



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 05:40 PM EDT

PDB ID : 3H7N / pdb_00003h7n
Title : Structure of Nup120
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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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

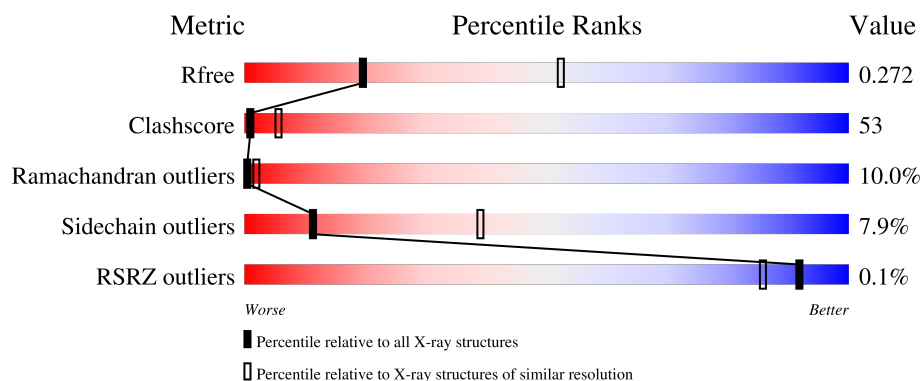
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

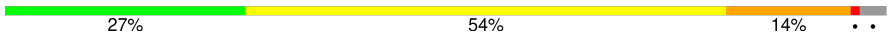
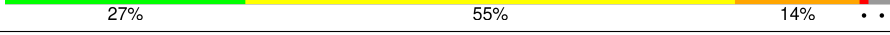
The reported resolution of this entry is 3.00 Å.

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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (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.

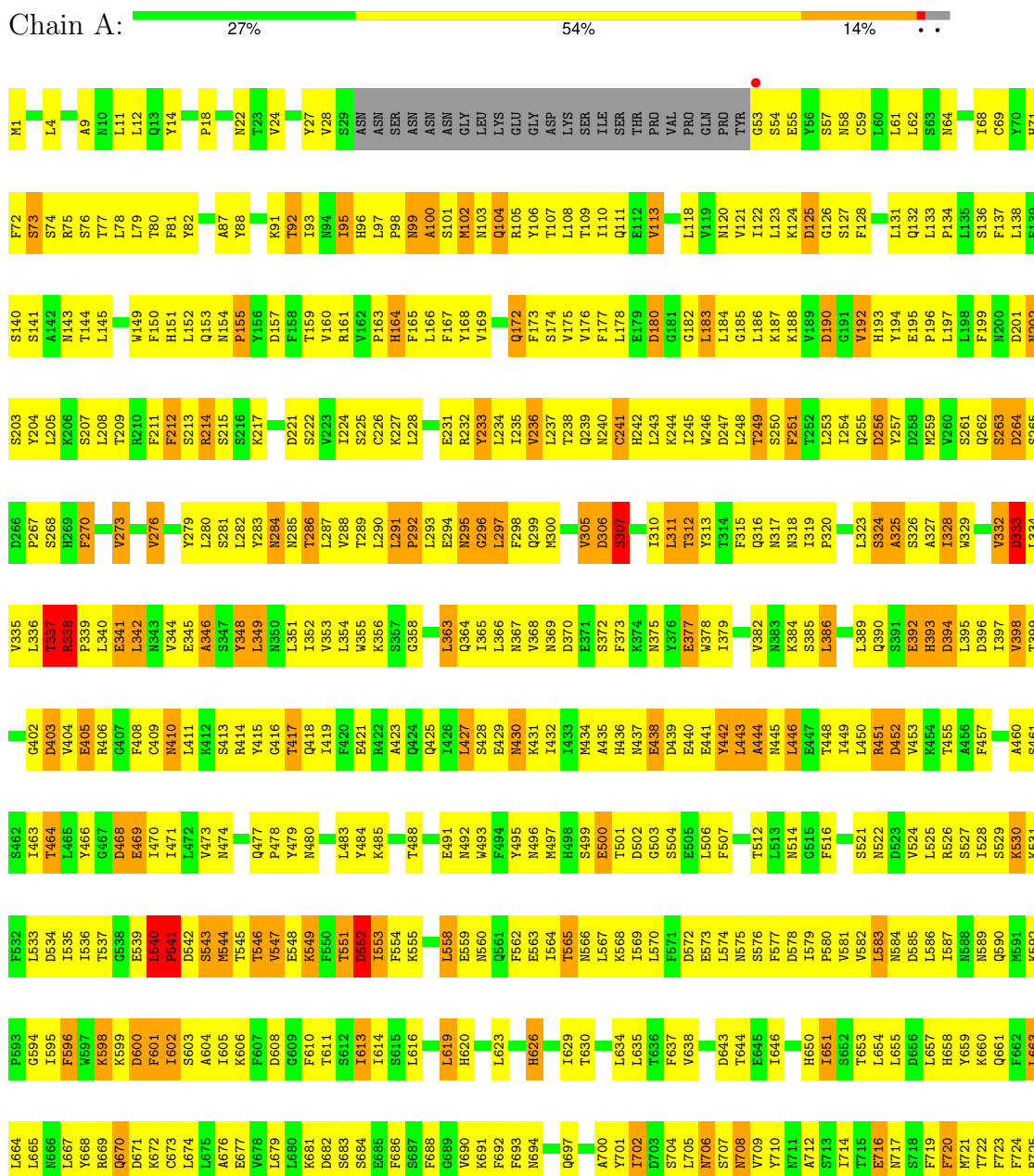
- Molecule 1 is a protein called Nucleoporin NUP120.

