Full wwPDB X-ray Structure Validation Report ⓘ

Mar 19, 2026 – 11:57 PM UTC

PDB ID	:	4EBA / pdb_00004eba
Title	:	Crystal structure of the Rna14-Rna15 complex
Authors	:	Paulson, A.R.; Tong, L.
Deposited on	:	2012-03-23
Resolution	:	3.30 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:

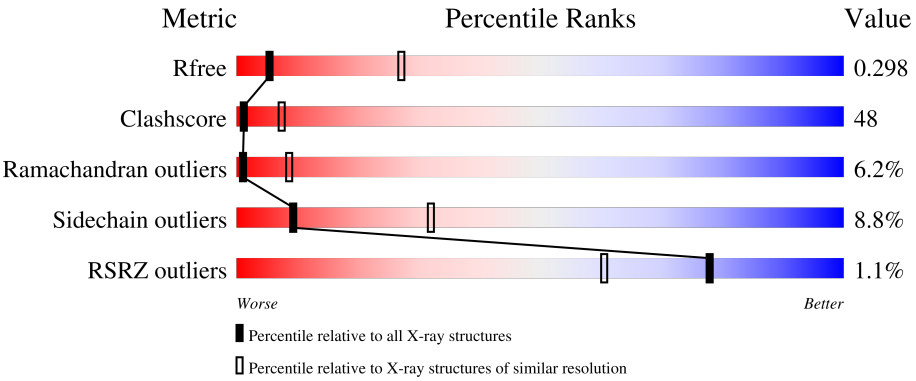
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



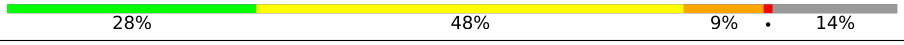
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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 <=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	645	25% 53% 12% • 9%
1	B	645	27% 48% 11% • 13%
1	C	645	% 31% 51% 8% 9%
1	D	645	29% 48% 8% 15%
1	E	645	5% 25% 52% 13% • 10%

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Mol	Chain	Length	Quality of chain
1	F	645	
2	G	174	
2	H	174	
2	I	174	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 30268 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 mRNA 3'-end-processing protein RNA14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	585	Total	C	N	O	S	0	0	0
			4874	3149	803	897	25			
1	B	558	Total	C	N	O	S	0	0	0
			4646	2990	772	859	25			
1	C	585	Total	C	N	O	S	0	0	0
			4874	3149	803	897	25			
1	D	551	Total	C	N	O	S	0	0	0
			4589	2957	759	848	25			
1	E	578	Total	C	N	O	S	0	0	0
			4823	3118	795	885	25			
1	F	553	Total	C	N	O	S	0	0	0
			4608	2967	764	852	25			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MET	-	expression tag	UNP Q6CII8
B	17	MET	-	expression tag	UNP Q6CII8
C	17	MET	-	expression tag	UNP Q6CII8
D	17	MET	-	expression tag	UNP Q6CII8
E	17	MET	-	expression tag	UNP Q6CII8
F	17	MET	-	expression tag	UNP Q6CII8

- Molecule 2 is a protein called Rna15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	81	Total	C	N	O	S	0	0	0
			618	395	98	119	6			
2	I	81	Total	C	N	O	S	0	0	0
			618	395	98	119	6			
2	H	81	Total	C	N	O	S	0	0	0
			618	395	98	119	6			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	85	MET	-	expression tag	UNP Q6CKN2
G	86	GLY	-	expression tag	UNP Q6CKN2
G	87	SER	-	expression tag	UNP Q6CKN2
G	88	SER	-	expression tag	UNP Q6CKN2
G	89	HIS	-	expression tag	UNP Q6CKN2
G	90	HIS	-	expression tag	UNP Q6CKN2
G	91	HIS	-	expression tag	UNP Q6CKN2
G	92	HIS	-	expression tag	UNP Q6CKN2
G	93	HIS	-	expression tag	UNP Q6CKN2
G	94	HIS	-	expression tag	UNP Q6CKN2
G	95	SER	-	expression tag	UNP Q6CKN2
G	96	SER	-	expression tag	UNP Q6CKN2
G	97	GLY	-	expression tag	UNP Q6CKN2
G	98	LEU	-	expression tag	UNP Q6CKN2
G	99	VAL	-	expression tag	UNP Q6CKN2
G	100	PRO	-	expression tag	UNP Q6CKN2
G	101	ARG	-	expression tag	UNP Q6CKN2
G	102	GLY	-	expression tag	UNP Q6CKN2
G	103	SER	-	expression tag	UNP Q6CKN2
G	104	HIS	-	expression tag	UNP Q6CKN2
I	85	MET	-	expression tag	UNP Q6CKN2
I	86	GLY	-	expression tag	UNP Q6CKN2
I	87	SER	-	expression tag	UNP Q6CKN2
I	88	SER	-	expression tag	UNP Q6CKN2
I	89	HIS	-	expression tag	UNP Q6CKN2
I	90	HIS	-	expression tag	UNP Q6CKN2
I	91	HIS	-	expression tag	UNP Q6CKN2
I	92	HIS	-	expression tag	UNP Q6CKN2
I	93	HIS	-	expression tag	UNP Q6CKN2
I	94	HIS	-	expression tag	UNP Q6CKN2
I	95	SER	-	expression tag	UNP Q6CKN2
I	96	SER	-	expression tag	UNP Q6CKN2
I	97	GLY	-	expression tag	UNP Q6CKN2
I	98	LEU	-	expression tag	UNP Q6CKN2
I	99	VAL	-	expression tag	UNP Q6CKN2
I	100	PRO	-	expression tag	UNP Q6CKN2
I	101	ARG	-	expression tag	UNP Q6CKN2
I	102	GLY	-	expression tag	UNP Q6CKN2
I	103	SER	-	expression tag	UNP Q6CKN2
I	104	HIS	-	expression tag	UNP Q6CKN2
H	85	MET	-	expression tag	UNP Q6CKN2
H	86	GLY	-	expression tag	UNP Q6CKN2

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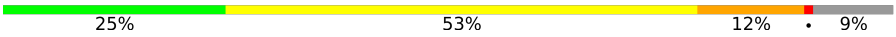
Chain	Residue	Modelled	Actual	Comment	Reference
H	87	SER	-	expression tag	UNP Q6CKN2
H	88	SER	-	expression tag	UNP Q6CKN2
H	89	HIS	-	expression tag	UNP Q6CKN2
H	90	HIS	-	expression tag	UNP Q6CKN2
H	91	HIS	-	expression tag	UNP Q6CKN2
H	92	HIS	-	expression tag	UNP Q6CKN2
H	93	HIS	-	expression tag	UNP Q6CKN2
H	94	HIS	-	expression tag	UNP Q6CKN2
H	95	SER	-	expression tag	UNP Q6CKN2
H	96	SER	-	expression tag	UNP Q6CKN2
H	97	GLY	-	expression tag	UNP Q6CKN2
H	98	LEU	-	expression tag	UNP Q6CKN2
H	99	VAL	-	expression tag	UNP Q6CKN2
H	100	PRO	-	expression tag	UNP Q6CKN2
H	101	ARG	-	expression tag	UNP Q6CKN2
H	102	GLY	-	expression tag	UNP Q6CKN2
H	103	SER	-	expression tag	UNP Q6CKN2
H	104	HIS	-	expression tag	UNP Q6CKN2

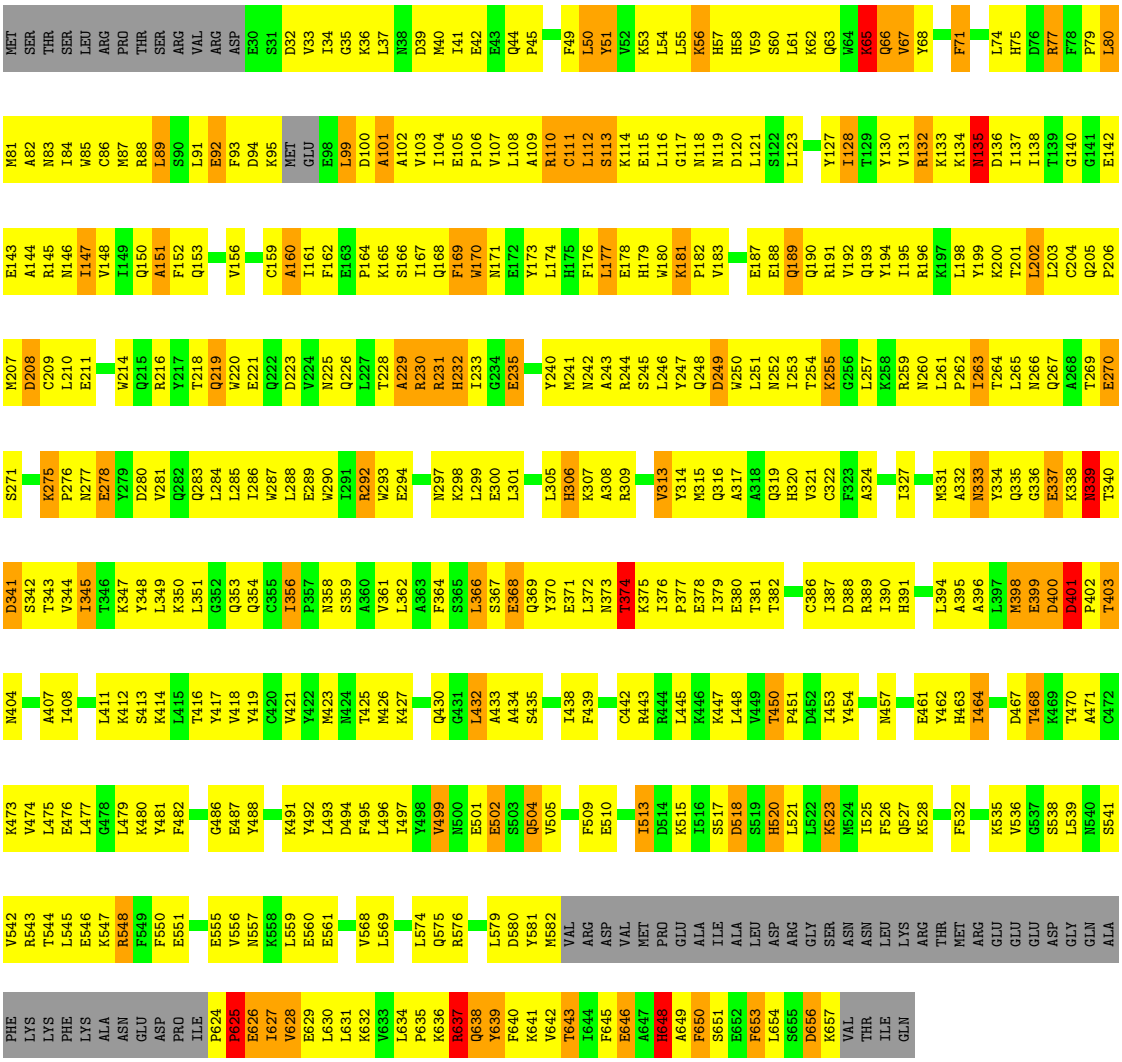
3 Residue-property plots (i)

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

• Molecule 1: mRNA 3'-end-processing protein RNA14

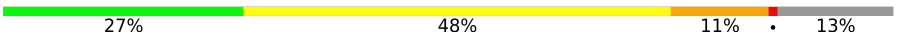
Chain A:

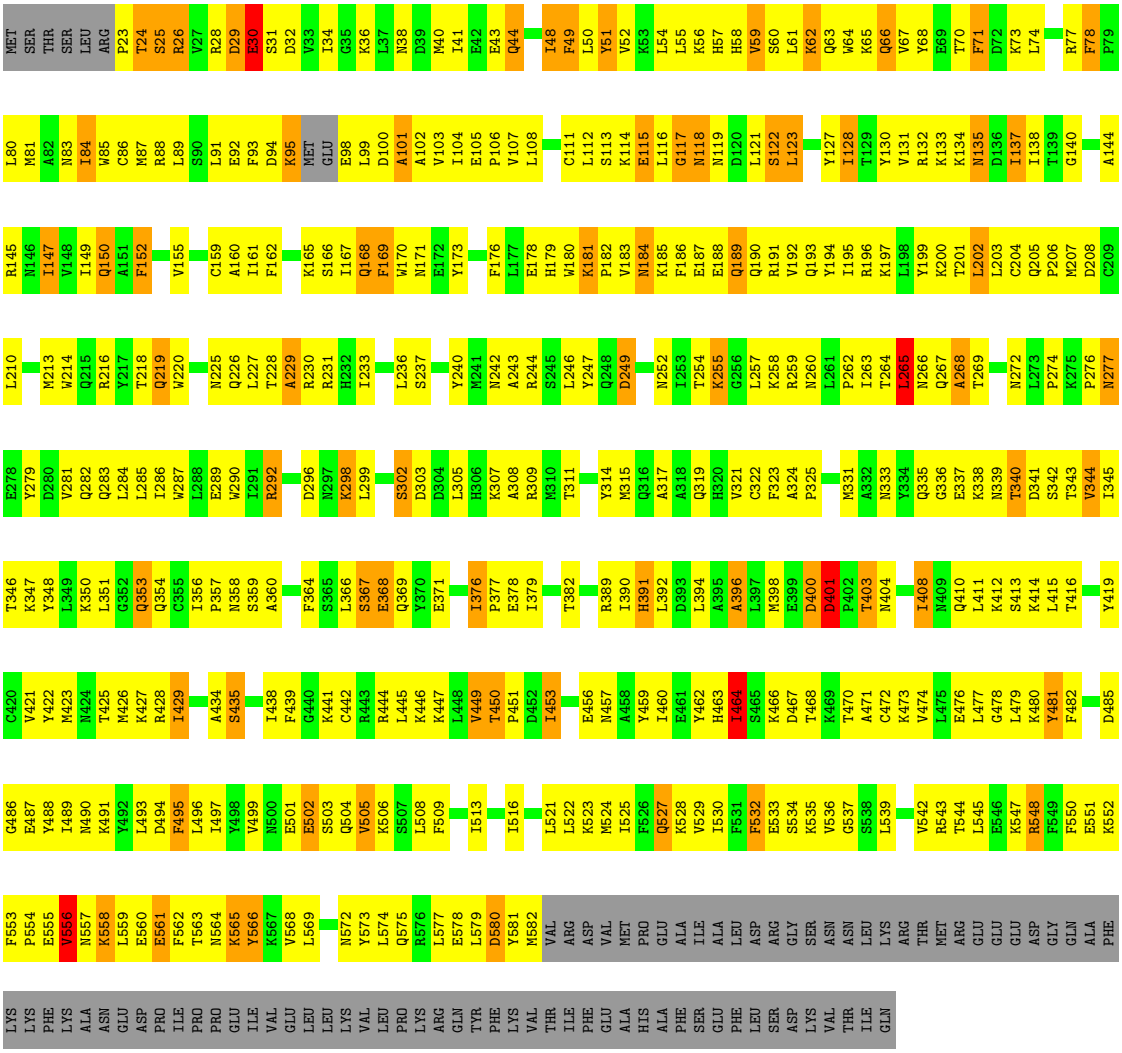




• Molecule 1: mRNA 3'-end-processing protein RNA14

Chain B:

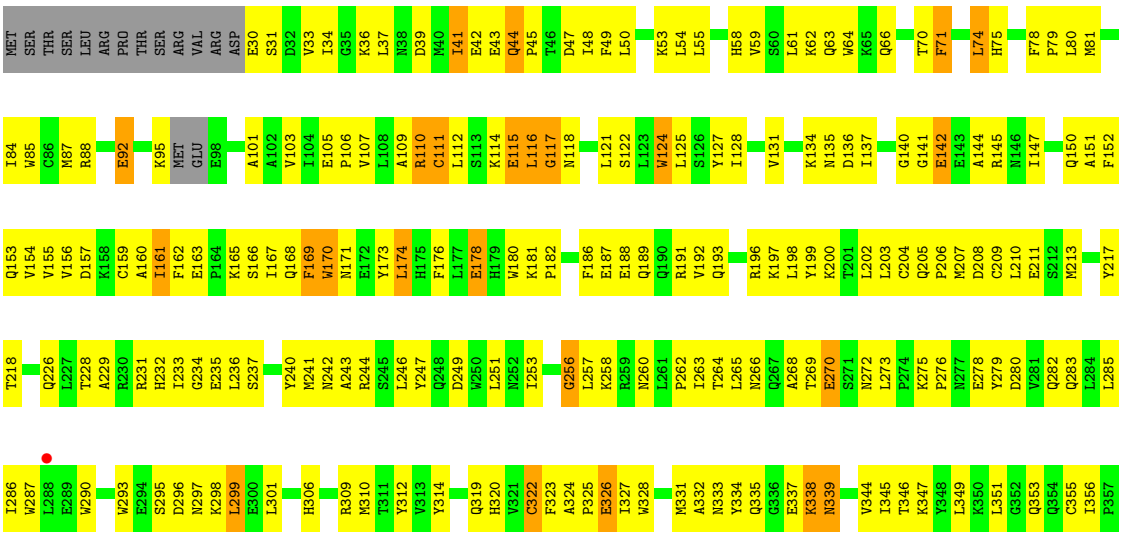


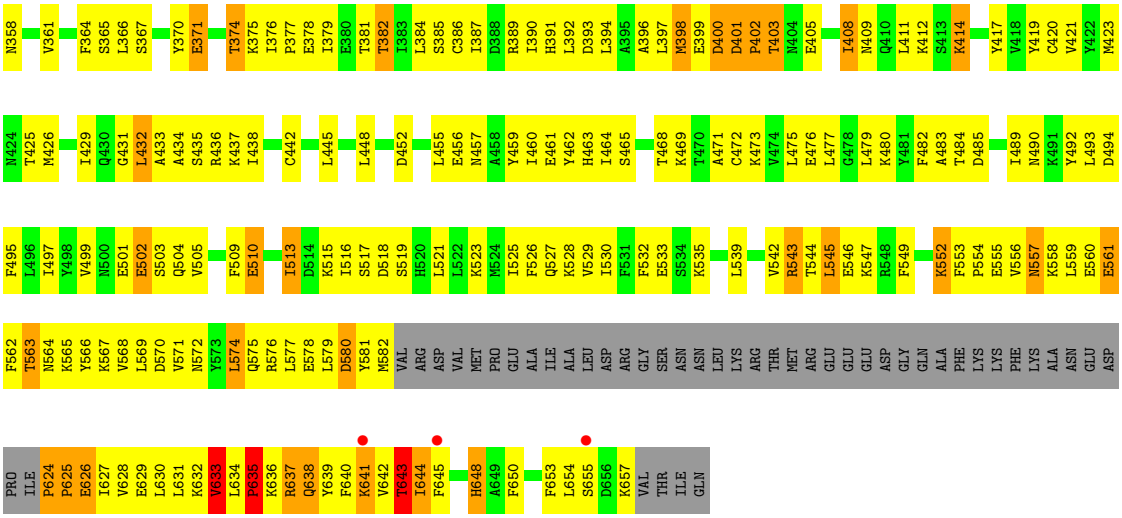


• Molecule 1: mRNA 3'-end-processing protein RNA14

Chain C:

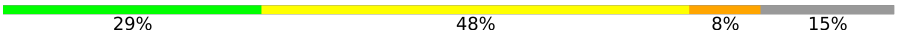


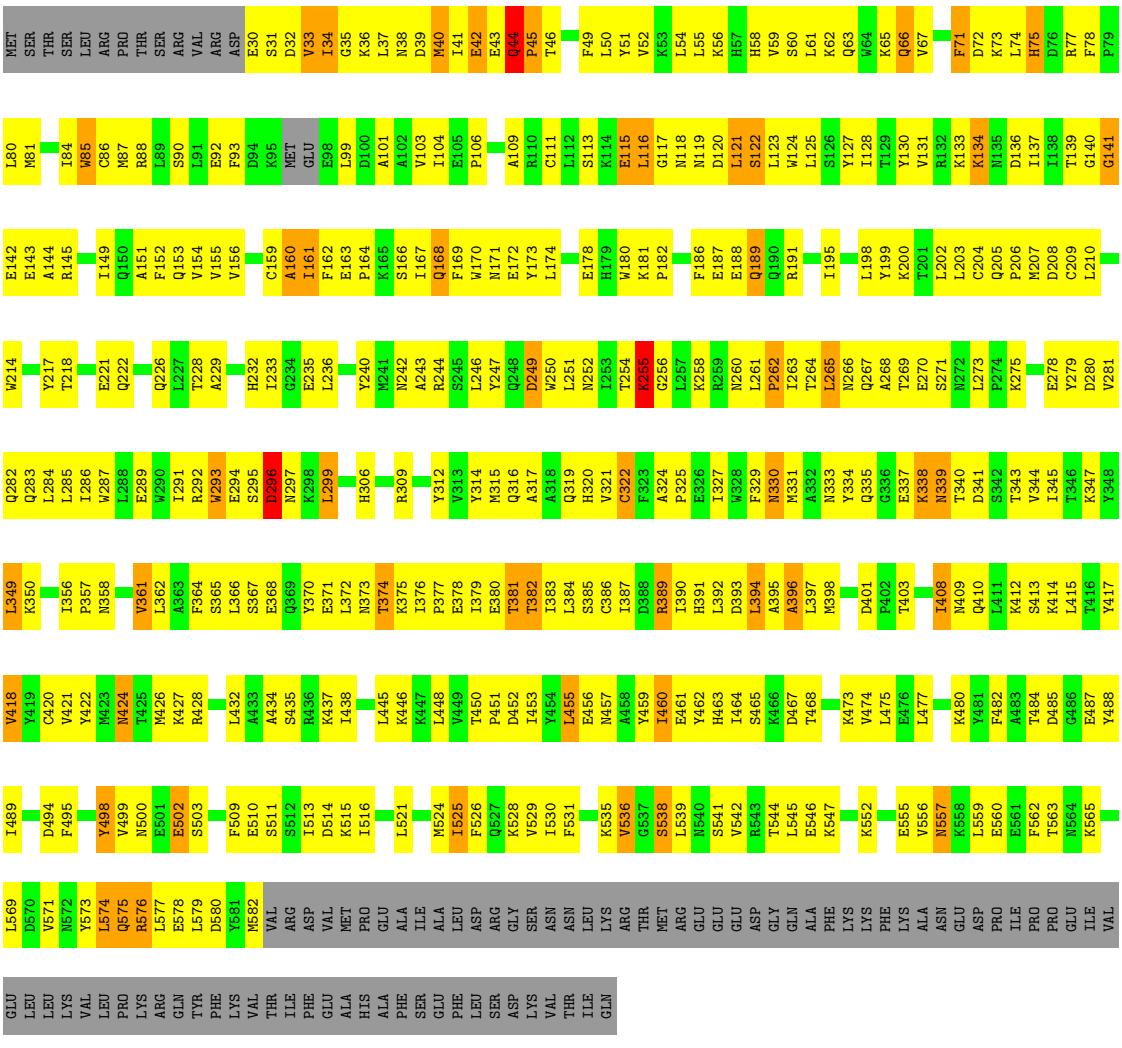




• Molecule 1: mRNA 3'-end-processing protein RNA14

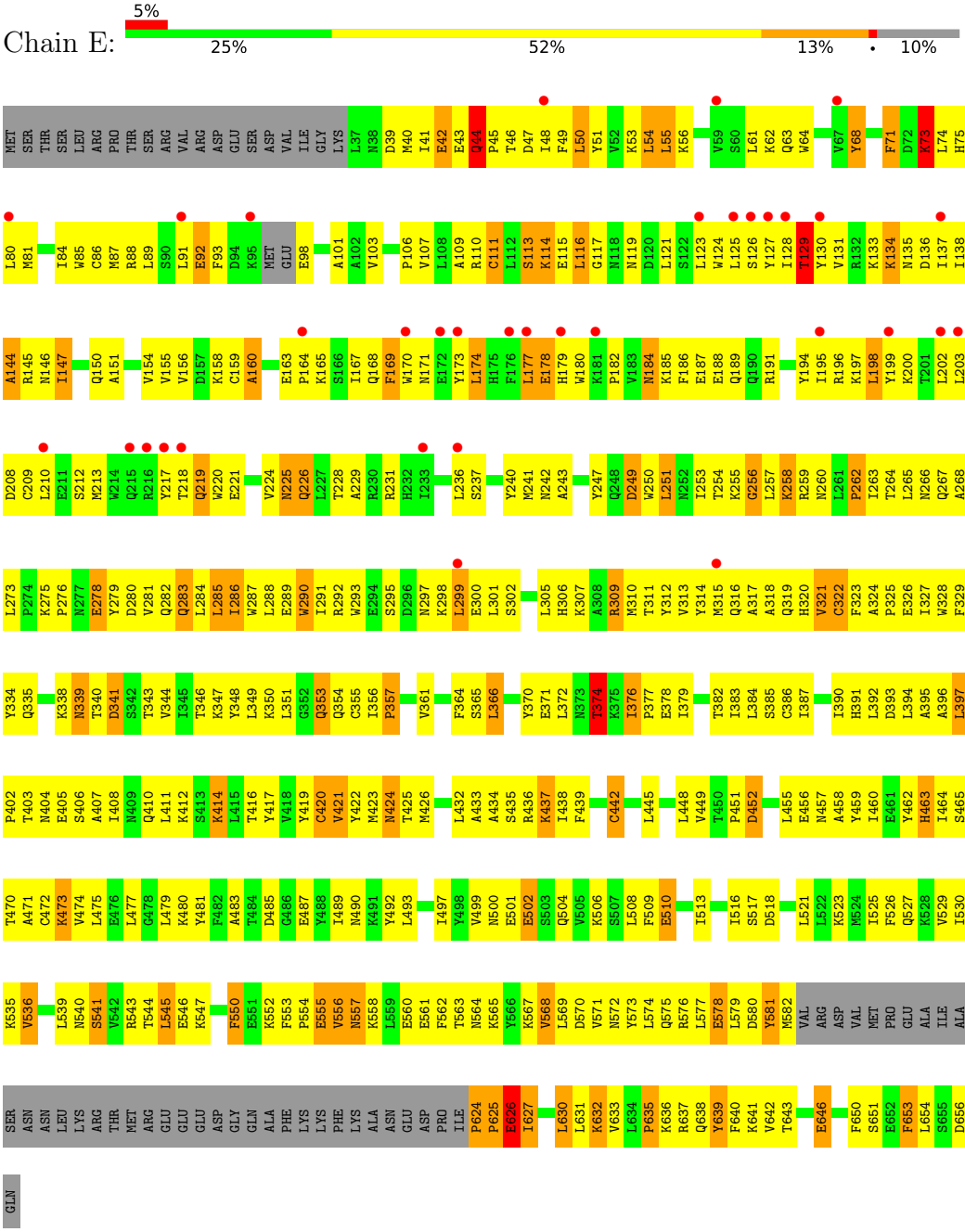
Chain D:





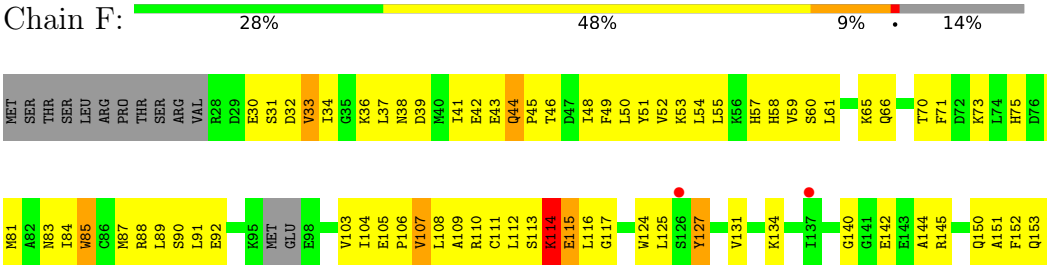
• Molecule 1: mRNA 3'-end-processing protein RNA14

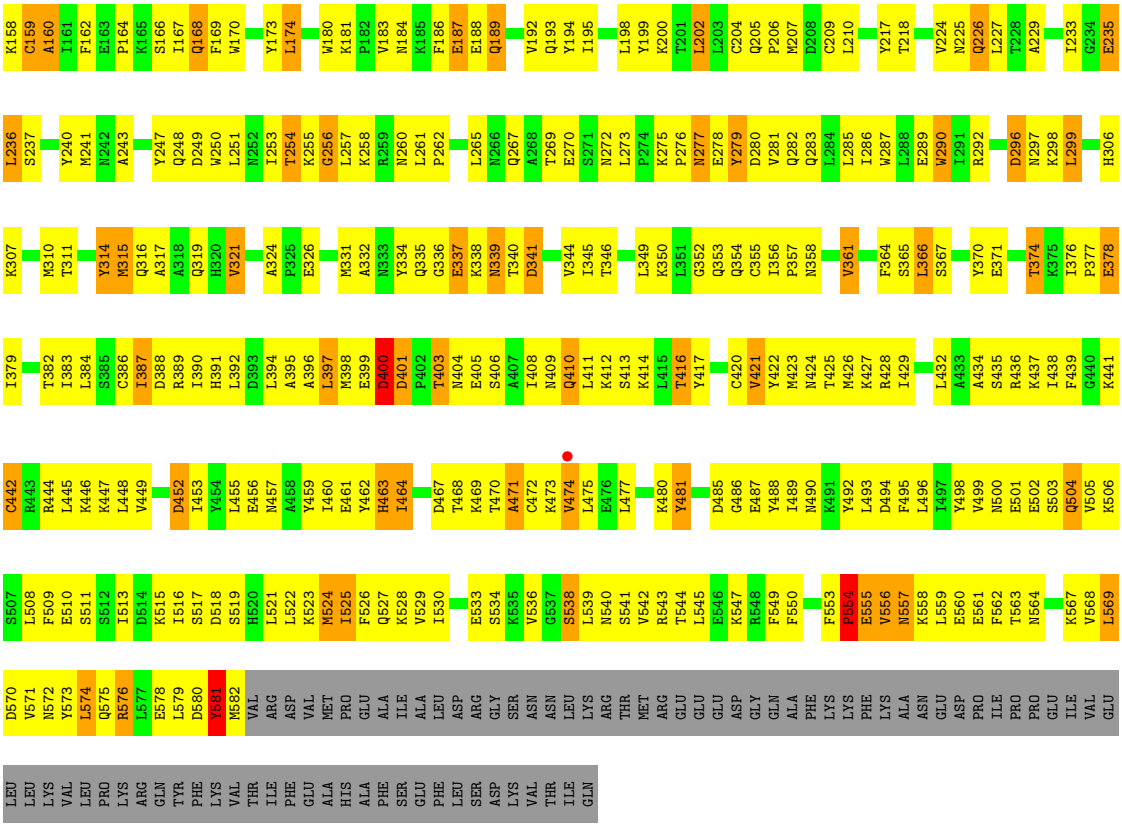
Chain E:



• Molecule 1: mRNA 3'-end-processing protein RNA14

Chain F:

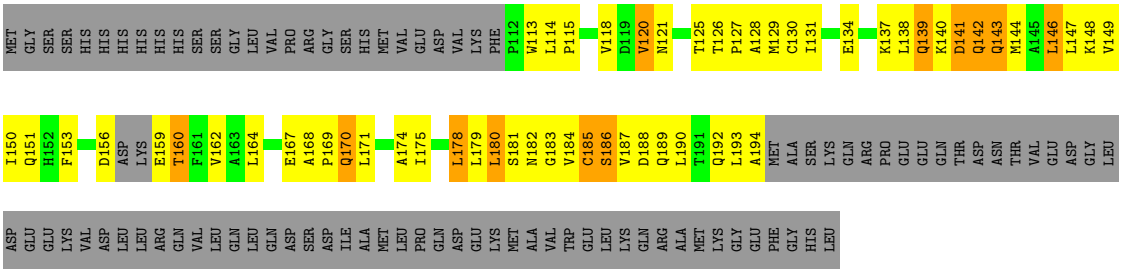




• Molecule 2: Rna15

Chain G:

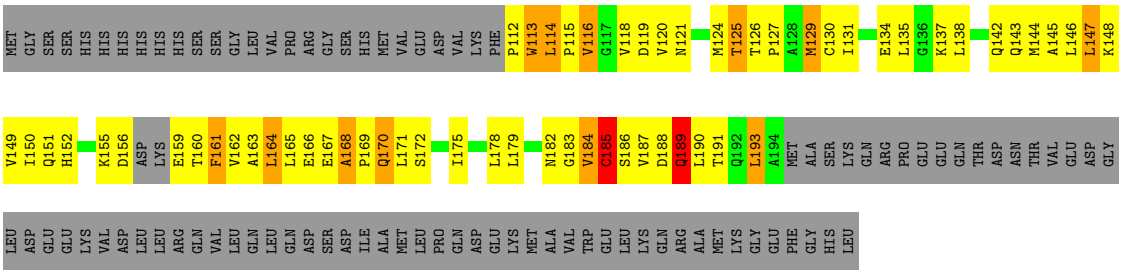




• Molecule 2: Rna15

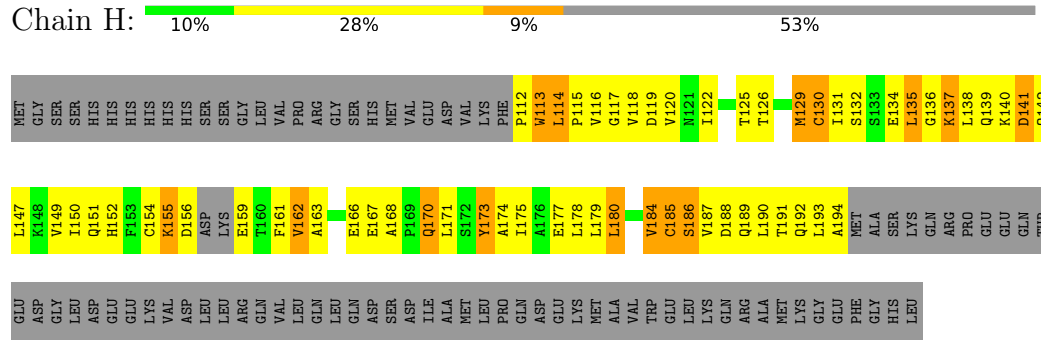
Chain I:





• Molecule 2: Rna15

Chain H:


10%
28%
9%
53%
MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET VAL GLU ASP VAL LYS PHE P112 W113 L114 P115 V116 G117 V118 D119 V120 N121 I122 T125 T126 M129 C130 I131 S132 S133 E134 L135 G136 K137 L138 Q139 K140 D141 Q142 Q143 H144 A145 L146
L147 K148 V149 I150 Q151 H152 F153 C154 K155 D156 ASP LYS E159 T160 F161 V162 A163 E166 E167 A168 P169 Q170 L171 S172 Y173 A174 I175 A176 E177 L178 L179 L180 V184 C185 S186 V187 D188 Q189 L190 T191 Q192 L193 A194 MET ALA SER LYS GLN ARG PRO GLU GLU GLN THR ASP ASN THR VAL
GLU ASP GLY LEU ASP GLU GLU LYS VAL ASP LEU LEU ARG GLN VAL LEU GLN LEU GLN ASP SER ASP ILE ALA MET LEU PRO GLN ASP GLU LYS MET ALA VAL TRP GLU LEU LYS GLN ARG ALA MET LYS GLY GLU PHE GLY HIS LEU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	162.04Å 162.04Å 177.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.79 – 3.30 47.79 – 3.30	Depositor EDS
% Data completeness (in resolution range)	86.4 (47.79-3.30) 86.4 (47.79-3.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.42 (at 3.33Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.226 , 0.298 0.226 , 0.298	Depositor DCC
R_{free} test set	3646 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	84.8	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 76.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l 0.038 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	30268	wwPDB-VP
Average B, all atoms (Å^2)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.09% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.56	0/4982	1.00	25/6732 (0.4%)
1	B	0.56	0/4747	1.03	26/6416 (0.4%)
1	C	0.47	0/4982	0.95	17/6732 (0.3%)
1	D	0.46	0/4689	0.92	15/6338 (0.2%)
1	E	0.55	0/4931	1.04	31/6664 (0.5%)
1	F	0.51	0/4708	0.96	16/6363 (0.3%)
2	G	0.48	0/626	1.12	3/849 (0.4%)
2	H	0.44	0/626	1.13	6/849 (0.7%)
2	I	0.46	0/626	1.05	6/849 (0.7%)
All	All	0.52	0/30917	0.99	145/41792 (0.3%)

There are no bond length outliers.

