Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2020 – 03:01 am BST

PDB ID	:	6GEF
Title	:	X-ray structure of the Yersinia pseudotuberculosis ATPase DotB
Authors	:	Prevost, M.S.; Waksman, G.
Deposited on	:	2018-04-26
Resolution	:	2.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

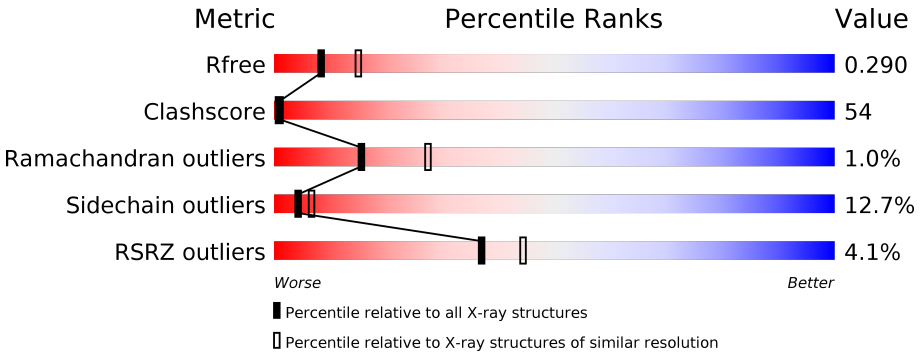
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.75 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}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	402	5% 42% 46% 9%
1	B	402	2% 38% 51% 6%
1	C	402	4% 40% 46% 10%
1	D	402	8% 40% 47% 9%
1	E	402	2% 43% 44% 8%
1	F	402	2% 46% 44% 6%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 18021 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 Type IV secretion system protein DotB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	0	0
			3027	1910	526	578	13			
1	B	384	Total	C	N	O	S	0	0	0
			2986	1884	516	573	13			
1	C	385	Total	C	N	O	S	0	0	0
			3009	1898	524	574	13			
1	D	385	Total	C	N	O	S	0	0	0
			2982	1883	516	570	13			
1	E	385	Total	C	N	O	S	0	0	0
			2995	1889	522	571	13			
1	F	386	Total	C	N	O	S	0	0	0
			3022	1907	526	576	13			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP A0A0U1QTI9
A	-12	ALA	-	expression tag	UNP A0A0U1QTI9
A	-11	SER	-	expression tag	UNP A0A0U1QTI9
A	-10	TRP	-	expression tag	UNP A0A0U1QTI9
A	-9	SER	-	expression tag	UNP A0A0U1QTI9
A	-8	HIS	-	expression tag	UNP A0A0U1QTI9
A	-7	PRO	-	expression tag	UNP A0A0U1QTI9
A	-6	GLN	-	expression tag	UNP A0A0U1QTI9
A	-5	PHE	-	expression tag	UNP A0A0U1QTI9
A	-4	GLU	-	expression tag	UNP A0A0U1QTI9
A	-3	LYS	-	expression tag	UNP A0A0U1QTI9
A	-2	ILE	-	expression tag	UNP A0A0U1QTI9
A	-1	GLU	-	expression tag	UNP A0A0U1QTI9
A	0	GLY	-	expression tag	UNP A0A0U1QTI9
A	1	ARG	-	expression tag	UNP A0A0U1QTI9
A	388	SER	-	expression tag	UNP A0A0U1QTI9
B	-13	MET	-	initiating methionine	UNP A0A0U1QTI9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	ALA	-	expression tag	UNP A0A0U1QTI9
B	-11	SER	-	expression tag	UNP A0A0U1QTI9
B	-10	TRP	-	expression tag	UNP A0A0U1QTI9
B	-9	SER	-	expression tag	UNP A0A0U1QTI9
B	-8	HIS	-	expression tag	UNP A0A0U1QTI9
B	-7	PRO	-	expression tag	UNP A0A0U1QTI9
B	-6	GLN	-	expression tag	UNP A0A0U1QTI9
B	-5	PHE	-	expression tag	UNP A0A0U1QTI9
B	-4	GLU	-	expression tag	UNP A0A0U1QTI9
B	-3	LYS	-	expression tag	UNP A0A0U1QTI9
B	-2	ILE	-	expression tag	UNP A0A0U1QTI9
B	-1	GLU	-	expression tag	UNP A0A0U1QTI9
B	0	GLY	-	expression tag	UNP A0A0U1QTI9
B	1	ARG	-	expression tag	UNP A0A0U1QTI9
B	388	SER	-	expression tag	UNP A0A0U1QTI9
C	-13	MET	-	initiating methionine	UNP A0A0U1QTI9
C	-12	ALA	-	expression tag	UNP A0A0U1QTI9
C	-11	SER	-	expression tag	UNP A0A0U1QTI9
C	-10	TRP	-	expression tag	UNP A0A0U1QTI9
C	-9	SER	-	expression tag	UNP A0A0U1QTI9
C	-8	HIS	-	expression tag	UNP A0A0U1QTI9
C	-7	PRO	-	expression tag	UNP A0A0U1QTI9
C	-6	GLN	-	expression tag	UNP A0A0U1QTI9
C	-5	PHE	-	expression tag	UNP A0A0U1QTI9
C	-4	GLU	-	expression tag	UNP A0A0U1QTI9
C	-3	LYS	-	expression tag	UNP A0A0U1QTI9
C	-2	ILE	-	expression tag	UNP A0A0U1QTI9
C	-1	GLU	-	expression tag	UNP A0A0U1QTI9
C	0	GLY	-	expression tag	UNP A0A0U1QTI9
C	1	ARG	-	expression tag	UNP A0A0U1QTI9
C	388	SER	-	expression tag	UNP A0A0U1QTI9
D	-13	MET	-	initiating methionine	UNP A0A0U1QTI9
D	-12	ALA	-	expression tag	UNP A0A0U1QTI9
D	-11	SER	-	expression tag	UNP A0A0U1QTI9
D	-10	TRP	-	expression tag	UNP A0A0U1QTI9
D	-9	SER	-	expression tag	UNP A0A0U1QTI9
D	-8	HIS	-	expression tag	UNP A0A0U1QTI9
D	-7	PRO	-	expression tag	UNP A0A0U1QTI9
D	-6	GLN	-	expression tag	UNP A0A0U1QTI9
D	-5	PHE	-	expression tag	UNP A0A0U1QTI9
D	-4	GLU	-	expression tag	UNP A0A0U1QTI9
D	-3	LYS	-	expression tag	UNP A0A0U1QTI9

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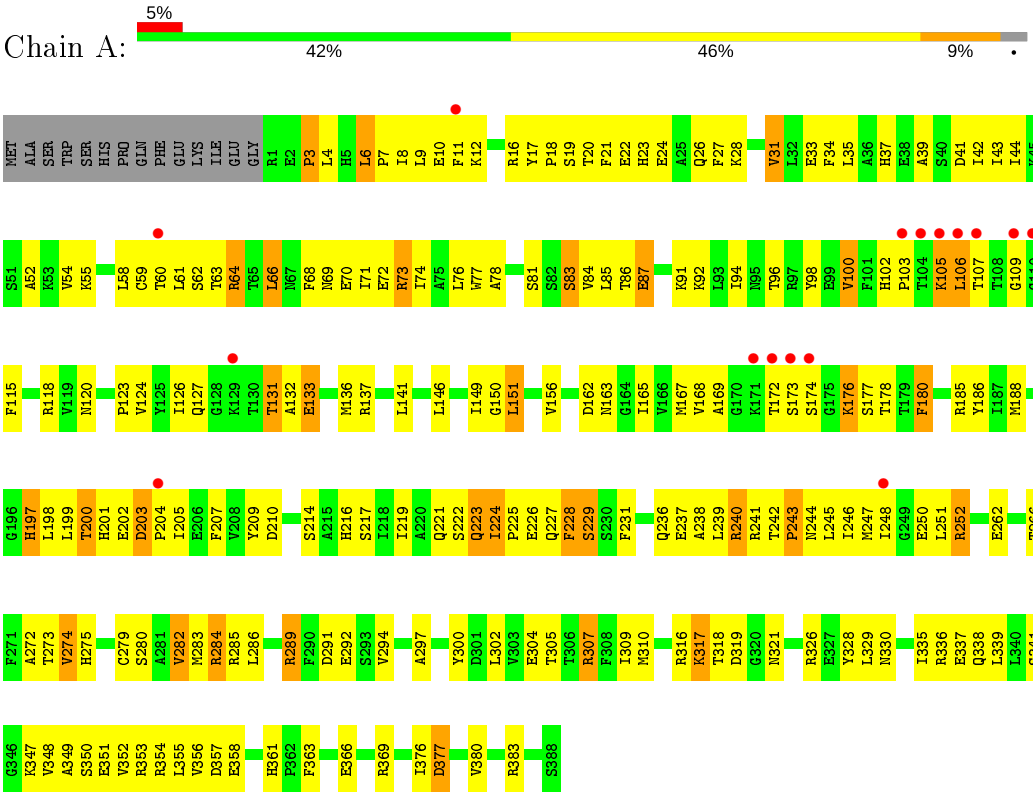
Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	ILE	-	expression tag	UNP A0A0U1QTI9
D	-1	GLU	-	expression tag	UNP A0A0U1QTI9
D	0	GLY	-	expression tag	UNP A0A0U1QTI9
D	1	ARG	-	expression tag	UNP A0A0U1QTI9
D	388	SER	-	expression tag	UNP A0A0U1QTI9
E	-13	MET	-	initiating methionine	UNP A0A0U1QTI9
E	-12	ALA	-	expression tag	UNP A0A0U1QTI9
E	-11	SER	-	expression tag	UNP A0A0U1QTI9
E	-10	TRP	-	expression tag	UNP A0A0U1QTI9
E	-9	SER	-	expression tag	UNP A0A0U1QTI9
E	-8	HIS	-	expression tag	UNP A0A0U1QTI9
E	-7	PRO	-	expression tag	UNP A0A0U1QTI9
E	-6	GLN	-	expression tag	UNP A0A0U1QTI9
E	-5	PHE	-	expression tag	UNP A0A0U1QTI9
E	-4	GLU	-	expression tag	UNP A0A0U1QTI9
E	-3	LYS	-	expression tag	UNP A0A0U1QTI9
E	-2	ILE	-	expression tag	UNP A0A0U1QTI9
E	-1	GLU	-	expression tag	UNP A0A0U1QTI9
E	0	GLY	-	expression tag	UNP A0A0U1QTI9
E	1	ARG	-	expression tag	UNP A0A0U1QTI9
E	388	SER	-	expression tag	UNP A0A0U1QTI9
F	-13	MET	-	initiating methionine	UNP A0A0U1QTI9
F	-12	ALA	-	expression tag	UNP A0A0U1QTI9
F	-11	SER	-	expression tag	UNP A0A0U1QTI9
F	-10	TRP	-	expression tag	UNP A0A0U1QTI9
F	-9	SER	-	expression tag	UNP A0A0U1QTI9
F	-8	HIS	-	expression tag	UNP A0A0U1QTI9
F	-7	PRO	-	expression tag	UNP A0A0U1QTI9
F	-6	GLN	-	expression tag	UNP A0A0U1QTI9
F	-5	PHE	-	expression tag	UNP A0A0U1QTI9
F	-4	GLU	-	expression tag	UNP A0A0U1QTI9
F	-3	LYS	-	expression tag	UNP A0A0U1QTI9
F	-2	ILE	-	expression tag	UNP A0A0U1QTI9
F	-1	GLU	-	expression tag	UNP A0A0U1QTI9
F	0	GLY	-	expression tag	UNP A0A0U1QTI9
F	1	ARG	-	expression tag	UNP A0A0U1QTI9
F	388	SER	-	expression tag	UNP A0A0U1QTI9

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

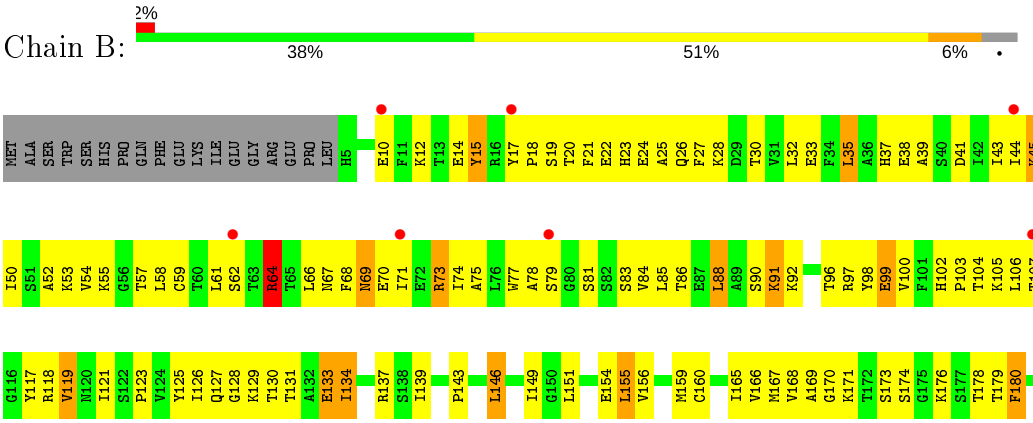
- Molecule 1: Type IV secretion system protein DotB

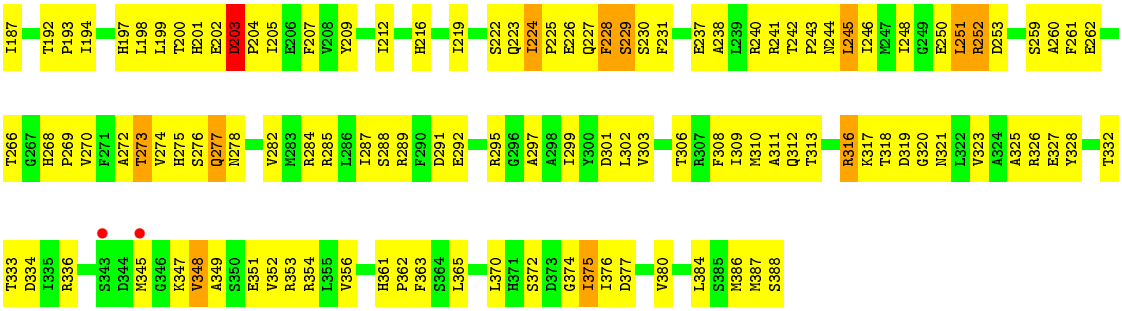
Chain A:

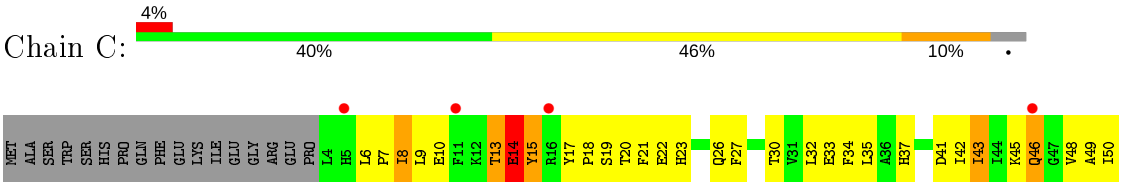


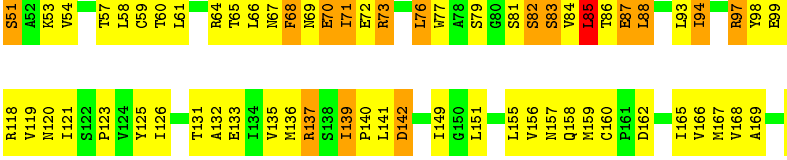
- Molecule 1: Type IV secretion system protein DotB

Chain B:



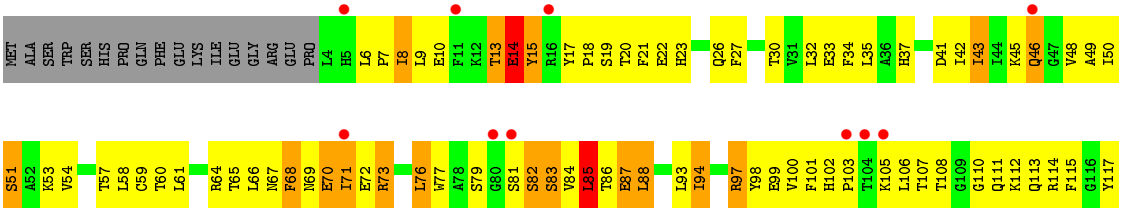


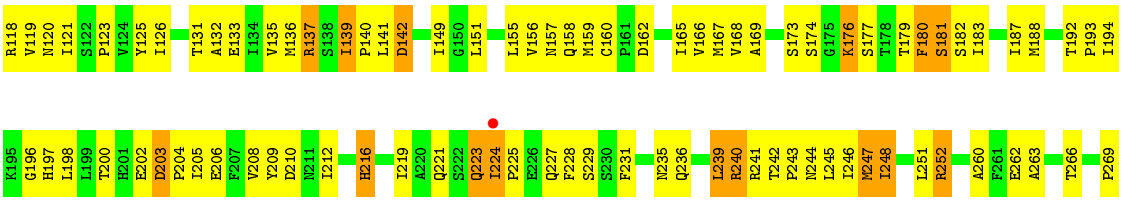


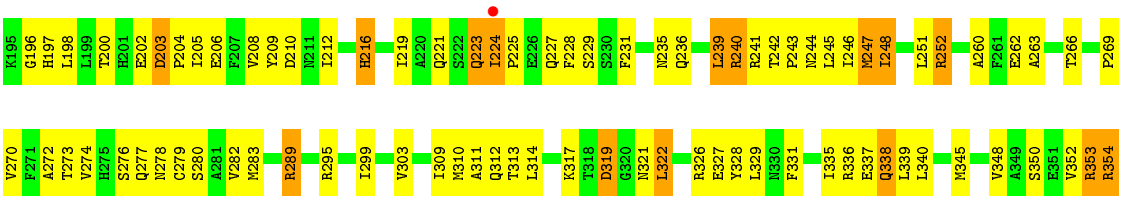


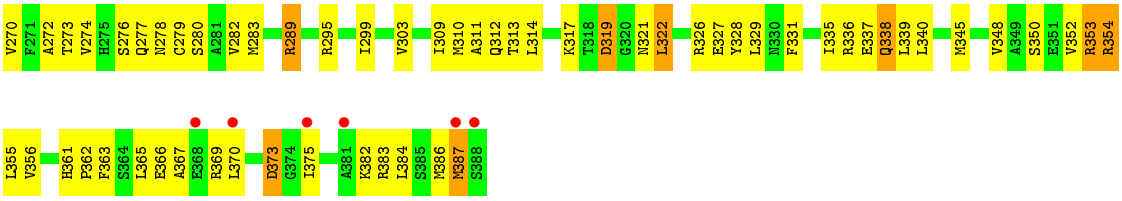
• Molecule 1: Type IV secretion system protein DotB

Chain C:



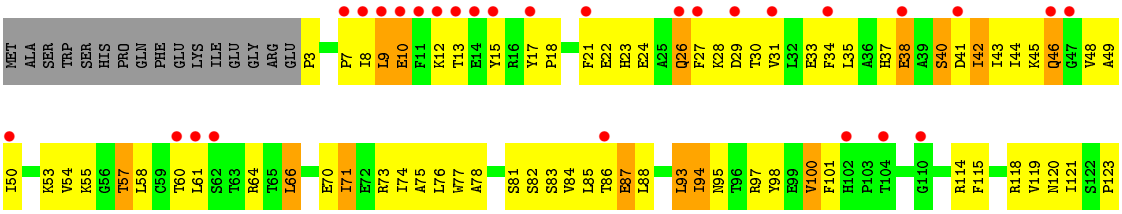


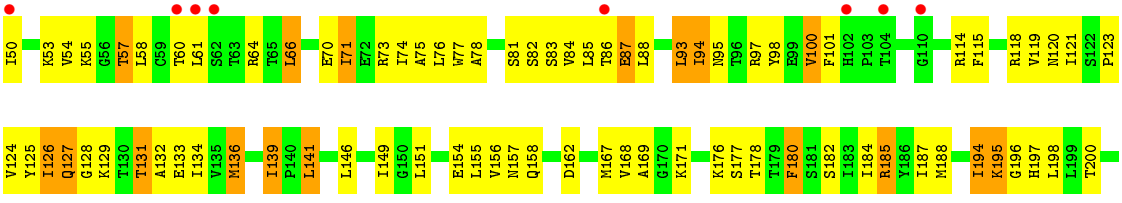


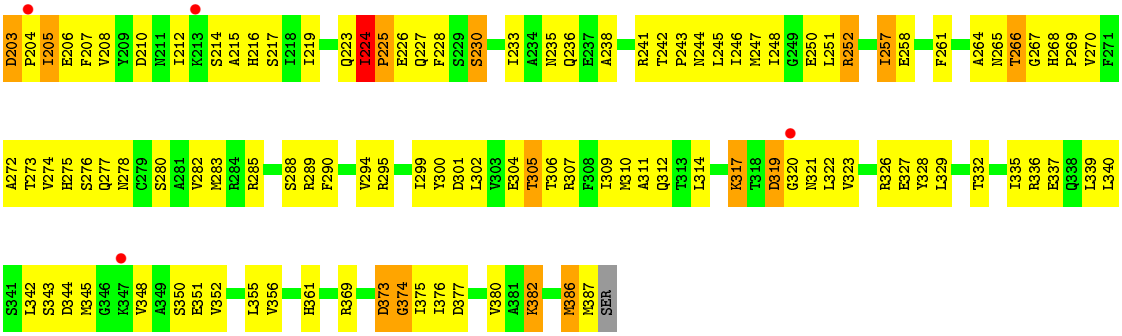


• Molecule 1: Type IV secretion system protein DotB

Chain D:

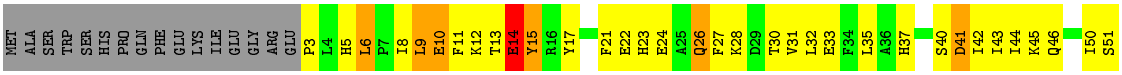


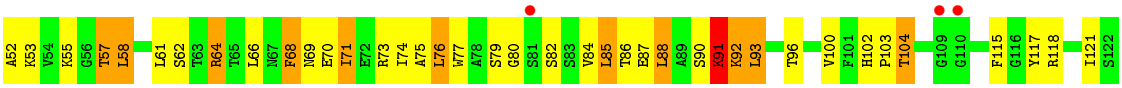


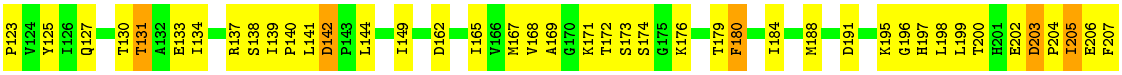


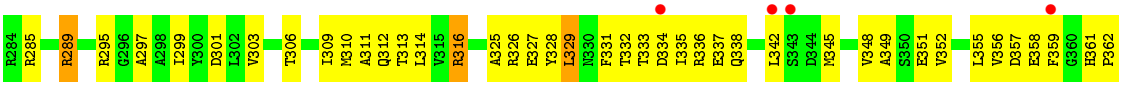
• Molecule 1: Type IV secretion system protein DotB

Chain E:



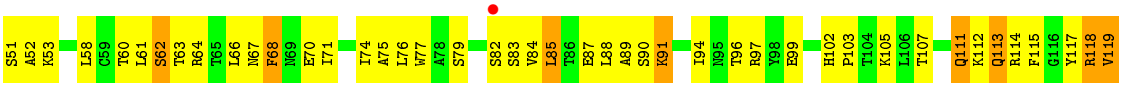


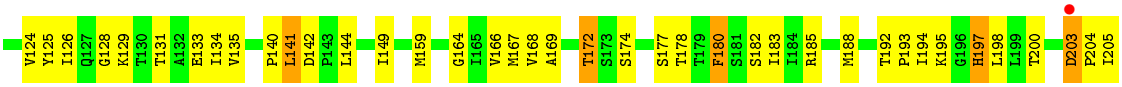


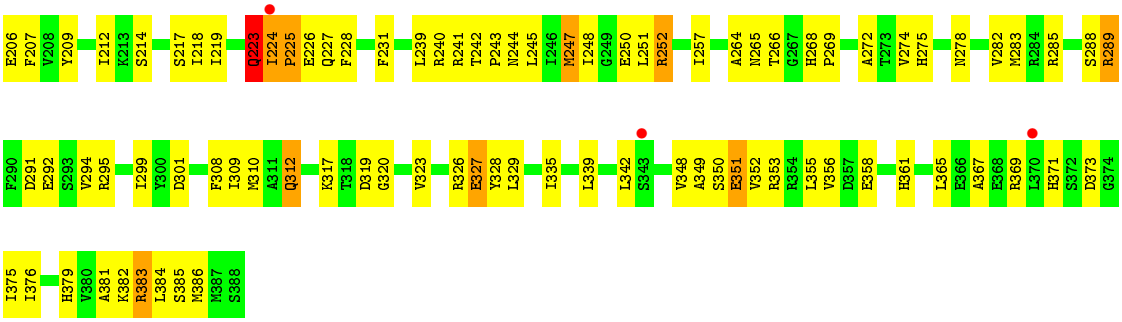


• Molecule 1: Type IV secretion system protein DotB

Chain F:






E206 F207 V208 Y209 I212 K213 S214 S217 I218 I219 Q223 I224 P225 E226 Q227 F228 F231 L239 R240 R241 T242 P243 N244 L245 I246 M247 I248 G249 E250 L251 R252 I257 A264 N265 T266 G267 H268 P269 A272 T273 V274 H275 N278 V282 M283 R284 R285 S288 R289
F290 D291 E292 S293 V294 R295 I299 Y300 D301 F308 I309 M310 A311 Q312 K317 T318 D319 G320 V323 R326 E327 Y328 L329 I335 L339 L342 S343 V348 A349 S350 E351 V352 R353 R354 L355 V356 D357 E358 H361 L365 E366 A367 E368 R369 L370 H371 S372 D373 G374
I375 I376 H379 V380 A381 K382 R383 L384 S385 M386 M387 S388

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	83.04Å 93.56Å 109.92Å 103.90° 101.98° 99.94°	Depositor
Resolution (Å)	40.56 – 2.75 45.71 – 2.75	Depositor EDS
% Data completeness (in resolution range)	97.8 (40.56-2.75) 97.9 (45.71-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.82 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.255 , 0.296 0.253 , 0.290	Depositor DCC
R_{free} test set	3866 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	70.0	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	18021	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.61% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.64	0/3081	0.61	2/4169 (0.0%)
1	B	0.64	0/3040	0.59	0/4117
1	C	0.63	0/3064	0.60	1/4147 (0.0%)
1	D	0.65	0/3036	0.61	1/4112 (0.0%)
1	E	0.68	0/3050	0.62	3/4129 (0.1%)
1	F	0.70	0/3077	0.63	2/4163 (0.0%)
All	All	0.66	0/18348	0.61	9/24837 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
1	C	0	3
1	D	0	5
1	F	0	2
All	All	0	13

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	3	PRO	N-CA-CB	7.53	112.33	103.30
1	F	3	PRO	N-CA-CB	6.92	111.61	103.30
1	A	210	ASP	CB-CG-OD2	6.89	124.50	118.30
1	D	3	PRO	N-CA-CB	6.86	111.53	103.30
1	E	289	ARG	NE-CZ-NH2	-6.06	117.27	120.30
1	E	41	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	E	3	PRO	N-CA-CB	5.71	110.15	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	85	LEU	CB-CG-CD1	5.40	120.18	111.00
1	F	383	ARG	NE-CZ-NH1	5.33	122.96	120.30

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	243	PRO	Peptide
1	B	203	ASP	Peptide
1	B	78	ALA	Peptide
1	C	105	LYS	Peptide
1	C	13	THR	Peptide
1	C	223	GLN	Peptide
1	D	225	PRO	Peptide
1	D	265	ASN	Peptide
1	D	266	THR	Peptide
1	D	267	GLY	Peptide
1	D	374	GLY	Peptide
1	F	223	GLN	Peptide
1	F	225	PRO	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3027	0	3036	282	1
1	B	2986	0	2977	371	0
1	C	3009	0	3010	364	0
1	D	2982	0	2961	385	1
1	E	2995	0	2976	328	0
1	F	3022	0	3035	282	0
All	All	18021	0	17995	1938	1

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 54.

