Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:11 AM GMT

PDB ID	:	3HI8
Title	:	Crystal structure of proliferating cell nuclear antigen (PCNA) from Haloferax volcanii
Authors	:	Morgunova, E.; Gray, F.C.; MacNeill S.A.; Ladenstein, R.
Deposited on	:	2009-05-19
Resolution	:	3.20 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 ⓘ symbol.

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

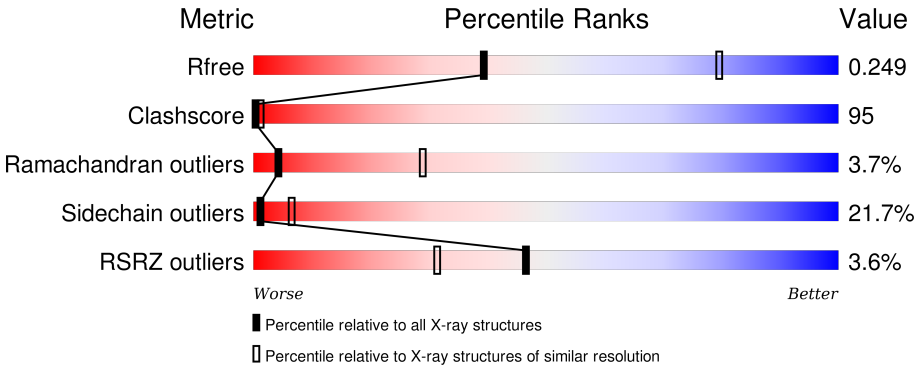
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	247	4% 23% 59% 14% .
1	B	247	4% 22% 60% 14% .
1	C	247	3% 22% 60% 14% .
1	D	247	5% 23% 60% 14% .
1	E	247	3% 23% 60% 14% .

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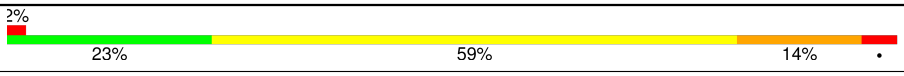
Mol	Chain	Length	Quality of chain
1	F	247	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11245 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 Proliferating cell nuclear antigen PcnA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	B	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	C	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	D	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	E	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			
1	F	247	Total	C	N	O	S	0	0	0
			1869	1167	308	386	8			

- Molecule 2 is water.

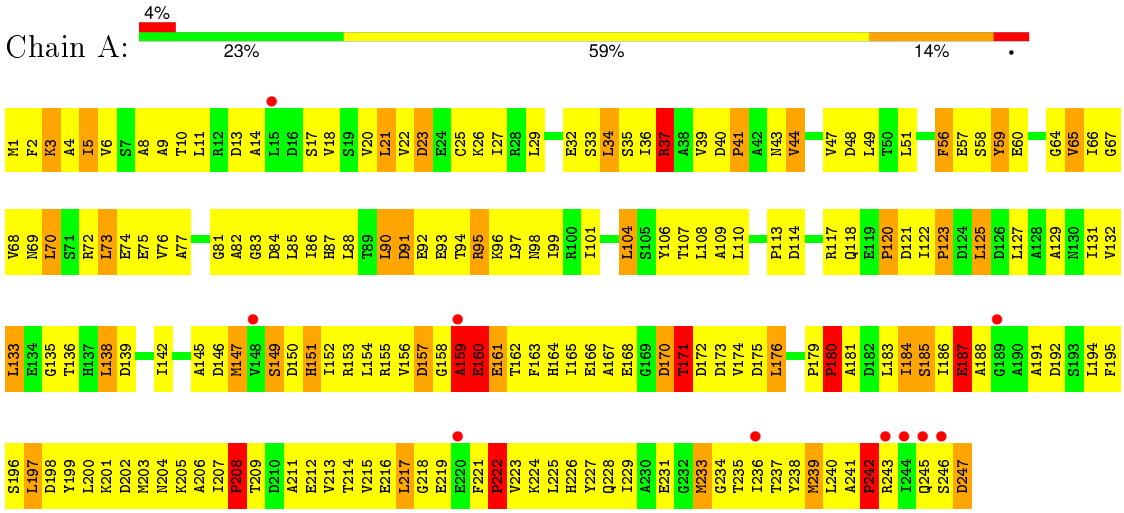
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	O	0	0
			5	5		
2	B	3	Total	O	0	0
			3	3		
2	C	2	Total	O	0	0
			2	2		
2	D	7	Total	O	0	0
			7	7		
2	E	5	Total	O	0	0
			5	5		
2	F	9	Total	O	0	0
			9	9		

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.

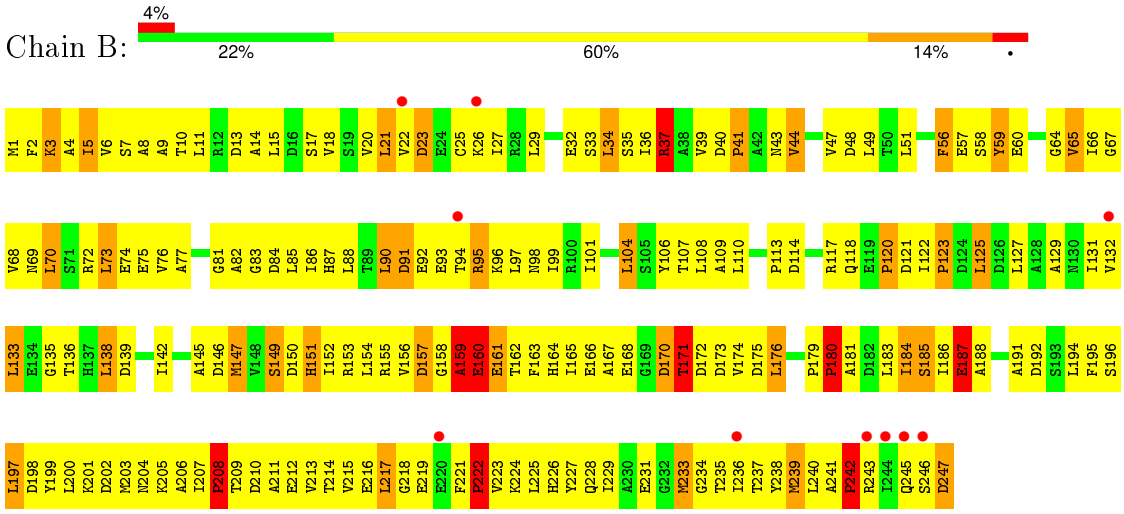
- Molecule 1: Proliferating cell nuclear antigen PcnA

Chain A:



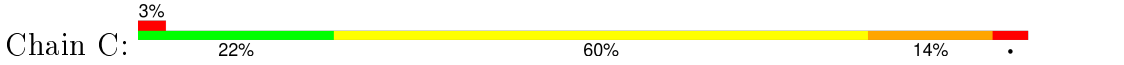
- Molecule 1: Proliferating cell nuclear antigen PcnA

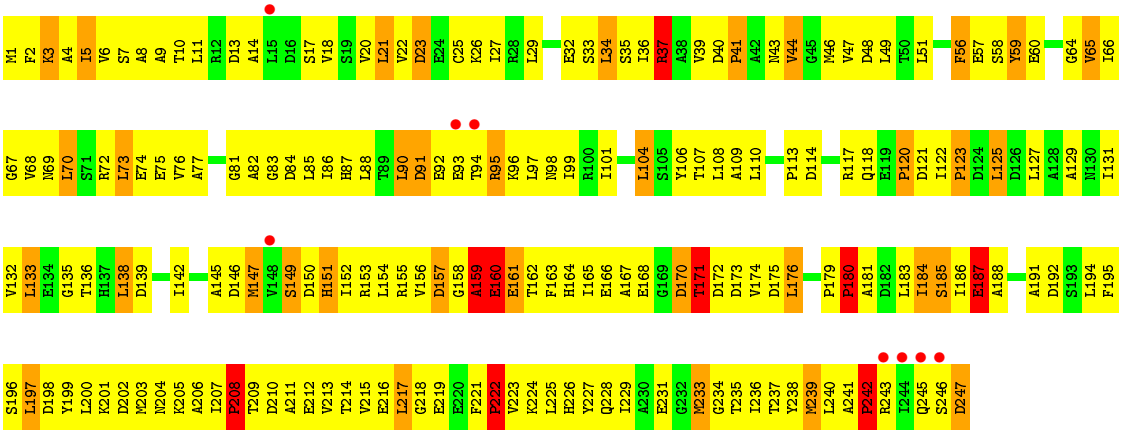
Chain B:



- Molecule 1: Proliferating cell nuclear antigen PcnA

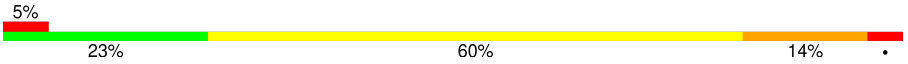
Chain C:

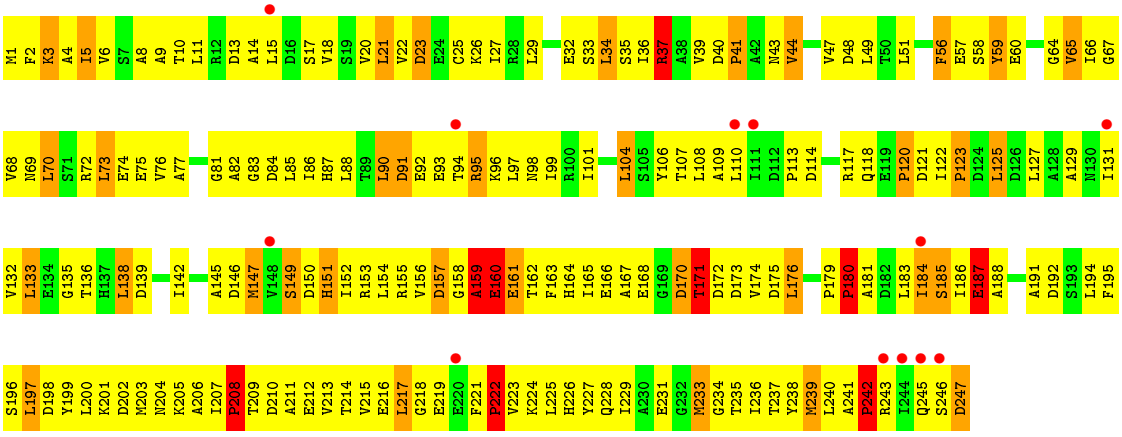




• Molecule 1: Proliferating cell nuclear antigen PcnA

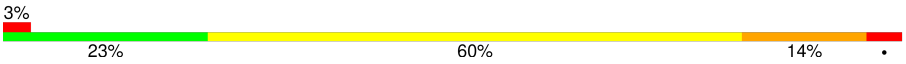
Chain D:

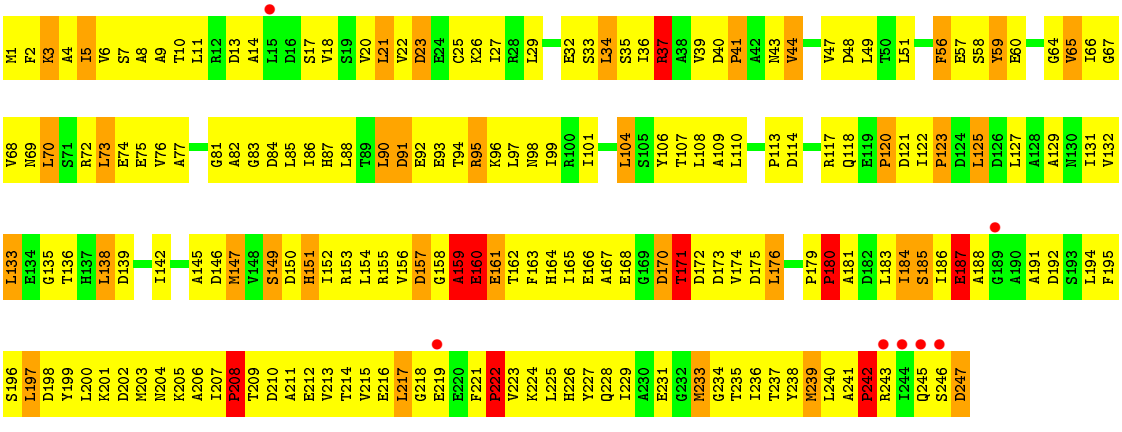




• Molecule 1: Proliferating cell nuclear antigen PcnA

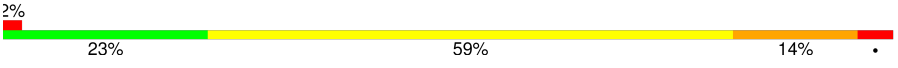
Chain E:

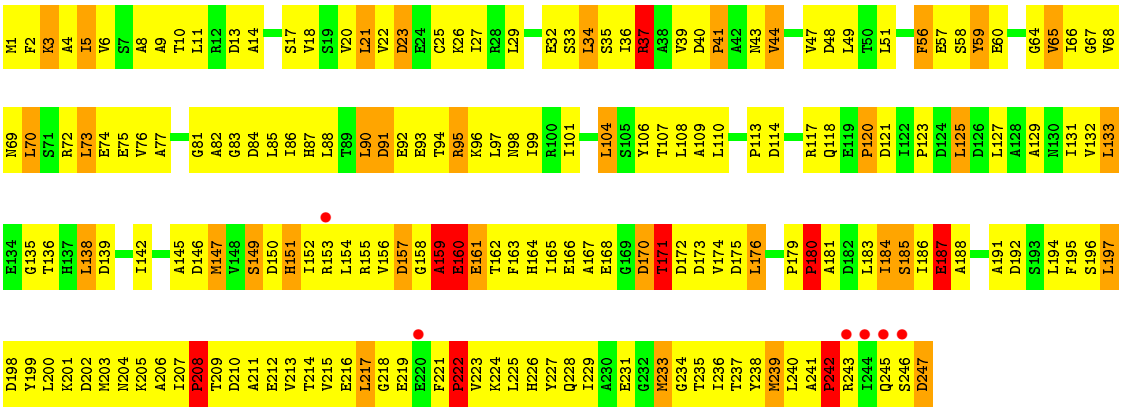




• Molecule 1: Proliferating cell nuclear antigen PcnA

Chain F:




M1 F2 K3 A4 I5 V6 S7 A8 A9 T10 L11 R12 D13 A14 S17 V18 S19 V20 L21 V22 D23 E24 C25 K26 I27 R28 L29 E32 S33 I34 S35 I36 R37 A38 V39 D40 P41 A42 N43 V44 V47 D48 L49 T50 L51 F56 E57 S58 Y59 E60 G64 V65 I66 G67 V68
N69 L70 S71 R72 L73 E74 E75 V76 A77 G81 A82 G83 D84 L85 I86 H87 L88 T89 L90 D91 E92 E93 T94 R95 K96 L97 N98 I99 R100 I101 L104 S105 Y106 T107 L108 A109 L110 P113 D114 R117 Q118 E119 P120 D121 I122 P123 D124 L125 D126 L127 A128 A129 N130 I131 V132 L133
E134 G135 T136 H137 L138 D139 I142 A145 D146 M147 V148 S149 D150 H151 I152 R153 L154 R155 V156 D157 G158 A159 E160 E161 T162 F163 H164 I165 E166 A167 E168 G169 D170 T171 D172 D173 V174 D175 L176 P179 P180 A181 D182 L183 I184 S185 I186 E187 A188 A191 D192 S193 L194 F195 S196 L197
D198 Y199 L200 K201 D202 M203 N204 K205 A206 I207 P208 T209 D210 A211 E212 V213 T214 V215 E216 L217 G218 E219 E220 F221 P222 V223 K224 L225 H226 Y227 Q228 I229 A230 E231 G232 M233 G234 T235 I236 T237 Y238 M239 L240 A241 P242 R243 I244 Q245 S246 D247

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	174.44Å 123.24Å 123.26Å 90.00° 135.00° 90.00°	Depositor
Resolution (Å)	32.95 – 3.20 32.96 – 3.20	Depositor EDS
% Data completeness (in resolution range)	86.6 (32.95-3.20) 86.5 (32.96-3.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	1.19 (at 3.18Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.237 , 0.250 0.236 , 0.249	Depositor DCC
R_{free} test set	1324 reflections (5.02%)	DCC
Wilson B-factor (Å^2)	138.1	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.23 , 88.6	EDS
Estimated twinning fraction	0.357 for -h-2*l,k,h+l 0.348 for k+l,h+l,-l 0.357 for -k+l,-h-l,-l 0.349 for -h-k-l,l,k 0.349 for -h+k-l,-l,-k 0.347 for -h-k-l,-l,h+l 0.347 for k+l,-h-l,-k 0.348 for -h+k-l,l,h+l 0.349 for -k+l,h+l,k 0.357 for -h,-k,h+l 0.358 for -h-2*l,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.34$, $< L^2 > = 0.17$	Xtriage
Outliers	0 of 26380 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11245	wwPDB-VP
Average B, all atoms (Å^2)	139.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% 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	0.71	0/1893	1.20	11/2572 (0.4%)
1	B	0.71	0/1893	1.20	11/2572 (0.4%)
1	C	0.71	0/1893	1.20	11/2572 (0.4%)
1	D	0.71	0/1893	1.20	11/2572 (0.4%)
1	E	0.71	0/1893	1.20	11/2572 (0.4%)
1	F	0.71	0/1893	1.20	11/2572 (0.4%)
All	All	0.71	0/11358	1.20	66/15432 (0.4%)

There are no bond length outliers.

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	180	PRO	CA-N-CD	-14.39	91.35	111.50
1	F	180	PRO	CA-N-CD	-14.37	91.38	111.50
1	C	180	PRO	CA-N-CD	-14.37	91.39	111.50
1	A	180	PRO	CA-N-CD	-14.36	91.39	111.50
1	E	180	PRO	CA-N-CD	-14.35	91.41	111.50
1	B	180	PRO	CA-N-CD	-14.35	91.41	111.50
1	E	120	PRO	CA-N-CD	-13.38	92.77	111.50
1	A	120	PRO	CA-N-CD	-13.36	92.80	111.50
1	F	120	PRO	CA-N-CD	-13.35	92.81	111.50
1	D	120	PRO	CA-N-CD	-13.35	92.81	111.50
1	B	120	PRO	CA-N-CD	-13.35	92.82	111.50
1	C	120	PRO	CA-N-CD	-13.33	92.83	111.50
1	D	242	PRO	CA-N-CD	-10.54	96.75	111.50
1	F	242	PRO	CA-N-CD	-10.53	96.76	111.50
1	E	242	PRO	CA-N-CD	-10.53	96.76	111.50
1	C	242	PRO	CA-N-CD	-10.52	96.78	111.50
1	A	242	PRO	CA-N-CD	-10.51	96.79	111.50
1	B	242	PRO	CA-N-CD	-10.51	96.79	111.50
1	B	171	THR	CA-CB-OG1	10.40	130.84	109.00
1	D	171	THR	CA-CB-OG1	10.40	130.83	109.00
1	C	171	THR	CA-CB-OG1	10.39	130.82	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	171	THR	CA-CB-OG1	10.38	130.79	109.00
1	F	171	THR	CA-CB-OG1	10.38	130.79	109.00
1	A	171	THR	CA-CB-OG1	10.37	130.77	109.00
1	E	222	PRO	CA-N-CD	-10.13	97.32	111.50
1	B	222	PRO	CA-N-CD	-10.13	97.32	111.50
1	F	222	PRO	CA-N-CD	-10.12	97.33	111.50
1	D	222	PRO	CA-N-CD	-10.10	97.36	111.50
1	A	222	PRO	CA-N-CD	-10.10	97.36	111.50
1	C	222	PRO	CA-N-CD	-10.10	97.36	111.50
1	F	208	PRO	CA-N-CD	-9.94	97.58	111.50
1	D	208	PRO	CA-N-CD	-9.93	97.60	111.50
1	C	208	PRO	CA-N-CD	-9.93	97.60	111.50
1	B	208	PRO	CA-N-CD	-9.92	97.61	111.50
1	A	208	PRO	CA-N-CD	-9.91	97.62	111.50
1	E	208	PRO	CA-N-CD	-9.90	97.64	111.50
1	F	41	PRO	CA-N-CD	-9.85	97.70	111.50
1	E	41	PRO	CA-N-CD	-9.84	97.73	111.50
1	D	41	PRO	CA-N-CD	-9.84	97.73	111.50
1	A	41	PRO	CA-N-CD	-9.83	97.74	111.50
1	C	41	PRO	CA-N-CD	-9.81	97.76	111.50
1	B	41	PRO	CA-N-CD	-9.81	97.76	111.50
1	E	160	GLU	CB-CA-C	7.18	124.76	110.40
1	C	160	GLU	CB-CA-C	7.17	124.74	110.40
1	A	160	GLU	CB-CA-C	7.17	124.73	110.40
1	F	160	GLU	CB-CA-C	7.16	124.73	110.40
1	B	160	GLU	CB-CA-C	7.16	124.72	110.40
1	D	160	GLU	CB-CA-C	7.16	124.72	110.40
1	B	123	PRO	CB-CA-C	5.91	126.78	112.00
1	A	123	PRO	CB-CA-C	5.91	126.77	112.00
1	D	123	PRO	CB-CA-C	5.91	126.77	112.00
1	C	123	PRO	CB-CA-C	5.90	126.76	112.00
1	E	123	PRO	CB-CA-C	5.90	126.76	112.00
1	F	123	PRO	CB-CA-C	5.90	126.74	112.00
1	D	159	ALA	O-C-N	5.53	131.54	122.70
1	A	159	ALA	O-C-N	5.52	131.54	122.70
1	C	159	ALA	O-C-N	5.51	131.52	122.70
1	F	159	ALA	O-C-N	5.51	131.52	122.70
1	E	159	ALA	O-C-N	5.50	131.50	122.70
1	B	159	ALA	O-C-N	5.50	131.49	122.70
1	E	187	GLU	N-CA-C	-5.26	96.80	111.00
1	A	187	GLU	N-CA-C	-5.25	96.82	111.00
1	D	187	GLU	N-CA-C	-5.25	96.82	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	187	GLU	N-CA-C	-5.25	96.83	111.00
1	C	187	GLU	N-CA-C	-5.24	96.84	111.00
1	B	187	GLU	N-CA-C	-5.24	96.86	111.00

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	1869	0	1847	373	0
1	B	1869	0	1847	377	0
1	C	1869	0	1847	372	0
1	D	1869	0	1847	374	0
1	E	1869	0	1847	365	0
1	F	1869	0	1847	358	0
2	A	5	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
2	D	7	0	0	0	0
2	E	5	0	0	0	0
2	F	9	0	0	0	0
All	All	11245	0	11082	2123	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 95.