All (145) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	31	SER	N-CA-C	-11.70	95.91	110.88
1	F	38	ASN	N-CA-C	-9.28	101.97	113.38
2	H	129	MET	N-CA-C	-9.27	101.97	113.38
1	C	641	LYS	N-CA-C	-9.13	101.21	111.71
1	F	85	TRP	N-CA-C	-8.85	102.05	113.12
2	G	187	VAL	N-CA-C	-8.78	103.86	113.43
1	C	626	GLU	N-CA-C	-8.46	103.15	113.97
1	E	627	ILE	N-CA-C	-7.87	103.54	113.22
1	C	445	LEU	N-CA-C	-7.83	103.79	112.72
2	I	189	GLN	N-CA-C	-7.81	103.90	113.19
1	A	44	GLN	CA-C-N	7.77	127.44	119.82
1	A	44	GLN	C-N-CA	7.77	127.44	119.82
1	E	73	LYS	N-CA-C	-7.69	101.90	111.75
1	E	393	ASP	N-CA-C	-7.68	102.88	111.71
2	H	130	CYS	N-CA-C	-7.67	103.92	113.28
1	A	535	LYS	N-CA-C	7.67	121.12	111.69
1	E	126	SER	N-CA-C	-7.36	104.39	113.15
1	F	127	TYR	N-CA-C	-7.33	104.86	113.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	435	SER	N-CA-C	-7.25	103.38	111.28
1	D	536	VAL	N-CA-C	7.15	118.13	112.12
1	A	92	GLU	N-CA-C	-7.14	104.70	113.41
1	E	147	ILE	N-CA-C	-7.00	104.23	112.98
2	H	185	CYS	N-CA-C	6.91	117.77	108.23
1	A	368	GLU	N-CA-C	-6.91	103.74	112.93
1	D	189	GLN	N-CA-C	-6.88	104.75	113.01
1	B	104	ILE	N-CA-C	6.80	119.55	111.05
1	A	580	ASP	N-CA-C	6.77	118.66	111.28
1	A	520	HIS	N-CA-C	6.61	119.31	111.71
2	I	129	MET	N-CA-C	-6.60	103.91	112.23
1	B	558	LYS	N-CA-C	6.58	119.00	111.11
1	E	178	GLU	N-CA-C	-6.58	105.88	114.04
1	E	536	VAL	CB-CA-C	-6.56	105.00	111.30
1	D	85	TRP	N-CA-C	-6.56	104.92	113.12
1	C	189	GLN	N-CA-C	-6.55	105.26	113.18
1	D	320	HIS	N-CA-C	6.53	120.45	112.23
1	B	44	GLN	CA-C-N	6.46	126.15	119.56
1	B	44	GLN	C-N-CA	6.46	126.15	119.56
1	F	65	LYS	N-CA-C	-6.46	104.89	112.89
1	F	90	SER	N-CA-C	-6.39	105.35	112.57
1	C	639	TYR	N-CA-C	-6.36	104.58	112.90
1	E	624	PRO	CA-C-N	6.35	127.78	119.84
1	E	624	PRO	C-N-CA	6.35	127.78	119.84
1	E	197	LYS	N-CA-C	-6.34	105.68	113.41
1	C	624	PRO	CA-C-N	6.28	127.69	119.84
1	C	624	PRO	C-N-CA	6.28	127.69	119.84
1	E	44	GLN	CA-C-N	6.21	126.33	119.87
1	E	44	GLN	C-N-CA	6.21	126.33	119.87
1	C	561	GLU	N-CA-C	-6.20	104.44	111.07
1	F	235	GLU	N-CA-C	-6.14	105.70	113.43
1	A	627	ILE	N-CA-C	-6.13	104.38	113.39
1	D	255	LYS	CB-CA-C	-6.12	109.53	116.63
1	C	320	HIS	N-CA-C	6.12	119.94	112.23
1	F	290	TRP	N-CA-C	-6.08	104.28	111.03
1	D	394	LEU	N-CA-C	-6.06	104.01	111.40
1	D	40	MET	N-CA-C	-5.99	106.51	113.88
1	A	231	ARG	N-CA-C	-5.97	106.33	113.97
1	F	361	VAL	N-CA-C	-5.97	104.51	110.30
2	H	173	TYR	N-CA-C	-5.94	106.03	113.28
1	C	178	GLU	N-CA-C	-5.93	106.21	113.50
1	A	523	LYS	N-CA-C	-5.91	104.84	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	73	LYS	N-CA-C	-5.90	103.82	111.02
1	F	236	LEU	N-CA-C	-5.89	106.34	112.93
1	E	249	ASP	N-CA-C	-5.81	104.54	111.69
1	D	446	LYS	CB-CA-C	-5.80	109.88	116.54
1	E	54	LEU	N-CA-C	-5.77	107.48	114.75
1	D	460	ILE	N-CA-C	-5.74	105.13	110.53
1	E	111	CYS	N-CA-C	5.73	118.47	111.82
1	A	235	GLU	N-CA-C	-5.68	107.59	114.75
1	B	73	LYS	N-CA-C	-5.67	104.46	111.33
1	D	498	TYR	N-CA-C	-5.66	106.33	113.18
2	I	191	THR	N-CA-C	-5.66	106.22	113.01
1	C	429	ILE	CB-CA-C	-5.66	106.90	111.71
1	E	169	PHE	N-CA-C	5.65	118.30	111.40
1	B	59	VAL	N-CA-C	-5.60	106.24	111.45
1	B	26	ARG	N-CA-C	-5.59	102.91	110.68
1	C	41	ILE	N-CA-C	-5.58	104.84	113.16
1	F	503	SER	N-CA-C	-5.57	105.31	111.71
1	B	401	ASP	CA-C-N	5.56	126.79	119.84
1	B	401	ASP	C-N-CA	5.56	126.79	119.84
1	E	550	PHE	N-CA-C	-5.56	105.75	112.54
1	C	197	LYS	N-CA-C	-5.56	104.91	110.97
1	A	249	ASP	N-CA-C	-5.55	104.45	111.11
1	B	376	ILE	CB-CA-C	-5.54	106.74	114.00
1	E	129	THR	N-CA-C	-5.51	105.81	112.54
1	A	356	ILE	CA-C-N	5.49	125.14	119.05
1	A	356	ILE	C-N-CA	5.49	125.14	119.05
2	I	125	THR	N-CA-C	5.49	116.97	109.18
1	B	51	TYR	N-CA-C	-5.48	106.44	113.23
1	A	223	ASP	N-CA-C	-5.48	106.27	113.17
1	C	270	GLU	N-CA-C	-5.45	106.67	113.38
1	B	249	ASP	N-CA-C	-5.45	105.24	111.07
2	H	191	THR	N-CA-C	-5.41	106.18	112.89
1	E	570	ASP	N-CA-C	5.41	118.70	111.24
1	A	111	CYS	N-CA-C	5.40	118.66	111.75
1	E	177	LEU	N-CA-C	-5.38	106.03	112.59
1	E	437	LYS	N-CA-C	-5.37	105.11	110.97
1	F	315	MET	N-CA-C	-5.36	105.55	112.68
1	C	64	TRP	N-CA-C	5.32	117.83	111.71
1	C	371	GLU	N-CA-C	-5.32	105.48	111.28
1	E	55	LEU	N-CA-C	-5.30	104.93	111.40
1	D	44	GLN	CA-C-N	5.30	126.47	119.84
1	D	44	GLN	C-N-CA	5.30	126.47	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	208	ASP	N-CA-C	-5.28	106.52	113.17
1	A	226	GLN	N-CA-C	-5.27	106.16	112.59
1	F	352	GLY	N-CA-C	-5.27	106.03	112.77
1	B	580	ASP	N-CA-C	5.26	117.70	111.33
1	F	378	GLU	N-CA-C	-5.25	105.45	111.07
1	B	410	GLN	N-CA-C	-5.24	104.82	111.11
1	A	35	GLY	N-CA-C	-5.24	108.46	115.32
1	F	296	ASP	N-CA-C	-5.23	106.16	112.54
1	A	65	LYS	N-CA-C	-5.23	106.75	113.23
1	E	47	ASP	N-CA-C	5.22	117.24	109.25
1	A	639	TYR	N-CA-C	-5.22	106.93	113.72
1	B	360	ALA	N-CA-C	-5.21	105.77	111.82
2	G	160	THR	N-CA-C	-5.21	106.76	113.01
2	I	161	PHE	N-CA-C	-5.21	105.52	111.14
1	E	220	TRP	N-CA-C	5.19	116.63	111.07
1	C	431	GLY	N-CA-C	5.19	119.40	112.65
1	B	532	PHE	N-CA-C	-5.18	105.71	111.36
1	F	229	ALA	N-CA-C	-5.17	106.12	112.90
1	A	306	HIS	N-CA-C	-5.16	104.72	111.02
2	I	193	LEU	N-CA-C	-5.16	106.94	113.18
1	B	344	VAL	CB-CA-C	-5.14	105.30	111.88
1	B	339	ASN	N-CA-C	5.13	116.72	110.41
1	B	123	LEU	N-CA-C	-5.13	105.85	112.68
1	B	505	VAL	N-CA-C	-5.11	105.72	110.53
1	E	144	ALA	N-CA-C	-5.11	107.11	113.19
2	G	131	ILE	N-CA-C	-5.10	105.00	110.36
1	E	286	ILE	N-CA-C	-5.10	106.82	111.67
1	E	414	LYS	N-CA-C	-5.10	105.61	111.07
1	E	376	ILE	N-CA-C	5.09	119.87	108.88
2	H	132	SER	N-CA-C	-5.09	105.92	111.82
1	A	230	ARG	N-CA-C	-5.09	106.85	113.16
1	E	290	TRP	N-CA-C	-5.08	105.39	111.03
1	B	226	GLN	N-CA-C	-5.06	106.24	112.72
1	B	566	TYR	N-CA-C	5.06	118.29	112.57
1	A	515	LYS	N-CA-C	5.06	119.16	112.89
1	A	648	HIS	N-CA-C	-5.06	107.06	113.18
1	D	249	ASP	N-CA-C	-5.06	105.95	111.82
1	E	189	GLN	N-CA-C	-5.05	107.06	113.18
1	D	445	LEU	N-CA-C	-5.05	106.71	112.92
1	E	630	LEU	N-CA-C	-5.04	106.31	112.90
1	B	565	LYS	N-CA-C	-5.03	105.25	111.33
1	A	278	GLU	N-CA-C	5.01	118.11	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	396	ALA	N-CA-C	-5.00	105.48	111.03

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	4874	0	4885	541	0
1	B	4646	0	4650	429	0
1	C	4874	0	4885	422	0
1	D	4589	0	4591	404	0
1	E	4823	0	4834	536	0
1	F	4608	0	4608	424	0
2	G	618	0	632	83	0
2	H	618	0	632	95	0
2	I	618	0	632	95	0
All	All	30268	0	30349	2905	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 48.