All (1938) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:224:ILE:HG23	1:D:225:PRO:CD	1.45	1.46
1:D:46:GLN:NE2	1:D:131:THR:HG21	1.42	1.29
1:F:75:ALA:HB1	1:F:85:LEU:CD2	1.63	1.27
1:E:204:PRO:HB2	1:E:206:GLU:OE1	1.34	1.27
1:E:224:ILE:CD1	1:E:225:PRO:HD3	1.65	1.27
1:E:204:PRO:O	1:E:205:ILE:HG22	1.19	1.26
1:D:203:ASP:OD1	1:D:204:PRO:HD3	1.29	1.25
1:E:275:HIS:HD2	1:F:265:ASN:O	1.18	1.24
1:E:277:GLN:HE21	1:E:387:MET:CE	1.53	1.21
1:B:18:PRO:CB	1:B:26:GLN:HE21	1.55	1.20
1:B:46:GLN:HG3	1:B:68:PHE:CE1	1.78	1.19
1:E:75:ALA:HB3	1:E:85:LEU:CD2	1.71	1.18
1:B:21:PHE:O	1:B:73:ARG:NE	1.74	1.18
1:A:248:ILE:CD1	1:A:270:VAL:HG13	1.73	1.18
1:E:224:ILE:O	1:E:228:PHE:O	1.60	1.18
1:F:203:ASP:HB3	1:F:204:PRO:CD	1.73	1.16
1:E:79:SER:HB3	1:E:121:ILE:HD11	1.28	1.16
1:B:245:LEU:HD23	1:B:269:PRO:HB2	1.22	1.16
1:E:79:SER:HB3	1:E:121:ILE:CD1	1.76	1.16
1:A:205:ILE:HG13	1:A:223:GLN:HG2	1.20	1.16
1:C:279:CYS:O	1:C:282:VAL:HG12	1.45	1.15
1:A:35:LEU:HD11	1:A:115:PHE:CD2	1.81	1.15
1:E:203:ASP:HB3	1:E:204:PRO:CD	1.77	1.15
1:C:224:ILE:CG2	1:C:225:PRO:HD3	1.75	1.14
1:A:248:ILE:HD13	1:A:270:VAL:HG13	1.17	1.14
1:D:203:ASP:CG	1:D:204:PRO:HD3	1.66	1.13
1:D:257:ILE:HD11	1:D:290:PHE:CE1	1.84	1.13
1:E:254:LYS:HD3	1:E:254:LYS:H	1.13	1.13
1:B:20:THR:O	1:B:26:GLN:NE2	1.80	1.13
1:E:204:PRO:O	1:E:205:ILE:CG2	1.96	1.13
1:A:203:ASP:HB3	1:A:204:PRO:HD2	1.23	1.12
1:C:224:ILE:HG22	1:C:225:PRO:CD	1.78	1.12
1:D:224:ILE:HG23	1:D:225:PRO:HD2	1.24	1.12
1:C:203:ASP:HB3	1:C:204:PRO:HD2	1.20	1.11
1:D:203:ASP:CG	1:D:204:PRO:CD	2.18	1.11
1:E:179:THR:HG21	1:E:312:GLN:OE1	1.46	1.11
1:D:317:LYS:HE2	1:D:321:ASN:HB2	1.17	1.11
1:F:224:ILE:HG22	1:F:225:PRO:HD3	1.11	1.11
1:B:316:ARG:NH1	1:B:320:GLY:O	1.85	1.10
1:F:75:ALA:HB1	1:F:85:LEU:HD23	1.24	1.10
1:D:46:GLN:NE2	1:D:131:THR:CG2	2.13	1.10
1:F:204:PRO:HA	1:F:223:GLN:HE21	1.15	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:46:GLN:HG3	1:D:71:ILE:CD1	1.82	1.10
1:F:76:LEU:HA	1:F:82:SER:HB2	1.22	1.10
1:B:203:ASP:HB3	1:B:204:PRO:HD2	1.15	1.10
1:D:48:VAL:O	1:D:66:LEU:HD11	1.52	1.09
1:E:102:HIS:CD2	1:E:103:PRO:HD2	1.88	1.08
1:A:151:LEU:HD21	1:A:326:ARG:CZ	1.84	1.07
1:C:194:ILE:HD11	1:C:245:LEU:HB2	1.36	1.07
1:D:141:LEU:H	1:D:141:LEU:HD12	1.07	1.07
1:D:224:ILE:HG23	1:D:225:PRO:HD3	1.13	1.07
1:E:203:ASP:HB3	1:E:204:PRO:HD3	1.31	1.07
1:E:275:HIS:CD2	1:F:265:ASN:O	2.09	1.06
1:D:118:ARG:HE	1:D:139:ILE:HD11	1.17	1.06
1:F:9:LEU:HD11	1:F:62:SER:HA	1.36	1.06
1:C:97:ARG:CB	1:C:97:ARG:HH11	1.68	1.06
1:B:45:LYS:NZ	1:B:46:GLN:O	1.88	1.05
1:D:46:GLN:HG3	1:D:71:ILE:HD13	1.31	1.05
1:F:19:SER:HA	1:F:64:ARG:HH12	1.16	1.04
1:C:97:ARG:HB2	1:C:97:ARG:HH11	1.18	1.03
1:D:257:ILE:HD11	1:D:290:PHE:CZ	1.93	1.03
1:D:46:GLN:CG	1:D:71:ILE:HD13	1.88	1.03
1:B:81:SER:O	1:B:84:VAL:HG13	1.58	1.03
1:B:192:THR:HG22	1:B:194:ILE:H	1.22	1.03
1:D:203:ASP:HA	1:D:224:ILE:HB	1.36	1.03
1:C:19:SER:HA	1:C:64:ARG:HH12	1.19	1.02
1:E:277:GLN:HE21	1:E:387:MET:HE1	1.22	1.02
1:D:224:ILE:CG2	1:D:225:PRO:CD	2.36	1.02
1:E:102:HIS:HD2	1:E:103:PRO:HD2	1.17	1.01
1:D:224:ILE:CG2	1:D:225:PRO:HD3	1.91	1.01
1:A:248:ILE:HD13	1:A:270:VAL:CG1	1.90	1.01
1:B:317:LYS:CD	1:B:375:ILE:HD11	1.90	1.01
1:E:224:ILE:HD12	1:E:225:PRO:HD3	1.41	1.01
1:A:10:GLU:OE2	1:A:59:CYS:SG	2.17	1.01
1:F:204:PRO:HA	1:F:223:GLN:NE2	1.76	1.01
1:F:203:ASP:HB3	1:F:204:PRO:HD2	1.02	1.01
1:B:317:LYS:HD2	1:B:375:ILE:HD11	1.04	1.00
1:D:230:SER:HB2	1:D:233:ILE:HG12	1.43	1.00
1:A:203:ASP:HB3	1:A:204:PRO:CD	1.91	1.00
1:C:94:ILE:HD11	1:C:121:ILE:HD12	1.42	1.00
1:A:149:ILE:HG13	1:A:151:LEU:HD23	1.39	1.00
1:D:118:ARG:NE	1:D:139:ILE:HD11	1.76	1.00
1:D:46:GLN:HE21	1:D:131:THR:CG2	1.69	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:35:LEU:HD11	1:E:117:TYR:OH	1.62	0.99
1:B:203:ASP:HB3	1:B:204:PRO:CD	1.93	0.99
1:C:139:ILE:HG13	1:C:140:PRO:HD2	1.42	0.99
1:E:379:HIS:O	1:E:382:LYS:HG2	1.63	0.99
1:B:68:PHE:HE2	1:B:129:LYS:HD3	1.25	0.99
1:D:95:ASN:HD21	1:D:120:ASN:HD22	1.11	0.98
1:D:141:LEU:CD1	1:D:141:LEU:H	1.75	0.98
1:D:335:ILE:HG23	1:D:355:LEU:HD13	1.44	0.98
1:C:165:ILE:HD13	1:C:270:VAL:HB	1.46	0.98
1:C:203:ASP:HB3	1:C:204:PRO:CD	1.93	0.98
1:C:239:LEU:HD12	1:C:240:ARG:N	1.78	0.98
1:B:370:LEU:O	1:B:375:ILE:HG22	1.64	0.98
1:E:224:ILE:CG1	1:E:225:PRO:HD3	1.92	0.98
1:F:6:LEU:HD22	1:F:63:THR:HG22	1.40	0.98
1:F:379:HIS:HA	1:F:382:LYS:HE2	1.43	0.98
1:F:224:ILE:HG22	1:F:225:PRO:CD	1.92	0.97
1:D:94:ILE:CG1	1:D:121:ILE:HB	1.93	0.97
1:A:243:PRO:HG2	1:A:246:ILE:HD11	1.45	0.97
1:F:6:LEU:HD22	1:F:63:THR:CG2	1.94	0.97
1:B:137:ARG:HG3	1:B:137:ARG:HH11	1.25	0.96
1:A:203:ASP:HA	1:A:225:PRO:CD	1.94	0.96
1:B:18:PRO:CB	1:B:26:GLN:NE2	2.27	0.96
1:D:203:ASP:OD1	1:D:204:PRO:CD	2.13	0.96
1:F:192:THR:HG22	1:F:194:ILE:H	1.25	0.96
1:E:331:PHE:HA	1:E:335:ILE:HG21	1.45	0.96
1:F:75:ALA:CB	1:F:85:LEU:HD23	1.96	0.96
1:E:204:PRO:CB	1:E:206:GLU:OE1	2.14	0.96
1:C:13:THR:O	1:C:14:GLU:HB2	1.64	0.95
1:C:125:TYR:OH	1:D:97:ARG:NH1	1.98	0.95
1:A:31:VAL:HG21	1:A:100:VAL:HG11	1.47	0.95
1:D:141:LEU:N	1:D:141:LEU:HD12	1.79	0.95
1:C:32:LEU:HD13	1:C:103:PRO:HD3	1.46	0.95
1:F:111:GLN:H	1:F:111:GLN:NE2	1.65	0.95
1:A:21:PHE:O	1:A:73:ARG:NE	1.99	0.95
1:A:244:ASN:O	1:A:269:PRO:HD2	1.67	0.95
1:B:55:LYS:HE2	1:B:321:ASN:HB3	1.46	0.95
1:A:18:PRO:O	1:A:64:ARG:NH2	1.99	0.94
1:B:35:LEU:HD13	1:B:117:TYR:OH	1.67	0.94
1:C:8:ILE:HD12	1:C:8:ILE:H	1.28	0.94
1:B:345:MET:O	1:B:348:VAL:HG22	1.68	0.94
1:C:19:SER:O	1:C:64:ARG:NH1	1.99	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:317:LYS:HE2	1:D:321:ASN:CB	1.97	0.94
1:B:46:GLN:HG3	1:B:68:PHE:HE1	1.24	0.94
1:D:317:LYS:CE	1:D:321:ASN:HB2	1.97	0.94
1:F:275:HIS:O	1:F:285:ARG:NH1	2.01	0.94
1:B:18:PRO:HB3	1:B:26:GLN:HE21	1.31	0.94
1:F:19:SER:HA	1:F:64:ARG:NH1	1.82	0.93
1:F:224:ILE:O	1:F:228:PHE:O	1.85	0.93
1:A:352:VAL:O	1:A:356:VAL:HG13	1.69	0.93
1:B:317:LYS:HD2	1:B:375:ILE:CD1	1.97	0.93
1:B:46:GLN:HG3	1:B:68:PHE:CD1	2.02	0.93
1:C:224:ILE:HG22	1:C:225:PRO:HD3	0.94	0.93
1:B:121:ILE:HD13	1:B:134:ILE:HB	1.49	0.93
1:B:35:LEU:HD21	1:B:115:PHE:CD1	2.04	0.92
1:A:106:LEU:HD12	1:A:113:GLN:HG2	1.48	0.92
1:B:318:THR:HG21	1:B:374:GLY:O	1.69	0.92
1:F:224:ILE:HG12	1:F:231:PHE:CE1	2.04	0.92
1:F:124:VAL:HG21	1:F:133:GLU:HB2	1.50	0.92
1:E:254:LYS:CD	1:E:254:LYS:H	1.82	0.91
1:B:205:ILE:HG22	1:B:223:GLN:OE1	1.69	0.91
1:D:301:ASP:O	1:D:305:THR:OG1	1.88	0.91
1:F:149:ILE:HD11	1:F:182:SER:OG	1.70	0.91
1:E:75:ALA:CB	1:E:85:LEU:CD2	2.49	0.91
1:C:108:THR:HG22	1:C:112:LYS:H	1.36	0.91
1:A:197:HIS:NE2	1:F:133:GLU:OE2	2.04	0.91
1:C:46:GLN:HE21	1:C:68:PHE:HA	1.35	0.91
1:D:118:ARG:HE	1:D:139:ILE:CD1	1.84	0.91
1:A:252:ARG:HB2	1:A:252:ARG:NH1	1.86	0.90
1:B:12:LYS:HZ3	1:B:17:TYR:H	1.18	0.90
1:F:105:LYS:HE2	1:F:113:GLN:OE1	1.69	0.90
1:D:9:LEU:HA	1:D:60:THR:O	1.71	0.90
1:B:174:SER:O	1:B:178:THR:HG23	1.71	0.90
1:B:15:TYR:OH	1:B:30:THR:HG22	1.71	0.90
1:D:48:VAL:O	1:D:66:LEU:CD1	2.19	0.90
1:A:6:LEU:HD22	1:A:6:LEU:O	1.71	0.90
1:B:149:ILE:HG13	1:B:151:LEU:HD23	1.54	0.90
1:D:83:SER:O	1:D:87:GLU:HG2	1.71	0.90
1:D:46:GLN:HE21	1:D:131:THR:HG21	1.20	0.90
1:E:254:LYS:N	1:E:254:LYS:HD3	1.84	0.89
1:F:149:ILE:HG22	1:F:326:ARG:HH22	1.37	0.89
1:E:75:ALA:HB3	1:E:85:LEU:HD21	1.53	0.89
1:D:94:ILE:HG12	1:D:121:ILE:HB	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:205:ILE:N	1:D:223:GLN:HE22	1.70	0.89
1:A:252:ARG:HH11	1:A:252:ARG:HB2	1.38	0.89
1:C:194:ILE:HD12	1:C:269:PRO:HG2	1.53	0.89
1:E:334:ASP:O	1:E:338:GLN:HG2	1.73	0.89
1:D:35:LEU:HD21	1:D:115:PHE:CD2	2.08	0.88
1:E:224:ILE:HD12	1:E:225:PRO:CD	2.03	0.88
1:F:79:SER:O	1:F:82:SER:OG	1.91	0.88
1:E:277:GLN:NE2	1:E:387:MET:CE	2.36	0.88
1:C:23:HIS:N	1:C:26:GLN:OE1	2.05	0.88
1:A:198:LEU:HB2	1:A:219:ILE:HD12	1.55	0.88
1:A:49:ALA:HB3	1:A:60:THR:HG21	1.55	0.88
1:E:58:LEU:HD12	1:E:58:LEU:O	1.74	0.88
1:A:297:ALA:HB1	1:F:383:ARG:HH22	1.36	0.88
1:C:34:PHE:CE1	1:C:61:LEU:CD2	2.57	0.88
1:F:99:GLU:OE1	1:F:114:ARG:NH2	2.07	0.87
1:D:205:ILE:H	1:D:223:GLN:HE22	0.89	0.87
1:C:19:SER:CA	1:C:64:ARG:HH12	1.88	0.87
1:D:81:SER:O	1:D:84:VAL:HG13	1.74	0.87
1:C:34:PHE:CZ	1:C:61:LEU:CD2	2.58	0.87
1:F:75:ALA:CB	1:F:85:LEU:CD2	2.51	0.87
1:A:60:THR:HG22	1:A:62:SER:H	1.39	0.86
1:D:203:ASP:OD1	1:D:224:ILE:HG21	1.75	0.86
1:E:102:HIS:HD2	1:E:103:PRO:CD	1.87	0.86
1:E:248:ILE:HG12	1:E:270:VAL:HG13	1.55	0.86
1:B:96:THR:HG23	1:B:119:VAL:HG22	1.55	0.86
1:C:32:LEU:CD1	1:C:103:PRO:HD3	2.05	0.86
1:D:95:ASN:ND2	1:D:120:ASN:HD22	1.73	0.86
1:A:203:ASP:HA	1:A:225:PRO:HD3	1.57	0.86
1:F:74:ILE:HD13	1:F:77:TRP:CZ3	2.11	0.86
1:B:102:HIS:HB2	1:B:115:PHE:CE2	2.09	0.85
1:B:192:THR:HG23	1:B:193:PRO:HD2	1.57	0.85
1:C:68:PHE:HA	1:C:71:ILE:HG12	1.56	0.85
1:A:151:LEU:HD21	1:A:326:ARG:NH2	1.90	0.85
1:D:326:ARG:HH11	1:D:326:ARG:HG3	1.41	0.85
1:B:68:PHE:CE2	1:B:129:LYS:HD3	2.11	0.85
1:A:297:ALA:HB1	1:F:383:ARG:NH2	1.92	0.85
1:C:162:ASP:O	1:C:269:PRO:HD3	1.77	0.84
1:D:118:ARG:NH2	1:D:139:ILE:HD11	1.93	0.84
1:F:76:LEU:CA	1:F:82:SER:HB2	2.07	0.84
1:B:46:GLN:CG	1:B:68:PHE:HE1	1.90	0.84
1:C:114:ARG:HG3	1:C:141:LEU:HD11	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:ASP:HA	1:D:224:ILE:CB	2.07	0.84
1:C:68:PHE:H	1:C:68:PHE:HD1	1.21	0.84
1:D:118:ARG:CZ	1:D:139:ILE:HD11	2.07	0.84
1:B:203:ASP:CB	1:B:204:PRO:HD2	2.03	0.84
1:C:239:LEU:HD12	1:C:240:ARG:H	1.43	0.84
1:D:246:ILE:HG13	1:D:268:HIS:CD2	2.13	0.84
1:C:97:ARG:NH1	1:C:97:ARG:HB2	1.92	0.84
1:E:118:ARG:HG3	1:E:139:ILE:HD11	1.60	0.84
1:B:24:GLU:O	1:B:27:PHE:N	2.11	0.83
1:B:100:VAL:HG12	1:B:115:PHE:HB2	1.60	0.83
1:A:64:ARG:NH1	1:A:70:GLU:OE2	2.11	0.83
1:D:250:GLU:HG2	1:D:273:THR:OG1	1.78	0.83
1:D:339:LEU:HD22	1:D:348:VAL:HG13	1.60	0.83
1:D:118:ARG:HH21	1:D:139:ILE:HD11	1.44	0.83
1:D:224:ILE:CG2	1:D:225:PRO:HD2	2.06	0.83
1:E:224:ILE:HG13	1:E:225:PRO:HD3	1.58	0.83
1:B:228:PHE:O	1:B:230:SER:N	2.11	0.83
1:C:99:GLU:CD	1:C:114:ARG:HH21	1.81	0.83
1:E:35:LEU:HD21	1:E:115:PHE:CG	2.14	0.83
1:A:167:MET:CE	1:A:286:LEU:HD11	2.09	0.83
1:A:35:LEU:HD11	1:A:115:PHE:CG	2.14	0.83
1:C:8:ILE:CD1	1:C:8:ILE:H	1.92	0.82
1:B:17:TYR:CE1	1:B:62:SER:HB3	2.14	0.82
1:B:79:SER:OG	1:B:97:ARG:O	1.96	0.82
1:D:24:GLU:OE1	1:D:28:LYS:NZ	2.11	0.82
1:E:79:SER:CB	1:E:121:ILE:CD1	2.57	0.82
1:C:8:ILE:HD12	1:C:8:ILE:N	1.95	0.82
1:D:35:LEU:HD21	1:D:115:PHE:CE2	2.14	0.82
1:F:317:LYS:HD3	1:F:323:VAL:CG1	2.09	0.82
1:B:384:LEU:HD23	1:B:384:LEU:O	1.78	0.82
1:B:349:ALA:O	1:B:352:VAL:HG12	1.78	0.82
1:E:203:ASP:CB	1:E:204:PRO:HD3	2.08	0.82
1:B:375:ILE:O	1:B:375:ILE:HD12	1.80	0.82
1:D:317:LYS:HD3	1:D:323:VAL:HG13	1.62	0.82
1:B:17:TYR:CZ	1:B:62:SER:HB3	2.14	0.81
1:B:376:ILE:HB	1:B:380:VAL:CG2	2.10	0.81
1:B:39:ALA:HB1	1:B:52:ALA:HB1	1.60	0.81
1:D:76:LEU:HD11	1:D:82:SER:HA	1.62	0.81
1:A:149:ILE:HG13	1:A:151:LEU:CD2	2.08	0.81
1:C:203:ASP:CB	1:C:204:PRO:CD	2.58	0.81
1:C:46:GLN:NE2	1:C:68:PHE:CB	2.43	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:ASP:CB	1:D:204:PRO:CD	2.58	0.81
1:D:8:ILE:HD12	1:D:8:ILE:H	1.44	0.81
1:E:224:ILE:CD1	1:E:225:PRO:CD	2.54	0.81
1:A:337:GLU:O	1:A:341:SER:OG	1.98	0.81
1:F:250:GLU:HG2	1:F:252:ARG:HG2	1.61	0.81
1:E:203:ASP:CB	1:E:204:PRO:CD	2.59	0.81
1:C:46:GLN:CD	1:C:131:THR:HG21	2.01	0.81
1:E:58:LEU:HD12	1:E:58:LEU:C	2.01	0.81
1:B:35:LEU:O	1:B:38:GLU:N	2.13	0.81
1:C:156:VAL:HA	1:C:159:MET:HG2	1.61	0.81
1:C:46:GLN:HG2	1:C:68:PHE:CD1	2.16	0.81
1:F:203:ASP:CB	1:F:204:PRO:HD2	1.99	0.81
1:F:66:LEU:HA	1:F:70:GLU:OE1	1.80	0.81
1:B:18:PRO:CG	1:B:26:GLN:HE21	1.94	0.81
1:C:139:ILE:HG13	1:C:140:PRO:CD	2.11	0.81
1:D:83:SER:O	1:D:86:THR:OG1	1.97	0.81
1:D:203:ASP:CG	1:D:204:PRO:HD2	2.01	0.80
1:D:304:GLU:O	1:D:307:ARG:NH1	2.12	0.80
1:C:274:VAL:HG11	1:C:282:VAL:HG23	1.62	0.80
1:F:192:THR:HG23	1:F:193:PRO:HD2	1.63	0.80
1:C:194:ILE:CD1	1:C:269:PRO:HG2	2.10	0.80
1:F:203:ASP:CB	1:F:204:PRO:CD	2.57	0.80
1:E:15:TYR:OH	1:E:30:THR:HG22	1.81	0.80
1:B:222:SER:HA	1:B:227:GLN:HE22	1.46	0.80
1:C:94:ILE:CD1	1:C:121:ILE:HD12	2.11	0.80
1:A:205:ILE:HG13	1:A:223:GLN:CG	2.07	0.80
1:B:102:HIS:HD2	1:B:105:LYS:CB	1.95	0.80
1:F:20:THR:O	1:F:70:GLU:HG2	1.81	0.80
1:E:79:SER:CB	1:E:121:ILE:HD12	2.11	0.80
1:E:327:GLU:HG3	1:E:362:PRO:HA	1.64	0.80
1:B:12:LYS:NZ	1:B:17:TYR:H	1.79	0.79
1:D:203:ASP:O	1:D:223:GLN:NE2	2.15	0.79
1:D:37:HIS:O	1:D:54:VAL:HG22	1.81	0.79
1:E:6:LEU:O	1:E:6:LEU:HD13	1.81	0.79
1:C:135:VAL:HG21	1:D:241:ARG:HA	1.65	0.79
1:F:35:LEU:HD21	1:F:115:PHE:CG	2.17	0.79
1:D:257:ILE:CD1	1:D:290:PHE:CE1	2.64	0.79
1:F:8:ILE:O	1:F:60:THR:OG1	2.01	0.79
1:A:124:VAL:HG23	1:A:131:THR:HG23	1.63	0.79
1:C:32:LEU:HD13	1:C:103:PRO:CD	2.13	0.79
1:C:194:ILE:HD12	1:C:269:PRO:CG	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:317:LYS:HD3	1:F:323:VAL:HG13	1.63	0.79
1:A:203:ASP:CB	1:A:204:PRO:CD	2.58	0.79
1:D:386:MET:CE	1:D:386:MET:HA	2.13	0.79
1:E:43:ILE:CG1	1:E:51:SER:OG	2.31	0.79
1:E:27:PHE:O	1:E:30:THR:OG1	2.00	0.78
1:F:15:TYR:CE1	1:F:61:LEU:HD13	2.19	0.78
1:D:188:MET:HB3	1:D:214:SER:OG	1.83	0.78
1:E:332:THR:O	1:E:335:ILE:HG22	1.82	0.78
1:B:23:HIS:O	1:B:26:GLN:CB	2.31	0.78
1:C:76:LEU:HD21	1:C:82:SER:HA	1.65	0.78
1:D:205:ILE:H	1:D:223:GLN:NE2	1.74	0.78
1:E:179:THR:CG2	1:E:326:ARG:HH21	1.97	0.78
1:A:149:ILE:CG1	1:A:151:LEU:HD23	2.13	0.78
1:B:48:VAL:O	1:B:66:LEU:HD23	1.84	0.78
1:D:203:ASP:O	1:D:224:ILE:HG22	1.82	0.78
1:F:149:ILE:HG22	1:F:326:ARG:NH2	1.98	0.78
1:B:102:HIS:HB2	1:B:115:PHE:HE2	1.46	0.78
1:F:17:TYR:CD1	1:F:18:PRO:HD2	2.18	0.78
1:D:120:ASN:ND2	1:E:237:GLU:OE1	2.16	0.78
1:F:376:ILE:CD1	1:F:381:ALA:HB2	2.12	0.78
1:C:194:ILE:CD1	1:C:245:LEU:HD13	2.14	0.78
1:D:84:VAL:O	1:D:87:GLU:HG3	1.84	0.78
1:C:19:SER:HA	1:C:64:ARG:NH1	1.97	0.77
1:D:40:SER:O	1:D:41:ASP:OD1	2.02	0.77
1:B:23:HIS:O	1:B:26:GLN:HB3	1.85	0.77
1:E:277:GLN:HE21	1:E:387:MET:HE3	1.48	0.77
1:E:335:ILE:CD1	1:E:355:LEU:HD13	2.13	0.77
1:A:43:ILE:CG2	1:A:133:GLU:OE2	2.31	0.77
1:B:155:LEU:HD22	1:B:155:LEU:O	1.84	0.77
1:C:34:PHE:CE1	1:C:61:LEU:HD21	2.18	0.77
1:E:204:PRO:HB2	1:E:206:GLU:CD	2.04	0.77
1:B:64:ARG:HB3	1:B:64:ARG:CZ	2.13	0.77
1:E:335:ILE:HD11	1:E:355:LEU:HD13	1.65	0.77
1:D:46:GLN:HE21	1:D:131:THR:CB	1.97	0.77
1:F:159:MET:SD	1:F:310:MET:HE3	2.25	0.77
1:C:66:LEU:HA	1:C:70:GLU:OE2	1.85	0.77
1:D:373:ASP:HB2	1:D:375:ILE:HD12	1.66	0.77
1:C:46:GLN:NE2	1:C:68:PHE:CG	2.53	0.77
1:A:167:MET:HE1	1:A:286:LEU:HD11	1.66	0.76
1:C:245:LEU:HD12	1:C:269:PRO:HB2	1.67	0.76
1:B:248:ILE:CG1	1:B:270:VAL:HG13	2.14	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:ARG:HG3	1:C:141:LEU:CD1	2.15	0.76
1:C:203:ASP:O	1:C:223:GLN:HG3	1.84	0.76
1:E:224:ILE:HG13	1:E:225:PRO:CD	2.14	0.76
1:B:248:ILE:HG13	1:B:270:VAL:HG13	1.67	0.76
1:B:118:ARG:NH2	1:B:205:ILE:O	2.18	0.76
1:C:46:GLN:HE21	1:C:71:ILE:HG12	1.49	0.76
1:D:146:LEU:HD13	1:D:156:VAL:HG11	1.67	0.76
1:F:149:ILE:CD1	1:F:182:SER:OG	2.34	0.76
1:A:35:LEU:O	1:A:35:LEU:HD23	1.86	0.76
1:C:17:TYR:CD1	1:C:18:PRO:HD2	2.21	0.76
1:C:345:MET:O	1:C:348:VAL:HG23	1.85	0.76
1:C:120:ASN:HB3	1:C:135:VAL:HG22	1.68	0.76
1:A:49:ALA:HB2	1:A:64:ARG:O	1.85	0.76
1:F:24:GLU:HG2	1:F:28:LYS:HE3	1.67	0.76
1:E:35:LEU:CD2	1:E:115:PHE:CG	2.69	0.75
1:E:306:THR:HG23	1:E:331:PHE:CD2	2.22	0.75
1:B:146:LEU:HD11	1:B:186:TYR:HB2	1.69	0.75
1:D:93:LEU:HD22	1:D:93:LEU:H	1.50	0.75
1:B:151:LEU:HD21	1:B:326:ARG:NH2	2.01	0.75
1:B:33:GLU:OE2	1:B:37:HIS:HE1	1.68	0.75
1:C:114:ARG:CG	1:C:141:LEU:HD11	2.15	0.75
1:C:99:GLU:OE1	1:C:114:ARG:NH2	2.19	0.75
1:A:302:LEU:C	1:A:302:LEU:HD13	2.07	0.75
1:A:34:PHE:HE2	1:A:50:ILE:HG22	1.50	0.75
1:B:176:LYS:NZ	1:B:275:HIS:CE1	2.55	0.75
1:B:18:PRO:HB3	1:B:26:GLN:NE2	1.94	0.75
1:E:204:PRO:C	1:E:205:ILE:HG22	2.05	0.75
1:B:244:ASN:O	1:B:269:PRO:HD2	1.85	0.75
1:D:203:ASP:CB	1:D:204:PRO:HD2	2.17	0.75
1:D:66:LEU:HD12	1:D:66:LEU:H	1.50	0.75
1:C:155:LEU:O	1:C:158:GLN:HB3	1.87	0.75
1:E:70:GLU:O	1:E:74:ILE:HG12	1.87	0.75
1:E:35:LEU:CD1	1:E:117:TYR:OH	2.34	0.75
1:A:107:THR:HG22	1:A:109:GLY:H	1.51	0.74
1:D:83:SER:HB2	1:D:86:THR:OG1	1.87	0.74
1:E:233:ILE:N	1:E:233:ILE:HD13	2.02	0.74
1:E:53:LYS:HA	1:E:57:THR:O	1.87	0.74
1:C:41:ASP:OD1	1:C:137:ARG:HG2	1.86	0.74
1:D:176:LYS:NZ	1:D:275:HIS:CE1	2.55	0.74
1:E:79:SER:HB3	1:E:121:ILE:HD12	1.64	0.74
1:C:71:ILE:HD13	1:C:131:THR:CG2	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:THR:N	1:B:111:GLN:O	2.19	0.74
1:E:248:ILE:HG12	1:E:270:VAL:CG1	2.18	0.74
1:F:9:LEU:HD11	1:F:62:SER:CA	2.15	0.74
1:C:22:GLU:O	1:C:77:TRP:CZ2	2.40	0.74
1:C:22:GLU:O	1:C:77:TRP:HZ2	1.71	0.74
1:D:53:LYS:NZ	1:E:242:THR:O	2.19	0.74
1:B:137:ARG:HG3	1:B:137:ARG:NH1	1.99	0.74
1:E:137:ARG:HH12	1:F:240:ARG:HB3	1.53	0.74
1:F:118:ARG:HG3	1:F:118:ARG:O	1.86	0.74
1:F:365:LEU:HD11	1:F:369:ARG:HE	1.52	0.74
1:B:102:HIS:ND1	1:B:103:PRO:HD2	2.03	0.74
1:B:317:LYS:HB3	1:B:375:ILE:CD1	2.17	0.74
1:C:68:PHE:O	1:C:71:ILE:HG13	1.86	0.74
1:C:97:ARG:CG	1:C:97:ARG:HH11	2.01	0.74
1:F:84:VAL:HG13	1:F:88:LEU:HG	1.68	0.74
1:C:387:MET:HA	1:C:387:MET:CE	2.18	0.74
1:F:85:LEU:C	1:F:85:LEU:HD12	2.09	0.74
1:A:203:ASP:HA	1:A:225:PRO:HD2	1.70	0.73
1:C:165:ILE:HD13	1:C:270:VAL:CB	2.16	0.73
1:C:194:ILE:HD13	1:C:245:LEU:HD13	1.69	0.73
1:E:376:ILE:HG23	1:E:380:VAL:CG2	2.18	0.73
1:E:6:LEU:H	1:E:6:LEU:HD12	1.54	0.73
1:B:12:LYS:HZ3	1:B:17:TYR:N	1.86	0.73
1:C:224:ILE:CG2	1:C:225:PRO:CD	2.52	0.73
1:E:199:LEU:HD11	1:E:241:ARG:HB2	1.69	0.73
1:F:44:ILE:HG12	1:F:50:ILE:CD1	2.18	0.73
1:C:97:ARG:HD3	1:C:98:TYR:N	2.04	0.73
1:D:9:LEU:H	1:D:9:LEU:HD12	1.52	0.73
1:D:203:ASP:HB3	1:D:204:PRO:HD2	1.70	0.73
1:B:17:TYR:CZ	1:B:62:SER:CB	2.72	0.73
1:E:176:LYS:CE	1:E:273:THR:HG23	2.18	0.73
1:A:246:ILE:HG22	1:A:248:ILE:HG13	1.71	0.73
1:D:55:LYS:O	1:D:55:LYS:HG3	1.88	0.73
1:F:18:PRO:O	1:F:64:ARG:NH1	2.21	0.73
1:D:200:THR:HA	1:D:247:MET:HB3	1.70	0.73
1:A:203:ASP:OD1	1:A:204:PRO:HD3	1.88	0.72
1:C:100:VAL:HG12	1:C:115:PHE:HB2	1.71	0.72
1:C:179:THR:HG21	1:C:310:MET:CE	2.18	0.72
1:D:246:ILE:CD1	1:D:268:HIS:NE2	2.52	0.72
1:C:21:PHE:CZ	1:C:50:ILE:HD12	2.25	0.72
1:A:342:LEU:HD12	1:A:351:GLU:HG3	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:95:ASN:HD21	1:D:120:ASN:ND2	1.86	0.72
1:E:224:ILE:CG1	1:E:225:PRO:CD	2.67	0.72
1:F:84:VAL:HG13	1:F:88:LEU:CG	2.18	0.72
1:B:45:LYS:C	1:B:71:ILE:HD11	2.10	0.72
1:D:9:LEU:CA	1:D:60:THR:O	2.37	0.72
1:B:12:LYS:HZ3	1:B:17:TYR:HB2	1.53	0.72
1:D:27:PHE:HB2	1:D:77:TRP:HZ3	1.52	0.72
1:F:102:HIS:CD2	1:F:105:LYS:HD3	2.23	0.72
1:B:203:ASP:CB	1:B:204:PRO:CD	2.61	0.72
1:E:335:ILE:HD11	1:E:355:LEU:HB3	1.72	0.71
1:F:224:ILE:HG21	1:F:231:PHE:CE2	2.25	0.71
1:D:257:ILE:HD11	1:D:290:PHE:HE1	1.47	0.71
1:A:248:ILE:HD11	1:A:270:VAL:HG13	1.70	0.71
1:B:284:ARG:HA	1:B:287:ILE:HG13	1.72	0.71
1:D:319:ASP:OD2	1:D:321:ASN:ND2	2.22	0.71
1:E:351:GLU:OE1	1:E:351:GLU:HA	1.91	0.71
1:B:107:THR:OG1	1:B:111:GLN:N	2.24	0.71
1:D:17:TYR:CD1	1:D:18:PRO:HD2	2.26	0.71
1:D:94:ILE:O	1:D:94:ILE:HG13	1.90	0.71
1:C:194:ILE:CD1	1:C:245:LEU:HB2	2.17	0.71
1:B:18:PRO:HB2	1:B:26:GLN:NE2	2.05	0.71
1:B:18:PRO:HB2	1:B:20:THR:O	1.89	0.71
1:B:317:LYS:HB3	1:B:375:ILE:HD12	1.72	0.71
1:B:245:LEU:HD22	1:B:246:ILE:H	1.55	0.71
1:C:46:GLN:CD	1:C:68:PHE:CG	2.64	0.71
1:D:12:LYS:N	1:D:12:LYS:HD2	2.06	0.71
1:F:74:ILE:CD1	1:F:77:TRP:CZ3	2.73	0.71
1:B:198:LEU:HB2	1:B:219:ILE:HD12	1.73	0.71
1:B:151:LEU:HD21	1:B:326:ARG:CZ	2.21	0.71
1:D:257:ILE:CD1	1:D:290:PHE:HE1	2.01	0.71
1:E:10:GLU:OE2	1:E:37:HIS:CD2	2.44	0.71
1:F:203:ASP:O	1:F:223:GLN:HG3	1.89	0.71
1:D:9:LEU:HB3	1:D:60:THR:O	1.90	0.71
1:E:75:ALA:HB3	1:E:85:LEU:HD22	1.73	0.71
1:C:68:PHE:N	1:C:68:PHE:HD1	1.89	0.70
1:B:302:LEU:O	1:B:306:THR:HG23	1.91	0.70
1:D:46:GLN:HG3	1:D:71:ILE:HD12	1.72	0.70
1:A:126:ILE:HG22	1:A:127:GLN:HG2	1.72	0.70
1:B:353:ARG:HH21	1:B:356:VAL:HG13	1.55	0.70
1:C:46:GLN:HE21	1:C:68:PHE:CA	2.03	0.70
1:F:33:GLU:OE2	1:F:37:HIS:HE1	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:LEU:CD2	1:A:326:ARG:CZ	2.66	0.70
1:D:124:VAL:HG11	1:D:133:GLU:HB2	1.74	0.70
1:D:13:THR:H	1:D:33:GLU:CD	1.93	0.70
1:D:27:PHE:O	1:D:30:THR:OG1	2.10	0.70
1:E:23:HIS:N	1:E:26:GLN:OE1	2.24	0.70
1:E:75:ALA:HB3	1:E:85:LEU:HD23	1.74	0.70
1:D:194:ILE:CD1	1:D:245:LEU:HB2	2.22	0.70
1:D:9:LEU:CB	1:D:60:THR:O	2.40	0.70
1:A:205:ILE:CG1	1:A:223:GLN:HG2	2.11	0.70
1:A:344:ASP:OD1	1:A:344:ASP:C	2.29	0.70
1:B:118:ARG:HG2	1:B:139:ILE:HD11	1.72	0.70
1:B:96:THR:HG23	1:B:119:VAL:CG2	2.21	0.70
1:D:94:ILE:CG1	1:D:94:ILE:O	2.38	0.70
1:F:84:VAL:CG2	1:F:87:GLU:HB3	2.21	0.70
1:D:329:LEU:HD11	1:D:335:ILE:CD1	2.22	0.69
1:B:176:LYS:HZ1	1:B:275:HIS:CE1	2.11	0.69
1:D:118:ARG:HH21	1:D:139:ILE:CD1	2.05	0.69
1:E:43:ILE:HG13	1:E:51:SER:OG	1.91	0.69
1:E:6:LEU:N	1:E:6:LEU:HD12	2.06	0.69
1:A:302:LEU:O	1:A:302:LEU:HD13	1.92	0.69
1:B:318:THR:CG2	1:B:374:GLY:O	2.38	0.69
1:B:37:HIS:O	1:B:38:GLU:HG2	1.92	0.69
1:C:277:GLN:N	1:C:277:GLN:OE1	2.24	0.69
1:A:18:PRO:HG2	1:A:21:PHE:CE1	2.27	0.69
1:C:43:ILE:O	1:C:43:ILE:HG13	1.90	0.69
1:C:112:LYS:HD2	1:C:113:GLN:H	1.57	0.69
1:D:169:ALA:N	1:D:310:MET:O	2.24	0.69
1:E:334:ASP:OD1	1:E:338:GLN:NE2	2.26	0.69
1:C:68:PHE:N	1:C:68:PHE:CD1	2.60	0.69
1:C:67:ASN:OD1	1:C:70:GLU:HG2	1.93	0.69
1:E:168:VAL:HG23	1:E:176:LYS:HG2	1.74	0.69
