



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:54 PM GMT

PDB ID : 1HQY  
Title : Nucleotide-Dependent Conformational Changes in a Protease-Associated ATPase HslU  
Authors : Wang, J.; Song, J.J.; Seong, I.S.; Franklin, M.C.; Kamtekar, S.; Eom, S.H.; Chung, C.H.  
Deposited on : 2000-12-20  
Resolution : 2.80 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

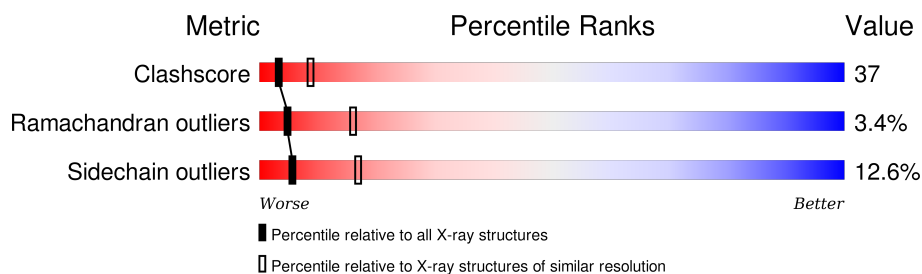
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)

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  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	175	 60% 34% 5% ..
1	B	175	 40% 50% 9% ..
1	C	175	 50% 40% 9% .
1	D	175	 43% 50% 6% ..
2	E	449	 45% 37% 8% • 9%
2	F	449	 39% 40% 11% • 9%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11818 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 HEAT SHOCK LOCUS HSLV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	B	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	C	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	D	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			

- Molecule 2 is a protein called HEAT SHOCK LOCUS HSLU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	408	Total	C	N	O	S	0	0	0
			3226	2014	577	625	10			
2	F	408	Total	C	N	O	S	0	0	0
			3226	2014	577	625	10			

There are 14 discrepancies between the modelled and reference sequences:

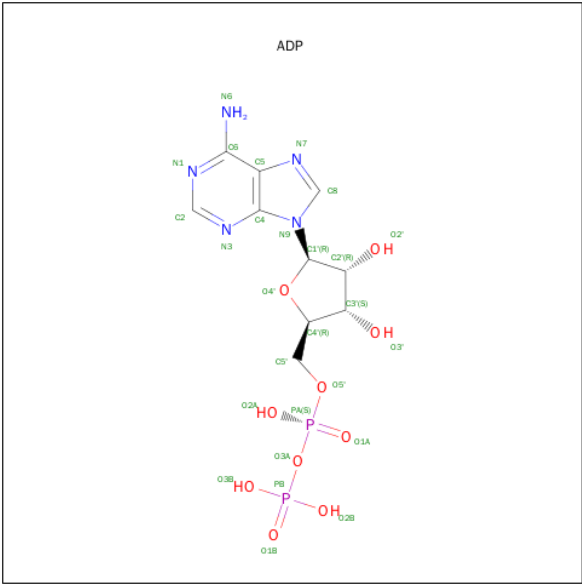
Chain	Residue	Modelled	Actual	Comment	Reference
E	-5	HIS	-	EXPRESSION TAG	UNP P0A6H5
E	-4	HIS	-	EXPRESSION TAG	UNP P0A6H5
E	-3	HIS	-	EXPRESSION TAG	UNP P0A6H5
E	-2	HIS	-	EXPRESSION TAG	UNP P0A6H5
E	-1	HIS	-	EXPRESSION TAG	UNP P0A6H5
E	0	HIS	-	EXPRESSION TAG	UNP P0A6H5
E	1	HIS	-	EXPRESSION TAG	UNP P0A6H5
F	-5	HIS	-	EXPRESSION TAG	UNP P0A6H5
F	-4	HIS	-	EXPRESSION TAG	UNP P0A6H5
F	-3	HIS	-	EXPRESSION TAG	UNP P0A6H5
F	-2	HIS	-	EXPRESSION TAG	UNP P0A6H5
F	-1	HIS	-	EXPRESSION TAG	UNP P0A6H5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	HIS	-	EXPRESSION TAG	UNP P0A6H5
F	1	HIS	-	EXPRESSION TAG	UNP P0A6H5

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).

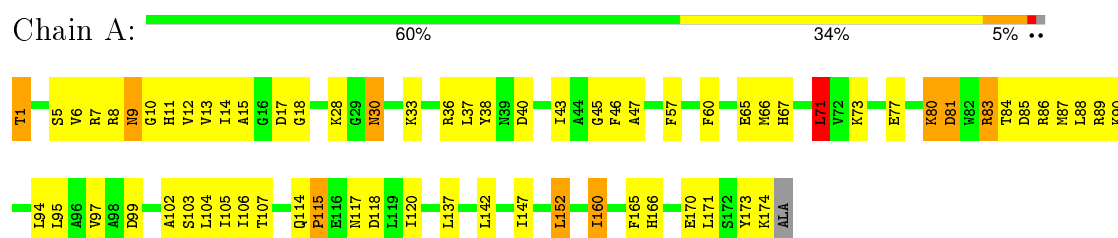


### 3 Residue-property plots

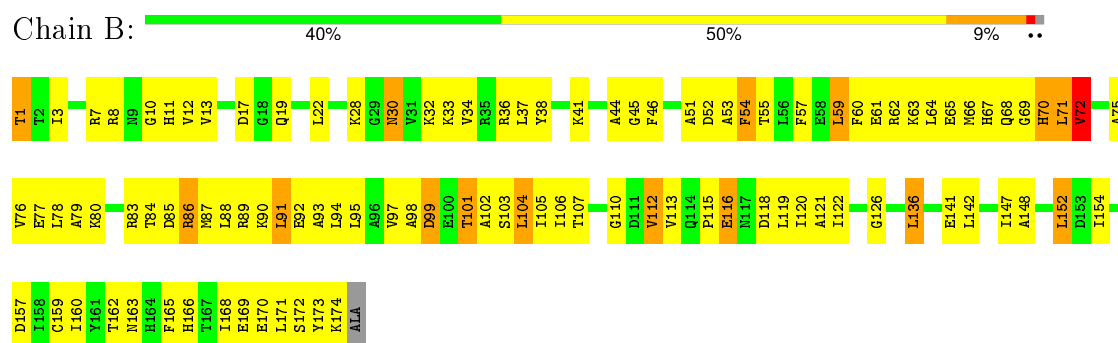
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

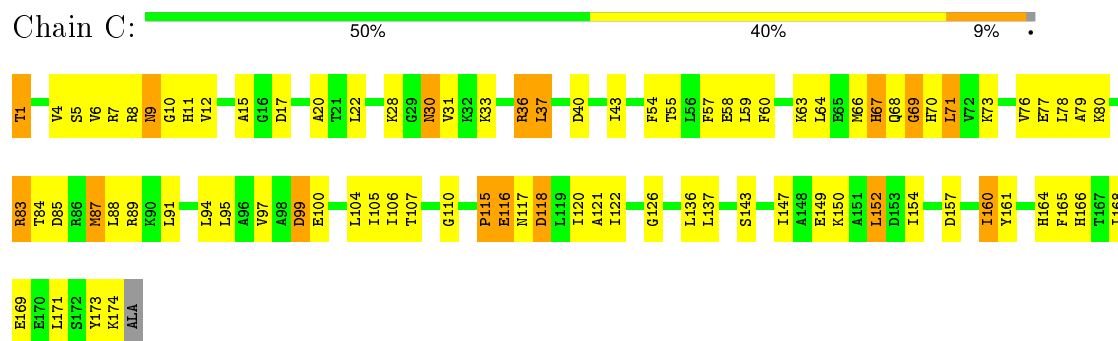
#### • Molecule 1: HEAT SHOCK LOCUS HSLV



#### • Molecule 1: HEAT SHOCK LOCUS HSLV

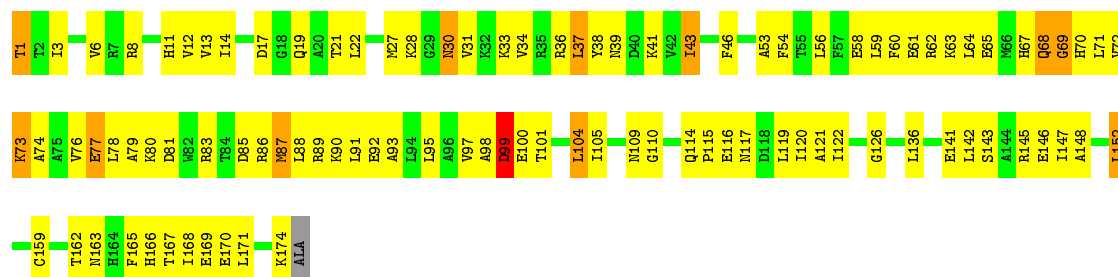


#### • Molecule 1: HEAT SHOCK LOCUS HSLV



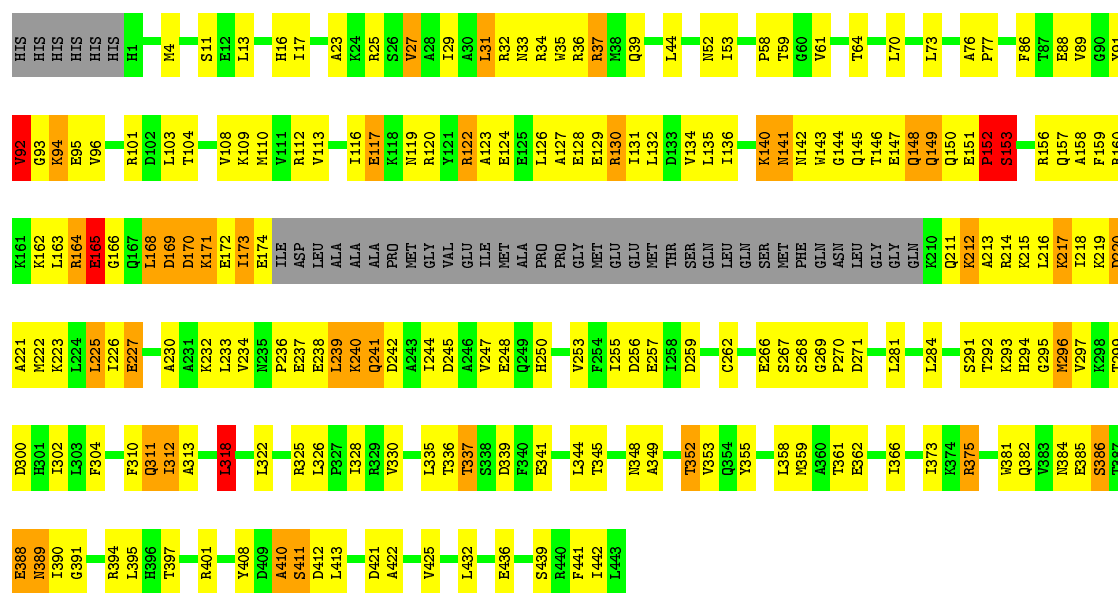
#### • Molecule 1: HEAT SHOCK LOCUS HSLV

Chain D:  43% 50% 6% ..



