1:B:589:ASN:HB2	2.14	0.47
1:C:55:GLU:OE1	1:C:74:SER:CA	2.60	0.47
1:C:101:SER:HB3	1:C:121:VAL:HG13	1.95	0.47
1:C:157:ASP:OD2	1:C:159:THR:HB	2.14	0.47
1:D:140:SER:OG	1:D:141:SER:N	2.44	0.47
1:D:157:ASP:OD2	1:D:159:THR:HB	2.14	0.47
1:D:180:ASP:C	1:D:182:GLY:H	2.18	0.47
1:D:293:LEU:HB2	1:D:297:LEU:CG	2.28	0.47
1:A:28:VAL:HG23	1:A:96:HIS:O	2.14	0.47
1:B:349:LEU:HB2	1:B:368:VAL:HG21	1.97	0.47
1:B:528:ILE:O	1:B:529:SER:C	2.50	0.47
1:C:73:SER:N	1:C:78:LEU:O	2.42	0.47
1:C:307:SER:O	1:C:308:SER:C	2.50	0.47
1:D:18:PRO:N	1:D:417:THR:HG21	2.29	0.47
1:D:243:LEU:HB3	1:D:259:MET:HE3	1.95	0.47
1:D:323:LEU:HD11	1:D:355:TRP:CD2	2.49	0.47
1:D:536:ILE:HD12	1:D:659:TYR:HB2	1.95	0.47
1:A:9:ALA:HB1	1:A:613:ILE:HD11	1.95	0.47
1:A:382:VAL:HG21	1:A:495:TYR:CD1	2.49	0.47
1:A:716:GLU:HG2	1:A:722:THR:CA	2.44	0.47
1:B:28:VAL:HG23	1:B:96:HIS:O	2.15	0.47
1:C:71:HIS:CE1	1:C:478:PRO:HA	2.50	0.47
1:C:317:ASN:CG	1:C:318:ASN:N	2.68	0.47
1:D:101:SER:HB2	1:D:107:THR:HG1	1.79	0.47
1:D:284:ASN:HB3	1:D:285:ASN:OD1	2.13	0.47
1:D:317:ASN:CG	1:D:318:ASN:N	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:491:GLU:O	1:D:495:TYR:HD2	1.96	0.47
1:D:579:ILE:O	1:D:583:LEU:HB2	2.14	0.47
1:A:157:ASP:OD2	1:A:159:THR:HB	2.15	0.47
1:A:326:SER:OG	1:A:328:ILE:HG13	2.13	0.47
1:A:506:LEU:HA	1:A:582:VAL:HG13	1.95	0.47
1:A:723:PHE:CD2	1:C:667:LEU:HD13	2.49	0.47
1:B:9:ALA:HB1	1:B:613:ILE:HD11	1.95	0.47
1:B:253:LEU:HG	1:B:255:GLN:O	2.14	0.47
1:B:443:LEU:C	1:B:445:ASN:N	2.65	0.47
1:B:579:ILE:O	1:B:583:LEU:HB2	2.14	0.47
1:B:719:PHE:O	1:B:720:PHE:C	2.52	0.47
1:D:629:ILE:O	1:D:630:THR:C	2.52	0.47
1:A:232:ARG:HG2	1:A:248:LEU:H	1.80	0.47
1:A:525:LEU:O	1:A:526:ARG:C	2.52	0.47
1:B:224:ILE:HD11	1:B:237:LEU:HG	1.97	0.47
1:B:284:ASN:HB3	1:B:285:ASN:OD1	2.13	0.47
1:B:619:LEU:HD11	1:B:623:LEU:HD11	1.97	0.47
1:C:323:LEU:HD11	1:C:355:TRP:CD2	2.49	0.47
1:C:579:ILE:O	1:C:583:LEU:HB2	2.14	0.47
1:D:349:LEU:HB2	1:D:368:VAL:HG21	1.97	0.47
1:D:443:LEU:C	1:D:445:ASN:N	2.65	0.47
1:D:224:ILE:HD11	1:D:237:LEU:HG	1.97	0.47
1:A:150:PHE:CD1	1:A:150:PHE:C	2.88	0.47
1:A:180:ASP:C	1:A:182:GLY:H	2.17	0.47
1:A:336:LEU:C	1:A:337:THR:HG22	2.34	0.47
1:A:569:ILE:HG22	1:A:573:GLU:OE1	2.15	0.47
1:B:9:ALA:CB	1:B:613:ILE:HD11	2.45	0.47
1:B:71:HIS:CE1	1:B:478:PRO:HA	2.49	0.47
1:B:124:LYS:O	1:B:126:GLY:N	2.48	0.47
1:B:283:TYR:O	1:B:284:ASN:O	2.33	0.47
1:B:396:ASP:C	1:B:396:ASP:OD1	2.52	0.47
1:B:533:LEU:HD13	1:B:729:ILE:CD1	2.45	0.47
1:B:566:ASN:HA	1:B:569:ILE:HD12	1.96	0.47
1:C:180:ASP:C	1:C:182:GLY:H	2.17	0.47
1:C:185:GLY:C	1:C:186:LEU:HD12	2.35	0.47
1:C:342:LEU:HD12	1:C:379:ILE:HD12	1.94	0.47
1:C:344:VAL:CG1	1:C:345:GLU:H	2.28	0.47
1:D:4:LEU:HA	1:D:485:LYS:O	2.14	0.47
1:D:95:ILE:CD1	1:D:133:LEU:HD11	2.43	0.47
1:D:244:LYS:HE2	1:D:256:ASP:OD1	2.14	0.47
1:A:71:HIS:CE1	1:A:478:PRO:HA	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:GLN:HG2	1:A:273:VAL:O	2.14	0.47
1:A:253:LEU:HG	1:A:255:GLN:O	2.15	0.47
1:A:342:LEU:HD12	1:A:379:ILE:HD12	1.94	0.47
1:A:579:ILE:O	1:A:583:LEU:HB2	2.15	0.47
1:B:18:PRO:HB3	1:B:417:THR:CG2	2.45	0.47
1:B:569:ILE:HG22	1:B:573:GLU:OE1	2.15	0.47
1:D:245:ILE:HG21	1:D:311:LEU:CD2	2.45	0.47
1:D:534:ASP:HA	1:D:537:THR:OG1	2.15	0.47
1:A:185:GLY:C	1:A:186:LEU:HD12	2.36	0.47
1:A:224:ILE:HD11	1:A:237:LEU:HG	1.96	0.47
1:A:236:VAL:HB	1:A:237:LEU:H	1.62	0.47
1:A:403:ASP:HB3	1:A:406:ARG:CB	2.44	0.47
1:A:585:ASP:OD1	1:A:589:ASN:HB2	2.14	0.47
1:B:241:CYS:O	1:B:259:MET:HG2	2.14	0.47
1:B:363:LEU:HG	1:B:364:GLN:N	2.29	0.47
1:C:239:GLN:HG2	1:C:273:VAL:O	2.14	0.47
1:C:563:GLU:HB3	1:C:565:THR:CG2	2.45	0.47
1:D:124:LYS:O	1:D:126:GLY:N	2.48	0.47
1:D:150:PHE:CD1	1:D:150:PHE:C	2.89	0.47
1:D:448:THR:O	1:D:452:ASP:OD2	2.33	0.47
1:D:506:LEU:HA	1:D:582:VAL:HG13	1.95	0.47
1:D:528:ILE:O	1:D:529:SER:C	2.51	0.47
1:A:224:ILE:CG2	1:A:276:VAL:HA	2.44	0.47
1:B:150:PHE:CD1	1:B:150:PHE:C	2.89	0.47
1:B:506:LEU:CD1	1:B:582:VAL:HG12	2.44	0.47
1:B:716:GLU:HG2	1:B:722:THR:CA	2.44	0.47
1:C:113:VAL:CG2	1:C:118:LEU:HB2	2.45	0.47
1:C:124:LYS:O	1:C:126:GLY:N	2.48	0.47
1:C:236:VAL:HB	1:C:237:LEU:H	1.61	0.47
1:C:445:ASN:O	1:C:446:LEU:C	2.53	0.47
1:C:506:LEU:HA	1:C:582:VAL:HG13	1.96	0.47
1:D:399:THR:O	1:D:526:ARG:NH2	2.48	0.47
1:D:403:ASP:HB3	1:D:406:ARG:CB	2.45	0.47
1:A:11:LEU:HB3	1:A:87:ALA:HB3	1.95	0.46
1:A:55:GLU:OE1	1:A:74:SER:CA	2.60	0.46
1:A:399:THR:O	1:A:526:ARG:NH2	2.48	0.46
1:A:563:GLU:HB3	1:A:565:THR:CG2	2.45	0.46
1:B:157:ASP:OD2	1:B:159:THR:HB	2.15	0.46
1:B:185:GLY:C	1:B:186:LEU:HD12	2.35	0.46
1:B:317:ASN:CG	1:B:318:ASN:N	2.68	0.46
1:B:344:VAL:CG1	1:B:345:GLU:H	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:326:SER:OG	1:C:328:ILE:HG13	2.14	0.46
1:C:336:LEU:C	1:C:337:THR:HG22	2.35	0.46
1:D:28:VAL:HG23	1:D:96:HIS:O	2.15	0.46
1:D:55:GLU:OE1	1:D:74:SER:CA	2.58	0.46
1:D:253:LEU:HG	1:D:255:GLN:O	2.15	0.46
1:A:349:LEU:N	1:A:368:VAL:HG22	2.26	0.46
1:B:95:ILE:CD1	1:B:133:LEU:HD11	2.43	0.46
1:C:68:ILE:HD11	1:C:81:PHE:HD1	1.80	0.46
1:C:585:ASP:OD1	1:C:589:ASN:HB2	2.14	0.46
1:D:71:HIS:CE1	1:D:478:PRO:HA	2.50	0.46
1:A:344:VAL:CG1	1:A:345:GLU:H	2.29	0.46
1:B:563:GLU:HB3	1:B:565:THR:CG2	2.45	0.46
1:C:150:PHE:CD1	1:C:150:PHE:C	2.89	0.46
1:C:172:GLN:HA	1:C:188:LYS:HB3	1.97	0.46
1:D:71:HIS:HE1	1:D:478:PRO:N	2.13	0.46
1:D:326:SER:OG	1:D:328:ILE:HG13	2.15	0.46
1:D:496:ASN:HA	1:D:499:SER:HB3	1.97	0.46
1:D:563:GLU:HB3	1:D:565:THR:CG2	2.45	0.46
1:D:716:GLU:HG2	1:D:722:THR:CA	2.44	0.46
1:A:255:GLN:OE1	1:A:257:TYR:CE2	2.69	0.46
1:B:4:LEU:HA	1:B:485:LYS:O	2.15	0.46
1:B:113:VAL:CG2	1:B:118:LEU:HB2	2.46	0.46
1:C:349:LEU:N	1:C:368:VAL:HG22	2.26	0.46
1:C:351:LEU:HG	1:C:353:VAL:CG2	2.44	0.46
1:D:14:TYR:CE2	1:D:613:ILE:HG22	2.50	0.46
1:D:243:LEU:HB3	1:D:259:MET:CE	2.45	0.46
1:D:250:SER:O	1:D:251:PHE:HB2	2.15	0.46
1:A:288:VAL:HG12	1:A:300:MET:HB3	1.98	0.46
1:B:18:PRO:N	1:B:417:THR:HG21	2.31	0.46
1:C:187:LYS:HD3	1:C:197:LEU:CD1	2.34	0.46
1:C:224:ILE:HD11	1:C:237:LEU:HG	1.97	0.46
1:D:344:VAL:CG1	1:D:345:GLU:H	2.28	0.46
1:A:71:HIS:HE1	1:A:478:PRO:N	2.13	0.46
1:A:280:LEU:HD12	1:A:280:LEU:O	2.15	0.46
1:B:157:ASP:C	1:B:159:THR:H	2.19	0.46
1:B:326:SER:O	1:B:327:ALA:HB3	2.15	0.46
1:B:445:ASN:O	1:B:446:LEU:C	2.53	0.46
1:B:569:ILE:O	1:B:573:GLU:HB2	2.15	0.46
1:C:293:LEU:HD13	1:C:297:LEU:HG	1.97	0.46
1:C:351:LEU:O	1:C:353:VAL:HG23	2.16	0.46
1:C:506:LEU:CD1	1:C:582:VAL:HG12	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:552:ASP:C	1:C:552:ASP:OD1	2.54	0.46
1:C:650:HIS:O	1:C:653:THR:HB	2.16	0.46
1:D:18:PRO:HB3	1:D:417:THR:HG22	1.97	0.46
1:D:255:GLN:OE1	1:D:257:TYR:CE2	2.68	0.46
1:D:363:LEU:HG	1:D:364:GLN:N	2.30	0.46
1:D:398:VAL:CB	1:D:669:ARG:NH1	2.55	0.46
1:A:187:LYS:HD3	1:A:197:LEU:CD1	2.34	0.46
1:A:491:GLU:O	1:A:495:TYR:HD2	1.98	0.46
1:A:506:LEU:CD1	1:A:582:VAL:HG12	2.46	0.46
1:B:265:SER:O	1:B:267:PRO:N	2.49	0.46
1:B:326:SER:OG	1:B:328:ILE:HG13	2.16	0.46
1:C:232:ARG:HD2	1:C:233:TYR:CE1	2.50	0.46
1:C:283:TYR:O	1:C:284:ASN:O	2.33	0.46
1:D:58:ASN:HA	1:D:474:ASN:HD22	1.79	0.46
1:D:157:ASP:C	1:D:159:THR:H	2.19	0.46
1:D:227:LYS:CG	1:D:282:LEU:HD22	2.45	0.46
1:D:227:LYS:HG3	1:D:282:LEU:HD22	1.98	0.46
1:A:232:ARG:HD2	1:A:233:TYR:CE1	2.50	0.46
1:A:445:ASN:O	1:A:446:LEU:C	2.54	0.46
1:A:650:HIS:O	1:A:653:THR:HB	2.16	0.46
1:B:341:GLU:HG3	1:B:341:GLU:O	2.16	0.46
1:B:427:LEU:HD21	1:B:449:ILE:HG13	1.98	0.46
1:B:500:GLU:HG2	1:B:501:THR:O	2.16	0.46
1:C:137:PHE:O	1:C:137:PHE:CG	2.68	0.46
1:C:233:TYR:O	1:C:235:ILE:HD12	2.16	0.46
1:C:280:LEU:HD12	1:C:280:LEU:O	2.15	0.46
1:C:525:LEU:O	1:C:526:ARG:C	2.54	0.46
1:C:619:LEU:HD11	1:C:623:LEU:HD11	1.97	0.46
1:D:113:VAL:CG2	1:D:118:LEU:HB2	2.46	0.46
1:D:185:GLY:C	1:D:186:LEU:HD12	2.36	0.46
1:D:427:LEU:HD21	1:D:449:ILE:HG13	1.97	0.46
1:D:506:LEU:CD1	1:D:582:VAL:HG12	2.45	0.46
1:A:113:VAL:CG2	1:A:118:LEU:HB2	2.46	0.46
1:A:124:LYS:O	1:A:126:GLY:N	2.49	0.46
1:A:227:LYS:HG3	1:A:282:LEU:HD22	1.98	0.46
1:A:245:ILE:HG21	1:A:311:LEU:CD2	2.46	0.46
1:A:351:LEU:O	1:A:353:VAL:HG23	2.16	0.46
1:A:694:ASN:N	1:A:697:GLN:NE2	2.64	0.46
1:B:95:ILE:HG21	1:B:131:LEU:HD11	1.98	0.46
1:D:569:ILE:HG22	1:D:573:GLU:OE1	2.16	0.46
1:A:172:GLN:HA	1:A:188:LYS:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:534:ASP:HA	1:A:537:THR:OG1	2.15	0.46
1:B:180:ASP:C	1:B:182:GLY:N	2.70	0.46
1:B:247:ASP:HB3	1:B:250:SER:HB2	1.98	0.46
1:B:293:LEU:HD22	1:B:297:LEU:CD1	2.44	0.46
1:B:436:HIS:CD2	1:B:438:GLU:HB2	2.51	0.46
1:C:288:VAL:HG12	1:C:300:MET:HB3	1.98	0.46
1:C:534:ASP:HA	1:C:537:THR:OG1	2.15	0.46
1:C:694:ASN:ND2	1:C:697:GLN:HG3	2.31	0.46
1:D:245:ILE:HG21	1:D:311:LEU:HD22	1.97	0.46
1:A:101:SER:HB2	1:A:107:THR:HG1	1.78	0.45
1:A:283:TYR:O	1:A:284:ASN:O	2.33	0.45
1:A:340:LEU:O	1:A:341:GLU:HB3	2.15	0.45
1:A:552:ASP:C	1:A:552:ASP:OD1	2.54	0.45
1:B:351:LEU:O	1:B:353:VAL:HG23	2.16	0.45
1:C:128:PHE:HB3	1:C:153:GLN:HB3	1.97	0.45
1:C:310:ILE:O	1:C:310:ILE:CG2	2.64	0.45
1:D:293:LEU:HD22	1:D:297:LEU:CD1	2.44	0.45
1:D:351:LEU:O	1:D:353:VAL:HG23	2.15	0.45
1:A:18:PRO:HB3	1:A:417:THR:CG2	2.46	0.45
1:A:71:HIS:CE1	1:A:478:PRO:HB3	2.52	0.45
1:A:128:PHE:HB3	1:A:153:GLN:HB3	1.97	0.45
1:A:157:ASP:C	1:A:159:THR:H	2.19	0.45
1:A:240:ASN:O	1:A:242:HIS:N	2.50	0.45
1:A:341:GLU:HG3	1:A:341:GLU:O	2.16	0.45
1:A:528:ILE:C	1:A:530:LYS:N	2.68	0.45
1:B:14:TYR:CE2	1:B:613:ILE:HG22	2.50	0.45
1:B:215:SER:HB3	1:B:216:SER:H	1.65	0.45
1:B:255:GLN:OE1	1:B:257:TYR:CE2	2.69	0.45
1:B:293:LEU:HD13	1:B:297:LEU:HG	1.97	0.45
1:C:28:VAL:HG13	1:C:150:PHE:CD1	2.51	0.45
1:C:403:ASP:HB3	1:C:406:ARG:CB	2.46	0.45
1:C:569:ILE:HG22	1:C:573:GLU:OE1	2.17	0.45
1:D:288:VAL:HG12	1:D:300:MET:HB3	1.97	0.45
1:D:326:SER:O	1:D:327:ALA:HB3	2.16	0.45
1:D:428:SER:O	1:D:429:GLU:C	2.54	0.45
1:A:103:ASN:H	1:A:107:THR:HG23	1.81	0.45
1:A:349:LEU:HB2	1:A:368:VAL:HG21	1.97	0.45
1:A:354:LEU:HD21	1:A:460:ALA:HB1	1.98	0.45
1:A:694:ASN:CG	1:A:697:GLN:HG3	2.36	0.45
1:B:128:PHE:HB3	1:B:153:GLN:HB3	1.97	0.45
1:B:172:GLN:HA	1:B:188:LYS:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:VAL:O	1:B:193:HIS:ND1	2.49	0.45
1:B:288:VAL:HG12	1:B:300:MET:HB3	1.98	0.45
1:C:71:HIS:CE1	1:C:478:PRO:HB3	2.51	0.45