All (2123) 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:A:149:SER:CB	1:A:167:ALA:HB1	1.53	1.38
1:B:149:SER:CB	1:B:167:ALA:HB1	1.53	1.37
1:C:149:SER:CB	1:C:167:ALA:HB1	1.53	1.36
1:F:149:SER:CB	1:F:167:ALA:HB1	1.53	1.35
1:E:149:SER:CB	1:E:167:ALA:HB1	1.53	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:149:SER:CB	1:D:167:ALA:HB1	1.53	1.35
1:D:156:VAL:HB	1:D:191:ALA:O	1.25	1.33
1:A:150:ASP:O	1:A:197:LEU:HD22	1.28	1.32
1:B:150:ASP:O	1:B:197:LEU:HD22	1.28	1.31
1:C:156:VAL:HB	1:C:191:ALA:O	1.25	1.31
1:F:95:ARG:O	1:F:109:ALA:HA	1.29	1.30
1:C:150:ASP:O	1:C:197:LEU:HD22	1.28	1.30
1:F:150:ASP:O	1:F:197:LEU:HD22	1.28	1.29
1:A:156:VAL:HB	1:A:191:ALA:O	1.25	1.29
1:D:8:ALA:HB3	1:D:82:ALA:O	1.32	1.29
1:E:95:ARG:O	1:E:109:ALA:HA	1.29	1.29
1:A:8:ALA:HB3	1:A:82:ALA:O	1.32	1.29
1:E:156:VAL:HB	1:E:191:ALA:O	1.25	1.29
1:A:95:ARG:O	1:A:109:ALA:HA	1.29	1.28
1:D:150:ASP:O	1:D:197:LEU:HD22	1.28	1.28
1:B:156:VAL:HB	1:B:191:ALA:O	1.25	1.27
1:E:8:ALA:HB3	1:E:82:ALA:O	1.33	1.26
1:E:150:ASP:O	1:E:197:LEU:HD22	1.28	1.26
1:D:95:ARG:O	1:D:109:ALA:HA	1.29	1.25
1:D:72:ARG:HH12	1:F:171:THR:CG2	1.48	1.25
1:B:47:VAL:HA	1:B:237:THR:O	1.36	1.25
1:C:8:ALA:HB3	1:C:82:ALA:O	1.32	1.25
1:C:47:VAL:HA	1:C:237:THR:O	1.36	1.25
1:C:95:ARG:O	1:C:109:ALA:HA	1.29	1.25
1:F:8:ALA:HB3	1:F:82:ALA:O	1.32	1.24
1:F:156:VAL:HB	1:F:191:ALA:O	1.25	1.24
1:B:8:ALA:HB3	1:B:82:ALA:O	1.32	1.24
1:B:95:ARG:O	1:B:109:ALA:HA	1.29	1.24
1:D:47:VAL:HA	1:D:237:THR:O	1.36	1.23
1:B:171:THR:CG2	1:C:72:ARG:HH12	1.50	1.22
1:E:47:VAL:HA	1:E:237:THR:O	1.36	1.21
1:E:171:THR:CG2	1:F:72:ARG:HH12	1.54	1.20
1:A:23:ASP:O	1:A:70:LEU:HB3	1.03	1.20
1:F:47:VAL:HA	1:F:237:THR:O	1.36	1.19
1:A:72:ARG:HH12	1:C:171:THR:CG2	1.55	1.18
1:A:47:VAL:HA	1:A:237:THR:O	1.36	1.18
1:C:195:PHE:CE2	1:C:242:PRO:HD3	1.79	1.18
1:C:23:ASP:O	1:C:70:LEU:HB3	1.03	1.18
1:B:23:ASP:O	1:B:70:LEU:HB3	1.03	1.18
1:E:23:ASP:O	1:E:70:LEU:HB3	1.03	1.17
1:D:23:ASP:O	1:D:70:LEU:HB3	1.03	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:PHE:CE2	1:A:242:PRO:HD3	1.79	1.17
1:F:23:ASP:O	1:F:70:LEU:HB3	1.03	1.17
1:D:195:PHE:CE2	1:D:242:PRO:HD3	1.79	1.17
1:A:195:PHE:HE2	1:A:242:PRO:HD3	1.00	1.17
1:F:222:PRO:HD3	1:F:242:PRO:HG2	1.23	1.17
1:E:195:PHE:CE2	1:E:242:PRO:HD3	1.79	1.16
1:A:171:THR:CG2	1:B:72:ARG:HH12	1.57	1.16
1:A:222:PRO:HD3	1:A:242:PRO:CG	1.75	1.16
1:F:195:PHE:CE2	1:F:242:PRO:HD3	1.79	1.16
1:F:222:PRO:HD3	1:F:242:PRO:CG	1.75	1.16
1:D:171:THR:CG2	1:E:72:ARG:HH12	1.57	1.16
1:B:195:PHE:CE2	1:B:242:PRO:HD3	1.79	1.16
1:E:222:PRO:HD3	1:E:242:PRO:CG	1.75	1.16
1:F:8:ALA:HB1	1:F:81:GLY:O	1.46	1.16
1:B:222:PRO:HD3	1:B:242:PRO:CG	1.75	1.15
1:C:222:PRO:HD3	1:C:242:PRO:CG	1.75	1.15
1:A:8:ALA:HB1	1:A:81:GLY:O	1.46	1.15
1:D:222:PRO:HD3	1:D:242:PRO:CG	1.75	1.15
1:E:2:PHE:O	1:E:88:LEU:O	1.66	1.14
1:B:2:PHE:O	1:B:88:LEU:O	1.66	1.14
1:F:2:PHE:O	1:F:88:LEU:O	1.66	1.14
1:C:222:PRO:HD3	1:C:242:PRO:HG2	1.23	1.13
1:E:195:PHE:HE2	1:E:242:PRO:HD3	1.00	1.13
1:E:149:SER:HB2	1:E:167:ALA:HB1	1.15	1.13
1:F:23:ASP:O	1:F:70:LEU:CB	1.97	1.13
1:C:2:PHE:O	1:C:88:LEU:O	1.66	1.13
1:B:23:ASP:O	1:B:70:LEU:CB	1.97	1.13
1:A:23:ASP:O	1:A:70:LEU:CB	1.97	1.13
1:E:8:ALA:HB1	1:E:81:GLY:O	1.46	1.12
1:D:23:ASP:O	1:D:70:LEU:CB	1.97	1.13
1:B:8:ALA:HB1	1:B:81:GLY:O	1.46	1.12
1:D:222:PRO:HD3	1:D:242:PRO:HG2	1.23	1.12
1:C:8:ALA:HB1	1:C:81:GLY:O	1.46	1.12
1:C:23:ASP:O	1:C:70:LEU:CB	1.97	1.12
1:B:149:SER:HB2	1:B:167:ALA:HB1	1.15	1.12
1:F:195:PHE:HE2	1:F:242:PRO:HD3	1.00	1.12
1:D:2:PHE:O	1:D:88:LEU:O	1.66	1.12
1:A:149:SER:HB3	1:A:167:ALA:HB1	1.32	1.12
1:B:222:PRO:HD3	1:B:242:PRO:HG2	1.23	1.12
1:C:152:ILE:HG23	1:C:165:ILE:CG2	1.80	1.12
1:D:8:ALA:HB1	1:D:81:GLY:O	1.46	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:PHE:O	1:A:88:LEU:O	1.66	1.12
1:E:222:PRO:HD3	1:E:242:PRO:HG2	1.23	1.12
1:E:152:ILE:HG23	1:E:165:ILE:CG2	1.80	1.12
1:D:149:SER:HB2	1:D:167:ALA:HB1	1.15	1.11
1:D:27:ILE:N	1:D:66:ILE:O	1.83	1.11
1:B:152:ILE:HG23	1:B:165:ILE:CG2	1.80	1.11
1:E:23:ASP:O	1:E:70:LEU:CB	1.97	1.11
1:C:195:PHE:HE2	1:C:242:PRO:HD3	1.00	1.11
1:C:149:SER:HB2	1:C:167:ALA:HB1	1.15	1.11
1:F:27:ILE:N	1:F:66:ILE:O	1.83	1.11
1:A:152:ILE:HG23	1:A:165:ILE:CG2	1.80	1.10
1:F:152:ILE:HG23	1:F:165:ILE:CG2	1.80	1.10
1:D:152:ILE:HG23	1:D:165:ILE:CG2	1.80	1.10
1:B:195:PHE:HE2	1:B:242:PRO:HD3	1.00	1.10
1:F:149:SER:HB2	1:F:167:ALA:HB1	1.15	1.10
1:A:27:ILE:N	1:A:66:ILE:O	1.83	1.09
1:A:149:SER:HB2	1:A:167:ALA:HB1	1.15	1.09
1:B:149:SER:HB3	1:B:167:ALA:HB1	1.32	1.09
1:B:27:ILE:N	1:B:66:ILE:O	1.83	1.09
1:E:27:ILE:N	1:E:66:ILE:O	1.83	1.09
1:A:96:LYS:HA	1:A:108:LEU:O	1.52	1.09
1:C:27:ILE:N	1:C:66:ILE:O	1.83	1.09
1:B:96:LYS:HA	1:B:108:LEU:O	1.53	1.09
1:F:96:LYS:HA	1:F:108:LEU:O	1.52	1.09
1:D:96:LYS:HA	1:D:108:LEU:O	1.53	1.09
1:D:195:PHE:HE2	1:D:242:PRO:HD3	1.00	1.09
1:A:222:PRO:HD3	1:A:242:PRO:HG2	1.23	1.08
1:C:96:LYS:HA	1:C:108:LEU:O	1.52	1.08
1:E:149:SER:HB3	1:E:167:ALA:HB1	1.32	1.08
1:F:149:SER:HB3	1:F:167:ALA:HB1	1.32	1.08
1:E:96:LYS:HA	1:E:108:LEU:O	1.52	1.07
1:C:149:SER:HB3	1:C:167:ALA:HB1	1.32	1.05
1:C:228:GLN:HA	1:C:234:GLY:O	1.57	1.04
1:A:228:GLN:HA	1:A:234:GLY:O	1.58	1.03
1:D:149:SER:HB3	1:D:167:ALA:HB1	1.32	1.03
1:C:191:ALA:HB1	1:C:218:GLY:C	1.80	1.02
1:E:191:ALA:HB1	1:E:218:GLY:C	1.79	1.02
1:D:228:GLN:HA	1:D:234:GLY:O	1.58	1.02
1:B:191:ALA:HB1	1:B:218:GLY:C	1.79	1.01
1:F:191:ALA:HB1	1:F:218:GLY:C	1.79	1.01
1:A:191:ALA:HB1	1:A:218:GLY:C	1.79	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:228:GLN:HA	1:F:234:GLY:O	1.58	1.01
1:B:228:GLN:HA	1:B:234:GLY:O	1.58	1.01
1:B:152:ILE:HG23	1:B:165:ILE:HG23	1.41	1.01
1:D:197:LEU:HD23	1:D:198:ASP:N	1.76	1.01
1:E:228:GLN:HA	1:E:234:GLY:O	1.58	1.01
1:B:149:SER:HB2	1:B:167:ALA:CB	1.91	1.01
1:F:149:SER:HB2	1:F:167:ALA:CB	1.91	1.01
1:D:191:ALA:HB1	1:D:218:GLY:C	1.79	1.01
1:E:149:SER:HB2	1:E:167:ALA:CB	1.91	1.00
1:B:197:LEU:HD23	1:B:198:ASP:N	1.76	1.00
1:B:171:THR:HG23	1:C:72:ARG:NH1	1.76	1.00
1:D:149:SER:HB2	1:D:167:ALA:CB	1.91	1.00
1:C:197:LEU:HD23	1:C:198:ASP:N	1.76	1.00
1:D:152:ILE:HG23	1:D:165:ILE:HG23	1.40	1.00
1:A:197:LEU:HD23	1:A:198:ASP:N	1.76	1.00
1:F:152:ILE:HG23	1:F:165:ILE:HG23	1.40	1.00
1:D:72:ARG:HH12	1:F:171:THR:HG23	1.25	0.99
1:C:149:SER:HB2	1:C:167:ALA:CB	1.91	0.99
1:F:197:LEU:HD23	1:F:198:ASP:N	1.76	0.99
1:E:156:VAL:HG21	1:E:217:LEU:HG	1.44	0.99
1:B:165:ILE:O	1:B:176:LEU:HD23	1.63	0.99
1:C:165:ILE:O	1:C:176:LEU:HD23	1.63	0.99
1:C:156:VAL:HG21	1:C:217:LEU:HG	1.44	0.99
1:A:149:SER:HB2	1:A:167:ALA:CB	1.91	0.99
1:D:171:THR:HG23	1:E:72:ARG:HH12	1.27	0.99
1:E:197:LEU:HD23	1:E:198:ASP:N	1.76	0.99
1:E:165:ILE:O	1:E:176:LEU:HD23	1.63	0.99
1:E:152:ILE:HG23	1:E:165:ILE:HG23	1.40	0.98
1:B:156:VAL:HG21	1:B:217:LEU:HG	1.44	0.98
1:A:165:ILE:O	1:A:176:LEU:HD23	1.63	0.98
1:D:165:ILE:O	1:D:176:LEU:HD23	1.63	0.98
1:A:152:ILE:HG23	1:A:165:ILE:HG23	1.40	0.98
1:C:152:ILE:HG23	1:C:165:ILE:HG23	1.40	0.97
1:D:72:ARG:NH1	1:F:171:THR:HG23	1.78	0.97
1:F:156:VAL:HG21	1:F:217:LEU:HG	1.44	0.97
1:E:171:THR:HG23	1:F:72:ARG:HH12	1.29	0.97
1:F:165:ILE:O	1:F:176:LEU:HD23	1.63	0.97
1:C:8:ALA:HB3	1:C:82:ALA:C	1.85	0.97
1:B:8:ALA:HB3	1:B:82:ALA:C	1.85	0.97
1:C:156:VAL:CB	1:C:191:ALA:O	2.13	0.97
1:A:37:ARG:HG2	1:A:37:ARG:O	1.65	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:THR:CG2	1:C:72:ARG:NH1	2.28	0.97
1:B:37:ARG:O	1:B:37:ARG:HG2	1.65	0.97
1:F:8:ALA:HB3	1:F:82:ALA:C	1.85	0.96
1:E:8:ALA:HB3	1:E:82:ALA:C	1.85	0.96
1:D:72:ARG:NH1	1:F:171:THR:CG2	2.27	0.96
1:B:171:THR:HG23	1:C:72:ARG:HH12	1.23	0.96
1:A:156:VAL:CB	1:A:191:ALA:O	2.13	0.96
1:B:156:VAL:CB	1:B:191:ALA:O	2.13	0.96
1:A:8:ALA:HB3	1:A:82:ALA:C	1.85	0.96
1:E:37:ARG:O	1:E:37:ARG:HG2	1.65	0.96
1:C:222:PRO:HD3	1:C:242:PRO:CD	1.95	0.95
1:A:222:PRO:HD3	1:A:242:PRO:CD	1.95	0.95
1:B:222:PRO:HD3	1:B:242:PRO:CD	1.95	0.95
1:E:156:VAL:CB	1:E:191:ALA:O	2.13	0.95
1:E:222:PRO:HD3	1:E:242:PRO:CD	1.95	0.95
1:D:37:ARG:O	1:D:37:ARG:HG2	1.65	0.95
1:F:156:VAL:CB	1:F:191:ALA:O	2.13	0.95
1:D:156:VAL:HG21	1:D:217:LEU:HG	1.44	0.95
1:D:156:VAL:CB	1:D:191:ALA:O	2.13	0.95
1:F:222:PRO:HD3	1:F:242:PRO:CD	1.95	0.95
1:F:37:ARG:O	1:F:37:ARG:HG2	1.65	0.95
1:A:156:VAL:HG21	1:A:217:LEU:HG	1.44	0.95
1:D:8:ALA:HB3	1:D:82:ALA:C	1.85	0.95
1:E:222:PRO:CD	1:E:242:PRO:HG2	1.97	0.94
1:C:222:PRO:CD	1:C:242:PRO:HG2	1.97	0.94
1:D:222:PRO:HD3	1:D:242:PRO:CD	1.95	0.94
1:C:37:ARG:O	1:C:37:ARG:HG2	1.65	0.94
1:A:222:PRO:CD	1:A:242:PRO:HG2	1.97	0.94
1:F:150:ASP:O	1:F:197:LEU:CD2	2.16	0.94
1:E:171:THR:HG23	1:F:72:ARG:NH1	1.82	0.94
1:F:156:VAL:CG2	1:F:217:LEU:HG	1.98	0.94
1:F:222:PRO:CD	1:F:242:PRO:HG2	1.97	0.94
1:E:133:LEU:HG	1:E:183:LEU:HD11	1.50	0.94
1:C:150:ASP:O	1:C:197:LEU:CD2	2.16	0.94
1:D:222:PRO:CD	1:D:242:PRO:HG2	1.97	0.93
1:B:133:LEU:HG	1:B:183:LEU:HD11	1.50	0.93
1:D:156:VAL:CG2	1:D:217:LEU:HG	1.98	0.93
1:C:156:VAL:CG2	1:C:217:LEU:HG	1.98	0.93
1:A:156:VAL:CG2	1:A:217:LEU:HG	1.98	0.93
1:B:150:ASP:O	1:B:197:LEU:CD2	2.16	0.93
1:B:222:PRO:CD	1:B:242:PRO:HG2	1.97	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:194:LEU:HD23	1:F:245:GLN:HG3	1.51	0.93
1:A:72:ARG:NH1	1:C:171:THR:HG23	1.83	0.93
1:E:171:THR:CG2	1:F:72:ARG:NH1	2.32	0.93
1:D:171:THR:HG23	1:E:72:ARG:NH1	1.83	0.93
1:A:133:LEU:HG	1:A:183:LEU:HD11	1.50	0.93
1:A:146:ASP:HA	1:A:197:LEU:HD11	1.51	0.93
1:A:72:ARG:NH1	1:C:171:THR:CG2	2.32	0.93
1:C:133:LEU:HG	1:C:183:LEU:HD11	1.50	0.93
1:A:150:ASP:O	1:A:197:LEU:CD2	2.16	0.93
1:E:156:VAL:CG2	1:E:217:LEU:HG	1.98	0.93
1:C:194:LEU:HD23	1:C:245:GLN:HG3	1.51	0.92
1:B:227:TYR:O	1:B:235:THR:HA	1.69	0.92
1:C:227:TYR:O	1:C:235:THR:HA	1.69	0.92
1:A:227:TYR:O	1:A:235:THR:HA	1.69	0.92
1:D:227:TYR:O	1:D:235:THR:HA	1.70	0.92
1:A:171:THR:HG23	1:B:72:ARG:HH12	1.33	0.92
1:D:194:LEU:HD23	1:D:245:GLN:HG3	1.51	0.92
1:F:95:ARG:O	1:F:109:ALA:CA	2.18	0.92
1:B:156:VAL:CG2	1:B:217:LEU:HG	1.98	0.92
1:E:95:ARG:O	1:E:109:ALA:CA	2.18	0.92
1:A:72:ARG:HH12	1:C:171:THR:HG23	1.31	0.91
1:F:133:LEU:HG	1:F:183:LEU:HD11	1.50	0.91
1:A:95:ARG:O	1:A:109:ALA:CA	2.18	0.91
1:E:194:LEU:HD23	1:E:245:GLN:HG3	1.51	0.91
1:F:227:TYR:O	1:F:235:THR:HA	1.69	0.91
1:C:95:ARG:O	1:C:109:ALA:CA	2.18	0.91
1:A:194:LEU:HD23	1:A:245:GLN:HG3	1.51	0.91
1:B:194:LEU:HD23	1:B:245:GLN:HG3	1.51	0.91
1:E:150:ASP:O	1:E:197:LEU:CD2	2.16	0.91
1:B:33:SER:CB	1:B:51:LEU:O	2.19	0.91
1:D:150:ASP:O	1:D:197:LEU:CD2	2.16	0.91
1:D:146:ASP:HA	1:D:197:LEU:HD11	1.51	0.91
1:C:33:SER:CB	1:C:51:LEU:O	2.19	0.91
1:C:146:ASP:HA	1:C:197:LEU:HD11	1.51	0.91
1:D:33:SER:CB	1:D:51:LEU:O	2.19	0.91
1:E:146:ASP:HA	1:E:197:LEU:HD11	1.51	0.90
1:E:227:TYR:O	1:E:235:THR:HA	1.69	0.90
1:D:133:LEU:HG	1:D:183:LEU:HD11	1.50	0.90
1:A:171:THR:HG23	1:B:72:ARG:NH1	1.85	0.90
1:D:21:LEU:HB3	1:D:40:ASP:HB3	1.54	0.90
1:E:33:SER:CB	1:E:51:LEU:O	2.19	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:153:ARG:O	1:E:165:ILE:HA	1.72	0.90
1:A:33:SER:CB	1:A:51:LEU:O	2.19	0.90
1:B:146:ASP:HA	1:B:197:LEU:HD11	1.51	0.90
1:A:153:ARG:O	1:A:165:ILE:HA	1.72	0.90
1:A:108:LEU:HD22	1:A:110:LEU:HD23	1.54	0.90
1:D:133:LEU:HG	1:D:183:LEU:CD1	2.02	0.90
1:B:153:ARG:O	1:B:165:ILE:HA	1.72	0.90
1:C:108:LEU:HD22	1:C:110:LEU:HD23	1.54	0.90
1:F:146:ASP:HA	1:F:197:LEU:HD11	1.51	0.89
1:E:6:VAL:HG22	1:E:56:PHE:HD2	1.38	0.89
1:A:21:LEU:HB3	1:A:40:ASP:HB3	1.54	0.89
1:A:6:VAL:HG22	1:A:56:PHE:HD2	1.37	0.89
1:A:171:THR:CG2	1:B:72:ARG:NH1	2.34	0.89
1:E:133:LEU:HG	1:E:183:LEU:CD1	2.02	0.89
1:F:21:LEU:HB3	1:F:40:ASP:HB3	1.54	0.89
1:E:21:LEU:HB3	1:E:40:ASP:HB3	1.54	0.89
1:F:133:LEU:HG	1:F:183:LEU:CD1	2.02	0.89
1:C:6:VAL:HG22	1:C:56:PHE:HD2	1.37	0.89
1:A:133:LEU:HG	1:A:183:LEU:CD1	2.02	0.89
1:F:33:SER:CB	1:F:51:LEU:O	2.19	0.89
1:F:108:LEU:HD22	1:F:110:LEU:HD23	1.54	0.89
1:D:95:ARG:O	1:D:109:ALA:CA	2.18	0.89
1:D:72:ARG:HH12	1:F:171:THR:HG21	1.35	0.88
1:F:8:ALA:N	1:F:84:ASP:O	2.06	0.88
1:C:153:ARG:O	1:C:165:ILE:HA	1.72	0.88
1:A:173:ASP:HB2	1:B:107:THR:CG2	2.02	0.88
1:D:153:ARG:O	1:D:165:ILE:HA	1.72	0.88
1:C:133:LEU:HG	1:C:183:LEU:CD1	2.02	0.88
1:B:6:VAL:HG22	1:B:56:PHE:HD2	1.37	0.88
1:B:142:ILE:HD13	1:B:152:ILE:HD12	1.56	0.88
1:F:153:ARG:O	1:F:165:ILE:HA	1.72	0.88
1:D:171:THR:CG2	1:E:72:ARG:NH1	2.35	0.88
1:B:173:ASP:HB2	1:C:107:THR:CG2	2.03	0.88
1:D:8:ALA:N	1:D:84:ASP:O	2.06	0.88
1:E:108:LEU:HD22	1:E:110:LEU:HD23	1.54	0.88
1:B:133:LEU:HG	1:B:183:LEU:CD1	2.02	0.88
1:F:213:VAL:HG22	1:F:227:TYR:CZ	2.09	0.88
1:D:170:ASP:O	1:D:171:THR:HG22	1.74	0.88
1:D:6:VAL:HG22	1:D:56:PHE:HD2	1.38	0.88
1:C:170:ASP:O	1:C:171:THR:HG22	1.74	0.88
1:C:213:VAL:HG22	1:C:227:TYR:CZ	2.09	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:ALA:N	1:B:84:ASP:O	2.06	0.88
1:B:95:ARG:O	1:B:109:ALA:CA	2.18	0.87
1:B:21:LEU:HB3	1:B:40:ASP:HB3	1.54	0.87
1:F:142:ILE:HD13	1:F:152:ILE:HD12	1.56	0.87
1:D:108:LEU:HD22	1:D:110:LEU:HD23	1.54	0.87
1:A:107:THR:CG2	1:C:173:ASP:HB2	2.04	0.87
1:A:213:VAL:HG22	1:A:227:TYR:CZ	2.09	0.87
1:C:142:ILE:HD13	1:C:152:ILE:HD12	1.56	0.87
1:E:213:VAL:HG22	1:E:227:TYR:CZ	2.09	0.87
1:A:8:ALA:N	1:A:84:ASP:O	2.06	0.87
1:E:152:ILE:CG2	1:E:165:ILE:HG23	2.05	0.87
1:B:213:VAL:HG22	1:B:227:TYR:CZ	2.09	0.87
1:C:8:ALA:N	1:C:84:ASP:O	2.06	0.87
1:B:170:ASP:O	1:B:171:THR:HG22	1.74	0.87
1:F:152:ILE:CG2	1:F:165:ILE:HG23	2.05	0.87
1:A:170:ASP:O	1:A:171:THR:HG22	1.74	0.87
1:E:8:ALA:N	1:E:84:ASP:O	2.06	0.86
1:C:152:ILE:CG2	1:C:165:ILE:HG23	2.05	0.86
1:E:142:ILE:HD13	1:E:152:ILE:HD12	1.56	0.86
1:E:146:ASP:HA	1:E:197:LEU:CD1	2.05	0.86
1:D:213:VAL:HG22	1:D:227:TYR:CZ	2.09	0.86
1:B:152:ILE:CG2	1:B:165:ILE:HG23	2.05	0.86
1:C:146:ASP:HA	1:C:197:LEU:CD1	2.05	0.86
1:B:146:ASP:HA	1:B:197:LEU:CD1	2.05	0.86
1:B:108:LEU:HD22	1:B:110:LEU:HD23	1.54	0.86
1:A:152:ILE:CG2	1:A:165:ILE:HG23	2.05	0.86
1:F:222:PRO:HD3	1:F:242:PRO:HD2	1.58	0.86
1:D:173:ASP:HB2	1:E:107:THR:CG2	2.05	0.86
1:A:222:PRO:HD3	1:A:242:PRO:HD2	1.58	0.86
1:D:146:ASP:HA	1:D:197:LEU:CD1	2.05	0.86
1:C:21:LEU:HB3	1:C:40:ASP:HB3	1.54	0.86
1:F:6:VAL:HG22	1:F:56:PHE:HD2	1.37	0.86
1:D:152:ILE:CG2	1:D:165:ILE:HG23	2.05	0.86
1:A:146:ASP:HA	1:A:197:LEU:CD1	2.05	0.86
1:C:152:ILE:CG2	1:C:165:ILE:CG2	2.54	0.86
1:F:170:ASP:O	1:F:171:THR:HG22	1.74	0.85
1:C:222:PRO:HD3	1:C:242:PRO:HD2	1.58	0.85
1:B:152:ILE:CG2	1:B:165:ILE:CG2	2.54	0.85
1:E:170:ASP:O	1:E:171:THR:HG22	1.74	0.85
1:D:142:ILE:HD13	1:D:152:ILE:HD12	1.56	0.85
1:D:152:ILE:CG2	1:D:165:ILE:CG2	2.54	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:146:ASP:HA	1:F:197:LEU:CD1	2.05	0.85
1:E:173:ASP:HB2	1:F:107:THR:CG2	2.06	0.85
1:A:152:ILE:CG2	1:A:165:ILE:CG2	2.54	0.84
1:F:152:ILE:CG2	1:F:165:ILE:CG2	2.54	0.84
1:E:129:ALA:HB1	1:E:156:VAL:HG11	1.59	0.84
1:A:142:ILE:HD13	1:A:152:ILE:HD12	1.56	0.84
1:E:152:ILE:CG2	1:E:165:ILE:CG2	2.54	0.84
1:F:135:GLY:N	1:F:211:ALA:O	2.10	0.84
1:B:129:ALA:HB1	1:B:156:VAL:HG11	1.59	0.84
1:C:135:GLY:N	1:C:211:ALA:O	2.10	0.84
1:E:135:GLY:N	1:E:211:ALA:O	2.10	0.84
1:A:129:ALA:HB1	1:A:156:VAL:HG11	1.59	0.84
1:C:34:LEU:O	1:C:51:LEU:HB2	1.78	0.84
1:A:34:LEU:O	1:A:51:LEU:HB2	1.78	0.84
1:F:34:LEU:O	1:F:51:LEU:HB2	1.78	0.83
1:E:222:PRO:HD3	1:E:242:PRO:HD2	1.58	0.83
1:A:135:GLY:N	1:A:211:ALA:O	2.10	0.83
1:B:222:PRO:HD3	1:B:242:PRO:HD2	1.58	0.83
1:D:8:ALA:CB	1:D:81:GLY:O	2.27	0.83
1:D:34:LEU:O	1:D:51:LEU:HB2	1.78	0.83
1:E:33:SER:HB2	1:E:51:LEU:O	1.79	0.83
1:D:135:GLY:N	1:D:211:ALA:O	2.10	0.83
1:B:135:GLY:N	1:B:211:ALA:O	2.10	0.83
1:A:72:ARG:HH12	1:C:171:THR:HG21	1.42	0.83
1:D:129:ALA:HB1	1:D:156:VAL:HG11	1.59	0.82
1:B:8:ALA:CB	1:B:81:GLY:O	2.27	0.82
1:C:8:ALA:CB	1:C:81:GLY:O	2.27	0.82
1:D:213:VAL:HG22	1:D:227:TYR:OH	1.80	0.82
1:A:213:VAL:HG22	1:A:227:TYR:OH	1.80	0.82
1:D:222:PRO:HD3	1:D:242:PRO:HD2	1.58	0.82
1:E:8:ALA:CB	1:E:81:GLY:O	2.27	0.82
1:B:33:SER:HB2	1:B:51:LEU:O	1.79	0.82
1:C:129:ALA:HB1	1:C:156:VAL:HG11	1.59	0.82
1:F:129:ALA:HB1	1:F:156:VAL:HG11	1.59	0.82
1:A:8:ALA:CB	1:A:81:GLY:O	2.27	0.82
1:E:34:LEU:O	1:E:51:LEU:HB2	1.78	0.82
1:C:213:VAL:HG22	1:C:227:TYR:OH	1.80	0.81
1:B:34:LEU:O	1:B:51:LEU:HB2	1.78	0.81
1:D:9:ALA:HB2	1:D:82:ALA:HB1	1.63	0.81
1:B:222:PRO:HB3	1:B:239:MET:HG2	1.61	0.81
1:C:222:PRO:HB3	1:C:239:MET:HG2	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:PRO:HB3	1:A:239:MET:HG2	1.61	0.81
1:F:33:SER:HB2	1:F:51:LEU:O	1.79	0.81
1:C:166:GLU:HB3	1:C:175:ASP:HA	1.63	0.81
1:F:213:VAL:HG22	1:F:227:TYR:OH	1.80	0.81
1:F:9:ALA:HB2	1:F:82:ALA:HB1	1.63	0.81
1:B:213:VAL:HG22	1:B:227:TYR:OH	1.80	0.81
1:E:171:THR:HG21	1:F:72:ARG:HH12	1.42	0.81
1:F:166:GLU:HB3	1:F:175:ASP:HA	1.63	0.81
1:D:151:HIS:HA	1:D:197:LEU:H	1.46	0.81
1:A:171:THR:HG21	1:B:72:ARG:HH12	1.46	0.81
1:B:152:ILE:HG23	1:B:165:ILE:HG22	1.63	0.81
1:F:222:PRO:HB3	1:F:239:MET:HG2	1.61	0.81
1:E:222:PRO:HB3	1:E:239:MET:HG2	1.61	0.81
1:D:33:SER:HB2	1:D:51:LEU:O	1.79	0.81
1:C:136:THR:HB	1:C:209:THR:HA	1.63	0.81
1:E:213:VAL:HG22	1:E:227:TYR:OH	1.80	0.80
1:E:166:GLU:HB3	1:E:175:ASP:HA	1.63	0.80
1:D:107:THR:CG2	1:F:173:ASP:HB2	2.12	0.80
1:C:33:SER:HB2	1:C:51:LEU:O	1.79	0.80
1:B:171:THR:HG21	1:C:72:ARG:HH12	1.43	0.80
1:A:33:SER:HB2	1:A:51:LEU:O	1.79	0.80
1:E:152:ILE:HG23	1:E:165:ILE:HG22	1.63	0.80
1:C:229:ILE:HD11	1:C:236:ILE:HD11	1.63	0.80
1:F:152:ILE:HG23	1:F:165:ILE:HG22	1.63	0.80
1:E:136:THR:HB	1:E:209:THR:HA	1.63	0.80
1:D:222:PRO:HB3	1:D:239:MET:HG2	1.61	0.80
1:E:195:PHE:HB3	1:E:240:LEU:HD22	1.64	0.80
1:F:8:ALA:CB	1:F:81:GLY:O	2.27	0.80
1:C:195:PHE:HB3	1:C:240:LEU:HD22	1.64	0.80
1:D:166:GLU:HB3	1:D:175:ASP:HA	1.63	0.80
1:F:229:ILE:HD11	1:F:236:ILE:HD11	1.63	0.79
1:D:195:PHE:HB3	1:D:240:LEU:HD22	1.64	0.79
1:B:9:ALA:HB2	1:B:82:ALA:HB1	1.63	0.79
1:A:229:ILE:HD11	1:A:236:ILE:HD11	1.63	0.79
1:F:195:PHE:HB3	1:F:240:LEU:HD22	1.64	0.79
1:D:152:ILE:HG23	1:D:165:ILE:HG22	1.63	0.79
1:F:4:ALA:O	1:F:87:HIS:HA	1.83	0.79
1:B:166:GLU:HB3	1:B:175:ASP:HA	1.63	0.79
1:B:136:THR:HB	1:B:209:THR:HA	1.63	0.79
1:E:9:ALA:HB2	1:E:82:ALA:HB1	1.63	0.79
1:E:4:ALA:O	1:E:87:HIS:HA	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:ILE:HG23	1:C:165:ILE:HG22	1.63	0.79
1:A:152:ILE:HG23	1:A:165:ILE:HG22	1.63	0.79
1:A:9:ALA:HB2	1:A:82:ALA:HB1	1.63	0.79
1:C:9:ALA:HB2	1:C:82:ALA:HB1	1.63	0.79
1:D:136:THR:HB	1:D:209:THR:HA	1.63	0.79
1:B:151:HIS:HA	1:B:197:LEU:H	1.46	0.79
1:C:4:ALA:O	1:C:87:HIS:HA	1.83	0.79
1:D:229:ILE:HD11	1:D:236:ILE:HD11	1.63	0.79
1:C:151:HIS:HA	1:C:197:LEU:H	1.46	0.79
1:F:136:THR:HB	1:F:209:THR:HA	1.63	0.79
1:F:151:HIS:HA	1:F:197:LEU:H	1.46	0.78
1:B:4:ALA:O	1:B:87:HIS:HA	1.83	0.78
1:D:4:ALA:O	1:D:87:HIS:HA	1.83	0.78
1:A:151:HIS:HA	1:A:197:LEU:H	1.46	0.78
1:B:204:ASN:HA	1:B:207:ILE:HD13	1.65	0.78
1:A:4:ALA:O	1:A:87:HIS:HA	1.83	0.78
1:A:166:GLU:HB3	1:A:175:ASP:HA	1.63	0.78
1:A:136:THR:HB	1:A:209:THR:HA	1.63	0.78
1:B:229:ILE:HD11	1:B:236:ILE:HD11	1.63	0.78
1:A:195:PHE:HB3	1:A:240:LEU:HD22	1.64	0.78
1:B:195:PHE:HB3	1:B:240:LEU:HD22	1.64	0.78
1:D:171:THR:HG21	1:E:72:ARG:HH12	1.47	0.78
1:B:171:THR:O	1:B:172:ASP:OD1	2.02	0.78
1:D:204:ASN:HA	1:D:207:ILE:HD13	1.66	0.78
1:F:204:ASN:HA	1:F:207:ILE:HD13	1.66	0.78
1:C:149:SER:CB	1:C:167:ALA:CB	2.49	0.78
1:C:171:THR:O	1:C:172:ASP:OD1	2.02	0.78
1:F:171:THR:O	1:F:172:ASP:OD1	2.02	0.78
1:A:171:THR:O	1:A:172:ASP:OD1	2.02	0.78
1:E:1:MET:HG3	1:E:91:ASP:CB	2.14	0.77
1:E:151:HIS:HA	1:E:197:LEU:H	1.46	0.77
1:E:229:ILE:HD11	1:E:236:ILE:HD11	1.63	0.77
1:F:1:MET:HG3	1:F:91:ASP:CB	2.14	0.77
1:D:157:ASP:O	1:D:157:ASP:CG	2.23	0.77
1:A:1:MET:HG3	1:A:91:ASP:CB	2.14	0.77
1:C:204:ASN:HA	1:C:207:ILE:HD13	1.66	0.77
1:D:1:MET:HG3	1:D:91:ASP:CB	2.14	0.77
1:B:1:MET:HG3	1:B:91:ASP:CB	2.14	0.77
1:D:20:VAL:HG13	1:D:202:ASP:HB3	1.67	0.77
1:C:1:MET:HG3	1:C:91:ASP:CB	2.14	0.77
1:A:39:VAL:CG1	1:A:43:ASN:HA	2.15	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:157:ASP:O	1:C:157:ASP:CG	2.23	0.77
1:A:20:VAL:HG13	1:A:202:ASP:HB3	1.67	0.77
1:C:39:VAL:CG1	1:C:43:ASN:HA	2.15	0.77
1:F:151:HIS:HB3	1:F:196:SER:HA	1.67	0.77
1:E:20:VAL:HG13	1:E:202:ASP:HB3	1.67	0.76
1:E:157:ASP:O	1:E:157:ASP:CG	2.23	0.76
1:D:171:THR:O	1:D:172:ASP:OD1	2.02	0.76
1:E:204:ASN:HA	1:E:207:ILE:HD13	1.66	0.76
1:E:39:VAL:CG1	1:E:43:ASN:HA	2.15	0.76
1:E:171:THR:O	1:E:172:ASP:OD1	2.02	0.76
1:A:151:HIS:HB3	1:A:196:SER:HA	1.67	0.76
1:A:8:ALA:CB	1:A:82:ALA:O	2.25	0.76
1:A:204:ASN:HA	1:A:207:ILE:HD13	1.65	0.76
1:B:3:LYS:O	1:B:58:SER:O	2.04	0.76
1:B:39:VAL:CG1	1:B:43:ASN:HA	2.15	0.76
1:F:3:LYS:O	1:F:58:SER:O	2.04	0.76
1:F:39:VAL:CG1	1:F:43:ASN:HA	2.15	0.76
1:F:157:ASP:CG	1:F:157:ASP:O	2.23	0.76
1:D:39:VAL:CG1	1:D:43:ASN:HA	2.15	0.76
1:B:157:ASP:O	1:B:157:ASP:CG	2.23	0.76
1:E:3:LYS:O	1:E:58:SER:O	2.04	0.76
1:E:25:CYS:SG	1:E:70:LEU:HG	2.26	0.75
1:E:151:HIS:HB3	1:E:196:SER:HA	1.68	0.75
1:C:3:LYS:O	1:C:58:SER:O	2.04	0.75
1:A:25:CYS:SG	1:A:70:LEU:HG	2.26	0.75
1:E:8:ALA:CB	1:E:82:ALA:O	2.26	0.75
1:B:8:ALA:CB	1:B:82:ALA:O	2.25	0.75
1:D:5:ILE:HG22	1:D:85:LEU:HB3	1.68	0.75
1:C:20:VAL:HG13	1:C:202:ASP:HB3	1.67	0.75
1:B:151:HIS:HB3	1:B:196:SER:HA	1.67	0.75
1:F:20:VAL:HG13	1:F:202:ASP:HB3	1.67	0.75
1:C:151:HIS:HB3	1:C:196:SER:HA	1.67	0.75
1:C:5:ILE:HG22	1:C:85:LEU:HB3	1.68	0.75
1:F:26:LYS:HE2	1:F:113:PRO:O	1.87	0.75
1:C:214:THR:OG1	1:C:226:HIS:HB2	1.87	0.75
1:F:191:ALA:CB	1:F:218:GLY:HA2	2.17	0.75
1:B:20:VAL:HG13	1:B:202:ASP:HB3	1.67	0.75
1:D:240:LEU:HD23	1:D:241:ALA:O	1.87	0.75
1:C:29:LEU:HD23	1:C:34:LEU:HD13	1.69	0.75
1:A:3:LYS:O	1:A:58:SER:O	2.04	0.75
1:F:29:LEU:HD23	1:F:34:LEU:HD13	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:ILE:HG22	1:B:85:LEU:HB3	1.68	0.75
1:F:5:ILE:HG22	1:F:85:LEU:HB3	1.68	0.75
1:B:240:LEU:HD23	1:B:241:ALA:O	1.87	0.74
1:F:25:CYS:SG	1:F:70:LEU:HG	2.26	0.74
1:A:108:LEU:HD22	1:A:110:LEU:CD2	2.17	0.74
1:D:25:CYS:SG	1:D:70:LEU:HG	2.26	0.74
1:F:214:THR:OG1	1:F:226:HIS:HB2	1.87	0.74
1:D:29:LEU:HD23	1:D:34:LEU:HD13	1.69	0.74
1:D:3:LYS:O	1:D:58:SER:O	2.04	0.74
1:C:240:LEU:HD23	1:C:241:ALA:O	1.87	0.74
1:C:191:ALA:CB	1:C:218:GLY:HA2	2.17	0.74
1:C:26:LYS:HE2	1:C:113:PRO:O	1.87	0.74
1:A:157:ASP:O	1:A:157:ASP:CG	2.23	0.74
1:D:214:THR:OG1	1:D:226:HIS:HB2	1.87	0.74
1:D:149:SER:CB	1:D:167:ALA:CB	2.49	0.74
1:E:108:LEU:HD22	1:E:110:LEU:CD2	2.17	0.74
1:E:240:LEU:HD23	1:E:241:ALA:O	1.87	0.74
1:D:191:ALA:CB	1:D:218:GLY:HA2	2.17	0.74
1:E:26:LYS:HE2	1:E:113:PRO:O	1.87	0.74
1:D:197:LEU:HA	1:D:200:LEU:HD12	1.70	0.74
1:B:25:CYS:SG	1:B:70:LEU:HG	2.26	0.74
1:E:29:LEU:HD23	1:E:34:LEU:HD13	1.69	0.74
1:F:108:LEU:HD22	1:F:110:LEU:CD2	2.17	0.74
1:A:96:LYS:CA	1:A:108:LEU:O	2.35	0.74
1:C:25:CYS:SG	1:C:70:LEU:HG	2.26	0.74
1:A:197:LEU:HA	1:A:200:LEU:HD12	1.70	0.74
1:C:197:LEU:HA	1:C:200:LEU:HD12	1.70	0.74
1:F:240:LEU:HD23	1:F:241:ALA:O	1.87	0.74
1:C:6:VAL:HG22	1:C:56:PHE:CD2	2.23	0.74
1:B:108:LEU:HD22	1:B:110:LEU:CD2	2.17	0.74
1:E:214:THR:OG1	1:E:226:HIS:HB2	1.87	0.74
1:A:29:LEU:HD23	1:A:34:LEU:HD13	1.69	0.74
1:D:108:LEU:HD22	1:D:110:LEU:CD2	2.17	0.74
1:D:6:VAL:HG22	1:D:56:PHE:CD2	2.23	0.74