1:C:34:PHE:CE1	1:C:61:LEU:HD22	2.27	0.69
1:B:35:LEU:CD1	1:B:117:TYR:OH	2.41	0.69
1:C:183:ILE:O	1:C:187:ILE:HG12	1.93	0.69
1:D:66:LEU:HA	1:D:70:GLU:OE2	1.92	0.69
1:E:283:MET:HG3	1:E:352:VAL:HG21	1.75	0.69
1:C:125:TYR:HH	1:D:97:ARG:NH1	1.90	0.68
1:B:12:LYS:NZ	1:B:17:TYR:HB2	2.07	0.68
1:E:209:TYR:HB2	1:E:219:ILE:HG21	1.75	0.68
1:B:180:PHE:HA	1:B:183:ILE:HG22	1.74	0.68
1:B:284:ARG:HA	1:B:287:ILE:CG1	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:35:LEU:HD21	1:E:115:PHE:CD1	2.28	0.68
1:B:70:GLU:O	1:B:74:ILE:HG13	1.92	0.68
1:A:6:LEU:N	1:A:6:LEU:HD13	2.09	0.68
1:B:67:ASN:OD1	1:B:69:ASN:N	2.26	0.68
1:D:246:ILE:HG13	1:D:268:HIS:HD2	1.58	0.68
1:A:317:LYS:HD3	1:A:319:ASP:HB3	1.75	0.68
1:A:6:LEU:HD23	1:A:7:PRO:O	1.94	0.68
1:C:67:ASN:OD1	1:C:70:GLU:N	2.26	0.68
1:F:373:ASP:HB2	1:F:375:ILE:CD1	2.23	0.68
1:F:9:LEU:HD21	1:F:63:THR:HG23	1.75	0.68
1:A:201:HIS:HB3	1:A:224:ILE:HD11	1.76	0.68
1:A:250:GLU:HA	1:A:273:THR:O	1.93	0.68
1:B:107:THR:OG1	1:B:111:GLN:CB	2.42	0.68
1:C:169:ALA:N	1:C:310:MET:O	2.24	0.68
1:F:12:LYS:HD2	1:F:15:TYR:O	1.94	0.68
1:A:8:ILE:HD12	1:A:8:ILE:H	1.59	0.68
1:B:35:LEU:HD13	1:B:117:TYR:HH	1.57	0.68
1:B:10:GLU:OE1	1:B:61:LEU:HD21	1.93	0.68
1:B:79:SER:HB2	1:B:96:THR:CG2	2.24	0.68
1:D:66:LEU:HD12	1:D:66:LEU:N	2.08	0.68
1:D:84:VAL:HA	1:D:87:GLU:OE2	1.94	0.68
1:A:279:CYS:O	1:A:282:VAL:HG13	1.95	0.67
1:F:278:ASN:O	1:F:282:VAL:HG23	1.94	0.67
1:D:278:ASN:OD1	1:D:280:SER:OG	2.11	0.67
1:D:94:ILE:HD12	1:D:94:ILE:O	1.94	0.67
1:B:19:SER:O	1:B:64:ARG:NE	2.28	0.67
1:C:54:VAL:O	1:C:57:THR:HG22	1.95	0.67
1:A:223:GLN:H	1:A:227:GLN:HE21	1.43	0.67
1:B:376:ILE:HB	1:B:380:VAL:HG21	1.75	0.67
1:C:168:VAL:HG23	1:C:176:LYS:HB3	1.77	0.67
1:C:187:ILE:HD12	1:C:194:ILE:CG2	2.24	0.67
1:D:224:ILE:O	1:D:228:PHE:O	2.12	0.67
1:E:252:ARG:HD3	1:E:285:ARG:HH21	1.59	0.67
1:B:96:THR:CG2	1:B:119:VAL:HG22	2.25	0.67
1:C:71:ILE:HD13	1:C:131:THR:HG22	1.76	0.67
1:B:228:PHE:O	1:B:229:SER:C	2.33	0.67
1:D:219:ILE:HD12	1:D:219:ILE:N	2.09	0.67
1:F:76:LEU:HD23	1:F:83:SER:N	2.09	0.67
1:A:243:PRO:CG	1:A:246:ILE:HD11	2.21	0.67
1:C:173:SER:O	1:C:314:LEU:HD12	1.95	0.67
1:D:155:LEU:O	1:D:158:GLN:HB2	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:THR:HG23	1:B:111:GLN:O	1.95	0.67
1:A:106:LEU:HD12	1:A:113:GLN:CG	2.24	0.67
1:C:15:TYR:OH	1:C:30:THR:HG22	1.94	0.67
1:A:297:ALA:CB	1:F:383:ARG:HH22	2.08	0.67
1:F:85:LEU:O	1:F:85:LEU:HD12	1.95	0.67
1:C:108:THR:HG22	1:C:112:LYS:O	1.95	0.67
1:F:224:ILE:CG1	1:F:231:PHE:CE1	2.78	0.67
1:B:246:ILE:HG22	1:B:248:ILE:HD13	1.74	0.66
1:D:188:MET:SD	1:D:219:ILE:HD11	2.35	0.66
1:D:176:LYS:NZ	1:D:250:GLU:OE2	2.29	0.66
1:A:27:PHE:O	1:A:31:VAL:HG13	1.96	0.66
1:B:55:LYS:CE	1:B:321:ASN:HB3	2.22	0.66
1:C:50:ILE:CG1	1:C:66:LEU:HD21	2.25	0.66
1:E:127:GLN:HA	1:F:114:ARG:NH1	2.10	0.66
1:F:376:ILE:HD12	1:F:376:ILE:O	1.94	0.66
1:A:279:CYS:HA	1:A:282:VAL:HG13	1.77	0.66
1:C:194:ILE:HD12	1:C:269:PRO:CB	2.24	0.66
1:C:46:GLN:NE2	1:C:68:PHE:HB3	2.09	0.66
1:E:206:GLU:N	1:E:206:GLU:OE2	2.28	0.66
1:F:45:LYS:HE2	1:F:126:ILE:HD11	1.76	0.66
1:D:94:ILE:HD11	1:D:121:ILE:HG13	1.76	0.66
1:D:244:ASN:O	1:D:269:PRO:HD2	1.95	0.66
1:F:53:LYS:HG2	1:F:58:LEU:HD23	1.78	0.66
1:A:224:ILE:HG21	1:A:231:PHE:CD2	2.31	0.66
1:F:35:LEU:HD21	1:F:115:PHE:CD1	2.31	0.66
1:A:202:GLU:O	1:A:223:GLN:HA	1.95	0.66
1:D:329:LEU:HD11	1:D:335:ILE:HD12	1.78	0.66
1:E:198:LEU:HB2	1:E:219:ILE:HD12	1.78	0.66
1:F:79:SER:OG	1:F:82:SER:OG	2.08	0.66
1:A:200:THR:HG22	1:A:221:GLN:HA	1.77	0.66
1:E:203:ASP:HB3	1:E:204:PRO:HD2	1.76	0.66
1:A:176:LYS:HZ3	1:A:273:THR:HB	1.58	0.66
1:B:81:SER:O	1:B:84:VAL:CG1	2.38	0.66
1:C:317:LYS:HB2	1:C:375:ILE:O	1.95	0.66
1:E:205:ILE:HG21	1:E:223:GLN:OE1	1.96	0.66
1:F:21:PHE:HA	1:F:26:GLN:NE2	2.11	0.66
1:C:94:ILE:HG12	1:C:94:ILE:O	1.95	0.65
1:E:85:LEU:HA	1:E:88:LEU:HB2	1.77	0.65
1:F:283:MET:HG3	1:F:352:VAL:HG21	1.78	0.65
1:F:84:VAL:HG23	1:F:87:GLU:HB3	1.78	0.65
1:B:223:GLN:HG2	1:B:226:GLU:OE1	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ILE:HG13	1:B:270:VAL:CG1	2.24	0.65
1:F:22:GLU:H	1:F:26:GLN:NE2	1.93	0.65
1:A:151:LEU:HD11	1:A:326:ARG:HD3	1.78	0.65
1:B:17:TYR:CE1	1:B:62:SER:CB	2.79	0.65
1:B:287:ILE:HD12	1:B:288:SER:N	2.12	0.65
1:F:82:SER:O	1:F:85:LEU:HB3	1.96	0.65
1:D:94:ILE:HD11	1:D:121:ILE:CG1	2.27	0.65
1:D:9:LEU:N	1:D:9:LEU:HD12	2.10	0.65
1:E:224:ILE:HG21	1:E:231:PHE:CE1	2.32	0.65
1:E:79:SER:OG	1:E:82:SER:HB2	1.97	0.65
1:A:198:LEU:HB2	1:A:219:ILE:CD1	2.24	0.65
1:A:226:GLU:O	1:F:91:LYS:NZ	2.30	0.65
1:B:12:LYS:HZ3	1:B:17:TYR:CB	2.08	0.65
1:E:90:SER:O	1:E:91:LYS:HB2	1.95	0.65
1:C:197:HIS:O	1:C:244:ASN:N	2.27	0.65
1:F:90:SER:O	1:F:91:LYS:HD3	1.96	0.65
1:E:348:VAL:HG13	1:E:349:ALA:H	1.60	0.65
1:F:19:SER:CA	1:F:64:ARG:HH22	2.08	0.65
1:F:74:ILE:HD13	1:F:77:TRP:CE3	2.32	0.65
1:D:94:ILE:CD1	1:D:94:ILE:O	2.45	0.65
1:F:114:ARG:HB2	1:F:141:LEU:HD11	1.78	0.65
1:F:19:SER:HA	1:F:64:ARG:CZ	2.27	0.65
1:A:167:MET:HE3	1:A:286:LEU:HD11	1.79	0.65
1:B:100:VAL:O	1:B:115:PHE:HD2	1.79	0.65
1:B:35:LEU:CD2	1:B:115:PHE:CD1	2.79	0.65
1:A:289:ARG:HA	1:B:297:ALA:HB2	1.78	0.65
1:C:203:ASP:CB	1:C:204:PRO:HD2	2.08	0.64
1:D:203:ASP:C	1:D:224:ILE:HG22	2.18	0.64
1:D:8:ILE:N	1:D:8:ILE:HD12	2.12	0.64
1:D:230:SER:HB2	1:D:233:ILE:CG1	2.24	0.64
1:E:75:ALA:HB1	1:E:121:ILE:HD13	1.78	0.64
1:A:12:LYS:HA	1:A:33:GLU:OE1	1.97	0.64
1:A:376:ILE:HB	1:A:380:VAL:CG2	2.27	0.64
1:C:119:VAL:HG22	1:C:136:MET:HG2	1.79	0.64
1:C:322:LEU:HD23	1:C:322:LEU:H	1.60	0.64
1:C:365:LEU:C	1:C:365:LEU:HD23	2.18	0.64
1:A:169:ALA:N	1:A:310:MET:O	2.24	0.64
1:A:353:ARG:O	1:A:356:VAL:HG22	1.97	0.64
1:B:332:THR:HG22	1:B:334:ASP:H	1.61	0.64
1:C:9:LEU:HA	1:C:60:THR:O	1.98	0.64
1:E:342:LEU:HD11	1:E:351:GLU:HG2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:124:VAL:CG2	1:F:133:GLU:HB2	2.27	0.64
1:A:42:ILE:HG23	1:A:136:MET:HB2	1.79	0.64
1:C:383:ARG:HD3	1:D:300:TYR:CD1	2.33	0.64
1:E:75:ALA:CB	1:E:85:LEU:HD22	2.28	0.64
1:F:118:ARG:HH21	1:F:206:GLU:CD	2.00	0.64
1:F:317:LYS:CD	1:F:323:VAL:HG13	2.28	0.64
1:C:46:GLN:OE1	1:C:131:THR:HG21	1.97	0.64
1:E:75:ALA:CB	1:E:85:LEU:HD23	2.28	0.64
1:B:376:ILE:HB	1:B:380:VAL:HG23	1.79	0.64
1:D:13:THR:N	1:D:33:GLU:OE1	2.31	0.64
1:F:169:ALA:N	1:F:310:MET:O	2.24	0.64
1:B:365:LEU:O	1:B:365:LEU:HD12	1.98	0.64
1:D:10:GLU:N	1:D:10:GLU:OE1	2.30	0.64
1:D:277:GLN:HE22	1:D:387:MET:CE	2.10	0.64
1:C:373:ASP:HB2	1:C:375:ILE:HD12	1.80	0.63
1:D:46:GLN:HE22	1:D:131:THR:HG21	1.53	0.63
1:E:203:ASP:O	1:E:223:GLN:HG3	1.97	0.63
1:E:35:LEU:CD2	1:E:115:PHE:CD1	2.81	0.63
1:A:31:VAL:CG2	1:A:100:VAL:HG11	2.27	0.63
1:B:99:GLU:HA	1:B:115:PHE:O	1.99	0.63
1:C:48:VAL:HA	1:C:65:THR:HG22	1.79	0.63
1:D:314:LEU:HD13	1:D:322:LEU:HD13	1.79	0.63
1:B:88:LEU:HD12	1:B:123:PRO:HD3	1.81	0.63
1:C:149:ILE:HD11	1:C:151:LEU:HD12	1.81	0.63
1:C:212:ILE:HD12	1:C:212:ILE:N	2.12	0.63
1:B:55:LYS:HD3	1:B:321:ASN:HA	1.79	0.63
1:C:203:ASP:HA	1:C:224:ILE:HG22	1.80	0.63
1:E:232:ALA:HB1	1:E:255:GLN:HE22	1.62	0.63
1:E:277:GLN:NE2	1:E:387:MET:HE1	2.04	0.63
1:A:205:ILE:N	1:A:223:GLN:OE1	2.19	0.63
1:B:245:LEU:HD22	1:B:246:ILE:N	2.12	0.63
1:E:169:ALA:N	1:E:310:MET:O	2.27	0.63
1:A:248:ILE:O	1:A:248:ILE:HG22	1.97	0.63
1:A:81:SER:OG	1:A:83:SER:OG	2.15	0.63
1:B:146:LEU:HB3	1:B:151:LEU:O	1.99	0.63
1:C:192:THR:HG23	1:C:194:ILE:O	1.98	0.63
1:C:295:ARG:O	1:C:299:ILE:HG13	1.98	0.63
1:D:176:LYS:HZ1	1:D:275:HIS:CE1	2.15	0.63
1:D:203:ASP:CA	1:D:224:ILE:HB	2.22	0.63
1:E:246:ILE:HG22	1:E:248:ILE:HG23	1.81	0.63
1:F:19:SER:CA	1:F:64:ARG:HH12	2.04	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:288:SER:OG	1:D:289:ARG:NH1	2.32	0.62
1:E:289:ARG:HH22	1:F:301:ASP:CG	2.02	0.62
1:F:19:SER:HA	1:F:64:ARG:HH22	1.63	0.62
1:A:238:ALA:HB1	1:A:246:ILE:HD13	1.80	0.62
1:B:155:LEU:HD13	1:B:159:MET:CE	2.28	0.62
1:C:108:THR:CG2	1:C:112:LYS:O	2.47	0.62
1:C:46:GLN:NE2	1:C:131:THR:HG23	2.14	0.62
1:F:21:PHE:HA	1:F:26:GLN:HE21	1.64	0.62
1:A:349:ALA:O	1:A:352:VAL:HG12	1.99	0.62
1:B:102:HIS:CD2	1:B:105:LYS:CB	2.81	0.62
1:B:45:LYS:HB2	1:B:133:GLU:CG	2.29	0.62
1:B:33:GLU:OE2	1:B:37:HIS:CE1	2.52	0.62
1:E:277:GLN:NE2	1:E:387:MET:HE3	2.10	0.62
1:A:329:LEU:HD12	1:A:356:VAL:HG12	1.81	0.62
1:C:111:GLN:O	1:C:111:GLN:HG2	1.99	0.62
1:D:285:ARG:O	1:D:288:SER:OG	2.13	0.62
1:E:179:THR:HG22	1:E:326:ARG:NH2	2.15	0.62
1:C:317:LYS:HG2	1:C:321:ASN:O	2.00	0.62
1:E:348:VAL:HG13	1:E:349:ALA:N	2.14	0.62
1:A:344:ASP:OD1	1:A:345:MET:CE	2.48	0.62
1:A:6:LEU:HD22	1:A:6:LEU:C	2.20	0.62
1:D:94:ILE:HD12	1:D:94:ILE:C	2.19	0.62
1:A:300:TYR:CE1	1:F:383:ARG:HB2	2.34	0.62
1:A:344:ASP:OD1	1:A:344:ASP:O	2.17	0.62
1:C:19:SER:C	1:C:64:ARG:NH1	2.52	0.62
1:C:365:LEU:O	1:C:365:LEU:HD23	1.99	0.62
1:D:171:LYS:HA	1:D:171:LYS:HE2	1.82	0.62
1:F:35:LEU:CD1	1:F:117:TYR:OH	2.48	0.62
1:C:48:VAL:O	1:C:66:LEU:HD13	1.98	0.62
1:E:241:ARG:HH21	1:E:241:ARG:HG3	1.64	0.62
1:F:7:PRO:O	1:F:8:ILE:CG1	2.48	0.62
1:A:246:ILE:HG13	1:A:268:HIS:CD2	2.34	0.62
1:C:97:ARG:CB	1:C:97:ARG:NH1	2.53	0.62
1:D:168:VAL:HG13	1:D:180:PHE:CZ	2.33	0.62
1:D:75:ALA:HB2	1:D:134:ILE:HD11	1.82	0.62
1:E:338:GLN:O	1:E:342:LEU:HD12	2.00	0.62
1:A:200:THR:HG21	1:A:202:GLU:OE2	1.99	0.62
1:B:245:LEU:CD2	1:B:269:PRO:HB2	2.15	0.62
1:B:43:ILE:N	1:B:43:ILE:HD12	2.13	0.62
1:A:194:ILE:HG12	1:A:269:PRO:HG2	1.82	0.61
1:C:322:LEU:CD2	1:C:322:LEU:H	2.12	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:GLN:CD	1:C:68:PHE:CD2	2.73	0.61
1:A:338:GLN:OE1	1:A:338:GLN:HA	2.00	0.61
1:C:46:GLN:CD	1:C:131:THR:CG2	2.69	0.61
1:C:50:ILE:HG12	1:C:66:LEU:HD21	1.82	0.61
1:C:67:ASN:OD1	1:C:69:ASN:HB2	1.99	0.61
1:D:246:ILE:HD11	1:D:268:HIS:NE2	2.15	0.61
1:F:251:LEU:HG	1:F:272:ALA:HB1	1.82	0.61
1:F:50:ILE:H	1:F:66:LEU:HD11	1.65	0.61
1:C:319:ASP:OD1	1:C:319:ASP:N	2.34	0.61
1:F:19:SER:HA	1:F:64:ARG:NH2	2.15	0.61
1:B:222:SER:HA	1:B:227:GLN:NE2	2.13	0.61
1:B:12:LYS:HA	1:B:33:GLU:OE2	2.01	0.61
1:B:45:LYS:HB2	1:B:133:GLU:HG3	1.81	0.61
1:D:37:HIS:O	1:D:38:GLU:C	2.38	0.61
1:C:125:TYR:OH	1:D:97:ARG:CZ	2.48	0.61
1:F:335:ILE:HG23	1:F:355:LEU:HD23	1.81	0.61
1:F:241:ARG:O	1:F:242:THR:HG22	2.01	0.61
1:A:245:LEU:HD13	1:A:269:PRO:HB2	1.83	0.61
1:C:79:SER:OG	1:C:84:VAL:HG11	2.01	0.61
1:D:76:LEU:CD1	1:D:82:SER:HA	2.30	0.61
1:D:84:VAL:HA	1:D:87:GLU:CG	2.31	0.61
1:F:20:THR:HG22	1:F:20:THR:O	2.01	0.61
1:A:167:MET:HE1	1:A:286:LEU:CD1	2.31	0.61
1:B:171:LYS:HE3	1:B:276:SER:C	2.21	0.61
1:D:176:LYS:HZ2	1:D:275:HIS:CE1	2.18	0.61
1:D:8:ILE:O	1:D:60:THR:N	2.23	0.61
1:E:75:ALA:HB1	1:E:121:ILE:CD1	2.31	0.61
1:E:233:ILE:N	1:E:233:ILE:CD1	2.63	0.61
1:A:106:LEU:CD1	1:A:113:GLN:HG2	2.26	0.60
1:B:35:LEU:C	1:B:38:GLU:H	2.04	0.60
1:F:342:LEU:HD21	1:F:351:GLU:HG2	1.81	0.60
1:C:114:ARG:NH1	1:C:210:ASP:OD2	2.34	0.60
1:F:84:VAL:HG13	1:F:88:LEU:CD1	2.31	0.60
1:B:317:LYS:HD3	1:B:323:VAL:HB	1.83	0.60
1:C:373:ASP:HB2	1:C:375:ILE:CD1	2.31	0.60
1:D:251:LEU:HB3	1:D:257:ILE:HG22	1.83	0.60
1:E:202:GLU:HB2	1:E:205:ILE:HA	1.83	0.60
1:B:278:ASN:O	1:B:282:VAL:HG23	2.02	0.60
1:B:179:THR:HG21	1:B:310:MET:CE	2.32	0.60
1:B:125:TYR:HB2	1:C:227:GLN:HE22	1.65	0.60
1:C:251:LEU:HG	1:C:272:ALA:HB1	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:264:ALA:O	1:D:266:THR:O	2.19	0.60
1:B:123:PRO:HB2	1:C:227:GLN:HB3	1.82	0.60
1:D:194:ILE:HD12	1:D:269:PRO:HG3	1.83	0.60
1:F:85:LEU:O	1:F:89:ALA:N	2.34	0.60
1:A:146:LEU:HD13	1:A:156:VAL:HG11	1.84	0.60
1:A:192:THR:HG23	1:A:194:ILE:O	2.01	0.60
1:A:64:ARG:HH11	1:A:70:GLU:CD	2.05	0.60
1:D:131:THR:OG1	1:D:132:ALA:N	2.34	0.60
1:F:44:ILE:HG12	1:F:50:ILE:HD13	1.83	0.60
1:B:58:LEU:HD23	1:C:196:GLY:HA2	1.83	0.60
1:F:329:LEU:HB2	1:F:356:VAL:HG22	1.83	0.60
1:B:224:ILE:HG21	1:B:231:PHE:CD2	2.36	0.60
1:B:45:LYS:HG2	1:B:46:GLN:N	2.16	0.60
1:E:205:ILE:O	1:E:205:ILE:HG23	2.02	0.60
1:B:21:PHE:O	1:B:73:ARG:CD	2.50	0.60
1:B:54:VAL:HG22	1:B:59:CYS:SG	2.41	0.60
1:E:44:ILE:HG23	1:E:50:ILE:HG12	1.84	0.60
1:E:24:GLU:OE1	1:E:77:TRP:HB3	2.01	0.60
1:A:81:SER:HG	1:A:83:SER:HG	1.50	0.60
1:B:66:LEU:HD22	1:B:66:LEU:H	1.67	0.60
1:F:75:ALA:O	1:F:82:SER:CB	2.50	0.60
1:A:245:LEU:CD1	1:A:269:PRO:HB2	2.32	0.59
1:B:15:TYR:HH	1:B:30:THR:HG22	1.66	0.59
1:B:66:LEU:HD22	1:B:66:LEU:N	2.17	0.59
1:B:91:LYS:HA	1:B:91:LYS:NZ	2.17	0.59
1:C:46:GLN:NE2	1:C:68:PHE:HA	2.10	0.59
1:D:197:HIS:H	1:D:244:ASN:HD22	1.48	0.59
1:D:277:GLN:HE22	1:D:387:MET:HE1	1.66	0.59
1:E:176:LYS:CE	1:E:273:THR:CG2	2.79	0.59
1:F:84:VAL:HG22	1:F:84:VAL:O	2.02	0.59
1:B:64:ARG:NH1	1:B:64:ARG:HB3	2.17	0.59
1:C:93:LEU:HD21	1:D:233:ILE:CG2	2.32	0.59
1:D:283:MET:HE1	1:D:302:LEU:HG	1.83	0.59
1:E:8:ILE:HD12	1:E:9:LEU:H	1.65	0.59
1:F:225:PRO:HB2	1:F:226:GLU:CD	2.22	0.59
1:A:209:TYR:HB2	1:A:219:ILE:HG21	1.84	0.59
1:D:118:ARG:NE	1:D:139:ILE:CD1	2.55	0.59
1:D:257:ILE:HD11	1:D:290:PHE:HZ	1.65	0.59
1:D:49:ALA:HB2	1:D:64:ARG:O	2.02	0.59
1:E:250:GLU:OE2	1:E:275:HIS:ND1	2.33	0.59
1:B:246:ILE:CG2	1:B:248:ILE:HD13	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:377:ASP:O	1:B:380:VAL:HG22	2.01	0.59
1:C:382:LYS:O	1:C:386:MET:HG3	2.02	0.59
1:C:387:MET:HA	1:C:387:MET:HE2	1.84	0.59
1:E:179:THR:HG22	1:E:326:ARG:HH21	1.66	0.59
1:A:151:LEU:CD2	1:A:326:ARG:NH1	2.65	0.59
1:B:155:LEU:HD13	1:B:159:MET:HE2	1.84	0.59
1:C:46:GLN:NE2	1:C:71:ILE:CD1	2.66	0.59
1:E:246:ILE:HG22	1:E:248:ILE:CG2	2.32	0.59
1:A:42:ILE:CG2	1:A:136:MET:HB2	2.32	0.59
1:D:386:MET:HE2	1:D:386:MET:HA	1.84	0.59
1:E:52:ALA:O	1:E:58:LEU:HA	2.02	0.59
1:F:13:THR:O	1:F:14:GLU:CB	2.51	0.59
1:B:167:MET:HE3	1:B:309:ILE:HG12	1.85	0.59
1:D:76:LEU:HD11	1:D:82:SER:CA	2.31	0.59
1:E:10:GLU:HB2	1:E:61:LEU:HD23	1.84	0.59
1:C:274:VAL:CG1	1:C:282:VAL:HG23	2.33	0.59
1:C:67:ASN:CG	1:C:70:GLU:HG2	2.22	0.59
1:E:303:VAL:O	1:E:336:ARG:HD2	2.03	0.59
1:A:228:PHE:O	1:A:229:SER:HB3	2.02	0.59
1:B:259:SER:O	1:B:262:GLU:HG2	2.03	0.59
1:B:370:LEU:HB3	1:B:375:ILE:CG2	2.33	0.59
1:D:194:ILE:HD11	1:D:245:LEU:HB2	1.83	0.59
1:D:46:GLN:CG	1:D:71:ILE:CD1	2.61	0.59
1:E:79:SER:OG	1:E:82:SER:CB	2.51	0.59
1:A:123:PRO:HB2	1:B:227:GLN:HB3	1.85	0.59
1:C:367:ALA:HB2	1:C:384:LEU:HB3	1.84	0.59
1:E:225:PRO:HB2	1:E:226:GLU:OE2	2.03	0.59
1:E:93:LEU:HD13	1:E:93:LEU:N	2.18	0.59
1:C:108:THR:HB	1:C:112:LYS:O	2.03	0.58
1:D:326:ARG:HG3	1:D:326:ARG:NH1	2.11	0.58
1:D:125:TYR:HB2	1:E:227:GLN:HE22	1.68	0.58
1:F:102:HIS:ND1	1:F:103:PRO:HD2	2.17	0.58
1:A:242:THR:HG22	1:F:135:VAL:HG11	1.85	0.58
1:B:10:GLU:HB2	1:B:61:LEU:HD23	1.85	0.58
1:E:200:THR:CG2	1:E:219:ILE:HD11	2.34	0.58
1:F:167:MET:HA	1:F:272:ALA:O	2.02	0.58
1:A:329:LEU:HD23	1:A:330:ASN:N	2.18	0.58
1:A:35:LEU:HD21	1:A:115:PHE:CE2	2.38	0.58
1:C:46:GLN:NE2	1:C:131:THR:CG2	2.67	0.58
1:E:327:GLU:CG	1:E:362:PRO:HA	2.33	0.58
1:E:331:PHE:HA	1:E:335:ILE:CG2	2.27	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:ASP:O	1:B:223:GLN:HG3	2.02	0.58
1:B:224:ILE:HG12	1:B:231:PHE:CE1	2.38	0.58
1:D:146:LEU:CD1	1:D:156:VAL:HG21	2.33	0.58
1:E:118:ARG:CG	1:E:139:ILE:HD11	2.32	0.58
1:A:248:ILE:N	1:A:248:ILE:HD12	2.19	0.58
1:B:325:ALA:HB1	1:B:384:LEU:HD11	1.85	0.58
1:B:384:LEU:C	1:B:384:LEU:HD23	2.24	0.58
1:C:142:ASP:N	1:C:142:ASP:OD1	2.35	0.58
1:D:94:ILE:CD1	1:D:121:ILE:HB	2.34	0.58
1:E:168:VAL:HG13	1:E:180:PHE:CZ	2.39	0.58
1:F:84:VAL:HG23	1:F:87:GLU:OE1	2.04	0.58
1:F:97:ARG:NH2	1:F:206:GLU:O	2.35	0.58
1:C:114:ARG:CG	1:C:141:LEU:CD1	2.78	0.58
1:C:188:MET:HA	1:C:216:HIS:HE1	1.68	0.58
1:C:353:ARG:O	1:C:356:VAL:HG12	2.03	0.58
1:C:94:ILE:HG23	1:C:121:ILE:O	2.04	0.58
1:A:151:LEU:HD22	1:A:151:LEU:N	2.19	0.58
1:C:66:LEU:HD12	1:C:66:LEU:N	2.19	0.58
1:C:97:ARG:C	1:C:97:ARG:HD3	2.24	0.58
1:C:209:TYR:CE1	1:C:221:GLN:NE2	2.72	0.58
1:F:35:LEU:HD13	1:F:117:TYR:OH	2.04	0.58
1:A:188:MET:HB3	1:A:214:SER:HB2	1.85	0.58
1:D:194:ILE:HD12	1:D:269:PRO:CG	2.34	0.58
1:D:373:ASP:HB2	1:D:375:ILE:CD1	2.33	0.58
1:D:84:VAL:O	1:D:87:GLU:CG	2.52	0.58
1:E:137:ARG:NH1	1:F:240:ARG:HB3	2.19	0.58
1:A:168:VAL:HA	1:A:310:MET:O	2.04	0.57
1:F:373:ASP:HB2	1:F:375:ILE:HD12	1.84	0.57
1:F:84:VAL:O	1:F:88:LEU:HG	2.04	0.57
1:A:44:ILE:N	1:A:44:ILE:HD12	2.19	0.57
1:B:169:ALA:N	1:B:310:MET:O	2.29	0.57
1:C:19:SER:CA	1:C:64:ARG:NH1	2.59	0.57
1:B:248:ILE:HG12	1:B:270:VAL:HG13	1.85	0.57
1:D:278:ASN:O	1:D:282:VAL:HG23	2.04	0.57
1:F:96:THR:OG1	1:F:97:ARG:N	2.36	0.57
1:A:178:THR:HG22	1:A:207:PHE:CZ	2.40	0.57
1:D:257:ILE:CD1	1:D:290:PHE:CZ	2.81	0.57
1:E:68:PHE:O	1:E:68:PHE:HD1	1.86	0.57
1:A:106:LEU:HB3	1:A:113:GLN:HB3	1.87	0.57
1:B:102:HIS:HB2	1:B:115:PHE:CZ	2.39	0.57
1:C:118:ARG:NH1	1:C:206:GLU:OE1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:203:ASP:C	1:D:224:ILE:CG2	2.72	0.57
1:E:329:LEU:HD12	1:E:356:VAL:HG23	1.86	0.57
1:C:168:VAL:CG2	1:C:176:LYS:HB3	2.34	0.57
1:C:27:PHE:O	1:C:30:THR:OG1	2.16	0.57
1:B:325:ALA:CB	1:B:384:LEU:HD11	2.35	0.57
1:B:79:SER:HB2	1:B:96:THR:OG1	2.04	0.57
1:C:279:CYS:O	1:C:282:VAL:CG1	2.37	0.57
1:C:174:SER:HA	1:C:314:LEU:HG	1.85	0.57
1:D:176:LYS:HD2	1:D:273:THR:HB	1.85	0.57
1:F:102:HIS:O	1:F:112:LYS:HD3	2.05	0.57
1:A:224:ILE:O	1:A:229:SER:N	2.36	0.57
1:B:137:ARG:CG	1:B:137:ARG:HH11	2.09	0.57
1:B:10:GLU:OE1	1:B:61:LEU:CD2	2.52	0.57
1:C:45:LYS:HG2	1:C:46:GLN:H	1.70	0.57
1:D:22:GLU:HB2	1:D:26:GLN:HE22	1.70	0.57
1:F:84:VAL:HG13	1:F:88:LEU:HD11	1.85	0.57
1:B:46:GLN:NE2	1:B:68:PHE:CE1	2.73	0.57
1:D:376:ILE:HB	1:D:380:VAL:CG2	2.35	0.57
1:E:241:ARG:NH2	1:E:241:ARG:HG3	2.18	0.57
1:F:295:ARG:O	1:F:299:ILE:HG13	2.05	0.57
1:B:151:LEU:N	1:B:151:LEU:HD22	2.20	0.57
1:C:21:PHE:CZ	1:C:50:ILE:CD1	2.88	0.57
1:F:317:LYS:HD3	1:F:323:VAL:HG11	1.85	0.57
1:F:75:ALA:HB1	1:F:85:LEU:HD21	1.75	0.57
1:B:44:ILE:HG12	1:B:50:ILE:HG12	1.87	0.56
1:B:66:LEU:H	1:B:66:LEU:CD2	2.17	0.56
1:C:102:HIS:O	1:C:112:LYS:NZ	2.37	0.56
1:C:209:TYR:HA	1:C:212:ILE:HD13	1.86	0.56
1:E:141:LEU:HD23	1:E:141:LEU:O	2.04	0.56
1:E:123:PRO:HB2	1:F:227:GLN:HB3	1.85	0.56
1:E:137:ARG:NH1	1:F:240:ARG:O	2.36	0.56
1:A:178:THR:HG22	1:A:207:PHE:HZ	1.70	0.56
1:B:18:PRO:HG3	1:B:26:GLN:HE21	1.70	0.56
1:B:46:GLN:NE2	1:B:68:PHE:HE1	2.03	0.56
1:C:85:LEU:O	1:C:85:LEU:HD12	2.04	0.56
1:D:167:MET:HA	1:D:272:ALA:O	2.05	0.56
1:D:46:GLN:HG2	1:D:71:ILE:HD13	1.81	0.56
1:E:6:LEU:O	1:E:6:LEU:CD1	2.52	0.56
1:F:84:VAL:O	1:F:88:LEU:N	2.23	0.56
1:A:146:LEU:HB3	1:A:151:LEU:O	2.05	0.56
1:D:126:ILE:HD12	1:D:127:GLN:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:LEU:CD1	1:E:58:LEU:C	2.71	0.56
1:F:35:LEU:HD21	1:F:115:PHE:CD2	2.40	0.56
1:A:335:ILE:HD13	1:A:355:LEU:HD22	1.86	0.56
1:E:198:LEU:HD22	1:E:245:LEU:HB3	1.88	0.56
1:E:93:LEU:CD1	1:E:93:LEU:N	2.69	0.56
1:F:6:LEU:CD2	1:F:63:THR:CG2	2.78	0.56
1:A:39:ALA:HB2	1:A:54:VAL:HG22	1.87	0.56
1:C:209:TYR:HE1	1:C:221:GLN:NE2	2.04	0.56
1:E:10:GLU:HA	1:E:10:GLU:OE1	2.05	0.56
1:E:82:SER:OG	1:E:88:LEU:HD13	2.05	0.56
1:F:185:ARG:HG3	1:F:212:ILE:HD12	1.86	0.56
1:A:262:GLU:O	1:A:266:THR:HG23	2.04	0.56
1:B:35:LEU:HD21	1:B:115:PHE:CG	2.40	0.56
1:B:176:LYS:NZ	1:B:275:HIS:ND1	2.52	0.56
1:C:34:PHE:CZ	1:C:61:LEU:HD23	2.39	0.56
1:E:149:ILE:HG22	1:E:149:ILE:O	2.06	0.56
1:F:376:ILE:HD11	1:F:381:ALA:HB2	1.88	0.56
1:F:41:ASP:O	1:F:52:ALA:HB1	2.05	0.56
1:A:11:PHE:O	1:A:37:HIS:NE2	2.36	0.56
1:B:259:SER:HA	1:B:262:GLU:HG2	1.87	0.56
1:E:74:ILE:HD13	1:E:77:TRP:CZ3	2.41	0.56
1:B:67:ASN:ND2	1:B:70:GLU:HG3	2.20	0.56
1:C:32:LEU:HD13	1:C:103:PRO:CG	2.36	0.56
1:C:50:ILE:H	1:C:66:LEU:HD11	1.71	0.56
1:E:233:ILE:H	1:E:233:ILE:HD13	1.70	0.56
1:F:20:THR:CG2	1:F:20:THR:O	2.54	0.56
1:B:96:THR:CG2	1:B:119:VAL:CG2	2.84	0.56
1:B:46:GLN:HB3	1:B:126:ILE:HD12	1.87	0.56
1:B:176:LYS:HZ2	1:B:275:HIS:CE1	2.23	0.56
1:D:194:ILE:HD11	1:D:245:LEU:HD22	1.88	0.56
1:F:291:ASP:OD1	1:F:292:GLU:N	2.38	0.56
1:F:74:ILE:CD1	1:F:77:TRP:HZ3	2.19	0.56
1:A:102:HIS:ND1	1:A:103:PRO:HD2	2.21	0.56
1:E:179:THR:HG21	1:E:312:GLN:CD	2.24	0.56
1:E:17:TYR:HE2	1:E:64:ARG:HH11	1.53	0.56
1:A:43:ILE:HG23	1:A:133:GLU:OE2	2.03	0.56
1:C:246:ILE:HD12	1:C:263:ALA:HB1	1.88	0.56
1:A:242:THR:OG1	1:F:53:LYS:NZ	2.34	0.55
1:A:73:ARG:O	1:A:76:LEU:HB3	2.06	0.55
1:D:203:ASP:HA	1:D:224:ILE:CG2	2.35	0.55
1:E:141:LEU:HD23	1:E:141:LEU:C	2.27	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:LEU:CD2	1:A:7:PRO:O	2.54	0.55
1:A:6:LEU:H	1:A:6:LEU:HD13	1.71	0.55
1:B:146:LEU:N	1:B:146:LEU:CD1	2.69	0.55
1:C:46:GLN:HE22	1:C:131:THR:HG23	1.71	0.55
1:D:319:ASP:C	1:D:319:ASP:OD1	2.45	0.55
1:A:377:ASP:OD1	1:A:377:ASP:N	2.38	0.55
1:E:379:HIS:O	1:E:382:LYS:CG	2.47	0.55
1:A:279:CYS:HA	1:A:282:VAL:CG1	2.37	0.55
1:B:291:ASP:OD1	1:B:292:GLU:N	2.40	0.55
1:B:46:GLN:OE1	1:B:47:GLY:N	2.39	0.55
1:C:33:GLU:OE1	1:C:37:HIS:NE2	2.39	0.55
1:C:97:ARG:NH1	1:C:97:ARG:CG	2.64	0.55
1:D:46:GLN:HE22	1:D:131:THR:CG2	2.10	0.55
1:E:12:LYS:NZ	1:E:61:LEU:O	2.39	0.55
1:C:71:ILE:CD1	1:C:131:THR:CG2	2.84	0.55
1:D:276:SER:OG	1:D:282:VAL:HG22	2.07	0.55
1:D:302:LEU:O	1:D:306:THR:OG1	2.15	0.55
1:F:15:TYR:HE1	1:F:61:LEU:HD13	1.72	0.55
1:B:224:ILE:HG21	1:B:231:PHE:CE2	2.41	0.55
1:C:97:ARG:NH1	1:C:205:ILE:O	2.40	0.55
1:C:7:PRO:HA	1:D:215:ALA:O	2.07	0.55
1:D:195:LYS:HB2	1:D:216:HIS:CD2	2.41	0.55
1:E:140:PRO:HB2	1:E:207:PHE:CE2	2.40	0.55
1:F:205:ILE:H	1:F:223:GLN:NE2	2.04	0.55