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

3 Residue-property plots

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

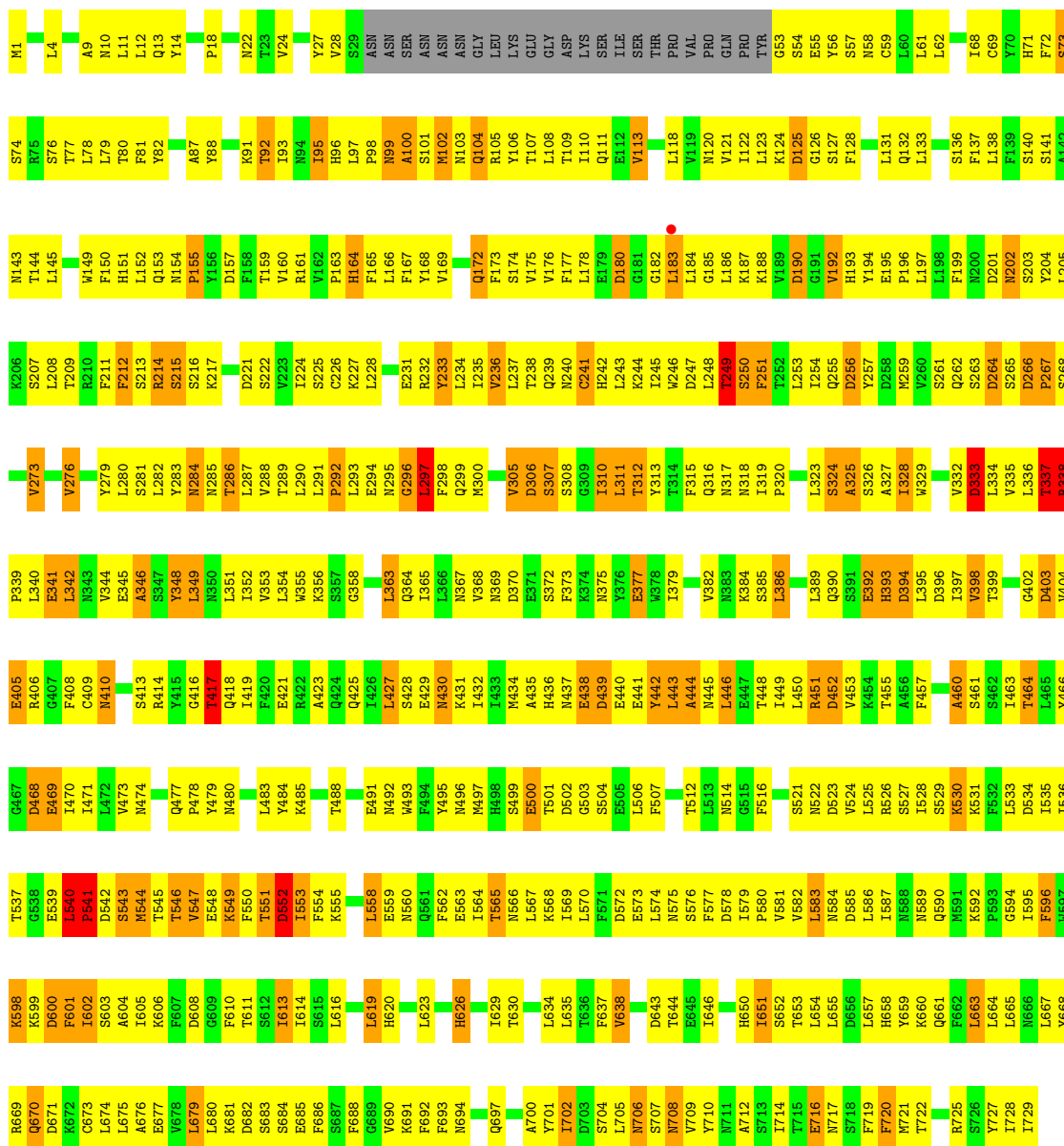
• Molecule 1: Nucleoporin NUP120



S726
Y727
I728
I729

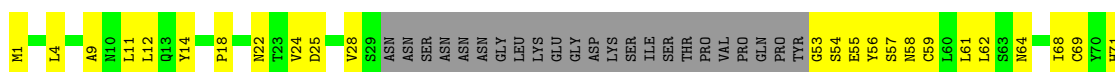
• Molecule 1: Nucleoporin NUP120

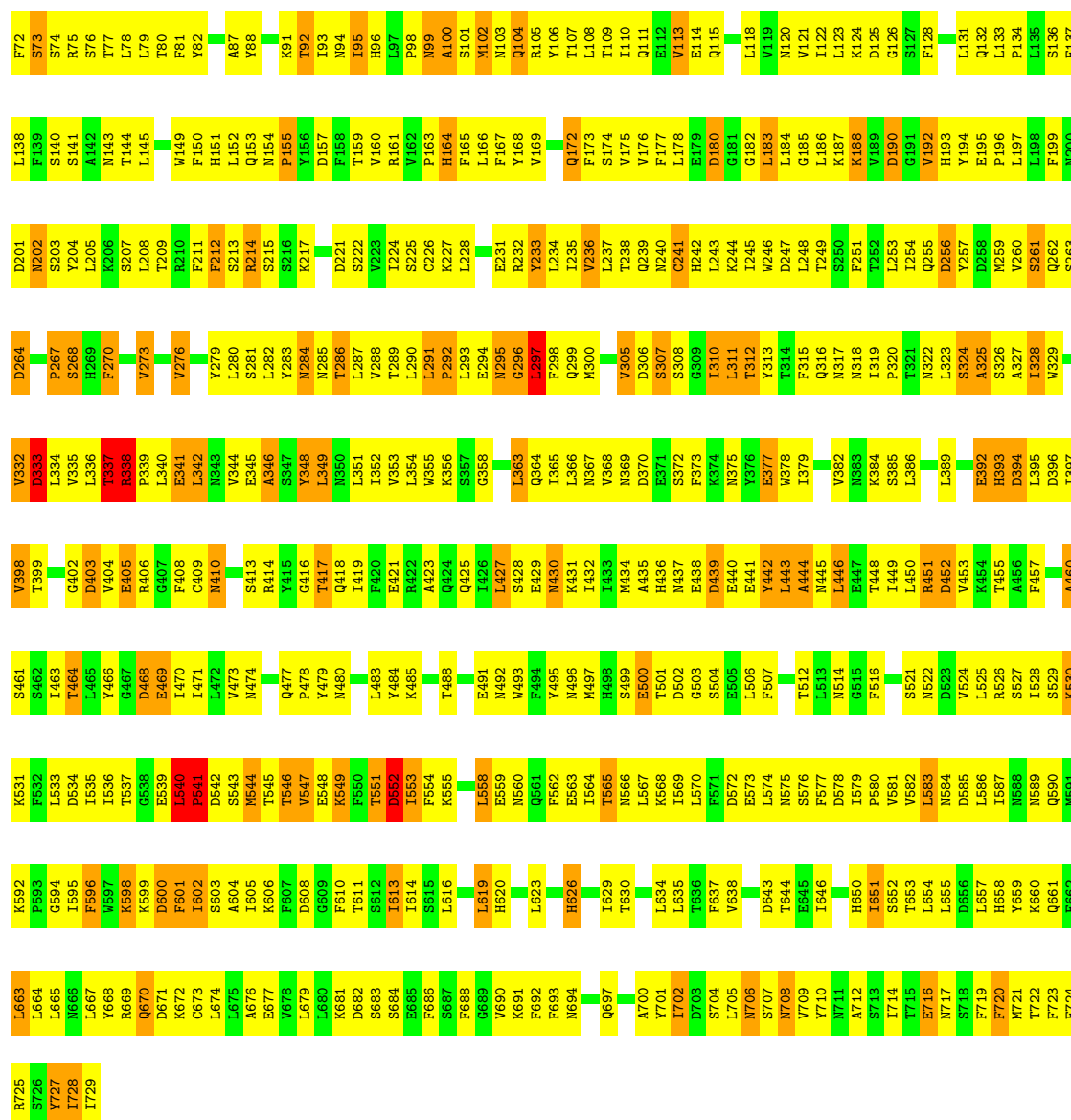
Chain B: 27% 54% 14% ..



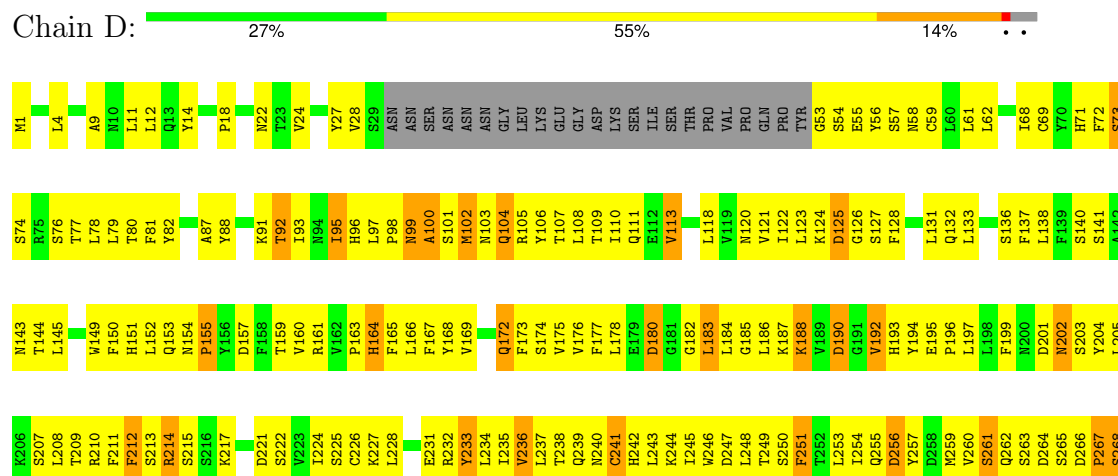
• Molecule 1: Nucleoporin NUP120

Chain C: 27% 55% 14% ..





• Molecule 1: Nucleoporin NUP120



I729	L667	K598	T537	G487	V404	H269
Y668	K599	K598	E538	D468	E405	V273
R669	D600	E539	L540	E469	G406	V276
Q670	F601	P541	D542	I470	F407	Y279
D671	I602	S603	S543	I471	F408	L280
K672	A604	R544	T545	L472	C409	S281
C673	L605	T546	V547	V473	N410	L282
L674	K606	E548	K549	N474	S413	Y283
L675	D607	F550	N480	Q477	R414	N284
A676	D608	T551	L483	P478	T417	N285
E677	G609	D552	Y484	Y479	Q418	T286
V678	F610	I553	K485	Y480	I419	L287
L679	T611	F554	T488		F420	V288
L680	L612	K555	E491		E421	T289
K681	I613	L558	N492		R422	L290
D682	T614	E559	W493		A423	L291
S683	L615	N560	F494		Q424	P292
S684	L616	F562	N496		Q425	L293
S685		E563	N497		L426	L294
F686		I564	H498		L427	E294
S687		T565	S499		S428	N295
F688		K568	T501		E429	G296
G689		I569	D502		N430	L287
V690		L570	G503		K431	F298
K691		F571	E505		I432	Q299
F692		D572	L506		I433	M300
F693		E573	F507		M434	L304
N694		L574	T512		A435	V305
Q697		N575	L513		N436	D306
A700		S576	N514		H437	S307
Y701		F577	G515		D370	S308
I702		D578	I579		E371	G309
D703		I579	F516		S372	I310
S704		P580	S521		F373	L311
L705		V581	N522		N375	T312
N706		V582	D523		Y376	T313
S707		L583	V524		E377	T314
N708		D584	R525		I378	F315
Y709		L586	R526		I379	Q316
E645		I587	S527		V382	N317
L646		N588	I528		N383	N318
		N589	S529		K384	I319
		Q590	K530		S385	P320
		N591	K531		L389	L323
N711		K592	F532		E392	S324
A712		P593	L533		I393	A325
S713		G594	D534		L394	S326
I714		F596	I535		A327	S327
T715		W597	I536		I328	W329
T716					W329	V332
E716					D332	D333
N717					L334	V335
S718					L336	L336
Y719						
F720						
N721						
T722						
F723						
F724						
N725						
S726						
Y727						
I728						

4 Data and refinement statistics

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 50.00 – 3.01	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.00) 85.3 (50.00-3.01)	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)	0.28 , 131.3	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	0.96	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	0.59	4/5878 (0.1%)	1.06	45/7981 (0.6%)
1	B	0.57	3/5878 (0.1%)	1.06	40/7981 (0.5%)
1	C	0.57	2/5878 (0.0%)	1.06	40/7981 (0.5%)
1	D	0.57	0/5878	1.07	44/7981 (0.6%)
All	All	0.58	9/23512 (0.0%)	1.06	169/31924 (0.5%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	307	SER	C-O	8.46	1.34	1.24
1	C	310	ILE	CA-C	6.36	1.59	1.52
1	A	306	ASP	CG-OD2	6.04	1.36	1.25
1	A	306	ASP	C-O	5.88	1.32	1.23
1	B	306	ASP	CA-C	5.73	1.60	1.53
1	A	306	ASP	N-CA	5.46	1.53	1.45
1	B	306	ASP	N-CA	5.37	1.52	1.45
1	B	306	ASP	C-O	5.29	1.31	1.23
1	C	310	ILE	C-O	5.18	1.30	1.24