All (2905) 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:D:563:THR:HG22	1:D:574:LEU:HD12	1.23	1.17
1:C:557:ASN:HD22	1:C:560:GLU:HB2	1.11	1.16
1:D:468:THR:HG21	1:D:499:VAL:HG11	1.31	1.07
2:G:125:THR:HG23	2:G:129:MET:HE2	1.39	1.04
1:A:345:ILE:H	1:A:345:ILE:HD12	1.19	1.03
1:A:225:ASN:HB2	1:A:229:ALA:HB2	1.37	1.02
2:H:170:GLN:N	2:H:170:GLN:HE21	1.56	1.02
1:A:548:ARG:HH11	1:A:548:ARG:HG2	1.23	1.01
1:F:299:LEU:H	1:F:299:LEU:HD12	1.21	1.01
1:D:468:THR:CG2	1:D:499:VAL:HG11	1.91	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:125:THR:HG22	2:G:126:THR:H	1.23	1.00
1:E:74:LEU:HD13	1:E:84:ILE:HG23	1.42	1.00
1:C:638:GLN:HA	1:C:641:LYS:HB3	1.44	0.99
1:E:311:THR:HG22	1:E:315:MET:HE2	1.41	0.99
1:F:398:MET:HG2	1:F:408:ILE:HD11	1.44	0.99
1:E:178:GLU:HA	1:E:191:ARG:NH2	1.79	0.98
1:B:258:LYS:HE2	2:H:152:HIS:HB2	1.46	0.97
1:A:364:PHE:CZ	1:A:421:VAL:HG11	1.99	0.97
1:E:335:GLN:HE21	1:E:348:TYR:HE1	1.10	0.97
1:E:125:LEU:HD23	1:E:128:ILE:HD12	1.43	0.97
1:D:489:ILE:HG13	1:D:516:ILE:HD11	1.46	0.95
1:A:638:GLN:HA	1:A:641:LYS:HG3	1.49	0.95
2:H:193:LEU:HD12	2:H:194:ALA:H	1.30	0.95
1:E:564:ASN:O	1:E:567:LYS:HG3	1.67	0.94
2:H:170:GLN:HE21	2:H:170:GLN:H	0.95	0.94
1:D:434:ALA:HA	1:D:437:LYS:HE3	1.49	0.93
1:C:81:MET:HE1	1:C:319:GLN:HA	1.50	0.93
1:D:260:ASN:HB3	2:I:152:HIS:NE2	1.84	0.93
1:A:99:LEU:HB2	1:A:134:LYS:NZ	1.84	0.92
1:E:563:THR:HG22	1:E:574:LEU:HD12	1.50	0.92
1:F:557:ASN:HD22	1:F:560:GLU:HB2	1.34	0.92
1:E:115:GLU:HG2	1:E:116:LEU:H	1.32	0.92
2:H:170:GLN:H	2:H:170:GLN:NE2	1.67	0.92
1:B:200:LYS:HG2	1:B:236:LEU:HD11	1.49	0.92
1:C:262:PRO:HG3	1:C:273:LEU:HD21	1.50	0.92
1:D:37:LEU:HA	1:D:40:MET:HE2	1.49	0.91
1:B:524:MET:HA	1:B:527:GLN:HE21	1.35	0.91
1:C:398:MET:HA	1:C:408:ILE:HD11	1.50	0.91
1:B:396:ALA:O	1:B:400:ASP:HB2	1.69	0.91
2:G:170:GLN:NE2	2:G:170:GLN:H	1.66	0.91
2:G:170:GLN:H	2:G:170:GLN:HE21	0.91	0.91
1:A:575:GLN:HE21	1:A:582:MET:HE3	1.37	0.90
1:A:137:ILE:HG23	1:A:145:ARG:HB2	1.54	0.90
1:F:390:ILE:HD13	1:F:414:LYS:HD3	1.51	0.90
1:F:489:ILE:HG13	1:F:516:ILE:HD11	1.53	0.90
1:B:548:ARG:HG2	1:B:548:ARG:HH11	1.36	0.89
2:G:170:GLN:HE21	2:G:170:GLN:N	1.71	0.89
1:F:576:ARG:HB3	1:F:576:ARG:HH11	1.36	0.89
1:F:48:ILE:HG22	1:F:273:LEU:HD13	1.53	0.89
1:A:568:VAL:HG12	1:A:569:LEU:HD22	1.55	0.89
2:G:185:CYS:SG	2:G:188:ASP:HB2	2.13	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:74:LEU:HD13	1:E:84:ILE:CG2	2.04	0.88
1:E:637:ARG:O	1:E:641:LYS:HB3	1.72	0.88
1:A:111:CYS:SG	1:A:112:LEU:HD23	2.11	0.88
1:F:314:TYR:HB3	1:F:331:MET:HE3	1.54	0.88
1:A:259:ARG:HG2	1:A:320:HIS:NE2	1.88	0.88
1:E:325:PRO:HD3	1:E:356:ILE:HD13	1.56	0.88
1:A:264:THR:HB	1:A:267:GLN:HG2	1.54	0.88
1:E:390:ILE:HD13	1:E:414:LYS:HD3	1.56	0.87
1:A:99:LEU:HB2	1:A:134:LYS:HZ3	1.39	0.87
1:A:180:TRP:HB3	1:A:191:ARG:HH12	1.40	0.87
2:I:170:GLN:HE21	2:I:170:GLN:H	1.21	0.87
1:C:425:THR:HG22	1:C:426:MET:HE2	1.57	0.87
1:E:475:LEU:HD12	1:E:475:LEU:H	1.40	0.87
1:C:364:PHE:CZ	1:C:421:VAL:HG11	2.10	0.87
1:A:180:TRP:CZ3	1:A:191:ARG:HA	2.10	0.87
1:A:631:LEU:HD21	2:G:171:LEU:HD22	1.56	0.87
1:E:364:PHE:CZ	1:E:421:VAL:HG11	2.10	0.87
1:C:572:ASN:ND2	1:C:575:GLN:HE21	1.73	0.86
1:A:180:TRP:HB3	1:A:191:ARG:NH1	1.91	0.86
1:A:283:GLN:HA	1:A:286:ILE:HD12	1.56	0.86
1:A:81:MET:HE1	1:A:319:GLN:HA	1.57	0.86
2:G:193:LEU:HG	2:G:194:ALA:H	1.41	0.86
2:H:185:CYS:HB3	2:H:188:ASP:HB3	1.58	0.86
2:H:179:LEU:HG	2:H:184:VAL:HG21	1.58	0.86
1:B:521:LEU:O	1:B:525:ILE:HG12	1.76	0.86
1:C:361:VAL:HG22	1:D:574:LEU:HD11	1.57	0.85
1:C:200:LYS:HG2	1:C:236:LEU:HD11	1.56	0.85
1:A:364:PHE:HZ	1:A:421:VAL:HG11	1.34	0.84
1:E:206:PRO:HA	1:E:210:LEU:HD11	1.57	0.84
1:A:65:LYS:O	1:A:65:LYS:HD3	1.76	0.84
1:C:61:LEU:HB2	1:C:63:GLN:HE21	1.42	0.84
2:G:143:GLN:HG2	2:G:182:ASN:HD21	1.43	0.84
1:C:468:THR:CG2	1:C:499:VAL:HG11	2.07	0.83
1:A:281:VAL:O	1:A:285:LEU:HD12	1.78	0.83
1:C:574:LEU:HD11	1:D:361:VAL:HG22	1.60	0.83
1:E:341:ASP:HB3	1:E:344:VAL:HG23	1.59	0.83
1:B:81:MET:HE1	1:B:319:GLN:HA	1.58	0.83
1:C:115:GLU:H	1:C:115:GLU:CD	1.86	0.83
1:F:140:GLY:HA3	1:F:144:ALA:HB3	1.60	0.83
2:I:170:GLN:H	2:I:170:GLN:NE2	1.74	0.83
1:A:33:VAL:HA	1:A:36:LYS:HD2	1.61	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:632:LYS:HG2	2:G:115:PRO:HG2	1.61	0.83
2:H:193:LEU:HD12	2:H:194:ALA:N	1.94	0.82
1:A:86:CYS:HB3	1:A:263:ILE:HG13	1.60	0.82
1:B:61:LEU:HB2	1:B:63:GLN:HE21	1.43	0.82
1:B:178:GLU:CD	1:B:216:ARG:HH22	1.88	0.82
1:C:557:ASN:ND2	1:C:560:GLU:HB2	1.92	0.82
1:E:81:MET:HE1	1:E:318:ALA:O	1.78	0.82
1:C:314:TYR:HB3	1:C:331:MET:HE3	1.61	0.82
1:E:546:GLU:OE2	1:E:565:LYS:HE2	1.80	0.82
2:H:155:LYS:H	2:H:155:LYS:HD3	1.44	0.82
1:C:299:LEU:H	1:C:299:LEU:HD12	1.45	0.81
1:D:124:TRP:O	1:D:127:TYR:HB3	1.78	0.81
1:F:43:GLU:O	1:F:44:GLN:HG2	1.80	0.81
2:G:147:LEU:HD11	2:G:178:LEU:HD22	1.60	0.81
1:D:90:SER:HB3	1:D:264:THR:HG23	1.60	0.81
1:E:557:ASN:HD22	1:E:560:GLU:HB2	1.44	0.81
1:F:115:GLU:H	1:F:115:GLU:CD	1.88	0.81
1:C:152:PHE:O	1:C:156:VAL:HG23	1.80	0.81
1:D:80:LEU:HA	1:D:118:ASN:HD21	1.43	0.81
1:A:81:MET:HB3	1:A:84:ILE:HD13	1.60	0.81
1:D:71:PHE:CE2	1:D:88:ARG:HB2	2.15	0.81
1:E:165:LYS:HD3	1:E:208:ASP:HB3	1.63	0.81
1:D:218:THR:HA	1:D:233:ILE:HD11	1.62	0.80
1:E:455:LEU:HB2	1:F:569:LEU:HD11	1.60	0.80
1:C:125:LEU:HD21	1:C:169:PHE:HD1	1.47	0.80
1:D:210:LEU:HD13	1:D:244:ARG:HA	1.62	0.80
1:D:299:LEU:H	1:D:299:LEU:HD12	1.46	0.80
1:D:557:ASN:HD22	1:D:560:GLU:H	1.26	0.80
1:A:108:LEU:O	1:A:112:LEU:HB2	1.81	0.80
1:E:502:GLU:OE2	1:E:536:VAL:HG11	1.81	0.80
1:E:434:ALA:HA	1:E:437:LYS:HZ3	1.46	0.80
1:C:378:GLU:O	1:C:382:THR:HG22	1.82	0.80
1:E:165:LYS:HE2	1:E:250:TRP:CZ3	2.17	0.80
1:A:140:GLY:HA3	1:A:144:ALA:HB2	1.64	0.79
2:H:135:LEU:HD22	2:H:178:LEU:HD21	1.63	0.79
1:B:89:LEU:HD21	1:B:107:VAL:HG11	1.65	0.79
1:E:521:LEU:O	1:E:525:ILE:HD13	1.83	0.79
1:F:557:ASN:ND2	1:F:560:GLU:H	1.79	0.79
1:F:51:TYR:O	1:F:55:LEU:HG	1.82	0.79
1:A:137:ILE:H	1:A:137:ILE:HD12	1.46	0.79
1:F:48:ILE:CG2	1:F:273:LEU:HD13	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:TRP:HZ3	1:A:191:ARG:HA	1.45	0.78
1:B:394:LEU:HA	1:B:411:LEU:HD23	1.64	0.78
1:D:115:GLU:CD	1:D:115:GLU:H	1.92	0.78
1:E:479:LEU:HD23	1:E:483:ALA:HA	1.65	0.78
1:E:557:ASN:ND2	1:E:560:GLU:H	1.80	0.78
1:A:447:LYS:HG2	1:A:481:TYR:HB3	1.63	0.78
1:E:124:TRP:CE3	1:E:155:VAL:HG22	2.18	0.78
1:B:145:ARG:NH2	1:B:180:TRP:HE1	1.82	0.78
1:B:496:LEU:HB3	1:B:505:VAL:HG22	1.65	0.78
1:D:560:GLU:HA	1:D:582:MET:HE1	1.66	0.78
1:E:327:ILE:HG23	1:E:328:TRP:N	1.99	0.78
1:F:79:PRO:HB2	1:F:116:LEU:HD13	1.66	0.78
2:I:190:LEU:O	2:I:193:LEU:HG	1.83	0.78
1:A:204:CYS:HB2	1:A:205:GLN:HE21	1.49	0.78
1:E:632:LYS:HG2	2:I:115:PRO:HB3	1.66	0.78
2:H:189:GLN:O	2:H:192:GLN:HB2	1.84	0.78
1:C:202:LEU:HB2	1:C:207:MET:HE1	1.66	0.77
1:D:51:TYR:O	1:D:55:LEU:HG	1.85	0.77
1:E:312:TYR:O	1:E:316:GLN:HG2	1.83	0.77
1:E:417:TYR:HB2	1:F:573:TYR:HD1	1.48	0.77
1:B:99:LEU:HB2	1:B:134:LYS:HZ3	1.49	0.77
1:E:327:ILE:CG2	1:E:328:TRP:H	1.98	0.77
1:E:423:MET:HA	1:E:438:ILE:HD12	1.66	0.77
1:B:145:ARG:CZ	1:B:180:TRP:HE1	1.98	0.77
1:C:529:VAL:HG12	1:C:545:LEU:HD11	1.67	0.77
1:E:631:LEU:HD23	2:I:171:LEU:HD13	1.65	0.77
1:A:632:LYS:HG2	2:G:115:PRO:CG	2.14	0.77
1:B:206:PRO:HB3	1:B:247:TYR:HB2	1.65	0.77
1:E:156:VAL:HA	1:E:160:ALA:CB	2.15	0.77
1:E:539:LEU:HD13	1:F:371:GLU:OE1	1.85	0.77
1:F:299:LEU:HD12	1:F:299:LEU:N	1.98	0.77
1:F:124:TRP:O	1:F:127:TYR:HB3	1.85	0.76
2:I:143:GLN:HG2	2:I:182:ASN:ND2	2.00	0.76
2:H:150:ILE:HD13	2:H:175:ILE:HG12	1.66	0.76
1:B:101:ALA:HB1	1:B:105:GLU:HG3	1.66	0.76
1:D:459:TYR:O	1:D:463:HIS:HB2	1.86	0.76
1:F:425:THR:HG22	1:F:426:MET:HE2	1.67	0.76
1:F:400:ASP:O	1:F:401:ASP:HB3	1.84	0.76
1:A:548:ARG:HG2	1:A:548:ARG:NH1	1.98	0.76
1:F:563:THR:HG22	1:F:572:ASN:HD21	1.51	0.76
1:C:629:GLU:HA	1:C:632:LYS:HE3	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:LEU:HA	1:A:411:LEU:HD23	1.67	0.76
1:C:624:PRO:N	1:C:625:PRO:HD3	2.00	0.76
1:A:462:TYR:CZ	1:A:499:VAL:HG11	2.19	0.76
1:E:93:PHE:HZ	1:E:130:TYR:HB2	1.51	0.76
1:D:330:ASN:N	1:D:330:ASN:HD22	1.84	0.76
1:E:364:PHE:HZ	1:E:421:VAL:HG11	1.47	0.76
1:D:573:TYR:O	1:D:577:LEU:HB2	1.85	0.75
2:G:193:LEU:HD23	2:G:193:LEU:H	1.52	0.75
2:I:185:CYS:SG	2:I:188:ASP:HB3	2.25	0.75
1:C:648:HIS:NE2	2:H:162:VAL:HB	2.01	0.75
1:D:557:ASN:ND2	1:D:560:GLU:H	1.85	0.75
1:E:109:ALA:O	1:E:113:SER:HB3	1.87	0.75
1:F:71:PHE:CE2	1:F:88:ARG:HB2	2.21	0.75
2:G:190:LEU:HA	2:G:193:LEU:HD21	1.67	0.75
1:C:181:LYS:O	1:C:181:LYS:HD2	1.85	0.75
1:F:579:LEU:O	1:F:582:MET:HB2	1.86	0.75
1:B:218:THR:HG22	1:B:233:ILE:HD13	1.68	0.75
1:C:282:GLN:O	1:C:286:ILE:HG13	1.86	0.75
1:A:579:LEU:HD13	1:A:582:MET:HE2	1.69	0.75
1:A:364:PHE:CE2	1:A:421:VAL:HG21	2.22	0.75
1:D:140:GLY:HA3	1:D:144:ALA:HB3	1.66	0.75
1:C:71:PHE:CE2	1:C:88:ARG:HB2	2.21	0.74
1:D:204:CYS:HB2	1:D:205:GLN:HE21	1.50	0.74
1:A:182:PRO:HG3	1:A:191:ARG:HD2	1.67	0.74
1:B:509:PHE:CD1	1:B:529:VAL:HG21	2.22	0.74
1:A:356:ILE:HG22	1:A:359:SER:HB2	1.69	0.74
1:A:396:ALA:O	1:A:400:ASP:HB2	1.86	0.74
1:E:295:SER:HB3	1:E:310:MET:HE1	1.69	0.74
1:B:61:LEU:O	1:B:63:GLN:HG3	1.87	0.74
1:E:398:MET:HA	1:E:408:ILE:HD11	1.69	0.74
1:C:115:GLU:C	1:C:117:GLY:H	1.95	0.74
1:B:218:THR:HA	1:B:233:ILE:HD11	1.68	0.74
1:B:524:MET:HA	1:B:527:GLN:NE2	2.03	0.74
1:C:111:CYS:O	1:C:118:ASN:HB2	1.88	0.74
1:C:574:LEU:O	1:C:574:LEU:HD13	1.86	0.74
1:C:635:PRO:HG3	2:H:120:VAL:HG21	1.70	0.74
1:E:269:THR:HG23	1:E:272:ASN:HD21	1.51	0.74
1:E:426:MET:HA	1:E:426:MET:HE2	1.69	0.74
1:F:405:GLU:HA	1:F:408:ILE:HG22	1.69	0.74
2:G:168:ALA:HA	2:G:170:GLN:HE22	1.53	0.74
1:A:378:GLU:O	1:A:382:THR:HG22	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:GLN:N	1:B:66:GLN:HE21	1.84	0.73
1:B:376:ILE:HB	1:B:377:PRO:HD3	1.70	0.73
1:E:465:SER:O	1:E:466:LYS:HB2	1.87	0.73
1:E:509:PHE:CZ	1:E:513:ILE:HD11	2.23	0.73
1:F:83:ASN:O	1:F:87:MET:HG3	1.88	0.73
1:F:200:LYS:HG2	1:F:236:LEU:HD11	1.69	0.73
1:A:205:GLN:O	1:A:207:MET:HG3	1.87	0.73
1:A:462:TYR:CE2	1:A:499:VAL:HG11	2.23	0.73
1:C:280:ASP:HB3	1:C:283:GLN:HB2	1.70	0.73
1:E:473:LYS:O	1:E:477:LEU:HD13	1.88	0.73
1:D:136:ASP:HB3	1:D:139:THR:HB	1.68	0.73
1:C:107:VAL:HA	1:C:110:ARG:HD3	1.70	0.73
1:E:200:LYS:HG2	1:E:236:LEU:HD11	1.69	0.73
1:F:181:LYS:O	1:F:181:LYS:HD2	1.89	0.73
1:E:287:TRP:O	1:E:290:TRP:HB3	1.89	0.73
1:E:468:THR:CG2	1:E:499:VAL:HG11	2.19	0.73
1:A:568:VAL:HG12	1:A:569:LEU:CD2	2.18	0.73
1:F:218:THR:HG23	1:F:233:ILE:HD13	1.69	0.73
2:I:179:LEU:O	2:I:184:VAL:HB	1.89	0.73
1:D:42:GLU:OE1	1:D:43:GLU:HG3	1.89	0.72
1:D:202:LEU:HD12	1:D:203:LEU:N	2.05	0.72
1:E:71:PHE:CE2	1:E:88:ARG:HB2	2.23	0.72
1:B:463:HIS:O	1:B:464:ILE:HG13	1.89	0.72
1:A:638:GLN:HA	1:A:641:LYS:CG	2.19	0.72
1:E:471:ALA:O	1:E:474:VAL:HB	1.90	0.72
1:F:371:GLU:HB2	1:F:379:ILE:HD11	1.71	0.72
1:A:654:LEU:HD21	2:G:150:ILE:HG22	1.72	0.72
1:B:137:ILE:H	1:B:137:ILE:HD12	1.53	0.72
1:B:351:LEU:HA	1:B:354:GLN:HG3	1.69	0.72
1:B:400:ASP:O	1:B:401:ASP:HB3	1.89	0.72
1:C:572:ASN:OD1	1:C:575:GLN:HG2	1.88	0.72
1:C:654:LEU:HD23	1:C:654:LEU:O	1.89	0.72
1:D:394:LEU:HD21	1:D:448:LEU:HD11	1.71	0.72
1:C:101:ALA:HB2	1:C:134:LYS:NZ	2.05	0.72
1:F:127:TYR:O	1:F:131:VAL:HG23	1.90	0.71
1:C:84:ILE:HA	1:C:87:MET:HE3	1.72	0.71
1:E:200:LYS:HG2	1:E:236:LEU:HD21	1.71	0.71
1:E:254:THR:HG23	1:E:257:LEU:HD22	1.71	0.71
1:A:75:HIS:HB3	1:A:110:ARG:HH21	1.54	0.71
1:E:313:VAL:O	1:E:316:GLN:HB2	1.90	0.71
1:E:578:GLU:O	1:E:579:LEU:HD23	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:289:GLU:HG3	1:F:292:ARG:HH21	1.55	0.71
1:B:444:ARG:HH21	2:G:167:GLU:CD	1.97	0.71
1:F:493:LEU:HD23	1:F:508:LEU:HD23	1.71	0.71
2:G:193:LEU:HG	2:G:194:ALA:N	2.05	0.71
1:C:226:GLN:NE2	1:C:226:GLN:H	1.89	0.71
1:A:61:LEU:HD12	1:A:63:GLN:NE2	2.05	0.71
1:B:43:GLU:HG2	2:G:113:TRP:HZ3	1.55	0.71
1:C:306:HIS:O	1:C:309:ARG:HB3	1.91	0.71
1:C:489:ILE:HG13	1:C:516:ILE:HD11	1.72	0.71
1:E:101:ALA:HB2	1:E:134:LYS:HE2	1.71	0.71
1:F:152:PHE:O	1:F:156:VAL:HG23	1.90	0.71
1:C:165:LYS:HD3	1:C:208:ASP:HB3	1.73	0.71
1:D:37:LEU:HD12	1:D:40:MET:CE	2.20	0.71
1:E:156:VAL:HA	1:E:160:ALA:HB3	1.73	0.71
1:F:563:THR:HG22	1:F:572:ASN:ND2	2.04	0.71
1:E:299:LEU:HD22	1:E:301:LEU:HD11	1.72	0.71
1:F:473:LYS:O	1:F:477:LEU:HD13	1.90	0.70
1:F:490:ASN:HB3	1:F:528:LYS:HZ1	1.56	0.70
1:A:285:LEU:HA	1:A:288:LEU:HD12	1.72	0.70
1:B:202:LEU:HD21	1:B:213:MET:HG2	1.72	0.70
1:F:299:LEU:H	1:F:299:LEU:CD1	2.01	0.70
1:B:51:TYR:O	1:B:55:LEU:HG	1.91	0.70
1:B:307:LYS:CE	1:B:338:LYS:HG3	2.22	0.70
1:E:264:THR:HG22	1:E:266:ASN:H	1.55	0.70
1:E:631:LEU:CD2	2:I:171:LEU:HD13	2.20	0.70
1:D:43:GLU:O	1:D:44:GLN:HG2	1.91	0.70
1:C:115:GLU:O	1:C:117:GLY:N	2.24	0.70
1:F:432:LEU:HD11	1:F:461:GLU:OE2	1.90	0.70
2:I:159:GLU:C	2:I:161:PHE:H	1.99	0.70
1:E:174:LEU:O	1:E:178:GLU:HG3	1.91	0.70
1:F:78:PHE:HB3	1:F:81:MET:CG	2.21	0.70
1:C:156:VAL:O	1:C:161:ILE:HG12	1.91	0.70
1:F:152:PHE:HB3	1:F:173:TYR:CE1	2.26	0.70
1:A:463:HIS:O	1:A:464:ILE:HG13	1.92	0.70
1:F:46:THR:HG23	1:F:276:PRO:HG3	1.72	0.70
2:I:145:ALA:O	2:I:149:VAL:HG23	1.92	0.70
1:B:128:ILE:O	1:B:132:ARG:HB2	1.92	0.70
1:B:366:LEU:C	1:B:368:GLU:H	1.98	0.70
1:A:336:GLY:O	1:A:338:LYS:N	2.25	0.70
1:C:627:ILE:HD11	2:H:171:LEU:HD11	1.72	0.70
1:D:41:ILE:HG12	1:D:50:LEU:HB3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:218:THR:HA	1:D:233:ILE:CD1	2.20	0.69
1:E:284:LEU:O	1:E:288:LEU:HG	1.91	0.69
1:E:293:TRP:CD1	1:E:298:LYS:HZ3	2.10	0.69
1:A:462:TYR:OH	1:A:499:VAL:HG11	1.90	0.69
1:A:641:LYS:HD2	1:A:642:VAL:N	2.06	0.69
1:D:222:GLN:HB3	1:D:226:GLN:HG2	1.73	0.69
1:F:572:ASN:OD1	1:F:575:GLN:HG2	1.91	0.69
2:H:125:THR:HG23	2:H:129:MET:HE2	1.72	0.69
2:H:134:GLU:C	2:H:136:GLY:H	2.01	0.69
1:D:152:PHE:O	1:D:156:VAL:HG23	1.91	0.69
1:D:575:GLN:C	1:D:577:LEU:H	1.99	0.69
1:E:638:GLN:HA	1:E:641:LYS:HG2	1.74	0.69
1:C:49:PHE:CE2	1:C:53:LYS:HD2	2.26	0.69
1:C:654:LEU:HD12	2:H:179:LEU:HD22	1.74	0.69
1:D:182:PRO:HD3	1:D:191:ARG:NH1	2.06	0.69
1:D:297:ASN:HB2	1:D:306:HIS:CE1	2.27	0.69
1:E:170:TRP:HE1	1:E:207:MET:HE3	1.56	0.69
1:E:341:ASP:OD2	1:E:343:THR:HG22	1.92	0.69
1:A:314:TYR:HB3	1:A:331:MET:HE2	1.75	0.69
1:D:434:ALA:HA	1:D:437:LYS:CE	2.22	0.69
1:E:205:GLN:O	1:E:210:LEU:HD21	1.92	0.69
1:F:576:ARG:HH11	1:F:576:ARG:CB	2.05	0.69
1:B:24:THR:HB	1:B:43:GLU:OE1	1.93	0.69
1:C:552:LYS:C	1:C:554:PRO:HD3	2.17	0.69
1:D:394:LEU:CD2	1:D:448:LEU:HD11	2.23	0.69
1:E:327:ILE:HG23	1:E:328:TRP:H	1.58	0.69
1:E:553:PHE:O	1:E:556:VAL:HG23	1.92	0.69
1:E:569:LEU:HD12	1:F:452:ASP:OD1	1.92	0.69
1:F:553:PHE:O	1:F:556:VAL:HG23	1.92	0.69
1:C:434:ALA:HA	1:C:437:LYS:HE2	1.75	0.69
1:A:247:TYR:HE1	1:A:251:LEU:HD22	1.56	0.69
1:D:349:LEU:HD11	1:D:365:SER:HB3	1.74	0.69
1:F:376:ILE:HB	1:F:377:PRO:HD3	1.75	0.69
1:F:557:ASN:HD22	1:F:560:GLU:CB	2.04	0.69
1:E:76:ASP:O	1:E:79:PRO:HD3	1.93	0.68
1:F:445:LEU:HD22	1:F:448:LEU:HD23	1.74	0.68
1:A:81:MET:CB	1:A:84:ILE:HD13	2.23	0.68
1:D:37:LEU:HD23	1:D:54:LEU:CD1	2.23	0.68
1:C:386:CYS:O	1:C:390:ILE:HG13	1.92	0.68
1:D:37:LEU:HD23	1:D:54:LEU:HD12	1.75	0.68
1:D:59:VAL:C	1:D:61:LEU:H	2.02	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:48:ILE:HG22	1:C:273:LEU:HD13	1.74	0.68
1:B:80:LEU:HA	1:B:118:ASN:HD21	1.58	0.68
1:F:501:GLU:HB3	1:F:504:GLN:HG3	1.75	0.68
2:I:126:THR:HB	2:I:129:MET:HB2	1.75	0.68
1:A:376:ILE:HB	1:A:377:PRO:HD3	1.74	0.68
1:A:394:LEU:HA	1:A:411:LEU:CD2	2.22	0.68
1:A:624:PRO:HB2	1:A:627:ILE:HG22	1.75	0.68
1:B:77:ARG:HD3	1:B:78:PHE:HE1	1.58	0.68
1:B:204:CYS:HB2	1:B:205:GLN:HE21	1.59	0.68
1:B:262:PRO:HB3	1:B:272:ASN:HD21	1.56	0.68
2:G:143:GLN:HG2	2:G:182:ASN:ND2	2.07	0.68
1:A:476:GLU:O	1:A:479:LEU:HB2	1.93	0.68
1:D:578:GLU:O	1:D:579:LEU:HD23	1.94	0.68
1:E:186:PHE:C	1:E:188:GLU:H	2.02	0.68
1:F:297:ASN:HD22	1:F:306:HIS:CG	2.12	0.68
1:F:366:LEU:HD22	1:F:370:TYR:CE1	2.29	0.68
1:B:64:TRP:HE3	1:B:68:TYR:HE2	1.42	0.68
1:B:145:ARG:CZ	1:B:180:TRP:NE1	2.57	0.68
1:F:36:LYS:C	1:F:37:LEU:HD12	2.19	0.68
1:F:506:LYS:HE2	1:F:533:GLU:OE2	1.93	0.68
2:G:125:THR:HG22	2:G:126:THR:N	2.04	0.68
1:B:404:ASN:O	1:B:408:ILE:HB	1.94	0.67
1:B:487:GLU:HG3	1:B:491:LYS:HE3	1.73	0.67
1:D:463:HIS:HE1	1:D:498:TYR:HE2	1.41	0.67
1:D:557:ASN:HD22	1:D:560:GLU:N	1.92	0.67
1:E:432:LEU:HD13	1:E:464:ILE:CD1	2.24	0.67
1:F:202:LEU:HB2	1:F:207:MET:HE1	1.75	0.67
1:A:576:ARG:HH11	1:A:576:ARG:HG3	1.58	0.67
1:B:26:ARG:HG3	1:B:26:ARG:O	1.94	0.67
1:B:130:TYR:C	1:B:132:ARG:H	2.02	0.67
1:E:361:VAL:HG23	1:F:578:GLU:OE2	1.94	0.67
1:E:405:GLU:HG3	1:E:406:SER:N	2.09	0.67
1:A:177:LEU:HB3	1:A:195:ILE:HG12	1.75	0.67
1:B:296:ASP:HB3	1:B:298:LYS:CD	2.24	0.67
1:C:567:LYS:HG2	1:C:572:ASN:HA	1.74	0.67
1:D:459:TYR:CE1	1:D:495:PHE:HD1	2.12	0.67
1:E:552:LYS:C	1:E:554:PRO:HD3	2.19	0.67
1:A:66:GLN:HE21	1:A:66:GLN:N	1.92	0.67
1:A:177:LEU:O	1:A:195:ILE:HD11	1.94	0.67
1:C:265:LEU:HD23	1:C:265:LEU:O	1.95	0.67
1:D:44:GLN:H	1:D:45:PRO:CD	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:572:ASN:C	1:B:572:ASN:HD22	2.02	0.67
1:A:42:GLU:O	1:A:45:PRO:HD3	1.94	0.67
1:C:364:PHE:HZ	1:C:421:VAL:HG11	1.59	0.67
2:I:183:GLY:O	2:I:184:VAL:HG23	1.95	0.67
2:H:147:LEU:HD22	2:H:179:LEU:HD13	1.76	0.67
1:A:634:LEU:HD11	2:G:174:ALA:HB2	1.77	0.67
1:D:282:GLN:O	1:D:286:ILE:HG13	1.94	0.67
1:E:170:TRP:CE3	1:E:202:LEU:HD23	2.30	0.67
1:B:427:LYS:HB2	1:B:435:SER:CB	2.24	0.67
1:C:389:ARG:HH21	1:C:392:LEU:HB2	1.59	0.67
1:E:228:THR:HG22	1:E:231:ARG:NE	2.10	0.67
1:B:24:THR:HG21	1:B:43:GLU:HG3	1.77	0.67
1:B:513:ILE:HA	1:B:522:LEU:HD11	1.75	0.67
1:C:196:ARG:HG2	1:C:200:LYS:HE2	1.76	0.67
1:C:497:ILE:HG23	1:C:532:PHE:CD1	2.30	0.67
1:E:217:TYR:CE2	1:E:236:LEU:HD12	2.30	0.67
1:E:254:THR:HG23	1:E:257:LEU:CD2	2.25	0.67
1:A:317:ALA:O	1:A:321:VAL:HG22	1.94	0.67
1:C:115:GLU:HG2	1:C:116:LEU:H	1.59	0.67
1:D:99:LEU:HD11	1:D:133:LYS:HD3	1.75	0.67
1:F:378:GLU:O	1:F:382:THR:HG22	1.94	0.67
1:A:71:PHE:CE1	1:A:88:ARG:HA	2.30	0.66
1:B:65:LYS:O	1:B:65:LYS:HD3	1.95	0.66
1:E:56:LYS:HE3	1:E:265:LEU:O	1.95	0.66
1:E:180:TRP:O	1:E:182:PRO:HD3	1.95	0.66
1:E:283:GLN:OE1	1:E:283:GLN:HA	1.94	0.66
1:A:100:ASP:OD1	1:A:103:VAL:HG23	1.95	0.66
1:B:434:ALA:O	1:B:438:ILE:HG13	1.94	0.66
1:C:626:GLU:HB3	2:H:149:VAL:HG11	1.75	0.66
1:D:127:TYR:O	1:D:131:VAL:HG23	1.95	0.66
1:E:401:ASP:C	1:E:403:THR:H	2.03	0.66
1:B:43:GLU:HG2	2:G:113:TRP:CZ3	2.30	0.66
1:B:202:LEU:HD12	1:B:202:LEU:C	2.20	0.66
1:F:254:THR:HG23	1:F:257:LEU:HB3	1.76	0.66
2:I:143:GLN:HG2	2:I:182:ASN:HD21	1.58	0.66
2:I:164:LEU:HD23	2:I:165:LEU:N	2.10	0.66
1:A:65:LYS:HD3	1:A:65:LYS:C	2.20	0.66
1:A:425:THR:HG22	1:A:426:MET:HE2	1.77	0.66
1:C:226:GLN:H	1:C:226:GLN:CD	2.02	0.66
1:E:452:ASP:HA	1:E:455:LEU:HD23	1.75	0.66
1:F:103:VAL:O	1:F:106:PRO:HD2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:654:LEU:HD22	2:H:154:CYS:SG	2.35	0.66
1:E:287:TRP:HZ2	1:E:320:HIS:CG	2.14	0.66
1:A:495:PHE:O	1:A:499:VAL:HG23	1.95	0.66
1:B:122:SER:HB3	1:B:263:ILE:HD12	1.78	0.66
1:E:554:PRO:O	1:E:555:GLU:HB3	1.96	0.66
1:E:115:GLU:HG2	1:E:116:LEU:N	2.07	0.66
1:E:335:GLN:NE2	1:E:348:TYR:HE1	1.88	0.66
1:A:225:ASN:HB2	1:A:229:ALA:CB	2.18	0.66
1:A:625:PRO:O	1:A:626:GLU:HB2	1.95	0.66
1:B:86:CYS:HB3	1:B:263:ILE:HG13	1.78	0.66
1:B:137:ILE:HG23	1:B:145:ARG:HB2	1.76	0.66
1:B:447:LYS:HG2	1:B:481:TYR:HB3	1.77	0.66
1:F:563:THR:HG23	1:F:574:LEU:HB3	1.78	0.66
1:B:390:ILE:HD13	1:B:414:LYS:HG2	1.78	0.66
1:D:262:PRO:HG3	1:D:273:LEU:HD21	1.77	0.66
1:E:501:GLU:HB3	1:E:504:GLN:HG3	1.78	0.66
1:A:140:GLY:HA3	1:A:144:ALA:CB	2.26	0.66
1:A:356:ILE:CG2	1:A:359:SER:HB2	2.25	0.66
1:B:23:PRO:HB3	1:B:26:ARG:NH1	2.11	0.66
1:C:275:LYS:HE2	1:C:275:LYS:H	1.61	0.66
1:D:396:ALA:O	1:D:398:MET:N	2.28	0.65
1:D:455:LEU:HA	1:D:475:LEU:HD21	1.77	0.65
1:F:41:ILE:CG1	1:F:50:LEU:HB3	2.26	0.65
1:D:299:LEU:HD12	1:D:299:LEU:N	2.12	0.65
1:F:392:LEU:HD13	2:I:113:TRP:CZ3	2.32	0.65
1:F:432:LEU:HA	1:F:435:SER:HB3	1.78	0.65
1:A:142:GLU:O	1:A:146:ASN:HB2	1.96	0.65
1:B:137:ILE:HD12	1:B:137:ILE:N	2.10	0.65
1:B:165:LYS:HD3	1:B:208:ASP:OD2	1.97	0.65
1:C:145:ARG:HD2	1:C:145:ARG:O	1.94	0.65
1:F:282:GLN:O	1:F:286:ILE:HG13	1.96	0.65
2:H:185:CYS:CB	2:H:188:ASP:HB3	2.24	0.65
1:B:204:CYS:HB2	1:B:205:GLN:NE2	2.11	0.65
1:B:206:PRO:HA	1:B:210:LEU:HD11	1.78	0.65
1:B:364:PHE:CZ	1:B:421:VAL:HG11	2.32	0.65
1:E:131:VAL:HG11	1:E:151:ALA:CB	2.26	0.65
1:F:280:ASP:O	1:F:283:GLN:HB2	1.97	0.65
2:G:174:ALA:O	2:G:178:LEU:HB2	1.95	0.65
1:E:489:ILE:HD12	1:E:508:LEU:HD11	1.78	0.65
1:A:173:TYR:CE2	1:A:198:LEU:HD22	2.32	0.65
1:A:462:TYR:HD2	1:A:463:HIS:NE2	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:434:ALA:HA	1:E:437:LYS:NZ	2.11	0.65
1:F:398:MET:CG	1:F:408:ILE:HD11	2.22	0.65
1:D:513:ILE:HG22	1:D:552:LYS:HE2	1.78	0.65
1:E:42:GLU:O	1:E:45:PRO:HD3	1.96	0.65
1:E:327:ILE:CG2	1:E:328:TRP:N	2.54	0.65
1:F:492:TYR:CE1	1:F:496:LEU:HD11	2.32	0.65
2:I:160:THR:O	2:I:163:ALA:HB3	1.96	0.65
1:A:646:GLU:HB2	1:A:650:PHE:HD2	1.61	0.65
1:E:468:THR:HG21	1:E:499:VAL:HG11	1.78	0.65
1:F:468:THR:CG2	1:F:499:VAL:HG11	2.26	0.65
1:C:237:SER:O	1:C:241:MET:HG2	1.96	0.65
1:C:455:LEU:N	1:C:455:LEU:HD22	2.12	0.65
1:C:468:THR:HG21	1:C:499:VAL:HG11	1.78	0.65
1:C:523:LYS:HB2	1:C:553:PHE:CE2	2.32	0.65
1:E:61:LEU:HB2	1:E:63:GLN:HE21	1.60	0.65
1:A:339:ASN:HD22	1:A:339:ASN:C	2.05	0.65
1:D:460:ILE:O	1:D:464:ILE:HG13	1.97	0.65
1:E:432:LEU:HD13	1:E:464:ILE:HD11	1.77	0.65
1:E:638:GLN:NE2	1:F:384:LEU:HD12	2.12	0.65
2:I:188:ASP:C	2:I:190:LEU:H	2.04	0.64
2:H:134:GLU:O	2:H:137:LYS:HG2	1.96	0.64
1:E:299:LEU:H	1:E:299:LEU:HD12	1.62	0.64
1:F:523:LYS:HB2	1:F:553:PHE:CE2	2.31	0.64
2:I:114:LEU:H	2:I:114:LEU:HD12	1.61	0.64
1:E:335:GLN:HG3	1:E:348:TYR:CE1	2.32	0.64
1:E:568:VAL:HG23	1:F:417:TYR:HE1	1.62	0.64
1:F:85:TRP:CE3	1:F:111:CYS:HB3	2.32	0.64
1:A:119:ASN:OD1	1:A:159:CYS:HB2	1.97	0.64
1:B:556:VAL:HG22	1:B:557:ASN:H	1.62	0.64
1:C:493:LEU:O	1:C:497:ILE:HG13	1.98	0.64
1:D:52:VAL:HG11	1:D:268:ALA:HB3	1.79	0.64
1:D:156:VAL:HG13	1:D:170:TRP:HH2	1.63	0.64
2:G:147:LEU:HD22	2:G:179:LEU:HD23	1.79	0.64
1:A:167:ILE:HG23	1:A:168:GLN:H	1.62	0.64
1:D:81:MET:HE1	1:D:319:GLN:O	1.98	0.64
1:E:255:LYS:O	1:E:257:LEU:N	2.29	0.64
1:E:335:GLN:HG3	1:E:348:TYR:CD1	2.33	0.64
1:E:574:LEU:HD11	1:F:361:VAL:HG22	1.79	0.64
1:B:426:MET:HG3	1:B:438:ILE:HD11	1.79	0.64
1:C:186:PHE:C	1:C:188:GLU:H	2.05	0.64
1:E:198:LEU:HD12	1:E:198:LEU:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:143:GLN:HG3	2:G:178:LEU:HD21	1.80	0.64
2:H:146:LEU:O	2:H:150:ILE:HG13	1.97	0.64
1:A:218:THR:HG22	1:A:233:ILE:HG21	1.80	0.64
1:C:140:GLY:HA3	1:C:144:ALA:HB3	1.79	0.64
1:C:400:ASP:O	1:C:401:ASP:HB3	1.97	0.64
1:C:563:THR:HG22	1:C:572:ASN:OD1	1.97	0.64
1:D:468:THR:HG21	1:D:499:VAL:CG1	2.20	0.64
1:E:384:LEU:HD23	1:E:387:ILE:HD12	1.80	0.64
1:A:99:LEU:H	1:A:99:LEU:HD12	1.61	0.64
1:C:631:LEU:HD12	2:H:115:PRO:HD2	1.79	0.64
2:H:143:GLN:CG	2:H:178:LEU:HD22	2.28	0.64
1:B:202:LEU:HD12	1:B:203:LEU:N	2.13	0.64
1:E:125:LEU:HD21	1:E:169:PHE:HD1	1.63	0.64
1:F:54:LEU:HG	1:F:54:LEU:O	1.97	0.64
1:F:485:ASP:HB3	1:F:488:TYR:HB3	1.80	0.64
2:I:189:GLN:NE2	2:I:189:GLN:H	1.96	0.64
1:A:345:ILE:H	1:A:345:ILE:CD1	1.97	0.64
1:D:287:TRP:O	1:D:291:ILE:HG13	1.97	0.64
1:E:631:LEU:HD21	2:I:171:LEU:HD22	1.79	0.64
1:A:32:ASP:O	1:A:36:LYS:HG3	1.99	0.63
1:A:462:TYR:HD2	1:A:463:HIS:CE1	2.16	0.63
1:C:174:LEU:O	1:C:178:GLU:HG3	1.98	0.63
1:C:283:GLN:HA	1:C:286:ILE:HD12	1.80	0.63
1:C:473:LYS:O	1:C:477:LEU:HD13	1.98	0.63
1:D:456:GLU:O	1:D:460:ILE:HG13	1.97	0.63
1:E:626:GLU:OE1	2:I:146:LEU:HG	1.98	0.63
1:A:108:LEU:HD13	1:A:127:TYR:HD1	1.61	0.63
1:D:152:PHE:HB3	1:D:173:TYR:CE1	2.34	0.63
1:E:412:LYS:HE2	1:E:448:LEU:HA	1.79	0.63
2:H:186:SER:HA	2:H:189:GLN:HE21	1.62	0.63
1:C:30:GLU:HG3	1:C:31:SER:H	1.64	0.63
1:C:644:ILE:HG23	2:H:173:TYR:HE1	1.64	0.63
1:D:55:LEU:HD13	1:D:265:LEU:HD11	1.80	0.63
1:E:207:MET:H	1:E:210:LEU:HG	1.63	0.63
1:E:650:PHE:HD2	2:I:165:LEU:HD21	1.63	0.63
1:A:280:ASP:OD2	1:A:283:GLN:HG2	1.98	0.63
1:C:635:PRO:HG3	2:H:120:VAL:CG2	2.28	0.63
1:E:200:LYS:CD	1:E:236:LEU:HD21	2.29	0.63
1:E:479:LEU:HD11	1:E:492:TYR:HE2	1.63	0.63
1:A:83:ASN:HB2	1:A:262:PRO:O	1.97	0.63
1:B:525:ILE:O	1:B:529:VAL:HG23	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:173:TYR:CD2	1:E:198:LEU:HD22	2.34	0.63
2:H:186:SER:O	2:H:190:LEU:HG	1.98	0.63
1:A:51:TYR:HD1	1:A:74:LEU:HB2	1.64	0.63
1:A:61:LEU:HB2	1:A:63:GLN:HE21	1.64	0.63
1:C:423:MET:HB2	1:C:438:ILE:HG21	1.79	0.63
1:D:542:VAL:O	1:D:546:GLU:HG3	1.97	0.63
1:E:43:GLU:O	1:E:44:GLN:HG2	1.98	0.63
1:E:136:ASP:HB3	1:E:139:THR:HB	1.81	0.63
1:A:265:LEU:HD23	1:A:265:LEU:O	1.98	0.63
1:D:378:GLU:O	1:D:382:THR:HG22	1.99	0.63
1:F:89:LEU:HD11	1:F:108:LEU:HD21	1.80	0.63
1:C:166:SER:HG	1:C:170:TRP:CD1	2.17	0.63
1:D:159:CYS:O	1:D:161:ILE:HG12	1.98	0.63
1:D:376:ILE:HB	1:D:377:PRO:HD3	1.80	0.63
1:A:202:LEU:HD12	1:A:203:LEU:N	2.13	0.63
1:B:59:VAL:HG13	1:B:60:SER:N	2.13	0.63
1:B:77:ARG:HB3	1:B:78:PHE:HD1	1.63	0.63
1:C:78:PHE:HB3	1:C:81:MET:HG2	1.78	0.63
1:D:180:TRP:CZ3	1:D:191:ARG:HB2	2.34	0.63
1:D:280:ASP:HB3	1:D:283:GLN:HB2	1.81	0.63
1:E:371:GLU:HA	1:E:379:ILE:HD11	1.81	0.63
1:A:341:ASP:O	1:A:344:VAL:HG23	1.99	0.62
1:A:395:ALA:O	1:A:399:GLU:HG3	1.99	0.62
1:A:470:THR:O	1:A:474:VAL:HG23	1.99	0.62
1:B:442:CYS:O	1:B:445:LEU:HB2	1.99	0.62
1:C:636:LYS:C	1:C:638:GLN:H	2.06	0.62
1:E:576:ARG:HH11	1:E:576:ARG:HB2	1.64	0.62
1:A:115:GLU:O	1:A:116:LEU:HD23	1.98	0.62
1:A:443:ARG:HD2	1:A:477:LEU:HG	1.81	0.62
1:A:626:GLU:OE1	2:G:149:VAL:HG21	1.98	0.62
1:E:170:TRP:NE1	1:E:207:MET:HE3	2.14	0.62
1:E:237:SER:O	1:E:241:MET:HG2	1.99	0.62
1:E:635:PRO:HB2	1:E:640:PHE:HE1	1.63	0.62
1:F:297:ASN:HB2	1:F:306:HIS:CE1	2.35	0.62
1:A:231:ARG:O	1:A:235:GLU:HG3	1.99	0.62
1:B:422:TYR:CE2	1:B:438:ILE:HD13	2.34	0.62
1:C:509:PHE:CD1	1:C:529:VAL:HG21	2.34	0.62
1:D:371:GLU:HA	1:D:379:ILE:HD11	1.81	0.62
1:E:48:ILE:HG22	1:E:273:LEU:HD13	1.80	0.62
1:E:253:ILE:HG23	1:E:289:GLU:HG2	1.80	0.62
1:F:574:LEU:O	1:F:578:GLU:HB3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:580:ASP:C	1:F:582:MET:H	2.05	0.62
1:A:639:TYR:CE2	2:G:120:VAL:HG23	2.35	0.62
1:C:509:PHE:CZ	1:C:513:ILE:HD11	2.34	0.62
1:D:103:VAL:O	1:D:106:PRO:HD2	1.98	0.62
1:E:125:LEU:CD2	1:E:128:ILE:HD12	2.23	0.62
1:F:456:GLU:O	1:F:460:ILE:HG13	1.99	0.62
1:B:85:TRP:CE3	1:B:111:CYS:HB3	2.33	0.62
1:B:346:THR:OG1	1:B:369:GLN:HB3	1.98	0.62
1:D:426:MET:HG3	1:D:438:ILE:HD11	1.82	0.62
1:A:79:PRO:C	1:A:80:LEU:HD23	2.24	0.62
1:A:398:MET:C	1:A:400:ASP:H	2.08	0.62
1:B:184:ASN:OD1	1:B:185:LYS:N	2.31	0.62
1:E:191:ARG:HE	1:E:195:ILE:HD11	1.64	0.62
2:H:186:SER:CA	2:H:189:GLN:HE21	2.11	0.62
1:C:178:GLU:HA	1:C:191:ARG:NH2	2.13	0.62
1:D:494:ASP:OD1	1:D:528:LYS:HD3	1.99	0.62
1:E:326:GLU:O	1:E:330:ASN:HB2	1.99	0.62
1:B:530:ILE:HG13	1:B:545:LEU:HD22	1.82	0.62
1:C:412:LYS:NZ	1:C:448:LEU:HA	2.14	0.62
1:F:371:GLU:OE2	1:F:429:ILE:HD11	2.00	0.62
2:G:186:SER:HA	2:G:189:GLN:OE1	1.99	0.62
1:A:174:LEU:HD11	1:A:199:TYR:CZ	2.35	0.62
1:A:202:LEU:HD13	1:A:207:MET:HE1	1.82	0.62
1:C:180:TRP:O	1:C:191:ARG:NH1	2.33	0.62
1:E:302:SER:OG	1:E:305:LEU:HG	1.99	0.62
1:E:573:TYR:HD1	1:F:417:TYR:HB2	1.64	0.62
1:A:513:ILE:N	1:A:513:ILE:HD12	2.15	0.62
1:D:41:ILE:O	1:D:41:ILE:HG22	1.99	0.62
1:E:200:LYS:CG	1:E:236:LEU:HD21	2.29	0.62
1:E:557:ASN:ND2	1:E:560:GLU:N	2.48	0.62
1:B:378:GLU:OE2	1:B:378:GLU:N	2.32	0.61
1:B:427:LYS:HB2	1:B:435:SER:HB2	1.82	0.61
1:C:559:LEU:HA	1:D:329:PHE:HE1	1.63	0.61
1:E:209:CYS:HB2	1:E:212:SER:HB3	1.82	0.61
1:E:426:MET:HG3	1:E:438:ILE:HD11	1.80	0.61
1:B:218:THR:HA	1:B:233:ILE:CD1	2.30	0.61
1:B:281:VAL:HG12	1:B:285:LEU:HD11	1.81	0.61
1:C:640:PHE:HA	1:C:642:VAL:HG22	1.82	0.61
1:E:400:ASP:O	1:E:401:ASP:HB3	2.00	0.61
1:E:560:GLU:O	1:E:563:THR:OG1	2.16	0.61
1:F:371:GLU:CB	1:F:379:ILE:HD11	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:144:MET:HE3	2:I:182:ASN:HB3	1.82	0.61
1:A:80:LEU:HD13	1:A:315:MET:HE1	1.82	0.61
1:A:92:GLU:OE2	1:A:103:VAL:HG11	2.00	0.61
1:A:165:LYS:HD3	1:A:208:ASP:HB3	1.81	0.61
1:B:341:ASP:C	1:B:343:THR:H	2.07	0.61
1:D:77:ARG:HB3	1:D:78:PHE:CD1	2.36	0.61
1:D:426:MET:HE2	1:D:426:MET:HA	1.82	0.61
1:C:460:ILE:O	1:C:464:ILE:HG13	2.00	0.61
1:B:140:GLY:HA3	1:B:144:ALA:HB2	1.83	0.61
1:C:74:LEU:HD13	1:C:84:ILE:CG2	2.31	0.61
1:C:569:LEU:O	1:C:571:VAL:HG23	2.01	0.61
1:D:186:PHE:C	1:D:188:GLU:H	2.07	0.61
1:E:137:ILE:HD12	1:E:179:HIS:NE2	2.15	0.61
1:E:159:CYS:SG	1:E:160:ALA:N	2.73	0.61
1:A:128:ILE:HG12	1:A:152:PHE:CE1	2.36	0.61
1:A:638:GLN:O	1:A:641:LYS:HE3	2.00	0.61
1:C:106:PRO:O	1:C:109:ALA:HB3	2.01	0.61
1:D:85:TRP:CE3	1:D:111:CYS:HB3	2.35	0.61
1:E:41:ILE:CG1	1:E:50:LEU:HD22	2.30	0.61
1:E:41:ILE:HG22	1:E:41:ILE:O	2.00	0.61
1:F:534:SER:HA	1:F:542:VAL:HG21	1.82	0.61
1:A:130:TYR:C	1:A:132:ARG:H	2.08	0.61
1:A:249:ASP:O	1:A:253:ILE:HG13	2.00	0.61
1:A:510:GLU:OE1	1:A:548:ARG:NH2	2.34	0.61
1:B:552:LYS:C	1:B:554:PRO:HD3	2.25	0.61
1:C:103:VAL:O	1:C:106:PRO:HD2	2.00	0.61
1:C:432:LEU:HD22	1:C:464:ILE:HD13	1.81	0.61
1:E:311:THR:O	1:E:315:MET:HG3	2.00	0.61
1:E:265:LEU:O	1:E:265:LEU:HD23	2.01	0.61
1:E:280:ASP:HB3	1:E:283:GLN:HB2	1.82	0.61
1:E:638:GLN:O	1:E:641:LYS:HG3	2.01	0.61
1:A:387:ILE:CD1	1:A:418:VAL:HG12	2.31	0.61
1:C:247:TYR:CZ	1:C:251:LEU:HD13	2.36	0.61
1:C:501:GLU:O	1:C:504:GLN:N	2.31	0.61
1:D:546:GLU:OE2	1:D:565:LYS:HE2	2.01	0.61
1:A:283:GLN:CA	1:A:286:ILE:HD12	2.30	0.60
1:A:634:LEU:HD11	2:G:174:ALA:CB	2.31	0.60
1:B:267:GLN:O	1:B:269:THR:HG23	2.00	0.60
1:B:390:ILE:HG22	1:B:415:LEU:HD13	1.81	0.60
1:B:506:LYS:NZ	1:B:545:LEU:HD12	2.16	0.60
1:E:135:ASN:ND2	1:E:147:ILE:HG21	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:PRO:O	1:A:109:ALA:HB3	2.00	0.60
1:A:270:GLU:O	1:A:270:GLU:HG2	2.01	0.60
1:C:205:GLN:O	1:C:207:MET:HG3	2.01	0.60
1:C:275:LYS:HE2	1:C:278:GLU:OE1	2.01	0.60
1:D:275:LYS:HD3	1:D:275:LYS:N	2.15	0.60
1:F:77:ARG:HB3	1:F:78:PHE:CD1	2.36	0.60
1:F:557:ASN:ND2	1:F:560:GLU:N	2.49	0.60
1:A:510:GLU:O	1:A:513:ILE:HD11	2.01	0.60
1:D:221:GLU:HB3	1:D:229:ALA:HB1	1.83	0.60
1:A:345:ILE:HD12	1:A:345:ILE:N	2.04	0.60
1:B:317:ALA:O	1:B:321:VAL:HG22	2.02	0.60
1:C:44:GLN:H	1:C:45:PRO:HD3	1.65	0.60
1:D:115:GLU:C	1:D:117:GLY:H	2.07	0.60
1:D:200:LYS:HG2	1:D:236:LEU:HD11	1.83	0.60
2:I:121:ASN:CG	2:I:124:MET:HE2	2.25	0.60
1:A:400:ASP:O	1:A:401:ASP:HB3	2.01	0.60
1:A:427:LYS:HB2	1:A:435:SER:OG	2.01	0.60
1:A:624:PRO:HB2	1:A:627:ILE:CG2	2.31	0.60
1:B:78:PHE:N	1:B:78:PHE:CD1	2.69	0.60
1:B:115:GLU:CD	1:B:115:GLU:H	2.10	0.60
1:F:254:THR:HG23	1:F:257:LEU:CB	2.30	0.60
1:F:509:PHE:O	1:F:513:ILE:HG13	2.01	0.60
2:I:125:THR:HG22	2:I:129:MET:CE	2.31	0.60
1:A:58:HIS:HB3	1:A:67:VAL:HG23	1.84	0.60
1:C:574:LEU:HD11	1:D:361:VAL:CG2	2.30	0.60
1:D:115:GLU:CD	1:D:115:GLU:N	2.60	0.60
1:D:295:SER:C	1:D:297:ASN:H	2.10	0.60
1:F:115:GLU:CD	1:F:115:GLU:N	2.59	0.60
2:H:114:LEU:H	2:H:114:LEU:HD12	1.66	0.60
2:H:134:GLU:HA	2:H:137:LYS:HE2	1.83	0.60
1:A:649:ALA:C	1:A:651:SER:H	2.10	0.60
1:B:86:CYS:CB	1:B:263:ILE:HG13	2.31	0.60
1:B:580:ASP:C	1:B:582:MET:H	2.10	0.60
1:E:41:ILE:HG13	1:E:50:LEU:HD22	1.82	0.60
1:E:263:ILE:HG22	1:E:267:GLN:NE2	2.17	0.60
1:E:325:PRO:HD3	1:E:356:ILE:CD1	2.30	0.60
1:F:71:PHE:CD2	1:F:88:ARG:HB2	2.36	0.60
1:F:156:VAL:HA	1:F:160:ALA:HB3	1.82	0.60
1:B:192:VAL:HG12	1:B:220:TRP:CH2	2.36	0.60
1:D:128:ILE:HA	1:D:131:VAL:HG23	1.84	0.60
1:E:631:LEU:HD12	2:I:115:PRO:HD2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:118:VAL:HG12	2:I:119:ASP:N	2.17	0.60
2:I:138:LEU:O	2:I:142:GLN:HB3	2.02	0.60
1:B:307:LYS:HE3	1:B:338:LYS:HG3	1.83	0.60
1:B:356:ILE:O	1:B:358:ASN:N	2.35	0.60
1:D:455:LEU:HD13	1:D:475:LEU:CD2	2.31	0.60
1:E:332:ALA:O	1:E:335:GLN:HB2	2.02	0.60
2:G:159:GLU:O	2:G:162:VAL:HG22	2.02	0.60
1:A:58:HIS:ND1	1:A:66:GLN:HB3	2.16	0.60
1:A:179:HIS:CG	1:A:179:HIS:O	2.55	0.60
1:B:227:LEU:HD23	1:B:227:LEU:O	2.02	0.60
1:B:364:PHE:HZ	1:B:421:VAL:HG11	1.65	0.60
1:B:559:LEU:HD21	1:B:579:LEU:HD11	1.84	0.60
1:C:553:PHE:O	1:C:556:VAL:HG23	2.00	0.60
1:A:99:LEU:HD12	1:A:99:LEU:N	2.16	0.59
1:B:252:ASN:O	1:B:255:LYS:HG2	2.02	0.59
1:C:44:GLN:H	1:C:45:PRO:CD	2.15	0.59
1:D:103:VAL:C	1:D:106:PRO:HD2	2.27	0.59
1:F:354:GLN:O	1:F:357:PRO:HD3	2.02	0.59
1:F:533:GLU:HB3	1:F:542:VAL:HG22	1.82	0.59
1:F:576:ARG:HB3	1:F:576:ARG:NH1	2.14	0.59
1:C:131:VAL:HG11	1:C:151:ALA:HB2	1.83	0.59
1:E:309:ARG:O	1:E:312:TYR:N	2.29	0.59
1:E:449:VAL:HG23	1:E:449:VAL:O	2.00	0.59
1:E:580:ASP:C	1:E:582:MET:H	2.08	0.59
1:C:542:VAL:O	1:C:546:GLU:HG3	2.02	0.59
1:E:74:LEU:HD22	1:E:84:ILE:HD13	1.84	0.59
1:E:394:LEU:O	1:E:398:MET:HG3	2.02	0.59
1:A:245:SER:O	1:A:248:GLN:HB2	2.02	0.59
1:B:548:ARG:HG2	1:B:548:ARG:NH1	2.10	0.59
1:C:30:GLU:HG3	1:C:31:SER:N	2.17	0.59
1:C:74:LEU:HD22	1:C:84:ILE:HD13	1.83	0.59
1:C:79:PRO:O	1:C:80:LEU:HD23	2.02	0.59
1:C:202:LEU:O	1:C:207:MET:HE2	2.02	0.59
1:C:371:GLU:HA	1:C:379:ILE:HD11	1.84	0.59
1:D:222:GLN:HA	1:D:226:GLN:HA	1.84	0.59
2:H:150:ILE:HG23	2:H:161:PHE:HE1	1.66	0.59
1:A:59:VAL:HG13	1:A:60:SER:N	2.16	0.59
1:A:99:LEU:HB2	1:A:134:LYS:HZ1	1.66	0.59
1:B:99:LEU:HB2	1:B:134:LYS:NZ	2.16	0.59
1:C:218:THR:HA	1:C:233:ILE:HD11	1.83	0.59
1:D:428:ARG:O	1:D:428:ARG:HG2	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:259:ARG:HH12	1:E:290:TRP:HH2	1.48	0.59
1:E:523:LYS:HB2	1:E:553:PHE:CE2	2.37	0.59
1:E:563:THR:HG22	1:E:574:LEU:CD1	2.26	0.59
1:A:89:LEU:N	1:A:89:LEU:HD23	2.17	0.59
1:A:264:THR:HB	1:A:267:GLN:CG	2.31	0.59
1:B:259:ARG:HD3	1:B:287:TRP:CH2	2.38	0.59
1:B:524:MET:O	1:B:528:LYS:HG3	2.03	0.59
1:D:37:LEU:HD12	1:D:40:MET:HE1	1.83	0.59
1:D:451:PRO:HG3	1:D:482:PHE:CD2	2.37	0.59
1:A:307:LYS:HD2	1:A:334:TYR:OH	2.03	0.59
1:B:89:LEU:HD21	1:B:107:VAL:CG1	2.31	0.59
1:C:153:GLN:O	1:C:156:VAL:HB	2.02	0.59
1:D:330:ASN:N	1:D:330:ASN:ND2	2.51	0.59
1:F:350:LYS:NZ	1:F:354:GLN:HE21	2.00	0.59
2:G:150:ILE:HG21	2:G:175:ILE:HD13	1.85	0.59
2:G:164:LEU:HD12	2:G:164:LEU:O	2.03	0.59
1:B:71:PHE:CE2	1:B:88:ARG:HB2	2.37	0.59
1:B:119:ASN:OD1	1:B:159:CYS:HB2	2.03	0.59
1:C:631:LEU:HD21	2:H:171:LEU:HD12	1.83	0.59
1:A:85:TRP:CD2	1:A:111:CYS:HB3	2.36	0.59
1:A:115:GLU:H	1:A:115:GLU:CD	2.11	0.59
1:A:517:SER:O	1:A:518:ASP:C	2.46	0.59
1:F:275:LYS:H	1:F:275:LYS:HE2	1.67	0.59
2:G:189:GLN:HG3	2:G:190:LEU:N	2.17	0.59
1:A:196:ARG:NH1	1:A:232:HIS:HE1	2.01	0.59
1:B:296:ASP:HB3	1:B:298:LYS:HD2	1.83	0.59
1:C:394:LEU:HA	1:C:411:LEU:HD23	1.84	0.59
1:D:455:LEU:HD22	1:D:455:LEU:N	2.18	0.59
1:E:44:GLN:H	1:E:45:PRO:HD3	1.68	0.59
1:E:284:LEU:HB2	1:E:321:VAL:HG11	1.85	0.59
1:C:85:TRP:CD2	1:C:111:CYS:HB3	2.38	0.58
1:C:361:VAL:HG22	1:D:574:LEU:CD1	2.30	0.58
1:C:563:THR:HG23	1:C:574:LEU:HD12	1.83	0.58
1:E:285:LEU:HD23	1:E:285:LEU:O	2.03	0.58
1:E:557:ASN:HD22	1:E:560:GLU:CB	2.13	0.58
2:G:125:THR:CG2	2:G:129:MET:HE2	2.26	0.58
1:A:451:PRO:HB3	1:A:488:TYR:CD1	2.38	0.58
1:D:284:LEU:O	1:D:287:TRP:N	2.35	0.58
1:D:412:LYS:O	1:D:415:LEU:HB3	2.04	0.58
1:E:165:LYS:HE2	1:E:250:TRP:HZ3	1.66	0.58
1:E:282:GLN:O	1:E:286:ILE:HG13	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:168:ALA:HB1	2:I:170:GLN:OE1	2.04	0.58
2:H:116:VAL:HG23	2:H:117:GLY:N	2.17	0.58
1:A:54:LEU:HG	1:A:58:HIS:HD2	1.68	0.58
1:A:173:TYR:CE2	1:A:198:LEU:HD13	2.38	0.58
1:A:280:ASP:HB3	1:A:283:GLN:HB2	1.84	0.58
1:A:492:TYR:CE1	1:A:496:LEU:HD11	2.37	0.58
1:B:305:LEU:O	1:B:308:ALA:HB3	2.03	0.58
1:E:470:THR:O	1:E:474:VAL:HG23	2.03	0.58
1:E:509:PHE:CD1	1:E:529:VAL:HG21	2.38	0.58
1:F:79:PRO:CB	1:F:116:LEU:HD13	2.33	0.58
1:F:167:ILE:HG13	1:F:209:CYS:HB3	1.84	0.58
1:A:521:LEU:O	1:A:525:ILE:HG12	2.03	0.58
1:B:180:TRP:CZ3	1:B:191:ARG:HA	2.37	0.58
1:B:219:GLN:NE2	1:B:220:TRP:N	2.51	0.58
1:C:34:ILE:HD13	1:C:58:HIS:CE1	2.38	0.58
1:D:262:PRO:CG	1:D:273:LEU:HD21	2.33	0.58
1:D:317:ALA:HB1	1:D:327:ILE:HD11	1.83	0.58
2:I:179:LEU:HG	2:I:184:VAL:HG21	1.84	0.58
1:A:336:GLY:C	1:A:338:LYS:N	2.62	0.58
1:B:77:ARG:HB3	1:B:78:PHE:CD1	2.37	0.58
1:C:501:GLU:O	1:C:502:GLU:C	2.47	0.58
1:C:543:ARG:CZ	1:D:372:LEU:HD11	2.34	0.58
1:D:32:ASP:O	1:D:34:ILE:N	2.36	0.58
2:I:147:LEU:HD23	2:I:148:LYS:N	2.19	0.58
1:A:432:LEU:O	1:A:432:LEU:HD12	2.03	0.58
1:A:579:LEU:CD1	1:A:582:MET:HE2	2.32	0.58
1:B:100:ASP:C	1:B:102:ALA:H	2.12	0.58
1:C:332:ALA:O	1:C:345:ILE:HG12	2.04	0.58
1:E:40:MET:HB3	1:E:50:LEU:HD21	1.85	0.58
1:F:490:ASN:OD1	1:F:524:MET:HE2	2.03	0.58
1:A:103:VAL:O	1:A:106:PRO:HD2	2.03	0.58
1:A:202:LEU:HD12	1:A:202:LEU:C	2.29	0.58
1:B:180:TRP:HB3	1:B:191:ARG:NH1	2.18	0.58
1:E:125:LEU:C	1:E:127:TYR:H	2.08	0.58
1:F:78:PHE:HB3	1:F:81:MET:HG2	1.85	0.58
1:D:502:GLU:OE2	1:D:536:VAL:HG11	2.03	0.58
1:E:48:ILE:HA	1:E:51:TYR:HD2	1.69	0.58
1:E:156:VAL:O	1:E:160:ALA:HB3	2.04	0.58
1:E:442:CYS:O	1:E:445:LEU:HB2	2.04	0.58
1:F:168:GLN:HG3	1:F:169:PHE:N	2.18	0.58
1:F:516:ILE:HG22	1:F:517:SER:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:LYS:NZ	1:A:448:LEU:HA	2.19	0.58
1:B:28:ARG:HH21	1:F:33:VAL:HG11	1.69	0.58
1:C:121:LEU:HG	1:C:159:CYS:SG	2.44	0.58
1:C:452:ASP:HA	1:C:455:LEU:HD23	1.86	0.58
1:D:136:ASP:HB3	1:D:139:THR:CB	2.32	0.58
1:D:358:ASN:HB3	1:D:389:ARG:HG3	1.85	0.58
1:A:210:LEU:HD11	1:A:243:ALA:HB1	1.85	0.58
1:A:351:LEU:HA	1:A:354:GLN:OE1	2.04	0.58
1:B:545:LEU:HA	1:B:548:ARG:HD3	1.86	0.58
1:C:370:TYR:CD1	1:C:378:GLU:HB3	2.39	0.58
1:C:371:GLU:OE2	1:D:539:LEU:HB2	2.04	0.58
1:F:336:GLY:HA3	1:F:345:ILE:HG13	1.86	0.58
1:F:486:GLY:C	1:F:521:LEU:HD22	2.29	0.58
1:A:66:GLN:HE21	1:A:66:GLN:CA	2.17	0.57
1:B:314:TYR:HB3	1:B:331:MET:CE	2.34	0.57
1:D:33:VAL:H	1:D:36:LYS:NZ	2.01	0.57
1:D:457:ASN:O	1:D:461:GLU:HG2	2.04	0.57
1:A:178:GLU:O	1:A:191:ARG:NH2	2.33	0.57
1:A:182:PRO:HB3	1:A:188:GLU:HB2	1.86	0.57
1:B:130:TYR:C	1:B:132:ARG:N	2.62	0.57
1:B:462:TYR:CE1	1:B:468:THR:HG23	2.39	0.57
1:C:78:PHE:HB3	1:C:81:MET:CG	2.33	0.57
1:C:483:ALA:HB1	1:C:515:LYS:NZ	2.19	0.57
1:E:320:HIS:O	1:E:322:CYS:N	2.37	0.57
1:F:167:ILE:HG23	1:F:168:GLN:N	2.18	0.57
1:F:371:GLU:CA	1:F:379:ILE:HD11	2.34	0.57
1:A:180:TRP:O	1:A:182:PRO:HD3	2.05	0.57
1:A:324:ALA:O	1:A:327:ILE:HG22	2.03	0.57
1:B:78:PHE:HD1	1:B:78:PHE:N	2.03	0.57
1:B:479:LEU:O	1:B:480:LYS:C	2.47	0.57
1:C:257:LEU:HD12	1:C:283:GLN:HE22	1.67	0.57
1:C:392:LEU:O	1:C:393:ASP:C	2.46	0.57
1:C:468:THR:O	1:C:469:LYS:C	2.47	0.57
1:C:636:LYS:O	1:C:638:GLN:N	2.36	0.57
1:D:221:GLU:HB3	1:D:229:ALA:CB	2.34	0.57
1:D:434:ALA:O	1:D:438:ILE:HG13	2.03	0.57
1:E:103:VAL:C	1:E:106:PRO:HD2	2.29	0.57
1:E:115:GLU:CG	1:E:116:LEU:H	2.12	0.57
1:E:258:LYS:HG3	1:E:260:ASN:OD1	2.04	0.57
1:E:299:LEU:HD21	1:E:309:ARG:NH1	2.19	0.57
1:B:401:ASP:CG	1:B:401:ASP:O	2.48	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:TYR:OH	1:B:441:LYS:HE3	2.03	0.57
1:D:269:THR:C	1:D:271:SER:H	2.12	0.57
1:A:173:TYR:HE2	1:A:198:LEU:HD13	1.68	0.57
1:B:191:ARG:HG3	1:B:191:ARG:HH11	1.70	0.57
1:C:325:PRO:HD3	1:C:356:ILE:HD13	1.87	0.57
1:C:394:LEU:HA	1:C:411:LEU:CD2	2.35	0.57
1:D:432:LEU:HD13	1:D:464:ILE:HD11	1.87	0.57
1:E:200:LYS:O	1:E:204:CYS:SG	2.57	0.57
1:E:394:LEU:HD12	1:E:411:LEU:HD23	1.87	0.57
1:F:240:TYR:O	1:F:243:ALA:HB3	2.05	0.57
1:A:79:PRO:HG3	1:A:351:LEU:HD22	1.86	0.57
1:A:85:TRP:CE3	1:A:111:CYS:HB3	2.39	0.57
1:E:173:TYR:HE2	1:E:198:LEU:HB2	1.69	0.57
1:E:275:LYS:HE2	1:E:275:LYS:H	1.70	0.57
1:E:568:VAL:O	1:E:569:LEU:C	2.47	0.57
1:A:191:ARG:HH11	1:A:191:ARG:HG3	1.68	0.57
1:A:284:LEU:HG	1:A:288:LEU:HD11	1.87	0.57
1:B:457:ASN:HB3	1:B:474:VAL:HG11	1.87	0.57
1:C:43:GLU:O	1:C:44:GLN:HG2	2.04	0.57
1:F:202:LEU:C	1:F:202:LEU:HD12	2.30	0.57
1:F:226:GLN:C	1:F:227:LEU:HD12	2.29	0.57
1:F:556:VAL:O	1:F:557:ASN:C	2.48	0.57
1:A:259:ARG:HG2	1:A:320:HIS:CD2	2.39	0.57
1:A:261:LEU:HD12	1:A:319:GLN:HE21	1.70	0.57
1:C:41:ILE:HG12	1:C:50:LEU:HB3	1.87	0.57
1:C:412:LYS:HZ1	1:C:448:LEU:HA	1.70	0.57
1:D:371:GLU:CA	1:D:379:ILE:HD11	2.35	0.57
1:F:278:GLU:O	1:F:279:TYR:HB3	2.03	0.57
1:F:341:ASP:HB3	1:F:344:VAL:HG23	1.87	0.57
1:F:386:CYS:O	1:F:390:ILE:HG13	2.05	0.57
1:D:128:ILE:HA	1:D:131:VAL:CG2	2.34	0.57
1:E:154:VAL:O	1:E:158:LYS:HG2	2.04	0.57
1:F:509:PHE:CE2	1:F:513:ILE:HD11	2.40	0.57
1:B:258:LYS:CE	2:H:152:HIS:HB2	2.29	0.57
1:B:476:GLU:HA	1:B:479:LEU:HD12	1.87	0.57
1:F:364:PHE:HZ	1:F:421:VAL:HG11	1.69	0.57
1:F:394:LEU:HD12	1:F:411:LEU:HD23	1.85	0.57
2:I:186:SER:N	2:I:189:GLN:HE22	2.03	0.57
2:I:187:VAL:O	2:I:190:LEU:HG	2.05	0.57
1:A:167:ILE:HG23	1:A:168:GLN:N	2.18	0.56
1:A:401:ASP:C	1:A:403:THR:H	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:425:THR:HG22	1:A:426:MET:CE	2.34	0.56
1:C:208:ASP:HA	1:C:247:TYR:CZ	2.40	0.56
1:C:626:GLU:OE1	2:H:149:VAL:HG21	2.04	0.56
1:A:81:MET:CE	1:A:319:GLN:HA	2.31	0.56
1:B:427:LYS:HB2	1:B:435:SER:HB3	1.86	0.56
1:C:37:LEU:HD23	1:C:54:LEU:HD13	1.87	0.56
1:D:167:ILE:HD12	1:D:209:CYS:HB3	1.86	0.56
1:E:145:ARG:NH2	1:E:180:TRP:CZ2	2.73	0.56
1:E:533:GLU:HG3	1:E:545:LEU:HD12	1.87	0.56
1:F:41:ILE:HD11	1:F:50:LEU:C	2.30	0.56
2:H:145:ALA:O	2:H:149:VAL:HG23	2.05	0.56
1:A:32:ASP:O	1:A:32:ASP:CG	2.48	0.56
1:A:93:PHE:HE2	1:A:104:ILE:HD13	1.70	0.56
1:A:115:GLU:N	1:A:115:GLU:OE2	2.36	0.56
1:A:228:THR:HG22	1:A:231:ARG:HH22	1.69	0.56
1:A:630:LEU:HD23	2:G:171:LEU:CD1	2.35	0.56
1:B:497:ILE:HG23	1:B:532:PHE:HD1	1.71	0.56
1:C:168:GLN:HG3	1:C:169:PHE:N	2.20	0.56
1:C:459:TYR:CE1	1:C:495:PHE:HD1	2.22	0.56
1:C:472:CYS:SG	1:C:504:GLN:NE2	2.78	0.56
1:D:530:ILE:HA	1:D:545:LEU:HD13	1.87	0.56
1:D:556:VAL:O	1:D:557:ASN:C	2.47	0.56
1:E:114:LYS:HD3	1:E:114:LYS:N	2.20	0.56
1:E:287:TRP:CZ2	1:E:320:HIS:CG	2.94	0.56
1:E:309:ARG:O	1:E:312:TYR:HB3	2.04	0.56
1:E:460:ILE:O	1:E:464:ILE:HG13	2.05	0.56
1:F:125:LEU:C	1:F:127:TYR:H	2.14	0.56
1:A:518:ASP:CG	1:A:521:LEU:HD13	2.30	0.56
1:B:167:ILE:HG23	1:B:168:GLN:N	2.21	0.56
1:C:54:LEU:HD23	1:C:70:THR:HG23	1.88	0.56
1:C:103:VAL:C	1:C:106:PRO:HD2	2.31	0.56
1:C:553:PHE:HB3	1:C:556:VAL:HG21	1.88	0.56
1:E:107:VAL:HA	1:E:110:ARG:CD	2.36	0.56
1:E:119:ASN:O	1:E:316:GLN:NE2	2.38	0.56
1:E:137:ILE:HG13	1:E:138:ILE:HG13	1.87	0.56
1:E:173:TYR:CE2	1:E:198:LEU:HD22	2.40	0.56
1:F:85:TRP:CD2	1:F:111:CYS:HB3	2.39	0.56
1:A:49:PHE:CE2	1:A:53:LYS:HD3	2.40	0.56
1:A:170:TRP:CZ3	1:A:202:LEU:HB3	2.41	0.56
1:B:178:GLU:CD	1:B:216:ARG:NH2	2.61	0.56
1:C:217:TYR:CE2	1:C:236:LEU:HD12	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:456:GLU:O	1:C:460:ILE:HG13	2.06	0.56
1:E:344:VAL:O	1:E:347:LYS:HB3	2.05	0.56
1:F:78:PHE:HB3	1:F:81:MET:HG3	1.86	0.56
2:I:184:VAL:O	2:I:185:CYS:HB2	2.05	0.56
1:A:387:ILE:HG22	1:A:388:ASP:N	2.20	0.56
1:B:180:TRP:HB3	1:B:191:ARG:HH12	1.69	0.56