1:B:197:LEU:HA	1:B:200:LEU:HD12	1.70	0.73
1:A:191:ALA:CB	1:A:218:GLY:HA2	2.17	0.73
1:B:214:THR:OG1	1:B:226:HIS:HB2	1.87	0.73
1:E:191:ALA:CB	1:E:218:GLY:HA2	2.17	0.73
1:D:151:HIS:HB3	1:D:196:SER:HA	1.68	0.73
1:B:191:ALA:CB	1:B:218:GLY:HA2	2.17	0.73
1:E:5:ILE:HG22	1:E:85:LEU:HB3	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:LYS:HE2	1:B:113:PRO:O	1.87	0.73
1:D:96:LYS:CA	1:D:108:LEU:O	2.35	0.73
1:D:26:LYS:HE2	1:D:113:PRO:O	1.87	0.73
1:A:6:VAL:HG22	1:A:56:PHE:CD2	2.23	0.73
1:A:26:LYS:HE2	1:A:113:PRO:O	1.87	0.73
1:E:1:MET:HG3	1:E:91:ASP:HB3	1.70	0.73
1:A:214:THR:OG1	1:A:226:HIS:HB2	1.87	0.73
1:B:1:MET:HG3	1:B:91:ASP:HB3	1.70	0.73
1:D:8:ALA:CB	1:D:82:ALA:O	2.26	0.73
1:C:8:ALA:CB	1:C:82:ALA:O	2.25	0.73
1:A:240:LEU:HD23	1:A:241:ALA:O	1.87	0.72
1:F:197:LEU:HA	1:F:200:LEU:HD12	1.70	0.72
1:C:108:LEU:HD22	1:C:110:LEU:CD2	2.17	0.72
1:F:8:ALA:CB	1:F:82:ALA:O	2.25	0.72
1:E:101:ILE:HD11	1:E:104:LEU:HD12	1.71	0.72
1:E:197:LEU:HA	1:E:200:LEU:HD12	1.70	0.72
1:E:6:VAL:HG22	1:E:56:PHE:CD2	2.23	0.72
1:B:96:LYS:CA	1:B:108:LEU:O	2.35	0.72
1:B:29:LEU:HD23	1:B:34:LEU:HD13	1.69	0.72
1:A:5:ILE:HG22	1:A:85:LEU:HB3	1.68	0.72
1:A:104:LEU:HD21	1:C:174:VAL:HG23	1.72	0.72
1:D:101:ILE:HD11	1:D:104:LEU:HD12	1.71	0.72
1:C:1:MET:HG3	1:C:91:ASP:HB3	1.70	0.72
1:B:101:ILE:HD11	1:B:104:LEU:HD12	1.71	0.72
1:F:96:LYS:CA	1:F:108:LEU:O	2.35	0.72
1:D:1:MET:HG3	1:D:91:ASP:HB3	1.70	0.72
1:A:101:ILE:HD11	1:A:104:LEU:HD12	1.71	0.72
1:E:96:LYS:CA	1:E:108:LEU:O	2.35	0.72
1:A:1:MET:HG3	1:A:91:ASP:HB3	1.70	0.72
1:A:197:LEU:HD23	1:A:198:ASP:H	1.55	0.71
1:B:197:LEU:HD23	1:B:198:ASP:H	1.55	0.71
1:C:104:LEU:HD13	1:C:104:LEU:O	1.90	0.71
1:E:104:LEU:HD13	1:E:104:LEU:O	1.90	0.71
1:C:29:LEU:HA	1:C:34:LEU:HB3	1.73	0.71
1:C:101:ILE:HD11	1:C:104:LEU:HD12	1.71	0.71
1:C:191:ALA:CB	1:C:218:GLY:CA	2.69	0.71
1:F:197:LEU:HD23	1:F:198:ASP:H	1.55	0.71
1:B:142:ILE:HD13	1:B:152:ILE:CD1	2.21	0.71
1:D:142:ILE:HD13	1:D:152:ILE:CD1	2.21	0.71
1:D:29:LEU:HA	1:D:34:LEU:HB3	1.73	0.71
1:B:104:LEU:HD13	1:B:104:LEU:O	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:142:ILE:HD13	1:C:152:ILE:CD1	2.21	0.71
1:D:197:LEU:HD23	1:D:198:ASP:H	1.55	0.71
1:F:191:ALA:HB1	1:F:218:GLY:CA	2.21	0.71
1:D:191:ALA:HB1	1:D:218:GLY:CA	2.21	0.71
1:E:191:ALA:HB1	1:E:218:GLY:CA	2.21	0.71
1:F:101:ILE:HD11	1:F:104:LEU:HD12	1.71	0.71
1:A:142:ILE:HD13	1:A:152:ILE:CD1	2.21	0.71
1:B:6:VAL:HG22	1:B:56:PHE:CD2	2.23	0.71
1:B:29:LEU:HA	1:B:34:LEU:HB3	1.73	0.71
1:D:191:ALA:CB	1:D:218:GLY:CA	2.69	0.71
1:A:191:ALA:HB1	1:A:218:GLY:CA	2.21	0.71
1:D:229:ILE:HD11	1:D:236:ILE:CD1	2.21	0.71
1:C:229:ILE:HD11	1:C:236:ILE:CD1	2.21	0.71
1:E:29:LEU:HA	1:E:34:LEU:HB3	1.73	0.71
1:B:191:ALA:HB1	1:B:218:GLY:CA	2.21	0.70
1:B:155:ARG:HA	1:B:192:ASP:HB2	1.73	0.70
1:E:142:ILE:HD13	1:E:152:ILE:CD1	2.21	0.70
1:F:104:LEU:O	1:F:104:LEU:HD13	1.90	0.70
1:F:155:ARG:HA	1:F:192:ASP:HB2	1.73	0.70
1:F:229:ILE:HD11	1:F:236:ILE:CD1	2.21	0.70
1:A:104:LEU:HD13	1:A:104:LEU:O	1.90	0.70
1:B:191:ALA:CB	1:B:218:GLY:CA	2.69	0.70
1:F:191:ALA:CB	1:F:218:GLY:CA	2.69	0.70
1:A:29:LEU:HA	1:A:34:LEU:HB3	1.73	0.70
1:C:125:LEU:HD12	1:C:224:LYS:HE3	1.74	0.70
1:F:142:ILE:HD13	1:F:152:ILE:CD1	2.21	0.70
1:C:155:ARG:HA	1:C:192:ASP:HB2	1.73	0.70
1:B:229:ILE:HD11	1:B:236:ILE:CD1	2.21	0.70
1:A:174:VAL:HG23	1:B:104:LEU:HD21	1.73	0.70
1:F:138:LEU:HG	1:F:213:VAL:HG11	1.74	0.70
1:E:155:ARG:HA	1:E:192:ASP:HB2	1.73	0.70
1:E:191:ALA:CB	1:E:218:GLY:CA	2.69	0.70
1:A:229:ILE:HD11	1:A:236:ILE:CD1	2.21	0.70
1:D:138:LEU:HG	1:D:213:VAL:HG11	1.74	0.70
1:F:125:LEU:HD12	1:F:224:LYS:HE3	1.73	0.70
1:F:1:MET:HG3	1:F:91:ASP:HB3	1.70	0.70
1:D:104:LEU:O	1:D:104:LEU:HD13	1.90	0.70
1:E:229:ILE:HD11	1:E:236:ILE:CD1	2.21	0.70
1:B:138:LEU:HG	1:B:213:VAL:HG11	1.74	0.70
1:F:29:LEU:HA	1:F:34:LEU:HB3	1.73	0.70
1:A:155:ARG:HA	1:A:192:ASP:HB2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:138:LEU:HG	1:C:213:VAL:HG11	1.74	0.70
1:F:6:VAL:HG22	1:F:56:PHE:CD2	2.23	0.70
1:A:191:ALA:CB	1:A:218:GLY:CA	2.69	0.69
1:A:125:LEU:HD12	1:A:224:LYS:HE3	1.74	0.69
1:E:197:LEU:HD23	1:E:198:ASP:H	1.55	0.69
1:B:125:LEU:HD12	1:B:224:LYS:HE3	1.74	0.69
1:C:191:ALA:HB1	1:C:218:GLY:CA	2.21	0.69
1:F:25:CYS:O	1:F:67:GLY:HA2	1.93	0.69
1:B:107:THR:HG23	1:B:107:THR:O	1.92	0.69
1:A:33:SER:HB3	1:A:51:LEU:O	1.92	0.69
1:A:25:CYS:O	1:A:68:VAL:N	2.26	0.69
1:D:155:ARG:HA	1:D:192:ASP:HB2	1.73	0.69
1:C:197:LEU:HD23	1:C:198:ASP:H	1.55	0.69
1:F:215:VAL:HG12	1:F:223:VAL:HG21	1.75	0.69
1:E:107:THR:O	1:E:107:THR:HG23	1.92	0.69
1:E:215:VAL:HG12	1:E:223:VAL:HG21	1.75	0.69
1:D:107:THR:HG23	1:D:107:THR:O	1.92	0.69
1:C:33:SER:HB3	1:C:51:LEU:O	1.92	0.69
1:B:174:VAL:HG23	1:C:104:LEU:HD21	1.75	0.69
1:E:138:LEU:HG	1:E:213:VAL:HG11	1.74	0.69
1:B:215:VAL:HG12	1:B:223:VAL:HG21	1.75	0.69
1:F:107:THR:HG23	1:F:107:THR:O	1.92	0.69
1:D:104:LEU:HD21	1:F:174:VAL:HG23	1.73	0.69
1:A:25:CYS:O	1:A:67:GLY:HA2	1.93	0.69
1:D:25:CYS:O	1:D:67:GLY:HA2	1.93	0.69
1:C:107:THR:O	1:C:107:THR:HG23	1.92	0.69
1:C:25:CYS:O	1:C:68:VAL:N	2.26	0.69
1:E:33:SER:HB3	1:E:51:LEU:O	1.92	0.69
1:A:138:LEU:HG	1:A:213:VAL:HG11	1.73	0.69
1:E:20:VAL:HG21	1:E:202:ASP:O	1.93	0.69
1:C:20:VAL:HG21	1:C:202:ASP:O	1.93	0.69
1:F:98:ASN:HA	1:F:106:TYR:O	1.93	0.69
1:A:98:ASN:HA	1:A:106:TYR:O	1.93	0.69
1:B:25:CYS:O	1:B:67:GLY:HA2	1.93	0.69
1:A:20:VAL:HG21	1:A:202:ASP:O	1.93	0.69
1:F:33:SER:HB3	1:F:51:LEU:O	1.92	0.69
1:A:215:VAL:HG12	1:A:223:VAL:HG21	1.75	0.68
1:F:25:CYS:O	1:F:68:VAL:N	2.26	0.68
1:C:98:ASN:HA	1:C:106:TYR:O	1.93	0.68
1:E:125:LEU:HD12	1:E:224:LYS:HE3	1.73	0.68
1:D:153:ARG:HG2	1:D:194:LEU:CD2	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:LYS:CA	1:C:108:LEU:O	2.35	0.68
1:D:125:LEU:HD12	1:D:224:LYS:HE3	1.73	0.68
1:D:20:VAL:HG21	1:D:202:ASP:O	1.93	0.68
1:C:25:CYS:O	1:C:67:GLY:HA2	1.93	0.68
1:D:215:VAL:HG12	1:D:223:VAL:HG21	1.75	0.68
1:B:3:LYS:O	1:B:59:TYR:HA	1.94	0.68
1:D:33:SER:HB3	1:D:51:LEU:O	1.92	0.68
1:C:153:ARG:HG2	1:C:194:LEU:CD2	2.24	0.68
1:E:191:ALA:HB1	1:E:218:GLY:O	1.94	0.68
1:F:191:ALA:HB1	1:F:218:GLY:O	1.94	0.68
1:F:20:VAL:HG21	1:F:202:ASP:O	1.93	0.68
1:F:149:SER:CB	1:F:167:ALA:CB	2.49	0.68
1:A:153:ARG:HG2	1:A:194:LEU:CD2	2.24	0.68
1:F:153:ARG:HG2	1:F:194:LEU:CD2	2.24	0.68
1:E:25:CYS:O	1:E:67:GLY:HA2	1.93	0.67
1:B:20:VAL:HG21	1:B:202:ASP:O	1.93	0.67
1:C:191:ALA:HB1	1:C:218:GLY:O	1.94	0.67
1:E:25:CYS:O	1:E:68:VAL:N	2.26	0.67
1:A:107:THR:HG23	1:A:107:THR:O	1.92	0.67
1:A:3:LYS:O	1:A:59:TYR:HA	1.94	0.67
1:D:222:PRO:CD	1:D:242:PRO:CG	2.64	0.67
1:E:174:VAL:HG23	1:F:104:LEU:HD21	1.75	0.67
1:C:3:LYS:O	1:C:59:TYR:HA	1.94	0.67
1:E:3:LYS:O	1:E:59:TYR:HA	1.94	0.67
1:E:161:GLU:HB3	1:E:188:ALA:HB1	1.76	0.67
1:E:153:ARG:HG2	1:E:194:LEU:CD2	2.24	0.67
1:D:191:ALA:HB1	1:D:218:GLY:O	1.94	0.67
1:C:215:VAL:HG12	1:C:223:VAL:HG21	1.75	0.67
1:A:191:ALA:HB1	1:A:218:GLY:O	1.94	0.67
1:C:136:THR:HB	1:C:209:THR:HG22	1.77	0.67
1:B:136:THR:HB	1:B:209:THR:HG22	1.77	0.67
1:B:153:ARG:HG2	1:B:194:LEU:CD2	2.24	0.67
1:A:73:LEU:HD22	1:A:77:ALA:HB2	1.77	0.67
1:A:180:PRO:HA	1:A:186:ILE:HD11	1.77	0.67
1:B:191:ALA:HB1	1:B:218:GLY:O	1.94	0.67
1:B:4:ALA:O	1:B:86:ILE:O	2.13	0.67
1:C:161:GLU:HB3	1:C:188:ALA:HB1	1.76	0.67
1:D:98:ASN:HA	1:D:106:TYR:O	1.93	0.67
1:A:47:VAL:CA	1:A:237:THR:O	2.30	0.67
1:F:3:LYS:O	1:F:59:TYR:HA	1.94	0.67
1:E:136:THR:HB	1:E:209:THR:HG22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:HIS:HE1	1:D:185:SER:HA	1.60	0.67
1:D:180:PRO:HA	1:D:186:ILE:HD11	1.77	0.67
1:F:231:GLU:HB2	1:F:233:MET:CE	2.25	0.67
1:F:180:PRO:HA	1:F:186:ILE:HD11	1.77	0.67
1:F:207:ILE:HD12	1:F:207:ILE:N	2.10	0.67
1:A:161:GLU:HB3	1:A:188:ALA:HB1	1.76	0.67
1:E:47:VAL:CA	1:E:237:THR:O	2.30	0.67
1:B:33:SER:HB3	1:B:51:LEU:O	1.92	0.67
1:E:98:ASN:HA	1:E:106:TYR:O	1.93	0.66
1:A:207:ILE:N	1:A:207:ILE:HD12	2.10	0.66
1:D:47:VAL:CA	1:D:237:THR:O	2.30	0.66
1:C:180:PRO:HA	1:C:186:ILE:HD11	1.77	0.66
1:B:161:GLU:HB3	1:B:188:ALA:HB1	1.76	0.66
1:C:236:ILE:O	1:C:236:ILE:HG13	1.95	0.66
1:B:236:ILE:O	1:B:236:ILE:HG13	1.95	0.66
1:D:3:LYS:O	1:D:59:TYR:HA	1.94	0.66
1:F:4:ALA:O	1:F:86:ILE:O	2.13	0.66
1:B:39:VAL:HG13	1:B:43:ASN:HA	1.78	0.66
1:E:231:GLU:HB2	1:E:233:MET:CE	2.25	0.66
1:B:149:SER:CB	1:B:167:ALA:CB	2.49	0.66
1:F:236:ILE:HG13	1:F:236:ILE:O	1.96	0.66
1:D:236:ILE:O	1:D:236:ILE:HG13	1.96	0.66
1:B:98:ASN:HA	1:B:106:TYR:O	1.93	0.66
1:A:231:GLU:HB2	1:A:233:MET:CE	2.25	0.66
1:A:236:ILE:O	1:A:236:ILE:HG13	1.96	0.66
1:E:180:PRO:HA	1:E:186:ILE:HD11	1.77	0.66
1:D:231:GLU:HB2	1:D:233:MET:CE	2.25	0.66
1:D:170:ASP:O	1:D:171:THR:CG2	2.44	0.66
1:A:4:ALA:O	1:A:86:ILE:O	2.13	0.66
1:F:136:THR:HB	1:F:209:THR:HG22	1.77	0.66
1:D:161:GLU:HB3	1:D:188:ALA:HB1	1.76	0.66
1:E:207:ILE:HD12	1:E:207:ILE:N	2.10	0.66
1:C:39:VAL:HG13	1:C:43:ASN:HA	1.78	0.66
1:D:25:CYS:O	1:D:68:VAL:N	2.26	0.66
1:C:73:LEU:HD22	1:C:77:ALA:HB2	1.77	0.66
1:B:73:LEU:HD22	1:B:77:ALA:HB2	1.77	0.66
1:E:39:VAL:HG13	1:E:43:ASN:HA	1.78	0.66
1:D:73:LEU:HD22	1:D:77:ALA:HB2	1.77	0.66
1:D:136:THR:HB	1:D:209:THR:HG22	1.77	0.66
1:C:4:ALA:O	1:C:86:ILE:O	2.13	0.66
1:B:47:VAL:CA	1:B:237:THR:O	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:ILE:N	1:B:207:ILE:HD12	2.10	0.66
1:B:25:CYS:O	1:B:68:VAL:N	2.26	0.66
1:D:32:GLU:N	1:D:32:GLU:OE1	2.29	0.65
1:F:170:ASP:O	1:F:171:THR:CG2	2.44	0.65
1:F:161:GLU:HB3	1:F:188:ALA:HB1	1.76	0.65
1:B:231:GLU:HB2	1:B:233:MET:CE	2.25	0.65
1:C:231:GLU:HB2	1:C:233:MET:CE	2.25	0.65
1:C:170:ASP:O	1:C:171:THR:CG2	2.44	0.65
1:E:4:ALA:O	1:E:86:ILE:O	2.13	0.65
1:A:29:LEU:CD2	1:A:34:LEU:HD13	2.26	0.65
1:D:207:ILE:HD12	1:D:207:ILE:N	2.10	0.65
1:C:29:LEU:CD2	1:C:34:LEU:HD13	2.26	0.65
1:D:4:ALA:O	1:D:86:ILE:O	2.13	0.65
1:C:136:THR:HB	1:C:209:THR:CA	2.27	0.65
1:A:39:VAL:HG13	1:A:43:ASN:HA	1.78	0.65
1:F:73:LEU:HD22	1:F:77:ALA:HB2	1.77	0.65
1:E:73:LEU:HD22	1:E:77:ALA:HB2	1.77	0.65
1:E:200:LEU:HA	1:E:203:MET:HE2	1.77	0.65
1:C:207:ILE:HD12	1:C:207:ILE:N	2.10	0.65
1:B:136:THR:HB	1:B:209:THR:CA	2.27	0.65
1:A:200:LEU:HA	1:A:203:MET:HE2	1.78	0.65
1:D:29:LEU:CD2	1:D:34:LEU:HD13	2.26	0.65
1:F:39:VAL:HG13	1:F:43:ASN:HA	1.78	0.65
1:B:180:PRO:HA	1:B:186:ILE:HD11	1.77	0.65
1:B:170:ASP:O	1:B:171:THR:CG2	2.44	0.65
1:A:170:ASP:O	1:A:171:THR:CG2	2.44	0.65
1:C:32:GLU:OE1	1:C:32:GLU:N	2.30	0.65
1:E:29:LEU:CD2	1:E:34:LEU:HD13	2.26	0.65
1:D:39:VAL:HG13	1:D:43:ASN:HA	1.77	0.65
1:A:149:SER:CB	1:A:167:ALA:CB	2.49	0.65
1:D:154:LEU:O	1:D:156:VAL:HG23	1.97	0.65
1:C:222:PRO:CD	1:C:242:PRO:CG	2.64	0.65
1:B:154:LEU:O	1:B:156:VAL:HG23	1.97	0.65
1:F:29:LEU:CD2	1:F:34:LEU:HD13	2.26	0.65
1:A:195:PHE:CE2	1:A:240:LEU:O	2.50	0.65
1:B:157:ASP:HA	1:B:160:GLU:O	1.97	0.65
1:B:136:THR:CB	1:B:209:THR:HG22	2.27	0.65
1:D:136:THR:HB	1:D:209:THR:CA	2.27	0.65
1:F:136:THR:HB	1:F:209:THR:CA	2.27	0.65
1:E:157:ASP:HA	1:E:160:GLU:O	1.97	0.65
1:E:73:LEU:CD2	1:E:77:ALA:HB2	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:HIS:CE1	1:D:185:SER:HA	2.31	0.64
1:E:136:THR:CB	1:E:209:THR:HG22	2.28	0.64
1:A:136:THR:HB	1:A:209:THR:HG22	1.77	0.64
1:A:154:LEU:O	1:A:156:VAL:HG23	1.97	0.64
1:E:236:ILE:HG13	1:E:236:ILE:O	1.95	0.64
1:D:196:SER:H	1:D:240:LEU:HD21	1.62	0.64
1:A:136:THR:CB	1:A:209:THR:HG22	2.28	0.64
1:C:157:ASP:HA	1:C:160:GLU:O	1.97	0.64
1:A:73:LEU:CD2	1:A:77:ALA:HB2	2.27	0.64
1:D:108:LEU:CD2	1:D:110:LEU:HD23	2.28	0.64
1:A:136:THR:HB	1:A:209:THR:CA	2.27	0.64
1:B:73:LEU:CD2	1:B:77:ALA:HB2	2.27	0.64
1:E:32:GLU:OE1	1:E:32:GLU:N	2.29	0.64
1:B:215:VAL:HG12	1:B:223:VAL:CG2	2.28	0.64
1:D:195:PHE:CE2	1:D:240:LEU:O	2.50	0.64
1:D:200:LEU:HA	1:D:203:MET:HE2	1.78	0.64
1:F:158:GLY:H	1:F:162:THR:HB	1.62	0.64
1:F:136:THR:CB	1:F:209:THR:HG22	2.27	0.64
1:C:195:PHE:CE2	1:C:240:LEU:O	2.50	0.64
1:C:200:LEU:HA	1:C:203:MET:HE2	1.80	0.64
1:D:215:VAL:HG12	1:D:223:VAL:CG2	2.28	0.64
1:E:195:PHE:CE2	1:E:240:LEU:O	2.50	0.64
1:F:32:GLU:N	1:F:32:GLU:OE1	2.30	0.64
1:E:136:THR:HB	1:E:209:THR:CB	2.28	0.64
1:D:157:ASP:HA	1:D:160:GLU:O	1.97	0.64
1:A:108:LEU:CD2	1:A:110:LEU:HD23	2.28	0.64
1:D:73:LEU:CD2	1:D:77:ALA:HB2	2.27	0.64
1:C:73:LEU:CD2	1:C:77:ALA:HB2	2.27	0.64
1:C:136:THR:CB	1:C:209:THR:HG22	2.27	0.64
1:E:136:THR:HB	1:E:209:THR:CA	2.27	0.64
1:B:136:THR:HB	1:B:209:THR:CB	2.28	0.64
1:B:195:PHE:CE2	1:B:240:LEU:O	2.50	0.64
1:F:215:VAL:HG12	1:F:223:VAL:CG2	2.28	0.64
1:E:215:VAL:HG12	1:E:223:VAL:CG2	2.28	0.64
1:A:136:THR:HB	1:A:209:THR:CB	2.28	0.64
1:D:158:GLY:H	1:D:162:THR:HB	1.62	0.64
1:A:215:VAL:HG12	1:A:223:VAL:CG2	2.28	0.64
1:E:170:ASP:O	1:E:171:THR:CG2	2.44	0.64
1:F:157:ASP:HA	1:F:160:GLU:O	1.97	0.64
1:A:32:GLU:OE1	1:A:32:GLU:N	2.30	0.64
1:E:2:PHE:HZ	1:E:64:GLY:HA3	1.64	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:THR:CB	1:D:209:THR:HG22	2.27	0.64
1:A:231:GLU:HB2	1:A:233:MET:HE2	1.80	0.64
1:B:196:SER:H	1:B:240:LEU:HD21	1.62	0.63
1:D:174:VAL:HG23	1:E:104:LEU:HD21	1.79	0.63
1:B:158:GLY:H	1:B:162:THR:HB	1.62	0.63
1:B:29:LEU:CD2	1:B:34:LEU:HD13	2.26	0.63
1:C:158:GLY:O	1:C:159:ALA:HB3	1.98	0.63
1:E:158:GLY:H	1:E:162:THR:HB	1.62	0.63
1:E:196:SER:H	1:E:240:LEU:HD21	1.62	0.63
1:A:157:ASP:HA	1:A:160:GLU:O	1.97	0.63
1:E:158:GLY:O	1:E:159:ALA:HB3	1.98	0.63
1:B:158:GLY:O	1:B:159:ALA:HB3	1.98	0.63
1:F:154:LEU:O	1:F:156:VAL:HG23	1.97	0.63
1:F:73:LEU:CD2	1:F:77:ALA:HB2	2.27	0.63
1:A:158:GLY:H	1:A:162:THR:HB	1.62	0.63
1:D:136:THR:HB	1:D:209:THR:CB	2.28	0.63
1:C:158:GLY:H	1:C:162:THR:HB	1.62	0.63
1:C:215:VAL:HG12	1:C:223:VAL:CG2	2.28	0.63
1:C:2:PHE:HZ	1:C:64:GLY:HA3	1.64	0.63
1:D:158:GLY:O	1:D:159:ALA:HB3	1.98	0.63
1:E:154:LEU:O	1:E:156:VAL:HG23	1.97	0.63
1:F:47:VAL:CA	1:F:237:THR:O	2.30	0.63
1:B:32:GLU:N	1:B:32:GLU:OE1	2.29	0.63
1:F:136:THR:HB	1:F:209:THR:CB	2.28	0.63
1:C:154:LEU:O	1:C:156:VAL:HG23	1.97	0.63
1:F:2:PHE:HZ	1:F:64:GLY:HA3	1.63	0.63
1:F:195:PHE:CE2	1:F:240:LEU:O	2.50	0.63
1:A:158:GLY:O	1:A:159:ALA:HB3	1.98	0.63
1:D:231:GLU:HB2	1:D:233:MET:HE3	1.80	0.63
1:F:94:THR:O	1:F:110:LEU:HB2	1.99	0.63
1:C:172:ASP:O	1:C:173:ASP:OD1	2.17	0.63
1:C:136:THR:HB	1:C:209:THR:CB	2.28	0.63
1:E:149:SER:CB	1:E:167:ALA:CB	2.49	0.62
1:D:2:PHE:HZ	1:D:64:GLY:HA3	1.64	0.62
1:F:158:GLY:O	1:F:159:ALA:HB3	1.98	0.62
1:D:154:LEU:O	1:D:155:ARG:C	2.38	0.62
1:D:172:ASP:O	1:D:173:ASP:OD1	2.17	0.62
1:E:108:LEU:CD2	1:E:110:LEU:HD23	2.28	0.62
1:C:196:SER:H	1:C:240:LEU:HD21	1.62	0.62
1:E:154:LEU:O	1:E:155:ARG:C	2.38	0.62
1:B:94:THR:O	1:B:110:LEU:HB2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:108:LEU:CD2	1:F:110:LEU:HD23	2.28	0.62
1:F:153:ARG:HG2	1:F:194:LEU:HD21	1.82	0.62
1:D:73:LEU:HA	1:D:76:VAL:CG1	2.29	0.62
1:B:97:LEU:HD12	1:B:110:LEU:HD21	1.81	0.62
1:F:195:PHE:HZ	1:F:221:PHE:O	1.83	0.62
1:B:2:PHE:HZ	1:B:64:GLY:HA3	1.64	0.62
1:A:196:SER:H	1:A:240:LEU:HD21	1.62	0.62
1:F:196:SER:H	1:F:240:LEU:HD21	1.62	0.62
1:E:195:PHE:HZ	1:E:221:PHE:O	1.83	0.62
1:F:154:LEU:O	1:F:155:ARG:C	2.38	0.62
1:E:94:THR:O	1:E:110:LEU:HB2	1.99	0.62
1:E:73:LEU:HA	1:E:76:VAL:CG1	2.29	0.62
1:F:172:ASP:O	1:F:173:ASP:OD1	2.17	0.62
1:A:154:LEU:O	1:A:155:ARG:C	2.38	0.62
1:C:108:LEU:CD2	1:C:110:LEU:HD23	2.28	0.62
1:A:2:PHE:HZ	1:A:64:GLY:HA3	1.64	0.62
1:D:153:ARG:HG2	1:D:194:LEU:HD21	1.81	0.62
1:C:73:LEU:HA	1:C:76:VAL:CG1	2.29	0.62
1:C:94:THR:O	1:C:110:LEU:HB2	1.99	0.62
1:A:172:ASP:O	1:A:173:ASP:OD1	2.17	0.62
1:A:222:PRO:CD	1:A:242:PRO:CG	2.64	0.62
1:C:153:ARG:HG2	1:C:194:LEU:HD21	1.82	0.62
1:E:153:ARG:HG2	1:E:194:LEU:HD21	1.82	0.61
1:B:108:LEU:CD2	1:B:110:LEU:HD23	2.28	0.61
1:B:73:LEU:HA	1:B:76:VAL:CG1	2.29	0.61
1:A:153:ARG:HG2	1:A:194:LEU:HD21	1.82	0.61
1:E:172:ASP:O	1:E:173:ASP:OD1	2.17	0.61
1:F:73:LEU:HA	1:F:76:VAL:CG1	2.29	0.61
1:A:73:LEU:HA	1:A:76:VAL:CG1	2.29	0.61
1:B:213:VAL:CG2	1:B:227:TYR:OH	2.48	0.61
1:A:195:PHE:HZ	1:A:221:PHE:O	1.83	0.61
1:D:213:VAL:CG2	1:D:227:TYR:OH	2.48	0.61
1:B:172:ASP:O	1:B:173:ASP:OD1	2.17	0.61
1:F:200:LEU:HA	1:F:203:MET:HE2	1.80	0.61
1:F:156:VAL:HG21	1:F:217:LEU:CG	2.27	0.61
1:B:176:LEU:HD13	1:C:104:LEU:HB2	1.81	0.61
1:C:154:LEU:O	1:C:155:ARG:C	2.38	0.61
1:F:179:PRO:O	1:F:183:LEU:HD22	2.01	0.61
1:A:213:VAL:CG2	1:A:227:TYR:OH	2.48	0.61
1:D:195:PHE:HZ	1:D:221:PHE:O	1.83	0.61
1:C:231:GLU:HB2	1:C:233:MET:HE2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:PHE:HZ	1:B:221:PHE:O	1.83	0.61
1:E:179:PRO:O	1:E:183:LEU:HD22	2.01	0.61
1:C:195:PHE:HZ	1:C:221:PHE:O	1.83	0.61
1:E:97:LEU:HD12	1:E:110:LEU:HD21	1.82	0.61
1:D:94:THR:O	1:D:110:LEU:HB2	1.99	0.61
1:E:156:VAL:HG23	1:E:217:LEU:HG	1.83	0.61
1:A:94:THR:O	1:A:110:LEU:HB2	1.99	0.61
1:B:185:SER:HA	1:E:87:HIS:CE1	2.35	0.61
1:C:97:LEU:HD12	1:C:110:LEU:HD21	1.82	0.61
1:B:153:ARG:HG2	1:B:194:LEU:HD21	1.82	0.61
1:B:154:LEU:O	1:B:155:ARG:C	2.38	0.61
1:B:185:SER:HA	1:E:87:HIS:HE1	1.66	0.61
1:F:133:LEU:HG	1:F:183:LEU:HD12	1.83	0.61
1:D:8:ALA:HB2	1:D:84:ASP:O	2.01	0.61
1:E:27:ILE:O	1:E:65:VAL:HG23	2.01	0.61
1:A:179:PRO:O	1:A:183:LEU:HD22	2.01	0.60
1:B:8:ALA:HB2	1:B:84:ASP:O	2.01	0.60
1:C:191:ALA:CB	1:C:218:GLY:C	2.66	0.60
1:F:198:ASP:O	1:F:201:LYS:HB2	2.01	0.60
1:A:97:LEU:HD12	1:A:110:LEU:HD21	1.81	0.60
1:B:179:PRO:O	1:B:183:LEU:HD22	2.01	0.60
1:C:156:VAL:HG23	1:C:217:LEU:HG	1.83	0.60
1:B:156:VAL:HG21	1:B:217:LEU:CG	2.27	0.60
1:E:198:ASP:O	1:E:201:LYS:HB2	2.01	0.60
1:B:27:ILE:O	1:B:65:VAL:HG23	2.01	0.60
1:E:133:LEU:HG	1:E:183:LEU:HD12	1.83	0.60
1:D:156:VAL:H	1:D:192:ASP:CB	2.15	0.60
1:F:213:VAL:CG2	1:F:227:TYR:OH	2.48	0.60
1:A:133:LEU:HG	1:A:183:LEU:HD12	1.83	0.60
1:B:156:VAL:H	1:B:192:ASP:CB	2.15	0.60
1:B:133:LEU:HG	1:B:183:LEU:HD12	1.83	0.60
1:D:133:LEU:HG	1:D:183:LEU:HD12	1.83	0.60
1:D:72:ARG:NH1	1:F:171:THR:HG21	2.08	0.60
1:F:231:GLU:HB2	1:F:233:MET:HE3	1.83	0.60
1:F:27:ILE:O	1:F:65:VAL:HG23	2.01	0.60
1:A:156:VAL:H	1:A:192:ASP:CB	2.15	0.60
1:A:8:ALA:HB2	1:A:84:ASP:O	2.01	0.60
1:A:27:ILE:O	1:A:65:VAL:HG23	2.01	0.60
1:D:27:ILE:O	1:D:65:VAL:HG23	2.01	0.60
1:B:198:ASP:O	1:B:201:LYS:HB2	2.01	0.60
1:D:97:LEU:HD12	1:D:110:LEU:HD21	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:47:VAL:CA	1:C:237:THR:O	2.30	0.60
1:E:156:VAL:H	1:E:192:ASP:CB	2.15	0.60
1:C:198:ASP:O	1:C:201:LYS:HB2	2.01	0.60
1:F:97:LEU:HD12	1:F:110:LEU:HD21	1.81	0.60
1:B:161:GLU:O	1:B:162:THR:OG1	2.20	0.60
1:C:179:PRO:O	1:C:183:LEU:HD22	2.01	0.60
1:D:179:PRO:O	1:D:183:LEU:HD22	2.01	0.60
1:C:213:VAL:CG2	1:C:227:TYR:OH	2.48	0.60
1:C:27:ILE:O	1:C:65:VAL:HG23	2.01	0.59
1:F:8:ALA:HB2	1:F:84:ASP:O	2.01	0.59
1:D:198:ASP:O	1:D:201:LYS:HB2	2.01	0.59
1:B:179:PRO:HG2	1:D:179:PRO:HG2	1.83	0.59
1:F:156:VAL:HG23	1:F:217:LEU:HG	1.83	0.59
1:C:8:ALA:HB2	1:C:84:ASP:O	2.01	0.59
1:F:156:VAL:H	1:F:192:ASP:CB	2.15	0.59
1:E:213:VAL:CG2	1:E:227:TYR:OH	2.48	0.59
1:B:175:ASP:O	1:C:104:LEU:HD22	2.03	0.59
1:A:198:ASP:O	1:A:201:LYS:HB2	2.01	0.59
1:B:195:PHE:CB	1:B:240:LEU:HD22	2.33	0.59
1:F:194:LEU:CD2	1:F:245:GLN:HG3	2.30	0.59
1:E:8:ALA:HB2	1:E:84:ASP:O	2.01	0.59
1:A:195:PHE:CB	1:A:240:LEU:HD22	2.33	0.59
1:C:195:PHE:CB	1:C:240:LEU:HD22	2.33	0.59
1:F:35:SER:O	1:F:36:ILE:HD13	2.03	0.59
1:A:157:ASP:HB2	1:A:160:GLU:O	2.03	0.59
1:A:156:VAL:HG23	1:A:217:LEU:HG	1.83	0.59
1:D:222:PRO:CD	1:D:242:PRO:HD2	2.32	0.59
1:E:222:PRO:CD	1:E:242:PRO:CG	2.64	0.59
1:D:87:HIS:O	1:D:99:ILE:HG13	2.03	0.59
1:D:157:ASP:HB2	1:D:160:GLU:O	2.03	0.59
1:E:231:GLU:HB2	1:E:233:MET:HE3	1.85	0.59
1:E:35:SER:O	1:E:36:ILE:HD13	2.03	0.59
1:B:200:LEU:HA	1:B:203:MET:HE2	1.83	0.59
1:A:87:HIS:O	1:A:99:ILE:HG13	2.03	0.59
1:E:157:ASP:HB2	1:E:160:GLU:O	2.03	0.59
1:C:156:VAL:H	1:C:192:ASP:CB	2.15	0.58
1:B:157:ASP:HB2	1:B:160:GLU:O	2.03	0.58
1:F:157:ASP:HB2	1:F:160:GLU:O	2.03	0.58
1:B:101:ILE:CD1	1:B:104:LEU:HD12	2.34	0.58
1:C:216:GLU:OE1	1:C:224:LYS:HD2	2.03	0.58
1:F:216:GLU:OE1	1:F:224:LYS:HD2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:ILE:CD1	1:C:104:LEU:HD12	2.34	0.58
1:C:157:ASP:HB2	1:C:160:GLU:O	2.03	0.58
1:A:101:ILE:CD1	1:A:104:LEU:HD12	2.34	0.58
1:C:222:PRO:CD	1:C:242:PRO:HD2	2.32	0.58
1:C:6:VAL:CG2	1:C:56:PHE:HD2	2.14	0.58
1:C:73:LEU:HA	1:C:76:VAL:HG12	1.86	0.58
1:A:216:GLU:OE1	1:A:224:LYS:HD2	2.03	0.58
1:D:156:VAL:HG23	1:D:217:LEU:HG	1.83	0.58
1:F:133:LEU:CG	1:F:183:LEU:CD1	2.80	0.58
1:E:216:GLU:OE1	1:E:224:LYS:HD2	2.03	0.58
1:A:191:ALA:CB	1:A:218:GLY:C	2.66	0.58
1:A:176:LEU:HD13	1:B:104:LEU:HB2	1.85	0.58
1:E:161:GLU:O	1:E:162:THR:OG1	2.20	0.58
1:A:73:LEU:HA	1:A:76:VAL:HG12	1.86	0.58
1:D:216:GLU:OE1	1:D:224:LYS:HD2	2.03	0.58
1:E:97:LEU:HB3	1:E:108:LEU:HB3	1.86	0.58
1:B:131:ILE:HD11	1:B:217:LEU:HB2	1.86	0.58
1:B:35:SER:O	1:B:36:ILE:HD13	2.03	0.58
1:C:87:HIS:O	1:C:99:ILE:HG13	2.03	0.58
1:E:195:PHE:CB	1:E:240:LEU:HD22	2.33	0.58
1:C:6:VAL:N	1:C:86:ILE:O	2.37	0.58
1:D:35:SER:O	1:D:36:ILE:HD13	2.03	0.58
1:B:87:HIS:O	1:B:99:ILE:HG13	2.03	0.58
1:A:131:ILE:HD11	1:A:217:LEU:HB2	1.86	0.58
1:E:11:LEU:HD11	1:E:77:ALA:HB1	1.86	0.58
1:E:191:ALA:CB	1:E:218:GLY:C	2.66	0.58
1:E:87:HIS:O	1:E:99:ILE:HG13	2.03	0.58
1:F:87:HIS:O	1:F:99:ILE:HG13	2.03	0.58
1:F:222:PRO:CD	1:F:242:PRO:HD2	2.32	0.57
1:E:101:ILE:CD1	1:E:104:LEU:HD12	2.34	0.57
1:E:194:LEU:CD2	1:E:245:GLN:HG3	2.30	0.57
1:D:97:LEU:HB3	1:D:108:LEU:HB3	1.86	0.57
1:D:73:LEU:HA	1:D:76:VAL:HG12	1.86	0.57
1:E:6:VAL:CG2	1:E:56:PHE:HD2	2.14	0.57
1:B:214:THR:O	1:B:225:LEU:HA	2.04	0.57
1:E:133:LEU:CG	1:E:183:LEU:CD1	2.80	0.57
1:B:216:GLU:OE1	1:B:224:LYS:HD2	2.03	0.57
1:F:97:LEU:HB3	1:F:108:LEU:HB3	1.86	0.57
1:F:73:LEU:HA	1:F:76:VAL:HG12	1.86	0.57
1:E:131:ILE:HD11	1:E:217:LEU:HB2	1.86	0.57
1:A:186:ILE:HG22	1:A:187:GLU:N	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:SER:O	1:A:36:ILE:HD13	2.03	0.57
1:B:191:ALA:CB	1:B:218:GLY:C	2.66	0.57
1:B:186:ILE:HG22	1:B:187:GLU:N	2.19	0.57
1:E:214:THR:O	1:E:225:LEU:HA	2.04	0.57
1:D:186:ILE:HG22	1:D:187:GLU:N	2.19	0.57
1:C:35:SER:O	1:C:36:ILE:HD13	2.03	0.57
1:F:214:THR:O	1:F:225:LEU:HA	2.04	0.57
1:A:214:THR:O	1:A:225:LEU:HA	2.04	0.57
1:E:73:LEU:HA	1:E:76:VAL:HG12	1.86	0.57
1:D:195:PHE:CB	1:D:240:LEU:HD22	2.33	0.57
1:C:214:THR:O	1:C:225:LEU:HA	2.04	0.57
1:C:133:LEU:HG	1:C:183:LEU:HD12	1.83	0.57
1:B:73:LEU:HA	1:B:76:VAL:HG12	1.86	0.57
1:D:157:ASP:O	1:D:157:ASP:OD1	2.23	0.57
1:A:104:LEU:HB2	1:C:176:LEU:HD13	1.87	0.57
1:D:195:PHE:CE1	1:D:223:VAL:HB	2.40	0.57
1:F:101:ILE:CD1	1:F:104:LEU:HD12	2.34	0.57
1:F:6:VAL:N	1:F:86:ILE:O	2.37	0.57
1:B:195:PHE:CE1	1:B:223:VAL:HB	2.40	0.57
1:C:194:LEU:CD2	1:C:245:GLN:HG3	2.30	0.57
1:F:152:ILE:HG13	1:F:197:LEU:HB2	1.87	0.57
1:B:157:ASP:O	1:B:157:ASP:OD1	2.23	0.57
1:E:152:ILE:HG13	1:E:197:LEU:HB2	1.87	0.57
1:C:97:LEU:HB3	1:C:108:LEU:HB3	1.86	0.57
1:C:145:ALA:O	1:C:197:LEU:CD1	2.53	0.57
1:D:101:ILE:CD1	1:D:104:LEU:HD12	2.34	0.57
1:F:195:PHE:CB	1:F:240:LEU:HD22	2.33	0.57
1:A:157:ASP:OD1	1:A:157:ASP:O	2.23	0.57
1:A:194:LEU:CD2	1:A:245:GLN:HG3	2.30	0.57
1:F:186:ILE:HG22	1:F:187:GLU:N	2.19	0.57
1:A:11:LEU:HD11	1:A:77:ALA:HB1	1.86	0.57
1:C:11:LEU:HD11	1:C:77:ALA:HB1	1.86	0.57
1:C:131:ILE:HD11	1:C:217:LEU:HB2	1.86	0.57
1:C:157:ASP:OD1	1:C:157:ASP:O	2.23	0.57