All (169) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	305	VAL	N-CA-C	9.61	120.80	111.67
1	A	305	VAL	N-CA-C	9.50	120.70	111.67
1	B	305	VAL	N-CA-C	9.21	120.42	111.67
1	D	308	SER	N-CA-C	-8.67	101.80	111.07
1	D	305	VAL	CB-CA-C	-8.42	101.87	111.80
1	D	452	ASP	N-CA-C	8.31	120.03	110.97
1	C	452	ASP	N-CA-C	8.16	119.86	110.97
1	C	552	ASP	N-CA-C	-8.14	102.36	111.07
1	A	503	GLY	N-CA-C	-8.12	104.24	111.95
1	A	452	ASP	N-CA-C	8.11	119.81	110.97
1	C	503	GLY	N-CA-C	-8.10	104.26	111.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	552	ASP	N-CA-C	-8.04	102.47	111.07
1	B	552	ASP	N-CA-C	-8.02	102.48	111.07
1	D	682	ASP	N-CA-C	-7.95	102.60	111.82
1	C	682	ASP	N-CA-C	-7.95	102.60	111.82
1	B	682	ASP	N-CA-C	-7.92	102.64	111.82
1	B	503	GLY	N-CA-C	-7.91	104.44	111.95
1	A	682	ASP	N-CA-C	-7.89	102.67	111.82
1	B	452	ASP	N-CA-C	7.88	119.56	110.97
1	D	503	GLY	N-CA-C	-7.80	104.54	111.95
1	A	681	LYS	N-CA-C	-7.76	104.97	114.75
1	D	681	LYS	N-CA-C	-7.73	105.01	114.75
1	A	552	ASP	N-CA-C	-7.73	102.80	111.07
1	C	681	LYS	N-CA-C	-7.63	105.13	114.75
1	B	681	LYS	N-CA-C	-7.60	105.18	114.75
1	D	305	VAL	N-CA-C	7.51	118.81	111.67
1	D	442	TYR	N-CA-C	-7.47	103.08	111.07
1	C	88	TYR	N-CA-C	7.36	119.20	111.03
1	B	88	TYR	N-CA-C	7.30	119.13	111.03
1	B	442	TYR	N-CA-C	-7.29	103.28	111.07
1	C	500	GLU	N-CA-C	7.28	118.20	108.38
1	B	425	GLN	N-CA-C	-7.25	101.89	111.24
1	C	442	TYR	N-CA-C	-7.23	103.33	111.07
1	A	442	TYR	N-CA-C	-7.23	103.34	111.07
1	B	358	GLY	N-CA-C	-7.23	98.58	112.02
1	D	88	TYR	N-CA-C	7.20	119.02	111.03
1	C	405	GLU	N-CA-C	-7.19	103.77	112.54
1	A	405	GLU	N-CA-C	-7.18	103.78	112.54
1	D	405	GLU	N-CA-C	-7.17	103.80	112.54
1	B	405	GLU	N-CA-C	-7.13	103.85	112.54
1	D	358	GLY	N-CA-C	-7.12	98.78	112.02
1	C	358	GLY	N-CA-C	-7.10	98.81	112.02
1	A	500	GLU	N-CA-C	7.09	117.95	108.38
1	C	425	GLN	N-CA-C	-7.07	102.12	111.24
1	D	500	GLU	N-CA-C	7.05	117.91	108.38
1	A	425	GLN	N-CA-C	-7.03	102.17	111.24
1	A	358	GLY	N-CA-C	-7.03	98.95	112.02
1	C	337	THR	N-CA-C	7.02	119.03	107.73
1	A	88	TYR	N-CA-C	7.01	118.81	111.03
1	D	337	THR	N-CA-C	7.00	118.99	107.73
1	B	500	GLU	N-CA-C	6.99	117.81	108.38
1	B	337	THR	N-CA-C	6.97	118.96	107.73
1	D	540	LEU	CA-C-N	6.94	128.51	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	540	LEU	C-N-CA	6.94	128.51	119.84
1	A	337	THR	N-CA-C	6.92	118.87	107.73
1	C	555	LYS	N-CA-C	-6.92	103.18	111.69
1	C	540	LEU	CA-C-N	6.91	128.48	119.84
1	C	540	LEU	C-N-CA	6.91	128.48	119.84
1	A	540	LEU	CA-C-N	6.88	128.44	119.84
1	A	540	LEU	C-N-CA	6.88	128.44	119.84
1	B	555	LYS	N-CA-C	-6.88	103.23	111.69
1	B	540	LEU	CA-C-N	6.86	128.41	119.84
1	B	540	LEU	C-N-CA	6.86	128.41	119.84
1	A	555	LYS	N-CA-C	-6.85	103.26	111.69
1	D	555	LYS	N-CA-C	-6.76	103.37	111.69
1	A	551	THR	N-CA-C	-6.63	105.32	113.41
1	C	551	THR	N-CA-C	-6.54	105.43	113.41
1	A	488	THR	N-CA-C	-6.53	101.34	110.35
1	D	551	THR	N-CA-C	-6.52	105.46	113.41
1	B	551	THR	N-CA-C	-6.49	105.50	113.41
1	C	208	LEU	N-CA-C	-6.48	105.44	113.15
1	B	208	LEU	N-CA-C	-6.45	105.47	113.15
1	A	208	LEU	N-CA-C	-6.45	105.48	113.15
1	A	249	THR	N-CA-C	-6.44	102.62	112.99
1	D	488	THR	N-CA-C	-6.43	101.48	110.35
1	B	488	THR	N-CA-C	-6.33	101.61	110.35
1	D	208	LEU	N-CA-C	-6.31	105.64	113.15
1	C	175	VAL	N-CA-C	6.25	116.87	110.05
1	D	175	VAL	N-CA-C	6.24	116.85	110.05
1	B	175	VAL	N-CA-C	6.21	116.82	110.05
1	B	251	PHE	N-CA-C	-6.16	105.07	112.58
1	A	175	VAL	N-CA-C	6.14	116.75	110.05
1	C	488	THR	N-CA-C	-6.11	101.92	110.35
1	D	425	GLN	N-CA-C	-5.94	101.83	111.04
1	D	619	LEU	N-CA-C	-5.88	104.56	110.97
1	B	195	GLU	CA-C-N	5.87	127.18	119.84
1	B	195	GLU	C-N-CA	5.87	127.18	119.84
1	C	365	ILE	N-CA-C	-5.80	99.99	108.11
1	A	195	GLU	CA-C-N	5.79	127.07	119.84
1	A	195	GLU	C-N-CA	5.79	127.07	119.84
1	A	305	VAL	CA-C-N	-5.78	110.19	121.06
1	A	305	VAL	C-N-CA	-5.78	110.19	121.06
1	B	365	ILE	N-CA-C	-5.78	100.02	108.11
1	D	195	GLU	CA-C-N	5.76	127.04	119.84
1	D	195	GLU	C-N-CA	5.76	127.04	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	195	GLU	CA-C-N	5.76	127.04	119.84
1	C	195	GLU	C-N-CA	5.76	127.04	119.84
1	D	213	SER	N-CA-C	5.72	122.99	110.80
1	A	213	SER	N-CA-C	5.72	122.98	110.80
1	B	213	SER	N-CA-C	5.70	122.93	110.80
1	C	213	SER	N-CA-C	5.69	122.92	110.80
1	C	451	ARG	N-CA-C	-5.68	104.30	111.11
1	D	365	ILE	N-CA-C	-5.66	100.18	108.11
1	B	333	ASP	N-CA-C	-5.60	98.86	110.80
1	A	451	ARG	N-CA-C	-5.60	104.39	111.11
1	C	286	THR	N-CA-C	5.60	117.92	110.53
1	D	286	THR	N-CA-C	5.59	117.92	110.53
1	C	333	ASP	N-CA-C	-5.59	98.90	110.80
1	A	333	ASP	N-CA-C	-5.58	98.91	110.80
1	B	601	PHE	N-CA-C	-5.58	106.46	113.72
1	A	365	ILE	N-CA-C	-5.57	100.32	108.11
1	A	601	PHE	N-CA-C	-5.54	106.52	113.72
1	B	619	LEU	N-CA-C	-5.53	104.94	110.97
1	B	286	THR	N-CA-C	5.51	117.80	110.53
1	D	601	PHE	N-CA-C	-5.50	106.58	113.72
1	B	626	HIS	N-CA-C	-5.49	104.98	110.97
1	C	601	PHE	N-CA-C	-5.49	106.58	113.72
1	D	333	ASP	N-CA-C	-5.49	99.11	110.80
1	B	233	TYR	N-CA-C	5.45	117.00	109.15
1	D	451	ARG	N-CA-C	-5.45	104.57	111.11
1	A	286	THR	N-CA-C	5.43	117.70	110.53
1	B	451	ARG	N-CA-C	-5.43	104.59	111.11
1	B	143	ASN	N-CA-C	-5.41	106.26	112.92
1	B	305	VAL	CA-C-N	-5.41	111.12	120.97
1	B	305	VAL	C-N-CA	-5.41	111.12	120.97
1	A	471	ILE	N-CA-C	5.40	116.54	108.54
1	D	251	PHE	N-CA-C	-5.40	105.99	112.58
1	D	143	ASN	N-CA-C	-5.39	106.29	112.92
1	C	143	ASN	N-CA-C	-5.39	106.29	112.92
1	D	332	VAL	N-CA-C	-5.39	108.25	113.53
1	D	626	HIS	N-CA-C	-5.39	105.10	110.97
1	A	672	LYS	N-CA-C	5.36	117.55	111.11
1	A	143	ASN	N-CA-C	-5.34	106.35	112.92
1	C	626	HIS	N-CA-C	-5.33	105.16	110.97
1	C	233	TYR	N-CA-C	5.33	116.83	109.15
1	D	471	ILE	N-CA-C	5.32	116.41	108.54
1	A	626	HIS	N-CA-C	-5.32	105.18	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	619	LEU	N-CA-C	-5.30	105.19	110.97
1	D	233	TYR	N-CA-C	5.29	116.78	109.15
1	A	307	SER	CB-CA-C	5.29	120.95	110.42
1	A	233	TYR	N-CA-C	5.28	116.76	109.15
1	D	706	ASN	N-CA-C	-5.28	104.99	111.75
1	C	332	VAL	N-CA-C	-5.21	108.42	113.53
1	A	503	GLY	CA-C-O	-5.18	118.85	122.22
1	A	619	LEU	N-CA-C	-5.18	105.33	110.97
1	B	471	ILE	N-CA-C	5.18	116.20	108.54
1	A	549	LYS	N-CA-C	-5.17	104.71	111.02
1	A	706	ASN	N-CA-C	-5.17	105.14	111.75
1	C	706	ASN	N-CA-C	-5.14	105.17	111.75
1	C	471	ILE	N-CA-C	5.11	116.11	108.54
1	B	706	ASN	N-CA-C	-5.09	105.24	111.75
1	D	672	LYS	N-CA-C	5.08	117.21	111.11
1	A	332	VAL	N-CA-C	-5.08	108.55	113.53
1	C	672	LYS	N-CA-C	5.08	117.20	111.11
1	D	503	GLY	CA-C-O	-5.08	118.92	122.22
1	C	549	LYS	N-CA-C	-5.07	104.84	111.02
1	C	291	LEU	CA-C-N	5.07	126.17	119.84
1	C	291	LEU	C-N-CA	5.07	126.17	119.84
1	B	549	LYS	N-CA-C	-5.06	104.84	111.02
1	D	297	LEU	N-CA-C	5.05	117.84	107.69
1	B	249	THR	N-CA-C	-5.04	100.06	110.80
1	C	297	LEU	N-CA-C	5.04	117.82	107.69
1	A	291	LEU	CA-C-N	5.02	126.12	119.84
1	A	291	LEU	C-N-CA	5.02	126.12	119.84
1	D	306	ASP	CA-C-N	5.02	131.13	121.54
1	D	306	ASP	C-N-CA	5.02	131.13	121.54
1	B	297	LEU	N-CA-C	5.02	117.78	107.69
1	D	549	LYS	N-CA-C	-5.02	104.90	111.02
1	A	251	PHE	N-CA-C	-5.00	105.84	112.24

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	630	0
1	B	5748	0	5657	599	0
1	C	5748	0	5657	624	0
1	D	5748	0	5657	603	0
All	All	22992	0	22628	2422	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 53.