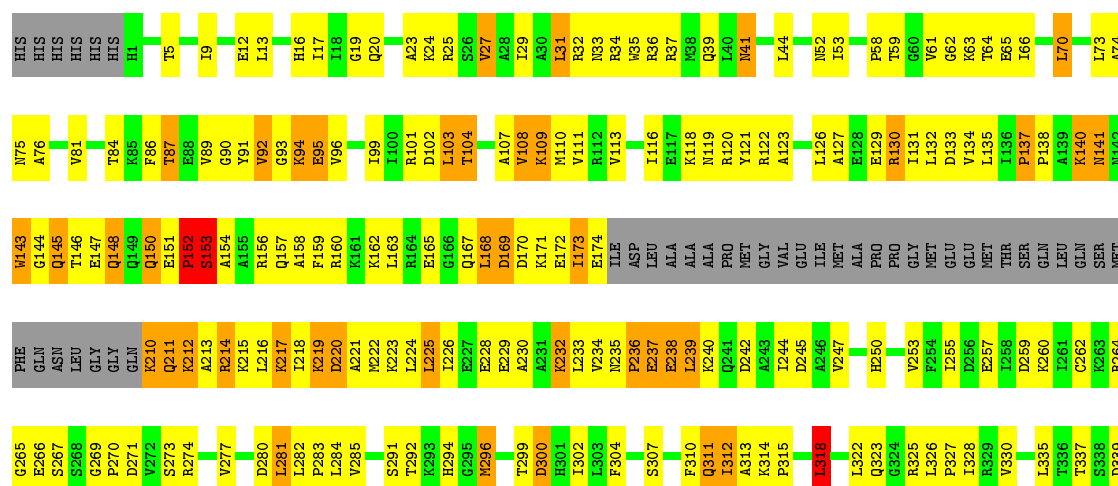
• Molecule 2: HEAT SHOCK LOCUS HSLU

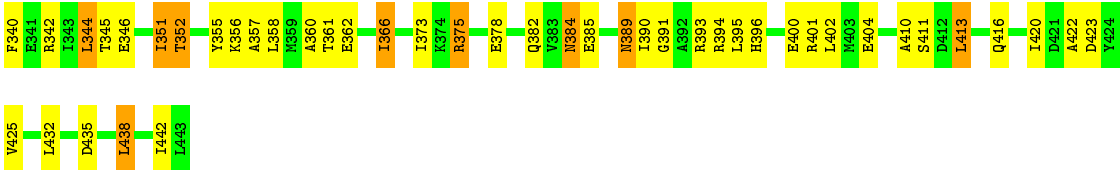
Chain E:  45% 37% 8% 9%



• Molecule 2: HEAT SHOCK LOCUS HSLU

Chain F:  39% 40% 11% 9%





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	172.02Å 172.02Å 276.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.62 – 2.80	Depositor
% Data completeness (in resolution range)	92.2 (29.62-2.80)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.287 , 0.333	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11818	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	0.47	0/1345	0.72	0/1817
1	B	0.43	0/1345	0.69	0/1817
1	C	0.38	0/1345	0.68	0/1817
1	D	0.38	0/1345	0.64	0/1817
2	E	0.46	2/3266 (0.1%)	0.72	4/4400 (0.1%)
2	F	0.48	2/3266 (0.1%)	0.72	5/4400 (0.1%)
All	All	0.45	4/11912 (0.0%)	0.70	9/16068 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	152	PRO	CA-C	-7.24	1.38	1.52
2	F	152	PRO	CA-C	-6.39	1.40	1.52
2	E	153	SER	N-CA	-6.12	1.34	1.46
2	F	152	PRO	C-N	-5.72	1.21	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	152	PRO	CA-N-CD	-8.50	99.61	111.50
2	E	152	PRO	C-N-CA	-7.76	102.31	121.70
2	F	153	SER	CB-CA-C	7.51	124.38	110.10
2	F	153	SER	C-N-CA	6.99	139.17	121.70
2	E	153	SER	CB-CA-C	6.80	123.03	110.10
2	E	318	LEU	CA-CB-CG	6.73	130.78	115.30
2	F	152	PRO	CA-N-CD	-6.49	102.42	111.50
2	F	318	LEU	CA-CB-CG	5.58	128.15	115.30
2	F	152	PRO	CA-C-N	-5.20	105.75	117.20

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	1328	0	1348	73	0
1	B	1328	0	1348	103	0
1	C	1328	0	1348	83	0
1	D	1328	0	1348	111	0
2	E	3226	0	3293	257	0
2	F	3226	0	3293	286	0
3	E	27	0	12	1	0
3	F	27	0	12	3	0
All	All	11818	0	12002	889	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 37.