1:C:95:ILE:HG21	1:C:131:LEU:CD1	2.47	0.45
1:C:157:ASP:C	1:C:159:THR:H	2.19	0.45
1:C:232:ARG:HG2	1:C:248:LEU:H	1.82	0.45
1:C:707:SER:C	1:C:709:VAL:N	2.70	0.45
1:D:28:VAL:HG13	1:D:150:PHE:CD1	2.51	0.45
1:D:341:GLU:HG3	1:D:341:GLU:O	2.16	0.45
1:A:291:LEU:HA	1:A:292:PRO:HD3	1.80	0.45
1:A:594:GLY:C	1:A:595:ILE:HD12	2.37	0.45
1:B:28:VAL:HG13	1:B:150:PHE:CD1	2.51	0.45
1:B:319:ILE:HG23	1:B:320:PRO:HD2	1.98	0.45
1:B:491:GLU:O	1:B:495:TYR:HD2	1.98	0.45
1:B:534:ASP:HA	1:B:537:THR:OG1	2.17	0.45
1:B:651:ILE:O	1:B:654:LEU:N	2.49	0.45
1:C:14:TYR:CZ	1:C:613:ILE:HG22	2.51	0.45
1:C:326:SER:O	1:C:327:ALA:HB3	2.17	0.45
1:C:500:GLU:HG2	1:C:501:THR:O	2.16	0.45
1:D:293:LEU:HD13	1:D:297:LEU:HG	1.97	0.45
1:D:351:LEU:HG	1:D:353:VAL:CG2	2.45	0.45
1:A:227:LYS:CG	1:A:282:LEU:HD22	2.46	0.45
1:A:293:LEU:HD13	1:A:297:LEU:HG	1.98	0.45
1:B:241:CYS:O	1:B:259:MET:CG	2.64	0.45
1:B:650:HIS:O	1:B:653:THR:HB	2.16	0.45
1:D:342:LEU:HD12	1:D:379:ILE:HD12	1.94	0.45
1:D:542:ASP:O	1:D:543:SER:C	2.55	0.45
1:A:500:GLU:HG2	1:A:501:THR:O	2.16	0.45
1:B:183:LEU:N	1:B:183:LEU:HD23	2.32	0.45
1:B:629:ILE:O	1:B:630:THR:C	2.54	0.45
1:C:180:ASP:O	1:C:182:GLY:N	2.50	0.45
1:C:594:GLY:C	1:C:595:ILE:HD12	2.37	0.45
1:D:172:GLN:H	1:D:172:GLN:NE2	2.15	0.45
1:D:707:SER:C	1:D:709:VAL:N	2.70	0.45
1:A:28:VAL:HG13	1:A:150:PHE:CD1	2.52	0.45
1:A:61:LEU:O	1:A:62:LEU:HD23	2.16	0.45
1:A:180:ASP:O	1:A:182:GLY:N	2.50	0.45
1:A:306:ASP:OD1	1:A:307:SER:N	2.38	0.45
1:A:323:LEU:HD11	1:A:355:TRP:CE3	2.52	0.45
1:B:346:ALA:HB1	1:B:369:ASN:HB3	1.99	0.45
1:C:226:CYS:O	1:C:227:LYS:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:227:LYS:HG3	1:C:282:LEU:HD22	1.99	0.45
1:C:694:ASN:N	1:C:697:GLN:NE2	2.65	0.45
1:C:716:GLU:HG2	1:C:721:MET:C	2.37	0.45
1:D:68:ILE:HD11	1:D:81:PHE:HD1	1.82	0.45
1:D:128:PHE:HB3	1:D:153:GLN:HB3	1.97	0.45
1:D:180:ASP:C	1:D:182:GLY:N	2.70	0.45
1:D:340:LEU:O	1:D:341:GLU:HB3	2.17	0.45
1:D:500:GLU:HG2	1:D:501:THR:O	2.17	0.45
1:A:9:ALA:HA	1:A:613:ILE:HD11	1.99	0.45
1:A:144:THR:HG22	1:A:145:LEU:N	2.32	0.45
1:B:180:ASP:O	1:B:182:GLY:N	2.50	0.45
1:B:594:GLY:C	1:B:595:ILE:HD12	2.37	0.45
1:C:14:TYR:OH	1:C:613:ILE:HA	2.16	0.45
1:C:201:ASP:O	1:C:202:ASN:C	2.55	0.45
1:C:240:ASN:O	1:C:242:HIS:N	2.50	0.45
1:A:326:SER:O	1:A:327:ALA:HB3	2.17	0.45
1:B:95:ILE:HG21	1:B:131:LEU:CD1	2.47	0.45
1:B:201:ASP:O	1:B:202:ASN:C	2.55	0.45
1:B:340:LEU:CD2	1:B:342:LEU:HD21	2.37	0.45
1:C:291:LEU:HA	1:C:292:PRO:HD3	1.81	0.45
1:C:315:PHE:CD1	1:C:316:GLN:N	2.85	0.45
1:C:569:ILE:O	1:C:573:GLU:HB2	2.16	0.45
1:C:694:ASN:CG	1:C:697:GLN:HG3	2.37	0.45
1:D:183:LEU:N	1:D:183:LEU:HD23	2.32	0.45
1:D:192:VAL:O	1:D:193:HIS:ND1	2.50	0.45
1:D:201:ASP:O	1:D:202:ASN:C	2.55	0.45
1:A:14:TYR:CE2	1:A:613:ILE:HG22	2.52	0.45
1:A:95:ILE:HG21	1:A:131:LEU:HD11	1.98	0.45
1:A:137:PHE:O	1:A:137:PHE:CG	2.70	0.45
1:A:707:SER:C	1:A:709:VAL:N	2.70	0.45
1:B:240:ASN:O	1:B:242:HIS:N	2.50	0.45
1:B:428:SER:O	1:B:429:GLU:C	2.55	0.45
1:B:528:ILE:O	1:B:531:LYS:N	2.50	0.45
1:B:542:ASP:O	1:B:543:SER:C	2.56	0.45
1:C:180:ASP:C	1:C:182:GLY:N	2.69	0.45
1:C:244:LYS:HD3	1:C:253:LEU:CD2	2.47	0.45
1:C:245:ILE:HG21	1:C:311:LEU:CD2	2.47	0.45
1:C:249:THR:HG22	1:C:249:THR:O	2.17	0.45
1:C:483:LEU:HD23	1:C:483:LEU:C	2.38	0.45
1:C:651:ILE:O	1:C:654:LEU:N	2.49	0.45
1:D:319:ILE:HG23	1:D:320:PRO:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:337:THR:OG1	1:D:338:ARG:N	2.50	0.45
1:D:552:ASP:C	1:D:552:ASP:OD1	2.55	0.45
1:D:697:GLN:O	1:D:700:ALA:HB3	2.17	0.45
1:A:95:ILE:HG21	1:A:131:LEU:CD1	2.47	0.44
1:A:201:ASP:O	1:A:202:ASN:C	2.55	0.44
1:A:427:LEU:HD21	1:A:449:ILE:HG13	1.99	0.44
1:A:637:PHE:CD2	1:A:651:ILE:HD11	2.50	0.44
1:B:111:GLN:HG3	1:B:168:TYR:CE2	2.52	0.44
1:B:144:THR:HG22	1:B:145:LEU:N	2.32	0.44
1:B:716:GLU:HG2	1:B:721:MET:C	2.38	0.44
1:C:349:LEU:HB2	1:C:368:VAL:HG21	1.98	0.44
1:C:427:LEU:HD21	1:C:449:ILE:HG13	1.99	0.44
1:C:629:ILE:O	1:C:630:THR:C	2.54	0.44
1:D:95:ILE:HG21	1:D:131:LEU:CD1	2.47	0.44
1:D:694:ASN:N	1:D:697:GLN:NE2	2.65	0.44
1:A:9:ALA:CA	1:A:613:ILE:HD11	2.47	0.44
1:A:528:ILE:O	1:A:531:LYS:N	2.50	0.44
1:B:61:LEU:O	1:B:62:LEU:HD23	2.17	0.44
1:B:340:LEU:O	1:B:341:GLU:HB3	2.17	0.44
1:C:244:LYS:HD3	1:C:253:LEU:HD22	1.97	0.44
1:C:382:VAL:HG12	1:C:384:LYS:H	1.83	0.44
1:D:172:GLN:HA	1:D:188:LYS:HB3	1.98	0.44
1:D:594:GLY:C	1:D:595:ILE:HD12	2.38	0.44
1:A:103:ASN:O	1:A:106:TYR:HB2	2.17	0.44
1:A:180:ASP:C	1:A:182:GLY:N	2.70	0.44
1:A:716:GLU:HG2	1:A:721:MET:C	2.38	0.44
1:B:496:ASN:HA	1:B:499:SER:HB3	1.99	0.44
1:B:552:ASP:C	1:B:552:ASP:OD1	2.55	0.44
1:B:694:ASN:N	1:B:697:GLN:NE2	2.65	0.44
1:B:707:SER:C	1:B:709:VAL:N	2.71	0.44
1:C:192:VAL:O	1:C:193:HIS:ND1	2.50	0.44
1:C:346:ALA:HB1	1:C:369:ASN:HB3	1.98	0.44
1:D:61:LEU:O	1:D:62:LEU:HD23	2.17	0.44
1:D:95:ILE:HG21	1:D:131:LEU:HD11	1.99	0.44
1:D:346:ALA:HB1	1:D:369:ASN:HB3	1.99	0.44
1:D:569:ILE:O	1:D:573:GLU:HB2	2.17	0.44
1:D:651:ILE:O	1:D:654:LEU:N	2.50	0.44
1:A:172:GLN:H	1:A:172:GLN:NE2	2.14	0.44
1:A:245:ILE:HG21	1:A:311:LEU:HD22	1.97	0.44
1:A:616:LEU:HD22	1:A:676:ALA:HB2	1.99	0.44
1:A:667:LEU:HD13	1:C:723:PHE:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:694:ASN:ND2	1:A:697:GLN:HG3	2.32	0.44
1:A:697:GLN:O	1:A:700:ALA:HB3	2.18	0.44
1:B:694:ASN:ND2	1:B:697:GLN:HG3	2.33	0.44
1:C:28:VAL:CB	1:C:98:PRO:HD3	2.47	0.44
1:C:61:LEU:O	1:C:62:LEU:HD23	2.16	0.44
1:C:382:VAL:HG21	1:C:495:TYR:CD1	2.52	0.44
1:C:491:GLU:O	1:C:495:TYR:HD2	2.00	0.44
1:C:705:LEU:O	1:C:709:VAL:HG23	2.17	0.44
1:D:14:TYR:OH	1:D:613:ILE:HA	2.17	0.44
1:D:335:VAL:HG13	1:D:335:VAL:O	2.17	0.44
1:D:445:ASN:O	1:D:446:LEU:C	2.54	0.44
1:D:564:ILE:HD12	1:D:564:ILE:HA	1.83	0.44
1:A:428:SER:O	1:A:429:GLU:C	2.54	0.44
1:A:569:ILE:O	1:A:573:GLU:HB2	2.17	0.44
1:A:705:LEU:O	1:A:706:ASN:C	2.56	0.44
1:A:719:PHE:CD1	1:A:720:PHE:N	2.86	0.44
1:B:100:ALA:O	1:B:124:LYS:HG3	2.18	0.44
1:C:154:ASN:N	1:C:155:PRO:CD	2.79	0.44
1:C:428:SER:O	1:C:429:GLU:C	2.54	0.44
1:D:144:THR:HG22	1:D:145:LEU:N	2.32	0.44
1:D:240:ASN:O	1:D:242:HIS:N	2.50	0.44
1:D:483:LEU:HD23	1:D:483:LEU:C	2.38	0.44
1:D:694:ASN:ND2	1:D:697:GLN:HG3	2.33	0.44
1:A:18:PRO:HB3	1:A:417:THR:HG22	1.99	0.44
1:A:68:ILE:HD11	1:A:81:PHE:HD1	1.82	0.44
1:A:315:PHE:CD1	1:A:316:GLN:N	2.86	0.44
1:A:477:GLN:O	1:A:480:ASN:HB2	2.18	0.44
1:B:68:ILE:HD11	1:B:81:PHE:HD1	1.83	0.44
1:B:351:LEU:HG	1:B:353:VAL:CG2	2.46	0.44
1:C:227:LYS:CG	1:C:282:LEU:HD22	2.47	0.44
1:D:168:TYR:HA	1:D:174:SER:CB	2.47	0.44
1:A:192:VAL:O	1:A:193:HIS:ND1	2.50	0.44
1:B:14:TYR:OH	1:B:613:ILE:HA	2.17	0.44
1:B:168:TYR:HA	1:B:174:SER:CB	2.47	0.44
1:B:199:PHE:HB3	1:B:251:PHE:O	2.18	0.44
1:B:477:GLN:O	1:B:480:ASN:HB2	2.17	0.44
1:B:559:GLU:O	1:B:560:ASN:HB2	2.17	0.44
1:C:177:PHE:CZ	1:C:234:LEU:HD21	2.40	0.44
1:C:183:LEU:N	1:C:183:LEU:HD23	2.32	0.44
1:C:286:THR:CG2	1:C:287:LEU:H	2.30	0.44
1:C:340:LEU:O	1:C:341:GLU:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:341:GLU:HG3	1:C:341:GLU:O	2.17	0.44
1:C:457:PHE:CG	1:C:477:GLN:HG2	2.53	0.44
1:D:265:SER:O	1:D:267:PRO:CD	2.66	0.44
1:D:297:LEU:CD1	1:D:318:ASN:HD21	2.31	0.44
1:D:528:ILE:O	1:D:531:LYS:N	2.51	0.44
1:D:650:HIS:O	1:D:653:THR:HB	2.18	0.44
1:A:183:LEU:N	1:A:183:LEU:HD23	2.32	0.44
1:A:319:ILE:HG23	1:A:320:PRO:HD2	1.98	0.44
1:A:629:ILE:O	1:A:630:THR:C	2.55	0.44
1:B:102:MET:CB	1:B:107:THR:HG21	2.35	0.44
1:B:172:GLN:H	1:B:172:GLN:NE2	2.16	0.44
1:B:564:ILE:HA	1:B:564:ILE:HD12	1.84	0.44
1:D:28:VAL:CB	1:D:98:PRO:HD3	2.48	0.44
1:D:233:TYR:O	1:D:235:ILE:HD12	2.18	0.44
1:D:265:SER:O	1:D:267:PRO:N	2.51	0.44
1:D:382:VAL:HG21	1:D:495:TYR:CD1	2.53	0.44
1:A:69:CYS:SG	1:A:82:TYR:CE1	3.11	0.44
1:A:233:TYR:O	1:A:235:ILE:HD12	2.18	0.44
1:A:286:THR:CG2	1:A:287:LEU:H	2.30	0.44
1:A:335:VAL:HG13	1:A:335:VAL:O	2.18	0.44
1:A:346:ALA:HB1	1:A:369:ASN:HB3	1.99	0.44
1:A:351:LEU:HG	1:A:353:VAL:CG2	2.46	0.44
1:B:315:PHE:CD1	1:B:316:GLN:N	2.86	0.44
1:B:337:THR:OG1	1:B:338:ARG:N	2.51	0.44
1:B:528:ILE:C	1:B:530:LYS:N	2.68	0.44
1:B:719:PHE:CD1	1:B:720:PHE:N	2.86	0.44
1:C:95:ILE:HG21	1:C:131:LEU:HD11	1.98	0.44
1:C:128:PHE:HE2	1:C:194:TYR:CE2	2.36	0.44
1:C:144:THR:HG22	1:C:145:LEU:N	2.33	0.44
1:C:443:LEU:O	1:C:444:ALA:C	2.56	0.44
1:C:719:PHE:CD1	1:C:720:PHE:N	2.86	0.44
1:D:180:ASP:O	1:D:182:GLY:N	2.51	0.44
1:D:226:CYS:O	1:D:227:LYS:HG2	2.17	0.44
1:D:260:VAL:O	1:D:261:SER:CB	2.65	0.44
1:D:306:ASP:OD1	1:D:307:SER:N	2.46	0.44
1:D:439:ASP:O	1:D:441:GLU:N	2.51	0.44
1:D:705:LEU:C	1:D:707:SER:N	2.70	0.44
1:D:716:GLU:HG2	1:D:721:MET:C	2.39	0.44
1:B:28:VAL:CB	1:B:98:PRO:HD3	2.48	0.43
1:B:478:PRO:O	1:B:479:TYR:HB2	2.18	0.43
1:C:9:ALA:CA	1:C:613:ILE:HD11	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:478:PRO:O	1:C:479:TYR:HB2	2.18	0.43
1:C:528:ILE:C	1:C:530:LYS:N	2.69	0.43
1:D:111:GLN:HG3	1:D:168:TYR:CE2	2.52	0.43
1:D:128:PHE:HE2	1:D:194:TYR:CE2	2.36	0.43
1:D:305:VAL:HG23	1:D:306:ASP:H	1.83	0.43
1:D:468:ASP:HB2	1:D:469:GLU:OE2	2.18	0.43
1:D:719:PHE:CD1	1:D:720:PHE:N	2.86	0.43
1:A:694:ASN:OD1	1:A:697:GLN:HG3	2.19	0.43
1:A:707:SER:O	1:A:710:TYR:N	2.50	0.43
1:B:71:HIS:CE1	1:B:478:PRO:N	2.86	0.43
1:B:128:PHE:HE2	1:B:194:TYR:CE2	2.36	0.43
1:B:233:TYR:O	1:B:235:ILE:HD12	2.18	0.43
1:C:293:LEU:HD22	1:C:297:LEU:CD1	2.45	0.43
1:C:319:ILE:HG23	1:C:320:PRO:HD2	1.99	0.43
1:C:496:ASN:HA	1:C:499:SER:HB3	1.99	0.43
1:D:110:ILE:O	1:D:111:GLN:NE2	2.51	0.43
1:D:382:VAL:HG12	1:D:384:LYS:H	1.83	0.43
1:D:541:PRO:HD2	1:D:544:MET:HE1	2.00	0.43
1:A:154:ASN:N	1:A:155:PRO:CD	2.80	0.43
1:A:293:LEU:HD22	1:A:297:LEU:CD1	2.45	0.43
1:A:323:LEU:CD1	1:A:329:TRP:HB2	2.40	0.43
1:A:559:GLU:O	1:A:560:ASN:HB2	2.17	0.43
1:B:18:PRO:HB3	1:B:417:THR:HG22	2.00	0.43
1:B:103:ASN:O	1:B:106:TYR:HB2	2.18	0.43
1:B:306:ASP:O	1:B:307:SER:CB	2.65	0.43
1:B:354:LEU:HD21	1:B:460:ALA:HB1	1.99	0.43
1:B:541:PRO:HD2	1:B:544:MET:HE1	2.01	0.43
1:B:637:PHE:CD2	1:B:651:ILE:HD11	2.52	0.43
1:C:18:PRO:HB3	1:C:417:THR:CG2	2.48	0.43
1:C:448:THR:O	1:C:452:ASP:OD2	2.36	0.43
1:C:533:LEU:CD1	1:C:729:ILE:HD11	2.49	0.43
1:D:53:GLY:HA3	1:D:71:HIS:HB3	2.00	0.43
1:D:443:LEU:O	1:D:444:ALA:C	2.56	0.43
1:A:402:GLY:O	1:A:403:ASP:O	2.36	0.43