1:F:84:VAL:HG22	1:F:87:GLU:HB3	1.88	0.55
1:C:177:SER:O	1:C:181:SER:OG	2.23	0.55
1:C:353:ARG:O	1:C:356:VAL:CG1	2.54	0.55
1:D:345:MET:O	1:D:348:VAL:HG23	2.06	0.55
1:D:55:LYS:HG3	1:D:57:THR:HG23	1.89	0.55
1:C:156:VAL:O	1:C:159:MET:HG2	2.07	0.55
1:C:168:VAL:HA	1:C:310:MET:O	2.07	0.55
1:D:208:VAL:HG13	1:D:210:ASP:OD1	2.07	0.55
1:E:278:ASN:O	1:E:282:VAL:HG23	2.07	0.55
1:E:41:ASP:O	1:E:52:ALA:HA	2.06	0.55
1:F:197:HIS:HB3	1:F:243:PRO:HA	1.88	0.55
1:F:76:LEU:O	1:F:76:LEU:HD22	2.06	0.55
1:B:224:ILE:HG22	1:B:225:PRO:HD3	1.89	0.55
1:B:251:LEU:HD11	1:B:260:ALA:HB2	1.89	0.55
1:B:55:LYS:HD3	1:B:321:ASN:CA	2.37	0.55
1:C:100:VAL:HG13	1:C:100:VAL:O	2.07	0.55
1:D:289:ARG:HD3	1:E:297:ALA:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:223:GLN:HG2	1:F:226:GLU:OE1	2.06	0.55
1:A:251:LEU:HG	1:A:272:ALA:HB1	1.87	0.55
1:D:154:GLU:O	1:D:157:ASN:HB2	2.07	0.55
1:E:35:LEU:HD11	1:E:117:TYR:HH	1.69	0.55
1:E:64:ARG:O	1:E:64:ARG:HG3	2.06	0.55
1:A:42:ILE:HD13	1:A:136:MET:HE2	1.89	0.54
1:B:319:ASP:OD2	1:B:321:ASN:ND2	2.40	0.54
1:B:27:PHE:HE1	1:B:44:ILE:HD11	1.72	0.54
1:C:99:GLU:OE1	1:C:114:ARG:NE	2.36	0.54
1:C:205:ILE:HD12	1:C:223:GLN:HB2	1.88	0.54
1:D:329:LEU:HB2	1:D:356:VAL:HG22	1.88	0.54
1:D:46:GLN:HB3	1:D:71:ILE:HG21	1.89	0.54
1:D:46:GLN:CB	1:D:71:ILE:HG21	2.37	0.54
1:E:224:ILE:HD11	1:E:225:PRO:HD3	1.75	0.54
1:C:159:MET:O	1:C:166:VAL:HG21	2.06	0.54
1:C:209:TYR:HE1	1:C:221:GLN:HE21	1.55	0.54
1:C:32:LEU:HD13	1:C:103:PRO:HG3	1.89	0.54
1:E:306:THR:HG21	1:E:331:PHE:CE2	2.42	0.54
1:E:329:LEU:HB2	1:E:356:VAL:HG22	1.88	0.54
1:F:111:GLN:H	1:F:111:GLN:CD	2.10	0.54
1:D:352:VAL:O	1:D:356:VAL:HG23	2.07	0.54
1:D:42:ILE:HG23	1:D:136:MET:HG3	1.88	0.54
1:E:316:ARG:CG	1:E:316:ARG:HH11	2.20	0.54
1:A:35:LEU:HD11	1:A:115:PHE:CE2	2.39	0.54
1:B:12:LYS:HE2	1:B:15:TYR:CE2	2.42	0.54
1:D:12:LYS:N	1:D:12:LYS:CD	2.71	0.54
1:D:27:PHE:CE2	1:D:74:ILE:HG23	2.42	0.54
1:D:8:ILE:H	1:D:8:ILE:CD1	2.17	0.54
1:E:224:ILE:HD12	1:E:225:PRO:N	2.23	0.54
1:A:197:HIS:CE1	1:F:133:GLU:OE2	2.60	0.54
1:F:68:PHE:O	1:F:71:ILE:HG13	2.07	0.54
1:A:224:ILE:HG12	1:A:231:PHE:CD1	2.42	0.54
1:B:67:ASN:HD21	1:B:70:GLU:HG3	1.73	0.54
1:E:306:THR:CG2	1:E:331:PHE:CD2	2.91	0.54
1:F:383:ARG:O	1:F:383:ARG:HD2	2.07	0.54
1:C:46:GLN:NE2	1:C:68:PHE:CA	2.66	0.54
1:D:257:ILE:HG13	1:D:258:GLU:N	2.21	0.54
1:E:328:TYR:CZ	1:E:361:HIS:HB2	2.43	0.54
1:A:105:LYS:O	1:A:105:LYS:HG3	2.07	0.54
1:C:159:MET:SD	1:C:183:ILE:HD13	2.48	0.54
1:D:7:PRO:HG2	1:D:60:THR:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:45:LYS:CE	1:F:126:ILE:HD11	2.37	0.54
1:A:297:ALA:CB	1:F:383:ARG:NH2	2.65	0.54
1:B:73:ARG:HD2	1:B:77:TRP:CH2	2.43	0.54
1:C:156:VAL:CA	1:C:159:MET:HG2	2.34	0.54
1:D:208:VAL:HG12	1:D:210:ASP:H	1.73	0.54
1:D:44:ILE:HG13	1:D:50:ILE:HD13	1.89	0.54
1:A:239:LEU:HD13	1:F:172:THR:HG22	1.90	0.54
1:B:127:GLN:NE2	1:C:210:ASP:HB3	2.23	0.54
1:B:20:THR:HG22	1:B:21:PHE:N	2.22	0.54
1:B:81:SER:HB2	1:B:83:SER:OG	2.08	0.54
1:E:363:PHE:CD2	1:E:387:MET:HB2	2.43	0.54
1:E:214:SER:OG	1:E:217:SER:HB2	2.09	0.54
1:F:20:THR:HA	1:F:70:GLU:OE2	2.08	0.54
1:A:199:LEU:HD12	1:A:243:PRO:HG3	1.90	0.53
1:C:179:THR:HG21	1:C:310:MET:HE3	1.89	0.53
1:D:76:LEU:CG	1:D:82:SER:HA	2.38	0.53
1:E:82:SER:OG	1:E:85:LEU:HB3	2.08	0.53
1:A:68:PHE:O	1:A:72:GLU:HG3	2.07	0.53
1:D:146:LEU:HD23	1:D:182:SER:HB3	1.89	0.53
1:E:176:LYS:HE2	1:E:273:THR:OG1	2.08	0.53
1:F:224:ILE:CG2	1:F:225:PRO:CD	2.79	0.53
1:B:192:THR:CG2	1:B:193:PRO:HD2	2.34	0.53
1:A:58:LEU:HD21	1:B:216:HIS:O	2.08	0.53
1:D:328:TYR:CZ	1:D:361:HIS:HB2	2.43	0.53
1:D:344:ASP:C	1:D:345:MET:HG3	2.28	0.53
1:F:114:ARG:CB	1:F:141:LEU:HD11	2.39	0.53
1:B:200:THR:HG23	1:B:219:ILE:HD11	1.89	0.53
1:B:363:PHE:CD1	1:B:384:LEU:HD21	2.43	0.53
1:C:235:ASN:ND2	1:C:248:ILE:HG22	2.24	0.53
1:F:45:LYS:HE2	1:F:126:ILE:CD1	2.39	0.53
1:A:41:ASP:OD2	1:A:137:ARG:HG2	2.08	0.53
1:C:100:VAL:CG1	1:C:100:VAL:O	2.56	0.53
1:D:319:ASP:O	1:D:319:ASP:OD1	2.27	0.53
1:B:176:LYS:HD2	1:B:273:THR:OG1	2.09	0.53
1:C:108:THR:CB	1:C:112:LYS:O	2.57	0.53
1:A:34:PHE:CE2	1:A:50:ILE:HG22	2.39	0.53
1:B:12:LYS:NZ	1:B:17:TYR:CB	2.71	0.53
1:B:46:GLN:N	1:B:71:ILE:CD1	2.72	0.53
1:E:15:TYR:C	1:E:15:TYR:CD1	2.82	0.53
1:B:316:ARG:HH11	1:B:316:ARG:CG	2.22	0.53
1:B:316:ARG:HG2	1:B:316:ARG:HH11	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:69:ASN:HB3	1:C:73:ARG:HH12	1.74	0.53
1:E:43:ILE:CG1	1:E:51:SER:HG	2.22	0.53
1:E:45:LYS:NZ	1:E:46:GLN:O	2.42	0.53
1:F:9:LEU:HD21	1:F:63:THR:CG2	2.37	0.53
1:A:151:LEU:HD22	1:A:326:ARG:NH1	2.24	0.53
1:A:146:LEU:HD11	1:A:156:VAL:HG21	1.91	0.53
1:B:102:HIS:CG	1:B:103:PRO:HD2	2.44	0.53
1:C:277:GLN:HG2	1:C:278:ASN:ND2	2.23	0.53
1:D:12:LYS:HA	1:D:33:GLU:OE2	2.09	0.53
1:D:194:ILE:HD12	1:D:245:LEU:HB2	1.90	0.53
1:E:43:ILE:HD11	1:F:218:ILE:HD13	1.91	0.53
1:F:7:PRO:O	1:F:8:ILE:CB	2.56	0.53
1:A:151:LEU:HD21	1:A:326:ARG:NH1	2.23	0.53
1:B:151:LEU:HD11	1:B:326:ARG:CD	2.38	0.53
1:D:187:ILE:HD13	1:D:194:ILE:HD13	1.91	0.53
1:D:124:VAL:O	1:E:227:GLN:OE1	2.26	0.53
1:E:35:LEU:CD2	1:E:115:PHE:CD2	2.91	0.52
1:F:174:SER:O	1:F:312:GLN:NE2	2.43	0.52
1:C:94:ILE:HD13	1:C:121:ILE:HB	1.89	0.52
1:D:194:ILE:HD11	1:D:245:LEU:CB	2.39	0.52
1:E:335:ILE:HD11	1:E:355:LEU:CD1	2.36	0.52
1:C:337:GLU:HA	1:C:340:LEU:HD12	1.90	0.52
1:D:119:VAL:HG22	1:D:136:MET:HE3	1.90	0.52
1:E:210:ASP:OD1	1:E:211:ASN:N	2.42	0.52
1:E:200:THR:HG23	1:E:219:ILE:HD11	1.90	0.52
1:A:200:THR:CG2	1:A:202:GLU:OE2	2.57	0.52
1:B:223:GLN:H	1:B:227:GLN:NE2	2.07	0.52
1:B:246:ILE:CG2	1:B:248:ILE:CD1	2.87	0.52
1:B:39:ALA:CB	1:B:52:ALA:HB1	2.34	0.52
1:C:46:GLN:HB2	1:C:126:ILE:HD12	1.90	0.52
1:E:327:GLU:HA	1:E:361:HIS:O	2.09	0.52
1:B:156:VAL:HG13	1:B:183:ILE:HG13	1.92	0.52
1:D:251:LEU:HG	1:D:272:ALA:HB1	1.91	0.52
1:D:373:ASP:N	1:D:373:ASP:OD1	2.43	0.52
1:E:285:ARG:HH11	1:E:285:ARG:HG3	1.75	0.52
1:F:319:ASP:OD1	1:F:320:GLY:N	2.42	0.52
1:A:354:ARG:NE	1:A:358:GLU:OE1	2.43	0.52
1:C:365:LEU:C	1:C:365:LEU:CD2	2.78	0.52
1:E:12:LYS:HA	1:E:33:GLU:OE1	2.09	0.52
1:A:224:ILE:HG12	1:A:231:PHE:CE1	2.45	0.52
1:A:284:ARG:HG2	1:A:349:ALA:CB	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:155:LEU:O	1:C:158:GLN:CB	2.58	0.52
1:D:205:ILE:HG22	1:D:205:ILE:O	2.09	0.52
1:D:76:LEU:HD21	1:D:82:SER:HA	1.91	0.52
1:E:176:LYS:HE3	1:E:273:THR:HG23	1.91	0.52
1:E:380:VAL:HA	1:E:383:ARG:HG3	1.91	0.52
1:F:71:ILE:HD12	1:F:71:ILE:C	2.30	0.52
1:A:291:ASP:OD1	1:A:292:GLU:N	2.43	0.52
1:C:224:ILE:HG12	1:C:231:PHE:CD1	2.44	0.52
1:E:289:ARG:NH2	1:F:301:ASP:OD2	2.39	0.52
1:B:201:HIS:HB3	1:B:224:ILE:HD11	1.92	0.52
1:B:79:SER:HB2	1:B:96:THR:HG21	1.90	0.52
1:C:168:VAL:HG23	1:C:168:VAL:O	2.10	0.52
1:D:141:LEU:N	1:D:141:LEU:CD1	2.49	0.52
1:D:24:GLU:O	1:D:28:LYS:HG3	2.10	0.52
1:E:44:ILE:HD13	1:E:74:ILE:HG21	1.91	0.52
1:A:246:ILE:O	1:A:248:ILE:HD12	2.10	0.52
1:B:102:HIS:CE1	1:B:103:PRO:HD2	2.44	0.52
1:B:146:LEU:N	1:B:146:LEU:HD12	2.25	0.52
1:B:58:LEU:CD2	1:C:196:GLY:HA2	2.40	0.52
1:E:102:HIS:CD2	1:E:103:PRO:CD	2.71	0.52
1:E:376:ILE:HG23	1:E:380:VAL:HG23	1.92	0.52
1:B:46:GLN:N	1:B:71:ILE:HD11	2.24	0.51
1:C:46:GLN:OE1	1:C:131:THR:CG2	2.57	0.51
1:D:75:ALA:CB	1:D:134:ILE:HD11	2.40	0.51
1:D:320:GLY:O	1:D:321:ASN:OD1	2.28	0.51
1:A:168:VAL:HG13	1:A:180:PHE:CZ	2.46	0.51
1:A:376:ILE:HB	1:A:380:VAL:HG23	1.92	0.51
1:C:118:ARG:NH2	1:C:204:PRO:HG3	2.25	0.51
1:C:46:GLN:OE1	1:C:68:PHE:CD2	2.64	0.51
1:E:118:ARG:NH1	1:E:139:ILE:CD1	2.73	0.51
1:F:24:GLU:CG	1:F:28:LYS:HE3	2.38	0.51
1:A:201:HIS:HB3	1:A:224:ILE:CD1	2.40	0.51
1:A:49:ALA:CB	1:A:60:THR:HG21	2.33	0.51
1:D:44:ILE:N	1:D:44:ILE:HD12	2.26	0.51
1:D:252:ARG:NH1	1:E:262:GLU:OE1	2.37	0.51
1:F:365:LEU:O	1:F:369:ARG:HG2	2.09	0.51
1:B:246:ILE:HG22	1:B:248:ILE:CD1	2.40	0.51
1:C:112:LYS:CD	1:C:113:GLN:H	2.23	0.51
1:C:277:GLN:H	1:C:277:GLN:CD	2.13	0.51
1:E:224:ILE:H	1:E:225:PRO:HD2	1.75	0.51
1:F:192:THR:O	1:F:195:LYS:HE3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:303:VAL:O	1:B:336:ARG:HG2	2.10	0.51
1:D:124:VAL:CG1	1:D:133:GLU:HB2	2.38	0.51
1:E:53:LYS:NZ	1:F:242:THR:OG1	2.44	0.51
1:F:376:ILE:HD13	1:F:381:ALA:HB2	1.92	0.51
1:A:228:PHE:O	1:A:229:SER:CB	2.58	0.51
1:A:4:LEU:O	1:A:6:LEU:HD12	2.11	0.51
1:B:363:PHE:CD2	1:B:387:MET:HB3	2.46	0.51
1:A:167:MET:HA	1:A:272:ALA:O	2.11	0.51
1:A:49:ALA:HB3	1:A:60:THR:CG2	2.36	0.51
1:A:87:GLU:HG3	1:A:94:ILE:HD11	1.92	0.51
1:B:154:GLU:H	1:B:154:GLU:CD	2.12	0.51
1:B:45:LYS:CG	1:B:46:GLN:N	2.73	0.51
1:C:202:GLU:O	1:C:223:GLN:HA	2.11	0.51
1:F:379:HIS:HA	1:F:382:LYS:CE	2.29	0.51
1:B:251:LEU:HD13	1:B:272:ALA:HB1	1.91	0.51
1:B:67:ASN:OD1	1:B:69:ASN:HB2	2.10	0.51
1:C:34:PHE:CZ	1:C:61:LEU:HD22	2.46	0.51
1:C:81:SER:OG	1:C:87:GLU:OE1	2.20	0.51
1:D:27:PHE:O	1:D:31:VAL:HG23	2.11	0.51
1:E:74:ILE:HA	1:E:77:TRP:CE3	2.45	0.51
1:C:46:GLN:NE2	1:C:71:ILE:HD11	2.25	0.51
1:C:10:GLU:CD	1:C:59:CYS:SG	2.90	0.51
1:D:224:ILE:HG12	1:D:225:PRO:N	2.25	0.51
1:D:73:ARG:HG3	1:D:73:ARG:HH11	1.75	0.51
1:E:40:SER:O	1:E:138:SER:HB2	2.11	0.51
1:F:35:LEU:CD2	1:F:115:PHE:CD2	2.94	0.51
1:F:285:ARG:O	1:F:288:SER:OG	2.19	0.51
1:A:44:ILE:HG23	1:A:66:LEU:CD2	2.41	0.50
1:B:224:ILE:N	1:B:225:PRO:HD2	2.26	0.50
1:C:46:GLN:HE21	1:C:71:ILE:CG1	2.22	0.50
1:D:10:GLU:CD	1:D:10:GLU:H	2.11	0.50
1:E:144:LEU:HD12	1:E:149:ILE:HD11	1.93	0.50
1:A:222:SER:HA	1:A:227:GLN:NE2	2.26	0.50
1:C:33:GLU:OE1	1:C:37:HIS:CD2	2.64	0.50
1:D:307:ARG:NH1	1:D:336:ARG:CZ	2.74	0.50
1:E:176:LYS:HE2	1:E:273:THR:CG2	2.41	0.50
1:E:232:ALA:CB	1:E:255:GLN:HE22	2.24	0.50
1:F:241:ARG:O	1:F:242:THR:CG2	2.59	0.50
1:A:39:ALA:HA	1:A:54:VAL:HA	1.93	0.50
1:A:46:GLN:HG3	1:A:68:PHE:CD1	2.47	0.50
1:A:64:ARG:NH1	1:A:70:GLU:CD	2.64	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:27:PHE:HD2	1:D:77:TRP:HE3	1.59	0.50
1:D:123:PRO:HB3	1:E:227:GLN:HG2	1.93	0.50
1:D:377:ASP:OD1	1:D:377:ASP:C	2.49	0.50
1:D:41:ASP:OD2	1:E:242:THR:OG1	2.21	0.50
1:E:35:LEU:HD23	1:E:115:PHE:CE1	2.47	0.50
1:F:119:VAL:O	1:F:119:VAL:CG2	2.59	0.50
1:B:107:THR:OG1	1:B:111:GLN:CA	2.59	0.50
1:B:185:ARG:HG3	1:B:212:ILE:HD12	1.93	0.50
1:C:167:MET:HA	1:C:272:ALA:O	2.12	0.50
1:F:111:GLN:HE21	1:F:111:GLN:H	1.52	0.50
1:A:279:CYS:CA	1:A:282:VAL:HG13	2.40	0.50
1:A:335:ILE:CD1	1:A:355:LEU:HD22	2.40	0.50
1:C:278:ASN:HA	1:C:311:ALA:CB	2.42	0.50
1:C:48:VAL:HG22	1:C:49:ALA:N	2.25	0.50
1:D:126:ILE:O	1:D:128:GLY:N	2.45	0.50
1:D:34:PHE:HE2	1:D:50:ILE:CG2	2.24	0.50
1:E:379:HIS:O	1:E:383:ARG:HG3	2.11	0.50
1:F:224:ILE:HG21	1:F:231:PHE:CZ	2.47	0.50
1:F:376:ILE:HD12	1:F:376:ILE:C	2.32	0.50
1:B:137:ARG:CG	1:B:137:ARG:NH1	2.69	0.50
1:B:384:LEU:C	1:B:384:LEU:CD2	2.80	0.50
1:C:367:ALA:HB2	1:C:384:LEU:CB	2.41	0.50
1:C:76:LEU:CD2	1:C:82:SER:HA	2.38	0.50
1:F:9:LEU:CD1	1:F:62:SER:HA	2.25	0.50
1:A:165:ILE:HG22	1:A:167:MET:HG3	1.94	0.50
1:A:52:ALA:O	1:A:58:LEU:HA	2.12	0.50
1:C:45:LYS:HB2	1:C:133:GLU:HG3	1.94	0.50
1:E:202:GLU:CB	1:E:205:ILE:HA	2.42	0.50
1:E:345:MET:O	1:E:348:VAL:HG12	2.11	0.50
1:E:74:ILE:HD13	1:E:77:TRP:HZ3	1.76	0.50
1:F:348:VAL:HG13	1:F:349:ALA:H	1.77	0.50
1:B:250:GLU:O	1:B:250:GLU:HG2	2.12	0.50
1:C:179:THR:HG21	1:C:310:MET:HE1	1.92	0.50
1:C:149:ILE:O	1:C:326:ARG:NH2	2.45	0.50
1:D:250:GLU:OE2	1:D:275:HIS:CE1	2.65	0.50
1:F:17:TYR:CD2	1:F:62:SER:HB3	2.47	0.50
1:F:192:THR:CG2	1:F:193:PRO:HD2	2.37	0.50
1:D:10:GLU:OE1	1:D:61:LEU:CD2	2.59	0.49
1:D:216:HIS:CD2	1:D:217:SER:HB3	2.47	0.49
1:F:7:PRO:O	1:F:8:ILE:HD12	2.12	0.49
1:C:212:ILE:CD1	1:C:212:ILE:N	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:245:LEU:CD1	1:C:269:PRO:HB2	2.40	0.49
1:D:154:GLU:N	1:D:154:GLU:OE1	2.32	0.49
1:D:185:ARG:HG3	1:D:212:ILE:HD12	1.94	0.49
1:E:184:ILE:O	1:E:188:MET:HG2	2.11	0.49
1:A:131:THR:OG1	1:A:132:ALA:N	2.45	0.49
1:A:165:ILE:HG13	1:A:305:THR:HG22	1.93	0.49
1:A:69:ASN:O	1:A:73:ARG:HG2	2.13	0.49
1:C:224:ILE:HG12	1:C:231:PHE:CE1	2.47	0.49
1:E:335:ILE:HD11	1:E:355:LEU:CB	2.40	0.49
1:E:43:ILE:HD11	1:E:51:SER:OG	2.11	0.49
1:F:371:HIS:HB2	1:F:376:ILE:HD11	1.93	0.49
1:F:46:GLN:O	1:F:66:LEU:O	2.30	0.49
1:A:83:SER:O	1:A:87:GLU:HG2	2.12	0.49
1:B:171:LYS:HE3	1:B:277:GLN:N	2.27	0.49
1:B:88:LEU:CD1	1:B:123:PRO:HD3	2.41	0.49
1:C:209:TYR:HB2	1:C:219:ILE:HG21	1.93	0.49
1:C:350:SER:O	1:C:353:ARG:HB2	2.12	0.49
1:C:352:VAL:O	1:C:356:VAL:HG12	2.12	0.49
1:C:9:LEU:HD12	1:C:9:LEU:O	2.13	0.49
1:D:35:LEU:HD21	1:D:115:PHE:CG	2.44	0.49
1:E:14:GLU:C	1:E:14:GLU:OE1	2.51	0.49
1:E:176:LYS:NZ	1:E:273:THR:HG23	2.28	0.49
1:A:198:LEU:HD22	1:A:245:LEU:HB3	1.94	0.49
1:B:22:GLU:HB2	1:B:23:HIS:HD2	1.77	0.49
1:C:248:ILE:HD13	1:C:270:VAL:CG1	2.42	0.49
1:D:54:VAL:O	1:D:55:LYS:HG2	2.12	0.49
1:E:203:ASP:HA	1:E:224:ILE:HG13	1.94	0.49
1:E:247:MET:HG3	1:E:247:MET:O	2.13	0.49
1:F:7:PRO:HB2	1:F:60:THR:HG23	1.94	0.49
1:A:329:LEU:HD23	1:A:329:LEU:C	2.33	0.49
1:B:146:LEU:H	1:B:146:LEU:CD1	2.26	0.49
1:C:159:MET:SD	1:C:183:ILE:CD1	3.01	0.49
1:C:83:SER:OG	1:C:83:SER:O	2.27	0.49
1:E:149:ILE:CG2	1:E:149:ILE:O	2.60	0.49
1:E:69:ASN:O	1:E:73:ARG:HG3	2.12	0.49
1:F:50:ILE:H	1:F:66:LEU:CD1	2.26	0.49
1:A:44:ILE:HG22	1:A:71:ILE:CD1	2.43	0.49
1:B:46:GLN:CG	1:B:68:PHE:CE1	2.65	0.49
1:C:223:GLN:O	1:C:227:GLN:HB2	2.13	0.49
1:C:165:ILE:HD12	1:C:260:ALA:HB1	1.95	0.49
1:C:303:VAL:HG21	1:C:340:LEU:HD23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:198:LEU:HB2	1:E:219:ILE:CD1	2.40	0.49
1:A:238:ALA:HB1	1:A:246:ILE:CD1	2.42	0.49
1:A:167:MET:HE2	1:A:274:VAL:HG21	1.95	0.49
1:C:135:VAL:HG23	1:C:135:VAL:O	2.12	0.49
1:C:322:LEU:CD2	1:C:322:LEU:N	2.74	0.49
1:C:328:TYR:CZ	1:C:361:HIS:HB2	2.47	0.49
1:C:20:THR:HG23	1:C:70:GLU:OE1	2.12	0.49
1:E:13:THR:O	1:E:14:GLU:CB	2.60	0.49
1:A:284:ARG:HG2	1:A:349:ALA:HB2	1.95	0.49
1:B:180:PHE:O	1:B:183:ILE:HG22	2.13	0.49
1:B:170:GLY:O	1:B:275:HIS:HA	2.13	0.49
1:B:309:ILE:O	1:B:328:TYR:HA	2.13	0.49
1:B:179:THR:HG21	1:B:310:MET:HE3	1.94	0.49
1:C:97:ARG:NE	1:C:99:GLU:OE2	2.43	0.49
1:C:33:GLU:HG3	1:C:61:LEU:HD11	1.95	0.49
1:C:71:ILE:HG13	1:C:72:GLU:N	2.28	0.49
1:D:40:SER:C	1:D:41:ASP:OD1	2.52	0.49
1:D:45:LYS:O	1:D:66:LEU:CD1	2.61	0.49
1:F:379:HIS:O	1:F:382:LYS:HG2	2.13	0.49
1:B:262:GLU:O	1:B:266:THR:HG23	2.13	0.48
1:C:53:LYS:HG2	1:C:58:LEU:CD2	2.42	0.48
1:D:317:LYS:HB3	1:D:375:ILE:HG22	1.94	0.48
1:D:64:ARG:NH1	1:D:70:GLU:OE2	2.46	0.48
1:E:28:LYS:O	1:E:32:LEU:HD13	2.13	0.48
1:B:180:PHE:HA	1:B:183:ILE:CG2	2.43	0.48
1:B:209:TYR:HB2	1:B:219:ILE:HG21	1.94	0.48
1:B:20:THR:CG2	1:B:21:PHE:N	2.76	0.48
1:D:118:ARG:HG3	1:D:139:ILE:HG12	1.94	0.48
1:D:317:LYS:HB3	1:D:375:ILE:CG2	2.43	0.48
1:E:309:ILE:O	1:E:328:TYR:HA	2.13	0.48
1:E:333:THR:O	1:E:337:GLU:HG3	2.13	0.48
1:F:339:LEU:HD22	1:F:348:VAL:HG23	1.96	0.48
1:F:367:ALA:HB2	1:F:384:LEU:HG	1.94	0.48
1:B:224:ILE:O	1:B:228:PHE:O	2.31	0.48
1:C:282:VAL:HG13	1:C:283:MET:N	2.28	0.48
1:D:27:PHE:HB2	1:D:77:TRP:CZ3	2.41	0.48
1:E:35:LEU:HD23	1:E:115:PHE:CZ	2.49	0.48
1:F:383:ARG:HA	1:F:386:MET:HE1	1.95	0.48
1:C:149:ILE:HD13	1:C:182:SER:OG	2.14	0.48
1:E:43:ILE:HG12	1:E:51:SER:HG	1.79	0.48
1:C:165:ILE:HD13	1:C:270:VAL:CG1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:159:MET:CE	1:C:183:ILE:CD1	2.91	0.48
1:C:373:ASP:N	1:C:373:ASP:OD1	2.46	0.48
1:C:46:GLN:NE2	1:C:68:PHE:CD2	2.80	0.48
1:D:93:LEU:HD22	1:D:93:LEU:N	2.24	0.48
1:E:75:ALA:HB2	1:E:134:ILE:HD11	1.95	0.48
1:F:310:MET:SD	1:F:326:ARG:HD3	2.53	0.48
1:B:179:THR:HG21	1:B:310:MET:HE1	1.96	0.48
1:D:252:ARG:HH22	1:E:262:GLU:CD	2.17	0.48
1:F:114:ARG:HB2	1:F:141:LEU:CD1	2.42	0.48
1:E:254:LYS:HE3	1:F:294:VAL:HG23	1.96	0.48
1:B:119:VAL:CG2	1:B:119:VAL:O	2.62	0.48
1:B:224:ILE:H	1:B:225:PRO:HD2	1.79	0.48
1:B:327:GLU:HG3	1:B:362:PRO:HA	1.96	0.48
1:B:377:ASP:OD1	1:B:377:ASP:C	2.52	0.48
1:B:70:GLU:O	1:B:73:ARG:HG3	2.14	0.48
1:E:274:VAL:HG11	1:E:282:VAL:HG13	1.94	0.48
1:E:299:ILE:CD1	1:E:345:MET:HB3	2.43	0.48
1:F:74:ILE:CD1	1:F:77:TRP:CE3	2.96	0.48
1:B:252:ARG:HG2	1:B:253:ASP:N	2.29	0.48
1:C:159:MET:CE	1:C:183:ILE:HD13	2.43	0.48
1:D:194:ILE:O	1:D:194:ILE:HG12	2.13	0.48
1:D:46:GLN:O	1:D:66:LEU:O	2.32	0.48
1:E:45:LYS:HB2	1:E:133:GLU:HG3	1.96	0.48
1:E:225:PRO:HB2	1:E:226:GLU:CD	2.34	0.48
1:F:198:LEU:O	1:F:219:ILE:HD12	2.13	0.48
1:F:241:ARG:C	1:F:242:THR:HG22	2.34	0.48
1:F:382:LYS:O	1:F:386:MET:HB2	2.14	0.48
1:F:67:ASN:OD1	1:F:70:GLU:HG3	2.14	0.48
1:A:246:ILE:CG2	1:A:248:ILE:HG13	2.43	0.48
1:A:380:VAL:HG12	1:A:383:ARG:NH2	2.29	0.48
1:B:224:ILE:HG22	1:B:225:PRO:CD	2.44	0.48
1:B:250:GLU:OE2	1:B:275:HIS:HD2	1.97	0.48
1:C:262:GLU:O	1:C:266:THR:HG23	2.14	0.48
1:C:329:LEU:HD11	1:C:335:ILE:HD13	1.96	0.48
1:C:283:MET:HG3	1:C:352:VAL:HG21	1.95	0.48
1:C:46:GLN:NE2	1:C:71:ILE:HG12	2.25	0.48
1:D:257:ILE:HD12	1:D:261:PHE:CZ	2.48	0.48
1:E:358:GLU:HG2	1:E:359:PHE:CD2	2.49	0.48
1:F:17:TYR:HE2	1:F:64:ARG:HB3	1.78	0.48
1:A:18:PRO:HB2	1:A:20:THR:O	2.14	0.47
1:A:344:ASP:OD1	1:A:345:MET:HE3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:LEU:HD11	1:C:179:THR:HG23	1.96	0.47
1:D:124:VAL:HG23	1:D:131:THR:HG23	1.95	0.47
1:A:6:LEU:CD1	1:A:6:LEU:N	2.75	0.47
1:B:302:LEU:HD12	1:B:306:THR:CG2	2.44	0.47
1:B:328:TYR:CZ	1:B:361:HIS:HB2	2.49	0.47
1:D:75:ALA:CA	1:D:134:ILE:HD11	2.44	0.47
1:E:6:LEU:N	1:E:6:LEU:CD1	2.75	0.47
1:F:34:PHE:HE2	1:F:50:ILE:CG2	2.27	0.47
1:A:302:LEU:C	1:A:302:LEU:CD1	2.79	0.47
1:A:307:ARG:HD3	1:A:336:ARG:NH2	2.28	0.47
1:A:376:ILE:HB	1:A:380:VAL:HG21	1.96	0.47
1:B:327:GLU:HA	1:B:361:HIS:O	2.14	0.47
1:B:64:ARG:NH2	1:B:70:GLU:OE1	2.47	0.47
1:C:35:LEU:HD21	1:C:117:TYR:OH	2.13	0.47
1:D:198:LEU:O	1:D:219:ILE:HA	2.14	0.47
1:D:76:LEU:CD1	1:D:84:VAL:HG22	2.45	0.47
1:A:195:LYS:HG2	1:A:216:HIS:CD2	2.50	0.47
1:B:17:TYR:CD1	1:B:62:SER:HB2	2.50	0.47
1:B:284:ARG:CA	1:B:287:ILE:HG13	2.42	0.47
1:C:224:ILE:HD12	1:C:228:PHE:HB2	1.95	0.47
1:C:339:LEU:HD22	1:C:348:VAL:HG13	1.96	0.47
1:C:34:PHE:CD2	1:C:42:ILE:HD13	2.49	0.47
1:D:243:PRO:CG	1:D:246:ILE:HD11	2.44	0.47
1:D:243:PRO:HG3	1:D:246:ILE:HD11	1.95	0.47
1:B:19:SER:O	1:B:64:ARG:CZ	2.63	0.47
1:B:332:THR:HG22	1:B:333:THR:N	2.29	0.47
1:C:125:TYR:OH	1:D:97:ARG:NH2	2.47	0.47
1:C:133:GLU:OE2	1:D:197:HIS:NE2	2.37	0.47
1:C:137:ARG:HH11	1:C:137:ARG:HB3	1.80	0.47
1:F:188:MET:HE3	1:F:212:ILE:HG21	1.95	0.47
1:B:27:PHE:O	1:B:30:THR:OG1	2.29	0.47
1:B:41:ASP:OD1	1:B:137:ARG:HA	2.14	0.47
1:D:204:PRO:HB2	1:D:206:GLU:OE1	2.14	0.47
1:D:235:ASN:OD1	1:D:248:ILE:HD12	2.15	0.47
1:D:34:PHE:CE2	1:D:50:ILE:HG22	2.49	0.47
1:D:376:ILE:HB	1:D:380:VAL:HG23	1.97	0.47
1:D:94:ILE:HD11	1:D:121:ILE:HB	1.96	0.47
1:E:376:ILE:HG22	1:E:377:ASP:O	2.15	0.47
1:E:43:ILE:O	1:E:43:ILE:HG13	2.14	0.47
1:F:111:GLN:N	1:F:111:GLN:NE2	2.48	0.47
1:F:266:THR:HG23	1:F:268:HIS:CD2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:244:ASN:O	1:F:269:PRO:CG	2.63	0.47
1:F:386:MET:HE2	1:F:386:MET:HB3	1.60	0.47
1:B:68:PHE:CZ	1:B:131:THR:HG21	2.50	0.47
1:C:353:ARG:O	1:C:354:ARG:C	2.53	0.47
1:D:119:VAL:HG22	1:D:136:MET:CE	2.45	0.47
1:D:248:ILE:HG12	1:D:270:VAL:HG13	1.97	0.47
1:F:12:LYS:HD2	1:F:15:TYR:CD1	2.50	0.47
1:A:102:HIS:CG	1:A:106:LEU:HB2	2.49	0.47
1:A:192:THR:O	1:A:195:LYS:HE3	2.13	0.47
1:C:188:MET:HE1	1:C:198:LEU:HD12	1.97	0.47
1:C:45:LYS:HG2	1:C:46:GLN:N	2.28	0.47
1:D:283:MET:CE	1:D:302:LEU:HG	2.44	0.47
1:E:43:ILE:CD1	1:E:51:SER:OG	2.61	0.47
1:F:188:MET:HB3	1:F:214:SER:HB2	1.97	0.47
1:A:21:PHE:O	1:A:73:ARG:CZ	2.60	0.47
1:A:246:ILE:O	1:A:248:ILE:CD1	2.63	0.47
1:B:224:ILE:O	1:B:228:PHE:C	2.53	0.47
1:B:66:LEU:HB3	1:B:71:ILE:HG13	1.97	0.47
1:C:141:LEU:CD2	1:C:208:VAL:CG2	2.93	0.47
1:C:289:ARG:N	1:C:289:ARG:HD2	2.30	0.47
1:C:46:GLN:OE1	1:C:68:PHE:CE2	2.68	0.47
1:C:67:ASN:OD1	1:C:69:ASN:N	2.47	0.47
1:D:98:TYR:CE2	1:D:100:VAL:HG12	2.50	0.47
1:D:198:LEU:HD22	1:D:245:LEU:HB3	1.97	0.47
1:D:289:ARG:NH2	1:E:301:ASP:OD1	2.47	0.47
1:D:294:VAL:HG12	1:D:294:VAL:O	2.15	0.47
1:D:278:ASN:HA	1:D:311:ALA:CB	2.45	0.47
1:F:15:TYR:CD1	1:F:33:GLU:HG2	2.49	0.47
1:A:198:LEU:CB	1:A:219:ILE:HD12	2.36	0.47
1:A:300:TYR:HB3	1:F:386:MET:HE3	1.97	0.47
1:A:328:TYR:CZ	1:A:361:HIS:HB2	2.50	0.47
1:B:317:LYS:HB3	1:B:375:ILE:HD11	1.96	0.47
1:B:351:GLU:OE2	1:B:351:GLU:HA	2.14	0.47
1:E:382:LYS:O	1:E:386:MET:HG3	2.15	0.47
1:F:46:GLN:OE1	1:F:131:THR:HG21	2.15	0.47
1:A:162:ASP:OD1	1:A:163:ASN:ND2	2.48	0.47
1:A:342:LEU:HD12	1:A:351:GLU:CG	2.43	0.47
1:B:375:ILE:HG23	1:B:376:ILE:HG23	1.96	0.47
1:C:141:LEU:HD23	1:C:208:VAL:HG22	1.97	0.47
1:C:187:ILE:HD12	1:C:194:ILE:HG22	1.97	0.47
1:C:280:SER:HB3	1:C:353:ARG:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:83:SER:CB	1:D:86:THR:OG1	2.60	0.47
1:D:94:ILE:HD11	1:D:121:ILE:CB	2.45	0.47
1:E:262:GLU:O	1:E:266:THR:HG23	2.15	0.47
1:E:179:THR:HG21	1:E:326:ARG:HH21	1.77	0.47
1:F:7:PRO:O	1:F:8:ILE:HG13	2.15	0.47
1:A:151:LEU:HD11	1:A:326:ARG:CD	2.44	0.46
1:B:370:LEU:HB3	1:B:375:ILE:HG23	1.97	0.46
1:B:317:LYS:CG	1:B:375:ILE:HD11	2.43	0.46
1:C:84:VAL:HA	1:C:87:GLU:HG3	1.97	0.46
1:E:21:PHE:O	1:E:73:ARG:HD2	2.15	0.46
1:F:209:TYR:HB2	1:F:219:ILE:HG21	1.97	0.46
1:A:226:GLU:C	1:F:91:LYS:NZ	2.69	0.46
1:B:127:GLN:HE21	1:C:210:ASP:HB3	1.80	0.46
1:C:114:ARG:CD	1:C:141:LEU:HD11	2.44	0.46
1:E:246:ILE:CG2	1:E:248:ILE:HG23	2.45	0.46
1:E:348:VAL:CG1	1:E:349:ALA:H	2.28	0.46