All (889) 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)
2:F:152:PRO:HB2	2:F:156:ARG:HB2	1.30	1.11
2:E:152:PRO:HB2	2:E:156:ARG:HB2	1.27	1.10
2:E:170:ASP:HA	2:E:217:LYS:HA	1.34	1.06
2:E:174:GLU:HB3	2:E:211:GLN:HG3	1.38	1.05
2:E:312:ILE:HD13	2:E:312:ILE:H	1.20	1.02
2:F:312:ILE:H	2:F:312:ILE:HD13	1.25	1.02
2:E:130:ARG:HD2	2:E:225:LEU:HD11	1.41	1.01
2:E:152:PRO:HB3	2:E:156:ARG:H	1.27	0.98
2:E:132:LEU:HD11	2:E:160:ARG:HG3	1.42	0.98
2:F:132:LEU:HD11	2:F:160:ARG:HG3	1.48	0.96
2:F:351:ILE:HD13	2:F:351:ILE:H	1.31	0.94
1:D:83:ARG:HH11	1:D:83:ARG:HB3	1.33	0.94
2:F:172:GLU:HB3	2:F:215:LYS:HD2	1.50	0.93
2:E:299:THR:HA	2:E:302:ILE:HD13	1.48	0.93
2:E:150:GLN:HA	2:E:153:SER:OG	1.70	0.91
1:A:10:GLY:HA3	1:A:174:LYS:HA	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:135:LEU:HD23	2:F:171:LYS:HE2	1.54	0.90
1:D:105:ILE:HD11	1:D:120:ILE:HG21	1.49	0.90
2:E:104:THR:HG21	2:E:292:THR:HG21	1.54	0.90
2:E:130:ARG:HB2	2:E:130:ARG:NH2	1.87	0.89
2:E:94:LYS:HE2	2:E:94:LYS:HA	1.51	0.89
2:E:168:LEU:HG	2:E:219:LYS:HD3	1.51	0.89
1:B:72:VAL:O	1:B:76:VAL:HG23	1.72	0.88
1:D:105:ILE:HD11	1:D:120:ILE:CG2	2.04	0.88
2:F:130:ARG:HD2	2:F:225:LEU:HD11	1.55	0.87
2:E:103:LEU:HD22	2:E:247:VAL:HG22	1.55	0.87
2:E:150:GLN:O	2:E:153:SER:HB2	1.75	0.86
2:E:64:THR:HB	3:E:450:ADP:O2A	1.75	0.86
2:E:212:LYS:HD3	2:E:216:LEU:HD21	1.55	0.86
1:A:80:LYS:HA	1:A:83:ARG:HH12	1.39	0.85
2:E:344:LEU:O	2:E:352:THR:HB	1.75	0.85
2:F:224:LEU:O	2:F:228:GLU:HB2	1.77	0.85
1:D:83:ARG:NH1	1:D:83:ARG:HB3	1.91	0.84
1:C:28:LYS:HE2	1:C:30:ASN:ND2	1.91	0.84
2:E:214:ARG:HD3	2:E:216:LEU:HD22	1.59	0.84
1:A:1:THR:HB	1:A:33:LYS:HZ3	1.42	0.84
2:F:174:GLU:HA	2:F:213:ALA:H	1.43	0.83
1:D:54:PHE:O	1:D:58:GLU:HB2	1.79	0.83
2:F:94:LYS:HE2	2:F:94:LYS:HA	1.59	0.82
2:F:389:ASN:ND2	2:F:391:GLY:H	1.78	0.82
2:F:91:TYR:O	2:F:92:VAL:HG13	1.79	0.82
2:F:223:LYS:HA	2:F:226:ILE:HG12	1.61	0.82
2:E:173:ILE:HG12	2:E:212:LYS:HD2	1.58	0.82
2:F:152:PRO:CB	2:F:156:ARG:HB2	2.08	0.82
1:A:83:ARG:HH11	1:A:83:ARG:HG2	1.43	0.82
2:E:211:GLN:HG2	2:E:212:LYS:H	1.43	0.82
2:F:64:THR:HB	3:F:1450:ADP:O2A	1.80	0.81
1:B:86:ARG:HA	1:B:89:ARG:NE	1.95	0.81
2:F:150:GLN:O	2:F:153:SER:HB2	1.79	0.81
2:F:123:ALA:HA	2:F:127:ALA:HB3	1.62	0.80
2:F:312:ILE:H	2:F:312:ILE:CD1	1.93	0.80
1:A:10:GLY:HA2	1:A:173:TYR:CE1	2.16	0.80
1:B:88:LEU:O	1:B:91:LEU:HD12	1.81	0.79
2:F:148:GLN:OE1	2:F:151:GLU:HG3	1.82	0.79
2:F:132:LEU:HD23	2:F:135:LEU:HD12	1.62	0.79
2:F:174:GLU:HA	2:F:212:LYS:HB3	1.65	0.78
2:F:173:ILE:HG12	2:F:212:LYS:HD2	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:LYS:HA	1:A:83:ARG:NH1	1.99	0.78
1:D:152:LEU:HD13	1:D:166:HIS:ND1	1.99	0.78
2:E:147:GLU:HA	2:E:150:GLN:HG3	1.66	0.78
1:D:14:ILE:HD13	1:D:43:ILE:HG12	1.66	0.77
2:E:389:ASN:ND2	2:E:391:GLY:H	1.82	0.77
2:F:393:ARG:HG2	2:F:393:ARG:HH11	1.49	0.77
1:B:1:THR:HB	1:B:33:LYS:NZ	2.00	0.77
2:E:312:ILE:CD1	2:E:312:ILE:H	1.94	0.76
2:F:132:LEU:HA	2:F:135:LEU:HD12	1.66	0.76
2:E:124:GLU:HA	2:E:127:ALA:HB3	1.66	0.75
1:C:83:ARG:CZ	1:C:83:ARG:HB3	2.16	0.75
2:E:152:PRO:HB2	2:E:156:ARG:CB	2.13	0.75
2:E:152:PRO:CB	2:E:156:ARG:H	1.98	0.75
2:E:152:PRO:CB	2:E:156:ARG:HB2	2.12	0.75
2:F:345:THR:CG2	2:F:373:ILE:HD13	2.16	0.75
2:E:359:MET:HG3	2:E:366:ILE:HG13	1.69	0.75
2:F:81:VAL:HG11	2:F:99:ILE:HG13	1.69	0.74
2:F:103:LEU:HD13	2:F:247:VAL:HG22	1.68	0.74
2:F:171:LYS:NZ	2:F:218:ILE:HD11	2.02	0.74
1:A:85:ASP:O	1:A:89:ARG:HB2	1.88	0.74
2:F:232:LYS:N	2:F:232:LYS:HZ1	1.86	0.74
2:E:361:THR:HG21	2:F:36:ARG:HA	1.70	0.73
2:F:27:VAL:HG13	2:F:70:LEU:HG	1.68	0.73
2:E:291:SER:HA	2:E:296:MET:HE2	1.71	0.73
2:F:219:LYS:HA	2:F:223:LYS:HZ3	1.54	0.73
2:E:91:TYR:O	2:E:92:VAL:HG13	1.89	0.73
1:D:73:LYS:NZ	1:D:77:GLU:HG2	2.02	0.73
2:E:174:GLU:HA	2:E:213:ALA:H	1.53	0.72
2:F:242:ASP:HA	2:F:245:ASP:OD1	1.89	0.72
1:A:67:HIS:HD2	1:A:73:LYS:HD2	1.55	0.72
1:A:83:ARG:NH1	1:A:83:ARG:HG2	2.01	0.72
1:B:88:LEU:HD12	1:B:91:LEU:HD11	1.71	0.71
1:D:43:ILE:H	1:D:43:ILE:HD13	1.53	0.71
2:E:174:GLU:CB	2:E:211:GLN:HG3	2.18	0.71
1:B:17:ASP:HA	1:B:165:PHE:O	1.90	0.71
1:C:7:ARG:HB2	1:C:12:VAL:HG23	1.73	0.71
1:A:88:LEU:HD12	1:A:88:LEU:H	1.54	0.71
2:E:362:GLU:HG2	2:E:410:ALA:HB1	1.73	0.71
2:F:344:LEU:O	2:F:352:THR:HB	1.91	0.70
1:A:77:GLU:O	1:A:80:LYS:HB2	1.92	0.70
2:F:147:GLU:HG2	2:F:150:GLN:NE2	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:384:ASN:ND2	2:E:394:ARG:HE	1.89	0.70
1:B:104:LEU:CD1	1:B:112:VAL:HG12	2.21	0.70
2:E:130:ARG:CD	2:E:225:LEU:HD11	2.19	0.70
1:C:28:LYS:HE2	1:C:30:ASN:HD21	1.54	0.70
2:E:389:ASN:C	2:E:389:ASN:HD22	1.94	0.70
2:E:150:GLN:CA	2:E:153:SER:OG	2.40	0.70
2:F:174:GLU:HB3	2:F:211:GLN:HB2	1.74	0.70
1:B:8:ARG:NH1	1:B:142:LEU:O	2.22	0.70
2:E:136:ILE:O	2:E:136:ILE:HG22	1.92	0.69
2:E:174:GLU:HA	2:E:212:LYS:HB3	1.72	0.69
1:D:14:ILE:HD13	1:D:43:ILE:CG1	2.22	0.69
1:B:170:GLU:HG2	1:B:171:LEU:H	1.56	0.69
1:D:28:LYS:HD3	1:D:31:VAL:HG22	1.73	0.69
1:A:13:VAL:HG12	1:A:170:GLU:HG3	1.75	0.69
2:E:130:ARG:HB2	2:E:130:ARG:HH21	1.58	0.69
1:C:85:ASP:HB3	1:C:88:LEU:HB2	1.73	0.69
2:F:86:PHE:CZ	2:F:99:ILE:HD11	2.28	0.69
1:A:117:ASN:O	1:A:118:ASP:HB2	1.92	0.69
1:B:105:ILE:HD11	1:B:120:ILE:HG23	1.75	0.69
1:C:136:LEU:HB3	1:C:147:ILE:HD12	1.74	0.69
2:E:375:ARG:CZ	2:E:422:ALA:HB1	2.22	0.69
2:E:91:TYR:HB2	2:F:90:GLY:O	1.93	0.68
2:E:168:LEU:CG	2:E:219:LYS:HD3	2.22	0.68
1:D:3:ILE:HB	1:D:122:ILE:HG12	1.76	0.68
1:A:1:THR:HB	1:A:33:LYS:NZ	2.07	0.68
2:F:152:PRO:HB2	2:F:156:ARG:CB	2.15	0.68
2:F:86:PHE:HZ	2:F:99:ILE:HD11	1.57	0.68
1:D:170:GLU:HG2	1:D:171:LEU:H	1.58	0.68
2:F:130:ARG:CD	2:F:225:LEU:HD11	2.22	0.68
2:E:293:LYS:HG3	2:E:294:HIS:CD2	2.28	0.68
1:B:86:ARG:HA	1:B:89:ARG:CZ	2.22	0.68
1:C:152:LEU:HD13	1:C:166:HIS:ND1	2.09	0.68
2:F:171:LYS:HZ2	2:F:218:ILE:HD11	1.58	0.68
2:E:389:ASN:HD22	2:E:391:GLY:H	1.41	0.68
1:A:67:HIS:CD2	1:A:73:LYS:HD2	2.29	0.68
2:F:389:ASN:HD22	2:F:391:GLY:H	1.40	0.67
2:F:147:GLU:O	2:F:151:GLU:HG2	1.94	0.67
2:E:173:ILE:N	2:E:173:ILE:HD13	2.10	0.67
1:D:79:ALA:HB1	1:D:110:GLY:HA2	1.75	0.67
1:C:55:THR:O	1:C:58:GLU:HB3	1.94	0.67
1:B:62:ARG:HA	1:B:65:GLU:HG3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:384:ASN:ND2	2:F:394:ARG:HE	1.92	0.67
2:F:236:PRO:HG2	2:F:237:GLU:H	1.60	0.67
2:E:345:THR:HG21	2:E:373:ILE:HD13	1.75	0.66
1:C:152:LEU:HD13	1:C:166:HIS:CE1	2.30	0.66
2:F:135:LEU:HB3	2:F:159:PHE:CD2	2.30	0.66
2:F:375:ARG:CZ	2:F:422:ALA:HB1	2.26	0.66
2:E:112:ARG:HH11	2:E:112:ARG:HG3	1.61	0.66
2:E:214:ARG:HG2	2:E:215:LYS:N	2.11	0.66
2:F:270:PRO:O	2:F:274:ARG:HD2	1.96	0.66
1:B:1:THR:HB	1:B:33:LYS:HZ3	1.61	0.66
1:B:57:PHE:O	1:B:61:GLU:HG3	1.96	0.66
1:B:36:ARG:O	1:B:37:LEU:HD23	1.94	0.66
1:D:115:PRO:HG3	1:D:120:ILE:HG12	1.77	0.65
1:B:104:LEU:HD12	1:B:112:VAL:HG12	1.78	0.65
2:F:235:ASN:HB2	2:F:236:PRO:HD2	1.77	0.65
2:F:239:LEU:HD23	2:F:240:LYS:N	2.12	0.65
1:C:11:HIS:CE1	1:C:174:LYS:HE2	2.32	0.65
1:C:105:ILE:HD11	1:C:120:ILE:HG23	1.79	0.65
2:E:211:GLN:HG2	2:E:212:LYS:N	2.12	0.65
2:E:217:LYS:HG3	2:E:219:LYS:HZ1	1.61	0.65
2:F:212:LYS:NZ	2:F:212:LYS:HB2	2.11	0.65
1:A:105:ILE:CD1	1:A:120:ILE:HG23	2.27	0.65
2:F:63:LYS:HE2	2:F:307:SER:OG	1.96	0.65
2:E:145:GLN:HB2	2:E:148:GLN:HB2	1.77	0.64
2:E:86:PHE:O	2:E:89:VAL:HG22	1.96	0.64
1:B:86:ARG:HA	1:B:89:ARG:HE	1.60	0.64
1:A:90:LYS:NZ	1:B:89:ARG:NH2	2.44	0.64
2:E:96:VAL:HG11	2:E:281:LEU:HD12	1.79	0.64
1:B:136:LEU:HB3	1:B:147:ILE:CD1	2.27	0.64
1:C:64:LEU:O	1:C:69:GLY:N	2.28	0.64
2:F:217:LYS:HB2	2:F:217:LYS:NZ	2.13	0.64
2:E:240:LYS:HE3	2:E:294:HIS:O	1.98	0.64
1:C:136:LEU:HB3	1:C:147:ILE:CD1	2.27	0.64
1:B:63:LYS:HA	1:B:66:MET:HE3	1.80	0.64
2:F:223:LYS:HD2	2:F:223:LYS:N	2.12	0.64
1:D:115:PRO:HB2	1:D:119:LEU:O	1.98	0.64
1:B:65:GLU:HB3	2:F:143:TRP:HA	1.80	0.64
2:F:232:LYS:H	2:F:232:LYS:HZ1	1.44	0.64
1:B:152:LEU:HD13	1:B:166:HIS:ND1	2.12	0.64
