



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:46 AM UTC

PDB ID : 7LZ4 / pdb_00007lz4
Title : Crystal structure of A211D mutant of Protein Kinase A RIa subunit, a Carney Complex mutation
Authors : Del Rio, J.; Wu, J.; Taylor, S.S.
Deposited on : 2021-03-08
Resolution : 4.16 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

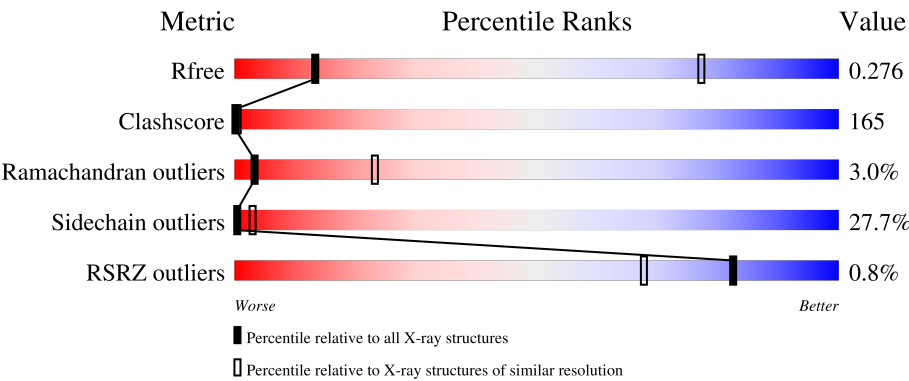
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.16 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



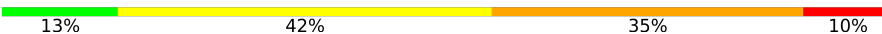
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1077 (4.50-3.82)
Clashscore	190562	1019 (4.48-3.84)
Ramachandran outliers	187476	1035 (4.50-3.82)
Sidechain outliers	187428	1022 (4.50-3.82)
RSRZ outliers	180081	1074 (4.50-3.82)

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

Mol	Chain	Length	Quality of chain
1	A	269	2% 12%47%31%9%
1	B	269	% 11%48%33%7%
1	C	269	% 12%44%32%12%
1	D	269	% 11%51%29%8%
1	E	269	11%55%29%

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Mol	Chain	Length	Quality of chain
1	F	269	
1	G	269	
1	H	269	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CMP	A	401	-	-	X	-
2	CMP	A	402	-	-	X	-
2	CMP	B	401	-	-	X	-
2	CMP	B	402	-	-	X	-
2	CMP	C	401	-	-	X	-
2	CMP	C	402	-	-	X	-
2	CMP	D	401	-	-	X	-
2	CMP	D	402	-	-	X	-
2	CMP	E	401	-	-	X	-
2	CMP	E	402	-	-	X	-
2	CMP	F	401	-	-	X	-
2	CMP	F	402	-	-	X	-
2	CMP	G	401	-	-	X	-
2	CMP	G	402	-	-	X	-
2	CMP	H	401	-	-	X	-
2	CMP	H	402	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 17138 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.

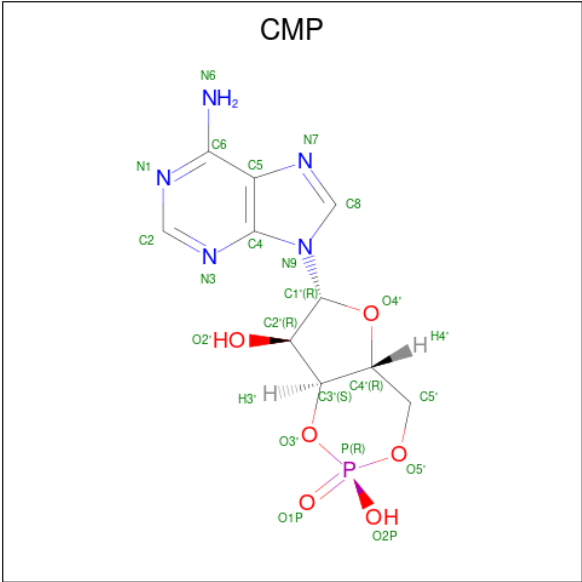
- Molecule 1 is a protein called cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	B	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	C	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	D	266	Total	C	N	O	S	0	0	0
			2086	1325	356	397	8			
1	E	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	F	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	G	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			
1	H	268	Total	C	N	O	S	0	0	0
			2100	1333	358	401	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	211	ASP	ALA	engineered mutation	UNP P00514
B	211	ASP	ALA	engineered mutation	UNP P00514
C	211	ASP	ALA	engineered mutation	UNP P00514
D	211	ASP	ALA	engineered mutation	UNP P00514
E	211	ASP	ALA	engineered mutation	UNP P00514
F	211	ASP	ALA	engineered mutation	UNP P00514
G	211	ASP	ALA	engineered mutation	UNP P00514
H	211	ASP	ALA	engineered mutation	UNP P00514

- Molecule 2 is ADENOSINE-3',5'-CYCLIC-MONOPHOSPHATE (CCD ID: CMP) (formula: $C_{10}H_{12}N_5O_6P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	C	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	C	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	D	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	D	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	E	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	E	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	F	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	F	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	G	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	G	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

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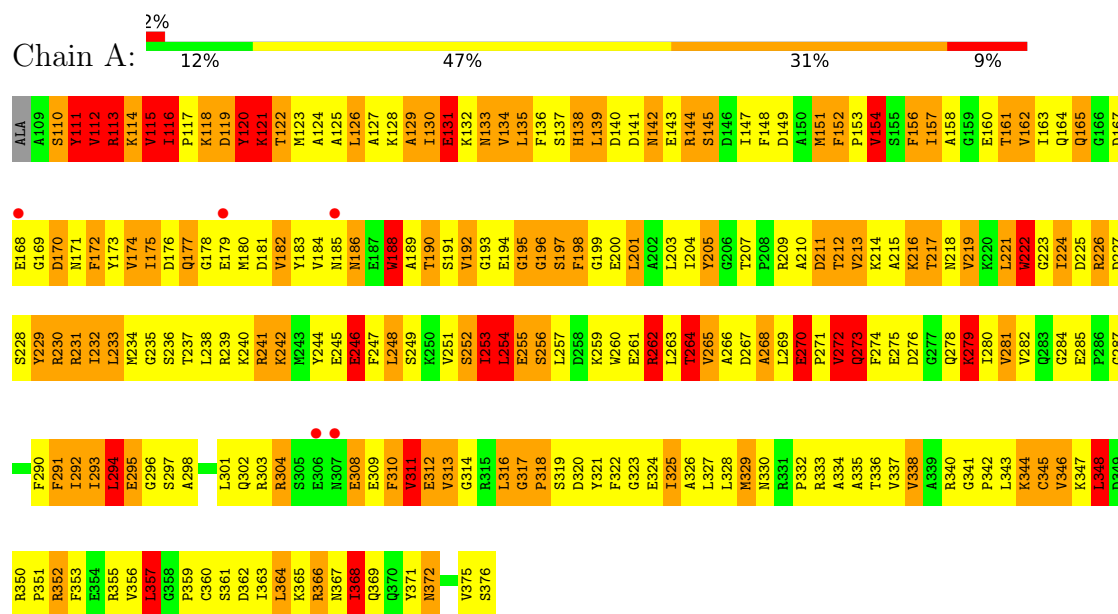
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	C	N	O	P	0	0
			22	10	5	6	1		
2	H	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

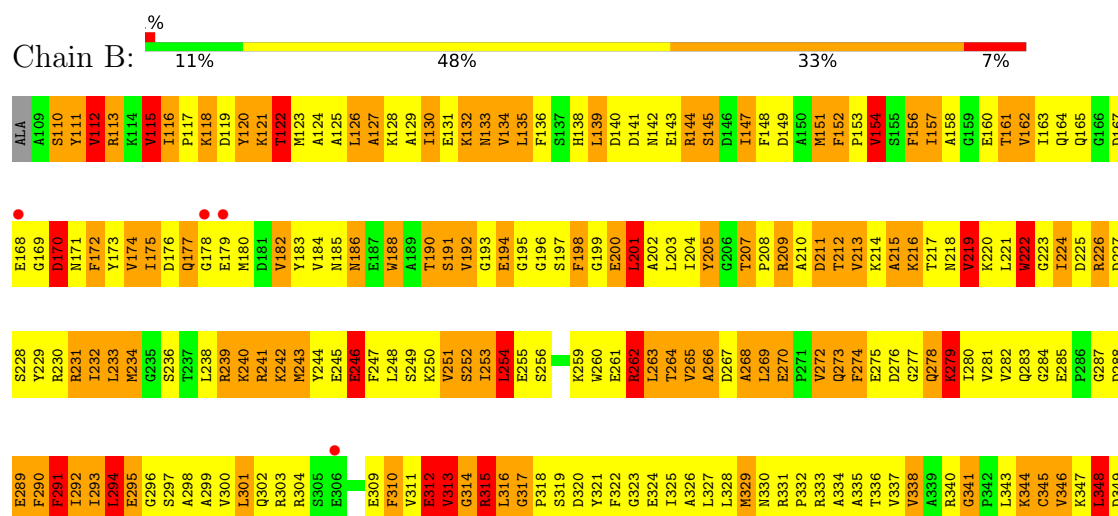
3 Residue-property plots

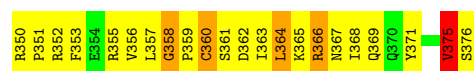
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

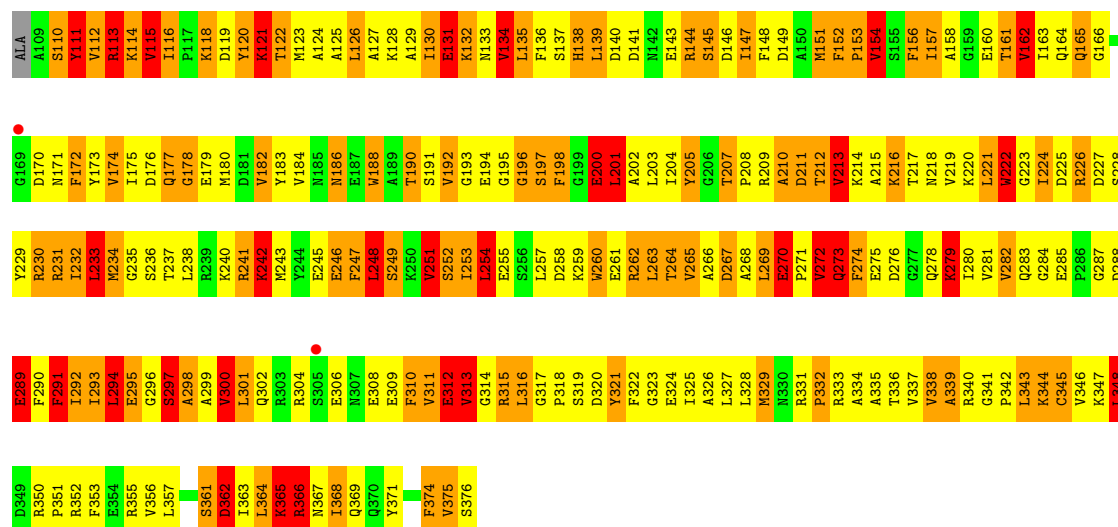


- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed

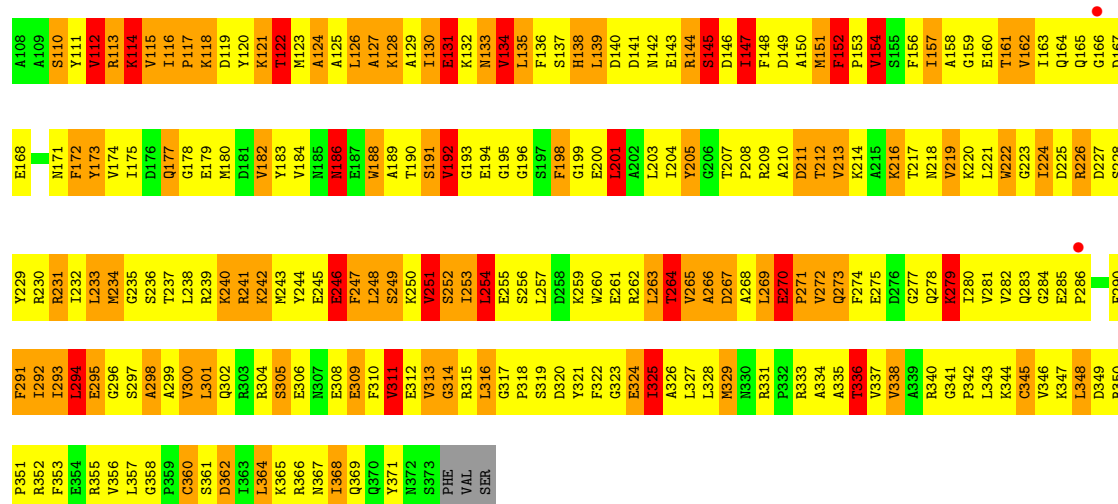
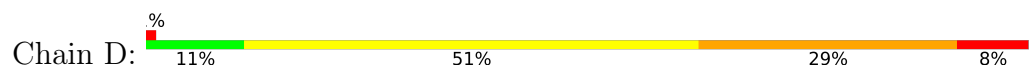




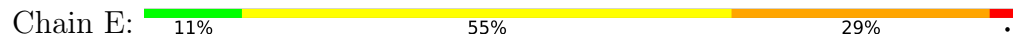
- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed





E354
R355
V356
L357
G358
P359
C360
S361
D362
I363
L364
K365
R366
N367
I368
Q369
Y371
N372
S373
F374
V375
S376

- Molecule 1: cAMP-dependent protein kinase type I-alpha regulatory subunit, N-terminally processed



ALA
A109
S110
Y111
V112
R113
K114
V115
I116
P117
K118
D119
M120
K121
T122
M123
A124
A125
L126
A127
K128
A129
I130
E131
K132
N133
V134
L135
F136
S137
H138
L139
D140
E141
N142
E143
R144
S145
D146
I147
F148
D149
A150
M151
F152
P153
V154
S155
F156
I157
A158
G159
E160
T161
L162
V163
Q164
Q165
G166
D167

E168
G169
D170
N171
F172
Y173
V174
I175
D176
Q177
K178
E179
M180
D181
V182
Y183
Y184
N185
L186
E187
W188
A189
T190
S191
V192
G193
E194
L195
G196
S197
F198
G199
E200
L201
A202
L203
I204
Y205
G206
T207
P208
R209
D210
D211
T212
V213
K214
A215
K216
T217
N218
V219
K220
L221
L222
G223
I224
D225
R226
D227

S228
Y229
R230
R231
I232
L233
M234
G235
S236
T237
L238
R239
K240
R241
K242
M243
Y244
E245
E246
F247
L248
S249
K250
V251
S252
L253
E254
E255
S256
L257
D258
K259
W260
E261
L262
L263
T264
V265
A266
D267
A268
L269
E270
P271
V272
Q273
F274
E275
D276
G277
Q278
K279
I280
V281
V282
Q283
G284
E285
P286
D287

D288
E289
F290
F291
I292
L293
L294
E295
G296
S297
A298
A299
V300
L301
Q302
R303
R304
S305
E306
R307
E308
E309
F310
V311
E312
K313
G314
R315
L316
G317
P318
S319
D320
Y321
F322
G323
E324
I325
A326
L327
M328
M329
N330
R331
P332
R333
A334
A335
T336
V337
V338
A339
R340
G341
P342
L343
K344
C345
V346
K347

L348
D349
R350
P351
R352
F353
E354
R355
V356
L357
C360
S361
D362
I363
L364
K365
R366
N367
I368
Q369
Y371
F374
V375
S376

4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	176.79Å 176.79Å 345.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.25 – 4.16 48.25 – 4.16	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.25-4.16) 99.4 (48.25-4.16)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.7 _650	Depositor
R, R_{free}	0.221 , 0.270 0.228 , 0.276	Depositor DCC
R_{free} test set	1539 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	125.7	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 158.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.418 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	17138	wwPDB-VP
Average B, all atoms (Å ²)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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 ⓘ

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

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	1.72	33/2138 (1.5%)	1.97	93/2887 (3.2%)
1	B	1.68	30/2138 (1.4%)	1.93	75/2887 (2.6%)
1	C	1.57	21/2138 (1.0%)	2.01	90/2887 (3.1%)
1	D	1.57	20/2124 (0.9%)	1.91	71/2869 (2.5%)
1	E	1.40	19/2138 (0.9%)	1.77	54/2887 (1.9%)
1	F	1.51	23/2138 (1.1%)	1.88	77/2887 (2.7%)
1	G	1.90	58/2138 (2.7%)	2.31	126/2887 (4.4%)
1	H	1.56	22/2138 (1.0%)	1.91	74/2887 (2.6%)
All	All	1.62	226/17090 (1.3%)	1.97	660/23078 (2.9%)

All (226) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	112	VAL	CA-CB	19.77	1.81	1.54
1	A	112	VAL	CA-C	17.31	1.74	1.52
1	G	272	VAL	CA-CB	-13.99	1.45	1.55
1	F	192	VAL	CA-CB	-13.03	1.37	1.54
1	B	113	ARG	CA-C	12.57	1.68	1.52
1	E	192	VAL	CA-CB	-11.61	1.40	1.54
1	F	375	VAL	CA-CB	11.21	1.65	1.55
1	B	241	ARG	CZ-NH1	11.15	1.48	1.32
1	G	131	GLU	CB-CG	-10.55	1.20	1.52
1	F	318	PRO	CG-CD	10.49	1.86	1.50
1	D	114	LYS	N-CA	10.45	1.59	1.46
1	G	131	GLU	N-CA	10.38	1.58	1.46
1	A	115	VAL	CA-CB	-10.24	1.40	1.54
1	G	121	LYS	CB-CG	-9.60	1.23	1.52
1	E	318	PRO	N-CA	9.58	1.59	1.47
1	G	130	ILE	CA-CB	9.02	1.64	1.54
1	G	361	SER	N-CA	9.00	1.57	1.46
1	F	317	GLY	C-O	-8.82	1.12	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	115	VAL	CA-CB	-8.82	1.43	1.54
1	B	154	VAL	CA-CB	-8.81	1.42	1.54
1	G	192	VAL	CA-CB	-8.71	1.43	1.54
1	D	152	PHE	CE1-CZ	-8.64	1.12	1.38
1	A	311	VAL	CA-CB	-8.63	1.46	1.55
1	G	141	ASP	C-N	8.58	1.45	1.33
1	B	241	ARG	CB-CG	-8.48	1.26	1.52
1	A	113	ARG	N-CA	8.44	1.56	1.46
1	D	115	VAL	N-CA	8.38	1.56	1.46
1	A	372	ASN	CG-ND2	-8.36	1.15	1.33
1	A	154	VAL	CA-CB	-8.30	1.43	1.54
1	A	113	ARG	CA-C	8.26	1.61	1.52
1	G	230	ARG	CA-C	-8.23	1.42	1.52
1	D	192	VAL	CA-CB	-8.19	1.43	1.54
1	H	288	ASP	CG-OD1	-8.13	1.09	1.25
1	A	172	PHE	CA-C	-8.13	1.43	1.52
1	D	152	PHE	CG-CD2	-8.12	1.21	1.38
1	D	269	LEU	CA-C	-8.07	1.42	1.53
1	C	265	VAL	CA-CB	-8.05	1.45	1.54
1	G	289	GLU	CB-CG	-7.82	1.28	1.52
1	G	240	LYS	CA-C	-7.80	1.42	1.52
1	H	288	ASP	CB-CG	-7.80	1.32	1.52
1	H	268	ALA	CA-CB	-7.69	1.40	1.53
1	G	141	ASP	C-O	-7.66	1.14	1.24
1	F	127	ALA	CA-CB	-7.64	1.41	1.53
1	G	172	PHE	CA-C	-7.63	1.43	1.52
1	C	192	VAL	CA-CB	-7.52	1.44	1.53
1	D	152	PHE	CE2-CZ	-7.50	1.16	1.38
1	B	172	PHE	CA-C	-7.37	1.43	1.52
1	A	192	VAL	CA-CB	-7.32	1.45	1.54
1	D	114	LYS	CA-C	7.30	1.62	1.52
1	D	152	PHE	CG-CD1	-7.30	1.23	1.38
1	G	127	ALA	CA-CB	-7.17	1.42	1.53
1	F	316	LEU	CA-C	-7.17	1.43	1.52
1	D	127	ALA	CA-CB	-7.16	1.41	1.53
1	H	192	VAL	CA-CB	-7.14	1.44	1.53
1	B	192	VAL	CA-CB	-7.13	1.44	1.53
1	E	318	PRO	CA-CB	7.09	1.63	1.53
1	B	113	ARG	N-CA	7.08	1.55	1.46
1	G	272	VAL	CA-C	7.07	1.59	1.52
1	G	131	GLU	CG-CD	-7.05	1.34	1.52
1	C	132	LYS	CA-C	-6.96	1.42	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	290	PHE	CA-C	-6.93	1.44	1.52
1	A	197	SER	CA-C	-6.89	1.44	1.52
1	A	175	ILE	CA-CB	6.88	1.62	1.54
1	B	241	ARG	CZ-NH2	6.86	1.42	1.33
1	D	130	ILE	C-O	-6.86	1.16	1.24
1	F	172	PHE	CA-C	-6.82	1.44	1.52
1	C	174	VAL	CA-CB	-6.78	1.45	1.54
1	G	241	ARG	N-CA	-6.74	1.38	1.46
1	G	131	GLU	CA-CB	-6.70	1.43	1.53
1	H	197	SER	CA-C	-6.67	1.44	1.52
1	B	182	VAL	CA-CB	-6.66	1.45	1.54
1	G	314	GLY	CA-C	6.58	1.58	1.51
1	G	174	VAL	CA-CB	-6.57	1.46	1.54
1	H	265	VAL	CA-CB	-6.54	1.47	1.54
1	G	252	SER	N-CA	6.53	1.54	1.46
1	G	279	LYS	CD-CE	-6.53	1.32	1.52
1	E	114	LYS	N-CA	6.50	1.53	1.45
1	E	158	ALA	CA-CB	-6.47	1.43	1.53
1	G	114	LYS	N-CA	6.45	1.54	1.46
1	H	278	GLN	CD-NE2	-6.45	1.19	1.33
1	E	118	LYS	CA-C	6.42	1.61	1.52
1	E	318	PRO	N-CD	6.41	1.56	1.47
1	H	278	GLN	CB-CG	-6.39	1.33	1.52
1	E	232	ILE	CA-CB	-6.38	1.46	1.54
1	F	317	GLY	CA-C	6.36	1.61	1.51
1	H	278	GLN	CD-OE1	-6.34	1.11	1.23
1	A	112	VAL	CB-CG2	6.33	1.73	1.52
1	F	318	PRO	N-CD	-6.28	1.39	1.47
1	B	118	LYS	CA-C	6.27	1.61	1.52
1	A	116	ILE	CA-CB	-6.27	1.46	1.54
1	A	130	ILE	C-O	-6.24	1.17	1.24
1	G	331	ARG	N-CA	-6.24	1.40	1.45
1	G	375	VAL	CA-CB	6.24	1.62	1.54
1	F	331	ARG	CB-CG	-6.21	1.33	1.52
1	F	127	ALA	N-CA	-6.21	1.39	1.46
1	A	142	ASN	CG-ND2	-6.21	1.20	1.33
1	G	234	MET	CA-C	-6.21	1.44	1.52
1	H	172	PHE	CA-C	-6.19	1.45	1.52
1	D	251	VAL	CA-CB	6.18	1.61	1.54
1	G	270	GLU	CB-CG	-6.18	1.33	1.52
1	B	222	TRP	N-CA	-6.16	1.38	1.46
1	G	278	GLN	CD-NE2	-6.15	1.20	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	141	ASP	CA-CB	-6.12	1.43	1.53
1	F	285	GLU	CG-CD	-6.12	1.36	1.52
1	C	321	TYR	CA-C	-6.11	1.45	1.52
1	D	115	VAL	CA-C	6.10	1.60	1.52
1	A	222	TRP	N-CA	-6.10	1.39	1.46
1	B	291	PHE	CA-C	-6.02	1.45	1.52
1	B	161	THR	CA-CB	-6.00	1.44	1.53
1	G	115	VAL	CA-C	5.99	1.60	1.52
1	B	246	GLU	CA-C	-5.98	1.44	1.52
1	G	241	ARG	CB-CG	-5.97	1.34	1.52
1	E	216	LYS	CA-C	-5.96	1.46	1.53
1	C	241	ARG	CA-C	-5.94	1.45	1.52
1	C	282	VAL	CA-CB	-5.92	1.47	1.54
1	E	190	THR	CA-CB	5.89	1.63	1.53
1	C	339	ALA	CA-CB	-5.88	1.45	1.53
1	G	270	GLU	C-O	-5.88	1.19	1.24
1	B	241	ARG	CA-CB	-5.88	1.44	1.53
1	G	154	VAL	CA-CB	-5.87	1.46	1.54
1	H	298	ALA	CA-CB	-5.87	1.43	1.53
1	C	172	PHE	CA-C	-5.87	1.45	1.52
1	C	298	ALA	CA-CB	-5.86	1.43	1.53
1	F	318	PRO	C-O	5.85	1.31	1.24
1	A	303	ARG	CA-C	5.83	1.59	1.52
1	F	124	ALA	CA-CB	-5.83	1.43	1.53
1	E	124	ALA	CA-CB	-5.83	1.43	1.53
1	A	188	TRP	CA-CB	5.82	1.62	1.53
1	H	375	VAL	CA-C	5.82	1.60	1.52
1	G	331	ARG	CA-C	-5.81	1.46	1.52
1	G	115	VAL	N-CA	5.79	1.53	1.46
1	G	173	TYR	CA-C	5.79	1.59	1.52
1	A	127	ALA	CA-CB	-5.79	1.44	1.53
1	H	189	ALA	CA-CB	-5.78	1.45	1.53
1	A	241	ARG	CA-C	-5.77	1.45	1.52
1	H	339	ALA	CA-CB	-5.76	1.45	1.53
1	C	291	PHE	CA-C	-5.75	1.45	1.52
1	D	131	GLU	CB-CG	-5.74	1.35	1.52
1	C	154	VAL	CA-CB	-5.74	1.46	1.54
1	E	213	VAL	CA-C	5.74	1.59	1.52
1	H	222	TRP	N-CA	-5.71	1.39	1.46
1	G	141	ASP	N-CA	5.71	1.53	1.46
1	G	348	LEU	CA-C	-5.70	1.46	1.52
1	B	303	ARG	CA-C	5.69	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	372	ASN	CG-ND2	-5.69	1.21	1.33
1	B	147	ILE	CA-CB	-5.66	1.47	1.54
1	C	253	ILE	CA-CB	-5.65	1.46	1.54
1	G	185	ASN	CG-ND2	-5.64	1.21	1.33
1	C	114	LYS	N-CA	5.63	1.53	1.45
1	H	216	LYS	C-O	-5.63	1.18	1.23
1	F	158	ALA	CA-CB	-5.62	1.44	1.53
1	G	265	VAL	CA-C	-5.62	1.46	1.52
1	E	189	ALA	CA-CB	-5.61	1.45	1.53
1	F	130	ILE	CA-CB	5.55	1.62	1.54
1	G	192	VAL	CA-C	-5.55	1.45	1.52
1	D	162	VAL	CA-CB	-5.54	1.46	1.54
1	D	271	PRO	CA-C	-5.54	1.46	1.52
1	A	129	ALA	CA-CB	-5.52	1.44	1.53
1	A	372	ASN	CG-OD1	-5.50	1.13	1.23
1	A	265	VAL	CA-CB	-5.50	1.48	1.54
1	G	141	ASP	CA-C	-5.48	1.45	1.52
1	C	222	TRP	N-CA	-5.46	1.39	1.46
1	E	375	VAL	CA-C	5.45	1.59	1.52
1	G	153	PRO	CA-C	-5.45	1.45	1.52
1	E	216	LYS	C-O	-5.45	1.18	1.23
1	A	142	ASN	CG-OD1	-5.43	1.13	1.23
1	A	318	PRO	CA-C	5.43	1.59	1.52
1	D	241	ARG	CA-C	-5.42	1.46	1.52
1	B	294	LEU	CA-C	-5.41	1.48	1.52
1	H	313	VAL	CA-CB	5.41	1.60	1.54
1	F	319	SER	CA-C	5.40	1.60	1.52
1	A	246	GLU	CA-C	-5.40	1.45	1.52
1	B	279	LYS	N-CA	-5.39	1.39	1.46
1	A	131	GLU	N-CA	5.37	1.53	1.46
1	H	230	ARG	CA-C	-5.37	1.45	1.52
1	F	269	LEU	CA-C	-5.37	1.46	1.53
1	B	215	ALA	CA-CB	-5.37	1.45	1.53
1	D	154	VAL	CA-C	-5.36	1.46	1.52
1	G	241	ARG	CA-C	-5.36	1.46	1.52
1	G	158	ALA	CA-CB	-5.36	1.44	1.53
1	G	288	ASP	CG-OD1	-5.34	1.15	1.25
1	G	242	LYS	CA-C	-5.33	1.46	1.52
1	G	278	GLN	CB-CG	-5.33	1.36	1.52
1	B	266	ALA	CA-CB	-5.33	1.45	1.53
1	G	127	ALA	CA-C	-5.32	1.46	1.52
1	C	190	THR	CA-CB	5.32	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	350	ARG	N-CA	-5.31	1.42	1.46
1	G	278	GLN	CG-CD	-5.30	1.38	1.52
1	F	375	VAL	CA-C	5.29	1.60	1.53
1	G	121	LYS	N-CA	-5.29	1.40	1.46
1	B	190	THR	CA-CB	5.28	1.62	1.53
1	G	357	LEU	N-CA	-5.26	1.39	1.46
1	C	197	SER	CA-C	-5.26	1.46	1.52
1	G	152	PHE	CG-CD2	-5.26	1.27	1.38
1	F	114	LYS	N-CA	5.24	1.52	1.46
1	A	219	VAL	CA-CB	-5.23	1.46	1.55
1	H	190	THR	CA-CB	5.22	1.62	1.53
1	B	132	LYS	CA-C	-5.22	1.45	1.52
1	D	266	ALA	CA-CB	-5.19	1.45	1.53
1	B	216	LYS	CA-C	-5.19	1.47	1.53
1	E	154	VAL	CA-CB	-5.19	1.47	1.54
1	A	118	LYS	CA-C	5.19	1.59	1.52
1	F	318	PRO	CA-C	5.18	1.59	1.52
1	F	285	GLU	CD-OE1	-5.16	1.15	1.25
1	B	175	ILE	CA-CB	5.15	1.60	1.54
1	G	152	PHE	CG-CD1	-5.14	1.28	1.38
1	B	239	ARG	CA-C	-5.14	1.47	1.53
1	A	161	THR	CA-CB	-5.12	1.46	1.53
1	C	240	LYS	CA-C	-5.11	1.46	1.52
1	E	318	PRO	CG-CD	5.11	1.68	1.50
1	G	190	THR	CA-C	5.10	1.59	1.52
1	B	127	ALA	CA-CB	-5.09	1.45	1.53
1	B	209	ARG	CA-C	-5.08	1.46	1.52
1	F	174	VAL	CA-CB	-5.07	1.48	1.54
1	C	313	VAL	N-CA	5.06	1.52	1.46
1	D	279	LYS	CA-CB	-5.06	1.45	1.53
1	H	273	GLN	CD-OE1	-5.06	1.14	1.23
1	E	265	VAL	CA-CB	-5.05	1.49	1.54
1	H	300	VAL	N-CA	-5.05	1.39	1.46
1	A	272	VAL	CA-CB	-5.04	1.47	1.54
1	E	375	VAL	N-CA	5.02	1.52	1.46
1	G	268	ALA	CA-CB	-5.02	1.45	1.53
1	C	210	ALA	CA-CB	-5.02	1.45	1.53
1	G	357	LEU	CG-CD1	-5.01	1.36	1.52
1	A	174	VAL	CA-CB	-5.01	1.48	1.54
1	C	272	VAL	CA-CB	-5.00	1.47	1.54