1:C:92:GLU:OE1	1:C:95:LYS:HE2	2.05	0.56
1:E:115:GLU:HG2	1:E:116:LEU:HG	1.87	0.56
1:E:206:PRO:HB3	1:E:247:TYR:CA	2.35	0.56
1:E:340:THR:O	1:E:341:ASP:C	2.48	0.56
1:E:557:ASN:HD22	1:E:560:GLU:H	1.49	0.56
1:A:439:PHE:CZ	1:A:474:VAL:HG13	2.40	0.56
1:C:218:THR:HA	1:C:233:ILE:CD1	2.35	0.56
1:C:523:LYS:O	1:C:527:GLN:HG3	2.05	0.56
1:E:405:GLU:C	1:E:407:ALA:N	2.63	0.56
1:E:555:GLU:C	1:E:555:GLU:CD	2.74	0.56
1:A:105:GLU:HB2	1:A:106:PRO:HD3	1.87	0.56
1:A:307:LYS:HE3	1:A:338:LYS:HG3	1.86	0.56
1:B:439:PHE:CZ	1:B:474:VAL:HG13	2.41	0.56
1:C:37:LEU:O	1:C:41:ILE:HG13	2.06	0.56
1:C:642:VAL:O	1:C:643:THR:HG23	2.06	0.56
1:D:181:LYS:HG3	1:D:181:LYS:O	2.06	0.56
1:D:531:PHE:CD1	1:D:531:PHE:C	2.84	0.56
2:I:159:GLU:C	2:I:161:PHE:N	2.64	0.56
1:A:33:VAL:HG12	1:A:37:LEU:HG	1.86	0.56
1:A:116:LEU:O	1:A:118:ASN:N	2.38	0.56
1:C:455:LEU:HB2	1:D:569:LEU:HD11	1.88	0.56
1:D:30:GLU:HG3	1:D:31:SER:N	2.21	0.56
1:D:289:GLU:OE2	1:D:292:ARG:NH2	2.39	0.56
1:D:297:ASN:HD22	1:D:306:HIS:CG	2.23	0.56
1:D:324:ALA:O	1:D:327:ILE:HG22	2.06	0.56
1:D:414:LYS:O	1:D:418:VAL:HG23	2.05	0.56
1:E:178:GLU:HA	1:E:191:ARG:HH22	1.66	0.56
1:E:568:VAL:CG2	1:F:417:TYR:HE1	2.19	0.56
1:F:270:GLU:O	1:F:270:GLU:HG2	2.06	0.56
1:F:493:LEU:CD2	1:F:508:LEU:HD23	2.35	0.56
1:B:183:VAL:HG23	1:B:187:GLU:OE1	2.06	0.56
1:B:391:HIS:CD2	1:B:415:LEU:HD21	2.41	0.56
1:B:398:MET:HA	1:B:408:ILE:HD11	1.87	0.56
1:D:463:HIS:HE1	1:D:498:TYR:CE2	2.23	0.56
1:E:101:ALA:CB	1:E:134:LYS:HE2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:83:ASN:ND2	1:F:261:LEU:HB3	2.21	0.56
1:F:432:LEU:HD22	1:F:464:ILE:CD1	2.35	0.56
1:F:563:THR:CG2	1:F:572:ASN:HD21	2.18	0.56
2:G:139:GLN:O	2:G:142:GLN:HG2	2.06	0.56
1:A:128:ILE:HG12	1:A:152:PHE:CD1	2.41	0.55
1:B:427:LYS:HA	1:B:435:SER:HB3	1.88	0.55
1:E:177:LEU:O	1:E:195:ILE:HD11	2.07	0.55
1:F:578:GLU:O	1:F:579:LEU:HD23	2.06	0.55
1:A:55:LEU:C	1:A:57:HIS:H	2.15	0.55
1:A:247:TYR:CE1	1:A:251:LEU:HD22	2.39	0.55
1:E:41:ILE:HD12	1:E:54:LEU:HD22	1.88	0.55
1:E:174:LEU:HD11	1:E:199:TYR:CZ	2.41	0.55
1:E:306:HIS:O	1:E:309:ARG:HB3	2.06	0.55
1:E:468:THR:HG23	1:E:499:VAL:HG11	1.87	0.55
1:E:553:PHE:O	1:E:554:PRO:C	2.49	0.55
1:E:574:LEU:O	1:E:574:LEU:HD13	2.07	0.55
1:F:571:VAL:HB	1:F:573:TYR:CE2	2.42	0.55
1:A:361:VAL:HG23	1:B:578:GLU:OE1	2.06	0.55
1:B:92:GLU:C	1:B:94:ASP:H	2.14	0.55
1:B:416:THR:OG1	1:B:450:THR:HG23	2.06	0.55
1:B:473:LYS:O	1:B:477:LEU:HB2	2.07	0.55
1:D:84:ILE:HA	1:D:87:MET:HE3	1.87	0.55
1:D:575:GLN:C	1:D:577:LEU:N	2.63	0.55
1:F:416:THR:OG1	1:F:449:VAL:HB	2.06	0.55
1:A:92:GLU:C	1:A:94:ASP:H	2.14	0.55
1:B:192:VAL:HG12	1:B:220:TRP:CZ2	2.40	0.55
1:C:575:GLN:C	1:C:577:LEU:H	2.14	0.55
1:E:489:ILE:HG13	1:E:516:ILE:HD11	1.88	0.55
1:F:521:LEU:O	1:F:525:ILE:HD13	2.06	0.55
1:F:557:ASN:ND2	1:F:560:GLU:HB2	2.15	0.55
1:B:336:GLY:C	1:B:338:LYS:H	2.14	0.55
1:C:171:ASN:OD1	1:C:213:MET:HE1	2.07	0.55
1:D:511:SER:O	1:D:515:LYS:HE2	2.07	0.55
1:F:364:PHE:CZ	1:F:421:VAL:HG11	2.42	0.55
2:I:188:ASP:C	2:I:190:LEU:N	2.64	0.55
1:A:84:ILE:HA	1:A:87:MET:HE3	1.87	0.55
1:A:480:LYS:HD3	1:A:480:LYS:N	2.22	0.55
1:B:559:LEU:O	1:B:562:PHE:HB3	2.07	0.55
1:C:566:TYR:OH	1:D:368:GLU:OE2	2.14	0.55
1:D:345:ILE:O	1:D:349:LEU:HB2	2.06	0.55
1:D:482:PHE:C	1:D:484:THR:H	2.15	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:115:GLU:H	1:E:115:GLU:CD	2.15	0.55
1:F:160:ALA:HB1	1:F:170:TRP:CZ2	2.42	0.55
1:A:54:LEU:HG	1:A:58:HIS:CD2	2.41	0.55
1:A:71:PHE:CD1	1:A:88:ARG:HD2	2.42	0.55
1:A:646:GLU:HG3	1:A:650:PHE:HE2	1.72	0.55
1:B:41:ILE:HD11	1:B:50:LEU:O	2.06	0.55
1:C:47:ASP:HB2	1:C:276:PRO:CG	2.37	0.55
1:D:269:THR:OG1	1:D:271:SER:HB3	2.07	0.55
1:D:279:TYR:CE2	1:D:324:ALA:HA	2.41	0.55
1:E:49:PHE:CE2	1:E:270:GLU:HB2	2.42	0.55
1:E:107:VAL:HA	1:E:110:ARG:HG3	1.89	0.55
1:E:555:GLU:C	1:E:555:GLU:OE1	2.49	0.55
1:F:401:ASP:CG	1:F:401:ASP:O	2.48	0.55
1:A:137:ILE:HD12	1:A:137:ILE:N	2.18	0.55
1:B:100:ASP:O	1:B:102:ALA:N	2.40	0.55
1:B:132:ARG:HG2	1:B:132:ARG:HH11	1.71	0.55
1:B:341:ASP:O	1:B:344:VAL:HG23	2.06	0.55
1:D:162:PHE:CD2	1:D:309:ARG:HG3	2.41	0.55
1:E:164:PRO:HG3	1:E:250:TRP:CZ2	2.41	0.55
1:E:471:ALA:O	1:E:475:LEU:HD12	2.06	0.55
1:F:561:GLU:O	1:F:562:PHE:C	2.48	0.55
2:I:175:ILE:O	2:I:179:LEU:HD13	2.07	0.55
1:B:58:HIS:CE1	1:B:66:GLN:HG2	2.41	0.55
1:B:59:VAL:CG1	1:B:60:SER:N	2.70	0.55
1:D:214:TRP:CH2	1:D:233:ILE:HG23	2.42	0.55
1:E:457:ASN:O	1:E:460:ILE:HB	2.07	0.55
1:B:246:LEU:CD1	1:B:299:LEU:HD23	2.37	0.55
1:D:44:GLN:N	1:D:45:PRO:CD	2.68	0.55
1:F:258:LYS:HG3	1:F:260:ASN:OD1	2.07	0.55
1:A:40:MET:HG2	1:A:50:LEU:CD1	2.36	0.54
1:A:147:ILE:O	1:A:150:GLN:HB2	2.07	0.54
1:A:366:LEU:HD22	1:A:370:TYR:CE1	2.41	0.54
1:A:371:GLU:HA	1:A:379:ILE:HD11	1.88	0.54
1:D:258:LYS:HG3	1:D:260:ASN:OD1	2.07	0.54
1:F:536:VAL:O	1:F:536:VAL:HG12	2.06	0.54
2:I:147:LEU:HD23	2:I:147:LEU:C	2.31	0.54
1:B:160:ALA:C	1:B:162:PHE:H	2.15	0.54
1:B:325:PRO:HD3	1:B:356:ILE:HD13	1.89	0.54
1:F:60:SER:O	1:F:61:LEU:HD23	2.06	0.54
1:F:563:THR:HG22	1:F:572:ASN:CG	2.32	0.54
2:I:167:GLU:O	2:I:168:ALA:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:179:LEU:O	2:H:184:VAL:HB	2.08	0.54
1:B:103:VAL:O	1:B:106:PRO:HD2	2.07	0.54
1:B:202:LEU:HB2	1:B:207:MET:HE1	1.88	0.54
1:C:455:LEU:HD22	1:C:455:LEU:H	1.71	0.54
1:C:561:GLU:O	1:C:562:PHE:C	2.50	0.54
1:E:568:VAL:CG2	1:F:417:TYR:CE1	2.91	0.54
1:F:145:ARG:NH2	1:F:180:TRP:CZ2	2.75	0.54
1:F:265:LEU:HD23	1:F:265:LEU:O	2.07	0.54
1:A:131:VAL:HG11	1:A:151:ALA:HB2	1.88	0.54
1:A:156:VAL:O	1:A:161:ILE:HG23	2.07	0.54
1:A:230:ARG:HG2	1:A:230:ARG:O	2.07	0.54
1:A:451:PRO:HG3	1:A:482:PHE:CD2	2.42	0.54
1:B:36:LYS:O	1:B:40:MET:HG3	2.06	0.54
1:B:451:PRO:HB3	1:B:488:TYR:CD1	2.43	0.54
1:D:167:ILE:HG12	1:D:171:ASN:ND2	2.22	0.54
1:E:459:TYR:O	1:E:463:HIS:HB2	2.07	0.54
1:B:61:LEU:HD12	1:B:63:GLN:NE2	2.22	0.54
1:B:121:LEU:HG	1:B:159:CYS:SG	2.47	0.54
1:C:529:VAL:HG12	1:C:545:LEU:CD1	2.37	0.54
1:D:59:VAL:HG22	1:D:67:VAL:HG21	1.88	0.54
1:D:71:PHE:HE2	1:D:88:ARG:HB2	1.68	0.54
1:D:557:ASN:HD22	1:D:560:GLU:HB2	1.73	0.54
1:F:460:ILE:O	1:F:464:ILE:HG13	2.07	0.54
2:I:170:GLN:HE21	2:I:170:GLN:N	1.98	0.54
1:D:74:LEU:O	1:D:75:HIS:C	2.48	0.54
1:D:167:ILE:HG23	1:D:168:GLN:N	2.22	0.54
1:D:557:ASN:ND2	1:D:560:GLU:N	2.55	0.54
1:E:335:GLN:OE1	1:E:335:GLN:HA	2.07	0.54
1:F:463:HIS:HE1	1:F:498:TYR:HE2	1.55	0.54
1:B:38:ASN:N	1:B:38:ASN:HD22	2.04	0.54
1:C:122:SER:OG	1:C:263:ILE:HD11	2.08	0.54
1:D:159:CYS:O	1:D:161:ILE:N	2.41	0.54
1:E:165:LYS:HE2	1:E:250:TRP:CH2	2.42	0.54
1:F:55:LEU:HD13	1:F:71:PHE:CE1	2.42	0.54
1:F:200:LYS:HG2	1:F:236:LEU:CD1	2.37	0.54
1:F:400:ASP:O	1:F:401:ASP:CB	2.55	0.54
1:A:417:TYR:HE1	1:B:568:VAL:HG23	1.72	0.54
1:B:523:LYS:HB2	1:B:553:PHE:CE2	2.43	0.54
1:D:217:TYR:CE2	1:D:236:LEU:HD12	2.43	0.54
1:E:637:ARG:CZ	2:I:116:VAL:HG12	2.38	0.54
1:F:296:ASP:HB3	1:F:298:LYS:HZ2	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:185:CYS:O	2:G:186:SER:HB2	2.07	0.54
1:A:334:TYR:O	1:A:335:GLN:C	2.51	0.54
1:D:384:LEU:O	1:D:387:ILE:N	2.41	0.54
1:E:81:MET:CE	1:E:319:GLN:HA	2.38	0.54
1:E:93:PHE:CZ	1:E:130:TYR:HB2	2.39	0.54
1:F:404:ASN:O	1:F:408:ILE:HB	2.08	0.54
2:H:155:LYS:O	2:H:159:GLU:N	2.41	0.54
2:H:178:LEU:C	2:H:180:LEU:H	2.15	0.54
1:A:254:THR:O	1:A:257:LEU:HB2	2.07	0.54
1:A:373:ASN:O	1:A:375:LYS:N	2.41	0.54
1:A:557:ASN:HB3	1:A:560:GLU:HB3	1.88	0.54
1:C:101:ALA:HB2	1:C:134:LYS:CE	2.38	0.54
1:C:633:VAL:HA	2:H:118:VAL:CG2	2.38	0.54
1:D:145:ARG:HH11	1:D:149:ILE:HD11	1.73	0.54
1:F:81:MET:CE	1:F:319:GLN:HA	2.37	0.54
2:G:138:LEU:HB3	2:G:142:GLN:HG3	1.90	0.54
2:I:187:VAL:N	2:I:189:GLN:HE22	2.06	0.54
1:A:629:GLU:OE1	1:A:632:LYS:HE2	2.09	0.53
1:E:167:ILE:HD12	1:E:209:CYS:HB3	1.90	0.53
1:E:225:ASN:O	1:E:229:ALA:HB2	2.08	0.53
1:F:413:SER:O	1:F:416:THR:N	2.42	0.53
2:H:134:GLU:C	2:H:136:GLY:N	2.61	0.53
1:B:496:LEU:HD22	1:B:501:GLU:CB	2.37	0.53
1:C:425:THR:HG22	1:C:426:MET:CE	2.33	0.53
1:E:324:ALA:O	1:E:325:PRO:C	2.51	0.53
1:F:151:ALA:O	1:F:154:VAL:HG12	2.08	0.53
1:F:353:GLN:O	1:F:357:PRO:HA	2.08	0.53
2:I:134:GLU:O	2:I:137:LYS:HE3	2.08	0.53
1:A:247:TYR:CD1	1:A:247:TYR:C	2.86	0.53
1:B:34:ILE:HG12	1:B:57:HIS:HD2	1.74	0.53
1:C:218:THR:HG23	1:C:233:ILE:CD1	2.38	0.53
1:E:314:TYR:HB3	1:E:331:MET:HG3	1.90	0.53
1:C:127:TYR:O	1:C:131:VAL:HG23	2.08	0.53
1:C:483:ALA:HB1	1:C:515:LYS:HZ1	1.73	0.53
1:C:521:LEU:O	1:C:525:ILE:HD13	2.07	0.53
1:E:195:ILE:O	1:E:199:TYR:CD2	2.62	0.53
2:H:171:LEU:HD23	2:H:171:LEU:O	2.09	0.53
1:A:264:THR:HG22	1:A:266:ASN:H	1.73	0.53
1:B:206:PRO:CB	1:B:247:TYR:HB2	2.36	0.53
1:D:473:LYS:O	1:D:477:LEU:HD13	2.07	0.53
1:D:502:GLU:CD	1:D:536:VAL:HG11	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:571:VAL:HB	1:E:573:TYR:CE2	2.43	0.53
1:F:75:HIS:HB3	1:F:110:ARG:HH21	1.73	0.53
2:H:147:LEU:HD22	2:H:179:LEU:CD1	2.38	0.53
1:A:135:ASN:CG	1:A:147:ILE:HG21	2.34	0.53
1:A:170:TRP:CE3	1:A:202:LEU:HD23	2.44	0.53
1:A:366:LEU:C	1:A:368:GLU:H	2.16	0.53
1:A:390:ILE:HD13	1:A:414:LYS:HG2	1.91	0.53
1:A:569:LEU:CD2	1:B:456:GLU:HG2	2.38	0.53
1:C:140:GLY:O	1:C:142:GLU:N	2.41	0.53
1:C:157:ASP:HA	1:C:161:ILE:HD11	1.90	0.53
1:C:490:ASN:ND2	1:C:525:ILE:CD1	2.72	0.53
1:D:74:LEU:HD13	1:D:84:ILE:HD13	1.91	0.53
1:D:81:MET:HE1	1:D:322:CYS:HB3	1.91	0.53
1:D:206:PRO:HB3	1:D:247:TYR:HB2	1.91	0.53
1:F:468:THR:HG21	1:F:499:VAL:HG11	1.90	0.53
1:A:162:PHE:HA	1:A:309:ARG:NH1	2.24	0.53
1:A:218:THR:HG22	1:A:233:ILE:CG2	2.38	0.53
1:A:542:VAL:HG12	1:A:546:GLU:HG3	1.90	0.53
1:B:132:ARG:HG2	1:B:132:ARG:NH1	2.24	0.53
1:B:530:ILE:CG1	1:B:545:LEU:HD22	2.38	0.53
1:C:471:ALA:HB1	1:C:495:PHE:CZ	2.44	0.53
1:D:121:LEU:HD12	1:D:163:GLU:HG2	1.90	0.53
1:E:87:MET:HG2	1:E:264:THR:C	2.33	0.53
1:F:166:SER:O	1:F:167:ILE:C	2.51	0.53
1:F:275:LYS:HE2	1:F:278:GLU:HG2	1.90	0.53
1:A:89:LEU:HD21	1:A:107:VAL:HG11	1.91	0.53
1:C:218:THR:HG23	1:C:233:ILE:HD13	1.91	0.53
1:C:398:MET:HA	1:C:408:ILE:CD1	2.33	0.53
1:D:341:ASP:HB3	1:D:344:VAL:HG23	1.91	0.53
1:F:145:ARG:NH2	1:F:180:TRP:HZ2	2.07	0.53
2:G:179:LEU:O	2:G:180:LEU:C	2.52	0.53
2:H:155:LYS:HE2	2:H:156:ASP:OD1	2.09	0.53
2:H:168:ALA:HA	2:H:170:GLN:HE22	1.74	0.53
1:A:189:GLN:O	1:A:192:VAL:HG22	2.09	0.53
1:B:61:LEU:HB2	1:B:63:GLN:NE2	2.20	0.53
1:B:467:ASP:OD1	1:B:470:THR:HG23	2.09	0.53
1:B:572:ASN:OD1	1:B:575:GLN:HG3	2.09	0.53
1:C:228:THR:O	1:C:231:ARG:HB3	2.09	0.53
1:C:262:PRO:CG	1:C:273:LEU:HD21	2.31	0.53
1:C:399:GLU:HG3	1:C:400:ASP:N	2.22	0.53
1:C:655:SER:O	2:H:151:GLN:NE2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:627:ILE:HD11	2:I:171:LEU:HD21	1.91	0.53
1:F:281:VAL:HG12	1:F:285:LEU:HD12	1.91	0.53
1:A:135:ASN:ND2	1:A:147:ILE:HG21	2.23	0.53
1:A:374:THR:O	1:A:376:ILE:N	2.42	0.53
1:B:24:THR:CG2	1:B:43:GLU:HG3	2.39	0.53
1:B:179:HIS:CG	1:B:179:HIS:O	2.59	0.53
1:C:192:VAL:HG23	1:C:193:GLN:H	1.74	0.53
1:C:206:PRO:HG3	1:C:246:LEU:HB2	1.90	0.53
1:E:281:VAL:O	1:E:285:LEU:HB2	2.10	0.53
1:F:81:MET:HE1	1:F:319:GLN:HA	1.90	0.53
1:F:553:PHE:O	1:F:554:PRO:O	2.27	0.53
1:F:553:PHE:O	1:F:554:PRO:C	2.51	0.53
2:I:146:LEU:HD23	2:I:146:LEU:O	2.08	0.53
1:B:55:LEU:HD21	1:B:70:THR:CG2	2.38	0.52
1:C:44:GLN:N	1:C:45:PRO:CD	2.73	0.52
1:C:401:ASP:C	1:C:403:THR:H	2.15	0.52
1:C:554:PRO:O	1:C:555:GLU:HB3	2.08	0.52
1:D:38:ASN:HD22	1:D:38:ASN:N	2.06	0.52
1:D:52:VAL:HA	1:D:55:LEU:HD12	1.91	0.52
1:E:398:MET:HA	1:E:408:ILE:CD1	2.37	0.52
1:F:186:PHE:C	1:F:188:GLU:H	2.17	0.52
2:G:114:LEU:CD2	2:G:164:LEU:HD13	2.39	0.52
2:H:135:LEU:HD13	2:H:177:GLU:HG2	1.91	0.52
1:A:41:ILE:HG23	1:A:51:TYR:CE2	2.45	0.52
1:A:132:ARG:HG2	1:A:132:ARG:HH11	1.74	0.52
1:A:432:LEU:O	1:A:435:SER:HB3	2.08	0.52
1:A:576:ARG:HG3	1:A:576:ARG:NH1	2.24	0.52
1:B:277:ASN:HD22	1:B:277:ASN:N	2.06	0.52
1:B:289:GLU:OE2	1:B:292:ARG:HD2	2.09	0.52
1:C:48:ILE:N	1:C:48:ILE:HD12	2.24	0.52
1:C:516:ILE:HG22	1:C:517:SER:O	2.10	0.52
1:C:628:VAL:C	1:C:630:LEU:H	2.17	0.52
1:D:210:LEU:CD1	1:D:244:ARG:HA	2.36	0.52
1:E:321:VAL:HG23	1:E:321:VAL:O	2.09	0.52
1:E:639:TYR:HB3	2:I:127:PRO:CG	2.38	0.52
1:F:49:PHE:O	1:F:52:VAL:HB	2.10	0.52
2:H:126:THR:HB	2:H:129:MET:HB2	1.90	0.52
1:A:77:ARG:HH11	1:A:77:ARG:HB2	1.74	0.52
1:A:130:TYR:C	1:A:132:ARG:N	2.66	0.52
1:A:462:TYR:CD2	1:A:463:HIS:CE1	2.97	0.52
1:B:423:MET:HA	1:B:438:ILE:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:627:ILE:CD1	2:H:171:LEU:HD11	2.38	0.52
1:D:125:LEU:C	1:D:127:TYR:H	2.15	0.52
1:D:392:LEU:HD13	2:H:113:TRP:CZ3	2.44	0.52
1:E:200:LYS:HD2	1:E:236:LEU:HD21	1.91	0.52
1:E:347:LYS:O	1:E:351:LEU:HG	2.09	0.52
1:E:396:ALA:O	1:E:397:LEU:C	2.51	0.52
1:E:485:ASP:OD1	1:E:487:GLU:HB3	2.08	0.52
1:E:580:ASP:O	1:E:582:MET:N	2.41	0.52
1:F:424:ASN:O	1:F:427:LYS:HB3	2.09	0.52
1:F:490:ASN:HB3	1:F:528:LYS:NZ	2.24	0.52
2:G:147:LEU:HD22	2:G:179:LEU:CD2	2.39	0.52
1:A:61:LEU:HB2	1:A:63:GLN:HG3	1.90	0.52
1:A:68:TYR:OH	1:A:92:GLU:OE2	2.27	0.52
1:B:376:ILE:O	1:B:379:ILE:HB	2.10	0.52
1:E:44:GLN:H	1:E:45:PRO:CD	2.22	0.52
1:E:88:ARG:CZ	1:E:107:VAL:HG21	2.38	0.52
1:E:206:PRO:HB3	1:E:247:TYR:HB2	1.90	0.52
1:E:456:GLU:O	1:E:460:ILE:HG13	2.08	0.52
1:F:37:LEU:HD21	1:F:53:LYS:HE3	1.90	0.52
1:F:45:PRO:O	1:F:51:TYR:HE2	1.93	0.52
1:F:55:LEU:HD22	1:F:71:PHE:CD1	2.44	0.52
1:A:37:LEU:HB2	1:A:54:LEU:HD13	1.91	0.52
1:A:341:ASP:HB3	1:A:344:VAL:HG23	1.90	0.52
1:A:387:ILE:HD11	1:A:418:VAL:HG12	1.91	0.52
1:A:510:GLU:C	1:A:513:ILE:HD11	2.34	0.52
1:B:99:LEU:N	1:B:99:LEU:HD12	2.25	0.52
1:B:262:PRO:HD3	1:B:272:ASN:ND2	2.24	0.52
1:B:364:PHE:HA	1:B:367:SER:OG	2.09	0.52
1:C:61:LEU:HB2	1:C:63:GLN:NE2	2.20	0.52
1:C:472:CYS:O	1:C:476:GLU:HG3	2.10	0.52
1:C:633:VAL:HA	2:H:118:VAL:HG23	1.92	0.52
1:D:275:LYS:N	1:D:275:LYS:CD	2.72	0.52
1:E:191:ARG:HE	1:E:195:ILE:CD1	2.22	0.52
1:E:299:LEU:HB2	1:E:301:LEU:HG	1.91	0.52
1:E:351:LEU:HA	1:E:354:GLN:OE1	2.09	0.52
1:E:557:ASN:HD22	1:E:560:GLU:N	2.07	0.52
1:F:167:ILE:CG2	1:F:168:GLN:N	2.73	0.52
1:F:189:GLN:O	1:F:193:GLN:HG3	2.10	0.52
1:F:341:ASP:HB3	1:F:344:VAL:CG2	2.40	0.52
1:A:89:LEU:HD11	1:A:108:LEU:HD21	1.92	0.52
1:C:180:TRP:O	1:C:182:PRO:HD3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:202:LEU:C	1:C:202:LEU:HD12	2.35	0.52
1:C:495:PHE:O	1:C:499:VAL:HG23	2.09	0.52
1:E:171:ASN:ND2	1:E:213:MET:HE1	2.25	0.52
1:E:196:ARG:NH2	1:E:221:GLU:OE1	2.43	0.52
1:E:207:MET:H	1:E:210:LEU:CD1	2.22	0.52
1:F:509:PHE:CD1	1:F:529:VAL:HG21	2.45	0.52
2:G:150:ILE:HG22	2:G:150:ILE:O	2.08	0.52
1:A:247:TYR:CD1	1:A:247:TYR:O	2.63	0.52
1:A:640:PHE:C	1:A:642:VAL:N	2.66	0.52
1:C:326:GLU:HG3	1:C:326:GLU:O	2.08	0.52
1:C:344:VAL:O	1:C:347:LYS:HB3	2.10	0.52
1:D:115:GLU:HG2	1:D:116:LEU:H	1.75	0.52
1:D:521:LEU:O	1:D:525:ILE:HD13	2.10	0.52
1:F:164:PRO:HG3	1:F:250:TRP:CE2	2.45	0.52
1:F:417:TYR:O	1:F:421:VAL:HG12	2.09	0.52
1:A:33:VAL:HA	1:A:36:LYS:CD	2.35	0.52
1:D:93:PHE:HZ	1:D:130:TYR:HB2	1.75	0.52
1:E:198:LEU:O	1:E:202:LEU:HG	2.10	0.52
1:E:284:LEU:HD22	1:E:324:ALA:HB1	1.91	0.52
1:F:55:LEU:O	1:F:59:VAL:HG23	2.10	0.52
1:F:262:PRO:CG	1:F:273:LEU:HD21	2.40	0.52
1:A:121:LEU:HG	1:A:159:CYS:SG	2.50	0.52
1:B:34:ILE:HG12	1:B:57:HIS:CD2	2.45	0.52
1:B:196:ARG:O	1:B:197:LYS:C	2.53	0.52
1:B:206:PRO:HB3	1:B:247:TYR:CB	2.36	0.52
1:B:371:GLU:OE1	1:B:428:ARG:NH2	2.43	0.52
1:D:49:PHE:O	1:D:52:VAL:N	2.41	0.52
1:E:151:ALA:O	1:E:155:VAL:HG23	2.09	0.52
1:E:259:ARG:NH1	1:E:290:TRP:CH2	2.78	0.52
1:F:311:THR:O	1:F:315:MET:HG2	2.09	0.52
1:F:472:CYS:O	1:F:473:LYS:C	2.51	0.52
1:F:526:PHE:CD2	1:F:549:PHE:HB2	2.45	0.52
1:F:557:ASN:HD22	1:F:560:GLU:H	1.56	0.52
2:I:159:GLU:OE2	2:I:160:THR:N	2.43	0.52
1:A:509:PHE:CD1	1:A:525:ILE:HG22	2.46	0.52
1:B:65:LYS:HD3	1:B:65:LYS:C	2.35	0.52
1:D:295:SER:C	1:D:297:ASN:N	2.68	0.52
1:F:564:ASN:HA	1:F:567:LYS:HD2	1.92	0.52
1:A:628:VAL:HG12	1:A:629:GLU:OE2	2.09	0.51
1:B:84:ILE:HA	1:B:87:MET:HE3	1.92	0.51
1:D:202:LEU:HD12	1:D:202:LEU:C	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:292:ARG:O	1:D:295:SER:N	2.40	0.51
1:D:338:LYS:O	1:D:339:ASN:HB3	2.10	0.51
1:E:405:GLU:C	1:E:407:ALA:H	2.17	0.51
1:F:486:GLY:HA3	1:F:521:LEU:HD13	1.92	0.51
1:A:343:THR:O	1:A:343:THR:HG22	2.08	0.51
1:B:366:LEU:O	1:B:368:GLU:N	2.42	0.51
1:D:58:HIS:CE1	1:D:66:GLN:HG2	2.44	0.51
1:D:366:LEU:O	1:D:367:SER:C	2.53	0.51
1:A:49:PHE:CZ	1:A:270:GLU:HB2	2.44	0.51
1:A:80:LEU:HD21	1:A:116:LEU:HD22	1.90	0.51
1:A:298:LYS:O	1:A:300:GLU:OE2	2.29	0.51
1:A:398:MET:O	1:A:402:PRO:HD3	2.10	0.51
1:B:95:LYS:HB2	1:B:95:LYS:NZ	2.25	0.51
1:C:645:PHE:O	2:H:193:LEU:HA	2.11	0.51
1:D:85:TRP:CD2	1:D:111:CYS:HB3	2.45	0.51
1:D:202:LEU:HD12	1:D:203:LEU:HG	1.92	0.51
1:D:413:SER:OG	1:D:450:THR:HG21	2.10	0.51
1:E:81:MET:HE1	1:E:319:GLN:HA	1.92	0.51
1:E:516:ILE:HG22	1:E:517:SER:O	2.09	0.51
1:E:556:VAL:O	1:E:557:ASN:C	2.51	0.51
2:G:189:GLN:HG3	2:G:190:LEU:H	1.75	0.51
1:A:369:GLN:O	1:A:372:LEU:HB3	2.11	0.51
1:A:635:PRO:HB3	2:G:120:VAL:HG21	1.92	0.51
1:B:259:ARG:HD3	1:B:287:TRP:CZ2	2.46	0.51
1:B:557:ASN:C	1:B:557:ASN:OD1	2.53	0.51
1:C:417:TYR:HE2	1:D:574:LEU:HD23	1.76	0.51
1:D:86:CYS:HB3	1:D:263:ILE:HG13	1.91	0.51
1:D:90:SER:CB	1:D:264:THR:HG23	2.36	0.51
1:D:178:GLU:HA	1:D:191:ARG:HH21	1.76	0.51
1:E:156:VAL:CA	1:E:160:ALA:HB3	2.40	0.51
1:E:165:LYS:HD3	1:E:208:ASP:CB	2.38	0.51
1:E:180:TRP:CZ3	1:E:191:ARG:HB2	2.44	0.51
1:F:310:MET:HE2	1:F:334:TYR:CE1	2.46	0.51
1:F:336:GLY:HA3	1:F:345:ILE:CG1	2.41	0.51
1:F:423:MET:HE3	1:F:460:ILE:HD12	1.93	0.51
1:A:457:ASN:O	1:A:461:GLU:HG2	2.10	0.51
1:B:314:TYR:HB3	1:B:331:MET:HE3	1.92	0.51
1:B:398:MET:C	1:B:400:ASP:H	2.18	0.51
1:C:338:LYS:O	1:C:339:ASN:HB3	2.10	0.51
1:C:409:ASN:O	1:C:412:LYS:HB2	2.11	0.51
1:D:560:GLU:HA	1:D:582:MET:CE	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:550:PHE:CD1	1:E:558:LYS:HE2	2.46	0.51
1:F:225:ASN:C	1:F:227:LEU:H	2.17	0.51
1:F:358:ASN:HB3	1:F:389:ARG:CG	2.41	0.51
2:I:185:CYS:HB3	2:I:189:GLN:HE21	1.74	0.51
1:A:49:PHE:CE2	1:A:270:GLU:HB2	2.45	0.51
1:B:84:ILE:HG22	1:B:85:TRP:N	2.25	0.51
1:C:641:LYS:O	1:C:642:VAL:C	2.53	0.51
1:C:642:VAL:HG23	1:C:643:THR:N	2.26	0.51
1:D:221:GLU:HG3	1:D:233:ILE:HG13	1.93	0.51
1:D:262:PRO:HG3	1:D:273:LEU:CD2	2.41	0.51
1:D:455:LEU:CD2	1:D:455:LEU:H	2.24	0.51
1:E:544:THR:O	1:E:547:LYS:HB3	2.11	0.51
2:G:150:ILE:N	2:G:150:ILE:HD12	2.25	0.51
2:G:185:CYS:SG	2:G:188:ASP:CB	2.94	0.51
2:I:125:THR:HG22	2:I:129:MET:SD	2.51	0.51
1:A:99:LEU:HD11	1:A:133:LYS:HD3	1.93	0.51
1:B:66:GLN:N	1:B:66:GLN:NE2	2.58	0.51
1:B:190:GLN:HA	1:B:193:GLN:HG3	1.91	0.51
1:B:202:LEU:C	1:B:202:LEU:CD1	2.84	0.51
1:D:59:VAL:C	1:D:61:LEU:N	2.63	0.51
1:D:86:CYS:SG	1:D:123:LEU:HA	2.51	0.51
1:D:408:ILE:HG22	1:D:409:ASN:N	2.25	0.51
1:E:51:TYR:O	1:E:54:LEU:N	2.43	0.51
1:E:88:ARG:HG2	1:E:88:ARG:O	2.11	0.51
1:F:49:PHE:O	1:F:52:VAL:N	2.43	0.51
1:F:89:LEU:HD11	1:F:108:LEU:CD2	2.39	0.51
1:F:310:MET:O	1:F:314:TYR:HB2	2.11	0.51
1:F:432:LEU:HD22	1:F:464:ILE:HD13	1.93	0.51
1:A:173:TYR:CD2	1:A:198:LEU:HD22	2.46	0.51
1:A:401:ASP:C	1:A:403:THR:N	2.68	0.51
1:A:575:GLN:HE21	1:A:582:MET:CE	2.16	0.51
1:A:641:LYS:HD2	1:A:641:LYS:C	2.35	0.51
1:B:51:TYR:CB	1:B:74:LEU:HD13	2.41	0.51
1:B:336:GLY:C	1:B:338:LYS:N	2.67	0.51
1:C:405:GLU:HA	1:C:408:ILE:HB	1.92	0.51
1:C:653:PHE:O	1:C:657:LYS:CG	2.59	0.51
1:E:275:LYS:HE2	1:E:275:LYS:N	2.26	0.51
1:E:299:LEU:HD21	1:E:309:ARG:CZ	2.41	0.51
1:B:296:ASP:HB3	1:B:298:LYS:HD3	1.91	0.51
1:B:353:GLN:HG3	1:B:353:GLN:O	2.10	0.51
1:B:425:THR:O	1:B:429:ILE:HG12	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:152:PHE:HB3	1:F:173:TYR:CD1	2.46	0.51
1:F:279:TYR:CE2	1:F:324:ALA:HA	2.46	0.51
1:F:468:THR:HG23	1:F:499:VAL:HG11	1.93	0.51
2:I:179:LEU:HB3	2:I:184:VAL:HB	1.92	0.51
1:B:122:SER:HB3	1:B:263:ILE:CD1	2.41	0.51
1:D:121:LEU:HD21	1:D:169:PHE:HB2	1.93	0.51
1:D:191:ARG:O	1:D:195:ILE:HG13	2.10	0.51
1:D:420:CYS:SG	1:D:453:ILE:HA	2.51	0.51
1:E:46:THR:HG23	1:E:276:PRO:HG3	1.93	0.51
1:F:444:ARG:HD2	2:I:166:GLU:OE2	2.11	0.51
1:F:455:LEU:H	1:F:455:LEU:CD2	2.24	0.51
1:A:417:TYR:O	1:A:421:VAL:HG12	2.11	0.50
1:B:65:LYS:HD2	1:B:66:GLN:HE22	1.76	0.50
1:E:81:MET:SD	1:E:319:GLN:O	2.69	0.50
1:E:249:ASP:O	1:E:253:ILE:HG13	2.11	0.50
1:E:420:CYS:HB3	1:F:568:VAL:HG11	1.93	0.50
1:E:432:LEU:O	1:E:435:SER:HB3	2.11	0.50
1:F:409:ASN:HA	1:F:412:LYS:HB2	1.93	0.50
2:G:192:GLN:OE1	2:G:192:GLN:HA	2.11	0.50
2:I:168:ALA:HA	2:I:170:GLN:HE22	1.75	0.50
1:A:166:SER:HG	1:A:170:TRP:CD1	2.28	0.50
1:C:37:LEU:HD23	1:C:54:LEU:CD1	2.41	0.50
1:D:280:ASP:O	1:D:283:GLN:HB2	2.12	0.50
1:E:129:THR:HG23	1:E:133:LYS:HE3	1.94	0.50
1:E:509:PHE:CG	1:E:529:VAL:HG21	2.46	0.50
1:E:624:PRO:N	1:E:625:PRO:HD3	2.26	0.50
1:F:55:LEU:HD22	1:F:71:PHE:CE1	2.46	0.50
1:F:173:TYR:CD2	1:F:198:LEU:HD22	2.47	0.50
1:F:455:LEU:CD2	1:F:455:LEU:N	2.74	0.50
1:A:166:SER:O	1:A:170:TRP:HD1	1.94	0.50
1:A:635:PRO:HB3	2:G:120:VAL:CG2	2.42	0.50
1:B:281:VAL:O	1:B:284:LEU:HB3	2.12	0.50
1:B:447:LYS:CG	1:B:481:TYR:HB3	2.41	0.50
1:B:481:TYR:N	1:B:481:TYR:CD1	2.80	0.50
1:B:506:LYS:HZ1	1:B:545:LEU:HD12	1.75	0.50
1:C:169:PHE:O	1:C:170:TRP:C	2.54	0.50
1:C:529:VAL:CG1	1:C:545:LEU:HD11	2.39	0.50
1:C:580:ASP:C	1:C:582:MET:H	2.18	0.50
1:D:125:LEU:C	1:D:127:TYR:N	2.69	0.50
1:D:166:SER:O	1:D:167:ILE:C	2.55	0.50
1:D:455:LEU:HD13	1:D:475:LEU:HD22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:351:LEU:O	1:E:354:GLN:HB2	2.11	0.50
1:F:502:GLU:OE2	1:F:536:VAL:HG11	2.11	0.50
2:G:180:LEU:HD12	2:G:185:CYS:O	2.11	0.50
1:B:168:GLN:O	1:B:169:PHE:C	2.54	0.50
1:B:390:ILE:HD11	1:B:414:LYS:HE2	1.94	0.50
1:B:472:CYS:HB3	1:B:504:GLN:HE22	1.75	0.50
1:D:93:PHE:CZ	1:D:130:TYR:HB2	2.46	0.50
1:D:218:THR:HG23	1:D:233:ILE:CD1	2.41	0.50
1:D:464:ILE:HG22	1:D:465:SER:N	2.26	0.50
1:E:125:LEU:HD23	1:E:128:ILE:CD1	2.29	0.50
1:E:378:GLU:N	1:E:378:GLU:OE2	2.42	0.50
1:E:641:LYS:O	1:E:643:THR:N	2.44	0.50
1:F:255:LYS:C	1:F:257:LEU:H	2.19	0.50
1:F:337:GLU:O	1:F:337:GLU:HG2	2.11	0.50
2:H:184:VAL:O	2:H:185:CYS:SG	2.67	0.50
1:A:336:GLY:C	1:A:338:LYS:H	2.18	0.50
1:A:640:PHE:C	1:A:642:VAL:H	2.18	0.50
1:C:115:GLU:C	1:C:117:GLY:N	2.60	0.50
1:D:65:LYS:HB3	1:D:66:GLN:OE1	2.12	0.50
1:D:222:GLN:O	1:D:226:GLN:HG3	2.10	0.50
1:E:85:TRP:CD2	1:E:111:CYS:HB3	2.47	0.50
1:E:424:ASN:ND2	1:E:456:GLU:OE1	2.45	0.50
1:F:522:LEU:O	1:F:525:ILE:N	2.44	0.50
2:G:184:VAL:O	2:G:185:CYS:SG	2.69	0.50
2:I:137:LYS:HG3	2:I:138:LEU:HG	1.92	0.50
1:A:486:GLY:C	1:A:521:LEU:HD23	2.36	0.50
1:B:335:GLN:HB3	1:B:344:VAL:HG11	1.94	0.50
1:D:44:GLN:H	1:D:45:PRO:HD3	1.76	0.50
1:D:275:LYS:H	1:D:275:LYS:HE2	1.76	0.50
1:D:314:TYR:O	1:D:317:ALA:HB3	2.12	0.50
1:E:306:HIS:O	1:E:310:MET:HG2	2.12	0.50
1:F:480:LYS:HB2	1:F:481:TYR:CD1	2.47	0.50
1:F:523:LYS:O	1:F:527:GLN:HG3	2.11	0.50
2:G:125:THR:HG23	2:G:129:MET:CE	2.28	0.50
2:I:179:LEU:CG	2:I:184:VAL:HG21	2.41	0.50
1:A:305:LEU:O	1:A:306:HIS:C	2.54	0.50
1:A:447:LYS:CG	1:A:481:TYR:HB3	2.37	0.50
1:B:89:LEU:CD2	1:B:107:VAL:HG11	2.39	0.50
1:C:543:ARG:NE	1:D:372:LEU:HD11	2.26	0.50
1:D:546:GLU:O	1:D:547:LYS:C	2.54	0.50
1:E:366:LEU:HD22	1:E:370:TYR:CE1	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:370:TYR:CE1	1:E:378:GLU:HB3	2.47	0.50
1:E:509:PHE:CE2	1:E:513:ILE:HD11	2.46	0.50
1:E:638:GLN:HA	1:E:641:LYS:CG	2.41	0.50
1:F:374:THR:O	1:F:374:THR:HG22	2.12	0.50
1:F:580:ASP:C	1:F:582:MET:N	2.66	0.50
1:A:259:ARG:HG2	1:A:320:HIS:CE1	2.46	0.50
1:C:475:LEU:HD13	1:C:492:TYR:CE1	2.47	0.50
1:E:68:TYR:N	1:E:68:TYR:HD2	2.10	0.50
1:E:207:MET:H	1:E:210:LEU:CG	2.24	0.50
1:F:78:PHE:CD1	1:F:78:PHE:N	2.80	0.50
1:F:481:TYR:CD1	1:F:481:TYR:N	2.79	0.50
1:F:494:ASP:O	1:F:498:TYR:HB2	2.12	0.50
1:A:173:TYR:O	1:A:176:PHE:HB3	2.12	0.50
1:A:462:TYR:CD2	1:A:463:HIS:NE2	2.78	0.50
1:A:463:HIS:O	1:A:464:ILE:CG1	2.60	0.50
1:B:501:GLU:O	1:B:505:VAL:HG23	2.12	0.50
1:C:358:ASN:HB3	1:C:389:ARG:HG3	1.93	0.50
1:D:200:LYS:HG2	1:D:236:LEU:CD1	2.41	0.50
1:D:370:TYR:HB2	1:D:379:ILE:HG12	1.94	0.50
1:D:530:ILE:HG12	1:D:545:LEU:HB3	1.93	0.50
1:E:56:LYS:HG3	1:E:265:LEU:HD21	1.93	0.50
1:E:432:LEU:O	1:E:433:ALA:C	2.54	0.50
1:F:474:VAL:HG12	1:F:475:LEU:N	2.25	0.50
2:G:144:MET:O	2:G:148:LYS:HG2	2.12	0.50
2:I:146:LEU:HD23	2:I:150:ILE:HD13	1.93	0.50
1:A:289:GLU:O	1:A:292:ARG:HG3	2.12	0.49
1:A:631:LEU:CD1	2:G:114:LEU:HD23	2.42	0.49
1:B:356:ILE:CG2	1:B:359:SER:HB2	2.41	0.49
1:B:568:VAL:HG12	1:B:569:LEU:HG	1.92	0.49
1:C:125:LEU:CD2	1:C:169:PHE:HD1	2.23	0.49
1:C:563:THR:HG23	1:C:574:LEU:HB3	1.94	0.49
1:D:390:ILE:HD13	1:D:414:LYS:CD	2.42	0.49
1:D:525:ILE:HG22	1:D:526:PHE:N	2.26	0.49
1:E:386:CYS:O	1:E:390:ILE:HG13	2.12	0.49
2:H:134:GLU:O	2:H:136:GLY:N	2.44	0.49
1:A:89:LEU:N	1:A:89:LEU:CD2	2.75	0.49
1:A:110:ARG:HG2	1:A:110:ARG:HH11	1.76	0.49
1:A:542:VAL:O	1:A:543:ARG:C	2.55	0.49
1:B:486:GLY:C	1:B:521:LEU:HD23	2.37	0.49
1:C:55:LEU:O	1:C:59:VAL:HG23	2.12	0.49
1:C:81:MET:CE	1:C:319:GLN:HA	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:173:TYR:CD2	1:C:198:LEU:HD22	2.47	0.49
1:C:247:TYR:O	1:C:251:LEU:HB2	2.12	0.49
1:C:501:GLU:HB3	1:C:504:GLN:HG3	1.93	0.49
1:E:574:LEU:CD1	1:F:361:VAL:HG22	2.42	0.49
1:F:388:ASP:OD2	2:I:116:VAL:HG11	2.11	0.49
1:F:529:VAL:HG12	1:F:545:LEU:HD11	1.94	0.49
1:B:496:LEU:HD22	1:B:501:GLU:HB2	1.93	0.49
1:B:539:LEU:HD23	1:B:539:LEU:C	2.37	0.49
1:C:74:LEU:HD13	1:C:84:ILE:HG21	1.94	0.49
1:C:563:THR:CG2	1:C:574:LEU:HB3	2.42	0.49
1:D:41:ILE:CG1	1:D:50:LEU:HB3	2.41	0.49
1:D:104:ILE:HG21	1:D:130:TYR:CE1	2.46	0.49
1:D:291:ILE:HD13	1:D:314:TYR:CE1	2.47	0.49
1:E:124:TRP:CZ3	1:E:155:VAL:HG22	2.48	0.49
1:F:41:ILE:HG13	1:F:50:LEU:HB3	1.94	0.49
1:F:394:LEU:CD1	1:F:411:LEU:HD23	2.42	0.49
1:A:305:LEU:O	1:A:308:ALA:HB3	2.12	0.49
1:A:544:THR:O	1:A:547:LYS:HB3	2.12	0.49
1:B:364:PHE:CZ	1:B:421:VAL:CG1	2.95	0.49
1:B:542:VAL:O	1:B:543:ARG:C	2.53	0.49
1:B:572:ASN:ND2	1:B:575:GLN:H	2.10	0.49
1:C:322:CYS:SG	1:C:323:PHE:N	2.86	0.49
1:C:563:THR:HB	1:C:572:ASN:HD21	1.78	0.49
1:C:578:GLU:HG2	1:C:578:GLU:O	2.12	0.49
1:D:434:ALA:CA	1:D:437:LYS:HE3	2.33	0.49
1:E:44:GLN:N	1:E:45:PRO:CD	2.75	0.49
1:E:121:LEU:CD1	1:E:163:GLU:HG2	2.42	0.49
1:E:156:VAL:HG13	1:E:170:TRP:CH2	2.48	0.49
1:F:568:VAL:O	1:F:569:LEU:C	2.56	0.49
2:H:116:VAL:CG2	2:H:117:GLY:N	2.76	0.49
2:H:143:GLN:HG3	2:H:178:LEU:HD22	1.93	0.49
1:B:185:LYS:HG2	1:B:186:PHE:N	2.26	0.49
1:C:347:LYS:O	1:C:351:LEU:HG	2.13	0.49
1:C:375:LYS:HB3	1:C:378:GLU:OE2	2.13	0.49
1:C:546:GLU:OE2	1:C:565:LYS:HE2	2.12	0.49
1:D:84:ILE:O	1:D:84:ILE:HG22	2.12	0.49
1:D:557:ASN:HD22	1:D:560:GLU:CB	2.24	0.49
1:E:40:MET:C	1:E:42:GLU:H	2.19	0.49
1:E:68:TYR:N	1:E:68:TYR:CD2	2.80	0.49
1:F:39:ASP:O	1:F:42:GLU:N	2.43	0.49
1:A:362:LEU:O	1:A:366:LEU:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:416:THR:OG1	1:A:450:THR:HG23	2.12	0.49
1:C:101:ALA:CB	1:C:134:LYS:HE2	2.43	0.49
1:C:376:ILE:HB	1:C:377:PRO:HD3	1.94	0.49
1:C:399:GLU:CG	1:C:400:ASP:N	2.75	0.49
1:C:559:LEU:HB2	1:D:329:PHE:HD1	1.78	0.49
1:D:169:PHE:CD2	1:D:170:TRP:N	2.81	0.49
1:D:247:TYR:CZ	1:D:251:LEU:HD13	2.47	0.49
1:D:541:SER:O	1:D:544:THR:HB	2.13	0.49
1:D:559:LEU:O	1:D:562:PHE:HB3	2.12	0.49
1:E:135:ASN:ND2	1:E:147:ILE:CG2	2.75	0.49
1:F:77:ARG:HB3	1:F:78:PHE:CE1	2.46	0.49
1:F:392:LEU:C	1:F:394:LEU:N	2.70	0.49
1:F:563:THR:HG22	1:F:572:ASN:OD1	2.12	0.49
1:A:315:MET:O	1:A:316:GLN:C	2.55	0.49
1:A:418:VAL:HA	1:A:421:VAL:CG1	2.43	0.49
1:A:646:GLU:HG3	1:A:650:PHE:CE2	2.46	0.49
1:B:74:LEU:HD21	1:B:84:ILE:HG12	1.94	0.49
1:B:137:ILE:H	1:B:137:ILE:CD1	2.24	0.49
1:E:384:LEU:O	1:E:385:SER:C	2.55	0.49
1:E:417:TYR:O	1:E:420:CYS:HB2	2.13	0.49
2:H:186:SER:HA	2:H:189:GLN:NE2	2.25	0.49
1:A:152:PHE:CD2	1:A:173:TYR:HD1	2.31	0.49
1:A:170:TRP:HE3	1:A:198:LEU:HD11	1.78	0.49
1:A:287:TRP:CH2	1:A:316:GLN:HB3	2.48	0.49
1:A:398:MET:O	1:A:400:ASP:N	2.43	0.49
1:B:162:PHE:CD2	1:B:309:ARG:HG3	2.48	0.49
1:B:166:SER:O	1:B:170:TRP:HD1	1.95	0.49
1:B:487:GLU:N	1:B:521:LEU:HD23	2.28	0.49
1:B:496:LEU:CB	1:B:505:VAL:HG22	2.41	0.49
1:C:125:LEU:C	1:C:127:TYR:H	2.19	0.49
1:C:371:GLU:CA	1:C:379:ILE:HD11	2.43	0.49
1:C:539:LEU:CD2	1:D:371:GLU:HB3	2.43	0.49
1:D:142:GLU:OE1	1:D:142:GLU:HA	2.12	0.49
1:D:427:LYS:HB2	1:D:435:SER:HB2	1.93	0.49
1:E:289:GLU:OE2	1:E:292:ARG:NH2	2.46	0.49
1:F:455:LEU:N	1:F:455:LEU:HD22	2.28	0.49
1:F:504:GLN:O	1:F:505:VAL:C	2.55	0.49
2:I:164:LEU:HD23	2:I:165:LEU:H	1.76	0.49
1:A:493:LEU:O	1:A:494:ASP:C	2.56	0.49
1:B:85:TRP:CZ3	1:B:111:CYS:HB3	2.48	0.49
1:B:99:LEU:CB	1:B:134:LYS:HZ3	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:SER:OG	1:B:303:ASP:N	2.44	0.49
1:B:351:LEU:CA	1:B:354:GLN:HG3	2.39	0.49
1:B:401:ASP:C	1:B:403:THR:H	2.21	0.49
1:E:313:VAL:O	1:E:316:GLN:CB	2.59	0.49
1:F:114:LYS:HG2	1:F:115:GLU:OE2	2.13	0.49
1:A:634:LEU:CD1	2:G:174:ALA:HB2	2.43	0.49
1:B:108:LEU:HD22	1:B:127:TYR:HD1	1.78	0.49
1:B:378:GLU:O	1:B:382:THR:OG1	2.28	0.49
1:C:309:ARG:O	1:C:312:TYR:HB3	2.12	0.49
1:C:624:PRO:O	1:C:627:ILE:HG22	2.11	0.49
1:D:299:LEU:H	1:D:299:LEU:CD1	2.23	0.49
1:E:103:VAL:O	1:E:106:PRO:HD2	2.13	0.49
1:E:292:ARG:HH11	1:E:292:ARG:HG3	1.78	0.49
1:E:316:GLN:O	1:E:319:GLN:HB3	2.12	0.49
1:E:419:TYR:O	1:E:422:TYR:HB3	2.12	0.49
1:A:196:ARG:HD3	1:A:232:HIS:CE1	2.48	0.48
1:A:387:ILE:HD12	1:A:418:VAL:HG12	1.95	0.48
1:B:25:SER:HB2	1:B:43:GLU:CD	2.38	0.48
1:B:57:HIS:C	1:B:59:VAL:N	2.70	0.48
1:C:34:ILE:HD13	1:C:58:HIS:HE1	1.77	0.48
1:C:526:PHE:O	1:C:530:ILE:HG13	2.12	0.48
1:C:653:PHE:CG	2:H:192:GLN:NE2	2.81	0.48
1:D:84:ILE:HG12	1:D:87:MET:CE	2.43	0.48
1:D:115:GLU:C	1:D:117:GLY:N	2.71	0.48
1:E:370:TYR:CD1	1:E:378:GLU:HB3	2.48	0.48
1:F:262:PRO:HD3	1:F:272:ASN:OD1	2.13	0.48
1:F:540:ASN:HD22	1:F:543:ARG:NH2	2.11	0.48
2:G:138:LEU:O	2:G:139:GLN:C	2.56	0.48
1:A:207:MET:C	1:A:209:CYS:H	2.21	0.48
1:A:569:LEU:HD22	1:B:456:GLU:HG2	1.95	0.48
1:B:572:ASN:C	1:B:572:ASN:ND2	2.70	0.48
1:D:77:ARG:HB3	1:D:78:PHE:HD1	1.77	0.48
1:D:392:LEU:O	1:D:395:ALA:N	2.46	0.48
1:E:55:LEU:HB3	1:E:265:LEU:HD11	1.94	0.48
1:E:167:ILE:HG23	1:E:168:GLN:N	2.28	0.48
1:E:262:PRO:HB3	1:E:268:ALA:HA	1.94	0.48
1:E:479:LEU:HD11	1:E:492:TYR:CE2	2.46	0.48
1:F:289:GLU:HG3	1:F:292:ARG:NH2	2.27	0.48
1:F:438:ILE:O	1:F:442:CYS:HB2	2.13	0.48
1:F:540:ASN:HD22	1:F:543:ARG:HH21	1.59	0.48
2:I:193:LEU:C	2:I:193:LEU:HD12	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:PRO:CG	1:A:351:LEU:HD22	2.43	0.48
1:A:335:GLN:HG3	1:A:348:TYR:CE1	2.48	0.48
1:B:192:VAL:O	1:B:193:GLN:C	2.55	0.48
1:C:192:VAL:HG23	1:C:193:GLN:N	2.28	0.48
1:D:81:MET:CE	1:D:319:GLN:HA	2.43	0.48
1:D:296:ASP:O	1:D:297:ASN:C	2.56	0.48
1:D:297:ASN:ND2	1:D:306:HIS:CG	2.81	0.48
1:D:390:ILE:HD13	1:D:414:LYS:HD3	1.94	0.48
1:E:125:LEU:HD11	1:E:169:PHE:HB2	1.94	0.48
1:E:143:GLU:C	1:E:145:ARG:H	2.20	0.48
1:E:177:LEU:HD11	1:E:194:TYR:HB3	1.96	0.48
1:F:394:LEU:O	1:F:395:ALA:C	2.57	0.48
2:I:159:GLU:O	2:I:162:VAL:HG22	2.14	0.48
1:A:275:LYS:O	1:A:278:GLU:HB3	2.13	0.48
1:B:61:LEU:O	1:B:62:LYS:C	2.57	0.48
1:B:145:ARG:O	1:B:145:ARG:HG2	2.12	0.48
1:B:155:VAL:HG11	1:B:169:PHE:CE1	2.49	0.48
1:C:180:TRP:HZ3	1:C:191:ARG:HA	1.77	0.48
1:C:432:LEU:HD13	1:C:464:ILE:HD11	1.94	0.48
1:D:40:MET:HE3	1:D:50:LEU:HD22	1.95	0.48
1:E:423:MET:HB2	1:E:438:ILE:CG2	2.43	0.48
1:F:52:VAL:HA	1:F:55:LEU:HD12	1.96	0.48
1:F:194:TYR:HD1	1:F:194:TYR:N	2.12	0.48
1:F:281:VAL:O	1:F:282:GLN:C	2.54	0.48
1:F:553:PHE:N	1:F:554:PRO:HD3	2.29	0.48
1:A:214:TRP:CH2	1:A:233:ILE:HG23	2.48	0.48
1:A:254:THR:O	1:A:255:LYS:C	2.56	0.48
1:A:341:ASP:OD2	1:A:343:THR:HB	2.12	0.48
1:A:358:ASN:HB3	1:A:389:ARG:CG	2.43	0.48
1:A:575:GLN:NE2	1:A:582:MET:HE3	2.17	0.48
1:C:554:PRO:O	1:C:555:GLU:CB	2.60	0.48
1:D:56:LYS:O	1:D:60:SER:HB2	2.13	0.48
1:D:269:THR:C	1:D:271:SER:N	2.71	0.48
1:D:455:LEU:HD22	1:D:455:LEU:H	1.77	0.48
1:E:71:PHE:CD2	1:E:88:ARG:HB2	2.49	0.48
1:E:86:CYS:SG	1:E:123:LEU:HA	2.54	0.48
1:F:46:THR:HG21	1:F:276:PRO:HB3	1.95	0.48
1:F:152:PHE:CG	1:F:173:TYR:CD1	3.02	0.48
2:G:139:GLN:O	2:G:141:ASP:N	2.46	0.48
2:I:165:LEU:HD11	2:I:172:SER:HB2	1.96	0.48
1:A:94:ASP:O	1:A:95:LYS:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:497:ILE:HG23	1:A:532:PHE:CD1	2.49	0.48
1:A:509:PHE:CE1	1:A:525:ILE:HG22	2.49	0.48
1:B:449:VAL:HG23	1:B:450:THR:O	2.12	0.48
1:B:560:GLU:O	1:B:562:PHE:N	2.47	0.48
1:C:202:LEU:HB2	1:C:207:MET:CE	2.40	0.48
1:C:296:ASP:O	1:C:297:ASN:C	2.57	0.48
1:D:264:THR:HG22	1:D:266:ASN:H	1.79	0.48
1:D:292:ARG:O	1:D:294:GLU:N	2.47	0.48
1:E:144:ALA:HA	1:E:147:ILE:CD1	2.42	0.48
1:F:563:THR:HG23	1:F:574:LEU:CB	2.43	0.48
2:H:131:ILE:CG2	2:H:135:LEU:HD12	2.44	0.48
1:A:59:VAL:CG1	1:A:60:SER:N	2.77	0.48
1:A:180:TRP:CZ3	1:A:191:ARG:CA	2.90	0.48
1:A:219:GLN:NE2	1:A:219:GLN:C	2.72	0.48
1:C:423:MET:HE3	1:C:460:ILE:CD1	2.44	0.48
1:D:101:ALA:HB2	1:D:134:LYS:HZ3	1.78	0.48
1:D:168:GLN:HG3	1:D:169:PHE:N	2.29	0.48
1:D:169:PHE:O	1:D:170:TRP:C	2.56	0.48
1:D:297:ASN:ND2	1:D:306:HIS:HB2	2.27	0.48
1:D:314:TYR:HB3	1:D:331:MET:HE3	1.96	0.48
1:E:61:LEU:O	1:E:63:GLN:HG3	2.13	0.48
1:F:421:VAL:HA	1:F:424:ASN:HD22	1.78	0.48
1:F:468:THR:O	1:F:469:LYS:C	2.56	0.48
1:A:80:LEU:HA	1:A:118:ASN:HD21	1.78	0.48
1:A:169:PHE:O	1:A:170:TRP:C	2.56	0.48
1:A:373:ASN:C	1:A:375:LYS:H	2.21	0.48
1:B:195:ILE:HG22	1:B:199:TYR:HD2	1.78	0.48
1:B:364:PHE:HZ	1:B:421:VAL:CG1	2.26	0.48
1:C:269:THR:HG23	1:C:272:ASN:HD21	1.79	0.48
1:C:569:LEU:HD12	1:D:452:ASP:OD1	2.13	0.48
1:D:156:VAL:HG22	1:D:170:TRP:CZ3	2.48	0.48
1:E:423:MET:HA	1:E:438:ILE:CD1	2.40	0.48
1:E:569:LEU:HD11	1:F:455:LEU:HB2	1.95	0.48
1:F:254:THR:CG2	1:F:257:LEU:HB3	2.44	0.48
1:A:51:TYR:CD1	1:A:74:LEU:HB2	2.47	0.48
1:A:559:LEU:HD21	1:A:579:LEU:HD11	1.95	0.48
1:B:333:ASN:O	1:B:337:GLU:HB2	2.14	0.48
1:B:516:ILE:CD1	1:B:525:ILE:HG13	2.43	0.48
1:C:135:ASN:ND2	1:C:147:ILE:HG21	2.28	0.48
1:C:533:GLU:HG3	1:C:545:LEU:HD12	1.95	0.48
1:C:653:PHE:O	1:C:657:LYS:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:120:ASP:O	1:D:121:LEU:C	2.57	0.48
1:E:501:GLU:O	1:E:504:GLN:N	2.47	0.48
2:G:134:GLU:O	2:G:137:LYS:HG2	2.14	0.48
1:A:57:HIS:C	1:A:59:VAL:N	2.72	0.48
1:A:101:ALA:HA	1:A:130:TYR:OH	2.14	0.48
1:A:169:PHE:CD2	1:A:170:TRP:N	2.82	0.48
1:A:231:ARG:NH1	1:A:231:ARG:HB3	2.28	0.48
1:A:536:VAL:O	1:A:536:VAL:HG22	2.13	0.48
1:B:74:LEU:HD21	1:B:84:ILE:CG1	2.44	0.48
1:C:125:LEU:C	1:C:127:TYR:N	2.70	0.48
1:C:265:LEU:HD23	1:C:265:LEU:C	2.38	0.48
1:C:275:LYS:HE2	1:C:275:LYS:N	2.28	0.48
1:D:247:TYR:CE1	1:D:251:LEU:HD13	2.49	0.48
1:D:499:VAL:O	1:D:499:VAL:HG12	2.14	0.48
1:E:398:MET:HG2	1:E:408:ILE:HD13	1.95	0.48
1:F:405:GLU:HA	1:F:408:ILE:CG2	2.42	0.48
1:F:442:CYS:SG	1:F:453:ILE:HG12	2.53	0.48
1:F:525:ILE:HG22	1:F:526:PHE:N	2.28	0.48
1:A:66:GLN:CA	1:A:66:GLN:NE2	2.76	0.47
1:A:182:PRO:HG2	1:A:188:GLU:HG3	1.95	0.47
1:A:283:GLN:HA	1:A:283:GLN:OE1	2.13	0.47
1:A:401:ASP:CG	1:A:401:ASP:O	2.55	0.47
1:B:341:ASP:O	1:B:343:THR:N	2.45	0.47
1:B:366:LEU:C	1:B:368:GLU:N	2.65	0.47
1:C:283:GLN:HA	1:C:286:ILE:CD1	2.44	0.47
1:C:628:VAL:C	1:C:630:LEU:N	2.68	0.47
1:D:153:GLN:O	1:D:156:VAL:N	2.47	0.47
1:E:154:VAL:HG13	1:E:155:VAL:HG23	1.95	0.47
1:E:170:TRP:CE3	1:E:198:LEU:CD1	2.97	0.47
1:E:364:PHE:CZ	1:E:421:VAL:CG1	2.92	0.47
1:F:109:ALA:O	1:F:113:SER:HB3	2.14	0.47
1:F:249:ASP:O	1:F:253:ILE:HG13	2.14	0.47
1:F:441:LYS:HA	1:F:444:ARG:HE	1.78	0.47
1:F:538:SER:O	1:F:541:SER:HB2	2.14	0.47
1:A:83:ASN:O	1:A:84:ILE:C	2.57	0.47
1:A:501:GLU:O	1:A:502:GLU:C	2.57	0.47
1:A:628:VAL:O	1:A:632:LYS:HG3	2.13	0.47
1:B:264:THR:O	1:B:266:ASN:N	2.47	0.47
1:B:408:ILE:O	1:B:412:LYS:HG3	2.14	0.47
1:C:293:TRP:CD1	1:C:298:LYS:HZ3	2.32	0.47
1:C:640:PHE:CA	1:C:642:VAL:HG22	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:204:CYS:HB2	1:D:205:GLN:NE2	2.25	0.47
1:D:255:LYS:HB3	1:D:256:GLY:H	1.46	0.47
1:D:392:LEU:HA	1:D:395:ALA:HB3	1.95	0.47
1:D:509:PHE:CD1	1:D:529:VAL:HG21	2.49	0.47
1:E:472:CYS:HB3	1:E:504:GLN:HE22	1.79	0.47
1:E:576:ARG:O	1:E:577:LEU:HD23	2.14	0.47
1:F:499:VAL:O	1:F:499:VAL:HG12	2.13	0.47
1:F:580:ASP:O	1:F:582:MET:N	2.32	0.47
2:I:112:PRO:N	2:I:114:LEU:CD1	2.77	0.47
2:I:189:GLN:H	2:I:189:GLN:CD	2.23	0.47
1:D:474:VAL:HG12	1:D:475:LEU:N	2.29	0.47
1:E:156:VAL:HA	1:E:160:ALA:HB2	1.93	0.47
1:E:462:TYR:HD2	1:E:463:HIS:HD1	1.61	0.47
1:F:32:ASP:O	1:F:34:ILE:N	2.38	0.47
2:H:120:VAL:HG22	2:H:130:CYS:SG	2.54	0.47
1:A:67:VAL:HG12	1:A:68:TYR:CD2	2.49	0.47
1:A:398:MET:C	1:A:400:ASP:N	2.72	0.47
1:A:646:GLU:HB2	1:A:650:PHE:CD2	2.47	0.47
1:B:44:GLN:HE22	1:B:389:ARG:NH2	2.12	0.47
1:B:356:ILE:HG21	1:B:359:SER:HB2	1.96	0.47
1:C:210:LEU:HD13	1:C:244:ARG:HA	1.96	0.47
1:C:452:ASP:OD1	1:D:569:LEU:HD12	2.14	0.47
1:D:455:LEU:HD13	1:D:475:LEU:HD21	1.95	0.47
1:E:131:VAL:HG11	1:E:151:ALA:HB3	1.95	0.47
1:E:575:GLN:C	1:E:577:LEU:H	2.23	0.47
1:E:640:PHE:CZ	2:I:131:ILE:HD11	2.49	0.47
1:F:459:TYR:CE1	1:F:495:PHE:HD1	2.32	0.47
1:F:522:LEU:O	1:F:525:ILE:HB	2.14	0.47
1:A:204:CYS:HB2	1:A:205:GLN:NE2	2.24	0.47
1:A:545:LEU:HD23	1:A:545:LEU:O	2.13	0.47
1:B:149:ILE:O	1:B:150:GLN:C	2.58	0.47
1:C:186:PHE:C	1:C:188:GLU:N	2.72	0.47
1:E:396:ALA:O	1:E:398:MET:N	2.48	0.47
1:E:465:SER:O	1:E:466:LYS:CB	2.58	0.47
1:F:49:PHE:O	1:F:50:LEU:C	2.55	0.47
1:F:124:TRP:CE3	1:F:155:VAL:HG22	2.49	0.47
1:A:67:VAL:O	1:A:71:PHE:HB2	2.14	0.47
1:B:83:ASN:HB2	1:B:262:PRO:O	2.15	0.47
1:C:417:TYR:HB2	1:D:573:TYR:CD1	2.49	0.47
1:D:160:ALA:HB1	1:D:170:TRP:CZ2	2.50	0.47
1:E:425:THR:HG22	1:E:426:MET:CE	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:553:PHE:N	1:E:554:PRO:HD3	2.30	0.47
1:F:277:ASN:HD22	1:F:277:ASN:N	2.13	0.47
2:G:147:LEU:CD1	2:G:178:LEU:HD22	2.38	0.47
1:A:209:CYS:O	1:A:210:LEU:C	2.57	0.47
1:A:400:ASP:O	1:A:401:ASP:CB	2.61	0.47
1:A:624:PRO:O	1:A:625:PRO:C	2.56	0.47
1:A:631:LEU:HD11	2:G:164:LEU:HD11	1.97	0.47
1:B:462:TYR:CD2	1:B:463:HIS:CE1	3.03	0.47
1:B:462:TYR:O	1:B:466:LYS:HA	2.14	0.47
1:B:503:SER:OG	1:B:504:GLN:N	2.46	0.47
1:C:206:PRO:HB3	1:C:247:TYR:CA	2.44	0.47
1:C:264:THR:HG22	1:C:266:ASN:H	1.79	0.47
1:C:264:THR:CG2	1:C:266:ASN:HD22	2.28	0.47
1:C:327:ILE:CG2	1:C:328:TRP:N	2.78	0.47
1:C:392:LEU:C	1:C:394:LEU:N	2.69	0.47
1:C:417:TYR:HB2	1:D:573:TYR:HD1	1.79	0.47
1:C:518:ASP:O	1:C:519:SER:C	2.57	0.47
1:C:627:ILE:CG1	2:H:171:LEU:HD11	2.44	0.47
1:C:644:ILE:HG23	2:H:173:TYR:CE1	2.47	0.47
1:D:140:GLY:C	1:D:142:GLU:H	2.23	0.47
1:D:169:PHE:O	1:D:172:GLU:N	2.47	0.47
1:D:267:GLN:O	1:D:269:THR:HG23	2.14	0.47
1:E:269:THR:HG23	1:E:272:ASN:ND2	2.24	0.47
1:E:284:LEU:HD11	1:E:288:LEU:HD21	1.97	0.47
1:E:417:TYR:HB2	1:F:573:TYR:CD1	2.39	0.47
1:E:455:LEU:CB	1:F:569:LEU:HD11	2.38	0.47
1:E:571:VAL:HB	1:E:573:TYR:CD2	2.50	0.47
1:F:55:LEU:HD21	1:F:70:THR:CG2	2.44	0.47
1:F:159:CYS:O	1:F:162:PHE:N	2.44	0.47
1:F:167:ILE:CG1	1:F:209:CYS:HB3	2.44	0.47
1:F:194:TYR:N	1:F:194:TYR:CD1	2.80	0.47
1:F:455:LEU:HD21	1:F:488:TYR:CD1	2.50	0.47
1:F:553:PHE:N	1:F:554:PRO:CD	2.78	0.47
2:I:137:LYS:O	2:I:138:LEU:HB2	2.13	0.47
2:I:169:PRO:O	2:I:172:SER:HB3	2.15	0.47
2:H:138:LEU:O	2:H:139:GLN:C	2.58	0.47
1:B:77:ARG:HD3	1:B:78:PHE:CE1	2.45	0.47
1:B:358:ASN:HB3	1:B:389:ARG:CG	2.45	0.47
1:C:420:CYS:O	1:C:423:MET:N	2.48	0.47
1:C:475:LEU:HB3	1:C:492:TYR:CZ	2.50	0.47
1:C:572:ASN:OD1	1:C:572:ASN:O	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:572:ASN:HD21	1:C:575:GLN:HE21	1.55	0.47
1:D:33:VAL:HA	1:D:36:LYS:NZ	2.30	0.47
1:D:41:ILE:HD11	1:D:50:LEU:O	2.15	0.47
1:D:333:ASN:O	1:D:334:TYR:C	2.57	0.47
1:D:380:GLU:O	1:D:381:THR:C	2.56	0.47
1:E:353:GLN:O	1:E:353:GLN:HG3	2.14	0.47
1:E:374:THR:O	1:E:376:ILE:HG12	2.15	0.47
1:E:378:GLU:O	1:E:382:THR:HG22	2.15	0.47
1:F:554:PRO:O	1:F:555:GLU:HB3	2.15	0.47
2:I:171:LEU:O	2:I:175:ILE:HG13	2.14	0.47
1:A:180:TRP:O	1:A:191:ARG:NH1	2.48	0.47
1:B:81:MET:HE2	1:B:81:MET:HA	1.96	0.47
1:C:400:ASP:O	1:C:401:ASP:CB	2.61	0.47
1:C:568:VAL:O	1:C:569:LEU:C	2.57	0.47
1:D:202:LEU:CD1	1:D:203:LEU:HG	2.45	0.47
1:D:392:LEU:O	1:D:393:ASP:C	2.58	0.47
1:D:524:MET:O	1:D:525:ILE:C	2.58	0.47
1:E:417:TYR:O	1:E:421:VAL:HG12	2.15	0.47
1:F:370:TYR:CG	1:F:378:GLU:HB3	2.49	0.47
1:A:132:ARG:HG2	1:A:132:ARG:NH1	2.30	0.47
1:A:221:GLU:HB3	1:A:229:ALA:HB1	1.96	0.47
1:A:245:SER:O	1:A:248:GLN:N	2.46	0.47
1:B:23:PRO:HD3	1:B:26:ARG:NH2	2.30	0.47
1:C:563:THR:HG21	1:C:575:GLN:HB3	1.97	0.47
1:D:119:ASN:HA	1:D:124:TRP:HE1	1.80	0.47
1:E:145:ARG:NH2	1:E:180:TRP:HZ2	2.12	0.47
1:E:279:TYR:CE2	1:E:324:ALA:HA	2.51	0.47
1:E:638:GLN:O	1:E:640:PHE:N	2.48	0.47
2:H:131:ILE:HG23	2:H:135:LEU:HD12	1.96	0.47
1:A:128:ILE:HD11	1:A:152:PHE:N	2.30	0.46
1:A:137:ILE:H	1:A:137:ILE:CD1	2.22	0.46
1:A:164:PRO:HG3	1:A:250:TRP:CE2	2.50	0.46
1:A:250:TRP:CH2	1:A:254:THR:HG21	2.51	0.46
1:A:276:PRO:C	1:A:278:GLU:H	2.24	0.46
1:C:167:ILE:HG23	1:C:168:GLN:N	2.30	0.46
1:C:299:LEU:HB2	1:C:301:LEU:HG	1.97	0.46
1:C:334:TYR:O	1:C:335:GLN:C	2.56	0.46
1:C:367:SER:OG	1:C:379:ILE:HG23	2.15	0.46
1:C:384:LEU:O	1:C:387:ILE:N	2.48	0.46
1:D:42:GLU:C	1:D:45:PRO:HD3	2.40	0.46
1:D:153:GLN:O	1:D:156:VAL:HB	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:366:LEU:HD23	1:D:366:LEU:HA	1.71	0.46
1:E:341:ASP:CG	1:E:343:THR:HG22	2.40	0.46
1:F:559:LEU:O	1:F:562:PHE:HB3	2.15	0.46
1:A:156:VAL:HA	1:A:160:ALA:HB3	1.96	0.46
1:A:167:ILE:HG12	1:A:171:ASN:ND2	2.30	0.46
1:A:294:GLU:HG3	1:A:313:VAL:HG21	1.97	0.46
1:A:542:VAL:CG1	1:A:546:GLU:HG3	2.44	0.46
1:C:462:TYR:C	1:C:464:ILE:H	2.24	0.46
1:C:624:PRO:N	1:C:625:PRO:CD	2.76	0.46
1:D:198:LEU:O	1:D:202:LEU:HG	2.15	0.46
1:D:275:LYS:H	1:D:275:LYS:CE	2.29	0.46
1:E:41:ILE:HG12	1:E:50:LEU:HD22	1.96	0.46
1:E:144:ALA:HA	1:E:147:ILE:HD12	1.97	0.46
1:E:163:GLU:OE2	1:E:165:LYS:N	2.46	0.46
1:E:226:GLN:HA	1:E:229:ALA:HB2	1.96	0.46
1:E:401:ASP:C	1:E:403:THR:N	2.72	0.46
1:E:561:GLU:O	1:E:562:PHE:C	2.57	0.46
1:F:183:VAL:O	1:F:183:VAL:HG12	2.16	0.46
1:A:100:ASP:C	1:A:102:ALA:H	2.23	0.46
1:A:289:GLU:OE2	1:A:292:ARG:HD2	2.15	0.46
1:A:417:TYR:HE1	1:B:568:VAL:CG2	2.28	0.46
1:B:290:TRP:CD1	1:B:290:TRP:C	2.93	0.46
1:C:634:LEU:O	1:C:635:PRO:C	2.58	0.46
1:D:122:SER:O	1:D:123:LEU:C	2.59	0.46
1:D:401:ASP:C	1:D:403:THR:N	2.73	0.46
1:E:125:LEU:C	1:E:127:TYR:N	2.74	0.46
1:E:200:LYS:HG2	1:E:236:LEU:CD2	2.43	0.46
2:G:114:LEU:HD21	2:G:164:LEU:HD13	1.96	0.46
2:I:112:PRO:O	2:I:113:TRP:CD1	2.68	0.46
2:I:184:VAL:O	2:I:185:CYS:CB	2.63	0.46
2:H:118:VAL:HG12	2:H:119:ASP:N	2.29	0.46
2:H:150:ILE:HG23	2:H:161:PHE:CE1	2.48	0.46
1:A:196:ARG:NH1	1:A:232:HIS:CE1	2.82	0.46
1:A:629:GLU:HA	1:A:632:LYS:HG3	1.97	0.46
1:B:230:ARG:O	1:B:230:ARG:HD3	2.15	0.46
1:B:480:LYS:HB2	1:B:481:TYR:CD1	2.51	0.46
1:B:529:VAL:O	1:B:532:PHE:HB3	2.16	0.46
1:D:121:LEU:O	1:D:124:TRP:HB2	2.15	0.46
1:D:143:GLU:C	1:D:145:ARG:H	2.24	0.46