1:A:6:VAL:CG2	1:A:56:PHE:HD2	2.14	0.57
1:B:194:LEU:CD2	1:B:245:GLN:HG3	2.30	0.56
1:A:222:PRO:CD	1:A:242:PRO:HD2	2.32	0.56
1:F:68:VAL:O	1:F:70:LEU:N	2.38	0.56
1:C:195:PHE:CE1	1:C:223:VAL:HB	2.40	0.56
1:A:156:VAL:H	1:A:192:ASP:HB3	1.71	0.56
1:D:68:VAL:O	1:D:70:LEU:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:186:ILE:HG22	1:E:187:GLU:N	2.19	0.56
1:D:149:SER:HB3	1:D:167:ALA:CB	2.22	0.56
1:D:156:VAL:H	1:D:192:ASP:HB3	1.71	0.56
1:D:131:ILE:HD11	1:D:217:LEU:HB2	1.86	0.56
1:A:152:ILE:HG13	1:A:197:LEU:HB2	1.87	0.56
1:F:195:PHE:CE1	1:F:223:VAL:HB	2.40	0.56
1:F:145:ALA:O	1:F:197:LEU:CD1	2.53	0.56
1:A:156:VAL:HG21	1:A:217:LEU:CG	2.27	0.56
1:A:97:LEU:HB3	1:A:108:LEU:HB3	1.86	0.56
1:A:70:LEU:O	1:A:74:GLU:HB2	2.06	0.56
1:D:145:ALA:O	1:D:197:LEU:CD1	2.53	0.56
1:E:145:ALA:O	1:E:197:LEU:CD1	2.53	0.56
1:B:97:LEU:HB3	1:B:108:LEU:HB3	1.86	0.56
1:B:70:LEU:O	1:B:74:GLU:HB2	2.06	0.56
1:B:231:GLU:HB2	1:B:233:MET:HE2	1.87	0.56
1:D:92:GLU:O	1:D:93:GLU:HG2	2.05	0.56
1:B:222:PRO:CB	1:B:239:MET:HG2	2.34	0.56
1:C:152:ILE:HG13	1:C:197:LEU:HB2	1.87	0.56
1:C:133:LEU:CG	1:C:183:LEU:CD1	2.80	0.56
1:C:186:ILE:HG22	1:C:187:GLU:N	2.19	0.56
1:D:214:THR:O	1:D:225:LEU:HA	2.04	0.56
1:E:92:GLU:O	1:E:93:GLU:HG2	2.06	0.56
1:C:222:PRO:CB	1:C:239:MET:HG2	2.34	0.56
1:F:131:ILE:HD11	1:F:217:LEU:HB2	1.86	0.56
1:F:157:ASP:OD1	1:F:157:ASP:O	2.23	0.56
1:B:11:LEU:HD11	1:B:77:ALA:HB1	1.86	0.56
1:D:6:VAL:CG2	1:D:56:PHE:HD2	2.14	0.56
1:D:6:VAL:N	1:D:86:ILE:O	2.37	0.56
1:E:157:ASP:O	1:E:157:ASP:OD1	2.23	0.56
1:A:195:PHE:CE1	1:A:223:VAL:HB	2.40	0.56
1:B:145:ALA:O	1:B:197:LEU:CD1	2.53	0.56
1:C:201:LYS:O	1:C:205:LYS:HB2	2.06	0.56
1:B:156:VAL:H	1:B:192:ASP:HB3	1.71	0.56
1:E:6:VAL:N	1:E:86:ILE:O	2.37	0.56
1:A:145:ALA:O	1:A:197:LEU:CD1	2.53	0.56
1:A:201:LYS:O	1:A:205:LYS:HB2	2.06	0.56
1:B:195:PHE:HE2	1:B:240:LEU:O	1.89	0.56
1:D:200:LEU:HG	1:D:240:LEU:HD13	1.88	0.56
1:E:222:PRO:CD	1:E:242:PRO:HD2	2.33	0.56
1:B:6:VAL:N	1:B:86:ILE:O	2.37	0.56
1:B:117:ARG:HG3	1:B:118:GLN:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:161:GLU:O	1:D:162:THR:OG1	2.20	0.56
1:D:127:LEU:HD22	1:D:218:GLY:HA3	1.88	0.56
1:B:200:LEU:HG	1:B:240:LEU:HD13	1.88	0.56
1:C:161:GLU:O	1:C:162:THR:OG1	2.20	0.56
1:F:11:LEU:HD11	1:F:77:ALA:HB1	1.86	0.56
1:F:222:PRO:CD	1:F:242:PRO:CG	2.64	0.56
1:D:201:LYS:O	1:D:205:LYS:HB2	2.06	0.56
1:B:222:PRO:CD	1:B:242:PRO:HD2	2.33	0.56
1:C:156:VAL:H	1:C:192:ASP:HB3	1.70	0.56
1:C:70:LEU:O	1:C:74:GLU:HB2	2.06	0.56
1:F:225:LEU:O	1:F:237:THR:HA	2.06	0.56
1:E:136:THR:HA	1:E:208:PRO:O	2.06	0.56
1:B:136:THR:HA	1:B:208:PRO:O	2.06	0.56
1:A:200:LEU:HG	1:A:240:LEU:HD13	1.88	0.56
1:C:200:LEU:HG	1:C:240:LEU:HD13	1.88	0.56
1:F:201:LYS:O	1:F:205:LYS:HB2	2.06	0.56
1:D:11:LEU:HD11	1:D:77:ALA:HB1	1.86	0.56
1:E:225:LEU:O	1:E:237:THR:HA	2.06	0.56
1:B:231:GLU:HB2	1:B:233:MET:HE3	1.88	0.56
1:B:92:GLU:O	1:B:93:GLU:HG2	2.05	0.56
1:F:149:SER:HB3	1:F:167:ALA:CB	2.22	0.55
1:B:201:LYS:O	1:B:205:LYS:HB2	2.06	0.55
1:F:49:LEU:HD21	1:F:236:ILE:HG22	1.88	0.55
1:D:104:LEU:HB2	1:F:176:LEU:HD13	1.88	0.55
1:D:152:ILE:HG13	1:D:197:LEU:HB2	1.87	0.55
1:E:195:PHE:HE2	1:E:240:LEU:O	1.89	0.55
1:E:195:PHE:CE1	1:E:223:VAL:HB	2.40	0.55
1:C:97:LEU:N	1:C:108:LEU:O	2.40	0.55
1:F:92:GLU:O	1:F:93:GLU:HG2	2.05	0.55
1:B:152:ILE:HG13	1:B:197:LEU:HB2	1.87	0.55
1:E:70:LEU:O	1:E:74:GLU:HB2	2.06	0.55
1:E:222:PRO:CB	1:E:239:MET:HG2	2.34	0.55
1:B:49:LEU:HD21	1:B:236:ILE:HG22	1.88	0.55
1:B:97:LEU:N	1:B:108:LEU:O	2.40	0.55
1:F:5:ILE:HA	1:F:86:ILE:O	2.07	0.55
1:C:136:THR:HA	1:C:208:PRO:O	2.06	0.55
1:A:92:GLU:O	1:A:93:GLU:HG2	2.05	0.55
1:D:156:VAL:HG21	1:D:217:LEU:CG	2.27	0.55
1:F:70:LEU:O	1:F:74:GLU:HB2	2.06	0.55
1:F:146:ASP:HA	1:F:197:LEU:HD12	1.87	0.55
1:E:156:VAL:H	1:E:192:ASP:HB3	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:VAL:O	1:A:70:LEU:N	2.37	0.55
1:A:97:LEU:N	1:A:108:LEU:O	2.40	0.55
1:E:201:LYS:O	1:E:205:LYS:HB2	2.06	0.55
1:F:161:GLU:O	1:F:162:THR:OG1	2.20	0.55
1:A:222:PRO:CB	1:A:239:MET:HG2	2.34	0.55
1:A:161:GLU:O	1:A:162:THR:OG1	2.20	0.55
1:E:97:LEU:N	1:E:108:LEU:O	2.40	0.55
1:D:136:THR:HA	1:D:208:PRO:O	2.06	0.55
1:A:117:ARG:HG3	1:A:118:GLN:N	2.21	0.55
1:F:97:LEU:N	1:F:108:LEU:O	2.40	0.55
1:D:176:LEU:HD13	1:E:104:LEU:HB2	1.88	0.55
1:F:8:ALA:CB	1:F:84:ASP:O	2.55	0.55
1:F:156:VAL:H	1:F:192:ASP:HB3	1.71	0.55
1:A:225:LEU:O	1:A:237:THR:HA	2.06	0.55
1:D:1:MET:HG3	1:D:91:ASP:HB2	1.89	0.55
1:F:117:ARG:HG3	1:F:118:GLN:N	2.21	0.55
1:A:127:LEU:HD22	1:A:218:GLY:HA3	1.88	0.55
1:E:127:LEU:HD22	1:E:218:GLY:HA3	1.88	0.55
1:B:127:LEU:HD22	1:B:218:GLY:HA3	1.88	0.55
1:D:70:LEU:O	1:D:74:GLU:HB2	2.06	0.55
1:F:136:THR:HB	1:F:209:THR:CG2	2.37	0.55
1:E:138:LEU:HD12	1:E:204:ASN:ND2	2.22	0.55
1:A:49:LEU:HD21	1:A:236:ILE:HG22	1.88	0.55
1:B:156:VAL:HG23	1:B:217:LEU:HG	1.83	0.55
1:E:8:ALA:CB	1:E:84:ASP:O	2.55	0.55
1:D:97:LEU:N	1:D:108:LEU:O	2.40	0.55
1:B:138:LEU:HD12	1:B:204:ASN:ND2	2.22	0.55
1:B:68:VAL:O	1:B:70:LEU:N	2.38	0.55
1:A:6:VAL:N	1:A:86:ILE:O	2.37	0.55
1:A:136:THR:HA	1:A:208:PRO:O	2.06	0.55
1:B:1:MET:HG3	1:B:91:ASP:HB2	1.89	0.55
1:D:117:ARG:HG3	1:D:118:GLN:N	2.21	0.55
1:C:127:LEU:HD22	1:C:218:GLY:HA3	1.88	0.55
1:C:5:ILE:HA	1:C:86:ILE:O	2.07	0.55
1:D:138:LEU:HD12	1:D:204:ASN:ND2	2.22	0.55
1:C:225:LEU:O	1:C:237:THR:HA	2.06	0.55
1:F:136:THR:HA	1:F:208:PRO:O	2.06	0.55
1:A:216:GLU:HB2	1:A:224:LYS:HB2	1.89	0.55
1:D:216:GLU:HB2	1:D:224:LYS:HB2	1.89	0.55
1:D:8:ALA:CB	1:D:84:ASP:O	2.55	0.55
1:E:49:LEU:HD21	1:E:236:ILE:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:LEU:HD21	1:D:236:ILE:HG22	1.88	0.55
1:A:5:ILE:HA	1:A:86:ILE:O	2.07	0.55
1:E:20:VAL:CG1	1:E:202:ASP:HB3	2.36	0.55
1:D:5:ILE:HA	1:D:86:ILE:O	2.07	0.55
1:B:20:VAL:CG1	1:B:202:ASP:HB3	2.36	0.55
1:C:195:PHE:HE2	1:C:240:LEU:O	1.89	0.54
1:D:195:PHE:HE2	1:D:240:LEU:O	1.89	0.54
1:C:8:ALA:CB	1:C:84:ASP:O	2.55	0.54
1:B:8:ALA:CB	1:B:84:ASP:O	2.55	0.54
1:C:216:GLU:HB2	1:C:224:LYS:HB2	1.89	0.54
1:A:138:LEU:HD12	1:A:204:ASN:ND2	2.22	0.54
1:E:5:ILE:HA	1:E:86:ILE:O	2.07	0.54
1:D:225:LEU:O	1:D:237:THR:HA	2.06	0.54
1:C:1:MET:HG3	1:C:91:ASP:HB2	1.89	0.54
1:C:92:GLU:O	1:C:93:GLU:HG2	2.05	0.54
1:F:138:LEU:HD12	1:F:204:ASN:ND2	2.22	0.54
1:A:1:MET:HG3	1:A:91:ASP:HB2	1.89	0.54
1:B:133:LEU:CG	1:B:183:LEU:HD11	2.32	0.54
1:C:94:THR:O	1:C:94:THR:HG22	2.08	0.54
1:B:20:VAL:HG13	1:B:202:ASP:CB	2.37	0.54
1:C:136:THR:HB	1:C:209:THR:CG2	2.37	0.54
1:B:149:SER:HB3	1:B:167:ALA:CB	2.22	0.54
1:B:136:THR:HB	1:B:209:THR:CG2	2.37	0.54
1:C:117:ARG:HG3	1:C:118:GLN:N	2.21	0.54
1:A:196:SER:H	1:A:240:LEU:CD2	2.21	0.54
1:C:146:ASP:HA	1:C:197:LEU:HD12	1.87	0.54
1:D:153:ARG:HG2	1:D:194:LEU:HD22	1.90	0.54
1:B:133:LEU:CG	1:B:183:LEU:CD1	2.80	0.54
1:D:94:THR:O	1:D:94:THR:HG22	2.08	0.54
1:B:225:LEU:O	1:B:237:THR:HA	2.06	0.54
1:C:156:VAL:HG21	1:C:217:LEU:CG	2.27	0.54
1:A:8:ALA:CB	1:A:84:ASP:O	2.55	0.54
1:B:5:ILE:HA	1:B:86:ILE:O	2.07	0.54
1:F:216:GLU:HB2	1:F:224:LYS:HB2	1.89	0.54
1:E:68:VAL:O	1:E:70:LEU:N	2.37	0.54
1:E:20:VAL:HG13	1:E:202:ASP:CB	2.37	0.54
1:E:136:THR:HB	1:E:209:THR:CG2	2.37	0.54
1:B:196:SER:H	1:B:240:LEU:CD2	2.21	0.54
1:F:183:LEU:O	1:F:185:SER:N	2.41	0.54
1:F:195:PHE:HE2	1:F:240:LEU:O	1.89	0.54
1:A:183:LEU:O	1:A:185:SER:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:127:LEU:HD22	1:F:218:GLY:HA3	1.88	0.54
1:D:136:THR:HB	1:D:209:THR:CG2	2.37	0.54
1:E:117:ARG:HG3	1:E:118:GLN:N	2.21	0.54
1:F:94:THR:HG22	1:F:94:THR:O	2.08	0.54
1:F:196:SER:H	1:F:240:LEU:CD2	2.21	0.54
1:F:200:LEU:HG	1:F:240:LEU:HD13	1.88	0.54
1:E:200:LEU:HG	1:E:240:LEU:HD13	1.88	0.54
1:B:183:LEU:O	1:B:185:SER:N	2.41	0.54
1:D:37:ARG:HB2	1:D:48:ASP:HA	1.90	0.54
1:C:49:LEU:HD21	1:C:236:ILE:HG22	1.88	0.54
1:E:37:ARG:HB2	1:E:48:ASP:HA	1.90	0.54
1:E:1:MET:HG3	1:E:91:ASP:HB2	1.89	0.54
1:C:138:LEU:HD12	1:C:204:ASN:ND2	2.22	0.54
1:C:183:LEU:O	1:C:185:SER:N	2.41	0.54
1:B:216:GLU:HB2	1:B:224:LYS:HB2	1.89	0.53
1:E:216:GLU:HB2	1:E:224:LYS:HB2	1.89	0.53
1:C:153:ARG:HG2	1:C:194:LEU:HD22	1.90	0.53
1:E:156:VAL:HG21	1:E:217:LEU:CG	2.27	0.53
1:D:146:ASP:HA	1:D:197:LEU:HD12	1.87	0.53
1:E:176:LEU:HD13	1:F:104:LEU:HB2	1.89	0.53
1:A:195:PHE:HE2	1:A:240:LEU:O	1.89	0.53
1:A:37:ARG:HB2	1:A:48:ASP:HA	1.90	0.53
1:A:146:ASP:HA	1:A:197:LEU:HD12	1.87	0.53
1:B:146:ASP:HA	1:B:197:LEU:HD12	1.87	0.53
1:E:11:LEU:HD21	1:E:77:ALA:HB1	1.91	0.53
1:B:37:ARG:HB2	1:B:48:ASP:HA	1.90	0.53
1:B:6:VAL:CG2	1:B:56:PHE:HD2	2.14	0.53
1:E:231:GLU:HB2	1:E:233:MET:HE2	1.90	0.53
1:E:94:THR:O	1:E:94:THR:HG22	2.08	0.53
1:E:153:ARG:HG2	1:E:194:LEU:HD22	1.90	0.53
1:E:183:LEU:O	1:E:185:SER:N	2.41	0.53
1:A:136:THR:HB	1:A:209:THR:CG2	2.37	0.53
1:D:191:ALA:CB	1:D:218:GLY:C	2.66	0.53
1:A:11:LEU:HD21	1:A:77:ALA:HB1	1.91	0.53
1:A:94:THR:O	1:A:94:THR:HG22	2.08	0.53
1:D:215:VAL:CG1	1:D:223:VAL:HG21	2.39	0.53
1:E:146:ASP:HA	1:E:197:LEU:HD12	1.87	0.53
1:F:6:VAL:CG2	1:F:56:PHE:HD2	2.14	0.53
1:E:171:THR:HG21	1:F:72:ARG:NH1	2.13	0.53
1:F:222:PRO:CB	1:F:239:MET:HG2	2.34	0.53
1:F:44:VAL:HG12	1:F:241:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:LEU:CG	1:A:183:LEU:CD1	2.80	0.53
1:D:44:VAL:HG12	1:D:241:ALA:HB2	1.91	0.53
1:C:3:LYS:O	1:C:59:TYR:CA	2.57	0.53
1:D:183:LEU:O	1:D:185:SER:N	2.41	0.53
1:D:20:VAL:CG1	1:D:202:ASP:HB3	2.36	0.53
1:E:149:SER:HB3	1:E:167:ALA:CB	2.22	0.53
1:B:153:ARG:HG2	1:B:194:LEU:HD22	1.90	0.53
1:D:196:SER:H	1:D:240:LEU:CD2	2.21	0.53
1:E:44:VAL:HG12	1:E:241:ALA:CB	2.39	0.53
1:B:94:THR:O	1:B:94:THR:HG22	2.08	0.53
1:C:20:VAL:HG13	1:C:202:ASP:CB	2.37	0.53
1:A:197:LEU:HD23	1:A:197:LEU:C	2.29	0.53
1:F:11:LEU:HD21	1:F:77:ALA:HB1	1.91	0.53
1:D:194:LEU:CD2	1:D:245:GLN:HG3	2.30	0.53
1:D:133:LEU:CG	1:D:183:LEU:CD1	2.80	0.53
1:B:11:LEU:HD21	1:B:77:ALA:HB1	1.91	0.53
1:F:1:MET:HG3	1:F:91:ASP:HB2	1.89	0.53
1:C:196:SER:H	1:C:240:LEU:CD2	2.21	0.53
1:F:104:LEU:C	1:F:104:LEU:HD13	2.30	0.53
1:E:133:LEU:CG	1:E:183:LEU:HD11	2.32	0.53
1:C:149:SER:OG	1:C:168:GLU:O	2.27	0.52
1:B:194:LEU:O	1:B:195:PHE:CG	2.63	0.52
1:F:215:VAL:CG1	1:F:223:VAL:HG21	2.39	0.52
1:D:44:VAL:HG12	1:D:241:ALA:CB	2.39	0.52
1:C:11:LEU:HD21	1:C:77:ALA:HB1	1.91	0.52
1:C:37:ARG:HB2	1:C:48:ASP:HA	1.90	0.52
1:F:20:VAL:HG13	1:F:202:ASP:CB	2.37	0.52
1:B:3:LYS:O	1:B:59:TYR:CA	2.57	0.52
1:A:149:SER:OG	1:A:168:GLU:O	2.27	0.52
1:B:215:VAL:CG1	1:B:223:VAL:HG21	2.39	0.52
1:C:131:ILE:CD1	1:C:217:LEU:HB2	2.40	0.52
1:E:131:ILE:CD1	1:E:217:LEU:HB2	2.40	0.52
1:E:196:SER:H	1:E:240:LEU:CD2	2.21	0.52
1:B:149:SER:OG	1:B:168:GLU:O	2.27	0.52
1:A:194:LEU:O	1:A:195:PHE:CG	2.63	0.52
1:F:44:VAL:HG12	1:F:241:ALA:CB	2.39	0.52
1:E:3:LYS:O	1:E:59:TYR:CA	2.57	0.52
1:F:131:ILE:CD1	1:F:217:LEU:HB2	2.40	0.52
1:F:3:LYS:O	1:F:59:TYR:CA	2.57	0.52
1:C:136:THR:OG1	1:C:209:THR:HG22	2.10	0.52
1:D:136:THR:OG1	1:D:209:THR:HG22	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:ASP:OD1	1:F:208:PRO:O	2.28	0.52
1:F:37:ARG:HB2	1:F:48:ASP:HA	1.90	0.52
1:C:44:VAL:HG12	1:C:241:ALA:CB	2.39	0.52
1:F:136:THR:OG1	1:F:209:THR:HG22	2.10	0.52
1:C:194:LEU:O	1:C:195:PHE:CG	2.62	0.52
1:C:197:LEU:C	1:C:197:LEU:HD23	2.29	0.52
1:B:136:THR:OG1	1:B:209:THR:HG22	2.10	0.52
1:A:139:ASP:OD1	1:A:208:PRO:O	2.28	0.52
1:B:44:VAL:HG12	1:B:241:ALA:CB	2.39	0.52
1:F:133:LEU:CG	1:F:183:LEU:HD11	2.32	0.52
1:A:104:LEU:HD13	1:A:104:LEU:C	2.30	0.52
1:E:194:LEU:O	1:E:195:PHE:CG	2.63	0.52
1:D:11:LEU:HD21	1:D:77:ALA:HB1	1.91	0.52
1:C:139:ASP:OD1	1:C:208:PRO:O	2.28	0.52
1:D:139:ASP:OD1	1:D:208:PRO:O	2.28	0.52
1:A:153:ARG:HG2	1:A:194:LEU:HD22	1.90	0.52
1:A:44:VAL:HG12	1:A:241:ALA:CB	2.39	0.52
1:F:106:TYR:HE2	1:F:108:LEU:HB2	1.75	0.52
1:D:175:ASP:O	1:E:104:LEU:HD22	2.09	0.52
1:E:104:LEU:HD13	1:E:104:LEU:C	2.30	0.52
1:C:133:LEU:CD2	1:C:183:LEU:HD12	2.40	0.52
1:D:104:LEU:C	1:D:104:LEU:HD13	2.30	0.52
1:F:197:LEU:HD23	1:F:197:LEU:C	2.29	0.52
1:E:44:VAL:HG12	1:E:241:ALA:HB2	1.91	0.52
1:C:37:ARG:CG	1:C:37:ARG:O	2.49	0.52
1:C:20:VAL:CG1	1:C:202:ASP:HB3	2.36	0.52
1:D:3:LYS:O	1:D:59:TYR:CA	2.57	0.52
1:F:133:LEU:CD2	1:F:183:LEU:HD12	2.40	0.52
1:A:131:ILE:CD1	1:A:217:LEU:HB2	2.40	0.52
1:A:8:ALA:HB3	1:A:84:ASP:H	1.75	0.52
1:D:194:LEU:O	1:D:195:PHE:CG	2.63	0.52
1:B:131:ILE:CD1	1:B:217:LEU:HB2	2.40	0.52
1:E:8:ALA:HB3	1:E:84:ASP:H	1.75	0.52
1:D:95:ARG:O	1:D:110:LEU:N	2.43	0.52
1:C:66:ILE:HG21	1:C:110:LEU:HD13	1.93	0.52
1:C:133:LEU:CG	1:C:183:LEU:HD11	2.32	0.52
1:B:139:ASP:OD1	1:B:208:PRO:O	2.28	0.52
1:B:197:LEU:HD23	1:B:197:LEU:C	2.29	0.51
1:B:222:PRO:CD	1:B:242:PRO:CG	2.64	0.51
1:D:8:ALA:HB3	1:D:84:ASP:H	1.75	0.51
1:B:106:TYR:HE2	1:B:108:LEU:HB2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:VAL:CG1	1:A:202:ASP:HB3	2.36	0.51
1:F:194:LEU:O	1:F:195:PHE:CG	2.62	0.51
1:E:95:ARG:O	1:E:110:LEU:N	2.43	0.51
1:A:106:TYR:HE2	1:A:108:LEU:HB2	1.75	0.51
1:D:222:PRO:CB	1:D:239:MET:HG2	2.34	0.51
1:D:133:LEU:CD2	1:D:183:LEU:HD12	2.40	0.51
1:A:57:GLU:OE1	1:A:57:GLU:N	2.44	0.51
1:F:20:VAL:CG1	1:F:202:ASP:HB3	2.36	0.51
1:B:133:LEU:CD2	1:B:183:LEU:HD12	2.40	0.51
1:C:57:GLU:OE1	1:C:57:GLU:N	2.44	0.51
1:C:8:ALA:HB3	1:C:84:ASP:H	1.75	0.51
1:F:8:ALA:HB3	1:F:84:ASP:H	1.75	0.51
1:A:20:VAL:HG13	1:A:202:ASP:CB	2.37	0.51
1:B:57:GLU:OE1	1:B:57:GLU:N	2.44	0.51
1:E:139:ASP:OD1	1:E:208:PRO:O	2.28	0.51
1:D:149:SER:OG	1:D:168:GLU:O	2.27	0.51
1:D:131:ILE:CD1	1:D:217:LEU:HB2	2.40	0.51
1:C:104:LEU:C	1:C:104:LEU:HD13	2.30	0.51
1:C:215:VAL:CG1	1:C:223:VAL:HG21	2.39	0.51
1:E:215:VAL:CG1	1:E:223:VAL:HG21	2.39	0.51
1:F:161:GLU:HB3	1:F:188:ALA:CB	2.41	0.51
1:E:133:LEU:CD2	1:E:183:LEU:HD12	2.40	0.51
1:A:3:LYS:O	1:A:59:TYR:CA	2.57	0.51
1:C:106:TYR:HE2	1:C:108:LEU:HB2	1.75	0.51
1:C:68:VAL:O	1:C:70:LEU:N	2.37	0.51
1:A:136:THR:OG1	1:A:209:THR:HG22	2.10	0.51
1:F:231:GLU:HB2	1:F:233:MET:HE2	1.91	0.51
1:D:161:GLU:HB3	1:D:188:ALA:CB	2.41	0.51
1:A:44:VAL:HG12	1:A:241:ALA:HB2	1.91	0.51
1:B:44:VAL:HG12	1:B:241:ALA:HB2	1.91	0.51
1:D:170:ASP:C	1:D:171:THR:HG22	2.31	0.51
1:C:95:ARG:O	1:C:110:LEU:N	2.43	0.51
1:A:29:LEU:HD12	1:A:29:LEU:N	2.26	0.51
1:E:136:THR:OG1	1:E:209:THR:HG22	2.10	0.51
1:E:149:SER:OG	1:E:168:GLU:O	2.27	0.51
1:E:56:PHE:N	1:E:56:PHE:CD1	2.79	0.51
1:B:8:ALA:HB3	1:B:84:ASP:H	1.75	0.51
1:B:95:ARG:O	1:B:110:LEU:N	2.43	0.51
1:A:58:SER:C	1:A:59:TYR:HD2	2.14	0.51
1:B:161:GLU:HB3	1:B:188:ALA:CB	2.41	0.51
1:E:58:SER:C	1:E:59:TYR:HD2	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:206:ALA:C	1:C:207:ILE:HD12	2.32	0.51
1:B:104:LEU:C	1:B:104:LEU:HD13	2.30	0.51
1:C:44:VAL:HG12	1:C:241:ALA:HB2	1.91	0.51
1:E:206:ALA:C	1:E:207:ILE:HD12	2.32	0.51
1:A:66:ILE:HG21	1:A:110:LEU:HD13	1.93	0.51
1:D:197:LEU:HD23	1:D:197:LEU:C	2.29	0.51
1:E:57:GLU:N	1:E:57:GLU:OE1	2.44	0.51
1:D:29:LEU:HD12	1:D:29:LEU:N	2.26	0.51
1:D:20:VAL:HG13	1:D:202:ASP:CB	2.37	0.51
1:F:153:ARG:HG2	1:F:194:LEU:HD22	1.90	0.50
1:D:57:GLU:OE1	1:D:57:GLU:N	2.44	0.50
1:F:58:SER:C	1:F:59:TYR:HD2	2.14	0.50
1:E:66:ILE:HG21	1:E:110:LEU:HD13	1.93	0.50
1:D:106:TYR:HE2	1:D:108:LEU:HB2	1.75	0.50
1:D:66:ILE:HG21	1:D:110:LEU:HD13	1.93	0.50
1:C:108:LEU:HD23	1:C:109:ALA:O	2.12	0.50
1:B:13:ASP:OD2	1:B:14:ALA:N	2.45	0.50
1:F:108:LEU:HD23	1:F:109:ALA:O	2.12	0.50
1:A:104:LEU:HD22	1:C:175:ASP:O	2.11	0.50
1:E:161:GLU:HB3	1:E:188:ALA:CB	2.41	0.50
1:A:95:ARG:O	1:A:110:LEU:N	2.43	0.50
1:A:107:THR:HG22	1:C:173:ASP:HB2	1.91	0.50
1:D:56:PHE:N	1:D:56:PHE:CD1	2.79	0.50
1:F:56:PHE:N	1:F:56:PHE:CD1	2.79	0.50
1:A:215:VAL:CG1	1:A:223:VAL:HG21	2.39	0.50
1:F:95:ARG:O	1:F:110:LEU:N	2.43	0.50
1:E:106:TYR:HE2	1:E:108:LEU:HB2	1.75	0.50
1:E:194:LEU:HD23	1:E:245:GLN:CG	2.34	0.50
1:B:66:ILE:HG21	1:B:110:LEU:HD13	1.92	0.50
1:C:184:ILE:HD13	1:C:212:GLU:OE2	2.12	0.50
1:B:184:ILE:HD13	1:B:212:GLU:OE2	2.12	0.50
1:C:58:SER:C	1:C:59:TYR:HD2	2.14	0.50
1:C:8:ALA:CB	1:C:84:ASP:H	2.25	0.50
1:B:29:LEU:N	1:B:29:LEU:HD12	2.26	0.50
1:F:29:LEU:N	1:F:29:LEU:HD12	2.26	0.50
1:D:13:ASP:OD2	1:D:14:ALA:N	2.45	0.50
1:E:13:ASP:OD2	1:E:14:ALA:N	2.45	0.50
1:A:133:LEU:CD2	1:A:183:LEU:HD12	2.40	0.50
1:A:206:ALA:C	1:A:207:ILE:HD12	2.32	0.50
1:E:8:ALA:CB	1:E:84:ASP:H	2.25	0.50
1:E:153:ARG:CG	1:E:194:LEU:HD21	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:184:ILE:HD13	1:D:212:GLU:OE2	2.12	0.50
1:A:173:ASP:HB2	1:B:107:THR:HG22	1.92	0.50
1:B:108:LEU:HD23	1:B:109:ALA:O	2.12	0.50
1:B:56:PHE:CD1	1:B:56:PHE:N	2.79	0.50
1:A:13:ASP:OD2	1:A:14:ALA:N	2.45	0.50
1:F:153:ARG:CG	1:F:194:LEU:HD21	2.42	0.50
1:D:194:LEU:HD23	1:D:245:GLN:CG	2.34	0.50
1:F:184:ILE:HD13	1:F:212:GLU:OE2	2.12	0.50
1:A:184:ILE:HD13	1:A:212:GLU:OE2	2.12	0.50
1:A:153:ARG:CG	1:A:194:LEU:HD21	2.42	0.50
1:D:108:LEU:HD23	1:D:109:ALA:O	2.12	0.50
1:F:8:ALA:CB	1:F:84:ASP:H	2.25	0.50
1:C:29:LEU:N	1:C:29:LEU:HD12	2.26	0.50
1:F:57:GLU:N	1:F:57:GLU:OE1	2.44	0.50
1:D:10:THR:HA	1:D:13:ASP:OD1	2.12	0.50
1:C:13:ASP:OD2	1:C:14:ALA:N	2.45	0.50
1:F:13:ASP:OD2	1:F:14:ALA:N	2.45	0.50
1:C:153:ARG:CG	1:C:194:LEU:HD21	2.42	0.50
1:D:206:ALA:C	1:D:207:ILE:HD12	2.32	0.50
1:F:191:ALA:CB	1:F:218:GLY:C	2.66	0.50
1:D:231:GLU:HB2	1:D:233:MET:HE2	1.94	0.50
1:B:10:THR:HA	1:B:13:ASP:OD1	2.12	0.50
1:A:10:THR:O	1:A:13:ASP:OD2	2.30	0.50
1:F:66:ILE:HG21	1:F:110:LEU:HD13	1.93	0.49
1:D:153:ARG:CG	1:D:194:LEU:HD21	2.42	0.49
1:D:58:SER:C	1:D:59:TYR:HD2	2.14	0.49
1:A:108:LEU:HD23	1:A:109:ALA:O	2.12	0.49
1:E:10:THR:HA	1:E:13:ASP:OD1	2.12	0.49
1:B:153:ARG:CG	1:B:194:LEU:HD21	2.42	0.49
1:C:194:LEU:HD23	1:C:245:GLN:CG	2.34	0.49
1:C:56:PHE:N	1:C:56:PHE:CD1	2.79	0.49
1:B:8:ALA:CB	1:B:84:ASP:H	2.25	0.49
1:B:58:SER:C	1:B:59:TYR:HD2	2.14	0.49
1:E:170:ASP:C	1:E:171:THR:HG22	2.31	0.49
1:E:108:LEU:HD23	1:E:109:ALA:O	2.12	0.49
1:F:206:ALA:C	1:F:207:ILE:HD12	2.32	0.49
1:A:8:ALA:CB	1:A:84:ASP:H	2.25	0.49
1:C:170:ASP:C	1:C:171:THR:HG22	2.31	0.49
1:E:29:LEU:N	1:E:29:LEU:HD12	2.26	0.49
1:B:10:THR:O	1:B:13:ASP:OD2	2.30	0.49
1:F:149:SER:OG	1:F:168:GLU:O	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:194:LEU:HD23	1:F:245:GLN:CG	2.34	0.49
1:C:56:PHE:HE1	1:C:59:TYR:CZ	2.31	0.49
1:E:56:PHE:HE1	1:E:59:TYR:CZ	2.31	0.49
1:B:56:PHE:HE1	1:B:59:TYR:CZ	2.31	0.49
1:A:10:THR:HA	1:A:13:ASP:OD1	2.12	0.49
1:A:194:LEU:HD23	1:A:245:GLN:CG	2.34	0.49
1:D:8:ALA:CB	1:D:84:ASP:H	2.25	0.49
1:C:162:THR:HG22	1:C:163:PHE:N	2.28	0.49
1:E:68:VAL:HG11	1:E:73:LEU:HD12	1.95	0.49
1:D:142:ILE:HA	1:D:152:ILE:HD11	1.95	0.49
1:C:68:VAL:HG11	1:C:73:LEU:HD12	1.95	0.49
1:D:56:PHE:HE1	1:D:59:TYR:CZ	2.31	0.49
1:C:231:GLU:HB2	1:C:233:MET:HE3	1.92	0.49
1:E:10:THR:O	1:E:13:ASP:OD2	2.30	0.49
1:E:184:ILE:HD13	1:E:212:GLU:OE2	2.12	0.49
1:B:195:PHE:HD2	1:B:240:LEU:CD2	2.26	0.49
1:C:195:PHE:HD2	1:C:240:LEU:CD2	2.26	0.49
1:D:68:VAL:HG11	1:D:73:LEU:HD12	1.95	0.49
1:A:231:GLU:HB2	1:A:233:MET:HE3	1.95	0.49
1:C:10:THR:O	1:C:13:ASP:OD2	2.30	0.49
1:F:68:VAL:HG11	1:F:73:LEU:HD12	1.95	0.49
1:F:195:PHE:HD2	1:F:240:LEU:CD2	2.26	0.49
1:F:194:LEU:HB3	1:F:243:ARG:HB2	1.95	0.49
1:E:142:ILE:HA	1:E:152:ILE:HD11	1.95	0.49
1:F:157:ASP:CA	1:F:160:GLU:O	2.61	0.49
1:B:206:ALA:C	1:B:207:ILE:HD12	2.32	0.49
1:D:10:THR:O	1:D:13:ASP:OD2	2.30	0.49
1:C:10:THR:HA	1:C:13:ASP:OD1	2.12	0.49
1:F:10:THR:HA	1:F:13:ASP:OD1	2.12	0.49
1:A:194:LEU:HB3	1:A:243:ARG:HB2	1.95	0.48
1:B:142:ILE:HA	1:B:152:ILE:HD11	1.95	0.48
1:A:56:PHE:HE1	1:A:59:TYR:CZ	2.31	0.48
1:F:10:THR:O	1:F:13:ASP:OD2	2.30	0.48
1:B:194:LEU:HB3	1:B:243:ARG:HB2	1.95	0.48
1:A:161:GLU:HB3	1:A:188:ALA:CB	2.41	0.48
1:E:162:THR:HG22	1:E:163:PHE:N	2.28	0.48
1:D:157:ASP:CA	1:D:160:GLU:O	2.61	0.48
1:C:194:LEU:HB3	1:C:243:ARG:HB2	1.95	0.48
1:A:68:VAL:HG11	1:A:73:LEU:HD12	1.95	0.48
1:C:5:ILE:HD13	1:D:184:ILE:O	2.13	0.48
1:C:107:THR:CG2	1:C:107:THR:O	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:157:ASP:CA	1:E:160:GLU:O	2.61	0.48
1:C:161:GLU:HB3	1:C:188:ALA:CB	2.41	0.48
1:C:142:ILE:HA	1:C:152:ILE:HD11	1.95	0.48
1:D:107:THR:O	1:D:107:THR:CG2	2.61	0.48
1:B:170:ASP:C	1:B:171:THR:HG22	2.31	0.48
1:A:170:ASP:C	1:A:171:THR:HG22	2.31	0.48
1:A:142:ILE:HA	1:A:152:ILE:HD11	1.95	0.48
1:A:195:PHE:HD2	1:A:240:LEU:CD2	2.26	0.48
1:C:157:ASP:CA	1:C:160:GLU:O	2.61	0.48
1:F:107:THR:CG2	1:F:107:THR:O	2.61	0.48
1:F:142:ILE:HA	1:F:152:ILE:HD11	1.95	0.48
1:D:195:PHE:HD2	1:D:240:LEU:CD2	2.26	0.48
1:B:162:THR:HG22	1:B:163:PHE:N	2.28	0.48
1:A:20:VAL:HG12	1:A:21:LEU:HD23	1.96	0.48
1:A:56:PHE:CD1	1:A:56:PHE:N	2.79	0.48
1:D:56:PHE:CD1	1:D:59:TYR:CD2	3.02	0.48
1:D:104:LEU:HD22	1:F:175:ASP:O	2.12	0.48
1:C:56:PHE:CD1	1:C:59:TYR:CD2	3.02	0.48
1:F:170:ASP:C	1:F:171:THR:HG22	2.31	0.48
1:F:162:THR:HG22	1:F:163:PHE:N	2.28	0.48
1:D:20:VAL:HG12	1:D:21:LEU:HD23	1.95	0.48
1:B:175:ASP:O	1:C:104:LEU:CD2	2.62	0.48
1:A:162:THR:HG22	1:A:163:PHE:N	2.28	0.48
1:E:156:VAL:CG1	1:E:191:ALA:O	2.62	0.48
1:E:56:PHE:CD1	1:E:59:TYR:CD2	3.02	0.48
1:F:56:PHE:HE1	1:F:59:TYR:CZ	2.31	0.48
1:A:152:ILE:HD13	1:A:165:ILE:HG21	1.96	0.48
1:F:152:ILE:HD13	1:F:165:ILE:HG21	1.96	0.48
1:D:195:PHE:CE2	1:D:242:PRO:CD	2.73	0.48
1:E:195:PHE:CE2	1:E:242:PRO:CD	2.73	0.48
1:B:47:VAL:HB	1:B:238:TYR:CE2	2.49	0.48
1:C:47:VAL:HB	1:C:238:TYR:CE2	2.49	0.48
1:C:20:VAL:HG12	1:C:21:LEU:HD23	1.96	0.48
1:F:56:PHE:CD1	1:F:59:TYR:CD2	3.02	0.48
1:C:149:SER:HB3	1:C:167:ALA:CB	2.22	0.48
1:C:156:VAL:CG1	1:C:191:ALA:O	2.62	0.48
1:E:97:LEU:HB2	1:E:110:LEU:HD21	1.96	0.48
1:D:152:ILE:HD13	1:D:165:ILE:HG21	1.96	0.48
1:F:156:VAL:CG1	1:F:191:ALA:O	2.62	0.48
1:F:47:VAL:HB	1:F:238:TYR:CE2	2.49	0.48
1:B:3:LYS:O	1:B:59:TYR:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:VAL:CG1	1:B:241:ALA:HB2	2.44	0.47
1:A:72:ARG:NH1	1:C:171:THR:HG21	2.13	0.47
1:D:194:LEU:HB3	1:D:243:ARG:HB2	1.95	0.47
1:B:56:PHE:CD1	1:B:59:TYR:CD2	3.02	0.47
1:F:3:LYS:O	1:F:59:TYR:HB3	2.14	0.47
1:C:151:HIS:CB	1:C:195:PHE:O	2.62	0.47
1:C:44:VAL:CG1	1:C:241:ALA:HB2	2.44	0.47
1:D:186:ILE:CG2	1:D:187:GLU:N	2.77	0.47
1:D:97:LEU:HB2	1:D:110:LEU:HD21	1.96	0.47
1:D:47:VAL:HB	1:D:238:TYR:CE2	2.49	0.47
1:B:152:ILE:HD13	1:B:165:ILE:HG21	1.96	0.47
1:B:151:HIS:CB	1:B:195:PHE:O	2.62	0.47
1:A:133:LEU:CG	1:A:183:LEU:HD11	2.32	0.47
1:D:151:HIS:CB	1:D:195:PHE:O	2.62	0.47
1:E:195:PHE:HD2	1:E:240:LEU:CD2	2.26	0.47
1:E:151:HIS:CB	1:E:195:PHE:O	2.62	0.47
1:B:68:VAL:HG11	1:B:73:LEU:HD12	1.95	0.47
1:E:65:VAL:HG22	1:E:113:PRO:CG	2.44	0.47
1:D:44:VAL:CG1	1:D:241:ALA:HB2	2.44	0.47
1:B:157:ASP:CA	1:B:160:GLU:O	2.61	0.47
1:E:186:ILE:CG2	1:E:187:GLU:N	2.78	0.47
1:A:5:ILE:O	1:A:56:PHE:HA	2.15	0.47
1:E:20:VAL:HG12	1:E:21:LEU:HD23	1.95	0.47
1:D:162:THR:HG22	1:D:163:PHE:N	2.28	0.47
1:A:44:VAL:CG1	1:A:241:ALA:HB2	2.44	0.47
1:F:240:LEU:HD23	1:F:241:ALA:N	2.30	0.47
1:A:65:VAL:HG22	1:A:113:PRO:CG	2.45	0.47
1:E:152:ILE:HD13	1:E:165:ILE:HG21	1.96	0.47
1:E:175:ASP:O	1:F:104:LEU:HD22	2.14	0.47
1:C:97:LEU:HB2	1:C:110:LEU:HD21	1.96	0.47
1:B:194:LEU:HD23	1:B:245:GLN:CG	2.34	0.47
1:F:151:HIS:CB	1:F:195:PHE:O	2.62	0.47
1:E:194:LEU:HB3	1:E:243:ARG:HB2	1.95	0.47
1:E:5:ILE:O	1:E:56:PHE:HA	2.15	0.47
1:B:173:ASP:HB2	1:C:107:THR:HG23	1.90	0.47