All (660) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	121	LYS	CA-CB-CG	19.01	152.12	114.10
1	C	115	VAL	CB-CA-C	-16.25	89.87	110.99
1	G	115	VAL	N-CA-C	14.97	129.07	108.11
1	G	121	LYS	CB-CA-C	-14.94	86.00	110.79
1	C	279	LYS	CD-CE-NZ	-14.40	65.81	111.90
1	D	131	GLU	N-CA-C	13.71	126.31	111.36
1	D	115	VAL	N-CA-C	13.39	127.51	108.36
1	A	110	SER	N-CA-C	13.35	125.28	108.45
1	A	113	ARG	N-CA-C	12.66	129.91	108.13
1	B	314	GLY	N-CA-C	12.35	127.11	110.69
1	A	357	LEU	CB-CG-CD1	-12.24	73.97	110.70
1	B	115	VAL	CB-CA-C	-12.22	90.98	110.28
1	E	313	VAL	N-CA-C	12.04	124.46	112.90
1	D	114	LYS	N-CA-C	11.82	128.42	108.20
1	A	279	LYS	CG-CD-CE	-11.72	84.35	111.30
1	G	130	ILE	N-CA-C	11.62	121.58	110.30
1	H	270	GLU	CA-C-N	-11.49	108.44	120.85
1	H	270	GLU	C-N-CA	-11.49	108.44	120.85
1	A	131	GLU	N-CA-C	11.40	125.71	111.69
1	H	240	LYS	N-CA-C	-11.37	98.88	111.28
1	A	115	VAL	CB-CA-C	-11.20	92.92	111.29
1	A	314	GLY	N-CA-C	11.13	129.84	110.80
1	D	270	GLU	CB-CA-C	11.09	125.00	109.92
1	G	231	ARG	CA-C-N	-11.05	109.48	122.63
1	G	231	ARG	C-N-CA	-11.05	109.48	122.63
1	F	110	SER	N-CA-C	-11.04	90.52	108.07
1	D	246	GLU	CB-CA-C	-10.78	93.95	110.88
1	H	231	ARG	CA-C-N	-10.73	112.24	123.08
1	H	231	ARG	C-N-CA	-10.73	112.24	123.08
1	G	121	LYS	N-CA-C	10.64	122.88	111.28
1	F	331	ARG	CB-CA-C	-10.62	93.53	109.56
1	E	216	LYS	N-CA-C	-10.49	94.78	111.04
1	C	242	LYS	CD-CE-NZ	-10.44	78.50	111.90
1	B	279	LYS	N-CA-CB	-10.29	93.10	110.49
1	H	278	GLN	CB-CA-C	-10.26	92.69	110.45
1	C	134	VAL	N-CA-C	10.21	121.08	110.36
1	G	120	TYR	CA-C-N	-10.18	106.64	120.28
1	G	120	TYR	C-N-CA	-10.18	106.64	120.28
1	G	216	LYS	N-CA-C	-10.04	91.07	110.56
1	A	172	PHE	N-CA-C	-9.91	93.87	109.72
1	C	270	GLU	N-CA-CB	9.80	120.90	109.72
1	F	115	VAL	CB-CA-C	-9.75	99.17	110.96
1	A	345	CYS	N-CA-C	9.72	123.62	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	110	SER	N-CA-C	9.72	124.24	108.99
1	F	240	LYS	N-CA-C	-9.69	100.72	111.28
1	E	345	CYS	N-CA-C	9.64	123.50	109.14
1	C	240	LYS	N-CA-C	-9.62	100.80	111.28
1	G	286	PRO	CA-C-N	-9.61	113.80	122.73
1	G	286	PRO	C-N-CA	-9.61	113.80	122.73
1	G	289	GLU	CA-CB-CG	9.51	133.12	114.10
1	C	231	ARG	CA-C-N	-9.50	113.49	123.08
1	C	231	ARG	C-N-CA	-9.50	113.49	123.08
1	C	216	LYS	N-CA-C	-9.34	96.56	111.04
1	G	131	GLU	CA-CB-CG	9.34	132.78	114.10
1	D	269	LEU	N-CA-C	-9.33	98.21	110.43
1	H	270	GLU	N-CA-C	9.31	119.05	108.25
1	F	285	GLU	CG-CD-OE1	-9.29	97.02	118.40
1	D	311	VAL	N-CA-C	9.27	121.70	108.17
1	C	310	PHE	N-CA-C	9.23	124.90	109.76
1	B	138	HIS	N-CA-C	9.23	124.73	113.38
1	B	262	ARG	N-CA-C	-9.23	101.22	111.28
1	F	114	LYS	N-CA-C	9.19	124.71	109.46
1	F	115	VAL	N-CA-C	9.18	122.27	108.23
1	C	174	VAL	N-CA-C	-9.16	95.29	108.48
1	B	279	LYS	CB-CG-CD	-9.10	90.36	111.30
1	E	118	LYS	N-CA-C	9.08	130.13	110.80
1	F	279	LYS	N-CA-C	9.05	122.13	108.46
1	B	172	PHE	N-CA-C	-9.03	95.23	109.50
1	A	279	LYS	CB-CG-CD	9.01	132.03	111.30
1	G	267	ASP	N-CA-C	-9.00	100.44	111.33
1	A	130	ILE	N-CA-C	8.99	118.98	110.53
1	B	270	GLU	N-CA-C	8.98	118.67	108.25
1	B	345	CYS	N-CA-C	8.97	123.43	109.52
1	B	192	VAL	CB-CA-C	-8.97	99.33	110.99
1	H	288	ASP	CB-CG-OD1	-8.96	97.79	118.40
1	G	140	ASP	N-CA-C	-8.90	96.62	110.42
1	H	216	LYS	N-CA-C	-8.84	97.33	111.04
1	H	138	HIS	N-CA-C	8.83	124.24	113.38
1	D	113	ARG	N-CA-C	8.82	122.79	108.41
1	C	138	HIS	N-CA-C	8.81	124.02	113.28
1	G	366	ARG	N-CA-C	-8.78	101.67	111.07
1	H	118	LYS	N-CA-C	8.77	129.48	110.80
1	H	344	LYS	CB-CA-C	-8.75	99.74	110.94
1	H	295	GLU	N-CA-C	8.74	122.44	109.24
1	F	345	CYS	N-CA-C	8.74	122.16	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	118	LYS	N-CA-C	8.73	129.41	110.80
1	F	138	HIS	N-CA-C	8.72	124.11	113.38
1	D	345	CYS	N-CA-C	8.70	122.38	109.24
1	D	265	VAL	N-CA-C	-8.70	101.18	110.23
1	G	213	VAL	N-CA-C	8.69	120.27	108.11
1	D	267	ASP	N-CA-C	-8.68	100.83	111.33
1	D	115	VAL	CB-CA-C	-8.65	99.08	110.84
1	B	201	LEU	CA-CB-CG	-8.61	86.17	116.30
1	E	374	PHE	N-CA-C	8.57	123.47	112.92
1	C	341	GLY	CA-C-N	8.52	129.76	120.13
1	C	341	GLY	C-N-CA	8.52	129.76	120.13
1	B	295	GLU	N-CA-C	8.40	121.92	109.24
1	B	132	LYS	N-CA-C	-8.38	102.82	112.87
1	B	313	VAL	N-CA-C	8.36	123.50	113.22
1	F	120	TYR	CA-C-N	-8.35	109.59	120.44
1	F	120	TYR	C-N-CA	-8.35	109.59	120.44
1	G	192	VAL	CA-C-N	-8.34	114.01	122.27
1	G	192	VAL	C-N-CA	-8.34	114.01	122.27
1	H	300	VAL	N-CA-C	-8.34	96.62	108.80
1	D	130	ILE	N-CA-CB	8.33	120.06	110.65
1	D	294	LEU	N-CA-C	-8.31	100.75	112.13
1	D	130	ILE	N-CA-C	8.27	118.19	110.42
1	G	131	GLU	N-CA-C	8.26	121.03	111.11
1	B	216	LYS	N-CA-C	-8.25	98.25	111.04
1	F	341	GLY	CA-C-N	8.24	129.44	120.13
1	F	341	GLY	C-N-CA	8.24	129.44	120.13
1	H	288	ASP	CB-CG-OD2	8.22	137.30	118.40
1	C	295	GLU	N-CA-C	8.21	121.64	109.24
1	B	113	ARG	N-CA-C	8.19	123.06	109.46
1	F	285	GLU	CG-CD-OE2	8.18	137.21	118.40
1	G	373	SER	N-CA-C	8.16	123.31	110.17
1	C	300	VAL	CB-CA-C	8.13	124.62	111.29
1	F	133	ASN	N-CA-C	8.13	121.50	108.41
1	G	219	VAL	N-CA-C	8.12	122.35	108.95
1	G	131	GLU	CB-CG-CD	-8.11	98.82	112.60
1	E	131	GLU	N-CA-C	8.10	120.19	111.36
1	D	172	PHE	N-CA-C	-8.09	96.57	109.59
1	F	269	LEU	N-CA-C	-8.08	99.84	110.43
1	E	133	ASN	N-CA-C	8.06	121.39	108.41
1	G	294	LEU	N-CA-C	-8.06	100.60	111.96
1	B	115	VAL	N-CA-C	8.05	119.93	108.17
1	F	231	ARG	CA-C-N	-8.04	115.09	122.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	231	ARG	C-N-CA	-8.04	115.09	122.97
1	A	138	HIS	N-CA-C	8.03	123.25	113.38
1	H	300	VAL	CB-CA-C	8.02	122.69	110.82
1	A	316	LEU	CA-CB-CG	-8.02	88.25	116.30
1	G	131	GLU	CB-CA-C	-7.97	98.06	110.81
1	G	240	LYS	N-CA-C	-7.96	102.58	111.82
1	C	254	LEU	CA-CB-CG	-7.93	88.54	116.30
1	C	200	GLU	CA-CB-CG	7.88	129.86	114.10
1	E	341	GLY	CA-C-N	7.88	129.03	120.13
1	E	341	GLY	C-N-CA	7.88	129.03	120.13
1	D	231	ARG	CA-C-N	-7.87	115.25	122.97
1	D	231	ARG	C-N-CA	-7.87	115.25	122.97
1	F	285	GLU	CB-CG-CD	-7.87	99.22	112.60
1	H	341	GLY	CA-C-N	7.87	129.02	120.13
1	H	341	GLY	C-N-CA	7.87	129.02	120.13
1	H	288	ASP	N-CA-CB	-7.86	100.03	110.88
1	G	140	ASP	N-CA-CB	7.85	122.81	110.56
1	A	265	VAL	CB-CA-C	-7.85	102.00	111.81
1	A	118	LYS	N-CA-C	7.83	127.49	110.80
1	E	138	HIS	N-CA-C	7.83	123.01	113.38
1	D	138	HIS	N-CA-C	7.82	122.82	113.28
1	H	254	LEU	CA-CB-CG	-7.80	88.98	116.30
1	F	216	LYS	N-CA-C	-7.79	98.97	111.04
1	F	113	ARG	N-CA-C	7.78	120.90	109.07
1	D	124	ALA	N-CA-C	-7.77	101.92	111.33
1	E	113	ARG	N-CA-C	7.76	121.89	109.24
1	F	118	LYS	N-CA-C	7.74	127.29	110.80
1	A	317	GLY	CA-C-N	7.74	127.79	119.90
1	A	317	GLY	C-N-CA	7.74	127.79	119.90
1	B	254	LEU	CA-CB-CG	-7.73	89.23	116.30
1	E	115	VAL	N-CA-C	7.72	118.98	108.17
1	G	246	GLU	N-CA-CB	7.72	121.21	110.01
1	A	312	GLU	N-CA-C	7.72	121.32	108.73
1	A	357	LEU	N-CA-C	7.67	121.52	112.93
1	F	192	VAL	N-CA-CB	-7.67	101.39	111.82
1	C	270	GLU	N-CA-C	7.66	119.50	110.31
1	E	115	VAL	CB-CA-C	-7.66	99.42	110.83
1	F	232	ILE	CB-CA-C	7.66	118.22	111.71
1	C	147	ILE	CB-CA-C	-7.61	102.23	111.97
1	B	241	ARG	N-CA-CB	-7.60	98.93	110.26
1	G	138	HIS	N-CA-C	7.60	122.72	113.38
1	E	302	GLN	N-CA-C	7.59	122.13	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	348	LEU	N-CA-C	-7.57	95.69	108.26
1	G	254	LEU	CA-CB-CG	-7.56	89.84	116.30
1	A	162	VAL	N-CA-C	-7.53	103.52	110.82
1	G	145	SER	N-CA-C	-7.53	103.02	111.07
1	A	317	GLY	N-CA-C	-7.49	97.06	112.34
1	A	219	VAL	N-CA-C	7.48	121.31	108.90
1	E	213	VAL	N-CA-C	7.47	119.60	108.46
1	G	113	ARG	N-CA-C	7.47	126.71	110.80
1	B	231	ARG	CA-C-N	-7.46	110.61	121.65
1	B	231	ARG	C-N-CA	-7.46	110.61	121.65
1	G	147	ILE	N-CA-CB	7.46	119.28	110.55
1	G	341	GLY	CA-C-N	7.45	128.54	120.13
1	G	341	GLY	C-N-CA	7.45	128.54	120.13
1	D	314	GLY	N-CA-C	7.44	124.95	111.03
1	H	174	VAL	N-CA-C	-7.42	97.79	108.48
1	B	170	ASP	N-CA-C	7.42	122.30	112.13
1	F	265	VAL	CB-CA-C	-7.42	102.20	111.70
1	C	345	CYS	N-CA-C	7.40	120.17	109.14
1	A	254	LEU	CA-CB-CG	-7.39	90.44	116.30
1	B	116	ILE	N-CA-C	7.38	115.45	108.15
1	A	192	VAL	CB-CA-C	-7.37	100.30	110.77
1	B	294	LEU	N-CA-C	-7.36	102.05	112.13
1	C	265	VAL	CB-CA-C	-7.34	102.31	111.70
1	D	248	LEU	N-CA-C	7.34	119.28	111.28
1	D	113	ARG	CA-C-N	7.33	132.37	122.84
1	D	113	ARG	C-N-CA	7.33	132.37	122.84
1	E	270	GLU	N-CA-CB	7.32	120.28	109.88
1	A	174	VAL	N-CA-C	-7.32	97.92	108.53
1	D	118	LYS	N-CA-C	7.31	126.37	110.80
1	C	273	GLN	CB-CA-C	-7.31	96.84	111.17
1	B	118	LYS	N-CA-C	7.30	126.35	110.80
1	H	345	CYS	N-CA-C	7.30	120.02	109.14
1	C	172	PHE	N-CA-C	-7.30	97.51	109.40
1	D	113	ARG	CB-CA-C	-7.29	98.06	110.16
1	F	130	ILE	CG1-CB-CG2	-7.29	88.83	110.70
1	H	375	VAL	N-CA-C	7.29	124.50	109.34
1	B	113	ARG	O-C-N	-7.29	114.92	123.22
1	C	312	GLU	N-CA-C	7.29	120.36	108.26
1	A	133	ASN	N-CA-C	7.28	120.13	108.41
1	C	182	VAL	CB-CA-C	-7.28	101.53	110.99
1	C	362	ASP	N-CA-C	7.26	126.27	110.80
1	G	141	ASP	CA-C-N	-7.25	110.00	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	141	ASP	C-N-CA	-7.25	110.00	120.29
1	D	141	ASP	N-CA-C	7.24	119.80	111.11
1	D	295	GLU	N-CA-C	7.24	119.46	109.18
1	C	267	ASP	N-CA-C	-7.24	102.58	111.33
1	F	248	LEU	N-CA-C	7.21	119.13	111.28
1	H	147	ILE	CB-CG1-CD1	-7.20	98.69	113.80
1	D	122	THR	N-CA-C	-7.19	102.63	111.33
1	A	112	VAL	N-CA-C	7.18	124.27	109.34
1	C	242	LYS	CA-CB-CG	-7.17	99.77	114.10
1	C	157	ILE	N-CA-C	7.13	119.33	108.71
1	G	270	GLU	CA-CB-CG	7.13	128.36	114.10
1	G	136	PHE	N-CA-C	-7.12	104.95	112.93
1	C	213	VAL	N-CA-C	7.12	119.06	108.46
1	E	254	LEU	CA-CB-CG	-7.11	91.40	116.30
1	C	374	PHE	N-CA-C	7.11	121.67	112.92
1	H	182	VAL	CB-CA-C	-7.10	101.77	110.99
1	D	112	VAL	N-CA-C	7.09	124.09	109.34
1	A	130	ILE	CA-C-O	-7.08	113.19	121.05
1	D	264	THR	N-CA-C	-7.07	103.58	111.71
1	E	219	VAL	N-CA-C	7.07	120.62	108.95
1	E	267	ASP	N-CA-C	-7.07	102.78	111.33
1	H	115	VAL	N-CA-C	7.07	117.83	107.37
1	B	269	LEU	N-CA-C	-7.06	101.19	110.43
1	A	253	ILE	N-CA-C	7.05	124.01	109.34
1	G	121	LYS	CB-CG-CD	-7.05	95.08	111.30
1	F	375	VAL	CB-CA-C	7.04	117.69	111.71
1	C	112	VAL	N-CA-C	7.02	117.72	107.75
1	G	331	ARG	CA-C-N	7.02	128.62	119.84
1	G	331	ARG	C-N-CA	7.02	128.62	119.84
1	G	348	LEU	N-CA-C	-7.00	96.10	108.13
1	E	172	PHE	N-CA-C	-6.99	98.34	109.59
1	G	330	ASN	N-CA-C	-6.99	101.74	111.52
1	E	262	ARG	N-CA-C	-6.98	103.67	111.28
1	F	237	THR	N-CA-C	-6.98	103.36	110.97
1	E	192	VAL	N-CA-CB	-6.97	101.78	111.41
1	G	352	ARG	N-CA-C	-6.95	103.76	111.82
1	G	174	VAL	N-CA-C	-6.94	98.47	108.53
1	G	361	SER	N-CA-CB	-6.93	99.97	110.01
1	D	113	ARG	CA-C-O	-6.88	112.94	120.30
1	F	324	GLU	N-CA-C	6.86	118.76	111.28
1	A	295	GLU	N-CA-C	6.84	119.80	109.41
1	D	341	GLY	CA-C-N	6.83	127.85	120.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	341	GLY	C-N-CA	6.83	127.85	120.13
1	H	122	THR	N-CA-C	-6.83	103.07	111.33
1	H	131	GLU	CB-CA-C	-6.83	100.16	110.88
1	E	270	GLU	N-CA-C	6.81	119.32	110.40
1	G	118	LYS	N-CA-C	6.80	125.28	110.80
1	A	201	LEU	CA-CB-CG	-6.79	92.52	116.30
1	G	279	LYS	N-CA-C	6.78	119.44	108.32
1	H	262	ARG	N-CA-C	-6.77	103.13	111.33
1	E	248	LEU	N-CA-C	6.77	118.32	111.07
1	G	192	VAL	N-CA-CB	-6.77	102.93	111.46
1	H	232	ILE	CB-CA-C	6.77	117.87	111.44
1	E	120	TYR	CA-C-N	-6.75	111.67	120.44
1	E	120	TYR	C-N-CA	-6.75	111.67	120.44
1	B	265	VAL	CB-CA-C	-6.75	103.07	111.70
1	F	111	TYR	CB-CA-C	-6.74	100.40	110.24
1	F	131	GLU	N-CA-C	6.72	118.26	111.07
1	F	114	LYS	CA-CB-CG	-6.71	100.67	114.10
1	A	112	VAL	O-C-N	-6.71	114.19	122.57
1	H	348	LEU	N-CA-C	-6.71	97.12	108.26
1	G	117	PRO	CB-CA-C	6.70	122.62	111.56
1	B	190	THR	N-CA-C	6.69	118.30	108.86
1	H	374	PHE	N-CA-C	6.69	121.05	113.02
1	G	165	GLN	N-CA-C	6.64	119.86	110.23
1	C	366	ARG	NE-CZ-NH2	6.63	125.17	119.20
1	A	294	LEU	N-CA-C	-6.62	103.06	112.13
1	E	231	ARG	CA-C-N	-6.62	111.85	121.65
1	E	231	ARG	C-N-CA	-6.62	111.85	121.65
1	H	147	ILE	N-CA-CB	6.62	117.86	110.51
1	G	239	ARG	CB-CG-CD	-6.62	96.08	111.30
1	G	253	ILE	N-CA-C	6.61	123.09	109.34
1	B	240	LYS	N-CA-C	-6.61	103.29	111.75
1	A	221	LEU	N-CA-C	6.60	120.45	109.95
1	A	311	VAL	N-CA-C	6.58	117.10	107.75
1	H	343	LEU	CB-CA-C	6.58	122.43	109.66
1	H	273	GLN	N-CA-C	6.57	118.19	108.60
1	B	174	VAL	N-CA-C	-6.56	99.04	108.48
1	B	161	THR	CB-CA-C	-6.55	100.11	110.79
1	A	161	THR	CB-CA-C	-6.53	100.33	110.78
1	F	294	LEU	N-CA-C	-6.53	103.19	112.13
1	C	248	LEU	N-CA-C	6.52	118.39	111.28
1	B	122	THR	N-CA-C	-6.51	103.30	111.11
1	F	114	LYS	CB-CA-C	-6.51	99.12	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	172	PHE	N-CA-C	-6.51	99.11	109.59
1	G	147	ILE	CB-CA-C	-6.51	103.64	111.97
1	C	113	ARG	N-CA-C	6.51	124.66	110.80
1	F	331	ARG	CA-CB-CG	6.51	127.12	114.10
1	G	342	PRO	CA-C-O	-6.50	113.36	120.97
1	C	147	ILE	CB-CG1-CD1	-6.50	100.15	113.80
1	E	159	GLY	N-CA-C	-6.49	103.73	114.76
1	F	277	GLY	N-CA-C	-6.47	107.00	115.47
1	B	241	ARG	NH1-CZ-NH2	6.46	127.70	119.30
1	C	192	VAL	N-CA-CB	-6.44	103.79	111.90
1	C	270	GLU	CB-CA-C	-6.42	100.33	109.96
1	H	201	LEU	CA-CB-CG	-6.42	93.82	116.30
1	G	248	LEU	N-CA-C	6.41	119.08	111.71
1	G	182	VAL	N-CA-C	6.41	117.10	107.75
1	C	113	ARG	CA-C-N	6.39	130.97	120.94
1	C	113	ARG	C-N-CA	6.39	130.97	120.94
1	D	360	CYS	N-CA-C	-6.39	104.68	113.18
1	E	232	ILE	N-CA-C	6.39	117.39	111.45
1	E	265	VAL	CB-CA-C	-6.36	103.55	111.70
1	C	132	LYS	N-CA-C	-6.35	104.63	112.38
1	E	117	PRO	CA-C-O	-6.35	110.00	119.34
1	B	317	GLY	CA-C-N	6.35	126.38	119.90
1	B	317	GLY	C-N-CA	6.35	126.38	119.90
1	F	121	LYS	N-CA-C	6.35	117.86	111.07
1	G	345	CYS	N-CA-C	6.35	118.20	109.18
1	G	159	GLY	N-CA-C	-6.34	104.68	115.08
1	G	208	PRO	N-CA-C	-6.32	101.97	111.57
1	H	115	VAL	CB-CA-C	-6.31	102.42	111.19
1	C	196	GLY	N-CA-C	6.30	122.89	112.30
1	A	348	LEU	N-CA-C	-6.30	98.01	108.34
1	G	134	VAL	N-CA-C	6.29	119.87	111.44
1	A	111	TYR	N-CA-C	6.28	124.18	110.80
1	G	276	ASP	N-CA-C	6.27	119.13	110.35
1	F	180	MET	N-CA-C	6.27	119.68	109.59
1	A	141	ASP	CA-C-N	-6.27	111.39	120.29
1	A	141	ASP	C-N-CA	-6.27	111.39	120.29
1	C	344	LYS	CB-CA-C	-6.27	102.92	110.94
1	A	112	VAL	CA-CB-CG2	6.24	121.01	110.40
1	F	201	LEU	CA-CB-CG	-6.24	94.46	116.30
1	H	219	VAL	N-CA-C	6.24	118.46	108.85
1	B	279	LYS	CD-CE-NZ	-6.23	91.98	111.90
1	B	344	LYS	N-CA-C	6.22	118.57	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	279	LYS	N-CA-C	6.22	118.63	108.55
1	F	254	LEU	CA-CB-CG	-6.22	94.51	116.30
1	G	273	GLN	N-CA-C	6.22	118.31	108.79
1	G	239	ARG	N-CA-C	6.22	120.07	112.23
1	F	274	PHE	N-CA-C	6.22	118.63	109.24
1	B	312	GLU	N-CA-C	6.21	120.39	109.96
1	H	192	VAL	N-CA-CB	-6.21	104.08	111.90
1	D	130	ILE	CA-C-O	-6.20	113.98	121.18
1	A	262	ARG	N-CA-C	-6.20	103.83	111.33
1	G	117	PRO	CA-C-O	-6.20	109.31	120.60
1	B	288	ASP	N-CA-C	6.20	121.68	112.94
1	H	134	VAL	N-CA-C	6.20	117.68	110.62
1	F	317	GLY	O-C-N	6.19	127.96	121.77
1	A	112	VAL	CB-CA-C	6.18	121.42	111.29
1	H	147	ILE	CB-CA-C	-6.17	103.98	111.88
1	C	375	VAL	N-CA-C	6.17	122.18	109.34
1	G	196	GLY	N-CA-C	6.17	122.66	112.66
1	C	147	ILE	N-CA-C	6.16	116.33	110.42
1	D	336	THR	N-CA-C	-6.16	99.68	109.59
1	F	296	GLY	N-CA-C	-6.15	102.96	111.76
1	H	157	ILE	N-CA-C	6.15	117.88	108.71
1	E	182	VAL	CB-CA-C	-6.15	103.41	110.73
1	G	246	GLU	CB-CA-C	-6.15	101.22	110.88
1	G	172	PHE	N-CA-C	-6.15	100.18	109.95
1	G	264	THR	N-CA-C	-6.15	104.69	111.82
1	F	331	ARG	CA-C-N	6.14	126.98	120.11
1	F	331	ARG	C-N-CA	6.14	126.98	120.11
1	C	200	GLU	N-CA-CB	6.13	119.21	110.13
1	D	201	LEU	N-CA-C	6.13	123.86	110.80
1	H	159	GLY	N-CA-C	-6.13	103.37	114.46
1	G	169	GLY	CA-C-N	-6.12	109.84	121.54
1	G	169	GLY	C-N-CA	-6.12	109.84	121.54
1	A	231	ARG	CA-C-N	-6.11	110.97	121.97
1	A	231	ARG	C-N-CA	-6.11	110.97	121.97
1	G	313	VAL	N-CA-CB	-6.11	103.87	112.12
1	A	248	LEU	N-CA-C	6.11	117.61	111.07
1	B	348	LEU	N-CA-C	-6.09	98.14	108.26
1	E	240	LYS	N-CA-C	-6.09	104.64	111.28
1	G	279	LYS	N-CA-CB	-6.09	100.28	110.57
1	D	216	LYS	N-CA-C	-6.09	101.61	111.04
1	H	313	VAL	N-CA-CB	6.08	117.53	110.65
1	B	213	VAL	N-CA-C	6.06	117.49	108.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	232	ILE	CB-CA-C	6.05	121.22	111.29
1	E	253	ILE	N-CA-CB	-6.04	101.26	111.23
1	F	186	ASN	N-CA-CB	-6.03	107.29	114.17
1	D	305	SER	N-CA-C	-6.02	99.98	109.50
1	C	366	ARG	NE-CZ-NH1	-6.02	115.48	121.50
1	A	157	ILE	N-CA-C	6.02	117.68	108.71
1	C	230	ARG	N-CA-C	-6.02	103.89	111.11
1	H	178	GLY	N-CA-C	6.01	120.36	111.76
1	C	274	PHE	N-CA-C	6.01	117.33	108.86
1	B	219	VAL	N-CA-C	6.01	118.87	108.90
1	C	233	LEU	N-CA-C	6.00	120.76	113.38
1	G	146	ASP	CA-C-O	-6.00	114.48	120.90
1	H	343	LEU	N-CA-C	-6.00	100.37	109.85
1	D	240	LYS	N-CA-C	-6.00	104.07	111.33
1	D	141	ASP	CA-C-N	-5.99	111.78	120.29
1	D	141	ASP	C-N-CA	-5.99	111.78	120.29
1	A	344	LYS	N-CA-C	5.98	118.15	107.80
1	G	274	PHE	N-CA-C	5.98	118.50	109.41
1	D	141	ASP	CB-CA-C	-5.98	101.25	110.81
1	A	169	GLY	CA-C-N	-5.97	112.97	122.17
1	A	169	GLY	C-N-CA	-5.97	112.97	122.17
1	D	133	ASN	N-CA-C	5.97	118.02	108.41
1	D	325	ILE	N-CA-C	5.97	121.76	109.34
1	G	370	GLN	N-CA-C	-5.96	105.11	112.38
1	G	307	ASN	CA-C-O	-5.96	115.52	122.37
1	B	157	ILE	CB-CA-C	-5.95	102.58	110.98
1	D	219	VAL	N-CA-C	5.95	118.77	108.95
1	E	289	GLU	N-CA-C	5.95	118.90	109.50
1	C	343	LEU	CB-CA-C	5.94	121.19	109.66
1	G	192	VAL	N-CA-C	5.94	116.42	107.80
1	G	221	LEU	N-CA-C	5.94	119.23	109.85
1	D	348	LEU	N-CA-C	-5.93	98.19	108.69
1	F	117	PRO	CA-C-O	-5.92	110.63	119.34
1	H	120	TYR	CA-C-N	-5.92	112.75	120.44
1	H	120	TYR	C-N-CA	-5.92	112.75	120.44
1	D	110	SER	N-CA-C	5.92	118.13	108.55
1	F	182	VAL	CB-CA-C	-5.91	103.69	110.73
1	H	192	VAL	N-CA-C	5.91	116.68	107.28
1	D	300	VAL	N-CA-C	5.90	116.66	107.28
1	G	349	ASP	N-CA-C	-5.90	102.04	110.59
1	C	153	PRO	CA-C-N	-5.88	114.24	122.71
1	C	153	PRO	C-N-CA	-5.88	114.24	122.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	357	LEU	CB-CG-CD1	-5.88	93.06	110.70
1	C	253	ILE	N-CA-CB	-5.88	101.53	111.23
1	D	114	LYS	CB-CA-C	-5.87	101.38	110.78
1	E	165	GLN	N-CA-C	5.87	118.34	110.35
1	A	134	VAL	N-CA-C	5.87	119.27	111.17
1	B	315	ARG	N-CA-C	5.87	118.46	108.90
1	H	172	PHE	N-CA-C	-5.86	99.85	109.40
1	H	265	VAL	CB-CA-C	-5.86	104.20	111.70
1	A	196	GLY	N-CA-C	5.85	121.55	112.60
1	G	300	VAL	CB-CA-C	-5.84	102.43	110.96
1	G	114	LYS	CA-C-N	-5.84	115.49	123.14
1	G	114	LYS	C-N-CA	-5.84	115.49	123.14
1	G	296	GLY	N-CA-C	-5.84	103.40	112.45
1	C	147	ILE	N-CA-CB	5.83	117.37	110.55
1	C	331	ARG	CA-C-N	5.83	126.64	120.11
1	C	331	ARG	C-N-CA	5.83	126.64	120.11
1	F	219	VAL	N-CA-C	5.83	118.56	108.95
1	F	285	GLU	N-CA-CB	-5.83	101.98	109.55
1	C	192	VAL	N-CA-C	5.82	116.53	107.28
1	C	270	GLU	CA-CB-CG	5.82	125.73	114.10
1	G	130	ILE	CA-C-O	-5.81	115.07	121.29
1	D	331	ARG	CA-C-N	5.80	127.10	119.84
1	D	331	ARG	C-N-CA	5.80	127.10	119.84
1	F	318	PRO	CB-CG-CD	-5.80	87.53	106.10
1	G	262	ARG	N-CA-C	-5.80	105.04	111.36
1	A	121	LYS	CD-CE-NZ	5.79	130.43	111.90
1	A	265	VAL	N-CA-C	-5.79	104.69	110.30
1	B	194	GLU	N-CA-C	-5.79	100.56	109.76
1	C	273	GLN	N-CA-C	5.78	117.03	108.60
1	A	264	THR	N-CA-C	-5.77	105.08	111.71
1	C	366	ARG	N-CA-CB	-5.77	100.74	110.49
1	G	347	LYS	N-CA-C	5.76	118.63	109.81
1	A	366	ARG	N-CA-C	-5.76	104.36	111.33
1	F	192	VAL	CB-CA-C	-5.75	102.66	110.42
1	A	216	LYS	N-CA-C	-5.75	102.13	111.04
1	C	120	TYR	CA-C-N	-5.74	112.97	120.44
1	C	120	TYR	C-N-CA	-5.74	112.97	120.44
1	G	200	GLU	CA-CB-CG	5.74	125.58	114.10
1	D	134	VAL	N-CA-C	5.73	117.15	110.62
1	B	169	GLY	CA-C-N	-5.72	113.97	122.56
1	B	169	GLY	C-N-CA	-5.72	113.97	122.56
1	G	190	THR	CA-C-O	5.72	127.42	121.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	344	LYS	N-CA-CB	5.72	118.72	110.37
1	H	141	ASP	N-CA-C	5.72	117.97	111.11
1	G	201	LEU	CA-CB-CG	-5.71	96.31	116.30
1	B	162	VAL	N-CA-C	-5.71	105.28	110.82
1	C	201	LEU	CA-CB-CG	-5.70	96.35	116.30
1	E	277	GLY	N-CA-C	-5.70	108.00	115.47
1	C	200	GLU	CB-CA-C	-5.70	101.22	110.79
1	A	213	VAL	N-CA-C	5.69	116.94	108.46
1	E	125	ALA	N-CA-C	5.69	118.34	111.40
1	H	128	LYS	CD-CE-NZ	5.69	130.10	111.90
1	A	195	GLY	N-CA-C	-5.69	107.92	114.69
1	F	152	PHE	CA-C-N	5.67	126.12	119.99
1	F	152	PHE	C-N-CA	5.67	126.12	119.99
1	G	260	TRP	N-CA-C	-5.67	105.11	111.28
1	A	341	GLY	CA-C-N	5.66	126.53	120.13
1	A	341	GLY	C-N-CA	5.66	126.53	120.13
1	C	141	ASP	N-CA-C	5.66	117.90	111.11
1	E	310	PHE	N-CA-C	-5.66	102.52	110.50
1	B	366	ARG	N-CA-C	-5.66	104.50	111.75
1	D	114	LYS	CA-C-O	-5.66	114.66	120.54
1	G	272	VAL	N-CA-CB	5.66	117.31	109.84
1	G	336	THR	N-CA-C	-5.66	100.48	109.59
1	C	111	TYR	O-C-N	-5.63	115.10	122.59
1	A	268	ALA	N-CA-C	5.62	120.14	113.28
1	H	274	PHE	N-CA-C	5.62	116.78	108.86
1	A	279	LYS	N-CA-C	5.61	117.38	108.79
1	G	224	ILE	N-CA-CB	5.60	120.55	111.36
1	A	199	GLY	N-CA-C	-5.60	106.28	114.90
1	G	258	ASP	N-CA-C	-5.59	101.69	110.36
1	B	239	ARG	CB-CG-CD	-5.59	98.45	111.30
1	E	201	LEU	CA-CB-CG	-5.59	96.75	116.30
1	F	239	ARG	CG-CD-NE	5.58	124.28	112.00
1	B	274	PHE	N-CA-C	5.58	117.89	109.41
1	A	116	ILE	CA-C-N	5.58	126.81	119.84
1	A	116	ILE	C-N-CA	5.58	126.81	119.84
1	F	295	GLU	N-CA-C	5.57	117.87	109.23
1	E	281	VAL	CB-CA-C	-5.57	102.39	110.63
1	A	219	VAL	CB-CA-C	-5.56	100.90	110.30
1	G	190	THR	N-CA-CB	5.56	120.50	111.21
1	F	213	VAL	N-CA-C	5.56	116.74	108.46
1	C	120	TYR	CB-CA-C	-5.55	99.38	110.42
1	G	137	SER	CA-C-N	-5.55	112.66	122.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	137	SER	C-N-CA	-5.55	112.66	122.26
1	B	232	ILE	N-CA-C	5.55	116.61	111.45
1	B	358	GLY	CA-C-N	-5.55	112.91	119.84
1	B	358	GLY	C-N-CA	-5.55	112.91	119.84
1	G	251	VAL	CB-CA-C	5.54	119.05	110.96
1	A	311	VAL	CB-CA-C	-5.53	103.61	111.40
1	A	165	GLN	N-CA-C	5.53	118.03	110.24
1	H	246	GLU	CB-CA-C	-5.52	100.07	110.67
1	C	222	TRP	N-CA-CB	-5.52	101.89	110.55
1	E	366	ARG	NE-CZ-NH2	5.52	124.17	119.20
1	G	158	ALA	CA-C-O	-5.49	115.46	120.95
1	H	213	VAL	N-CA-C	5.48	116.63	108.46
1	D	279	LYS	N-CA-C	5.47	117.42	108.55
1	G	301	LEU	N-CA-CB	5.47	119.61	110.85
1	E	349	ASP	N-CA-C	-5.46	102.82	110.35
1	H	127	ALA	N-CA-C	-5.45	104.57	111.11
1	A	217	THR	CB-CA-C	-5.43	101.06	113.33
1	C	178	GLY	N-CA-C	5.42	119.51	111.76
1	C	289	GLU	N-CA-C	5.42	118.06	109.50
1	E	121	LYS	N-CA-C	5.40	116.85	111.07
1	D	263	LEU	CA-CB-CG	-5.40	97.40	116.30
1	A	182	VAL	CB-CA-C	-5.39	104.31	110.73
1	B	239	ARG	CG-CD-NE	5.39	123.87	112.00
1	B	277	GLY	CA-C-O	5.39	125.04	119.00
1	H	300	VAL	N-CA-CB	-5.39	104.97	112.52
1	D	246	GLU	CA-CB-CG	5.39	124.88	114.10
1	D	147	ILE	N-CA-CB	5.38	117.86	110.54
1	E	175	ILE	N-CA-C	-5.38	100.13	107.99
1	D	298	ALA	N-CA-C	5.36	116.43	108.60
1	F	162	VAL	CB-CA-C	-5.36	105.06	112.24
1	F	366	ARG	N-CA-C	-5.36	105.54	111.71
1	H	131	GLU	N-CA-CB	5.36	117.78	110.01
1	H	114	LYS	N-CA-C	5.36	122.21	110.80
1	A	357	LEU	CB-CA-C	5.36	120.08	110.81
1	F	289	GLU	N-CA-C	5.35	117.96	109.50
1	G	129	ALA	N-CA-C	-5.35	105.44	111.28
1	B	141	ASP	CA-C-N	-5.35	113.11	120.28
1	B	141	ASP	C-N-CA	-5.35	113.11	120.28
1	G	180	MET	N-CA-C	5.35	118.43	110.14
1	A	170	ASP	N-CA-C	5.34	119.28	112.12
1	G	269	LEU	CA-C-N	-5.34	114.18	124.01
1	G	269	LEU	C-N-CA	-5.34	114.18	124.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	114	LYS	CD-CE-NZ	5.34	128.99	111.90
1	A	229	TYR	CB-CA-C	-5.33	102.28	110.81
1	H	280	ILE	N-CA-CB	-5.33	102.84	110.52
1	F	196	GLY	N-CA-C	5.32	120.76	112.31
1	F	360	CYS	N-CA-C	-5.31	106.12	113.18
1	H	331	ARG	CA-C-N	5.31	126.47	119.84
1	H	331	ARG	C-N-CA	5.31	126.47	119.84
1	C	366	ARG	CD-NE-CZ	-5.30	116.98	124.40
1	A	192	VAL	N-CA-CB	-5.29	104.76	111.64
1	H	266	ALA	N-CA-C	-5.29	104.56	111.02
1	E	182	VAL	N-CA-C	5.29	116.12	107.24
1	G	123	MET	CB-CG-SD	-5.28	96.87	112.70
1	A	190	THR	N-CA-C	5.27	116.67	109.18
1	C	294	LEU	N-CA-C	-5.26	104.92	112.13
1	A	221	LEU	CA-C-O	5.25	127.10	121.16
1	D	251	VAL	CB-CA-C	5.25	117.98	110.84
1	C	121	LYS	N-CA-C	5.25	116.68	111.07
1	H	313	VAL	N-CA-C	-5.24	105.50	110.42
1	F	365	LYS	CD-CE-NZ	-5.24	95.14	111.90
1	C	297	SER	CB-CA-C	5.23	121.70	110.45
1	A	304	ARG	N-CA-C	5.23	121.94	110.80
1	C	242	LYS	N-CA-C	5.23	117.40	111.02
1	F	317	GLY	N-CA-C	-5.22	101.69	112.34
1	H	366	ARG	N-CA-C	-5.22	105.01	111.33
1	B	263	LEU	CA-CB-CG	-5.22	98.03	116.30
1	F	348	LEU	N-CA-C	-5.22	99.94	108.76
1	G	263	LEU	N-CA-CB	-5.22	102.45	110.12
1	G	161	THR	OG1-CB-CG2	5.22	119.73	109.30
1	C	260	TRP	N-CA-C	-5.21	105.03	111.33
1	G	253	ILE	CA-CB-CG1	-5.21	101.55	110.40
1	H	170	ASP	N-CA-C	5.21	121.89	110.80
1	A	279	LYS	N-CA-CB	-5.20	103.50	111.56
1	D	213	VAL	N-CA-C	5.20	116.21	108.46
1	D	277	GLY	N-CA-C	-5.20	108.66	115.47
1	F	124	ALA	N-CA-C	-5.20	105.10	111.75
1	G	278	GLN	CA-CB-CG	-5.20	103.70	114.10
1	A	115	VAL	N-CA-C	5.20	120.15	109.34
1	E	163	ILE	CB-CA-C	-5.20	103.41	110.42
1	B	277	GLY	N-CA-C	-5.19	108.67	115.47
1	G	274	PHE	N-CA-CB	-5.19	103.18	111.43
1	A	352	ARG	N-CA-C	-5.19	105.80	111.82
1	G	239	ARG	CG-CD-NE	5.19	123.41	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	273	GLN	N-CA-C	5.19	116.41	108.42
1	F	163	ILE	N-CA-C	5.19	115.45	107.77
1	C	162	VAL	N-CA-C	-5.18	105.79	110.82
1	C	232	ILE	CB-CA-C	5.18	116.36	111.44
1	G	368	ILE	N-CA-C	-5.18	106.26	113.00
1	B	133	ASN	N-CA-C	5.18	117.06	108.20
1	F	113	ARG	CA-C-N	5.18	129.49	122.19
1	F	113	ARG	C-N-CA	5.18	129.49	122.19
1	C	251	VAL	CB-CA-C	5.18	118.55	110.83
1	E	317	GLY	C-N-CD	-5.17	103.81	125.00
1	B	246	GLU	N-CA-CB	5.16	118.28	110.28
1	D	145	SER	N-CA-C	-5.16	105.08	111.33
1	G	130	ILE	CB-CA-C	-5.16	105.36	111.81
1	B	341	GLY	CA-C-N	5.16	125.96	120.13
1	B	341	GLY	C-N-CA	5.16	125.96	120.13
1	A	281	VAL	CA-C-N	-5.15	115.54	122.91
1	A	281	VAL	C-N-CA	-5.15	115.54	122.91
1	B	278	GLN	CA-C-N	-5.15	111.71	121.54
1	B	278	GLN	C-N-CA	-5.15	111.71	121.54
1	H	128	LYS	N-CA-CB	-5.15	102.55	110.12
1	F	355	ARG	NE-CZ-NH1	-5.14	116.36	121.50
1	A	270	GLU	N-CA-C	5.14	116.57	108.55
1	E	373	SER	N-CA-C	5.14	117.97	109.85
1	G	281	VAL	CA-C-N	-5.14	116.46	122.93
1	G	281	VAL	C-N-CA	-5.14	116.46	122.93
1	H	153	PRO	CA-C-N	-5.13	114.19	122.25
1	H	153	PRO	C-N-CA	-5.13	114.19	122.25
1	B	222	TRP	N-CA-C	-5.13	100.54	108.90
1	D	117	PRO	CA-C-O	-5.13	111.27	120.60
1	H	194	GLU	N-CA-C	-5.13	103.27	110.50
1	D	270	GLU	N-CA-C	5.12	114.72	108.11
1	E	141	ASP	N-CA-C	5.12	117.25	111.11
1	C	221	LEU	CA-C-O	5.12	126.94	121.16
1	G	192	VAL	CG1-CB-CG2	5.12	122.06	110.80
1	B	375	VAL	N-CA-C	5.11	115.06	108.82
1	D	186	ASN	N-CA-CB	-5.11	108.35	114.17
1	E	296	GLY	N-CA-C	-5.11	104.46	111.76
1	D	182	VAL	N-CA-C	5.10	115.32	107.77
1	D	271	PRO	O-C-N	5.10	129.88	123.05
1	B	268	ALA	N-CA-C	5.10	119.50	113.28
1	F	159	GLY	N-CA-C	-5.10	106.02	114.48
1	F	141	ASP	N-CA-C	5.09	117.22	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	344	LYS	CD-CE-NZ	5.08	128.17	111.90
1	C	365	LYS	CB-CA-C	-5.08	102.90	110.88
1	B	360	CYS	N-CA-C	-5.08	106.43	113.18
1	H	248	LEU	N-CA-C	5.08	116.81	111.28
1	G	172	PHE	CA-C-O	-5.07	115.43	121.16
1	A	308	GLU	N-CA-C	-5.07	106.23	112.72
1	H	347	LYS	CG-CD-CE	-5.07	99.64	111.30
1	D	147	ILE	CB-CA-C	-5.07	105.30	112.14
1	G	203	LEU	N-CA-C	5.06	116.61	111.14
1	G	226	ARG	N-CA-CB	5.06	118.80	110.39
1	G	141	ASP	N-CA-C	5.06	121.58	110.80
1	A	230	ARG	N-CA-C	-5.06	104.84	111.02
1	A	368	ILE	N-CA-C	-5.05	106.21	113.07
1	D	173	TYR	N-CA-C	5.04	117.66	109.24
1	C	165	GLN	N-CA-C	5.04	117.54	110.23
1	A	120	TYR	CB-CA-C	-5.04	102.48	110.84
1	B	113	ARG	CB-CG-CD	5.04	122.89	111.30
1	B	192	VAL	N-CA-CB	-5.04	105.55	111.90
1	E	239	ARG	CB-CG-CD	-5.03	99.72	111.30
1	H	269	LEU	N-CA-C	-5.03	103.84	110.43
1	F	285	GLU	N-CA-C	5.03	117.41	110.07
1	A	230	ARG	CD-NE-CZ	-5.02	117.37	124.40
1	F	263	LEU	CA-CB-CG	-5.02	98.73	116.30
1	A	246	GLU	N-CA-CB	5.02	118.06	110.28
1	C	294	LEU	CA-C-N	-5.01	114.09	122.21
1	C	294	LEU	C-N-CA	-5.01	114.09	122.21
1	G	341	GLY	N-CA-C	-5.01	102.12	112.34
1	A	115	VAL	N-CA-CB	-5.01	102.97	111.23
1	B	330	ASN	N-CA-C	-5.00	104.49	111.39

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2100	0	2069	752	0
1	B	2100	0	2071	729	0
1	C	2100	0	2069	808	0
1	D	2086	0	2060	726	0
1	E	2100	0	2071	703	0
1	F	2100	0	2071	708	0
1	G	2100	0	2071	619	0
1	H	2100	0	2071	760	0
2	A	44	0	22	40	0
2	B	44	0	22	55	0
2	C	44	0	22	36	0
2	D	44	0	22	37	0
2	E	44	0	22	35	0
2	F	44	0	22	29	0
2	G	44	0	22	30	0
2	H	44	0	22	38	0
All	All	17138	0	16729	5572	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 165.