1:A:443:LEU:O	1:A:444:ALA:C	2.56	0.43
1:A:496:ASN:HA	1:A:499:SER:HB3	1.99	0.43
1:B:61:LEU:HD12	1:B:62:LEU:H	1.83	0.43
1:B:184:LEU:HD11	1:B:196:PRO:CB	2.49	0.43
1:B:187:LYS:HE2	1:B:197:LEU:HD21	2.01	0.43
1:B:630:THR:HG22	1:B:634:LEU:HD11	2.00	0.43
1:C:61:LEU:HD12	1:C:62:LEU:H	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:559:GLU:O	1:D:560:ASN:HB2	2.18	0.43
1:A:177:PHE:CZ	1:A:234:LEU:HD21	2.40	0.43
1:A:533:LEU:CD1	1:A:729:ILE:HD11	2.49	0.43
1:A:673:CYS:O	1:A:677:GLU:HG2	2.18	0.43
1:B:439:ASP:O	1:B:441:GLU:N	2.51	0.43
1:C:245:ILE:HG21	1:C:311:LEU:HD22	1.98	0.43
1:C:665:LEU:O	1:C:668:TYR:HB3	2.17	0.43
1:D:100:ALA:O	1:D:124:LYS:HG3	2.19	0.43
1:D:102:MET:CB	1:D:107:THR:HG21	2.36	0.43
1:D:608:ASP:HB2	1:D:691:LYS:HZ3	1.81	0.43
1:D:707:SER:O	1:D:710:TYR:N	2.51	0.43
1:A:28:VAL:CB	1:A:98:PRO:HD3	2.48	0.43
1:A:100:ALA:O	1:A:124:LYS:HG3	2.18	0.43
1:A:104:GLN:C	1:A:106:TYR:N	2.71	0.43
1:B:297:LEU:CD1	1:B:318:ASN:HD21	2.31	0.43
1:B:430:ASN:O	1:B:432:ILE:HG13	2.18	0.43
1:B:694:ASN:CG	1:B:697:GLN:HG3	2.38	0.43
1:B:697:GLN:O	1:B:700:ALA:HB3	2.19	0.43
1:C:9:ALA:HA	1:C:613:ILE:HD11	2.00	0.43
1:C:103:ASN:O	1:C:106:TYR:HB2	2.19	0.43
1:C:111:GLN:HG3	1:C:168:TYR:CE2	2.53	0.43
1:D:9:ALA:CA	1:D:613:ILE:HD11	2.48	0.43
1:D:297:LEU:HD13	1:D:318:ASN:ND2	2.33	0.43
1:D:315:PHE:CD1	1:D:316:GLN:N	2.87	0.43
1:A:128:PHE:HE2	1:A:194:TYR:CE2	2.37	0.43
1:A:667:LEU:HD22	1:C:723:PHE:HE2	1.75	0.43
1:B:73:SER:HB3	1:B:78:LEU:N	2.30	0.43
1:B:137:PHE:CG	1:B:137:PHE:O	2.71	0.43
1:B:228:LEU:HA	1:B:233:TYR:O	2.19	0.43
1:B:243:LEU:HD23	1:B:259:MET:HE3	2.01	0.43
1:B:448:THR:O	1:B:452:ASP:OD2	2.37	0.43
1:B:572:ASP:O	1:B:575:ASN:HB2	2.18	0.43
1:B:719:PHE:O	1:B:722:THR:N	2.51	0.43
1:C:439:ASP:O	1:C:441:GLU:N	2.51	0.43
1:C:651:ILE:O	1:C:653:THR:N	2.52	0.43
1:D:73:SER:CB	1:D:78:LEU:H	2.31	0.43
1:D:103:ASN:O	1:D:106:TYR:HB2	2.19	0.43
1:D:572:ASP:O	1:D:575:ASN:HB2	2.18	0.43
1:A:22:ASN:HD21	1:A:91:LYS:HD3	1.84	0.43
1:A:61:LEU:HD12	1:A:62:LEU:H	1.82	0.43
1:A:547:VAL:HG22	1:A:644:THR:CG2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:719:PHE:O	1:A:722:THR:N	2.51	0.43
1:C:73:SER:O	1:C:76:SER:N	2.48	0.43
1:C:477:GLN:O	1:C:480:ASN:HB2	2.19	0.43
1:C:547:VAL:HG22	1:C:644:THR:CG2	2.48	0.43
1:C:616:LEU:HD22	1:C:676:ALA:HB2	2.00	0.43
1:D:22:ASN:HD22	1:D:91:LYS:HB2	1.84	0.43
1:D:61:LEU:HD12	1:D:62:LEU:H	1.84	0.43
1:D:457:PHE:CG	1:D:477:GLN:HG2	2.53	0.43
1:D:477:GLN:O	1:D:480:ASN:HB2	2.18	0.43
1:D:657:LEU:O	1:D:660:LYS:N	2.52	0.43
1:A:244:LYS:HD3	1:A:253:LEU:HD22	2.00	0.43
1:A:287:LEU:HD12	1:A:288:VAL:H	1.84	0.43
1:A:382:VAL:HG12	1:A:384:LYS:H	1.84	0.43
1:A:406:ARG:C	1:A:408:PHE:N	2.70	0.43
1:A:457:PHE:CG	1:A:477:GLN:HG2	2.54	0.43
1:B:227:LYS:HG3	1:B:282:LEU:HD22	2.01	0.43
1:C:335:VAL:HG13	1:C:335:VAL:O	2.19	0.43
1:D:73:SER:HB3	1:D:78:LEU:N	2.30	0.43
1:A:14:TYR:OH	1:A:613:ILE:HA	2.19	0.43
1:A:111:GLN:HG3	1:A:168:TYR:CE2	2.54	0.43
1:A:199:PHE:HB3	1:A:251:PHE:O	2.19	0.43
1:A:226:CYS:O	1:A:227:LYS:HG2	2.19	0.43
1:A:439:ASP:O	1:A:441:GLU:N	2.51	0.43
1:A:535:ILE:CG2	1:A:655:LEU:HD13	2.49	0.43
1:A:535:ILE:HG21	1:A:655:LEU:HD13	2.00	0.43
1:B:27:TYR:N	1:B:27:TYR:CD1	2.87	0.43
1:B:250:SER:O	1:B:251:PHE:HB2	2.18	0.43
1:B:483:LEU:HD23	1:B:483:LEU:C	2.39	0.43
1:B:602:ILE:HG22	1:B:602:ILE:O	2.18	0.43
1:B:705:LEU:C	1:B:707:SER:N	2.71	0.43
1:C:177:PHE:CD1	1:C:183:LEU:HB3	2.54	0.43
1:C:187:LYS:HE2	1:C:197:LEU:HD21	2.01	0.43
1:C:246:TRP:HA	1:C:253:LEU:HA	2.00	0.43
1:C:270:PHE:HE2	1:C:292:PRO:HG2	1.84	0.43
1:C:528:ILE:O	1:C:531:LYS:N	2.52	0.43
1:D:398:VAL:CG2	1:D:669:ARG:HH12	2.32	0.43
1:D:402:GLY:O	1:D:403:ASP:O	2.37	0.43
1:D:637:PHE:CD2	1:D:651:ILE:HD11	2.52	0.43
1:A:564:ILE:HD12	1:A:564:ILE:HA	1.84	0.42
1:A:602:ILE:O	1:A:602:ILE:HG22	2.18	0.42
1:B:185:GLY:O	1:B:196:PRO:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:ILE:HG21	1:B:311:LEU:CD2	2.49	0.42
1:B:348:TYR:HB3	1:B:368:VAL:HG23	2.01	0.42
1:B:443:LEU:O	1:B:444:ALA:C	2.57	0.42
1:C:71:HIS:CE1	1:C:478:PRO:N	2.87	0.42
1:C:270:PHE:C	1:C:270:PHE:CD2	2.91	0.42
1:C:297:LEU:CD1	1:C:318:ASN:HD21	2.31	0.42
1:C:402:GLY:O	1:C:403:ASP:O	2.37	0.42
1:C:630:THR:HG22	1:C:634:LEU:HD11	2.00	0.42
1:C:705:LEU:O	1:C:706:ASN:C	2.58	0.42
1:C:727:TYR:HB3	1:C:728:ILE:H	1.70	0.42
1:D:187:LYS:HE2	1:D:197:LEU:HD21	2.01	0.42
1:D:528:ILE:C	1:D:530:LYS:N	2.69	0.42
1:D:602:ILE:O	1:D:602:ILE:HG22	2.18	0.42
1:D:694:ASN:CG	1:D:697:GLN:HG3	2.38	0.42
1:A:18:PRO:N	1:A:417:THR:HG21	2.33	0.42
1:A:398:VAL:CG2	1:A:669:ARG:HH12	2.33	0.42
1:B:287:LEU:HD12	1:B:288:VAL:H	1.84	0.42
1:B:335:VAL:O	1:B:335:VAL:HG13	2.18	0.42
1:B:406:ARG:C	1:B:408:PHE:N	2.71	0.42
1:B:468:ASP:HB2	1:B:469:GLU:OE2	2.19	0.42
1:B:705:LEU:O	1:B:709:VAL:HG23	2.18	0.42
1:C:398:VAL:HG21	1:C:665:LEU:HD13	2.01	0.42
1:C:406:ARG:C	1:C:408:PHE:N	2.71	0.42
1:D:104:GLN:C	1:D:106:TYR:N	2.72	0.42
1:D:255:GLN:OE1	1:D:257:TYR:HE2	2.02	0.42
1:A:12:LEU:HD13	1:A:18:PRO:O	2.18	0.42
1:A:187:LYS:HE2	1:A:197:LEU:HD21	2.01	0.42
1:A:564:ILE:O	1:A:567:LEU:HB3	2.19	0.42
1:B:104:GLN:C	1:B:106:TYR:N	2.71	0.42
1:B:187:LYS:CE	1:B:197:LEU:HD21	2.49	0.42
1:B:226:CYS:O	1:B:227:LYS:HG2	2.19	0.42
1:B:398:VAL:CB	1:B:669:ARG:NH1	2.58	0.42
1:B:436:HIS:C	1:B:438:GLU:H	2.22	0.42
1:B:616:LEU:HD22	1:B:676:ALA:HB2	2.00	0.42
1:B:665:LEU:O	1:B:668:TYR:HB3	2.18	0.42
1:C:12:LEU:HD13	1:C:18:PRO:O	2.18	0.42
1:C:104:GLN:C	1:C:106:TYR:N	2.72	0.42
1:C:110:ILE:O	1:C:111:GLN:NE2	2.52	0.42
1:C:172:GLN:H	1:C:172:GLN:NE2	2.16	0.42
1:C:430:ASN:N	1:C:430:ASN:ND2	2.66	0.42
1:C:441:GLU:O	1:C:445:ASN:ND2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:VAL:CG1	1:D:177:PHE:N	2.78	0.42
1:D:184:LEU:HD11	1:D:196:PRO:CB	2.50	0.42
1:D:367:ASN:HB3	1:D:377:GLU:O	2.20	0.42
1:D:705:LEU:O	1:D:706:ASN:C	2.57	0.42
1:D:719:PHE:O	1:D:722:THR:N	2.52	0.42
1:A:64:ASN:OD1	1:A:64:ASN:N	2.48	0.42
1:B:73:SER:CB	1:B:78:LEU:H	2.32	0.42
1:B:297:LEU:HD13	1:B:318:ASN:ND2	2.34	0.42
1:C:64:ASN:OD1	1:C:64:ASN:N	2.48	0.42
1:C:187:LYS:CE	1:C:197:LEU:HD21	2.50	0.42
1:C:287:LEU:HD12	1:C:288:VAL:H	1.85	0.42
1:C:430:ASN:O	1:C:432:ILE:HG13	2.19	0.42
1:C:602:ILE:O	1:C:602:ILE:HG22	2.18	0.42
1:D:137:PHE:O	1:D:137:PHE:CG	2.71	0.42
1:D:228:LEU:HA	1:D:233:TYR:O	2.20	0.42
1:D:354:LEU:HD21	1:D:460:ALA:HB1	2.00	0.42
1:A:53:GLY:HA3	1:A:71:HIS:HB3	2.02	0.42
1:A:254:ILE:CB	1:A:311:LEU:HD12	2.49	0.42
1:A:310:ILE:HG22	1:A:310:ILE:O	2.19	0.42
1:B:177:PHE:CD1	1:B:183:LEU:HB3	2.55	0.42
1:B:651:ILE:O	1:B:653:THR:N	2.52	0.42
1:C:468:ASP:HB2	1:C:469:GLU:OE2	2.20	0.42
1:D:27:TYR:N	1:D:27:TYR:CD1	2.88	0.42
1:D:340:LEU:CD2	1:D:342:LEU:HD21	2.39	0.42
1:A:619:LEU:HD11	1:A:623:LEU:HD11	2.01	0.42
1:B:245:ILE:HG21	1:B:311:LEU:HD22	2.01	0.42
1:B:707:SER:O	1:B:710:TYR:N	2.53	0.42
1:C:69:CYS:SG	1:C:82:TYR:CE1	3.12	0.42
1:C:187:LYS:HD3	1:C:197:LEU:HD21	2.02	0.42
1:C:323:LEU:CD1	1:C:329:TRP:HB2	2.41	0.42
1:C:337:THR:OG1	1:C:338:ARG:N	2.51	0.42
1:D:466:TYR:O	1:D:470:ILE:HB	2.19	0.42
1:A:102:MET:CB	1:A:107:THR:HG21	2.36	0.42
1:A:297:LEU:CD1	1:A:318:ASN:HD21	2.32	0.42
1:A:337:THR:OG1	1:A:338:ARG:N	2.51	0.42
1:A:441:GLU:O	1:A:445:ASN:ND2	2.53	0.42
1:A:542:ASP:O	1:A:543:SER:C	2.57	0.42
1:A:568:LYS:HZ2	1:D:210:ARG:NH2	2.15	0.42
1:B:53:GLY:HA3	1:B:71:HIS:HB3	2.02	0.42
1:B:367:ASN:HB3	1:B:377:GLU:O	2.20	0.42
1:B:430:ASN:N	1:B:430:ASN:ND2	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:466:TYR:O	1:B:470:ILE:HB	2.20	0.42
1:B:705:LEU:O	1:B:706:ASN:C	2.58	0.42
1:C:367:ASN:HB3	1:C:377:GLU:O	2.19	0.42
1:C:559:GLU:O	1:C:560:ASN:HB2	2.18	0.42
1:C:596:PHE:C	1:C:598:LYS:N	2.73	0.42
1:D:177:PHE:CD1	1:D:183:LEU:HB3	2.55	0.42
1:D:342:LEU:HD23	1:D:342:LEU:N	2.35	0.42
1:D:348:TYR:HB3	1:D:368:VAL:HG23	2.01	0.42
1:D:630:THR:HG22	1:D:634:LEU:HD11	2.01	0.42
1:D:694:ASN:N	1:D:697:GLN:HE21	2.18	0.42
1:A:73:SER:O	1:A:76:SER:N	2.49	0.42
1:A:110:ILE:O	1:A:111:GLN:NE2	2.53	0.42
1:A:430:ASN:N	1:A:430:ASN:ND2	2.66	0.42
1:A:536:ILE:HD11	1:A:655:LEU:CB	2.49	0.42
1:A:549:LYS:O	1:A:552:ASP:N	2.53	0.42
1:A:596:PHE:C	1:A:598:LYS:N	2.73	0.42
1:B:441:GLU:O	1:B:445:ASN:ND2	2.53	0.42
1:C:102:MET:CB	1:C:107:THR:HG21	2.36	0.42
1:C:466:TYR:O	1:C:470:ILE:HB	2.19	0.42
1:C:690:VAL:CG1	1:C:691:LYS:H	2.33	0.42
1:D:9:ALA:HA	1:D:613:ILE:HD11	2.00	0.42
1:D:185:GLY:O	1:D:196:PRO:HA	2.20	0.42
1:D:550:PHE:CD2	1:D:638:VAL:HG12	2.55	0.42
1:D:651:ILE:O	1:D:653:THR:N	2.52	0.42
1:D:665:LEU:O	1:D:668:TYR:HB3	2.19	0.42
1:A:24:VAL:CG2	1:A:93:ILE:HG12	2.50	0.42
1:A:187:LYS:HD3	1:A:197:LEU:HD21	2.02	0.42
1:A:187:LYS:CE	1:A:197:LEU:HD21	2.50	0.42
1:A:250:SER:O	1:A:251:PHE:HB2	2.19	0.42
1:A:670:GLN:HG3	1:C:727:TYR:CZ	2.55	0.42
1:B:69:CYS:SG	1:B:82:TYR:CE1	3.13	0.42
1:B:176:VAL:CG1	1:B:177:PHE:N	2.79	0.42
1:B:255:GLN:OE1	1:B:257:TYR:HE2	2.03	0.42
1:B:382:VAL:HG12	1:B:384:LYS:H	1.84	0.42
1:C:323:LEU:HD11	1:C:355:TRP:CE3	2.55	0.42
1:C:346:ALA:HB3	1:C:369:ASN:HD22	1.85	0.42
1:C:354:LEU:HD21	1:C:460:ALA:HB1	2.01	0.42
1:C:637:PHE:CD2	1:C:651:ILE:HG12	2.55	0.42
1:D:287:LEU:HD12	1:D:288:VAL:H	1.85	0.42
1:D:430:ASN:N	1:D:430:ASN:ND2	2.66	0.42
1:D:553:ILE:O	1:D:553:ILE:CG2	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:673:CYS:O	1:D:677:GLU:HG2	2.20	0.42
1:A:228:LEU:HA	1:A:233:TYR:O	2.20	0.42
1:A:317:ASN:ND2	1:A:319:ILE:CG1	2.70	0.42
1:A:340:LEU:O	1:A:341:GLU:CB	2.68	0.42
1:A:348:TYR:HB3	1:A:368:VAL:HG23	2.01	0.42
1:A:541:PRO:HD2	1:A:544:MET:HE1	2.01	0.42
1:B:110:ILE:O	1:B:111:GLN:NE2	2.53	0.42
1:B:187:LYS:HD3	1:B:197:LEU:HD21	2.01	0.42
1:B:637:PHE:CD2	1:B:651:ILE:HG12	2.55	0.42
1:C:24:VAL:CG2	1:C:93:ILE:HG12	2.50	0.42
1:C:124:LYS:C	1:C:126:GLY:H	2.23	0.42
1:C:237:LEU:CD1	1:C:241:CYS:HA	2.50	0.42
1:C:254:ILE:CG2	1:C:311:LEU:HB2	2.45	0.42
1:C:290:LEU:HD13	1:C:298:PHE:CE1	2.55	0.42
1:C:436:HIS:CD2	1:C:438:GLU:HB2	2.55	0.42
1:C:564:ILE:O	1:C:567:LEU:HB3	2.20	0.42
1:D:263:SER:O	1:D:264:ASP:C	2.57	0.42
1:D:334:LEU:CD1	1:D:351:LEU:HD11	2.37	0.42
1:D:566:ASN:HA	1:D:569:ILE:CD1	2.50	0.42
1:A:367:ASN:HB3	1:A:377:GLU:O	2.20	0.41
1:A:411:LEU:O	1:A:415:TYR:HB2	2.20	0.41
1:A:423:ALA:HB2	1:A:453:VAL:HG21	2.02	0.41
1:A:637:PHE:CD2	1:A:651:ILE:HG12	2.55	0.41