1:E:27:PHE:CD1	1:E:74:ILE:HD12	2.50	0.46
1:F:245:LEU:HA	1:F:269:PRO:HG2	1.97	0.46
1:A:203:ASP:OD2	1:A:225:PRO:HG3	2.16	0.46
1:B:155:LEU:HD22	1:B:155:LEU:C	2.35	0.46
1:B:91:LYS:HA	1:B:91:LYS:HZ3	1.78	0.46
1:C:125:TYR:HH	1:D:97:ARG:CZ	2.28	0.46
1:C:99:GLU:OE1	1:C:114:ARG:CZ	2.63	0.46
1:F:24:GLU:O	1:F:28:LYS:HG3	2.14	0.46
1:A:202:GLU:HB3	1:A:204:PRO:O	2.15	0.46
1:A:87:GLU:O	1:A:91:LYS:N	2.48	0.46
1:B:46:GLN:HB3	1:B:126:ILE:CD1	2.45	0.46
1:C:97:ARG:CD	1:C:97:ARG:C	2.83	0.46
1:D:84:VAL:HA	1:D:87:GLU:HG3	1.98	0.46
1:E:22:GLU:N	1:E:26:GLN:OE1	2.48	0.46
1:B:238:ALA:O	1:B:243:PRO:HD3	2.14	0.46
1:B:319:ASP:HB3	1:B:321:ASN:OD1	2.16	0.46
1:B:17:TYR:CE2	1:B:62:SER:CB	2.98	0.46
1:B:96:THR:OG1	1:B:97:ARG:N	2.49	0.46
1:D:12:LYS:H	1:D:12:LYS:CD	2.28	0.46
1:D:208:VAL:CG1	1:D:210:ASP:OD1	2.64	0.46
1:C:123:PRO:HB2	1:D:227:GLN:HG2	1.97	0.46
1:A:241:ARG:HG2	1:F:135:VAL:HG21	1.98	0.46
1:B:21:PHE:HZ	1:B:30:THR:HG21	1.81	0.46
1:C:51:SER:HA	1:C:59:CYS:O	2.16	0.46
1:E:53:LYS:NZ	1:F:242:THR:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:32:LEU:HD13	1:F:103:PRO:HD3	1.96	0.46
1:B:318:THR:HG23	1:B:375:ILE:O	2.16	0.46
1:E:169:ALA:HA	1:E:274:VAL:O	2.16	0.46
1:C:111:GLN:O	1:C:111:GLN:CG	2.64	0.46
1:C:303:VAL:O	1:C:336:ARG:HD2	2.16	0.46
1:C:49:ALA:HA	1:C:66:LEU:CD1	2.46	0.46
1:C:10:GLU:HG2	1:C:59:CYS:SG	2.55	0.46
1:E:295:ARG:O	1:E:299:ILE:HG13	2.16	0.46
1:E:342:LEU:CD1	1:E:351:GLU:HG2	2.44	0.46
1:E:9:LEU:HD21	1:E:62:SER:HA	1.98	0.46
1:F:49:ALA:HB2	1:F:64:ARG:O	2.15	0.46
1:A:150:GLY:C	1:A:151:LEU:HD22	2.36	0.46
1:A:192:THR:OG1	1:A:193:PRO:HD2	2.16	0.46
1:B:224:ILE:HG22	1:B:225:PRO:N	2.31	0.46
1:B:46:GLN:CD	1:B:68:PHE:HE1	2.18	0.46
1:B:75:ALA:HB1	1:B:84:VAL:HG21	1.98	0.46
1:C:108:THR:HG23	1:C:110:GLY:N	2.31	0.46
1:C:313:THR:HG22	1:C:314:LEU:N	2.31	0.46
1:D:216:HIS:HD2	1:D:217:SER:HB3	1.81	0.46
1:F:17:TYR:HE2	1:F:64:ARG:CB	2.29	0.46
1:A:252:ARG:O	1:A:289:ARG:HD3	2.15	0.46
1:B:156:VAL:HA	1:B:159:MET:HE3	1.98	0.46
1:C:6:LEU:HD23	1:C:6:LEU:H	1.80	0.46
1:E:23:HIS:O	1:E:26:GLN:HG3	2.16	0.46
1:A:329:LEU:CD1	1:A:356:VAL:HG12	2.45	0.45
1:C:280:SER:CB	1:C:353:ARG:HG3	2.46	0.45
1:D:78:ALA:HB1	1:D:119:VAL:HG11	1.97	0.45
1:D:245:LEU:HB2	1:D:269:PRO:HG2	1.98	0.45
1:E:377:ASP:OD1	1:E:380:VAL:HG22	2.16	0.45
1:A:78:ALA:HA	1:A:98:TYR:CD1	2.52	0.45
1:B:156:VAL:HA	1:B:159:MET:CE	2.46	0.45
1:B:86:THR:O	1:B:90:SER:N	2.49	0.45
1:B:79:SER:CB	1:B:96:THR:OG1	2.65	0.45
1:C:131:THR:HG22	1:C:132:ALA:N	2.31	0.45
1:C:331:PHE:HB3	1:C:336:ARG:HG3	1.97	0.45
1:C:48:VAL:O	1:C:66:LEU:CD1	2.64	0.45
1:D:154:GLU:H	1:D:154:GLU:CD	2.18	0.45
1:D:176:LYS:CD	1:D:273:THR:HB	2.46	0.45
1:D:230:SER:CB	1:D:233:ILE:HG12	2.30	0.45
1:D:332:THR:CG2	1:D:335:ILE:HG13	2.45	0.45
1:D:95:ASN:ND2	1:D:120:ASN:HB2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:285:ARG:NH1	1:E:285:ARG:HG3	2.31	0.45
1:E:335:ILE:CD1	1:E:355:LEU:HD22	2.47	0.45
1:E:358:GLU:HG2	1:E:359:PHE:CE2	2.51	0.45
1:E:71:ILE:HD12	1:E:71:ILE:C	2.37	0.45
1:F:275:HIS:HB3	1:F:285:ARG:HH12	1.81	0.45
1:C:338:GLN:OE1	1:C:355:LEU:HD21	2.16	0.45
1:D:168:VAL:HA	1:D:310:MET:O	2.16	0.45
1:D:13:THR:HB	1:D:33:GLU:OE1	2.16	0.45
1:E:176:LYS:NZ	1:E:275:HIS:CE1	2.83	0.45
1:E:179:THR:CG2	1:E:312:GLN:OE1	2.40	0.45
1:A:203:ASP:OD1	1:A:204:PRO:CD	2.62	0.45
1:B:353:ARG:NH2	1:B:356:VAL:HG13	2.28	0.45
1:D:289:ARG:HD3	1:E:297:ALA:CB	2.46	0.45
1:B:202:GLU:OE1	1:B:205:ILE:HA	2.16	0.45
1:C:112:LYS:CG	1:C:113:GLN:H	2.29	0.45
1:C:99:GLU:CD	1:C:114:ARG:NH2	2.61	0.45
1:D:88:LEU:HD22	1:D:123:PRO:HD3	1.99	0.45
1:D:203:ASP:HB3	1:D:204:PRO:CD	2.35	0.45
1:D:326:ARG:CG	1:D:326:ARG:NH1	2.75	0.45
1:D:84:VAL:HG23	1:D:85:LEU:H	1.82	0.45
1:D:87:GLU:H	1:D:87:GLU:HG2	1.54	0.45
1:E:205:ILE:CG2	1:E:223:GLN:OE1	2.64	0.45
1:B:266:THR:OG1	1:B:268:HIS:NE2	2.44	0.45
1:B:50:ILE:HG13	1:B:66:LEU:HD21	1.98	0.45
1:C:101:PHE:HB3	1:C:112:LYS:HE3	1.99	0.45
1:C:131:THR:HG22	1:C:132:ALA:H	1.81	0.45
1:D:118:ARG:NH2	1:D:139:ILE:CD1	2.69	0.45
1:E:246:ILE:CG2	1:E:248:ILE:CG2	2.94	0.45
1:F:119:VAL:HG23	1:F:119:VAL:O	2.16	0.45
1:A:18:PRO:HG2	1:A:21:PHE:CD1	2.51	0.45
1:A:238:ALA:O	1:A:243:PRO:HD3	2.17	0.45
1:A:24:GLU:O	1:A:28:LYS:HG3	2.17	0.45
1:D:250:GLU:OE2	1:D:275:HIS:CD2	2.69	0.45
1:A:185:ARG:HG3	1:A:186:TYR:N	2.30	0.45
1:C:188:MET:HE1	1:C:219:ILE:HB	1.98	0.45
1:C:46:GLN:CG	1:C:68:PHE:CD1	2.94	0.45
1:E:238:ALA:O	1:E:243:PRO:HD3	2.16	0.45
1:E:31:VAL:HG13	1:E:42:ILE:HD11	1.98	0.45
1:E:24:GLU:OE1	1:E:77:TRP:CB	2.64	0.45
1:F:11:PHE:CD1	1:F:11:PHE:N	2.85	0.45
1:A:43:ILE:HG22	1:A:133:GLU:OE2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:LEU:CD1	1:A:156:VAL:HG21	2.47	0.45
1:A:214:SER:OG	1:A:217:SER:HB2	2.16	0.45
1:A:294:VAL:O	1:A:294:VAL:HG12	2.17	0.45
1:A:9:LEU:HA	1:A:60:THR:O	2.16	0.45
1:B:316:ARG:CG	1:B:316:ARG:NH1	2.78	0.45
1:C:168:VAL:HG13	1:C:180:PHE:CZ	2.52	0.45
1:E:203:ASP:HA	1:E:224:ILE:CG1	2.47	0.45
1:E:55:LYS:O	1:E:316:ARG:NH2	2.45	0.45
1:B:155:LEU:HD13	1:B:159:MET:HE1	1.98	0.45
1:B:192:THR:HG22	1:B:194:ILE:N	2.08	0.45
1:B:199:LEU:N	1:B:199:LEU:CD1	2.80	0.45
1:B:223:GLN:N	1:B:227:GLN:NE2	2.65	0.45
1:C:200:THR:HA	1:C:247:MET:HB3	1.99	0.45
1:C:303:VAL:HG21	1:C:340:LEU:CD2	2.47	0.45
1:D:168:VAL:O	1:D:273:THR:HA	2.16	0.45
1:E:191:ASP:HA	1:E:195:LYS:HE2	1.98	0.45
1:A:338:GLN:CA	1:A:338:GLN:OE1	2.65	0.44
1:E:142:ASP:OD1	1:E:142:ASP:N	2.48	0.44
1:F:159:MET:CE	1:F:183:ILE:HD11	2.47	0.44
1:A:195:LYS:HB3	1:A:216:HIS:HD2	1.83	0.44
1:A:347:LYS:HD3	1:A:347:LYS:HA	1.72	0.44
1:B:224:ILE:HA	1:B:224:ILE:HD12	1.73	0.44
1:C:135:VAL:O	1:C:135:VAL:CG2	2.66	0.44
1:D:139:ILE:O	1:D:139:ILE:HG22	2.17	0.44
1:D:203:ASP:CA	1:D:224:ILE:CG2	2.95	0.44
1:D:34:PHE:HE2	1:D:50:ILE:HG22	1.82	0.44
1:D:75:ALA:HA	1:D:134:ILE:HD11	1.98	0.44
1:E:316:ARG:CG	1:E:316:ARG:NH1	2.79	0.44
1:F:198:LEU:HB2	1:F:219:ILE:HD12	1.99	0.44
1:A:176:LYS:NZ	1:A:273:THR:HB	2.31	0.44
1:A:55:LYS:HD3	1:A:321:ASN:ND2	2.32	0.44
1:B:242:THR:O	1:B:242:THR:HG23	2.17	0.44
1:B:99:GLU:C	1:B:99:GLU:OE1	2.55	0.44
1:F:111:GLN:CD	1:F:111:GLN:N	2.70	0.44
1:F:75:ALA:HB2	1:F:134:ILE:HD11	1.99	0.44
1:A:17:TYR:CD2	1:A:62:SER:CB	3.01	0.44
1:C:98:TYR:O	1:C:117:TYR:HB2	2.18	0.44
1:C:59:CYS:SG	1:C:60:THR:N	2.91	0.44
1:C:83:SER:O	1:C:86:THR:HG22	2.17	0.44
1:D:58:LEU:HD23	1:E:196:GLY:HA2	1.99	0.44
1:E:327:GLU:HG3	1:E:362:PRO:CA	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:224:ILE:HA	1:F:224:ILE:HD12	1.70	0.44
1:A:60:THR:HG21	1:A:62:SER:O	2.18	0.44
1:A:84:VAL:HG23	1:A:85:LEU:HD12	1.98	0.44
1:B:165:ILE:HG22	1:B:167:MET:HG3	1.99	0.44
1:C:27:PHE:HZ	1:C:136:MET:CE	2.31	0.44
1:C:309:ILE:O	1:C:328:TYR:HA	2.17	0.44
1:D:248:ILE:HA	1:D:248:ILE:HD13	1.86	0.44
1:D:250:GLU:HA	1:D:273:THR:O	2.18	0.44
1:E:141:LEU:CD2	1:E:141:LEU:C	2.86	0.44
1:E:165:ILE:HG22	1:E:167:MET:HG3	1.99	0.44
1:E:335:ILE:HD11	1:E:355:LEU:CG	2.47	0.44
1:E:376:ILE:HG23	1:E:380:VAL:HG22	1.98	0.44
1:E:84:VAL:O	1:E:84:VAL:HG22	2.18	0.44
1:A:361:HIS:NE2	1:A:366:GLU:OE1	2.50	0.44
1:B:143:PRO:HA	1:B:207:PHE:CD2	2.53	0.44
1:B:66:LEU:CD2	1:B:66:LEU:N	2.79	0.44
1:C:46:GLN:HG2	1:C:68:PHE:CE1	2.52	0.44
1:F:205:ILE:N	1:F:223:GLN:NE2	2.65	0.44
1:B:102:HIS:ND1	1:B:103:PRO:CD	2.77	0.44
1:B:12:LYS:HD3	1:B:15:TYR:O	2.17	0.44
1:B:363:PHE:O	1:B:384:LEU:HD22	2.17	0.44
1:C:50:ILE:N	1:C:66:LEU:HD11	2.32	0.44
1:D:196:GLY:HA3	1:D:244:ASN:ND2	2.32	0.44
1:D:307:ARG:NH1	1:D:336:ARG:NH2	2.66	0.44
1:D:335:ILE:CG2	1:D:355:LEU:HD13	2.32	0.44
1:E:103:PRO:HG2	1:E:104:THR:HG23	2.00	0.44
1:F:350:SER:O	1:F:353:ARG:HB3	2.17	0.44
1:F:383:ARG:HA	1:F:386:MET:CE	2.48	0.44
1:B:151:LEU:HD11	1:B:326:ARG:NE	2.32	0.44
1:C:21:PHE:CZ	1:C:30:THR:HG21	2.52	0.44
1:E:245:LEU:HD12	1:E:269:PRO:HB2	2.00	0.44
1:E:32:LEU:HD11	1:E:100:VAL:HG23	2.00	0.44
1:F:96:THR:HG23	1:F:119:VAL:HG22	2.00	0.44
1:F:168:VAL:HA	1:F:310:MET:O	2.18	0.44
1:F:166:VAL:HG13	1:F:308:PHE:HB3	1.99	0.44
1:A:339:LEU:HD22	1:A:348:VAL:HG13	2.00	0.44
1:B:250:GLU:HA	1:B:273:THR:HG22	2.00	0.44
1:C:205:ILE:CD1	1:C:223:GLN:HB2	2.48	0.44
1:E:306:THR:CG2	1:E:331:PHE:CE2	3.01	0.44
1:E:328:TYR:CZ	1:E:361:HIS:CB	3.01	0.44
1:F:168:VAL:HG23	1:F:180:PHE:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:GLN:HA	1:A:113:GLN:OE1	2.18	0.43
1:A:279:CYS:C	1:A:282:VAL:HG13	2.39	0.43
1:C:22:GLU:O	1:C:77:TRP:CH2	2.71	0.43
1:C:239:LEU:CD1	1:C:240:ARG:N	2.66	0.43
1:D:208:VAL:CG1	1:D:210:ASP:CG	2.87	0.43
1:F:34:PHE:CE2	1:F:50:ILE:CG2	3.00	0.43
1:A:151:LEU:N	1:A:151:LEU:CD2	2.82	0.43
1:A:307:ARG:HD3	1:A:336:ARG:CZ	2.49	0.43
1:A:44:ILE:HG23	1:A:66:LEU:HD23	2.00	0.43
1:A:87:GLU:HG2	1:A:87:GLU:H	1.51	0.43
1:A:123:PRO:CB	1:B:227:GLN:HB3	2.48	0.43
1:D:94:ILE:HG13	1:D:121:ILE:HB	1.92	0.43
1:D:343:SER:O	1:D:345:MET:HG3	2.18	0.43
1:E:80:GLY:O	1:E:82:SER:N	2.49	0.43
1:E:85:LEU:HD12	1:E:86:THR:N	2.34	0.43
1:A:200:THR:CG2	1:A:200:THR:O	2.65	0.43
1:A:236:GLN:O	1:A:240:ARG:NH1	2.51	0.43
1:A:304:GLU:O	1:A:336:ARG:NH2	2.50	0.43
1:B:168:VAL:HG12	1:B:176:LYS:HG2	2.01	0.43
1:B:180:PHE:CA	1:B:183:ILE:HG22	2.45	0.43
1:C:239:LEU:C	1:C:239:LEU:HD12	2.37	0.43
1:D:126:ILE:O	1:D:127:GLN:C	2.57	0.43
1:D:12:LYS:H	1:D:12:LYS:HD2	1.79	0.43
1:D:196:GLY:HA3	1:D:244:ASN:HD22	1.83	0.43
1:D:332:THR:HG23	1:D:335:ILE:HG13	2.00	0.43
1:E:44:ILE:HG23	1:E:66:LEU:HD22	2.00	0.43
1:F:22:GLU:H	1:F:26:GLN:HE22	1.65	0.43
1:F:365:LEU:O	1:F:365:LEU:HD12	2.17	0.43
1:F:53:LYS:HG2	1:F:58:LEU:CD2	2.47	0.43
1:A:9:LEU:HD11	1:A:63:THR:HG23	2.00	0.43
1:C:194:ILE:CD1	1:C:245:LEU:CD1	2.91	0.43
1:D:188:MET:SD	1:D:219:ILE:CD1	3.04	0.43
1:D:76:LEU:HD11	1:D:82:SER:O	2.19	0.43
1:E:35:LEU:HD23	1:E:115:PHE:CD1	2.52	0.43
1:E:316:ARG:HH11	1:E:316:ARG:HG3	1.82	0.43
1:E:76:LEU:HD22	1:E:76:LEU:O	2.18	0.43
1:F:102:HIS:CG	1:F:105:LYS:HB3	2.53	0.43
1:F:169:ALA:HA	1:F:274:VAL:O	2.19	0.43
1:C:157:ASN:HA	1:C:160:CYS:SG	2.58	0.43
1:C:231:PHE:CE2	1:C:252:ARG:NH2	2.86	0.43
1:D:180:PHE:O	1:D:184:ILE:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:224:ILE:CB	1:D:225:PRO:CD	2.89	0.43
1:D:95:ASN:OD1	1:E:237:GLU:OE2	2.36	0.43
1:E:167:MET:HA	1:E:272:ALA:O	2.18	0.43
1:E:171:LYS:O	1:F:266:THR:HA	2.19	0.43
1:C:141:LEU:CD2	1:C:208:VAL:HG22	2.49	0.43
1:C:242:THR:O	1:C:242:THR:HG23	2.18	0.43
1:D:44:ILE:HB	1:D:134:ILE:HB	2.01	0.43
1:D:348:VAL:O	1:D:352:VAL:HG23	2.18	0.43
1:E:14:GLU:CA	1:E:14:GLU:OE1	2.66	0.43
1:E:162:ASP:N	1:E:162:ASP:OD1	2.52	0.43
1:E:277:GLN:HG2	1:E:387:MET:HE3	2.01	0.43
1:E:70:GLU:O	1:E:74:ILE:CG1	2.61	0.43
1:F:200:THR:HA	1:F:247:MET:HB3	2.01	0.43
1:A:118:ARG:O	1:A:136:MET:HA	2.18	0.43
1:B:224:ILE:HG12	1:B:231:PHE:CZ	2.53	0.43
1:C:322:LEU:HD23	1:C:322:LEU:O	2.18	0.43
1:C:338:GLN:HE22	1:C:354:ARG:HH12	1.64	0.43
1:D:121:ILE:HG12	1:D:134:ILE:HG12	1.99	0.43
1:D:289:ARG:HA	1:D:289:ARG:HD3	1.79	0.43
1:F:85:LEU:CD1	1:F:85:LEU:C	2.80	0.43
1:A:16:ARG:HA	1:A:16:ARG:HD2	1.71	0.43
1:B:171:LYS:O	1:C:266:THR:C	2.57	0.43
1:B:352:VAL:O	1:B:356:VAL:HG12	2.19	0.43
1:B:85:LEU:HD23	1:B:85:LEU:O	2.17	0.43
1:D:188:MET:HE2	1:D:212:ILE:CG2	2.49	0.43
1:D:35:LEU:HD21	1:D:115:PHE:CZ	2.52	0.43
1:F:11:PHE:N	1:F:11:PHE:HD1	2.17	0.43
1:C:194:ILE:CG1	1:C:269:PRO:HG2	2.48	0.43
1:B:125:TYR:OH	1:C:99:GLU:HG3	2.18	0.43
1:D:101:PHE:CE2	1:D:114:ARG:CB	3.02	0.43
1:D:339:LEU:HD21	1:D:352:VAL:HG23	2.00	0.43
1:D:37:HIS:O	1:D:54:VAL:CG2	2.61	0.43
1:E:179:THR:CG2	1:E:326:ARG:NH2	2.70	0.43
1:E:198:LEU:O	1:E:219:ILE:HD12	2.19	0.43
1:E:247:MET:CE	1:E:249:GLY:N	2.82	0.43
1:B:90:SER:O	1:B:90:SER:OG	2.35	0.43
1:C:108:THR:HG22	1:C:112:LYS:N	2.18	0.43
1:C:248:ILE:HD13	1:C:270:VAL:HG13	2.01	0.43
1:D:22:GLU:H	1:D:26:GLN:NE2	2.16	0.43
1:F:348:VAL:HG13	1:F:349:ALA:N	2.34	0.43
1:B:377:ASP:OD1	1:B:380:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:GLU:O	1:B:99:GLU:OE1	2.37	0.42
1:C:192:THR:OG1	1:C:193:PRO:HD2	2.19	0.42
1:C:69:ASN:O	1:C:72:GLU:HB3	2.19	0.42
1:A:242:THR:HG23	1:A:242:THR:O	2.19	0.42
1:A:309:ILE:O	1:A:328:TYR:HA	2.19	0.42
1:B:347:LYS:HA	1:B:347:LYS:HE2	2.00	0.42
1:C:370:LEU:HD22	1:C:375:ILE:HG21	2.00	0.42
1:C:34:PHE:CD1	1:C:61:LEU:HD21	2.53	0.42
1:D:23:HIS:C	1:D:77:TRP:CH2	2.93	0.42
1:D:250:GLU:OE1	1:D:275:HIS:CD2	2.72	0.42
1:E:199:LEU:HG	1:E:243:PRO:HB3	2.01	0.42
1:F:30:THR:HG23	1:F:61:LEU:HD12	1.99	0.42
1:B:151:LEU:CD2	1:B:326:ARG:NH2	2.78	0.42
1:B:35:LEU:HA	1:B:35:LEU:HD12	1.89	0.42
1:D:205:ILE:HG13	1:D:223:GLN:NE2	2.33	0.42
1:E:299:ILE:HD12	1:E:345:MET:HB3	2.01	0.42
1:F:13:THR:O	1:F:14:GLU:HB2	2.19	0.42
1:F:85:LEU:HD13	1:F:94:ILE:CD1	2.49	0.42
1:A:20:THR:HG23	1:A:22:GLU:HG3	2.01	0.42
1:A:344:ASP:OD1	1:A:345:MET:HE2	2.20	0.42
1:C:361:HIS:NE2	1:C:366:GLU:OE2	2.51	0.42
1:D:84:VAL:HA	1:D:87:GLU:CD	2.39	0.42
1:E:92:LYS:HD2	1:E:92:LYS:HA	1.48	0.42
1:F:84:VAL:C	1:F:88:LEU:HG	2.40	0.42
1:A:242:THR:N	1:A:243:PRO:HD3	2.34	0.42
1:B:156:VAL:HG22	1:B:159:MET:HE3	2.00	0.42
1:D:176:LYS:NZ	1:D:275:HIS:ND1	2.51	0.42
1:F:159:MET:HG2	1:F:308:PHE:CD1	2.55	0.42
1:A:321:ASN:HD22	1:A:321:ASN:N	2.18	0.42
1:A:50:ILE:HG13	1:A:66:LEU:HD21	2.01	0.42
1:D:310:MET:SD	1:D:326:ARG:HD2	2.60	0.42
1:E:248:ILE:HG13	1:E:248:ILE:H	1.62	0.42
1:E:169:ALA:O	1:E:311:ALA:HA	2.19	0.42
1:E:361:HIS:NE2	1:E:366:GLU:OE2	2.53	0.42
1:E:68:PHE:CD1	1:E:68:PHE:C	2.93	0.42
1:F:17:TYR:CD2	1:F:62:SER:CB	3.02	0.42
1:F:251:LEU:HD22	1:F:257:ILE:HA	2.02	0.42
1:B:151:LEU:CD2	1:B:151:LEU:N	2.83	0.42
1:B:375:ILE:C	1:B:375:ILE:HD12	2.31	0.42
1:C:141:LEU:HD21	1:C:208:VAL:CG2	2.50	0.42
1:D:151:LEU:HG	1:D:326:ARG:HH12	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:202:GLU:HB2	1:E:205:ILE:CA	2.47	0.42
1:E:250:GLU:OE1	1:E:252:ARG:HG2	2.19	0.42
1:E:313:THR:HG22	1:E:314:LEU:N	2.35	0.42
1:F:141:LEU:HD23	1:F:141:LEU:HA	1.85	0.42
1:F:164:GLY:HA2	1:F:264:ALA:HB1	2.02	0.42
1:A:246:ILE:HG13	1:A:268:HIS:NE2	2.33	0.42
1:A:33:GLU:HA	1:A:33:GLU:OE2	2.19	0.42
1:A:60:THR:CG2	1:A:62:SER:O	2.67	0.42
1:B:28:LYS:O	1:B:32:LEU:HG	2.20	0.42
1:B:79:SER:O	1:B:96:THR:HG21	2.19	0.42
1:C:121:ILE:HG23	1:C:132:ALA:HB1	2.02	0.42
1:C:168:VAL:CG2	1:C:168:VAL:O	2.67	0.42
1:E:14:GLU:O	1:E:14:GLU:OE1	2.38	0.42
1:E:202:GLU:O	1:E:223:GLN:HA	2.20	0.42
1:F:242:THR:O	1:F:242:THR:HG23	2.20	0.42
1:F:289:ARG:HD3	1:F:289:ARG:HA	1.64	0.42
1:A:17:TYR:CD2	1:A:62:SER:HB3	2.55	0.42
1:B:192:THR:CG2	1:B:193:PRO:CD	2.97	0.42
1:D:242:THR:O	1:D:242:THR:HG23	2.19	0.42
1:E:348:VAL:CG1	1:E:349:ALA:N	2.82	0.42
1:B:259:SER:O	1:B:262:GLU:CG	2.67	0.42
1:C:100:VAL:CG1	1:C:115:PHE:HB2	2.43	0.42
1:D:235:ASN:O	1:D:238:ALA:HB3	2.20	0.42
1:D:235:ASN:OD1	1:D:248:ILE:CD1	2.68	0.42
1:D:246:ILE:HD12	1:D:268:HIS:NE2	2.31	0.42
1:B:100:VAL:CG1	1:B:115:PHE:HB2	2.41	0.41
1:B:12:LYS:HZ3	1:B:17:TYR:CA	2.33	0.41
1:A:120:ASN:ND2	1:B:237:GLU:OE2	2.52	0.41
1:E:325:ALA:CB	1:E:384:LEU:HD21	2.50	0.41
1:A:329:LEU:HD12	1:A:356:VAL:CG1	2.49	0.41
1:B:192:THR:HG23	1:B:193:PRO:CD	2.38	0.41
1:C:361:HIS:CE1	1:C:365:LEU:HD22	2.55	0.41
1:C:88:LEU:HD12	1:C:88:LEU:HA	1.82	0.41
1:D:24:GLU:HG3	1:D:24:GLU:O	2.20	0.41
1:D:250:GLU:HG2	1:D:273:THR:HG1	1.80	0.41
1:D:246:ILE:CG1	1:D:268:HIS:CD2	2.96	0.41
1:E:46:GLN:OE1	1:E:131:THR:HG21	2.20	0.41
1:F:242:THR:N	1:F:243:PRO:CD	2.83	0.41
1:F:244:ASN:O	1:F:269:PRO:HG2	2.20	0.41
1:A:228:PHE:CE1	1:A:237:GLU:HG3	2.55	0.41
1:A:120:ASN:OD1	1:B:241:ARG:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:VAL:HG11	1:B:282:VAL:HG13	2.02	0.41
1:B:388:SER:OG	1:B:388:SER:O	2.32	0.41
1:B:128:GLY:HA2	1:C:114:ARG:NH2	2.35	0.41
1:C:68:PHE:O	1:C:71:ILE:CG1	2.63	0.41
1:D:27:PHE:CB	1:D:77:TRP:HZ3	2.28	0.41
1:E:68:PHE:HD1	1:E:68:PHE:C	2.23	0.41
1:F:124:VAL:HG21	1:F:133:GLU:CB	2.37	0.41
1:E:137:ARG:NH1	1:F:240:ARG:CA	2.84	0.41
1:F:384:LEU:O	1:F:384:LEU:HD12	2.20	0.41
1:F:19:SER:CB	1:F:64:ARG:HH22	2.33	0.41
1:A:23:HIS:O	1:A:26:GLN:HG2	2.20	0.41
1:C:27:PHE:HZ	1:C:136:MET:HE2	1.85	0.41
1:C:194:ILE:HG23	1:C:194:ILE:O	2.20	0.41
1:C:282:VAL:CG1	1:C:283:MET:N	2.83	0.41
1:D:178:THR:HA	1:D:207:PHE:CE2	2.55	0.41
1:D:24:GLU:HA	1:D:77:TRP:CZ3	2.54	0.41
1:D:277:GLN:OE1	1:D:387:MET:HE2	2.20	0.41
1:E:351:GLU:OE1	1:E:351:GLU:CA	2.62	0.41
1:F:327:GLU:HA	1:F:361:HIS:O	2.20	0.41
1:F:75:ALA:HB1	1:F:85:LEU:HD22	1.81	0.41
1:A:172:THR:HG22	1:A:174:SER:H	1.84	0.41
1:A:284:ARG:HD3	1:A:349:ALA:HB2	2.02	0.41
1:C:42:ILE:O	1:C:135:VAL:HA	2.20	0.41
1:C:203:ASP:CG	1:C:204:PRO:CD	2.89	0.41
1:F:102:HIS:ND1	1:F:103:PRO:CD	2.82	0.41
1:F:214:SER:OG	1:F:217:SER:HB2	2.20	0.41
1:A:124:VAL:CG2	1:A:131:THR:HG23	2.44	0.41
1:A:141:LEU:HD23	1:A:141:LEU:C	2.41	0.41
1:A:200:THR:HG22	1:A:200:THR:O	2.21	0.41
1:A:18:PRO:CG	1:A:21:PHE:CE1	3.02	0.41
1:B:129:LYS:HG2	1:B:130:THR:N	2.35	0.41
1:B:261:PHE:CE1	1:B:302:LEU:HA	2.56	0.41
1:A:289:ARG:HH22	1:B:301:ASP:CG	2.24	0.41
1:B:91:LYS:CA	1:B:91:LYS:NZ	2.83	0.41
1:C:102:HIS:ND1	1:C:106:LEU:CB	2.83	0.41
1:C:156:VAL:HA	1:C:159:MET:CG	2.41	0.41
1:D:139:ILE:HD13	1:D:139:ILE:HA	1.67	0.41
1:D:18:PRO:HB3	1:D:26:GLN:HG2	2.03	0.41
1:D:317:LYS:H	1:D:317:LYS:HG2	1.55	0.41
1:D:13:THR:O	1:D:33:GLU:OE1	2.38	0.41
1:D:55:LYS:CG	1:D:57:THR:HG23	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:45:LYS:O	1:D:66:LEU:HD11	2.21	0.41
1:D:7:PRO:HG2	1:D:60:THR:CG2	2.51	0.41
1:E:375:ILE:HG22	1:E:375:ILE:O	2.19	0.41
1:E:75:ALA:O	1:E:79:SER:OG	2.30	0.41
1:F:140:PRO:HG2	1:F:207:PHE:CE1	2.56	0.41
1:A:83:SER:H	1:A:83:SER:HG	1.52	0.41
1:B:146:LEU:H	1:B:146:LEU:HD13	1.84	0.41
1:B:261:PHE:HZ	1:B:302:LEU:HB2	1.86	0.41
1:B:97:ARG:HG2	1:B:98:TYR:N	2.34	0.41
1:C:224:ILE:HA	1:C:224:ILE:HD12	1.78	0.41
1:D:21:PHE:HE1	1:D:27:PHE:HA	1.84	0.41
1:B:149:ILE:O	1:B:326:ARG:NH2	2.51	0.41
1:B:17:TYR:CG	1:B:62:SER:HB2	2.55	0.41
1:B:24:GLU:O	1:B:25:ALA:C	2.58	0.41
1:B:370:LEU:O	1:B:375:ILE:CG2	2.52	0.41
1:C:327:GLU:HG3	1:C:362:PRO:HA	2.02	0.41
1:D:382:LYS:HD3	1:D:382:LYS:HA	1.86	0.41
1:D:45:LYS:O	1:D:66:LEU:HD13	2.21	0.41
1:E:125:TYR:OH	1:F:97:ARG:HD3	2.21	0.41
1:F:309:ILE:O	1:F:328:TYR:HA	2.21	0.41
1:A:329:LEU:HD23	1:A:330:ASN:C	2.41	0.41
1:B:23:HIS:O	1:B:26:GLN:HB2	2.14	0.41
1:B:284:ARG:O	1:B:287:ILE:HG13	2.21	0.41
1:D:53:LYS:HA	1:D:57:THR:O	2.21	0.41
1:D:55:LYS:O	1:D:55:LYS:CG	2.62	0.41
1:D:76:LEU:HD11	1:D:82:SER:C	2.40	0.41
1:D:27:PHE:CB	1:D:77:TRP:CZ3	3.03	0.41
1:F:224:ILE:HG12	1:F:231:PHE:CZ	2.54	0.41
1:F:386:MET:HG2	1:F:386:MET:O	2.21	0.41
1:A:35:LEU:C	1:A:35:LEU:HD23	2.39	0.41
1:B:295:ARG:O	1:B:299:ILE:HG13	2.20	0.41
1:B:332:THR:CG2	1:B:333:THR:N	2.84	0.41
1:C:112:LYS:CG	1:C:113:GLN:N	2.84	0.41
1:C:34:PHE:CZ	1:C:61:LEU:HD21	2.44	0.41
1:D:15:TYR:OH	1:D:26:GLN:HG3	2.20	0.41
1:D:95:ASN:HD22	1:D:120:ASN:HB2	1.86	0.41
1:E:213:LYS:H	1:E:213:LYS:HG2	1.57	0.41
1:E:85:LEU:HD12	1:E:86:THR:H	1.86	0.41
1:F:328:TYR:CZ	1:F:361:HIS:HB2	2.56	0.41
1:A:239:LEU:HD13	1:F:172:THR:CG2	2.50	0.41
1:A:354:ARG:O	1:A:357:ASP:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ILE:HG12	1:A:77:TRP:CZ3	2.56	0.41
1:B:160:CYS:HB3	1:B:192:THR:CG2	2.51	0.41
1:B:202:GLU:O	1:B:223:GLN:HA	2.21	0.41
1:B:287:ILE:C	1:B:287:ILE:HD12	2.41	0.41
1:B:21:PHE:CZ	1:B:30:THR:HG21	2.56	0.41
1:B:35:LEU:O	1:B:38:GLU:CA	2.68	0.41
1:C:203:ASP:CG	1:C:204:PRO:HD3	2.41	0.41
1:C:241:ARG:C	1:C:243:PRO:HD3	2.41	0.41
1:E:197:HIS:CE1	1:E:199:LEU:HD21	2.56	0.41
1:E:197:HIS:O	1:E:244:ASN:N	2.52	0.41
1:E:168:VAL:HA	1:E:310:MET:O	2.21	0.41
1:B:169:ALA:O	1:B:311:ALA:HA	2.21	0.40
1:C:94:ILE:CD1	1:C:121:ILE:HB	2.50	0.40
1:C:97:ARG:HG2	1:C:97:ARG:NH1	2.36	0.40
1:D:123:PRO:HG2	1:E:227:GLN:O	2.21	0.40
1:D:309:ILE:O	1:D:328:TYR:HA	2.20	0.40
1:E:188:MET:HB2	1:E:214:SER:HB2	2.02	0.40
1:A:176:LYS:HZ1	1:A:275:HIS:CE1	2.39	0.40
1:A:6:LEU:CD2	1:A:6:LEU:C	2.88	0.40
1:B:104:THR:O	1:B:106:LEU:CD1	2.70	0.40
1:B:166:VAL:HG13	1:B:308:PHE:HB3	2.02	0.40
1:B:168:VAL:HA	1:B:310:MET:O	2.21	0.40
1:B:194:ILE:HG12	1:B:269:PRO:HG2	2.03	0.40
1:D:195:LYS:HE3	1:D:195:LYS:HB3	1.51	0.40
1:D:314:LEU:CD1	1:D:322:LEU:HD13	2.50	0.40
1:D:43:ILE:C	1:D:44:ILE:HD12	2.42	0.40
1:D:27:PHE:CD2	1:D:77:TRP:HE3	2.38	0.40
1:A:149:ILE:O	1:A:326:ARG:NH1	2.32	0.40
1:B:154:GLU:OE1	1:B:154:GLU:N	2.33	0.40
1:B:43:ILE:H	1:B:43:ILE:HD12	1.84	0.40
1:B:53:LYS:HE2	1:C:244:ASN:OD1	2.21	0.40
1:D:274:VAL:HG11	1:D:282:VAL:HG13	2.02	0.40
1:D:250:GLU:CD	1:D:275:HIS:CD2	2.95	0.40
1:D:295:ARG:O	1:D:299:ILE:HG13	2.21	0.40
1:D:322:LEU:HD23	1:D:322:LEU:HA	1.89	0.40
1:E:252:ARG:HA	1:E:252:ARG:HD2	1.68	0.40
1:A:223:GLN:NE2	1:A:226:GLU:OE2	2.54	0.40
1:C:139:ILE:HD13	1:C:206:GLU:HG2	2.04	0.40
1:D:43:ILE:HD13	1:E:197:HIS:CD2	2.57	0.40
1:D:10:GLU:OE1	1:D:61:LEU:HD23	2.21	0.40
1:D:76:LEU:CD2	1:D:82:SER:HA	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:205:ILE:N	1:E:206:GLU:OE2	2.54	0.40
1:F:125:TYR:CZ	1:F:128:GLY:HA2	2.56	0.40
1:F:198:LEU:HB2	1:F:219:ILE:CD1	2.51	0.40
1:F:44:ILE:HD13	1:F:74:ILE:HG21	2.04	0.40
1:A:60:THR:HG22	1:A:61:LEU:N	2.37	0.40
1:B:159:MET:HG2	1:B:308:PHE:CD1	2.57	0.40
1:B:251:LEU:HD13	1:B:272:ALA:CB	2.52	0.40
1:C:27:PHE:CZ	1:C:136:MET:HE1	2.57	0.40
1:D:24:GLU:HA	1:D:77:TRP:CE3	2.57	0.40
1:E:223:GLN:H	1:E:227:GLN:NE2	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:THR:CG2	1:D:374:GLY:CA[1_656]	2.19	0.01