1:D:373:ASN:O	1:D:375:LYS:HG2	2.16	0.46
1:D:417:TYR:O	1:D:420:CYS:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:131:VAL:HG21	1:E:151:ALA:HB1	1.97	0.46
1:E:355:CYS:O	1:E:357:PRO:HD2	2.16	0.46
1:E:390:ILE:CD1	1:E:414:LYS:HD3	2.39	0.46
1:E:438:ILE:O	1:E:442:CYS:HB2	2.15	0.46
1:F:350:LYS:HZ1	1:F:354:GLN:HE21	1.62	0.46
1:F:462:TYR:C	1:F:464:ILE:H	2.23	0.46
2:I:126:THR:HG23	2:I:127:PRO:HD2	1.97	0.46
1:C:232:HIS:C	1:C:234:GLY:N	2.72	0.46
1:C:295:SER:C	1:C:297:ASN:H	2.23	0.46
1:D:571:VAL:HG11	1:D:573:TYR:CE2	2.50	0.46
1:F:156:VAL:HG13	1:F:170:TRP:CH2	2.50	0.46
2:H:135:LEU:HD22	2:H:178:LEU:HD11	1.98	0.46
1:A:137:ILE:HG23	1:A:145:ARG:CB	2.36	0.46
1:A:169:PHE:O	1:A:171:ASN:N	2.48	0.46
1:A:181:LYS:O	1:A:182:PRO:C	2.58	0.46
1:B:100:ASP:C	1:B:102:ALA:N	2.74	0.46
1:B:206:PRO:HB3	1:B:247:TYR:CA	2.46	0.46
1:E:41:ILE:O	1:E:41:ILE:CG2	2.63	0.46
1:E:107:VAL:HG13	1:E:110:ARG:HD3	1.98	0.46
1:E:159:CYS:O	1:E:160:ALA:C	2.57	0.46
1:E:576:ARG:HB2	1:E:576:ARG:NH1	2.28	0.46
1:F:111:CYS:SG	1:F:112:LEU:HG	2.55	0.46
1:F:153:GLN:O	1:F:156:VAL:N	2.42	0.46
2:I:146:LEU:HA	2:I:149:VAL:HG23	1.97	0.46
1:A:113:SER:HB2	1:A:115:GLU:CD	2.40	0.46
1:A:351:LEU:O	1:A:354:GLN:HB2	2.16	0.46
1:A:427:LYS:HB2	1:A:435:SER:CB	2.46	0.46
1:B:314:TYR:HB3	1:B:331:MET:HE2	1.98	0.46
1:B:485:ASP:O	1:B:489:ILE:HG12	2.15	0.46
1:C:36:LYS:O	1:C:39:ASP:HB2	2.14	0.46
1:C:74:LEU:O	1:C:75:HIS:C	2.59	0.46
1:C:324:ALA:O	1:C:325:PRO:C	2.59	0.46
1:C:436:ARG:NH2	1:C:461:GLU:OE1	2.46	0.46
1:D:247:TYR:O	1:D:250:TRP:HB3	2.15	0.46
1:D:482:PHE:C	1:D:484:THR:N	2.74	0.46
1:E:530:ILE:O	1:E:531:PHE:C	2.59	0.46
1:F:59:VAL:C	1:F:61:LEU:H	2.23	0.46
1:F:518:ASP:O	1:F:519:SER:C	2.59	0.46
2:I:186:SER:CA	2:I:189:GLN:HE22	2.29	0.46
1:A:401:ASP:O	1:A:403:THR:N	2.49	0.46
1:A:473:LYS:O	1:A:477:LEU:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568:VAL:CG1	1:A:569:LEU:HD22	2.37	0.46
1:B:279:TYR:CE2	1:B:324:ALA:HA	2.51	0.46
1:D:199:TYR:O	1:D:203:LEU:HG	2.16	0.46
1:D:455:LEU:N	1:D:455:LEU:CD2	2.79	0.46
1:F:55:LEU:HD21	1:F:70:THR:HG22	1.98	0.46
1:F:81:MET:HG3	1:F:84:ILE:HD12	1.97	0.46
1:F:578:GLU:C	1:F:579:LEU:HD23	2.40	0.46
2:I:138:LEU:HB3	2:I:142:GLN:CG	2.46	0.46
2:I:175:ILE:O	2:I:175:ILE:HG22	2.15	0.46
2:H:180:LEU:HD22	2:H:189:GLN:OE1	2.16	0.46
1:A:121:LEU:C	1:A:123:LEU:H	2.23	0.46
1:B:81:MET:HE1	1:B:319:GLN:CA	2.37	0.46
1:B:113:SER:OG	1:B:115:GLU:HG2	2.15	0.46
1:C:124:TRP:O	1:C:127:TYR:HB3	2.16	0.46
1:C:242:ASN:O	1:C:246:LEU:HG	2.16	0.46
1:E:191:ARG:NE	1:E:195:ILE:HD11	2.31	0.46
1:E:200:LYS:HG2	1:E:236:LEU:CD1	2.43	0.46
1:F:370:TYR:CD1	1:F:378:GLU:HB3	2.51	0.46
1:F:446:LYS:C	1:F:448:LEU:H	2.24	0.46
2:I:162:VAL:O	2:I:166:GLU:HB2	2.16	0.46
2:H:180:LEU:HD13	2:H:189:GLN:HE22	1.80	0.46
1:A:178:GLU:CD	1:A:216:ARG:NH2	2.74	0.46
1:A:248:GLN:O	1:A:249:ASP:C	2.59	0.46
1:A:345:ILE:HB	1:A:369:GLN:OE1	2.16	0.46
1:A:358:ASN:HB3	1:A:389:ARG:HG3	1.98	0.46
1:B:52:VAL:HG11	1:B:268:ALA:CB	2.45	0.46
1:B:71:PHE:HB3	1:B:88:ARG:NH1	2.30	0.46
1:B:116:LEU:O	1:B:118:ASN:N	2.44	0.46
1:B:181:LYS:HD2	1:B:181:LYS:N	2.31	0.46
1:B:493:LEU:O	1:B:494:ASP:C	2.59	0.46
1:C:544:THR:O	1:C:547:LYS:HB3	2.16	0.46
1:D:186:PHE:C	1:D:188:GLU:N	2.74	0.46
1:E:135:ASN:HB3	1:E:144:ALA:O	2.16	0.46
1:E:170:TRP:CD2	1:E:202:LEU:HD23	2.51	0.46
1:E:579:LEU:HD22	1:E:581:TYR:OH	2.16	0.46
1:F:315:MET:O	1:F:316:GLN:C	2.58	0.46
2:I:160:THR:O	2:I:160:THR:HG22	2.16	0.46
2:H:150:ILE:O	2:H:154:CYS:SG	2.67	0.46
1:A:177:LEU:HD11	1:A:194:TYR:HB3	1.97	0.45
1:A:334:TYR:C	1:A:336:GLY:N	2.71	0.45
1:A:442:CYS:HA	1:A:445:LEU:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:ILE:O	1:B:49:PHE:C	2.59	0.45
1:B:199:TYR:O	1:B:203:LEU:HG	2.16	0.45
1:C:55:LEU:HD13	1:C:71:PHE:CE1	2.50	0.45
1:C:61:LEU:O	1:C:62:LYS:C	2.59	0.45
1:C:61:LEU:HD12	1:C:63:GLN:NE2	2.31	0.45
1:C:384:LEU:O	1:C:385:SER:C	2.57	0.45
1:D:207:MET:O	1:D:247:TYR:CD2	2.69	0.45
1:E:119:ASN:HD22	1:E:312:TYR:HD1	1.64	0.45
1:E:170:TRP:CE2	1:E:202:LEU:HB3	2.51	0.45
1:E:191:ARG:O	1:E:195:ILE:HG13	2.16	0.45
1:E:333:ASN:HD22	1:F:558:LYS:HD3	1.81	0.45
1:E:394:LEU:HD12	1:E:411:LEU:CD2	2.46	0.45
1:F:326:GLU:O	1:F:326:GLU:HG3	2.15	0.45
1:A:39:ASP:O	1:A:42:GLU:HB3	2.17	0.45
1:A:89:LEU:C	1:A:91:LEU:H	2.23	0.45
1:B:145:ARG:NE	1:B:180:TRP:NE1	2.64	0.45
1:B:242:ASN:O	1:B:246:LEU:HG	2.15	0.45
1:B:444:ARG:NH2	2:G:167:GLU:OE2	2.49	0.45
1:C:211:GLU:HA	1:C:240:TYR:OH	2.16	0.45
1:C:567:LYS:HG2	1:C:572:ASN:CA	2.45	0.45
1:D:249:ASP:O	1:D:252:ASN:HB2	2.15	0.45
1:D:356:ILE:O	1:D:358:ASN:N	2.50	0.45
1:F:255:LYS:HB3	1:F:256:GLY:H	1.44	0.45
1:F:355:CYS:C	1:F:356:ILE:HG13	2.41	0.45
1:A:241:MET:O	1:A:244:ARG:N	2.50	0.45
1:A:252:ASN:O	1:A:255:LYS:HG2	2.16	0.45
1:B:71:PHE:HB3	1:B:88:ARG:HH11	1.81	0.45
1:B:335:GLN:OE1	1:B:335:GLN:HA	2.17	0.45
1:B:478:GLY:O	1:B:482:PHE:HB2	2.16	0.45
1:C:203:LEU:HD12	1:C:236:LEU:HD13	1.99	0.45
1:C:249:ASP:O	1:C:253:ILE:HG13	2.16	0.45
1:C:346:THR:HG21	1:C:370:TYR:HE2	1.82	0.45
1:C:642:VAL:HG23	1:C:643:THR:H	1.81	0.45
1:D:207:MET:H	1:D:210:LEU:HG	1.81	0.45
1:D:401:ASP:C	1:D:403:THR:H	2.23	0.45
1:D:462:TYR:HA	1:D:467:ASP:O	2.16	0.45
1:E:41:ILE:HD11	1:E:51:TYR:HA	1.98	0.45
1:E:458:ALA:C	1:E:460:ILE:N	2.74	0.45
1:E:577:LEU:O	1:E:578:GLU:HB2	2.15	0.45
1:A:113:SER:HB2	1:A:115:GLU:OE1	2.16	0.45
1:A:127:TYR:O	1:A:131:VAL:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:ASN:HB2	1:A:306:HIS:CE1	2.52	0.45
1:A:423:MET:HA	1:A:438:ILE:HD12	1.99	0.45
1:D:384:LEU:O	1:D:385:SER:C	2.59	0.45
1:E:78:PHE:N	1:E:78:PHE:CD1	2.83	0.45
1:E:392:LEU:HA	1:E:395:ALA:HB3	1.98	0.45
1:F:420:CYS:O	1:F:423:MET:N	2.49	0.45
1:A:49:PHE:HE2	1:A:53:LYS:NZ	2.14	0.45
1:A:61:LEU:HB2	1:A:63:GLN:NE2	2.28	0.45
1:A:153:GLN:O	1:A:156:VAL:HB	2.16	0.45
1:A:179:HIS:O	1:A:179:HIS:ND1	2.49	0.45
1:A:182:PRO:CG	1:A:191:ARG:HD2	2.43	0.45
1:B:30:GLU:HG2	1:F:61:LEU:HD22	1.99	0.45
1:B:191:ARG:NH1	1:B:191:ARG:HG3	2.31	0.45
1:C:455:LEU:H	1:C:455:LEU:CD2	2.29	0.45
1:C:494:ASP:OD1	1:C:528:LYS:HD3	2.16	0.45
1:D:306:HIS:O	1:D:306:HIS:CD2	2.70	0.45
1:E:314:TYR:CD1	1:E:331:MET:HB2	2.51	0.45
1:F:202:LEU:O	1:F:207:MET:HE2	2.16	0.45
1:A:135:ASN:O	1:A:136:ASP:C	2.60	0.45
1:A:538:SER:O	1:A:539:LEU:C	2.60	0.45
1:B:121:LEU:C	1:B:123:LEU:H	2.24	0.45
1:B:495:PHE:O	1:B:499:VAL:HG22	2.17	0.45
1:C:54:LEU:HD23	1:C:70:THR:CG2	2.46	0.45
1:C:178:GLU:HA	1:C:191:ARG:HH21	1.78	0.45
1:C:240:TYR:O	1:C:243:ALA:HB3	2.16	0.45
1:C:392:LEU:O	1:C:394:LEU:N	2.50	0.45
1:E:568:VAL:HG21	1:F:417:TYR:CE1	2.51	0.45
1:E:641:LYS:C	1:E:643:THR:N	2.71	0.45
1:A:202:LEU:C	1:A:202:LEU:CD1	2.90	0.45
1:A:636:LYS:C	1:A:638:GLN:H	2.25	0.45
1:B:162:PHE:HD2	1:B:309:ARG:HG3	1.81	0.45
1:B:182:PRO:HB3	1:B:188:GLU:HB2	1.99	0.45
1:B:564:ASN:O	1:B:565:LYS:C	2.59	0.45
1:C:79:PRO:HB2	1:C:116:LEU:HD22	1.98	0.45
1:C:564:ASN:HA	1:C:567:LYS:HE2	1.99	0.45
1:E:178:GLU:HA	1:E:191:ARG:CZ	2.43	0.45
1:E:630:LEU:CD1	2:I:135:LEU:HD21	2.46	0.45
1:F:199:TYR:CD1	1:F:217:TYR:HB2	2.51	0.45
2:G:126:THR:HB	2:G:129:MET:H	1.82	0.45
1:A:101:ALA:O	1:A:105:GLU:HG3	2.17	0.45
1:A:336:GLY:O	1:A:337:GLU:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:THR:O	1:B:229:ALA:C	2.60	0.45
1:B:240:TYR:O	1:B:243:ALA:HB3	2.17	0.45
1:B:264:THR:C	1:B:266:ASN:N	2.74	0.45
1:C:140:GLY:C	1:C:142:GLU:N	2.74	0.45
1:C:337:GLU:C	1:C:339:ASN:H	2.24	0.45
1:C:455:LEU:N	1:C:455:LEU:CD2	2.80	0.45
1:E:71:PHE:CE1	1:E:265:LEU:HD12	2.52	0.45
1:E:171:ASN:HD21	1:E:213:MET:HE1	1.82	0.45
1:E:372:LEU:CD1	1:F:543:ARG:NE	2.80	0.45
1:E:426:MET:HE2	1:E:426:MET:CA	2.45	0.45
1:E:533:GLU:OE1	1:E:541:SER:HB3	2.16	0.45
1:F:124:TRP:O	1:F:127:TYR:N	2.43	0.45
1:F:307:LYS:HD3	1:F:338:LYS:HG3	1.99	0.45
2:H:163:ALA:O	2:H:167:GLU:HG2	2.17	0.45
1:B:180:TRP:HZ3	1:B:191:ARG:HA	1.82	0.45
1:B:281:VAL:O	1:B:285:LEU:HD12	2.17	0.45
1:B:573:TYR:O	1:B:574:LEU:C	2.59	0.45
1:B:580:ASP:C	1:B:582:MET:N	2.74	0.45
1:C:112:LEU:HD23	1:C:112:LEU:HA	1.82	0.45
1:C:128:ILE:HD11	1:C:155:VAL:HG21	1.98	0.45
1:E:131:VAL:HG11	1:E:151:ALA:HB2	1.99	0.45
1:E:164:PRO:CG	1:E:250:TRP:CZ2	2.99	0.45
1:E:210:LEU:HD21	1:E:243:ALA:HB1	1.98	0.45
1:E:451:PRO:O	1:E:452:ASP:C	2.60	0.45
1:E:540:ASN:ND2	1:E:543:ARG:NH2	2.65	0.45
1:F:180:TRP:CZ2	1:F:187:GLU:HG2	2.51	0.45
1:F:563:THR:CG2	1:F:572:ASN:OD1	2.65	0.45
2:I:144:MET:HA	2:I:147:LEU:HB3	1.98	0.45
1:A:105:GLU:OE1	1:A:105:GLU:HA	2.17	0.45
1:A:199:TYR:C	1:A:201:THR:H	2.23	0.45
1:B:95:LYS:O	1:B:98:GLU:N	2.49	0.45
1:C:181:LYS:O	1:C:181:LYS:CD	2.61	0.45
1:C:572:ASN:CG	1:C:575:GLN:HG2	2.41	0.45
1:D:84:ILE:O	1:D:84:ILE:CG2	2.64	0.45
1:D:137:ILE:O	1:D:141:GLY:HA2	2.17	0.45
1:E:40:MET:C	1:E:42:GLU:N	2.74	0.45
1:E:317:ALA:O	1:E:321:VAL:HG22	2.16	0.45
1:F:204:CYS:HB2	1:F:205:GLN:HE21	1.82	0.45
1:A:93:PHE:HE2	1:A:104:ILE:CD1	2.29	0.44
1:B:105:GLU:HB2	1:B:106:PRO:HD3	1.99	0.44
1:B:135:ASN:ND2	1:B:147:ILE:HG21	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:TYR:CZ	1:B:244:ARG:HD2	2.52	0.44
1:B:556:VAL:HG22	1:B:557:ASN:N	2.30	0.44
1:C:125:LEU:HD21	1:C:169:PHE:CD1	2.38	0.44
1:C:509:PHE:CG	1:C:529:VAL:HG21	2.51	0.44
1:D:221:GLU:O	1:D:229:ALA:HB2	2.17	0.44
1:D:242:ASN:O	1:D:246:LEU:HG	2.16	0.44
1:E:173:TYR:O	1:E:173:TYR:CG	2.70	0.44
1:E:262:PRO:CB	1:E:268:ALA:HA	2.47	0.44
1:E:401:ASP:O	1:E:403:THR:N	2.49	0.44
1:F:114:LYS:O	1:F:115:GLU:C	2.60	0.44
1:F:145:ARG:CZ	1:F:180:TRP:CZ2	3.00	0.44
1:F:226:GLN:O	1:F:226:GLN:HG2	2.17	0.44
1:F:332:ALA:O	1:F:345:ILE:HG12	2.16	0.44
1:F:358:ASN:HB3	1:F:389:ARG:HG3	1.99	0.44
2:I:137:LYS:O	2:I:138:LEU:CB	2.65	0.44
1:A:178:GLU:CD	1:A:216:ARG:HH22	2.25	0.44
1:A:220:TRP:HZ3	1:A:221:GLU:OE2	1.99	0.44
1:A:332:ALA:C	1:A:334:TYR:H	2.24	0.44
1:A:492:TYR:HE1	1:A:496:LEU:HD11	1.81	0.44
1:B:83:ASN:ND2	1:B:84:ILE:HD12	2.32	0.44
1:C:417:TYR:CE2	1:D:574:LEU:HD23	2.52	0.44
1:C:633:VAL:O	2:H:134:GLU:HG3	2.17	0.44
1:D:33:VAL:H	1:D:36:LYS:HZ3	1.65	0.44
1:D:330:ASN:ND2	1:D:330:ASN:H	2.15	0.44
1:E:124:TRP:O	1:E:127:TYR:HB3	2.17	0.44
1:A:88:ARG:O	1:A:88:ARG:HG3	2.16	0.44
1:A:334:TYR:O	1:A:336:GLY:N	2.51	0.44
1:B:117:GLY:O	1:B:119:ASN:N	2.50	0.44
1:C:265:LEU:O	1:C:268:ALA:HB3	2.17	0.44
1:C:306:HIS:CD2	1:C:310:MET:HG2	2.52	0.44
1:D:136:ASP:CB	1:D:139:THR:HB	2.44	0.44
1:E:247:TYR:CZ	1:E:251:LEU:HD13	2.53	0.44
1:E:287:TRP:CZ2	1:E:320:HIS:ND1	2.86	0.44
1:E:529:VAL:O	1:E:532:PHE:HB3	2.17	0.44
1:A:351:LEU:HD23	1:A:354:GLN:OE1	2.18	0.44
1:A:418:VAL:HG12	1:A:418:VAL:O	2.16	0.44
1:B:203:LEU:HD13	1:B:214:TRP:CE3	2.52	0.44
1:B:527:GLN:HE21	1:B:527:GLN:HB2	1.61	0.44
1:B:559:LEU:O	1:B:563:THR:HG23	2.17	0.44
1:C:55:LEU:HD22	1:C:71:PHE:CD1	2.53	0.44
1:C:137:ILE:HG21	1:C:176:PHE:HE1	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:262:PRO:HG3	1:C:273:LEU:CD2	2.36	0.44
1:C:576:ARG:O	1:C:577:LEU:HD23	2.17	0.44
1:D:432:LEU:O	1:D:435:SER:HB3	2.17	0.44
1:E:327:ILE:O	1:E:328:TRP:C	2.60	0.44
2:H:135:LEU:CD1	2:H:177:GLU:HG2	2.47	0.44
2:H:142:GLN:O	2:H:145:ALA:HB3	2.17	0.44
1:A:152:PHE:HB3	1:A:173:TYR:CD1	2.53	0.44
1:A:225:ASN:O	1:A:229:ALA:HB3	2.17	0.44
1:A:364:PHE:N	1:A:364:PHE:CD1	2.85	0.44
1:A:630:LEU:HD23	2:G:171:LEU:HD13	1.99	0.44
1:B:51:TYR:CG	1:B:74:LEU:HD13	2.53	0.44
1:B:77:ARG:CD	1:B:78:PHE:HE1	2.27	0.44
1:B:225:ASN:CB	1:B:228:THR:HB	2.48	0.44
1:B:459:TYR:O	1:B:460:ILE:C	2.57	0.44
1:C:199:TYR:O	1:C:203:LEU:HG	2.18	0.44
1:C:517:SER:O	1:C:518:ASP:HB3	2.18	0.44
1:D:37:LEU:HA	1:D:40:MET:CE	2.35	0.44
1:D:261:LEU:HD23	1:D:261:LEU:HA	1.76	0.44
1:E:77:ARG:HG3	1:E:77:ARG:HH11	1.81	0.44
1:E:265:LEU:HD23	1:E:265:LEU:C	2.43	0.44
1:E:477:LEU:HD12	1:E:477:LEU:N	2.33	0.44
1:F:383:ILE:HG21	1:F:422:TYR:CG	2.53	0.44
1:F:533:GLU:OE1	1:F:541:SER:HB3	2.17	0.44
2:G:179:LEU:O	2:G:181:SER:N	2.50	0.44
2:I:186:SER:C	2:I:189:GLN:HE22	2.26	0.44
1:A:87:MET:HE2	1:A:262:PRO:O	2.18	0.44
1:A:162:PHE:HA	1:A:309:ARG:HH12	1.82	0.44
1:A:183:VAL:HG23	1:A:187:GLU:OE1	2.18	0.44
1:A:404:ASN:OD1	1:A:407:ALA:N	2.45	0.44
1:A:574:LEU:HD12	1:A:574:LEU:HA	1.61	0.44
1:A:624:PRO:HG3	2:G:153:PHE:CE1	2.52	0.44
1:B:204:CYS:O	1:B:205:GLN:C	2.59	0.44
1:B:205:GLN:NE2	1:B:205:GLN:H	2.15	0.44
1:B:580:ASP:O	1:B:582:MET:N	2.50	0.44
1:C:167:ILE:HD12	1:C:209:CYS:HB3	1.99	0.44
1:C:475:LEU:HB3	1:C:492:TYR:CE1	2.53	0.44
1:C:572:ASN:ND2	1:C:575:GLN:NE2	2.53	0.44
1:D:33:VAL:C	1:D:35:GLY:N	2.71	0.44
1:D:49:PHE:O	1:D:50:LEU:C	2.60	0.44
1:D:59:VAL:C	1:D:62:LYS:H	2.23	0.44
1:D:295:SER:O	1:D:297:ASN:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:477:LEU:O	1:D:480:LYS:HG2	2.18	0.44
1:E:297:ASN:HB2	1:E:306:HIS:CE1	2.53	0.44
1:F:405:GLU:HG3	1:F:406:SER:N	2.32	0.44
2:G:168:ALA:CA	2:G:170:GLN:HE22	2.27	0.44
1:A:100:ASP:OD1	1:A:100:ASP:O	2.35	0.44
1:A:538:SER:N	1:A:541:SER:OG	2.50	0.44
1:B:281:VAL:O	1:B:282:GLN:C	2.61	0.44
1:B:427:LYS:CA	1:B:435:SER:HB3	2.48	0.44
1:C:502:GLU:O	1:C:503:SER:C	2.59	0.44
1:C:546:GLU:O	1:C:547:LYS:C	2.58	0.44
1:D:292:ARG:C	1:D:294:GLU:N	2.74	0.44
1:D:361:VAL:HG12	1:D:362:LEU:N	2.33	0.44
1:E:313:VAL:O	1:E:316:GLN:N	2.51	0.44
1:E:361:VAL:HG11	1:F:559:LEU:HD11	1.98	0.44
1:E:651:SER:HB2	2:I:162:VAL:CG1	2.48	0.44
1:F:346:THR:O	1:F:350:LYS:HB2	2.17	0.44
1:F:470:THR:O	1:F:472:CYS:N	2.50	0.44
1:F:568:VAL:O	1:F:570:ASP:N	2.50	0.44
1:A:300:GLU:OE2	1:A:300:GLU:N	2.51	0.44
1:B:86:CYS:HB3	1:B:263:ILE:CG1	2.46	0.44
1:B:274:PRO:HB2	1:B:323:PHE:CE1	2.53	0.44
1:C:279:TYR:CE2	1:C:324:ALA:HA	2.53	0.44
1:C:579:LEU:HD22	1:C:581:TYR:CZ	2.53	0.44
1:D:337:GLU:C	1:D:339:ASN:H	2.26	0.44
1:D:575:GLN:O	1:D:577:LEU:N	2.51	0.44
1:E:103:VAL:O	1:E:103:VAL:HG12	2.17	0.44
1:E:119:ASN:O	1:E:312:TYR:CE1	2.70	0.44
1:E:219:GLN:HE21	1:E:219:GLN:HB3	1.58	0.44
1:E:474:VAL:O	1:E:477:LEU:HB2	2.18	0.44
1:E:493:LEU:O	1:E:497:ILE:HG13	2.18	0.44
1:E:631:LEU:O	1:E:633:VAL:N	2.51	0.44
1:F:54:LEU:HG	1:F:58:HIS:CD2	2.52	0.44
1:F:349:LEU:HD11	1:F:365:SER:HB3	1.99	0.44
1:F:401:ASP:C	1:F:403:THR:N	2.76	0.44
1:F:529:VAL:CG1	1:F:545:LEU:HD11	2.48	0.44
1:A:196:ARG:CG	1:A:200:LYS:HE2	2.48	0.44
1:A:386:CYS:O	1:A:387:ILE:C	2.61	0.44
1:A:636:LYS:O	1:A:638:GLN:N	2.46	0.44
1:B:89:LEU:C	1:B:91:LEU:N	2.74	0.44
1:B:366:LEU:HB3	1:B:382:THR:HG21	1.99	0.44
1:C:110:ARG:HG2	1:C:110:ARG:HH11	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:LYS:HE3	1:C:260:ASN:CG	2.43	0.44
1:C:327:ILE:HG23	1:C:328:TRP:N	2.33	0.44
1:C:504:GLN:O	1:C:505:VAL:C	2.61	0.44
1:D:232:HIS:HA	1:D:235:GLU:OE1	2.17	0.44
1:D:364:PHE:O	1:D:365:SER:C	2.60	0.44
1:D:424:ASN:O	1:D:427:LYS:HB3	2.18	0.44
1:E:282:GLN:HA	1:E:282:GLN:NE2	2.32	0.44
1:E:371:GLU:OE2	1:F:539:LEU:HB2	2.17	0.44
1:E:497:ILE:HG23	1:E:532:PHE:CD1	2.53	0.44
1:F:410:GLN:HE21	1:F:410:GLN:HB3	1.52	0.44
1:A:51:TYR:CD2	1:A:51:TYR:N	2.86	0.43
1:A:269:THR:O	1:A:271:SER:N	2.42	0.43
1:B:181:LYS:O	1:B:181:LYS:HD3	2.18	0.43
1:B:376:ILE:HB	1:B:377:PRO:CD	2.45	0.43
1:C:297:ASN:HB2	1:C:306:HIS:CE1	2.53	0.43
1:C:314:TYR:CD1	1:C:331:MET:HB2	2.53	0.43
1:C:432:LEU:O	1:C:433:ALA:C	2.60	0.43
1:C:464:ILE:HG22	1:C:465:SER:N	2.33	0.43
1:D:315:MET:O	1:D:316:GLN:C	2.60	0.43
1:D:386:CYS:O	1:D:390:ILE:HG13	2.18	0.43
1:E:423:MET:HB2	1:E:438:ILE:HG21	2.00	0.43
1:E:462:TYR:C	1:E:464:ILE:H	2.26	0.43
1:E:554:PRO:O	1:E:555:GLU:CB	2.64	0.43
1:E:631:LEU:CD1	2:I:115:PRO:HD2	2.47	0.43
1:F:287:TRP:CZ3	1:F:290:TRP:CZ3	3.06	0.43
1:F:345:ILE:O	1:F:346:THR:C	2.60	0.43
1:F:436:ARG:O	1:F:437:LYS:C	2.61	0.43
2:H:118:VAL:CG1	2:H:119:ASP:N	2.81	0.43
1:A:269:THR:C	1:A:271:SER:H	2.24	0.43
1:A:532:PHE:O	1:A:536:VAL:HG12	2.17	0.43
1:B:68:TYR:OH	1:B:103:VAL:HG11	2.18	0.43
1:B:128:ILE:C	1:B:130:TYR:H	2.25	0.43
1:B:345:ILE:O	1:B:346:THR:C	2.60	0.43
1:C:174:LEU:HD11	1:C:199:TYR:CZ	2.52	0.43
1:C:644:ILE:HA	2:H:173:TYR:OH	2.18	0.43
1:D:162:PHE:HA	1:D:309:ARG:NH1	2.34	0.43
1:E:121:LEU:HG	1:E:163:GLU:HG2	1.99	0.43
1:E:164:PRO:HG2	1:E:165:LYS:H	1.83	0.43
1:E:412:LYS:CE	1:E:448:LEU:HA	2.46	0.43
1:F:183:VAL:HG23	1:F:187:GLU:OE1	2.18	0.43
1:F:240:TYR:O	1:F:241:MET:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:487:GLU:N	1:F:521:LEU:HD22	2.33	0.43
1:A:364:PHE:CZ	1:A:421:VAL:CG1	2.86	0.43
1:A:462:TYR:HD1	1:A:471:ALA:HB3	1.84	0.43
1:B:225:ASN:HB2	1:B:228:THR:HB	2.00	0.43
1:B:281:VAL:O	1:B:284:LEU:N	2.51	0.43
1:C:160:ALA:C	1:C:162:PHE:H	2.26	0.43
1:C:527:GLN:HE21	1:C:561:GLU:CD	2.22	0.43
1:C:572:ASN:CG	1:C:575:GLN:HE21	2.26	0.43
1:D:164:PRO:HG3	1:D:250:TRP:CE2	2.54	0.43
1:D:275:LYS:CD	1:D:275:LYS:H	2.31	0.43
1:D:455:LEU:HD21	1:D:488:TYR:CD1	2.52	0.43
1:E:371:GLU:CA	1:E:379:ILE:HD11	2.45	0.43
1:F:105:GLU:HB2	1:F:106:PRO:HD3	2.00	0.43
2:G:169:PRO:HD2	2:G:170:GLN:NE2	2.32	0.43
1:A:41:ILE:HD11	1:A:51:TYR:HA	1.99	0.43
1:A:128:ILE:CD1	1:A:151:ALA:HB1	2.49	0.43
1:A:334:TYR:HA	1:A:337:GLU:HB3	2.01	0.43
1:A:418:VAL:HA	1:A:421:VAL:HG12	2.00	0.43
1:B:61:LEU:O	1:B:63:GLN:CG	2.63	0.43
1:B:254:THR:O	1:B:255:LYS:C	2.60	0.43
1:B:559:LEU:HD21	1:B:579:LEU:CD1	2.47	0.43
1:B:560:GLU:O	1:B:563:THR:N	2.51	0.43
1:D:52:VAL:HG21	1:D:268:ALA:HB1	2.00	0.43
1:D:167:ILE:CD1	1:D:209:CYS:HB3	2.49	0.43
1:D:168:GLN:O	1:D:169:PHE:C	2.60	0.43
1:D:240:TYR:O	1:D:243:ALA:HB3	2.19	0.43
1:E:206:PRO:HB3	1:E:247:TYR:CB	2.48	0.43
1:E:394:LEU:HA	1:E:411:LEU:CD2	2.49	0.43
1:E:420:CYS:C	1:E:422:TYR:N	2.77	0.43
1:F:125:LEU:HD11	1:F:168:GLN:HG3	2.01	0.43
1:F:434:ALA:HA	1:F:437:LYS:HE3	2.01	0.43
1:F:540:ASN:ND2	1:F:543:ARG:NH2	2.67	0.43
2:G:186:SER:C	2:G:189:GLN:HG2	2.42	0.43
2:I:185:CYS:HB3	2:I:189:GLN:NE2	2.33	0.43
1:A:51:TYR:CB	1:A:74:LEU:HD12	2.48	0.43
1:A:132:ARG:HH21	1:A:176:PHE:HD1	1.67	0.43
1:A:513:ILE:HD12	1:A:513:ILE:H	1.84	0.43
1:B:59:VAL:O	1:B:62:LYS:N	2.51	0.43
1:B:66:GLN:HE21	1:B:66:GLN:CA	2.31	0.43
1:B:489:ILE:HD12	1:B:508:LEU:HD11	2.01	0.43
1:F:125:LEU:C	1:F:127:TYR:N	2.74	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:341:ASP:CG	1:F:344:VAL:HG23	2.44	0.43
1:F:349:LEU:HB3	1:F:366:LEU:HG	2.01	0.43
1:F:387:ILE:HG22	1:F:388:ASP:N	2.33	0.43
1:A:87:MET:HG2	1:A:265:LEU:N	2.33	0.43
1:A:339:ASN:C	1:A:339:ASN:ND2	2.74	0.43
1:A:350:LYS:HA	1:A:366:LEU:HD11	2.00	0.43
1:A:579:LEU:HD23	1:A:579:LEU:HA	1.82	0.43
1:B:111:CYS:SG	1:B:112:LEU:HD23	2.58	0.43
1:B:127:TYR:O	1:B:131:VAL:HG23	2.19	0.43
1:C:479:LEU:O	1:C:480:LYS:C	2.60	0.43
1:D:80:LEU:HA	1:D:118:ASN:ND2	2.23	0.43
1:E:327:ILE:HG22	1:E:328:TRP:H	1.78	0.43
1:E:394:LEU:HD23	1:E:448:LEU:HD11	2.00	0.43
1:E:580:ASP:C	1:E:582:MET:N	2.75	0.43
1:F:254:THR:HG22	1:F:255:LYS:N	2.32	0.43
1:F:428:ARG:O	1:F:428:ARG:HG2	2.17	0.43
2:G:128:ALA:C	2:G:130:CYS:H	2.27	0.43
1:A:147:ILE:HG22	1:A:148:VAL:N	2.33	0.43
1:A:247:TYR:O	1:A:251:LEU:HB2	2.18	0.43
1:A:387:ILE:HD12	1:A:418:VAL:CG1	2.49	0.43
1:A:414:LYS:HB2	1:B:577:LEU:HD13	2.00	0.43
1:A:509:PHE:O	1:A:513:ILE:HG13	2.19	0.43
1:B:70:THR:O	1:B:71:PHE:C	2.61	0.43
1:B:121:LEU:O	1:B:123:LEU:N	2.52	0.43
1:B:350:LYS:NZ	1:B:354:GLN:HE21	2.15	0.43
1:B:501:GLU:HB3	1:B:504:GLN:HB2	2.00	0.43
1:C:335:GLN:OE1	1:C:335:GLN:HA	2.18	0.43
1:C:414:LYS:HA	1:D:577:LEU:HD13	2.00	0.43
1:D:54:LEU:HG	1:D:58:HIS:CD2	2.53	0.43
1:D:413:SER:O	1:D:414:LYS:C	2.62	0.43
1:E:203:LEU:HD22	1:E:240:TYR:CD1	2.54	0.43
1:E:331:MET:O	1:E:332:ALA:C	2.61	0.43
1:F:296:ASP:CB	1:F:298:LYS:HZ2	2.31	0.43
1:F:511:SER:O	1:F:515:LYS:HG3	2.19	0.43
1:F:533:GLU:HG3	1:F:545:LEU:HD12	2.01	0.43
1:F:567:LYS:HG2	1:F:572:ASN:HA	2.01	0.43
2:H:162:VAL:O	2:H:166:GLU:HG3	2.19	0.43
1:A:240:TYR:O	1:A:243:ALA:HB3	2.18	0.43
1:A:432:LEU:HD12	1:A:432:LEU:C	2.44	0.43
1:B:93:PHE:O	1:B:94:ASP:OD1	2.37	0.43
1:B:94:ASP:O	1:B:95:LYS:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:394:LEU:HD11	1:C:412:LYS:HG3	2.01	0.43
1:C:546:GLU:O	1:C:549:PHE:N	2.52	0.43
1:D:60:SER:O	1:D:61:LEU:HD23	2.18	0.43
1:D:339:ASN:ND2	1:D:340:THR:O	2.52	0.43
1:E:87:MET:SD	1:E:268:ALA:HB2	2.59	0.43
1:E:376:ILE:HB	1:E:377:PRO:HD3	1.99	0.43
1:F:392:LEU:C	1:F:394:LEU:H	2.25	0.43
1:F:471:ALA:HB1	1:F:495:PHE:CZ	2.54	0.43
1:A:333:ASN:HD22	1:A:333:ASN:HA	1.68	0.43
1:A:394:LEU:HD12	1:A:411:LEU:HD23	2.01	0.43
1:A:496:LEU:HB3	1:A:505:VAL:HG22	2.01	0.43
1:B:133:LYS:C	1:B:135:ASN:H	2.27	0.43
1:B:550:PHE:HE2	1:B:558:LYS:HD2	1.84	0.43
1:C:131:VAL:HG11	1:C:151:ALA:CB	2.47	0.43
1:C:323:PHE:CE2	1:C:355:CYS:O	2.72	0.43
1:D:170:TRP:HA	1:D:170:TRP:CE3	2.53	0.43
1:D:513:ILE:CG2	1:D:552:LYS:HE2	2.49	0.43
1:E:107:VAL:HA	1:E:110:ARG:CG	2.47	0.43
1:E:324:ALA:O	1:E:327:ILE:HG22	2.18	0.43
1:E:394:LEU:HA	1:E:411:LEU:HD21	2.01	0.43
1:E:532:PHE:O	1:E:535:LYS:N	2.49	0.43
1:E:573:TYR:C	1:E:575:GLN:N	2.72	0.43
1:E:653:PHE:O	1:E:657:LYS:HB3	2.18	0.43
1:F:54:LEU:HG	1:F:58:HIS:HD2	1.84	0.43
1:F:248:GLN:O	1:F:251:LEU:N	2.51	0.43
2:I:135:LEU:HD22	2:I:178:LEU:HD21	2.01	0.43
1:A:49:PHE:CZ	1:A:53:LYS:HD3	2.54	0.43
1:A:246:LEU:HD23	1:A:246:LEU:HA	1.78	0.43
1:A:542:VAL:HG12	1:A:543:ARG:N	2.34	0.43
1:B:128:ILE:HD13	1:B:152:PHE:CE1	2.54	0.43
1:B:490:ASN:OD1	1:B:525:ILE:HD13	2.18	0.43
1:B:501:GLU:O	1:B:502:GLU:C	2.61	0.43
1:C:398:MET:O	1:C:402:PRO:HD3	2.18	0.43
1:D:36:LYS:HA	1:D:39:ASP:OD2	2.18	0.43
1:D:294:GLU:OE1	1:D:309:ARG:NE	2.45	0.43
1:D:574:LEU:HD22	1:D:574:LEU:HA	1.78	0.43
1:E:170:TRP:CZ3	1:E:198:LEU:HD13	2.54	0.43
1:E:281:VAL:HG21	1:F:581:TYR:CD2	2.54	0.43
1:E:560:GLU:O	1:E:561:GLU:C	2.62	0.43
1:F:81:MET:HE1	1:F:319:GLN:O	2.19	0.43
1:F:125:LEU:HD11	1:F:168:GLN:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:140:GLY:C	1:F:142:GLU:H	2.27	0.43
1:F:156:VAL:HG13	1:F:170:TRP:HH2	1.83	0.43
2:I:118:VAL:CG1	2:I:119:ASP:N	2.82	0.43
1:A:150:GLN:O	1:A:151:ALA:C	2.61	0.42
1:A:462:TYR:HD1	1:A:471:ALA:CB	2.32	0.42
1:B:56:LYS:C	1:B:59:VAL:HG12	2.43	0.42
1:B:195:ILE:HG22	1:B:199:TYR:CD2	2.54	0.42
1:B:553:PHE:N	1:B:554:PRO:HD3	2.34	0.42
1:C:295:SER:C	1:C:297:ASN:N	2.76	0.42
1:D:160:ALA:C	1:D:162:PHE:N	2.76	0.42
1:E:439:PHE:CD2	1:E:457:ASN:OD1	2.72	0.42
1:E:539:LEU:HD22	1:F:371:GLU:HB3	2.01	0.42
2:I:155:LYS:O	2:I:156:ASP:HB3	2.18	0.42
2:I:170:GLN:NE2	2:I:170:GLN:N	2.55	0.42
1:A:101:ALA:HB1	1:A:105:GLU:CG	2.49	0.42
1:A:244:ARG:O	1:A:247:TYR:N	2.51	0.42
1:A:290:TRP:O	1:A:293:TRP:HB3	2.19	0.42
1:A:493:LEU:O	1:A:497:ILE:HG13	2.19	0.42
1:A:557:ASN:OD1	1:A:557:ASN:C	2.62	0.42
1:B:66:GLN:NE2	1:B:66:GLN:CA	2.82	0.42
1:B:149:ILE:O	1:B:152:PHE:N	2.51	0.42
1:B:553:PHE:O	1:B:556:VAL:HB	2.19	0.42
1:B:560:GLU:O	1:B:561:GLU:C	2.61	0.42
1:C:121:LEU:HD12	1:C:163:GLU:HG2	2.02	0.42
1:C:628:VAL:O	1:C:630:LEU:N	2.52	0.42
1:D:63:GLN:O	1:D:67:VAL:HG23	2.19	0.42
1:D:182:PRO:HD3	1:D:191:ARG:HH11	1.81	0.42
1:E:88:ARG:NH2	1:E:107:VAL:HG21	2.34	0.42
1:E:349:LEU:CD1	1:E:365:SER:HB3	2.49	0.42
1:E:526:PHE:O	1:E:527:GLN:C	2.60	0.42
1:E:641:LYS:C	1:E:643:THR:H	2.27	0.42
1:F:152:PHE:CG	1:F:173:TYR:HD1	2.37	0.42
1:F:286:ILE:O	1:F:287:TRP:C	2.60	0.42
2:G:148:LYS:O	2:G:151:GLN:HB3	2.19	0.42
1:A:182:PRO:HB3	1:A:188:GLU:CB	2.48	0.42
1:A:191:ARG:NH1	1:A:191:ARG:HG3	2.32	0.42
1:A:412:LYS:NZ	1:A:447:LYS:O	2.49	0.42
1:A:636:LYS:HG3	2:G:118:VAL:O	2.20	0.42
1:B:347:LYS:HG2	1:B:348:TYR:N	2.33	0.42
1:C:48:ILE:O	1:C:49:PHE:C	2.61	0.42
1:D:81:MET:HE2	1:D:319:GLN:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:122:SER:O	1:D:125:LEU:N	2.51	0.42
1:E:255:LYS:HB3	1:E:256:GLY:H	1.67	0.42
1:E:348:TYR:O	1:E:349:LEU:C	2.61	0.42
1:E:349:LEU:HD11	1:E:365:SER:HB3	2.01	0.42
1:E:432:LEU:HD21	1:E:436:ARG:HH21	1.84	0.42
1:F:432:LEU:HD13	1:F:464:ILE:CD1	2.49	0.42
1:F:462:TYR:HA	1:F:467:ASP:O	2.19	0.42
2:H:125:THR:HG22	2:H:126:THR:N	2.33	0.42
2:H:135:LEU:HD13	2:H:177:GLU:HB3	2.01	0.42
2:H:174:ALA:O	2:H:177:GLU:HB3	2.19	0.42
2:H:187:VAL:O	2:H:187:VAL:HG12	2.19	0.42
1:A:71:PHE:CZ	1:A:88:ARG:HA	2.53	0.42
1:A:167:ILE:CG1	1:A:171:ASN:HD21	2.32	0.42
1:A:174:LEU:HD11	1:A:199:TYR:CE1	2.54	0.42
1:A:340:THR:HB	1:A:341:ASP:H	1.63	0.42
1:B:99:LEU:CD2	1:B:133:LYS:HD2	2.49	0.42
1:B:203:LEU:HD13	1:B:214:TRP:HE3	1.83	0.42
1:B:544:THR:O	1:B:547:LYS:HB3	2.19	0.42
1:C:101:ALA:HB2	1:C:134:LYS:HZ1	1.83	0.42
1:C:349:LEU:CD1	1:C:365:SER:HB3	2.49	0.42
1:C:562:PHE:CZ	1:C:566:TYR:CE2	3.08	0.42
1:D:106:PRO:O	1:D:109:ALA:HB3	2.20	0.42
1:D:292:ARG:O	1:D:293:TRP:C	2.62	0.42
1:D:468:THR:HG23	1:D:499:VAL:HG11	1.90	0.42
1:E:88:ARG:O	1:E:92:GLU:OE1	2.38	0.42
1:F:247:TYR:O	1:F:250:TRP:HB3	2.19	0.42
1:F:398:MET:HG2	1:F:408:ILE:CD1	2.33	0.42
1:F:399:GLU:C	1:F:401:ASP:H	2.28	0.42
1:F:413:SER:O	1:F:414:LYS:C	2.63	0.42
1:F:436:ARG:O	1:F:439:PHE:N	2.50	0.42
2:H:138:LEU:HD22	2:H:142:GLN:CD	2.44	0.42
1:A:156:VAL:O	1:A:161:ILE:HG12	2.19	0.42
1:B:38:ASN:HD21	1:B:54:LEU:CD2	2.33	0.42
1:B:543:ARG:HD3	1:B:543:ARG:HA	1.82	0.42
1:B:560:GLU:C	1:B:562:PHE:N	2.75	0.42
1:D:78:PHE:CD1	1:D:78:PHE:N	2.87	0.42
1:D:140:GLY:O	1:D:142:GLU:N	2.53	0.42
1:D:580:ASP:C	1:D:582:MET:H	2.28	0.42
1:E:41:ILE:HD11	1:E:50:LEU:O	2.19	0.42
1:E:325:PRO:C	1:E:327:ILE:N	2.77	0.42
1:E:479:LEU:CD1	1:E:492:TYR:HE2	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:84:ILE:O	1:F:84:ILE:HG22	2.18	0.42
1:F:107:VAL:HG12	1:F:108:LEU:N	2.33	0.42
1:F:235:GLU:C	1:F:237:SER:H	2.26	0.42
1:F:272:ASN:OD1	1:F:273:LEU:HG	2.20	0.42
1:F:321:VAL:O	1:F:321:VAL:HG23	2.19	0.42
1:F:489:ILE:HG13	1:F:516:ILE:CD1	2.37	0.42
1:A:89:LEU:HD11	1:A:108:LEU:CD2	2.49	0.42
1:A:434:ALA:O	1:A:435:SER:C	2.61	0.42
1:A:638:GLN:HE21	1:A:638:GLN:HB2	1.66	0.42
1:A:648:HIS:O	1:A:651:SER:HB2	2.20	0.42
1:B:425:THR:HG22	1:B:426:MET:CE	2.50	0.42
1:C:121:LEU:HD11	1:C:166:SER:HB3	2.01	0.42
1:C:135:ASN:ND2	1:C:147:ILE:CG2	2.83	0.42
1:D:59:VAL:HG22	1:D:67:VAL:CG2	2.49	0.42
1:D:154:VAL:HG13	1:D:155:VAL:N	2.34	0.42
1:E:305:LEU:O	1:E:306:HIS:C	2.63	0.42
1:E:405:GLU:HG3	1:E:406:SER:H	1.84	0.42
1:E:499:VAL:O	1:E:499:VAL:HG12	2.18	0.42
1:E:572:ASN:ND2	1:E:575:GLN:NE2	2.67	0.42
1:E:573:TYR:C	1:E:575:GLN:H	2.27	0.42
1:F:206:PRO:HA	1:F:210:LEU:HD11	2.01	0.42
1:F:267:GLN:O	1:F:269:THR:HG23	2.19	0.42
1:A:51:TYR:N	1:A:51:TYR:HD2	2.17	0.42
1:A:151:ALA:O	1:A:152:PHE:C	2.62	0.42
1:A:181:LYS:CD	1:A:181:LYS:H	2.32	0.42
1:A:219:GLN:NE2	1:A:220:TRP:N	2.68	0.42
1:A:349:LEU:HD23	1:A:349:LEU:HA	1.71	0.42
1:A:467:ASP:OD1	1:A:467:ASP:O	2.38	0.42
1:B:169:PHE:O	1:B:170:TRP:C	2.62	0.42
1:C:30:GLU:CG	1:C:31:SER:H	2.27	0.42
1:C:167:ILE:CD1	1:C:209:CYS:HB3	2.50	0.42
1:C:256:GLY:O	1:C:283:GLN:OE1	2.37	0.42
1:C:270:GLU:O	1:C:270:GLU:HG2	2.19	0.42
1:C:546:GLU:HA	1:C:549:PHE:HB3	2.01	0.42
1:E:136:ASP:HB3	1:E:139:THR:CB	2.49	0.42
1:E:142:GLU:O	1:E:146:ASN:ND2	2.53	0.42
1:E:434:ALA:HB2	1:E:437:LYS:HZ1	1.85	0.42
1:E:506:LYS:O	1:E:510:GLU:HB2	2.19	0.42
1:E:523:LYS:HB2	1:E:553:PHE:HE2	1.85	0.42
1:E:653:PHE:CD1	1:E:657:LYS:HD3	2.55	0.42
1:F:169:PHE:O	1:F:170:TRP:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:LEU:HD12	1:A:203:LEU:HG	2.02	0.42
1:A:248:GLN:O	1:A:251:LEU:N	2.53	0.42
1:A:327:ILE:HD12	1:A:327:ILE:HA	1.81	0.42
1:A:348:TYR:O	1:A:349:LEU:C	2.63	0.42
1:A:656:ASP:OD2	1:A:657:LYS:HG3	2.19	0.42
1:B:99:LEU:CD1	1:B:133:LYS:HD3	2.49	0.42
1:B:167:ILE:O	1:B:171:ASN:ND2	2.53	0.42
1:B:194:TYR:N	1:B:194:TYR:CD1	2.88	0.42
1:B:356:ILE:C	1:B:358:ASN:N	2.78	0.42
1:C:55:LEU:HB3	1:C:265:LEU:HD11	2.02	0.42
1:C:140:GLY:C	1:C:142:GLU:H	2.27	0.42
1:C:641:LYS:HE3	1:D:437:LYS:NZ	2.35	0.42
1:D:420:CYS:SG	1:D:453:ILE:HD12	2.60	0.42
1:D:502:GLU:O	1:D:503:SER:C	2.63	0.42
1:E:56:LYS:HG3	1:E:265:LEU:CD2	2.49	0.42
1:E:263:ILE:HG22	1:E:267:GLN:HE22	1.84	0.42
1:E:405:GLU:O	1:E:407:ALA:N	2.52	0.42
1:E:654:LEU:HG	2:I:151:GLN:OE1	2.20	0.42
1:F:57:HIS:O	1:F:57:HIS:HD2	2.03	0.42
1:F:115:GLU:C	1:F:117:GLY:H	2.27	0.42
1:F:262:PRO:HG3	1:F:273:LEU:HD21	2.01	0.42
1:F:335:GLN:O	1:F:339:ASN:OD1	2.38	0.42
1:F:383:ILE:HG21	1:F:422:TYR:HB2	2.01	0.42
1:F:462:TYR:CZ	1:F:499:VAL:HG22	2.54	0.42
2:I:130:CYS:O	2:I:134:GLU:HB2	2.19	0.42
1:A:404:ASN:OD1	1:A:404:ASN:C	2.62	0.42
1:A:526:PHE:O	1:A:527:GLN:C	2.63	0.42
1:C:101:ALA:HB2	1:C:134:LYS:HE2	2.01	0.42
1:C:432:LEU:O	1:C:435:SER:HB3	2.20	0.42
1:D:104:ILE:HG21	1:D:130:TYR:CD1	2.54	0.42
1:D:337:GLU:O	1:D:339:ASN:N	2.52	0.42
1:E:350:LYS:O	1:E:354:GLN:HG3	2.20	0.42
1:E:401:ASP:OD2	1:E:404:ASN:HB2	2.20	0.42
1:E:439:PHE:CG	1:E:457:ASN:OD1	2.73	0.42
1:F:104:ILE:O	1:F:107:VAL:HB	2.20	0.42
2:G:150:ILE:HG21	2:G:175:ILE:CD1	2.48	0.42
2:I:179:LEU:HB3	2:I:184:VAL:CB	2.49	0.42
1:A:178:GLU:C	1:A:180:TRP:N	2.78	0.42
1:A:253:ILE:HG23	1:A:289:GLU:HG3	2.02	0.42
1:A:376:ILE:O	1:A:377:PRO:C	2.61	0.42
1:A:579:LEU:HD13	1:A:582:MET:CE	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:VAL:CG1	1:B:60:SER:H	2.32	0.42
1:B:219:GLN:HE21	1:B:220:TRP:N	2.18	0.42
1:C:229:ALA:C	1:C:231:ARG:H	2.27	0.42
1:C:552:LYS:HB2	1:C:552:LYS:NZ	2.35	0.42
1:C:556:VAL:O	1:C:558:LYS:N	2.52	0.42
1:C:569:LEU:O	1:C:571:VAL:N	2.53	0.42
1:D:261:LEU:HD22	1:D:262:PRO:HD2	2.02	0.42
1:D:347:LYS:O	1:D:350:LYS:HB3	2.19	0.42
1:D:383:ILE:HG21	1:D:422:TYR:CD1	2.54	0.42
1:E:135:ASN:HD21	1:E:147:ILE:HG21	1.85	0.42
1:E:323:PHE:C	1:E:356:ILE:HD11	2.45	0.42
1:F:383:ILE:HG21	1:F:422:TYR:CD1	2.55	0.42
1:F:401:ASP:O	1:F:403:THR:N	2.53	0.42
2:H:112:PRO:O	2:H:114:LEU:N	2.53	0.42
1:A:128:ILE:HD12	1:A:151:ALA:HB1	2.02	0.41
1:A:174:LEU:O	1:A:178:GLU:N	2.51	0.41
1:A:202:LEU:O	1:A:207:MET:HE2	2.20	0.41
1:A:269:THR:C	1:A:271:SER:N	2.78	0.41
1:A:442:CYS:O	1:A:445:LEU:N	2.51	0.41
1:B:56:LYS:HE3	1:B:265:LEU:O	2.19	0.41
1:B:64:TRP:CH2	1:B:95:LYS:HD2	2.55	0.41
1:B:257:LEU:HB2	1:B:286:ILE:HG21	2.02	0.41
1:B:311:THR:O	1:B:315:MET:HG2	2.20	0.41
1:B:335:GLN:HB3	1:B:344:VAL:CG1	2.50	0.41
1:B:439:PHE:O	1:B:442:CYS:HB2	2.20	0.41
1:C:232:HIS:C	1:C:234:GLY:H	2.28	0.41
1:C:401:ASP:C	1:C:403:THR:N	2.78	0.41
1:C:509:PHE:O	1:C:510:GLU:C	2.63	0.41
1:C:559:LEU:HA	1:D:329:PHE:CE1	2.50	0.41
1:D:44:GLN:N	1:D:45:PRO:HD2	2.34	0.41
1:D:72:ASP:C	1:D:74:LEU:N	2.76	0.41
1:D:124:TRP:CE3	1:D:155:VAL:HG22	2.54	0.41
1:D:169:PHE:CD2	1:D:169:PHE:C	2.97	0.41
1:D:485:ASP:OD1	1:D:487:GLU:HB3	2.19	0.41
1:D:509:PHE:CE2	1:D:513:ILE:HD11	2.55	0.41
1:E:372:LEU:HD11	1:F:543:ARG:CZ	2.49	0.41
1:E:577:LEU:HD13	1:F:414:LYS:HB2	2.02	0.41
1:F:48:ILE:O	1:F:49:PHE:C	2.62	0.41
1:F:258:LYS:HE3	1:F:260:ASN:CG	2.45	0.41
2:G:169:PRO:HD2	2:G:170:GLN:HE22	1.85	0.41
1:A:202:LEU:HD13	1:A:207:MET:CE	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:501:GLU:HB3	1:A:504:GLN:HB2	2.01	0.41
1:A:632:LYS:CG	2:G:115:PRO:HG2	2.42	0.41
1:B:89:LEU:C	1:B:91:LEU:H	2.28	0.41
1:B:149:ILE:HD13	1:B:194:TYR:CE2	2.55	0.41
1:B:501:GLU:C	1:B:505:VAL:HG23	2.45	0.41
1:C:287:TRP:CZ3	1:C:290:TRP:CZ3	3.08	0.41
1:C:378:GLU:O	1:C:379:ILE:C	2.62	0.41
1:C:423:MET:CB	1:C:438:ILE:HG21	2.48	0.41
1:C:482:PHE:C	1:C:484:THR:H	2.27	0.41
1:E:64:TRP:HE3	1:E:68:TYR:HE2	1.68	0.41
1:E:143:GLU:C	1:E:145:ARG:N	2.78	0.41
1:E:228:THR:HG22	1:E:231:ARG:HE	1.80	0.41
1:E:275:LYS:O	1:E:278:GLU:HB2	2.19	0.41
1:E:555:GLU:CD	1:E:555:GLU:O	2.63	0.41
1:F:509:PHE:CG	1:F:529:VAL:HG21	2.54	0.41
1:F:560:GLU:O	1:F:561:GLU:C	2.62	0.41
2:G:127:PRO:O	2:G:130:CYS:HB3	2.21	0.41
2:G:139:GLN:C	2:G:141:ASP:N	2.79	0.41
1:A:335:GLN:OE1	1:A:335:GLN:HA	2.20	0.41
1:A:475:LEU:HD13	1:A:492:TYR:CD1	2.56	0.41
1:A:548:ARG:NH1	1:A:548:ARG:CG	2.73	0.41
1:A:556:VAL:HG22	1:A:561:GLU:HG2	2.01	0.41
1:B:101:ALA:HB2	1:B:130:TYR:OH	2.20	0.41
1:B:340:THR:OG1	1:B:341:ASP:N	2.53	0.41
1:B:427:LYS:CB	1:B:435:SER:HB3	2.50	0.41
1:C:229:ALA:C	1:C:231:ARG:N	2.76	0.41
1:C:366:LEU:HD23	1:C:366:LEU:HA	1.82	0.41
1:C:370:TYR:HB2	1:C:379:ILE:HG12	2.02	0.41
1:D:80:LEU:CA	1:D:118:ASN:HD21	2.22	0.41
1:E:442:CYS:HA	1:E:445:LEU:HD12	2.01	0.41
1:E:479:LEU:HD23	1:E:483:ALA:CA	2.42	0.41
1:F:59:VAL:C	1:F:61:LEU:N	2.78	0.41
1:F:71:PHE:HE2	1:F:88:ARG:HB2	1.79	0.41
1:F:154:VAL:O	1:F:158:LYS:HB2	2.20	0.41
1:F:195:ILE:HG22	1:F:199:TYR:HD2	1.84	0.41
1:F:316:GLN:O	1:F:319:GLN:HB3	2.20	0.41
1:F:408:ILE:O	1:F:412:LYS:HB2	2.20	0.41
1:F:494:ASP:O	1:F:498:TYR:N	2.52	0.41
2:H:190:LEU:O	2:H:193:LEU:HG	2.20	0.41
1:A:166:SER:OG	1:A:170:TRP:NE1	2.53	0.41
1:A:367:SER:HB2	1:A:379:ILE:HG23	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:33:VAL:O	1:D:35:GLY:N	2.53	0.41
1:D:54:LEU:HG	1:D:58:HIS:HD2	1.85	0.41
1:D:167:ILE:CG2	1:D:168:GLN:N	2.84	0.41
1:D:167:ILE:CG1	1:D:171:ASN:ND2	2.84	0.41
1:E:339:ASN:ND2	1:E:340:THR:H	2.18	0.41
1:E:412:LYS:HE2	1:E:448:LEU:CA	2.47	0.41
1:E:638:GLN:OE1	1:E:638:GLN:N	2.53	0.41
1:F:401:ASP:C	1:F:403:THR:H	2.27	0.41
1:F:471:ALA:O	1:F:475:LEU:HD12	2.20	0.41
1:F:550:PHE:O	1:F:554:PRO:HG3	2.19	0.41
2:H:155:LYS:HE2	2:H:155:LYS:HB2	1.91	0.41
2:H:185:CYS:HB3	2:H:186:SER:H	1.56	0.41
1:A:103:VAL:C	1:A:106:PRO:HD2	2.46	0.41
1:A:344:VAL:O	1:A:347:LYS:HB3	2.20	0.41
1:B:202:LEU:HD13	1:B:207:MET:CE	2.50	0.41
1:B:236:LEU:O	1:B:237:SER:C	2.61	0.41
1:C:48:ILE:HD12	1:C:48:ILE:H	1.84	0.41
1:C:80:LEU:HD23	1:C:80:LEU:HA	1.75	0.41
1:C:150:GLN:O	1:C:154:VAL:HG12	2.21	0.41
1:D:140:GLY:C	1:D:142:GLU:N	2.79	0.41
1:E:115:GLU:C	1:E:117:GLY:H	2.28	0.41
1:E:346:THR:O	1:E:350:LYS:HB2	2.20	0.41
1:E:479:LEU:O	1:E:480:LYS:C	2.64	0.41
1:A:34:ILE:HD11	1:A:57:HIS:NE2	2.36	0.41
1:A:81:MET:O	1:A:84:ILE:HB	2.21	0.41
1:A:167:ILE:HG12	1:A:171:ASN:HD21	1.85	0.41
1:A:523:LYS:O	1:A:527:GLN:HG3	2.20	0.41
1:A:550:PHE:N	1:A:550:PHE:CD2	2.89	0.41
1:A:637:ARG:H	1:A:637:ARG:HG3	1.46	0.41
1:B:121:LEU:C	1:B:123:LEU:N	2.78	0.41
1:B:123:LEU:HD12	1:B:123:LEU:HA	1.82	0.41
1:C:173:TYR:CE2	1:C:198:LEU:HD22	2.56	0.41
1:C:579:LEU:O	1:C:581:TYR:N	2.54	0.41
1:D:33:VAL:O	1:D:34:ILE:C	2.64	0.41
1:D:74:LEU:O	1:D:77:ARG:N	2.43	0.41
1:D:218:THR:HG23	1:D:233:ILE:HD13	2.02	0.41
1:E:150:GLN:O	1:E:154:VAL:HG12	2.21	0.41
1:E:284:LEU:CD1	1:E:288:LEU:HD21	2.50	0.41
1:E:539:LEU:HD22	1:F:371:GLU:CG	2.51	0.41
1:F:492:TYR:O	1:F:492:TYR:HD1	2.04	0.41
2:G:138:LEU:O	2:G:139:GLN:O	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:HIS:C	1:B:59:VAL:H	2.29	0.41
1:B:152:PHE:HB3	1:B:173:TYR:CE1	2.55	0.41
1:B:190:GLN:O	1:B:193:GLN:HB2	2.21	0.41
1:B:228:THR:O	1:B:230:ARG:N	2.54	0.41
1:B:281:VAL:HG12	1:B:285:LEU:CD1	2.48	0.41
1:B:564:ASN:C	1:B:566:TYR:N	2.75	0.41
1:C:180:TRP:CZ3	1:C:191:ARG:HB2	2.55	0.41
1:C:210:LEU:CD1	1:C:244:ARG:HA	2.49	0.41
1:D:71:PHE:CD2	1:D:88:ARG:HD2	2.55	0.41
1:D:125:LEU:HD23	1:D:125:LEU:HA	1.87	0.41
1:D:160:ALA:O	1:D:162:PHE:N	2.53	0.41
1:D:242:ASN:O	1:D:242:ASN:ND2	2.54	0.41
1:D:251:LEU:HD12	1:D:251:LEU:HA	1.81	0.41
1:D:270:GLU:O	1:D:270:GLU:HG2	2.21	0.41
1:D:394:LEU:HD23	1:D:448:LEU:HD11	2.01	0.41
1:E:74:LEU:O	1:E:75:HIS:C	2.63	0.41
1:E:174:LEU:HD11	1:E:199:TYR:OH	2.21	0.41
1:E:228:THR:HA	1:E:231:ARG:HG2	2.01	0.41
1:E:254:THR:HG23	1:E:257:LEU:HB2	2.02	0.41
1:E:299:LEU:O	1:E:300:GLU:HB2	2.20	0.41
1:F:501:GLU:O	1:F:504:GLN:N	2.40	0.41
1:F:574:LEU:HD23	1:F:574:LEU:HA	1.81	0.41
1:A:57:HIS:C	1:A:59:VAL:H	2.28	0.41
1:A:199:TYR:C	1:A:201:THR:N	2.79	0.41
1:A:261:LEU:CD1	1:A:319:GLN:HE21	2.33	0.41
1:B:194:TYR:O	1:B:195:ILE:C	2.64	0.41
1:B:502:GLU:OE1	1:B:502:GLU:HA	2.21	0.41
1:C:235:GLU:C	1:C:237:SER:H	2.29	0.41
1:C:396:ALA:O	1:C:397:LEU:C	2.63	0.41
2:G:190:LEU:HA	2:G:193:LEU:CD2	2.45	0.41
1:A:40:MET:HG2	1:A:50:LEU:HD11	2.03	0.41
1:A:82:ALA:HB1	1:A:120:ASP:OD2	2.21	0.41
1:A:83:ASN:HB2	1:A:87:MET:HE2	2.03	0.41
1:A:85:TRP:CE2	1:A:111:CYS:HB3	2.56	0.41
1:A:181:LYS:H	1:A:181:LYS:HD2	1.85	0.41
1:A:241:MET:HE1	1:A:244:ARG:HD3	2.03	0.41
1:A:520:HIS:ND1	1:A:520:HIS:C	2.77	0.41
1:B:64:TRP:CE3	1:B:68:TYR:HE2	2.29	0.41
1:B:259:ARG:HD3	1:B:287:TRP:HH2	1.83	0.41
1:B:262:PRO:CB	1:B:272:ASN:HD21	2.29	0.41
1:B:398:MET:C	1:B:400:ASP:N	2.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:468:THR:O	1:B:471:ALA:HB3	2.21	0.41
1:B:493:LEU:O	1:B:497:ILE:HG13	2.20	0.41
1:B:495:PHE:HB3	1:B:496:LEU:H	1.76	0.41
1:B:533:GLU:O	1:B:534:SER:C	2.63	0.41
1:B:536:VAL:HG13	1:B:537:GLY:N	2.35	0.41
1:C:457:ASN:HA	1:C:460:ILE:HD12	2.03	0.41
1:C:579:LEU:O	1:C:580:ASP:C	2.64	0.41
1:D:101:ALA:HB2	1:D:134:LYS:NZ	2.35	0.41
1:D:163:GLU:OE1	1:D:312:TYR:OH	2.34	0.41
1:D:169:PHE:HD2	1:D:170:TRP:N	2.18	0.41
1:D:341:ASP:C	1:D:343:THR:H	2.28	0.41
1:D:542:VAL:C	1:D:544:THR:N	2.78	0.41
1:E:42:GLU:OE1	1:E:43:GLU:HG3	2.21	0.41
1:E:43:GLU:O	1:E:44:GLN:CG	2.69	0.41
1:E:48:ILE:O	1:E:51:TYR:HB2	2.20	0.41
1:E:49:PHE:CZ	1:E:270:GLU:HB2	2.56	0.41
1:E:54:LEU:HD12	1:E:54:LEU:HA	1.78	0.41
1:E:458:ALA:C	1:E:460:ILE:H	2.29	0.41
1:E:636:LYS:HG2	2:I:116:VAL:O	2.20	0.41
1:F:37:LEU:HD12	1:F:37:LEU:N	2.35	0.41
1:F:227:LEU:HD12	1:F:227:LEU:N	2.36	0.41
1:F:317:ALA:O	1:F:321:VAL:HG22	2.21	0.41
1:F:339:ASN:HD22	1:F:340:THR:H	1.69	0.41
1:F:358:ASN:HB3	1:F:389:ARG:HG2	2.02	0.41
1:F:399:GLU:CG	1:F:400:ASP:N	2.84	0.41
1:F:463:HIS:HE1	1:F:498:TYR:CE2	2.36	0.41
1:F:544:THR:O	1:F:547:LYS:HB3	2.21	0.41
1:F:563:THR:HG21	1:F:575:GLN:HE21	1.86	0.41
1:F:572:ASN:OD1	1:F:572:ASN:O	2.38	0.41
2:G:139:GLN:HB2	2:G:142:GLN:OE1	2.21	0.41
2:H:185:CYS:SG	2:H:188:ASP:CB	3.09	0.41
1:A:80:LEU:CD1	1:A:315:MET:HE1	2.49	0.41
1:A:178:GLU:C	1:A:180:TRP:H	2.29	0.41
1:B:23:PRO:HA	1:B:26:ARG:HG2	2.03	0.41
1:B:189:GLN:HE21	1:B:189:GLN:HB3	1.54	0.41
1:B:462:TYR:CZ	1:B:468:THR:HG23	2.54	0.41
1:B:503:SER:O	1:B:506:LYS:N	2.54	0.41
1:C:59:VAL:C	1:C:61:LEU:N	2.79	0.41
1:C:217:TYR:CZ	1:C:236:LEU:HD12	2.56	0.41
1:C:434:ALA:O	1:C:435:SER:C	2.64	0.41
1:C:457:ASN:O	1:C:461:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:LEU:CD2	1:D:54:LEU:HA	2.50	0.41
1:E:262:PRO:HG3	1:E:273:LEU:CD2	2.50	0.41
1:E:291:ILE:HG21	1:E:314:TYR:CZ	2.56	0.41
1:E:525:ILE:O	1:E:529:VAL:HG23	2.21	0.41
1:E:656:ASP:O	1:E:657:LYS:HB2	2.20	0.41
1:F:107:VAL:C	1:F:109:ALA:N	2.77	0.41
1:F:115:GLU:HG2	1:F:116:LEU:H	1.86	0.41
1:F:170:TRP:NE1	1:F:207:MET:SD	2.94	0.41
1:F:339:ASN:ND2	1:F:340:THR:H	2.18	0.41
1:F:367:SER:O	1:F:379:ILE:HG12	2.21	0.41
1:F:470:THR:O	1:F:471:ALA:C	2.64	0.41
2:G:146:LEU:O	2:G:149:VAL:N	2.54	0.41
2:G:168:ALA:HA	2:G:170:GLN:NE2	2.30	0.41
2:H:113:TRP:O	2:H:114:LEU:C	2.64	0.41
1:A:231:ARG:HB3	1:A:231:ARG:HH11	1.86	0.40
1:A:284:LEU:HG	1:A:288:LEU:CD1	2.50	0.40
1:A:307:LYS:CE	1:A:338:LYS:HG3	2.51	0.40
1:A:638:GLN:C	1:A:641:LYS:HE3	2.46	0.40
1:B:173:TYR:O	1:B:176:PHE:HB3	2.21	0.40
1:B:305:LEU:HA	1:B:305:LEU:HD23	1.86	0.40
1:B:307:LYS:CD	1:B:338:LYS:HG3	2.51	0.40
1:C:134:LYS:HD3	1:C:134:LYS:HA	1.80	0.40
1:C:539:LEU:HD22	1:D:371:GLU:HB3	2.02	0.40
1:D:72:ASP:O	1:D:73:LYS:C	2.64	0.40
1:D:186:PHE:HE1	1:D:189:GLN:NE2	2.18	0.40
1:D:206:PRO:HA	1:D:210:LEU:HD11	2.04	0.40
1:D:451:PRO:HG3	1:D:482:PHE:CG	2.56	0.40
1:D:538:SER:O	1:D:539:LEU:C	2.64	0.40
1:E:184:ASN:HB2	1:E:185:LYS:H	1.58	0.40
1:E:477:LEU:N	1:E:477:LEU:CD1	2.84	0.40
1:E:639:TYR:CE1	2:I:120:VAL:HB	2.56	0.40
1:F:174:LEU:HD11	1:F:199:TYR:CZ	2.55	0.40
1:F:225:ASN:O	1:F:227:LEU:N	2.54	0.40
1:F:376:ILE:O	1:F:379:ILE:HB	2.21	0.40
1:F:530:ILE:CG1	1:F:545:LEU:HD22	2.51	0.40
2:G:156:ASP:O	2:G:159:GLU:N	2.54	0.40
1:A:56:LYS:HE3	1:A:265:LEU:O	2.22	0.40
1:A:190:GLN:O	1:A:193:GLN:HB2	2.21	0.40
1:A:211:GLU:HA	1:A:240:TYR:OH	2.20	0.40
1:A:299:LEU:HB2	1:A:301:LEU:HG	2.04	0.40
1:A:394:LEU:HD21	1:A:448:LEU:HD11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:LEU:HD12	1:B:299:LEU:HD23	2.04	0.40
1:B:453:ILE:HA	1:B:453:ILE:HD12	1.81	0.40
1:C:124:TRP:NE1	1:C:159:CYS:HB2	2.36	0.40
1:C:509:PHE:CE2	1:C:513:ILE:HD11	2.56	0.40
1:D:81:MET:CE	1:D:322:CYS:HB3	2.51	0.40
1:D:131:VAL:HG11	1:D:151:ALA:CB	2.51	0.40
1:E:134:LYS:HA	1:E:134:LYS:HD3	1.87	0.40
1:E:307:LYS:HD2	1:E:334:TYR:OH	2.21	0.40
1:E:382:THR:HG23	1:E:383:ILE:N	2.35	0.40
2:I:179:LEU:HD23	2:I:184:VAL:HG11	2.02	0.40
2:H:112:PRO:N	2:H:114:LEU:CD1	2.84	0.40
1:A:68:TYR:CD2	1:A:68:TYR:N	2.89	0.40
1:A:299:LEU:O	1:A:300:GLU:C	2.65	0.40
1:A:376:ILE:HB	1:A:377:PRO:CD	2.49	0.40
1:A:487:GLU:HG3	1:A:491:LYS:HE3	2.02	0.40
1:B:29:ASP:OD1	1:B:32:ASP:OD2	2.39	0.40
1:B:59:VAL:O	1:B:60:SER:C	2.64	0.40
1:B:99:LEU:HD11	1:B:133:LYS:HD3	2.03	0.40
1:B:128:ILE:C	1:B:130:TYR:N	2.79	0.40
1:B:444:ARG:C	1:B:446:LYS:H	2.29	0.40
1:C:182:PRO:HD3	1:C:191:ARG:HH11	1.86	0.40
1:C:196:ARG:CG	1:C:200:LYS:HE2	2.48	0.40
1:C:275:LYS:CE	1:C:278:GLU:OE1	2.68	0.40
1:C:543:ARG:NH2	1:D:372:LEU:HD11	2.37	0.40
1:E:91:LEU:HB3	1:E:92:GLU:OE1	2.21	0.40
1:F:353:GLN:O	1:F:357:PRO:CA	2.70	0.40
1:F:439:PHE:HB2	1:F:457:ASN:ND2	2.35	0.40
1:F:502:GLU:H	1:F:502:GLU:HG2	1.69	0.40
1:F:561:GLU:O	1:F:564:ASN:N	2.55	0.40
2:I:155:LYS:O	2:I:156:ASP:CB	2.70	0.40
2:H:150:ILE:O	2:H:154:CYS:N	2.53	0.40
2:H:155:LYS:HB2	2:H:156:ASP:H	1.77	0.40
1:A:56:LYS:CE	1:A:265:LEU:O	2.70	0.40
1:A:121:LEU:C	1:A:123:LEU:N	2.80	0.40
1:A:181:LYS:HD2	1:A:181:LYS:N	2.36	0.40
1:A:196:ARG:HH11	1:A:232:HIS:HE1	1.70	0.40
1:A:205:GLN:O	1:A:206:PRO:C	2.64	0.40
1:A:221:GLU:O	1:A:229:ALA:CB	2.69	0.40
1:A:299:LEU:O	1:A:301:LEU:HD23	2.21	0.40
1:A:453:ILE:HG23	1:A:454:TYR:N	2.36	0.40
1:A:653:PHE:CD1	1:A:657:LYS:HD3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:ARG:HA	1:B:28:ARG:HD2	1.92	0.40
1:B:66:GLN:O	1:B:67:VAL:C	2.64	0.40
1:B:200:LYS:O	1:B:201:THR:C	2.65	0.40
1:B:206:PRO:HA	1:B:210:LEU:CD1	2.49	0.40
1:C:105:GLU:N	1:C:106:PRO:CD	2.84	0.40
1:C:394:LEU:HD21	1:C:448:LEU:HD11	2.03	0.40
1:D:125:LEU:HD21	1:D:169:PHE:CD1	2.56	0.40
1:E:49:PHE:CE2	1:E:53:LYS:HD2	2.56	0.40
1:E:71:PHE:HE1	1:E:265:LEU:HD12	1.87	0.40
1:E:73:LYS:HE2	1:E:73:LYS:HB2	1.99	0.40
1:E:198:LEU:HD12	1:E:202:LEU:HD23	2.03	0.40
1:E:327:ILE:HD12	1:E:327:ILE:HA	1.80	0.40
1:E:501:GLU:O	1:E:502:GLU:C	2.63	0.40
1:F:350:LYS:NZ	1:F:354:GLN:NE2	2.68	0.40
1:F:517:SER:O	1:F:518:ASP:HB3	2.21	0.40
1:A:250:TRP:CE2	1:A:254:THR:OG1	2.73	0.40
1:A:344:VAL:O	1:A:347:LYS:N	2.54	0.40
1:C:482:PHE:C	1:C:484:THR:N	2.78	0.40
1:C:650:PHE:HD1	1:C:650:PHE:O	2.04	0.40
1:C:650:PHE:O	1:C:650:PHE:CD1	2.74	0.40
1:D:324:ALA:O	1:D:325:PRO:C	2.65	0.40
1:E:329:PHE:CD1	1:E:329:PHE:C	2.99	0.40
1:F:192:VAL:HG23	1:F:193:GLN:N	2.36	0.40
1:F:397:LEU:O	1:F:397:LEU:HG	2.22	0.40
2:H:139:GLN:O	2:H:141:ASP:N	2.54	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	579/645 (90%)	433 (75%)	110 (19%)	36 (6%)	1 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	554/645 (86%)	414 (75%)	108 (20%)	32 (6%)	1	9
1	C	579/645 (90%)	435 (75%)	110 (19%)	34 (6%)	1	9
1	D	547/645 (85%)	398 (73%)	117 (21%)	32 (6%)	1	9
1	E	572/645 (89%)	429 (75%)	106 (18%)	37 (6%)	1	8
1	F	549/645 (85%)	422 (77%)	95 (17%)	32 (6%)	1	9
2	G	77/174 (44%)	57 (74%)	12 (16%)	8 (10%)	0	2
2	H	77/174 (44%)	56 (73%)	12 (16%)	9 (12%)	0	1
2	I	77/174 (44%)	58 (75%)	14 (18%)	5 (6%)	1	8
All	All	3611/4392 (82%)	2702 (75%)	684 (19%)	225 (6%)	1	9