1:B:103:ASN:H	1:B:107:THR:HG23	1.80	0.41
1:B:227:LYS:CG	1:B:282:LEU:HD22	2.49	0.41
1:B:323:LEU:HD11	1:B:355:TRP:CE3	2.55	0.41
1:C:18:PRO:HB3	1:C:417:THR:HG22	2.01	0.41
1:C:53:GLY:HA3	1:C:71:HIS:HB3	2.02	0.41
1:C:541:PRO:HD2	1:C:544:MET:HE1	2.02	0.41
1:D:12:LEU:HD13	1:D:18:PRO:O	2.19	0.41
1:D:69:CYS:SG	1:D:82:TYR:CE1	3.13	0.41
1:D:536:ILE:HD11	1:D:655:LEU:CB	2.50	0.41
1:A:124:LYS:C	1:A:126:GLY:H	2.23	0.41
1:A:572:ASP:O	1:A:575:ASN:HB2	2.19	0.41
1:A:727:TYR:HB3	1:A:728:ILE:H	1.71	0.41
1:B:402:GLY:O	1:B:403:ASP:O	2.38	0.41
1:B:457:PHE:CG	1:B:477:GLN:HG2	2.55	0.41
1:B:530:LYS:O	1:B:533:LEU:HB2	2.19	0.41
1:B:620:HIS:CD2	1:B:668:TYR:CD2	3.07	0.41
1:C:291:LEU:N	1:C:297:LEU:O	2.53	0.41
1:C:348:TYR:HB3	1:C:368:VAL:HG23	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:542:ASP:O	1:C:543:SER:C	2.57	0.41
1:C:591:MET:HB3	1:C:591:MET:HE2	1.91	0.41
1:C:707:SER:O	1:C:710:TYR:N	2.52	0.41
1:D:184:LEU:O	1:D:199:PHE:CE1	2.73	0.41
1:D:237:LEU:CD1	1:D:241:CYS:HA	2.50	0.41
1:D:535:ILE:HG21	1:D:655:LEU:HD13	2.02	0.41
1:A:237:LEU:CD1	1:A:241:CYS:HA	2.50	0.41
1:A:244:LYS:HE2	1:A:256:ASP:OD1	2.19	0.41
1:A:290:LEU:HD13	1:A:298:PHE:CE1	2.56	0.41
1:A:386:LEU:O	1:A:390:GLN:HG3	2.20	0.41
1:A:430:ASN:O	1:A:432:ILE:HG13	2.20	0.41
1:A:530:LYS:O	1:A:533:LEU:HB2	2.20	0.41
1:A:694:ASN:N	1:A:697:GLN:HE21	2.18	0.41
1:A:705:LEU:O	1:A:709:VAL:HG23	2.20	0.41
1:B:55:GLU:HB3	1:B:56:TYR:H	1.74	0.41
1:B:124:LYS:C	1:B:126:GLY:H	2.23	0.41
1:B:184:LEU:O	1:B:199:PHE:CE1	2.73	0.41
1:B:423:ALA:HB2	1:B:453:VAL:HG21	2.01	0.41
1:B:616:LEU:HD11	1:B:675:LEU:CD2	2.50	0.41
1:B:694:ASN:N	1:B:697:GLN:HE21	2.18	0.41
1:C:182:GLY:C	1:C:183:LEU:HD23	2.41	0.41
1:C:297:LEU:HD13	1:C:318:ASN:ND2	2.34	0.41
1:C:549:LYS:O	1:C:552:ASP:N	2.54	0.41
1:C:673:CYS:O	1:C:677:GLU:HG2	2.20	0.41
1:D:24:VAL:CG2	1:D:93:ILE:HG12	2.50	0.41
1:D:71:HIS:CE1	1:D:478:PRO:HB3	2.55	0.41
1:D:71:HIS:CE1	1:D:478:PRO:N	2.88	0.41
1:D:187:LYS:CE	1:D:197:LEU:HD21	2.50	0.41
1:D:406:ARG:C	1:D:408:PHE:N	2.72	0.41
1:D:530:LYS:O	1:D:533:LEU:HB2	2.20	0.41
1:A:58:ASN:HA	1:A:474:ASN:HD22	1.81	0.41
1:A:177:PHE:CD1	1:A:183:LEU:HB3	2.55	0.41
1:A:184:LEU:HD11	1:A:196:PRO:CB	2.50	0.41
1:A:184:LEU:O	1:A:199:PHE:CE1	2.73	0.41
1:A:255:GLN:OE1	1:A:257:TYR:HE2	2.03	0.41
1:A:291:LEU:N	1:A:297:LEU:O	2.53	0.41
1:A:651:ILE:O	1:A:654:LEU:N	2.52	0.41
1:B:22:ASN:HD21	1:B:91:LYS:HD3	1.86	0.41
1:B:73:SER:O	1:B:76:SER:N	2.50	0.41
1:B:237:LEU:CD1	1:B:241:CYS:HA	2.50	0.41
1:B:535:ILE:HG21	1:B:655:LEU:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:550:PHE:CD2	1:B:638:VAL:HG12	2.56	0.41
1:B:553:ILE:O	1:B:553:ILE:CG2	2.61	0.41
1:C:22:ASN:HD21	1:C:91:LYS:HD3	1.86	0.41
1:C:99:ASN:O	1:C:100:ALA:O	2.39	0.41
1:C:697:GLN:O	1:C:700:ALA:HB3	2.20	0.41
1:D:55:GLU:HB3	1:D:56:TYR:H	1.75	0.41
1:D:268:SER:OG	1:D:269:HIS:N	2.54	0.41
1:D:436:HIS:C	1:D:438:GLU:H	2.24	0.41
1:A:77:THR:O	1:A:97:LEU:HB2	2.20	0.41
1:A:483:LEU:C	1:A:483:LEU:HD23	2.41	0.41
1:A:630:THR:HG22	1:A:634:LEU:HD11	2.01	0.41
1:A:667:LEU:HD22	1:C:723:PHE:CD2	2.54	0.41
1:A:690:VAL:CG1	1:A:691:LYS:H	2.34	0.41
1:A:705:LEU:C	1:A:707:SER:N	2.69	0.41
1:B:22:ASN:HD22	1:B:91:LYS:HB2	1.86	0.41
1:B:77:THR:O	1:B:97:LEU:HB2	2.21	0.41
1:B:199:PHE:HA	1:B:251:PHE:HB3	2.03	0.41
1:C:22:ASN:HD22	1:C:91:LYS:HB2	1.84	0.41
1:C:262:GLN:OE1	1:C:315:PHE:HB2	2.21	0.41
1:C:366:LEU:HD13	1:C:378:TRP:CE2	2.56	0.41
1:C:535:ILE:HG21	1:C:655:LEU:HD13	2.01	0.41
1:C:563:GLU:HB3	1:C:565:THR:HG22	2.02	0.41
1:D:291:LEU:N	1:D:297:LEU:O	2.53	0.41
1:A:22:ASN:ND2	1:A:91:LYS:HD3	2.35	0.41
1:A:466:TYR:O	1:A:470:ILE:HB	2.20	0.41
1:B:24:VAL:CG2	1:B:93:ILE:HG12	2.50	0.41
1:B:342:LEU:HD23	1:B:342:LEU:N	2.36	0.41
1:B:605:ILE:CG1	1:B:606:LYS:H	2.19	0.41
1:C:228:LEU:HA	1:C:233:TYR:O	2.21	0.41
1:C:317:ASN:ND2	1:C:319:ILE:CG1	2.71	0.41
1:C:535:ILE:CG2	1:C:655:LEU:HD13	2.51	0.41
1:C:549:LYS:O	1:C:552:ASP:HB3	2.20	0.41
1:C:694:ASN:OD1	1:C:697:GLN:HG3	2.21	0.41
1:C:719:PHE:O	1:C:722:THR:N	2.53	0.41
1:D:73:SER:O	1:D:76:SER:N	2.50	0.41
1:D:323:LEU:HD11	1:D:355:TRP:CE3	2.55	0.41
1:D:405:GLU:CD	1:D:437:ASN:ND2	2.74	0.41
1:D:563:GLU:HB3	1:D:565:THR:HG22	2.02	0.41
1:A:182:GLY:C	1:A:183:LEU:HD23	2.41	0.41
1:B:657:LEU:O	1:B:660:LYS:N	2.54	0.41
1:C:28:VAL:HG13	1:C:150:PHE:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:GLU:HB3	1:C:56:TYR:H	1.75	0.41
1:C:184:LEU:HD11	1:C:196:PRO:CB	2.50	0.41
1:C:185:GLY:O	1:C:196:PRO:HA	2.21	0.41
1:C:199:PHE:HA	1:C:251:PHE:HB3	2.03	0.41
1:C:396:ASP:OD2	1:C:399:THR:OG1	2.36	0.41
1:D:679:LEU:O	1:D:680:LEU:HD12	2.21	0.41
1:A:27:TYR:N	1:A:27:TYR:CD1	2.87	0.41
1:A:73:SER:HB3	1:A:78:LEU:N	2.30	0.41
1:A:270:PHE:CD2	1:A:270:PHE:C	2.94	0.41
1:A:297:LEU:HD13	1:A:318:ASN:ND2	2.34	0.41
1:A:468:ASP:HB2	1:A:469:GLU:OE2	2.21	0.41
1:B:165:PHE:HB3	1:B:177:PHE:HB2	2.03	0.41
1:B:291:LEU:N	1:B:297:LEU:O	2.53	0.41
1:B:398:VAL:HG21	1:B:665:LEU:HD13	2.02	0.41
1:B:614:ILE:HD13	1:B:614:ILE:HA	1.89	0.41
1:B:673:CYS:O	1:B:677:GLU:HG2	2.21	0.41
1:C:124:LYS:C	1:C:126:GLY:N	2.74	0.41
1:C:322:ASN:OD1	1:C:322:ASN:N	2.50	0.41
1:C:637:PHE:CD2	1:C:651:ILE:HD11	2.53	0.41
1:D:286:THR:CG2	1:D:287:LEU:H	2.30	0.41
1:D:535:ILE:CG2	1:D:655:LEU:HD13	2.51	0.41
1:A:71:HIS:CE1	1:A:478:PRO:N	2.89	0.41
1:A:133:LEU:HA	1:A:134:PRO:HD3	1.98	0.41
1:A:185:GLY:O	1:A:196:PRO:HA	2.21	0.41
1:A:563:GLU:HB3	1:A:565:THR:HG22	2.03	0.41
1:A:665:LEU:O	1:A:668:TYR:HB3	2.21	0.41
1:B:71:HIS:CE1	1:B:478:PRO:HB3	2.56	0.41
1:B:307:SER:O	1:B:308:SER:C	2.58	0.41
1:B:346:ALA:HB3	1:B:369:ASN:HD22	1.85	0.41
1:B:536:ILE:HD11	1:B:655:LEU:CB	2.51	0.41
1:B:549:LYS:O	1:B:552:ASP:HB3	2.21	0.41
1:B:563:GLU:HB3	1:B:565:THR:HG22	2.03	0.41
1:B:566:ASN:HA	1:B:569:ILE:CD1	2.51	0.41
1:B:596:PHE:C	1:B:598:LYS:N	2.73	0.41
1:B:679:LEU:O	1:B:680:LEU:HD12	2.21	0.41
1:C:25:ASP:OD1	1:C:94:ASN:HB2	2.21	0.41
1:C:58:ASN:HA	1:C:474:ASN:HD22	1.81	0.41
1:C:100:ALA:O	1:C:124:LYS:HG3	2.20	0.41
1:C:184:LEU:O	1:C:199:PHE:CE1	2.73	0.41
1:C:283:TYR:N	1:C:336:LEU:HD23	2.36	0.41
1:C:340:LEU:O	1:C:341:GLU:CB	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:423:ALA:HB2	1:C:453:VAL:HG21	2.03	0.41
1:C:620:HIS:CD2	1:C:668:TYR:CD2	3.09	0.41
1:D:11:LEU:HD23	1:D:11:LEU:HA	1.82	0.41
1:D:77:THR:O	1:D:97:LEU:HB2	2.21	0.41
1:D:103:ASN:H	1:D:107:THR:HG23	1.81	0.41
1:D:124:LYS:C	1:D:126:GLY:H	2.23	0.41
1:D:187:LYS:HD3	1:D:197:LEU:HD21	2.02	0.41
1:D:283:TYR:N	1:D:336:LEU:HD23	2.36	0.41
1:D:547:VAL:HG22	1:D:644:THR:CG2	2.48	0.41
1:D:564:ILE:O	1:D:567:LEU:HB3	2.21	0.41
1:D:569:ILE:H	1:D:569:ILE:HG13	1.67	0.41
1:A:346:ALA:HB3	1:A:369:ASN:HD22	1.86	0.41
1:A:549:LYS:O	1:A:552:ASP:HB3	2.21	0.41
1:B:10:ASN:O	1:B:13:GLN:HB2	2.21	0.41
1:B:182:GLY:C	1:B:183:LEU:HD23	2.42	0.41
1:B:247:ASP:OD1	1:B:249:THR:HB	2.21	0.41
1:B:283:TYR:N	1:B:336:LEU:HD23	2.36	0.41
1:B:398:VAL:CG2	1:B:669:ARG:HH12	2.34	0.41
1:C:73:SER:O	1:C:74:SER:C	2.59	0.41
1:C:352:ILE:HG22	1:C:463:ILE:CD1	2.51	0.41
1:C:398:VAL:CG2	1:C:669:ARG:HH12	2.34	0.41
1:D:340:LEU:O	1:D:341:GLU:CB	2.69	0.41
1:D:430:ASN:O	1:D:432:ILE:HG13	2.20	0.41
1:D:549:LYS:O	1:D:552:ASP:HB3	2.21	0.41
1:A:478:PRO:O	1:A:479:TYR:HB2	2.21	0.40
1:A:674:LEU:HB3	1:C:723:PHE:CE1	2.56	0.40
1:B:91:LYS:HE2	1:B:91:LYS:HB3	1.94	0.40
1:B:386:LEU:O	1:B:390:GLN:HG3	2.20	0.40
1:C:22:ASN:ND2	1:C:91:LYS:HD3	2.36	0.40
1:C:82:TYR:CD1	1:C:82:TYR:C	2.95	0.40
1:C:260:VAL:O	1:C:261:SER:HB3	2.21	0.40
1:C:608:ASP:HB2	1:C:691:LYS:HZ3	1.84	0.40
1:D:22:ASN:HD21	1:D:91:LYS:HD3	1.87	0.40
1:D:423:ALA:HB2	1:D:453:VAL:HG21	2.02	0.40
1:D:534:ASP:C	1:D:536:ILE:N	2.75	0.40
1:D:596:PHE:C	1:D:598:LYS:N	2.74	0.40
1:D:620:HIS:CD2	1:D:668:TYR:CD2	3.08	0.40
1:D:663:LEU:HD12	1:D:729:ILE:HD12	2.03	0.40
1:A:124:LYS:C	1:A:126:GLY:N	2.75	0.40
1:A:161:ARG:NH2	1:A:178:LEU:HD12	2.36	0.40
1:A:657:LEU:O	1:A:660:LYS:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:701:TYR:O	1:A:702:ILE:C	2.59	0.40
1:B:694:ASN:OD1	1:B:697:GLN:HG3	2.21	0.40
1:C:73:SER:HB3	1:C:78:LEU:N	2.31	0.40
1:C:133:LEU:HA	1:C:134:PRO:HD3	1.98	0.40
1:C:199:PHE:HD2	1:C:251:PHE:HA	1.86	0.40
1:D:182:GLY:C	1:D:183:LEU:HD23	2.42	0.40
1:A:283:TYR:N	1:A:336:LEU:HD23	2.36	0.40
1:A:366:LEU:HD13	1:A:378:TRP:CE2	2.56	0.40
1:B:124:LYS:C	1:B:126:GLY:N	2.74	0.40
1:B:265:SER:O	1:B:266:ASP:C	2.59	0.40
1:B:663:LEU:HD12	1:B:729:ILE:HD12	2.03	0.40
1:B:690:VAL:CG1	1:B:691:LYS:H	2.32	0.40
1:B:693:PHE:CA	1:B:697:GLN:NE2	2.84	0.40
1:C:165:PHE:CD2	1:C:177:PHE:CD2	3.05	0.40
1:C:566:ASN:HA	1:C:569:ILE:CD1	2.51	0.40
1:D:290:LEU:HD13	1:D:298:PHE:CE1	2.56	0.40
1:D:441:GLU:O	1:D:445:ASN:ND2	2.55	0.40
1:D:540:LEU:HD23	1:D:544:MET:HE1	2.03	0.40
1:D:604:ALA:CB	1:D:691:LYS:HE2	2.50	0.40
1:D:616:LEU:HD11	1:D:675:LEU:HD23	2.04	0.40
1:D:632:GLN:O	1:D:635:LEU:HB3	2.21	0.40
1:A:723:PHE:CD2	1:C:667:LEU:HD22	2.55	0.40
1:A:723:PHE:HE2	1:C:667:LEU:HD22	1.78	0.40
1:B:286:THR:CG2	1:B:287:LEU:H	2.31	0.40
1:B:530:LYS:HE2	1:B:530:LYS:CA	2.50	0.40
1:B:564:ILE:O	1:B:567:LEU:HB3	2.21	0.40
1:B:616:LEU:HD11	1:B:675:LEU:HD23	2.04	0.40
1:C:114:GLU:O	1:C:115:GLN:HB2	2.22	0.40
1:C:161:ARG:NH2	1:C:178:LEU:HD12	2.37	0.40
1:C:165:PHE:HB3	1:C:177:PHE:HB2	2.04	0.40
1:C:657:LEU:O	1:C:660:LYS:N	2.55	0.40
1:C:663:LEU:HD12	1:C:729:ILE:HD12	2.03	0.40
1:D:124:LYS:C	1:D:126:GLY:N	2.74	0.40
1:A:165:PHE:CD2	1:A:177:PHE:CD2	3.06	0.40
1:A:352:ILE:HG22	1:A:463:ILE:CD1	2.52	0.40
1:A:614:ILE:HD13	1:A:614:ILE:HA	1.92	0.40
1:A:663:LEU:HD12	1:A:729:ILE:HD12	2.03	0.40
1:A:693:PHE:CA	1:A:697:GLN:NE2	2.85	0.40
1:A:727:TYR:CZ	1:C:670:GLN:HG3	2.57	0.40
1:B:12:LEU:HD13	1:B:18:PRO:O	2.21	0.40
1:B:184:LEU:HD11	1:B:196:PRO:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:549:LYS:O	1:B:552:ASP:N	2.54	0.40
1:C:324:SER:O	1:C:325:ALA:C	2.60	0.40
1:C:572:ASP:O	1:C:575:ASN:HB2	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	702/729 (96%)	463 (66%)	169 (24%)	70 (10%)	0	2
1	B	702/729 (96%)	469 (67%)	159 (23%)	74 (10%)	0	2
1	C	702/729 (96%)	467 (66%)	165 (24%)	70 (10%)	0	2
1	D	702/729 (96%)	469 (67%)	165 (24%)	68 (10%)	0	2
All	All	2808/2916 (96%)	1868 (66%)	658 (23%)	282 (10%)	0	2