1:C:133:LEU:O	1:C:213:VAL:N	2.29	0.47
1:E:47:VAL:HB	1:E:238:TYR:CE2	2.49	0.47
1:A:56:PHE:CD1	1:A:59:TYR:CD2	3.02	0.47
1:D:5:ILE:O	1:D:56:PHE:HA	2.15	0.47
1:A:151:HIS:CB	1:A:195:PHE:O	2.62	0.47
1:B:146:ASP:C	1:B:147:MET:HG3	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:133:LEU:HD23	1:F:133:LEU:HA	1.74	0.47
1:F:65:VAL:HG22	1:F:113:PRO:CG	2.45	0.47
1:C:146:ASP:C	1:C:147:MET:HG3	2.35	0.47
1:F:44:VAL:CG1	1:F:241:ALA:HB2	2.44	0.47
1:A:157:ASP:CA	1:A:160:GLU:O	2.61	0.47
1:A:97:LEU:HB2	1:A:110:LEU:HD21	1.96	0.47
1:B:186:ILE:CG2	1:B:187:GLU:N	2.78	0.47
1:D:65:VAL:HG22	1:D:113:PRO:CG	2.44	0.47
1:C:65:VAL:HG22	1:C:113:PRO:CG	2.45	0.47
1:B:97:LEU:HB2	1:B:110:LEU:HD21	1.96	0.47
1:A:47:VAL:HB	1:A:238:TYR:CE2	2.49	0.47
1:A:3:LYS:O	1:A:59:TYR:HB3	2.14	0.47
1:D:3:LYS:O	1:D:59:TYR:HB3	2.14	0.47
1:B:20:VAL:HG12	1:B:21:LEU:HD23	1.96	0.47
1:F:4:ALA:HB1	1:F:56:PHE:CD2	2.50	0.47
1:A:240:LEU:HD23	1:A:241:ALA:N	2.30	0.47
1:D:240:LEU:HD23	1:D:241:ALA:N	2.30	0.47
1:E:4:ALA:HB1	1:E:56:PHE:CD2	2.50	0.47
1:F:20:VAL:HG12	1:F:21:LEU:HD23	1.96	0.47
1:B:4:ALA:HB1	1:B:56:PHE:CD2	2.50	0.47
1:B:195:PHE:CE2	1:B:242:PRO:CD	2.73	0.47
1:B:240:LEU:HD23	1:B:241:ALA:N	2.30	0.47
1:E:44:VAL:CG1	1:E:241:ALA:HB2	2.44	0.47
1:C:3:LYS:O	1:C:59:TYR:HB3	2.14	0.47
1:E:3:LYS:O	1:E:59:TYR:HB3	2.14	0.47
1:B:65:VAL:HG22	1:B:113:PRO:CG	2.44	0.47
1:C:4:ALA:HB1	1:C:56:PHE:CD2	2.50	0.47
1:C:5:ILE:O	1:C:56:PHE:HA	2.15	0.47
1:F:8:ALA:HB3	1:F:82:ALA:CA	2.45	0.47
1:A:4:ALA:HB1	1:A:56:PHE:CD2	2.50	0.47
1:F:5:ILE:O	1:F:56:PHE:HA	2.15	0.47
1:D:156:VAL:HA	1:D:162:THR:O	2.16	0.46
1:A:175:ASP:O	1:B:104:LEU:HD22	2.14	0.46
1:C:152:ILE:HD13	1:C:165:ILE:HG21	1.96	0.46
1:C:8:ALA:HB3	1:C:82:ALA:CA	2.45	0.46
1:F:158:GLY:O	1:F:159:ALA:CB	2.63	0.46
1:C:240:LEU:HD23	1:C:241:ALA:N	2.30	0.46
1:E:107:THR:O	1:E:107:THR:CG2	2.61	0.46
1:D:146:ASP:C	1:D:147:MET:HG3	2.35	0.46
1:D:133:LEU:CG	1:D:183:LEU:HD11	2.32	0.46
1:F:156:VAL:HA	1:F:162:THR:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:146:ASP:C	1:F:147:MET:HG3	2.35	0.46
1:A:186:ILE:CG2	1:A:187:GLU:N	2.78	0.46
1:C:5:ILE:HB	1:C:57:GLU:OE1	2.15	0.46
1:B:172:ASP:OD1	1:C:108:LEU:HG	2.15	0.46
1:B:5:ILE:O	1:B:56:PHE:HA	2.15	0.46
1:D:4:ALA:HB1	1:D:56:PHE:CD2	2.50	0.46
1:A:146:ASP:C	1:A:147:MET:HG3	2.35	0.46
1:F:97:LEU:HB2	1:F:110:LEU:HD21	1.96	0.46
1:F:186:ILE:CG2	1:F:187:GLU:N	2.78	0.46
1:A:173:ASP:HB2	1:B:107:THR:HG23	1.93	0.46
1:B:73:LEU:O	1:B:76:VAL:HG12	2.16	0.46
1:E:133:LEU:HD23	1:E:133:LEU:HA	1.74	0.46
1:B:5:ILE:HB	1:B:57:GLU:OE1	2.15	0.46
1:C:131:ILE:HD13	1:C:217:LEU:HD23	1.98	0.46
1:E:156:VAL:HA	1:E:162:THR:O	2.16	0.46
1:E:146:ASP:C	1:E:147:MET:HG3	2.35	0.46
1:C:47:VAL:HG13	1:C:47:VAL:O	2.16	0.46
1:B:107:THR:O	1:B:107:THR:CG2	2.61	0.46
1:A:149:SER:HB3	1:A:167:ALA:CB	2.22	0.46
1:C:195:PHE:CE2	1:C:242:PRO:CD	2.73	0.46
1:A:156:VAL:CG1	1:A:191:ALA:O	2.62	0.46
1:E:5:ILE:HB	1:E:57:GLU:OE1	2.15	0.46
1:C:8:ALA:HB2	1:C:84:ASP:HB2	1.98	0.46
1:C:186:ILE:CG2	1:C:187:GLU:N	2.78	0.46
1:D:47:VAL:O	1:D:47:VAL:HG13	2.16	0.46
1:F:47:VAL:O	1:F:47:VAL:HG13	2.16	0.46
1:F:5:ILE:HB	1:F:57:GLU:OE1	2.15	0.46
1:A:133:LEU:CG	1:A:183:LEU:HD12	2.45	0.46
1:B:156:VAL:CG1	1:B:191:ALA:O	2.62	0.46
1:B:8:ALA:HB2	1:B:84:ASP:HB2	1.98	0.46
1:D:5:ILE:HB	1:D:57:GLU:OE1	2.16	0.46
1:B:65:VAL:HG22	1:B:113:PRO:HG2	1.98	0.46
1:A:47:VAL:HG13	1:A:47:VAL:O	2.16	0.46
1:D:8:ALA:HB3	1:D:82:ALA:CA	2.45	0.46
1:A:8:ALA:HB2	1:A:84:ASP:HB2	1.98	0.46
1:E:131:ILE:HG22	1:E:132:VAL:N	2.31	0.46
1:A:107:THR:O	1:A:107:THR:CG2	2.61	0.46
1:B:156:VAL:HA	1:B:162:THR:O	2.16	0.46
1:D:133:LEU:HA	1:D:133:LEU:HD23	1.74	0.46
1:C:133:LEU:CG	1:C:183:LEU:HD12	2.45	0.46
1:B:29:LEU:HB3	1:B:34:LEU:HD22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:VAL:HB	1:B:22:VAL:HG22	1.98	0.46
1:F:133:LEU:CG	1:F:183:LEU:HD12	2.45	0.46
1:D:133:LEU:CG	1:D:183:LEU:HD12	2.45	0.46
1:F:131:ILE:HG22	1:F:132:VAL:N	2.31	0.46
1:B:8:ALA:HB3	1:B:82:ALA:CA	2.45	0.46
1:A:5:ILE:HB	1:A:57:GLU:OE1	2.15	0.46
1:A:18:VAL:HB	1:A:22:VAL:HG22	1.98	0.46
1:D:131:ILE:HD13	1:D:217:LEU:HD23	1.98	0.45
1:C:131:ILE:HG22	1:C:132:VAL:N	2.31	0.45
1:C:156:VAL:HA	1:C:162:THR:O	2.16	0.45
1:F:138:LEU:O	1:F:138:LEU:HD13	2.17	0.45
1:A:131:ILE:HG22	1:A:132:VAL:N	2.31	0.45
1:A:8:ALA:HB3	1:A:82:ALA:CA	2.45	0.45
1:D:176:LEU:HD13	1:E:104:LEU:HD23	1.97	0.45
1:B:131:ILE:HG22	1:B:132:VAL:N	2.31	0.45
1:B:47:VAL:HG13	1:B:47:VAL:O	2.16	0.45
1:C:65:VAL:HG22	1:C:113:PRO:HG2	1.98	0.45
1:F:131:ILE:HD13	1:F:217:LEU:HD23	1.98	0.45
1:E:73:LEU:O	1:E:76:VAL:HG12	2.16	0.45
1:A:180:PRO:O	1:A:183:LEU:CB	2.65	0.45
1:A:69:ASN:HB2	1:A:108:LEU:HD21	1.99	0.45
1:B:131:ILE:HD13	1:B:217:LEU:HD23	1.98	0.45
1:B:173:ASP:HB2	1:C:107:THR:HG22	1.92	0.45
1:C:180:PRO:O	1:C:183:LEU:CB	2.65	0.45
1:E:133:LEU:CG	1:E:183:LEU:HD12	2.45	0.45
1:F:29:LEU:HB3	1:F:34:LEU:HD22	1.98	0.45
1:E:18:VAL:HB	1:E:22:VAL:HG22	1.98	0.45
1:F:73:LEU:O	1:F:76:VAL:HG12	2.16	0.45
1:E:131:ILE:HD13	1:E:217:LEU:HD23	1.98	0.45
1:E:47:VAL:HG13	1:E:47:VAL:O	2.16	0.45
1:C:18:VAL:HB	1:C:22:VAL:HG22	1.98	0.45
1:D:240:LEU:CD2	1:D:241:ALA:O	2.62	0.45
1:D:65:VAL:HG22	1:D:113:PRO:HG2	1.98	0.45
1:D:138:LEU:O	1:D:138:LEU:HD13	2.17	0.45
1:E:180:PRO:O	1:E:183:LEU:CB	2.65	0.45
1:A:156:VAL:HA	1:A:162:THR:O	2.16	0.45
1:D:73:LEU:O	1:D:76:VAL:HG12	2.16	0.45
1:F:8:ALA:HB2	1:F:84:ASP:HB2	1.98	0.45
1:A:29:LEU:HB3	1:A:34:LEU:HD22	1.98	0.45
1:F:65:VAL:HG22	1:F:113:PRO:HG2	1.98	0.45
1:B:158:GLY:O	1:B:159:ALA:CB	2.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:PRO:O	1:B:183:LEU:CB	2.65	0.45
1:D:49:LEU:CD2	1:D:236:ILE:HG22	2.47	0.45
1:C:69:ASN:HB2	1:C:108:LEU:HD21	1.99	0.45
1:C:73:LEU:O	1:C:76:VAL:HG12	2.16	0.45
1:B:138:LEU:O	1:B:138:LEU:HD13	2.17	0.45
1:E:29:LEU:HB3	1:E:34:LEU:HD22	1.98	0.45
1:D:155:ARG:O	1:D:163:PHE:HA	2.17	0.45
1:B:176:LEU:HD13	1:C:104:LEU:HD23	1.98	0.45
1:E:155:ARG:O	1:E:163:PHE:HA	2.17	0.45
1:E:240:LEU:HD23	1:E:241:ALA:N	2.30	0.45
1:D:180:PRO:O	1:D:183:LEU:CB	2.65	0.45
1:C:29:LEU:HB3	1:C:34:LEU:HD22	1.98	0.45
1:F:95:ARG:C	1:F:110:LEU:H	2.20	0.45
1:C:240:LEU:O	1:C:242:PRO:HD3	2.17	0.45
1:A:108:LEU:HG	1:C:172:ASP:OD1	2.17	0.45
1:A:107:THR:HG23	1:C:173:ASP:HB2	1.95	0.45
1:C:106:TYR:CE2	1:C:108:LEU:HB2	2.52	0.45
1:B:26:LYS:HA	1:B:67:GLY:HA2	1.99	0.45
1:F:180:PRO:O	1:F:183:LEU:CB	2.65	0.45
1:D:8:ALA:HB2	1:D:84:ASP:HB2	1.98	0.45
1:D:173:ASP:HB2	1:E:107:THR:HG23	1.93	0.45
1:E:138:LEU:HD13	1:E:138:LEU:O	2.17	0.45
1:E:69:ASN:HB2	1:E:108:LEU:HD21	1.98	0.45
1:E:199:TYR:O	1:E:203:MET:HG3	2.17	0.45
1:C:49:LEU:CD2	1:C:236:ILE:HG22	2.47	0.45
1:B:240:LEU:O	1:B:242:PRO:HD3	2.17	0.45
1:A:155:ARG:O	1:A:163:PHE:HA	2.17	0.45
1:A:49:LEU:CD2	1:A:236:ILE:HG22	2.47	0.45
1:A:26:LYS:HA	1:A:67:GLY:HA2	1.99	0.45
1:D:133:LEU:O	1:D:213:VAL:N	2.29	0.45
1:C:26:LYS:HA	1:C:67:GLY:HA2	1.99	0.45
1:F:155:ARG:O	1:F:163:PHE:HA	2.17	0.45
1:D:156:VAL:CG1	1:D:191:ALA:O	2.62	0.44
1:C:151:HIS:HB3	1:C:195:PHE:O	2.18	0.44
1:C:199:TYR:O	1:C:203:MET:HG3	2.17	0.44
1:F:240:LEU:O	1:F:242:PRO:HD3	2.17	0.44
1:A:131:ILE:HG12	1:A:163:PHE:CD1	2.52	0.44
1:E:65:VAL:HG22	1:E:113:PRO:HG2	1.98	0.44
1:A:95:ARG:C	1:A:110:LEU:H	2.20	0.44
1:B:155:ARG:O	1:B:163:PHE:HA	2.17	0.44
1:E:197:LEU:C	1:E:197:LEU:HD23	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:66:ILE:CD1	1:D:90:LEU:HD13	2.47	0.44
1:B:49:LEU:CD2	1:B:236:ILE:HG22	2.47	0.44
1:D:131:ILE:HG22	1:D:132:VAL:N	2.31	0.44
1:F:106:TYR:CE2	1:F:108:LEU:HB2	2.52	0.44
1:A:66:ILE:CD1	1:A:90:LEU:HD13	2.47	0.44
1:D:106:TYR:CE2	1:D:108:LEU:HB2	2.52	0.44
1:B:66:ILE:CD1	1:B:90:LEU:HD13	2.47	0.44
1:F:18:VAL:HB	1:F:22:VAL:HG22	1.98	0.44
1:D:18:VAL:HB	1:D:22:VAL:HG22	1.98	0.44
1:F:26:LYS:HA	1:F:67:GLY:HA2	1.99	0.44
1:F:66:ILE:CD1	1:F:90:LEU:HD13	2.48	0.44
1:A:158:GLY:O	1:A:159:ALA:CB	2.63	0.44
1:A:73:LEU:O	1:A:76:VAL:HG12	2.16	0.44
1:D:240:LEU:O	1:D:242:PRO:HD3	2.17	0.44
1:E:8:ALA:HB2	1:E:84:ASP:HB2	1.98	0.44
1:B:179:PRO:HG2	1:D:179:PRO:CG	2.47	0.44
1:C:138:LEU:HD13	1:C:138:LEU:O	2.17	0.44
1:C:95:ARG:C	1:C:110:LEU:H	2.20	0.44
1:D:131:ILE:HG12	1:D:163:PHE:CD1	2.52	0.44
1:A:199:TYR:O	1:A:203:MET:HG3	2.17	0.44
1:E:106:TYR:CE2	1:E:108:LEU:HB2	2.52	0.44
1:E:158:GLY:O	1:E:159:ALA:CB	2.64	0.44
1:A:138:LEU:HD13	1:A:138:LEU:O	2.17	0.44
1:D:69:ASN:HB2	1:D:108:LEU:HD21	1.99	0.44
1:B:95:ARG:C	1:B:110:LEU:H	2.20	0.44
1:D:29:LEU:HB3	1:D:34:LEU:HD22	1.98	0.44
1:B:151:HIS:HB3	1:B:195:PHE:O	2.18	0.44
1:C:155:ARG:O	1:C:163:PHE:HA	2.17	0.44
1:E:66:ILE:CD1	1:E:90:LEU:HD13	2.48	0.44
1:E:131:ILE:HG12	1:E:163:PHE:CD1	2.52	0.44
1:A:65:VAL:HG22	1:A:113:PRO:HG2	1.98	0.44
1:D:95:ARG:C	1:D:110:LEU:H	2.20	0.44
1:D:2:PHE:CD1	1:D:90:LEU:HD12	2.53	0.44
1:C:207:ILE:N	1:C:207:ILE:CD1	2.81	0.44
1:F:69:ASN:HB2	1:F:108:LEU:HD21	1.99	0.44
1:F:151:HIS:HB3	1:F:195:PHE:O	2.18	0.44
1:D:151:HIS:HB3	1:D:195:PHE:O	2.18	0.44
1:E:240:LEU:O	1:E:242:PRO:HD3	2.17	0.44
1:C:2:PHE:CD1	1:C:90:LEU:HD12	2.53	0.44
1:B:69:ASN:HB2	1:B:108:LEU:HD21	1.98	0.44
1:B:199:TYR:O	1:B:203:MET:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:49:LEU:CD2	1:F:236:ILE:HG22	2.47	0.44
1:A:131:ILE:HD13	1:A:217:LEU:HD23	1.98	0.44
1:E:95:ARG:C	1:E:110:LEU:H	2.20	0.44
1:E:8:ALA:HB3	1:E:82:ALA:CA	2.45	0.44
1:D:155:ARG:HB3	1:D:164:HIS:HB2	2.00	0.44
1:A:240:LEU:O	1:A:242:PRO:HD3	2.17	0.44
1:A:133:LEU:O	1:A:213:VAL:N	2.28	0.44
1:E:150:ASP:O	1:E:197:LEU:HB3	2.18	0.44
1:C:66:ILE:CD1	1:C:90:LEU:HD13	2.47	0.44
1:A:173:ASP:HB2	1:B:107:THR:HG21	1.93	0.44
1:B:207:ILE:N	1:B:207:ILE:CD1	2.81	0.44
1:D:157:ASP:CB	1:D:160:GLU:O	2.66	0.44
1:C:150:ASP:O	1:C:197:LEU:HB3	2.18	0.44
1:F:195:PHE:CE2	1:F:242:PRO:CD	2.73	0.44
1:E:207:ILE:CD1	1:E:207:ILE:N	2.81	0.44
1:B:131:ILE:HG12	1:B:163:PHE:CD1	2.52	0.44
1:D:26:LYS:HA	1:D:67:GLY:HA2	1.99	0.44
1:F:29:LEU:HG	1:F:34:LEU:HB3	2.00	0.44
1:A:240:LEU:CD2	1:A:241:ALA:O	2.62	0.43
1:C:155:ARG:HB3	1:C:164:HIS:HB2	2.00	0.43
1:F:35:SER:HB2	1:F:49:LEU:O	2.18	0.43
1:A:155:ARG:HB3	1:A:164:HIS:HB2	2.00	0.43
1:D:173:ASP:HB2	1:E:107:THR:HG21	1.96	0.43
1:A:207:ILE:HG21	1:A:227:TYR:OH	2.18	0.43
1:A:2:PHE:CD1	1:A:90:LEU:HD12	2.53	0.43
1:D:199:TYR:O	1:D:203:MET:HG3	2.17	0.43
1:B:106:TYR:CE2	1:B:108:LEU:HB2	2.52	0.43
1:A:195:PHE:CE2	1:A:242:PRO:CD	2.73	0.43
1:C:131:ILE:HG12	1:C:163:PHE:CD1	2.52	0.43
1:C:157:ASP:CB	1:C:160:GLU:O	2.66	0.43
1:F:73:LEU:HD23	1:F:76:VAL:HG13	2.00	0.43
1:F:150:ASP:O	1:F:197:LEU:HB3	2.18	0.43
1:F:199:TYR:O	1:F:203:MET:HG3	2.17	0.43
1:E:207:ILE:HG21	1:E:227:TYR:OH	2.18	0.43
1:D:150:ASP:O	1:D:197:LEU:HB3	2.18	0.43
1:B:157:ASP:CB	1:B:160:GLU:O	2.66	0.43
1:C:73:LEU:HD23	1:C:76:VAL:HG13	2.00	0.43
1:F:131:ILE:HG12	1:F:163:PHE:CD1	2.52	0.43
1:A:172:ASP:OD1	1:B:108:LEU:HG	2.18	0.43
1:C:122:ILE:O	1:C:123:PRO:C	2.56	0.43
1:A:198:ASP:C	1:A:200:LEU:H	2.22	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:ALA:O	1:C:84:ASP:N	2.51	0.43
1:C:207:ILE:HG21	1:C:227:TYR:OH	2.19	0.43
1:B:35:SER:HB2	1:B:49:LEU:O	2.18	0.43
1:A:150:ASP:O	1:A:197:LEU:HB3	2.18	0.43
1:E:49:LEU:CD2	1:E:236:ILE:HG22	2.47	0.43
1:A:235:THR:HG22	1:A:236:ILE:N	2.34	0.43
1:D:207:ILE:HG21	1:D:227:TYR:OH	2.18	0.43
1:D:107:THR:HG22	1:F:173:ASP:HB2	1.98	0.43
1:B:82:ALA:O	1:B:84:ASP:N	2.51	0.43
1:D:20:VAL:HG12	1:D:21:LEU:CD2	2.49	0.43
1:E:20:VAL:HG12	1:E:21:LEU:CD2	2.49	0.43
1:A:176:LEU:HD13	1:B:104:LEU:HD23	2.00	0.43
1:B:184:ILE:O	1:E:5:ILE:HD13	2.18	0.43
1:F:155:ARG:HB3	1:F:164:HIS:HB2	2.00	0.43
1:F:157:ASP:CB	1:F:160:GLU:O	2.66	0.43
1:B:2:PHE:CD1	1:B:90:LEU:HD12	2.53	0.43
1:F:20:VAL:HG12	1:F:21:LEU:CD2	2.49	0.43
1:F:235:THR:HG22	1:F:236:ILE:N	2.34	0.43
1:F:145:ALA:O	1:F:197:LEU:HD13	2.19	0.43
1:D:171:THR:HG21	1:E:72:ARG:NH1	2.19	0.43
1:E:2:PHE:CD1	1:E:90:LEU:HD12	2.53	0.43
1:B:155:ARG:HB3	1:B:164:HIS:HB2	2.00	0.43
1:B:133:LEU:HD23	1:B:133:LEU:HA	1.74	0.43
1:F:82:ALA:O	1:F:84:ASP:N	2.51	0.43
1:B:27:ILE:HD12	1:B:68:VAL:HG21	2.01	0.43
1:B:73:LEU:HD23	1:B:76:VAL:HG13	2.00	0.43
1:C:20:VAL:HG12	1:C:21:LEU:CD2	2.49	0.43
1:E:122:ILE:O	1:E:123:PRO:C	2.56	0.43
1:C:145:ALA:O	1:C:197:LEU:HD13	2.19	0.43
1:C:240:LEU:CD2	1:C:241:ALA:O	2.62	0.43
1:F:198:ASP:C	1:F:200:LEU:H	2.22	0.43
1:E:82:ALA:O	1:E:84:ASP:N	2.51	0.43
1:D:73:LEU:CA	1:D:76:VAL:HG12	2.49	0.43
1:E:56:PHE:CD1	1:E:59:TYR:CE2	3.07	0.43
1:B:56:PHE:CD1	1:B:59:TYR:CE2	3.07	0.43
1:F:56:PHE:CD1	1:F:59:TYR:CE2	3.07	0.43
1:A:151:HIS:HB3	1:A:195:PHE:O	2.18	0.43
1:B:145:ALA:O	1:B:197:LEU:HD13	2.19	0.43
1:F:73:LEU:CA	1:F:76:VAL:HG12	2.49	0.43
1:E:235:THR:HG22	1:E:236:ILE:N	2.34	0.43
1:E:73:LEU:HD23	1:E:76:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:151:HIS:HB3	1:E:195:PHE:O	2.18	0.43
1:C:56:PHE:CD1	1:C:59:TYR:CE2	3.07	0.43
1:D:27:ILE:HD12	1:D:68:VAL:HG21	2.01	0.43
1:A:20:VAL:HG12	1:A:21:LEU:CD2	2.49	0.43
1:B:150:ASP:O	1:B:197:LEU:HB3	2.18	0.43
1:F:207:ILE:HG21	1:F:227:TYR:OH	2.18	0.43
1:F:27:ILE:HG23	1:F:36:ILE:HD11	2.01	0.43
1:F:2:PHE:CD1	1:F:90:LEU:HD12	2.53	0.43
1:C:198:ASP:C	1:C:200:LEU:H	2.22	0.43
1:E:70:LEU:HD22	1:E:70:LEU:O	2.19	0.43
1:D:73:LEU:HD23	1:D:76:VAL:HG13	2.00	0.43
1:B:171:THR:HG21	1:C:72:ARG:NH1	2.13	0.43
1:C:35:SER:HB2	1:C:49:LEU:O	2.19	0.43
1:A:171:THR:HG21	1:B:72:ARG:NH1	2.16	0.43
1:B:235:THR:HG22	1:B:236:ILE:N	2.34	0.43
1:E:157:ASP:CB	1:E:160:GLU:O	2.66	0.43
1:F:133:LEU:O	1:F:213:VAL:N	2.28	0.43
1:E:131:ILE:HD12	1:E:131:ILE:N	2.34	0.43
1:A:27:ILE:HD12	1:A:68:VAL:HG21	2.01	0.43
1:A:73:LEU:HD23	1:A:76:VAL:HG13	2.00	0.43
1:A:109:ALA:HB3	1:C:171:THR:OG1	2.19	0.43
1:D:145:ALA:O	1:D:197:LEU:HD13	2.19	0.43
1:D:35:SER:HB2	1:D:49:LEU:O	2.18	0.43
1:D:27:ILE:HG23	1:D:36:ILE:HD11	2.01	0.43
1:E:5:ILE:HD12	1:E:57:GLU:HB2	2.01	0.43
1:A:171:THR:OG1	1:B:109:ALA:HB3	2.19	0.43
1:E:26:LYS:HA	1:E:67:GLY:HA2	1.99	0.42
1:B:131:ILE:HD12	1:B:131:ILE:N	2.34	0.42
1:C:70:LEU:O	1:C:70:LEU:HD22	2.19	0.42
1:D:5:ILE:HD12	1:D:57:GLU:HB2	2.01	0.42
1:B:20:VAL:HG12	1:B:21:LEU:CD2	2.49	0.42
1:E:35:SER:HB2	1:E:49:LEU:O	2.18	0.42
1:E:27:ILE:HD12	1:E:68:VAL:HG21	2.01	0.42
1:A:35:SER:HB2	1:A:49:LEU:O	2.19	0.42
1:C:27:ILE:HD12	1:C:68:VAL:HG21	2.01	0.42
1:B:207:ILE:HG21	1:B:227:TYR:OH	2.18	0.42
1:A:106:TYR:CE2	1:A:108:LEU:HB2	2.52	0.42
1:D:207:ILE:CD1	1:D:207:ILE:N	2.81	0.42
1:F:82:ALA:C	1:F:84:ASP:H	2.23	0.42
1:D:131:ILE:N	1:D:131:ILE:HD12	2.34	0.42
1:A:145:ALA:O	1:A:197:LEU:HD13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:MET:HB3	1:A:239:MET:HE2	1.96	0.42
1:C:131:ILE:HD12	1:C:131:ILE:N	2.34	0.42
1:F:27:ILE:HD12	1:F:68:VAL:HG21	2.01	0.42
1:A:17:SER:OG	1:A:236:ILE:HG21	2.20	0.42
1:D:235:THR:HG22	1:D:236:ILE:N	2.34	0.42
1:C:82:ALA:C	1:C:84:ASP:H	2.23	0.42
1:C:17:SER:OG	1:C:236:ILE:HG21	2.20	0.42
1:F:131:ILE:HD12	1:F:131:ILE:N	2.34	0.42
1:C:43:ASN:HD22	1:C:43:ASN:N	2.18	0.42
1:E:27:ILE:HG23	1:E:36:ILE:HD11	2.01	0.42
1:C:27:ILE:HG23	1:C:36:ILE:HD11	2.01	0.42
1:A:29:LEU:HG	1:A:34:LEU:HB3	2.00	0.42
1:B:198:ASP:C	1:B:200:LEU:H	2.22	0.42
1:A:157:ASP:CB	1:A:160:GLU:O	2.66	0.42
1:A:82:ALA:O	1:A:84:ASP:N	2.51	0.42
1:B:133:LEU:CG	1:B:183:LEU:HD12	2.45	0.42
1:B:27:ILE:HG23	1:B:36:ILE:HD11	2.01	0.42
1:C:29:LEU:HG	1:C:34:LEU:HB3	2.00	0.42
1:D:29:LEU:HG	1:D:34:LEU:HB3	2.00	0.42
1:A:73:LEU:CA	1:A:76:VAL:HG12	2.49	0.42
1:E:82:ALA:C	1:E:84:ASP:H	2.23	0.42
1:B:70:LEU:HD22	1:B:70:LEU:O	2.19	0.42
1:B:29:LEU:HG	1:B:34:LEU:HB3	2.00	0.42
1:A:56:PHE:CD1	1:A:59:TYR:CE2	3.07	0.42
1:D:56:PHE:CD1	1:D:59:TYR:CE2	3.07	0.42
1:F:5:ILE:HD12	1:F:57:GLU:HB2	2.01	0.42
1:A:122:ILE:O	1:A:123:PRO:C	2.56	0.42
1:D:82:ALA:O	1:D:84:ASP:N	2.51	0.42
1:E:17:SER:OG	1:E:236:ILE:HG21	2.20	0.42
1:E:25:CYS:O	1:E:67:GLY:CA	2.66	0.42
1:E:73:LEU:CA	1:E:76:VAL:HG12	2.49	0.42
1:E:155:ARG:HB3	1:E:164:HIS:HB2	2.00	0.42
1:D:122:ILE:O	1:D:123:PRO:C	2.56	0.42
1:C:49:LEU:HD23	1:C:235:THR:O	2.20	0.42
1:C:25:CYS:O	1:C:67:GLY:CA	2.66	0.42
1:C:73:LEU:CA	1:C:76:VAL:HG12	2.49	0.42
1:E:29:LEU:HG	1:E:34:LEU:HB3	2.00	0.42
1:E:172:ASP:OD1	1:F:108:LEU:HG	2.19	0.42
1:F:17:SER:OG	1:F:236:ILE:HG21	2.20	0.42
1:A:131:ILE:N	1:A:131:ILE:HD12	2.34	0.42
1:D:198:ASP:C	1:D:200:LEU:H	2.22	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70:LEU:O	1:D:70:LEU:HD22	2.19	0.42
1:D:20:VAL:CG2	1:D:202:ASP:O	2.66	0.42
1:B:122:ILE:O	1:B:123:PRO:C	2.56	0.42
1:E:173:ASP:HB2	1:F:107:THR:HG22	1.95	0.42
1:F:49:LEU:HD23	1:F:235:THR:O	2.20	0.42
1:C:5:ILE:CA	1:C:86:ILE:O	2.68	0.42
1:C:235:THR:HG22	1:C:236:ILE:N	2.34	0.42
1:B:73:LEU:CA	1:B:76:VAL:HG12	2.49	0.42
1:F:47:VAL:HB	1:F:238:TYR:CD2	2.55	0.42
1:B:43:ASN:N	1:B:43:ASN:HD22	2.18	0.42
1:A:246:SER:O	1:A:247:ASP:HB2	2.20	0.42
1:B:240:LEU:CD2	1:B:241:ALA:O	2.62	0.41
1:C:158:GLY:O	1:C:159:ALA:CB	2.63	0.41
1:D:82:ALA:C	1:D:84:ASP:H	2.23	0.41
1:E:240:LEU:CD2	1:E:241:ALA:O	2.62	0.41
1:B:49:LEU:HD23	1:B:235:THR:O	2.20	0.41
1:E:47:VAL:HB	1:E:238:TYR:CD2	2.55	0.41
1:F:5:ILE:CA	1:F:86:ILE:O	2.68	0.41
1:E:145:ALA:O	1:E:197:LEU:HD13	2.19	0.41
1:C:86:ILE:HG21	1:C:99:ILE:HD11	2.02	0.41
1:D:17:SER:OG	1:D:236:ILE:HG21	2.20	0.41
1:D:49:LEU:HD23	1:D:235:THR:O	2.20	0.41
1:E:5:ILE:CA	1:E:86:ILE:O	2.68	0.41
1:B:32:GLU:O	1:B:33:SER:OG	2.35	0.41
1:A:5:ILE:HD12	1:A:57:GLU:HB2	2.01	0.41
1:C:246:SER:O	1:C:247:ASP:HB2	2.20	0.41
1:A:27:ILE:HG23	1:A:36:ILE:HD11	2.01	0.41
1:A:70:LEU:HD22	1:A:70:LEU:O	2.19	0.41
1:D:175:ASP:O	1:E:104:LEU:CD2	2.68	0.41
1:D:123:PRO:HG3	1:D:239:MET:HE1	2.02	0.41
1:E:198:ASP:C	1:E:200:LEU:H	2.22	0.41
1:D:47:VAL:HB	1:D:238:TYR:CD2	2.55	0.41
1:A:34:LEU:HD23	1:A:34:LEU:N	2.35	0.41
1:A:86:ILE:HG21	1:A:99:ILE:HD11	2.02	0.41
1:D:158:GLY:O	1:D:159:ALA:CB	2.63	0.41
1:A:174:VAL:CG2	1:B:104:LEU:HD21	2.47	0.41
1:E:49:LEU:HD23	1:E:235:THR:O	2.20	0.41
1:B:17:SER:OG	1:B:236:ILE:HG21	2.20	0.41
1:A:214:THR:HG1	1:A:226:HIS:HB2	1.82	0.41
1:D:34:LEU:HD23	1:D:34:LEU:N	2.35	0.41
1:F:240:LEU:CD2	1:F:241:ALA:O	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:ILE:HD12	1:C:57:GLU:HB2	2.01	0.41
1:B:179:PRO:CG	1:D:179:PRO:HG2	2.48	0.41
1:C:32:GLU:O	1:C:33:SER:OG	2.35	0.41
1:E:43:ASN:N	1:E:43:ASN:HD22	2.18	0.41
1:F:246:SER:O	1:F:247:ASP:HB2	2.20	0.41
1:F:36:ILE:HG22	1:F:37:ARG:N	2.36	0.41
1:E:131:ILE:HD11	1:E:156:VAL:HG21	2.03	0.41
1:B:76:VAL:HG13	1:B:77:ALA:N	2.36	0.41
1:B:209:THR:O	1:B:210:ASP:HB2	2.21	0.41
1:D:209:THR:O	1:D:210:ASP:HB2	2.21	0.41
1:F:70:LEU:O	1:F:70:LEU:HD22	2.19	0.41
1:E:2:PHE:HA	1:E:60:GLU:O	2.21	0.41
1:A:76:VAL:HG13	1:A:77:ALA:N	2.36	0.41
1:D:25:CYS:O	1:D:67:GLY:CA	2.66	0.41
1:B:82:ALA:C	1:B:84:ASP:H	2.23	0.41
1:D:176:LEU:N	1:D:176:LEU:HD22	2.36	0.41
1:D:36:ILE:HG22	1:D:37:ARG:N	2.36	0.41
1:D:37:ARG:O	1:D:37:ARG:CG	2.49	0.41
1:C:47:VAL:HB	1:C:238:TYR:CD2	2.55	0.41
1:D:86:ILE:HG21	1:D:99:ILE:HD11	2.02	0.41
1:E:246:SER:O	1:E:247:ASP:HB2	2.20	0.41
1:A:123:PRO:HG3	1:A:239:MET:HE1	2.03	0.41
1:F:2:PHE:HA	1:F:60:GLU:O	2.21	0.41
1:F:176:LEU:HD22	1:F:176:LEU:N	2.36	0.41
1:F:221:PHE:C	1:F:242:PRO:HG3	2.42	0.41
1:A:159:ALA:O	1:A:160:GLU:HB2	2.21	0.41
1:A:131:ILE:HD11	1:A:156:VAL:HG21	2.03	0.41
1:A:82:ALA:C	1:A:84:ASP:H	2.23	0.41
1:A:49:LEU:HD23	1:A:235:THR:O	2.20	0.41
1:D:199:TYR:HB2	1:D:240:LEU:HD11	2.03	0.41
1:B:159:ALA:O	1:B:160:GLU:HB2	2.21	0.41
1:E:176:LEU:N	1:E:176:LEU:HD22	2.36	0.41
1:C:76:VAL:HG13	1:C:77:ALA:N	2.36	0.41
1:B:36:ILE:HG22	1:B:37:ARG:N	2.36	0.41
1:E:180:PRO:O	1:E:183:LEU:HB2	2.21	0.41
1:A:5:ILE:CA	1:A:86:ILE:O	2.68	0.41
1:F:34:LEU:N	1:F:34:LEU:HD23	2.35	0.41
1:E:209:THR:O	1:E:210:ASP:HB2	2.21	0.41
1:D:246:SER:O	1:D:247:ASP:HB2	2.20	0.41
1:F:69:ASN:CG	1:F:108:LEU:HD21	2.42	0.41
1:A:180:PRO:O	1:A:183:LEU:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:THR:HG21	1:C:173:ASP:HB2	1.96	0.41
1:D:69:ASN:CG	1:D:108:LEU:HD21	2.42	0.41
1:B:69:ASN:CG	1:B:108:LEU:HD21	2.42	0.41
1:A:47:VAL:HB	1:A:238:TYR:CD2	2.55	0.41
1:B:7:SER:HA	1:B:85:LEU:HD23	2.04	0.41
1:F:209:THR:O	1:F:210:ASP:HB2	2.21	0.41
1:A:199:TYR:HB2	1:A:240:LEU:HD11	2.03	0.40
1:B:239:MET:HB3	1:B:239:MET:HE2	1.96	0.40
1:A:104:LEU:CD2	1:C:175:ASP:O	2.69	0.40
1:D:104:LEU:CD2	1:F:175:ASP:O	2.69	0.40
1:A:2:PHE:HA	1:A:60:GLU:O	2.21	0.40
1:C:7:SER:HA	1:C:85:LEU:HD23	2.04	0.40
1:C:2:PHE:HA	1:C:60:GLU:O	2.21	0.40
1:E:34:LEU:HD23	1:E:34:LEU:N	2.35	0.40
1:B:5:ILE:HD12	1:B:57:GLU:HB2	2.01	0.40
1:D:5:ILE:CA	1:D:86:ILE:O	2.68	0.40
1:A:43:ASN:HD22	1:A:43:ASN:N	2.18	0.40
1:E:43:ASN:HD21	1:E:117:ARG:HH22	1.69	0.40
1:F:43:ASN:HD21	1:F:117:ARG:HH22	1.69	0.40
1:F:43:ASN:N	1:F:43:ASN:HD22	2.18	0.40
1:D:117:ARG:CG	1:D:118:GLN:N	2.84	0.40
1:A:176:LEU:N	1:A:176:LEU:HD22	2.36	0.40
1:B:176:LEU:N	1:B:176:LEU:HD22	2.36	0.40
1:F:76:VAL:HG13	1:F:77:ALA:N	2.36	0.40
1:C:145:ALA:C	1:C:197:LEU:HD12	2.42	0.40
1:E:69:ASN:CG	1:E:108:LEU:HD21	2.42	0.40
1:A:36:ILE:HG22	1:A:37:ARG:N	2.36	0.40
1:A:73:LEU:C	1:A:76:VAL:HG12	2.42	0.40
1:E:195:PHE:HD2	1:E:240:LEU:HD23	1.86	0.40
1:D:76:VAL:HG13	1:D:77:ALA:N	2.36	0.40
1:C:69:ASN:CG	1:C:108:LEU:HD21	2.42	0.40
1:B:34:LEU:HD23	1:B:34:LEU:N	2.35	0.40
1:B:145:ALA:C	1:B:197:LEU:HD12	2.42	0.40
1:B:195:PHE:HD2	1:B:240:LEU:HD23	1.86	0.40
1:C:176:LEU:HD22	1:C:176:LEU:N	2.36	0.40
1:C:199:TYR:HB2	1:C:240:LEU:HD11	2.03	0.40
1:A:69:ASN:CG	1:A:108:LEU:HD21	2.42	0.40
1:D:221:PHE:C	1:D:242:PRO:HG3	2.42	0.40
1:E:7:SER:HA	1:E:85:LEU:HD23	2.04	0.40
1:F:159:ALA:O	1:F:160:GLU:HB2	2.21	0.40
1:D:43:ASN:HD21	1:D:117:ARG:HH22	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:15:LEU:N	1:D:15:LEU:HD23	2.37	0.40
1:B:246:SER:O	1:B:247:ASP:HB2	2.20	0.40
1:F:1:MET:O	1:F:60:GLU:O	2.40	0.40
1:A:131:ILE:HD13	1:A:163:PHE:HE1	1.87	0.40
1:D:172:ASP:OD1	1:E:108:LEU:HG	2.22	0.40
1:B:131:ILE:HD13	1:B:163:PHE:HE1	1.87	0.40
1:E:86:ILE:HG21	1:E:99:ILE:HD11	2.02	0.40
1:B:47:VAL:HB	1:B:238:TYR:CD2	2.55	0.40
1:C:34:LEU:HD23	1:C:34:LEU:N	2.35	0.40
1:C:209:THR:O	1:C:210:ASP:HB2	2.21	0.40
1:B:1:MET:O	1:B:60:GLU:O	2.40	0.40
1:C:46:MET:HE2	1:C:46:MET:HB3	1.97	0.40
1:B:15:LEU:HD23	1:B:15:LEU:N	2.37	0.40
1:A:221:PHE:C	1:A:242:PRO:HG3	2.42	0.40
1:B:199:TYR:HB2	1:B:240:LEU:HD11	2.03	0.40
1:C:159:ALA:O	1:C:160:GLU:HB2	2.21	0.40
1:A:1:MET:O	1:A:60:GLU:O	2.40	0.40
1:D:195:PHE:HD2	1:D:240:LEU:HD23	1.86	0.40
1:E:221:PHE:C	1:E:242:PRO:HG3	2.42	0.40
1:C:58:SER:C	1:C:59:TYR:CD2	2.94	0.40
1:D:2:PHE:HA	1:D:60:GLU:O	2.21	0.40
1:B:25:CYS:O	1:B:67:GLY:CA	2.66	0.40
1:D:32:GLU:O	1:D:33:SER:OG	2.35	0.40
1:F:32:GLU:O	1:F:33:SER:OG	2.35	0.40
1:B:86:ILE:HG21	1:B:99:ILE:HD11	2.02	0.40
1:F:86:ILE:HG21	1:F:99:ILE:HD11	2.02	0.40
1:A:43:ASN:HD21	1:A:117:ARG:HH22	1.69	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	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	4	29
1	B	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	4	29
1	C	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	4	29
1	D	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	4	29
1	E	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	4	29
1	F	245/247 (99%)	206 (84%)	30 (12%)	9 (4%)	4	29
All	All	1470/1482 (99%)	1236 (84%)	180 (12%)	54 (4%)	4	29