All (225) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	LYS
1	A	110	ARG
1	A	135	ASN
1	A	255	LYS
1	A	337	GLU
1	A	374	THR
1	A	401	ASP
1	A	464	ILE
1	A	625	PRO
1	A	626	GLU
1	B	30	GLU
1	B	101	ALA
1	B	118	ASN
1	B	229	ALA
1	B	255	LYS
1	B	401	ASP
1	B	464	ILE
1	B	502	GLU
1	C	44	GLN
1	C	169	PHE
1	C	339	ASN
1	C	401	ASP
1	C	570	ASP
1	C	637	ARG
1	D	33	VAL
1	D	44	GLN

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Mol	Chain	Res	Type
1	D	113	SER
1	D	160	ALA
1	D	338	LYS
1	D	374	THR
1	D	396	ALA
1	D	397	LEU
1	E	44	GLN
1	E	160	ALA
1	E	625	PRO
1	E	639	TYR
1	F	30	GLU
1	F	339	ASN
1	F	341	ASP
1	F	401	ASP
1	F	569	LEU
2	G	139	GLN
2	G	186	SER
2	I	168	ALA
2	H	137	LYS
1	A	113	SER
1	A	138	ILE
1	A	160	ALA
1	A	339	ASN
1	A	433	ALA
1	A	502	GLU
1	A	581	TYR
1	A	637	ARG
1	A	653	PHE
1	B	62	LYS
1	B	135	ASN
1	B	168	GLN
1	B	265	LEU
1	B	340	THR
1	B	342	SER
1	B	556	VAL
1	B	581	TYR
1	C	116	LEU
1	C	141	GLY
1	C	170	TRP
1	C	400	ASP
1	C	463	HIS
1	C	485	ASP