2:F:291:SER:HA	2:F:296:MET:HE2	1.80	0.64
2:E:116:ILE:O	2:E:120:ARG:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:64:LEU:HA	1:D:74:ALA:HB2	1.80	0.64
1:C:8:ARG:NH2	1:C:137:LEU:HD12	2.13	0.63
2:E:255:ILE:HD13	2:E:281:LEU:HD21	1.80	0.63
1:A:7:ARG:HB2	1:A:12:VAL:HG23	1.80	0.63
1:C:15:ALA:HB1	1:C:152:LEU:HD12	1.81	0.63
2:E:52:ASN:HB2	2:E:325:ARG:O	1.99	0.63
2:F:86:PHE:HB2	2:F:277:VAL:HG13	1.79	0.63
1:A:105:ILE:HD11	1:A:120:ILE:HG23	1.81	0.63
1:A:8:ARG:NH1	1:A:142:LEU:O	2.23	0.63
2:E:174:GLU:HB3	2:E:211:GLN:CG	2.22	0.63
1:C:100:GLU:OE2	1:C:173:TYR:HB2	1.99	0.63
2:F:151:GLU:HB2	2:F:152:PRO:CD	2.29	0.63
2:F:214:ARG:HE	2:F:216:LEU:HB3	1.63	0.63
1:C:59:LEU:HD23	1:C:78:LEU:HD12	1.81	0.62
2:F:132:LEU:HD23	2:F:135:LEU:CD1	2.30	0.62
1:A:15:ALA:HB1	1:A:152:LEU:HD12	1.81	0.62
1:B:38:TYR:HB2	1:B:64:LEU:CD1	2.29	0.62
2:F:211:GLN:NE2	2:F:212:LYS:H	1.97	0.62
1:A:38:TYR:HE1	1:A:65:GLU:HG2	1.63	0.62
1:D:30:ASN:H	1:D:30:ASN:HD22	1.47	0.62
2:F:108:VAL:C	2:F:110:MET:H	2.02	0.62
2:E:293:LYS:HG3	2:E:294:HIS:HD2	1.64	0.61
1:B:38:TYR:HB2	1:B:64:LEU:HD12	1.81	0.61
2:E:140:LYS:HD3	2:E:140:LYS:H	1.65	0.61
2:F:116:ILE:O	2:F:120:ARG:HB2	2.00	0.61
2:F:174:GLU:CA	2:F:212:LYS:HB3	2.29	0.61
2:F:389:ASN:HD22	2:F:389:ASN:C	2.03	0.61
2:E:269:GLY:N	2:E:270:PRO:HD2	2.15	0.61
2:E:89:VAL:HG12	2:E:93:GLY:HA3	1.81	0.61
2:F:401:ARG:NH2	2:F:442:ILE:HG13	2.14	0.61
2:F:122:ARG:HH11	2:F:126:LEU:HD23	1.65	0.61
2:F:393:ARG:NH2	3:F:1450:ADP:O1B	2.33	0.61
1:A:87:MET:CE	1:B:84:THR:HG23	2.31	0.61
2:F:101:ARG:HG2	2:F:292:THR:HG22	1.82	0.61
2:F:345:THR:HG21	2:F:373:ILE:HD13	1.82	0.61
2:F:362:GLU:HG3	2:F:411:SER:HA	1.83	0.61
2:E:148:GLN:HA	2:E:151:GLU:HG2	1.82	0.60
1:D:67:HIS:CD2	1:D:73:LYS:HE2	2.36	0.60
1:D:30:ASN:HD22	1:D:30:ASN:N	1.98	0.60
1:D:121:ALA:HB1	1:D:126:GLY:O	2.01	0.60
1:B:28:LYS:NZ	1:B:30:ASN:HD21	1.98	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:123:ALA:HA	2:F:127:ALA:CB	2.30	0.60
2:E:311:GLN:HE21	2:E:311:GLN:CA	2.14	0.60
1:D:73:LYS:HZ1	1:D:77:GLU:HG2	1.65	0.60
1:B:28:LYS:NZ	1:B:30:ASN:ND2	2.49	0.60
2:F:127:ALA:HA	2:F:130:ARG:NH2	2.17	0.60
1:A:88:LEU:CD1	1:A:88:LEU:H	2.13	0.60
2:E:220:ASP:O	2:E:221:ALA:C	2.38	0.60
2:F:389:ASN:HD22	2:F:390:ILE:N	1.99	0.60
2:F:123:ALA:CA	2:F:127:ALA:HB3	2.30	0.60
1:D:71:LEU:HD21	1:D:97:VAL:CG1	2.32	0.60
2:F:108:VAL:HG21	2:F:294:HIS:CD2	2.37	0.60
1:C:10:GLY:HA3	1:C:174:LYS:HA	1.82	0.60
2:F:140:LYS:HD3	2:F:140:LYS:H	1.66	0.60
1:C:36:ARG:HD3	1:C:40:ASP:OD1	2.01	0.60
2:E:345:THR:CG2	2:E:373:ILE:HD13	2.31	0.60
1:C:95:LEU:HB2	1:C:106:ILE:HB	1.83	0.60
2:E:173:ILE:HG12	2:E:212:LYS:CD	2.31	0.59
2:E:122:ARG:CZ	2:E:126:LEU:HD21	2.32	0.59
1:A:10:GLY:HA2	1:A:173:TYR:CZ	2.36	0.59
1:B:60:PHE:CD1	1:B:78:LEU:HD22	2.37	0.59
2:F:148:GLN:HA	2:F:151:GLU:CG	2.32	0.59
2:F:432:LEU:N	2:F:432:LEU:HD12	2.17	0.59
2:E:140:LYS:O	2:E:141:ASN:HB2	2.03	0.59
2:E:216:LEU:HD23	2:E:216:LEU:H	1.67	0.59
1:D:6:VAL:HG21	1:D:147:ILE:HG22	1.84	0.59
2:F:131:ILE:HD11	2:F:218:ILE:HD13	1.83	0.59
2:F:269:GLY:N	2:F:270:PRO:HD2	2.17	0.59
2:F:153:SER:N	2:F:156:ARG:HB3	2.18	0.59
1:D:68:GLN:O	1:D:70:HIS:N	2.35	0.59
2:F:76:ALA:HB1	2:F:250:HIS:O	2.02	0.59
2:F:108:VAL:C	2:F:110:MET:N	2.56	0.59
2:F:393:ARG:HG2	2:F:393:ARG:NH1	2.18	0.59
1:B:168:ILE:HD12	1:B:168:ILE:N	2.18	0.59
2:E:312:ILE:HG12	2:E:313:ALA:H	1.68	0.59
1:C:10:GLY:HA2	1:C:173:TYR:CZ	2.38	0.58
2:F:163:LEU:HD11	2:F:222:MET:CE	2.33	0.58
2:E:153:SER:HA	2:E:157:GLN:HG3	1.85	0.58
1:A:88:LEU:N	1:A:88:LEU:HD12	2.16	0.58
1:D:73:LYS:HA	1:D:76:VAL:HG12	1.84	0.58
1:D:38:TYR:HE1	1:D:65:GLU:HB3	1.69	0.58
2:E:257:GLU:HG3	2:E:257:GLU:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:86:ARG:HA	1:D:89:ARG:CZ	2.34	0.58
2:F:130:ARG:HG2	2:F:225:LEU:HD21	1.84	0.58
1:B:59:LEU:HD12	1:B:59:LEU:O	2.04	0.58
2:F:413:LEU:O	2:F:416:GLN:HG3	2.03	0.58
2:F:130:ARG:HH21	2:F:229:GLU:HG3	1.68	0.58
1:A:90:LYS:HZ1	1:B:89:ARG:NH2	2.02	0.58
2:F:108:VAL:HG21	2:F:294:HIS:HD2	1.69	0.58
2:F:356:LYS:HG3	2:F:366:ILE:HG22	1.84	0.58
1:C:30:ASN:H	1:C:30:ASN:ND2	2.00	0.58
1:B:99:ASP:OD1	1:B:101:THR:HB	2.04	0.58
2:E:131:ILE:O	2:E:134:VAL:HG12	2.04	0.57
1:B:79:ALA:HB2	1:B:106:ILE:HG23	1.86	0.57
2:E:33:ASN:ND2	2:E:36:ARG:HD2	2.19	0.57
2:F:167:GLN:O	2:F:168:LEU:HB3	2.03	0.57
1:B:141:GLU:OE2	1:B:141:GLU:HA	2.04	0.57
2:E:170:ASP:HB3	2:E:217:LYS:HD3	1.85	0.57
1:C:8:ARG:HG2	1:C:9:ASN:ND2	2.19	0.57
2:E:147:GLU:HA	2:E:150:GLN:CG	2.34	0.57
2:E:153:SER:O	2:E:157:GLN:NE2	2.38	0.57
2:F:147:GLU:HG2	2:F:150:GLN:HE21	1.68	0.57
2:E:362:GLU:HG2	2:E:410:ALA:CB	2.34	0.57
1:C:105:ILE:CD1	1:C:120:ILE:HG23	2.35	0.57
2:E:442:ILE:O	2:E:442:ILE:HG22	2.04	0.57
2:E:432:LEU:HD12	2:E:432:LEU:H	1.70	0.57
2:F:312:ILE:HG12	2:F:313:ALA:N	2.20	0.56
1:A:10:GLY:HA3	1:A:174:LYS:CA	2.29	0.56
2:F:130:ARG:NH2	2:F:229:GLU:HG3	2.20	0.56
2:E:147:GLU:CA	2:E:150:GLN:HG3	2.34	0.56
1:B:65:GLU:HG2	2:F:143:TRP:CD1	2.40	0.56
2:F:375:ARG:HB3	2:F:425:VAL:HG11	1.87	0.56
2:F:163:LEU:HD11	2:F:222:MET:HE3	1.86	0.56
1:D:170:GLU:HG2	1:D:171:LEU:N	2.21	0.56
2:F:96:VAL:HG11	2:F:281:LEU:HD12	1.87	0.56
1:B:98:ALA:CB	1:B:103:SER:HB3	2.34	0.56
2:E:168:LEU:CD2	2:E:219:LYS:HD3	2.36	0.56
2:F:86:PHE:O	2:F:89:VAL:HG22	2.05	0.56
1:C:11:HIS:NE2	1:C:174:LYS:HE2	2.20	0.56
2:F:52:ASN:HB2	2:F:325:ARG:O	2.06	0.56
1:D:17:ASP:HA	1:D:165:PHE:O	2.05	0.56
2:F:211:GLN:HE21	2:F:212:LYS:H	1.54	0.56
1:D:174:LYS:HA	1:D:174:LYS:HZ2	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:151:GLU:CB	2:F:152:PRO:CD	2.83	0.56
2:E:108:VAL:HG21	2:E:294:HIS:ND1	2.20	0.56
1:B:28:LYS:HZ2	1:B:30:ASN:HD21	1.54	0.56
2:F:129:GLU:HB2	2:F:130:ARG:NH1	2.21	0.56
1:B:86:ARG:HA	1:B:89:ARG:NH1	2.21	0.56
1:D:73:LYS:HZ2	1:D:77:GLU:HG2	1.70	0.56
1:B:101:THR:HG22	1:B:102:ALA:N	2.21	0.56
2:E:58:PRO:HG2	2:E:61:VAL:HG11	1.88	0.55
2:E:35:TRP:O	2:E:39:GLN:HG2	2.06	0.55
2:E:89:VAL:HG12	2:E:93:GLY:CA	2.36	0.55
1:C:79:ALA:HB1	1:C:110:GLY:HA2	1.88	0.55
2:E:132:LEU:HB3	2:E:156:ARG:NH1	2.22	0.55
1:D:3:ILE:HB	1:D:122:ILE:CG1	2.37	0.55
1:D:14:ILE:HD11	1:D:98:ALA:HB3	1.89	0.55
2:E:109:LYS:HD3	2:F:296:MET:HB3	1.88	0.55
1:B:7:ARG:NE	1:B:118:ASP:OD2	2.39	0.55
2:F:25:ARG:O	2:F:29:ILE:HG12	2.07	0.55
2:E:150:GLN:O	2:E:153:SER:CB	2.52	0.55
1:B:1:THR:HB	1:B:33:LYS:HZ2	1.71	0.55
2:E:212:LYS:NZ	2:E:212:LYS:HB2	2.22	0.55
2:F:232:LYS:H	2:F:232:LYS:NZ	2.05	0.54
2:E:408:TYR:HA	2:F:29:ILE:CD1	2.37	0.54
1:B:19:GLN:HB2	1:B:163:ASN:ND2	2.22	0.54
2:F:232:LYS:N	2:F:232:LYS:NZ	2.55	0.54
2:E:130:ARG:HB2	2:E:130:ARG:CZ	2.36	0.54
2:F:89:VAL:HA	2:F:92:VAL:C	2.27	0.54
1:B:115:PRO:HG3	1:B:120:ILE:HG12	1.88	0.54
2:E:432:LEU:N	2:E:432:LEU:HD12	2.21	0.54
1:A:80:LYS:CA	1:A:83:ARG:HH12	2.15	0.54
1:C:30:ASN:H	1:C:30:ASN:HD22	1.52	0.54
2:E:89:VAL:HG12	2:E:93:GLY:C	2.28	0.54
2:F:262:CYS:SG	2:F:318:LEU:HD13	2.47	0.54
2:F:217:LYS:HG3	2:F:218:ILE:H	1.72	0.54
2:F:384:ASN:HD21	2:F:390:ILE:HG12	1.71	0.54
1:C:59:LEU:HD11	1:C:63:LYS:HE2	1.89	0.54
2:F:31:LEU:HD11	2:F:74:ALA:HB2	1.89	0.54
2:E:124:GLU:HA	2:E:127:ALA:CB	2.35	0.54
2:F:264:ARG:NE	2:F:265:GLY:H	2.04	0.54
2:E:220:ASP:HA	2:E:223:LYS:HD2	1.88	0.54
1:B:63:LYS:HD2	1:B:77:GLU:HB3	1.90	0.54
1:B:98:ALA:HB2	1:B:103:SER:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:408:TYR:HB2	2:F:29:ILE:HD11	1.89	0.54
2:F:223:LYS:HA	2:F:226:ILE:CG1	2.35	0.54
1:B:72:VAL:O	1:B:75:ALA:HB3	2.08	0.54
2:F:41:ASN:C	2:F:41:ASN:HD22	2.10	0.54
2:F:65:GLU:HG3	3:F:1450:ADP:H2'	1.90	0.54
1:D:37:LEU:HD11	1:D:60:PHE:HD2	1.72	0.54
2:F:96:VAL:HG12	2:F:284:LEU:HD11	1.89	0.54
1:D:56:LEU:HD13	1:D:95:LEU:HD11	1.89	0.54
2:F:257:GLU:HB2	2:F:260:LYS:HG3	1.90	0.54
2:F:27:VAL:CG1	2:F:70:LEU:HG	2.37	0.54
2:E:123:ALA:O	2:E:127:ALA:HB2	2.08	0.54
1:B:106:ILE:HD12	1:B:106:ILE:N	2.23	0.54