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	ILE
1	A	208	PRO
1	B	184	ILE
1	B	208	PRO
1	C	184	ILE
1	C	208	PRO
1	D	184	ILE
1	D	208	PRO
1	E	184	ILE
1	E	208	PRO
1	F	184	ILE
1	F	208	PRO
1	A	83	GLY
1	A	160	GLU
1	A	180	PRO
1	B	83	GLY
1	B	160	GLU
1	B	180	PRO
1	C	83	GLY
1	C	160	GLU
1	C	180	PRO
1	D	83	GLY
1	D	160	GLU
1	D	180	PRO
1	E	83	GLY
1	E	160	GLU
1	E	180	PRO
1	F	83	GLY
1	F	160	GLU
1	F	180	PRO

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Mol	Chain	Res	Type
1	A	37	ARG
1	A	159	ALA
1	B	37	ARG
1	B	159	ALA
1	C	37	ARG
1	C	159	ALA
1	D	37	ARG
1	D	159	ALA
1	E	37	ARG
1	F	37	ARG
1	F	159	ALA
1	E	159	ALA
1	A	181	ALA
1	B	181	ALA
1	C	181	ALA
1	D	181	ALA
1	E	181	ALA
1	F	181	ALA
1	A	242	PRO
1	B	242	PRO
1	C	242	PRO
1	D	242	PRO
1	E	242	PRO
1	F	242	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	203/203 (100%)	159 (78%)	44 (22%)	1 6
1	B	203/203 (100%)	159 (78%)	44 (22%)	1 6
1	C	203/203 (100%)	159 (78%)	44 (22%)	1 6
1	D	203/203 (100%)	159 (78%)	44 (22%)	1 6
1	E	203/203 (100%)	159 (78%)	44 (22%)	1 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	F	203/203 (100%)	159 (78%)	44 (22%)	1 6
All	All	1218/1218 (100%)	954 (78%)	264 (22%)	1 6

