Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:18 PM GMT

PDB ID	:	4EBA
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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

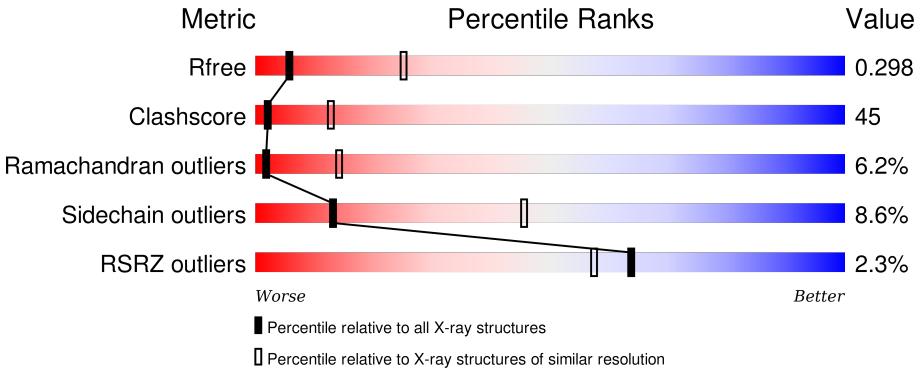
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance

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}	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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

Mol	Chain	Length	Quality of chain
1	A	645	27% 53% 9% • 9%
1	B	645	29% 49% 8% • 13%
1	C	645	2% 35% 49% 6% • 9%
1	D	645	% 32% 47% 7% 15%
1	E	645	7% 27% 52% 10% 10%

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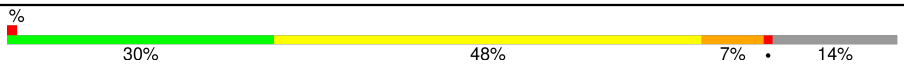
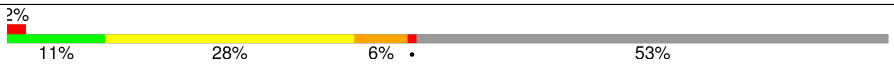
Mol	Chain	Length	Quality of chain
1	F	645	
2	G	174	
2	H	174	
2	I	174	

2 Entry composition

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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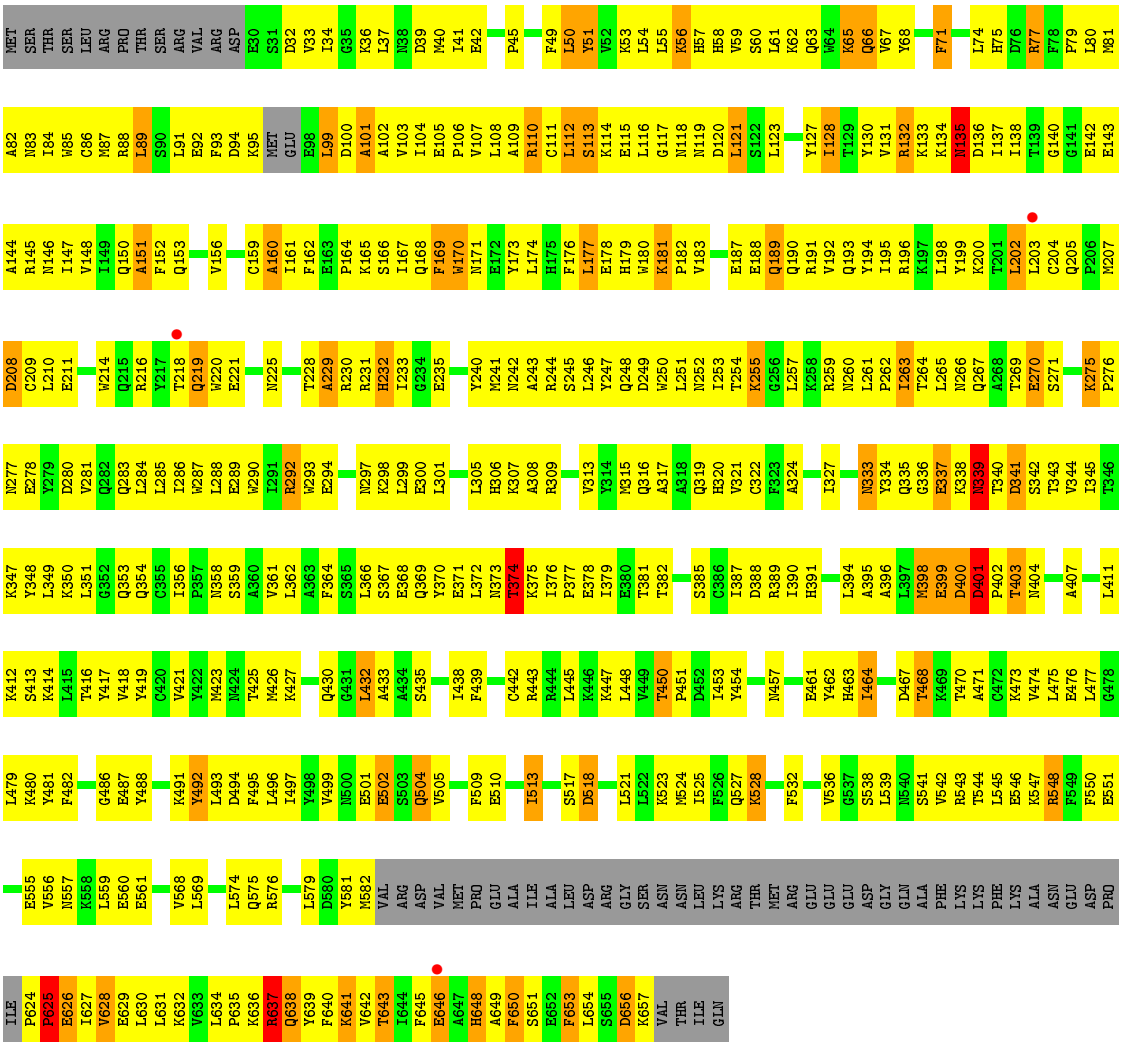
Chain	Residue	Modelled	Actual	Comment	Reference
H	87	SER	-	EXPRESSION TAG	UNP Q6CKN2
H	88	SER	-	EXPRESSION TAG	UNP Q6CKN2
H	89	HIS	-	EXPRESSION TAG	UNP Q6CKN2
H	90	HIS	-	EXPRESSION TAG	UNP Q6CKN2
H	91	HIS	-	EXPRESSION TAG	UNP Q6CKN2
H	92	HIS	-	EXPRESSION TAG	UNP Q6CKN2
H	93	HIS	-	EXPRESSION TAG	UNP Q6CKN2
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 and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

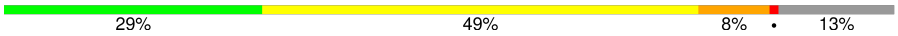
- Molecule 1: mRNA 3'-end-processing protein RNA14

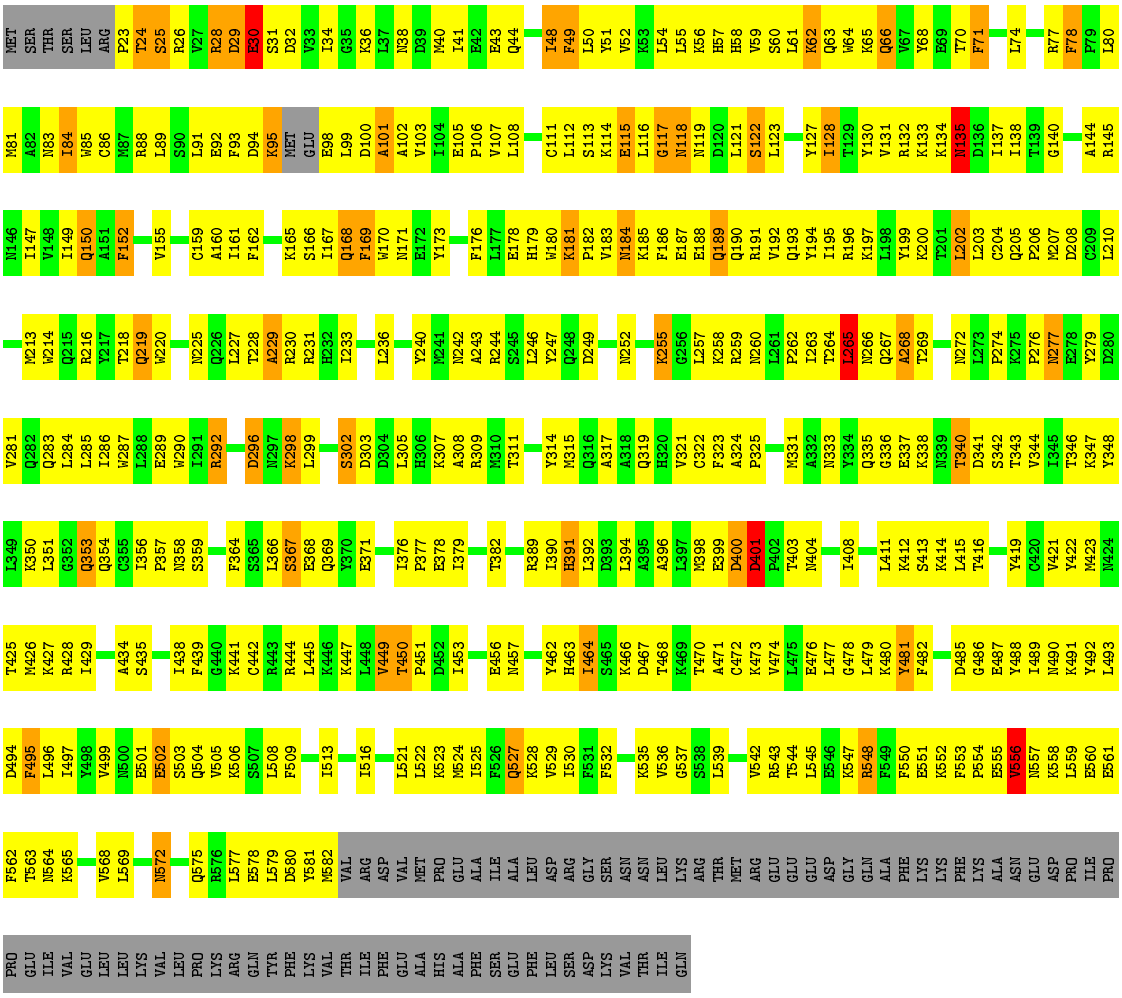
Chain A:



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

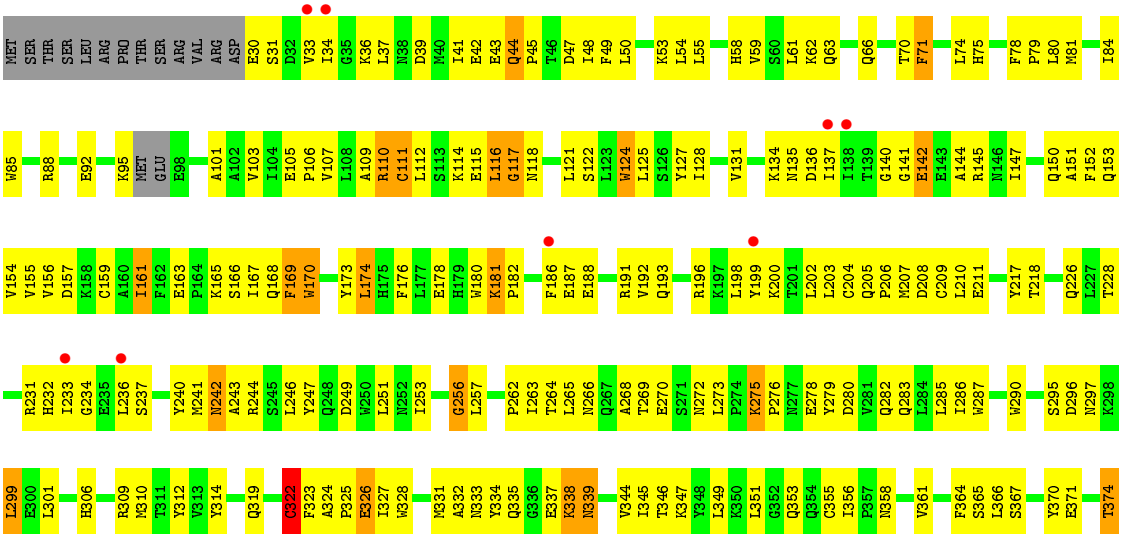
Chain B:

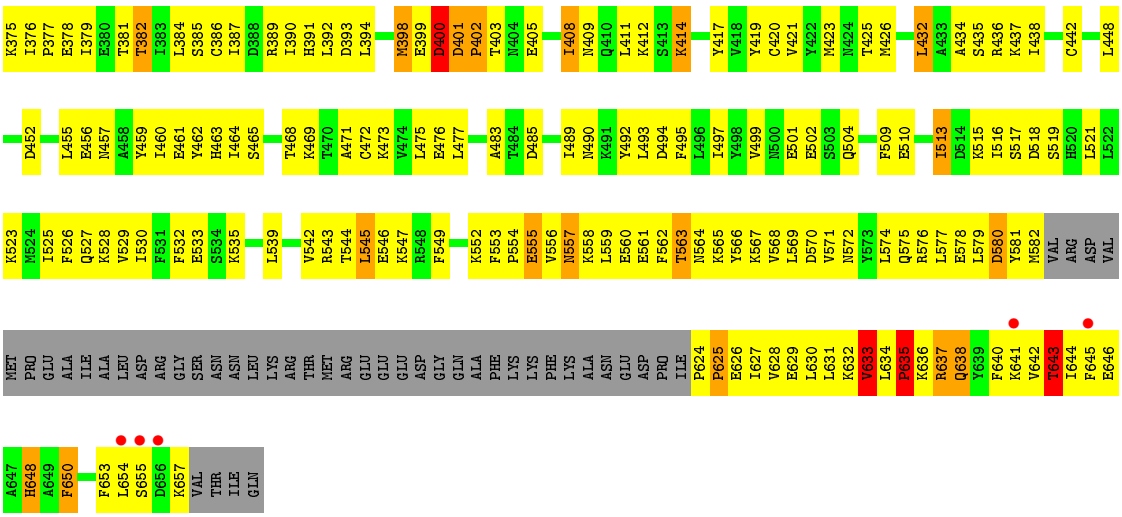




• Molecule 1: mRNA 3'-end-processing protein RNA14

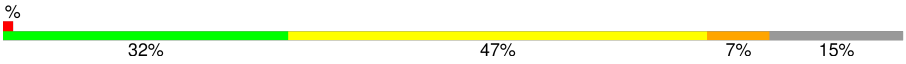
Chain C:

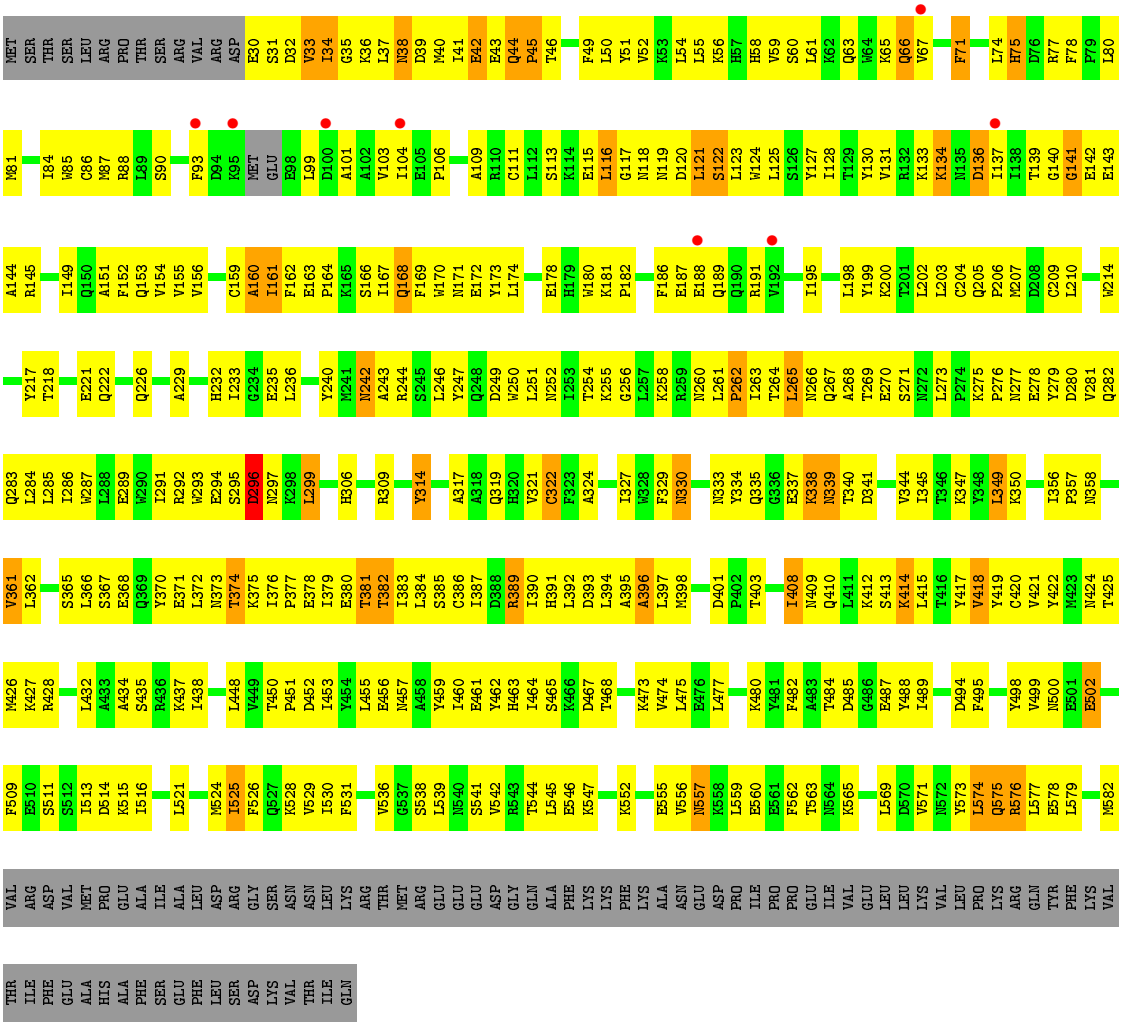




• Molecule 1: mRNA 3'-end-processing protein RNA14

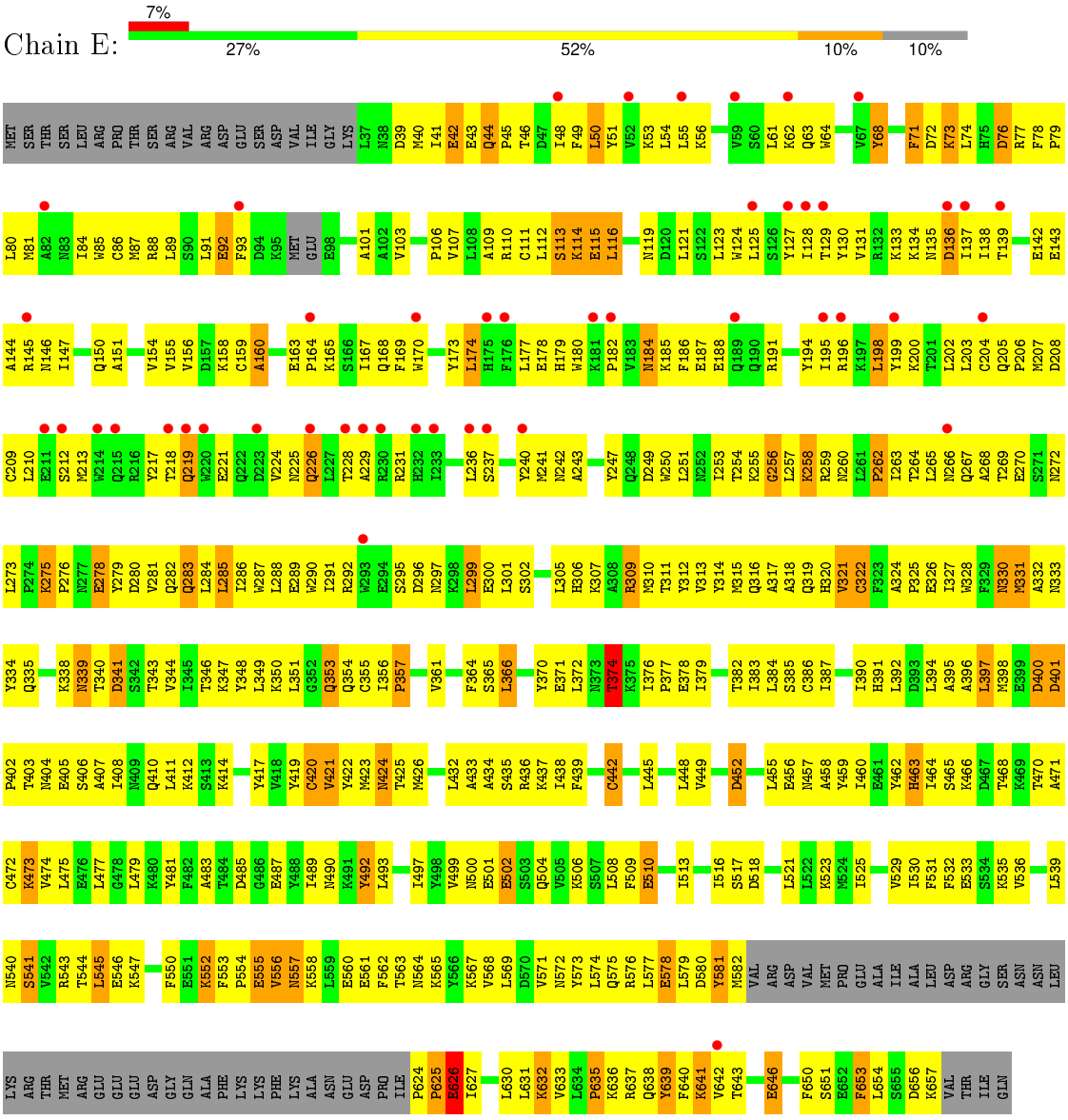
Chain D:





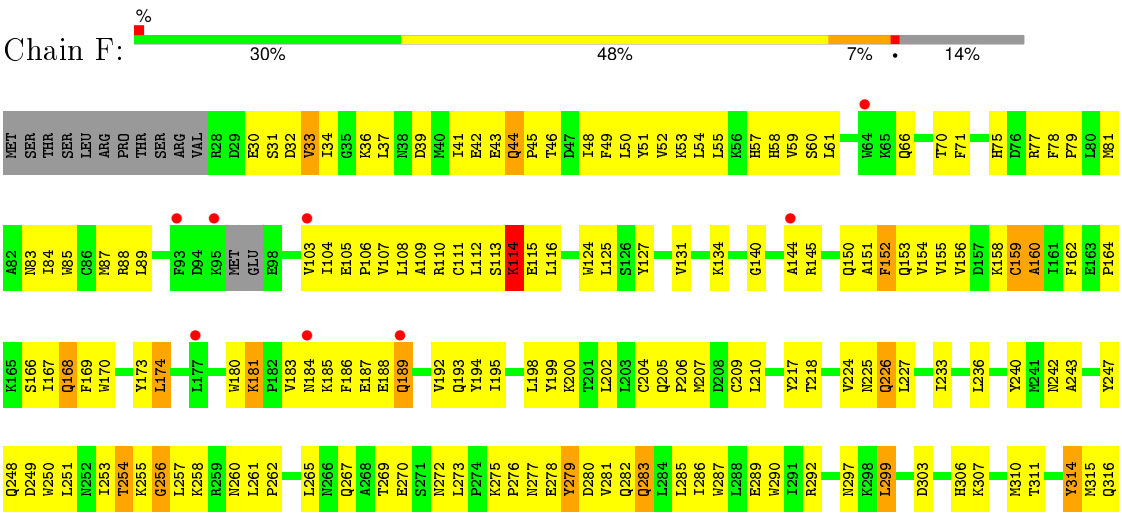
• Molecule 1: mRNA 3'-end-processing protein RNA14

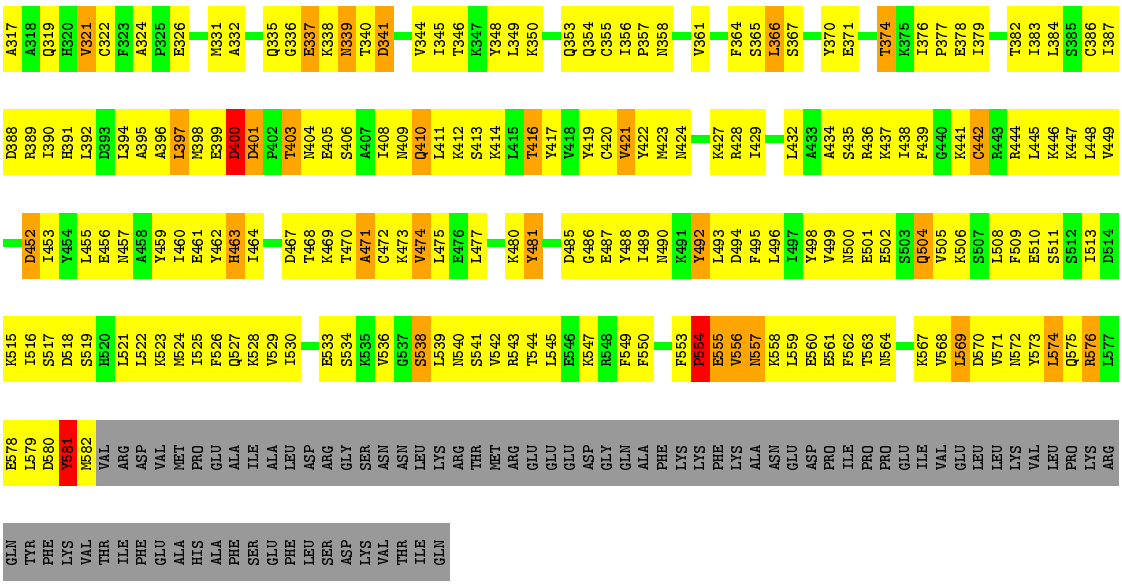
Chain E:



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

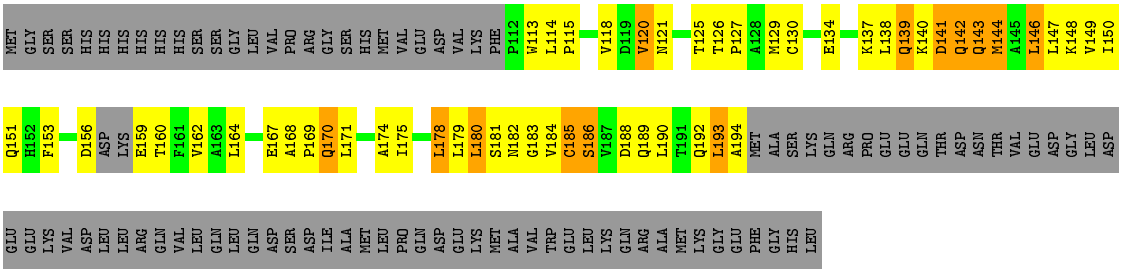
Chain F:





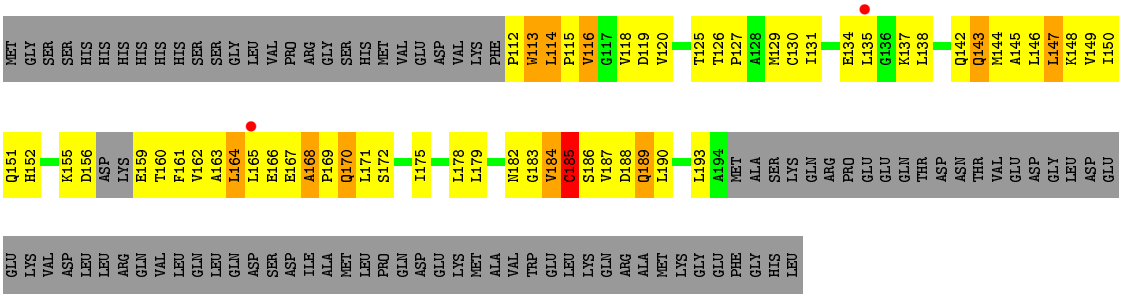
- Molecule 2: Rna15

Chain G:



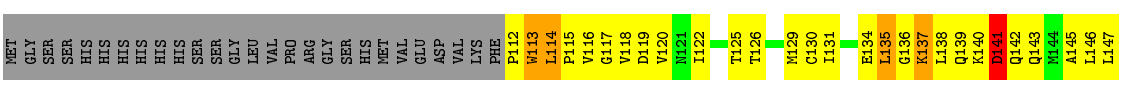
- Molecule 2: Rna15

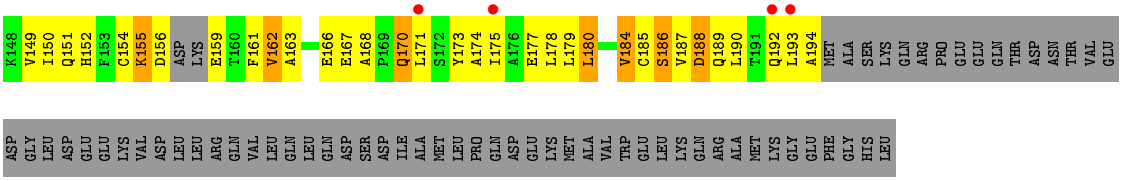
Chain I:



- Molecule 2: Rna15

Chain H:




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) 86.3 (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	3446 reflections (5.09%)	DCC
Wilson B-factor (Å^2)	84.8	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 76.8	EDS
Estimated twinning fraction	0.018 for -h,-k,l 0.038 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Outliers	0 of 71798 reflections	Xtriage
F_o,F_c correlation	0.92	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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.46	0/4982	0.64	0/6732
1	B	0.44	0/4747	0.67	1/6416 (0.0%)
1	C	0.40	0/4982	0.60	0/6732
1	D	0.40	0/4689	0.59	0/6338
1	E	0.46	0/4931	0.66	1/6664 (0.0%)
1	F	0.42	0/4708	0.61	0/6363
2	G	0.39	0/626	0.71	0/849
2	H	0.37	0/626	0.67	0/849
2	I	0.38	0/626	0.63	0/849
All	All	0.43	0/30917	0.63	2/41792 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	31	SER	N-CA-C	-5.59	95.91	111.00
1	E	112	LEU	CA-CB-CG	5.05	126.91	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4874	0	4885	509	0
1	B	4646	0	4650	399	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4874	0	4885	391	0
1	D	4589	0	4591	385	0
1	E	4823	0	4834	511	0
1	F	4608	0	4608	398	0
2	G	618	0	632	81	0
2	H	618	0	632	93	0
2	I	618	0	632	92	0
All	All	30268	0	30349	2735	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 45.