All (5572) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:VAL:CA	1:A:112:VAL:C	1.74	1.54
1:A:112:VAL:CA	1:A:112:VAL:CB	1.81	1.53
2:C:402:CMP:H2	2:C:402:CMP:C2	0.97	1.50
2:A:401:CMP:H2	2:A:401:CMP:C2	0.97	1.49
2:A:402:CMP:H2	2:A:402:CMP:C2	0.97	1.49
2:E:401:CMP:H2	2:E:401:CMP:C2	0.97	1.49
2:G:402:CMP:C2	2:G:402:CMP:H2	0.97	1.49
2:H:402:CMP:H2	2:H:402:CMP:C2	0.97	1.49
2:D:401:CMP:H2	2:D:401:CMP:C2	0.97	1.48
2:H:401:CMP:H2	2:H:401:CMP:C2	0.97	1.48
2:D:402:CMP:H2	2:D:402:CMP:C2	0.97	1.48
2:B:401:CMP:H2	2:B:401:CMP:C2	0.97	1.48
2:C:401:CMP:H2	2:C:401:CMP:C2	0.97	1.48
2:B:402:CMP:H2	2:B:402:CMP:C2	0.97	1.48
2:F:401:CMP:H2	2:F:401:CMP:C2	0.97	1.48
2:E:402:CMP:H2	2:E:402:CMP:C2	0.97	1.48
2:G:401:CMP:C2	2:G:401:CMP:H2	0.97	1.47
2:F:402:CMP:H2	2:F:402:CMP:C2	0.97	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:273:GLN:HE21	1:G:273:GLN:N	1.06	1.42
1:C:273:GLN:HE21	1:C:273:GLN:N	1.14	1.40
1:F:318:PRO:CG	1:F:318:PRO:CD	1.86	1.36
1:A:165:GLN:N	1:A:212:THR:HG23	1.41	1.30
1:B:165:GLN:N	1:B:212:THR:HG23	1.48	1.28
1:A:230:ARG:NH1	1:A:234:MET:HE1	1.43	1.28
1:C:156:PHE:CE2	1:C:162:VAL:HG12	1.67	1.28
1:H:294:LEU:HD12	1:H:295:GLU:N	1.46	1.28
1:C:280:ILE:CD1	1:C:322:PHE:HE2	1.47	1.27
1:H:302:GLN:HE22	1:H:374:PHE:CB	1.48	1.26
1:D:165:GLN:N	1:D:212:THR:HG23	1.52	1.25
1:G:273:GLN:N	1:G:273:GLN:NE2	1.80	1.25
1:H:175:ILE:O	1:H:175:ILE:HD12	1.29	1.24
1:E:111:TYR:CE2	1:H:111:TYR:HE2	1.56	1.24
1:B:313:VAL:HG21	2:B:402:CMP:N6	1.50	1.24
1:A:175:ILE:HD12	1:A:175:ILE:O	1.37	1.23
1:C:230:ARG:NH1	1:C:234:MET:HE1	1.53	1.23
1:E:273:GLN:N	1:E:273:GLN:HE21	1.33	1.23
1:B:175:ILE:HD12	1:B:175:ILE:O	1.36	1.22
1:H:280:ILE:CD1	1:H:322:PHE:HE2	1.51	1.22
1:C:284:GLY:C	1:C:332:PRO:HB3	1.65	1.21
1:F:157:ILE:HD12	1:H:243:MET:CE	1.69	1.21
1:H:284:GLY:O	1:H:332:PRO:HB3	1.41	1.21
1:A:273:GLN:N	1:A:273:GLN:HE21	1.35	1.20
1:G:165:GLN:N	1:G:212:THR:HG23	1.56	1.20
1:E:182:VAL:HG22	1:E:190:THR:O	1.39	1.20
1:H:156:PHE:CE2	1:H:162:VAL:HG12	1.76	1.20
1:F:175:ILE:HD12	1:F:175:ILE:O	1.42	1.20
1:C:280:ILE:HD13	1:C:322:PHE:CE2	1.77	1.19
1:D:156:PHE:CD2	1:D:162:VAL:HG12	1.76	1.19
1:E:156:PHE:CD2	1:E:162:VAL:HG12	1.77	1.19
1:A:165:GLN:H	1:A:212:THR:CG2	1.55	1.19
1:G:265:VAL:HG12	1:G:269:LEU:HD11	1.20	1.19
1:E:165:GLN:N	1:E:212:THR:HG23	1.55	1.18
1:F:182:VAL:HG22	1:F:190:THR:O	1.39	1.18
1:C:196:GLY:HA2	1:C:355:ARG:NH2	1.57	1.18
1:G:273:GLN:NE2	1:G:273:GLN:H	1.35	1.18
1:H:156:PHE:CD2	1:H:162:VAL:HG12	1.78	1.18
1:B:273:GLN:N	1:B:273:GLN:NE2	1.92	1.18
1:C:243:MET:CE	1:E:157:ILE:HD12	1.73	1.18
1:D:126:LEU:HD12	1:D:126:LEU:O	1.42	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:293:ILE:HG13	1:G:345:CYS:SG	1.83	1.18
1:B:273:GLN:NE2	1:B:273:GLN:H	1.40	1.17
1:E:196:GLY:HA2	1:E:355:ARG:NH2	1.56	1.17
1:G:175:ILE:HD12	1:G:175:ILE:O	1.40	1.17
1:C:178:GLY:HA3	1:C:219:VAL:HG12	1.22	1.17
1:E:265:VAL:CG1	1:E:269:LEU:HD21	1.73	1.17
1:F:157:ILE:HD12	1:H:243:MET:HE1	1.26	1.17
1:C:249:SER:CA	1:C:262:ARG:HH22	1.58	1.17
1:D:175:ILE:HD12	1:D:175:ILE:O	1.42	1.17
1:E:112:VAL:HG12	1:E:231:ARG:CZ	1.72	1.17
1:E:156:PHE:CE2	1:E:162:VAL:HG12	1.79	1.17
1:C:279:LYS:HE2	1:C:336:THR:HG23	1.23	1.17
1:E:300:VAL:HG21	2:E:402:CMP:H8	1.25	1.17
1:C:272:VAL:C	1:C:273:GLN:HE21	1.52	1.16
1:C:273:GLN:N	1:C:273:GLN:NE2	1.93	1.16
1:A:182:VAL:HG22	1:A:190:THR:O	1.43	1.16
1:B:158:ALA:HB2	1:B:217:THR:C	1.70	1.16
1:C:284:GLY:O	1:C:332:PRO:HB3	1.45	1.16
1:G:293:ILE:HD11	1:G:343:LEU:CD1	1.76	1.16
1:A:301:LEU:HB3	1:A:310:PHE:HE2	1.02	1.16
1:C:157:ILE:HD12	1:C:157:ILE:O	1.46	1.16
1:F:251:VAL:CG1	1:F:254:LEU:HD21	1.75	1.16
1:C:265:VAL:O	1:C:269:LEU:HG	1.44	1.16
1:F:289:GLU:HG3	1:F:347:LYS:HZ3	1.01	1.15
1:G:265:VAL:HG13	1:G:269:LEU:HD21	1.20	1.15
1:D:279:LYS:HB2	1:D:279:LYS:NZ	1.33	1.15
1:D:353:PHE:CE1	1:D:357:LEU:HD22	1.82	1.15
1:D:251:VAL:HG13	1:D:254:LEU:HD11	1.16	1.15
1:C:113:ARG:HG3	1:F:112:VAL:HG11	1.28	1.14
1:F:165:GLN:N	1:F:212:THR:HG23	1.60	1.14
1:C:182:VAL:HG22	1:C:190:THR:O	1.47	1.14
1:G:265:VAL:O	1:G:269:LEU:HG	1.42	1.14
1:E:111:TYR:HE2	1:H:112:VAL:HG12	1.10	1.14
1:H:272:VAL:HA	1:H:273:GLN:NE2	1.63	1.14
1:D:301:LEU:HD21	1:D:310:PHE:HB3	1.17	1.14
1:H:111:TYR:CD2	1:H:112:VAL:N	2.14	1.14
1:H:230:ARG:NH1	1:H:234:MET:HE1	1.63	1.14
1:A:115:VAL:CG2	1:D:112:VAL:HG23	1.79	1.13
1:C:113:ARG:HG3	1:F:112:VAL:CG1	1.79	1.13
1:C:266:ALA:HA	1:C:269:LEU:HD12	1.13	1.12
1:F:156:PHE:CD2	1:F:162:VAL:HG12	1.84	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:GLY:HA3	1:A:219:VAL:HG12	1.24	1.12
1:E:175:ILE:HD12	1:E:175:ILE:O	1.47	1.12
1:C:175:ILE:HD12	1:C:175:ILE:O	1.48	1.12
1:C:285:GLU:O	1:C:332:PRO:HA	1.49	1.12
1:C:294:LEU:HD13	1:C:344:LYS:O	1.44	1.12
1:C:356:VAL:HG23	1:C:357:LEU:HD13	1.29	1.12
1:D:259:LYS:O	1:D:262:ARG:HG2	1.45	1.12
1:D:165:GLN:H	1:D:212:THR:CG2	1.63	1.11
1:G:294:LEU:HD12	1:G:294:LEU:N	1.62	1.11
1:B:269:LEU:HB3	1:B:346:VAL:CG2	1.81	1.11
1:C:294:LEU:HD11	1:C:345:CYS:HA	1.21	1.11
1:C:294:LEU:HD12	1:C:294:LEU:N	1.61	1.11
1:F:162:VAL:HG23	1:F:163:ILE:HG13	1.19	1.11
1:C:115:VAL:HG23	1:F:110:SER:HB2	1.29	1.11
1:D:251:VAL:CG1	1:D:254:LEU:HD11	1.81	1.11
1:E:279:LYS:HB2	1:E:279:LYS:NZ	1.45	1.11
1:C:280:ILE:HD13	1:C:322:PHE:HE2	1.08	1.11
1:H:165:GLN:N	1:H:212:THR:HG23	1.65	1.11
1:A:325:ILE:HD11	2:A:402:CMP:O2P	1.49	1.10
1:B:294:LEU:HD11	1:B:345:CYS:HA	1.30	1.10
1:D:294:LEU:HD11	1:D:345:CYS:HA	1.28	1.10
1:D:293:ILE:HD11	1:D:343:LEU:HD11	1.21	1.10
1:D:156:PHE:CE2	1:D:162:VAL:HG12	1.86	1.10
1:B:165:GLN:H	1:B:212:THR:CG2	1.63	1.10
1:C:165:GLN:N	1:C:212:THR:HG23	1.66	1.10
1:D:294:LEU:HD12	1:D:294:LEU:H	1.12	1.10
1:F:156:PHE:CE2	1:F:162:VAL:HG12	1.86	1.10
1:G:266:ALA:HA	1:G:269:LEU:HD12	1.14	1.10
1:E:265:VAL:O	1:E:269:LEU:HG	1.50	1.10
1:G:182:VAL:HG22	1:G:190:THR:O	1.51	1.10
1:C:249:SER:HA	1:C:262:ARG:HH22	1.11	1.09
1:F:196:GLY:HA2	1:F:355:ARG:NH2	1.67	1.09
1:G:265:VAL:CG1	1:G:269:LEU:HD21	1.82	1.09
1:A:113:ARG:NE	1:D:113:ARG:HB3	1.66	1.09
1:C:274:PHE:HD2	1:C:343:LEU:HD23	1.12	1.09
1:D:233:LEU:H	1:D:233:LEU:HD12	1.15	1.09
1:D:324:GLU:OE2	1:D:371:TYR:HE2	1.35	1.09
1:F:279:LYS:HB2	1:F:279:LYS:HZ3	1.13	1.09
1:G:126:LEU:HD12	1:G:126:LEU:O	1.49	1.09
1:G:294:LEU:HD11	1:G:345:CYS:HA	1.33	1.09
1:E:162:VAL:HG23	1:E:163:ILE:HG13	1.32	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:273:GLN:N	1:F:273:GLN:HE21	1.50	1.09
1:E:324:GLU:O	1:E:328:LEU:HD12	1.52	1.09
1:H:182:VAL:HG22	1:H:190:THR:O	1.51	1.09
1:A:115:VAL:HG21	1:D:112:VAL:HG23	1.24	1.09
1:B:294:LEU:HD13	1:B:344:LYS:O	1.51	1.09
1:F:280:ILE:CD1	1:F:322:PHE:HE2	1.65	1.09
1:A:156:PHE:CD2	1:A:162:VAL:HG12	1.88	1.08
1:B:324:GLU:O	1:B:328:LEU:HD12	1.51	1.08
1:D:356:VAL:HG23	1:D:357:LEU:HD12	1.30	1.08
1:D:365:LYS:O	1:D:368:ILE:HG13	1.53	1.08
1:F:114:LYS:HZ2	1:F:115:VAL:HG22	1.07	1.08
1:F:229:TYR:CD1	1:F:233:LEU:HD13	1.88	1.08
1:H:260:TRP:HE1	2:H:401:CMP:H2'	1.13	1.08
1:A:190:THR:HG22	1:A:191:SER:H	1.15	1.08
1:E:251:VAL:HG13	1:E:254:LEU:HD21	1.28	1.08
1:B:229:TYR:CD1	1:B:233:LEU:HD13	1.88	1.08
1:D:182:VAL:HG22	1:D:190:THR:O	1.51	1.08
1:D:253:ILE:HG13	1:D:254:LEU:HD13	1.35	1.08
1:E:293:ILE:HD13	1:E:317:GLY:O	1.54	1.08
1:G:365:LYS:O	1:G:368:ILE:HG13	1.54	1.08
1:A:116:ILE:O	1:A:118:LYS:HG3	1.50	1.08
1:A:198:PHE:HD1	1:A:198:PHE:C	1.57	1.08
1:B:161:THR:HA	1:B:214:LYS:HD2	1.30	1.08
1:G:165:GLN:H	1:G:212:THR:CG2	1.67	1.08
1:H:178:GLY:HA3	1:H:219:VAL:HG12	1.31	1.08
1:A:269:LEU:HD22	1:A:346:VAL:HG21	1.36	1.07
1:E:112:VAL:HG12	1:E:231:ARG:NE	1.68	1.07
1:E:294:LEU:N	1:E:294:LEU:HD12	1.57	1.07
1:G:294:LEU:CD1	1:G:345:CYS:HA	1.84	1.07
1:A:126:LEU:HD12	1:A:126:LEU:O	1.51	1.07
1:A:294:LEU:CD1	1:A:345:CYS:HA	1.85	1.07
1:B:294:LEU:H	1:B:294:LEU:HD12	1.13	1.07
1:C:265:VAL:HG12	1:C:269:LEU:HD11	1.12	1.07
1:G:293:ILE:HD11	1:G:343:LEU:HD11	1.08	1.07
1:H:228:SER:O	1:H:232:ILE:HG22	1.54	1.07
1:H:273:GLN:HB3	1:H:344:LYS:HA	1.36	1.07
1:H:356:VAL:HG23	1:H:357:LEU:HD13	1.32	1.07
1:D:251:VAL:HG23	1:D:319:SER:O	1.55	1.07
1:E:175:ILE:HD11	1:E:196:GLY:H	1.17	1.07
1:G:279:LYS:HB2	1:G:279:LYS:NZ	1.53	1.07
1:B:175:ILE:HA	1:B:221:LEU:CD2	1.85	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:134:VAL:HG11	1:D:268:ALA:HA	1.36	1.07
1:D:273:GLN:HE21	1:D:273:GLN:N	1.51	1.07
1:C:134:VAL:HG11	1:C:268:ALA:HA	1.33	1.07
1:D:294:LEU:CD1	1:D:345:CYS:HA	1.85	1.07
1:E:226:ARG:HH11	1:E:226:ARG:HG3	1.18	1.07
1:E:294:LEU:CD1	1:E:345:CYS:HA	1.85	1.07
1:F:255:GLU:OE1	1:F:255:GLU:HA	1.53	1.07
1:A:294:LEU:HD11	1:A:345:CYS:HA	1.34	1.06
1:F:226:ARG:HH11	1:F:226:ARG:HG3	1.15	1.06
1:H:134:VAL:HG11	1:H:268:ALA:HA	1.36	1.06
1:B:196:GLY:HA2	1:B:355:ARG:NH2	1.70	1.06
1:D:298:ALA:HB1	1:D:338:VAL:O	1.56	1.06
1:F:126:LEU:HD12	1:F:126:LEU:O	1.56	1.06
1:H:165:GLN:H	1:H:212:THR:HG23	0.93	1.06
1:A:175:ILE:HA	1:A:221:LEU:CD2	1.85	1.06
1:H:157:ILE:HD12	1:H:157:ILE:O	1.56	1.06
1:A:273:GLN:N	1:A:273:GLN:NE2	2.01	1.06
1:C:229:TYR:HD1	1:C:233:LEU:CD1	1.69	1.06
1:E:165:GLN:H	1:E:212:THR:CG2	1.68	1.06
1:H:280:ILE:CD1	1:H:322:PHE:CE2	2.39	1.06
1:B:116:ILE:O	1:B:118:LYS:HG3	1.55	1.06
1:C:111:TYR:HE1	1:F:111:TYR:CE2	1.75	1.05
1:C:294:LEU:CD1	1:C:345:CYS:HA	1.84	1.05
1:F:294:LEU:HD12	1:F:294:LEU:N	1.70	1.05
1:F:324:GLU:O	1:F:328:LEU:HD12	1.55	1.05
1:G:226:ARG:HG3	1:G:226:ARG:HH11	1.15	1.05
1:C:111:TYR:CE1	1:F:111:TYR:CE2	2.44	1.05
1:D:200:GLU:HG2	1:D:201:LEU:H	1.15	1.05
1:G:211:ASP:CG	2:G:401:CMP:H5'1	1.81	1.05
1:C:278:GLN:HG3	1:C:279:LYS:N	1.66	1.05
1:D:291:PHE:CE1	1:D:347:LYS:NZ	2.25	1.05
1:H:279:LYS:NZ	1:H:336:THR:HG23	1.72	1.05
1:F:289:GLU:HG3	1:F:347:LYS:NZ	1.69	1.04
1:A:114:LYS:HG3	1:A:115:VAL:H	1.22	1.04
1:G:294:LEU:HD12	1:G:294:LEU:H	0.99	1.04
1:A:371:TYR:CE1	2:A:402:CMP:C8	2.41	1.04
1:C:272:VAL:HA	1:C:273:GLN:NE2	1.72	1.04
1:F:251:VAL:HG12	1:F:254:LEU:CD2	1.88	1.04
1:G:279:LYS:HZ3	1:G:279:LYS:CB	1.54	1.04
1:C:113:ARG:HD2	1:F:112:VAL:HB	1.37	1.04
1:C:243:MET:HE1	1:E:157:ILE:HD12	1.37	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:190:THR:HG22	1:D:191:SER:H	1.21	1.04
1:D:279:LYS:NZ	1:D:279:LYS:CB	2.06	1.04
1:D:324:GLU:HG2	1:D:325:ILE:N	1.70	1.04
1:D:356:VAL:HG23	1:D:357:LEU:CD1	1.86	1.04
1:G:161:THR:HA	1:G:214:LYS:HD2	1.40	1.04
1:G:233:LEU:H	1:G:233:LEU:HD12	1.22	1.04
1:H:272:VAL:CA	1:H:273:GLN:NE2	2.21	1.04
1:A:262:ARG:O	1:A:265:VAL:HB	1.56	1.04
1:C:158:ALA:HB2	1:C:217:THR:C	1.83	1.04
1:C:275:GLU:O	1:C:278:GLN:HB3	1.56	1.04
1:A:294:LEU:H	1:A:294:LEU:HD12	1.13	1.03
1:B:182:VAL:HG22	1:B:190:THR:O	1.56	1.03
1:C:156:PHE:CD2	1:C:162:VAL:HG12	1.91	1.03
1:C:281:VAL:HG11	1:C:333:ARG:HD2	1.35	1.03
1:D:293:ILE:HG13	1:D:345:CYS:SG	1.98	1.03
1:D:294:LEU:HD12	1:D:294:LEU:N	1.68	1.03
1:A:365:LYS:O	1:A:368:ILE:HG13	1.58	1.03
1:B:153:PRO:HB3	1:B:222:TRP:CZ3	1.92	1.03
1:B:356:VAL:HG23	1:B:357:LEU:HD13	1.34	1.03
1:G:302:GLN:CG	1:G:313:VAL:HG11	1.87	1.03
1:H:280:ILE:HD13	1:H:322:PHE:CE2	1.92	1.03
1:F:112:VAL:HG13	1:F:113:ARG:H	1.24	1.03
1:F:172:PHE:HB3	1:F:224:ILE:HD11	1.40	1.03
1:B:280:ILE:CD1	1:B:322:PHE:HE2	1.72	1.03
1:C:113:ARG:CG	1:F:112:VAL:HG11	1.88	1.03
1:C:269:LEU:HB3	1:C:346:VAL:CG2	1.89	1.03
1:D:293:ILE:HD11	1:D:343:LEU:CD1	1.88	1.03
1:G:251:VAL:HG13	1:G:254:LEU:HD21	1.37	1.03
1:H:251:VAL:O	1:H:254:LEU:HD11	1.57	1.03
1:B:251:VAL:HG13	1:B:254:LEU:HD21	1.35	1.03
1:E:266:ALA:HA	1:E:269:LEU:HD12	1.33	1.03
1:F:175:ILE:HD11	1:F:196:GLY:H	1.21	1.03
1:G:190:THR:HG22	1:G:191:SER:H	1.23	1.03
1:A:115:VAL:HG21	1:D:112:VAL:H	1.20	1.02
1:D:279:LYS:CB	1:D:279:LYS:HZ3	1.68	1.02
1:E:299:ALA:HB1	1:E:312:GLU:OE2	1.56	1.02
1:G:266:ALA:HA	1:G:269:LEU:CD1	1.89	1.02
1:C:165:GLN:H	1:C:212:THR:CG2	1.71	1.02
1:E:175:ILE:HA	1:E:221:LEU:CD2	1.90	1.02
1:E:265:VAL:HG13	1:E:269:LEU:HD21	1.36	1.02
1:E:325:ILE:HD11	2:E:402:CMP:O2P	1.59	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:279:LYS:NZ	1:H:279:LYS:HB2	1.75	1.02
1:A:113:ARG:HE	1:D:113:ARG:HB3	0.89	1.02
1:B:111:TYR:O	1:B:112:VAL:HG22	1.58	1.02
1:B:280:ILE:HD11	1:B:322:PHE:HE2	1.17	1.02
1:C:249:SER:HA	1:C:262:ARG:NH2	1.73	1.02
1:C:280:ILE:CD1	1:C:322:PHE:CE2	2.38	1.02
1:E:229:TYR:CD1	1:E:233:LEU:HD13	1.94	1.02
1:A:266:ALA:HA	1:A:269:LEU:HD12	1.37	1.02
1:B:280:ILE:CD1	1:B:322:PHE:CE2	2.43	1.02
1:B:294:LEU:HD12	1:B:294:LEU:N	1.73	1.02
1:D:273:GLN:N	1:D:273:GLN:NE2	2.06	1.02
1:E:294:LEU:HD12	1:E:294:LEU:H	1.06	1.02
1:F:114:LYS:NZ	1:F:115:VAL:HG22	1.74	1.02
1:B:180:MET:HB2	1:B:192:VAL:HB	1.40	1.02
1:C:115:VAL:HA	1:C:149:ASP:HB3	1.39	1.02
1:C:226:ARG:HH11	1:C:226:ARG:HG3	1.19	1.02
1:E:273:GLN:N	1:E:273:GLN:NE2	2.06	1.02
1:H:114:LYS:NZ	1:H:115:VAL:H	1.55	1.02
1:H:226:ARG:HH11	1:H:226:ARG:HG3	1.22	1.02
1:H:229:TYR:CD1	1:H:233:LEU:HD13	1.95	1.02
1:H:284:GLY:C	1:H:332:PRO:HB3	1.85	1.02
1:A:114:LYS:CG	1:A:115:VAL:H	1.72	1.01
1:B:126:LEU:HD12	1:B:126:LEU:O	1.59	1.01
1:B:172:PHE:HB3	1:B:224:ILE:HD11	1.40	1.01
1:E:111:TYR:CE2	1:H:111:TYR:CE2	2.47	1.01
1:H:161:THR:HA	1:H:214:LYS:HD2	1.42	1.01
1:A:301:LEU:HB3	1:A:310:PHE:CE2	1.94	1.01
1:E:348:LEU:HD21	1:E:356:VAL:HG21	1.43	1.01
1:H:251:VAL:HG13	1:H:254:LEU:HD21	1.38	1.01
1:A:229:TYR:CD1	1:A:233:LEU:HD13	1.95	1.01
1:C:229:TYR:CD1	1:C:233:LEU:CD1	2.43	1.01
1:D:162:VAL:HG23	1:D:163:ILE:HG13	1.39	1.01
1:D:260:TRP:HE1	2:D:401:CMP:H2'	1.23	1.01
1:F:165:GLN:H	1:F:212:THR:HG23	0.84	1.01
1:G:162:VAL:HG23	1:G:163:ILE:HG13	1.40	1.01
1:H:112:VAL:HG13	1:H:113:ARG:H	1.25	1.01
1:C:279:LYS:HE2	1:C:336:THR:CG2	1.90	1.01
1:D:135:LEU:HD12	1:D:136:PHE:H	1.25	1.01
1:E:243:MET:HE1	1:G:157:ILE:HD12	1.42	1.01
1:B:156:PHE:CD2	1:B:162:VAL:HG12	1.95	1.00
1:B:190:THR:HG22	1:B:191:SER:H	1.24	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:165:GLN:H	1:C:212:THR:HG23	0.86	1.00
1:C:175:ILE:HA	1:C:221:LEU:CD2	1.91	1.00
1:E:294:LEU:HD11	1:E:345:CYS:HA	1.43	1.00
1:F:260:TRP:HE1	2:F:401:CMP:H2'	1.26	1.00
1:G:230:ARG:NH1	1:G:234:MET:HE1	1.74	1.00
1:H:165:GLN:H	1:H:212:THR:CG2	1.74	1.00
1:H:272:VAL:HA	1:H:273:GLN:HE22	1.13	1.00
1:A:115:VAL:CB	1:D:112:VAL:HG23	1.90	1.00
1:A:260:TRP:CE2	2:A:401:CMP:C8	2.43	1.00
1:H:190:THR:HG22	1:H:191:SER:H	1.25	1.00
1:H:274:PHE:HD2	1:H:343:LEU:HD23	1.22	1.00
1:A:161:THR:HA	1:A:214:LYS:HD2	1.44	1.00
1:A:198:PHE:C	1:A:198:PHE:CD1	2.32	1.00
1:A:371:TYR:HE1	2:A:402:CMP:C8	1.74	1.00
1:B:269:LEU:HB3	1:B:346:VAL:HG21	1.38	1.00
1:F:165:GLN:H	1:F:212:THR:CG2	1.75	1.00
1:G:196:GLY:HA2	1:G:355:ARG:NH2	1.76	1.00
1:G:302:GLN:HG3	1:G:313:VAL:CG1	1.92	1.00
1:H:158:ALA:HB2	1:H:217:THR:C	1.86	1.00
1:H:211:ASP:CG	2:H:401:CMP:H5'1	1.85	1.00
1:H:249:SER:CA	1:H:262:ARG:HH22	1.74	1.00
1:C:266:ALA:HA	1:C:269:LEU:CD1	1.92	1.00
1:F:233:LEU:HD12	1:F:233:LEU:H	1.26	1.00
1:B:139:LEU:HD12	1:B:139:LEU:H	1.26	1.00
1:C:139:LEU:H	1:C:139:LEU:HD12	1.24	1.00
1:E:126:LEU:O	1:E:126:LEU:HD12	1.60	1.00
1:E:265:VAL:HG12	1:E:269:LEU:HD11	1.41	1.00
1:E:280:ILE:CD1	1:E:322:PHE:HE2	1.75	1.00
1:G:229:TYR:CD1	1:G:233:LEU:HD13	1.96	1.00
1:C:282:VAL:O	1:C:285:GLU:HG2	1.62	1.00
1:D:229:TYR:CD1	1:D:233:LEU:HD13	1.97	1.00
1:E:279:LYS:NZ	1:E:279:LYS:CB	2.21	1.00
1:A:255:GLU:OE1	1:A:255:GLU:HA	1.56	1.00
1:B:294:LEU:CD1	1:B:345:CYS:HA	1.91	0.99
1:C:293:ILE:HD11	1:C:343:LEU:HD11	1.43	0.99
1:G:251:VAL:CG1	1:G:254:LEU:HD21	1.92	0.99
1:H:300:VAL:O	1:H:301:LEU:HD23	1.61	0.99
1:F:280:ILE:CD1	1:F:322:PHE:CE2	2.45	0.99
1:H:226:ARG:HG3	1:H:226:ARG:NH1	1.75	0.99
1:A:357:LEU:N	1:A:357:LEU:HD12	1.55	0.99
1:H:182:VAL:HG23	1:H:182:VAL:O	1.61	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:ARG:HE	1:D:113:ARG:CB	1.73	0.99
1:A:269:LEU:HB3	1:A:346:VAL:CG2	1.93	0.99
1:D:371:TYR:CE1	2:D:402:CMP:N7	2.30	0.99
1:A:158:ALA:HB2	1:A:217:THR:C	1.87	0.99
1:A:233:LEU:H	1:A:233:LEU:HD12	1.26	0.99
1:A:112:VAL:C	1:A:112:VAL:HA	1.86	0.99
1:A:294:LEU:HD12	1:A:294:LEU:N	1.75	0.99
1:B:226:ARG:HG3	1:B:226:ARG:HH11	1.27	0.99
1:E:282:VAL:O	1:E:285:GLU:HG2	1.63	0.99
1:G:293:ILE:CD1	1:G:343:LEU:HD11	1.92	0.99
1:A:175:ILE:HD13	1:A:194:GLU:HA	1.45	0.99
1:C:110:SER:HB3	1:F:114:LYS:HE2	1.40	0.99
1:D:247:PHE:HE1	1:D:294:LEU:HA	1.27	0.99
1:G:356:VAL:HG23	1:G:357:LEU:CD1	1.93	0.98
1:A:172:PHE:HB3	1:A:224:ILE:HD11	1.44	0.98
1:E:111:TYR:CE2	1:H:112:VAL:HG12	1.98	0.98
1:A:135:LEU:HD12	1:A:136:PHE:H	1.24	0.98
1:E:111:TYR:HE2	1:H:112:VAL:CG1	1.76	0.98
1:A:157:ILE:O	1:A:157:ILE:HD12	1.64	0.98
1:C:265:VAL:HG13	1:C:269:LEU:HD21	1.45	0.98
1:E:365:LYS:O	1:E:368:ILE:HG13	1.63	0.98
1:H:269:LEU:HB3	1:H:346:VAL:HG21	1.45	0.98
1:D:259:LYS:HG3	1:D:260:TRP:N	1.79	0.98
1:C:273:GLN:HB3	1:C:343:LEU:O	1.63	0.98
1:H:154:VAL:HG12	1:H:221:LEU:HB2	1.45	0.98
1:A:251:VAL:HG23	1:A:319:SER:O	1.63	0.98
1:B:200:GLU:HG2	1:B:201:LEU:H	1.29	0.98
1:C:229:TYR:CD1	1:C:233:LEU:HD13	1.98	0.98
1:D:226:ARG:HH11	1:D:226:ARG:HG3	1.23	0.98
1:H:196:GLY:HA2	1:H:355:ARG:NH2	1.77	0.98
1:D:247:PHE:CE1	1:D:294:LEU:HA	1.98	0.98
1:H:229:TYR:CD1	1:H:233:LEU:CD1	2.47	0.98
1:B:233:LEU:H	1:B:233:LEU:HD12	1.26	0.97
1:E:251:VAL:HG23	1:E:319:SER:O	1.63	0.97
1:H:230:ARG:CZ	1:H:234:MET:HE1	1.92	0.97
1:A:135:LEU:HD12	1:A:136:PHE:N	1.80	0.97
1:A:293:ILE:HD11	1:A:343:LEU:HD11	1.42	0.97
1:A:230:ARG:NH1	1:A:234:MET:CE	2.26	0.97
1:C:281:VAL:CG1	1:C:333:ARG:HD2	1.93	0.97
1:D:301:LEU:HD23	1:D:310:PHE:HD1	1.28	0.97
1:B:260:TRP:HE1	2:B:401:CMP:H2'	1.29	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:229:TYR:HD1	1:H:233:LEU:CD1	1.77	0.97
1:C:204:ILE:HG22	1:C:205:TYR:CD2	2.00	0.97
1:F:293:ILE:HD11	1:F:343:LEU:HD11	1.47	0.97
1:A:198:PHE:HD1	1:A:198:PHE:O	1.46	0.97
1:A:361:SER:C	1:A:365:LYS:HZ2	1.73	0.97
1:H:253:ILE:HG13	1:H:254:LEU:H	1.30	0.96
1:A:139:LEU:H	1:A:139:LEU:HD12	1.28	0.96
1:A:226:ARG:HH11	1:A:226:ARG:HG3	1.28	0.96
1:G:148:PHE:CD1	1:H:120:TYR:CE1	2.52	0.96
1:B:229:TYR:HD1	1:B:233:LEU:HD13	1.27	0.96
1:C:294:LEU:HD12	1:C:294:LEU:H	1.16	0.96
1:D:182:VAL:HG12	1:D:213:VAL:HG22	1.43	0.96
1:A:153:PRO:HB3	1:A:222:TRP:CZ3	2.01	0.96
1:C:265:VAL:HG12	1:C:269:LEU:CD1	1.93	0.96
1:E:178:GLY:HA3	1:E:219:VAL:HG12	1.45	0.96
1:B:260:TRP:CE2	2:B:401:CMP:C8	2.48	0.96
1:C:283:GLN:HA	1:C:333:ARG:O	1.66	0.96
1:G:172:PHE:HB3	1:G:224:ILE:HD11	1.46	0.96
1:G:247:PHE:HE1	1:G:294:LEU:HA	1.29	0.96
1:E:249:SER:N	1:E:262:ARG:HH22	1.61	0.96
1:H:294:LEU:HD12	1:H:294:LEU:C	1.87	0.96
1:A:247:PHE:HE1	1:A:294:LEU:HA	1.28	0.96
1:B:273:GLN:N	1:B:273:GLN:HE21	1.53	0.96
1:C:156:PHE:HE2	1:C:162:VAL:HG12	1.19	0.96
1:C:324:GLU:O	1:C:328:LEU:HD12	1.65	0.96
1:D:172:PHE:HB3	1:D:224:ILE:HD11	1.47	0.96
1:F:269:LEU:HB3	1:F:346:VAL:CG2	1.95	0.96
1:F:273:GLN:N	1:F:273:GLN:NE2	2.13	0.96
1:A:280:ILE:HD11	1:A:322:PHE:HE2	1.31	0.96
1:G:279:LYS:HB2	1:G:279:LYS:HZ3	0.79	0.96
1:D:153:PRO:HB3	1:D:222:TRP:CZ3	2.01	0.96
1:F:118:LYS:HE2	1:F:148:PHE:O	1.65	0.96
1:H:114:LYS:HZ1	1:H:115:VAL:H	1.06	0.96
1:C:120:TYR:HB2	1:D:149:ASP:OD1	1.66	0.95
1:H:279:LYS:HE3	1:H:282:VAL:HG22	1.47	0.95
1:A:154:VAL:HG12	1:A:221:LEU:HB2	1.44	0.95
1:C:190:THR:HG22	1:C:191:SER:H	1.30	0.95
1:E:280:ILE:CD1	1:E:322:PHE:CE2	2.50	0.95
1:G:134:VAL:HG11	1:G:268:ALA:HA	1.44	0.95
1:A:251:VAL:HG13	1:A:254:LEU:HD21	1.45	0.95
1:C:120:TYR:CE1	1:D:148:PHE:CD1	2.53	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:274:PHE:CD2	1:C:343:LEU:HD23	1.99	0.95
1:F:113:ARG:HD3	1:F:146:ASP:CG	1.91	0.95
1:G:255:GLU:OE1	1:G:255:GLU:HA	1.65	0.95
1:B:230:ARG:O	1:B:234:MET:HB3	1.63	0.95
1:C:182:VAL:HG23	1:C:182:VAL:O	1.66	0.95
1:G:148:PHE:CB	1:H:120:TYR:HD1	1.79	0.95
1:G:165:GLN:H	1:G:212:THR:HG23	0.80	0.95
1:A:112:VAL:HG22	1:D:115:VAL:HG21	1.46	0.95
1:E:251:VAL:O	1:E:254:LEU:HD11	1.65	0.95
1:F:329:MET:HB2	1:F:331:ARG:HG3	1.48	0.95
1:A:291:PHE:N	1:A:291:PHE:HD1	1.60	0.95
1:B:175:ILE:HD13	1:B:194:GLU:HA	1.45	0.95
1:C:365:LYS:O	1:C:368:ILE:HG13	1.64	0.95
1:H:329:MET:HA	1:H:329:MET:HE3	1.48	0.95
1:A:269:LEU:HD22	1:A:346:VAL:CG2	1.97	0.95
1:B:200:GLU:HG2	1:B:201:LEU:N	1.78	0.95
1:F:259:LYS:O	1:F:262:ARG:HG3	1.63	0.95
1:G:226:ARG:HG3	1:G:226:ARG:NH1	1.72	0.95
1:H:172:PHE:HB3	1:H:224:ILE:HD11	1.49	0.95
1:C:272:VAL:CA	1:C:273:GLN:NE2	2.30	0.95
1:D:279:LYS:HB2	1:D:279:LYS:HZ2	1.31	0.95
1:G:259:LYS:O	1:G:262:ARG:HG3	1.66	0.95
1:A:196:GLY:HA2	1:A:355:ARG:NH2	1.81	0.94
1:C:120:TYR:HD1	1:D:148:PHE:CB	1.80	0.94
1:B:200:GLU:CG	1:B:201:LEU:H	1.79	0.94
1:B:251:VAL:HG23	1:B:319:SER:O	1.66	0.94
1:E:255:GLU:OE1	1:E:255:GLU:HA	1.65	0.94
1:C:172:PHE:HB3	1:C:224:ILE:HD11	1.46	0.94
1:D:279:LYS:HB2	1:D:279:LYS:HZ3	0.88	0.94
1:F:300:VAL:HG22	1:F:337:VAL:HG22	1.48	0.94
1:G:148:PHE:CD1	1:H:120:TYR:HE1	1.85	0.94
1:G:173:TYR:HB2	1:G:198:PHE:CE1	2.02	0.94
1:H:229:TYR:CE1	1:H:233:LEU:HD13	2.01	0.94
1:H:233:LEU:H	1:H:233:LEU:HD12	1.32	0.94
1:B:259:LYS:HG3	1:B:260:TRP:N	1.80	0.94
1:C:265:VAL:CG1	1:C:269:LEU:HD21	1.98	0.94
1:A:259:LYS:HG3	1:A:260:TRP:N	1.78	0.94
1:B:157:ILE:HD12	1:B:157:ILE:O	1.68	0.94
1:B:253:ILE:HG13	1:B:254:LEU:H	1.30	0.94
1:F:175:ILE:HA	1:F:221:LEU:CD2	1.97	0.94
1:G:260:TRP:HE1	2:G:401:CMP:H2'	1.27	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:365:LYS:O	1:H:368:ILE:HG13	1.66	0.94
1:E:273:GLN:HE21	1:E:273:GLN:H	1.07	0.94
1:A:115:VAL:HG21	1:D:112:VAL:N	1.83	0.94
1:B:291:PHE:N	1:B:291:PHE:HD1	1.66	0.94
1:C:356:VAL:HG23	1:C:357:LEU:CD1	1.96	0.94
1:F:114:LYS:NZ	1:F:115:VAL:CG2	2.30	0.94
1:F:279:LYS:HB2	1:F:279:LYS:NZ	1.81	0.94
1:F:300:VAL:CG1	1:F:335:ALA:HB1	1.96	0.94
1:B:350:ARG:HB3	1:B:351:PRO:HD3	1.47	0.94
1:C:120:TYR:HE1	1:D:148:PHE:CD1	1.86	0.94
1:E:211:ASP:OD2	2:E:401:CMP:H3'	1.67	0.94
1:H:198:PHE:CD1	1:H:198:PHE:C	2.43	0.94
1:A:123:MET:HE3	1:B:123:MET:HE3	1.48	0.93
1:A:294:LEU:HD13	1:A:344:LYS:O	1.67	0.93
1:F:229:TYR:HD1	1:F:233:LEU:CD1	1.81	0.93
1:F:294:LEU:HD12	1:F:294:LEU:H	1.31	0.93
1:G:204:ILE:HG12	1:G:234:MET:SD	2.08	0.93
1:H:114:LYS:HZ1	1:H:115:VAL:N	1.65	0.93
1:B:120:TYR:HD2	1:B:120:TYR:C	1.75	0.93
1:C:251:VAL:HG13	1:C:254:LEU:HD21	1.50	0.93
1:D:165:GLN:H	1:D:212:THR:HG23	0.78	0.93
1:E:171:ASN:HB3	1:E:224:ILE:O	1.68	0.93
1:E:173:TYR:HB2	1:E:198:PHE:CE1	2.04	0.93
1:F:294:LEU:CD1	1:F:345:CYS:HA	1.98	0.93
1:H:300:VAL:HG11	2:H:402:CMP:C8	1.98	0.93
1:A:156:PHE:CE2	1:A:162:VAL:HG12	2.03	0.93
1:C:182:VAL:HG12	1:C:213:VAL:HG13	1.51	0.93
1:D:188:TRP:HH2	1:D:191:SER:HG	1.14	0.93
1:B:259:LYS:HG3	1:B:260:TRP:H	1.34	0.93
1:F:171:ASN:HB3	1:F:224:ILE:O	1.69	0.93
1:A:175:ILE:CD1	1:A:194:GLU:HA	1.98	0.93
1:A:182:VAL:HG12	1:A:213:VAL:HG22	1.48	0.93
1:C:115:VAL:CG2	1:F:110:SER:HB2	1.98	0.93
1:D:161:THR:HA	1:D:214:LYS:HD2	1.49	0.93
1:D:324:GLU:HG2	1:D:325:ILE:H	1.21	0.93
1:F:162:VAL:CG2	1:F:163:ILE:HG13	1.99	0.93
1:F:179:GLU:HG2	1:F:216:LYS:HD3	1.50	0.93
1:A:162:VAL:HG23	1:A:163:ILE:HG13	1.49	0.93
1:B:182:VAL:O	1:B:182:VAL:HG23	1.69	0.93
1:G:251:VAL:O	1:G:254:LEU:HD11	1.68	0.93
1:H:182:VAL:HG12	1:H:213:VAL:HG22	1.48	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:ASP:OD2	2:A:401:CMP:H3'	1.69	0.93
1:B:255:GLU:OE1	1:B:255:GLU:HA	1.66	0.93
1:D:175:ILE:HA	1:D:221:LEU:CD2	1.99	0.93
1:D:371:TYR:HE1	2:D:402:CMP:N7	1.66	0.93
1:G:371:TYR:CE1	2:G:402:CMP:C5	2.56	0.93
1:H:269:LEU:HB3	1:H:346:VAL:CG2	1.99	0.93
1:H:272:VAL:C	1:H:273:GLN:HE21	1.75	0.93
1:B:247:PHE:CE1	1:B:294:LEU:HA	2.03	0.93
1:D:273:GLN:HE21	1:D:273:GLN:H	0.99	0.93
1:H:262:ARG:O	1:H:265:VAL:HB	1.69	0.93
1:D:325:ILE:HD11	2:D:402:CMP:O1P	1.69	0.92
1:E:233:LEU:H	1:E:233:LEU:HD12	1.32	0.92
1:F:226:ARG:HG3	1:F:226:ARG:NH1	1.74	0.92
1:H:156:PHE:CD2	1:H:162:VAL:CG1	2.52	0.92
1:H:279:LYS:HZ1	1:H:336:THR:HG23	1.31	0.92
1:B:279:LYS:HE3	1:B:282:VAL:HG22	1.51	0.92
1:C:161:THR:HA	1:C:214:LYS:HD2	1.51	0.92
1:C:179:GLU:HG2	1:C:216:LYS:HD2	1.52	0.92
1:D:293:ILE:CD1	1:D:343:LEU:HD11	1.99	0.92
1:F:161:THR:HA	1:F:214:LYS:HD2	1.49	0.92
1:B:325:ILE:HG13	1:B:326:ALA:H	1.34	0.92
1:D:157:ILE:HB	1:D:218:ASN:OD1	1.70	0.92
1:H:294:LEU:CD1	1:H:295:GLU:N	2.32	0.92
1:A:120:TYR:C	1:A:120:TYR:CD2	2.46	0.92
1:A:357:LEU:HD12	1:A:357:LEU:H	1.31	0.92
1:C:270:GLU:O	1:C:346:VAL:HA	1.68	0.92
1:D:361:SER:C	1:D:365:LYS:HZ2	1.78	0.92
1:C:126:LEU:HD12	1:C:126:LEU:O	1.68	0.92
1:E:172:PHE:HB3	1:E:224:ILE:HD11	1.47	0.92
1:H:356:VAL:HG23	1:H:357:LEU:CD1	1.98	0.92
1:A:280:ILE:CD1	1:A:322:PHE:HE2	1.80	0.92
1:E:265:VAL:HG12	1:E:269:LEU:HD21	1.50	0.92
1:F:280:ILE:HD11	1:F:322:PHE:HE2	1.33	0.92
1:H:139:LEU:H	1:H:139:LEU:HD12	1.35	0.92
1:B:266:ALA:HA	1:B:269:LEU:HD12	1.51	0.92
1:D:204:ILE:HG12	1:D:234:MET:SD	2.08	0.92
1:G:247:PHE:CE1	1:G:294:LEU:HA	2.05	0.92
1:A:249:SER:N	1:A:262:ARG:HH22	1.67	0.92
1:A:259:LYS:HG3	1:A:260:TRP:H	1.31	0.92
1:E:211:ASP:CG	2:E:401:CMP:H5'1	1.95	0.92
1:G:120:TYR:C	1:G:120:TYR:CD2	2.48	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:302:GLN:NE2	1:H:374:PHE:CB	2.32	0.92
1:B:280:ILE:HD13	1:B:322:PHE:CZ	2.04	0.92
1:C:175:ILE:HA	1:C:221:LEU:HD22	1.51	0.92
1:G:302:GLN:HG3	1:G:313:VAL:HG11	0.96	0.92
1:D:118:LYS:HE2	1:D:148:PHE:O	1.70	0.92
1:F:294:LEU:HD11	1:F:345:CYS:HA	1.50	0.92
1:G:153:PRO:HB3	1:G:222:TRP:CZ3	2.05	0.92