All (264) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	5	ILE
1	A	21	LEU
1	A	23	ASP
1	A	34	LEU
1	A	37	ARG
1	A	41	PRO
1	A	44	VAL
1	A	56	PHE
1	A	59	TYR
1	A	65	VAL
1	A	70	LEU
1	A	73	LEU
1	A	75	GLU
1	A	90	LEU
1	A	91	ASP
1	A	95	ARG
1	A	104	LEU
1	A	114	ASP
1	A	120	PRO
1	A	121	ASP
1	A	125	LEU
1	A	133	LEU
1	A	138	LEU
1	A	147	MET
1	A	149	SER
1	A	151	HIS
1	A	157	ASP
1	A	161	GLU
1	A	170	ASP
1	A	171	THR
1	A	176	LEU
1	A	180	PRO
1	A	185	SER
1	A	187	GLU
1	A	197	LEU

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Mol	Chain	Res	Type
1	A	208	PRO
1	A	217	LEU
1	A	219	GLU
1	A	222	PRO
1	A	233	MET
1	A	239	MET
1	A	242	PRO
1	A	247	ASP
1	B	3	LYS
1	B	5	ILE
1	B	21	LEU
1	B	23	ASP
1	B	34	LEU
1	B	37	ARG
1	B	41	PRO
1	B	44	VAL
1	B	56	PHE
1	B	59	TYR
1	B	65	VAL
1	B	70	LEU
1	B	73	LEU
1	B	75	GLU
1	B	90	LEU
1	B	91	ASP
1	B	95	ARG
1	B	104	LEU
1	B	114	ASP
1	B	120	PRO
1	B	121	ASP
1	B	125	LEU
1	B	133	LEU
1	B	138	LEU
1	B	147	MET
1	B	149	SER
1	B	151	HIS
1	B	157	ASP
1	B	161	GLU
1	B	170	ASP
1	B	171	THR
1	B	176	LEU
1	B	180	PRO
1	B	185	SER