2:F:151:GLU:HB2	2:F:152:PRO:HD2	1.90	0.53
2:E:311:GLN:HA	2:E:311:GLN:NE2	2.24	0.53
2:F:211:GLN:HE21	2:F:212:LYS:N	2.07	0.53
2:E:92:VAL:HG21	2:F:92:VAL:CG1	2.38	0.53
1:A:28:LYS:NZ	1:A:30:ASN:ND2	2.55	0.53
1:D:83:ARG:HD3	1:D:109:ASN:O	2.08	0.53
2:F:174:GLU:HB3	2:F:211:GLN:NE2	2.23	0.53
2:F:35:TRP:O	2:F:39:GLN:HG2	2.09	0.53
2:E:147:GLU:HG3	2:E:150:GLN:CD	2.28	0.53
2:F:32:ARG:O	2:F:36:ARG:HG3	2.09	0.53
2:F:101:ARG:O	2:F:104:THR:HB	2.09	0.53
2:F:292:THR:C	2:F:294:HIS:H	2.11	0.53
2:F:12:GLU:HG2	2:F:73:LEU:CD1	2.38	0.53
1:D:19:GLN:HB2	1:D:163:ASN:ND2	2.24	0.53
2:F:150:GLN:O	2:F:153:SER:CB	2.54	0.53
2:F:148:GLN:HA	2:F:151:GLU:HG2	1.91	0.53
1:D:71:LEU:C	1:D:71:LEU:HD13	2.29	0.53
1:A:152:LEU:HD13	1:A:166:HIS:ND1	2.23	0.53
2:F:264:ARG:CZ	2:F:265:GLY:H	2.22	0.53
2:E:131:ILE:HD11	2:E:218:ILE:HG12	1.90	0.53
2:E:311:GLN:HA	2:E:311:GLN:HE21	1.72	0.53
2:E:122:ARG:O	2:E:126:LEU:HD23	2.08	0.53
1:D:13:VAL:C	1:D:14:ILE:HD12	2.29	0.53
1:D:43:ILE:HD13	1:D:98:ALA:O	2.08	0.53
1:C:36:ARG:HH12	1:C:40:ASP:C	2.11	0.53
2:E:312:ILE:HG12	2:E:313:ALA:N	2.24	0.53
1:C:66:MET:HB3	1:C:67:HIS:ND1	2.24	0.53
1:A:47:ALA:HB3	1:A:94:LEU:HB2	1.91	0.53
2:F:218:ILE:C	2:F:220:ASP:H	2.10	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:103:LEU:O	2:F:107:ALA:HB2	2.09	0.53
2:F:103:LEU:CD1	2:F:247:VAL:HG13	2.39	0.52
1:C:6:VAL:HG21	1:C:147:ILE:CG2	2.38	0.52
2:E:212:LYS:CD	2:E:216:LEU:HD21	2.35	0.52
1:D:28:LYS:NZ	1:D:30:ASN:ND2	2.57	0.52
2:E:92:VAL:HG21	2:F:92:VAL:HG13	1.91	0.52
1:C:43:ILE:HG13	1:C:43:ILE:O	2.10	0.52
2:F:148:GLN:HA	2:F:151:GLU:HG3	1.91	0.52
2:F:312:ILE:HD13	2:F:312:ILE:N	2.08	0.52
1:A:84:THR:HG23	1:A:85:ASP:N	2.25	0.52
2:F:214:ARG:NE	2:F:216:LEU:HB3	2.25	0.52
1:D:86:ARG:HA	1:D:89:ARG:NH1	2.24	0.52
1:A:115:PRO:HG3	1:A:120:ILE:HG12	1.91	0.52
2:F:108:VAL:HA	2:F:111:VAL:HG22	1.91	0.52
1:D:143:SER:OG	1:D:146:GLU:HG3	2.10	0.52
2:E:242:ASP:HA	2:E:245:ASP:OD1	2.09	0.52
2:F:210:LYS:N	2:F:210:LYS:HD3	2.23	0.52
1:D:22:LEU:HD12	1:D:27:MET:CE	2.39	0.52
1:D:97:VAL:HB	1:D:104:LEU:CD1	2.39	0.52
1:C:87:MET:N	1:C:87:MET:SD	2.83	0.52
2:E:174:GLU:CA	2:E:212:LYS:HB3	2.39	0.52
2:F:119:ASN:OD1	2:F:234:VAL:HG23	2.09	0.52
2:F:232:LYS:HZ2	2:F:232:LYS:HB2	1.75	0.52
2:E:232:LYS:HB3	2:E:232:LYS:NZ	2.25	0.52
2:E:408:TYR:CB	2:F:29:ILE:HD11	2.40	0.52
2:E:76:ALA:HB1	2:E:250:HIS:O	2.10	0.52
2:F:145:GLN:CA	2:F:145:GLN:HE21	2.22	0.52
2:F:402:LEU:HD11	2:F:425:VAL:HA	1.91	0.52
1:A:152:LEU:HD13	1:A:166:HIS:CE1	2.45	0.52
2:F:129:GLU:HB2	2:F:130:ARG:HH11	1.75	0.51
2:F:108:VAL:O	2:F:110:MET:N	2.43	0.51
2:F:62:GLY:O	2:F:66:ILE:HG13	2.10	0.51
1:A:12:VAL:HG12	1:A:171:LEU:HB3	1.93	0.51
1:C:6:VAL:HG21	1:C:147:ILE:HG22	1.92	0.51
1:B:44:ALA:HB2	1:B:97:VAL:HG23	1.92	0.51
1:B:95:LEU:N	1:B:95:LEU:HD12	2.25	0.51
1:D:86:ARG:HG2	1:D:89:ARG:HH22	1.76	0.51
2:E:33:ASN:HD22	2:E:36:ARG:HD2	1.76	0.51
1:B:159:CYS:HB3	1:B:162:THR:HB	1.93	0.51
2:F:255:ILE:HD12	2:F:255:ILE:N	2.26	0.51
2:E:108:VAL:C	2:E:110:MET:H	2.12	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:337:THR:O	2:E:341:GLU:HG3	2.10	0.51
2:F:335:LEU:HD22	2:F:339:ASP:HB3	1.93	0.51
1:B:28:LYS:HZ1	1:B:30:ASN:ND2	2.09	0.51
1:D:85:ASP:OD1	1:D:87:MET:HB2	2.11	0.51
2:F:130:ARG:CG	2:F:225:LEU:HD11	2.40	0.51
1:D:71:LEU:HD21	1:D:97:VAL:HG12	1.93	0.51
1:A:5:SER:HB3	1:A:120:ILE:HB	1.92	0.51
2:F:163:LEU:HD21	2:F:222:MET:HE1	1.93	0.51
1:D:71:LEU:HD21	1:D:97:VAL:HG11	1.93	0.51
2:F:315:PRO:O	2:F:318:LEU:HB2	2.11	0.51
2:F:58:PRO:HG2	2:F:61:VAL:HG11	1.93	0.51
1:B:92:GLU:O	1:B:93:ALA:HB2	2.11	0.51
2:F:170:ASP:HA	2:F:217:LYS:HA	1.92	0.50
1:C:8:ARG:HH21	1:C:137:LEU:HD12	1.76	0.50
1:B:60:PHE:CE2	1:B:97:VAL:HG21	2.46	0.50
2:E:442:ILE:CG2	2:E:442:ILE:O	2.58	0.50
2:F:170:ASP:HB3	2:F:217:LYS:HD3	1.92	0.50
2:E:148:GLN:OE1	2:E:151:GLU:HG3	2.11	0.50
1:B:59:LEU:HG	1:B:78:LEU:HD13	1.94	0.50
2:E:234:VAL:O	2:E:236:PRO:HD3	2.11	0.50
2:E:108:VAL:C	2:E:110:MET:N	2.64	0.50
1:B:60:PHE:HD1	1:B:78:LEU:HD22	1.75	0.50
2:E:408:TYR:HA	2:F:29:ILE:HD11	1.93	0.50
2:E:89:VAL:HA	2:E:92:VAL:C	2.32	0.50
1:C:5:SER:HB3	1:C:120:ILE:HB	1.93	0.50
1:D:8:ARG:NH1	1:D:142:LEU:O	2.42	0.50
1:A:95:LEU:HB2	1:A:106:ILE:HB	1.94	0.50
2:F:135:LEU:HD13	2:F:159:PHE:HD2	1.76	0.50
2:E:131:ILE:CD1	2:E:218:ILE:HG12	2.41	0.50
1:D:41:LYS:O	1:D:171:LEU:HD21	2.11	0.50
1:C:152:LEU:HD22	1:C:166:HIS:HE1	1.77	0.50
2:E:140:LYS:HD3	2:E:140:LYS:N	2.26	0.50
2:E:408:TYR:CA	2:F:29:ILE:HD11	2.41	0.50
2:F:312:ILE:HG12	2:F:313:ALA:H	1.77	0.50
2:E:122:ARG:NE	2:E:126:LEU:HD21	2.27	0.50
2:F:118:LYS:C	2:F:119:ASN:HD22	2.15	0.50
1:C:28:LYS:CE	1:C:30:ASN:HD21	2.22	0.50
1:D:37:LEU:N	1:D:37:LEU:HD23	2.26	0.50
1:D:30:ASN:ND2	1:D:30:ASN:N	2.59	0.50
2:E:96:VAL:CG1	2:E:281:LEU:HD12	2.41	0.50
1:D:64:LEU:HD23	1:D:74:ALA:CB	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:84:THR:O	1:C:89:ARG:NH1	2.42	0.50
2:E:77:PRO:HB2	2:E:103:LEU:HD21	1.94	0.50
2:E:89:VAL:HA	2:E:93:GLY:N	2.27	0.50
1:D:13:VAL:HG12	1:D:170:GLU:HA	1.93	0.50
1:B:136:LEU:HB3	1:B:147:ILE:HD12	1.94	0.50
2:F:122:ARG:NE	2:F:122:ARG:HA	2.27	0.49
1:C:67:HIS:ND1	1:C:67:HIS:N	2.60	0.49
2:E:151:GLU:CB	2:E:152:PRO:CD	2.90	0.49
2:F:344:LEU:HD21	2:F:395:LEU:HD22	1.94	0.49
1:C:85:ASP:OD1	1:C:87:MET:HG2	2.12	0.49
1:C:36:ARG:HH11	1:C:36:ARG:HB3	1.77	0.49
1:B:10:GLY:HA2	1:B:173:TYR:CZ	2.47	0.49
2:E:143:TRP:O	2:E:145:GLN:N	2.45	0.49
2:E:345:THR:HG22	2:E:352:THR:HG21	1.94	0.49
2:E:389:ASN:ND2	2:E:389:ASN:C	2.65	0.49
1:B:38:TYR:CE2	1:B:41:LYS:HD2	2.46	0.49
1:B:71:LEU:HB2	1:B:99:ASP:OD1	2.13	0.49
2:F:131:ILE:O	2:F:134:VAL:HG12	2.11	0.49
1:A:87:MET:HE3	1:B:84:THR:HG23	1.92	0.49
2:F:135:LEU:HB3	2:F:159:PHE:CE2	2.47	0.49
2:E:127:ALA:HA	2:E:130:ARG:HH22	1.77	0.49
1:D:59:LEU:HG	1:D:78:LEU:HD13	1.94	0.49
2:F:235:ASN:OD1	2:F:238:GLU:HB2	2.13	0.49
2:F:108:VAL:HA	2:F:111:VAL:CG2	2.43	0.49
2:F:34:ARG:CZ	2:F:250:HIS:HA	2.43	0.49
1:D:28:LYS:HG2	1:D:30:ASN:ND2	2.27	0.49
1:B:98:ALA:HB2	1:B:103:SER:CB	2.42	0.49
2:E:168:LEU:HG	2:E:219:LYS:CD	2.34	0.49
2:E:397:THR:HG22	2:F:327:PRO:HA	1.94	0.49
2:E:389:ASN:HD22	2:E:390:ILE:N	2.10	0.49
1:C:10:GLY:HA2	1:C:173:TYR:CE1	2.48	0.49
2:F:173:ILE:N	2:F:173:ILE:HD13	2.27	0.49
1:C:150:LYS:O	1:C:154:ILE:HD13	2.13	0.49
2:F:145:GLN:NE2	2:F:145:GLN:HA	2.28	0.49
1:A:90:LYS:HZ2	1:B:89:ARG:NH2	2.11	0.49
2:E:34:ARG:CZ	2:E:250:HIS:HA	2.43	0.48
2:F:5:THR:O	2:F:9:ILE:HG12	2.12	0.48
2:F:236:PRO:O	2:F:238:GLU:N	2.44	0.48
2:E:96:VAL:HG12	2:E:284:LEU:HD11	1.95	0.48
2:E:382:GLN:O	2:E:386:SER:HB3	2.12	0.48
2:F:151:GLU:CB	2:F:152:PRO:HD3	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:171:LYS:HA	2:E:171:LYS:NZ	2.28	0.48
2:E:169:ASP:O	2:E:218:ILE:HG13	2.13	0.48
2:E:112:ARG:HG3	2:E:112:ARG:NH1	2.26	0.48
1:C:1:THR:N	1:C:161:TYR:O	2.47	0.48
2:E:145:GLN:O	2:E:147:GLU:N	2.46	0.48
2:F:340:PHE:O	2:F:344:LEU:HD22	2.14	0.48
1:C:143:SER:O	1:C:147:ILE:HG12	2.14	0.48
1:B:70:HIS:HE1	1:B:72:VAL:HB	1.78	0.48
1:A:81:ASP:HA	1:A:84:THR:CG2	2.43	0.48
1:A:33:LYS:HA	1:A:46:PHE:CE1	2.48	0.48
1:B:3:ILE:HB	1:B:122:ILE:CG1	2.44	0.48
2:E:149:GLN:HE21	2:E:149:GLN:HB2	1.54	0.48
1:B:154:ILE:O	1:B:157:ASP:HB2	2.14	0.48
2:E:335:LEU:O	2:E:381:TRP:HZ3	1.97	0.48
2:E:163:LEU:HG	2:E:163:LEU:O	2.13	0.48
1:A:60:PHE:CE2	1:A:97:VAL:HG21	2.49	0.48
2:E:344:LEU:HD23	2:E:373:ILE:HG23	1.95	0.48
1:C:36:ARG:NH1	1:C:40:ASP:CA	2.76	0.48
1:B:71:LEU:HD13	1:B:71:LEU:C	2.34	0.48
1:A:30:ASN:ND2	1:A:30:ASN:H	2.12	0.48
1:B:53:ALA:C	1:B:55:THR:H	2.17	0.48
1:A:8:ARG:O	1:A:11:HIS:HB2	2.13	0.48
1:C:68:GLN:O	1:C:70:HIS:N	2.46	0.48
1:A:17:ASP:HA	1:A:165:PHE:O	2.12	0.48
1:A:86:ARG:HA	1:A:89:ARG:CZ	2.44	0.48
1:C:64:LEU:HB3	1:C:69:GLY:HA2	1.96	0.48
1:D:36:ARG:NE	1:D:169:GLU:OE2	2.47	0.48
1:D:46:PHE:CE2	1:D:53:ALA:HB2	2.49	0.48
2:E:171:LYS:HB3	2:E:172:GLU:H	1.52	0.47