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	386/402 (96%)	364 (94%)	18 (5%)	4 (1%)	15	27
1	B	382/402 (95%)	363 (95%)	16 (4%)	3 (1%)	19	34
1	C	383/402 (95%)	358 (94%)	21 (6%)	4 (1%)	15	27
1	D	383/402 (95%)	366 (96%)	12 (3%)	5 (1%)	12	21
1	E	383/402 (95%)	358 (94%)	21 (6%)	4 (1%)	15	27
1	F	384/402 (96%)	356 (93%)	24 (6%)	4 (1%)	15	27
All	All	2301/2412 (95%)	2165 (94%)	112 (5%)	24 (1%)	15	27

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	PRO
1	A	203	ASP
1	B	203	ASP
1	B	229	SER
1	C	14	GLU
1	C	203	ASP
1	D	127	GLN
1	D	203	ASP
1	D	205	ILE
1	E	14	GLU
1	E	203	ASP
1	F	8	ILE
1	F	203	ASP
1	A	342	LEU
1	D	38	GLU
1	F	14	GLU
1	F	91	LYS
1	A	229	SER
1	B	64	ARG
1	E	91	LYS
1	C	353	ARG
1	E	205	ILE
1	C	248	ILE
1	D	224	ILE

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	334/351 (95%)	289 (86%)	45 (14%)	4 5
1	B	329/351 (94%)	289 (88%)	40 (12%)	5 7
1	C	332/351 (95%)	287 (86%)	45 (14%)	3 5
1	D	325/351 (93%)	278 (86%)	47 (14%)	3 4
1	E	327/351 (93%)	285 (87%)	42 (13%)	4 6
1	F	335/351 (95%)	303 (90%)	32 (10%)	8 14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1982/2106 (94%)	1731 (87%)	251 (13%)	4 7