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Mol	Chain	Res	Type
1	C	513	ILE
1	C	557	ASN
1	C	635	PRO
1	C	643	THR
1	D	168	GLN
1	D	293	TRP
1	D	339	ASN
1	D	382	THR
1	E	113	SER
1	E	256	GLY
1	E	258	LYS
1	E	321	VAL
1	E	339	ASN
1	E	374	THR
1	E	401	ASP
1	E	452	ASP
1	E	578	GLU
1	E	581	TYR
1	E	626	GLU
1	E	632	LYS
1	F	160	ALA
1	F	184	ASN
1	F	224	VAL
1	F	226	GLN
1	F	400	ASP
1	F	452	ASP
1	F	463	HIS
2	G	140	LYS
2	G	183	GLY
2	I	184	VAL
2	H	113	TRP
2	H	140	LYS
2	H	141	ASP
1	A	56	LYS
1	A	117	GLY
1	A	151	ALA
1	A	169	PHE
1	A	170	TRP
1	A	208	ASP
1	A	277	ASN
1	B	122	SER
1	B	169	PHE

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Mol	Chain	Res	Type
1	B	322	CYS
1	B	367	SER
1	B	561	GLU
1	C	110	ARG
1	C	117	GLY
1	C	187	GLU
1	C	322	CYS
1	C	326	GLU
1	C	580	ASP
1	D	122	SER
1	D	254	THR
1	D	322	CYS
1	D	389	ARG
1	D	557	ASN
1	E	62	LYS
1	E	76	ASP
1	E	116	LEU
1	E	224	VAL
1	E	309	ARG
1	E	341	ASP
1	E	397	LEU
1	E	642	VAL
1	E	646	GLU
1	E	653	PHE
1	F	114	LYS
1	F	254	THR
1	F	396	ALA
1	F	471	ALA
1	F	554	PRO
1	F	557	ASN
1	F	581	TYR
2	G	121	ASN
2	G	180	LEU
2	I	185	CYS
2	H	135	LEU
1	A	229	ALA
1	A	322	CYS
1	A	398	MET
1	A	399	GLU
1	A	468	THR
1	A	518	ASP
1	A	643	THR