2:F:169:ASP:O	2:F:218:ILE:HG13	2.14	0.47
2:E:168:LEU:HG	2:E:219:LYS:HB3	1.95	0.47
2:E:212:LYS:C	2:E:214:ARG:H	2.15	0.47
1:D:148:ALA:O	1:D:152:LEU:HB2	2.14	0.47
1:D:13:VAL:O	1:D:14:ILE:HD12	2.14	0.47
2:E:23:ALA:HA	2:E:330:VAL:HG21	1.96	0.47
1:D:91:LEU:HD12	1:D:91:LEU:O	2.14	0.47
2:E:95:GLU:OE1	2:E:101:ARG:NH1	2.44	0.47
2:E:32:ARG:O	2:E:36:ARG:HG3	2.13	0.47
2:F:12:GLU:HG2	2:F:73:LEU:HD13	1.95	0.47
1:D:105:ILE:HD11	1:D:120:ILE:HG23	1.93	0.47
2:F:393:ARG:NH1	2:F:393:ARG:CG	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:MET:HB3	1:A:67:HIS:ND1	2.29	0.47
2:E:109:LYS:HG3	2:E:109:LYS:O	2.13	0.47
2:F:109:LYS:O	2:F:113:VAL:HG23	2.14	0.47
2:F:135:LEU:CD2	2:F:171:LYS:HE2	2.35	0.47
2:F:41:ASN:ND2	2:F:44:LEU:HB2	2.29	0.47
2:E:151:GLU:HB2	2:E:152:PRO:HD2	1.96	0.47
2:E:88:GLU:HB3	2:F:90:GLY:HA2	1.97	0.47
1:B:34:VAL:HA	1:B:45:GLY:HA2	1.97	0.47
1:C:149:GLU:OE1	1:C:166:HIS:CD2	2.67	0.47
1:A:87:MET:HE1	1:B:84:THR:HG23	1.96	0.47
2:F:23:ALA:HA	2:F:330:VAL:HG21	1.97	0.47
2:F:229:GLU:OE2	2:F:232:LYS:HD2	2.14	0.47
2:F:216:LEU:HD11	2:F:221:ALA:HA	1.96	0.47
2:F:20:GLN:O	2:F:24:LYS:HG3	2.14	0.47
2:F:358:LEU:O	2:F:361:THR:HB	2.14	0.47
2:E:152:PRO:HB3	2:E:156:ARG:N	2.11	0.47
1:D:115:PRO:CB	1:D:119:LEU:O	2.63	0.47
1:D:99:ASP:OD1	1:D:100:GLU:N	2.48	0.47
1:A:65:GLU:OE2	2:E:141:ASN:HB2	2.14	0.47
2:E:436:GLU:O	2:E:439:SER:HB2	2.15	0.47
1:D:1:THR:HB	1:D:33:LYS:HZ3	1.78	0.47
1:B:87:MET:O	1:B:90:LYS:HD2	2.15	0.47
2:E:95:GLU:OE1	2:E:101:ARG:NH2	2.44	0.47
1:A:86:ARG:HG2	1:A:89:ARG:NH2	2.30	0.47
1:D:99:ASP:HA	1:D:171:LEU:CD2	2.45	0.47
2:E:109:LYS:O	2:E:113:VAL:HG23	2.14	0.47
1:C:30:ASN:N	1:C:30:ASN:HD22	2.08	0.47
2:F:396:HIS:O	2:F:400:GLU:HB2	2.15	0.47
2:E:211:GLN:O	2:E:212:LYS:HB2	2.15	0.46
2:E:256:ASP:O	2:E:257:GLU:HG2	2.16	0.46
1:D:1:THR:HB	1:D:33:LYS:NZ	2.30	0.46
2:F:357:ALA:O	2:F:360:ALA:HB3	2.16	0.46
2:F:167:GLN:NE2	2:F:219:LYS:HD2	2.30	0.46
1:A:18:GLY:HA2	1:A:33:LYS:HE3	1.97	0.46
2:E:91:TYR:C	2:E:92:VAL:HG22	2.35	0.46
1:C:71:LEU:HD12	1:C:104:LEU:HD21	1.96	0.46
2:E:103:LEU:HD13	2:E:247:VAL:HG13	1.98	0.46
2:F:140:LYS:O	2:F:141:ASN:HB3	2.16	0.46
2:E:248:GLU:HG2	2:E:297:VAL:HG13	1.97	0.46
1:D:81:ASP:HB3	1:D:88:LEU:CD1	2.44	0.46
2:E:127:ALA:HA	2:E:130:ARG:NH2	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:LYS:HE3	1:B:32:LYS:HB2	1.77	0.46
2:E:237:GLU:OE2	2:E:237:GLU:HA	2.16	0.46
2:F:167:GLN:O	2:F:168:LEU:CB	2.63	0.46
1:C:28:LYS:HG2	1:C:30:ASN:ND2	2.30	0.46
2:E:109:LYS:HB2	2:F:296:MET:HG2	1.98	0.46
2:E:335:LEU:HD22	2:E:339:ASP:HB3	1.97	0.46
1:D:92:GLU:O	1:D:93:ALA:HB2	2.15	0.46
2:F:119:ASN:ND2	2:F:233:LEU:HD23	2.31	0.46
2:E:34:ARG:NH2	2:E:250:HIS:HA	2.30	0.46
1:B:85:ASP:HB3	1:B:88:LEU:HB2	1.98	0.46
2:F:285:VAL:HG12	2:F:304:PHE:CD1	2.51	0.46
2:E:150:GLN:HA	2:E:153:SER:HG	1.74	0.46
1:D:168:ILE:HG22	1:D:169:GLU:N	2.30	0.46
2:E:384:ASN:HD21	2:E:390:ILE:HG12	1.81	0.46
1:C:8:ARG:O	1:C:11:HIS:HB2	2.16	0.46
2:F:255:ILE:H	2:F:255:ILE:HD12	1.80	0.46
2:E:4:MET:HE1	2:E:73:LEU:HD11	1.98	0.46
2:F:123:ALA:C	2:F:127:ALA:HB3	2.36	0.46
2:F:151:GLU:HB2	2:F:152:PRO:HD3	1.96	0.46
2:E:344:LEU:HD13	2:E:395:LEU:HD13	1.98	0.46
2:F:390:ILE:HD12	2:F:393:ARG:HB2	1.98	0.46
1:B:59:LEU:C	1:B:59:LEU:HD12	2.36	0.46
2:F:269:GLY:N	2:F:270:PRO:CD	2.79	0.45
1:D:64:LEU:HA	1:D:74:ALA:CB	2.47	0.45
1:D:62:ARG:O	1:D:65:GLU:HG2	2.15	0.45
2:F:362:GLU:HG2	2:F:410:ALA:CB	2.47	0.45
1:D:70:HIS:CE1	1:D:72:VAL:HB	2.51	0.45
2:F:366:ILE:HG13	2:F:420:ILE:HD11	1.97	0.45
1:C:91:LEU:O	1:C:91:LEU:HD12	2.16	0.45
2:F:345:THR:HG23	2:F:373:ILE:HD13	1.97	0.45
2:E:382:GLN:HA	2:E:382:GLN:NE2	2.30	0.45
1:D:60:PHE:CZ	1:D:97:VAL:HG11	2.52	0.45
2:F:345:THR:HG22	2:F:352:THR:HG21	1.99	0.45
1:D:79:ALA:HB1	1:D:110:GLY:CA	2.44	0.45
1:D:38:TYR:CG	1:D:64:LEU:HD13	2.51	0.45
2:F:122:ARG:HG3	2:F:233:LEU:CD2	2.47	0.45
1:A:14:ILE:HD12	1:A:43:ILE:HG13	1.99	0.45
2:E:130:ARG:HG2	2:E:225:LEU:HD21	1.99	0.45
2:E:362:GLU:HG3	2:E:411:SER:HA	1.98	0.45
1:B:104:LEU:HB2	1:B:113:VAL:O	2.16	0.45
2:F:17:ILE:HD12	2:F:17:ILE:N	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:MET:C	1:B:67:HIS:ND1	2.70	0.45
2:E:117:GLU:OE2	2:E:120:ARG:NH1	2.49	0.45
2:F:102:ASP:C	2:F:104:THR:H	2.20	0.45
2:E:267:SER:HB3	2:E:270:PRO:CG	2.47	0.45
2:E:31:LEU:HD12	2:E:70:LEU:CD2	2.47	0.45
2:E:134:VAL:CG1	2:E:171:LYS:HD3	2.47	0.45
2:F:212:LYS:HZ3	2:F:212:LYS:HB2	1.79	0.45
1:B:46:PHE:CE2	1:B:53:ALA:HB2	2.51	0.45
2:E:158:ALA:O	2:E:162:LYS:HG3	2.16	0.45
2:E:95:GLU:H	2:E:95:GLU:CD	2.20	0.45
2:E:432:LEU:H	2:E:432:LEU:CD1	2.28	0.45
1:B:53:ALA:O	1:B:55:THR:N	2.50	0.45
1:C:71:LEU:HD21	1:C:97:VAL:CG1	2.47	0.45
1:D:141:GLU:OE2	1:D:141:GLU:HA	2.17	0.45
1:D:105:ILE:HD12	1:D:122:ILE:HG21	1.99	0.45
2:E:358:LEU:O	2:E:361:THR:HB	2.16	0.45
2:F:74:ALA:O	2:F:75:ASN:C	2.56	0.45
2:F:41:ASN:HD21	2:F:44:LEU:HB2	1.82	0.45
1:C:60:PHE:CZ	1:C:97:VAL:HG11	2.52	0.45
2:F:280:ASP:O	2:F:283:PRO:HD2	2.16	0.45
1:C:20:ALA:HB2	1:C:31:VAL:HG21	1.97	0.45
1:D:11:HIS:HA	1:D:171:LEU:O	2.17	0.45
1:D:174:LYS:HA	1:D:174:LYS:NZ	2.32	0.45
1:C:77:GLU:O	1:C:80:LYS:HB3	2.17	0.45
2:E:27:VAL:HG13	2:E:70:LEU:HG	1.99	0.45
2:E:230:ALA:O	2:E:233:LEU:HB3	2.17	0.45
2:E:37:ARG:HB3	2:E:37:ARG:HH11	1.80	0.45
2:E:311:GLN:H	2:E:312:ILE:HD13	1.82	0.44
1:A:102:ALA:HB1	1:A:114:GLN:OE1	2.18	0.44
1:B:78:LEU:C	1:B:80:LYS:N	2.70	0.44
2:F:432:LEU:H	2:F:432:LEU:HD12	1.82	0.44
2:E:401:ARG:HD2	2:E:432:LEU:CD2	2.47	0.44
2:E:165:GLU:HG2	2:E:166:GLY:N	2.32	0.44
2:F:95:GLU:H	2:F:95:GLU:CD	2.21	0.44
2:F:220:ASP:O	2:F:224:LEU:HB2	2.17	0.44
2:E:168:LEU:HA	2:E:219:LYS:HB3	1.98	0.44
1:C:30:ASN:N	1:C:30:ASN:ND2	2.63	0.44
1:D:36:ARG:HG2	1:D:43:ILE:HG22	1.98	0.44
2:F:432:LEU:N	2:F:432:LEU:CD1	2.80	0.44
2:E:253:VAL:HB	2:E:304:PHE:CD2	2.52	0.44
2:E:16:HIS:HB2	2:E:17:ILE:HD12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:160:ARG:HG2	2:F:160:ARG:HH11	1.83	0.44
2:E:215:LYS:HG3	2:E:215:LYS:O	2.17	0.44
2:E:108:VAL:O	2:E:110:MET:N	2.51	0.44
1:C:83:ARG:NH1	1:C:83:ARG:HB3	2.32	0.44
2:F:19:GLY:O	2:F:24:LYS:HE3	2.18	0.44
2:E:219:LYS:HG3	2:E:220:ASP:H	1.83	0.44
1:D:145:ARG:NH1	1:D:168:ILE:HD12	2.33	0.44
2:F:103:LEU:HD13	2:F:247:VAL:CG2	2.45	0.44
1:B:77:GLU:OE2	1:B:80:LYS:HD2	2.18	0.44
2:F:158:ALA:O	2:F:162:LYS:HG3	2.18	0.44
1:C:116:GLU:C	1:C:118:ASP:H	2.21	0.44
2:E:312:ILE:N	2:E:312:ILE:CD1	2.72	0.44
1:A:80:LYS:O	1:A:81:ASP:C	2.55	0.44
1:D:99:ASP:OD1	1:D:101:THR:N	2.46	0.44
1:C:160:ILE:HD13	1:C:160:ILE:HA	1.74	0.44
2:E:142:ASN:ND2	2:E:149:GLN:HE22	2.15	0.44
1:D:28:LYS:HZ3	1:D:30:ASN:HD21	1.65	0.44
2:F:122:ARG:HG2	2:F:122:ARG:HH21	1.82	0.44
1:D:87:MET:O	1:D:90:LYS:HG2	2.17	0.44
1:D:81:ASP:HB3	1:D:88:LEU:HD12	1.99	0.44
2:E:348:ASN:O	2:E:349:ALA:HB3	2.18	0.44
2:E:222:MET:O	2:E:226:ILE:HG12	2.18	0.44
1:C:37:LEU:HD13	1:C:57:PHE:HB3	1.99	0.44
2:F:267:SER:O	2:F:271:ASP:OD2	2.36	0.44
2:F:135:LEU:HD23	2:F:171:LYS:CE	2.34	0.44
2:E:212:LYS:HB2	2:E:212:LYS:HZ2	1.83	0.44
1:A:85:ASP:CG	1:A:88:LEU:HD13	2.38	0.44
2:F:86:PHE:HZ	2:F:99:ILE:CD1	2.29	0.44
1:B:104:LEU:HD11	1:B:112:VAL:HG12	1.99	0.44
1:C:105:ILE:HD12	1:C:122:ILE:CG2	2.47	0.44
2:E:269:GLY:N	2:E:270:PRO:CD	2.80	0.44
2:F:96:VAL:HG12	2:F:284:LEU:CD1	2.48	0.44
1:A:99:ASP:C	1:A:99:ASP:OD1	2.55	0.44
1:D:58:GLU:O	1:D:61:GLU:HB2	2.17	0.44
1:D:97:VAL:HB	1:D:104:LEU:HD11	2.00	0.44
2:E:388:GLU:O	2:E:394:ARG:NH2	2.50	0.44
1:D:73:LYS:HD2	1:D:76:VAL:CG1	2.47	0.44
1:B:13:VAL:HG12	1:B:170:GLU:HG3	2.00	0.44
1:D:38:TYR:HB2	1:D:64:LEU:HD13	2.00	0.44
2:F:223:LYS:CD	2:F:223:LYS:N	2.81	0.44
2:F:253:VAL:HB	2:F:304:PHE:CD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:435:ASP:CG	2:F:438:LEU:HB2	2.38	0.44
1:C:73:LYS:HA	1:C:76:VAL:HG12	2.00	0.44
2:F:168:LEU:O	2:F:217:LYS:HD2	2.18	0.43
2:F:318:LEU:O	2:F:323:GLN:NE2	2.50	0.43