All (251) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	19	SER
1	A	31	VAL
1	A	64	ARG
1	A	66	LEU
1	A	73	ARG
1	A	83	SER
1	A	86	THR
1	A	87	GLU
1	A	92	LYS
1	A	96	THR
1	A	100	VAL
1	A	105	LYS
1	A	106	LEU
1	A	131	THR
1	A	133	GLU
1	A	151	LEU
1	A	173	SER
1	A	176	LYS
1	A	177	SER
1	A	180	PHE
1	A	197	HIS
1	A	200	THR
1	A	223	GLN
1	A	224	ILE
1	A	228	PHE
1	A	240	ARG
1	A	247	MET
1	A	252	ARG
1	A	274	VAL
1	A	280	SER
1	A	282	VAL
1	A	283	MET
1	A	284	ARG
1	A	285	ARG
1	A	289	ARG
1	A	307	ARG

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Mol	Chain	Res	Type
1	A	316	ARG
1	A	317	LYS
1	A	344	ASP
1	A	345	MET
1	A	350	SER
1	A	363	PHE
1	A	369	ARG
1	A	377	ASP
1	B	14	GLU
1	B	15	TYR
1	B	35	LEU
1	B	45	LYS
1	B	57	THR
1	B	64	ARG
1	B	69	ASN
1	B	73	ARG
1	B	88	LEU
1	B	91	LYS
1	B	92	LYS
1	B	99	GLU
1	B	119	VAL
1	B	133	GLU
1	B	134	ILE
1	B	146	LEU
1	B	155	LEU
1	B	173	SER
1	B	180	PHE
1	B	185	ARG
1	B	187	ILE
1	B	197	HIS
1	B	224	ILE
1	B	228	PHE
1	B	240	ARG
1	B	245	LEU
1	B	251	LEU
1	B	252	ARG
1	B	273	THR
1	B	277	GLN
1	B	285	ARG
1	B	289	ARG
1	B	312	GLN
1	B	313	THR