All (2422) 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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:404:VAL:HG11	1:C:438:GLU:HA	1.57	0.86
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:243:LEU:HB3	1:D:259:MET:HE3	1.62	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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:605:ILE:HG13	1:B:606:LYS:N	1.96	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:D:605:ILE:HG13	1:D:606:LYS:N	1.97	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
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:721:MET:HB3	1:C:721:MET:HE1	1.64	0.77
1:A:55:GLU:OE1	1:A:74:SER:HA	1.85	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:721:MET:HE1	1:C:721:MET:HB3	1.67	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
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:B:243:LEU:HB3	1:B:259:MET:HE3	1.70	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:608:ASP:HB2	1:C:691:LYS:HZ1	1.54	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:553:ILE:O	1:D:553:ILE:HG22	1.89	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: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:286:THR:HG22	1:D:287:LEU:N	2.04	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:A:243:LEU:HB3	1:A:259:MET:HE3	1.72	0.70
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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:102:MET:HE2	1:D:122:ILE:HG22	1.74	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:C:243:LEU:HB3	1:C:259:MET:HE3	1.72	0.69
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:102:MET:HE2	1:A:122:ILE:HG22	1.74	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: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: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:D:341:GLU:C	1:D:342:LEU:HD23	2.18	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:MET:HE2	1:C:122:ILE:HG22	1.75	0.69
1:A:154:ASN:N	1:A:155:PRO:HD3	2.07	0.68
1:B:341:GLU:C	1:B:342:LEU:HD23	2.18	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:B:102:MET:HE2	1:B:122:ILE:HG22	1.76	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:226:CYS:SG	1:B:227:LYS:N	2.66	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: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:A:341:GLU:C	1:A:342:LEU:HD23	2.19	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:701:TYR:O	1:D:705:LEU:HD12	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:ARG:HB2	1:A:339:PRO:CD	2.22	0.67
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:341:GLU:C	1:C:342:LEU:HD23	2.19	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:D:226:CYS:SG	1:D:227:LYS:N	2.67	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:A:73:SER:HB3	1:A:78:LEU:H	1.60	0.66
1:A:545:THR:C	1:A:547:VAL:H	2.02	0.66
1:C:368:VAL:HG23	1:C:368:VAL:O	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:B:185:GLY:O	1:B:186:LEU:HD12	1.94	0.66
1:B:545:THR:C	1:B:547:VAL:H	2.03	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:D:545:THR:C	1:D:547:VAL:H	2.03	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:259:MET:HE1	1:B:313:TYR:CE2	2.30	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:C:545:THR:C	1:C:547:VAL:H	2.03	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:D:338:ARG:HB2	1:D:339:PRO:CD	2.23	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: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: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: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:D:292:PRO:C	1:D:293:LEU:HD12	2.23	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:B:292:PRO:C	1:B:293:LEU:HD12	2.23	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:B:108:LEU:HD23	1:B:108:LEU:C	2.24	0.62
1:B:417:THR:HG22	1:B:418:GLN:N	2.15	0.62
1:B:596:PHE:C	1:B:598:LYS:H	2.07	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:D:596:PHE:C	1:D:598:LYS:H	2.07	0.62
1:C:291:LEU:HB2	1:C:297:LEU:CB	2.30	0.62
1:C:596:PHE:C	1:C:598:LYS:H	2.07	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:A:568:LYS:HZ3	1:D:210:ARG:HH22	1.46	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:D:403:ASP:CG	1:D:404:VAL:H	2.08	0.62
1:A:596:PHE:C	1:A:598:LYS:H	2.07	0.61
1:A:637:PHE:HD2	1:A:651:ILE:HD11	1.65	0.61
1:C:292:PRO:C	1:C:293:LEU:HD12	2.24	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:D:608:ASP:HB2	1:D:691:LYS:HZ1	1.64	0.61
1:A:132:GLN:NE2	1:A:151:HIS:NE2	2.49	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:292:PRO:C	1:A:293:LEU:HD12	2.24	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:305:VAL:HG23	1:D:306:ASP:N	2.14	0.61
1:B:101:SER:HB2	1:B:107:THR:OG1	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: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
1:D:417:THR:HG22	1:D:418:GLN:N	2.16	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:108:LEU:HD23	1:D:108:LEU:C	2.25	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:C:108:LEU:HD23	1:C:108:LEU:C	2.25	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:B:403:ASP:CG	1:B:404:VAL:H	2.09	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:D:552:ASP:C	1:D:554:PHE:H	2.10	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:LEU:HD23	1:A:108:LEU:C	2.26	0.60
1:A:167:PHE:CD2	1:A:168:TYR:N	2.69	0.60
1:A:403:ASP:CG	1:A:404:VAL:H	2.09	0.60
1:A:552:ASP:C	1:A:554:PHE:H	2.10	0.60
1:B:332:VAL:HB	1:B:354:LEU:HD23	1.84	0.60
1:B:552:ASP:C	1:B:554:PHE:H	2.10	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:450:LEU:O	1:C:451:ARG:C	2.44	0.59
1:C:539:GLU:O	1:C:541:PRO:HD3	2.02	0.59
1:D:165:PHE:HD2	1:D:177:PHE:CD2	2.20	0.59
1:D:217:LYS:HG3	1:D:217:LYS:O	2.00	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:B:217:LYS:HG3	1:B:217:LYS:O	2.00	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:403:ASP:CG	1:C:404:VAL:H	2.09	0.59
1:C:533:LEU:HD13	1:C:729:ILE:HD11	1.84	0.59
1:C:552:ASP:C	1:C:554:PHE:H	2.11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:102:MET:HE3	1:A:163:PRO:HD2	1.85	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: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
1:C:332:VAL:O	1:C:333:ASP:HB2	2.03	0.59
1:D:719:PHE:C	1:D:721:MET:N	2.60	0.59
1:A:165:PHE:HD2	1:A:177:PHE:CD2	2.20	0.59
1:C:102:MET:HE3	1:C:163:PRO:HD2	1.85	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:A:545:THR:C	1:A:547:VAL:N	2.60	0.58
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:B:719:PHE:C	1:B:721:MET:N	2.61	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:545:THR:C	1:C:547:VAL:N	2.61	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: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:172:GLN:CD	1:A:172:GLN:H	2.11	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
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:A:259:MET:HE1	1:A:313:TYR:CE2	2.38	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:102:MET:HE3	1:B:163:PRO:HD2	1.86	0.58
1:C:694:ASN:ND2	1:C:697:GLN:NE2	2.50	0.58
1:D:450:LEU:O	1:D:451:ARG:C	2.44	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:A:450:LEU:O	1:A:451:ARG:C	2.46	0.57
1:B:512:THR:HG22	1:B:573:GLU:OE2	2.04	0.57
1:C:72:PHE:O	1:C:73:SER:C	2.46	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
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:B:450:LEU:O	1:B:451:ARG:C	2.44	0.57
1:C:397:ILE:HG23	1:C:526:ARG:HG2	1.87	0.57
1:D:72:PHE:O	1:D:73:SER:C	2.45	0.57
1:D:78:LEU:HD12	1:D:79:LEU:N	2.20	0.57
1:D:172:GLN:CD	1:D:172:GLN:H	2.12	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:72:PHE:O	1:A:73:SER:C	2.46	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: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:A:259:MET:HE2	1:A:262:GLN:HE22	1.69	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:297:LEU:HD13	1:A:318:ASN:HD21	1.70	0.56
1:B:72:PHE:O	1:B:73:SER:C	2.46	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:102:MET:HE3	1:D:163:PRO:HD2	1.87	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:GLN:C	1:A:106:TYR:H	2.13	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:D:393:HIS:O	1:D:394:ASP:C	2.48	0.56
1:A:393:HIS:O	1:A:395:LEU:HG	2.04	0.56
1:B:172:GLN:H	1:B:172:GLN:CD	2.13	0.56
1:B:650:HIS:O	1:B:651:ILE:C	2.48	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: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
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:A:719:PHE:C	1:A:721:MET:N	2.60	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:C:172:GLN:H	1:C:172:GLN:CD	2.14	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:104:GLN:C	1:B:106:TYR:H	2.13	0.56
1:B:332:VAL:HG22	1:B:356:LYS:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:244:LYS:HB3	1:D:253:LEU:CD1	2.36	0.56
1:B:393:HIS:O	1:B:394:ASP:C	2.49	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:536:ILE:HD11	1:D:655:LEU:C	2.32	0.55
1:D:650:HIS:O	1:D:651:ILE:C	2.49	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:434:MET:HE3	1:D:442:TYR:HD1	1.71	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:D:104:GLN:C	1:D:106:TYR:H	2.14	0.55
1:A:558:LEU:HD11	1:A:635:LEU:CD1	2.36	0.55
1:C:104:GLN:C	1:C:106:TYR:H	2.14	0.55
1:C:558:LEU:HD11	1:C:635:LEU:CD1	2.36	0.55
1:C:719:PHE:C	1:C:721:MET:N	2.61	0.55
1:D:419:ILE:HG12	1:D:457:PHE:CD2	2.41	0.55
1:D:707:SER:O	1:D:708:ASN:C	2.50	0.55
1:A:149:TRP:CE3	1:A:150:PHE:HB3	2.42	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:575:ASN:C	1:D:577:PHE:H	2.14	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
1:D:259:MET:HE1	1:D:313:TYR:CE2	2.42	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:A:528:ILE:O	1:A:529:SER:C	2.50	0.55
1:B:403:ASP:HB3	1:B:406:ARG:HB3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:428:SER:O	1:C:431:LYS:N	2.39	0.55
1:C:719:PHE:O	1:C:720:PHE:C	2.50	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:D:657:LEU:O	1:D:658:HIS:C	2.50	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:536:ILE:HD11	1:A:655:LEU:C	2.32	0.54
1:B:71:HIS:CE1	1:B:478:PRO:CA	2.90	0.54
1:B:536:ILE:HD11	1:B:655:LEU:C	2.32	0.54
1:B:545:THR:C	1:B:547:VAL:N	2.60	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:C:528:ILE:O	1:C:529:SER:C	2.50	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:B:122:ILE:CD1	1:B:166:LEU:HD13	2.33	0.54
1:C:575:ASN:C	1:C:577:PHE:H	2.14	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:D:525:LEU:O	1:D:526:ARG:C	2.49	0.54
1:A:393:HIS:O	1:A:394:ASP:C	2.49	0.54
1:A:443:LEU:C	1:A:445:ASN:N	2.64	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:B:575:ASN:C	1:B:577:PHE:H	2.14	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:A:575:ASN:C	1:A:577:PHE:H	2.14	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:443:LEU:C	1:C:445:ASN:N	2.64	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
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:C:707:SER:O	1:C:708:ASN:C	2.50	0.54
1:D:11:LEU:HB3	1:D:87:ALA:CB	2.38	0.54
1:D:545:THR:C	1:D:547:VAL:N	2.61	0.54
1:A:396:ASP:C	1:A:396:ASP:OD1	2.50	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:396:ASP:C	1:C:396:ASP:OD1	2.50	0.54
1:C:404:VAL:HG13	1:C:405:GLU:N	2.23	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:D:719:PHE:O	1:D:720:PHE:C	2.50	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:C:393:HIS:O	1:C:394:ASP:C	2.50	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:D:396:ASP:C	1:D:396:ASP:OD1	2.50	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:259:MET:HE1	1:C:313:TYR:CE2	2.42	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:546:THR:O	1:D:546:THR:CG2	2.54	0.54
1:A:707:SER:O	1:A:708:ASN:C	2.51	0.54
1:A:719:PHE:O	1:A:720:PHE:C	2.51	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:C:536:ILE:HD11	1:C:655:LEU:C	2.33	0.53
1:D:28:VAL:HB	1:D:98:PRO:HD3	1.90	0.53
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:650:HIS:O	1:C:651:ILE:C	2.50	0.53
1:A:207:SER:C	1:A:209:THR:H	2.15	0.53
1:A:657:LEU:O	1:A:658:HIS:C	2.52	0.53
1:B:525:LEU:O	1:B:526:ARG:C	2.50	0.53
1:B:707:SER:O	1:B:708:ASN:C	2.51	0.53
1:C:601:PHE:O	1:C:602:ILE:HB	2.09	0.53
1:D:336:LEU:C	1:D:337:THR:HG22	2.33	0.53
1:A:78:LEU:HD12	1:A:79:LEU:N	2.21	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:207:SER:C	1:B:209:THR:H	2.15	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:A:650:HIS:O	1:A:651:ILE:C	2.50	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:C:657:LEU:O	1:C:658:HIS:C	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:109:THR:HG23	1:D:120:ASN:HD22	1.74	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:207:SER:C	1:C:209:THR:H	2.16	0.53
1:C:263:SER:O	1:C:264:ASP:C	2.51	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: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: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:B:263:SER:O	1:B:264:ASP:C	2.51	0.53
1:B:657:LEU:O	1:B:658:HIS:C	2.52	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: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:B:434:MET:HE3	1:B:442:TYR:HD1	1.74	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:336:LEU:C	1:B:337:THR:HG22	2.34	0.52
1:C:293:LEU:HB2	1:C:297:LEU:CG	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:B:528:ILE:O	1:B:529:SER:C	2.50	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:207:SER:C	1:D:209:THR:H	2.16	0.52
1:A:263:SER:O	1:A:264:ASP:C	2.51	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
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: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:443:LEU:C	1:B:445:ASN:N	2.65	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:434:MET:HE3	1:A:442:TYR:HD1	1.75	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:B:719:PHE:O	1:B:720:PHE:C	2.52	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:D:629:ILE:O	1:D:630:THR:C	2.52	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:525:LEU:O	1:A:526:ARG:C	2.52	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:D:317:ASN:CG	1:D:318:ASN:N	2.67	0.52
1:D:443:LEU:C	1:D:445:ASN:N	2.65	0.52
1:A:317:ASN:CG	1:A:318:ASN:N	2.67	0.52
1:B:521:SER:O	1:B:524:VAL:HB	2.09	0.52
1:B:541:PRO:HB2	1:B:544:MET:HE2	1.92	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:A:150:PHE:CD1	1:A:150:PHE:C	2.88	0.52
1:B:180:ASP:C	1:B:182:GLY:H	2.17	0.52
1:B:368:VAL:O	1:B:368:VAL:CG2	2.57	0.52
1:B:396:ASP:C	1:B:396:ASP:OD1	2.52	0.52
1:C:14:TYR:HB3	1:C:673:CYS:HB2	1.91	0.52
1:C:185:GLY:C	1:C:186:LEU:HD12	2.35	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
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:336:LEU:C	1:A:337:THR:HG22	2.34	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:180:ASP:C	1:C:182:GLY:H	2.17	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:708:ASN:O	1:D:712:ALA:HB2	2.09	0.52