All (2735) 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
1:A:345:ILE:HD12	1:A:345:ILE:H	1.19	1.03
1:A:225:ASN:HB2	1:A:229:ALA:HB2	1.37	1.02
2:H:170:GLN:HE21	2:H:170:GLN:N	1.56	1.02
1:A:548:ARG:HG2	1:A:548:ARG:HH11	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
2:G:125:THR:HG22	2:G:126:THR:H	1.23	1.00
1:E:311:THR:HG22	1:E:315:MET:HE2	1.40	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:C:202:LEU:HB2	1:C:207:MET:HE1	1.44	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:H	2:H:170:GLN:HE21	0.95	0.94
1:D:434:ALA:HA	1:D:437:LYS:HE3	1.49	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:H:170:GLN:NE2	2:H:170:GLN:H	1.67	0.92
1:E:115:GLU:HG2	1:E:116:LEU:H	1.32	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:C:398:MET:HA	1:C:408:ILE:HD11	1.50	0.91
1:B:524:MET:HA	1:B:527:GLN:HE21	1.35	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:HE21	2:G:170:GLN:H	0.91	0.91
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:N	2:G:170:GLN:HE21	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
2:G:185:CYS:SG	2:G:188:ASP:HB2	2.13	0.89
1:A:568:VAL:HG12	1:A:569:LEU:HD22	1.55	0.89
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: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:F:314:TYR:HB3	1:F:331:MET:HE3	1.55	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: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:E:475:LEU:H	1:E:475:LEU:HD12	1.40	0.87
1:A:579:LEU:HD13	1:A:582:MET:HE1	1.57	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:E:364:PHE:CZ	1:E:421:VAL:HG11	2.10	0.87
1:A:631:LEU:HD21	2:G:171:LEU:HD22	1.56	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:185:CYS:HB3	2:H:188:ASP:HB3	1.58	0.86
2:G:193:LEU:HG	2:G:194:ALA:H	1.41	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:A:99:LEU:HB2	1:A:134:LYS:HZ3	1.42	0.84
1:E:206:PRO:HA	1:E:210:LEU:HD11	1.57	0.84
1:A:65:LYS:HD3	1:A:65:LYS:O	1.76	0.84
2:G:143:GLN:HG2	2:G:182:ASN:HD21	1.43	0.84
1:C:61:LEU:HB2	1:C:63:GLN:HE21	1.42	0.84
1:C:468:THR:CG2	1:C:499:VAL:HG11	2.07	0.83
1:C:574:LEU:HD11	1:D:361:VAL:HG22	1.60	0.83
1:A:281:VAL:O	1:A:285:LEU:HD12	1.78	0.83
1:E:341:ASP:HB3	1:E:344:VAL:HG23	1.59	0.83
2:I:170:GLN:NE2	2:I:170:GLN:H	1.74	0.83
1:F:140:GLY:HA3	1:F:144:ALA:HB3	1.60	0.83
1:A:33:VAL:HA	1:A:36:LYS:HD2	1.61	0.83
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:F:202:LEU:HB2	1:F:207:MET:HE1	1.60	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:C:557:ASN:ND2	1:C:560:GLU:HB2	1.92	0.82
1:E:546:GLU:OE2	1:E:565:LYS:HE2	1.80	0.82
2:H:155:LYS:HD3	2:H:155:LYS:H	1.44	0.82
2:G:147:LEU:HD11	2:G:178:LEU:HD22	1.60	0.81
1:E:81:MET:HE1	1:E:318:ALA:O	1.80	0.81
1:F:43:GLU:O	1:F:44:GLN:HG2	1.80	0.81
1:C:299:LEU:HD12	1:C:299:LEU:H	1.45	0.81
1:D:124:TRP:O	1:D:127:TYR:HB3	1.78	0.81
1:E:557:ASN:HD22	1:E:560:GLU:HB2	1.44	0.81
1:D:90:SER:HB3	1:D:264:THR:HG23	1.60	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: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:A:81:MET:HB3	1:A:84:ILE:HD13	1.60	0.81
1:E:455:LEU:HB2	1:F:569:LEU:HD11	1.60	0.80
1:D:218:THR:HA	1:D:233:ILE:HD11	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:557:ASN:HD22	1:D:560:GLU:H	1.26	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: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: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:F:557:ASN:ND2	1:F:560:GLU:H	1.79	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: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
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:C:115:GLU:H	1:C:115:GLU:CD	1.86	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:E:124:TRP:CE3	1:E:155:VAL:HG22	2.18	0.78
1:A:447:LYS:HG2	1:A:481:TYR:HB3	1.63	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: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
2:H:189:GLN:O	2:H:192:GLN:HB2	1.84	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
1:E:312:TYR:O	1:E:316:GLN:HG2	1.83	0.77
1:D:51:TYR:O	1:D:55:LEU:HG	1.85	0.77
1:E:417:TYR:HB2	1:F:573:TYR:HD1	1.48	0.77
1:B:178:GLU:CD	1:B:216:ARG:HH22	1.88	0.77
1:B:99:LEU:HB2	1:B:134:LYS:HZ3	1.48	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:E:631:LEU:HD23	2:I:171:LEU:HD13	1.65	0.77
1:C:529:VAL:HG12	1:C:545:LEU:HD11	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:632:LYS:HG2	2:G:115:PRO:CG	2.14	0.77
1:E:156:VAL:HA	1:E:160:ALA:CB	2.15	0.77
1:B:206:PRO:HB3	1:B:247:TYR:HB2	1.65	0.77
1:F:299:LEU:N	1:F:299:LEU:HD12	1.98	0.77
1:E:539:LEU:HD13	1:F:371:GLU:OE1	1.85	0.77
2:H:150:ILE:HD13	2:H:175:ILE:HG12	1.66	0.76
1:F:115:GLU:CD	1:F:115:GLU:H	1.88	0.76
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
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: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
1:C:624:PRO:N	1:C:625:PRO:HD3	2.00	0.76
1:A:394:LEU:HA	1:A:411:LEU:HD23	1.67	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:E:364:PHE:HZ	1:E:421:VAL:HG11	1.47	0.76
1:D:330:ASN:HD22	1:D:330:ASN:N	1.84	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:D:557:ASN:ND2	1:D:560:GLU:H	1.85	0.75
1:C:648:HIS:NE2	2:H:162:VAL:HB	2.01	0.75
2:G:190:LEU:HA	2:G:193:LEU:HD21	1.67	0.75
1:F:71:PHE:CE2	1:F:88:ARG:HB2	2.21	0.75
1:E:109:ALA:O	1:E:113:SER:HB3	1.87	0.75
1:F:579:LEU:O	1:F:582:MET:HB2	1.86	0.75
1:C:181:LYS:O	1:C:181:LYS:HD2	1.85	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: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:D:204:CYS:HB2	1:D:205:GLN:HE21	1.50	0.74
1:C:71:PHE:CE2	1:C:88:ARG:HB2	2.21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:E:269:THR:HG23	1:E:272:ASN:HD21	1.51	0.74
1:C:635:PRO:HG3	2:H:120:VAL:HG21	1.70	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:D:115:GLU:CD	1:D:115:GLU:H	1.92	0.74
1:E:509:PHE:CZ	1:E:513:ILE:HD11	2.23	0.73
1:E:465:SER:O	1:E:466:LYS:HB2	1.87	0.73
1:A:378:GLU:O	1:A:382:THR:HG22	1.88	0.73
1:F:200:LYS:HG2	1:F:236:LEU:HD11	1.69	0.73
1:B:66:GLN:HE21	1:B:66:GLN:N	1.84	0.73
1:B:376:ILE:HB	1:B:377:PRO:HD3	1.70	0.73
1:F:83:ASN:O	1:F:87:MET:HG3	1.88	0.73
1:A:205:GLN:O	1:A:207:MET:HG3	1.87	0.73
1:E:473:LYS:O	1:E:477:LEU:HD13	1.88	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: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:468:THR:CG2	1:E:499:VAL:HG11	2.19	0.73
1:E:287:TRP:O	1:E:290:TRP:HB3	1.89	0.73
1:A:568:VAL:HG12	1:A:569:LEU:CD2	2.18	0.73
2:I:179:LEU:O	2:I:184:VAL:HB	1.89	0.73
1:F:218:THR:HG23	1:F:233:ILE:HD13	1.69	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:B:400:ASP:O	1:B:401:ASP:HB3	1.89	0.72
1:B:137:ILE:HD12	1:B:137:ILE:H	1.53	0.72
1:A:654:LEU:HD21	2:G:150:ILE:HG22	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:351:LEU:HA	1:B:354:GLN:HG3	1.69	0.72
1:C:572:ASN:OD1	1:C:575:GLN:HG2	1.88	0.72
1:C:654:LEU:O	1:C:654:LEU:HD23	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: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:578:GLU:O	1:E:579:LEU:HD23	1.90	0.71
1:E:313:VAL:O	1:E:316:GLN:HB2	1.90	0.71
1:F:289:GLU:HG3	1:F:292:ARG:HH21	1.55	0.71
2:G:193:LEU:HG	2:G:194:ALA:N	2.05	0.71
1:F:493:LEU:HD23	1:F:508:LEU:HD23	1.71	0.71
1:C:226:GLN:H	1:C:226:GLN:NE2	1.89	0.71
1:E:327:ILE:CG2	1:E:328:TRP:N	2.54	0.71
1:F:152:PHE:O	1:F:156:VAL:HG23	1.90	0.71
1:C:489:ILE:HG13	1:C:516:ILE:HD11	1.72	0.71
1:B:43:GLU:HG2	2:G:113:TRP:HZ3	1.55	0.71
1:E:101:ALA:HB2	1:E:134:LYS:HE2	1.71	0.71
1:A:61:LEU:HD12	1:A:63:GLN:NE2	2.05	0.71
1:C:306:HIS:O	1:C:309:ARG:HB3	1.91	0.71
1:E:425:THR:HG22	1:E:426:MET:HE3	1.71	0.71
1:E:156:VAL:HA	1:E:160:ALA:HB3	1.73	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: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:299:LEU:CD1	1:F:299:LEU:H	2.01	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:E:631:LEU:CD2	2:I:171:LEU:HD13	2.20	0.70
1:B:51:TYR:O	1:B:55:LEU:HG	1.91	0.70
1:E:264:THR:HG22	1:E:266:ASN:H	1.55	0.70
1:B:307:LYS:CE	1:B:338:LYS:HG3	2.22	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:152:PHE:HB3	1:F:173:TYR:CE1	2.26	0.70
1:C:156:VAL:O	1:C:161:ILE:HG12	1.91	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:C:627:ILE:HD11	2:H:171:LEU:HD11	1.72	0.70
1:A:336:GLY:O	1:A:338:LYS:N	2.25	0.70
1:E:284:LEU:O	1:E:288:LEU:HG	1.91	0.69
1:D:218:THR:HA	1:D:233:ILE:CD1	2.20	0.69
1:D:41:ILE:HG12	1:D:50:LEU:HB3	1.73	0.69
1:A:641:LYS:HD2	1:A:642:VAL:N	2.06	0.69
1:C:115:GLU:C	1:C:117:GLY:H	1.95	0.69
1:F:572:ASN:OD1	1:F:575:GLN:HG2	1.91	0.69
1:A:462:TYR:OH	1:A:499:VAL:HG11	1.90	0.69
1:D:222:GLN:HB3	1:D:226:GLN:HG2	1.73	0.69
1:E:638:GLN:HA	1:E:641:LYS:HG2	1.74	0.69
1:D:152:PHE:O	1:D:156:VAL:HG23	1.91	0.69
1:C:654:LEU:HD12	2:H:179:LEU:HD22	1.74	0.69
1:D:297:ASN:HB2	1:D:306:HIS:CE1	2.27	0.69
1:D:182:PRO:HD3	1:D:191:ARG:NH1	2.06	0.69
1:C:49:PHE:CE2	1:C:53:LYS:HD2	2.26	0.69
1:E:341:ASP:OD2	1:E:343:THR:HG22	1.92	0.69
1:D:434:ALA:HA	1:D:437:LYS:CE	2.22	0.69
1:F:576:ARG:HH11	1:F:576:ARG:CB	2.05	0.69
1:E:205:GLN:O	1:E:210:LEU:HD21	1.92	0.69
1:E:553:PHE:O	1:E:556:VAL:HG23	1.92	0.69
1:F:553:PHE:O	1:F:556:VAL:HG23	1.92	0.69
1:E:569:LEU:HD12	1:F:452:ASP:OD1	1.92	0.69
1:E:327:ILE:HG23	1:E:328:TRP:H	1.58	0.69
1:D:394:LEU:CD2	1:D:448:LEU:HD11	2.23	0.69
1:B:24:THR:HB	1:B:43:GLU:OE1	1.93	0.69
1:C:434:ALA:HA	1:C:437:LYS:HE2	1.75	0.69
1:F:557:ASN:HD22	1:F:560:GLU:CB	2.04	0.69
1:F:376:ILE:HB	1:F:377:PRO:HD3	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:445:LEU:HD22	1:F:448:LEU:HD23	1.74	0.68
1:E:76:ASP:O	1:E:79:PRO:HD3	1.93	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:48:ILE:HG22	1:C:273:LEU:HD13	1.74	0.68
1:F:501:GLU:HB3	1:F:504:GLN:HG3	1.75	0.68
1:B:80:LEU:HA	1:B:118:ASN:HD21	1.58	0.68
2:I:126:THR:HB	2:I:129:MET:HB2	1.75	0.68
2:G:143:GLN:HG2	2:G:182:ASN:ND2	2.07	0.68
1:A:394:LEU:HA	1:A:411:LEU:CD2	2.22	0.68
1:B:262:PRO:HB3	1:B:272:ASN:HD21	1.56	0.68
1:B:77:ARG:HD3	1:B:78:PHE:HE1	1.58	0.68
1:A:624:PRO:HB2	1:A:627:ILE:HG22	1.75	0.68
1:A:376:ILE:HB	1:A:377:PRO:HD3	1.74	0.68
1:B:204:CYS:HB2	1:B:205:GLN:HE21	1.59	0.68
1:D:578:GLU:O	1:D:579:LEU:HD23	1.94	0.68
1:F:366:LEU:HD22	1:F:370:TYR:CE1	2.29	0.68
1:F:297:ASN:HD22	1:F:306:HIS:CG	2.12	0.68
1:A:476:GLU:O	1:A:479:LEU:HB2	1.93	0.68
2:G:125:THR:HG22	2:G:126:THR:N	2.04	0.68
1:A:81:MET:HE1	1:A:319:GLN:HA	1.75	0.68
1:B:145:ARG:CZ	1:B:180:TRP:NE1	2.57	0.68
1:B:64:TRP:HE3	1:B:68:TYR:HE2	1.42	0.68
1:F:506:LYS:HE2	1:F:533:GLU:OE2	1.93	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:557:ASN:HD22	1:D:560:GLU:N	1.92	0.67
1:D:463:HIS:HE1	1:D:498:TYR:HE2	1.41	0.67
1:E:432:LEU:HD13	1:E:464:ILE:CD1	2.24	0.67
1:E:361:VAL:HG23	1:F:578:GLU:OE2	1.94	0.67
1:B:26:ARG:HG3	1:B:26:ARG:O	1.94	0.67
1:E:405:GLU:HG3	1:E:406:SER:N	2.09	0.67
1:A:576:ARG:HG3	1:A:576:ARG:HH11	1.58	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: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:A:66:GLN:HE21	1:A:66:GLN:N	1.92	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
1:A:177:LEU:O	1:A:195:ILE:HD11	1.94	0.67
2:H:147:LEU:HD22	2:H:179:LEU:HD13	1.76	0.67
1:C:364:PHE:HZ	1:C:421:VAL:HG11	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:183:GLY:O	2:I:184:VAL:HG23	1.95	0.67
1:A:42:GLU:O	1:A:45:PRO:HD3	1.94	0.67
1:A:634:LEU:HD11	2:G:174:ALA:HB2	1.77	0.67
1:E:170:TRP:CE3	1:E:202:LEU:HD23	2.30	0.67
1:D:282:GLN:O	1:D:286:ILE:HG13	1.94	0.67
1:C:389:ARG:HH21	1:C:392:LEU:HB2	1.59	0.67
1:B:427:LYS:HB2	1:B:435:SER:CB	2.24	0.67
1:E:228:THR:HG22	1:E:231:ARG:NE	2.10	0.67
1:C:196:ARG:HG2	1:C:200:LYS:HE2	1.76	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: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:497:ILE:HG23	1:C:532:PHE:CD1	2.30	0.67
1:C:115:GLU:HG2	1:C:116:LEU:H	1.59	0.67
1:F:378:GLU:O	1:F:382:THR:HG22	1.94	0.67
1:A:317:ALA:O	1:A:321:VAL:HG22	1.94	0.67
1:D:99:LEU:HD11	1:D:133:LYS:HD3	1.75	0.67
1:E:180:TRP:O	1:E:182:PRO:HD3	1.95	0.66
1:A:71:PHE:CE1	1:A:88:ARG:HA	2.30	0.66
1:B:65:LYS:HD3	1:B:65:LYS:O	1.95	0.66
1:E:56:LYS:HE3	1:E:265:LEU:O	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:D:127:TYR:O	1:D:131:VAL:HG23	1.95	0.66
1:A:625:PRO:O	1:A:626:GLU:HB2	1.95	0.66
1:C:626:GLU:HB3	2:H:149:VAL:HG11	1.75	0.66
1:B:434:ALA:O	1:B:438:ILE:HG13	1.94	0.66
1:B:444:ARG:HH21	2:G:167:GLU:CD	1.97	0.66
2:I:143:GLN:HG2	2:I:182:ASN:HD21	1.58	0.66
1:B:43:GLU:HG2	2:G:113:TRP:CZ3	2.30	0.66
1:F:254:THR:HG23	1:F:257:LEU:HB3	1.76	0.66
2:I:164:LEU:HD23	2:I:165:LEU:N	2.10	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
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:E:554:PRO:O	1:E:555:GLU:HB3	1.96	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:335:GLN:NE2	1:E:348:TYR:HE1	1.88	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:115:GLU:HG2	1:E:116:LEU:N	2.07	0.66
1:A:225:ASN:HB2	1:A:229:ALA:CB	2.18	0.66
1:B:137:ILE:HG23	1:B:145:ARG:HB2	1.76	0.66
1:F:563:THR:HG23	1:F:574:LEU:HB3	1.78	0.66
1:B:86:CYS:HB3	1:B:263:ILE:HG13	1.78	0.66
1:B:447:LYS:HG2	1:B:481:TYR:HB3	1.77	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
2:I:159:GLU:C	2:I:161:PHE:H	1.99	0.66
1:C:275:LYS:H	1:C:275:LYS:HE2	1.61	0.66
1:F:41:ILE:CG1	1:F:50:LEU:HB3	2.26	0.65
1:D:455:LEU:HA	1:D:475:LEU:HD21	1.77	0.65
1:D:396:ALA:O	1:D:398:MET:N	2.28	0.65
1:D:299:LEU:N	1:D:299:LEU:HD12	2.12	0.65
1:F:432:LEU:HA	1:F:435:SER:HB3	1.78	0.65
1:F:392:LEU:HD13	2:I:113:TRP:CZ3	2.32	0.65
2:H:185:CYS:CB	2:H:188:ASP:HB3	2.24	0.65
1:B:137:ILE:HD12	1:B:137:ILE:N	2.10	0.65
1:A:142:GLU:O	1:A:146:ASN:HB2	1.96	0.65
1:F:282:GLN:O	1:F:286:ILE:HG13	1.96	0.65
1:B:165:LYS:HD3	1:B:208:ASP:OD2	1.97	0.65
1:B:366:LEU:C	1:B:368:GLU:H	1.98	0.65
1:C:145:ARG:O	1:C:145:ARG:HD2	1.94	0.65
1:E:131:VAL:HG11	1:E:151:ALA:CB	2.26	0.65
2:G:174:ALA:O	2:G:178:LEU:HB2	1.95	0.65
1:B:206:PRO:HA	1:B:210:LEU:HD11	1.78	0.65
1:B:204:CYS:HB2	1:B:205:GLN:NE2	2.11	0.65
1:B:364:PHE:CZ	1:B:421:VAL:HG11	2.32	0.65
1:F:280:ASP:O	1:F:283:GLN:HB2	1.97	0.65
1:E:489:ILE:HD12	1:E:508:LEU:HD11	1.78	0.65
1:F:398:MET:CG	1:F:408:ILE:HD11	2.22	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
1:E:434:ALA:HA	1:E:437:LYS:NZ	2.11	0.65
1:E:42:GLU:O	1:E:45:PRO:HD3	1.96	0.65
2:I:160:THR:O	2:I:163:ALA:HB3	1.96	0.65
1:F:492:TYR:CE1	1:F:496:LEU:HD11	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:513:ILE:HG22	1:D:552:LYS:HE2	1.78	0.65
1:A:111:CYS:HG	1:A:112:LEU:HD23	1.60	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:A:646:GLU:HB2	1:A:650:PHE:HD2	1.61	0.65
1:D:575:GLN:C	1:D:577:LEU:H	1.99	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:C:237:SER:O	1:C:241:MET:HG2	1.96	0.65
2:H:134:GLU:C	2:H:136:GLY:H	2.01	0.65
1:C:455:LEU:HD22	1:C:455:LEU:N	2.12	0.65
1:E:638:GLN:NE2	1:F:384:LEU:HD12	2.12	0.65
1:E:432:LEU:HD13	1:E:464:ILE:HD11	1.77	0.65
1:D:460:ILE:O	1:D:464:ILE:HG13	1.97	0.65
2:H:134:GLU:O	2:H:137:LYS:HG2	1.96	0.64
1:F:523:LYS:HB2	1:F:553:PHE:CE2	2.31	0.64
1:E:299:LEU:H	1:E:299:LEU:HD12	1.62	0.64
2:I:114:LEU:HD12	2:I:114:LEU:H	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
2:G:147:LEU:HD22	2:G:179:LEU:HD23	1.79	0.64
1:D:156:VAL:HG13	1:D:170:TRP:HH2	1.63	0.64
1:D:52:VAL:HG11	1:D:268:ALA:HB3	1.79	0.64
1:C:493:LEU:O	1:C:497:ILE:HG13	1.98	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: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:A:167:ILE:HG23	1:A:168:GLN:H	1.62	0.64
1:E:255:LYS:O	1:E:257:LEU:N	2.29	0.64
1:D:81:MET:HE1	1:D:319:GLN:O	1.98	0.64
1:C:552:LYS:C	1:C:554:PRO:HD3	2.17	0.64
2:H:146:LEU:O	2:H:150:ILE:HG13	1.97	0.64
2:G:143:GLN:HG3	2:G:178:LEU:HD21	1.80	0.64
1:E:198:LEU:O	1:E:198:LEU:HD12	1.98	0.64
1:B:426:MET:HG3	1:B:438:ILE:HD11	1.79	0.64
1:D:468:THR:HG21	1:D:499:VAL:CG1	2.20	0.64
1:C:563:THR:HG22	1:C:572:ASN:OD1	1.97	0.64
1:A:218:THR:HG22	1:A:233:ILE:HG21	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:400:ASP:O	1:C:401:ASP:HB3	1.97	0.64
1:E:384:LEU:HD23	1:E:387:ILE:HD12	1.80	0.64
1:C:140:GLY:HA3	1:C:144:ALA:HB3	1.79	0.64
2:H:143:GLN:CG	2:H:178:LEU:HD22	2.28	0.64
1:A:99:LEU:HD12	1:A:99:LEU:H	1.61	0.64
1:C:631:LEU:HD12	2:H:115:PRO:HD2	1.79	0.64
1:E:125:LEU:HD21	1:E:169:PHE:HD1	1.63	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:B:202:LEU:HD12	1:B:203:LEU:N	2.13	0.64
1:F:54:LEU:O	1:F:54:LEU:HG	1.97	0.64
1:A:345:ILE:CD1	1:A:345:ILE:H	1.97	0.64
2:G:125:THR:HG23	2:G:129:MET:HE3	1.80	0.64
1:E:631:LEU:HD21	2:I:171:LEU:HD22	1.79	0.64
1:D:287:TRP:O	1:D:291:ILE:HG13	1.97	0.64
1:A:32:ASP:O	1:A:36:LYS:HG3	1.99	0.63
1:C:174:LEU:O	1:C:178:GLU:HG3	1.98	0.63
1:A:462:TYR:HD2	1:A:463:HIS:CE1	2.16	0.63
1:C:283:GLN:HA	1:C:286:ILE:HD12	1.80	0.63
1:E:626:GLU:OE1	2:I:146:LEU:HG	1.98	0.63
1:E:434:ALA:HA	1:E:437:LYS:HZ3	1.63	0.63
1:D:456:GLU:O	1:D:460:ILE:HG13	1.97	0.63
1:C:473:LYS:O	1:C:477:LEU:HD13	1.98	0.63
2:G:125:THR:HG23	2:G:129:MET:CE	2.28	0.63
2:H:186:SER:HA	2:H:189:GLN:HE21	1.62	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
1:E:207:MET:H	1:E:210:LEU:HG	1.63	0.63
1:D:55:LEU:HD13	1:D:265:LEU:HD11	1.80	0.63
1:E:650:PHE:HD2	2:I:165:LEU:HD21	1.63	0.63
1:D:59:VAL:C	1:D:61:LEU:H	2.02	0.63
1:C:644:ILE:HG23	2:H:173:TYR:HE1	1.64	0.63
1:C:30:GLU:HG3	1:C:31:SER:H	1.64	0.63
1:A:280:ASP:OD2	1:A:283:GLN:HG2	1.98	0.63
1:B:59:VAL:HG13	1:B:60:SER:N	2.13	0.63
1:E:479:LEU:HD11	1:E:492:TYR:HE2	1.63	0.63
1:B:130:TYR:C	1:B:132:ARG:H	2.02	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
2:H:186:SER:O	2:H:190:LEU:HG	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:525:ILE:O	1:B:529:VAL:HG23	1.98	0.63
1:A:83:ASN:HB2	1:A:262:PRO:O	1.97	0.63
1:E:173:TYR:CD2	1:E:198:LEU:HD22	2.34	0.63
1:A:61:LEU:HB2	1:A:63:GLN:HE21	1.64	0.63
1:E:43:GLU:O	1:E:44:GLN:HG2	1.98	0.63
1:E:186:PHE:C	1:E:188:GLU:H	2.02	0.63
1:D:542:VAL:O	1:D:546:GLU:HG3	1.97	0.63
1:C:423:MET:HB2	1:C:438:ILE:HG21	1.79	0.63
1:E:136:ASP:HB3	1:E:139:THR:HB	1.81	0.63
1:A:51:TYR:HD1	1:A:74:LEU:HB2	1.64	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:36:LYS:C	1:F:37:LEU:HD12	2.19	0.63
1:F:89:LEU:HD11	1:F:108:LEU:HD21	1.80	0.63
1:D:376:ILE:HB	1:D:377:PRO:HD3	1.80	0.63