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Mol	Chain	Res	Type
1	B	24	THR
1	B	184	ASN
1	B	357	PRO
1	B	495	PHE
1	C	111	CYS
1	C	142	GLU
1	C	338	LYS
1	C	374	THR
1	C	432	LEU
1	D	45	PRO
1	D	75	HIS
1	D	141	GLY
1	D	296	ASP
1	E	187	GLU
1	E	262	PRO
1	E	518	ASP
1	F	44	GLN
1	F	168	GLN
1	F	279	TYR
1	F	397	LEU
1	F	447	LYS
1	F	556	VAL
2	H	186	SER
1	A	101	ALA
1	A	270	GLU
1	A	341	ASP
1	B	117	GLY
1	B	161	ILE
1	B	268	ALA
1	B	302	SER
1	C	625	PRO
1	D	187	GLU
1	D	357	PRO
1	E	184	ASN
1	E	338	LYS
1	E	420	CYS
1	E	556	VAL
1	E	557	ASN
1	F	321	VAL
1	F	374	THR
2	G	141	ASP
2	G	185	CYS

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Mol	Chain	Res	Type
2	I	113	TRP
2	I	114	LEU
2	H	180	LEU
1	B	49	PHE
1	C	161	ILE
1	C	256	GLY
1	C	398	MET
1	D	116	LEU
1	D	161	ILE
1	D	262	PRO
1	D	381	THR
1	D	525	ILE
1	D	576	ARG
1	F	159	CYS
1	F	474	VAL
1	C	33	VAL
1	C	402	PRO
1	C	633	VAL
1	E	357	PRO
1	E	402	PRO
1	F	33	VAL
1	F	421	VAL
2	H	114	LEU
2	H	184	VAL
1	D	361	VAL
1	D	418	VAL
1	F	256	GLY
1	B	138	ILE
1	D	34	ILE
1	B	48	ILE
1	E	635	PRO

5.3.2 Protein sidechains (i)

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

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	544/598 (91%)	478 (88%)	66 (12%)	5 20
1	B	519/598 (87%)	470 (91%)	49 (9%)	8 30
1	C	544/598 (91%)	505 (93%)	39 (7%)	13 40
1	D	512/598 (86%)	474 (93%)	38 (7%)	13 38
1	E	538/598 (90%)	486 (90%)	52 (10%)	8 28
1	F	514/598 (86%)	476 (93%)	38 (7%)	13 38
2	G	71/154 (46%)	64 (90%)	7 (10%)	7 27
2	H	71/154 (46%)	67 (94%)	4 (6%)	19 47
2	I	71/154 (46%)	65 (92%)	6 (8%)	10 33
All	All	3384/4050 (84%)	3085 (91%)	299 (9%)	9 32

All (299) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LEU
1	A	51	TYR
1	A	65	LYS
1	A	66	GLN
1	A	67	VAL
1	A	71	PHE
1	A	77	ARG
1	A	80	LEU
1	A	89	LEU
1	A	99	LEU
1	A	112	LEU
1	A	114	LYS
1	A	128	ILE
1	A	132	ARG
1	A	135	ASN
1	A	143	GLU
1	A	147	ILE
1	A	177	LEU
1	A	181	LYS
1	A	189	GLN
1	A	202	LEU
1	A	219	GLN
1	A	232	HIS

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Mol	Chain	Res	Type
1	A	242	ASN
1	A	260	ASN
1	A	263	ILE
1	A	275	LYS
1	A	292	ARG
1	A	313	VAL
1	A	333	ASN
1	A	339	ASN
1	A	342	SER
1	A	345	ILE
1	A	353	GLN
1	A	366	LEU
1	A	374	THR
1	A	380	GLU
1	A	381	THR
1	A	391	HIS
1	A	400	ASP
1	A	401	ASP
1	A	403	THR
1	A	408	ILE
1	A	413	SER
1	A	419	TYR
1	A	430	GLN
1	A	432	LEU
1	A	450	THR
1	A	468	THR
1	A	499	VAL
1	A	504	GLN
1	A	513	ILE
1	A	528	LYS
1	A	548	ARG
1	A	551	GLU
1	A	555	GLU
1	A	625	PRO
1	A	628	VAL
1	A	637	ARG
1	A	638	GLN
1	A	643	THR
1	A	645	PHE
1	A	646	GLU
1	A	648	HIS
1	A	650	PHE

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Mol	Chain	Res	Type
1	A	656	ASP
1	B	25	SER
1	B	29	ASP
1	B	30	GLU
1	B	66	GLN
1	B	71	PHE
1	B	78	PHE
1	B	84	ILE
1	B	95	LYS
1	B	114	LYS
1	B	115	GLU
1	B	128	ILE
1	B	137	ILE
1	B	147	ILE
1	B	150	GLN
1	B	152	PHE
1	B	181	LYS
1	B	189	GLN
1	B	202	LEU
1	B	219	GLN
1	B	231	ARG
1	B	249	ASP
1	B	260	ASN
1	B	265	LEU
1	B	276	PRO
1	B	277	ASN
1	B	283	GLN
1	B	292	ARG
1	B	298	LYS
1	B	353	GLN
1	B	368	GLU
1	B	391	HIS
1	B	392	LEU
1	B	400	ASP
1	B	401	ASP
1	B	403	THR
1	B	408	ILE
1	B	413	SER
1	B	429	ILE
1	B	449	VAL
1	B	450	THR
1	B	453	ILE

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Mol	Chain	Res	Type
1	B	464	ILE
1	B	481	TYR
1	B	527	GLN
1	B	535	LYS
1	B	548	ARG
1	B	551	GLU
1	B	555	GLU
1	B	556	VAL
1	C	42	GLU
1	C	66	GLN
1	C	71	PHE
1	C	74	LEU
1	C	92	GLU
1	C	114	LYS
1	C	115	GLU
1	C	124	TRP
1	C	136	ASP
1	C	174	LEU
1	C	204	CYS
1	C	285	LEU
1	C	299	LEU
1	C	333	ASN
1	C	353	GLN
1	C	374	THR
1	C	381	THR
1	C	382	THR
1	C	391	HIS
1	C	403	THR
1	C	408	ILE
1	C	414	LYS
1	C	419	TYR
1	C	442	CYS
1	C	502	GLU
1	C	510	GLU
1	C	535	LYS
1	C	543	ARG
1	C	545	LEU
1	C	552	LYS
1	C	563	THR
1	C	574	LEU
1	C	633	VAL
1	C	635	PRO

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Mol	Chain	Res	Type
1	C	637	ARG
1	C	638	GLN
1	C	643	THR
1	C	644	ILE
1	C	648	HIS
1	D	42	GLU
1	D	46	THR
1	D	66	GLN
1	D	71	PHE
1	D	92	GLU
1	D	115	GLU
1	D	121	LEU
1	D	134	LYS
1	D	174	LEU
1	D	228	THR
1	D	255	LYS
1	D	265	LEU
1	D	278	GLU
1	D	281	VAL
1	D	285	LEU
1	D	296	ASP
1	D	299	LEU
1	D	321	VAL
1	D	330	ASN
1	D	335	GLN
1	D	349	LEU
1	D	374	THR
1	D	391	HIS
1	D	408	ILE
1	D	410	GLN
1	D	421	VAL
1	D	424	ASN
1	D	455	LEU
1	D	500	ASN
1	D	502	GLU
1	D	510	GLU
1	D	514	ASP
1	D	535	LYS
1	D	538	SER
1	D	555	GLU
1	D	574	LEU
1	D	575	GLN

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Mol	Chain	Res	Type
1	D	576	ARG
1	E	39	ASP
1	E	42	GLU
1	E	50	LEU
1	E	68	TYR
1	E	71	PHE
1	E	73	LYS
1	E	80	LEU
1	E	89	LEU
1	E	92	GLU
1	E	98	GLU
1	E	114	LYS
1	E	129	THR
1	E	134	LYS
1	E	174	LEU
1	E	198	LEU
1	E	207	MET
1	E	218	THR
1	E	219	GLN
1	E	225	ASN
1	E	226	GLN
1	E	242	ASN
1	E	251	LEU
1	E	278	GLU
1	E	283	GLN
1	E	285	LEU
1	E	299	LEU
1	E	322	CYS
1	E	330	ASN
1	E	331	MET
1	E	353	GLN
1	E	366	LEU
1	E	374	THR
1	E	391	HIS
1	E	400	ASP
1	E	410	GLN
1	E	416	THR
1	E	421	VAL
1	E	424	ASN
1	E	442	CYS
1	E	463	HIS
1	E	473	LYS

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Mol	Chain	Res	Type
1	E	481	TYR
1	E	490	ASN
1	E	500	ASN
1	E	502	GLU
1	E	510	GLU
1	E	541	SER
1	E	545	LEU
1	E	555	GLU
1	E	568	VAL
1	E	626	GLU
1	E	646	GLU
1	F	31	SER
1	F	66	GLN
1	F	91	LEU
1	F	92	GLU
1	F	107	VAL
1	F	114	LYS
1	F	115	GLU
1	F	134	LYS
1	F	150	GLN
1	F	174	LEU
1	F	187	GLU
1	F	189	GLN
1	F	202	LEU
1	F	277	ASN
1	F	299	LEU
1	F	314	TYR
1	F	337	GLU
1	F	366	LEU
1	F	387	ILE
1	F	391	HIS
1	F	400	ASP
1	F	403	THR
1	F	410	GLN
1	F	416	THR
1	F	442	CYS
1	F	464	ILE
1	F	481	TYR
1	F	500	ASN
1	F	504	GLN
1	F	510	GLU
1	F	524	MET

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Mol	Chain	Res	Type
1	F	525	ILE
1	F	538	SER
1	F	554	PRO
1	F	555	GLU
1	F	574	LEU
1	F	576	ARG
1	F	581	TYR
2	G	120	VAL
2	G	142	GLN
2	G	143	GLN
2	G	146	LEU
2	G	160	THR
2	G	170	GLN
2	G	178	LEU
2	I	116	VAL
2	I	147	LEU
2	I	164	LEU
2	I	170	GLN
2	I	185	CYS
2	I	189	GLN
2	H	122	ILE
2	H	155	LYS
2	H	162	VAL
2	H	170	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (172) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	63	GLN
1	A	66	GLN
1	A	118	ASN
1	A	171	ASN
1	A	189	GLN
1	A	190	GLN
1	A	205	GLN
1	A	219	GLN
1	A	232	HIS
1	A	242	ASN
1	A	252	ASN
1	A	266	ASN
1	A	267	GLN

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Mol	Chain	Res	Type
1	A	282	GLN
1	A	297	ASN
1	A	306	HIS
1	A	316	GLN
1	A	333	ASN
1	A	339	ASN
1	A	373	ASN
1	A	527	GLN
1	A	540	ASN
1	A	575	GLN
1	B	38	ASN
1	B	44	GLN
1	B	57	HIS
1	B	58	HIS
1	B	63	GLN
1	B	66	GLN
1	B	118	ASN
1	B	135	ASN
1	B	153	GLN
1	B	171	ASN
1	B	189	GLN
1	B	205	GLN
1	B	219	GLN
1	B	232	HIS
1	B	266	ASN
1	B	277	ASN
1	B	330	ASN
1	B	333	ASN
1	B	354	GLN
1	B	391	HIS
1	B	463	HIS
1	B	504	GLN
1	B	527	GLN
1	B	564	ASN
1	B	572	ASN
1	C	38	ASN
1	C	57	HIS
1	C	58	HIS
1	C	63	GLN
1	C	75	HIS
1	C	118	ASN
1	C	135	ASN

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Mol	Chain	Res	Type
1	C	146	ASN
1	C	175	HIS
1	C	189	GLN
1	C	219	GLN
1	C	222	GLN
1	C	226	GLN
1	C	232	HIS
1	C	242	ASN
1	C	266	ASN
1	C	267	GLN
1	C	282	GLN
1	C	330	ASN
1	C	430	GLN
1	C	457	ASN
1	C	463	HIS
1	C	504	GLN
1	C	540	ASN
1	C	557	ASN
1	C	564	ASN
1	C	572	ASN
1	C	638	GLN
1	D	38	ASN
1	D	58	HIS
1	D	118	ASN
1	D	146	ASN
1	D	168	GLN
1	D	171	ASN
1	D	189	GLN
1	D	190	GLN
1	D	205	GLN
1	D	219	GLN
1	D	226	GLN
1	D	242	ASN
1	D	267	GLN
1	D	277	ASN
1	D	330	ASN
1	D	339	ASN
1	D	354	GLN
1	D	373	ASN
1	D	391	HIS
1	D	410	GLN
1	D	463	HIS

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Mol	Chain	Res	Type
1	D	504	GLN
1	D	540	ASN
1	D	557	ASN
1	D	564	ASN
1	D	575	GLN
1	E	63	GLN
1	E	75	HIS
1	E	118	ASN
1	E	146	ASN
1	E	171	ASN
1	E	189	GLN
1	E	190	GLN
1	E	215	GLN
1	E	219	GLN
1	E	242	ASN
1	E	248	GLN
1	E	267	GLN
1	E	277	ASN
1	E	282	GLN
1	E	316	GLN
1	E	319	GLN
1	E	330	ASN
1	E	333	ASN
1	E	358	ASN
1	E	410	GLN
1	E	430	GLN
1	E	457	ASN
1	E	504	GLN
1	E	527	GLN
1	E	540	ASN
1	E	557	ASN
1	E	564	ASN
1	E	575	GLN
1	F	38	ASN
1	F	57	HIS
1	F	58	HIS
1	F	75	HIS
1	F	83	ASN
1	F	118	ASN
1	F	189	GLN
1	F	190	GLN
1	F	205	GLN

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Mol	Chain	Res	Type
1	F	219	GLN
1	F	226	GLN
1	F	242	ASN
1	F	252	ASN
1	F	282	GLN
1	F	330	ASN
1	F	354	GLN
1	F	404	ASN
1	F	410	GLN
1	F	424	ASN
1	F	430	GLN
1	F	457	ASN
1	F	463	HIS
1	F	504	GLN
1	F	540	ASN
1	F	557	ASN
1	F	575	GLN
2	G	143	GLN
2	G	170	GLN
2	G	182	ASN
2	I	143	GLN
2	I	170	GLN
2	I	182	ASN
2	I	189	GLN
2	H	139	GLN
2	H	142	GLN
2	H	143	GLN
2	H	151	GLN
2	H	152	HIS
2	H	170	GLN
2	H	189	GLN
2	H	192	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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	585/645 (90%)	-0.53	0 100 100	39, 76, 136, 149	0
1	B	558/645 (86%)	-0.55	0 100 100	36, 73, 136, 148	0
1	C	585/645 (90%)	-0.27	4 (0%) 84 70	60, 106, 149, 151	0
1	D	551/645 (85%)	-0.29	0 100 100	58, 104, 149, 151	0
1	E	578/645 (89%)	0.17	35 (6%) 27 18	57, 106, 150, 151	0
1	F	553/645 (85%)	-0.17	3 (0%) 87 76	55, 104, 148, 151	0
2	G	81/174 (46%)	-0.31	0 100 100	63, 102, 138, 151	0
2	H	81/174 (46%)	-0.20	0 100 100	90, 128, 148, 151	0
2	I	81/174 (46%)	-0.16	0 100 100	96, 125, 147, 151	0
All	All	3653/4392 (83%)	-0.27	42 (1%) 78 60	36, 99, 148, 151	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	164	PRO	3.9
1	E	137	ILE	3.9
1	E	233	ILE	3.6
1	E	173	TYR	3.5
1	E	80	LEU	3.3
1	E	125	LEU	3.2
1	E	181	LYS	3.1
1	E	127	TYR	3.1
1	C	641	LYS	2.9
1	E	199	TYR	2.9
1	E	195	ILE	2.8
1	E	126	SER	2.7
1	E	177	LEU	2.7
1	E	172	GLU	2.6
1	E	202	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	F	474	VAL	2.6
1	E	210	LEU	2.5
1	E	170	TRP	2.5
1	E	59	VAL	2.5
1	C	645	PHE	2.4
1	E	236	LEU	2.4
1	E	299	LEU	2.4
1	F	126	SER	2.4
1	E	203	LEU	2.4
1	E	48	ILE	2.3
1	E	216	ARG	2.3
1	E	91	LEU	2.3
1	E	176	PHE	2.3
1	E	179	HIS	2.3
1	E	123	LEU	2.3
1	E	217	TYR	2.3
1	C	288	LEU	2.2
1	E	218	THR	2.2
1	E	95	LYS	2.2
1	E	315	MET	2.2
1	C	655	SER	2.1
1	E	207	MET	2.1
1	E	215	GLN	2.1
1	F	137	ILE	2.1
1	E	130	TYR	2.1
1	E	67	VAL	2.0
1	E	128	ILE	2.0

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

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

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.