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Mol	Chain	Res	Type
1	B	187	GLU
1	B	197	LEU
1	B	208	PRO
1	B	217	LEU
1	B	219	GLU
1	B	222	PRO
1	B	233	MET
1	B	239	MET
1	B	242	PRO
1	B	247	ASP
1	C	3	LYS
1	C	5	ILE
1	C	21	LEU
1	C	23	ASP
1	C	34	LEU
1	C	37	ARG
1	C	41	PRO
1	C	44	VAL
1	C	56	PHE
1	C	59	TYR
1	C	65	VAL
1	C	70	LEU
1	C	73	LEU
1	C	75	GLU
1	C	90	LEU
1	C	91	ASP
1	C	95	ARG
1	C	104	LEU
1	C	114	ASP
1	C	120	PRO
1	C	121	ASP
1	C	125	LEU
1	C	133	LEU
1	C	138	LEU
1	C	147	MET
1	C	149	SER
1	C	151	HIS
1	C	157	ASP
1	C	161	GLU
1	C	170	ASP
1	C	171	THR
1	C	176	LEU

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Mol	Chain	Res	Type
1	C	180	PRO
1	C	185	SER
1	C	187	GLU
1	C	197	LEU
1	C	208	PRO
1	C	217	LEU
1	C	219	GLU
1	C	222	PRO
1	C	233	MET
1	C	239	MET
1	C	242	PRO
1	C	247	ASP
1	D	3	LYS
1	D	5	ILE
1	D	21	LEU
1	D	23	ASP
1	D	34	LEU
1	D	37	ARG
1	D	41	PRO
1	D	44	VAL
1	D	56	PHE
1	D	59	TYR
1	D	65	VAL
1	D	70	LEU
1	D	73	LEU
1	D	75	GLU
1	D	90	LEU
1	D	91	ASP
1	D	95	ARG
1	D	104	LEU
1	D	114	ASP
1	D	120	PRO
1	D	121	ASP
1	D	125	LEU
1	D	133	LEU
1	D	138	LEU
1	D	147	MET
1	D	149	SER
1	D	151	HIS
1	D	157	ASP
1	D	161	GLU
1	D	170	ASP

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Mol	Chain	Res	Type
1	D	171	THR
1	D	176	LEU
1	D	180	PRO
1	D	185	SER
1	D	187	GLU
1	D	197	LEU
1	D	208	PRO
1	D	217	LEU
1	D	219	GLU
1	D	222	PRO
1	D	233	MET
1	D	239	MET
1	D	242	PRO
1	D	247	ASP
1	E	3	LYS
1	E	5	ILE
1	E	21	LEU
1	E	23	ASP
1	E	34	LEU
1	E	37	ARG
1	E	41	PRO
1	E	44	VAL
1	E	56	PHE
1	E	59	TYR
1	E	65	VAL
1	E	70	LEU
1	E	73	LEU
1	E	75	GLU
1	E	90	LEU
1	E	91	ASP
1	E	95	ARG
1	E	104	LEU
1	E	114	ASP
1	E	120	PRO
1	E	121	ASP
1	E	125	LEU
1	E	133	LEU
1	E	138	LEU
1	E	147	MET
1	E	149	SER
1	E	151	HIS
1	E	157	ASP

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Mol	Chain	Res	Type
1	E	161	GLU
1	E	170	ASP
1	E	171	THR
1	E	176	LEU
1	E	180	PRO
1	E	185	SER
1	E	187	GLU
1	E	197	LEU
1	E	208	PRO
1	E	217	LEU
1	E	219	GLU
1	E	222	PRO
1	E	233	MET
1	E	239	MET
1	E	242	PRO
1	E	247	ASP
1	F	3	LYS
1	F	5	ILE
1	F	21	LEU
1	F	23	ASP
1	F	34	LEU
1	F	37	ARG
1	F	41	PRO
1	F	44	VAL
1	F	56	PHE
1	F	59	TYR
1	F	65	VAL
1	F	70	LEU
1	F	73	LEU
1	F	75	GLU
1	F	90	LEU
1	F	91	ASP
1	F	95	ARG
1	F	104	LEU
1	F	114	ASP
1	F	120	PRO
1	F	121	ASP
1	F	125	LEU
1	F	133	LEU
1	F	138	LEU
1	F	147	MET
1	F	149	SER

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Mol	Chain	Res	Type
1	F	151	HIS
1	F	157	ASP
1	F	161	GLU
1	F	170	ASP
1	F	171	THR
1	F	176	LEU
1	F	180	PRO
1	F	185	SER
1	F	187	GLU
1	F	197	LEU
1	F	208	PRO
1	F	217	LEU
1	F	219	GLU
1	F	222	PRO
1	F	233	MET
1	F	239	MET
1	F	242	PRO
1	F	247	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	B	43	ASN
1	C	43	ASN
1	C	87	HIS
1	D	43	ASN
1	E	43	ASN
1	E	87	HIS
1	F	43	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

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	247/247 (100%)	-0.20	10 (4%) 42 27	93, 138, 172, 203	0
1	B	247/247 (100%)	-0.13	10 (4%) 42 27	95, 139, 172, 204	0
1	C	247/247 (100%)	-0.20	8 (3%) 51 36	94, 139, 172, 203	0
1	D	247/247 (100%)	-0.19	12 (4%) 33 20	94, 138, 173, 204	0
1	E	247/247 (100%)	-0.20	7 (2%) 56 42	95, 139, 172, 203	0
1	F	247/247 (100%)	-0.21	6 (2%) 62 47	94, 139, 172, 205	0
All	All	1482/1482 (100%)	-0.19	53 (3%) 46 31	93, 139, 175, 205	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	246	SER	5.8
1	F	244	ILE	5.8
1	D	244	ILE	5.5
1	F	243	ARG	5.2
1	D	245	GLN	5.1
1	E	244	ILE	4.9
1	A	244	ILE	4.9
1	B	245	GLN	4.7
1	B	244	ILE	4.6
1	A	245	GLN	4.5
1	C	243	ARG	4.4
1	A	148	VAL	4.3
1	A	246	SER	4.3
1	F	246	SER	4.3
1	C	148	VAL	4.1
1	B	94	THR	4.0
1	B	243	ARG	3.9
1	C	245	GLN	3.9
1	D	243	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	220	GLU	3.8
1	E	246	SER	3.7
1	F	245	GLN	3.7
1	D	246	SER	3.6
1	A	220	GLU	3.3
1	C	244	ILE	3.3
1	F	220	GLU	3.3
1	A	159	ALA	3.3
1	A	243	ARG	3.3
1	C	15	LEU	3.3
1	E	245	GLN	3.1
1	D	94	THR	3.0
1	E	243	ARG	3.0
1	E	219	GLU	3.0
1	D	15	LEU	2.9
1	D	131	ILE	2.9
1	A	15	LEU	2.8
1	B	220	GLU	2.6
1	C	93	GLU	2.6
1	E	189	GLY	2.6
1	D	111	ILE	2.6
1	C	246	SER	2.6
1	E	15	LEU	2.5
1	B	26	LYS	2.5
1	B	132	VAL	2.5
1	C	94	THR	2.4
1	D	148	VAL	2.4
1	B	22	VAL	2.3
1	B	236	ILE	2.3
1	F	153	ARG	2.2
1	A	236	ILE	2.2
1	D	110	LEU	2.1
1	D	184	ILE	2.0
1	A	189	GLY	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

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.