1:D:159:CYS:O	1:D:161:ILE:HG12	1.98	0.63
1:A:202:LEU:HD12	1:A:203:LEU:N	2.13	0.63
1:A:579:LEU:CD1	1:A:582:MET:HE1	2.29	0.63
1:D:180:TRP:CZ3	1:D:191:ARG:HB2	2.34	0.63
1:B:77:ARG:HB3	1:B:78:PHE:HD1	1.63	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:C:78:PHE:HB3	1:C:81:MET:HG2	1.78	0.63
1:E:552:LYS:C	1:E:554:PRO:HD3	2.19	0.62
1:E:576:ARG:HB2	1:E:576:ARG:HH11	1.64	0.62
1:A:341:ASP:O	1:A:344:VAL:HG23	1.99	0.62
1:B:442:CYS:O	1:B:445:LEU:HB2	1.99	0.62
1:A:470:THR:O	1:A:474:VAL:HG23	1.99	0.62
1:A:395:ALA:O	1:A:399:GLU:HG3	1.99	0.62
1:E:635:PRO:HB2	1:E:640:PHE:HE1	1.63	0.62
1:A:626:GLU:OE1	2:G:149:VAL:HG21	1.98	0.62
1:F:297:ASN:HB2	1:F:306:HIS:CE1	2.35	0.62
1:A:443:ARG:HD2	1:A:477:LEU:HG	1.81	0.62
1:A:49:PHE:HE2	1:A:53:LYS:HZ2	1.46	0.62
1:A:115:GLU:O	1:A:116:LEU:HD23	1.98	0.62
1:E:237:SER:O	1:E:241:MET:HG2	1.99	0.62
1:C:509:PHE:CD1	1:C:529:VAL:HG21	2.34	0.62
1:F:574:LEU:O	1:F:578:GLU:HB3	1.99	0.62
1:E:48:ILE:HG22	1:E:273:LEU:HD13	1.80	0.62
1:B:422:TYR:CE2	1:B:438:ILE:HD13	2.34	0.62
1:D:371:GLU:HA	1:D:379:ILE:HD11	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:ARG:O	1:A:235:GLU:HG3	1.99	0.62
1:E:253:ILE:HG23	1:E:289:GLU:HG2	1.80	0.62
1:E:125:LEU:CD2	1:E:128:ILE:HD12	2.23	0.62
1:C:509:PHE:CZ	1:C:513:ILE:HD11	2.34	0.62
1:F:456:GLU:O	1:F:460:ILE:HG13	1.99	0.62
1:D:103:VAL:O	1:D:106:PRO:HD2	1.98	0.62
1:B:572:ASN:HD22	1:B:572:ASN:C	2.02	0.62
1:A:639:TYR:CE2	2:G:120:VAL:HG23	2.35	0.62
1:D:426:MET:HG3	1:D:438:ILE:HD11	1.82	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: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:D:37:LEU:HA	1:D:40:MET:HE2	1.81	0.62
1:B:184:ASN:OD1	1:B:185:LYS:N	2.31	0.62
1:C:178:GLU:HA	1:C:191:ARG:NH2	2.13	0.62
1:E:326:GLU:O	1:E:330:ASN:HB2	1.99	0.62
1:D:494:ASP:OD1	1:D:528:LYS:HD3	1.99	0.62
1:B:530:ILE:HG13	1:B:545:LEU:HD22	1.82	0.62
2:G:186:SER:HA	2:G:189:GLN:OE1	1.99	0.62
1:F:371:GLU:OE2	1:F:429:ILE:HD11	2.00	0.62
1:C:412:LYS:NZ	1:C:448:LEU:HA	2.14	0.62
1:A:99:LEU:HB2	1:A:134:LYS:HZ1	1.63	0.62
1:E:573:TYR:HD1	1:F:417:TYR:HB2	1.64	0.62
1:A:174:LEU:HD11	1:A:199:TYR:CZ	2.35	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:A:513:ILE:N	1:A:513:ILE:HD12	2.15	0.62
1:E:557:ASN:ND2	1:E:560:GLU:N	2.48	0.62
1:E:200:LYS:CG	1:E:236:LEU:HD21	2.29	0.62
1:D:41:ILE:O	1:D:41:ILE:HG22	1.99	0.62
1:E:401:ASP:C	1:E:403:THR:H	2.03	0.62
1:E:426:MET:HG3	1:E:438:ILE:HD11	1.80	0.61
1:B:427:LYS:HB2	1:B:435:SER:HB2	1.82	0.61
1:B:378:GLU:N	1:B:378:GLU:OE2	2.32	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:C:640:PHE:HA	1:C:642:VAL:HG22	1.82	0.61
1:E:560:GLU:O	1:E:563:THR:OG1	2.16	0.61
1:A:65:LYS:HD3	1:A:65:LYS:C	2.20	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)
1:B:218:THR:HA	1:B:233:ILE:CD1	2.30	0.61
1:E:400:ASP:O	1:E:401:ASP:HB3	2.00	0.61
1:B:281:VAL:HG12	1:B:285:LEU:HD11	1.81	0.61
1:A:92:GLU:OE2	1:A:103:VAL:HG11	2.00	0.61
1:C:226:GLN:CD	1:C:226:GLN:H	2.02	0.61
1:D:77:ARG:HB3	1:D:78:PHE:CD1	2.36	0.61
1:A:165:LYS:HD3	1:A:208:ASP:HB3	1.81	0.61
1:C:460:ILE:O	1:C:464:ILE:HG13	2.00	0.61
1:E:159:CYS:SG	1:E:160:ALA:N	2.73	0.61
1:E:41:ILE:HG22	1:E:41:ILE:O	2.00	0.61
1:E:137:ILE:HD12	1:E:179:HIS:NE2	2.15	0.61
1:C:569:LEU:O	1:C:571:VAL:HG23	2.01	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:A:59:VAL:HG13	1:A:60:SER:N	2.16	0.61
1:A:638:GLN:O	1:A:641:LYS:HE3	2.00	0.61
1:A:128:ILE:HG12	1:A:152:PHE:CE1	2.36	0.61
1:E:41:ILE:CG1	1:E:50:LEU:HD22	2.30	0.61
1:F:534:SER:HA	1:F:542:VAL:HG21	1.82	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:A:81:MET:CE	1:A:319:GLN:HA	2.31	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:E:311:THR:O	1:E:315:MET:HG3	2.00	0.61
1:C:432:LEU:HD22	1:C:464:ILE:HD13	1.81	0.61
1:C:103:VAL:O	1:C:106:PRO:HD2	2.00	0.61
1:E:638:GLN:O	1:E:641:LYS:HG3	2.01	0.61
1:E:265:LEU:HD23	1:E:265:LEU:O	2.01	0.61
1:E:280:ASP:HB3	1:E:283:GLN:HB2	1.82	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:D:546:GLU:OE2	1:D:565:LYS:HE2	2.01	0.61
1:C:501:GLU:O	1:C:504:GLN:N	2.31	0.61
1:B:506:LYS:NZ	1:B:545:LEU:HD12	2.16	0.60
1:A:634:LEU:HD11	2:G:174:ALA:CB	2.31	0.60
1:A:283:GLN:CA	1:A:286:ILE:HD12	2.30	0.60
1:B:390:ILE:HG22	1:B:415:LEU:HD13	1.81	0.60
1:B:267:GLN:O	1:B:269:THR:HG23	2.00	0.60
1:E:135:ASN:ND2	1:E:147:ILE:HG21	2.15	0.60
1:C:205:GLN:O	1:C:207:MET:HG3	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:557:ASN:ND2	1:F:560:GLU:N	2.49	0.60
1:A:106:PRO:O	1:A:109:ALA:HB3	2.00	0.60
1:B:202:LEU:HD12	1:B:202:LEU:C	2.20	0.60
1:F:77:ARG:HB3	1:F:78:PHE:CD1	2.36	0.60
1:C:275:LYS:HE2	1:C:278:GLU:OE1	2.01	0.60
1:A:270:GLU:HG2	1:A:270:GLU:O	2.01	0.60
1:D:275:LYS:N	1:D:275:LYS:HD3	2.15	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:N	1:A:345:ILE:HD12	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:200:LYS:HG2	1:D:236:LEU:HD11	1.83	0.60
1:A:400:ASP:O	1:A:401:ASP:HB3	2.01	0.60
2:I:125:THR:HG22	2:I:129:MET:CE	2.31	0.60
1:B:78:PHE:N	1:B:78:PHE:CD1	2.69	0.60
1:A:624:PRO:HB2	1:A:627:ILE:CG2	2.31	0.60
1:F:509:PHE:O	1:F:513:ILE:HG13	2.01	0.60
1:F:254:THR:HG23	1:F:257:LEU:CB	2.30	0.60
1:A:427:LYS:HB2	1:A:435:SER:OG	2.01	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
2:H:134:GLU:HA	2:H:137:LYS:HE2	1.83	0.60
2:H:114:LEU:H	2:H:114:LEU:HD12	1.66	0.60
1:E:325:PRO:HD3	1:E:356:ILE:CD1	2.30	0.60
1:F:156:VAL:HA	1:F:160:ALA:HB3	1.82	0.60
1:F:71:PHE:CD2	1:F:88:ARG:HB2	2.36	0.60
1:E:41:ILE:HG13	1:E:50:LEU:HD22	1.82	0.60
1:B:86:CYS:CB	1:B:263:ILE:HG13	2.31	0.60
1:E:263:ILE:HG22	1:E:267:GLN:NE2	2.17	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
2:I:188:ASP:C	2:I:190:LEU:H	2.04	0.60
1:B:192:VAL:HG12	1:B:220:TRP:CH2	2.36	0.60
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:E:332:ALA:O	1:E:335:GLN:HB2	2.02	0.60
1:B:307:LYS:HE3	1:B:338:LYS:HG3	1.83	0.60
1:D:455:LEU:HD13	1:D:475:LEU:CD2	2.31	0.60
1:C:81:MET:CE	1:C:319:GLN:HA	2.32	0.60
2:G:159:GLU:O	2:G:162:VAL:HG22	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:ILE:O	1:B:358:ASN:N	2.35	0.60
1:A:339:ASN:HD22	1:A:339:ASN:C	2.05	0.60
1:A:58:HIS:ND1	1:A:66:GLN:HB3	2.16	0.60
1:D:560:GLU:HA	1:D:582:MET:HE3	1.84	0.60
1:B:364:PHE:HZ	1:B:421:VAL:HG11	1.65	0.60
1:C:553:PHE:O	1:C:556:VAL:HG23	2.00	0.60
1:B:559:LEU:HD21	1:B:579:LEU:HD11	1.84	0.60
1:C:186:PHE:C	1:C:188:GLU:H	2.05	0.60
1:B:227:LEU:O	1:B:227:LEU:HD23	2.02	0.60
1:A:179:HIS:CG	1:A:179:HIS:O	2.55	0.60
1:A:99:LEU:N	1:A:99:LEU:HD12	2.16	0.59
1:F:576:ARG:NH1	1:F:576:ARG:HB3	2.14	0.59
1:F:533:GLU:HB3	1:F:542:VAL:HG22	1.82	0.59
1:C:44:GLN:H	1:C:45:PRO:CD	2.15	0.59
1:F:354:GLN:O	1:F:357:PRO:HD3	2.02	0.59
1:B:252:ASN:O	1:B:255:LYS:HG2	2.02	0.59
1:E:309:ARG:O	1:E:312:TYR:N	2.29	0.59
1:C:131:VAL:HG11	1:C:151:ALA:HB2	1.83	0.59
1:E:449:VAL:O	1:E:449:VAL:HG23	2.00	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:C:542:VAL:O	1:C:546:GLU:HG3	2.02	0.59
2:H:150:ILE:HG23	2:H:161:PHE:HE1	1.66	0.59
1:B:548:ARG:NH1	1:B:548:ARG:HG2	2.10	0.59
1:C:371:GLU:HA	1:C:379:ILE:HD11	1.84	0.59
1:C:79:PRO:O	1:C:80:LEU:HD23	2.02	0.59
1:D:222:GLN:HA	1:D:226:GLN:HA	1.84	0.59
1:A:245:SER:O	1:A:248:GLN:HB2	2.02	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: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:B:99:LEU:HB2	1:B:134:LYS:NZ	2.16	0.59
1:E:259:ARG:HH12	1:E:290:TRP:HH2	1.48	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
1:B:524:MET:O	1:B:528:LYS:HG3	2.03	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:D:451:PRO:HG3	1:D:482:PHE:CD2	2.37	0.59
1:B:259:ARG:HD3	1:B:287:TRP:CH2	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:164:LEU:HD12	2:G:164:LEU:O	2.03	0.59
1:C:153:GLN:O	1:C:156:VAL:HB	2.02	0.59
1:B:89:LEU:HD21	1:B:107:VAL:CG1	2.31	0.59
1:D:330:ASN:ND2	1:D:330:ASN:N	2.51	0.59
2:G:150:ILE:HG21	2:G:175:ILE:HD13	1.85	0.59
1:A:307:LYS:HD2	1:A:334:TYR:OH	2.03	0.59
1:F:350:LYS:NZ	1:F:354:GLN:HE21	2.00	0.59
1:C:425:THR:HG22	1:C:426:MET:CE	2.33	0.59
1:C:631:LEU:HD21	2:H:171:LEU:HD12	1.83	0.59
1:B:119:ASN:OD1	1:B:159:CYS:HB2	2.03	0.59
1:B:71:PHE:CE2	1:B:88:ARG:HB2	2.37	0.59
2:G:189:GLN:HG3	2:G:190:LEU:N	2.17	0.59
1:A:85:TRP:CD2	1:A:111:CYS:HB3	2.36	0.59
1:F:275:LYS:HE2	1:F:275:LYS:H	1.67	0.59
1:E:284:LEU:HB2	1:E:321:VAL:HG11	1.85	0.59
1:A:575:GLN:HE21	1:A:582:MET:CE	2.16	0.59
1:E:44:GLN:H	1:E:45:PRO:HD3	1.68	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:N	1:D:455:LEU:HD22	2.18	0.59
1:A:196:ARG:NH1	1:A:232:HIS:HE1	2.01	0.59
1:C:361:VAL:HG22	1:D:574:LEU:CD1	2.30	0.58
1:E:557:ASN:HD22	1:E:560:GLU:CB	2.13	0.58
1:C:563:THR:HG23	1:C:574:LEU:HD12	1.83	0.58
1:C:85:TRP:CD2	1:C:111:CYS:HB3	2.38	0.58
1:E:285:LEU:HD23	1:E:285:LEU:O	2.03	0.58
2:I:168:ALA:HB1	2:I:170:GLN:OE1	2.04	0.58
1:E:165:LYS:HE2	1:E:250:TRP:HZ3	1.66	0.58
1:D:284:LEU:O	1:D:287:TRP:N	2.35	0.58
1:E:282:GLN:O	1:E:286:ILE:HG13	2.02	0.58
1:D:412:LYS:O	1:D:415:LEU:HB3	2.04	0.58
2:H:116:VAL:HG23	2:H:117:GLY:N	2.17	0.58
1:A:451:PRO:HB3	1:A:488:TYR:CD1	2.38	0.58
1:A:173:TYR:CE2	1:A:198:LEU:HD13	2.38	0.58
1:A:54:LEU:HG	1:A:58:HIS:HD2	1.68	0.58
1:E:470:THR:O	1:E:474:VAL:HG23	2.03	0.58
1:A:280:ASP:HB3	1:A:283:GLN:HB2	1.84	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:B:305:LEU:O	1:B:308:ALA:HB3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:492:TYR:CE1	1:A:496:LEU:HD11	2.37	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
2:I:179:LEU:HG	2:I:184:VAL:HG21	1.84	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
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:B:77:ARG:HB3	1:B:78:PHE:CD1	2.37	0.58
1:C:543:ARG:CZ	1:D:372:LEU:HD11	2.34	0.58
1:F:490:ASN:HB3	1:F:528:LYS:HZ1	1.67	0.58
2:I:147:LEU:HD23	2:I:148:LYS:N	2.19	0.58
1:D:32:ASP:O	1:D:34:ILE:N	2.36	0.58
1:E:40:MET:HB3	1:E:50:LEU:HD21	1.85	0.58
1:A:432:LEU:O	1:A:432:LEU:HD12	2.03	0.58
1:C:332:ALA:O	1:C:345:ILE:HG12	2.04	0.58
1:A:103:VAL:O	1:A:106:PRO:HD2	2.03	0.58
1:B:180:TRP:HB3	1:B:191:ARG:NH1	2.18	0.58
1:F:78:PHE:HB3	1:F:81:MET:HG2	1.85	0.58
1:B:341:ASP:C	1:B:343:THR:H	2.07	0.58
1:C:636:LYS:C	1:C:638:GLN:H	2.06	0.58
1:F:516:ILE:HG22	1:F:517:SER:O	2.04	0.58
1:E:442:CYS:O	1:E:445:LEU:HB2	2.04	0.58
1:E:156:VAL:O	1:E:160:ALA:HB3	2.04	0.58
1:F:168:GLN:HG3	1:F:169:PHE:N	2.18	0.58
1:E:48:ILE:HA	1:E:51:TYR:HD2	1.69	0.58
1:A:79:PRO:C	1:A:80:LEU:HD23	2.24	0.58
1:D:502:GLU:OE2	1:D:536:VAL:HG11	2.03	0.58
1:C:121:LEU:HG	1:C:159:CYS:SG	2.44	0.58
1:A:412:LYS:NZ	1:A:448:LEU:HA	2.19	0.58
1:D:136:ASP:HB3	1:D:139:THR:CB	2.32	0.58
1:F:81:MET:HE2	1:F:319:GLN:HA	1.86	0.58
1:C:452:ASP:HA	1:C:455:LEU:HD23	1.86	0.58
1:B:28:ARG:HH21	1:F:33:VAL:HG11	1.69	0.58
1:D:358:ASN:HB3	1:D:389:ARG:HG3	1.85	0.58
1:D:186:PHE:C	1:D:188:GLU:H	2.07	0.58
1:B:545:LEU:HA	1:B:548:ARG:HD3	1.86	0.58
1:A:210:LEU:HD11	1:A:243:ALA:HB1	1.85	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:580:ASP:C	1:F:582:MET:H	2.05	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:LEU:HA	1:A:354:GLN:OE1	2.04	0.58
1:F:336:GLY:HA3	1:F:345:ILE:HG13	1.86	0.58
1:A:66:GLN:HE21	1:A:66:GLN:CA	2.17	0.57
1:D:457:ASN:O	1:D:461:GLU:HG2	2.04	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: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:F:371:GLU:CA	1:F:379:ILE:HD11	2.34	0.57
1:F:167:ILE:HG23	1:F:168:GLN:N	2.18	0.57
1:E:320:HIS:O	1:E:322:CYS:N	2.37	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:C:636:LYS:O	1:C:638:GLN:N	2.36	0.57
1:D:434:ALA:O	1:D:438:ILE:HG13	2.03	0.57
1:E:115:GLU:CG	1:E:116:LEU:H	2.12	0.57
1:A:180:TRP:O	1:A:182:PRO:HD3	2.05	0.57
1:E:299:LEU:HD21	1:E:309:ARG:NH1	2.19	0.57
1:D:221:GLU:HB3	1:D:229:ALA:CB	2.34	0.57
1:C:257:LEU:HD12	1:C:283:GLN:HE22	1.67	0.57
1:A:398:MET:C	1:A:400:ASP:H	2.08	0.57
1:F:81:MET:HE1	1:F:322:CYS:HB3	1.86	0.57
1:B:78:PHE:N	1:B:78:PHE:HD1	2.03	0.57
1:A:324:ALA:O	1:A:327:ILE:HG22	2.03	0.57
1:E:258:LYS:HG3	1:E:260:ASN:OD1	2.04	0.57
1:B:419:TYR:OH	1:B:441:LYS:HE3	2.03	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:E:394:LEU:HD12	1:E:411:LEU:HD23	1.87	0.57
1:E:200:LYS:O	1:E:204:CYS:SG	2.57	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:A:524:MET:HE2	1:A:528:LYS:HE2	1.86	0.57
1:C:325:PRO:HD3	1:C:356:ILE:HD13	1.87	0.57
1:F:240:TYR:O	1:F:243:ALA:HB3	2.05	0.57
1:A:85:TRP:CE3	1:A:111:CYS:HB3	2.39	0.57
1:A:202:LEU:HD13	1:A:207:MET:HE1	1.87	0.57
1:A:84:ILE:HA	1:A:87:MET:HE3	1.86	0.57
1:E:173:TYR:HE2	1:E:198:LEU:HB2	1.69	0.57
1:A:79:PRO:HG3	1:A:351:LEU:HD22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:275:LYS:HE2	1:E:275:LYS:H	1.70	0.57
1:A:191:ARG:HG3	1:A:191:ARG:HH11	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:386:CYS:O	1:F:390:ILE:HG13	2.05	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: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:C:41:ILE:HG12	1:C:50:LEU:HB3	1.87	0.57
1:E:154:VAL:O	1:E:158:LYS:HG2	2.04	0.57
1:D:128:ILE:HA	1:D:131:VAL:CG2	2.34	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:F:364:PHE:HZ	1:F:421:VAL:HG11	1.69	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:B:476:GLU:HA	1:B:479:LEU:HD12	1.87	0.57
1:F:394:LEU:HD12	1:F:411:LEU:HD23	1.85	0.57
1:A:167:ILE:HG23	1:A:168:GLN:N	2.18	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:425:THR:HG22	1:A:426:MET:CE	2.34	0.56
1:E:145:ARG:NH2	1:E:180:TRP:CZ2	2.73	0.56
1:D:167:ILE:HD12	1:D:209:CYS:HB3	1.86	0.56
1:D:115:GLU:C	1:D:117:GLY:H	2.07	0.56
1:B:427:LYS:HB2	1:B:435:SER:HB3	1.86	0.56
2:H:145:ALA:O	2:H:149:VAL:HG23	2.05	0.56
1:C:37:LEU:HD23	1:C:54:LEU:HD13	1.87	0.56
1:E:533:GLU:HG3	1:E:545:LEU:HD12	1.87	0.56
1:A:130:TYR:C	1:A:132:ARG:H	2.08	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:459:TYR:CE1	1:C:495:PHE:HD1	2.22	0.56
1:E:309:ARG:O	1:E:312:TYR:HB3	2.04	0.56
1:C:168:GLN:HG3	1:C:169:PHE:N	2.20	0.56
1:F:115:GLU:N	1:F:115:GLU:CD	2.59	0.56
1:E:287:TRP:CZ2	1:E:320:HIS:CG	2.94	0.56
1:E:460:ILE:O	1:E:464:ILE:HG13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:552:LYS:C	1:B:554:PRO:HD3	2.25	0.56
1:A:115:GLU:OE2	1:A:115:GLU:N	2.36	0.56
1:A:228:THR:HG22	1:A:231:ARG:HH22	1.69	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:A:93:PHE:HE2	1:A:104:ILE:HD13	1.70	0.56
1:E:114:LYS:N	1:E:114:LYS:HD3	2.20	0.56
1:E:119:ASN:O	1:E:316:GLN:NE2	2.38	0.56
1:E:173:TYR:CE2	1:E:198:LEU:HD22	2.40	0.56
1:E:107:VAL:HA	1:E:110:ARG:CD	2.36	0.56
1:C:553:PHE:HB3	1:C:556:VAL:HG21	1.88	0.56
1:F:85:TRP:CD2	1:F:111:CYS:HB3	2.39	0.56
1:E:137:ILE:HG13	1:E:138:ILE:HG13	1.87	0.56
1:C:54:LEU:HD23	1:C:70:THR:HG23	1.88	0.56
1:B:167:ILE:HG23	1:B:168:GLN:N	2.21	0.56
1:A:170:TRP:CZ3	1:A:202:LEU:HB3	2.41	0.56
1:C:217:TYR:CE2	1:C:236:LEU:HD12	2.41	0.56
1:E:344:VAL:O	1:E:347:LYS:HB3	2.05	0.56
2:I:184:VAL:O	2:I:185:CYS:HB2	2.05	0.56
1:F:78:PHE:HB3	1:F:81:MET:HG3	1.86	0.56
1:A:49:PHE:CE2	1:A:53:LYS:HD3	2.40	0.56
1:C:456:GLU:O	1:C:460:ILE:HG13	2.06	0.56
1:A:387:ILE:HG22	1:A:388:ASP:N	2.20	0.56
1:E:557:ASN:HD22	1:E:560:GLU:H	1.49	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: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:C:523:LYS:O	1:C:527:GLN:HG3	2.05	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:642:VAL:O	1:C:643:THR:HG23	2.06	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:425:THR:HG22	1:C:426:MET:HE2	1.87	0.56
1:C:37:LEU:O	1:C:41:ILE:HG13	2.06	0.56
1:D:181:LYS:O	1:D:181:LYS:HG3	2.06	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:A:33:VAL:HG12	1:A:37:LEU:HG	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:F:493:LEU:CD2	1:F:508:LEU:HD23	2.35	0.56
1:C:455:LEU:HB2	1:D:569:LEU:HD11	1.88	0.56
1:D:324:ALA:O	1:D:327:ILE:HG22	2.06	0.56
1:A:116:LEU:O	1:A:118:ASN:N	2.38	0.56
1:D:414:LYS:O	1:D:418:VAL:HG23	2.05	0.56
1:A:649:ALA:C	1:A:651:SER:H	2.10	0.56
1:D:30:GLU:HG3	1:D:31:SER:N	2.21	0.56
1:F:270:GLU:O	1:F:270:GLU:HG2	2.06	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:F:563:THR:CG2	1:F:572:ASN:HD21	2.18	0.56
1:F:83:ASN:ND2	1:F:261:LEU:HB3	2.21	0.56
1:E:101:ALA:CB	1:E:134:LYS:HE2	2.36	0.56
1:F:432:LEU:HD22	1:F:464:ILE:CD1	2.35	0.56
1:B:391:HIS:CD2	1:B:415:LEU:HD21	2.41	0.56
2:G:139:GLN:O	2:G:142:GLN:HG2	2.06	0.56
1:B:183:VAL:HG23	1:B:187:GLU:OE1	2.06	0.56
1:E:177:LEU:O	1:E:195:ILE:HD11	2.07	0.55
1:A:128:ILE:HG12	1:A:152:PHE:CD1	2.41	0.55
1:F:578:GLU:O	1:F:579:LEU:HD23	2.06	0.55
1:B:427:LYS:HA	1:B:435:SER:HB3	1.88	0.55
1:B:115:GLU:CD	1:B:115:GLU:H	2.10	0.55
1:E:174:LEU:HD11	1:E:199:TYR:CZ	2.41	0.55
1:E:574:LEU:HD13	1:E:574:LEU:O	2.07	0.55
1:F:571:VAL:HB	1:F:573:TYR:CE2	2.42	0.55
1:E:306:HIS:O	1:E:309:ARG:HB3	2.06	0.55
1:D:295:SER:C	1:D:297:ASN:H	2.10	0.55
1:E:468:THR:HG23	1:E:499:VAL:HG11	1.87	0.55
1:D:37:LEU:HA	1:D:40:MET:CE	2.35	0.55
1:E:41:ILE:HD12	1:E:54:LEU:HD22	1.88	0.55
1:A:247:TYR:CE1	1:A:251:LEU:HD22	2.39	0.55
1:F:416:THR:OG1	1:F:449:VAL:HB	2.06	0.55
1:A:361:VAL:HG23	1:B:578:GLU:OE1	2.06	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:B:580:ASP:C	1:B:582:MET:H	2.10	0.55
1:F:557:ASN:ND2	1:F:560:GLU:HB2	2.15	0.55
1:E:489:ILE:HG13	1:E:516:ILE:HD11	1.88	0.55
1:B:192:VAL:HG12	1:B:220:TRP:CZ2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:521:LEU:O	1:F:525:ILE:HD13	2.06	0.55
1:F:364:PHE:CZ	1:F:421:VAL:HG11	2.42	0.55
1:D:511:SER:O	1:D:515:LYS:HE2	2.07	0.55
1:F:160:ALA:HB1	1:F:170:TRP:CZ2	2.42	0.55
1:D:345:ILE:O	1:D:349:LEU:HB2	2.06	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:A:480:LYS:HD3	1:A:480:LYS:N	2.22	0.55
2:G:125:THR:HA	2:G:129:MET:HE2	1.89	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:E:107:VAL:HA	1:E:110:ARG:HG3	1.89	0.55
1:A:646:GLU:HG3	1:A:650:PHE:HE2	1.72	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:C:47:ASP:HB2	1:C:276:PRO:CG	2.37	0.55
1:B:41:ILE:HD11	1:B:50:LEU:O	2.06	0.55
1:D:269:THR:OG1	1:D:271:SER:HB3	2.07	0.55
1:A:137:ILE:N	1:A:137:ILE:HD12	2.18	0.55
1:E:471:ALA:O	1:E:475:LEU:HD12	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
2:I:175:ILE:O	2:I:179:LEU:HD13	2.07	0.55
1:B:132:ARG:HH11	1:B:132:ARG:HG2	1.71	0.55
1:B:341:ASP:O	1:B:344:VAL:HG23	2.06	0.55