All (282) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	ALA
1	A	104	GLN
1	A	113	VAL
1	A	214	ARG
1	A	241	CYS
1	A	256	ASP
1	A	261	SER
1	A	264	ASP
1	A	267	PRO
1	A	268	SER
1	A	284	ASN
1	A	307	SER

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Mol	Chain	Res	Type
1	A	324	SER
1	A	338	ARG
1	A	341	GLU
1	A	403	ASP
1	A	417	THR
1	A	435	ALA
1	A	576	SER
1	B	100	ALA
1	B	104	GLN
1	B	113	VAL
1	B	214	ARG
1	B	241	CYS
1	B	256	ASP
1	B	261	SER
1	B	284	ASN
1	B	307	SER
1	B	324	SER
1	B	338	ARG
1	B	341	GLU
1	B	403	ASP
1	B	417	THR
1	B	435	ALA
1	B	576	SER
1	B	651	ILE
1	C	100	ALA
1	C	113	VAL
1	C	214	ARG
1	C	241	CYS
1	C	256	ASP
1	C	261	SER
1	C	268	SER
1	C	284	ASN
1	C	324	SER
1	C	338	ARG
1	C	341	GLU
1	C	403	ASP
1	C	417	THR
1	C	435	ALA
1	C	576	SER
1	C	651	ILE
1	D	100	ALA
1	D	104	GLN