1:B:111:TYR:C	1:B:112:VAL:HG22	1.92	0.91
1:B:118:LYS:HE2	1:B:148:PHE:O	1.70	0.91
1:E:113:ARG:O	1:H:112:VAL:HB	1.69	0.91
1:G:265:VAL:HG12	1:G:269:LEU:CD1	1.99	0.91
1:G:279:LYS:NZ	1:G:279:LYS:CB	2.16	0.91
1:G:350:ARG:HB3	1:G:351:PRO:HD3	1.52	0.91
1:H:234:MET:HG3	1:H:238:LEU:HD12	1.52	0.91
1:H:285:GLU:OE1	1:H:285:GLU:HA	1.69	0.91
1:D:196:GLY:HA2	1:D:355:ARG:NH2	1.84	0.91
1:E:289:GLU:HG3	1:E:347:LYS:NZ	1.83	0.91
1:G:301:LEU:HD13	1:G:310:PHE:HB3	1.50	0.91
1:H:274:PHE:CD2	1:H:343:LEU:HD23	2.05	0.91
1:A:247:PHE:CE1	1:A:294:LEU:HA	2.05	0.91
1:B:200:GLU:HG2	1:B:201:LEU:CD1	1.98	0.91
1:C:226:ARG:HG3	1:C:226:ARG:NH1	1.74	0.91
1:E:230:ARG:CZ	1:E:234:MET:HE1	2.00	0.91
1:H:272:VAL:C	1:H:273:GLN:NE2	2.28	0.91
1:B:175:ILE:CD1	1:B:194:GLU:HA	2.00	0.91
1:A:115:VAL:HG21	1:D:112:VAL:CG2	2.00	0.91
1:B:259:LYS:O	1:B:262:ARG:HG3	1.70	0.91
1:B:313:VAL:HG23	1:B:313:VAL:O	1.67	0.91
1:E:228:SER:O	1:E:232:ILE:HG22	1.70	0.91
1:E:230:ARG:NH1	1:E:234:MET:HE1	1.85	0.91
1:F:152:PHE:HE2	1:F:223:GLY:HA3	1.33	0.91
1:B:247:PHE:HE1	1:B:294:LEU:HA	1.33	0.91
1:C:156:PHE:CD2	1:C:162:VAL:CG1	2.53	0.91
1:E:280:ILE:HD11	1:E:322:PHE:HE2	1.34	0.91
1:F:179:GLU:HG2	1:F:216:LYS:CD	1.99	0.91
1:G:251:VAL:HG23	1:G:319:SER:O	1.70	0.91
1:C:198:PHE:C	1:C:198:PHE:CD1	2.38	0.91
1:F:293:ILE:HG13	1:F:345:CYS:SG	2.09	0.91
1:H:280:ILE:HG13	1:H:281:VAL:N	1.82	0.91
1:A:273:GLN:HE21	1:A:273:GLN:H	0.99	0.91
1:C:253:ILE:HG13	1:C:254:LEU:H	1.36	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:111:TYR:HE2	1:H:111:TYR:HE2	1.06	0.91
1:A:180:MET:HB2	1:A:192:VAL:HB	1.51	0.91
1:C:224:ILE:HD12	1:C:224:ILE:N	1.86	0.91
1:H:293:ILE:HD11	1:H:343:LEU:HD11	1.51	0.91
1:A:230:ARG:O	1:A:234:MET:HB3	1.71	0.91
1:B:278:GLN:CG	1:B:279:LYS:H	1.84	0.91
1:C:111:TYR:CE1	1:F:111:TYR:HE2	1.87	0.91
1:D:211:ASP:CG	2:D:401:CMP:H5'1	1.95	0.91
1:D:301:LEU:CD2	1:D:310:PHE:HB3	2.00	0.91
1:E:279:LYS:HB2	1:E:279:LYS:HZ2	1.00	0.91
1:F:251:VAL:O	1:F:254:LEU:HD11	1.70	0.91
1:A:188:TRP:CZ3	1:A:190:THR:C	2.48	0.90
1:B:111:TYR:CD2	1:B:112:VAL:N	2.39	0.90
1:B:365:LYS:O	1:B:368:ILE:HG13	1.70	0.90
1:D:324:GLU:OE2	1:D:371:TYR:CE2	2.24	0.90
1:E:161:THR:HA	1:E:214:LYS:HD2	1.52	0.90
1:H:114:LYS:HZ2	1:H:114:LYS:HA	1.33	0.90
1:A:134:VAL:HG11	1:A:268:ALA:HA	1.53	0.90
1:E:274:PHE:CE2	1:E:280:ILE:HG22	2.05	0.90
1:F:278:GLN:HG3	1:F:279:LYS:H	1.34	0.90
1:H:259:LYS:HG3	1:H:260:TRP:N	1.84	0.90
1:C:228:SER:O	1:C:232:ILE:HG22	1.72	0.90
1:C:233:LEU:HD12	1:C:233:LEU:H	1.36	0.90
1:C:243:MET:HE3	1:E:157:ILE:HD12	1.52	0.90
1:D:131:GLU:OE1	1:D:131:GLU:N	2.03	0.90
1:D:347:LYS:O	1:D:348:LEU:HD12	1.71	0.90
1:H:281:VAL:HG11	1:H:333:ARG:HD2	1.54	0.90
1:H:298:ALA:O	1:H:315:ARG:HA	1.70	0.90
1:B:371:TYR:CE1	2:B:402:CMP:C8	2.54	0.90
1:H:173:TYR:HD2	1:H:198:PHE:CE1	1.90	0.90
1:H:175:ILE:O	1:H:175:ILE:CD1	2.18	0.90
1:A:371:TYR:CE1	2:A:402:CMP:N7	2.39	0.90
1:E:111:TYR:CG	1:E:112:VAL:N	2.37	0.90
1:F:291:PHE:CE1	1:F:347:LYS:NZ	2.40	0.90
1:F:294:LEU:O	1:F:318:PRO:HB3	1.72	0.90
1:G:175:ILE:HA	1:G:221:LEU:CD2	2.02	0.90
1:A:293:ILE:HG13	1:A:345:CYS:SG	2.12	0.90
1:D:200:GLU:CG	1:D:201:LEU:H	1.84	0.90
1:F:175:ILE:HA	1:F:221:LEU:HD22	1.54	0.90
1:G:198:PHE:CD1	1:G:198:PHE:C	2.45	0.90
1:A:230:ARG:HH12	1:A:234:MET:HE1	1.36	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:PHE:N	1:C:291:PHE:HD1	1.69	0.90
1:F:365:LYS:O	1:F:368:ILE:HG13	1.72	0.90
1:B:158:ALA:HB2	1:B:217:THR:O	1.70	0.89
1:B:301:LEU:HD13	1:B:310:PHE:HB2	1.52	0.89
1:E:294:LEU:CD1	1:E:294:LEU:H	1.85	0.89
1:C:280:ILE:HG13	1:C:281:VAL:N	1.84	0.89
1:E:262:ARG:O	1:E:265:VAL:HB	1.70	0.89
1:F:130:ILE:HG13	1:F:136:PHE:CD2	2.06	0.89
1:G:249:SER:N	1:G:262:ARG:HH22	1.68	0.89
1:H:175:ILE:HA	1:H:221:LEU:CD2	2.01	0.89
1:A:325:ILE:CD1	2:A:402:CMP:O2P	2.20	0.89
1:C:259:LYS:HG3	1:C:260:TRP:N	1.88	0.89
1:C:272:VAL:C	1:C:273:GLN:NE2	2.29	0.89
1:D:234:MET:HG3	1:D:238:LEU:HD12	1.53	0.89
1:C:269:LEU:CB	1:C:346:VAL:CG2	2.49	0.89
1:A:139:LEU:HD12	1:A:139:LEU:N	1.87	0.89
1:D:233:LEU:H	1:D:233:LEU:CD1	1.78	0.89
1:D:371:TYR:CE1	2:D:402:CMP:C8	2.55	0.89
1:E:164:GLN:HA	1:E:212:THR:HG22	1.54	0.89
1:E:303:ARG:HA	1:E:309:GLU:O	1.72	0.89
1:H:323:GLY:HA2	2:H:402:CMP:O2P	1.72	0.89
1:B:175:ILE:HA	1:B:221:LEU:HD22	1.52	0.89
1:B:229:TYR:HD1	1:B:233:LEU:CD1	1.85	0.89
1:C:272:VAL:HA	1:C:273:GLN:HE22	1.33	0.89
1:F:247:PHE:HE1	1:F:294:LEU:HA	1.34	0.89
1:B:249:SER:N	1:B:262:ARG:HH22	1.69	0.89
1:E:118:LYS:HE2	1:E:148:PHE:O	1.71	0.89
1:E:182:VAL:O	1:E:182:VAL:HG23	1.71	0.89
1:A:280:ILE:HG13	1:A:281:VAL:N	1.87	0.89
1:F:229:TYR:CD1	1:F:233:LEU:CD1	2.56	0.89
1:C:260:TRP:HE1	2:C:401:CMP:H2'	1.36	0.89
1:E:280:ILE:HG13	1:E:281:VAL:H	1.36	0.89
1:F:263:LEU:O	1:F:266:ALA:HB3	1.73	0.89
1:A:113:ARG:HH21	1:D:115:VAL:HG13	1.35	0.88
1:B:211:ASP:OD2	2:B:401:CMP:H3'	1.73	0.88
1:B:226:ARG:HG3	1:B:226:ARG:NH1	1.83	0.88
1:D:200:GLU:HG2	1:D:201:LEU:N	1.78	0.88
1:E:266:ALA:HA	1:E:269:LEU:CD1	2.02	0.88
1:F:251:VAL:HG12	1:F:254:LEU:HD21	0.92	0.88
1:G:280:ILE:HG13	1:G:281:VAL:N	1.88	0.88
1:H:115:VAL:HA	1:H:149:ASP:HB3	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:255:GLU:HA	1:H:255:GLU:OE1	1.73	0.88
1:H:280:ILE:HD11	1:H:337:VAL:HB	1.54	0.88
1:A:114:LYS:CG	1:A:115:VAL:N	2.30	0.88
1:A:269:LEU:HB3	1:A:346:VAL:HG23	1.54	0.88
1:A:313:VAL:HG13	1:A:313:VAL:O	1.73	0.88
1:B:154:VAL:HG12	1:B:221:LEU:HB2	1.54	0.88
1:D:324:GLU:CG	1:D:325:ILE:H	1.85	0.88
1:D:371:TYR:CE1	2:D:402:CMP:C5	2.61	0.88
1:E:226:ARG:HG3	1:E:226:ARG:NH1	1.80	0.88
1:E:279:LYS:HE3	1:E:282:VAL:HG22	1.54	0.88
1:A:111:TYR:O	1:A:112:VAL:HG22	1.73	0.88
1:D:269:LEU:HD22	1:D:346:VAL:CG2	2.04	0.88
1:F:260:TRP:HE1	2:F:401:CMP:C2'	1.86	0.88
1:E:356:VAL:HG23	1:E:357:LEU:CD1	2.02	0.88
1:F:356:VAL:HG23	1:F:357:LEU:HD13	1.55	0.88
1:E:259:LYS:O	1:E:262:ARG:HG3	1.72	0.88
1:E:356:VAL:HG23	1:E:357:LEU:HD13	1.56	0.88
1:F:152:PHE:O	1:F:152:PHE:HD2	1.56	0.88
1:H:180:MET:HB2	1:H:192:VAL:HB	1.55	0.88
1:H:260:TRP:NE1	2:H:401:CMP:H2'	1.87	0.88
1:H:302:GLN:O	1:H:310:PHE:CD1	2.26	0.88
1:A:272:VAL:HG22	1:A:273:GLN:H	1.39	0.88
1:B:260:TRP:CD1	2:B:401:CMP:C5	2.62	0.88
1:C:300:VAL:O	1:C:301:LEU:HD12	1.74	0.88
1:E:111:TYR:CE2	1:H:112:VAL:CG1	2.54	0.88
1:G:229:TYR:HD1	1:G:233:LEU:CD1	1.86	0.88
1:H:122:THR:O	1:H:125:ALA:HB3	1.72	0.88
1:C:247:PHE:HE1	1:C:294:LEU:HA	1.36	0.88
1:D:226:ARG:HG3	1:D:226:ARG:NH1	1.81	0.88
1:F:182:VAL:HG23	1:F:182:VAL:O	1.71	0.88
1:F:229:TYR:CE1	1:F:233:LEU:HD13	2.09	0.88
1:A:280:ILE:CD1	1:A:322:PHE:CE2	2.57	0.88
1:B:371:TYR:CE1	2:B:402:CMP:N7	2.42	0.88
1:C:234:MET:HG3	1:C:238:LEU:HD12	1.56	0.88
1:E:165:GLN:H	1:E:212:THR:HG23	0.75	0.88
1:F:229:TYR:HD1	1:F:233:LEU:HD13	1.32	0.88
1:B:280:ILE:HD13	1:B:322:PHE:CE2	2.08	0.87
1:F:178:GLY:HA3	1:F:219:VAL:HG12	1.54	0.87
1:G:148:PHE:HB3	1:H:120:TYR:HD1	1.39	0.87
1:A:131:GLU:OE1	1:A:131:GLU:N	2.07	0.87
1:C:229:TYR:CE1	1:C:233:LEU:HD13	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:139:LEU:H	1:E:139:LEU:HD12	1.39	0.87
1:B:134:VAL:HG11	1:B:268:ALA:HA	1.55	0.87
1:C:329:MET:HA	1:C:329:MET:HE3	1.56	0.87
1:E:249:SER:N	1:E:262:ARG:NH2	2.22	0.87
1:F:280:ILE:HD13	1:F:322:PHE:CE2	2.09	0.87
1:E:269:LEU:HB3	1:E:346:VAL:CG2	2.05	0.87
1:F:139:LEU:H	1:F:139:LEU:HD12	1.39	0.87
1:C:255:GLU:HA	1:C:255:GLU:OE1	1.75	0.87
1:E:203:LEU:HD22	1:E:226:ARG:HB3	1.57	0.87
1:F:350:ARG:O	1:F:353:PHE:HB3	1.73	0.87
1:H:291:PHE:CE1	1:H:347:LYS:NZ	2.43	0.87
1:H:300:VAL:HG23	1:H:314:GLY:H	1.39	0.87
1:B:356:VAL:HG23	1:B:357:LEU:CD1	2.04	0.87
1:C:173:TYR:HD2	1:C:198:PHE:CZ	1.92	0.87
1:H:162:VAL:HG23	1:H:163:ILE:HG13	1.55	0.87
1:H:273:GLN:NE2	1:H:273:GLN:N	2.22	0.87
1:A:118:LYS:HE2	1:A:148:PHE:O	1.73	0.87
1:C:266:ALA:CA	1:C:269:LEU:HD12	2.02	0.87
1:D:175:ILE:HD11	1:D:196:GLY:H	1.38	0.87
1:E:251:VAL:CG1	1:E:254:LEU:HD21	2.03	0.87
1:H:126:LEU:HD12	1:H:126:LEU:O	1.74	0.87
1:A:115:VAL:CG2	1:D:112:VAL:H	1.88	0.87
1:A:120:TYR:HD1	1:B:148:PHE:HB2	1.37	0.87
1:A:230:ARG:O	1:A:234:MET:CB	2.22	0.87
1:A:324:GLU:HG2	1:A:325:ILE:N	1.89	0.87
1:C:158:ALA:HB1	1:C:216:LYS:O	1.75	0.87
1:C:329:MET:HA	1:C:329:MET:CE	2.05	0.86
1:D:204:ILE:HG22	1:D:205:TYR:CD2	2.09	0.86
1:B:262:ARG:O	1:B:265:VAL:HB	1.75	0.86
1:B:325:ILE:HD11	2:B:402:CMP:O1P	1.75	0.86
1:C:300:VAL:HG21	1:C:313:VAL:HG12	1.56	0.86
1:E:229:TYR:HD1	1:E:233:LEU:HD13	1.40	0.86
1:G:204:ILE:HG22	1:G:205:TYR:CD2	2.09	0.86
1:G:229:TYR:CD1	1:G:233:LEU:CD1	2.58	0.86
1:H:230:ARG:O	1:H:234:MET:HB3	1.74	0.86
1:A:152:PHE:HE2	1:A:223:GLY:HA3	1.40	0.86
1:B:158:ALA:HB1	1:B:216:LYS:O	1.75	0.86
1:C:139:LEU:HD12	1:C:139:LEU:N	1.89	0.86
1:C:269:LEU:CB	1:C:346:VAL:HG21	2.06	0.86
1:D:230:ARG:NH1	1:D:234:MET:HE1	1.89	0.86
1:F:278:GLN:CG	1:F:279:LYS:H	1.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:275:GLU:O	1:H:278:GLN:HB2	1.73	0.86
1:F:273:GLN:HE21	1:F:273:GLN:H	1.15	0.86
1:A:226:ARG:HG3	1:A:226:ARG:NH1	1.84	0.86
1:F:190:THR:HG22	1:F:191:SER:H	1.39	0.86
1:B:139:LEU:HD12	1:B:139:LEU:N	1.86	0.86
1:G:139:LEU:HD12	1:G:139:LEU:N	1.91	0.86
1:C:198:PHE:CD1	1:C:198:PHE:O	2.27	0.86
1:E:353:PHE:CE1	1:E:357:LEU:HD22	2.10	0.86
1:F:274:PHE:CE2	1:F:280:ILE:HG22	2.11	0.86
1:B:279:LYS:HZ3	1:B:279:LYS:HB2	1.40	0.86
1:G:246:GLU:O	1:G:247:PHE:C	2.18	0.86
1:G:178:GLY:HA3	1:G:219:VAL:HG12	1.57	0.86
1:B:371:TYR:HE1	2:B:402:CMP:N7	1.74	0.85
1:E:328:LEU:CD2	1:E:365:LYS:HE3	2.06	0.85
1:D:300:VAL:CG2	1:D:335:ALA:HB1	2.05	0.85
1:E:291:PHE:N	1:E:291:PHE:HD1	1.74	0.85
1:G:294:LEU:CD1	1:G:294:LEU:H	1.88	0.85
1:A:114:LYS:C	1:A:115:VAL:HG22	2.00	0.85
1:E:293:ILE:CD1	1:E:317:GLY:O	2.24	0.85
1:F:152:PHE:O	1:F:152:PHE:CD2	2.28	0.85
1:F:165:GLN:HA	1:F:211:ASP:O	1.76	0.85
1:D:301:LEU:HD21	1:D:310:PHE:CB	2.04	0.85
1:E:131:GLU:N	1:E:131:GLU:OE1	2.09	0.85
1:F:279:LYS:HZ3	1:F:279:LYS:CB	1.89	0.85
1:G:131:GLU:OE1	1:G:131:GLU:N	2.08	0.85
1:A:188:TRP:HZ3	1:A:190:THR:C	1.83	0.85
1:B:120:TYR:C	1:B:120:TYR:CD2	2.45	0.85
1:F:291:PHE:N	1:F:291:PHE:HD1	1.68	0.85
1:H:175:ILE:HA	1:H:221:LEU:HD22	1.59	0.85
1:H:204:ILE:HG22	1:H:205:TYR:CD2	2.12	0.85
1:B:112:VAL:HG12	1:B:231:ARG:NE	1.91	0.85
1:G:229:TYR:HD1	1:G:233:LEU:HD13	1.41	0.85
1:H:114:LYS:NZ	1:H:115:VAL:N	2.21	0.85
1:A:293:ILE:HD11	1:A:343:LEU:CD1	2.05	0.85
1:B:249:SER:CA	1:B:262:ARG:HH22	1.90	0.85
1:G:249:SER:CA	1:G:262:ARG:HH22	1.89	0.85
1:A:111:TYR:HA	1:D:115:VAL:HG23	1.59	0.85
1:A:175:ILE:HD11	1:A:193:GLY:O	1.76	0.85
1:B:230:ARG:NH1	1:B:234:MET:HE1	1.92	0.85
1:C:278:GLN:HG3	1:C:279:LYS:H	1.42	0.85
1:D:273:GLN:NE2	1:D:273:GLN:H	1.70	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:182:VAL:CG2	1:F:190:THR:O	2.24	0.85
1:H:156:PHE:HE2	1:H:162:VAL:HG12	1.40	0.85
1:A:120:TYR:C	1:A:120:TYR:HD2	1.84	0.85
1:C:198:PHE:O	1:C:198:PHE:HD1	1.60	0.85
1:C:363:ILE:O	1:C:366:ARG:HG2	1.75	0.85
1:D:126:LEU:HB2	1:D:222:TRP:CZ2	2.11	0.85
1:D:198:PHE:CD1	1:D:198:PHE:C	2.53	0.85
1:E:259:LYS:HG3	1:E:260:TRP:N	1.92	0.85
1:F:348:LEU:HD21	1:F:356:VAL:HG21	1.57	0.85
1:D:230:ARG:O	1:D:234:MET:HB3	1.76	0.85
1:E:156:PHE:CD2	1:E:162:VAL:CG1	2.59	0.85
1:G:118:LYS:HE2	1:G:148:PHE:O	1.75	0.85
1:G:291:PHE:N	1:G:291:PHE:HD1	1.74	0.85
1:C:163:ILE:HB	1:C:213:VAL:HG23	1.59	0.84
1:C:170:ASP:H	1:C:209:ARG:NH2	1.75	0.84
1:D:269:LEU:HB3	1:D:346:VAL:CG2	2.07	0.84
1:E:173:TYR:HB2	1:E:198:PHE:HE1	1.42	0.84
1:F:325:ILE:HD11	2:F:402:CMP:O1P	1.76	0.84
1:C:112:VAL:O	1:F:112:VAL:CG1	2.25	0.84
1:C:299:ALA:HB1	1:C:312:GLU:CD	2.02	0.84
1:E:279:LYS:HB2	1:E:279:LYS:HZ3	1.40	0.84
1:F:164:GLN:HA	1:F:212:THR:HG22	1.59	0.84
1:F:259:LYS:HG3	1:F:260:TRP:N	1.91	0.84
1:F:293:ILE:HD11	1:F:343:LEU:CD1	2.06	0.84
1:H:172:PHE:HB3	1:H:224:ILE:CD1	2.07	0.84
1:E:175:ILE:HA	1:E:221:LEU:HD22	1.57	0.84
1:H:251:VAL:CG1	1:H:254:LEU:HD21	2.07	0.84
1:B:165:GLN:HA	1:B:211:ASP:O	1.78	0.84
1:B:200:GLU:HG2	1:B:201:LEU:HD12	1.57	0.84
1:B:278:GLN:HG2	1:B:279:LYS:H	1.41	0.84
1:E:156:PHE:HD2	1:E:162:VAL:HG12	1.42	0.84
1:E:175:ILE:HD11	1:E:196:GLY:N	1.90	0.84
1:F:280:ILE:HD13	1:F:322:PHE:CZ	2.12	0.84
1:G:361:SER:C	1:G:365:LYS:HZ2	1.85	0.84
1:H:296:GLY:O	1:H:318:PRO:HD3	1.78	0.84
1:C:293:ILE:HD11	1:C:343:LEU:CD1	2.07	0.84
1:D:301:LEU:HD23	1:D:310:PHE:CD1	2.12	0.84
1:F:114:LYS:HZ2	1:F:115:VAL:CG2	1.88	0.84
1:F:153:PRO:HB3	1:F:222:TRP:CZ3	2.12	0.84
1:A:182:VAL:HG23	1:A:182:VAL:O	1.76	0.84
1:E:190:THR:HG22	1:E:191:SER:H	1.41	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:300:VAL:HG21	2:E:402:CMP:C8	2.05	0.84
1:G:259:LYS:HG3	1:G:260:TRP:N	1.90	0.84
1:A:115:VAL:HG11	1:D:112:VAL:CG2	2.08	0.84
1:B:198:PHE:CD1	1:B:198:PHE:C	2.49	0.84
1:C:120:TYR:CB	1:D:149:ASP:OD1	2.25	0.84
1:E:278:GLN:HG3	1:E:279:LYS:H	1.43	0.84
1:F:173:TYR:HB2	1:F:198:PHE:CE1	2.13	0.84
1:F:247:PHE:CE1	1:F:294:LEU:HA	2.11	0.84
1:G:175:ILE:HD11	1:G:196:GLY:H	1.40	0.84
1:H:113:ARG:CD	1:H:114:LYS:H	1.91	0.84
1:D:139:LEU:HD12	1:D:139:LEU:N	1.91	0.84
1:D:280:ILE:HG13	1:D:281:VAL:N	1.93	0.84
1:A:350:ARG:O	1:A:353:PHE:HB3	1.78	0.84
1:E:123:MET:HE3	1:F:123:MET:CE	2.08	0.84
1:H:247:PHE:HE1	1:H:294:LEU:HA	1.41	0.84
1:H:260:TRP:CE2	2:H:401:CMP:C8	2.60	0.84
1:A:190:THR:CG2	1:A:191:SER:H	1.91	0.83
1:C:188:TRP:CZ3	1:C:190:THR:C	2.56	0.83
1:D:139:LEU:HD12	1:D:139:LEU:H	1.42	0.83
1:B:321:TYR:CD1	1:B:321:TYR:C	2.56	0.83
1:C:179:GLU:HG2	1:C:216:LYS:CD	2.07	0.83
1:C:269:LEU:HD23	1:C:348:LEU:HD13	1.60	0.83
1:C:323:GLY:HA2	2:C:402:CMP:O1P	1.78	0.83
1:F:139:LEU:HD12	1:F:139:LEU:N	1.93	0.83
1:A:229:TYR:CE1	1:A:233:LEU:HD13	2.14	0.83
1:C:110:SER:HB3	1:F:114:LYS:CE	2.08	0.83
1:C:122:THR:O	1:C:125:ALA:HB3	1.78	0.83
1:C:173:TYR:HD2	1:C:198:PHE:CE1	1.95	0.83
1:A:313:VAL:O	1:A:313:VAL:CG1	2.26	0.83
1:B:182:VAL:HG12	1:B:213:VAL:HG22	1.60	0.83
1:B:291:PHE:N	1:B:291:PHE:CD1	2.37	0.83
1:B:312:GLU:CD	1:B:314:GLY:H	1.85	0.83
1:B:350:ARG:O	1:B:353:PHE:HB3	1.78	0.83
1:F:157:ILE:CD1	1:H:243:MET:CE	2.53	0.83
1:H:249:SER:N	1:H:262:ARG:HH22	1.75	0.83
1:A:273:GLN:HB2	1:A:343:LEU:O	1.78	0.83
1:C:211:ASP:OD2	2:C:401:CMP:H3'	1.77	0.83
1:D:259:LYS:HG3	1:D:260:TRP:H	1.37	0.83
1:A:147:ILE:HG23	1:A:232:ILE:HD13	1.61	0.83
1:E:242:LYS:N	1:E:242:LYS:HD3	1.92	0.83
1:E:247:PHE:HE1	1:E:294:LEU:HA	1.42	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:179:GLU:HG2	1:H:216:LYS:CD	2.08	0.83
1:C:120:TYR:HD1	1:D:148:PHE:HB2	1.42	0.83
1:D:163:ILE:HD12	1:D:213:VAL:HB	1.59	0.83
1:D:175:ILE:HA	1:D:221:LEU:HD22	1.60	0.83
1:F:157:ILE:HD12	1:H:243:MET:HE3	1.56	0.83
1:G:148:PHE:CB	1:H:120:TYR:CD1	2.61	0.83
1:H:175:ILE:HD13	1:H:194:GLU:HA	1.60	0.83
1:H:279:LYS:HB2	1:H:279:LYS:HZ2	1.41	0.83
1:B:280:ILE:HG13	1:B:281:VAL:N	1.91	0.83
1:C:224:ILE:HD12	1:C:224:ILE:H	1.41	0.83
1:C:284:GLY:O	1:C:332:PRO:CB	2.26	0.83
1:D:120:TYR:C	1:D:120:TYR:CD2	2.54	0.83
1:D:249:SER:CA	1:D:262:ARG:HH22	1.91	0.83
1:C:204:ILE:HG22	1:C:205:TYR:HD2	1.40	0.83
1:E:123:MET:HE3	1:F:123:MET:HE3	1.61	0.83
1:F:175:ILE:HD11	1:F:196:GLY:N	1.93	0.83
1:G:120:TYR:C	1:G:120:TYR:HD2	1.87	0.83
1:H:156:PHE:HD2	1:H:162:VAL:CG1	1.92	0.83
1:B:324:GLU:OE2	1:B:371:TYR:HE2	1.61	0.83
1:C:312:GLU:OE1	1:C:312:GLU:HA	1.79	0.83
1:H:300:VAL:C	1:H:301:LEU:HD23	2.02	0.83
1:G:198:PHE:O	1:G:198:PHE:HD1	1.62	0.82
1:A:203:LEU:HD22	1:A:226:ARG:HB3	1.60	0.82
1:C:279:LYS:CE	1:C:336:THR:HG23	2.06	0.82
1:F:347:LYS:O	1:F:348:LEU:HD12	1.78	0.82
1:G:139:LEU:HD12	1:G:139:LEU:H	1.45	0.82
1:G:234:MET:HG3	1:G:238:LEU:HD12	1.61	0.82
1:G:266:ALA:CA	1:G:269:LEU:HD12	2.05	0.82
1:C:259:LYS:HG3	1:C:260:TRP:H	1.44	0.82
1:H:259:LYS:HG3	1:H:260:TRP:H	1.40	0.82
1:H:294:LEU:O	1:H:318:PRO:HB3	1.77	0.82
1:A:147:ILE:CG2	1:A:232:ILE:HD13	2.09	0.82
1:A:224:ILE:O	1:A:224:ILE:HD13	1.79	0.82
1:B:130:ILE:CG2	1:B:131:GLU:N	2.41	0.82
1:D:135:LEU:HD12	1:D:136:PHE:N	1.94	0.82
1:D:156:PHE:HD2	1:D:162:VAL:HG12	1.43	0.82
1:A:229:TYR:HD1	1:A:233:LEU:CD1	1.92	0.82
1:A:259:LYS:O	1:A:262:ARG:HG3	1.78	0.82
1:B:135:LEU:HD12	1:B:136:PHE:H	1.45	0.82
1:D:294:LEU:HD13	1:D:344:LYS:O	1.79	0.82
1:D:300:VAL:HG12	1:D:314:GLY:O	1.78	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:111:TYR:CG	1:H:112:VAL:N	2.46	0.82
1:C:241:ARG:NH1	1:C:263:LEU:HG	1.94	0.82
1:D:260:TRP:NE1	2:D:401:CMP:H2'	1.93	0.82
1:D:325:ILE:HG12	2:D:402:CMP:O3'	1.80	0.82
1:E:243:MET:HE2	1:G:159:GLY:O	1.79	0.82
1:E:260:TRP:CE2	2:E:401:CMP:C8	2.62	0.82
1:G:279:LYS:HE3	1:G:282:VAL:HG22	1.59	0.82
1:B:165:GLN:H	1:B:212:THR:HG23	0.71	0.82
1:E:263:LEU:O	1:E:266:ALA:HB3	1.78	0.82
1:G:229:TYR:CE1	1:G:233:LEU:HD13	2.14	0.82
1:A:249:SER:N	1:A:262:ARG:NH2	2.27	0.82
1:B:246:GLU:O	1:B:247:PHE:C	2.18	0.82
1:B:263:LEU:O	1:B:266:ALA:HB3	1.77	0.82
1:C:230:ARG:O	1:C:234:MET:HB3	1.80	0.82
1:D:291:PHE:N	1:D:291:PHE:HD1	1.72	0.82
1:E:139:LEU:HD12	1:E:139:LEU:N	1.91	0.82
1:A:316:LEU:C	1:A:316:LEU:HD12	2.05	0.82
1:C:259:LYS:O	1:C:262:ARG:HG3	1.79	0.82
1:D:255:GLU:OE1	1:D:255:GLU:HA	1.78	0.82
1:E:243:MET:HE1	1:G:157:ILE:CD1	2.10	0.82
1:F:246:GLU:O	1:F:247:PHE:C	2.22	0.82
1:F:269:LEU:HB3	1:F:346:VAL:HG21	1.62	0.82
1:G:347:LYS:O	1:G:348:LEU:HD12	1.80	0.82
1:G:350:ARG:O	1:G:353:PHE:HB3	1.79	0.82
1:A:228:SER:O	1:A:232:ILE:HG22	1.80	0.82
1:B:251:VAL:O	1:B:254:LEU:HD11	1.80	0.82
1:C:247:PHE:CE1	1:C:294:LEU:HA	2.15	0.82
1:C:350:ARG:O	1:C:353:PHE:HB3	1.79	0.82
1:D:156:PHE:CD2	1:D:162:VAL:CG1	2.60	0.82
1:F:356:VAL:HG23	1:F:357:LEU:CD1	2.09	0.82
1:H:280:ILE:HD13	1:H:322:PHE:CZ	2.15	0.82
1:A:158:ALA:HB1	1:A:216:LYS:O	1.80	0.81
1:E:246:GLU:O	1:E:247:PHE:C	2.20	0.81
1:H:266:ALA:HA	1:H:269:LEU:HD12	1.60	0.81
1:B:156:PHE:HD2	1:B:162:VAL:HG12	1.43	0.81
1:B:281:VAL:HG11	1:B:333:ARG:HD2	1.59	0.81
1:C:230:ARG:CZ	1:C:234:MET:HE1	2.09	0.81
1:E:229:TYR:CD1	1:E:233:LEU:CD1	2.63	0.81
1:E:229:TYR:CE1	1:E:233:LEU:HD13	2.15	0.81
1:F:157:ILE:O	1:F:160:GLU:HB2	1.78	0.81
1:H:280:ILE:HD11	1:H:322:PHE:HE2	1.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:ARG:HB3	1:A:351:PRO:HD3	1.61	0.81
1:A:365:LYS:HA	1:A:368:ILE:HG13	1.62	0.81
1:B:211:ASP:N	1:B:211:ASP:OD1	2.13	0.81
1:B:269:LEU:HD22	1:B:346:VAL:HG21	1.62	0.81
1:B:325:ILE:HG13	1:B:326:ALA:N	1.93	0.81
1:C:120:TYR:CD1	1:D:148:PHE:CB	2.62	0.81
1:C:316:LEU:HA	1:C:320:ASP:OD2	1.81	0.81
1:D:229:TYR:CD1	1:D:233:LEU:CD1	2.63	0.81
1:E:247:PHE:CE1	1:E:294:LEU:HA	2.14	0.81
1:G:261:GLU:O	1:G:265:VAL:HG23	1.79	0.81
1:H:285:GLU:O	1:H:332:PRO:HA	1.79	0.81
1:B:179:GLU:HG2	1:B:216:LYS:CD	2.11	0.81
1:B:348:LEU:HD21	1:B:356:VAL:HG21	1.62	0.81
1:E:243:MET:CE	1:G:157:ILE:CD1	2.59	0.81
1:B:156:PHE:CE2	1:B:162:VAL:HG12	2.15	0.81
1:C:120:TYR:CD1	1:D:148:PHE:HB2	2.15	0.81
1:D:178:GLY:HA3	1:D:219:VAL:HG12	1.61	0.81
1:D:229:TYR:CE1	1:D:233:LEU:HD13	2.14	0.81
1:G:324:GLU:HG2	1:G:325:ILE:N	1.95	0.81
1:H:188:TRP:CZ3	1:H:190:THR:C	2.58	0.81
1:H:294:LEU:HD12	1:H:295:GLU:H	1.44	0.81
1:B:230:ARG:O	1:B:234:MET:CB	2.28	0.81
1:C:233:LEU:CD1	1:C:233:LEU:H	1.90	0.81
1:D:251:VAL:O	1:D:252:SER:O	1.98	0.81
1:F:230:ARG:O	1:F:234:MET:HB3	1.81	0.81
1:A:142:ASN:HB2	1:C:121:LYS:HE3	1.61	0.81
1:A:249:SER:CA	1:A:262:ARG:HH22	1.92	0.81
1:C:180:MET:HB2	1:C:192:VAL:HB	1.62	0.81
1:G:196:GLY:HA2	1:G:355:ARG:HH21	1.43	0.81
1:H:350:ARG:O	1:H:353:PHE:HB3	1.80	0.81
1:A:148:PHE:HB2	1:B:120:TYR:HD1	1.45	0.81
1:A:371:TYR:HE1	2:A:402:CMP:N7	1.77	0.81
1:C:111:TYR:HE1	1:F:111:TYR:CD2	1.99	0.81
1:E:292:ILE:HB	1:E:346:VAL:HG13	1.62	0.81
1:A:173:TYR:HD2	1:A:198:PHE:CE1	1.98	0.81
1:B:153:PRO:CB	1:B:222:TRP:CZ3	2.64	0.81
1:B:251:VAL:CG1	1:B:254:LEU:HD21	2.10	0.81
1:H:247:PHE:C	1:H:247:PHE:CD2	2.59	0.81
1:F:156:PHE:HD2	1:F:162:VAL:HG12	1.46	0.80
1:C:154:VAL:HG12	1:C:221:LEU:HB2	1.63	0.80
1:C:251:VAL:O	1:C:254:LEU:HD11	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:272:VAL:HG22	1:C:273:GLN:H	1.47	0.80
1:E:204:ILE:HG22	1:E:205:TYR:CD2	2.15	0.80
1:E:280:ILE:HG13	1:E:281:VAL:N	1.94	0.80
1:E:294:LEU:HD13	1:E:344:LYS:O	1.81	0.80
1:G:211:ASP:OD2	2:G:401:CMP:H5'1	1.82	0.80
1:A:113:ARG:NH2	1:D:114:LYS:C	2.39	0.80
1:A:280:ILE:HD13	1:A:322:PHE:CZ	2.16	0.80
1:A:325:ILE:HG13	1:A:326:ALA:H	1.47	0.80
1:B:371:TYR:HE1	2:B:402:CMP:C8	1.93	0.80
1:C:172:PHE:HB3	1:C:224:ILE:CD1	2.12	0.80
1:C:280:ILE:HD13	1:C:322:PHE:CZ	2.16	0.80
1:D:144:ARG:HG2	1:D:145:SER:N	1.94	0.80
1:D:353:PHE:CE1	1:D:357:LEU:CD2	2.63	0.80
1:F:279:LYS:NZ	1:F:279:LYS:CB	2.36	0.80
1:F:280:ILE:HG13	1:F:281:VAL:N	1.95	0.80
1:G:116:ILE:HG22	1:G:118:LYS:HG3	1.63	0.80
1:B:162:VAL:HG23	1:B:163:ILE:HG13	1.64	0.80
1:C:300:VAL:O	1:C:301:LEU:CD1	2.30	0.80
1:F:329:MET:CB	1:F:331:ARG:HG3	2.10	0.80
1:B:175:ILE:HD11	1:B:193:GLY:O	1.81	0.80
1:B:273:GLN:H	1:B:273:GLN:HE21	0.82	0.80
1:C:365:LYS:HA	1:C:368:ILE:HD11	1.64	0.80
1:G:249:SER:N	1:G:262:ARG:NH2	2.29	0.80
1:G:291:PHE:CE1	1:G:347:LYS:NZ	2.50	0.80
1:D:126:LEU:HD12	1:D:126:LEU:C	2.07	0.80
1:D:291:PHE:CD1	1:D:347:LYS:NZ	2.48	0.80
1:E:293:ILE:HG21	1:E:317:GLY:O	1.82	0.80
1:F:228:SER:O	1:F:232:ILE:HG22	1.81	0.80
1:A:251:VAL:O	1:A:254:LEU:HD11	1.80	0.80
1:A:291:PHE:N	1:A:291:PHE:CD1	2.38	0.80
1:B:229:TYR:CD1	1:B:233:LEU:CD1	2.63	0.80
1:B:249:SER:N	1:B:262:ARG:NH2	2.29	0.80
1:C:211:ASP:CG	2:C:401:CMP:H5'1	2.06	0.80
1:E:229:TYR:HD1	1:E:233:LEU:CD1	1.93	0.80
1:E:265:VAL:HG12	1:E:269:LEU:CD1	2.12	0.80
1:A:111:TYR:C	1:D:115:VAL:CG2	2.55	0.80
1:C:165:GLN:HA	1:C:211:ASP:O	1.81	0.80
1:G:228:SER:O	1:G:232:ILE:HG22	1.82	0.80
1:G:253:ILE:HD13	1:G:321:TYR:CD2	2.17	0.80
1:A:375:VAL:HG13	1:A:376:SER:N	1.97	0.80
1:C:249:SER:N	1:C:262:ARG:HH22	1.79	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:224:ILE:O	1:D:224:ILE:HD13	1.82	0.80
1:B:323:GLY:HA2	2:B:402:CMP:O2P	1.82	0.80
1:B:375:VAL:CG2	1:B:376:SER:H	1.95	0.80
1:C:120:TYR:C	1:C:120:TYR:CD2	2.59	0.80
1:C:175:ILE:O	1:C:175:ILE:CD1	2.29	0.80
1:D:269:LEU:HD22	1:D:346:VAL:HG21	1.64	0.80
1:E:156:PHE:HE2	1:E:162:VAL:HG12	1.46	0.80
1:F:112:VAL:HG13	1:F:113:ARG:N	1.96	0.80
1:F:278:GLN:CG	1:F:279:LYS:N	2.45	0.80
1:B:229:TYR:CE1	1:B:233:LEU:HD13	2.17	0.79
1:C:278:GLN:O	1:C:338:VAL:HA	1.82	0.79
1:C:291:PHE:N	1:C:291:PHE:CD1	2.46	0.79
1:G:182:VAL:HG23	1:G:182:VAL:O	1.79	0.79
1:G:325:ILE:HG23	1:G:329:MET:HG3	1.65	0.79
1:H:279:LYS:HB2	1:H:279:LYS:HZ3	1.47	0.79
1:A:260:TRP:CD1	2:A:401:CMP:C5	2.70	0.79
1:C:287:GLY:HA3	1:C:326:ALA:HB1	1.64	0.79
1:C:371:TYR:HE1	2:C:402:CMP:C8	1.94	0.79
1:D:251:VAL:HG13	1:D:254:LEU:CD1	2.06	0.79
1:E:111:TYR:HE2	1:H:111:TYR:CE2	1.94	0.79
1:E:280:ILE:HD11	1:E:322:PHE:CE2	2.14	0.79
1:G:120:TYR:HD2	1:G:121:LYS:HA	1.46	0.79
1:H:249:SER:N	1:H:262:ARG:NH2	2.29	0.79
1:H:281:VAL:CG1	1:H:333:ARG:HD2	2.11	0.79
1:C:281:VAL:CG1	1:C:333:ARG:CD	2.59	0.79
1:E:350:ARG:O	1:E:353:PHE:HB3	1.81	0.79
1:F:324:GLU:HB2	1:F:364:LEU:HD13	1.62	0.79
1:G:198:PHE:C	1:G:198:PHE:HD1	1.91	0.79
1:C:321:TYR:CD1	1:C:321:TYR:C	2.59	0.79
1:F:175:ILE:CD1	1:F:195:GLY:H	1.95	0.79
1:A:135:LEU:CD1	1:A:136:PHE:N	2.45	0.79
1:A:253:ILE:HG13	1:A:254:LEU:H	1.47	0.79
1:C:243:MET:CE	1:E:157:ILE:CD1	2.58	0.79
1:C:280:ILE:CG1	1:C:337:VAL:HB	2.13	0.79
1:D:291:PHE:N	1:D:291:PHE:CD1	2.47	0.79
1:E:239:ARG:HH11	1:G:157:ILE:HG23	1.46	0.79
1:F:204:ILE:HG22	1:F:205:TYR:CD2	2.18	0.79
1:F:291:PHE:N	1:F:291:PHE:CD1	2.44	0.79
1:B:190:THR:CG2	1:B:191:SER:H	1.96	0.79
1:B:211:ASP:OD2	2:B:401:CMP:C3'	2.31	0.79
1:C:196:GLY:CA	1:C:355:ARG:NH2	2.42	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:LEU:CD1	1:C:294:LEU:H	1.95	0.79
1:D:112:VAL:HG12	1:D:231:ARG:CZ	2.11	0.79
1:D:157:ILE:CD1	1:F:243:MET:HE1	2.12	0.79
1:A:165:GLN:H	1:A:212:THR:HG23	0.67	0.79
1:A:190:THR:HG22	1:A:191:SER:N	1.95	0.79
1:E:175:ILE:HG22	1:E:221:LEU:HD21	1.65	0.79
1:E:196:GLY:HA2	1:E:355:ARG:HH21	1.48	0.79
1:F:262:ARG:O	1:F:265:VAL:HB	1.83	0.79
1:G:348:LEU:HD21	1:G:356:VAL:HG21	1.65	0.79
1:E:291:PHE:CE1	1:E:347:LYS:NZ	2.50	0.79
1:F:134:VAL:HG11	1:F:268:ALA:HA	1.62	0.79
1:F:203:LEU:HD13	1:F:226:ARG:HB3	1.63	0.79
1:A:113:ARG:HH21	1:D:115:VAL:CG1	1.94	0.79
1:E:179:GLU:HG2	1:E:216:LYS:CD	2.13	0.79
1:F:156:PHE:CD2	1:F:162:VAL:CG1	2.65	0.79
1:G:188:TRP:CZ3	1:G:190:THR:C	2.61	0.79
1:H:112:VAL:HG13	1:H:113:ARG:N	1.98	0.79
1:H:139:LEU:HD12	1:H:139:LEU:N	1.97	0.79
1:A:114:LYS:HG2	1:A:115:VAL:N	1.96	0.78
1:B:175:ILE:CD1	1:B:193:GLY:O	2.31	0.78
1:C:198:PHE:C	1:C:198:PHE:HD1	1.91	0.78
1:C:281:VAL:HG13	1:C:333:ARG:CD	2.13	0.78
1:D:233:LEU:HD12	1:D:233:LEU:N	1.92	0.78
1:F:230:ARG:NH1	1:F:234:MET:HE1	1.97	0.78
1:H:198:PHE:C	1:H:198:PHE:HD1	1.88	0.78
1:A:156:PHE:HD2	1:A:162:VAL:HG12	1.40	0.78
1:A:246:GLU:O	1:A:247:PHE:C	2.20	0.78
1:B:211:ASP:CG	2:B:401:CMP:H5'1	2.07	0.78
1:C:269:LEU:HD23	1:C:348:LEU:CD1	2.13	0.78
1:E:198:PHE:CD1	1:E:198:PHE:C	2.58	0.78
1:F:172:PHE:HB3	1:F:224:ILE:CD1	2.12	0.78
1:F:269:LEU:HB3	1:F:346:VAL:HG23	1.63	0.78
1:G:262:ARG:O	1:G:265:VAL:HB	1.83	0.78
1:H:249:SER:HA	1:H:262:ARG:HH22	1.48	0.78
1:H:279:LYS:NZ	1:H:279:LYS:CB	2.44	0.78
1:H:287:GLY:HA3	1:H:326:ALA:HB1	1.65	0.78
1:A:229:TYR:CD1	1:A:233:LEU:CD1	2.65	0.78
1:C:234:MET:O	1:C:238:LEU:HD12	1.83	0.78
1:D:165:GLN:HA	1:D:211:ASP:O	1.83	0.78