1:B:100:ASP:O	1:B:102:ALA:N	2.40	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:B:58:HIS:CE1	1:B:66:GLN:HG2	2.41	0.55
1:E:457:ASN:O	1:E:460:ILE:HB	2.07	0.55
1:E:580:ASP:C	1:E:582:MET:H	2.08	0.55
1:E:125:LEU:C	1:E:127:TYR:H	2.08	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:B:246:LEU:CD1	1:B:299:LEU:HD23	2.37	0.55
1:D:258:LYS:HG3	1:D:260:ASN:OD1	2.07	0.54
1:D:560:GLU:HA	1:D:582:MET:CE	2.37	0.54
1:D:103:VAL:C	1:D:106:PRO:HD2	2.27	0.54
1:F:536:VAL:HG12	1:F:536:VAL:O	2.06	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:H:179:LEU:O	2:H:184:VAL:HB	2.08	0.54
2:I:167:GLU:O	2:I:168:ALA:HB2	2.08	0.54
1:F:60:SER:O	1:F:61:LEU:HD23	2.06	0.54
1:B:325:PRO:HD3	1:B:356:ILE:HD13	1.89	0.54
1:E:568:VAL:CG2	1:F:417:TYR:CE1	2.91	0.54
1:B:103:VAL:O	1:B:106:PRO:HD2	2.07	0.54
1:C:455:LEU:H	1:C:455:LEU:HD22	1.71	0.54
1:F:145:ARG:NH2	1:F:180:TRP:CZ2	2.75	0.54
1:F:265:LEU:O	1:F:265:LEU:HD23	2.07	0.54
1:A:131:VAL:HG11	1:A:151:ALA:HB2	1.88	0.54
1:D:167:ILE:HG12	1:D:171:ASN:ND2	2.22	0.54
1:C:399:GLU:HG3	1:C:400:ASP:N	2.22	0.54
1:A:451:PRO:HG3	1:A:482:PHE:CD2	2.42	0.54
1:A:156:VAL:O	1:A:161:ILE:HG23	2.07	0.54
1:E:459:TYR:O	1:E:463:HIS:HB2	2.07	0.54
1:B:451:PRO:HB3	1:B:488:TYR:CD1	2.43	0.54
1:B:36:LYS:O	1:B:40:MET:HG3	2.06	0.54
1:A:230:ARG:O	1:A:230:ARG:HG2	2.07	0.54
1:A:517:SER:O	1:A:518:ASP:C	2.46	0.54
2:I:170:GLN:N	2:I:170:GLN:HE21	1.98	0.54
1:B:61:LEU:HD12	1:B:63:GLN:NE2	2.22	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:C:529:VAL:HG12	1:C:545:LEU:CD1	2.37	0.54
1:F:460:ILE:O	1:F:464:ILE:HG13	2.07	0.54
2:H:134:GLU:C	2:H:136:GLY:N	2.61	0.54
1:D:59:VAL:HG22	1:D:67:VAL:HG21	1.88	0.54
1:B:121:LEU:HG	1:B:159:CYS:SG	2.47	0.54
1:B:314:TYR:HB3	1:B:331:MET:HE3	1.89	0.54
1:E:335:GLN:HA	1:E:335:GLN:OE1	2.07	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:A:115:GLU:CD	1:A:115:GLU:H	2.11	0.54
1:F:463:HIS:HE1	1:F:498:TYR:HE2	1.55	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:400:ASP:O	1:F:401:ASP:CB	2.55	0.54
1:F:200:LYS:HG2	1:F:236:LEU:CD1	2.37	0.54
1:D:159:CYS:O	1:D:161:ILE:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:122:SER:OG	1:C:263:ILE:HD11	2.08	0.54
1:B:38:ASN:N	1:B:38:ASN:HD22	2.04	0.54
1:A:417:TYR:HE1	1:B:568:VAL:HG23	1.72	0.54
2:G:185:CYS:O	2:G:186:SER:HB2	2.07	0.54
1:E:637:ARG:CZ	2:I:116:VAL:HG12	2.38	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: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
1:E:81:MET:CE	1:E:319:GLN:HA	2.38	0.54
1:A:81:MET:HE2	1:A:319:GLN:HG3	1.90	0.54
1:E:93:PHE:CZ	1:E:130:TYR:HB2	2.39	0.54
1:B:100:ASP:C	1:B:102:ALA:H	2.12	0.54
1:D:384:LEU:O	1:D:387:ILE:N	2.41	0.54
2:I:187:VAL:N	2:I:189:GLN:HE22	2.06	0.54
1:C:101:ALA:HB2	1:C:134:LYS:CE	2.38	0.54
1:F:81:MET:CE	1:F:319:GLN:HA	2.37	0.54
1:C:633:VAL:HA	2:H:118:VAL:CG2	2.38	0.54
2:G:138:LEU:HB3	2:G:142:GLN:HG3	1.90	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:D:145:ARG:HH11	1:D:149:ILE:HD11	1.73	0.54
1:A:557:ASN:HB3	1:A:560:GLU:HB3	1.88	0.54
1:A:629:GLU:OE1	1:A:632:LYS:HE2	2.09	0.53
1:C:115:GLU:C	1:C:117:GLY:N	2.60	0.53
1:D:37:LEU:HD12	1:D:40:MET:HE2	1.88	0.53
1:E:167:ILE:HD12	1:E:209:CYS:HB3	1.90	0.53
1:C:501:GLU:O	1:C:502:GLU:C	2.47	0.53
1:F:413:SER:O	1:F:416:THR:N	2.42	0.53
1:E:225:ASN:O	1:E:229:ALA:HB2	2.08	0.53
1:B:496:LEU:HD22	1:B:501:GLU:CB	2.37	0.53
1:A:336:GLY:C	1:A:338:LYS:N	2.62	0.53
2:I:134:GLU:O	2:I:137:LYS:HE3	2.08	0.53
1:F:353:GLN:O	1:F:357:PRO:HA	2.08	0.53
1:F:151:ALA:O	1:F:154:VAL:HG12	2.08	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:E:195:ILE:O	1:E:199:TYR:CD2	2.62	0.53
1:C:127:TYR:O	1:C:131:VAL:HG23	2.08	0.53
2:H:171:LEU:O	2:H:171:LEU:HD23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:521:LEU:O	1:C:525:ILE:HD13	2.07	0.53
2:H:147:LEU:HD22	2:H:179:LEU:CD1	2.38	0.53
1:E:571:VAL:HB	1:E:573:TYR:CE2	2.43	0.53
1:A:202:LEU:HD12	1:A:202:LEU:C	2.29	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:E:434:ALA:HB2	1:E:437:LYS:HZ1	1.74	0.53
1:A:343:THR:O	1:A:343:THR:HG22	2.08	0.53
1:D:473:LYS:O	1:D:477:LEU:HD13	2.07	0.53
1:F:75:HIS:HB3	1:F:110:ARG:HH21	1.73	0.53
1:A:569:LEU:CD2	1:B:456:GLU:HG2	2.38	0.53
1:A:170:TRP:CE3	1:A:202:LEU:HD23	2.44	0.53
1:C:157:ASP:HA	1:C:161:ILE:HD11	1.90	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:D:81:MET:HE1	1:D:322:CYS:HB3	1.91	0.53
1:C:140:GLY:O	1:C:142:GLU:N	2.41	0.53
1:D:74:LEU:HD13	1:D:84:ILE:HD13	1.91	0.53
1:F:486:GLY:C	1:F:521:LEU:HD22	2.29	0.53
1:C:490:ASN:ND2	1:C:525:ILE:CD1	2.72	0.53
1:A:390:ILE:HD13	1:A:414:LYS:HG2	1.91	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:B:130:TYR:C	1:B:132:ARG:N	2.62	0.53
1:B:132:ARG:NH1	1:B:132:ARG:HG2	2.24	0.53
1:A:218:THR:HG22	1:A:233:ILE:CG2	2.38	0.53
1:F:275:LYS:HE2	1:F:278:GLU:HG2	1.90	0.53
1:A:162:PHE:HA	1:A:309:ARG:NH1	2.24	0.53
1:E:103:VAL:C	1:E:106:PRO:HD2	2.29	0.53
1:A:542:VAL:HG12	1:A:546:GLU:HG3	1.90	0.53
2:H:168:ALA:HA	2:H:170:GLN:HE22	1.74	0.53
1:C:398:MET:HA	1:C:408:ILE:CD1	2.33	0.53
1:A:89:LEU:HD21	1:A:107:VAL:HG11	1.91	0.53
2:H:155:LYS:HE2	2:H:156:ASP:OD1	2.09	0.53
1:C:218:THR:HG23	1:C:233:ILE:HD13	1.91	0.53
1:F:145:ARG:NH2	1:F:180:TRP:HZ2	2.07	0.53
1:D:341:ASP:HB3	1:D:344:VAL:HG23	1.91	0.53
1:C:262:PRO:CG	1:C:273:LEU:HD21	2.31	0.53
1:C:468:THR:O	1:C:469:LYS:C	2.47	0.53
1:B:61:LEU:HB2	1:B:63:GLN:NE2	2.20	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:C:392:LEU:O	1:C:393:ASP:C	2.46	0.53
1:B:479:LEU:O	1:B:480:LYS:C	2.47	0.53
1:F:281:VAL:HG12	1:F:285:LEU:HD12	1.91	0.53
1:B:572:ASN:OD1	1:B:575:GLN:HG3	2.09	0.53
1:D:269:THR:C	1:D:271:SER:H	2.12	0.53
1:C:655:SER:O	2:H:151:GLN:NE2	2.42	0.53
1:C:228:THR:O	1:C:231:ARG:HB3	2.09	0.53
1:A:189:GLN:O	1:A:192:VAL:HG22	2.09	0.53
1:B:467:ASP:OD1	1:B:470:THR:HG23	2.09	0.53
1:F:226:GLN:C	1:F:227:LEU:HD12	2.29	0.53
1:F:553:PHE:O	1:F:554:PRO:O	2.27	0.53
1:B:401:ASP:O	1:B:401:ASP:CG	2.48	0.53
1:A:68:TYR:OH	1:A:92:GLU:OE2	2.27	0.53
1:D:115:GLU:N	1:D:115:GLU:CD	2.60	0.53
1:B:24:THR:CG2	1:B:43:GLU:HG3	2.39	0.53
1:C:206:PRO:HG3	1:C:246:LEU:HB2	1.90	0.53
2:I:146:LEU:HD23	2:I:146:LEU:O	2.08	0.53
1:A:374:THR:O	1:A:376:ILE:N	2.42	0.53
1:E:281:VAL:O	1:E:285:LEU:HB2	2.10	0.53
1:A:135:ASN:ND2	1:A:147:ILE:HG21	2.23	0.53
1:C:192:VAL:HG23	1:C:193:GLN:H	1.74	0.53
1:B:179:HIS:CG	1:B:179:HIS:O	2.59	0.53
2:H:135:LEU:HD13	2:H:177:GLU:HG2	1.91	0.52
2:G:114:LEU:CD2	2:G:164:LEU:HD13	2.39	0.52
1:F:202:LEU:HD12	1:F:202:LEU:C	2.30	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:B:55:LEU:HD21	1:B:70:THR:CG2	2.38	0.52
1:C:554:PRO:O	1:C:555:GLU:HB3	2.08	0.52
1:C:44:GLN:N	1:C:45:PRO:CD	2.73	0.52
1:D:38:ASN:HD22	1:D:38:ASN:N	2.06	0.52
1:C:48:ILE:N	1:C:48:ILE:HD12	2.24	0.52
1:E:568:VAL:O	1:E:569:LEU:C	2.47	0.52
1:A:132:ARG:HH11	1:A:132:ARG:HG2	1.74	0.52
1:E:321:VAL:HG23	1:E:321:VAL:O	2.09	0.52
1:D:210:LEU:CD1	1:D:244:ARG:HA	2.36	0.52
1:F:49:PHE:O	1:F:52:VAL:HB	2.10	0.52
1:C:516:ILE:HG22	1:C:517:SER:O	2.10	0.52
1:E:639:TYR:HB3	2:I:127:PRO:CG	2.38	0.52
1:A:576:ARG:HG3	1:A:576:ARG:NH1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ILE:HG23	1:A:51:TYR:CE2	2.45	0.52
1:A:432:LEU:O	1:A:435:SER:HB3	2.08	0.52
2:H:126:THR:HB	2:H:129:MET:HB2	1.90	0.52
1:B:289:GLU:OE2	1:B:292:ARG:HD2	2.09	0.52
1:B:277:ASN:N	1:B:277:ASN:HD22	2.06	0.52
1:F:556:VAL:O	1:F:557:ASN:C	2.48	0.52
1:F:424:ASN:O	1:F:427:LYS:HB3	2.09	0.52
2:G:147:LEU:HD22	2:G:179:LEU:CD2	2.39	0.52
1:E:347:LYS:O	1:E:351:LEU:HG	2.09	0.52
1:C:627:ILE:CD1	2:H:171:LEU:HD11	2.38	0.52
1:A:462:TYR:CD2	1:A:463:HIS:CE1	2.97	0.52
1:E:200:LYS:HD2	1:E:236:LEU:HD21	1.91	0.52
1:B:423:MET:HA	1:B:438:ILE:HD12	1.91	0.52
1:F:490:ASN:HB3	1:F:528:LYS:NZ	2.24	0.52
1:E:580:ASP:O	1:E:582:MET:N	2.41	0.52
1:D:392:LEU:HD13	2:H:113:TRP:CZ3	2.44	0.52
1:E:485:ASP:OD1	1:E:487:GLU:HB3	2.08	0.52
1:A:77:ARG:HB2	1:A:77:ARG:HH11	1.74	0.52
1:E:206:PRO:HB3	1:E:247:TYR:HB2	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:B:376:ILE:O	1:B:379:ILE:HB	2.10	0.52
1:E:88:ARG:CZ	1:E:107:VAL:HG21	2.38	0.52
1:A:61:LEU:HB2	1:A:63:GLN:HG3	1.90	0.52
1:E:44:GLN:H	1:E:45:PRO:CD	2.22	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:E:191:ARG:HE	1:E:195:ILE:CD1	2.22	0.52
1:A:387:ILE:HD11	1:A:418:VAL:HG12	1.91	0.52
1:E:557:ASN:HD22	1:E:560:GLU:N	2.07	0.52
1:A:37:LEU:HB2	1:A:54:LEU:HD13	1.91	0.52
1:C:61:LEU:HB2	1:C:63:GLN:NE2	2.20	0.52
1:E:351:LEU:HA	1:E:354:GLN:OE1	2.09	0.52
1:E:299:LEU:HB2	1:E:301:LEU:HG	1.91	0.52
1:B:99:LEU:HD12	1:B:99:LEU:N	2.25	0.52
1:F:167:ILE:CG2	1:F:168:GLN:N	2.73	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:633:VAL:HA	2:H:118:VAL:HG23	1.92	0.52
1:A:341:ASP:HB3	1:A:344:VAL:HG23	1.90	0.52
1:C:472:CYS:O	1:C:476:GLU:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:275:LYS:N	1:D:275:LYS:CD	2.72	0.52
1:F:341:ASP:HB3	1:F:344:VAL:CG2	2.40	0.52
1:F:189:GLN:O	1:F:193:GLN:HG3	2.10	0.52
1:D:575:GLN:C	1:D:577:LEU:N	2.63	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
1:E:207:MET:H	1:E:210:LEU:CD1	2.22	0.52
1:C:495:PHE:O	1:C:499:VAL:HG23	2.09	0.52
1:A:401:ASP:C	1:A:403:THR:H	2.13	0.52
2:G:150:ILE:HG22	2:G:150:ILE:O	2.08	0.52
1:F:509:PHE:CD1	1:F:529:VAL:HG21	2.45	0.52
1:E:196:ARG:NH2	1:E:221:GLU:OE1	2.43	0.52
1:F:417:TYR:O	1:F:421:VAL:HG12	2.09	0.52
1:D:115:GLU:HG2	1:D:116:LEU:H	1.75	0.52
1:A:247:TYR:CD1	1:A:247:TYR:O	2.63	0.52
1:F:164:PRO:HG3	1:F:250:TRP:CE2	2.45	0.52
1:C:344:VAL:O	1:C:347:LYS:HB3	2.10	0.52
1:D:521:LEU:O	1:D:525:ILE:HD13	2.10	0.52
1:C:326:GLU:O	1:C:326:GLU:HG3	2.08	0.52
1:F:262:PRO:CG	1:F:273:LEU:HD21	2.40	0.52
1:A:33:VAL:HA	1:A:36:LYS:CD	2.35	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:E:198:LEU:O	1:E:202:LEU:HG	2.10	0.52
1:C:412:LYS:HZ1	1:C:448:LEU:HA	1.75	0.52
1:D:93:PHE:HZ	1:D:130:TYR:HB2	1.75	0.52
1:E:151:ALA:O	1:E:155:VAL:HG23	2.09	0.52
1:F:557:ASN:HD22	1:F:560:GLU:H	1.56	0.52
1:A:32:ASP:CG	1:A:32:ASP:O	2.48	0.52
1:B:34:ILE:HG12	1:B:57:HIS:CD2	2.45	0.52
1:D:556:VAL:O	1:D:557:ASN:C	2.47	0.52
1:D:49:PHE:O	1:D:52:VAL:N	2.41	0.52
1:B:206:PRO:HB3	1:B:247:TYR:CB	2.36	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
2:I:159:GLU:OE2	2:I:160:THR:N	2.43	0.52
1:A:121:LEU:HG	1:A:159:CYS:SG	2.50	0.52
1:C:81:MET:HE2	1:C:319:GLN:HA	1.91	0.52
1:F:526:PHE:CD2	1:F:549:PHE:HB2	2.45	0.52
1:B:371:GLU:OE1	1:B:428:ARG:NH2	2.43	0.52
1:A:509:PHE:CD1	1:A:525:ILE:HG22	2.46	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:178:GLU:CD	1:B:216:ARG:NH2	2.61	0.52
1:F:564:ASN:HA	1:F:567:LYS:HD2	1.92	0.52
1:A:518:ASP:CG	1:A:521:LEU:HD13	2.30	0.51
1:E:340:THR:O	1:E:341:ASP:C	2.48	0.51
1:A:628:VAL:HG12	1:A:629:GLU:OE2	2.09	0.51
1:D:292:ARG:O	1:D:295:SER:N	2.40	0.51
1:F:486:GLY:HA3	1:F:521:LEU:HD13	1.92	0.51
1:D:338:LYS:O	1:D:339:ASN:HB3	2.10	0.51
1:D:58:HIS:CE1	1:D:66:GLN:HG2	2.44	0.51
1:B:366:LEU:O	1:B:368:GLU:N	2.42	0.51
1:C:645:PHE:O	2:H:193:LEU:HA	2.11	0.51
2:G:189:GLN:HG3	2:G:190:LEU:H	1.75	0.51
1:F:41:ILE:HD11	1:F:50:LEU:C	2.30	0.51
1:B:95:LYS:HB2	1:B:95:LYS:NZ	2.25	0.51
1:A:398:MET:O	1:A:402:PRO:HD3	2.10	0.51
1:D:202:LEU:HD12	1:D:203:LEU:HG	1.92	0.51
1:E:405:GLU:C	1:E:407:ALA:N	2.63	0.51
2:I:159:GLU:C	2:I:161:PHE:N	2.64	0.51
1:E:516:ILE:HG22	1:E:517:SER:O	2.09	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:C:103:VAL:C	1:C:106:PRO:HD2	2.31	0.51
1:D:85:TRP:CD2	1:D:111:CYS:HB3	2.45	0.51
1:D:413:SER:OG	1:D:450:THR:HG21	2.10	0.51
1:A:298:LYS:O	1:A:300:GLU:OE2	2.29	0.51
1:C:417:TYR:HE2	1:D:574:LEU:HD23	1.76	0.51
1:A:369:GLN:O	1:A:372:LEU:HB3	2.11	0.51
1:E:180:TRP:CZ3	1:E:191:ARG:HB2	2.44	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:E:165:LYS:HD3	1:E:208:ASP:CB	2.38	0.51
1:E:156:VAL:CA	1:E:160:ALA:HB3	2.40	0.51
1:D:178:GLU:HA	1:D:191:ARG:HH21	1.76	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:F:336:GLY:HA3	1:F:345:ILE:CG1	2.41	0.51
2:I:185:CYS:HB3	2:I:189:GLN:HE21	1.74	0.51
1:C:409:ASN:O	1:C:412:LYS:HB2	2.11	0.51
1:E:550:PHE:CD1	1:E:558:LYS:HE2	2.46	0.51
1:A:457:ASN:O	1:A:461:GLU:HG2	2.10	0.51
1:F:358:ASN:HB3	1:F:389:ARG:CG	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:338:LYS:O	1:C:339:ASN:HB3	2.10	0.51
1:C:642:VAL:HG23	1:C:643:THR:N	2.26	0.51
2:G:185:CYS:SG	2:G:188:ASP:CB	2.94	0.51
1:D:221:GLU:HG3	1:D:233:ILE:HG13	1.93	0.51
2:G:150:ILE:N	2:G:150:ILE:HD12	2.25	0.51
1:B:84:ILE:HG22	1:B:85:TRP:N	2.25	0.51
2:I:125:THR:HG22	2:I:129:MET:SD	2.51	0.51
1:D:262:PRO:HG3	1:D:273:LEU:CD2	2.41	0.51
1:D:455:LEU:H	1:D:455:LEU:CD2	2.24	0.51
1:A:49:PHE:CE2	1:A:270:GLU:HB2	2.45	0.51
1:E:544:THR:O	1:E:547:LYS:HB3	2.11	0.51
1:D:531:PHE:CD1	1:D:531:PHE:C	2.84	0.51
1:A:99:LEU:HD11	1:A:133:LYS:HD3	1.93	0.51
1:F:310:MET:O	1:F:314:TYR:HB2	2.11	0.51
1:D:86:CYS:SG	1:D:123:LEU:HA	2.51	0.51
1:F:49:PHE:O	1:F:52:VAL:N	2.43	0.51
1:F:125:LEU:C	1:F:127:TYR:H	2.14	0.51
1:B:66:GLN:NE2	1:B:66:GLN:N	2.58	0.51
1:E:88:ARG:O	1:E:88:ARG:HG2	2.11	0.51
1:E:51:TYR:O	1:E:54:LEU:N	2.43	0.51
1:F:432:LEU:HD22	1:F:464:ILE:HD13	1.93	0.51
1:F:89:LEU:HD11	1:F:108:LEU:CD2	2.39	0.51
1:B:190:GLN:HA	1:B:193:GLN:HG3	1.91	0.51
1:D:408:ILE:HG22	1:D:409:ASN:N	2.25	0.51
1:C:653:PHE:O	1:C:657:LYS:CG	2.59	0.51
1:C:405:GLU:HA	1:C:408:ILE:HB	1.92	0.51
1:A:173:TYR:CD2	1:A:198:LEU:HD22	2.46	0.51
1:E:299:LEU:HD21	1:E:309:ARG:CZ	2.41	0.51
1:B:51:TYR:CB	1:B:74:LEU:HD13	2.41	0.51
1:E:275:LYS:N	1:E:275:LYS:HE2	2.26	0.51
1:E:553:PHE:O	1:E:554:PRO:C	2.49	0.51
1:F:152:PHE:HB3	1:F:173:TYR:CD1	2.46	0.51
2:I:179:LEU:HB3	2:I:184:VAL:HB	1.92	0.51
1:F:468:THR:HG23	1:F:499:VAL:HG11	1.93	0.51
1:B:296:ASP:HB3	1:B:298:LYS:HD3	1.91	0.51
1:B:425:THR:O	1:B:429:ILE:HG12	2.11	0.51
1:A:55:LEU:C	1:A:57:HIS:H	2.15	0.51
1:F:279:TYR:CE2	1:F:324:ALA:HA	2.46	0.51
1:B:353:GLN:HG3	1:B:353:GLN:O	2.10	0.51
1:F:455:LEU:CD2	1:F:455:LEU:H	2.24	0.51
1:A:92:GLU:C	1:A:94:ASP:H	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:575:GLN:C	1:C:577:LEU:H	2.14	0.51
1:D:121:LEU:HD21	1:D:169:PHE:HB2	1.93	0.51
1:B:92:GLU:C	1:B:94:ASP:H	2.14	0.51
1:D:191:ARG:O	1:D:195:ILE:HG13	2.10	0.51
1:B:122:SER:HB3	1:B:263:ILE:CD1	2.41	0.51
1:F:444:ARG:HD2	2:I:166:GLU:OE2	2.11	0.51
1:E:46:THR:HG23	1:E:276:PRO:HG3	1.93	0.51
1:D:420:CYS:SG	1:D:453:ILE:HA	2.51	0.51
1:F:409:ASN:HA	1:F:412:LYS:HB2	1.93	0.50
1:A:417:TYR:O	1:A:421:VAL:HG12	2.11	0.50
2:I:168:ALA:HA	2:I:170:GLN:HE22	1.75	0.50
1:E:420:CYS:HB3	1:F:568:VAL:HG11	1.93	0.50
1:E:81:MET:SD	1:E:319:GLN:O	2.69	0.50
2:I:188:ASP:C	2:I:190:LEU:N	2.64	0.50
1:B:65:LYS:HD2	1:B:66:GLN:HE22	1.76	0.50
1:B:336:GLY:C	1:B:338:LYS:H	2.14	0.50
1:E:432:LEU:O	1:E:435:SER:HB3	2.11	0.50
1:E:249:ASP:O	1:E:253:ILE:HG13	2.11	0.50
2:G:192:GLN:HA	2:G:192:GLN:OE1	2.11	0.50
1:F:455:LEU:CD2	1:F:455:LEU:N	2.74	0.50
1:F:173:TYR:CD2	1:F:198:LEU:HD22	2.47	0.50
1:E:509:PHE:CG	1:E:529:VAL:HG21	2.46	0.50
1:F:55:LEU:HD22	1:F:71:PHE:CE1	2.46	0.50
1:F:315:MET:HE1	1:F:348:TYR:HE2	1.76	0.50
1:D:280:ASP:O	1:D:283:GLN:HB2	2.12	0.50
1:C:37:LEU:HD23	1:C:54:LEU:CD1	2.41	0.50
1:E:129:THR:HG23	1:E:133:LYS:HE3	1.94	0.50
1:E:624:PRO:N	1:E:625:PRO:HD3	2.26	0.50
1:E:115:GLU:H	1:E:115:GLU:CD	2.15	0.50
2:G:180:LEU:HD12	2:G:185:CYS:O	2.11	0.50
1:A:166:SER:O	1:A:170:TRP:HD1	1.94	0.50
1:E:351:LEU:O	1:E:354:GLN:HB2	2.11	0.50
1:C:529:VAL:CG1	1:C:545:LEU:HD11	2.39	0.50
1:B:447:LYS:CG	1:B:481:TYR:HB3	2.41	0.50
1:B:481:TYR:CD1	1:B:481:TYR:N	2.80	0.50
1:D:455:LEU:HD13	1:D:475:LEU:HD22	1.93	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:F:502:GLU:OE2	1:F:536:VAL:HG11	2.11	0.50
1:E:125:LEU:HD23	1:E:128:ILE:CD1	2.29	0.50
2:H:184:VAL:O	2:H:185:CYS:SG	2.67	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:555:GLU:OE1	1:E:555:GLU:C	2.49	0.50
1:B:472:CYS:HB3	1:B:504:GLN:HE22	1.75	0.50
1:E:641:LYS:O	1:E:643:THR:N	2.44	0.50
1:D:218:THR:HG23	1:D:233:ILE:CD1	2.41	0.50
1:F:401:ASP:CG	1:F:401:ASP:O	2.48	0.50
1:B:390:ILE:HD11	1:B:414:LYS:HE2	1.94	0.50
1:D:464:ILE:HG22	1:D:465:SER:N	2.26	0.50
1:D:93:PHE:CZ	1:D:130:TYR:HB2	2.46	0.50
1:E:378:GLU:OE2	1:E:378:GLU:N	2.42	0.50
1:F:337:GLU:HG2	1:F:337:GLU:O	2.11	0.50
2:G:184:VAL:O	2:G:185:CYS:SG	2.69	0.50
1:F:561:GLU:O	1:F:562:PHE:C	2.48	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:424:ASN:ND2	1:E:456:GLU:OE1	2.45	0.50
1:B:366:LEU:C	1:B:368:GLU:N	2.65	0.50
2:I:137:LYS:HG3	2:I:138:LEU:HG	1.92	0.50
1:F:522:LEU:O	1:F:525:ILE:N	2.44	0.50
1:E:85:TRP:CD2	1:E:111:CYS:HB3	2.47	0.50
1:F:523:LYS:O	1:F:527:GLN:HG3	2.11	0.50
1:E:306:HIS:O	1:E:310:MET:HG2	2.12	0.50
2:I:179:LEU:CG	2:I:184:VAL:HG21	2.41	0.50
1:D:44:GLN:H	1:D:45:PRO:HD3	1.76	0.50
1:D:314:TYR:O	1:D:317:ALA:HB3	2.12	0.50
1:D:275:LYS:HE2	1:D:275:LYS:H	1.76	0.50
1:B:335:GLN:HB3	1:B:344:VAL:HG11	1.94	0.50
1:F:480:LYS:HB2	1:F:481:TYR:CD1	2.47	0.50
1:E:638:GLN:HA	1:E:641:LYS:CG	2.41	0.50
1:B:89:LEU:CD2	1:B:107:VAL:HG11	2.39	0.50
1:E:509:PHE:CE2	1:E:513:ILE:HD11	2.46	0.50
1:A:447:LYS:CG	1:A:481:TYR:HB3	2.37	0.50
1:C:543:ARG:NE	1:D:372:LEU:HD11	2.26	0.50
1:D:525:ILE:HG22	1:D:526:PHE:N	2.26	0.50
1:E:366:LEU:HD22	1:E:370:TYR:CE1	2.47	0.50
1:E:370:TYR:CE1	1:E:378:GLU:HB3	2.47	0.50
1:F:374:THR:O	1:F:374:THR:HG22	2.12	0.50
1:A:259:ARG:HG2	1:A:320:HIS:CE1	2.46	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
2:I:147:LEU:HD23	2:I:147:LEU:C	2.31	0.50
1:F:494:ASP:O	1:F:498:TYR:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:481:TYR:CD1	1:F:481:TYR:N	2.79	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:B:501:GLU:O	1:B:505:VAL:HG23	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:E:56:LYS:HG3	1:E:265:LEU:HD21	1.93	0.50
1:B:202:LEU:HB2	1:B:207:MET:HE1	1.93	0.50
2:I:146:LEU:HD23	2:I:150:ILE:HD13	1.93	0.50
1:C:358:ASN:HB3	1:C:389:ARG:HG3	1.93	0.50
1:D:370:TYR:HB2	1:D:379:ILE:HG12	1.94	0.50
1:D:200:LYS:HG2	1:D:236:LEU:CD1	2.41	0.50
1:D:530:ILE:HG12	1:D:545:LEU:HB3	1.93	0.50
2:G:144:MET:O	2:G:148:LYS:HG2	2.12	0.50
1:B:160:ALA:C	1:B:162:PHE:H	2.15	0.50
1:F:474:VAL:HG12	1:F:475:LEU:N	2.25	0.50
1:B:568:VAL:HG12	1:B:569:LEU:HG	1.92	0.49
1:E:386:CYS:O	1:E:390:ILE:HG13	2.12	0.49
1:A:631:LEU:CD1	2:G:114:LEU:HD23	2.42	0.49
1:C:563:THR:HG23	1:C:574:LEU:HB3	1.94	0.49
1:C:125:LEU:CD2	1:C:169:PHE:HD1	2.23	0.49