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Mol	Chain	Res	Type
1	B	316	ARG
1	B	348	VAL
1	B	354	ARG
1	B	372	SER
1	B	375	ILE
1	B	386	MET
1	C	8	ILE
1	C	14	GLU
1	C	15	TYR
1	C	43	ILE
1	C	46	GLN
1	C	51	SER
1	C	68	PHE
1	C	70	GLU
1	C	71	ILE
1	C	73	ARG
1	C	76	LEU
1	C	82	SER
1	C	83	SER
1	C	85	LEU
1	C	87	GLU
1	C	88	LEU
1	C	94	ILE
1	C	97	ARG
1	C	107	THR
1	C	137	ARG
1	C	139	ILE
1	C	142	ASP
1	C	176	LYS
1	C	180	PHE
1	C	181	SER
1	C	216	HIS
1	C	224	ILE
1	C	229	SER
1	C	236	GLN
1	C	239	LEU
1	C	240	ARG
1	C	247	MET
1	C	252	ARG
1	C	273	THR
1	C	276	SER
1	C	289	ARG

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Mol	Chain	Res	Type
1	C	312	GLN
1	C	319	ASP
1	C	322	LEU
1	C	338	GLN
1	C	354	ARG
1	C	363	PHE
1	C	369	ARG
1	C	373	ASP
1	C	387	MET
1	D	9	LEU
1	D	10	GLU
1	D	26	GLN
1	D	29	ASP
1	D	40	SER
1	D	42	ILE
1	D	46	GLN
1	D	57	THR
1	D	66	LEU
1	D	71	ILE
1	D	87	GLU
1	D	93	LEU
1	D	94	ILE
1	D	100	VAL
1	D	126	ILE
1	D	129	LYS
1	D	131	THR
1	D	136	MET
1	D	139	ILE
1	D	141	LEU
1	D	149	ILE
1	D	162	ASP
1	D	177	SER
1	D	180	PHE
1	D	185	ARG
1	D	194	ILE
1	D	195	LYS
1	D	224	ILE
1	D	226	GLU
1	D	230	SER
1	D	236	GLN
1	D	252	ARG
1	D	257	ILE

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Mol	Chain	Res	Type
1	D	305	THR
1	D	312	GLN
1	D	317	LYS
1	D	319	ASP
1	D	327	GLU
1	D	337	GLU
1	D	340	LEU
1	D	342	LEU
1	D	350	SER
1	D	351	GLU
1	D	369	ARG
1	D	373	ASP
1	D	382	LYS
1	D	386	MET
1	E	5	HIS
1	E	6	LEU
1	E	9	LEU
1	E	10	GLU
1	E	11	PHE
1	E	14	GLU
1	E	15	TYR
1	E	26	GLN
1	E	57	THR
1	E	58	LEU
1	E	64	ARG
1	E	68	PHE
1	E	71	ILE
1	E	76	LEU
1	E	85	LEU
1	E	87	GLU
1	E	88	LEU
1	E	91	LYS
1	E	92	LYS
1	E	93	LEU
1	E	96	THR
1	E	104	THR
1	E	130	THR
1	E	131	THR
1	E	142	ASP
1	E	172	THR
1	E	173	SER
1	E	174	SER

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Mol	Chain	Res	Type
1	E	180	PHE
1	E	211	ASN
1	E	213	LYS
1	E	229	SER
1	E	233	ILE
1	E	241	ARG
1	E	252	ARG
1	E	254	LYS
1	E	273	THR
1	E	316	ARG
1	E	329	LEU
1	E	357	ASP
1	E	377	ASP
1	E	383	ARG
1	F	5	HIS
1	F	14	GLU
1	F	51	SER
1	F	62	SER
1	F	68	PHE
1	F	85	LEU
1	F	107	THR
1	F	111	GLN
1	F	113	GLN
1	F	118	ARG
1	F	119	VAL
1	F	129	LYS
1	F	141	LEU
1	F	142	ASP
1	F	144	LEU
1	F	172	THR
1	F	177	SER
1	F	178	THR
1	F	180	PHE
1	F	197	HIS
1	F	223	GLN
1	F	224	ILE
1	F	239	LEU
1	F	247	MET
1	F	248	ILE
1	F	252	ARG
1	F	289	ARG
1	F	312	GLN

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Mol	Chain	Res	Type
1	F	327	GLU
1	F	351	GLU
1	F	358	GLU
1	F	385	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	GLN
1	A	216	HIS
1	A	227	GLN
1	A	278	ASN
1	A	321	ASN
1	B	23	HIS
1	B	26	GLN
1	B	37	HIS
1	B	69	ASN
1	B	102	HIS
1	B	197	HIS
1	B	227	GLN
1	B	275	HIS
1	B	338	GLN
1	C	46	GLN
1	C	69	ASN
1	C	235	ASN
1	C	312	GLN
1	C	338	GLN
1	D	26	GLN
1	D	95	ASN
1	D	216	HIS
1	D	223	GLN
1	D	244	ASN
1	D	277	GLN
1	E	102	HIS
1	E	255	GLN
1	E	275	HIS
1	E	277	GLN
1	F	26	GLN
1	F	37	HIS
1	F	111	GLN
1	F	157	ASN
1	F	197	HIS

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Mol	Chain	Res	Type
1	F	223	GLN
1	F	379	HIS

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	388/402 (96%)	0.24	19 (4%)	29	36	48, 71, 107, 135	0
1	B	384/402 (95%)	0.20	10 (2%)	56	65	49, 76, 112, 128	0
1	C	385/402 (95%)	0.29	17 (4%)	34	41	50, 71, 100, 117	0
1	D	385/402 (95%)	0.52	32 (8%)	11	13	51, 79, 131, 156	0
1	E	385/402 (95%)	0.18	8 (2%)	63	72	47, 71, 99, 144	0
1	F	386/402 (96%)	0.22	8 (2%)	63	72	40, 66, 99, 120	0
All	All	2313/2412 (95%)	0.27	94 (4%)	37	44	40, 72, 113, 156	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	34	PHE	5.7
1	D	61	LEU	5.6
1	E	109	GLY	5.4
1	D	29	ASP	5.3
1	A	109	GLY	5.2
1	A	113	GLN	4.8
1	A	112	LYS	4.6
1	E	81	SER	4.6
1	D	27	PHE	4.5
1	A	173	SER	4.2
1	A	174	SER	4.1
1	F	82	SER	4.1
1	D	11	PHE	4.1
1	A	105	LYS	4.0
1	D	10	GLU	4.0
1	A	103	PRO	3.9
1	A	107	THR	3.5
1	D	50	ILE	3.5
1	F	343	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	80	GLY	3.5
1	D	46	GLN	3.2
1	F	31	VAL	3.2
1	A	343	SER	3.2
1	D	86	THR	3.1
1	B	17	TYR	3.1
1	D	17	TYR	3.0
1	D	104	THR	3.0
1	C	105	LYS	2.9
1	E	110	GLY	2.9
1	B	115	PHE	2.9
1	A	104	THR	2.9
1	E	334	ASP	2.9
1	D	60	THR	2.9
1	C	46	GLN	2.8
1	E	342	LEU	2.8
1	C	5	HIS	2.7
1	A	110	GLY	2.7
1	C	103	PRO	2.6
1	D	14	GLU	2.6
1	C	381	ALA	2.6
1	D	204	PRO	2.6
1	A	106	LEU	2.6
1	F	370	LEU	2.5
1	D	21	PHE	2.5
1	F	20	THR	2.5
1	F	203	ASP	2.5
1	A	172	THR	2.5
1	D	47	GLY	2.5
1	B	343	SER	2.5
1	D	62	SER	2.4
1	C	368	GLU	2.4
1	E	359	PHE	2.4
1	B	10	GLU	2.4
1	D	110	GLY	2.4
1	D	320	GLY	2.4
1	B	345	MET	2.4
1	A	204	PRO	2.4
1	C	375	ILE	2.4
1	E	343	SER	2.3
1	A	11	PHE	2.3
1	C	71	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	129	LYS	2.3
1	D	102	HIS	2.3
1	C	81	SER	2.3
1	D	9	LEU	2.3
1	F	224	ILE	2.3
1	C	11	PHE	2.3
1	F	21	PHE	2.3
1	A	171	LYS	2.3
1	A	60	THR	2.3
1	C	224	ILE	2.2
1	D	41	ASP	2.2
1	B	107	THR	2.2
1	D	15	TYR	2.2
1	B	71	ILE	2.2
1	D	8	ILE	2.2
1	C	387	MET	2.2
1	B	62	SER	2.2
1	C	16	ARG	2.2
1	C	370	LEU	2.2
1	D	26	GLN	2.2
1	E	379	HIS	2.2
1	D	13	THR	2.2
1	D	213	LYS	2.1
1	D	38	GLU	2.1
1	B	44	ILE	2.1
1	D	7	PRO	2.1
1	D	347	LYS	2.1
1	C	104	THR	2.1
1	D	31	VAL	2.1
1	A	248	ILE	2.1
1	D	12	LYS	2.0
1	C	388	SER	2.0
1	B	79	SER	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.