1:E:126:LEU:HD12	1:E:126:LEU:C	2.08	0.78
1:E:204:ILE:HG22	1:E:205:TYR:HD2	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:290:PHE:C	1:F:291:PHE:HD1	1.89	0.78
1:A:172:PHE:HB3	1:A:224:ILE:CD1	2.14	0.78
1:A:201:LEU:HD12	1:A:201:LEU:H	1.49	0.78
1:A:269:LEU:HB3	1:A:346:VAL:HG21	1.64	0.78
1:B:203:LEU:HD13	1:B:226:ARG:HB3	1.63	0.78
1:B:312:GLU:OE1	1:B:312:GLU:HA	1.81	0.78
1:B:313:VAL:CG2	2:B:402:CMP:N6	2.42	0.78
1:C:246:GLU:O	1:C:247:PHE:C	2.23	0.78
1:D:269:LEU:HB3	1:D:346:VAL:HG23	1.65	0.78
1:E:260:TRP:HE1	2:E:401:CMP:H2'	1.47	0.78
1:F:196:GLY:HA2	1:F:355:ARG:HH21	1.44	0.78
1:H:280:ILE:HG13	1:H:281:VAL:H	1.48	0.78
1:E:203:LEU:HD12	1:E:229:TYR:CD2	2.19	0.78
1:F:325:ILE:HG13	1:F:326:ALA:H	1.46	0.78
1:G:368:ILE:O	1:G:371:TYR:HB2	1.82	0.78
1:H:328:LEU:CD2	1:H:365:LYS:HE3	2.12	0.78
1:A:266:ALA:HA	1:A:269:LEU:CD1	2.11	0.78
1:C:112:VAL:O	1:F:112:VAL:HG12	1.83	0.78
1:C:294:LEU:N	1:C:294:LEU:CD1	2.42	0.78
1:D:279:LYS:CB	1:D:279:LYS:HZ2	1.90	0.78
1:F:175:ILE:CD1	1:F:195:GLY:N	2.46	0.78
1:G:120:TYR:CD1	1:H:148:PHE:CD1	2.71	0.78
1:G:224:ILE:HD13	1:G:224:ILE:O	1.83	0.78
1:E:112:VAL:CG1	1:E:231:ARG:CZ	2.60	0.78
1:F:294:LEU:HD13	1:F:344:LYS:O	1.83	0.78
1:G:269:LEU:HD23	1:G:348:LEU:CD1	2.14	0.78
1:G:356:VAL:HG23	1:G:357:LEU:HD13	1.64	0.78
1:H:224:ILE:H	1:H:224:ILE:HD12	1.47	0.78
1:H:324:GLU:O	1:H:328:LEU:HD12	1.83	0.78
1:A:144:ARG:HD2	1:B:120:TYR:OH	1.84	0.78
1:C:171:ASN:HB3	1:C:224:ILE:O	1.83	0.78
1:E:203:LEU:HD13	1:E:226:ARG:HB3	1.66	0.78
1:F:242:LYS:HD3	1:F:242:LYS:N	1.90	0.78
1:G:116:ILE:HG21	1:G:118:LYS:HZ2	1.46	0.78
1:H:158:ALA:HB1	1:H:216:LYS:O	1.84	0.78
1:H:198:PHE:HD1	1:H:198:PHE:O	1.67	0.78
1:H:224:ILE:HD12	1:H:224:ILE:N	1.99	0.78
1:H:234:MET:O	1:H:238:LEU:HD12	1.83	0.78
1:A:165:GLN:HA	1:A:211:ASP:O	1.82	0.78
1:C:324:GLU:HB2	1:C:364:LEU:HD13	1.66	0.78
1:D:203:LEU:HD22	1:D:226:ARG:HB3	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:249:SER:CA	1:E:262:ARG:HH22	1.97	0.78
1:F:203:LEU:HD12	1:F:229:TYR:CD2	2.19	0.78
1:G:294:LEU:HD11	1:G:345:CYS:CA	2.13	0.78
1:H:260:TRP:CD2	2:H:401:CMP:C8	2.67	0.78
1:H:293:ILE:HD11	1:H:343:LEU:CD1	2.14	0.78
1:D:112:VAL:HG12	1:D:231:ARG:NE	1.99	0.78
1:D:302:GLN:HG3	1:D:313:VAL:HG11	1.64	0.78
1:G:280:ILE:CD1	1:G:322:PHE:HE2	1.96	0.78
1:H:153:PRO:HB3	1:H:222:TRP:CZ3	2.19	0.78
1:C:293:ILE:HG21	1:C:317:GLY:O	1.84	0.77
1:E:260:TRP:CD1	2:E:401:CMP:C5	2.72	0.77
1:F:173:TYR:HB2	1:F:198:PHE:HE1	1.49	0.77
1:F:230:ARG:CZ	1:F:234:MET:HE1	2.14	0.77
1:F:255:GLU:OE1	1:F:255:GLU:CA	2.28	0.77
1:B:325:ILE:CG1	2:B:402:CMP:O1P	2.32	0.77
1:E:123:MET:CE	1:F:123:MET:HE3	2.13	0.77
1:E:175:ILE:CD1	1:E:195:GLY:N	2.47	0.77
1:G:253:ILE:HD13	1:G:321:TYR:CE2	2.18	0.77
1:H:201:LEU:H	1:H:201:LEU:HD12	1.49	0.77
1:B:111:TYR:C	1:B:112:VAL:CG2	2.57	0.77
1:C:204:ILE:HG12	1:C:234:MET:SD	2.24	0.77
1:E:289:GLU:HG3	1:E:347:LYS:HZ3	1.46	0.77
1:G:164:GLN:HA	1:G:212:THR:HG22	1.65	0.77
1:B:278:GLN:CG	1:B:279:LYS:N	2.39	0.77
1:E:135:LEU:HD12	1:E:136:PHE:H	1.48	0.77
1:F:300:VAL:HG21	2:F:402:CMP:H8	1.66	0.77
1:A:301:LEU:HD13	1:A:310:PHE:CE2	2.19	0.77
1:B:260:TRP:HE1	2:B:401:CMP:C2'	1.97	0.77
1:E:272:VAL:HA	1:E:273:GLN:NE2	1.99	0.77
1:F:175:ILE:HD13	1:F:194:GLU:HA	1.66	0.77
1:G:203:LEU:HD22	1:G:226:ARG:HB3	1.66	0.77
1:A:224:ILE:CD1	1:A:224:ILE:N	2.48	0.77
1:A:247:PHE:HZ	1:A:293:ILE:O	1.67	0.77
1:C:313:VAL:HG11	2:C:402:CMP:HN61	1.50	0.77
1:H:295:GLU:HA	1:H:318:PRO:HG3	1.67	0.77
1:A:269:LEU:CD2	1:A:346:VAL:HG21	2.13	0.77
1:C:144:ARG:CG	1:C:145:SER:N	2.48	0.77
1:E:325:ILE:HG13	1:E:326:ALA:H	1.47	0.77
1:F:318:PRO:O	1:F:319:SER:HB3	1.85	0.77
1:G:179:GLU:HG2	1:G:216:LYS:CD	2.15	0.77
1:G:233:LEU:HD12	1:G:233:LEU:N	1.96	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:237:THR:O	1:G:241:ARG:HG3	1.84	0.77
1:C:294:LEU:CD1	1:C:344:LYS:O	2.30	0.77
1:C:325:ILE:CG1	2:C:402:CMP:O2P	2.32	0.77
1:D:198:PHE:HD1	1:D:198:PHE:O	1.67	0.77
1:E:172:PHE:HB3	1:E:224:ILE:CD1	2.15	0.77
1:E:175:ILE:CD1	1:E:195:GLY:H	1.98	0.77
1:F:180:MET:HB2	1:F:192:VAL:HB	1.67	0.77
1:H:120:TYR:C	1:H:120:TYR:CD2	2.63	0.77
1:H:247:PHE:CE1	1:H:294:LEU:HA	2.20	0.77
1:A:281:VAL:CG1	1:A:333:ARG:HG3	2.15	0.77
1:C:265:VAL:CG1	1:C:269:LEU:HD11	2.07	0.77
1:E:280:ILE:HD13	1:E:322:PHE:CZ	2.19	0.77
1:F:157:ILE:CD1	1:H:243:MET:HE3	2.13	0.77
1:D:296:GLY:HA3	1:D:342:PRO:O	1.85	0.77
1:E:126:LEU:HB2	1:E:222:TRP:CZ2	2.20	0.77
1:G:116:ILE:CG2	1:G:118:LYS:HZ2	1.97	0.77
1:G:173:TYR:HD2	1:G:198:PHE:CE1	2.03	0.77
1:A:170:ASP:H	1:A:209:ARG:NH2	1.83	0.76
1:A:324:GLU:HB2	1:A:364:LEU:CD1	2.15	0.76
1:D:229:TYR:HD1	1:D:233:LEU:HD13	1.49	0.76
1:D:290:PHE:C	1:D:291:PHE:HD1	1.92	0.76
1:H:285:GLU:OE1	1:H:285:GLU:CA	2.33	0.76
1:A:280:ILE:HD13	1:A:322:PHE:CE2	2.20	0.76
1:B:294:LEU:CD1	1:B:344:LYS:O	2.31	0.76
1:C:111:TYR:CD1	1:F:111:TYR:CE2	2.73	0.76
1:C:281:VAL:HG13	1:C:333:ARG:CG	2.16	0.76
1:H:200:GLU:OE1	1:H:201:LEU:HD12	1.84	0.76
1:B:175:ILE:HG22	1:B:221:LEU:HD21	1.66	0.76
1:E:154:VAL:HG12	1:E:221:LEU:HB2	1.66	0.76
1:E:165:GLN:HA	1:E:211:ASP:O	1.84	0.76
1:E:299:ALA:CB	1:E:312:GLU:OE2	2.33	0.76
1:F:293:ILE:HG23	1:F:318:PRO:HA	1.66	0.76
1:H:211:ASP:OD1	2:H:401:CMP:H5'1	1.85	0.76
1:A:179:GLU:HG2	1:A:216:LYS:HD2	1.66	0.76
1:A:365:LYS:C	1:A:368:ILE:HG13	2.09	0.76
1:C:110:SER:O	1:F:114:LYS:HD3	1.85	0.76
1:E:328:LEU:HD22	1:E:365:LYS:HE3	1.66	0.76
1:A:274:PHE:HD2	1:A:343:LEU:HD23	1.50	0.76
1:B:224:ILE:O	1:B:224:ILE:HD13	1.84	0.76
1:B:375:VAL:CG2	1:B:376:SER:N	2.48	0.76
1:B:376:SER:N	1:C:306:GLU:HA	1.99	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:SER:OG	1:C:253:ILE:HG23	1.84	0.76
1:C:278:GLN:O	1:C:338:VAL:HG22	1.85	0.76
1:D:157:ILE:CD1	1:F:243:MET:CE	2.63	0.76
1:D:190:THR:HG22	1:D:191:SER:N	1.99	0.76
1:E:152:PHE:HE2	1:E:223:GLY:HA3	1.51	0.76
1:E:175:ILE:HD13	1:E:194:GLU:HA	1.65	0.76
1:E:300:VAL:CG1	1:E:335:ALA:HB1	2.16	0.76
1:H:115:VAL:HG23	1:H:115:VAL:O	1.85	0.76
1:H:311:VAL:HG23	1:H:312:GLU:N	1.99	0.76
1:C:224:ILE:N	1:C:224:ILE:CD1	2.47	0.76
1:C:243:MET:HE3	1:E:157:ILE:CD1	2.15	0.76
1:C:249:SER:CA	1:C:262:ARG:NH2	2.38	0.76
1:G:294:LEU:HD13	1:G:344:LYS:O	1.85	0.76
1:H:173:TYR:HD2	1:H:198:PHE:CZ	2.03	0.76
1:A:115:VAL:HG11	1:D:112:VAL:HG21	1.66	0.76
1:A:153:PRO:CB	1:A:222:TRP:CZ3	2.69	0.76
1:B:190:THR:HG22	1:B:191:SER:N	1.99	0.76
1:C:279:LYS:CE	1:C:336:THR:CG2	2.63	0.76
1:C:298:ALA:O	1:C:315:ARG:HA	1.85	0.76
1:E:179:GLU:HB3	1:E:217:THR:HG23	1.68	0.76
1:F:184:VAL:O	1:F:184:VAL:HG13	1.85	0.76
1:G:131:GLU:OE1	1:G:131:GLU:CA	2.24	0.76
1:G:365:LYS:HA	1:G:368:ILE:HG13	1.67	0.76
1:H:131:GLU:N	1:H:131:GLU:OE1	2.19	0.76
1:A:113:ARG:O	1:A:113:ARG:HG2	1.84	0.76
1:A:253:ILE:HG13	1:A:254:LEU:CD2	2.16	0.76
1:C:135:LEU:HD12	1:C:136:PHE:H	1.49	0.76
1:C:226:ARG:HH11	1:C:226:ARG:CG	1.98	0.76
1:C:280:ILE:HD11	1:C:322:PHE:HE2	1.49	0.76
1:F:156:PHE:HE2	1:F:162:VAL:HG12	1.50	0.76
1:F:251:VAL:HG22	1:F:319:SER:O	1.86	0.76
1:A:157:ILE:HG13	1:A:160:GLU:OE1	1.86	0.76
1:B:282:VAL:O	1:B:285:GLU:HG2	1.84	0.76
1:E:111:TYR:O	1:E:112:VAL:HG13	1.86	0.76
1:F:157:ILE:HG13	1:F:160:GLU:OE1	1.85	0.76
1:G:291:PHE:N	1:G:291:PHE:CD1	2.54	0.76
1:H:144:ARG:CG	1:H:145:SER:N	2.49	0.76
1:H:293:ILE:HG21	1:H:317:GLY:O	1.85	0.76
1:A:321:TYR:C	1:A:321:TYR:CD1	2.64	0.76
1:B:173:TYR:HD2	1:B:198:PHE:CZ	2.04	0.76
1:B:197:SER:O	1:B:198:PHE:HB3	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:113:ARG:HD2	1:F:112:VAL:CB	2.12	0.76
1:D:316:LEU:HA	1:D:320:ASP:OD2	1.85	0.76
1:D:325:ILE:HG13	1:D:326:ALA:H	1.50	0.76
1:E:291:PHE:N	1:E:291:PHE:CD1	2.51	0.76
1:H:260:TRP:CG	2:H:401:CMP:N7	2.54	0.76
1:B:234:MET:HG3	1:B:238:LEU:HD12	1.68	0.75
1:C:224:ILE:O	1:C:224:ILE:HD13	1.86	0.75
1:C:375:VAL:HG23	1:C:376:SER:H	1.51	0.75
1:E:134:VAL:HG11	1:E:268:ALA:HA	1.68	0.75
1:F:293:ILE:CG2	1:F:318:PRO:HA	2.15	0.75
1:H:305:SER:O	1:H:306:GLU:O	2.04	0.75
1:D:292:ILE:HB	1:D:346:VAL:HG13	1.68	0.75
1:E:112:VAL:HG12	1:E:231:ARG:NH2	2.01	0.75
1:E:329:MET:HA	1:E:329:MET:CE	2.17	0.75
1:F:260:TRP:CD1	2:F:401:CMP:C5	2.75	0.75
1:H:284:GLY:O	1:H:332:PRO:CB	2.29	0.75
1:A:324:GLU:HG2	1:A:325:ILE:H	1.51	0.75
1:D:196:GLY:HA2	1:D:355:ARG:HH21	1.49	0.75
1:F:224:ILE:O	1:F:224:ILE:HD13	1.85	0.75
1:G:173:TYR:HB2	1:G:198:PHE:HE1	1.47	0.75
1:C:175:ILE:HD13	1:C:194:GLU:HA	1.67	0.75
1:C:273:GLN:HE21	1:C:273:GLN:H	1.33	0.75
1:A:140:ASP:C	1:A:140:ASP:OD1	2.29	0.75
1:B:291:PHE:HD1	1:B:291:PHE:H	1.34	0.75
1:C:269:LEU:HB2	1:C:346:VAL:HG21	1.68	0.75
1:E:204:ILE:HG12	1:E:234:MET:SD	2.26	0.75
1:G:226:ARG:HH11	1:G:226:ARG:CG	1.97	0.75
1:H:113:ARG:HD3	1:H:114:LYS:H	1.49	0.75
1:A:115:VAL:CB	1:D:112:VAL:CG2	2.65	0.75
1:C:251:VAL:CG1	1:C:254:LEU:HD21	2.16	0.75
1:E:348:LEU:HD21	1:E:356:VAL:CG2	2.17	0.75
1:G:230:ARG:CZ	1:G:234:MET:HE1	2.16	0.75
1:G:365:LYS:C	1:G:368:ILE:HG13	2.11	0.75
1:H:179:GLU:HG2	1:H:216:LYS:HD2	1.69	0.75
1:D:179:GLU:HG2	1:D:216:LYS:HD3	1.69	0.75
1:E:301:LEU:HD21	1:E:338:VAL:HB	1.69	0.75
1:F:126:LEU:HB2	1:F:222:TRP:CZ2	2.22	0.75
1:G:211:ASP:N	1:G:211:ASP:OD1	2.19	0.75
1:G:230:ARG:O	1:G:234:MET:HB3	1.87	0.75
1:B:251:VAL:CG2	1:B:319:SER:O	2.34	0.75
1:B:298:ALA:O	1:B:316:LEU:HB2	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:283:GLN:HG3	1:C:334:ALA:C	2.11	0.75
1:D:253:ILE:CG1	1:D:254:LEU:HD13	2.16	0.75
1:D:294:LEU:CD1	1:D:344:LYS:O	2.34	0.75
1:D:371:TYR:HE1	2:D:402:CMP:C8	1.98	0.75
1:F:154:VAL:HG12	1:F:221:LEU:HB2	1.67	0.75
1:F:274:PHE:HD2	1:F:343:LEU:HD23	1.51	0.75
1:G:324:GLU:HG2	1:G:325:ILE:H	1.50	0.75
1:B:179:GLU:HG2	1:B:216:LYS:HD3	1.68	0.75
1:C:156:PHE:HD2	1:C:162:VAL:CG1	1.99	0.75
1:C:365:LYS:HA	1:C:368:ILE:CD1	2.16	0.75
1:E:200:GLU:OE2	1:E:241:ARG:NH2	2.20	0.75
1:A:325:ILE:CG1	2:A:402:CMP:O2P	2.35	0.74
1:B:375:VAL:HG22	1:B:376:SER:N	2.02	0.74
1:C:203:LEU:HD22	1:C:226:ARG:HB3	1.68	0.74
1:E:184:VAL:HG13	1:E:184:VAL:O	1.85	0.74
1:E:269:LEU:CB	1:E:346:VAL:CG2	2.65	0.74
1:F:325:ILE:HG13	1:F:326:ALA:N	2.00	0.74
1:F:328:LEU:HD13	1:F:364:LEU:HD11	1.69	0.74
1:G:190:THR:CG2	1:G:191:SER:H	1.99	0.74
1:B:293:ILE:HD11	1:B:343:LEU:HD11	1.69	0.74
1:C:201:LEU:H	1:C:201:LEU:HD12	1.52	0.74
1:D:249:SER:HA	1:D:262:ARG:HH22	1.53	0.74
1:F:204:ILE:HG12	1:F:234:MET:SD	2.27	0.74
1:G:280:ILE:CD1	1:G:322:PHE:CE2	2.70	0.74
1:C:273:GLN:NE2	1:C:273:GLN:H	1.83	0.74
1:E:182:VAL:CG2	1:E:190:THR:O	2.29	0.74
1:F:294:LEU:N	1:F:294:LEU:CD1	2.49	0.74
1:G:198:PHE:CD1	1:G:198:PHE:O	2.39	0.74
1:G:295:GLU:HB2	1:G:344:LYS:HB3	1.69	0.74
1:H:293:ILE:HG13	1:H:345:CYS:SG	2.26	0.74
1:A:234:MET:HG3	1:A:238:LEU:HD12	1.69	0.74
1:A:291:PHE:CE1	1:A:347:LYS:NZ	2.56	0.74
1:C:120:TYR:HD1	1:D:148:PHE:HB3	1.53	0.74
1:C:325:ILE:HD11	2:C:402:CMP:O2P	1.85	0.74
1:D:204:ILE:HD13	1:D:238:LEU:HD11	1.68	0.74
1:D:251:VAL:CG2	1:D:319:SER:O	2.35	0.74
1:G:171:ASN:HB3	1:G:224:ILE:O	1.86	0.74
1:G:210:ALA:N	1:G:211:ASP:OD1	2.21	0.74
1:H:175:ILE:HD11	1:H:196:GLY:H	1.53	0.74
1:H:269:LEU:HD22	1:H:346:VAL:HG21	1.69	0.74
1:H:293:ILE:CG2	1:H:317:GLY:O	2.36	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:ASP:OD1	1:A:211:ASP:N	2.21	0.74
1:A:253:ILE:HD13	1:A:321:TYR:CE2	2.23	0.74
1:B:140:ASP:C	1:B:140:ASP:OD1	2.31	0.74
1:B:300:VAL:CG1	1:B:335:ALA:HB1	2.18	0.74
1:B:361:SER:C	1:B:365:LYS:HZ2	1.95	0.74
1:B:365:LYS:HA	1:B:368:ILE:HG13	1.68	0.74
1:C:247:PHE:C	1:C:247:PHE:CD2	2.63	0.74
1:C:293:ILE:CG2	1:C:317:GLY:O	2.35	0.74
1:C:324:GLU:HB2	1:C:364:LEU:CD1	2.18	0.74
1:D:120:TYR:C	1:D:120:TYR:HD2	1.92	0.74
1:D:260:TRP:HA	1:D:263:LEU:HD12	1.70	0.74
1:D:328:LEU:HD22	1:D:365:LYS:HE3	1.69	0.74
1:E:135:LEU:HD12	1:E:136:PHE:N	2.01	0.74
1:E:353:PHE:CE1	1:E:357:LEU:CD2	2.70	0.74
1:G:261:GLU:OE2	1:G:359:PRO:HG2	1.86	0.74
1:A:114:LYS:HA	1:D:111:TYR:HE2	1.51	0.74
1:B:130:ILE:CG2	1:B:131:GLU:H	2.01	0.74
1:C:200:GLU:OE1	1:C:201:LEU:HD12	1.87	0.74
1:C:366:ARG:HG3	1:C:367:ASN:N	2.00	0.74
1:D:152:PHE:H	1:D:152:PHE:HD1	1.35	0.74
1:F:158:ALA:HB2	1:F:217:THR:C	2.12	0.74
1:G:204:ILE:HG22	1:G:205:TYR:HD2	1.49	0.74
1:H:175:ILE:CD1	1:H:194:GLU:HA	2.17	0.74
1:A:211:ASP:OD2	2:A:401:CMP:C3'	2.36	0.74
1:C:280:ILE:HG12	1:C:337:VAL:HB	1.70	0.74
1:C:284:GLY:CA	1:C:332:PRO:HB3	2.17	0.74
1:E:347:LYS:O	1:E:348:LEU:HD12	1.87	0.74
1:F:211:ASP:OD2	2:F:401:CMP:N3	2.21	0.74
1:B:313:VAL:HG21	2:B:402:CMP:HN61	1.49	0.74
1:D:153:PRO:HB3	1:D:222:TRP:HZ3	1.48	0.74
1:E:157:ILE:O	1:E:160:GLU:HB2	1.88	0.74
1:F:306:GLU:CB	1:G:307:ASN:CB	2.65	0.74
1:A:156:PHE:CD2	1:A:162:VAL:CG1	2.70	0.74
1:B:269:LEU:HB3	1:B:346:VAL:HG23	1.66	0.74
1:C:111:TYR:CD1	1:F:111:TYR:HE2	2.06	0.74
1:D:192:VAL:O	1:D:192:VAL:HG12	1.88	0.74
1:D:280:ILE:HG13	1:D:281:VAL:H	1.51	0.74
1:F:289:GLU:CG	1:F:347:LYS:HZ3	1.93	0.74
1:H:173:TYR:CD2	1:H:198:PHE:CE1	2.75	0.74
1:D:198:PHE:CD1	1:D:198:PHE:O	2.41	0.73
1:D:204:ILE:HG22	1:D:205:TYR:HD2	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:294:LEU:H	1:D:294:LEU:CD1	1.98	0.73
1:D:301:LEU:CD2	1:D:310:PHE:CD1	2.70	0.73
1:F:254:LEU:HD12	1:F:255:GLU:N	2.02	0.73
1:F:260:TRP:NE1	2:F:401:CMP:H2'	2.02	0.73
1:G:112:VAL:HG12	1:G:231:ARG:NH2	2.03	0.73
1:G:172:PHE:HB3	1:G:224:ILE:CD1	2.18	0.73
1:H:316:LEU:HA	1:H:320:ASP:OD2	1.88	0.73
1:A:144:ARG:NH1	1:A:144:ARG:HB2	2.03	0.73
1:C:113:ARG:HG3	1:F:112:VAL:HG12	1.69	0.73
1:C:175:ILE:HD11	1:C:196:GLY:H	1.53	0.73
1:F:234:MET:HG3	1:F:238:LEU:HD12	1.71	0.73
1:G:371:TYR:HE1	2:G:402:CMP:N7	1.86	0.73
1:A:112:VAL:O	1:A:231:ARG:NH1	2.21	0.73
1:A:115:VAL:CG1	1:D:112:VAL:HG23	2.19	0.73
1:A:135:LEU:HD13	1:A:136:PHE:CD1	2.23	0.73
1:A:365:LYS:CA	1:A:368:ILE:HG13	2.18	0.73
1:C:234:MET:HG3	1:C:238:LEU:CD1	2.17	0.73
1:F:114:LYS:HD2	1:F:115:VAL:H	1.52	0.73
1:F:301:LEU:HD22	1:F:311:VAL:O	1.86	0.73
1:G:183:TYR:CE1	1:G:188:TRP:HB2	2.23	0.73
1:H:233:LEU:CD1	1:H:233:LEU:H	1.95	0.73
1:A:204:ILE:HG22	1:A:205:TYR:CD2	2.24	0.73
1:D:162:VAL:HG22	1:D:213:VAL:O	1.88	0.73
1:E:173:TYR:CB	1:E:198:PHE:HE1	2.01	0.73
1:A:328:LEU:HD22	1:A:365:LYS:HE3	1.68	0.73
1:B:252:SER:O	1:B:254:LEU:HG	1.88	0.73
1:C:153:PRO:HB3	1:C:222:TRP:CZ3	2.24	0.73
1:C:280:ILE:HD11	1:C:337:VAL:HB	1.68	0.73
1:G:211:ASP:OD2	2:G:401:CMP:H3'	1.88	0.73
1:H:204:ILE:HG22	1:H:205:TYR:HD2	1.49	0.73
1:H:280:ILE:HB	1:H:291:PHE:HE2	1.53	0.73
1:H:291:PHE:CD2	1:H:322:PHE:CZ	2.76	0.73
1:A:111:TYR:HA	1:D:115:VAL:CG2	2.19	0.73
1:C:280:ILE:HG13	1:C:281:VAL:H	1.53	0.73
1:E:152:PHE:CD2	1:E:152:PHE:O	2.41	0.73
1:F:204:ILE:HD13	1:F:238:LEU:HD11	1.69	0.73
1:H:273:GLN:HB2	1:H:343:LEU:O	1.89	0.73
1:H:280:ILE:CD1	1:H:337:VAL:HB	2.19	0.73
1:A:325:ILE:HG13	1:A:326:ALA:N	2.03	0.73
1:B:254:LEU:C	1:B:254:LEU:HD12	2.13	0.73
1:B:278:GLN:HG2	1:B:279:LYS:N	2.01	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:LEU:H	1:B:294:LEU:CD1	1.97	0.73
1:C:194:GLU:O	1:C:355:ARG:HD2	1.88	0.73
1:F:175:ILE:HD11	1:F:195:GLY:N	2.02	0.73
1:H:249:SER:CA	1:H:262:ARG:NH2	2.52	0.73
1:H:290:PHE:C	1:H:291:PHE:HD1	1.97	0.73
1:A:279:LYS:HB3	1:A:338:VAL:HG23	1.69	0.73
1:B:147:ILE:HG23	1:B:232:ILE:HD13	1.69	0.73
1:B:325:ILE:CD1	2:B:402:CMP:O1P	2.35	0.73
1:C:120:TYR:HD2	1:C:121:LYS:HA	1.52	0.73
1:C:130:ILE:HG23	1:C:131:GLU:N	2.04	0.73
1:C:269:LEU:HB3	1:C:346:VAL:HG22	1.70	0.73
1:C:287:GLY:HA3	1:C:326:ALA:CB	2.18	0.73
1:A:260:TRP:CG	2:A:401:CMP:N7	2.57	0.73
1:B:269:LEU:HD22	1:B:346:VAL:CG2	2.19	0.73
1:B:273:GLN:HB2	1:B:343:LEU:O	1.87	0.73
1:B:312:GLU:OE1	1:B:313:VAL:N	2.21	0.73
1:C:111:TYR:O	1:C:112:VAL:CG1	2.36	0.73
1:C:275:GLU:O	1:C:339:ALA:HB3	1.89	0.73
1:E:294:LEU:O	1:E:318:PRO:HB3	1.89	0.73
1:G:148:PHE:HB3	1:H:120:TYR:CD1	2.24	0.73
1:G:161:THR:CA	1:G:214:LYS:HD2	2.18	0.73
1:A:175:ILE:HA	1:A:221:LEU:HD22	1.69	0.73
1:A:280:ILE:HD12	1:A:281:VAL:HG23	1.71	0.73
1:B:130:ILE:HG23	1:B:131:GLU:N	2.03	0.73
1:C:293:ILE:HG13	1:C:345:CYS:SG	2.29	0.73
1:C:371:TYR:CE1	2:C:402:CMP:C8	2.71	0.73
1:D:172:PHE:HB3	1:D:224:ILE:CD1	2.19	0.73
1:E:239:ARG:NH1	1:G:157:ILE:HG23	2.02	0.73
1:F:279:LYS:HE3	1:F:282:VAL:HG22	1.70	0.73
1:F:280:ILE:HD11	1:F:322:PHE:CE2	2.20	0.73
1:A:203:LEU:HD12	1:A:229:TYR:CD2	2.24	0.72
1:C:204:ILE:CG2	1:C:205:TYR:CD2	2.71	0.72
1:F:301:LEU:HD12	1:F:310:PHE:HB3	1.71	0.72
1:G:272:VAL:C	1:G:273:GLN:NE2	2.46	0.72
1:H:135:LEU:HD12	1:H:136:PHE:H	1.52	0.72
1:A:272:VAL:HA	1:A:273:GLN:NE2	2.03	0.72
1:B:302:GLN:O	1:B:310:PHE:HA	1.90	0.72
1:D:157:ILE:CB	1:D:218:ASN:OD1	2.36	0.72
1:G:165:GLN:HA	1:G:211:ASP:O	1.89	0.72
1:A:112:VAL:O	1:A:231:ARG:CZ	2.37	0.72
1:A:365:LYS:HA	1:A:368:ILE:CG1	2.19	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:135:LEU:HD13	1:B:136:PHE:CD1	2.23	0.72
1:C:283:GLN:HG3	1:C:335:ALA:N	2.04	0.72
1:D:153:PRO:CB	1:D:222:TRP:CZ3	2.73	0.72
1:E:158:ALA:N	1:E:218:ASN:OD1	2.22	0.72
1:E:179:GLU:HG2	1:E:216:LYS:HD3	1.69	0.72
1:E:265:VAL:HG12	1:E:269:LEU:CD2	2.18	0.72
1:F:328:LEU:CD2	1:F:365:LYS:HE3	2.20	0.72
1:F:328:LEU:CD1	1:F:364:LEU:HD11	2.19	0.72
1:G:152:PHE:CD2	1:G:152:PHE:O	2.42	0.72
1:H:111:TYR:CE2	1:H:112:VAL:HG12	2.24	0.72
1:H:237:THR:O	1:H:241:ARG:HG3	1.89	0.72
1:A:142:ASN:HB2	1:C:121:LYS:CE	2.20	0.72
1:B:130:ILE:HG22	1:B:131:GLU:H	1.54	0.72
1:B:172:PHE:HB3	1:B:224:ILE:CD1	2.17	0.72
1:B:280:ILE:HD11	1:B:322:PHE:CE2	2.08	0.72
1:B:327:LEU:HD23	1:B:353:PHE:CE2	2.25	0.72
1:C:152:PHE:CD2	1:C:152:PHE:O	2.42	0.72
1:C:156:PHE:CE2	1:C:162:VAL:CG1	2.60	0.72
1:C:290:PHE:C	1:C:291:PHE:HD1	1.96	0.72
1:C:313:VAL:HG13	1:C:313:VAL:O	1.87	0.72
1:D:156:PHE:HD2	1:D:162:VAL:CG1	2.01	0.72
1:G:233:LEU:H	1:G:233:LEU:CD1	1.87	0.72
1:B:228:SER:O	1:B:232:ILE:HG22	1.89	0.72
1:D:171:ASN:HB3	1:D:224:ILE:O	1.88	0.72
1:H:288:ASP:C	1:H:288:ASP:OD1	2.23	0.72
1:A:165:GLN:N	1:A:212:THR:CG2	2.30	0.72
1:C:280:ILE:CD1	1:C:337:VAL:HB	2.20	0.72
1:C:291:PHE:CE1	1:C:347:LYS:NZ	2.58	0.72
1:E:112:VAL:CG1	1:E:231:ARG:NH2	2.53	0.72
1:E:278:GLN:CG	1:E:279:LYS:H	2.02	0.72
1:E:324:GLU:HB2	1:E:364:LEU:HD13	1.72	0.72
1:H:246:GLU:O	1:H:247:PHE:C	2.30	0.72
1:H:304:ARG:H	1:H:308:GLU:CB	2.00	0.72
1:A:153:PRO:CA	1:A:222:TRP:CZ3	2.73	0.72
1:A:182:VAL:CG2	1:A:190:THR:O	2.32	0.72
1:C:281:VAL:HG13	1:C:333:ARG:HG3	1.69	0.72
1:D:131:GLU:OE1	1:D:131:GLU:CA	2.34	0.72
1:D:157:ILE:O	1:D:160:GLU:HB2	1.89	0.72
1:D:280:ILE:CD1	1:D:322:PHE:CE2	2.73	0.72
1:E:279:LYS:CB	1:E:279:LYS:HZ2	1.83	0.72
1:F:162:VAL:HG23	1:F:163:ILE:N	2.04	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:211:ASP:OD2	2:F:401:CMP:H3'	1.89	0.72
1:A:260:TRP:CD2	2:A:401:CMP:N7	2.57	0.72
1:A:347:LYS:O	1:A:348:LEU:HD12	1.89	0.72
1:B:188:TRP:CZ3	1:B:190:THR:C	2.67	0.72
1:B:203:LEU:HD12	1:B:229:TYR:CD2	2.24	0.72
1:D:190:THR:CG2	1:D:191:SER:H	1.97	0.72
1:E:293:ILE:CG2	1:E:317:GLY:O	2.37	0.72
1:F:266:ALA:O	1:F:267:ASP:C	2.31	0.72
1:F:280:ILE:HD11	1:F:337:VAL:HB	1.71	0.72
1:F:301:LEU:HA	1:F:311:VAL:O	1.89	0.72
1:G:328:LEU:CD2	1:G:365:LYS:HE3	2.20	0.72
1:A:175:ILE:HG22	1:A:221:LEU:HD21	1.70	0.72
1:B:152:PHE:CD2	1:B:152:PHE:O	2.43	0.72
1:B:170:ASP:H	1:B:209:ARG:NH2	1.88	0.72
1:C:361:SER:C	1:C:365:LYS:HZ2	1.97	0.72
1:E:272:VAL:HG22	1:E:273:GLN:H	1.55	0.72
1:G:148:PHE:HB2	1:H:120:TYR:CD1	2.25	0.72
1:H:265:VAL:O	1:H:269:LEU:HG	1.90	0.72
1:C:144:ARG:HG2	1:C:145:SER:N	2.03	0.72
1:C:348:LEU:HD21	1:C:356:VAL:HG21	1.72	0.72
1:E:230:ARG:O	1:E:234:MET:HB3	1.89	0.72
1:A:147:ILE:HG23	1:A:232:ILE:CD1	2.19	0.71
1:A:183:TYR:CD1	1:A:188:TRP:HB2	2.24	0.71
1:A:222:TRP:CE3	1:A:222:TRP:HA	2.25	0.71
1:D:247:PHE:C	1:D:247:PHE:CD2	2.68	0.71
1:F:113:ARG:CD	1:F:146:ASP:CG	2.63	0.71
1:H:365:LYS:HA	1:H:368:ILE:HG13	1.71	0.71
1:A:179:GLU:HG2	1:A:216:LYS:CD	2.19	0.71
1:A:183:TYR:CE1	1:A:188:TRP:HB2	2.25	0.71
1:B:126:LEU:HD12	1:B:126:LEU:C	2.15	0.71
1:B:175:ILE:O	1:B:175:ILE:CD1	2.28	0.71
1:B:275:GLU:O	1:B:278:GLN:HB3	1.90	0.71
1:C:130:ILE:CG2	1:C:131:GLU:H	2.02	0.71
1:C:249:SER:N	1:C:262:ARG:NH2	2.39	0.71
1:G:328:LEU:HD22	1:G:365:LYS:HE3	1.72	0.71
1:H:251:VAL:HG23	1:H:319:SER:O	1.89	0.71
1:B:272:VAL:HG22	1:B:273:GLN:H	1.55	0.71
1:E:203:LEU:HD22	1:E:226:ARG:CB	2.20	0.71
1:F:198:PHE:C	1:F:198:PHE:CD1	2.66	0.71
1:C:188:TRP:CH2	1:C:190:THR:HA	2.25	0.71
1:D:368:ILE:O	1:D:371:TYR:HB2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:158:ALA:HB2	1:E:217:THR:C	2.15	0.71
1:E:280:ILE:CD1	1:E:281:VAL:HG23	2.20	0.71
1:F:272:VAL:HG22	1:F:273:GLN:H	1.55	0.71
1:G:253:ILE:HG21	1:G:321:TYR:CE2	2.25	0.71
1:H:184:VAL:O	1:H:184:VAL:HG13	1.88	0.71
1:H:270:GLU:O	1:H:346:VAL:HA	1.89	0.71
1:H:284:GLY:N	1:H:333:ARG:O	2.23	0.71
1:B:120:TYR:HD2	1:B:120:TYR:O	1.72	0.71
1:C:113:ARG:CG	1:F:112:VAL:CG1	2.59	0.71
1:F:259:LYS:HG3	1:F:260:TRP:H	1.55	0.71
1:G:126:LEU:HD12	1:G:126:LEU:C	2.15	0.71
1:G:280:ILE:HD11	1:G:337:VAL:HB	1.71	0.71
1:H:135:LEU:HD12	1:H:136:PHE:N	2.05	0.71
1:H:365:LYS:C	1:H:368:ILE:HG13	2.16	0.71
1:A:113:ARG:HH22	1:D:115:VAL:HA	1.55	0.71
1:B:247:PHE:HZ	1:B:293:ILE:O	1.73	0.71
1:D:325:ILE:HG12	2:D:402:CMP:P	2.31	0.71
1:E:183:TYR:CE1	1:E:188:TRP:HB2	2.26	0.71
1:E:251:VAL:CG2	1:E:319:SER:O	2.37	0.71
1:H:171:ASN:HB3	1:H:224:ILE:O	1.91	0.71
1:H:273:GLN:N	1:H:273:GLN:CD	2.49	0.71
1:A:224:ILE:N	1:A:224:ILE:HD12	2.06	0.71
1:A:281:VAL:HG13	1:A:333:ARG:HG3	1.72	0.71
1:C:356:VAL:CG2	1:C:357:LEU:HD13	2.16	0.71
1:D:159:GLY:O	1:F:243:MET:HE2	1.90	0.71
1:E:156:PHE:HD2	1:E:162:VAL:CG1	1.98	0.71
1:G:278:GLN:HG2	1:G:279:LYS:H	1.56	0.71
1:G:280:ILE:HG13	1:G:281:VAL:H	1.53	0.71
1:H:313:VAL:HG11	2:H:402:CMP:HN61	1.56	0.71
1:A:156:PHE:HD2	1:A:162:VAL:CG1	2.03	0.71
1:B:157:ILE:HG22	1:B:218:ASN:OD1	1.89	0.71
1:B:158:ALA:CB	1:B:217:THR:O	2.36	0.71
1:G:148:PHE:HD1	1:H:120:TYR:CE1	2.08	0.71
1:G:278:GLN:HG2	1:G:279:LYS:N	2.06	0.71
1:G:278:GLN:CG	1:G:279:LYS:H	2.03	0.71
1:A:111:TYR:O	1:D:115:VAL:HG21	1.90	0.71
1:A:113:ARG:NH1	1:D:114:LYS:N	2.39	0.71
1:A:254:LEU:HD12	1:A:254:LEU:C	2.15	0.71
1:A:290:PHE:C	1:A:291:PHE:HD1	1.98	0.71
1:B:198:PHE:CD1	1:B:198:PHE:O	2.43	0.71
1:B:210:ALA:N	1:B:211:ASP:OD1	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:300:VAL:O	1:C:301:LEU:CG	2.38	0.71
1:D:175:ILE:HD13	1:D:194:GLU:HA	1.70	0.71
1:E:325:ILE:HG13	1:E:326:ALA:N	2.03	0.71
1:G:265:VAL:O	1:G:269:LEU:CG	2.32	0.71
1:H:179:GLU:HG2	1:H:216:LYS:HD3	1.71	0.71
1:H:253:ILE:HG13	1:H:254:LEU:N	2.03	0.71
1:H:259:LYS:O	1:H:262:ARG:HG3	1.89	0.71
1:H:260:TRP:HE1	2:H:401:CMP:C2'	1.99	0.71
1:A:175:ILE:CD1	1:A:193:GLY:O	2.38	0.71
1:C:298:ALA:HB1	1:C:338:VAL:O	1.91	0.71
1:D:365:LYS:C	1:D:368:ILE:HG13	2.15	0.71
1:F:278:GLN:HG3	1:F:279:LYS:N	2.03	0.71
1:G:126:LEU:HB2	1:G:222:TRP:CZ2	2.26	0.71
1:G:282:VAL:O	1:G:285:GLU:HG2	1.91	0.71
1:A:239:ARG:NH2	1:C:156:PHE:CE1	2.58	0.70
1:A:251:VAL:CG1	1:A:254:LEU:HD21	2.20	0.70
1:A:294:LEU:CD1	1:A:344:LYS:O	2.38	0.70
1:C:130:ILE:HG23	1:C:131:GLU:H	1.54	0.70
1:C:182:VAL:CG2	1:C:190:THR:H	2.02	0.70
1:F:254:LEU:HD12	1:F:254:LEU:C	2.15	0.70
1:H:198:PHE:CD1	1:H:198:PHE:O	2.43	0.70
1:H:302:GLN:C	1:H:310:PHE:CE1	2.69	0.70
1:A:293:ILE:CD1	1:A:343:LEU:HD11	2.21	0.70
1:B:175:ILE:HD11	1:B:195:GLY:N	2.05	0.70
1:B:211:ASP:OD2	2:B:401:CMP:C4'	2.40	0.70
1:B:293:ILE:HG13	1:B:345:CYS:SG	2.30	0.70
1:C:182:VAL:HG12	1:C:213:VAL:CG1	2.19	0.70
1:C:230:ARG:HG2	1:C:230:ARG:HH11	1.56	0.70
1:D:224:ILE:CD1	1:D:224:ILE:N	2.52	0.70
1:F:247:PHE:C	1:F:247:PHE:CD2	2.69	0.70
1:F:260:TRP:CD1	2:F:401:CMP:C4	2.79	0.70
1:H:220:LYS:O	1:H:221:LEU:HD23	1.91	0.70
1:H:328:LEU:HD23	1:H:365:LYS:HE3	1.71	0.70
1:A:197:SER:O	1:A:198:PHE:HB3	1.90	0.70
1:F:114:LYS:CD	1:F:115:VAL:H	2.05	0.70
1:F:293:ILE:CD1	1:F:343:LEU:HD11	2.21	0.70
1:F:321:TYR:CD1	1:F:321:TYR:C	2.69	0.70
1:G:116:ILE:CG2	1:G:118:LYS:NZ	2.53	0.70
1:A:182:VAL:HG12	1:A:213:VAL:CG2	2.21	0.70
1:A:251:VAL:CG2	1:A:319:SER:O	2.38	0.70
1:B:175:ILE:CD1	1:B:195:GLY:H	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:157:ILE:HD12	1:C:157:ILE:C	2.16	0.70
1:D:246:GLU:O	1:D:249:SER:N	2.24	0.70
1:E:162:VAL:CG2	1:E:163:ILE:HG13	2.16	0.70
1:E:247:PHE:C	1:E:247:PHE:CD2	2.69	0.70
1:F:200:GLU:OE2	1:F:241:ARG:NH2	2.24	0.70
1:G:117:PRO:O	1:G:118:LYS:HB2	1.90	0.70
1:D:282:VAL:O	1:D:285:GLU:HG2	1.91	0.70
1:D:327:LEU:HD23	1:D:353:PHE:CD2	2.26	0.70
1:E:321:TYR:CD1	1:E:321:TYR:C	2.69	0.70
1:F:179:GLU:HG2	1:F:216:LYS:HD2	1.73	0.70
1:G:324:GLU:HB2	1:G:364:LEU:CD1	2.20	0.70
1:H:301:LEU:O	1:H:302:GLN:HG3	1.91	0.70
1:A:211:ASP:CG	2:A:401:CMP:H5'1	2.15	0.70
1:D:211:ASP:OD1	2:D:401:CMP:H5'1	1.91	0.70
1:E:175:ILE:HD11	1:E:195:GLY:N	2.05	0.70
1:G:175:ILE:HD13	1:G:194:GLU:HA	1.71	0.70
1:C:300:VAL:HG11	2:C:402:CMP:C8	2.21	0.70
1:D:280:ILE:HD11	1:D:337:VAL:HB	1.72	0.70
1:G:135:LEU:HD12	1:G:136:PHE:N	2.06	0.70
1:H:247:PHE:CD2	1:H:247:PHE:O	2.44	0.70
1:H:291:PHE:N	1:H:291:PHE:CD1	2.59	0.70
1:A:130:ILE:CD1	1:A:151:MET:CE	2.70	0.70
1:A:348:LEU:HD21	1:A:356:VAL:HG21	1.71	0.70
1:B:295:GLU:O	1:B:344:LYS:N	2.23	0.70
1:E:153:PRO:HB3	1:E:222:TRP:CZ3	2.27	0.70
1:E:278:GLN:CG	1:E:279:LYS:N	2.55	0.70
1:G:135:LEU:HD12	1:G:136:PHE:H	1.56	0.70
1:B:246:GLU:O	1:B:249:SER:N	2.24	0.70
1:C:265:VAL:O	1:C:269:LEU:CG	2.31	0.70
1:D:246:GLU:O	1:D:247:PHE:C	2.35	0.70
1:E:211:ASP:OD1	2:E:401:CMP:H5'1	1.91	0.70