1:A:289:GLU:O	1:A:292:ARG:HG3	2.12	0.49
2:H:134:GLU:O	2:H:136:GLY:N	2.44	0.49
1:B:356:ILE:CG2	1:B:359:SER:HB2	2.41	0.49
1:D:390:ILE:HD13	1:D:414:LYS:CD	2.42	0.49
1:C:561:GLU:O	1:C:562:PHE:C	2.50	0.49
1:B:81:MET:HE2	1:B:319:GLN:HG3	1.93	0.49
2:H:178:LEU:C	2:H:180:LEU:H	2.15	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:A:89:LEU:N	1:A:89:LEU:CD2	2.75	0.49
1:C:55:LEU:O	1:C:59:VAL:HG23	2.12	0.49
1:A:110:ARG:HG2	1:A:110:ARG:HH11	1.76	0.49
1:C:247:TYR:O	1:C:251:LEU:HB2	2.12	0.49
1:F:529:VAL:HG12	1:F:545:LEU:HD11	1.94	0.49
1:C:501:GLU:HB3	1:C:504:GLN:HG3	1.93	0.49
1:C:173:TYR:CD2	1:C:198:LEU:HD22	2.47	0.49
1:E:124:TRP:CZ3	1:E:155:VAL:HG22	2.48	0.49
1:B:496:LEU:HD22	1:B:501:GLU:HB2	1.93	0.49
1:C:563:THR:CG2	1:C:574:LEU:HB3	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:41:ILE:HG13	1:F:50:LEU:HB3	1.94	0.49
1:D:41:ILE:CG1	1:D:50:LEU:HB3	2.41	0.49
1:F:394:LEU:CD1	1:F:411:LEU:HD23	2.42	0.49
1:D:291:ILE:HD13	1:D:314:TYR:CE1	2.47	0.49
1:C:74:LEU:HD13	1:C:84:ILE:HG21	1.94	0.49
1:D:104:ILE:HG21	1:D:130:TYR:CE1	2.46	0.49
1:D:434:ALA:CA	1:D:437:LYS:HE3	2.33	0.49
1:A:640:PHE:C	1:A:642:VAL:N	2.66	0.49
2:H:143:GLN:HG3	2:H:178:LEU:HD22	1.93	0.49
1:C:563:THR:HB	1:C:572:ASN:HD21	1.78	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:563:THR:HG22	1:F:572:ASN:CG	2.32	0.49
1:E:44:GLN:N	1:E:45:PRO:CD	2.75	0.49
1:B:364:PHE:CZ	1:B:421:VAL:CG1	2.95	0.49
1:B:572:ASN:ND2	1:B:575:GLN:H	2.10	0.49
2:H:116:VAL:CG2	2:H:117:GLY:N	2.76	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:C:322:CYS:SG	1:C:323:PHE:N	2.86	0.49
1:C:578:GLU:HG2	1:C:578:GLU:O	2.12	0.49
1:D:557:ASN:HD22	1:D:560:GLU:CB	2.24	0.49
1:C:375:LYS:HB3	1:C:378:GLU:OE2	2.13	0.49
1:F:580:ASP:O	1:F:582:MET:N	2.32	0.49
1:B:185:LYS:HG2	1:B:186:PHE:N	2.26	0.49
1:D:74:LEU:O	1:D:75:HIS:C	2.48	0.49
1:D:84:ILE:O	1:D:84:ILE:HG22	2.12	0.49
1:C:546:GLU:OE2	1:C:565:LYS:HE2	2.12	0.49
1:C:347:LYS:O	1:C:351:LEU:HG	2.13	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: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:F:563:THR:HG22	1:F:572:ASN:OD1	2.12	0.49
1:C:101:ALA:CB	1:C:134:LYS:HE2	2.43	0.49
1:F:77:ARG:HB3	1:F:78:PHE:CE1	2.46	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:E:135:ASN:ND2	1:E:147:ILE:CG2	2.75	0.49
1:A:362:LEU:O	1:A:366:LEU:HB2	2.12	0.49
1:B:81:MET:HE1	1:B:319:GLN:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:559:LEU:O	1:D:562:PHE:HB3	2.12	0.49
1:C:376:ILE:HB	1:C:377:PRO:HD3	1.94	0.49
1:A:416:THR:OG1	1:A:450:THR:HG23	2.12	0.49
1:D:541:SER:O	1:D:544:THR:HB	2.13	0.49
1:A:418:VAL:HA	1:A:421:VAL:CG1	2.43	0.49
2:H:186:SER:HA	2:H:189:GLN:NE2	2.25	0.49
1:E:417:TYR:O	1:E:420:CYS:HB2	2.13	0.49
1:B:137:ILE:CD1	1:B:137:ILE:H	2.24	0.49
1:B:74:LEU:HD21	1:B:84:ILE:HG12	1.94	0.49
1:A:334:TYR:O	1:A:335:GLN:C	2.51	0.49
1:A:646:GLU:HG3	1:A:650:PHE:CE2	2.46	0.49
1:D:482:PHE:C	1:D:484:THR:H	2.15	0.49
1:A:425:THR:HG22	1:A:426:MET:HE1	1.94	0.49
1:B:81:MET:CE	1:B:319:GLN:HA	2.43	0.49
1:F:455:LEU:HD22	1:F:455:LEU:N	2.28	0.49
1:B:496:LEU:CB	1:B:505:VAL:HG22	2.41	0.49
1:A:170:TRP:HE3	1:A:198:LEU:HD11	1.78	0.49
1:A:152:PHE:CD2	1:A:173:TYR:HD1	2.31	0.49
1:B:487:GLU:N	1:B:521:LEU:HD23	2.28	0.49
1:C:371:GLU:CA	1:C:379:ILE:HD11	2.43	0.49
1:D:142:GLU:HA	1:D:142:GLU:OE1	2.12	0.49
1:A:398:MET:O	1:A:400:ASP:N	2.43	0.49
2:I:164:LEU:HD23	2:I:165:LEU:H	1.76	0.49
1:D:427:LYS:HB2	1:D:435:SER:HB2	1.93	0.49
1:C:539:LEU:CD2	1:D:371:GLU:HB3	2.43	0.49
1:E:289:GLU:OE2	1:E:292:ARG:NH2	2.46	0.49
2:H:125:THR:HA	2:H:129:MET:HE2	1.94	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:A:287:TRP:CH2	1:A:316:GLN:HB3	2.48	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:B:351:LEU:CA	1:B:354:GLN:HG3	2.39	0.49
1:B:85:TRP:CZ3	1:B:111:CYS:HB3	2.48	0.49
1:B:302:SER:OG	1:B:303:ASP:N	2.44	0.49
1:A:634:LEU:CD1	2:G:174:ALA:HB2	2.43	0.49
1:E:324:ALA:O	1:E:325:PRO:C	2.51	0.49
1:E:316:GLN:O	1:E:319:GLN:HB3	2.12	0.49
1:D:299:LEU:H	1:D:299:LEU:CD1	2.23	0.49
1:C:624:PRO:O	1:C:627:ILE:HG22	2.11	0.49
1:C:309:ARG:O	1:C:312:TYR:HB3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:292:ARG:HG3	1:E:292:ARG:HH11	1.78	0.49
1:E:103:VAL:O	1:E:106:PRO:HD2	2.13	0.49
1:B:108:LEU:HD22	1:B:127:TYR:HD1	1.78	0.49
1:E:419:TYR:O	1:E:422:TYR:HB3	2.12	0.49
1:A:387:ILE:HD12	1:A:418:VAL:HG12	1.95	0.48
1:C:653:PHE:CG	2:H:192:GLN:NE2	2.81	0.48
1:F:262:PRO:HD3	1:F:272:ASN:OD1	2.13	0.48
1:A:247:TYR:CD1	1:A:247:TYR:C	2.86	0.48
1:D:84:ILE:HG12	1:D:87:MET:CE	2.43	0.48
1:A:196:ARG:HD3	1:A:232:HIS:CE1	2.48	0.48
1:C:34:ILE:HD13	1:C:58:HIS:HE1	1.77	0.48
1:E:370:TYR:CD1	1:E:378:GLU:HB3	2.48	0.48
1:F:540:ASN:HD22	1:F:543:ARG:NH2	2.11	0.48
1:C:526:PHE:O	1:C:530:ILE:HG13	2.12	0.48
1:A:569:LEU:HD22	1:B:456:GLU:HG2	1.95	0.48
1:E:479:LEU:HD11	1:E:492:TYR:CE2	2.46	0.48
1:E:55:LEU:HB3	1:E:265:LEU:HD11	1.94	0.48
1:F:289:GLU:HG3	1:F:292:ARG:NH2	2.27	0.48
1:E:262:PRO:HB3	1:E:268:ALA:HA	1.94	0.48
1:E:167:ILE:HG23	1:E:168:GLN:N	2.28	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:F:540:ASN:HD22	1:F:543:ARG:HH21	1.59	0.48
1:F:438:ILE:O	1:F:442:CYS:HB2	2.13	0.48
1:E:177:LEU:HD11	1:E:194:TYR:HB3	1.96	0.48
1:E:125:LEU:HD11	1:E:169:PHE:HB2	1.94	0.48
1:D:297:ASN:ND2	1:D:306:HIS:CG	2.81	0.48
1:F:580:ASP:C	1:F:582:MET:N	2.66	0.48
1:A:335:GLN:HG3	1:A:348:TYR:CE1	2.48	0.48
2:I:159:GLU:O	2:I:162:VAL:HG22	2.14	0.48
1:D:81:MET:CE	1:D:319:GLN:HA	2.43	0.48
1:A:79:PRO:CG	1:A:351:LEU:HD22	2.43	0.48
1:D:390:ILE:HD13	1:D:414:LYS:HD3	1.94	0.48
1:A:366:LEU:C	1:A:368:GLU:H	2.16	0.48
1:C:192:VAL:HG23	1:C:193:GLN:N	2.28	0.48
1:F:553:PHE:N	1:F:554:PRO:HD3	2.29	0.48
1:C:180:TRP:HZ3	1:C:191:ARG:HA	1.77	0.48
1:F:52:VAL:HA	1:F:55:LEU:HD12	1.96	0.48
1:B:145:ARG:O	1:B:145:ARG:HG2	2.12	0.48
1:E:423:MET:HB2	1:E:438:ILE:CG2	2.43	0.48
1:C:432:LEU:HD13	1:C:464:ILE:HD11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:VAL:HG11	1:B:169:PHE:CE1	2.49	0.48
1:A:275:LYS:O	1:A:278:GLU:HB3	2.13	0.48
1:F:194:TYR:N	1:F:194:TYR:HD1	2.12	0.48
1:F:152:PHE:CG	1:F:173:TYR:CD1	3.02	0.48
1:F:166:SER:O	1:F:167:ILE:C	2.51	0.48
1:E:71:PHE:CD2	1:E:88:ARG:HB2	2.49	0.48
1:F:46:THR:HG21	1:F:276:PRO:HB3	1.95	0.48
2:I:165:LEU:HD11	2:I:172:SER:HB2	1.96	0.48
1:D:455:LEU:H	1:D:455:LEU:HD22	1.77	0.48
1:E:434:ALA:CB	1:E:437:LYS:HZ1	2.26	0.48
1:C:554:PRO:O	1:C:555:GLU:CB	2.60	0.48
1:A:214:TRP:CH2	1:A:233:ILE:HG23	2.48	0.48
1:D:56:LYS:O	1:D:60:SER:HB2	2.13	0.48
1:A:341:ASP:OD2	1:A:343:THR:HB	2.12	0.48
2:G:139:GLN:O	2:G:141:ASP:N	2.46	0.48
1:E:86:CYS:SG	1:E:123:LEU:HA	2.54	0.48
1:A:358:ASN:HB3	1:A:389:ARG:CG	2.43	0.48
1:A:509:PHE:CE1	1:A:525:ILE:HG22	2.49	0.48
2:H:131:ILE:CG2	2:H:135:LEU:HD12	2.44	0.48
2:G:179:LEU:O	2:G:180:LEU:C	2.52	0.48
1:A:94:ASP:O	1:A:95:LYS:HB3	2.14	0.48
1:D:292:ARG:O	1:D:294:GLU:N	2.47	0.48
1:D:264:THR:HG22	1:D:266:ASN:H	1.79	0.48
1:F:563:THR:HG23	1:F:574:LEU:CB	2.43	0.48
1:E:144:ALA:HA	1:E:147:ILE:CD1	2.42	0.48
1:B:560:GLU:O	1:B:562:PHE:N	2.47	0.48
1:B:449:VAL:HG23	1:B:450:THR:O	2.12	0.48
1:A:497:ILE:HG23	1:A:532:PHE:CD1	2.49	0.48
2:H:150:ILE:O	2:H:154:CYS:SG	2.67	0.48
1:F:421:VAL:HA	1:F:424:ASN:HD22	1.78	0.48
1:A:180:TRP:CZ3	1:A:191:ARG:CA	2.90	0.48
1:D:168:GLN:HG3	1:D:169:PHE:N	2.29	0.48
1:D:297:ASN:ND2	1:D:306:HIS:HB2	2.27	0.48
1:E:61:LEU:O	1:E:63:GLN:HG3	2.13	0.48
1:A:59:VAL:CG1	1:A:60:SER:N	2.77	0.48
1:E:569:LEU:HD11	1:F:455:LEU:HB2	1.95	0.48
1:D:125:LEU:C	1:D:127:TYR:H	2.15	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:B:195:ILE:HG22	1:B:199:TYR:HD2	1.78	0.48
1:F:254:THR:CG2	1:F:257:LEU:HB3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:PHE:HZ	1:B:421:VAL:CG1	2.26	0.48
1:A:80:LEU:HA	1:A:118:ASN:HD21	1.78	0.48
1:C:569:LEU:HD12	1:D:452:ASP:OD1	2.13	0.48
1:C:269:THR:HG23	1:C:272:ASN:HD21	1.79	0.48
1:C:653:PHE:O	1:C:657:LYS:HG3	2.14	0.48
1:F:553:PHE:O	1:F:554:PRO:C	2.51	0.48
1:A:559:LEU:HD21	1:A:579:LEU:HD11	1.95	0.48
1:B:516:ILE:CD1	1:B:525:ILE:HG13	2.43	0.48
1:C:533:GLU:HG3	1:C:545:LEU:HD12	1.95	0.48
1:E:87:MET:HG2	1:E:264:THR:C	2.33	0.48
1:E:501:GLU:O	1:E:504:GLN:N	2.47	0.48
1:C:401:ASP:C	1:C:403:THR:H	2.15	0.48
1:A:51:TYR:CD1	1:A:74:LEU:HB2	2.47	0.48
1:C:135:ASN:ND2	1:C:147:ILE:HG21	2.28	0.48
1:B:333:ASN:O	1:B:337:GLU:HB2	2.14	0.48
2:G:134:GLU:O	2:G:137:LYS:HG2	2.14	0.48
1:D:499:VAL:O	1:D:499:VAL:HG12	2.14	0.48
1:F:405:GLU:HA	1:F:408:ILE:CG2	2.42	0.48
1:A:101:ALA:HA	1:A:130:TYR:OH	2.14	0.48
1:A:130:TYR:C	1:A:132:ARG:N	2.66	0.48
1:A:169:PHE:CD2	1:A:170:TRP:N	2.82	0.48
1:D:247:TYR:CE1	1:D:251:LEU:HD13	2.49	0.48
1:E:398:MET:HG2	1:E:408:ILE:HD13	1.95	0.48
1:B:74:LEU:HD21	1:B:84:ILE:CG1	2.44	0.48
1:C:275:LYS:N	1:C:275:LYS:HE2	2.28	0.48
1:A:231:ARG:HB3	1:A:231:ARG:NH1	2.28	0.48
1:F:525:ILE:HG22	1:F:526:PHE:N	2.28	0.48
1:F:442:CYS:SG	1:F:453:ILE:HG12	2.53	0.48
1:A:536:VAL:O	1:A:536:VAL:HG22	2.13	0.48
1:F:186:PHE:C	1:F:188:GLU:H	2.17	0.48
1:E:154:VAL:HG13	1:E:155:VAL:HG23	1.95	0.47
1:A:66:GLN:NE2	1:A:66:GLN:CA	2.76	0.47
1:A:182:PRO:HG2	1:A:188:GLU:HG3	1.95	0.47
1:E:364:PHE:CZ	1:E:421:VAL:CG1	2.92	0.47
1:A:283:GLN:OE1	1:A:283:GLN:HA	2.13	0.47
1:D:153:GLN:O	1:D:156:VAL:N	2.47	0.47
1:E:170:TRP:CE3	1:E:198:LEU:CD1	2.97	0.47
1:C:283:GLN:HA	1:C:286:ILE:CD1	2.44	0.47
1:E:396:ALA:O	1:E:397:LEU:C	2.51	0.47
1:F:538:SER:O	1:F:541:SER:HB2	2.14	0.47
1:F:441:LYS:HA	1:F:444:ARG:HE	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:ASP:O	1:B:343:THR:N	2.45	0.47
1:F:249:ASP:O	1:F:253:ILE:HG13	2.14	0.47
1:F:109:ALA:O	1:F:113:SER:HB3	2.14	0.47
1:C:640:PHE:CA	1:C:642:VAL:HG22	2.44	0.47
1:B:408:ILE:O	1:B:412:LYS:HG3	2.14	0.47
1:E:576:ARG:O	1:E:577:LEU:HD23	2.14	0.47
1:A:628:VAL:O	1:A:632:LYS:HG3	2.13	0.47
1:D:204:CYS:HB2	1:D:205:GLN:NE2	2.25	0.47
1:F:472:CYS:O	1:F:473:LYS:C	2.51	0.47
1:F:499:VAL:O	1:F:499:VAL:HG12	2.13	0.47
1:E:472:CYS:HB3	1:E:504:GLN:HE22	1.79	0.47
2:I:112:PRO:N	2:I:114:LEU:CD1	2.77	0.47
1:D:509:PHE:CD1	1:D:529:VAL:HG21	2.49	0.47
1:D:502:GLU:CD	1:D:536:VAL:HG11	2.34	0.47
1:A:135:ASN:CG	1:A:147:ILE:HG21	2.34	0.47
1:D:392:LEU:HA	1:D:395:ALA:HB3	1.95	0.47
1:B:264:THR:O	1:B:266:ASN:N	2.47	0.47
1:D:255:LYS:HB3	1:D:256:GLY:H	1.46	0.47
1:A:510:GLU:C	1:A:513:ILE:HD11	2.34	0.47
1:E:156:VAL:HA	1:E:160:ALA:HB2	1.93	0.47
2:H:120:VAL:HG22	2:H:130:CYS:SG	2.54	0.47
1:D:474:VAL:HG12	1:D:475:LEU:N	2.29	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
1:C:628:VAL:C	1:C:630:LEU:H	2.17	0.47
1:C:202:LEU:HD12	1:C:202:LEU:C	2.35	0.47
1:E:131:VAL:HG11	1:E:151:ALA:HB3	1.95	0.47
1:E:640:PHE:CZ	2:I:131:ILE:HD11	2.49	0.47
1:A:67:VAL:HG12	1:A:68:TYR:CD2	2.49	0.47
1:D:455:LEU:HD13	1:D:475:LEU:HD21	1.95	0.47
1:A:646:GLU:HB2	1:A:650:PHE:CD2	2.47	0.47
1:C:452:ASP:OD1	1:D:569:LEU:HD12	2.14	0.47
1:B:356:ILE:HG21	1:B:359:SER:HB2	1.96	0.47
1:B:44:GLN:HE22	1:B:389:ARG:NH2	2.12	0.47
1:F:522:LEU:O	1:F:525:ILE:HB	2.14	0.47
1:F:459:TYR:CE1	1:F:495:PHE:HD1	2.32	0.47
1:C:210:LEU:HD13	1:C:244:ARG:HA	1.96	0.47
1:A:204:CYS:HB2	1:A:205:GLN:NE2	2.24	0.47
1:F:124:TRP:CE3	1:F:155:VAL:HG22	2.49	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:545:LEU:O	1:A:545:LEU:HD23	2.13	0.47
1:C:417:TYR:HB2	1:D:573:TYR:CD1	2.49	0.47
1:E:553:PHE:N	1:E:554:PRO:HD3	2.30	0.47
2:G:147:LEU:CD1	2:G:178:LEU:HD22	2.38	0.47
1:A:67:VAL:O	1:A:71:PHE:HB2	2.14	0.47
1:D:160:ALA:HB1	1:D:170:TRP:CZ2	2.50	0.47
1:B:83:ASN:HB2	1:B:262:PRO:O	2.15	0.47
1:B:425:THR:HG22	1:B:426:MET:HE3	1.96	0.47
1:F:277:ASN:N	1:F:277:ASN:HD22	2.13	0.47
1:C:417:TYR:HB2	1:D:573:TYR:HD1	1.79	0.47
1:F:553:PHE:N	1:F:554:PRO:CD	2.78	0.47
1:E:571:VAL:HB	1:E:573:TYR:CD2	2.50	0.47
1:F:455:LEU:HD21	1:F:488:TYR:CD1	2.50	0.47
1:B:503:SER:OG	1:B:504:GLN:N	2.46	0.47
1:E:284:LEU:HD11	1:E:288:LEU:HD21	1.97	0.47
1:E:455:LEU:CB	1:F:569:LEU:HD11	2.38	0.47
1:E:417:TYR:HB2	1:F:573:TYR:CD1	2.39	0.47
1:A:631:LEU:HD11	2:G:164:LEU:HD11	1.97	0.47
1:D:169:PHE:O	1:D:172:GLU:N	2.47	0.47
1:F:55:LEU:HD21	1:F:70:THR:CG2	2.44	0.47
1:F:167:ILE:CG1	1:F:209:CYS:HB3	2.44	0.47
1:C:627:ILE:CG1	2:H:171:LEU:HD11	2.44	0.47
1:A:400:ASP:O	1:A:401:ASP:CB	2.61	0.47
1:E:269:THR:HG23	1:E:272:ASN:ND2	2.24	0.47
1:B:65:LYS:HD3	1:B:65:LYS:C	2.35	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:C:206:PRO:HB3	1:C:247:TYR:CA	2.44	0.47
2:I:169:PRO:O	2:I:172:SER:HB3	2.15	0.47
1:C:644:ILE:HG23	2:H:173:TYR:CE1	2.47	0.47
2:I:137:LYS:O	2:I:138:LEU:HB2	2.13	0.47
1:D:267:GLN:O	1:D:269:THR:HG23	2.14	0.47
1:F:194:TYR:CD1	1:F:194:TYR:N	2.80	0.47
1:C:314:TYR:HB3	1:C:331:MET:CE	2.45	0.47
1:C:264:THR:HG22	1:C:266:ASN:H	1.79	0.47
1:B:196:ARG:O	1:B:197:LYS:C	2.53	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:F:159:CYS:O	1:F:162:PHE:N	2.44	0.47
1:F:554:PRO:O	1:F:555:GLU:HB3	2.15	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
2:I:171:LEU:O	2:I:175:ILE:HG13	2.14	0.47
1:D:202:LEU:HD12	1:D:202:LEU:C	2.35	0.47
1:D:41:ILE:HD11	1:D:50:LEU:O	2.15	0.47
1:B:77:ARG:HD3	1:B:78:PHE:CE1	2.45	0.47
1:E:405:GLU:C	1:E:407:ALA:H	2.17	0.47
1:C:420:CYS:O	1:C:423:MET:N	2.48	0.47
1:B:358:ASN:HB3	1:B:389:ARG:CG	2.45	0.47
1:D:33:VAL:HA	1:D:36:LYS:NZ	2.30	0.47
1:E:378:GLU:O	1:E:382:THR:HG22	2.15	0.47
1:C:475:LEU:HB3	1:C:492:TYR:CZ	2.50	0.47
1:E:374:THR:O	1:E:376:ILE:HG12	2.15	0.47
1:E:353:GLN:O	1:E:353:GLN:HG3	2.14	0.47
1:A:180:TRP:O	1:A:191:ARG:NH1	2.48	0.47
1:E:417:TYR:O	1:E:421:VAL:HG12	2.15	0.47
1:D:202:LEU:CD1	1:D:203:LEU:HG	2.45	0.47
1:F:370:TYR:CG	1:F:378:GLU:HB3	2.49	0.47
1:C:400:ASP:O	1:C:401:ASP:CB	2.61	0.47
1:F:524:MET:HE2	1:F:528:LYS:HE3	1.97	0.47
1:C:628:VAL:C	1:C:630:LEU:N	2.68	0.47
1:D:366:LEU:O	1:D:367:SER:C	2.53	0.47
1:A:221:GLU:HB3	1:A:229:ALA:HB1	1.96	0.47
1:E:145:ARG:NH2	1:E:180:TRP:HZ2	2.12	0.47
2:H:131:ILE:HG23	2:H:135:LEU:HD12	1.96	0.47
1:E:556:VAL:O	1:E:557:ASN:C	2.51	0.47
1:E:638:GLN:O	1:E:640:PHE:N	2.48	0.47
1:A:132:ARG:NH1	1:A:132:ARG:HG2	2.30	0.47
1:A:202:LEU:O	1:A:207:MET:HE2	2.15	0.47
1:E:279:TYR:CE2	1:E:324:ALA:HA	2.51	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: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:D:59:VAL:C	1:D:61:LEU:N	2.63	0.47
1:F:225:ASN:C	1:F:227:LEU:H	2.17	0.47
1:A:137:ILE:H	1:A:137:ILE:CD1	2.22	0.46
1:A:128:ILE:HD11	1:A:152:PHE:N	2.30	0.46
1:C:299:LEU:HB2	1:C:301:LEU:HG	1.97	0.46
1:D:153:GLN:O	1:D:156:VAL:HB	2.15	0.46
1:C:167:ILE:HG23	1:C:168:GLN:N	2.30	0.46
1:C:367:SER:OG	1:C:379:ILE:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:559:LEU:O	1:F:562:PHE:HB3	2.15	0.46
1:F:350:LYS:HZ1	1:F:354:GLN:HE21	1.61	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:D:366:LEU:HD23	1:D:366:LEU:HA	1.71	0.46
1:C:384:LEU:O	1:C:387:ILE:N	2.48	0.46
1:E:555:GLU:C	1:E:555:GLU:CD	2.74	0.46
1:B:398:MET:C	1:B:400:ASP:H	2.18	0.46
1:A:167:ILE:HG12	1:A:171:ASN:ND2	2.30	0.46
1:E:163:GLU:OE2	1:E:165:LYS:N	2.46	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:E:41:ILE:HG12	1:E:50:LEU:HD22	1.96	0.46
1:B:557:ASN:OD1	1:B:557:ASN:C	2.53	0.46
1:E:144:ALA:HA	1:E:147:ILE:HD12	1.97	0.46
1:D:275:LYS:CE	1:D:275:LYS:H	2.29	0.46
1:F:183:VAL:O	1:F:183:VAL:HG12	2.16	0.46
1:A:156:VAL:HA	1:A:160:ALA:HB3	1.96	0.46
1:E:226:GLN:HA	1:E:229:ALA:HB2	1.96	0.46
1:A:542:VAL:CG1	1:A:546:GLU:HG3	2.44	0.46
1:A:294:GLU:HG3	1:A:313:VAL:HG21	1.97	0.46
1:C:641:LYS:O	1:C:642:VAL:C	2.53	0.46
1:A:417:TYR:HE1	1:B:568:VAL:CG2	2.28	0.46
2:H:150:ILE:HG23	2:H:161:PHE:CE1	2.48	0.46
2:G:114:LEU:HD21	2:G:164:LEU:HD13	1.96	0.46
2:I:184:VAL:O	2:I:185:CYS:CB	2.63	0.46
1:A:401:ASP:C	1:A:403:THR:N	2.68	0.46
1:E:200:LYS:HG2	1:E:236:LEU:CD2	2.43	0.46
1:A:289:GLU:OE2	1:A:292:ARG:HD2	2.15	0.46
2:I:112:PRO:O	2:I:113:TRP:CD1	2.68	0.46
2:H:118:VAL:HG12	2:H:119:ASP:N	2.29	0.46
1:D:425:THR:HG22	1:D:426:MET:HE3	1.97	0.46
1:E:131:VAL:HG21	1:E:151:ALA:HB1	1.97	0.46
1:E:390:ILE:CD1	1:E:414:LYS:HD3	2.39	0.46
1:B:529:VAL:O	1:B:532:PHE:HB3	2.16	0.46
1:A:629:GLU:HA	1:A:632:LYS:HG3	1.97	0.46
1:D:121:LEU:O	1:D:124:TRP:HB2	2.15	0.46
1:E:438:ILE:O	1:E:442:CYS:HB2	2.15	0.46
1:B:202:LEU:CD1	1:B:202:LEU:C	2.84	0.46
2:I:126:THR:HG23	2:I:127:PRO:HD2	1.97	0.46
1:B:480:LYS:HB2	1:B:481:TYR:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:ARG:NH1	1:A:232:HIS:CE1	2.82	0.46
1:D:417:TYR:O	1:D:420:CYS:N	2.48	0.46
1:D:373:ASN:O	1:D:375:LYS:HG2	2.16	0.46
1:B:230:ARG:HD3	1:B:230:ARG:O	2.15	0.46
1:E:355:CYS:O	1:E:357:PRO:HD2	2.16	0.46
1:D:571:VAL:HG11	1:D:573:TYR:CE2	2.50	0.46
1:A:641:LYS:HD2	1:A:641:LYS:C	2.35	0.46
2:H:135:LEU:HD22	2:H:178:LEU:HD11	1.98	0.46
1:F:156:VAL:HG13	1:F:170:TRP:CH2	2.50	0.46
1:D:37:LEU:O	1:D:40:MET:HE3	2.16	0.46
1:B:336:GLY:C	1:B:338:LYS:N	2.67	0.46
1:A:137:ILE:HG23	1:A:145:ARG:CB	2.36	0.46
1:E:576:ARG:HB2	1:E:576:ARG:NH1	2.28	0.46
1:A:169:PHE:O	1:A:171:ASN:N	2.48	0.46
1:F:153:GLN:O	1:F:156:VAL:N	2.42	0.46
1:E:81:MET:HE2	1:E:319:GLN:HA	1.97	0.46
1:B:206:PRO:HB3	1:B:247:TYR:CA	2.46	0.46
1:E:107:VAL:HG13	1:E:110:ARG:HD3	1.98	0.46
1:E:41:ILE:CG2	1:E:41:ILE:O	2.63	0.46
2:I:146:LEU:HA	2:I:149:VAL:HG23	1.97	0.46
1:F:111:CYS:SG	1:F:112:LEU:HG	2.55	0.46
1:D:295:SER:C	1:D:297:ASN:N	2.68	0.46
1:D:247:TYR:O	1:D:250:TRP:HB3	2.15	0.46
2:I:186:SER:CA	2:I:189:GLN:HE22	2.29	0.46
1:A:351:LEU:O	1:A:354:GLN:HB2	2.16	0.46
1:C:436:ARG:NH2	1:C:461:GLU:OE1	2.46	0.46
1:A:427:LYS:HB2	1:A:435:SER:CB	2.46	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
2:H:180:LEU:HD22	2:H:189:GLN:OE1	2.16	0.46
1:A:568:VAL:CG1	1:A:569:LEU:HD22	2.37	0.46
1:F:55:LEU:HD21	1:F:70:THR:HG22	1.98	0.46
2:I:175:ILE:HG22	2:I:175:ILE:O	2.15	0.46
1:A:401:ASP:O	1:A:403:THR:N	2.49	0.46
1:D:199:TYR:O	1:D:203:LEU:HG	2.16	0.46
1:F:81:MET:HG3	1:F:84:ILE:HD12	1.97	0.46
1:D:455:LEU:N	1:D:455:LEU:CD2	2.79	0.46
1:A:473:LYS:O	1:A:477:LEU:HB2	2.16	0.46
2:I:138:LEU:HB3	2:I:142:GLN:CG	2.46	0.46
1:B:279:TYR:CE2	1:B:324:ALA:HA	2.51	0.46
1:E:191:ARG:NE	1:E:195:ILE:HD11	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:180:LEU:HD13	2:H:189:GLN:HE22	1.80	0.46
1:C:124:TRP:O	1:C:127:TYR:HB3	2.16	0.46
1:E:200:LYS:HG2	1:E:236:LEU:CD1	2.43	0.46
1:C:242:ASN:O	1:C:246:LEU:HG	2.16	0.46
1:F:370:TYR:CD1	1:F:378:GLU:HB3	2.51	0.46