1:A:180:ASP:C	1:A:182:GLY:H	2.17	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:C:317:ASN:CG	1:C:318:ASN:N	2.68	0.51
1:C:434:MET:HE3	1:C:442:TYR:HD1	1.76	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:185:GLY:C	1:A:186:LEU:HD12	2.36	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:ILE:HG21	1:D:203:SER:HB2	1.93	0.51
1:B:150:PHE:CD1	1:B:150:PHE:C	2.89	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:D:150:PHE:CD1	1:D:150:PHE:C	2.89	0.51
1:D:528:ILE:O	1:D:529:SER:C	2.51	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:601:PHE:O	1:B:602:ILE:HB	2.09	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:C:445:ASN:O	1:C:446:LEU:C	2.53	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:185:GLY:C	1:B:186:LEU:HD12	2.35	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: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:336:LEU:C	1:C:337:THR:HG22	2.35	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
1:D:506:LEU:HA	1:D:582:VAL:CG1	2.41	0.51
1:D:601:PHE:O	1:D:602:ILE:HB	2.09	0.51
1:A:317:ASN:HB3	1:A:373:PHE:HB3	1.93	0.51
1:B:317:ASN:CG	1:B:318:ASN:N	2.68	0.51
1:B:707:SER:O	1:B:709:VAL:N	2.43	0.51
1:C:150:PHE:C	1:C:150:PHE:CD1	2.89	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:690:VAL:CG1	1:D:691:LYS:N	2.74	0.51
1:A:1:MET:O	1:A:1:MET:HG2	2.10	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:B:232:ARG:NH1	1:B:233:TYR:OH	2.44	0.51
1:B:445:ASN:O	1:B:446:LEU:C	2.53	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:C:552:ASP:C	1:C:552:ASP:OD1	2.54	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: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
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:A:541:PRO:HB2	1:A:544:MET:CE	2.40	0.51
1:A:568:LYS:HZ3	1:D:210:ARG:NH2	2.09	0.51
1:C:553:ILE:O	1:C:553:ILE:CG2	2.59	0.51
1:D:180:ASP:C	1:D:182:GLY:H	2.18	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:445:ASN:O	1:A:446:LEU:C	2.54	0.50
1:A:620:HIS:CD2	1:A:668:TYR:CD2	2.99	0.50
1:B:157:ASP:C	1:B:159:THR:H	2.19	0.50
1:B:280:LEU:O	1:B:280:LEU:HD12	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:525:LEU:O	1:C:526:ARG:C	2.54	0.50
1:C:541:PRO:HB2	1:C:544:MET:CE	2.40	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:185:GLY:C	1:D:186:LEU:HD12	2.36	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:307:SER:O	1:C:308:SER:C	2.50	0.50
1:C:541:PRO:HB2	1:C:544:MET:HE2	1.92	0.50
1:C:708:ASN:O	1:C:712:ALA:HB2	2.10	0.50
1:D:157:ASP:C	1:D:159:THR:H	2.19	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:663:LEU:CD1	1:D:729:ILE:HD12	2.41	0.50
1:A:157:ASP:C	1:A:159:THR:H	2.19	0.50
1:A:552:ASP:C	1:A:552:ASP:OD1	2.54	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:B:55:GLU:OE1	1:B:74:SER:CA	2.59	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
1:C:690:VAL:CG1	1:C:691:LYS:N	2.74	0.50
1:D:172:GLN:NE2	1:D:172:GLN:N	2.60	0.50
1:D:304:LEU:O	1:D:312:THR:OG1	2.26	0.50
1:D:370:ASP:OD1	1:D:372:SER:HB3	2.11	0.50
1:D:428:SER:O	1:D:429:GLU:C	2.54	0.50
1:A:214:ARG:O	1:A:214:ARG:HG2	2.11	0.50
1:A:694:ASN:CG	1:A:697:GLN:HG3	2.36	0.50
1:B:225:SER:OG	1:B:279:TYR:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:157:ASP:C	1:C:159:THR:H	2.19	0.50
1:C:214:ARG:O	1:C:214:ARG:HG2	2.10	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:C:707:SER:C	1:C:709:VAL:N	2.70	0.50
1:A:594:GLY:C	1:A:595:ILE:HD12	2.37	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: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: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: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: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:D:542:ASP:O	1:D:543:SER:C	2.55	0.50
1:D:707:SER:C	1:D:709:VAL:N	2.70	0.50
1:A:125:ASP:OD1	1:A:127:SER:OG	2.29	0.50
1:A:225:SER:OG	1:A:279:TYR:HB2	2.12	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
1:B:629:ILE:O	1:B:630:THR:C	2.54	0.50
1:C:57:SER:HB2	1:C:71:HIS:CD2	2.47	0.50
1:C:506:LEU:HA	1:C:582:VAL:CG1	2.41	0.50
1:C:594:GLY:C	1:C:595:ILE:HD12	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:404:VAL:O	1:D:408:PHE:HB2	2.12	0.50
1:D:541:PRO:HB2	1:D:544:MET:HE2	1.94	0.50
1:A:290:LEU:O	1:A:291:LEU:HD23	2.12	0.49
1:C:716:GLU:HG2	1:C:721:MET:C	2.37	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: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:B:192:VAL:O	1:B:192:VAL:HG12	2.11	0.49
1:B:594:GLY:C	1:B:595:ILE:HD12	2.37	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:201:ASP:O	1:C:202:ASN:C	2.55	0.49
1:C:287:LEU:HG	1:C:288:VAL:N	2.26	0.49
1:C:694:ASN:CG	1:C:697:GLN:HG3	2.37	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:B:201:ASP:O	1:B:202:ASN:C	2.55	0.49
1:B:542:ASP:O	1:B:543:SER:C	2.56	0.49
1:C:172:GLN:N	1:C:172:GLN:NE2	2.61	0.49
1:D:192:VAL:O	1:D:192:VAL:HG12	2.12	0.49
1:D:201:ASP:O	1:D:202:ASN:C	2.55	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:568:LYS:NZ	1:D:210:ARG:NH2	2.57	0.49
1:A:707:SER:C	1:A:709:VAL:N	2.70	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:B:428:SER:O	1:B:429:GLU:C	2.55	0.49
1:C:1:MET:O	1:C:1:MET:HG2	2.12	0.49
1:C:9:ALA:CB	1:C:613:ILE:HD11	2.42	0.49
1:C:483:LEU:HD23	1:C:483:LEU:C	2.38	0.49
1:D:287:LEU:HG	1:D:288:VAL:N	2.27	0.49
1:D:552:ASP:C	1:D:552:ASP:OD1	2.55	0.49
1:A:201:ASP:O	1:A:202:ASN:C	2.55	0.49
1:A:344:VAL:CG1	1:A:345:GLU:N	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:C:221:ASP:O	1:C:238:THR:HB	2.12	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:C:629:ILE:O	1:C:630:THR:C	2.54	0.49
1:D:483:LEU:HD23	1:D:483:LEU:C	2.38	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:552:ASP:C	1:B:552:ASP:OD1	2.55	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:D:594:GLY:C	1:D:595:ILE:HD12	2.38	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:A:716:GLU:HG2	1:A:721:MET:C	2.38	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:B:707:SER:C	1:B:709:VAL:N	2.71	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:B:1:MET:HG2	1:B:1:MET:O	2.12	0.49
1:B:180:ASP:C	1:B:182:GLY:N	2.70	0.49
1:C:9:ALA:HB1	1:C:613:ILE:HD11	1.93	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:D:445:ASN:O	1:D:446:LEU:C	2.54	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:VAL:O	1:A:408:PHE:HB2	2.12	0.49
1:A:428:SER:O	1:A:429:GLU:C	2.54	0.49
1:A:705:LEU:O	1:A:706:ASN:C	2.56	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:428:SER:O	1:C:429:GLU:C	2.54	0.49
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:541:PRO:HB2	1:A:544:MET:HE2	1.94	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: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:192:VAL:O	1:A:192:VAL:HG12	2.12	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:536:ILE:HD12	1:B:659:TYR:HB2	1.93	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: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:A:629:ILE:O	1:A:630:THR:C	2.55	0.48
1:A:690:VAL:CG1	1:A:691:LYS:N	2.75	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:D:608:ASP:HB2	1:D:691:LYS:HZ3	1.75	0.48
1:A:370:ASP:OD1	1:A:372:SER:HB3	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:THR:O	1:A:452:ASP:OD2	2.31	0.48
1:B:247:ASP:HB2	1:B:254:ILE:HG13	1.94	0.48
1:B:323:LEU:HD11	1:B:355:TRP:CD2	2.48	0.48
1:B:528:ILE:C	1:B:530:LYS:N	2.68	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:C:443:LEU:O	1:C:444:ALA:C	2.56	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: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: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: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:180:ASP:C	1:D:182:GLY:N	2.70	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:104:GLN:C	1:B:106:TYR:N	2.71	0.48
1:B:254:ILE:CG2	1:B:311:LEU:HB2	2.44	0.48
1:B:716:GLU:HG2	1:B:721:MET:C	2.38	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:443:LEU:O	1:D:444:ALA:C	2.56	0.48
1:D:533:LEU:HD13	1:D:729:ILE:CD1	2.44	0.48
1:A:443:LEU:O	1:A:444:ALA:C	2.56	0.48
1:B:232:ARG:HD2	1:B:233:TYR:CE1	2.49	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: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:D:104:GLN:C	1:D:106:TYR:N	2.72	0.48
1:A:536:ILE:HD12	1:A:659:TYR:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:B:483:LEU:HD23	1:B:483:LEU:C	2.39	0.48
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: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:694:ASN:CG	1:B:697:GLN:HG3	2.38	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: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:C:73:SER:N	1:C:78:LEU:O	2.42	0.47
1:D:18:PRO:N	1:D:417:THR:HG21	2.29	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:180:ASP:C	1:C:182:GLY:N	2.69	0.47
1:D:284:ASN:HB3	1:D:285:ASN:OD1	2.13	0.47
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:O	1:B:444:ALA:C	2.57	0.47
1:B:579:ILE:O	1:B:583:LEU:HB2	2.14	0.47
1:C:270:PHE:C	1:C:270:PHE:CD2	2.91	0.47
1:C:705:LEU:O	1:C:706:ASN:C	2.58	0.47
1:D:528:ILE:C	1:D:530:LYS:N	2.69	0.47
1:A:232:ARG:HG2	1:A:248:LEU:H	1.80	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:694:ASN:CG	1:D:697:GLN:HG3	2.38	0.47
1:A:180:ASP:C	1:A:182:GLY:N	2.70	0.47
1:B:406:ARG:C	1:B:408:PHE:N	2.71	0.47
1:C:259:MET:HE2	1:C:262:GLN:HE22	1.80	0.47
1:D:224:ILE:HD11	1:D:237:LEU:HG	1.97	0.47
1:D:705:LEU:O	1:D:706:ASN:C	2.57	0.47
1:D:716:GLU:HG2	1:D:721:MET:C	2.39	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: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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:406:ARG:C	1:A:408:PHE:N	2.70	0.47
1:A:542:ASP:O	1:A:543:SER:C	2.57	0.47
1:A:585:ASP:OD1	1:A:589:ASN:HB2	2.14	0.47
1:B:125:ASP:OD1	1:B:127:SER:OG	2.29	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:B:705:LEU:O	1:B:706:ASN:C	2.58	0.47
1:C:239:GLN:HG2	1:C:273:VAL:O	2.14	0.47
1:C:406:ARG:C	1:C:408:PHE:N	2.71	0.47
1:C:563:GLU:HB3	1:C:565:THR:CG2	2.45	0.47
1:C:596:PHE:C	1:C:598:LYS:N	2.73	0.47
1:D:124:LYS:O	1:D:126:GLY:N	2.48	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:A:224:ILE:CG2	1:A:276:VAL:HA	2.44	0.47
1:A:596:PHE:C	1:A:598:LYS:N	2.73	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: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:104:GLN:C	1:A:106:TYR:N	2.71	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:344:VAL:CG1	1:B:345:GLU:H	2.27	0.46
1:C:326:SER:OG	1:C:328:ILE:HG13	2.14	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:B:259:MET:HE2	1:B:262:GLN:HE22	1.80	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:D:263:SER:O	1:D:264:ASP:C	2.57	0.46
1:D:705:LEU:C	1:D:707:SER:N	2.70	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:124:LYS:C	1:C:126:GLY:H	2.23	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:125:ASP:OD1	1:D:127:SER:OG	2.29	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:B:436:HIS:C	1:B:438:GLU:H	2.22	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:C:542:ASP:O	1:C:543:SER:C	2.57	0.46
1:D:14:TYR:CE2	1:D:613:ILE:HG22	2.50	0.46
1:D:250:SER:O	1:D:251:PHE:HB2	2.15	0.46
1:A:124:LYS:C	1:A:126:GLY:H	2.23	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:B:124:LYS:C	1:B:126:GLY:H	2.23	0.46
1:C:182:GLY:C	1:C:183:LEU:HD23	2.41	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:140:SER:OG	1:A:141:SER:N	2.44	0.46
1:A:280:LEU:HD12	1:A:280:LEU:O	2.15	0.46
1:B:326:SER:O	1:B:327:ALA:HB3	2.15	0.46
1:B:569:ILE:O	1:B:573:GLU:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:SER:OG	1:C:141:SER:N	2.43	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
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:D:436:HIS:C	1:D:438:GLU:H	2.24	0.46
1:A:187:LYS:HD3	1:A:197:LEU:CD1	2.34	0.46
1:A:483:LEU:C	1:A:483:LEU:HD23	2.41	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:A:705:LEU:C	1:A:707:SER:N	2.69	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:104:GLN:C	1:C:106:TYR:N	2.72	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: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:D:406:ARG:C	1:D:408:PHE:N	2.72	0.46
1:A:232:ARG:HD2	1:A:233:TYR:CE1	2.50	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: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:405:GLU:CD	1:D:437:ASN:ND2	2.74	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:182:GLY:C	1:A:183:LEU:HD23	2.41	0.46
1:A:227:LYS:HG3	1:A:282:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:270:PHE:C	1:A:270:PHE:CD2	2.94	0.46
1:A:534:ASP:HA	1:A:537:THR:OG1	2.15	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:B:705:LEU:C	1:B:707:SER:N	2.71	0.46
1:C:124:LYS:C	1:C:126:GLY:N	2.74	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: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: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:124:LYS:C	1:D:126:GLY:H	2.23	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: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:B:14:TYR:CE2	1:B:613:ILE:HG22	2.50	0.45
1:B:207:SER:C	1:B:209:THR:N	2.74	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:B:307:SER:O	1:B:308:SER:C	2.58	0.45
1:C:28:VAL:HG13	1:C:150:PHE:CD1	2.51	0.45
1:C:73:SER:O	1:C:74:SER:C	2.59	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:326:SER:O	1:D:327:ALA:HB3	2.16	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: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
1:B:182:GLY:C	1:B:183:LEU:HD23	2.42	0.45
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:B:596:PHE:C	1:B:598:LYS:N	2.73	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:232:ARG:HG2	1:C:248:LEU:H	1.82	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:528:ILE:C	1:A:530:LYS:N	2.68	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:82:TYR:CD1	1:C:82:TYR:C	2.95	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:124:LYS:C	1:A:126:GLY:N	2.75	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:A:701:TYR:O	1:A:702:ILE:C	2.59	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:C:540:LEU:HD23	1:C:544:MET:HE1	1.99	0.45
1:D:182:GLY:C	1:D:183:LEU:HD23	2.42	0.45
1:D:342:LEU:HD12	1:D:379:ILE:HD12	1.94	0.45
1:D:596:PHE:C	1:D:598:LYS:N	2.74	0.45
1:A:500:GLU:HG2	1:A:501:THR:O	2.16	0.45
1:B:183:LEU:HD23	1:B:183:LEU:N	2.32	0.45
1:B:265:SER:O	1:B:266:ASP:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:180:ASP:O	1:C:182:GLY:N	2.50	0.45
1:D:172:GLN:H	1:D:172:GLN:NE2	2.15	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:124:LYS:C	1:B:126:GLY:N	2.74	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
1:C:227:LYS:HG3	1:C:282:LEU:HD22	1.99	0.45
1:C:324:SER:O	1:C:325:ALA:C	2.60	0.45
1:C:694:ASN:N	1:C:697:GLN:NE2	2.65	0.45