1:B:280:ILE:HG13	1:B:281:VAL:H	1.56	0.70
1:D:269:LEU:HD22	1:D:346:VAL:HG22	1.73	0.70
1:E:120:TYR:C	1:E:120:TYR:CD2	2.68	0.70
1:G:182:VAL:HG12	1:G:213:VAL:HG22	1.73	0.70
1:A:203:LEU:HD13	1:A:226:ARG:HB3	1.73	0.69
1:C:183:TYR:HD1	1:C:188:TRP:HA	1.57	0.69
1:C:285:GLU:O	1:C:332:PRO:CA	2.36	0.69
1:C:311:VAL:HG23	1:C:312:GLU:N	2.07	0.69
1:D:252:SER:O	1:D:254:LEU:HD22	1.91	0.69
1:D:325:ILE:CD1	2:D:402:CMP:O1P	2.39	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:156:PHE:HD2	1:G:162:VAL:HG12	1.56	0.69
1:G:175:ILE:CD1	1:G:195:GLY:H	2.05	0.69
1:H:234:MET:HG3	1:H:238:LEU:CD1	2.20	0.69
1:H:253:ILE:HG13	1:H:254:LEU:CD2	2.21	0.69
1:A:175:ILE:O	1:A:175:ILE:CD1	2.29	0.69
1:A:224:ILE:CD1	1:A:224:ILE:H	2.04	0.69
1:B:198:PHE:O	1:B:198:PHE:HD1	1.75	0.69
1:C:224:ILE:H	1:C:224:ILE:CD1	2.04	0.69
1:D:162:VAL:CG2	1:D:163:ILE:HG13	2.18	0.69
1:D:280:ILE:CD1	1:D:322:PHE:HE2	2.05	0.69
1:E:245:GLU:OE1	1:E:246:GLU:OE1	2.08	0.69
1:H:203:LEU:HD12	1:H:229:TYR:CD2	2.27	0.69
1:A:263:LEU:O	1:A:267:ASP:N	2.24	0.69
1:C:174:VAL:O	1:C:174:VAL:HG13	1.90	0.69
1:C:365:LYS:O	1:C:368:ILE:CG1	2.39	0.69
1:D:194:GLU:O	1:D:355:ARG:HD2	1.92	0.69
1:H:182:VAL:HG12	1:H:213:VAL:CG2	2.22	0.69
1:H:361:SER:C	1:H:365:LYS:HZ2	1.99	0.69
1:D:222:TRP:CE3	1:D:222:TRP:HA	2.26	0.69
1:D:285:GLU:OE1	1:D:285:GLU:HA	1.93	0.69
1:E:243:MET:CE	1:G:157:ILE:HD12	2.15	0.69
1:F:130:ILE:HG13	1:F:136:PHE:CG	2.27	0.69
1:G:179:GLU:HG2	1:G:216:LYS:HD3	1.74	0.69
1:G:266:ALA:CA	1:G:269:LEU:CD1	2.68	0.69
1:G:275:GLU:O	1:G:278:GLN:HB3	1.92	0.69
1:H:347:LYS:O	1:H:348:LEU:HD12	1.93	0.69
1:A:113:ARG:NE	1:D:113:ARG:C	2.51	0.69
1:A:282:VAL:O	1:A:285:GLU:HG2	1.93	0.69
1:D:259:LYS:O	1:D:262:ARG:CG	2.33	0.69
1:D:329:MET:CE	1:D:329:MET:HA	2.21	0.69
1:E:116:ILE:HG22	1:E:118:LYS:HG3	1.74	0.69
1:F:222:TRP:CE3	1:F:222:TRP:HA	2.27	0.69
1:F:328:LEU:HD22	1:F:365:LYS:HE3	1.74	0.69
1:H:288:ASP:OD1	1:H:288:ASP:O	2.10	0.69
1:B:266:ALA:HA	1:B:269:LEU:CD1	2.23	0.69
1:C:266:ALA:CA	1:C:269:LEU:CD1	2.66	0.69
1:F:266:ALA:HA	1:F:269:LEU:HD12	1.74	0.69
1:A:204:ILE:HG22	1:A:205:TYR:HD2	1.57	0.69
1:A:253:ILE:HG21	1:A:321:TYR:CE2	2.27	0.69
1:B:153:PRO:CA	1:B:222:TRP:CZ3	2.75	0.69
1:C:190:THR:CG2	1:C:191:SER:H	2.03	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:GLN:HA	1:D:212:THR:HG22	1.75	0.69
1:G:152:PHE:O	1:G:152:PHE:HD2	1.74	0.69
1:G:175:ILE:O	1:G:175:ILE:CD1	2.32	0.69
1:G:280:ILE:HD11	1:G:322:PHE:HE2	1.56	0.69
1:G:280:ILE:HD13	1:G:322:PHE:CZ	2.27	0.69
1:G:298:ALA:HB1	1:G:338:VAL:O	1.93	0.69
1:A:188:TRP:CH2	1:A:190:THR:HA	2.27	0.69
1:A:323:GLY:HA2	2:A:402:CMP:O1P	1.93	0.69
1:B:135:LEU:HD12	1:B:136:PHE:N	2.07	0.69
1:B:161:THR:CA	1:B:214:LYS:HD2	2.17	0.69
1:B:211:ASP:OD2	2:B:401:CMP:H5'1	1.91	0.69
1:B:280:ILE:HD11	1:B:337:VAL:HB	1.73	0.69
1:C:327:LEU:HD23	1:C:353:PHE:CE2	2.27	0.69
1:D:111:TYR:OH	1:D:113:ARG:C	2.35	0.69
1:D:153:PRO:CB	1:D:222:TRP:HZ3	2.05	0.69
1:D:161:THR:CA	1:D:214:LYS:HD2	2.20	0.69
1:D:173:TYR:HB2	1:D:198:PHE:CE1	2.27	0.69
1:D:296:GLY:CA	1:D:342:PRO:O	2.40	0.69
1:D:298:ALA:CB	1:D:338:VAL:O	2.38	0.69
1:D:321:TYR:C	1:D:321:TYR:CD1	2.71	0.69
1:E:152:PHE:H	1:E:152:PHE:HD2	1.39	0.69
1:E:253:ILE:HG21	1:E:321:TYR:CE2	2.27	0.69
1:F:211:ASP:CG	2:F:401:CMP:H5'1	2.18	0.69
1:F:253:ILE:HG13	1:F:254:LEU:H	1.57	0.69
1:H:144:ARG:O	1:H:147:ILE:HG12	1.93	0.69
1:H:156:PHE:HD2	1:H:162:VAL:HG12	1.45	0.69
1:H:289:GLU:HB3	1:H:347:LYS:HZ1	1.56	0.69
1:H:365:LYS:HA	1:H:368:ILE:CG1	2.23	0.69
1:D:183:TYR:CE1	1:D:188:TRP:HB2	2.28	0.69
1:F:158:ALA:N	1:F:218:ASN:OD1	2.25	0.69
1:F:260:TRP:CE2	2:F:401:CMP:C8	2.76	0.69
1:G:148:PHE:HB2	1:H:120:TYR:HD1	1.55	0.69
1:G:290:PHE:C	1:G:291:PHE:HD1	2.01	0.69
1:H:222:TRP:HA	1:H:222:TRP:CE3	2.26	0.69
1:C:173:TYR:CD2	1:C:198:PHE:CZ	2.80	0.69
1:C:365:LYS:C	1:C:368:ILE:HG13	2.17	0.69
1:E:224:ILE:O	1:E:224:ILE:HD13	1.93	0.69
1:A:111:TYR:O	1:A:112:VAL:CG2	2.40	0.68
1:B:171:ASN:H	1:B:209:ARG:HH22	1.41	0.68
1:E:148:PHE:CD1	1:F:120:TYR:CD1	2.80	0.68
1:E:365:LYS:HA	1:E:368:ILE:HG13	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:371:TYR:CE1	2:G:402:CMP:C4	2.81	0.68
1:H:224:ILE:CD1	1:H:224:ILE:H	2.06	0.68
1:H:226:ARG:HH11	1:H:226:ARG:CG	2.02	0.68
1:H:300:VAL:O	1:H:312:GLU:HB2	1.93	0.68
1:B:321:TYR:CD1	1:B:321:TYR:O	2.46	0.68
1:C:300:VAL:N	1:C:312:GLU:OE2	2.25	0.68
1:D:173:TYR:HD2	1:D:198:PHE:CE1	2.11	0.68
1:E:116:ILE:N	1:E:149:ASP:O	2.25	0.68
1:E:123:MET:CE	1:F:123:MET:CE	2.72	0.68
1:E:308:GLU:C	1:E:309:GLU:HG2	2.17	0.68
1:G:182:VAL:CG2	1:G:190:THR:H	2.06	0.68
1:G:253:ILE:HG13	1:G:254:LEU:H	1.57	0.68
1:H:249:SER:HA	1:H:262:ARG:NH2	2.08	0.68
1:A:183:TYR:CD1	1:A:188:TRP:CB	2.77	0.68
1:C:233:LEU:HD12	1:C:233:LEU:N	2.06	0.68
1:D:123:MET:O	1:D:127:ALA:N	2.20	0.68
1:E:360:CYS:O	1:E:364:LEU:HD23	1.92	0.68
1:G:157:ILE:O	1:G:160:GLU:HB2	1.92	0.68
1:G:251:VAL:CG2	1:G:319:SER:O	2.39	0.68
1:G:371:TYR:HE1	2:G:402:CMP:C5	2.09	0.68
1:H:182:VAL:O	1:H:182:VAL:CG2	2.37	0.68
1:H:283:GLN:HG3	1:H:335:ALA:N	2.09	0.68
1:B:183:TYR:CE1	1:B:188:TRP:HB2	2.29	0.68
1:D:329:MET:HA	1:D:329:MET:HE3	1.74	0.68
1:F:174:VAL:HG23	1:F:196:GLY:O	1.94	0.68
1:H:301:LEU:HA	1:H:311:VAL:O	1.94	0.68
1:A:126:LEU:HD12	1:A:126:LEU:C	2.18	0.68
1:A:126:LEU:HB2	1:A:222:TRP:CZ2	2.28	0.68
1:A:209:ARG:HD2	2:A:401:CMP:O5'	1.93	0.68
1:B:135:LEU:CD1	1:B:136:PHE:N	2.57	0.68
1:B:254:LEU:HD12	1:B:255:GLU:N	2.09	0.68
1:B:269:LEU:CB	1:B:346:VAL:HG21	2.20	0.68
1:C:173:TYR:CD2	1:C:198:PHE:CE1	2.80	0.68
1:E:300:VAL:HA	1:E:336:THR:O	1.93	0.68
1:F:265:VAL:O	1:F:269:LEU:HG	1.93	0.68
1:G:269:LEU:HB3	1:G:346:VAL:CG2	2.23	0.68
1:H:190:THR:CG2	1:H:191:SER:H	2.00	0.68
1:B:324:GLU:HB2	1:B:364:LEU:CD1	2.24	0.68
1:F:260:TRP:NE1	2:F:401:CMP:C2'	2.57	0.68
1:H:365:LYS:HA	1:H:368:ILE:CD1	2.24	0.68
1:B:279:LYS:O	1:B:279:LYS:HG3	1.91	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:SER:HA	1:C:316:LEU:O	1.94	0.68
1:E:148:PHE:CD1	1:F:120:TYR:CE1	2.82	0.68
1:F:156:PHE:HD2	1:F:162:VAL:CG1	2.02	0.68
1:F:280:ILE:HD12	1:F:281:VAL:HG23	1.74	0.68
1:H:282:VAL:O	1:H:285:GLU:HG2	1.94	0.68
1:H:294:LEU:CD1	1:H:295:GLU:H	2.01	0.68
1:H:294:LEU:O	1:H:295:GLU:HG3	1.93	0.68
1:A:164:GLN:HA	1:A:212:THR:HG22	1.76	0.68
1:B:111:TYR:CG	1:B:112:VAL:N	2.47	0.68
1:C:144:ARG:O	1:C:147:ILE:HG12	1.94	0.68
1:D:278:GLN:HG3	1:D:279:LYS:H	1.58	0.68
1:E:253:ILE:HD13	1:E:321:TYR:CD2	2.29	0.68
1:E:294:LEU:HD13	1:E:345:CYS:HA	1.74	0.68
1:E:361:SER:C	1:E:365:LYS:HZ2	2.02	0.68
1:F:114:LYS:HD2	1:F:115:VAL:N	2.09	0.68
1:G:203:LEU:HD12	1:G:229:TYR:CD2	2.29	0.68
1:H:112:VAL:HG22	1:H:113:ARG:N	2.08	0.68
1:H:183:TYR:CE1	1:H:188:TRP:HB2	2.28	0.68
1:A:327:LEU:HD23	1:A:353:PHE:CE1	2.29	0.68
1:D:229:TYR:HD1	1:D:233:LEU:CD1	2.03	0.68
1:D:254:LEU:HD22	1:D:255:GLU:N	2.09	0.68
1:D:263:LEU:O	1:D:266:ALA:HB3	1.94	0.68
1:D:266:ALA:HA	1:D:269:LEU:HD12	1.76	0.68
1:F:135:LEU:HD12	1:F:135:LEU:N	2.08	0.68
1:F:226:ARG:HH11	1:F:226:ARG:CG	1.98	0.68
1:F:249:SER:CA	1:F:262:ARG:HH22	2.06	0.68
1:F:353:PHE:CE1	1:F:357:LEU:HD22	2.29	0.68
1:A:152:PHE:O	1:A:152:PHE:CD2	2.47	0.68
1:C:183:TYR:CE1	1:C:188:TRP:HB2	2.28	0.68
1:C:362:ASP:N	1:C:365:LYS:NZ	2.42	0.68
1:D:126:LEU:O	1:D:126:LEU:CD1	2.32	0.68
1:D:188:TRP:CZ3	1:D:190:THR:C	2.71	0.68
1:D:254:LEU:HD13	1:D:254:LEU:H	1.59	0.68
1:D:275:GLU:O	1:D:278:GLN:HB3	1.94	0.68
1:E:300:VAL:HG12	1:E:335:ALA:HB1	1.76	0.68
1:G:200:GLU:OE2	1:G:241:ARG:NH2	2.26	0.68
1:H:120:TYR:HD2	1:H:121:LYS:HA	1.58	0.68
1:A:260:TRP:HA	1:A:263:LEU:HD12	1.76	0.67
1:A:275:GLU:O	1:A:278:GLN:HB3	1.94	0.67
1:B:157:ILE:HG13	1:B:160:GLU:OE1	1.94	0.67
1:C:196:GLY:HA2	1:C:355:ARG:HH21	1.57	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:LEU:O	1:C:295:GLU:HG3	1.93	0.67
1:D:135:LEU:CD1	1:D:136:PHE:H	2.03	0.67
1:D:203:LEU:HD13	1:D:226:ARG:HB3	1.77	0.67
1:D:278:GLN:CG	1:D:279:LYS:H	2.07	0.67
1:E:328:LEU:HD23	1:E:365:LYS:HE3	1.74	0.67
1:F:112:VAL:HG22	1:F:113:ARG:N	2.09	0.67
1:F:131:GLU:OE1	1:F:132:LYS:N	2.28	0.67
1:G:116:ILE:HB	1:G:118:LYS:NZ	2.09	0.67
1:G:157:ILE:HB	1:G:218:ASN:OD1	1.94	0.67
1:H:170:ASP:H	1:H:209:ARG:NH2	1.92	0.67
1:H:224:ILE:CD1	1:H:224:ILE:N	2.55	0.67
1:A:112:VAL:CG2	1:D:115:VAL:HG21	2.21	0.67
1:A:226:ARG:HH11	1:A:226:ARG:CG	2.05	0.67
1:D:348:LEU:HD21	1:D:356:VAL:HG21	1.76	0.67
1:F:173:TYR:CB	1:F:198:PHE:HE1	2.07	0.67
1:F:177:GLN:HA	1:F:194:GLU:CG	2.24	0.67
1:F:249:SER:N	1:F:262:ARG:HH22	1.91	0.67
1:A:183:TYR:HD1	1:A:188:TRP:HA	1.58	0.67
1:A:230:ARG:O	1:A:234:MET:HB2	1.93	0.67
1:B:281:VAL:HG11	1:B:333:ARG:CD	2.23	0.67
1:C:115:VAL:CA	1:C:149:ASP:HB3	2.21	0.67
1:D:294:LEU:HD11	1:D:345:CYS:CA	2.17	0.67
1:F:130:ILE:HG21	1:F:148:PHE:HE2	1.59	0.67
1:F:275:GLU:O	1:F:278:GLN:HB3	1.94	0.67
1:G:260:TRP:CD1	2:G:401:CMP:C5	2.83	0.67
1:H:200:GLU:OE1	1:H:201:LEU:CD1	2.42	0.67
1:B:175:ILE:HD11	1:B:196:GLY:H	1.60	0.67
1:D:262:ARG:O	1:D:265:VAL:HB	1.94	0.67
1:E:131:GLU:OE1	1:E:131:GLU:CA	2.42	0.67
1:E:175:ILE:HD12	1:E:195:GLY:H	1.58	0.67
1:G:274:PHE:CE2	1:G:280:ILE:HG22	2.30	0.67
1:H:371:TYR:CE1	2:H:402:CMP:C5	2.82	0.67
1:B:224:ILE:CD1	1:B:224:ILE:N	2.57	0.67
1:E:163:ILE:HD12	1:E:213:VAL:HB	1.76	0.67
1:E:188:TRP:CZ3	1:E:190:THR:C	2.71	0.67
1:F:126:LEU:HD12	1:F:126:LEU:C	2.19	0.67
1:F:300:VAL:HG21	2:F:402:CMP:C8	2.24	0.67
1:G:263:LEU:O	1:G:266:ALA:HB3	1.94	0.67
1:G:278:GLN:CG	1:G:279:LYS:N	2.56	0.67
1:H:299:ALA:HA	1:H:314:GLY:O	1.95	0.67
1:A:120:TYR:CE1	1:B:148:PHE:CD1	2.81	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:ILE:CD1	1:B:151:MET:CE	2.73	0.67
1:C:158:ALA:HB2	1:C:217:THR:O	1.94	0.67
1:C:283:GLN:CA	1:C:333:ARG:O	2.40	0.67
1:D:198:PHE:C	1:D:198:PHE:HD1	1.98	0.67
1:E:173:TYR:HD2	1:E:198:PHE:CE1	2.12	0.67
1:F:365:LYS:HA	1:F:368:ILE:HG13	1.76	0.67
1:G:120:TYR:HD1	1:H:148:PHE:CD1	2.12	0.67
1:G:246:GLU:O	1:G:249:SER:N	2.26	0.67
1:B:278:GLN:O	1:B:338:VAL:HG22	1.94	0.67
1:B:300:VAL:HG12	1:B:335:ALA:HB1	1.77	0.67
1:D:224:ILE:CD1	1:D:224:ILE:H	2.06	0.67
1:F:114:LYS:CD	1:F:115:VAL:N	2.58	0.67
1:F:175:ILE:HD12	1:F:195:GLY:H	1.57	0.67
1:A:175:ILE:HD11	1:A:196:GLY:H	1.58	0.67
1:G:149:ASP:OD1	1:H:120:TYR:CB	2.43	0.67
1:G:294:LEU:CD1	1:G:344:LYS:O	2.41	0.67
1:B:135:LEU:HD12	1:B:135:LEU:N	2.10	0.67
1:B:175:ILE:CD1	1:B:194:GLU:CA	2.73	0.67
1:B:226:ARG:HH11	1:B:226:ARG:CG	2.06	0.67
1:C:237:THR:O	1:C:241:ARG:HG3	1.95	0.67
1:F:203:LEU:HD22	1:F:226:ARG:HB3	1.76	0.67
1:G:175:ILE:HD11	1:G:195:GLY:N	2.10	0.67
1:G:260:TRP:NE1	2:G:401:CMP:H2'	2.07	0.67
1:H:287:GLY:HA3	1:H:326:ALA:CB	2.24	0.67
1:H:293:ILE:HG23	1:H:318:PRO:HA	1.77	0.67
1:A:158:ALA:HB2	1:A:217:THR:O	1.95	0.67
1:B:153:PRO:HB3	1:B:222:TRP:HZ3	1.55	0.67
1:B:253:ILE:HG13	1:B:254:LEU:N	2.08	0.67
1:C:293:ILE:CD1	1:C:343:LEU:HD11	2.22	0.67
1:D:247:PHE:HE1	1:D:294:LEU:CA	2.04	0.67
1:D:249:SER:N	1:D:262:ARG:NH2	2.43	0.67
1:G:365:LYS:HA	1:G:368:ILE:CG1	2.25	0.67
1:A:239:ARG:HH22	1:C:156:PHE:HD1	1.42	0.66
1:A:350:ARG:O	1:A:353:PHE:N	2.28	0.66
1:C:274:PHE:CE2	1:C:280:ILE:HG22	2.30	0.66
1:C:353:PHE:O	1:C:357:LEU:HB2	1.93	0.66
1:D:298:ALA:O	1:D:316:LEU:HD22	1.94	0.66
1:E:182:VAL:HG12	1:E:213:VAL:HG22	1.76	0.66
1:E:325:ILE:CD1	2:E:402:CMP:O2P	2.38	0.66
1:G:153:PRO:CB	1:G:222:TRP:CZ3	2.78	0.66
1:H:188:TRP:CH2	1:H:190:THR:HA	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:279:LYS:HZ3	1:H:279:LYS:CB	2.06	0.66
1:B:252:SER:O	1:B:253:ILE:CG1	2.43	0.66
1:D:136:PHE:O	1:D:139:LEU:HD11	1.95	0.66
1:D:228:SER:O	1:D:232:ILE:HG22	1.96	0.66
1:D:245:GLU:OE1	1:D:246:GLU:OE1	2.12	0.66
1:A:269:LEU:CD2	1:A:346:VAL:CG2	2.72	0.66
1:B:179:GLU:HG2	1:B:216:LYS:HD2	1.76	0.66
1:C:269:LEU:HB3	1:C:346:VAL:HG21	1.68	0.66
1:D:179:GLU:HG2	1:D:216:LYS:CD	2.26	0.66
1:D:300:VAL:HG22	1:D:335:ALA:HB1	1.76	0.66
1:D:316:LEU:HD22	1:D:316:LEU:O	1.95	0.66
1:E:280:ILE:HD13	1:E:322:PHE:CE2	2.29	0.66
1:F:252:SER:O	1:F:255:GLU:HB2	1.95	0.66
1:G:175:ILE:HA	1:G:221:LEU:HD22	1.76	0.66
1:G:269:LEU:HD23	1:G:348:LEU:HD13	1.76	0.66
1:B:296:GLY:O	1:B:318:PRO:HD3	1.96	0.66
1:D:183:TYR:HD1	1:D:188:TRP:HA	1.59	0.66
1:E:173:TYR:HD2	1:E:198:PHE:CZ	2.13	0.66
1:F:203:LEU:HD12	1:F:229:TYR:HD2	1.58	0.66
1:A:198:PHE:CD1	1:A:198:PHE:O	2.39	0.66
1:A:210:ALA:N	1:A:211:ASP:OD1	2.28	0.66
1:B:324:GLU:O	1:B:328:LEU:CD1	2.37	0.66
1:D:165:GLN:N	1:D:212:THR:CG2	2.38	0.66
1:F:131:GLU:OE1	1:F:131:GLU:N	2.28	0.66
1:F:144:ARG:CG	1:F:145:SER:N	2.58	0.66
1:F:158:ALA:O	1:H:243:MET:SD	2.54	0.66
1:F:175:ILE:O	1:F:175:ILE:CD1	2.34	0.66
1:G:283:GLN:HB2	1:G:336:THR:OG1	1.96	0.66
1:H:260:TRP:HZ2	2:H:401:CMP:HO2'	1.44	0.66
1:A:175:ILE:CD1	1:A:194:GLU:CA	2.72	0.66
1:B:173:TYR:HD2	1:B:198:PHE:CE1	2.12	0.66
1:B:331:ARG:NH2	1:B:376:SER:HB3	2.11	0.66
1:E:152:PHE:HE2	1:E:223:GLY:CA	2.08	0.66
1:G:162:VAL:CG2	1:G:163:ILE:HG13	2.22	0.66
1:H:327:LEU:HD23	1:H:353:PHE:CE2	2.30	0.66
1:A:375:VAL:HG13	1:A:376:SER:H	1.61	0.66
1:C:200:GLU:OE1	1:C:201:LEU:CD1	2.43	0.66
1:C:243:MET:SD	1:E:158:ALA:O	2.54	0.66
1:C:258:ASP:O	1:C:262:ARG:CG	2.43	0.66
1:C:353:PHE:CE1	1:C:357:LEU:CD2	2.78	0.66
1:D:120:TYR:O	1:D:121:LYS:C	2.36	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ILE:HD13	1:A:321:TYR:CD2	2.29	0.66
1:A:261:GLU:OE2	1:A:359:PRO:HG2	1.96	0.66
1:A:285:GLU:OE1	1:A:285:GLU:HA	1.96	0.66
1:D:278:GLN:CG	1:D:279:LYS:N	2.58	0.66
1:D:371:TYR:CD1	2:D:402:CMP:C5	2.84	0.66
1:E:254:LEU:C	1:E:254:LEU:HD12	2.21	0.66
1:E:260:TRP:CD1	2:E:401:CMP:C4	2.83	0.66
1:F:140:ASP:C	1:F:140:ASP:OD1	2.38	0.66
1:G:365:LYS:CA	1:G:368:ILE:HG13	2.26	0.66
1:A:253:ILE:HG13	1:A:254:LEU:HD23	1.78	0.66
1:A:280:ILE:HB	1:A:291:PHE:HE2	1.61	0.66
1:B:184:VAL:HG13	1:B:184:VAL:O	1.95	0.66
1:B:242:LYS:N	1:B:242:LYS:HD3	2.09	0.66
1:B:263:LEU:O	1:B:267:ASP:N	2.27	0.66
1:F:144:ARG:HG2	1:F:145:SER:N	2.11	0.66
1:F:179:GLU:HB3	1:F:217:THR:HG23	1.76	0.66
1:H:305:SER:O	1:H:306:GLU:C	2.37	0.66
1:H:321:TYR:CD1	1:H:321:TYR:C	2.73	0.66
1:A:272:VAL:C	1:A:273:GLN:NE2	2.54	0.66
1:C:152:PHE:HE2	1:C:223:GLY:HA3	1.59	0.66
1:C:175:ILE:CD1	1:C:193:GLY:O	2.44	0.66
1:C:347:LYS:O	1:C:348:LEU:HD12	1.96	0.66
1:D:251:VAL:O	1:D:254:LEU:HD21	1.96	0.66
1:E:295:GLU:O	1:E:344:LYS:N	2.29	0.66
1:F:114:LYS:NZ	1:F:115:VAL:HG23	2.11	0.66
1:F:230:ARG:O	1:F:234:MET:CB	2.44	0.66
1:G:175:ILE:CD1	1:G:195:GLY:N	2.59	0.66
1:G:260:TRP:HA	1:G:263:LEU:HD12	1.78	0.66
1:H:365:LYS:HA	1:H:368:ILE:HD11	1.78	0.66
1:A:148:PHE:HB2	1:B:120:TYR:CD1	2.31	0.65
1:B:153:PRO:HB3	1:B:222:TRP:CH2	2.31	0.65
1:B:200:GLU:CG	1:B:201:LEU:CD1	2.74	0.65
1:C:148:PHE:CD1	1:D:120:TYR:CD1	2.84	0.65
1:C:371:TYR:HE1	2:C:402:CMP:N7	1.94	0.65
1:G:224:ILE:CD1	1:G:224:ILE:N	2.59	0.65
1:H:266:ALA:O	1:H:269:LEU:N	2.24	0.65
1:A:222:TRP:HA	1:A:222:TRP:HE3	1.62	0.65
1:B:312:GLU:OE2	1:B:314:GLY:N	2.29	0.65
1:C:263:LEU:O	1:C:266:ALA:HB3	1.96	0.65
1:C:292:ILE:HB	1:C:346:VAL:HG13	1.78	0.65
1:D:274:PHE:CE2	1:D:280:ILE:HG22	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:178:GLY:H	1:F:194:GLU:HG3	1.61	0.65
1:F:224:ILE:N	1:F:224:ILE:HD12	2.10	0.65
1:G:247:PHE:C	1:G:247:PHE:CD2	2.74	0.65
1:G:266:ALA:O	1:G:267:ASP:C	2.38	0.65
1:G:293:ILE:CG1	1:G:345:CYS:SG	2.75	0.65
1:H:298:ALA:HB1	1:H:338:VAL:O	1.95	0.65
1:A:280:ILE:HG13	1:A:281:VAL:H	1.60	0.65
1:A:324:GLU:O	1:A:328:LEU:HD12	1.97	0.65
1:B:203:LEU:HD12	1:B:229:TYR:HD2	1.61	0.65
1:B:265:VAL:O	1:B:269:LEU:HG	1.96	0.65
1:B:278:GLN:HG3	1:B:279:LYS:H	1.60	0.65
1:C:111:TYR:O	1:C:112:VAL:HG13	1.97	0.65
1:E:130:ILE:HD13	1:E:151:MET:HE3	1.78	0.65
1:F:245:GLU:OE1	1:F:246:GLU:OE1	2.12	0.65
1:H:120:TYR:C	1:H:120:TYR:HD2	2.04	0.65
1:H:126:LEU:HB2	1:H:222:TRP:CZ2	2.31	0.65
1:H:222:TRP:HA	1:H:222:TRP:HE3	1.60	0.65
1:H:273:GLN:CB	1:H:343:LEU:O	2.44	0.65
1:A:115:VAL:CG1	1:D:112:VAL:CG2	2.73	0.65
1:A:272:VAL:HG22	1:A:273:GLN:N	2.09	0.65
1:B:183:TYR:HD1	1:B:188:TRP:HA	1.62	0.65
1:B:301:LEU:HB2	1:B:336:THR:HB	1.77	0.65
1:F:173:TYR:HD2	1:F:198:PHE:CE1	2.14	0.65
1:C:251:VAL:HG23	1:C:319:SER:O	1.95	0.65
1:E:198:PHE:CD1	1:E:198:PHE:O	2.49	0.65
1:E:296:GLY:HA2	1:E:342:PRO:HG2	1.79	0.65
1:F:170:ASP:H	1:F:209:ARG:NH2	1.94	0.65
1:G:179:GLU:HG2	1:G:216:LYS:HD2	1.77	0.65
1:G:269:LEU:HD23	1:G:348:LEU:HD11	1.78	0.65
1:G:329:MET:HA	1:G:329:MET:CE	2.26	0.65
1:G:375:VAL:HG12	1:G:376:SER:H	1.59	0.65
1:H:175:ILE:CD1	1:H:193:GLY:O	2.45	0.65
1:H:247:PHE:HE1	1:H:294:LEU:CA	2.10	0.65
1:A:120:TYR:O	1:A:121:LYS:C	2.39	0.65
1:A:229:TYR:HD1	1:A:233:LEU:HD13	1.42	0.65
1:A:272:VAL:CA	1:A:273:GLN:NE2	2.60	0.65
1:A:350:ARG:O	1:A:353:PHE:CB	2.44	0.65
1:B:153:PRO:HA	1:B:222:TRP:CE3	2.31	0.65
1:B:161:THR:HA	1:B:214:LYS:CD	2.19	0.65
1:B:222:TRP:CE3	1:B:222:TRP:HA	2.31	0.65
1:B:294:LEU:HD11	1:B:345:CYS:CA	2.19	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:135:LEU:CD1	1:D:136:PHE:N	2.60	0.65
1:D:151:MET:HA	1:D:224:ILE:HG22	1.77	0.65
1:E:246:GLU:O	1:E:249:SER:N	2.30	0.65
1:E:353:PHE:HE1	1:E:357:LEU:HD22	1.61	0.65
1:F:173:TYR:HD2	1:F:198:PHE:CZ	2.14	0.65
1:H:252:SER:O	1:H:255:GLU:HB2	1.96	0.65
1:H:269:LEU:CB	1:H:346:VAL:HG21	2.25	0.65
1:A:115:VAL:HG11	1:D:112:VAL:HG23	1.78	0.65
1:A:184:VAL:O	1:A:184:VAL:HG13	1.95	0.65
1:A:280:ILE:HD11	1:A:337:VAL:HB	1.78	0.65
1:B:294:LEU:O	1:B:318:PRO:HB3	1.96	0.65
1:B:327:LEU:HD23	1:B:353:PHE:CD2	2.32	0.65
1:B:366:ARG:HG2	1:B:367:ASN:N	2.12	0.65
1:C:300:VAL:O	1:C:301:LEU:HG	1.96	0.65
1:F:183:TYR:CE1	1:F:188:TRP:HB2	2.31	0.65
1:F:289:GLU:CG	1:F:347:LYS:NZ	2.55	0.65
1:G:123:MET:CE	1:H:123:MET:HE3	2.27	0.65
1:A:356:VAL:HG23	1:A:357:LEU:N	2.12	0.65
1:B:165:GLN:N	1:B:212:THR:CG2	2.38	0.65
1:B:325:ILE:HG13	2:B:402:CMP:O1P	1.96	0.65
1:B:365:LYS:C	1:B:368:ILE:HG13	2.21	0.65
1:C:209:ARG:HD2	2:C:401:CMP:O5'	1.97	0.65
1:C:253:ILE:HG13	1:C:254:LEU:N	2.08	0.65
1:D:293:ILE:CG1	1:D:345:CYS:SG	2.80	0.65
1:D:327:LEU:HD23	1:D:353:PHE:CE2	2.32	0.65
1:F:114:LYS:HZ1	1:F:115:VAL:HG23	1.61	0.65
1:A:130:ILE:HD13	1:A:151:MET:HE3	1.78	0.65
1:B:273:GLN:N	1:B:273:GLN:CD	2.50	0.65
1:D:222:TRP:HA	1:D:222:TRP:HE3	1.62	0.65
1:G:184:VAL:HG13	1:G:184:VAL:O	1.96	0.65
1:G:301:LEU:HD13	1:G:310:PHE:CB	2.26	0.65
1:H:329:MET:HA	1:H:329:MET:CE	2.23	0.65
1:H:365:LYS:CA	1:H:368:ILE:HG13	2.27	0.65
1:A:113:ARG:HG2	1:D:113:ARG:O	1.97	0.65
1:A:158:ALA:N	1:A:218:ASN:OD1	2.28	0.65
1:C:152:PHE:O	1:C:152:PHE:HD2	1.79	0.65
1:C:252:SER:O	1:C:255:GLU:HB2	1.97	0.65
1:D:234:MET:O	1:D:238:LEU:HD12	1.97	0.65
1:D:328:LEU:CD2	1:D:365:LYS:HE3	2.26	0.65
1:A:280:ILE:HD11	1:A:322:PHE:CE2	2.22	0.64
1:B:188:TRP:CH2	1:B:190:THR:HA	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:233:LEU:HD12	1:B:233:LEU:N	2.02	0.64
1:B:260:TRP:CD1	2:B:401:CMP:C4	2.84	0.64
1:D:230:ARG:CZ	1:D:234:MET:HE1	2.25	0.64
1:F:224:ILE:CD1	1:F:224:ILE:N	2.59	0.64
1:G:203:LEU:HD13	1:G:226:ARG:HB3	1.78	0.64
1:A:131:GLU:OE1	1:A:131:GLU:CA	2.42	0.64
1:B:224:ILE:CD1	1:B:224:ILE:H	2.10	0.64
1:F:272:VAL:O	1:F:345:CYS:N	2.27	0.64
1:H:356:VAL:CG2	1:H:357:LEU:HD13	2.19	0.64
1:B:287:GLY:HA3	1:B:326:ALA:HB1	1.79	0.64
1:C:182:VAL:O	1:C:182:VAL:CG2	2.42	0.64
1:E:164:GLN:HA	1:E:212:THR:CG2	2.25	0.64
1:E:325:ILE:O	1:E:328:LEU:N	2.31	0.64
1:F:262:ARG:HA	1:F:265:VAL:CG2	2.27	0.64
1:F:274:PHE:CD2	1:F:343:LEU:HD23	2.32	0.64
1:G:161:THR:OG1	1:G:214:LYS:NZ	2.22	0.64
1:A:260:TRP:HE1	2:A:401:CMP:H2'	1.60	0.64
1:B:224:ILE:HD13	1:B:224:ILE:H	1.61	0.64
1:B:272:VAL:HA	1:B:273:GLN:NE2	2.12	0.64
1:C:243:MET:HE2	1:E:159:GLY:C	2.23	0.64
1:C:260:TRP:CE2	2:C:401:CMP:C8	2.80	0.64
1:D:188:TRP:CH2	1:D:190:THR:HA	2.33	0.64
1:E:253:ILE:HG13	1:E:254:LEU:H	1.61	0.64
1:E:254:LEU:HD12	1:E:255:GLU:N	2.12	0.64
1:B:252:SER:O	1:B:253:ILE:HG13	1.97	0.64
1:B:293:ILE:HG21	1:B:317:GLY:O	1.97	0.64
1:B:375:VAL:HG23	1:B:376:SER:H	1.63	0.64
1:D:273:GLN:HB2	1:D:343:LEU:O	1.98	0.64
1:D:325:ILE:HG13	1:D:326:ALA:N	2.13	0.64
1:E:224:ILE:HD12	1:E:224:ILE:N	2.12	0.64
1:E:272:VAL:C	1:E:273:GLN:NE2	2.55	0.64
1:F:205:TYR:HD2	1:F:205:TYR:N	1.96	0.64
1:G:272:VAL:HA	1:G:273:GLN:NE2	2.11	0.64
1:H:246:GLU:O	1:H:249:SER:N	2.30	0.64
1:A:114:LYS:HA	1:D:111:TYR:CE2	2.32	0.64
1:A:200:GLU:OE2	1:A:241:ARG:NH2	2.31	0.64
1:B:356:VAL:CG2	1:B:357:LEU:HD13	2.20	0.64
1:C:184:VAL:O	1:C:184:VAL:HG13	1.97	0.64
1:C:325:ILE:CD1	2:C:402:CMP:O2P	2.45	0.64
1:E:260:TRP:HE1	2:E:401:CMP:C2'	2.10	0.64
1:E:272:VAL:CA	1:E:273:GLN:NE2	2.60	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:152:PHE:HE2	1:F:223:GLY:CA	2.07	0.64
1:F:233:LEU:HD12	1:F:233:LEU:N	2.05	0.64
1:F:233:LEU:H	1:F:233:LEU:CD1	2.02	0.64
1:B:147:ILE:CG2	1:B:232:ILE:HD13	2.26	0.64
1:B:152:PHE:O	1:B:152:PHE:HD2	1.81	0.64
1:C:120:TYR:CE1	1:D:148:PHE:HD1	2.11	0.64
1:C:130:ILE:CG2	1:C:131:GLU:N	2.60	0.64
1:C:147:ILE:HG13	1:C:148:PHE:HD2	1.63	0.64
1:C:266:ALA:O	1:C:267:ASP:C	2.39	0.64
1:E:230:ARG:O	1:E:234:MET:CB	2.45	0.64
1:H:263:LEU:O	1:H:266:ALA:HB3	1.98	0.64
1:B:135:LEU:CD1	1:B:136:PHE:H	2.11	0.64
1:C:279:LYS:HB3	1:C:338:VAL:HG23	1.78	0.64
1:E:260:TRP:CG	2:E:401:CMP:C5	2.85	0.64
1:E:289:GLU:HG3	1:E:347:LYS:HZ1	1.60	0.64
1:E:290:PHE:C	1:E:291:PHE:HD1	2.05	0.64
1:E:365:LYS:C	1:E:368:ILE:HG13	2.21	0.64
1:F:153:PRO:CB	1:F:222:TRP:CZ3	2.81	0.64
1:G:156:PHE:CD2	1:G:162:VAL:HG12	2.32	0.64
1:H:230:ARG:HB3	1:H:234:MET:HE2	1.79	0.64
1:H:260:TRP:NE1	2:H:401:CMP:C2'	2.60	0.64
1:H:291:PHE:HD1	1:H:291:PHE:N	1.93	0.64
1:H:335:ALA:HB3	2:H:402:CMP:H5'1	1.80	0.64
1:B:118:LYS:HB2	1:B:123:MET:HE1	1.79	0.64
1:D:325:ILE:CG1	2:D:402:CMP:O1P	2.46	0.64
1:E:183:TYR:CD1	1:E:188:TRP:HB2	2.33	0.64
1:E:280:ILE:HD11	1:E:337:VAL:HB	1.79	0.64
1:E:280:ILE:HB	1:E:291:PHE:HE2	1.63	0.64
1:F:165:GLN:CA	1:F:211:ASP:O	2.45	0.64
1:F:198:PHE:CD1	1:F:198:PHE:N	2.64	0.64
1:F:329:MET:HA	1:F:329:MET:CE	2.27	0.64
1:G:152:PHE:CD2	1:G:152:PHE:C	2.73	0.64
1:G:272:VAL:CA	1:G:273:GLN:NE2	2.61	0.64
1:A:173:TYR:CD2	1:A:198:PHE:HE1	2.16	0.64
1:E:274:PHE:HD2	1:E:343:LEU:HD23	1.62	0.64
1:E:313:VAL:HG22	1:E:313:VAL:O	1.98	0.64
1:B:260:TRP:CG	2:B:401:CMP:N7	2.66	0.63
1:C:260:TRP:HE1	2:C:401:CMP:C2'	2.09	0.63
1:E:162:VAL:HG23	1:E:163:ILE:N	2.12	0.63
1:E:177:GLN:HA	1:E:194:GLU:CG	2.28	0.63
1:E:328:LEU:CD1	1:E:364:LEU:HD11	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:272:VAL:CA	1:H:273:GLN:HE21	2.00	0.63
1:H:363:ILE:O	1:H:366:ARG:HG2	1.98	0.63
1:A:183:TYR:CE1	1:A:188:TRP:CB	2.81	0.63
1:A:316:LEU:HA	1:A:320:ASP:OD2	1.98	0.63
1:A:375:VAL:CG1	1:A:376:SER:N	2.61	0.63
1:B:183:TYR:CD1	1:B:188:TRP:HB2	2.33	0.63
1:B:200:GLU:HG2	1:B:201:LEU:CG	2.28	0.63
1:B:312:GLU:OE1	1:B:312:GLU:CA	2.46	0.63
1:C:211:ASP:OD2	2:C:401:CMP:N3	2.32	0.63
1:C:222:TRP:HA	1:C:222:TRP:CE3	2.33	0.63
1:E:239:ARG:NH2	1:G:156:PHE:HD1	1.96	0.63
1:E:272:VAL:HA	1:E:273:GLN:HE22	1.60	0.63
1:F:163:ILE:HD12	1:F:213:VAL:HB	1.81	0.63
1:H:260:TRP:HA	1:H:263:LEU:HD12	1.80	0.63
1:B:126:LEU:HB2	1:B:222:TRP:CZ2	2.34	0.63
1:D:350:ARG:O	1:D:353:PHE:HB3	1.97	0.63
1:E:179:GLU:HG2	1:E:216:LYS:HD2	1.78	0.63
1:E:280:ILE:HG13	1:E:281:VAL:HG23	1.80	0.63
1:E:284:GLY:O	1:E:332:PRO:HB3	1.98	0.63
1:B:156:PHE:HD2	1:B:162:VAL:CG1	2.10	0.63
1:B:164:GLN:HA	1:B:212:THR:HG22	1.80	0.63
1:D:153:PRO:CA	1:D:222:TRP:CZ3	2.81	0.63
1:E:178:GLY:H	1:E:194:GLU:HG3	1.63	0.63
1:E:328:LEU:HD13	1:E:364:LEU:HD11	1.81	0.63
1:G:154:VAL:HG12	1:G:221:LEU:HB2	1.80	0.63
1:G:175:ILE:HD12	1:G:195:GLY:H	1.63	0.63
1:G:183:TYR:HD1	1:G:188:TRP:HA	1.64	0.63
1:H:183:TYR:HD1	1:H:188:TRP:HA	1.63	0.63
1:H:230:ARG:CB	1:H:234:MET:HE2	2.28	0.63
1:H:293:ILE:HG21	1:H:317:GLY:C	2.23	0.63
1:A:274:PHE:CD2	1:A:343:LEU:HD23	2.33	0.63
1:B:200:GLU:HG2	1:B:201:LEU:HG	1.80	0.63
1:C:293:ILE:HG21	1:C:317:GLY:C	2.23	0.63
1:E:246:GLU:O	1:E:248:LEU:N	2.31	0.63
1:G:165:GLN:N	1:G:212:THR:CG2	2.42	0.63
1:G:183:TYR:CD1	1:G:188:TRP:HB2	2.34	0.63
1:G:321:TYR:C	1:G:321:TYR:CD1	2.77	0.63
1:H:204:ILE:CG2	1:H:205:TYR:CD2	2.81	0.63
1:B:230:ARG:CZ	1:B:234:MET:HE1	2.28	0.63
1:B:280:ILE:HD13	1:B:322:PHE:HZ	1.63	0.63
1:C:110:SER:HB3	1:F:114:LYS:NZ	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:247:PHE:CD2	1:C:247:PHE:O	2.51	0.63
1:C:253:ILE:HG13	1:C:254:LEU:CD2	2.27	0.63
1:C:285:GLU:OE1	1:C:285:GLU:HA	1.98	0.63
1:D:144:ARG:O	1:D:145:SER:C	2.40	0.63
1:E:224:ILE:CD1	1:E:224:ILE:N	2.61	0.63
1:F:135:LEU:HD12	1:F:136:PHE:H	1.62	0.63
1:F:183:TYR:HD1	1:F:188:TRP:HA	1.63	0.63
1:G:162:VAL:HG22	1:G:213:VAL:O	1.99	0.63
1:G:262:ARG:HA	1:G:265:VAL:CG2	2.29	0.63
1:H:203:LEU:HD13	1:H:226:ARG:HB3	1.80	0.63
1:A:114:LYS:HG3	1:A:115:VAL:N	2.01	0.63
1:C:123:MET:HE3	1:D:123:MET:HE3	1.81	0.63
1:C:164:GLN:HA	1:C:212:THR:HG22	1.81	0.63
1:E:269:LEU:HD23	1:E:348:LEU:CD1	2.28	0.63
1:E:350:ARG:HB3	1:E:351:PRO:HD3	1.81	0.63
1:F:230:ARG:CB	1:F:234:MET:HE2	2.29	0.63
1:F:290:PHE:HB2	1:F:327:LEU:CD2	2.29	0.63
1:F:301:LEU:CD1	1:F:310:PHE:HB3	2.28	0.63
1:B:175:ILE:CD1	1:B:195:GLY:N	2.62	0.63
1:F:152:PHE:CD2	1:F:152:PHE:C	2.76	0.63
1:F:247:PHE:HZ	1:F:293:ILE:O	1.81	0.63
1:G:224:ILE:N	1:G:224:ILE:HD12	2.13	0.63
1:G:324:GLU:O	1:G:328:LEU:HD12	1.97	0.63
1:H:281:VAL:CG1	1:H:333:ARG:CD	2.76	0.63