2:I:162:VAL:O	2:I:166:GLU:HB2	2.16	0.46
1:B:113:SER:OG	1:B:115:GLU:HG2	2.15	0.46
1:A:345:ILE:HB	1:A:369:GLN:OE1	2.16	0.46
1:E:579:LEU:HD22	1:E:581:TYR:OH	2.16	0.46
1:D:125:LEU:C	1:D:127:TYR:N	2.69	0.46
1:D:166:SER:O	1:D:167:ILE:C	2.55	0.46
1:E:170:TRP:CD2	1:E:202:LEU:HD23	2.51	0.46
1:A:336:GLY:C	1:A:338:LYS:H	2.18	0.46
1:B:116:LEU:O	1:B:118:ASN:N	2.44	0.46
2:I:160:THR:O	2:I:160:THR:HG22	2.16	0.46
1:E:135:ASN:HB3	1:E:144:ALA:O	2.16	0.46
1:B:71:PHE:HB3	1:B:88:ARG:NH1	2.30	0.46
1:A:358:ASN:HB3	1:A:389:ARG:HG3	1.98	0.46
1:C:580:ASP:C	1:C:582:MET:H	2.18	0.46
1:B:52:VAL:HG11	1:B:268:ALA:CB	2.45	0.46
1:C:544:THR:O	1:C:547:LYS:HB3	2.16	0.46
1:B:181:LYS:HD2	1:B:181:LYS:N	2.31	0.46
1:E:191:ARG:O	1:E:195:ILE:HG13	2.16	0.45
1:C:61:LEU:HD12	1:C:63:GLN:NE2	2.31	0.45
1:E:119:ASN:HD22	1:E:312:TYR:HD1	1.64	0.45
1:C:169:PHE:O	1:C:170:TRP:C	2.54	0.45
1:D:207:MET:O	1:D:247:TYR:CD2	2.69	0.45
1:E:170:TRP:CE2	1:E:202:LEU:HB3	2.51	0.45
1:C:55:LEU:HD13	1:C:71:PHE:CE1	2.50	0.45
1:E:394:LEU:HD12	1:E:411:LEU:CD2	2.46	0.45
1:B:199:TYR:O	1:B:203:LEU:HG	2.16	0.45
1:A:177:LEU:HD11	1:A:194:TYR:HB3	1.97	0.45
1:F:255:LYS:C	1:F:257:LEU:H	2.19	0.45
1:B:168:GLN:O	1:B:169:PHE:C	2.54	0.45
1:A:442:CYS:HA	1:A:445:LEU:HD12	1.98	0.45
1:E:333:ASN:HD22	1:F:558:LYS:HD3	1.81	0.45
1:F:326:GLU:HG3	1:F:326:GLU:O	2.15	0.45
1:A:640:PHE:C	1:A:642:VAL:H	2.18	0.45
1:C:567:LYS:HG2	1:C:572:ASN:CA	2.45	0.45
1:B:145:ARG:NE	1:B:180:TRP:NE1	2.64	0.45
1:A:39:ASP:O	1:A:42:GLU:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:444:ARG:NH2	2:G:167:GLU:OE2	2.49	0.45
1:F:255:LYS:HB3	1:F:256:GLY:H	1.44	0.45
1:D:356:ILE:O	1:D:358:ASN:N	2.50	0.45
1:B:242:ASN:O	1:B:246:LEU:HG	2.15	0.45
1:C:211:GLU:HA	1:C:240:TYR:OH	2.16	0.45
1:D:249:ASP:O	1:D:252:ASN:HB2	2.15	0.45
1:A:486:GLY:C	1:A:521:LEU:HD23	2.36	0.45
1:C:642:VAL:HG23	1:C:643:THR:H	1.81	0.45
1:E:577:LEU:O	1:E:578:GLU:HB2	2.15	0.45
1:C:203:LEU:HD12	1:C:236:LEU:HD13	1.99	0.45
1:B:57:HIS:C	1:B:59:VAL:N	2.70	0.45
1:D:207:MET:H	1:D:210:LEU:HG	1.81	0.45
1:C:346:THR:HG21	1:C:370:TYR:HE2	1.82	0.45
1:E:41:ILE:HD11	1:E:51:TYR:HA	1.98	0.45
1:A:241:MET:O	1:A:244:ARG:N	2.50	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:A:252:ASN:O	1:A:255:LYS:HG2	2.16	0.45
1:D:462:TYR:HA	1:D:467:ASP:O	2.16	0.45
1:B:478:GLY:O	1:B:482:PHE:HB2	2.16	0.45
1:C:249:ASP:O	1:C:253:ILE:HG13	2.16	0.45
1:A:127:TYR:O	1:A:131:VAL:HG23	2.17	0.45
1:A:113:SER:HB2	1:A:115:GLU:OE1	2.16	0.45
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:E:392:LEU:HA	1:E:395:ALA:HB3	1.98	0.45
1:E:78:PHE:N	1:E:78:PHE:CD1	2.83	0.45
1:F:420:CYS:O	1:F:423:MET:N	2.49	0.45
1:A:182:PRO:CG	1:A:191:ARG:HD2	2.43	0.45
1:D:306:HIS:CD2	1:D:306:HIS:O	2.70	0.45
1:B:30:GLU:HG2	1:F:61:LEU:HD22	1.99	0.45
1:B:191:ARG:HG3	1:B:191:ARG:NH1	2.31	0.45
1:A:61:LEU:HB2	1:A:63:GLN:NE2	2.28	0.45
1:C:455:LEU:CD2	1:C:455:LEU:H	2.29	0.45
1:D:546:GLU:O	1:D:547:LYS:C	2.54	0.45
1:A:49:PHE:HE2	1:A:53:LYS:NZ	2.14	0.45
1:A:179:HIS:O	1:A:179:HIS:ND1	2.49	0.45
1:A:153:GLN:O	1:A:156:VAL:HB	2.16	0.45
1:E:314:TYR:CD1	1:E:331:MET:HB2	2.51	0.45
1:A:305:LEU:O	1:A:306:HIS:C	2.54	0.45
1:C:494:ASP:OD1	1:C:528:LYS:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:568:VAL:HG21	1:F:417:TYR:CE1	2.51	0.45
1:B:495:PHE:O	1:B:499:VAL:HG22	2.17	0.45
1:C:178:GLU:HA	1:C:191:ARG:HH21	1.78	0.45
1:E:432:LEU:O	1:E:433:ALA:C	2.54	0.45
1:C:392:LEU:O	1:C:394:LEU:N	2.50	0.45
1:E:282:GLN:NE2	1:E:282:GLN:HA	2.32	0.45
1:C:54:LEU:HD23	1:C:70:THR:CG2	2.46	0.45
1:C:240:TYR:O	1:C:243:ALA:HB3	2.16	0.45
2:G:126:THR:HB	2:G:129:MET:H	1.82	0.45
1:E:178:GLU:HA	1:E:191:ARG:CZ	2.43	0.45
1:B:506:LYS:HZ1	1:B:545:LEU:HD12	1.82	0.45
1:C:564:ASN:HA	1:C:567:LYS:HE2	1.99	0.45
1:C:79:PRO:HB2	1:C:116:LEU:HD22	1.98	0.45
1:B:162:PHE:HD2	1:B:309:ARG:HG3	1.81	0.45
1:E:630:LEU:CD1	2:I:135:LEU:HD21	2.46	0.45
1:B:182:PRO:HB3	1:B:188:GLU:HB2	1.99	0.45
1:F:199:TYR:CD1	1:F:217:TYR:HB2	2.51	0.45
1:A:101:ALA:O	1:A:105:GLU:HG3	2.17	0.45
1:B:486:GLY:C	1:B:521:LEU:HD23	2.37	0.45
1:F:124:TRP:O	1:F:127:TYR:N	2.43	0.45
1:E:71:PHE:CE1	1:E:265:LEU:HD12	2.52	0.45
1:E:40:MET:C	1:E:42:GLU:H	2.19	0.45
1:C:455:LEU:CD2	1:C:455:LEU:N	2.80	0.45
1:E:533:GLU:OE1	1:E:541:SER:HB3	2.16	0.45
1:A:542:VAL:O	1:A:543:ARG:C	2.55	0.45
1:E:372:LEU:CD1	1:F:543:ARG:NE	2.80	0.45
1:B:240:TYR:O	1:B:243:ALA:HB3	2.17	0.45
2:H:163:ALA:O	2:H:167:GLU:HG2	2.17	0.45
1:B:539:LEU:HD23	1:B:539:LEU:C	2.37	0.45
1:F:307:LYS:HD3	1:F:338:LYS:HG3	1.99	0.45
1:E:131:VAL:HG11	1:E:151:ALA:HB2	1.99	0.45
1:E:210:LEU:HD21	1:E:243:ALA:HB1	1.98	0.45
1:E:164:PRO:CG	1:E:250:TRP:CZ2	2.99	0.45
1:B:180:TRP:HZ3	1:B:191:ARG:HA	1.82	0.45
1:F:563:THR:CG2	1:F:572:ASN:OD1	2.65	0.45
1:B:281:VAL:O	1:B:285:LEU:HD12	2.17	0.45
2:I:144:MET:HA	2:I:147:LEU:HB3	1.98	0.45
1:F:180:TRP:CZ2	1:F:187:GLU:HG2	2.51	0.45
1:E:540:ASN:ND2	1:E:543:ARG:NH2	2.65	0.45
1:C:128:ILE:HD11	1:C:155:VAL:HG21	1.98	0.45
1:C:112:LEU:HA	1:C:112:LEU:HD23	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:GLU:OE1	1:A:105:GLU:HA	2.17	0.45
1:E:317:ALA:O	1:E:321:VAL:HG22	2.16	0.45
1:F:568:VAL:O	1:F:569:LEU:C	2.56	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: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:F:204:CYS:HB2	1:F:205:GLN:HE21	1.82	0.45
1:D:221:GLU:O	1:D:229:ALA:HB2	2.17	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:E:173:TYR:O	1:E:173:TYR:CG	2.70	0.44
1:B:105:GLU:HB2	1:B:106:PRO:HD3	1.99	0.44
1:E:262:PRO:CB	1:E:268:ALA:HA	2.47	0.44
1:F:392:LEU:C	1:F:394:LEU:N	2.70	0.44
1:B:556:VAL:HG22	1:B:557:ASN:N	2.30	0.44
1:E:401:ASP:O	1:E:403:THR:N	2.49	0.44
2:I:137:LYS:O	2:I:138:LEU:CB	2.65	0.44
1:F:332:ALA:O	1:F:345:ILE:HG12	2.16	0.44
1:A:93:PHE:HE2	1:A:104:ILE:CD1	2.29	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:358:ASN:HB3	1:F:389:ARG:HG3	1.99	0.44
1:B:240:TYR:CZ	1:B:244:ARG:HD2	2.52	0.44
1:B:135:ASN:ND2	1:B:147:ILE:HG21	2.32	0.44
1:B:542:VAL:O	1:B:543:ARG:C	2.53	0.44
1:D:242:ASN:O	1:D:246:LEU:HG	2.16	0.44
1:C:417:TYR:CE2	1:D:574:LEU:HD23	2.52	0.44
1:A:220:TRP:HZ3	1:A:221:GLU:OE2	1.99	0.44
1:E:124:TRP:O	1:E:127:TYR:HB3	2.17	0.44
1:C:125:LEU:C	1:C:127:TYR:H	2.19	0.44
1:E:426:MET:CE	1:E:426:MET:HA	2.48	0.44
1:D:330:ASN:H	1:D:330:ASN:ND2	2.15	0.44
1:B:83:ASN:ND2	1:B:84:ILE:HD12	2.32	0.44
1:B:378:GLU:O	1:B:382:THR:OG1	2.28	0.44
1:C:633:VAL:O	2:H:134:GLU:HG3	2.17	0.44
1:A:492:TYR:HE1	1:A:496:LEU:HD11	1.81	0.44
1:D:33:VAL:H	1:D:36:LYS:HZ3	1.65	0.44
1:A:88:ARG:HG3	1:A:88:ARG:O	2.16	0.44
1:E:247:TYR:CZ	1:E:251:LEU:HD13	2.53	0.44
1:E:529:VAL:O	1:E:532:PHE:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:265:LEU:O	1:C:268:ALA:HB3	2.17	0.44
1:D:136:ASP:CB	1:D:139:THR:HB	2.44	0.44
1:E:287:TRP:CZ2	1:E:320:HIS:ND1	2.86	0.44
1:C:306:HIS:CD2	1:C:310:MET:HG2	2.52	0.44
1:A:334:TYR:O	1:A:336:GLY:N	2.51	0.44
1:E:384:LEU:O	1:E:385:SER:C	2.55	0.44
1:B:572:ASN:C	1:B:572:ASN:ND2	2.70	0.44
1:B:117:GLY:O	1:B:119:ASN:N	2.50	0.44
1:A:315:MET:O	1:A:316:GLN:C	2.55	0.44
1:A:418:VAL:O	1:A:418:VAL:HG12	2.16	0.44
2:H:135:LEU:CD1	2:H:177:GLU:HG2	2.47	0.44
1:C:262:PRO:HG3	1:C:273:LEU:CD2	2.36	0.44
1:B:527:GLN:HB2	1:B:527:GLN:HE21	1.61	0.44
1:B:401:ASP:C	1:B:403:THR:H	2.21	0.44
1:C:576:ARG:O	1:C:577:LEU:HD23	2.17	0.44
1:C:55:LEU:HD22	1:C:71:PHE:CD1	2.53	0.44
1:B:203:LEU:HD13	1:B:214:TRP:CE3	2.52	0.44
1:F:504:GLN:O	1:F:505:VAL:C	2.55	0.44
2:H:142:GLN:O	2:H:145:ALA:HB3	2.17	0.44
1:D:432:LEU:O	1:D:435:SER:HB3	2.17	0.44
1:A:351:LEU:HD23	1:A:354:GLN:OE1	2.18	0.44
1:B:559:LEU:O	1:B:563:THR:HG23	2.17	0.44
1:C:137:ILE:HG21	1:C:176:PHE:HE1	1.81	0.44
1:A:225:ASN:O	1:A:229:ALA:HB3	2.17	0.44
1:A:364:PHE:CD1	1:A:364:PHE:N	2.85	0.44
2:G:179:LEU:O	2:G:181:SER:N	2.50	0.44
1:A:152:PHE:HB3	1:A:173:TYR:CD1	2.53	0.44
1:E:477:LEU:HD12	1:E:477:LEU:N	2.33	0.44
1:A:630:LEU:HD23	2:G:171:LEU:HD13	1.99	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: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:F:533:GLU:OE1	1:F:541:SER:HB3	2.17	0.44
1:D:261:LEU:HD23	1:D:261:LEU:HA	1.76	0.44
1:A:493:LEU:O	1:A:494:ASP:C	2.56	0.44
1:B:225:ASN:CB	1:B:228:THR:HB	2.48	0.44
1:C:335:GLN:HA	1:C:335:GLN:OE1	2.18	0.44
1:E:77:ARG:HH11	1:E:77:ARG:HG3	1.81	0.44
1:F:383:ILE:HG21	1:F:422:TYR:CG	2.53	0.44
1:F:405:GLU:HG3	1:F:406:SER:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:168:ALA:CA	2:G:170:GLN:HE22	2.27	0.44
1:C:572:ASN:ND2	1:C:575:GLN:NE2	2.53	0.44
1:E:297:ASN:HB2	1:E:306:HIS:CE1	2.53	0.44
1:D:295:SER:O	1:D:297:ASN:N	2.51	0.44
1:C:167:ILE:HD12	1:C:209:CYS:HB3	1.99	0.44
1:A:624:PRO:HG3	2:G:153:PHE:CE1	2.52	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:A:147:ILE:HG22	1:A:148:VAL:N	2.33	0.44
1:D:477:LEU:O	1:D:480:LYS:HG2	2.18	0.44
1:A:162:PHE:HA	1:A:309:ARG:HH12	1.82	0.44
1:C:475:LEU:HB3	1:C:492:TYR:CE1	2.53	0.44
1:A:183:VAL:HG23	1:A:187:GLU:OE1	2.18	0.44
1:A:574:LEU:HA	1:A:574:LEU:HD12	1.61	0.44
1:A:404:ASN:OD1	1:A:407:ALA:N	2.45	0.44
1:E:143:GLU:C	1:E:145:ARG:H	2.20	0.44
1:A:100:ASP:O	1:A:100:ASP:OD1	2.35	0.44
1:F:568:VAL:O	1:F:570:ASP:N	2.50	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:D:115:GLU:C	1:D:117:GLY:N	2.71	0.44
1:B:25:SER:HB2	1:B:43:GLU:CD	2.38	0.44
1:F:470:THR:O	1:F:472:CYS:N	2.50	0.44
1:B:427:LYS:CA	1:B:435:SER:HB3	2.48	0.44
1:E:651:SER:HB2	2:I:162:VAL:CG1	2.48	0.44
1:E:186:PHE:C	1:E:188:GLU:N	2.69	0.44
1:F:346:THR:O	1:F:350:LYS:HB2	2.17	0.44
2:G:138:LEU:O	2:G:139:GLN:C	2.56	0.44
1:A:538:SER:N	1:A:541:SER:OG	2.50	0.44
1:D:575:GLN:O	1:D:577:LEU:N	2.51	0.44
1:E:474:VAL:O	1:E:477:LEU:HB2	2.18	0.44
1:E:119:ASN:O	1:E:312:TYR:CE1	2.70	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
2:I:193:LEU:HD12	2:I:193:LEU:C	2.38	0.44
1:F:349:LEU:HD11	1:F:365:SER:HB3	1.99	0.44
1:F:529:VAL:CG1	1:F:545:LEU:HD11	2.48	0.44
1:B:86:CYS:HB3	1:B:263:ILE:CG1	2.46	0.44
1:F:54:LEU:HG	1:F:58:HIS:CD2	2.52	0.44
1:C:279:TYR:CE2	1:C:324:ALA:HA	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:103:VAL:O	1:E:103:VAL:HG12	2.17	0.44
1:A:300:GLU:N	1:A:300:GLU:OE2	2.51	0.44
1:C:579:LEU:HD22	1:C:581:TYR:CZ	2.53	0.44
1:B:274:PRO:HB2	1:B:323:PHE:CE1	2.53	0.44
1:E:219:GLN:HE21	1:E:219:GLN:HB3	1.58	0.44
1:A:636:LYS:O	1:A:638:GLN:N	2.46	0.44
1:A:207:MET:C	1:A:209:CYS:H	2.21	0.44
1:D:296:ASP:O	1:D:297:ASN:C	2.56	0.44
1:E:497:ILE:HG23	1:E:532:PHE:CD1	2.53	0.44
1:C:110:ARG:HH11	1:C:110:ARG:HG2	1.82	0.44
1:F:394:LEU:O	1:F:395:ALA:C	2.57	0.44
1:B:366:LEU:HB3	1:B:382:THR:HG21	1.99	0.44
1:D:424:ASN:O	1:D:427:LYS:HB3	2.18	0.44
1:E:371:GLU:OE2	1:F:539:LEU:HB2	2.17	0.44
1:B:192:VAL:O	1:B:193:GLN:C	2.55	0.44
1:A:196:ARG:CG	1:A:200:LYS:HE2	2.48	0.44
1:C:327:ILE:HG23	1:C:328:TRP:N	2.33	0.44
1:D:101:ALA:HB2	1:D:134:LYS:HZ3	1.83	0.44
1:D:232:HIS:HA	1:D:235:GLU:OE1	2.17	0.44
1:F:410:GLN:HB3	1:F:410:GLN:HE21	1.52	0.44
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:E:423:MET:HB2	1:E:438:ILE:HG21	2.00	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:F:281:VAL:O	1:F:282:GLN:C	2.54	0.43
2:H:118:VAL:CG1	2:H:119:ASP:N	2.81	0.43
1:A:51:TYR:N	1:A:51:TYR:CD2	2.86	0.43
1:C:464:ILE:HG22	1:C:465:SER:N	2.33	0.43
1:D:386:CYS:O	1:D:390:ILE:HG13	2.18	0.43
1:D:269:THR:C	1:D:271:SER:N	2.71	0.43
1:C:314:TYR:CD1	1:C:331:MET:HB2	2.53	0.43
1:B:181:LYS:HD3	1:B:181:LYS:O	2.18	0.43
1:F:287:TRP:CZ3	1:F:290:TRP:CZ3	3.06	0.43
1:A:269:THR:O	1:A:271:SER:N	2.42	0.43
1:C:174:LEU:HD11	1:C:199:TYR:CZ	2.52	0.43
1:B:61:LEU:O	1:B:62:LYS:C	2.57	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:B:68:TYR:OH	1:B:103:VAL:HG11	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:412:LYS:CE	1:E:448:LEU:HA	2.46	0.43
1:C:644:ILE:HA	2:H:173:TYR:OH	2.18	0.43
1:F:487:GLU:N	1:F:521:LEU:HD22	2.33	0.43
1:F:183:VAL:HG23	1:F:187:GLU:OE1	2.18	0.43
1:A:254:THR:O	1:A:255:LYS:C	2.56	0.43
1:A:532:PHE:O	1:A:536:VAL:HG12	2.17	0.43
1:A:219:GLN:C	1:A:219:GLN:NE2	2.72	0.43
1:A:364:PHE:CZ	1:A:421:VAL:CG1	2.86	0.43
2:G:169:PRO:HD2	2:G:170:GLN:NE2	2.32	0.43
1:A:575:GLN:HE21	1:A:582:MET:HE3	1.83	0.43
1:D:164:PRO:HG3	1:D:250:TRP:CE2	2.54	0.43
1:A:462:TYR:HD1	1:A:471:ALA:HB3	1.84	0.43
1:C:296:ASP:O	1:C:297:ASN:C	2.57	0.43
1:F:105:GLU:HB2	1:F:106:PRO:HD3	2.00	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:B:281:VAL:O	1:B:284:LEU:N	2.51	0.43
1:D:275:LYS:CD	1:D:275:LYS:H	2.31	0.43
1:A:373:ASN:C	1:A:375:LYS:H	2.21	0.43
1:B:225:ASN:HB2	1:B:228:THR:HB	2.00	0.43
1:A:418:VAL:HA	1:A:421:VAL:HG12	2.00	0.43
1:A:128:ILE:CD1	1:A:151:ALA:HB1	2.49	0.43
1:E:206:PRO:HB3	1:E:247:TYR:CB	2.48	0.43
1:B:61:LEU:O	1:B:63:GLN:CG	2.63	0.43
1:D:169:PHE:O	1:D:170:TRP:C	2.56	0.43
1:D:167:ILE:CD1	1:D:209:CYS:HB3	2.49	0.43
2:I:185:CYS:HB3	2:I:189:GLN:NE2	2.33	0.43
1:D:52:VAL:HG21	1:D:268:ALA:HB1	2.00	0.43
1:F:125:LEU:HD11	1:F:168:GLN:HG3	2.01	0.43
1:E:394:LEU:HA	1:E:411:LEU:CD2	2.49	0.43
1:A:334:TYR:HA	1:A:337:GLU:HB3	2.01	0.43
1:A:41:ILE:HD11	1:A:51:TYR:HA	1.99	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:F:540:ASN:ND2	1:F:543:ARG:NH2	2.67	0.43
1:F:434:ALA:HA	1:F:437:LYS:HE3	2.01	0.43
1:D:240:TYR:O	1:D:243:ALA:HB3	2.19	0.43
1:A:513:ILE:H	1:A:513:ILE:HD12	1.84	0.43
1:F:387:ILE:HG22	1:F:388:ASP:N	2.33	0.43
1:A:169:PHE:O	1:A:170:TRP:C	2.56	0.43
1:A:132:ARG:HH21	1:A:176:PHE:HD1	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:VAL:O	1:B:62:LYS:N	2.51	0.43
1:C:125:LEU:C	1:C:127:TYR:N	2.70	0.43
1:B:66:GLN:HE21	1:B:66:GLN:CA	2.31	0.43
1:F:468:THR:O	1:F:469:LYS:C	2.56	0.43
1:F:349:LEU:HB3	1:F:366:LEU:HG	2.01	0.43
1:A:51:TYR:CB	1:A:74:LEU:HD12	2.48	0.43
1:B:489:ILE:HD12	1:B:508:LEU:HD11	2.01	0.43
1:E:573:TYR:C	1:E:575:GLN:N	2.72	0.43
1:E:327:ILE:HG22	1:E:328:TRP:H	1.78	0.43
1:A:579:LEU:HA	1:A:579:LEU:HD23	1.82	0.43
1:D:120:ASP:O	1:D:121:LEU:C	2.57	0.43
1:D:80:LEU:HA	1:D:118:ASN:ND2	2.23	0.43
1:A:87:MET:HG2	1:A:265:LEU:N	2.33	0.43
1:E:394:LEU:HD23	1:E:448:LEU:HD11	2.00	0.43
1:B:111:CYS:SG	1:B:112:LEU:HD23	2.58	0.43
1:F:254:THR:HG22	1:F:255:LYS:N	2.32	0.43
1:D:33:VAL:HA	1:D:36:LYS:HZ1	1.83	0.43
1:A:350:LYS:HA	1:A:366:LEU:HD11	2.00	0.43
1:B:127:TYR:O	1:B:131:VAL:HG23	2.19	0.43
1:F:428:ARG:HG2	1:F:428:ARG:O	2.17	0.43
1:C:414:LYS:HA	1:D:577:LEU:HD13	2.00	0.43
1:A:509:PHE:O	1:A:513:ILE:HG13	2.19	0.43
1:A:387:ILE:HD12	1:A:418:VAL:CG1	2.49	0.43
1:B:501:GLU:HB3	1:B:504:GLN:HB2	2.00	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:C:265:LEU:C	1:C:265:LEU:HD23	2.38	0.43
1:B:350:LYS:NZ	1:B:354:GLN:HE21	2.15	0.43
1:D:54:LEU:HG	1:D:58:HIS:CD2	2.53	0.43
1:A:247:TYR:O	1:A:251:LEU:HB2	2.18	0.43
1:F:533:GLU:HG3	1:F:545:LEU:HD12	2.01	0.43
1:A:57:HIS:C	1:A:59:VAL:N	2.72	0.43
1:B:121:LEU:O	1:B:123:LEU:N	2.52	0.43
1:A:414:LYS:HB2	1:B:577:LEU:HD13	2.00	0.43
1:E:203:LEU:HD22	1:E:240:TYR:CD1	2.54	0.43
1:F:511:SER:O	1:F:515:LYS:HG3	2.19	0.43
1:A:240:TYR:O	1:A:243:ALA:HB3	2.18	0.43
1:B:94:ASP:O	1:B:95:LYS:HB3	2.18	0.43
1:B:93:PHE:O	1:B:94:ASP:OD1	2.37	0.43
1:A:401:ASP:O	1:A:401:ASP:CG	2.55	0.43
1:E:87:MET:SD	1:E:268:ALA:HB2	2.59	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:D:60:SER:O	1:D:61:LEU:HD23	2.18	0.43
1:C:546:GLU:O	1:C:549:PHE:N	2.52	0.43
1:B:314:TYR:HB3	1:B:331:MET:HE2	2.01	0.43
1:D:339:ASN:ND2	1:D:340:THR:O	2.52	0.43
1:F:471:ALA:HB1	1:F:495:PHE:CZ	2.54	0.43
1:E:376:ILE:HB	1:E:377:PRO:HD3	1.99	0.43
1:E:324:ALA:O	1:E:327:ILE:HG22	2.18	0.43
1:D:170:TRP:CE3	1:D:170:TRP:HA	2.53	0.43
1:C:131:VAL:HG11	1:C:151:ALA:CB	2.47	0.43
1:E:532:PHE:O	1:E:535:LYS:N	2.49	0.43
2:I:189:GLN:CD	2:I:189:GLN:H	2.23	0.43
1:A:394:LEU:HD12	1:A:411:LEU:HD23	2.01	0.43
1:E:394:LEU:HA	1:E:411:LEU:HD21	2.01	0.43
1:E:107:VAL:HA	1:E:110:ARG:CG	2.47	0.43
1:D:513:ILE:CG2	1:D:552:LYS:HE2	2.49	0.43
1:F:54:LEU:HG	1:F:58:HIS:HD2	1.84	0.43
1:A:496:LEU:HB3	1:A:505:VAL:HG22	2.01	0.43
1:C:323:PHE:CE2	1:C:355:CYS:O	2.72	0.43
2:I:135:LEU:HD22	2:I:178:LEU:HD21	2.01	0.43
1:E:653:PHE:O	1:E:657:LYS:HB3	2.18	0.43
1:B:550:PHE:HE2	1:B:558:LYS:HD2	1.84	0.43
1:A:333:ASN:HA	1:A:333:ASN:HD22	1.68	0.43
1:F:248:GLN:O	1:F:251:LEU:N	2.51	0.43
1:D:574:LEU:HA	1:D:574:LEU:HD22	1.78	0.43
1:C:398:MET:O	1:C:402:PRO:HD3	2.18	0.43
1:B:490:ASN:OD1	1:B:525:ILE:HD13	2.18	0.43
1:F:156:VAL:HG13	1:F:170:TRP:HH2	1.83	0.43
1:D:294:GLU:OE1	1:D:309:ARG:NE	2.45	0.43
1:A:83:ASN:O	1:A:84:ILE:C	2.57	0.43
1:D:560:GLU:CA	1:D:582:MET:HE3	2.48	0.43
1:E:170:TRP:CZ3	1:E:198:LEU:HD13	2.54	0.43
1:F:125:LEU:HD11	1:F:168:GLN:CG	2.49	0.43
1:B:128:ILE:HD13	1:B:152:PHE:CE1	2.54	0.43
1:A:398:MET:C	1:A:400:ASP:N	2.72	0.43
1:F:84:ILE:O	1:F:84:ILE:HG22	2.18	0.43
1:A:49:PHE:CZ	1:A:53:LYS:HD3	2.54	0.43
2:I:118:VAL:CG1	2:I:119:ASP:N	2.82	0.43
1:E:281:VAL:HG21	1:F:581:TYR:CD2	2.54	0.43
1:D:36:LYS:HA	1:D:39:ASP:OD2	2.18	0.43
1:A:542:VAL:HG12	1:A:543:ARG:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:501:GLU:O	1:A:502:GLU:C	2.57	0.43
1:A:246:LEU:HA	1:A:246:LEU:HD23	1.78	0.43
1:E:575:GLN:C	1:E:577:LEU:H	2.23	0.42
1:A:209:CYS:O	1:A:210:LEU:C	2.57	0.42
2:I:170:GLN:N	2:I:170:GLN:NE2	2.55	0.42
1:E:539:LEU:HD22	1:F:371:GLU:HB3	2.01	0.42
1:A:462:TYR:HD1	1:A:471:ALA:CB	2.32	0.42
1:B:195:ILE:HG22	1:B:199:TYR:CD2	2.54	0.42
1:E:439:PHE:CD2	1:E:457:ASN:OD1	2.72	0.42
1:B:553:PHE:N	1:B:554:PRO:HD3	2.34	0.42
1:D:33:VAL:C	1:D:35:GLY:N	2.71	0.42
2:I:155:LYS:O	2:I:156:ASP:HB3	2.18	0.42
1:A:101:ALA:HB1	1:A:105:GLU:CG	2.49	0.42
1:F:152:PHE:CG	1:F:173:TYR:HD1	2.37	0.42
1:C:121:LEU:HD12	1:C:163:GLU:HG2	2.02	0.42
1:F:49:PHE:O	1:F:50:LEU:C	2.55	0.42
1:B:149:ILE:O	1:B:152:PHE:N	2.51	0.42
1:B:149:ILE:O	1:B:150:GLN:C	2.58	0.42
1:B:66:GLN:NE2	1:B:66:GLN:CA	2.82	0.42
1:E:88:ARG:NH2	1:E:107:VAL:HG21	2.34	0.42
1:D:182:PRO:HD3	1:D:191:ARG:HH11	1.81	0.42
1:A:244:ARG:O	1:A:247:TYR:N	2.51	0.42
1:B:553:PHE:O	1:B:556:VAL:HB	2.19	0.42
1:D:63:GLN:O	1:D:67:VAL:HG23	2.19	0.42
2:G:148:LYS:O	2:G:151:GLN:HB3	2.19	0.42
1:A:493:LEU:O	1:A:497:ILE:HG13	2.19	0.42
1:C:628:VAL:O	1:C:630:LEU:N	2.52	0.42
1:E:349:LEU:CD1	1:E:365:SER:HB3	2.49	0.42
1:A:290:TRP:O	1:A:293:TRP:HB3	2.19	0.42
1:C:270:GLU:HG2	1:C:270:GLU:O	2.19	0.42