1:D:68:ILE:HD11	1:D:81:PHE:HD1	1.82	0.45
1:D:124:LYS:C	1:D:126:GLY:N	2.74	0.45
1:D:128:PHE:HB3	1:D:153:GLN:HB3	1.97	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:B:180:ASP:O	1:B:182:GLY:N	2.50	0.45
1:C:14:TYR:OH	1:C:613:ILE:HA	2.16	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: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:D:183:LEU:HD23	1:D:183:LEU:N	2.32	0.45
1:D:192:VAL:O	1:D:193:HIS:ND1	2.50	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:514:ASN:C	1:A:516:PHE:H	2.25	0.45
1:B:240:ASN:O	1:B:242:HIS:N	2.50	0.45
1:B:528:ILE:O	1:B:531:LYS:N	2.50	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: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:697:GLN:O	1:D:700:ALA:HB3	2.17	0.45
1:A:73:SER:O	1:A:74:SER:C	2.60	0.44
1:A:82:TYR:CD1	1:A:82:TYR:C	2.96	0.44
1:A:95:ILE:HG21	1:A:131:LEU:CD1	2.47	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: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: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:232:ARG:HD3	1:C:247:ASP:CG	2.42	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:C:534:ASP:C	1:C:536:ILE:N	2.75	0.44
1:D:172:GLN:HA	1:D:188:LYS:HB3	1.98	0.44
1:D:267:PRO:O	1:D:268:SER:C	2.60	0.44
1:D:540:LEU:HD23	1:D:544:MET:HE1	1.99	0.44
1:A:103:ASN:O	1:A:106:TYR:HB2	2.17	0.44
1:A:144:THR:HG22	1:A:145:LEU:N	2.32	0.44
1:B:496:ASN:HA	1:B:499:SER:HB3	1.99	0.44
1:B:694:ASN:N	1:B:697:GLN:NE2	2.65	0.44
1:C:108:LEU:C	1:C:108:LEU:CD2	2.90	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:C:701:TYR:O	1:C:702:ILE:C	2.60	0.44
1:C:705:LEU:C	1:C:707:SER:N	2.71	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:D:671:ASP:C	1:D:671:ASP:OD1	2.61	0.44
1:A:102:MET:HE2	1:A:122:ILE:CG2	2.46	0.44
1:A:172:GLN:H	1:A:172:GLN:NE2	2.14	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ILE:HG21	1:A:311:LEU:HD22	1.97	0.44
1:A:406:ARG:C	1:A:408:PHE:H	2.26	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
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:207:SER:C	1:D:209:THR:N	2.75	0.44
1:D:335:VAL:HG13	1:D:335:VAL:O	2.17	0.44
1:D:564:ILE:HD12	1:D:564:ILE:HA	1.83	0.44
1:A:569:ILE:O	1:A:573:GLU:HB2	2.17	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:B:108:LEU:C	1:B:108:LEU:CD2	2.89	0.44
1:C:154:ASN:N	1:C:155:PRO:CD	2.79	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: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:207:SER:C	1:A:209:THR:N	2.74	0.44
1:A:232:ARG:HD3	1:A:247:ASP:CG	2.43	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:A:540:LEU:HD23	1:A:544:MET:HE1	2.00	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:C:436:HIS:C	1:C:438:GLU:H	2.25	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:A:324:SER:O	1:A:325:ALA:C	2.61	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HD23	1:C:183:LEU:N	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
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:324:SER:O	1:D:325:ALA:C	2.60	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:HD23	1:A:183:LEU:N	2.32	0.44
1:A:319:ILE:HG23	1:A:320:PRO:HD2	1.98	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:540:LEU:HD23	1:B:544:MET:HE1	2.00	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:A:581:VAL:O	1:A:582:VAL:C	2.61	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: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:207:SER:C	1:C:209:THR:N	2.75	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:534:ASP:C	1:D:536:ILE:N	2.75	0.44
1:D:552:ASP:C	1:D:554:PHE:N	2.75	0.44
1:D:581:VAL:O	1:D:582:VAL:C	2.61	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
1:C:406:ARG:C	1:C:408:PHE:H	2.26	0.43
1:C:478:PRO:O	1:C:479:TYR:HB2	2.18	0.43
1:C:514:ASN:C	1:C:516:PHE:H	2.26	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:552:ASP:C	1:A:554:PHE:N	2.76	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:82:TYR:CD1	1:B:82:TYR:C	2.96	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:B:552:ASP:C	1:B:554:PHE:N	2.76	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:82:TYR:C	1:D:82:TYR:CD1	2.95	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: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:A:669:ARG:O	1:A:670:GLN:C	2.62	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:637:PHE:CD2	1:B:651:ILE:HD11	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:402:GLY:O	1:A:403:ASP:O	2.36	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:73:SER:O	1:B:74:SER:C	2.60	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:581:VAL:O	1:B:582:VAL:C	2.61	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
1:D:559:GLU:O	1:D:560:ASN:HB2	2.18	0.43
1:A:108:LEU:C	1:A:108:LEU:CD2	2.91	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:534:ASP:C	1:A:536:ILE:N	2.76	0.43
1:A:673:CYS:O	1:A:677:GLU:HG2	2.18	0.43
1:B:406:ARG:C	1:B:408:PHE:H	2.26	0.43
1:B:439:ASP:O	1:B:441:GLU:N	2.51	0.43
1:B:701:TYR:O	1:B:702:ILE:C	2.60	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:707:SER:O	1:D:710:TYR:N	2.51	0.43
1:D:719:PHE:C	1:D:721:MET:H	2.26	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:610:PHE:O	1:A:611:THR:C	2.62	0.43
1:A:719:PHE:C	1:A:721:MET:H	2.24	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: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:102:MET:HE2	1:C:122:ILE:CG2	2.48	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:102:MET:HE2	1:D:122:ILE:CG2	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:D:514:ASN:C	1:D:516:PHE:H	2.26	0.43
1:D:522:ASN:O	1:D:523:ASP:C	2.61	0.43
1:D:610:PHE:O	1:D:611:THR:C	2.62	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: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:552:ASP:C	1:C:554:PHE:N	2.76	0.43
1:C:643:ASP:CG	1:C:646:ILE:HG13	2.44	0.43
1:C:651:ILE:C	1:C:653:THR:N	2.76	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
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:108:LEU:C	1:D:108:LEU:CD2	2.91	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:457:PHE:CG	1:A:477:GLN:HG2	2.54	0.43
1:A:541:PRO:HD2	1:A:544:MET:HE1	2.01	0.43
1:B:227:LYS:HG3	1:B:282:LEU:HD22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:610:PHE:O	1:B:611:THR:C	2.62	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:D:73:SER:O	1:D:74:SER:C	2.61	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:436:HIS:C	1:A:438:GLU:H	2.27	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:232:ARG:HD3	1:B:247:ASP:CG	2.43	0.43
1:B:250:SER:O	1:B:251:PHE:HB2	2.18	0.43
1:B:602:ILE:HG22	1:B:602:ILE:O	2.18	0.43
1:B:719:PHE:C	1:B:721:MET:H	2.26	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:232:ARG:HD3	1:D:247:ASP:CG	2.43	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:D:701:TYR:O	1:D:702:ILE:C	2.61	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
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:C:71:HIS:CE1	1:C:478:PRO:N	2.87	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: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:406:ARG:C	1:D:408:PHE:H	2.27	0.42
1:D:602:ILE:O	1:D:602:ILE:HG22	2.18	0.42
1:A:18:PRO:N	1:A:417:THR:HG21	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:VAL:CG2	1:A:669:ARG:HH12	2.33	0.42
1:A:405:GLU:CD	1:A:437:ASN:HD22	2.26	0.42
1:A:643:ASP:CG	1:A:646:ILE:HG13	2.44	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:443:LEU:C	1:B:445:ASN:H	2.27	0.42
1:B:468:ASP:HB2	1:B:469:GLU:OE2	2.19	0.42
1:B:562:PHE:CD1	1:B:562:PHE:C	2.97	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:D:255:GLN:OE1	1:D:257:TYR:HE2	2.02	0.42
1:D:562:PHE:CD1	1:D:562:PHE:C	2.97	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: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: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: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:441:GLU:O	1:C:445:ASN:ND2	2.52	0.42
1:C:581:VAL:O	1:C:582:VAL:C	2.62	0.42
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:599:LYS:O	1:D:600:ASP:C	2.62	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:A:404:VAL:C	1:A:406:ARG:N	2.76	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:B:599:LYS:O	1:B:600:ASP:C	2.62	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:671:ASP:C	1:A:671:ASP:OD1	2.62	0.42
1:B:177:PHE:CD1	1:B:183:LEU:HB3	2.55	0.42
1:B:534:ASP:C	1:B:536:ILE:N	2.76	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:C:669:ARG:O	1:C:670:GLN:C	2.63	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:541:PRO:HD2	1:B:544:MET:HE1	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:C:404:VAL:C	1:C:406:ARG:N	2.76	0.42
1:C:541:PRO:HD2	1:C:544:MET:HE1	2.02	0.42
1:C:723:PHE:O	1:C:724:PHE:C	2.63	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:403:ASP:CG	1:A:404:VAL:N	2.75	0.42
1:A:441:GLU:O	1:A:445:ASN:ND2	2.53	0.42
1:B:53:GLY:HA3	1:B:71:HIS:HB3	2.02	0.42
1:B:324:SER:O	1:B:325:ALA:C	2.62	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
1:B:466:TYR:O	1:B:470:ILE:HB	2.20	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: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:443:LEU:C	1:D:445:ASN:H	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:541:PRO:HD2	1:D:544:MET:HE1	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:75:ARG:C	1:A:77:THR:N	2.77	0.42
1:A:110:ILE:O	1:A:111:GLN:NE2	2.53	0.42
1:A:443:LEU:C	1:A:445:ASN:H	2.27	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:599:LYS:O	1:A:600:ASP:C	2.62	0.42
1:B:441:GLU:O	1:B:445:ASN:ND2	2.53	0.42
1:B:514:ASN:C	1:B:516:PHE:H	2.26	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:D:669:ARG:O	1:D:670:GLN:C	2.62	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:579:ILE:O	1:A:580:PRO:C	2.62	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:403:ASP:CG	1:C:404:VAL:N	2.76	0.42
1:C:579:ILE:O	1:C:580:PRO:C	2.62	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:SER:O	1:A:251:PHE:HB2	2.19	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: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: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:293:LEU:C	1:C:295:ASN:N	2.78	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:C:599:LYS:O	1:C:600:ASP:C	2.62	0.42
1:C:610:PHE:O	1:C:611:THR:C	2.63	0.42
1:C:671:ASP:C	1:C:671:ASP:OD1	2.63	0.42
1:D:334:LEU:CD1	1:D:351:LEU:HD11	2.37	0.42
1:D:404:VAL:C	1:D:406:ARG:N	2.75	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:562:PHE:CD1	1:C:562:PHE:C	2.98	0.41
1:C:578:ASP:O	1:C:579:ILE:C	2.63	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:293:LEU:C	1:A:295:ASN:N	2.78	0.41
1:A:562:PHE:CD1	1:A:562:PHE:C	2.98	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:259:MET:CE	1:A:262:GLN:HE22	2.33	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: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:267:PRO:O	1:C:268:SER:C	2.62	0.41
1:C:297:LEU:HD13	1:C:318:ASN:ND2	2.34	0.41
1:C:443:LEU:C	1:C:445:ASN:H	2.28	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: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:102:MET:HE2	1:B:122:ILE:CG2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:237:LEU:CD1	1:B:241:CYS:HA	2.50	0.41
1:B:404:VAL:C	1:B:406:ARG:N	2.75	0.41
1:B:535:ILE:HG21	1:B:655:LEU:HD13	2.02	0.41
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:B:674:LEU:O	1:B:675:LEU:C	2.62	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:C:719:PHE:C	1:C:721:MET:H	2.26	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:643:ASP:CG	1:D:646:ILE:HG13	2.44	0.41
1:A:77:THR:O	1:A:97:LEU:HB2	2.20	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: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:B:651:ILE:C	1:B:653:THR:N	2.77	0.41
1:B:669:ARG:O	1:B:670:GLN:C	2.62	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:534:ASP:HA	1:C:537:THR:HG1	1.85	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:B:671:ASP:OD1	1:B:671:ASP:C	2.64	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:73:SER:O	1:D:76:SER:N	2.50	0.41
1:D:234:LEU:O	1:D:235:ILE:C	2.64	0.41
1:D:323:LEU:HD11	1:D:355:TRP:CE3	2.55	0.41
1:D:563:GLU:HB3	1:D:565:THR:HG22	2.02	0.41
1:D:674:LEU:O	1:D:675:LEU:C	2.62	0.41
1:B:643:ASP:CG	1:B:646:ILE:HG13	2.45	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
1:C:55:GLU:HB3	1:C:56:TYR:H	1.75	0.41
1:C:75:ARG:C	1:C:77:THR:N	2.78	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: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: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:A:578:ASP:O	1:A:579:ILE:C	2.64	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: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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:C:396:ASP:OD2	1:C:399:THR:OG1	2.36	0.41
1:C:423:ALA:HB2	1:C:453:VAL:HG21	2.03	0.41
1:C:439:ASP:C	1:C:441:GLU:N	2.79	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: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:403:ASP:CG	1:D:404:VAL:N	2.74	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: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: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:D:651:ILE:C	1:D:653:THR:N	2.77	0.41
1:A:478:PRO:O	1:A:479:TYR:HB2	2.21	0.40
1:A:514:ASN:C	1:A:516:PHE:N	2.79	0.40
1:A:651:ILE:C	1:A:653:THR:N	2.79	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:B:598:LYS:NZ	1:B:685:GLU:OE1	2.49	0.40
1:C:22:ASN:ND2	1:C:91:LYS:HD3	2.36	0.40
1:C:260:VAL:O	1:C:261:SER:HB3	2.21	0.40
1:C:514:ASN:C	1:C:516:PHE:N	2.79	0.40
1:D:22:ASN:HD21	1:D:91:LYS:HD3	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:423:ALA:HB2	1:D:453:VAL:HG21	2.02	0.40
1:D:439:ASP:C	1:D:441:GLU:N	2.79	0.40
1:D:579:ILE:O	1:D:580:PRO:C	2.63	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: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
1:B:234:LEU:O	1:B:235:ILE:C	2.64	0.40
1:B:439:ASP:C	1:B:441:GLU:N	2.79	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:723:PHE:O	1:D:724:PHE:C	2.63	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:A:439:ASP:C	1:A:441:GLU:N	2.79	0.40
1:A:723:PHE:O	1:A:724:PHE:C	2.64	0.40
1:B:575:ASN:C	1:B:577:PHE:N	2.79	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: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:578:ASP:O	1:D:579:ILE:C	2.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:610:PHE:C	1:D:612:SER:N	2.79	0.40
1:D:694:ASN:CG	1:D:697:GLN:HE21	2.30	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
1:B:522:ASN:O	1:B:523:ASP:C	2.64	0.40
1:B:549:LYS:O	1:B:552:ASP:N	2.54	0.40
1:B:578:ASP:O	1:B:579:ILE:C	2.63	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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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 ⓘ