1:A:237:THR:O	1:A:241:ARG:HG3	1.98	0.63
1:A:295:GLU:O	1:A:343:LEU:HD12	1.98	0.63
1:B:131:GLU:C	1:B:133:ASN:H	2.06	0.63
1:B:157:ILE:CB	1:B:218:ASN:OD1	2.47	0.63
1:B:274:PHE:HD2	1:B:343:LEU:HD23	1.64	0.63
1:B:365:LYS:CA	1:B:368:ILE:HG13	2.29	0.63
1:C:135:LEU:HD13	1:C:136:PHE:CD1	2.34	0.63
1:C:258:ASP:O	1:C:262:ARG:HG2	1.98	0.63
1:D:269:LEU:HB3	1:D:346:VAL:HG21	1.79	0.63
1:G:158:ALA:HB2	1:G:217:THR:C	2.24	0.63
1:H:247:PHE:C	1:H:247:PHE:HD2	2.05	0.63
1:H:294:LEU:HG	1:H:344:LYS:O	1.98	0.63
1:A:272:VAL:HA	1:A:273:GLN:HE22	1.62	0.62
1:B:324:GLU:OE2	1:B:371:TYR:CE2	2.47	0.62
1:B:350:ARG:HB3	1:B:351:PRO:CD	2.25	0.62
1:C:276:ASP:HA	1:C:339:ALA:O	1.99	0.62
1:D:211:ASP:OD2	2:D:401:CMP:N3	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:ILE:HD13	1:D:321:TYR:CD2	2.34	0.62
1:D:362:ASP:OD1	1:D:362:ASP:N	2.30	0.62
1:F:272:VAL:HA	1:F:273:GLN:NE2	2.14	0.62
1:F:280:ILE:HG13	1:F:281:VAL:H	1.61	0.62
1:H:229:TYR:HE1	1:H:233:LEU:HD13	1.62	0.62
1:A:260:TRP:CD2	2:A:401:CMP:C8	2.82	0.62
1:B:175:ILE:HD12	1:B:195:GLY:H	1.64	0.62
1:B:253:ILE:HG13	1:B:254:LEU:CD2	2.29	0.62
1:D:116:ILE:HG22	1:D:118:LYS:HG3	1.81	0.62
1:D:247:PHE:HZ	1:D:293:ILE:O	1.82	0.62
1:E:111:TYR:C	1:E:112:VAL:HG22	2.24	0.62
1:E:296:GLY:HA3	1:E:342:PRO:O	1.99	0.62
1:F:204:ILE:HG22	1:F:205:TYR:HD2	1.61	0.62
1:G:265:VAL:HA	1:G:356:VAL:HG11	1.79	0.62
1:G:273:GLN:HE21	1:G:273:GLN:CA	2.07	0.62
1:H:173:TYR:HB2	1:H:198:PHE:CE1	2.34	0.62
1:A:176:ASP:O	1:A:194:GLU:HG2	1.99	0.62
1:C:279:LYS:CE	1:C:282:VAL:HG22	2.30	0.62
1:C:365:LYS:O	1:C:368:ILE:N	2.27	0.62
1:D:365:LYS:HA	1:D:368:ILE:HG13	1.80	0.62
1:F:153:PRO:CA	1:F:222:TRP:CZ3	2.82	0.62
1:F:284:GLY:O	1:F:332:PRO:HB3	2.00	0.62
1:H:130:ILE:CD1	1:H:136:PHE:CD2	2.82	0.62
1:H:165:GLN:HA	1:H:211:ASP:O	1.99	0.62
1:H:302:GLN:C	1:H:310:PHE:CD1	2.77	0.62
1:A:153:PRO:HA	1:A:222:TRP:CE3	2.34	0.62
1:B:248:LEU:CB	1:B:262:ARG:HH21	2.13	0.62
1:C:116:ILE:HB	1:C:149:ASP:O	2.00	0.62
1:D:120:TYR:HE2	1:D:124:ALA:HB2	1.64	0.62
1:D:192:VAL:O	1:D:192:VAL:CG1	2.42	0.62
1:D:298:ALA:HB3	1:D:316:LEU:HD21	1.80	0.62
1:E:211:ASP:OD2	2:E:401:CMP:N3	2.32	0.62
1:F:222:TRP:HA	1:F:222:TRP:HE3	1.61	0.62
1:G:111:TYR:CD1	1:G:112:VAL:N	2.66	0.62
1:H:147:ILE:O	1:H:148:PHE:C	2.37	0.62
1:A:255:GLU:OE1	1:A:255:GLU:CA	2.37	0.62
1:B:156:PHE:CD2	1:B:162:VAL:CG1	2.78	0.62
1:B:279:LYS:NZ	1:B:279:LYS:CB	2.62	0.62
1:E:174:VAL:HG23	1:E:196:GLY:O	1.98	0.62
1:E:279:LYS:CB	1:E:279:LYS:HZ3	2.03	0.62
1:G:175:ILE:HD11	1:G:196:GLY:N	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:202:ALA:HB1	1:H:207:THR:O	2.00	0.62
1:A:154:VAL:O	1:A:221:LEU:N	2.28	0.62
1:A:366:ARG:HG2	1:A:367:ASN:N	2.15	0.62
1:C:230:ARG:CB	1:C:234:MET:HE2	2.30	0.62
1:C:302:GLN:O	1:C:310:PHE:CD1	2.52	0.62
1:C:325:ILE:CD1	1:C:334:ALA:HB3	2.28	0.62
1:D:253:ILE:HG21	1:D:321:TYR:CE2	2.35	0.62
1:E:211:ASP:OD2	2:E:401:CMP:C3'	2.44	0.62
1:E:266:ALA:CA	1:E:269:LEU:HD12	2.19	0.62
1:G:253:ILE:CG2	1:G:321:TYR:HE2	2.12	0.62
1:G:254:LEU:C	1:G:254:LEU:HD12	2.25	0.62
1:G:329:MET:HA	1:G:329:MET:HE3	1.82	0.62
1:H:325:ILE:CG1	2:H:402:CMP:O1P	2.47	0.62
1:B:312:GLU:CD	1:B:313:VAL:N	2.57	0.62
1:C:174:VAL:HG13	1:C:222:TRP:HB2	1.80	0.62
1:C:260:TRP:CD1	2:C:401:CMP:C5	2.87	0.62
1:D:347:LYS:O	1:D:348:LEU:CD1	2.46	0.62
1:D:356:VAL:CG2	1:D:357:LEU:CD1	2.73	0.62
1:G:247:PHE:HZ	1:G:293:ILE:O	1.81	0.62
1:G:265:VAL:HG12	1:G:269:LEU:HD21	1.80	0.62
1:H:162:VAL:CG2	1:H:163:ILE:HG13	2.29	0.62
1:H:283:GLN:HA	1:H:333:ARG:O	2.00	0.62
1:H:353:PHE:CE1	1:H:357:LEU:CD2	2.82	0.62
1:A:242:LYS:HD3	1:A:242:LYS:N	2.09	0.62
1:A:247:PHE:HE1	1:A:294:LEU:CA	2.06	0.62
1:A:311:VAL:HG22	1:A:312:GLU:N	2.15	0.62
1:C:158:ALA:N	1:C:218:ASN:OD1	2.33	0.62
1:C:230:ARG:NH1	1:C:230:ARG:HG2	2.15	0.62
1:D:162:VAL:HG23	1:D:163:ILE:N	2.15	0.62
1:E:198:PHE:O	1:E:198:PHE:HD1	1.83	0.62
1:E:259:LYS:HG3	1:E:260:TRP:H	1.63	0.62
1:G:152:PHE:HE2	1:G:223:GLY:HA3	1.65	0.62
1:H:260:TRP:CD1	2:H:401:CMP:C5	2.88	0.62
1:A:115:VAL:HB	1:D:112:VAL:CG2	2.29	0.62
1:B:248:LEU:HB2	1:B:262:ARG:HH21	1.65	0.62
1:D:234:MET:HG3	1:D:238:LEU:CD1	2.28	0.62
1:E:366:ARG:HG3	1:E:367:ASN:N	2.15	0.62
1:F:182:VAL:HG12	1:F:213:VAL:HG22	1.81	0.62
1:G:292:ILE:HB	1:G:346:VAL:HG13	1.81	0.62
1:H:246:GLU:HA	1:H:249:SER:OG	1.99	0.62
1:A:173:TYR:HD2	1:A:198:PHE:CZ	2.18	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:ILE:HD11	1:A:195:GLY:N	2.15	0.62
1:B:375:VAL:O	1:B:376:SER:OXT	2.18	0.62
1:C:247:PHE:HE1	1:C:294:LEU:CA	2.08	0.62
1:C:265:VAL:HG12	1:C:269:LEU:HD21	1.82	0.62
1:C:296:GLY:O	1:C:318:PRO:HD3	1.99	0.62
1:D:205:TYR:HD2	1:D:205:TYR:N	1.98	0.62
1:D:259:LYS:CG	1:D:260:TRP:N	2.56	0.62
1:D:350:ARG:HB3	1:D:351:PRO:HD3	1.80	0.62
1:H:175:ILE:HD11	1:H:193:GLY:O	2.00	0.62
1:H:298:ALA:O	1:H:315:ARG:CA	2.46	0.62
1:A:152:PHE:O	1:A:152:PHE:HD2	1.82	0.61
1:A:153:PRO:HB3	1:A:222:TRP:CH2	2.34	0.61
1:A:260:TRP:CE2	2:A:401:CMP:H8	2.35	0.61
1:A:263:LEU:O	1:A:266:ALA:HB3	2.00	0.61
1:B:161:THR:HG23	1:B:214:LYS:HD3	1.82	0.61
1:B:204:ILE:HG22	1:B:205:TYR:CD2	2.34	0.61
1:C:174:VAL:HA	1:C:196:GLY:O	1.99	0.61
1:E:115:VAL:CG2	1:H:110:SER:HB3	2.31	0.61
1:E:190:THR:CG2	1:E:191:SER:H	2.13	0.61
1:F:230:ARG:HB3	1:F:234:MET:HE2	1.81	0.61
1:F:327:LEU:HD23	1:F:353:PHE:CZ	2.35	0.61
1:G:260:TRP:HE1	2:G:401:CMP:C2'	2.07	0.61
1:H:173:TYR:CD2	1:H:198:PHE:CZ	2.86	0.61
1:H:269:LEU:HD22	1:H:346:VAL:CG2	2.30	0.61
1:A:120:TYR:CD2	1:A:120:TYR:O	2.53	0.61
1:B:265:VAL:HA	1:B:356:VAL:HG11	1.82	0.61
1:B:279:LYS:HB2	1:B:279:LYS:NZ	2.12	0.61
1:C:174:VAL:O	1:C:174:VAL:CG1	2.47	0.61
1:E:135:LEU:CD1	1:E:136:PHE:N	2.62	0.61
1:G:140:ASP:OD1	1:G:140:ASP:C	2.43	0.61
1:H:112:VAL:CG1	1:H:113:ARG:H	2.01	0.61
1:H:280:ILE:CG1	1:H:337:VAL:HB	2.30	0.61
1:A:115:VAL:CG2	1:D:112:VAL:CG2	2.67	0.61
1:A:280:ILE:HD13	1:A:322:PHE:HZ	1.66	0.61
1:B:289:GLU:HG3	1:B:347:LYS:NZ	2.14	0.61
1:C:321:TYR:CD1	1:C:321:TYR:O	2.53	0.61
1:E:140:ASP:C	1:E:140:ASP:OD1	2.43	0.61
1:E:152:PHE:O	1:E:152:PHE:HD2	1.80	0.61
1:F:114:LYS:HZ1	1:F:115:VAL:CG2	2.10	0.61
1:F:165:GLN:N	1:F:212:THR:CG2	2.46	0.61
1:G:316:LEU:HD12	1:G:316:LEU:N	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:375:VAL:HG12	1:G:376:SER:N	2.14	0.61
1:H:260:TRP:O	1:H:263:LEU:HB2	2.00	0.61
1:H:279:LYS:CE	1:H:336:THR:HG23	2.30	0.61
1:A:181:ASP:OD1	1:A:191:SER:HB3	2.00	0.61
1:B:196:GLY:HA2	1:B:355:ARG:HH21	1.61	0.61
1:B:324:GLU:HB2	1:B:364:LEU:HD13	1.82	0.61
1:F:260:TRP:HA	1:F:263:LEU:HD12	1.83	0.61
1:F:294:LEU:H	1:F:294:LEU:CD1	2.08	0.61
1:G:116:ILE:HB	1:G:118:LYS:HZ3	1.64	0.61
1:G:158:ALA:N	1:G:218:ASN:OD1	2.30	0.61
1:H:144:ARG:HG2	1:H:145:SER:N	2.14	0.61
1:H:147:ILE:HG13	1:H:148:PHE:HD2	1.65	0.61
1:A:247:PHE:C	1:A:247:PHE:CD2	2.77	0.61
1:A:327:LEU:HD23	1:A:353:PHE:CZ	2.35	0.61
1:C:120:TYR:C	1:C:120:TYR:HD2	2.04	0.61
1:C:130:ILE:CD1	1:C:136:PHE:CD2	2.83	0.61
1:C:234:MET:HG3	1:C:234:MET:O	2.00	0.61
1:C:324:GLU:N	1:C:324:GLU:OE1	2.33	0.61
1:D:182:VAL:HG23	1:D:182:VAL:O	2.00	0.61
1:E:157:ILE:HG13	1:E:160:GLU:OE1	2.01	0.61
1:C:112:VAL:HB	1:C:231:ARG:CZ	2.31	0.61
1:C:177:GLN:HA	1:C:194:GLU:HG3	1.82	0.61
1:C:247:PHE:HZ	1:C:293:ILE:O	1.82	0.61
1:C:315:ARG:NH2	1:C:340:ARG:HH22	1.97	0.61
1:D:183:TYR:CD1	1:D:188:TRP:HB2	2.36	0.61
1:D:198:PHE:CD1	1:D:198:PHE:N	2.66	0.61
1:D:224:ILE:N	1:D:224:ILE:HD12	2.15	0.61
1:E:246:GLU:C	1:E:248:LEU:N	2.55	0.61
1:H:350:ARG:HB3	1:H:351:PRO:HD3	1.83	0.61
1:A:362:ASP:O	1:A:365:LYS:HG3	2.01	0.61
1:B:266:ALA:O	1:B:267:ASP:C	2.43	0.61
1:B:371:TYR:CE1	2:B:402:CMP:C5	2.88	0.61
1:C:243:MET:CE	1:E:158:ALA:O	2.49	0.61
1:D:324:GLU:O	1:D:325:ILE:C	2.42	0.61
1:E:165:GLN:N	1:E:212:THR:CG2	2.42	0.61
1:G:173:TYR:CB	1:G:198:PHE:HE1	2.12	0.61
1:G:211:ASP:OD2	2:G:401:CMP:C3'	2.49	0.61
1:G:222:TRP:HA	1:G:222:TRP:CE3	2.34	0.61
1:A:113:ARG:CG	1:D:113:ARG:HB2	2.31	0.61
1:A:260:TRP:CG	2:A:401:CMP:C5	2.89	0.61
1:B:205:TYR:N	1:B:205:TYR:HD2	1.96	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:353:PHE:CE1	1:C:357:LEU:HD22	2.36	0.61
1:H:194:GLU:O	1:H:355:ARG:HD2	2.01	0.61
1:A:120:TYR:HB2	1:B:149:ASP:OD1	2.00	0.61
1:A:175:ILE:HD12	1:A:175:ILE:C	2.22	0.61
1:A:229:TYR:O	1:A:233:LEU:HD12	2.00	0.61
1:B:165:GLN:CA	1:B:211:ASP:O	2.49	0.61
1:B:239:ARG:C	1:B:241:ARG:N	2.53	0.61
1:B:246:GLU:C	1:B:248:LEU:N	2.59	0.61
1:C:220:LYS:O	1:C:221:LEU:HD23	2.01	0.61
1:D:247:PHE:CE1	1:D:294:LEU:HB3	2.36	0.61
1:E:222:TRP:HA	1:E:222:TRP:CE3	2.36	0.61
1:E:260:TRP:HA	1:E:263:LEU:HD12	1.82	0.61
1:E:329:MET:HA	1:E:329:MET:HE3	1.82	0.61
1:G:316:LEU:HA	1:G:320:ASP:OD2	2.01	0.61
1:A:171:ASN:HB3	1:A:224:ILE:O	2.01	0.61
1:B:201:LEU:O	1:B:204:ILE:N	2.34	0.61
1:B:222:TRP:HA	1:B:222:TRP:HE3	1.66	0.61
1:C:298:ALA:N	1:C:316:LEU:O	2.32	0.61
1:C:353:PHE:CE1	1:C:357:LEU:HD23	2.36	0.61
1:D:279:LYS:HG3	1:D:279:LYS:O	1.99	0.61
1:E:280:ILE:HD13	1:E:322:PHE:HZ	1.66	0.61
1:E:293:ILE:HA	1:E:345:CYS:SG	2.40	0.61
1:G:209:ARG:HD2	2:G:401:CMP:O5'	2.00	0.61
1:H:115:VAL:CA	1:H:149:ASP:HB3	2.29	0.61
1:A:120:TYR:CD1	1:B:148:PHE:HB2	2.27	0.60
1:A:233:LEU:HD12	1:A:233:LEU:N	2.03	0.60
1:A:362:ASP:N	1:A:365:LYS:HZ2	1.99	0.60
1:B:158:ALA:CA	1:B:217:THR:O	2.49	0.60
1:B:182:VAL:HG12	1:B:213:VAL:CG2	2.31	0.60
1:B:375:VAL:HG22	1:B:376:SER:OG	2.00	0.60
1:C:205:TYR:HD2	1:C:205:TYR:N	1.99	0.60
1:C:300:VAL:C	1:C:301:LEU:HD12	2.24	0.60
1:H:152:PHE:CD2	1:H:152:PHE:O	2.54	0.60
1:H:242:LYS:HD3	1:H:242:LYS:N	2.07	0.60
1:H:263:LEU:O	1:H:267:ASP:N	2.30	0.60
1:H:275:GLU:O	1:H:339:ALA:HB3	2.01	0.60
1:H:311:VAL:CG2	1:H:312:GLU:N	2.64	0.60
1:A:203:LEU:HD22	1:A:226:ARG:CB	2.30	0.60
1:A:246:GLU:C	1:A:248:LEU:N	2.53	0.60
1:A:248:LEU:CB	1:A:262:ARG:HH21	2.14	0.60
1:B:111:TYR:O	1:B:112:VAL:CG2	2.42	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:241:ARG:CZ	1:C:263:LEU:HG	2.31	0.60
1:D:325:ILE:CG1	2:D:402:CMP:P	2.89	0.60
1:G:157:ILE:HD12	1:G:157:ILE:O	2.01	0.60
1:G:253:ILE:CG2	1:G:321:TYR:CE2	2.84	0.60
1:G:356:VAL:HG23	1:G:357:LEU:HD12	1.80	0.60
1:H:211:ASP:OD2	2:H:401:CMP:H3'	2.00	0.60
1:H:247:PHE:HZ	1:H:293:ILE:O	1.82	0.60
1:H:328:LEU:HD22	1:H:365:LYS:HE3	1.82	0.60
1:A:139:LEU:CD2	1:A:147:ILE:HD13	2.32	0.60
1:A:316:LEU:C	1:A:316:LEU:CD1	2.69	0.60
1:B:120:TYR:HE2	1:B:124:ALA:HB2	1.66	0.60
1:C:123:MET:HE3	1:D:123:MET:CE	2.32	0.60
1:C:282:VAL:O	1:C:285:GLU:CG	2.46	0.60
1:C:294:LEU:HD11	1:C:345:CYS:CA	2.14	0.60
1:G:230:ARG:O	1:G:234:MET:CB	2.49	0.60
1:G:257:LEU:HD21	1:G:360:CYS:SG	2.41	0.60
1:G:299:ALA:HB3	1:G:338:VAL:HG12	1.82	0.60
1:A:260:TRP:CZ2	2:A:401:CMP:H8	2.37	0.60
1:C:151:MET:HA	1:C:224:ILE:HG22	1.83	0.60
1:C:178:GLY:CA	1:C:219:VAL:HG12	2.15	0.60
1:D:112:VAL:HG12	1:D:231:ARG:NH2	2.15	0.60
1:D:175:ILE:HD11	1:D:196:GLY:N	2.12	0.60
1:D:232:ILE:HG23	1:D:233:LEU:HG	1.83	0.60
1:E:294:LEU:N	1:E:294:LEU:CD1	2.38	0.60
1:A:294:LEU:CD1	1:A:294:LEU:H	2.01	0.60
1:B:260:TRP:CD2	2:B:401:CMP:C8	2.85	0.60
1:B:327:LEU:HD23	1:B:353:PHE:CZ	2.37	0.60
1:E:300:VAL:HG22	1:E:337:VAL:HG22	1.84	0.60
1:F:177:GLN:HA	1:F:194:GLU:HG3	1.82	0.60
1:F:325:ILE:CD1	2:F:402:CMP:O1P	2.49	0.60
1:G:262:ARG:HA	1:G:265:VAL:HG23	1.83	0.60
1:H:272:VAL:O	1:H:345:CYS:N	2.32	0.60
1:A:152:PHE:HE2	1:A:223:GLY:CA	2.11	0.60
1:B:130:ILE:HD13	1:B:151:MET:HE3	1.84	0.60
1:B:152:PHE:CD2	1:B:152:PHE:C	2.77	0.60
1:B:209:ARG:HD2	2:B:401:CMP:O5'	2.01	0.60
1:C:126:LEU:HB2	1:C:222:TRP:CZ2	2.37	0.60
1:C:229:TYR:CD1	1:C:233:LEU:HD12	2.36	0.60
1:D:283:GLN:OE1	1:D:302:GLN:HA	2.02	0.60
1:G:190:THR:HG22	1:G:191:SER:N	2.07	0.60
1:G:272:VAL:HA	1:G:273:GLN:HE22	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:325:ILE:HG23	1:G:329:MET:CG	2.31	0.60
1:H:281:VAL:HG13	1:H:333:ARG:CD	2.31	0.60
1:A:139:LEU:HD21	1:A:147:ILE:HD13	1.83	0.60
1:A:188:TRP:CZ3	1:A:190:THR:CA	2.84	0.60
1:A:362:ASP:N	1:A:362:ASP:OD1	2.32	0.60
1:B:120:TYR:O	1:B:121:LYS:C	2.41	0.60
1:B:152:PHE:HE2	1:B:223:GLY:HA3	1.65	0.60
1:C:140:ASP:C	1:C:140:ASP:OD1	2.45	0.60
1:C:361:SER:HB2	1:C:365:LYS:HZ1	1.65	0.60
1:D:184:VAL:HG13	1:D:184:VAL:O	2.01	0.60
1:E:113:ARG:O	1:H:112:VAL:CB	2.47	0.60
1:E:115:VAL:HG23	1:H:110:SER:HB3	1.84	0.60
1:F:114:LYS:CE	1:F:115:VAL:H	2.15	0.60
1:G:173:TYR:HD2	1:G:198:PHE:CZ	2.18	0.60
1:G:175:ILE:HD11	1:G:193:GLY:O	2.01	0.60
1:G:327:LEU:HD23	1:G:353:PHE:CE2	2.36	0.60
1:H:230:ARG:HH11	1:H:230:ARG:HG2	1.66	0.60
1:H:322:PHE:CD1	1:H:322:PHE:N	2.68	0.60
1:A:230:ARG:HH11	1:A:234:MET:HE1	1.57	0.60
1:A:254:LEU:HD12	1:A:255:GLU:N	2.17	0.60
1:A:266:ALA:O	1:A:267:ASP:C	2.44	0.60
1:A:366:ARG:O	1:A:369:GLN:HB2	2.02	0.60
1:B:273:GLN:HB3	1:B:344:LYS:HA	1.84	0.60
1:B:310:PHE:O	1:B:311:VAL:HG23	2.02	0.60
1:C:131:GLU:C	1:C:133:ASN:N	2.58	0.60
1:C:182:VAL:CG2	1:C:190:THR:O	2.38	0.60
1:C:301:LEU:HA	1:C:311:VAL:O	2.02	0.60
1:C:371:TYR:CE1	2:C:402:CMP:N7	2.69	0.60
1:D:205:TYR:CD2	1:D:205:TYR:N	2.70	0.60
1:D:353:PHE:CD1	1:D:357:LEU:HD22	2.33	0.60
1:F:130:ILE:CG1	1:F:136:PHE:CD2	2.81	0.60
1:F:158:ALA:O	1:H:243:MET:CE	2.49	0.60
1:F:190:THR:CG2	1:F:191:SER:H	2.12	0.60
1:H:200:GLU:OE2	1:H:241:ARG:NH2	2.35	0.60
1:A:211:ASP:OD2	2:A:401:CMP:N3	2.34	0.60
1:A:298:ALA:HB1	1:A:338:VAL:O	2.02	0.60
1:B:165:GLN:HE22	1:B:185:ASN:ND2	2.00	0.60
1:B:229:TYR:O	1:B:233:LEU:HD12	2.02	0.60
1:C:130:ILE:HG13	1:C:136:PHE:CD2	2.36	0.60
1:D:179:GLU:HB3	1:D:217:THR:HG23	1.84	0.60
1:D:298:ALA:O	1:D:316:LEU:CD2	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:266:ALA:CA	1:E:269:LEU:CD1	2.76	0.60
1:F:249:SER:N	1:F:262:ARG:NH2	2.49	0.60
1:B:182:VAL:O	1:B:182:VAL:CG2	2.44	0.60
1:B:210:ALA:C	1:B:211:ASP:OD1	2.45	0.60
1:B:253:ILE:C	1:B:255:GLU:H	2.10	0.60
1:C:284:GLY:N	1:C:333:ARG:O	2.32	0.60
1:D:175:ILE:HD11	1:D:195:GLY:N	2.17	0.60
1:D:249:SER:N	1:D:262:ARG:HH22	2.00	0.60
1:D:280:ILE:HD13	1:D:322:PHE:CZ	2.37	0.60
1:E:116:ILE:CG2	1:E:118:LYS:HZ2	2.14	0.60
1:E:123:MET:HE3	1:F:123:MET:HE2	1.83	0.60
1:F:175:ILE:HG22	1:F:221:LEU:HD21	1.83	0.60
1:A:311:VAL:CG2	1:A:312:GLU:N	2.65	0.59
1:A:316:LEU:CA	1:A:320:ASP:OD2	2.50	0.59
1:B:273:GLN:CB	1:B:344:LYS:HA	2.31	0.59
1:B:333:ARG:NH1	2:B:402:CMP:O2P	2.34	0.59
1:F:131:GLU:O	1:F:133:ASN:N	2.35	0.59
1:F:301:LEU:HD13	1:F:311:VAL:O	2.02	0.59
1:F:361:SER:C	1:F:365:LYS:HZ2	2.09	0.59
1:G:111:TYR:CG	1:G:112:VAL:N	2.70	0.59
1:H:266:ALA:O	1:H:267:ASP:C	2.45	0.59
1:H:325:ILE:HD11	2:H:402:CMP:O1P	2.02	0.59
1:A:117:PRO:HG2	1:D:110:SER:CB	2.32	0.59
1:A:329:MET:CE	1:A:329:MET:HA	2.32	0.59
1:B:135:LEU:HD13	1:B:136:PHE:CG	2.37	0.59
1:B:203:LEU:HD22	1:B:226:ARG:HB3	1.84	0.59
1:B:211:ASP:OD2	2:B:401:CMP:C5'	2.49	0.59
1:C:243:MET:HE2	1:E:159:GLY:O	2.02	0.59
1:C:293:ILE:HA	1:C:345:CYS:SG	2.42	0.59
1:C:312:GLU:OE1	1:C:312:GLU:CA	2.46	0.59
1:D:294:LEU:CD1	1:D:294:LEU:N	2.49	0.59
1:G:260:TRP:CD1	2:G:401:CMP:C4	2.90	0.59
1:H:295:GLU:HG2	1:H:318:PRO:HG3	1.83	0.59
1:B:153:PRO:CB	1:B:222:TRP:HZ3	2.13	0.59
1:C:259:LYS:O	1:C:260:TRP:C	2.45	0.59
1:C:278:GLN:O	1:C:338:VAL:CG2	2.49	0.59
1:D:111:TYR:CG	1:D:112:VAL:N	2.70	0.59
1:E:131:GLU:H	1:E:131:GLU:CD	2.09	0.59
1:E:177:GLN:HA	1:E:194:GLU:HG3	1.83	0.59
1:F:313:VAL:O	1:F:313:VAL:HG22	2.01	0.59
1:G:246:GLU:C	1:G:248:LEU:N	2.53	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:182:VAL:CG2	1:H:190:THR:H	2.13	0.59
1:H:203:LEU:HD22	1:H:226:ARG:HB3	1.84	0.59
1:A:162:VAL:CG2	1:A:163:ILE:HG13	2.29	0.59
1:A:173:TYR:HD2	1:A:198:PHE:HE1	1.43	0.59
1:B:272:VAL:CG2	1:B:273:GLN:NE2	2.66	0.59
1:C:118:LYS:HE2	1:C:148:PHE:O	2.01	0.59
1:C:298:ALA:CB	1:C:338:VAL:O	2.50	0.59
1:F:174:VAL:HG13	1:F:222:TRP:HB2	1.84	0.59
1:H:279:LYS:HB3	1:H:338:VAL:HG23	1.84	0.59
1:H:376:SER:O	1:H:376:SER:OG	2.14	0.59
1:A:157:ILE:CA	1:A:218:ASN:OD1	2.51	0.59
1:A:158:ALA:CA	1:A:217:THR:O	2.50	0.59
1:B:144:ARG:O	1:B:147:ILE:HG12	2.02	0.59
1:B:293:ILE:HD11	1:B:343:LEU:CD1	2.32	0.59
1:C:204:ILE:CG2	1:C:205:TYR:HD2	2.10	0.59
1:E:120:TYR:C	1:E:120:TYR:HD2	2.09	0.59
1:F:152:PHE:CE2	1:F:223:GLY:HA3	2.25	0.59
1:H:157:ILE:O	1:H:160:GLU:HB2	2.02	0.59
1:H:247:PHE:HE1	1:H:294:LEU:CB	2.14	0.59
1:H:348:LEU:HD21	1:H:356:VAL:HG21	1.83	0.59
1:A:116:ILE:HB	1:A:118:LYS:NZ	2.17	0.59
1:A:145:SER:HA	1:B:120:TYR:CD1	2.36	0.59
1:B:247:PHE:CE1	1:B:294:LEU:HB3	2.38	0.59
1:B:272:VAL:CA	1:B:273:GLN:NE2	2.66	0.59
1:B:313:VAL:HG21	2:B:402:CMP:C6	2.32	0.59
1:C:165:GLN:CA	1:C:211:ASP:O	2.49	0.59
1:D:235:GLY:O	1:D:239:ARG:HG3	2.02	0.59
1:E:183:TYR:HD1	1:E:188:TRP:HA	1.68	0.59
1:F:205:TYR:CD2	1:F:205:TYR:N	2.69	0.59
1:F:296:GLY:HA3	1:F:342:PRO:O	2.02	0.59
1:G:151:MET:HA	1:G:224:ILE:HG22	1.84	0.59
1:H:113:ARG:HB3	1:H:231:ARG:HH12	1.66	0.59
1:H:183:TYR:CD1	1:H:188:TRP:HB2	2.37	0.59
1:H:294:LEU:O	1:H:318:PRO:CB	2.47	0.59
1:H:353:PHE:CE1	1:H:357:LEU:HD23	2.38	0.59
1:B:205:TYR:CD2	1:B:205:TYR:N	2.68	0.59
1:B:260:TRP:CG	2:B:401:CMP:C5	2.90	0.59
1:C:129:ALA:HA	1:C:132:LYS:HE3	1.85	0.59
1:C:271:PRO:HA	1:C:345:CYS:O	2.02	0.59
1:D:291:PHE:CZ	1:D:347:LYS:NZ	2.71	0.59
1:G:173:TYR:CD2	1:G:198:PHE:CE1	2.87	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:365:LYS:O	1:G:368:ILE:CG1	2.42	0.59
1:H:252:SER:OG	1:H:253:ILE:N	2.34	0.59
1:H:278:GLN:O	1:H:338:VAL:HG22	2.00	0.59
1:A:112:VAL:CB	1:A:112:VAL:N	2.62	0.59
1:A:375:VAL:CG1	1:A:376:SER:H	2.15	0.59
1:B:253:ILE:HG13	1:B:254:LEU:HG	1.84	0.59
1:D:293:ILE:CG1	1:D:343:LEU:HD11	2.32	0.59
1:E:353:PHE:HE1	1:E:357:LEU:CD2	2.12	0.59
1:F:176:ASP:O	1:F:194:GLU:HG2	2.03	0.59
1:G:120:TYR:CD2	1:G:121:LYS:HA	2.35	0.59
1:H:284:GLY:CA	1:H:332:PRO:HB3	2.32	0.59
1:A:111:TYR:O	1:D:115:VAL:CG2	2.51	0.59
1:A:152:PHE:CE2	1:A:223:GLY:HA3	2.31	0.59
1:A:188:TRP:HZ3	1:A:190:THR:O	1.85	0.59
1:A:260:TRP:NE1	2:A:401:CMP:C8	2.65	0.59
1:A:262:ARG:HA	1:A:265:VAL:CG2	2.32	0.59
1:A:278:GLN:O	1:A:338:VAL:HG22	2.03	0.59
1:D:175:ILE:CD1	1:D:195:GLY:N	2.66	0.59
1:E:259:LYS:CG	1:E:260:TRP:N	2.66	0.59
1:H:204:ILE:HG12	1:H:234:MET:SD	2.43	0.59
1:H:205:TYR:HD2	1:H:205:TYR:N	2.00	0.59
1:B:173:TYR:HD1	1:B:223:GLY:HA3	1.68	0.59
1:D:200:GLU:HG2	1:D:201:LEU:HG	1.84	0.59
1:D:211:ASP:OD2	2:D:401:CMP:H3'	2.03	0.59
1:D:247:PHE:CE1	1:D:294:LEU:CA	2.79	0.59
1:D:293:ILE:HA	1:D:345:CYS:SG	2.43	0.59
1:F:365:LYS:C	1:F:368:ILE:HG13	2.26	0.59
1:H:173:TYR:CD2	1:H:198:PHE:HE1	2.18	0.59
1:H:177:GLN:HA	1:H:194:GLU:HG3	1.84	0.59
1:H:294:LEU:HD11	1:H:344:LYS:HG2	1.85	0.59
1:H:365:LYS:O	1:H:368:ILE:CG1	2.48	0.59
1:A:113:ARG:NH2	1:D:115:VAL:HA	2.16	0.58
1:A:273:GLN:NE2	1:A:273:GLN:H	1.79	0.58
1:B:375:VAL:C	1:C:306:GLU:HA	2.28	0.58
1:D:361:SER:C	1:D:365:LYS:NZ	2.57	0.58
1:D:366:ARG:HG2	1:D:367:ASN:N	2.17	0.58
1:E:362:ASP:OD1	1:E:362:ASP:N	2.36	0.58
1:F:131:GLU:OE1	1:F:131:GLU:CA	2.50	0.58
1:F:194:GLU:O	1:F:355:ARG:HD2	2.03	0.58
1:F:230:ARG:CA	1:F:234:MET:HE2	2.32	0.58
1:G:180:MET:HB2	1:G:192:VAL:HB	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:161:THR:CA	1:H:214:LYS:HD2	2.25	0.58
1:H:253:ILE:HG13	1:H:254:LEU:HG	1.85	0.58
1:A:144:ARG:HD2	1:B:120:TYR:HH	1.68	0.58
1:A:175:ILE:CD1	1:A:195:GLY:N	2.66	0.58
1:A:262:ARG:O	1:A:265:VAL:CB	2.43	0.58
1:A:294:LEU:HD11	1:A:345:CYS:CA	2.22	0.58
1:B:292:ILE:HB	1:B:346:VAL:HG13	1.84	0.58
1:C:143:GLU:HB3	1:C:232:ILE:HD11	1.85	0.58
1:C:281:VAL:CG1	1:C:333:ARG:CG	2.81	0.58
1:D:296:GLY:HA3	1:D:343:LEU:HA	1.85	0.58
1:E:198:PHE:CD1	1:E:198:PHE:N	2.70	0.58
1:F:220:LYS:O	1:F:221:LEU:HD23	2.03	0.58
1:G:117:PRO:HA	1:H:119:ASP:HA	1.84	0.58
1:A:135:LEU:HD13	1:A:136:PHE:CG	2.37	0.58
1:B:310:PHE:O	1:B:310:PHE:HD2	1.86	0.58
1:B:322:PHE:CD2	1:B:337:VAL:HG21	2.38	0.58
1:C:246:GLU:C	1:C:248:LEU:N	2.60	0.58
1:E:165:GLN:CA	1:E:211:ASP:O	2.50	0.58
1:F:120:TYR:C	1:F:120:TYR:CD2	2.81	0.58
1:F:180:MET:O	1:F:191:SER:HA	2.02	0.58
1:F:188:TRP:CZ3	1:F:190:THR:C	2.81	0.58
1:F:198:PHE:N	1:F:198:PHE:HD1	2.01	0.58
1:F:246:GLU:C	1:F:248:LEU:N	2.57	0.58
1:B:133:ASN:O	1:B:135:LEU:HD12	2.02	0.58
1:B:262:ARG:HA	1:B:265:VAL:CG2	2.34	0.58
1:B:281:VAL:CG1	1:B:333:ARG:CD	2.81	0.58
1:C:173:TYR:HB2	1:C:198:PHE:CE1	2.38	0.58
1:C:350:ARG:O	1:C:353:PHE:CB	2.51	0.58
1:E:120:TYR:CD1	1:F:148:PHE:CD1	2.92	0.58
1:E:203:LEU:HD12	1:E:229:TYR:HD2	1.67	0.58
1:G:112:VAL:HG12	1:G:231:ARG:CZ	2.33	0.58
1:G:144:ARG:O	1:G:147:ILE:HG12	2.02	0.58
1:G:164:GLN:HA	1:G:212:THR:CG2	2.32	0.58
1:H:280:ILE:HD11	1:H:337:VAL:CB	2.29	0.58
1:H:300:VAL:O	1:H:301:LEU:CD2	2.44	0.58
1:H:325:ILE:HG13	2:H:402:CMP:O1P	2.04	0.58
1:A:120:TYR:OH	1:B:144:ARG:HD2	2.03	0.58
1:A:259:LYS:CG	1:A:260:TRP:N	2.57	0.58
1:B:247:PHE:C	1:B:247:PHE:CD2	2.81	0.58
1:B:325:ILE:CD1	1:B:334:ALA:HB3	2.34	0.58
1:C:112:VAL:O	1:C:113:ARG:HG3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:247:PHE:CE1	1:C:294:LEU:HB3	2.38	0.58
1:C:263:LEU:O	1:C:267:ASP:N	2.33	0.58
1:C:292:ILE:HB	1:C:346:VAL:CG1	2.33	0.58
1:D:122:THR:O	1:D:125:ALA:HB3	2.03	0.58
1:D:200:GLU:HG2	1:D:201:LEU:HD12	1.84	0.58
1:E:144:ARG:CG	1:E:145:SER:N	2.67	0.58
1:E:161:THR:CA	1:E:214:LYS:HD2	2.32	0.58
1:E:173:TYR:CD2	1:E:198:PHE:CE1	2.91	0.58
1:E:182:VAL:CG2	1:E:190:THR:H	2.16	0.58
1:E:248:LEU:CB	1:E:262:ARG:HH21	2.17	0.58
1:G:269:LEU:CB	1:G:346:VAL:CG2	2.81	0.58
1:H:308:GLU:O	1:H:309:GLU:OE2	2.21	0.58
1:A:113:ARG:HE	1:D:113:ARG:C	2.10	0.58
1:C:205:TYR:CD2	1:C:205:TYR:N	2.71	0.58
1:C:247:PHE:C	1:C:247:PHE:HD2	2.08	0.58
1:C:272:VAL:HG22	1:C:273:GLN:N	2.14	0.58
1:D:318:PRO:O	1:D:319:SER:HB3	2.03	0.58
1:E:201:LEU:HD13	2:E:401:CMP:H2'	1.83	0.58
1:F:175:ILE:HD12	1:F:175:ILE:C	2.27	0.58
1:A:188:TRP:CZ3	1:A:190:THR:HA	2.38	0.58
1:B:163:ILE:O	1:B:212:THR:HG22	2.04	0.58
1:C:302:GLN:NE2	1:C:374:PHE:CB	2.67	0.58
1:D:162:VAL:CG2	1:D:213:VAL:O	2.50	0.58
1:D:175:ILE:CD1	1:D:194:GLU:HA	2.33	0.58
1:E:243:MET:HE3	1:G:157:ILE:CD1	2.33	0.58
1:E:262:ARG:HA	1:E:265:VAL:CG2	2.33	0.58
1:E:266:ALA:O	1:E:267:ASP:C	2.46	0.58
1:F:113:ARG:HD3	1:F:146:ASP:CB	2.34	0.58
1:G:254:LEU:HD12	1:G:255:GLU:N	2.18	0.58
1:A:142:ASN:CB	1:C:121:LYS:HE3	2.33	0.58
1:B:260:TRP:HA	1:B:263:LEU:HD12	1.84	0.58
1:C:139:LEU:N	1:C:139:LEU:CD1	2.63	0.58
1:D:161:THR:HG23	1:D:214:LYS:CD	2.34	0.58
1:D:199:GLY:HA2	2:D:401:CMP:P	2.44	0.58
1:D:204:ILE:CG2	1:D:205:TYR:CD2	2.83	0.58
1:E:180:MET:HB2	1:E:192:VAL:HB	1.86	0.58
1:E:274:PHE:CD2	1:E:280:ILE:HG22	2.39	0.58
1:E:296:GLY:CA	1:E:342:PRO:O	2.51	0.58
1:G:157:ILE:CB	1:G:218:ASN:OD1	2.51	0.58
1:H:325:ILE:O	1:H:328:LEU:N	2.36	0.58
1:A:113:ARG:HG2	1:D:113:ARG:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:ARG:CZ	1:D:114:LYS:N	2.67	0.58
1:B:120:TYR:CD2	1:B:120:TYR:O	2.52	0.58
1:B:177:GLN:HA	1:B:194:GLU:HG3	1.84	0.58
1:B:260:TRP:NE1	2:B:401:CMP:H2'	2.12	0.58
1:B:348:LEU:HD21	1:B:356:VAL:CG2	2.32	0.58
1:C:126:LEU:HD12	1:C:126:LEU:C	2.29	0.58
1:C:161:THR:OG1	1:C:214:LYS:NZ	2.32	0.58
1:C:371:TYR:CE1	2:C:402:CMP:C5	2.92	0.58
1:D:142:ASN:O	1:D:143:GLU:C	2.43	0.58
1:D:152:PHE:HD1	1:D:152:PHE:N	1.97	0.58
1:D:226:ARG:HH11	1:D:226:ARG:CG	2.04	0.58
1:D:254:LEU:C	1:D:254:LEU:CD2	2.76	0.58
1:E:152:PHE:CE2	1:E:223:GLY:C	2.82	0.58
1:E:293:ILE:CG1	1:E:317:GLY:O	2.51	0.58
1:E:300:VAL:HG11	2:E:402:CMP:C8	2.33	0.58
1:F:270:GLU:O	1:F:346:VAL:HA	2.04	0.58
1:G:276:ASP:C	1:G:278:GLN:H	2.09	0.58
1:B:269:LEU:CD2	1:B:346:VAL:HG21	2.34	0.58
1:B:294:LEU:O	1:B:295:GLU:HG3	2.03	0.58
1:C:175:ILE:HD11	1:C:193:GLY:O	2.04	0.58
1:C:229:TYR:HD1	1:C:233:LEU:HD11	1.66	0.58
1:D:129:ALA:CB	1:D:222:TRP:HE1	2.17	0.58
1:D:292:ILE:HB	1:D:346:VAL:CG1	2.33	0.58
1:E:151:MET:HA	1:E:224:ILE:HG22	1.85	0.58
1:E:152:PHE:CD2	1:E:152:PHE:N	2.68	0.58
1:F:300:VAL:HG11	1:F:335:ALA:HB1	1.85	0.58
1:F:361:SER:O	1:F:365:LYS:HD2	2.03	0.58
1:H:158:ALA:HA	1:H:215:ALA:CB	2.34	0.58
1:A:175:ILE:HA	1:A:221:LEU:HD23	1.81	0.57
1:D:135:LEU:HD12	1:D:135:LEU:N	2.19	0.57
1:D:242:LYS:N	1:D:242:LYS:HD3	2.11	0.57
1:E:269:LEU:CB	1:E:346:VAL:HG21	2.32	0.57
1:E:290:PHE:HB2	1:E:327:LEU:CD2	2.34	0.57
1:F:118:LYS:NZ	1:F:151:MET:O	2.32	0.57
1:F:183:TYR:CD1	1:F:188:TRP:HB2	2.38	0.57
1:F:230:ARG:HG2	1:F:230:ARG:HH11	1.69	0.57
1:G:247:PHE:HE1	1:G:294:LEU:CA	2.10	0.57
1:H:152:PHE:O	1:H:152:PHE:HD2	1.87	0.57
1:H:205:TYR:CD2	1:H:205:TYR:N	2.71	0.57
1:A:111:TYR:O	1:A:112:VAL:CB	2.52	0.57
1:A:138:HIS:CD2	1:C:157:ILE:CG2	2.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:233:LEU:O	1:B:234:MET:C	2.47	0.57
1:B:321:TYR:C	1:B:321:TYR:HD1	2.09	0.57
1:D:113:ARG:CZ	1:D:146:ASP:OD1	2.51	0.57
1:D:120:TYR:CE2	1:D:124:ALA:HB2	2.39	0.57
1:D:299:ALA:HB3	1:D:338:VAL:HG12	1.85	0.57
1:H:140:ASP:C	1:H:140:ASP:OD1	2.47	0.57
1:A:151:MET:HG2	1:A:224:ILE:CG2	2.34	0.57
1:B:261:GLU:O	1:B:262:ARG:C	2.47	0.57
1:B:347:LYS:O	1:B:348:LEU:HD12	2.04	0.57
1:C:158:ALA:HA	1:C:215:ALA:CB	2.34	0.57
1:D:157:ILE:HD12	1:F:243:MET:HE1	1.84	0.57
1:F:188:TRP:CH2	1:F:190:THR:HA	2.39	0.57
1:G:126:LEU:O	1:G:126:LEU:CD1	2.39	0.57
1:G:130:ILE:CG2	1:G:131:GLU:N	2.67	0.57
1:A:313:VAL:HG11	2:A:402:CMP:N6	2.19	0.57
1:B:157:ILE:CG2	1:B:218:ASN:OD1	2.52	0.57
1:B:246:GLU:O	1:B:248:LEU:N	2.37	0.57
1:C:222:TRP:HA	1:C:222:TRP:HE3	1.67	0.57
1:C:260:TRP:O	1:C:263:LEU:HB2	2.04	0.57
1:C:344:LYS:HE2	1:E:216:LYS:HA	1.86	0.57