1:A:636:LYS:HG3	2:G:118:VAL:O	2.20	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
1:A:182:PRO:HB3	1:A:188:GLU:CB	2.48	0.42
1:A:191:ARG:HG3	1:A:191:ARG:NH1	2.32	0.42
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: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
1:E:432:LEU:HD21	1:E:436:ARG:HH21	1.84	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)
2:H:125:THR:HG22	2:H:126:THR:N	2.33	0.42
1:E:349:LEU:HD11	1:E:365:SER:HB3	2.01	0.42
1:B:347:LYS:HG2	1:B:348:TYR:N	2.33	0.42
2:H:187:VAL:HG12	2:H:187:VAL:O	2.19	0.42
1:D:468:THR:HG23	1:D:499:VAL:HG11	1.90	0.42
1:E:72:ASP:C	1:E:74:LEU:N	2.72	0.42
1:F:398:MET:HG2	1:F:408:ILE:CD1	2.33	0.42
1:A:167:ILE:CG1	1:A:171:ASN:HD21	2.32	0.42
1:A:71:PHE:CZ	1:A:88:ARG:HA	2.53	0.42
1:A:174:LEU:HD11	1:A:199:TYR:CE1	2.54	0.42
1:B:99:LEU:CD2	1:B:133:LYS:HD2	2.49	0.42
1:E:88:ARG:O	1:E:92:GLU:OE1	2.38	0.42
1:C:101:ALA:HB2	1:C:134:LYS:HZ1	1.83	0.42
1:B:203:LEU:HD13	1:B:214:TRP:HE3	1.83	0.42
1:A:624:PRO:O	1:A:625:PRO:C	2.56	0.42
1:A:340:THR:HB	1:A:341:ASP:H	1.63	0.42
1:D:106:PRO:O	1:D:109:ALA:HB3	2.20	0.42
1:C:562:PHE:CZ	1:C:566:TYR:CE2	3.08	0.42
1:F:247:TYR:O	1:F:250:TRP:HB3	2.19	0.42
1:F:436:ARG:O	1:F:439:PHE:N	2.50	0.42
2:H:138:LEU:O	2:H:139:GLN:C	2.58	0.42
1:B:544:THR:O	1:B:547:LYS:HB3	2.19	0.42
1:C:349:LEU:CD1	1:C:365:SER:HB3	2.49	0.42
1:F:489:ILE:HG13	1:F:516:ILE:CD1	2.37	0.42
1:F:272:ASN:OD1	1:F:273:LEU:HG	2.20	0.42
1:E:295:SER:HB3	1:E:310:MET:CE	2.49	0.42
1:E:479:LEU:CD1	1:E:492:TYR:HE2	2.28	0.42
1:D:140:GLY:C	1:D:142:GLU:H	2.23	0.42
1:D:140:GLY:O	1:D:142:GLU:N	2.53	0.42
1:C:518:ASP:O	1:C:519:SER:C	2.57	0.42
1:E:41:ILE:HD11	1:E:50:LEU:O	2.19	0.42
1:C:392:LEU:C	1:C:394:LEU:N	2.69	0.42
1:F:107:VAL:HG12	1:F:108:LEU:N	2.33	0.42
1:D:78:PHE:N	1:D:78:PHE:CD1	2.87	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:F:321:VAL:HG23	1:F:321:VAL:O	2.19	0.42
1:A:638:GLN:HB2	1:A:638:GLN:HE21	1.66	0.42
1:E:572:ASN:ND2	1:E:575:GLN:NE2	2.67	0.42
1:A:89:LEU:HD11	1:A:108:LEU:CD2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:154:VAL:HG13	1:D:155:VAL:N	2.34	0.42
1:C:121:LEU:HD11	1:C:166:SER:HB3	2.01	0.42
1:E:499:VAL:HG12	1:E:499:VAL:O	2.18	0.42
1:E:405:GLU:HG3	1:E:406:SER:H	1.84	0.42
1:B:425:THR:HG22	1:B:426:MET:CE	2.50	0.42
1:D:59:VAL:HG22	1:D:67:VAL:CG2	2.49	0.42
1:A:648:HIS:O	1:A:651:SER:HB2	2.20	0.42
1:C:135:ASN:ND2	1:C:147:ILE:CG2	2.83	0.42
1:D:380:GLU:O	1:D:381:THR:C	2.56	0.42
1:F:267:GLN:O	1:F:269:THR:HG23	2.19	0.42
1:C:232:HIS:C	1:C:234:GLY:N	2.72	0.42
1:D:333:ASN:O	1:D:334:TYR:C	2.57	0.42
1:F:206:PRO:HA	1:F:210:LEU:HD11	2.01	0.42
1:A:219:GLN:NE2	1:A:220:TRP:N	2.68	0.42
1:E:523:LYS:HB2	1:E:553:PHE:HE2	1.85	0.42
1:A:181:LYS:CD	1:A:181:LYS:H	2.32	0.42
1:D:582:MET:HE2	1:D:582:MET:HB3	1.96	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:30:GLU:CG	1:C:31:SER:H	2.27	0.42
1:E:136:ASP:HB3	1:E:139:THR:CB	2.49	0.42
1:A:51:TYR:HD2	1:A:51:TYR:N	2.17	0.42
1:C:568:VAL:O	1:C:569:LEU:C	2.57	0.42
1:C:546:GLU:HA	1:C:549:PHE:HB3	2.01	0.42
1:D:392:LEU:O	1:D:393:ASP:C	2.58	0.42
1:E:653:PHE:CD1	1:E:657:LYS:HD3	2.55	0.42
1:E:506:LYS:O	1:E:510:GLU:HB2	2.19	0.42
1:E:142:GLU:O	1:E:146:ASN:ND2	2.53	0.42
1:A:349:LEU:HA	1:A:349:LEU:HD23	1.71	0.42
1:A:467:ASP:OD1	1:A:467:ASP:O	2.38	0.42
1:C:641:LYS:HE3	1:D:437:LYS:NZ	2.35	0.42
1:F:262:PRO:HG3	1:F:273:LEU:HD21	2.01	0.42
1:A:202:LEU:HD12	1:A:203:LEU:HG	2.02	0.42
1:B:99:LEU:CD1	1:B:133:LYS:HD3	2.49	0.42
1:E:425:THR:HG22	1:E:426:MET:CE	2.44	0.42
1:B:194:TYR:CD1	1:B:194:TYR:N	2.88	0.42
1:C:55:LEU:HB3	1:C:265:LEU:HD11	2.02	0.42
1:E:56:LYS:HG3	1:E:265:LEU:CD2	2.49	0.42
1:F:462:TYR:CZ	1:F:499:VAL:HG22	2.54	0.42
1:A:248:GLN:O	1:A:251:LEU:N	2.53	0.42
1:E:405:GLU:O	1:E:407:ALA:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:263:ILE:HG22	1:E:267:GLN:HE22	1.84	0.42
2:I:130:CYS:O	2:I:134:GLU:HB2	2.19	0.42
1:A:327:ILE:HA	1:A:327:ILE:HD12	1.81	0.42
1:B:167:ILE:O	1:B:171:ASN:ND2	2.53	0.42
1:D:524:MET:O	1:D:525:ILE:C	2.58	0.42
1:D:420:CYS:SG	1:D:453:ILE:HD12	2.60	0.42
1:F:383:ILE:HG21	1:F:422:TYR:HB2	2.01	0.42
1:F:335:GLN:O	1:F:339:ASN:OD1	2.38	0.42
1:E:654:LEU:HG	2:I:151:GLN:OE1	2.20	0.42
1:A:656:ASP:OD2	1:A:657:LYS:HG3	2.19	0.42
1:F:57:HIS:HD2	1:F:57:HIS:O	2.03	0.42
1:E:341:ASP:CG	1:E:343:THR:HG22	2.40	0.42
1:E:350:LYS:O	1:E:354:GLN:HG3	2.20	0.42
2:I:179:LEU:HB3	2:I:184:VAL:CB	2.49	0.42
1:D:42:GLU:C	1:D:45:PRO:HD3	2.40	0.42
2:G:150:ILE:HG21	2:G:175:ILE:CD1	2.48	0.42
1:C:101:ALA:HB2	1:C:134:LYS:HE2	2.01	0.42
1:C:295:SER:C	1:C:297:ASN:H	2.23	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
1:E:401:ASP:C	1:E:403:THR:N	2.72	0.42
1:E:401:ASP:OD2	1:E:404:ASN:HB2	2.20	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:A:276:PRO:C	1:A:278:GLU:H	2.24	0.42
1:C:334:TYR:O	1:C:335:GLN:C	2.56	0.42
1:D:101:ALA:HB2	1:D:134:LYS:NZ	2.35	0.42
1:B:290:TRP:C	1:B:290:TRP:CD1	2.93	0.42
1:B:59:VAL:CG1	1:B:60:SER:H	2.32	0.42
1:F:401:ASP:O	1:F:403:THR:N	2.53	0.42
1:A:412:LYS:HZ1	1:A:448:LEU:HA	1.83	0.42
1:A:253:ILE:HG23	1:A:289:GLU:HG3	2.02	0.42
1:D:261:LEU:HD22	1:D:262:PRO:HD2	2.02	0.42
1:C:556:VAL:O	1:C:558:LYS:N	2.52	0.42
1:C:552:LYS:HB2	1:C:552:LYS:NZ	2.35	0.42
1:C:462:TYR:C	1:C:464:ILE:H	2.24	0.42
1:C:569:LEU:O	1:C:571:VAL:N	2.53	0.42
1:E:135:ASN:HD21	1:E:147:ILE:HG21	1.85	0.42
2:H:112:PRO:O	2:H:114:LEU:N	2.53	0.42
1:B:219:GLN:HE21	1:B:220:TRP:N	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:383:ILE:HG21	1:F:422:TYR:CD1	2.55	0.42
1:E:561:GLU:O	1:E:562:PHE:C	2.57	0.42
1:D:383:ILE:HG21	1:D:422:TYR:CD1	2.54	0.42
1:D:347:LYS:O	1:D:350:LYS:HB3	2.19	0.42
2:G:169:PRO:HD2	2:G:170:GLN:HE22	1.85	0.41
1:E:577:LEU:HD13	1:F:414:LYS:HB2	2.02	0.41
1:E:641:LYS:C	1:E:643:THR:N	2.71	0.41
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:D:122:SER:O	1:D:123:LEU:C	2.59	0.41
1:D:124:TRP:CE3	1:D:155:VAL:HG22	2.54	0.41
1:B:64:TRP:CH2	1:B:95:LYS:HD2	2.55	0.41
1:C:634:LEU:O	1:C:635:PRO:C	2.58	0.41
1:D:44:GLN:N	1:D:45:PRO:HD2	2.34	0.41
1:F:462:TYR:C	1:F:464:ILE:H	2.23	0.41
1:D:509:PHE:CE2	1:D:513:ILE:HD11	2.55	0.41
1:B:439:PHE:O	1:B:442:CYS:HB2	2.20	0.41
1:C:559:LEU:HA	1:D:329:PHE:CE1	2.50	0.41
1:B:335:GLN:HB3	1:B:344:VAL:CG1	2.50	0.41
1:E:372:LEU:HD11	1:F:543:ARG:CZ	2.49	0.41
1:A:442:CYS:O	1:A:445:LEU:N	2.51	0.41
1:B:311:THR:O	1:B:315:MET:HG2	2.20	0.41
1:D:485:ASP:OD1	1:D:487:GLU:HB3	2.19	0.41
1:D:401:ASP:C	1:D:403:THR:N	2.73	0.41
1:B:257:LEU:HB2	1:B:286:ILE:HG21	2.02	0.41
1:B:56:LYS:HE3	1:B:265:LEU:O	2.19	0.41
2:G:125:THR:HG23	2:G:129:MET:HE2	2.01	0.41
1:A:202:LEU:HD13	1:A:207:MET:CE	2.50	0.41
1:A:632:LYS:CG	2:G:115:PRO:HG2	2.42	0.41
1:E:159:CYS:O	1:E:160:ALA:C	2.57	0.41
1:B:149:ILE:HD13	1:B:194:TYR:CE2	2.55	0.41
1:F:509:PHE:CG	1:F:529:VAL:HG21	2.54	0.41
1:E:228:THR:HG22	1:E:231:ARG:HE	1.80	0.41
1:C:423:MET:CB	1:C:438:ILE:HG21	2.48	0.41
1:E:275:LYS:O	1:E:278:GLU:HB2	2.19	0.41
1:E:64:TRP:HE3	1:E:68:TYR:HE2	1.68	0.41
1:A:501:GLU:HB3	1:A:504:GLN:HB2	2.01	0.41
2:G:127:PRO:O	2:G:130:CYS:HB3	2.21	0.41
1:C:287:TRP:CZ3	1:C:290:TRP:CZ3	3.08	0.41
1:A:548:ARG:NH1	1:A:548:ARG:CG	2.73	0.41
1:F:408:ILE:O	1:F:412:LYS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:190:LEU:O	2:H:193:LEU:HG	2.20	0.41
1:A:100:ASP:C	1:A:102:ALA:H	2.23	0.41
1:D:80:LEU:CA	1:D:118:ASN:HD21	2.22	0.41
1:D:560:GLU:CB	1:D:582:MET:HE3	2.50	0.41
1:C:370:TYR:HB2	1:C:379:ILE:HG12	2.02	0.41
1:F:71:PHE:HE2	1:F:88:ARG:HB2	1.79	0.41
1:E:479:LEU:HD23	1:E:483:ALA:CA	2.42	0.41
1:E:442:CYS:HA	1:E:445:LEU:HD12	2.01	0.41
1:B:101:ALA:HB2	1:B:130:TYR:OH	2.20	0.41
1:F:316:GLN:O	1:F:319:GLN:HB3	2.20	0.41
1:A:335:GLN:HA	1:A:335:GLN:OE1	2.20	0.41
1:A:334:TYR:C	1:A:336:GLY:N	2.71	0.41
1:E:458:ALA:C	1:E:460:ILE:N	2.74	0.41
1:B:427:LYS:CB	1:B:435:SER:HB3	2.50	0.41
1:A:475:LEU:HD13	1:A:492:TYR:CD1	2.56	0.41
1:B:340:THR:OG1	1:B:341:ASP:N	2.53	0.41
1:F:494:ASP:O	1:F:498:TYR:N	2.52	0.41
1:F:154:VAL:O	1:F:158:LYS:HB2	2.20	0.41
1:B:264:THR:C	1:B:266:ASN:N	2.74	0.41
1:F:195:ILE:HG22	1:F:199:TYR:HD2	1.84	0.41
1:A:556:VAL:HG22	1:A:561:GLU:HG2	2.01	0.41
1:C:366:LEU:HD23	1:C:366:LEU:HA	1.82	0.41
2:H:185:CYS:HB3	2:H:186:SER:H	1.56	0.41
1:F:550:PHE:O	1:F:554:PRO:HG3	2.19	0.41
1:E:638:GLN:N	1:E:638:GLN:OE1	2.53	0.41
1:E:339:ASN:ND2	1:E:340:THR:H	2.18	0.41
2:H:155:LYS:HE2	2:H:155:LYS:HB2	1.91	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:412:LYS:HE2	1:E:448:LEU:CA	2.47	0.41
1:D:54:LEU:HG	1:D:58:HIS:HD2	1.85	0.41
1:F:446:LYS:C	1:F:448:LEU:H	2.24	0.41
1:D:33:VAL:O	1:D:35:GLY:N	2.53	0.41
1:C:324:ALA:O	1:C:325:PRO:C	2.59	0.41
1:B:100:ASP:C	1:B:102:ALA:N	2.74	0.41
1:A:367:SER:HB2	1:A:379:ILE:HG23	2.01	0.41
1:F:471:ALA:O	1:F:475:LEU:HD12	2.20	0.41
1:C:48:ILE:H	1:C:48:ILE:HD12	1.84	0.41
1:A:181:LYS:O	1:A:182:PRO:C	2.58	0.41
1:E:346:THR:O	1:E:350:LYS:HB2	2.20	0.41
1:B:89:LEU:C	1:B:91:LEU:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:LEU:HD23	1:C:80:LEU:HA	1.75	0.41
1:B:202:LEU:HD13	1:B:207:MET:CE	2.50	0.41
1:A:344:VAL:O	1:A:347:LYS:HB3	2.20	0.41
1:E:382:THR:HG23	1:E:383:ILE:N	2.35	0.41
1:C:150:GLN:O	1:C:154:VAL:HG12	2.21	0.41
1:E:530:ILE:O	1:E:531:PHE:C	2.59	0.41
1:E:150:GLN:O	1:E:154:VAL:HG12	2.21	0.41
1:F:518:ASP:O	1:F:519:SER:C	2.59	0.41
1:A:167:ILE:HG12	1:A:171:ASN:HD21	1.85	0.41
1:E:284:LEU:CD1	1:E:288:LEU:HD21	2.50	0.41
1:A:81:MET:O	1:A:84:ILE:HB	2.21	0.41
1:D:218:THR:HG23	1:D:233:ILE:HD13	2.02	0.41
1:E:539:LEU:HD22	1:F:371:GLU:CG	2.51	0.41
1:F:578:GLU:C	1:F:579:LEU:HD23	2.40	0.41
1:F:492:TYR:HD1	1:F:492:TYR:O	2.04	0.41
1:D:74:LEU:O	1:D:77:ARG:N	2.43	0.41
1:C:74:LEU:O	1:C:75:HIS:C	2.59	0.41
1:A:34:ILE:HD11	1:A:57:HIS:NE2	2.36	0.41
1:B:123:LEU:HA	1:B:123:LEU:HD12	1.82	0.41
2:G:138:LEU:O	2:G:139:GLN:O	2.38	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:A:523:LYS:O	1:A:527:GLN:HG3	2.20	0.41
1:A:637:ARG:H	1:A:637:ARG:HG3	1.46	0.41
1:A:550:PHE:CD2	1:A:550:PHE:N	2.89	0.41
1:E:174:LEU:HD11	1:E:199:TYR:OH	2.21	0.41
1:C:180:TRP:CZ3	1:C:191:ARG:HB2	2.55	0.41
1:E:299:LEU:O	1:E:300:GLU:HB2	2.20	0.41
1:D:125:LEU:HA	1:D:125:LEU:HD23	1.87	0.41
1:D:160:ALA:O	1:D:162:PHE:N	2.53	0.41
1:D:292:ARG:C	1:D:294:GLU:N	2.74	0.41
1:D:71:PHE:CD2	1:D:88:ARG:HD2	2.55	0.41
1:D:251:LEU:HD12	1:D:251:LEU:HA	1.81	0.41
1:B:152:PHE:HB3	1:B:173:TYR:CE1	2.55	0.41
1:F:574:LEU:HA	1:F:574:LEU:HD23	1.81	0.41
1:D:394:LEU:HD23	1:D:448:LEU:HD11	2.01	0.41
1:E:254:THR:HG23	1:E:257:LEU:HB2	2.02	0.41
1:F:501:GLU:O	1:F:504:GLN:N	2.40	0.41
1:E:228:THR:HA	1:E:231:ARG:HG2	2.01	0.41
1:A:121:LEU:C	1:A:123:LEU:H	2.23	0.41
1:A:113:SER:HB2	1:A:115:GLU:CD	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:VAL:HG12	1:B:285:LEU:CD1	2.48	0.41
1:B:190:GLN:O	1:B:193:GLN:HB2	2.21	0.41
1:C:210:LEU:CD1	1:C:244:ARG:HA	2.49	0.41
1:B:228:THR:O	1:B:230:ARG:N	2.54	0.41
1:D:242:ASN:O	1:D:242:ASN:ND2	2.54	0.41
1:D:270:GLU:O	1:D:270:GLU:HG2	2.21	0.41
2:G:190:LEU:HA	2:G:193:LEU:CD2	2.45	0.41
1:A:178:GLU:CD	1:A:216:ARG:NH2	2.74	0.41
1:B:493:LEU:O	1:B:494:ASP:C	2.59	0.41
1:C:61:LEU:O	1:C:62:LYS:C	2.59	0.41
1:A:261:LEU:CD1	1:A:319:GLN:HE21	2.33	0.41
1:A:248:GLN:O	1:A:249:ASP:C	2.59	0.41
1:B:502:GLU:HA	1:B:502:GLU:OE1	2.21	0.41
2:H:185:CYS:SG	2:H:188:ASP:CB	3.09	0.41
1:B:495:PHE:HB3	1:B:496:LEU:H	1.76	0.41
1:E:636:LYS:HG2	2:I:116:VAL:O	2.20	0.41
1:A:85:TRP:CE2	1:A:111:CYS:HB3	2.56	0.41
1:A:181:LYS:HD2	1:A:181:LYS:H	1.85	0.41
1:B:493:LEU:O	1:B:497:ILE:HG13	2.20	0.41
1:D:169:PHE:HD2	1:D:170:TRP:N	2.18	0.41
1:B:64:TRP:CE3	1:B:68:TYR:HE2	2.29	0.41
1:F:399:GLU:CG	1:F:400:ASP:N	2.84	0.41
1:F:572:ASN:OD1	1:F:572:ASN:O	2.38	0.41
1:F:563:THR:HG21	1:F:575:GLN:HE21	1.86	0.41
1:B:468:THR:O	1:B:471:ALA:HB3	2.21	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:54:LEU:HA	1:E:54:LEU:HD12	1.78	0.41
1:B:262:PRO:CB	1:B:272:ASN:HD21	2.29	0.41
1:F:315:MET:O	1:F:316:GLN:C	2.58	0.41
1:F:37:LEU:N	1:F:37:LEU:HD12	2.35	0.41
1:C:457:ASN:HA	1:C:460:ILE:HD12	2.03	0.41
1:C:186:PHE:C	1:C:188:GLU:N	2.72	0.41
1:B:259:ARG:HD3	1:B:287:TRP:HH2	1.83	0.41
1:C:483:ALA:HB1	1:C:515:LYS:HZ2	1.83	0.41
2:G:139:GLN:HB2	2:G:142:GLN:OE1	2.21	0.41
1:E:49:PHE:CZ	1:E:270:GLU:HB2	2.56	0.41
1:A:40:MET:HG2	1:A:50:LEU:HD11	2.03	0.41
1:F:463:HIS:HE1	1:F:498:TYR:CE2	2.36	0.41
1:F:227:LEU:HD12	1:F:227:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:358:ASN:HB3	1:F:389:ARG:HG2	2.02	0.41
1:C:384:LEU:O	1:C:385:SER:C	2.57	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:D:401:ASP:C	1:D:403:THR:H	2.23	0.41
1:A:82:ALA:HB1	1:A:120:ASP:OD2	2.21	0.41
1:F:355:CYS:C	1:F:356:ILE:HG13	2.41	0.41
1:F:544:THR:O	1:F:547:LYS:HB3	2.21	0.41
1:B:536:VAL:HG13	1:B:537:GLY:N	2.35	0.41
1:B:48:ILE:O	1:B:49:PHE:C	2.59	0.41
2:G:168:ALA:HA	2:G:170:GLN:NE2	2.30	0.41
1:B:503:SER:O	1:B:506:LYS:N	2.54	0.41
1:A:89:LEU:C	1:A:91:LEU:H	2.23	0.41
1:C:217:TYR:CZ	1:C:236:LEU:HD12	2.56	0.41
1:F:170:TRP:NE1	1:F:207:MET:SD	2.94	0.41
1:E:525:ILE:O	1:E:529:VAL:HG23	2.21	0.41
1:F:115:GLU:HG2	1:F:116:LEU:H	1.86	0.41
1:F:367:SER:O	1:F:379:ILE:HG12	2.21	0.41
1:B:462:TYR:CZ	1:B:468:THR:HG23	2.54	0.41
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
2:G:146:LEU:O	2:G:149:VAL:N	2.54	0.41
1:B:23:PRO:HA	1:B:26:ARG:HG2	2.03	0.41
1:C:457:ASN:O	1:C:461:GLU:HG2	2.21	0.41
1:D:143:GLU:C	1:D:145:ARG:H	2.24	0.41
1:E:291:ILE:HG21	1:E:314:TYR:CZ	2.56	0.41
1:E:656:ASP:O	1:E:657:LYS:HB2	2.20	0.41
1:F:339:ASN:ND2	1:F:340:THR:H	2.18	0.41
1:B:189:GLN:HE21	1:B:189:GLN:HB3	1.54	0.41
1:E:477:LEU:CD1	1:E:477:LEU:N	2.84	0.40
1:A:284:LEU:HG	1:A:288:LEU:CD1	2.50	0.40
1:D:206:PRO:HA	1:D:210:LEU:HD11	2.04	0.40
1:F:376:ILE:O	1:F:379:ILE:HB	2.21	0.40
1:B:173:TYR:O	1:B:176:PHE:HB3	2.21	0.40
1:C:134:LYS:HA	1:C:134:LYS:HD3	1.80	0.40
1:E:40:MET:C	1:E:42:GLU:N	2.74	0.40
1:B:307:LYS:CD	1:B:338:LYS:HG3	2.51	0.40
1:A:307:LYS:CE	1:A:338:LYS:HG3	2.51	0.40
1:E:639:TYR:CE1	2:I:120:VAL:HB	2.56	0.40
1:F:530:ILE:CG1	1:F:545:LEU:HD22	2.51	0.40
1:C:539:LEU:HD22	1:D:371:GLU:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:ARG:HH11	1:A:231:ARG:HB3	1.86	0.40
2:G:156:ASP:O	2:G:159:GLU:N	2.54	0.40
1:D:451:PRO:HG3	1:D:482:PHE:CG	2.56	0.40
1:B:305:LEU:HD23	1:B:305:LEU:HA	1.86	0.40
1:D:186:PHE:HE1	1:D:189:GLN:NE2	2.18	0.40
1:B:580:ASP:C	1:B:582:MET:N	2.74	0.40
1:D:384:LEU:O	1:D:385:SER:C	2.59	0.40
1:F:225:ASN:O	1:F:227:LEU:N	2.54	0.40
1:F:174:LEU:HD11	1:F:199:TYR:CZ	2.55	0.40
1:E:184:ASN:HB2	1:E:185:LYS:H	1.58	0.40
1:D:276:PRO:O	1:D:277:ASN:HB2	2.21	0.40
1:A:211:GLU:HA	1:A:240:TYR:OH	2.20	0.40
1:D:131:VAL:HG11	1:D:151:ALA:CB	2.51	0.40
1:A:56:LYS:HE3	1:A:265:LEU:O	2.22	0.40
1:C:124:TRP:NE1	1:C:159:CYS:HB2	2.36	0.40
1:F:59:VAL:C	1:F:61:LEU:H	2.23	0.40
2:I:179:LEU:HD23	2:I:184:VAL:HG11	2.02	0.40
1:C:509:PHE:CE2	1:C:513:ILE:HD11	2.56	0.40
1:A:394:LEU:HD21	1:A:448:LEU:HD11	2.03	0.40
1:E:134:LYS:HA	1:E:134:LYS:HD3	1.87	0.40
1:D:81:MET:CE	1:D:322:CYS:HB3	2.51	0.40
2:H:112:PRO:N	2:H:114:LEU:CD1	2.84	0.40
1:B:246:LEU:HD12	1:B:299:LEU:HD23	2.04	0.40
1:A:299:LEU:HB2	1:A:301:LEU:HG	2.04	0.40
1:A:190:GLN:O	1:A:193:GLN:HB2	2.21	0.40
1:E:307:LYS:HD2	1:E:334:TYR:OH	2.21	0.40
1:B:453:ILE:HD12	1:B:453:ILE:HA	1.81	0.40
2:H:150:ILE:O	2:H:154:CYS:N	2.53	0.40
1:A:68:TYR:CD2	1:A:68:TYR:N	2.89	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
2:H:155:LYS:HB2	2:H:156:ASP:H	1.77	0.40
1:B:99:LEU:HD11	1:B:133:LYS:HD3	2.03	0.40
1:F:561:GLU:O	1:F:564:ASN:N	2.55	0.40
1:E:91:LEU:HB3	1:E:92:GLU:OE1	2.21	0.40
1:A:376:ILE:HB	1:A:377:PRO:CD	2.49	0.40
1:C:275:LYS:CE	1:C:278:GLU:OE1	2.68	0.40
1:F:353:GLN:O	1:F:357:PRO:CA	2.70	0.40
1:B:121:LEU:C	1:B:123:LEU:H	2.24	0.40
1:C:543:ARG:NH2	1:D:372:LEU:HD11	2.37	0.40
1:F:502:GLU:H	1:F:502:GLU:HG2	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:ASN:O	1:A:136:ASP:C	2.60	0.40
1:A:538:SER:O	1:A:539:LEU:C	2.60	0.40
2:I:155:LYS:O	2:I:156:ASP:CB	2.70	0.40
1:F:439:PHE:HB2	1:F:457:ASN:ND2	2.35	0.40
1:B:29:ASP:OD1	1:B:32:ASP:OD2	2.39	0.40
1:A:487:GLU:HG3	1:A:491:LYS:HE3	2.02	0.40
1:A:221:GLU:O	1:A:229:ALA:CB	2.69	0.40
1:A:636:LYS:C	1:A:638:GLN:H	2.25	0.40
1:F:517:SER:O	1:F:518:ASP:HB3	2.21	0.40
1:A:202:LEU:CD1	1:A:202:LEU:C	2.90	0.40
1:E:327:ILE:HD12	1:E:327:ILE:HA	1.80	0.40
1:A:181:LYS:HD2	1:A:181:LYS:N	2.36	0.40
1:D:125:LEU:HD21	1:D:169:PHE:CD1	2.56	0.40
1:A:56:LYS:CE	1:A:265:LEU:O	2.70	0.40
1:C:115:GLU:N	1:C:115:GLU:CD	2.66	0.40
1:E:198:LEU:HD12	1:E:202:LEU:HD23	2.03	0.40
1:B:206:PRO:HA	1:B:210:LEU:CD1	2.49	0.40
1:E:71:PHE:HE1	1:E:265:LEU:HD12	1.87	0.40
1:C:394:LEU:HD21	1:C:448:LEU:HD11	2.03	0.40
1:C:81:MET:HE1	1:C:319:GLN:HA	2.02	0.40
1:C:105:GLU:N	1:C:106:PRO:CD	2.84	0.40
1:F:350:LYS:NZ	1:F:354:GLN:NE2	2.68	0.40
1:D:482:PHE:C	1:D:484:THR:N	2.74	0.40
1:A:196:ARG:HH11	1:A:232:HIS:HE1	1.70	0.40
1:B:28:ARG:HD2	1:B:28:ARG:HA	1.92	0.40
1:E:49:PHE:CE2	1:E:53:LYS:HD2	2.56	0.40
1:C:337:GLU:C	1:C:339:ASN:H	2.24	0.40
1:A:653:PHE:CD1	1:A:657:LYS:HD3	2.56	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:B:564:ASN:O	1:B:565:LYS:C	2.59	0.40
1:E:73:LYS:HE2	1:E:73:LYS:HB2	1.99	0.40
1:C:636:LYS:C	1:C:638:GLN:N	2.73	0.40
1:F:125:LEU:C	1:F:127:TYR:N	2.74	0.40
1:A:336:GLY:O	1:A:337:GLU:C	2.60	0.40
1:A:344:VAL:O	1:A:347:LYS:N	2.54	0.40
1:E:209:CYS:SG	1:E:213:MET:HE2	2.62	0.40
1:A:250:TRP:CE2	1:A:254:THR:OG1	2.73	0.40
1:F:192:VAL:HG23	1:F:193:GLN:N	2.36	0.40
1:B:228:THR:O	1:B:229:ALA:C	2.60	0.40
2:H:139:GLN:O	2:H:141:ASP:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:650:PHE:HD1	1:C:650:PHE:O	2.04	0.40
1:C:650:PHE:CD1	1:C:650:PHE:O	2.74	0.40
1:F:397:LEU:O	1:F:397:LEU:HG	2.22	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%)	2 14
1	B	554/645 (86%)	414 (75%)	108 (20%)	32 (6%)	2 15
1	C	579/645 (90%)	435 (75%)	110 (19%)	34 (6%)	2 15
1	D	547/645 (85%)	398 (73%)	117 (21%)	32 (6%)	2 15
1	E	572/645 (89%)	429 (75%)	106 (18%)	37 (6%)	1 13
1	F	549/645 (85%)	422 (77%)	95 (17%)	32 (6%)	2 15
2	G	77/174 (44%)	57 (74%)	12 (16%)	8 (10%)	1 4
2	H	77/174 (44%)	56 (73%)	12 (16%)	9 (12%)	0 3
2	I	77/174 (44%)	58 (75%)	14 (18%)	5 (6%)	1 13
All	All	3611/4392 (82%)	2702 (75%)	684 (19%)	225 (6%)	2 14