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%)	609 (92%)	52 (8%)	11	39
1	B	661/682 (97%)	608 (92%)	53 (8%)	11	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	661/682 (97%)	609 (92%)	52 (8%)	11	39
1	D	661/682 (97%)	609 (92%)	52 (8%)	11	39
All	All	2644/2728 (97%)	2435 (92%)	209 (8%)	11	39

All (209) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	THR
1	A	99	ASN
1	A	164	HIS
1	A	172	GLN
1	A	180	ASP
1	A	183	LEU
1	A	236	VAL
1	A	270	PHE
1	A	294	GLU
1	A	297	LEU
1	A	311	LEU
1	A	312	THR
1	A	328	ILE
1	A	337	THR
1	A	338	ARG
1	A	342	LEU
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	389	LEU
1	A	393	HIS
1	A	398	VAL
1	A	409	CYS
1	A	427	LEU
1	A	430	ASN
1	A	438	GLU
1	A	446	LEU
1	A	455	THR
1	A	464	THR
1	A	469	GLU
1	A	530	LYS

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Mol	Chain	Res	Type
1	A	540	LEU
1	A	541	PRO
1	A	546	THR
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	613	ILE
1	A	638	VAL
1	A	663	LEU
1	A	670	GLN
1	A	679	LEU
1	A	683	SER
1	A	692	PHE
1	A	716	GLU
1	A	717	ASN
1	B	92	THR
1	B	99	ASN
1	B	164	HIS
1	B	172	GLN
1	B	180	ASP
1	B	183	LEU
1	B	236	VAL
1	B	294	GLU
1	B	297	LEU
1	B	310	ILE
1	B	311	LEU
1	B	312	THR
1	B	328	ILE
1	B	337	THR
1	B	338	ARG
1	B	342	LEU
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	389	LEU
1	B	393	HIS