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Mol	Chain	Res	Type
1	D	113	VAL
1	D	214	ARG
1	D	241	CYS
1	D	256	ASP
1	D	261	SER
1	D	268	SER
1	D	284	ASN
1	D	307	SER
1	D	324	SER
1	D	341	GLU
1	D	403	ASP
1	D	417	THR
1	D	435	ALA
1	D	576	SER
1	D	651	ILE
1	A	105	ARG
1	A	202	ASN
1	A	231	GLU
1	A	265	SER
1	A	346	ALA
1	A	443	LEU
1	A	444	ALA
1	A	504	SER
1	A	541	PRO
1	A	553	ILE
1	A	600	ASP
1	A	651	ILE
1	A	684	SER
1	A	727	TYR
1	B	105	ARG
1	B	125	ASP
1	B	202	ASN
1	B	231	GLU
1	B	264	ASP
1	B	346	ALA
1	B	443	LEU
1	B	444	ALA
1	B	504	SER
1	B	541	PRO
1	B	553	ILE
1	B	600	ASP
1	B	684	SER

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Mol	Chain	Res	Type
1	B	727	TYR
1	C	104	GLN
1	C	105	ARG
1	C	202	ASN
1	C	231	GLU
1	C	264	ASP
1	C	267	PRO
1	C	307	SER
1	C	346	ALA
1	C	443	LEU
1	C	444	ALA
1	C	504	SER
1	C	541	PRO
1	C	553	ILE
1	C	600	ASP
1	C	684	SER
1	C	727	TYR
1	D	105	ARG
1	D	202	ASN
1	D	231	GLU
1	D	338	ARG
1	D	346	ALA
1	D	443	LEU
1	D	444	ALA
1	D	504	SER
1	D	541	PRO
1	D	553	ILE
1	D	600	ASP
1	D	684	SER
1	D	727	TYR
1	A	73	SER
1	A	125	ASP
1	A	212	PHE
1	A	333	ASP
1	A	440	GLU
1	A	461	SER
1	A	468	ASP
1	A	497	MET
1	A	544	MET
1	A	708	ASN
1	A	720	PHE
1	B	73	SER