1:B:3:ILE:HB	1:B:122:ILE:HG12	2.00	0.43
1:A:6:VAL:HG21	1:A:147:ILE:HG22	1.99	0.43
2:F:89:VAL:HG12	2:F:93:GLY:C	2.38	0.43
2:F:345:THR:HG21	2:F:373:ILE:CD1	2.46	0.43
2:E:116:ILE:HG22	2:E:116:ILE:O	2.18	0.43
1:D:38:TYR:CB	1:D:64:LEU:HD13	2.48	0.43
1:B:38:TYR:CD2	1:B:41:LYS:HD2	2.53	0.43
2:E:131:ILE:HD11	2:E:218:ILE:CD1	2.48	0.43
2:E:173:ILE:N	2:E:173:ILE:CD1	2.80	0.43
1:D:83:ARG:HG2	1:D:83:ARG:O	2.18	0.43
2:F:211:GLN:O	2:F:212:LYS:HB2	2.18	0.43
2:E:135:LEU:HB3	2:E:159:PHE:CE2	2.53	0.43
2:E:336:THR:O	2:E:339:ASP:HB2	2.18	0.43
2:E:421:ASP:O	2:E:425:VAL:HG23	2.18	0.43
1:C:94:LEU:CD2	1:C:107:THR:HG22	2.48	0.43
2:E:292:THR:HG22	2:E:293:LYS:N	2.33	0.43
1:A:33:LYS:O	1:A:45:GLY:HA2	2.17	0.43
1:B:36:ARG:NE	1:B:169:GLU:OE2	2.48	0.43
2:F:122:ARG:CZ	2:F:122:ARG:HA	2.48	0.43
1:C:36:ARG:NH1	1:C:40:ASP:HA	2.33	0.43
1:C:17:ASP:HA	1:C:165:PHE:O	2.17	0.43
1:B:51:ALA:O	1:B:52:ASP:C	2.56	0.43
1:C:22:LEU:C	1:C:22:LEU:HD23	2.39	0.43
2:E:130:ARG:HD2	2:E:225:LEU:CD1	2.29	0.43
1:A:86:ARG:HG2	1:A:89:ARG:HH22	1.82	0.43
2:F:86:PHE:HB2	2:F:277:VAL:CG1	2.47	0.43
1:D:69:GLY:O	1:D:71:LEU:N	2.52	0.43
1:A:36:ARG:NH1	1:A:40:ASP:O	2.45	0.43
2:F:167:GLN:OE1	2:F:219:LYS:HB2	2.19	0.43
2:F:236:PRO:C	2:F:238:GLU:H	2.21	0.43
2:F:299:THR:O	2:F:302:ILE:HG12	2.18	0.43
2:E:53:ILE:HA	2:E:328:ILE:HB	2.00	0.43
1:D:38:TYR:HB2	1:D:64:LEU:CD1	2.49	0.43
1:D:21:THR:HG22	1:D:22:LEU:N	2.34	0.43
2:E:322:LEU:HD12	2:E:322:LEU:HA	1.87	0.43
1:B:147:ILE:HG22	1:B:148:ALA:N	2.33	0.43
1:A:28:LYS:HZ1	1:A:30:ASN:ND2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ILE:HA	1:A:160:ILE:HD13	1.92	0.43
2:F:384:ASN:ND2	2:F:390:ILE:H	2.17	0.43
2:F:432:LEU:H	2:F:432:LEU:CD1	2.31	0.43
1:A:71:LEU:HD12	1:A:104:LEU:HD21	2.00	0.43
2:E:170:ASP:CB	2:E:217:LYS:HD3	2.48	0.42
2:F:235:ASN:ND2	2:F:238:GLU:OE1	2.52	0.42
2:F:84:THR:O	2:F:87:THR:OG1	2.37	0.42
2:E:293:LYS:C	2:E:294:HIS:HD2	2.22	0.42
2:F:16:HIS:HB2	2:F:17:ILE:HD12	2.01	0.42
2:E:259:ASP:HB3	2:E:310:PHE:CZ	2.54	0.42
2:E:126:LEU:O	2:E:130:ARG:NH2	2.44	0.42
2:F:53:ILE:HG12	2:F:328:ILE:HB	2.01	0.42
2:F:311:GLN:HA	2:F:311:GLN:NE2	2.34	0.42
2:F:145:GLN:HB2	2:F:148:GLN:HG2	2.01	0.42
2:E:292:THR:HB	2:E:295:GLY:O	2.19	0.42
2:E:91:TYR:O	2:E:92:VAL:HG22	2.19	0.42
1:B:61:GLU:O	1:B:65:GLU:HG3	2.20	0.42
2:F:244:ILE:HD12	2:F:244:ILE:N	2.34	0.42
1:A:84:THR:HG23	1:A:85:ASP:H	1.84	0.42
2:F:270:PRO:O	2:F:273:SER:HB3	2.19	0.42
2:F:257:GLU:HB2	2:F:260:LYS:CG	2.49	0.42
1:D:12:VAL:HG13	1:D:12:VAL:O	2.19	0.42
2:F:172:GLU:O	2:F:173:ILE:HG23	2.20	0.42
2:F:96:VAL:CG1	2:F:281:LEU:HD12	2.50	0.42
2:F:174:GLU:C	2:F:212:LYS:HB3	2.39	0.42
2:F:86:PHE:CZ	2:F:99:ILE:CD1	3.01	0.42
1:D:99:ASP:HA	1:D:171:LEU:HD23	2.01	0.42
2:E:361:THR:HG23	2:F:39:GLN:HG3	2.01	0.42
1:C:168:ILE:HG22	1:C:169:GLU:N	2.34	0.42
1:D:34:VAL:HB	1:D:167:THR:HG22	2.01	0.42
2:F:225:LEU:HA	2:F:228:GLU:HB3	2.02	0.42
2:F:345:THR:CG2	2:F:373:ILE:CD1	2.93	0.42
2:F:33:ASN:ND2	2:F:36:ARG:HD2	2.34	0.42
2:E:117:GLU:OE2	2:E:120:ARG:NH2	2.53	0.42
2:E:257:GLU:O	2:E:257:GLU:CG	2.63	0.42
1:C:1:THR:HB	1:C:33:LYS:HZ3	1.85	0.42
1:C:121:ALA:HB1	1:C:126:GLY:O	2.19	0.42
2:F:131:ILE:HG23	2:F:132:LEU:N	2.34	0.42
1:C:115:PRO:HG3	1:C:120:ILE:HG12	2.01	0.42
1:B:94:LEU:HB3	1:B:122:ILE:HD12	2.02	0.42
2:F:342:ARG:O	2:F:346:GLU:HB2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:145:GLN:CA	2:F:145:GLN:NE2	2.83	0.42
2:E:128:GLU:O	2:E:129:GLU:C	2.58	0.42
2:E:130:ARG:CG	2:E:225:LEU:HD11	2.49	0.42
2:E:103:LEU:HD23	2:E:103:LEU:O	2.20	0.42
1:B:33:LYS:O	1:B:45:GLY:HA2	2.20	0.42
1:C:99:ASP:HA	1:C:171:LEU:HD22	2.02	0.42
1:A:13:VAL:CG1	1:A:170:GLU:HG3	2.46	0.42
2:E:117:GLU:HG3	2:E:120:ARG:NH2	2.35	0.42
2:F:102:ASP:C	2:F:104:THR:N	2.73	0.42
2:E:441:PHE:CE2	2:F:314:LYS:HG2	2.55	0.42
2:E:149:GLN:C	2:E:151:GLU:H	2.23	0.41
2:E:101:ARG:O	2:E:104:THR:HB	2.20	0.41
1:A:7:ARG:NE	1:A:118:ASP:OD2	2.53	0.41
1:C:71:LEU:CD1	1:C:104:LEU:HD21	2.49	0.41
2:E:164:ARG:HA	2:E:164:ARG:HH11	1.84	0.41
2:F:131:ILE:HG21	2:F:222:MET:HE1	2.02	0.41
2:E:134:VAL:HG22	2:E:134:VAL:O	2.20	0.41
1:D:152:LEU:HB3	1:D:166:HIS:CE1	2.55	0.41
1:D:59:LEU:HD11	1:D:63:LYS:HE3	2.02	0.41
1:B:170:GLU:CG	1:B:171:LEU:H	2.28	0.41
1:D:28:LYS:HZ3	1:D:30:ASN:ND2	2.17	0.41
1:C:59:LEU:HD23	1:C:78:LEU:CD1	2.49	0.41
2:E:244:ILE:HG13	2:E:297:VAL:HG22	2.00	0.41
2:F:322:LEU:HA	2:F:322:LEU:HD12	1.81	0.41
2:E:268:SER:HA	2:E:271:ASP:OD2	2.19	0.41
1:B:95:LEU:HD12	1:B:95:LEU:H	1.84	0.41
2:F:311:GLN:CA	2:F:311:GLN:HE21	2.33	0.41
1:C:157:ASP:OD2	1:C:164:HIS:NE2	2.53	0.41
2:F:282:LEU:HA	2:F:282:LEU:HD12	1.75	0.41
1:B:121:ALA:HB1	1:B:126:GLY:O	2.20	0.41
2:F:153:SER:HA	2:F:157:GLN:H	1.86	0.41
2:E:219:LYS:O	2:E:223:LYS:HG3	2.21	0.41
1:A:77:GLU:HA	1:A:80:LYS:HD2	2.01	0.41
1:D:98:ALA:O	1:D:99:ASP:HB3	2.20	0.41
2:F:375:ARG:HA	2:F:378:GLU:HB2	2.02	0.41
1:C:73:LYS:HA	1:C:73:LYS:HD2	1.85	0.41
2:F:152:PRO:HB3	2:F:156:ARG:H	1.85	0.41
2:F:217:LYS:HZ2	2:F:217:LYS:HB2	1.86	0.41
1:B:88:LEU:HA	1:B:91:LEU:CD1	2.51	0.41
1:D:59:LEU:O	1:D:59:LEU:HD12	2.21	0.41
1:C:67:HIS:NE2	1:C:77:GLU:HG3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:152:PRO:CB	2:E:156:ARG:CB	2.89	0.41
1:A:10:GLY:HA2	1:A:173:TYR:CD1	2.55	0.41
1:D:36:ARG:C	1:D:37:LEU:HD23	2.41	0.41
1:C:12:VAL:HG12	1:C:171:LEU:HB3	2.03	0.41
1:B:8:ARG:O	1:B:11:HIS:HB2	2.20	0.41
2:F:235:ASN:HB2	2:F:236:PRO:CD	2.47	0.41
1:A:114:GLN:HA	1:A:115:PRO:HD2	1.89	0.41
2:E:173:ILE:HD11	2:E:221:ALA:CB	2.50	0.41
1:B:85:ASP:O	1:B:86:ARG:C	2.59	0.41
1:D:60:PHE:HB2	1:D:78:LEU:HD22	2.02	0.41
1:B:78:LEU:O	1:B:80:LYS:N	2.54	0.41
2:F:119:ASN:HD22	2:F:119:ASN:N	2.17	0.41
2:E:119:ASN:OD1	2:E:234:VAL:HG23	2.20	0.41
2:E:227:GLU:O	2:E:230:ALA:N	2.52	0.41
2:F:132:LEU:HB3	2:F:156:ARG:CZ	2.51	0.41
1:B:115:PRO:HB2	1:B:119:LEU:O	2.21	0.41
1:B:148:ALA:O	1:B:152:LEU:HB2	2.21	0.41
2:E:25:ARG:O	2:E:29:ILE:CD1	2.68	0.41
2:F:145:GLN:C	2:F:147:GLU:H	2.25	0.41
2:E:150:GLN:C	2:E:153:SER:OG	2.58	0.41
1:A:81:ASP:HA	1:A:84:THR:HG22	2.03	0.41
2:F:389:ASN:C	2:F:389:ASN:ND2	2.73	0.41
1:D:43:ILE:HD12	1:D:171:LEU:HD22	2.03	0.41
2:F:216:LEU:HD21	2:F:221:ALA:HB2	2.03	0.41
1:D:159:CYS:HB3	1:D:162:THR:HB	2.03	0.41
2:E:262:CYS:SG	2:E:318:LEU:HD13	2.61	0.41
2:F:133:ASP:O	2:F:137:PRO:HA	2.21	0.41
1:D:169:GLU:HA	1:D:169:GLU:OE2	2.22	0.41
1:B:12:VAL:HG12	1:B:171:LEU:HB3	2.03	0.41
1:A:103:SER:O	1:A:104:LEU:HB3	2.21	0.41
2:E:140:LYS:O	2:E:141:ASN:CB	2.67	0.40
1:B:79:ALA:HB1	1:B:110:GLY:C	2.42	0.40
1:A:37:LEU:CD2	1:A:57:PHE:HB3	2.52	0.40
1:D:117:ASN:C	1:D:119:LEU:N	2.73	0.40
2:F:384:ASN:HD22	2:F:384:ASN:HA	1.58	0.40
2:F:89:VAL:HA	2:F:92:VAL:O	2.20	0.40
1:B:11:HIS:CE1	1:B:172:SER:OG	2.74	0.40
2:E:128:GLU:O	2:E:131:ILE:HG22	2.22	0.40
2:E:172:GLU:O	2:E:173:ILE:HG23	2.22	0.40
2:E:362:GLU:HG2	2:E:411:SER:N	2.36	0.40
2:E:135:LEU:O	2:E:136:ILE:HG12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:LEU:HD22	1:C:166:HIS:CE1	2.55	0.40
1:B:30:ASN:C	1:B:30:ASN:HD22	2.24	0.40
2:F:259:ASP:HB3	2:F:310:PHE:CZ	2.57	0.40
2:E:241:GLN:HB3	2:E:241:GLN:HE21	1.63	0.40
2:E:147:GLU:O	2:E:150:GLN:HG3	2.21	0.40
2:F:351:ILE:N	2:F:351:ILE:HD13	2.15	0.40
2:E:135:LEU:HB3	2:E:159:PHE:CD2	2.56	0.40
2:F:217:LYS:HB2	2:F:217:LYS:HZ3	1.87	0.40
2:E:171:LYS:HE3	2:E:172:GLU:N	2.37	0.40
1:C:10:GLY:HA3	1:C:174:LYS:H	1.86	0.40
1:B:79:ALA:HB1	1:B:110:GLY:HA2	2.03	0.40
2:E:239:LEU:O	2:E:242:ASP:HB2	2.21	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	172/175 (98%)	148 (86%)	19 (11%)	5 (3%)	6	19
1	B	172/175 (98%)	138 (80%)	25 (14%)	9 (5%)	2	7
1	C	172/175 (98%)	150 (87%)	18 (10%)	4 (2%)	8	26
1	D	172/175 (98%)	140 (81%)	28 (16%)	4 (2%)	8	26
2	E	404/449 (90%)	355 (88%)	36 (9%)	13 (3%)	5	17
2	F	404/449 (90%)	340 (84%)	48 (12%)	16 (4%)	4	12
All	All	1496/1598 (94%)	1271 (85%)	174 (12%)	51 (3%)	5	16