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Mol	Chain	Res	Type
1	B	398	VAL
1	B	409	CYS
1	B	417	THR
1	B	427	LEU
1	B	430	ASN
1	B	438	GLU
1	B	446	LEU
1	B	455	THR
1	B	464	THR
1	B	469	GLU
1	B	530	LYS
1	B	540	LEU
1	B	541	PRO
1	B	546	THR
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	613	ILE
1	B	638	VAL
1	B	663	LEU
1	B	670	GLN
1	B	679	LEU
1	B	683	SER
1	B	692	PHE
1	B	716	GLU
1	B	717	ASN
1	C	92	THR
1	C	99	ASN
1	C	164	HIS
1	C	172	GLN
1	C	180	ASP
1	C	183	LEU
1	C	188	LYS
1	C	236	VAL
1	C	270	PHE
1	C	294	GLU
1	C	297	LEU
1	C	311	LEU
1	C	312	THR

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Mol	Chain	Res	Type
1	C	328	ILE
1	C	337	THR
1	C	338	ARG
1	C	342	LEU
1	C	349	LEU
1	C	363	LEU
1	C	375	ASN
1	C	377	GLU
1	C	385	SER
1	C	386	LEU
1	C	389	LEU
1	C	393	HIS
1	C	398	VAL
1	C	409	CYS
1	C	427	LEU
1	C	430	ASN
1	C	446	LEU
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	546	THR
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	613	ILE
1	C	638	VAL
1	C	663	LEU
1	C	670	GLN
1	C	679	LEU
1	C	683	SER
1	C	692	PHE
1	C	716	GLU
1	C	717	ASN
1	D	92	THR
1	D	99	ASN
1	D	164	HIS

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Mol	Chain	Res	Type
1	D	172	GLN
1	D	180	ASP
1	D	183	LEU
1	D	188	LYS
1	D	236	VAL
1	D	294	GLU
1	D	297	LEU
1	D	311	LEU
1	D	312	THR
1	D	328	ILE
1	D	337	THR
1	D	338	ARG
1	D	342	LEU
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	389	LEU
1	D	393	HIS
1	D	398	VAL
1	D	409	CYS
1	D	427	LEU
1	D	430	ASN
1	D	438	GLU
1	D	446	LEU
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	546	THR
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	613	ILE
1	D	638	VAL

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Mol	Chain	Res	Type
1	D	663	LEU
1	D	670	GLN
1	D	679	LEU
1	D	683	SER
1	D	692	PHE
1	D	716	GLU
1	D	717	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (121) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	22	ASN
1	A	71	HIS
1	A	89	HIS
1	A	99	ASN
1	A	111	GLN
1	A	115	GLN
1	A	120	ASN
1	A	132	GLN
1	A	172	GLN
1	A	262	GLN
1	A	299	GLN
1	A	318	ASN
1	A	425	GLN
1	A	430	ASN
1	A	458	ASN
1	A	474	ASN
1	A	492	ASN
1	A	514	ASN
1	A	561	GLN
1	A	575	ASN
1	A	588	ASN
1	A	589	ASN
1	A	590	GLN
1	A	620	HIS
1	A	621	GLN
1	A	632	GLN
1	A	670	GLN
1	A	697	GLN
1	B	22	ASN
1	B	71	HIS

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Mol	Chain	Res	Type
1	B	89	HIS
1	B	111	GLN
1	B	115	GLN
1	B	120	ASN
1	B	132	GLN
1	B	172	GLN
1	B	318	ASN
1	B	369	ASN
1	B	425	GLN
1	B	430	ASN
1	B	437	ASN
1	B	458	ASN
1	B	474	ASN
1	B	487	ASN
1	B	492	ASN
1	B	514	ASN
1	B	561	GLN
1	B	575	ASN
1	B	584	ASN
1	B	588	ASN
1	B	589	ASN
1	B	590	GLN
1	B	620	HIS
1	B	632	GLN
1	B	670	GLN
1	B	697	GLN
1	C	13	GLN
1	C	22	ASN
1	C	71	HIS
1	C	89	HIS
1	C	103	ASN
1	C	111	GLN
1	C	115	GLN
1	C	120	ASN
1	C	132	GLN
1	C	172	GLN
1	C	242	HIS
1	C	262	GLN
1	C	299	GLN
1	C	318	ASN
1	C	425	GLN
1	C	430	ASN

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Mol	Chain	Res	Type
1	C	437	ASN
1	C	458	ASN
1	C	474	ASN
1	C	487	ASN
1	C	492	ASN
1	C	514	ASN
1	C	561	GLN
1	C	575	ASN
1	C	584	ASN
1	C	588	ASN
1	C	589	ASN
1	C	590	GLN
1	C	620	HIS
1	C	632	GLN
1	C	670	GLN
1	C	697	GLN
1	D	13	GLN
1	D	22	ASN
1	D	71	HIS
1	D	89	HIS
1	D	99	ASN
1	D	103	ASN
1	D	111	GLN
1	D	115	GLN
1	D	120	ASN
1	D	132	GLN
1	D	172	GLN
1	D	242	HIS
1	D	299	GLN
1	D	318	ASN
1	D	369	ASN
1	D	425	GLN
1	D	430	ASN
1	D	458	ASN
1	D	474	ASN
1	D	487	ASN
1	D	492	ASN
1	D	514	ASN
1	D	561	GLN
1	D	575	ASN
1	D	588	ASN
1	D	589	ASN

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Mol	Chain	Res	Type
1	D	590	GLN
1	D	620	HIS
1	D	621	GLN
1	D	632	GLN
1	D	670	GLN
1	D	697	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	706/729 (96%)	-0.90	1 (0%) 92 86	51, 121, 174, 188	0
1	B	706/729 (96%)	-0.89	1 (0%) 92 86	54, 121, 174, 188	0
1	C	706/729 (96%)	-0.92	0 100 100	52, 122, 174, 191	0
1	D	706/729 (96%)	-0.85	1 (0%) 92 86	50, 121, 174, 186	0
All	All	2824/2916 (96%)	-0.89	3 (0%) 92 86	50, 122, 174, 191	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	53	GLY	3.2
1	D	558	LEU	2.7
1	B	183	LEU	2.2

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.