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Mol	Chain	Res	Type
1	B	333	ASP
1	B	440	GLU
1	B	461	SER
1	B	468	ASP
1	B	497	MET
1	B	544	MET
1	B	708	ASN
1	B	720	PHE
1	C	73	SER
1	C	125	ASP
1	C	212	PHE
1	C	333	ASP
1	C	439	ASP
1	C	440	GLU
1	C	461	SER
1	C	468	ASP
1	C	497	MET
1	C	544	MET
1	C	708	ASN
1	C	720	PHE
1	D	73	SER
1	D	125	ASP
1	D	212	PHE
1	D	333	ASP
1	D	440	GLU
1	D	461	SER
1	D	468	ASP
1	D	497	MET
1	D	544	MET
1	D	708	ASN
1	D	720	PHE
1	A	102	MET
1	A	192	VAL
1	A	215	SER
1	A	222	SER
1	A	263	SER
1	A	325	ALA
1	A	348	TYR
1	A	392	GLU
1	A	394	ASP
1	A	598	LYS
1	A	602	ILE

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Mol	Chain	Res	Type
1	B	102	MET
1	B	164	HIS
1	B	192	VAL
1	B	212	PHE
1	B	215	SER
1	B	222	SER
1	B	249	THR
1	B	268	SER
1	B	348	TYR
1	B	392	GLU
1	B	394	ASP
1	B	598	LYS
1	B	602	ILE
1	B	652	SER
1	C	102	MET
1	C	192	VAL
1	C	222	SER
1	C	325	ALA
1	C	348	TYR
1	C	392	GLU
1	C	394	ASP
1	C	410	ASN
1	C	598	LYS
1	C	602	ILE
1	D	102	MET
1	D	192	VAL
1	D	222	SER
1	D	267	PRO
1	D	348	TYR
1	D	392	GLU
1	D	394	ASP
1	D	598	LYS
1	D	602	ILE
1	D	652	SER
1	A	155	PRO
1	A	164	HIS
1	A	190	ASP
1	A	410	ASN
1	B	155	PRO
1	B	190	ASP
1	B	250	SER
1	B	267	PRO

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Mol	Chain	Res	Type
1	B	276	VAL
1	B	325	ALA
1	B	410	ASN
1	B	460	ALA
1	B	543	SER
1	C	155	PRO
1	C	164	HIS
1	C	190	ASP
1	C	215	SER
1	C	460	ALA
1	C	652	SER
1	D	155	PRO
1	D	164	HIS
1	D	190	ASP
1	D	215	SER
1	D	266	ASP
1	D	276	VAL
1	D	325	ALA
1	D	410	ASN
1	A	273	VAL
1	A	276	VAL
1	A	295	ASN
1	A	543	SER
1	B	266	ASP
1	B	273	VAL
1	B	295	ASN
1	B	439	ASP
1	C	273	VAL
1	C	276	VAL
1	C	295	ASN
1	D	273	VAL
1	D	295	ASN
1	D	543	SER
1	A	296	GLY
1	B	296	GLY
1	C	296	GLY
1	C	702	ILE
1	C	728	ILE
1	D	296	GLY
1	A	95	ILE
1	A	292	PRO
1	A	547	VAL

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Mol	Chain	Res	Type
1	A	702	ILE
1	A	728	ILE
1	B	95	ILE
1	B	292	PRO
1	B	547	VAL
1	B	702	ILE
1	C	95	ILE
1	C	292	PRO
1	C	547	VAL
1	D	95	ILE
1	D	292	PRO
1	D	547	VAL
1	D	702	ILE
1	D	728	ILE
1	A	416	GLY
1	B	728	ILE
1	C	416	GLY
1	B	416	GLY

5.3.2 Protein sidechains [i](#)

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	661/682 (97%)	608 (92%)	53 (8%)	12	40
1	B	661/682 (97%)	607 (92%)	54 (8%)	11	39
1	C	661/682 (97%)	609 (92%)	52 (8%)	12	41
1	D	661/682 (97%)	610 (92%)	51 (8%)	13	42
All	All	2644/2728 (97%)	2434 (92%)	210 (8%)	12	41

All (210) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	PHE
1	A	92	THR
1	A	99	ASN

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Mol	Chain	Res	Type
1	A	150	PHE
1	A	151	HIS
1	A	164	HIS
1	A	172	GLN
1	A	180	ASP
1	A	183	LEU
1	A	211	PHE
1	A	236	VAL
1	A	270	PHE
1	A	280	LEU
1	A	294	GLU
1	A	297	LEU
1	A	312	THR
1	A	328	ILE
1	A	337	THR
1	A	338	ARG
1	A	349	LEU
1	A	363	LEU
1	A	375	ASN
1	A	377	GLU
1	A	385	SER
1	A	386	LEU
1	A	393	HIS
1	A	409	CYS
1	A	427	LEU
1	A	430	ASN
1	A	438	GLU
1	A	446	LEU
1	A	447	GLU
1	A	455	THR
1	A	464	THR
1	A	469	GLU
1	A	530	LYS
1	A	540	LEU
1	A	541	PRO
1	A	552	ASP
1	A	558	LEU
1	A	565	THR
1	A	583	LEU
1	A	590	GLN
1	A	596	PHE
1	A	597	TRP

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Mol	Chain	Res	Type
1	A	613	ILE
1	A	623	LEU
1	A	663	LEU
1	A	670	GLN
1	A	679	LEU
1	A	692	PHE
1	A	706	ASN
1	A	717	ASN
1	B	72	PHE
1	B	92	THR
1	B	99	ASN
1	B	150	PHE
1	B	151	HIS
1	B	164	HIS
1	B	172	GLN
1	B	180	ASP
1	B	183	LEU
1	B	211	PHE
1	B	236	VAL
1	B	270	PHE
1	B	280	LEU
1	B	294	GLU
1	B	297	LEU
1	B	312	THR
1	B	328	ILE
1	B	337	THR
1	B	338	ARG
1	B	349	LEU
1	B	363	LEU
1	B	375	ASN
1	B	377	GLU
1	B	385	SER
1	B	386	LEU
1	B	393	HIS
1	B	409	CYS
1	B	427	LEU
1	B	430	ASN
1	B	437	ASN
1	B	438	GLU
1	B	446	LEU
1	B	447	GLU
1	B	455	THR

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Mol	Chain	Res	Type
1	B	464	THR
1	B	469	GLU
1	B	530	LYS
1	B	540	LEU
1	B	541	PRO
1	B	552	ASP
1	B	558	LEU
1	B	565	THR
1	B	583	LEU
1	B	590	GLN
1	B	596	PHE
1	B	597	TRP
1	B	613	ILE
1	B	623	LEU
1	B	663	LEU
1	B	670	GLN
1	B	679	LEU
1	B	692	PHE
1	B	706	ASN
1	B	717	ASN
1	C	72	PHE
1	C	99	ASN
1	C	150	PHE
1	C	151	HIS
1	C	164	HIS
1	C	172	GLN
1	C	180	ASP
1	C	183	LEU
1	C	211	PHE
1	C	236	VAL
1	C	270	PHE
1	C	280	LEU
1	C	294	GLU
1	C	297	LEU
1	C	312	THR
1	C	328	ILE
1	C	337	THR
1	C	338	ARG
1	C	349	LEU
1	C	363	LEU
1	C	375	ASN
1	C	377	GLU

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Mol	Chain	Res	Type
1	C	385	SER
1	C	386	LEU
1	C	393	HIS
1	C	409	CYS
1	C	427	LEU
1	C	430	ASN
1	C	441	GLU
1	C	446	LEU
1	C	447	GLU
1	C	455	THR
1	C	464	THR
1	C	469	GLU
1	C	530	LYS
1	C	540	LEU
1	C	541	PRO
1	C	552	ASP
1	C	558	LEU
1	C	565	THR
1	C	583	LEU
1	C	590	GLN
1	C	596	PHE
1	C	597	TRP
1	C	613	ILE
1	C	623	LEU
1	C	663	LEU
1	C	670	GLN
1	C	679	LEU
1	C	692	PHE
1	C	706	ASN
1	C	717	ASN
1	D	72	PHE
1	D	99	ASN
1	D	150	PHE
1	D	151	HIS
1	D	164	HIS
1	D	172	GLN
1	D	180	ASP
1	D	183	LEU
1	D	211	PHE
1	D	236	VAL
1	D	280	LEU
1	D	294	GLU