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	544/598 (91%)	483 (89%)	61 (11%)	7 30
1	B	519/598 (87%)	472 (91%)	47 (9%)	12 41
1	C	544/598 (91%)	506 (93%)	38 (7%)	19 56
1	D	512/598 (86%)	476 (93%)	36 (7%)	19 56
1	E	538/598 (90%)	487 (90%)	51 (10%)	11 38
1	F	514/598 (86%)	479 (93%)	35 (7%)	20 57
2	G	71/154 (46%)	62 (87%)	9 (13%)	5 24
2	H	71/154 (46%)	65 (92%)	6 (8%)	13 46
2	I	71/154 (46%)	64 (90%)	7 (10%)	10 37
All	All	3384/4050 (84%)	3094 (91%)	290 (9%)	13 45

All (290) 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

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Mol	Chain	Res	Type
1	A	71	PHE
1	A	77	ARG
1	A	89	LEU
1	A	99	LEU
1	A	112	LEU
1	A	114	LYS
1	A	121	LEU
1	A	128	ILE
1	A	132	ARG
1	A	135	ASN
1	A	143	GLU
1	A	177	LEU
1	A	181	LYS
1	A	189	GLN
1	A	202	LEU
1	A	219	GLN
1	A	232	HIS
1	A	242	ASN
1	A	260	ASN
1	A	263	ILE
1	A	275	LYS
1	A	292	ARG
1	A	333	ASN
1	A	339	ASN
1	A	342	SER
1	A	353	GLN
1	A	374	THR
1	A	381	THR
1	A	385	SER
1	A	391	HIS
1	A	400	ASP
1	A	401	ASP
1	A	403	THR
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	492	TYR
1	A	504	GLN
1	A	513	ILE

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Mol	Chain	Res	Type
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	641	LYS
1	A	643	THR
1	A	645	PHE
1	A	646	GLU
1	A	648	HIS
1	A	650	PHE
1	A	656	ASP
1	B	25	SER
1	B	28	ARG
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	135	ASN
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

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Mol	Chain	Res	Type
1	B	296	ASP
1	B	298	LYS
1	B	353	GLN
1	B	391	HIS
1	B	392	LEU
1	B	399	GLU
1	B	400	ASP
1	B	401	ASP
1	B	413	SER
1	B	449	VAL
1	B	450	THR
1	B	481	TYR
1	B	492	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	B	572	ASN
1	C	42	GLU
1	C	66	GLN
1	C	71	PHE
1	C	114	LYS
1	C	124	TRP
1	C	136	ASP
1	C	174	LEU
1	C	181	LYS
1	C	204	CYS
1	C	242	ASN
1	C	275	LYS
1	C	285	LEU
1	C	299	LEU
1	C	322	CYS
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	400	ASP
1	C	408	ILE

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Mol	Chain	Res	Type
1	C	414	LYS
1	C	419	TYR
1	C	442	CYS
1	C	510	GLU
1	C	535	LYS
1	C	545	LEU
1	C	555	GLU
1	C	563	THR
1	C	633	VAL
1	C	635	PRO
1	C	637	ARG
1	C	638	GLN
1	C	643	THR
1	C	646	GLU
1	C	648	HIS
1	C	650	PHE
1	D	38	ASN
1	D	42	GLU
1	D	46	THR
1	D	66	GLN
1	D	71	PHE
1	D	121	LEU
1	D	134	LYS
1	D	136	ASP
1	D	174	LEU
1	D	242	ASN
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	314	TYR
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	414	LYS

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Mol	Chain	Res	Type
1	D	419	TYR
1	D	421	VAL
1	D	500	ASN
1	D	502	GLU
1	D	514	ASP
1	D	538	SER
1	D	555	GLU
1	D	574	LEU
1	D	575	GLN
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	114	LYS
1	E	115	GLU
1	E	136	ASP
1	E	174	LEU
1	E	198	LEU
1	E	218	THR
1	E	219	GLN
1	E	226	GLN
1	E	242	ASN
1	E	275	LYS
1	E	278	GLU
1	E	283	GLN
1	E	285	LEU
1	E	296	ASP
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

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Mol	Chain	Res	Type
1	E	410	GLN
1	E	421	VAL
1	E	424	ASN
1	E	442	CYS
1	E	463	HIS
1	E	473	LYS
1	E	481	TYR
1	E	490	ASN
1	E	492	TYR
1	E	500	ASN
1	E	502	GLU
1	E	510	GLU
1	E	541	SER
1	E	545	LEU
1	E	552	LYS
1	E	555	GLU
1	E	626	GLU
1	E	641	LYS
1	E	646	GLU
1	F	31	SER
1	F	66	GLN
1	F	114	LYS
1	F	134	LYS
1	F	150	GLN
1	F	152	PHE
1	F	174	LEU
1	F	181	LYS
1	F	185	LYS
1	F	189	GLN
1	F	242	ASN
1	F	283	GLN
1	F	299	LEU
1	F	303	ASP
1	F	314	TYR
1	F	337	GLU
1	F	366	LEU
1	F	391	HIS
1	F	400	ASP
1	F	403	THR
1	F	410	GLN
1	F	416	THR
1	F	419	TYR

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Mol	Chain	Res	Type
1	F	442	CYS
1	F	481	TYR
1	F	492	TYR
1	F	500	ASN
1	F	504	GLN
1	F	510	GLU
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	144	MET
2	G	146	LEU
2	G	160	THR
2	G	170	GLN
2	G	178	LEU
2	G	193	LEU
2	I	116	VAL
2	I	143	GLN
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	141	ASP
2	H	155	LYS
2	H	162	VAL
2	H	170	GLN
2	H	188	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (144) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	58	HIS
1	A	63	GLN
1	A	66	GLN

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Mol	Chain	Res	Type
1	A	118	ASN
1	A	171	ASN
1	A	189	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
1	A	277	ASN
1	A	282	GLN
1	A	306	HIS
1	A	316	GLN
1	A	333	ASN
1	A	339	ASN
1	A	504	GLN
1	A	527	GLN
1	A	540	ASN
1	A	564	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	189	GLN
1	B	205	GLN
1	B	215	GLN
1	B	219	GLN
1	B	232	HIS
1	B	266	ASN
1	B	277	ASN
1	B	354	GLN
1	B	391	HIS
1	B	463	HIS
1	B	500	ASN
1	B	504	GLN
1	B	527	GLN

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Mol	Chain	Res	Type
1	B	572	ASN
1	C	38	ASN
1	C	57	HIS
1	C	58	HIS
1	C	63	GLN
1	C	135	ASN
1	C	189	GLN
1	C	219	GLN
1	C	226	GLN
1	C	232	HIS
1	C	242	ASN
1	C	266	ASN
1	C	267	GLN
1	C	409	ASN
1	C	463	HIS
1	C	504	GLN
1	C	540	ASN
1	C	557	ASN
1	C	564	ASN
1	C	575	GLN
1	D	38	ASN
1	D	58	HIS
1	D	118	ASN
1	D	146	ASN
1	D	171	ASN
1	D	189	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	391	HIS
1	D	410	GLN
1	D	463	HIS
1	D	504	GLN
1	D	540	ASN
1	D	557	ASN
1	D	575	GLN

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Mol	Chain	Res	Type
1	E	63	GLN
1	E	75	HIS
1	E	118	ASN
1	E	135	ASN
1	E	146	ASN
1	E	171	ASN
1	E	189	GLN
1	E	215	GLN
1	E	219	GLN
1	E	225	ASN
1	E	242	ASN
1	E	267	GLN
1	E	282	GLN
1	E	316	GLN
1	E	330	ASN
1	E	333	ASN
1	E	410	GLN
1	E	504	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	83	ASN
1	F	118	ASN
1	F	189	GLN
1	F	205	GLN
1	F	219	GLN
1	F	226	GLN
1	F	242	ASN
1	F	282	GLN
1	F	330	ASN
1	F	354	GLN
1	F	373	ASN
1	F	410	GLN
1	F	424	ASN
1	F	463	HIS
1	F	504	GLN
1	F	540	ASN
1	F	557	ASN

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Mol	Chain	Res	Type
1	F	575	GLN
2	G	170	GLN
2	G	182	ASN
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	170	GLN
2	H	182	ASN
2	H	189	GLN
2	H	192	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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%)	-0.28	3 (0%) 91 90	39, 76, 136, 149	0
1	B	558/645 (86%)	-0.27	0 100 100	36, 73, 136, 148	0
1	C	585/645 (90%)	-0.08	13 (2%) 65 59	60, 106, 149, 151	0
1	D	551/645 (85%)	-0.11	8 (1%) 76 71	58, 104, 149, 151	0
1	E	578/645 (89%)	0.23	47 (8%) 15 11	57, 106, 150, 151	0
1	F	553/645 (85%)	-0.06	8 (1%) 78 73	55, 104, 148, 151	0
2	G	81/174 (46%)	-0.28	0 100 100	63, 102, 138, 151	0
2	H	81/174 (46%)	0.08	4 (4%) 33 27	90, 128, 148, 151	0
2	I	81/174 (46%)	-0.01	2 (2%) 61 54	96, 125, 147, 151	0
All	All	3653/4392 (83%)	-0.09	85 (2%) 64 57	36, 99, 148, 151	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	125	LEU	5.1
1	E	214	TRP	4.4
1	E	215	GLN	4.3
1	E	218	THR	4.3
1	C	655	SER	4.1
1	E	195	ILE	4.0
1	E	164	PRO	4.0
1	E	189	GLN	3.9
1	E	199	TYR	3.8
1	E	233	ILE	3.6
1	E	181	LYS	3.5
1	F	189	GLN	3.5
1	F	144	ALA	3.5
1	E	236	LEU	3.5
1	C	641	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	E	230	ARG	3.4
1	E	229	ALA	3.3
1	E	226	GLN	3.3
1	D	104	ILE	3.2
1	E	237	SER	3.1
1	C	645	PHE	3.1
1	E	204	CYS	3.1
1	E	128	ILE	3.1
1	E	67	VAL	3.0
1	C	34	ILE	2.9
1	E	228	THR	2.9
1	C	33	VAL	2.9
1	E	93	PHE	2.9
1	E	170	TRP	2.8
1	E	220	TRP	2.7
1	C	186	PHE	2.7
1	C	236	LEU	2.7
1	E	219	GLN	2.7
1	E	52	VAL	2.6
1	D	67	VAL	2.6
1	C	233	ILE	2.6
1	A	203	LEU	2.5
1	E	139	THR	2.5
1	E	266	ASN	2.5
1	E	55	LEU	2.5
1	C	199	TYR	2.5
1	F	177	LEU	2.5
1	D	137	ILE	2.5
1	F	95	LYS	2.5
1	C	137	ILE	2.4
1	C	656	ASP	2.4
1	E	240	TYR	2.4
1	A	218	THR	2.4
1	E	59	VAL	2.4
2	I	165	LEU	2.4
2	H	192	GLN	2.4
1	E	62	LYS	2.4
1	D	93	PHE	2.4
1	C	138	ILE	2.4
1	E	127	TYR	2.4
2	I	135	LEU	2.3
1	E	129	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	211	GLU	2.3
2	H	171	LEU	2.3
1	E	293	TRP	2.3
1	F	184	ASN	2.3
1	E	145	ARG	2.3
1	E	137	ILE	2.3
2	H	175	ILE	2.3
1	C	654	LEU	2.3
1	F	64	TRP	2.3
1	E	175	HIS	2.3
1	E	196	ARG	2.2
1	D	100	ASP	2.2
1	F	93	PHE	2.2
1	D	188	GLU	2.2
1	E	212	SER	2.2
1	E	232	HIS	2.2
1	D	192	VAL	2.2
2	H	193	LEU	2.2
1	E	642	VAL	2.2
1	E	176	PHE	2.1
1	F	103	VAL	2.1
1	E	136	ASP	2.1
1	E	223	ASP	2.1
1	E	182	PRO	2.0
1	D	95	LYS	2.0
1	E	82	ALA	2.0
1	A	646	GLU	2.0
1	E	48	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 carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.