All (51) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	116	GLU

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Mol	Chain	Res	Type
1	D	69	GLY
2	E	92	VAL
2	E	144	GLY
2	E	146	THR
2	E	153	SER
2	E	170	ASP
2	E	212	LYS
2	F	92	VAL
2	F	153	SER
2	F	165	GLU
2	F	212	LYS
2	F	236	PRO
2	F	237	GLU
1	A	9	ASN
1	B	54	PHE
1	B	116	GLU
2	E	165	GLU
2	E	217	LYS
2	E	227	GLU
2	E	410	ALA
2	F	143	TRP
2	F	144	GLY
2	F	146	THR
2	F	230	ALA
2	F	300	ASP
1	A	80	LYS
1	B	68	GLN
1	B	71	LEU
1	C	69	GLY
1	C	115	PRO
1	D	68	GLN
2	F	154	ALA
1	A	71	LEU
1	B	69	GLY
1	B	70	HIS
1	B	101	THR
1	C	117	ASN
2	F	137	PRO
2	F	138	PRO
2	F	168	LEU
1	A	81	ASP
1	A	115	PRO

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Mol	Chain	Res	Type
1	D	87	MET
2	E	44	LEU
2	E	141	ASN
2	E	239	LEU
2	F	109	LYS
1	B	86	ARG
1	D	99	ASP
1	B	72	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	136/136 (100%)	127 (93%)	9 (7%)	21	51
1	B	136/136 (100%)	119 (88%)	17 (12%)	6	17
1	C	136/136 (100%)	121 (89%)	15 (11%)	8	23
1	D	136/136 (100%)	122 (90%)	14 (10%)	9	26
2	E	350/383 (91%)	305 (87%)	45 (13%)	5	16
2	F	350/383 (91%)	293 (84%)	57 (16%)	3	8
All	All	1244/1310 (95%)	1087 (87%)	157 (13%)	5	17

All (157) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	THR
1	A	9	ASN
1	A	30	ASN
1	A	71	LEU
1	A	83	ARG
1	A	107	THR
1	A	137	LEU
1	A	152	LEU
1	A	160	ILE
1	B	1	THR

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Mol	Chain	Res	Type
1	B	22	LEU
1	B	30	ASN
1	B	54	PHE
1	B	59	LEU
1	B	72	VAL
1	B	83	ARG
1	B	91	LEU
1	B	99	ASP
1	B	104	LEU
1	B	107	THR
1	B	112	VAL
1	B	116	GLU
1	B	136	LEU
1	B	152	LEU
1	B	160	ILE
1	B	174	LYS
1	C	1	THR
1	C	4	VAL
1	C	9	ASN
1	C	30	ASN
1	C	36	ARG
1	C	37	LEU
1	C	54	PHE
1	C	67	HIS
1	C	71	LEU
1	C	83	ARG
1	C	87	MET
1	C	99	ASP
1	C	118	ASP
1	C	152	LEU
1	C	160	ILE
1	D	1	THR
1	D	30	ASN
1	D	37	LEU
1	D	39	ASN
1	D	43	ILE
1	D	73	LYS
1	D	77	GLU
1	D	80	LYS
1	D	99	ASP
1	D	104	LEU
1	D	114	GLN

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Mol	Chain	Res	Type
1	D	116	GLU
1	D	136	LEU
1	D	152	LEU
2	E	11	SER
2	E	13	LEU
2	E	27	VAL
2	E	31	LEU
2	E	37	ARG
2	E	59	THR
2	E	92	VAL
2	E	94	LYS
2	E	117	GLU
2	E	122	ARG
2	E	130	ARG
2	E	140	LYS
2	E	148	GLN
2	E	149	GLN
2	E	152	PRO
2	E	164	ARG
2	E	165	GLU
2	E	168	LEU
2	E	169	ASP
2	E	171	LYS
2	E	173	ILE
2	E	220	ASP
2	E	225	LEU
2	E	238	GLU
2	E	240	LYS
2	E	241	GLN
2	E	266	GLU
2	E	296	MET
2	E	300	ASP
2	E	311	GLN
2	E	312	ILE
2	E	318	LEU
2	E	326	LEU
2	E	337	THR
2	E	352	THR
2	E	353	VAL
2	E	355	TYR
2	E	375	ARG
2	E	385	GLU

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Mol	Chain	Res	Type
2	E	386	SER
2	E	388	GLU
2	E	389	ASN
2	E	411	SER
2	E	412	ASP
2	E	413	LEU
2	F	13	LEU
2	F	27	VAL
2	F	31	LEU
2	F	37	ARG
2	F	41	ASN
2	F	59	THR
2	F	70	LEU
2	F	87	THR
2	F	94	LYS
2	F	95	GLU
2	F	103	LEU
2	F	104	THR
2	F	108	VAL
2	F	121	TYR
2	F	130	ARG
2	F	140	LYS
2	F	141	ASN
2	F	145	GLN
2	F	148	GLN
2	F	150	GLN
2	F	152	PRO
2	F	153	SER
2	F	169	ASP
2	F	173	ILE
2	F	210	LYS
2	F	211	GLN
2	F	214	ARG
2	F	217	LYS
2	F	219	LYS
2	F	220	ASP
2	F	225	LEU
2	F	232	LYS
2	F	238	GLU
2	F	239	LEU
2	F	266	GLU
2	F	281	LEU

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Mol	Chain	Res	Type
2	F	296	MET
2	F	300	ASP
2	F	311	GLN
2	F	312	ILE
2	F	318	LEU
2	F	326	LEU
2	F	337	THR
2	F	344	LEU
2	F	351	ILE
2	F	352	THR
2	F	355	TYR
2	F	366	ILE
2	F	375	ARG
2	F	382	GLN
2	F	384	ASN
2	F	385	GLU
2	F	389	ASN
2	F	404	GLU
2	F	413	LEU
2	F	423	ASP
2	F	438	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	39	ASN
1	A	109	ASN
1	B	11	HIS
1	B	30	ASN
1	B	109	ASN
1	B	130	GLN
1	C	9	ASN
1	C	30	ASN
1	D	11	HIS
1	D	30	ASN
1	D	114	GLN
2	E	22	ASN
2	E	33	ASN
2	E	75	ASN
2	E	114	GLN
2	E	149	GLN

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Mol	Chain	Res	Type
2	E	150	GLN
2	E	241	GLN
2	E	294	HIS
2	E	311	GLN
2	E	348	ASN
2	E	382	GLN
2	E	384	ASN
2	E	389	ASN
2	E	416	GLN
2	E	428	HIS
2	F	22	ASN
2	F	33	ASN
2	F	41	ASN
2	F	75	ASN
2	F	114	GLN
2	F	119	ASN
2	F	142	ASN
2	F	145	GLN
2	F	149	GLN
2	F	150	GLN
2	F	211	GLN
2	F	311	GLN
2	F	348	ASN
2	F	365	ASN
2	F	384	ASN
2	F	389	ASN
2	F	416	GLN
2	F	417	ASN

### 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

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	ADP	E	450	-	22,29,29	1.53	6 (27%)	27,45,45	2.08	5 (18%)
3	ADP	F	1450	-	22,29,29	1.54	5 (22%)	27,45,45	2.00	5 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	E	450	-	-	0/12/32/32	0/3/3/3
3	ADP	F	1450	-	-	0/12/32/32	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1450	ADP	C8-N7	-3.97	1.27	1.34
3	E	450	ADP	C8-N7	-3.97	1.27	1.34
3	E	450	ADP	PA-O1A	-2.24	1.43	1.51
3	E	450	ADP	PA-O2A	-2.15	1.45	1.54
3	E	450	ADP	PB-O3B	-2.08	1.47	1.54
3	F	1450	ADP	PA-O2A	-2.08	1.46	1.54
3	F	1450	ADP	PA-O1A	-2.01	1.43	1.51
3	E	450	ADP	C2-N3	2.18	1.36	1.32
3	E	450	ADP	C4-N3	2.27	1.39	1.35
3	F	1450	ADP	C2-N3	2.31	1.36	1.32
3	F	1450	ADP	C4-N3	2.63	1.39	1.35

All (10) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	F	1450	ADP	N3-C2-N1	-5.21	124.90	128.89
3	E	450	ADP	N3-C2-N1	-4.82	125.20	128.89
3	E	450	ADP	C2'-C1'-N9	-4.26	107.79	114.29
3	F	1450	ADP	C2'-C1'-N9	-3.16	109.47	114.29
3	F	1450	ADP	O3A-PA-O5'	2.61	109.85	102.94
3	E	450	ADP	O3A-PA-O5'	2.92	110.68	102.94
3	F	1450	ADP	C2'-C3'-C4'	2.94	108.66	102.61
3	E	450	ADP	C2'-C3'-C4'	3.01	108.81	102.61
3	F	1450	ADP	C4'-O4'-C1'	6.35	116.70	109.72
3	E	450	ADP	C4'-O4'-C1'	6.53	116.89	109.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	450	ADP	1	0
3	F	1450	ADP	3	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.