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Mol	Chain	Res	Type
1	D	297	LEU
1	D	312	THR
1	D	328	ILE
1	D	337	THR
1	D	338	ARG
1	D	349	LEU
1	D	363	LEU
1	D	375	ASN
1	D	377	GLU
1	D	385	SER
1	D	386	LEU
1	D	393	HIS
1	D	409	CYS
1	D	427	LEU
1	D	430	ASN
1	D	438	GLU
1	D	446	LEU
1	D	447	GLU
1	D	455	THR
1	D	464	THR
1	D	469	GLU
1	D	530	LYS
1	D	540	LEU
1	D	541	PRO
1	D	552	ASP
1	D	558	LEU
1	D	565	THR
1	D	583	LEU
1	D	590	GLN
1	D	596	PHE
1	D	597	TRP
1	D	613	ILE
1	D	623	LEU
1	D	663	LEU
1	D	670	GLN
1	D	679	LEU
1	D	692	PHE
1	D	706	ASN
1	D	717	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (81) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	71	HIS
1	A	111	GLN
1	A	120	ASN
1	A	132	GLN
1	A	172	GLN
1	A	240	ASN
1	A	262	GLN
1	A	299	GLN
1	A	318	ASN
1	A	430	ASN
1	A	437	ASN
1	A	445	ASN
1	A	458	ASN
1	A	487	ASN
1	A	514	ASN
1	A	575	ASN
1	A	589	ASN
1	A	620	HIS
1	A	632	GLN
1	A	697	GLN
1	B	22	ASN
1	B	71	HIS
1	B	111	GLN
1	B	120	ASN
1	B	132	GLN
1	B	172	GLN
1	B	240	ASN
1	B	262	GLN
1	B	299	GLN
1	B	318	ASN
1	B	430	ASN
1	B	437	ASN
1	B	445	ASN
1	B	487	ASN
1	B	514	ASN
1	B	575	ASN
1	B	589	ASN
1	B	620	HIS
1	B	632	GLN
1	B	697	GLN
1	C	22	ASN
1	C	71	HIS

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Mol	Chain	Res	Type
1	C	111	GLN
1	C	120	ASN
1	C	132	GLN
1	C	172	GLN
1	C	240	ASN
1	C	242	HIS
1	C	262	GLN
1	C	299	GLN
1	C	318	ASN
1	C	430	ASN
1	C	445	ASN
1	C	458	ASN
1	C	487	ASN
1	C	514	ASN
1	C	575	ASN
1	C	589	ASN
1	C	620	HIS
1	C	632	GLN
1	C	697	GLN
1	D	22	ASN
1	D	71	HIS
1	D	111	GLN
1	D	120	ASN
1	D	132	GLN
1	D	172	GLN
1	D	240	ASN
1	D	262	GLN
1	D	299	GLN
1	D	318	ASN
1	D	430	ASN
1	D	445	ASN
1	D	487	ASN
1	D	514	ASN
1	D	575	ASN
1	D	589	ASN
1	D	620	HIS
1	D	632	GLN
1	D	697	GLN

5.3.3 RNA ⓘ

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 monosaccharides 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	706/729 (96%)	0.50	79 (11%) 5 1	51, 121, 174, 188	0
1	B	706/729 (96%)	0.51	69 (9%) 7 2	54, 121, 174, 188	0
1	C	706/729 (96%)	0.54	74 (10%) 6 2	52, 122, 174, 191	0
1	D	706/729 (96%)	0.48	68 (9%) 8 2	50, 121, 174, 186	0
All	All	2824/2916 (96%)	0.51	290 (10%) 6 2	50, 122, 174, 191	0

All (290) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	600	ASP	9.5
1	C	174	SER	9.3
1	B	244	LYS	9.3
1	C	186	LEU	8.5
1	B	194	TYR	7.9
1	D	558	LEU	7.8
1	C	185	GLY	7.7
1	C	184	LEU	7.7
1	A	600	ASP	7.6
1	B	197	LEU	7.6
1	C	175	VAL	7.4
1	A	183	LEU	7.0
1	D	237	LEU	6.7
1	A	313	TYR	6.6
1	B	166	LEU	6.5
1	C	313	TYR	6.5
1	D	186	LEU	6.4
1	C	176	VAL	6.2
1	B	155	PRO	6.0
1	B	198	LEU	5.8
1	A	184	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
1	C	601	PHE	5.6
1	A	186	LEU	5.5
1	B	288	VAL	5.3
1	D	270	PHE	5.2
1	C	215	SER	5.2
1	B	558	LEU	5.1
1	C	112	GLU	5.1
1	B	237	LEU	5.1
1	B	600	ASP	5.0
1	D	133	LEU	4.9
1	A	244	LYS	4.9
1	A	486	LEU	4.9
1	B	349	LEU	4.9
1	B	133	LEU	4.8
1	B	236	VAL	4.8
1	B	199	PHE	4.7
1	D	194	TYR	4.7
1	A	601	PHE	4.7
1	D	197	LEU	4.7
1	A	596	PHE	4.6
1	C	692	PHE	4.6
1	C	306	ASP	4.6
1	C	253	LEU	4.5
1	B	498	HIS	4.5
1	C	557	CYS	4.5
1	A	271	ARG	4.4
1	B	602	ILE	4.4
1	C	270	PHE	4.4
1	C	231	GLU	4.3
1	A	166	LEU	4.3
1	C	301	GLY	4.3
1	A	352	ILE	4.3
1	A	231	GLU	4.3
1	B	607	PHE	4.2
1	B	318	ASN	4.2
1	D	155	PRO	4.2
1	D	269	HIS	4.1
1	D	185	GLY	4.1
1	D	113	VAL	4.1
1	B	113	VAL	4.0
1	D	600	ASP	4.0
1	A	682	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	176	VAL	4.0
1	D	607	PHE	3.9
1	C	599	LYS	3.9
1	C	183	LEU	3.9
1	D	163	PRO	3.9
1	D	196	PRO	3.9
1	A	692	PHE	3.8
1	B	145	LEU	3.8
1	A	287	LEU	3.8
1	D	102	MET	3.8
1	B	287	LEU	3.8
1	B	550	PHE	3.8
1	A	365	ILE	3.7
1	D	112	GLU	3.7
1	B	601	PHE	3.7
1	C	607	PHE	3.7
1	A	353	VAL	3.7
1	A	113	VAL	3.7
1	A	685	GLU	3.7
1	D	14	TYR	3.7
1	C	292	PRO	3.6
1	A	174	SER	3.6
1	A	546	THR	3.6
1	B	196	PRO	3.5
1	B	183	LEU	3.5
1	B	285	ASN	3.5
1	D	376	TYR	3.5
1	C	598	LYS	3.5
1	C	259	MET	3.5
1	A	53	GLY	3.5
1	C	241	CYS	3.4
1	C	133	LEU	3.4
1	D	379	ILE	3.4
1	C	220	TYR	3.4
1	C	113	VAL	3.3
1	A	158	PHE	3.3
1	C	685	GLU	3.3
1	D	118	LEU	3.3
1	C	302	THR	3.3
1	D	261	SER	3.3
1	D	689	GLY	3.3
1	B	603	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	117	LEU	3.3
1	A	2	ALA	3.3
1	A	305	VAL	3.3
1	B	300	MET	3.3
1	A	427	LEU	3.3
1	B	269	HIS	3.3
1	C	246	TRP	3.2
1	B	466	TYR	3.2
1	A	245	ILE	3.2
1	B	242	HIS	3.2
1	D	729	ILE	3.2
1	A	498	HIS	3.2
1	C	152	LEU	3.1
1	D	599	LYS	3.1
1	B	379	ILE	3.1
1	A	119	VAL	3.1
1	C	2	ALA	3.1
1	B	401	THR	3.1
1	A	189	VAL	3.1
1	D	691	LYS	3.1
1	C	158	PHE	3.1
1	C	53	GLY	3.0
1	A	163	PRO	3.0
1	C	606	LYS	3.0
1	A	607	PHE	3.0
1	A	243	LEU	3.0
1	C	118	LEU	3.0
1	A	695	TYR	3.0
1	D	692	PHE	3.0
1	A	241	CYS	3.0
1	D	119	VAL	3.0
1	A	684	SER	3.0
1	D	378	TRP	2.9
1	A	318	ASN	2.9
1	D	129	LEU	2.9
1	C	724	PHE	2.9
1	D	134	PRO	2.9
1	A	311	LEU	2.9
1	A	263	SER	2.8
1	B	348	TYR	2.8
1	C	311	LEU	2.8
1	B	599	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	145	LEU	2.8
1	A	169	VAL	2.8
1	D	248	LEU	2.8
1	A	599	LYS	2.8
1	C	132	GLN	2.8
1	A	300	MET	2.8
1	C	637	PHE	2.8
1	D	139	PHE	2.8
1	A	348	TYR	2.7
1	B	574	LEU	2.7
1	A	291	LEU	2.7
1	B	153	GLN	2.7
1	C	682	ASP	2.7
1	D	640	PHE	2.7
1	D	166	LEU	2.7
1	B	365	ILE	2.7
1	A	297	LEU	2.7
1	A	558	LEU	2.7
1	A	185	GLY	2.7
1	A	259	MET	2.7
1	D	727	TYR	2.7
1	A	175	VAL	2.7
1	C	166	LEU	2.6
1	B	192	VAL	2.6
1	C	128	PHE	2.6
1	A	606	LYS	2.6
1	D	176	VAL	2.6
1	D	131	LEU	2.6
1	A	637	PHE	2.6
1	B	268	SER	2.6
1	B	72	PHE	2.6
1	A	605	ILE	2.6
1	B	228	LEU	2.6
1	C	596	PHE	2.6
1	D	381	SER	2.6
1	D	639	LEU	2.6
1	B	295	ASN	2.6
1	C	19	GLU	2.6
1	C	117	LEU	2.6
1	B	271	ARG	2.5
1	C	197	LEU	2.5
1	A	272	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	590	GLN	2.5
1	A	198	LEU	2.5
1	A	501	THR	2.5
1	B	169	VAL	2.5
1	D	9	ALA	2.5
1	B	378	TRP	2.5
1	A	591	MET	2.5
1	D	158	PHE	2.5
1	D	285	ASN	2.5
1	A	709	VAL	2.5
1	A	512	THR	2.5
1	B	270	PHE	2.5
1	B	596	PHE	2.5
1	C	299	GLN	2.5
1	D	650	HIS	2.5
1	C	129	LEU	2.5
1	D	463	ILE	2.5
1	B	186	LEU	2.4
1	C	639	LEU	2.4
1	A	437	ASN	2.4
1	C	127	SER	2.4
1	C	177	PHE	2.4
1	D	298	PHE	2.4
1	C	222	SER	2.4
1	C	427	LEU	2.4
1	B	342	LEU	2.4
1	A	246	TRP	2.4
1	C	310	ILE	2.4
1	D	359	THR	2.4
1	A	131	LEU	2.4
1	D	280	LEU	2.4
1	A	319	ILE	2.3
1	D	164	HIS	2.3
1	A	431	LYS	2.3
1	A	117	LEU	2.3
1	B	546	THR	2.3
1	C	263	SER	2.3
1	B	245	ILE	2.3
1	A	81	PHE	2.3
1	C	349	LEU	2.3
1	A	299	GLN	2.3
1	B	685	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	118	LEU	2.2
1	D	303	LEU	2.2
1	C	493	TRP	2.2
1	D	355	TRP	2.2
1	D	618	SER	2.2
1	B	367	ASN	2.2
1	C	18	PRO	2.2
1	C	254	ILE	2.2
1	B	376	TYR	2.2
1	C	271	ARG	2.2
1	A	514	ASN	2.2
1	A	309	GLY	2.2
1	D	288	VAL	2.2
1	B	375	ASN	2.2
1	D	184	LEU	2.2
1	A	577	PHE	2.2
1	B	156	TYR	2.2
1	C	77	THR	2.2
1	B	729	ILE	2.2
1	A	683	SER	2.2
1	A	379	ILE	2.2
1	B	160	VAL	2.2
1	C	433	ILE	2.2
1	C	272	LYS	2.2
1	C	374	LYS	2.2
1	A	133	LEU	2.1
1	B	243	LEU	2.1
1	B	66	GLU	2.1
1	A	138	LEU	2.1
1	A	366	LEU	2.1
1	C	342	LEU	2.1
1	C	446	LEU	2.1
1	D	287	LEU	2.1
1	D	663	LEU	2.1
1	A	639	LEU	2.1
1	D	97	LEU	2.1
1	A	310	ILE	2.1
1	C	110	ILE	2.1
1	D	506	LEU	2.1
1	D	333	ASP	2.1
1	B	138	LEU	2.1
1	D	375	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	355	TRP	2.1
1	B	639	LEU	2.1
1	B	231	GLU	2.1
1	D	321	THR	2.1
1	D	198	LEU	2.1
1	D	614	ILE	2.1
1	B	75	ARG	2.0
1	D	659	TYR	2.0
1	C	437	ASN	2.0
1	D	281	SER	2.0
1	C	198	LEU	2.0
1	C	223	VAL	2.0
1	D	510	LEU	2.0
1	B	164	HIS	2.0
1	B	606	LYS	2.0
1	C	119	VAL	2.0
1	C	615	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 monosaccharides 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.