1:D:365:LYS:CA	1:D:368:ILE:HG13	2.34	0.57
1:F:131:GLU:O	1:F:132:LYS:C	2.44	0.57
1:F:235:GLY:O	1:F:236:SER:C	2.46	0.57
1:H:129:ALA:CB	1:H:222:TRP:HE1	2.18	0.57
1:H:220:LYS:C	1:H:221:LEU:HD23	2.28	0.57
1:H:297:SER:O	1:H:340:ARG:HB2	2.04	0.57
1:A:175:ILE:HD12	1:A:195:GLY:H	1.69	0.57
1:B:133:ASN:C	1:B:133:ASN:OD1	2.47	0.57
1:B:152:PHE:HE2	1:B:223:GLY:CA	2.17	0.57
1:B:365:LYS:HA	1:B:368:ILE:CG1	2.35	0.57
1:D:201:LEU:O	1:D:204:ILE:N	2.38	0.57
1:E:233:LEU:HD12	1:E:233:LEU:N	2.08	0.57
1:F:164:GLN:HA	1:F:212:THR:CG2	2.31	0.57
1:F:363:ILE:O	1:F:366:ARG:HG2	2.04	0.57
1:G:234:MET:HG3	1:G:238:LEU:CD1	2.33	0.57
1:G:246:GLU:O	1:G:248:LEU:N	2.38	0.57
1:G:265:VAL:CG1	1:G:269:LEU:CD2	2.70	0.57
1:G:348:LEU:HD21	1:G:356:VAL:CG2	2.34	0.57
1:A:138:HIS:CD2	1:C:157:ILE:HG21	2.39	0.57
1:B:251:VAL:O	1:B:252:SER:O	2.21	0.57
1:C:120:TYR:HD2	1:C:121:LYS:CA	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:157:ILE:O	1:C:157:ILE:CD1	2.37	0.57
1:C:172:PHE:O	1:C:224:ILE:HD12	2.05	0.57
1:C:204:ILE:CG2	1:C:205:TYR:CE2	2.88	0.57
1:C:325:ILE:HG13	2:C:402:CMP:O2P	2.02	0.57
1:D:139:LEU:HD21	1:D:147:ILE:HD11	1.87	0.57
1:D:174:VAL:CG1	1:D:222:TRP:HB2	2.35	0.57
1:E:127:ALA:O	1:E:130:ILE:N	2.38	0.57
1:E:356:VAL:HG23	1:E:357:LEU:HD12	1.86	0.57
1:F:114:LYS:HE3	1:F:115:VAL:N	2.19	0.57
1:F:122:THR:O	1:F:125:ALA:HB3	2.04	0.57
1:F:198:PHE:CD1	1:F:198:PHE:O	2.57	0.57
1:F:294:LEU:CD1	1:F:344:LYS:O	2.52	0.57
1:F:312:GLU:OE1	1:F:340:ARG:NH1	2.37	0.57
1:G:112:VAL:HG12	1:G:231:ARG:HH21	1.69	0.57
1:G:153:PRO:HB3	1:G:222:TRP:HZ3	1.61	0.57
1:G:249:SER:CA	1:G:262:ARG:NH2	2.66	0.57
1:G:375:VAL:CG1	1:G:376:SER:N	2.68	0.57
1:H:111:TYR:CE2	1:H:112:VAL:CG1	2.86	0.57
1:A:248:LEU:HB2	1:A:262:ARG:HH21	1.69	0.57
1:B:293:ILE:HG23	1:B:318:PRO:HA	1.87	0.57
1:C:152:PHE:CD2	1:C:152:PHE:C	2.81	0.57
1:C:230:ARG:CA	1:C:234:MET:HE2	2.34	0.57
1:C:248:LEU:HD21	1:C:265:VAL:HG11	1.87	0.57
1:C:253:ILE:C	1:C:255:GLU:H	2.11	0.57
1:F:224:ILE:HD13	1:F:224:ILE:C	2.28	0.57
1:G:182:VAL:O	1:G:182:VAL:CG2	2.52	0.57
1:G:285:GLU:OE1	1:G:285:GLU:HA	2.04	0.57
1:H:153:PRO:CA	1:H:222:TRP:CZ3	2.88	0.57
1:H:269:LEU:HB3	1:H:346:VAL:HG23	1.84	0.57
1:H:278:GLN:O	1:H:338:VAL:HA	2.04	0.57
1:H:368:ILE:O	1:H:371:TYR:HB2	2.04	0.57
1:A:153:PRO:CB	1:A:222:TRP:HZ3	2.16	0.57
1:A:233:LEU:O	1:A:234:MET:C	2.48	0.57
1:A:309:GLU:HG3	1:A:310:PHE:N	2.19	0.57
1:C:135:LEU:HD12	1:C:136:PHE:N	2.19	0.57
1:C:172:PHE:O	1:C:224:ILE:CD1	2.52	0.57
1:D:113:ARG:NH2	1:D:146:ASP:OD1	2.38	0.57
1:D:247:PHE:CE1	1:D:294:LEU:CB	2.87	0.57
1:E:365:LYS:CA	1:E:368:ILE:HG13	2.34	0.57
1:F:293:ILE:HA	1:F:345:CYS:SG	2.45	0.57
1:G:252:SER:O	1:G:255:GLU:HB2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:253:ILE:HG23	1:G:321:TYR:HE2	1.70	0.57
1:A:171:ASN:H	1:A:209:ARG:HH22	1.53	0.57
1:A:292:ILE:HB	1:A:346:VAL:HG13	1.86	0.57
1:A:324:GLU:CG	1:A:325:ILE:N	2.67	0.57
1:B:121:LYS:O	1:B:124:ALA:N	2.38	0.57
1:B:200:GLU:O	1:B:201:LEU:C	2.45	0.57
1:B:284:GLY:O	1:B:332:PRO:HB3	2.05	0.57
1:C:281:VAL:O	1:C:336:THR:HA	2.04	0.57
1:D:136:PHE:O	1:D:139:LEU:CD1	2.52	0.57
1:E:170:ASP:H	1:E:209:ARG:NH2	2.02	0.57
1:E:269:LEU:HB3	1:E:346:VAL:HG22	1.85	0.57
1:E:291:PHE:CD1	1:E:347:LYS:NZ	2.73	0.57
1:F:153:PRO:HB3	1:F:222:TRP:HZ3	1.67	0.57
1:F:366:ARG:CG	1:F:367:ASN:N	2.67	0.57
1:G:118:LYS:NZ	1:G:151:MET:O	2.34	0.57
1:G:175:ILE:CD1	1:G:194:GLU:HA	2.34	0.57
1:H:162:VAL:HG22	1:H:213:VAL:O	2.05	0.57
1:H:327:LEU:HD23	1:H:353:PHE:CD2	2.40	0.57
1:B:272:VAL:HG22	1:B:273:GLN:N	2.20	0.57
1:B:329:MET:HA	1:B:329:MET:CE	2.35	0.57
1:C:247:PHE:HE1	1:C:294:LEU:HB3	1.70	0.57
1:C:325:ILE:HG13	1:C:326:ALA:H	1.70	0.57
1:D:152:PHE:N	1:D:152:PHE:CD1	2.68	0.57
1:E:178:GLY:HA3	1:E:219:VAL:CG1	2.26	0.57
1:E:226:ARG:HA	1:E:229:TYR:HB3	1.86	0.57
1:E:243:MET:HE1	1:G:158:ALA:O	2.05	0.57
1:E:294:LEU:CD1	1:E:344:LYS:O	2.51	0.57
1:E:365:LYS:HA	1:E:368:ILE:CG1	2.35	0.57
1:F:151:MET:HA	1:F:224:ILE:HG22	1.85	0.57
1:F:278:GLN:O	1:F:338:VAL:HG22	2.05	0.57
1:H:211:ASP:OD2	2:H:401:CMP:N3	2.38	0.57
1:A:224:ILE:HD12	1:A:224:ILE:H	1.68	0.56
1:B:274:PHE:CD2	1:B:343:LEU:HD23	2.40	0.56
1:D:131:GLU:H	1:D:131:GLU:CD	2.13	0.56
1:E:241:ARG:O	1:E:242:LYS:C	2.47	0.56
1:F:129:ALA:CB	1:F:222:TRP:HE1	2.18	0.56
1:F:269:LEU:HD23	1:F:348:LEU:CD1	2.35	0.56
1:G:177:GLN:HA	1:G:194:GLU:HG3	1.86	0.56
1:G:296:GLY:HA3	1:G:342:PRO:O	2.05	0.56
1:G:324:GLU:HB2	1:G:364:LEU:HD13	1.86	0.56
1:H:253:ILE:C	1:H:255:GLU:H	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:293:ILE:CD1	1:H:343:LEU:HD11	2.32	0.56
1:A:180:MET:O	1:A:191:SER:HA	2.05	0.56
1:B:162:VAL:CG2	1:B:163:ILE:HG13	2.34	0.56
1:C:110:SER:C	1:F:114:LYS:HD3	2.30	0.56
1:C:111:TYR:C	1:C:112:VAL:HG13	2.30	0.56
1:E:281:VAL:HG12	1:E:333:ARG:HG3	1.86	0.56
1:F:131:GLU:C	1:F:133:ASN:N	2.60	0.56
1:G:222:TRP:HA	1:G:222:TRP:HE3	1.69	0.56
1:H:152:PHE:HD2	1:H:152:PHE:H	1.54	0.56
1:H:154:VAL:O	1:H:221:LEU:N	2.29	0.56
1:A:113:ARG:CZ	1:D:114:LYS:C	2.78	0.56
1:A:194:GLU:O	1:A:355:ARG:HD2	2.05	0.56
1:A:201:LEU:HD13	2:A:401:CMP:H2'	1.87	0.56
1:A:366:ARG:O	1:A:369:GLN:CB	2.54	0.56
1:B:253:ILE:C	1:B:255:GLU:N	2.64	0.56
1:C:118:LYS:NZ	1:C:151:MET:O	2.32	0.56
1:C:252:SER:OG	1:C:253:ILE:N	2.37	0.56
1:C:266:ALA:N	1:C:269:LEU:HD11	2.20	0.56
1:C:294:LEU:O	1:C:318:PRO:HB3	2.04	0.56
1:D:263:LEU:O	1:D:266:ALA:N	2.39	0.56
1:D:365:LYS:HA	1:D:368:ILE:CG1	2.36	0.56
1:E:253:ILE:HD13	1:E:321:TYR:CE2	2.40	0.56
1:F:210:ALA:N	1:F:211:ASP:OD1	2.38	0.56
1:G:139:LEU:HD22	1:G:144:ARG:HA	1.88	0.56
1:G:204:ILE:CG2	1:G:205:TYR:CD2	2.84	0.56
1:G:259:LYS:HG3	1:G:260:TRP:H	1.68	0.56
1:G:293:ILE:HG23	1:G:318:PRO:HA	1.87	0.56
1:G:366:ARG:O	1:G:369:GLN:HB2	2.05	0.56
1:H:114:LYS:HZ2	1:H:114:LYS:CA	2.11	0.56
1:H:130:ILE:HD13	1:H:151:MET:CE	2.35	0.56
1:H:157:ILE:HD12	1:H:157:ILE:C	2.26	0.56
1:H:172:PHE:HD2	1:H:224:ILE:HD11	1.70	0.56
1:H:253:ILE:HG13	1:H:254:LEU:HD23	1.87	0.56
1:H:301:LEU:HB3	1:H:311:VAL:O	2.04	0.56
1:H:371:TYR:CE1	2:H:402:CMP:C4	2.94	0.56
1:A:175:ILE:CD1	1:A:195:GLY:H	2.18	0.56
1:F:130:ILE:CD1	1:F:136:PHE:CD2	2.89	0.56
1:F:133:ASN:ND2	1:F:174:VAL:HG21	2.19	0.56
1:A:298:ALA:HB3	1:A:316:LEU:HD11	1.86	0.56
1:A:325:ILE:CD1	1:A:334:ALA:CB	2.84	0.56
1:B:198:PHE:C	1:B:198:PHE:HD1	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:365:LYS:HA	1:C:368:ILE:CG1	2.36	0.56
1:D:153:PRO:HA	1:D:222:TRP:CE3	2.40	0.56
1:D:266:ALA:O	1:D:267:ASP:C	2.48	0.56
1:H:190:THR:HG22	1:H:191:SER:N	2.07	0.56
1:H:291:PHE:HB2	1:H:322:PHE:CE1	2.40	0.56
1:H:362:ASP:N	1:H:365:LYS:HZ2	2.03	0.56
1:A:152:PHE:CD2	1:A:152:PHE:C	2.78	0.56
1:A:183:TYR:HD1	1:A:188:TRP:CB	2.19	0.56
1:A:246:GLU:O	1:A:249:SER:N	2.38	0.56
1:B:139:LEU:HD21	1:B:147:ILE:HD13	1.86	0.56
1:B:362:ASP:OD1	1:B:362:ASP:N	2.38	0.56
1:C:350:ARG:HB3	1:C:351:PRO:HD3	1.87	0.56
1:D:118:LYS:NZ	1:D:151:MET:O	2.32	0.56
1:D:324:GLU:HB2	1:D:364:LEU:CD1	2.36	0.56
1:E:203:LEU:CD2	1:E:226:ARG:HB3	2.31	0.56
1:F:161:THR:HG23	1:F:214:LYS:HD3	1.87	0.56
1:F:329:MET:HA	1:F:329:MET:HE3	1.87	0.56
1:H:158:ALA:HB2	1:H:217:THR:O	2.05	0.56
1:H:266:ALA:O	1:H:268:ALA:N	2.39	0.56
1:A:120:TYR:HD1	1:B:148:PHE:CB	2.14	0.56
1:A:163:ILE:O	1:A:212:THR:HG22	2.06	0.56
1:A:278:GLN:HG3	1:A:279:LYS:H	1.69	0.56
1:A:279:LYS:HB2	1:A:337:VAL:O	2.05	0.56
1:A:290:PHE:HB2	1:A:327:LEU:CD2	2.36	0.56
1:B:239:ARG:O	1:B:240:LYS:C	2.46	0.56
1:B:278:GLN:HG3	1:B:279:LYS:N	2.17	0.56
1:B:281:VAL:CG1	1:B:333:ARG:HG3	2.35	0.56
1:C:325:ILE:O	1:C:328:LEU:N	2.39	0.56
1:D:171:ASN:OD1	1:D:225:ASP:HA	2.06	0.56
1:D:230:ARG:O	1:D:234:MET:CB	2.52	0.56
1:E:188:TRP:CH2	1:E:190:THR:HA	2.40	0.56
1:E:247:PHE:CD2	1:E:247:PHE:O	2.58	0.56
1:E:260:TRP:CG	2:E:401:CMP:N7	2.74	0.56
1:E:327:LEU:HD23	1:E:353:PHE:CE2	2.40	0.56
1:F:365:LYS:CA	1:F:368:ILE:HG13	2.35	0.56
1:G:280:ILE:HD13	1:G:322:PHE:CE2	2.41	0.56
1:G:280:ILE:HD13	1:G:322:PHE:HZ	1.69	0.56
1:H:172:PHE:O	1:H:224:ILE:CD1	2.53	0.56
1:H:283:GLN:HG3	1:H:334:ALA:C	2.31	0.56
1:H:289:GLU:HB3	1:H:347:LYS:NZ	2.21	0.56
1:A:113:ARG:O	1:D:113:ARG:O	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:VAL:HG13	1:B:333:ARG:HG3	1.86	0.56
1:B:353:PHE:O	1:B:357:LEU:HB2	2.06	0.56
1:C:224:ILE:HD13	1:C:224:ILE:C	2.31	0.56
1:E:130:ILE:CD1	1:E:151:MET:CE	2.84	0.56
1:E:148:PHE:CD1	1:F:120:TYR:HD1	2.24	0.56
1:E:203:LEU:CD1	1:E:226:ARG:HB3	2.36	0.56
1:E:204:ILE:CG2	1:E:205:TYR:CD2	2.88	0.56
1:G:245:GLU:OE1	1:G:246:GLU:OE1	2.23	0.56
1:A:158:ALA:CB	1:A:217:THR:O	2.54	0.56
1:B:272:VAL:CG2	1:B:273:GLN:HE22	2.19	0.56
1:B:350:ARG:O	1:B:353:PHE:CB	2.51	0.56
1:C:139:LEU:HD22	1:C:144:ARG:HA	1.86	0.56
1:C:175:ILE:HD11	1:C:196:GLY:N	2.20	0.56
1:C:282:VAL:O	1:C:333:ARG:HB2	2.06	0.56
1:C:295:GLU:O	1:C:344:LYS:N	2.39	0.56
1:D:158:ALA:HB2	1:D:217:THR:C	2.31	0.56
1:D:293:ILE:HG23	1:D:318:PRO:HA	1.88	0.56
1:E:269:LEU:HD23	1:E:348:LEU:HD11	1.87	0.56
1:F:269:LEU:HD23	1:F:348:LEU:HD11	1.87	0.56
1:G:170:ASP:H	1:G:209:ARG:NH2	2.03	0.56
1:G:366:ARG:CG	1:G:367:ASN:N	2.68	0.56
1:H:350:ARG:O	1:H:353:PHE:CB	2.54	0.56
1:A:157:ILE:HA	1:A:218:ASN:OD1	2.06	0.56
1:B:247:PHE:CE1	1:B:294:LEU:CA	2.86	0.56
1:B:311:VAL:CG1	1:B:312:GLU:N	2.69	0.56
1:B:366:ARG:O	1:B:369:GLN:CB	2.54	0.56
1:C:162:VAL:HG23	1:C:163:ILE:HG13	1.86	0.56
1:E:120:TYR:CE1	1:F:148:PHE:CD1	2.94	0.56
1:E:203:LEU:HD22	1:E:226:ARG:CG	2.36	0.56
1:G:265:VAL:C	1:G:269:LEU:HG	2.26	0.56
1:H:174:VAL:HA	1:H:196:GLY:O	2.06	0.56
1:H:182:VAL:HA	1:H:212:THR:O	2.06	0.56
1:A:261:GLU:O	1:A:262:ARG:C	2.49	0.55
1:B:226:ARG:O	1:B:227:ASP:C	2.50	0.55
1:B:282:VAL:O	1:B:285:GLU:CG	2.51	0.55
1:C:179:GLU:HG2	1:C:216:LYS:HD3	1.86	0.55
1:C:196:GLY:HA2	1:C:355:ARG:HH22	1.62	0.55
1:D:200:GLU:HG2	1:D:201:LEU:CD1	2.36	0.55
1:D:295:GLU:O	1:D:343:LEU:HD12	2.06	0.55
1:D:366:ARG:O	1:D:369:GLN:CB	2.54	0.55
1:E:278:GLN:HG3	1:E:279:LYS:N	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:113:ARG:HD3	1:F:146:ASP:OD2	2.05	0.55
1:G:162:VAL:HG23	1:G:163:ILE:N	2.21	0.55
1:G:174:VAL:CG1	1:G:222:TRP:HB2	2.37	0.55
1:A:144:ARG:CG	1:A:145:SER:N	2.69	0.55
1:A:158:ALA:HA	1:A:217:THR:O	2.07	0.55
1:A:183:TYR:HD1	1:A:188:TRP:CA	2.19	0.55
1:B:122:THR:O	1:B:125:ALA:HB3	2.07	0.55
1:B:260:TRP:CD2	2:B:401:CMP:N7	2.75	0.55
1:B:260:TRP:NE1	2:B:401:CMP:C8	2.68	0.55
1:C:158:ALA:CB	1:C:217:THR:O	2.54	0.55
1:C:321:TYR:C	1:C:321:TYR:HD1	2.14	0.55
1:F:159:GLY:C	1:H:243:MET:HE2	2.31	0.55
1:F:300:VAL:HA	1:F:336:THR:O	2.06	0.55
1:G:226:ARG:NH1	1:G:226:ARG:CG	2.56	0.55
1:H:182:VAL:CG2	1:H:190:THR:O	2.41	0.55
1:A:134:VAL:O	1:A:137:SER:HB3	2.07	0.55
1:A:205:TYR:HD2	1:A:205:TYR:N	2.04	0.55
1:A:273:GLN:CB	1:A:344:LYS:HA	2.36	0.55
1:A:278:GLN:CG	1:A:279:LYS:N	2.69	0.55
1:B:249:SER:CA	1:B:262:ARG:NH2	2.65	0.55
1:C:230:ARG:HA	1:C:234:MET:HE2	1.89	0.55
1:C:285:GLU:OE1	1:C:285:GLU:CA	2.54	0.55
1:C:293:ILE:HG23	1:C:318:PRO:HA	1.87	0.55
1:D:173:TYR:HB2	1:D:198:PHE:HE1	1.70	0.55
1:G:350:ARG:HB3	1:G:351:PRO:CD	2.32	0.55
1:H:224:ILE:O	1:H:224:ILE:HD13	2.07	0.55
1:H:353:PHE:O	1:H:357:LEU:HB2	2.05	0.55
1:C:158:ALA:CA	1:C:217:THR:O	2.54	0.55
1:C:171:ASN:H	1:C:209:ARG:HH22	1.53	0.55
1:C:327:LEU:HD23	1:C:353:PHE:CZ	2.41	0.55
1:D:259:LYS:C	1:D:262:ARG:HG2	2.25	0.55
1:E:260:TRP:NE1	2:E:401:CMP:H2'	2.20	0.55
1:G:242:LYS:HD3	1:G:242:LYS:N	2.15	0.55
1:G:371:TYR:OH	2:G:402:CMP:C2'	2.55	0.55
1:H:127:ALA:O	1:H:130:ILE:HG22	2.07	0.55
1:H:153:PRO:CB	1:H:222:TRP:CZ3	2.88	0.55
1:H:303:ARG:CB	1:H:310:PHE:CZ	2.90	0.55
1:H:353:PHE:CE1	1:H:357:LEU:HD22	2.41	0.55
1:A:112:VAL:CA	1:A:112:VAL:HB	2.17	0.55
1:A:144:ARG:O	1:A:147:ILE:HG12	2.06	0.55
1:A:173:TYR:CD2	1:A:198:PHE:CE1	2.85	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:LEU:HA	1:A:360:CYS:SG	2.46	0.55
1:B:131:GLU:C	1:B:133:ASN:N	2.59	0.55
1:B:182:VAL:CG2	1:B:190:THR:H	2.20	0.55
1:B:291:PHE:CD2	1:B:347:LYS:NZ	2.66	0.55
1:B:366:ARG:O	1:B:369:GLN:HB2	2.07	0.55
1:C:188:TRP:CZ3	1:C:190:THR:O	2.59	0.55
1:C:278:GLN:O	1:C:338:VAL:CA	2.53	0.55
1:D:300:VAL:HG12	1:D:314:GLY:C	2.30	0.55
1:E:154:VAL:O	1:E:221:LEU:N	2.29	0.55
1:E:260:TRP:CD2	2:E:401:CMP:C8	2.90	0.55
1:F:111:TYR:CD2	1:F:111:TYR:C	2.81	0.55
1:F:342:PRO:O	1:F:342:PRO:HG2	2.06	0.55
1:G:353:PHE:CE1	1:G:357:LEU:CD2	2.89	0.55
1:H:172:PHE:CE1	1:H:200:GLU:HB3	2.41	0.55
1:H:283:GLN:CG	1:H:333:ARG:O	2.55	0.55
1:A:126:LEU:O	1:A:126:LEU:CD1	2.41	0.55
1:A:135:LEU:CD1	1:A:135:LEU:C	2.78	0.55
1:C:247:PHE:HE1	1:C:294:LEU:CB	2.18	0.55
1:C:254:LEU:C	1:C:254:LEU:HD12	2.31	0.55
1:D:175:ILE:HG21	1:D:180:MET:HG3	1.87	0.55
1:D:239:ARG:O	1:D:240:LYS:C	2.49	0.55
1:E:131:GLU:N	1:E:131:GLU:CD	2.65	0.55
1:E:280:ILE:HB	1:E:291:PHE:CE2	2.41	0.55
1:F:133:ASN:O	1:F:135:LEU:HD12	2.07	0.55
1:F:173:TYR:CD2	1:F:198:PHE:CE1	2.94	0.55
1:F:310:PHE:O	1:F:311:VAL:HG13	2.07	0.55
1:G:153:PRO:CA	1:G:222:TRP:CZ3	2.89	0.55
1:G:247:PHE:CE1	1:G:294:LEU:HB3	2.41	0.55
1:G:256:SER:OG	1:G:363:ILE:CD1	2.55	0.55
1:A:111:TYR:CA	1:D:115:VAL:HG23	2.33	0.55
1:A:175:ILE:HD11	1:A:194:GLU:C	2.32	0.55
1:A:270:GLU:O	1:A:346:VAL:HA	2.06	0.55
1:B:152:PHE:CE2	1:B:223:GLY:C	2.84	0.55
1:B:260:TRP:NE1	2:B:401:CMP:N9	2.54	0.55
1:C:138:HIS:HD1	1:C:138:HIS:H	1.54	0.55
1:D:220:LYS:O	1:D:221:LEU:HD23	2.06	0.55
1:D:224:ILE:HD13	1:D:224:ILE:H	1.71	0.55
1:D:260:TRP:NE1	2:D:401:CMP:C2'	2.69	0.55
1:E:148:PHE:HD1	1:F:120:TYR:CD1	2.24	0.55
1:E:175:ILE:HD12	1:E:175:ILE:C	2.29	0.55
1:F:134:VAL:O	1:F:137:SER:HB3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:246:GLU:O	1:F:248:LEU:N	2.39	0.55
1:H:247:PHE:CE1	1:H:294:LEU:CB	2.89	0.55
1:H:274:PHE:CE2	1:H:280:ILE:HG22	2.42	0.55
1:H:365:LYS:O	1:H:368:ILE:N	2.30	0.55
1:A:113:ARG:NH2	1:D:115:VAL:CA	2.70	0.55
1:A:203:LEU:HD12	1:A:229:TYR:HD2	1.70	0.55
1:B:272:VAL:HG23	1:B:273:GLN:HE22	1.71	0.55
1:C:174:VAL:CG1	1:C:222:TRP:HB2	2.37	0.55
1:C:183:TYR:CD1	1:C:188:TRP:HB2	2.41	0.55
1:C:198:PHE:CD1	1:C:198:PHE:N	2.73	0.55
1:D:111:TYR:HH	1:D:113:ARG:C	2.14	0.55
1:D:127:ALA:O	1:D:130:ILE:N	2.38	0.55
1:D:152:PHE:CD1	1:D:152:PHE:O	2.60	0.55
1:E:162:VAL:HG22	1:E:213:VAL:O	2.07	0.55
1:E:302:GLN:O	1:E:309:GLU:O	2.24	0.55
1:F:179:GLU:CG	1:F:216:LYS:HD2	2.37	0.55
1:F:353:PHE:CE1	1:F:357:LEU:CD2	2.90	0.55
1:G:291:PHE:CD1	1:G:347:LYS:NZ	2.74	0.55
1:A:113:ARG:NH2	1:D:115:VAL:N	2.55	0.55
1:B:352:ARG:O	1:B:355:ARG:HB2	2.07	0.55
1:C:160:GLU:O	1:C:214:LYS:HA	2.06	0.55
1:C:260:TRP:NE1	2:C:401:CMP:H2'	2.16	0.55
1:D:317:GLY:O	1:D:320:ASP:HB2	2.06	0.55
1:E:175:ILE:HG22	1:E:221:LEU:CD2	2.37	0.55
1:E:282:VAL:O	1:E:285:GLU:CG	2.47	0.55
1:F:251:VAL:CG1	1:F:254:LEU:CD2	2.66	0.55
1:G:149:ASP:OD1	1:H:120:TYR:N	2.39	0.55
1:G:149:ASP:OD1	1:H:120:TYR:HB2	2.06	0.55
1:G:300:VAL:CG1	1:G:335:ALA:HB1	2.36	0.55
1:H:175:ILE:CD1	1:H:194:GLU:CA	2.85	0.55
1:H:196:GLY:HA2	1:H:355:ARG:HH21	1.70	0.55
1:A:111:TYR:CE2	1:A:113:ARG:N	2.75	0.55
1:A:151:MET:HA	1:A:224:ILE:HG22	1.88	0.55
1:A:175:ILE:HA	1:A:221:LEU:HD21	1.83	0.55
1:A:224:ILE:HD13	1:A:224:ILE:C	2.30	0.55
1:B:139:LEU:CD2	1:B:147:ILE:HD13	2.36	0.55
1:C:280:ILE:HD12	1:C:281:VAL:HG23	1.88	0.55
1:D:353:PHE:HE1	1:D:357:LEU:HD22	1.61	0.55
1:E:265:VAL:HG12	1:E:269:LEU:CG	2.36	0.55
1:G:123:MET:HE3	1:H:123:MET:HE3	1.90	0.55
1:H:300:VAL:CG2	1:H:314:GLY:O	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:301:LEU:CB	1:A:310:PHE:HE2	1.95	0.54
1:A:328:LEU:CD2	1:A:365:LYS:HE3	2.34	0.54
1:B:253:ILE:O	1:B:255:GLU:N	2.40	0.54
1:C:179:GLU:CG	1:C:216:LYS:HD2	2.32	0.54
1:E:147:ILE:O	1:E:148:PHE:C	2.50	0.54
1:G:188:TRP:CH2	1:G:190:THR:HA	2.42	0.54
1:A:115:VAL:CG2	1:D:111:TYR:CD2	2.90	0.54
1:A:253:ILE:CG2	1:A:321:TYR:HE2	2.21	0.54
1:A:325:ILE:CD1	1:A:334:ALA:HB3	2.37	0.54
1:B:134:VAL:HG11	1:B:268:ALA:CA	2.33	0.54
1:B:368:ILE:O	1:B:371:TYR:HB2	2.08	0.54
1:C:114:LYS:HD2	1:C:225:ASP:CG	2.32	0.54
1:C:329:MET:CE	1:C:329:MET:CA	2.81	0.54
1:D:175:ILE:HD11	1:D:193:GLY:O	2.07	0.54
1:E:270:GLU:HB2	1:E:271:PRO:CD	2.37	0.54
1:E:289:GLU:CG	1:E:347:LYS:NZ	2.66	0.54
1:E:318:PRO:O	1:E:319:SER:HB3	2.07	0.54
1:F:159:GLY:O	1:H:243:MET:HE2	2.08	0.54
1:F:211:ASP:OD1	1:F:211:ASP:N	2.39	0.54
1:F:300:VAL:O	1:F:312:GLU:HA	2.07	0.54
1:G:198:PHE:CD1	1:G:198:PHE:N	2.73	0.54
1:H:172:PHE:CD2	1:H:224:ILE:HD11	2.43	0.54
1:A:111:TYR:C	1:D:115:VAL:HG21	2.27	0.54
1:A:118:LYS:HB2	1:A:123:MET:HE1	1.89	0.54
1:A:177:GLN:HA	1:A:194:GLU:HG3	1.88	0.54
1:D:153:PRO:CA	1:D:222:TRP:HZ3	2.20	0.54
1:D:264:THR:O	1:D:265:VAL:C	2.49	0.54
1:A:239:ARG:O	1:A:240:LYS:C	2.48	0.54
1:B:204:ILE:HG23	1:B:234:MET:SD	2.47	0.54
1:C:120:TYR:CD1	1:D:148:PHE:HB3	2.37	0.54
1:C:135:LEU:CD1	1:C:136:PHE:N	2.71	0.54
1:C:363:ILE:O	1:C:366:ARG:CG	2.54	0.54
1:D:226:ARG:O	1:D:227:ASP:C	2.51	0.54
1:D:247:PHE:CZ	1:D:294:LEU:HA	2.41	0.54
1:D:357:LEU:O	1:D:360:CYS:HB2	2.08	0.54
1:E:280:ILE:HD12	1:E:281:VAL:CG2	2.37	0.54
1:F:153:PRO:CB	1:F:222:TRP:HZ3	2.19	0.54
1:F:253:ILE:HG21	1:F:321:TYR:CE2	2.42	0.54
1:F:260:TRP:CG	2:F:401:CMP:N7	2.75	0.54
1:F:325:ILE:O	1:F:328:LEU:N	2.41	0.54
1:G:116:ILE:CB	1:G:118:LYS:NZ	2.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:294:LEU:C	1:H:294:LEU:CD1	2.69	0.54
1:A:164:GLN:HA	1:A:212:THR:CG2	2.38	0.54
1:A:294:LEU:O	1:A:295:GLU:HG3	2.07	0.54
1:B:173:TYR:CD2	1:B:198:PHE:CE1	2.94	0.54
1:C:110:SER:CB	1:F:114:LYS:NZ	2.71	0.54
1:C:144:ARG:O	1:C:145:SER:C	2.49	0.54
1:C:171:ASN:OD1	1:C:225:ASP:HA	2.07	0.54
1:C:294:LEU:HD13	1:C:344:LYS:C	2.28	0.54
1:E:220:LYS:O	1:E:221:LEU:HD23	2.08	0.54
1:E:226:ARG:NH1	1:E:226:ARG:CG	2.61	0.54
1:E:348:LEU:CD2	1:E:356:VAL:CG2	2.86	0.54
1:E:368:ILE:O	1:E:371:TYR:HB2	2.07	0.54
1:F:130:ILE:CD1	1:F:151:MET:CE	2.85	0.54
1:F:182:VAL:O	1:F:182:VAL:CG2	2.45	0.54
1:G:224:ILE:HD13	1:G:224:ILE:C	2.30	0.54
1:G:260:TRP:CE2	2:G:401:CMP:C8	2.90	0.54
1:G:363:ILE:O	1:G:366:ARG:HG2	2.08	0.54
1:H:131:GLU:CD	1:H:131:GLU:H	2.15	0.54
1:H:164:GLN:HA	1:H:212:THR:HG22	1.89	0.54
1:H:291:PHE:HD2	1:H:322:PHE:CZ	2.20	0.54
1:H:295:GLU:HG2	1:H:318:PRO:CG	2.37	0.54
1:A:175:ILE:HD11	1:A:194:GLU:CA	2.37	0.54
1:A:226:ARG:O	1:A:227:ASP:C	2.50	0.54
1:A:316:LEU:CB	1:A:320:ASP:OD2	2.55	0.54
1:B:289:GLU:HG3	1:B:347:LYS:HZ1	1.71	0.54
1:C:131:GLU:O	1:C:133:ASN:N	2.40	0.54
1:C:246:GLU:O	1:C:249:SER:N	2.40	0.54
1:C:327:LEU:HD23	1:C:353:PHE:CD2	2.42	0.54
1:E:116:ILE:CG2	1:E:118:LYS:NZ	2.70	0.54
1:E:175:ILE:HD11	1:E:193:GLY:O	2.07	0.54
1:F:280:ILE:HD13	1:F:322:PHE:HZ	1.68	0.54
1:H:188:TRP:CZ3	1:H:190:THR:O	2.60	0.54
1:B:120:TYR:CE2	1:B:124:ALA:HB2	2.41	0.54
1:B:147:ILE:HG23	1:B:232:ILE:CD1	2.38	0.54
1:B:350:ARG:O	1:B:353:PHE:N	2.40	0.54
1:C:211:ASP:OD1	1:C:211:ASP:N	2.41	0.54
1:D:262:ARG:HA	1:D:265:VAL:CG2	2.38	0.54
1:D:300:VAL:HG13	1:D:314:GLY:H	1.72	0.54
1:E:152:PHE:HE2	1:E:223:GLY:C	2.16	0.54
1:E:265:VAL:O	1:E:269:LEU:CG	2.42	0.54
1:E:280:ILE:CD1	1:E:281:VAL:CG2	2.86	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:365:LYS:HA	1:F:368:ILE:CG1	2.38	0.54
1:G:183:TYR:HE1	1:G:188:TRP:HB2	1.70	0.54
1:G:255:GLU:OE1	1:G:255:GLU:CA	2.44	0.54
1:A:113:ARG:NH2	1:D:115:VAL:CG1	2.68	0.54
1:A:139:LEU:HB3	1:A:143:GLU:HB2	1.90	0.54
1:A:265:VAL:O	1:A:269:LEU:HG	2.08	0.54
1:A:273:GLN:HB3	1:A:344:LYS:HA	1.89	0.54
1:A:365:LYS:O	1:A:368:ILE:CG1	2.45	0.54
1:C:115:VAL:HA	1:C:149:ASP:CB	2.27	0.54
1:D:151:MET:HA	1:D:224:ILE:CG2	2.37	0.54
1:E:165:GLN:HG2	1:E:166:GLY:N	2.22	0.54
1:E:182:VAL:O	1:E:182:VAL:CG2	2.45	0.54
1:E:299:ALA:HB3	1:E:338:VAL:HG12	1.89	0.54
1:G:130:ILE:HG23	1:G:131:GLU:N	2.23	0.54
1:G:201:LEU:H	1:G:201:LEU:HD12	1.72	0.54
1:G:201:LEU:HD13	2:G:401:CMP:H2'	1.89	0.54
1:G:251:VAL:CG1	1:G:254:LEU:CD2	2.78	0.54
1:G:282:VAL:O	1:G:285:GLU:CG	2.56	0.54
1:H:300:VAL:O	1:H:312:GLU:CB	2.55	0.54
1:B:188:TRP:HH2	1:B:191:SER:HG	1.54	0.54
1:B:360:CYS:O	1:B:364:LEU:HD23	2.08	0.54
1:C:175:ILE:CD1	1:C:194:GLU:HA	2.35	0.54
1:C:329:MET:HA	1:C:329:MET:HE2	1.88	0.54
1:D:147:ILE:HG23	1:D:232:ILE:HD13	1.89	0.54
1:D:157:ILE:HD13	1:F:243:MET:HE1	1.88	0.54
1:E:226:ARG:HH11	1:E:226:ARG:CG	2.02	0.54
1:E:263:LEU:O	1:E:267:ASP:N	2.34	0.54
1:E:280:ILE:CG1	1:E:281:VAL:HG23	2.37	0.54
1:E:366:ARG:CG	1:E:367:ASN:N	2.70	0.54
1:F:241:ARG:O	1:F:242:LYS:C	2.45	0.54
1:G:121:LYS:O	1:G:122:THR:C	2.50	0.54
1:H:152:PHE:CD2	1:H:152:PHE:N	2.76	0.54
1:H:172:PHE:O	1:H:224:ILE:HD12	2.08	0.54
1:H:252:SER:OG	1:H:253:ILE:HG23	2.08	0.54
1:H:261:GLU:O	1:H:262:ARG:C	2.48	0.54
1:H:270:GLU:OE1	1:H:347:LYS:HB2	2.08	0.54
1:H:324:GLU:HB2	1:H:364:LEU:HD13	1.90	0.54
1:B:147:ILE:O	1:B:148:PHE:C	2.47	0.54
1:B:247:PHE:CZ	1:B:294:LEU:HA	2.43	0.54
1:C:112:VAL:HB	1:C:231:ARG:NH2	2.23	0.54
1:C:202:ALA:HB1	1:C:207:THR:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279:LYS:CE	1:C:336:THR:HG21	2.37	0.54
1:D:198:PHE:HD1	1:D:198:PHE:N	2.05	0.54
1:D:260:TRP:CD1	2:D:401:CMP:C5	2.96	0.54
1:E:285:GLU:OE1	1:E:285:GLU:HA	2.07	0.54
1:E:361:SER:O	1:E:364:LEU:HG	2.08	0.54
1:F:201:LEU:HD13	2:F:401:CMP:H2'	1.89	0.54
1:F:230:ARG:NH1	1:F:230:ARG:HG2	2.23	0.54
1:G:289:GLU:HG2	1:G:347:LYS:HZ3	1.73	0.54
1:H:165:GLN:HG2	1:H:166:GLY:N	2.21	0.54
1:H:245:GLU:OE1	1:H:246:GLU:N	2.40	0.54
1:H:273:GLN:HG3	1:H:344:LYS:HD2	1.90	0.54
1:H:325:ILE:HG13	1:H:326:ALA:H	1.72	0.54
1:A:153:PRO:HB3	1:A:222:TRP:HZ3	1.64	0.53
1:A:224:ILE:HD13	1:A:224:ILE:H	1.72	0.53
1:A:269:LEU:HD22	1:A:346:VAL:HG22	1.88	0.53
1:C:118:LYS:O	1:D:117:PRO:O	2.26	0.53
1:C:131:GLU:C	1:C:133:ASN:H	2.14	0.53
1:C:328:LEU:CD2	1:C:365:LYS:HE3	2.37	0.53
1:C:365:LYS:CA	1:C:368:ILE:HG13	2.37	0.53
1:D:175:ILE:HG22	1:D:221:LEU:HD21	1.89	0.53
1:E:135:LEU:HD12	1:E:135:LEU:N	2.23	0.53
1:E:173:TYR:CD2	1:E:198:PHE:CZ	2.96	0.53
1:F:274:PHE:CD2	1:F:280:ILE:HG22	2.43	0.53
1:F:316:LEU:HA	1:F:320:ASP:OD2	2.08	0.53
1:H:300:VAL:HA	1:H:336:THR:O	2.08	0.53
1:A:324:GLU:HB2	1:A:364:LEU:HD13	1.90	0.53
1:C:147:ILE:O	1:C:148:PHE:C	2.48	0.53
1:C:361:SER:C	1:C:365:LYS:NZ	2.67	0.53
1:E:224:ILE:CD1	1:E:224:ILE:H	2.22	0.53
1:F:175:ILE:HD11	1:F:193:GLY:O	2.08	0.53
1:F:224:ILE:CD1	1:F:224:ILE:H	2.20	0.53
1:F:263:LEU:O	1:F:267:ASP:N	2.35	0.53
1:G:153:PRO:CB	1:G:222:TRP:HZ3	2.19	0.53
1:G:253:ILE:HG13	1:G:254:LEU:CD2	2.38	0.53
1:H:131:GLU:C	1:H:133:ASN:N	2.65	0.53
1:H:162:VAL:CG2	1:H:213:VAL:O	2.56	0.53
1:H:230:ARG:NH1	1:H:230:ARG:HG2	2.23	0.53
1:A:120:TYR:HD2	1:A:120:TYR:O	1.86	0.53
1:A:153:PRO:HA	1:A:222:TRP:CZ3	2.42	0.53
1:A:269:LEU:CB	1:A:346:VAL:HG21	2.36	0.53
1:B:116:ILE:N	1:B:149:ASP:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:272:VAL:HG22	1:B:273:GLN:NE2	2.23	0.53
1:B:315:ARG:O	1:B:316:LEU:HD13	2.09	0.53
1:C:203:LEU:HD13	1:C:226:ARG:HB3	1.89	0.53
1:C:270:GLU:OE1	1:C:347:LYS:HB2	2.08	0.53
1:D:293:ILE:HG21	1:D:317:GLY:C	2.34	0.53
1:F:290:PHE:HB2	1:F:327:LEU:HD21	1.90	0.53
1:F:357:LEU:O	1:F:360:CYS:HB2	2.08	0.53
1:G:186:ASN:OD1	1:G:186:ASN:N	2.41	0.53
1:G:263:LEU:O	1:G:267:ASP:N	2.33	0.53
1:G:279:LYS:CB	1:G:279:LYS:HZ2	2.16	0.53
1:G:362:ASP:OD1	1:G:362:ASP:N	2.38	0.53
1:G:366:ARG:HG2	1:G:367:ASN:H	1.73	0.53
1:H:118:LYS:NZ	1:H:151:MET:O	2.35	0.53
1:H:253:ILE:O	1:H:255:GLU:N	2.41	0.53
1:H:325:ILE:CD1	1:H:334:ALA:HB3	2.37	0.53
1:A:165:GLN:CA	1:A:211:ASP:O	2.54	0.53
1:B:200:GLU:CD	1:B:201:LEU:HD11	2.33	0.53
1:B:302:GLN:O	1:B:310:PHE:HB3	2.09	0.53
1:D:200:GLU:OE2	1:D:201:LEU:HD11	2.08	0.53
1:D:229:TYR:O	1:D:233:LEU:HD12	2.08	0.53
1:E:116:ILE:HG13	1:E:152:PHE:HB3	1.89	0.53
1:F:158:ALA:HB1	1:F:216:LYS:O	2.08	0.53
1:F:362:ASP:N	1:F:362:ASP:OD1	2.41	0.53
1:G:203:LEU:HD12	1:G:229:TYR:HD2	1.73	0.53
1:G:371:TYR:HE1	2:G:402:CMP:C8	2.22	0.53
1:H:114:LYS:HZ2	1:H:115:VAL:N	2.05	0.53
1:H:241:ARG:O	1:H:242:LYS:C	2.50	0.53
1:H:265:VAL:HG12	1:H:269:LEU:HD11	1.91	0.53
1:A:144:ARG:HG2	1:A:145:SER:N	2.22	0.53
1:A:309:GLU:CG	1:A:310:PHE:N	2.72	0.53
1:B:158:ALA:CB	1:B:216:LYS:O	2.53	0.53
1:B:311:VAL:HG12	1:B:312:GLU:N	2.23	0.53
1:C:210:ALA:N	1:C:211:ASP:OD1	2.42	0.53
1:D:175:ILE:O	1:D:175:ILE:CD1	2.34	0.53
1:E:198:PHE:HD1	1:E:198:PHE:N	2.06	0.53
1:E:222:TRP:HA	1:E:222:TRP:HE3	1.73	0.53
1:E:247:PHE:HZ	1:E:293:ILE:O	1.92	0.53
1:F:293:ILE:HG21	1:F:317:GLY:C	2.34	0.53
1:G:175:ILE:CD1	1:G:193:GLY:O	2.57	0.53
1:H:229:TYR:CE1	1:H:233:LEU:CD1	2.79	0.53
1:A:111:TYR:O	1:A:112:VAL:HG13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:ILE:HG21	1:A:317:GLY:O	2.08	0.53
1:B:152:PHE:HD2	1:B:152:PHE:H	1.57	0.53
1:B:249:SER:HA	1:B:262:ARG:HH22	1.72	0.53
1:B:285:GLU:HA	1:B:285:GLU:OE1	2.08	0.53
1:B:325:ILE:CD1	1:B:334:ALA:CB	2.86	0.53
1:C:325:ILE:HG13	1:C:326:ALA:N	2.23	0.53
1:E:128:LYS:O	1:E:131:GLU:OE1	2.27	0.53
1:E:270:GLU:CB	1:E:271:PRO:CD	2.83	0.53
1:F:247:PHE:CD2	1:F:247:PHE:O	2.61	0.53
1:G:129:ALA:HA	1:G:132:LYS:HE3	1.89	0.53
1:G:280:ILE:HB	1:G:291:PHE:HE2	1.73	0.53
1:H:120:TYR:HD2	1:H:121:LYS:CA	2.20	0.53
1:H:204:ILE:CG2	1:H:205:TYR:HD2	2.18	0.53
1:H:279:LYS:HZ3	1:H:336:THR:HG23	1.70	0.53
1:A:260:TRP:CZ2	2:A:401:CMP:C8	2.91	0.53
1:C:246:GLU:O	1:C:248:LEU:N	2.40	0.53
1:C:300:VAL:HG23	1:C:313:VAL:H	1.73	0.53
1:D:201:LEU:HD13	2:D:401:CMP:H2'	1.90	0.53
1:D:211:ASP:OD1	1:D:211:ASP:N	2.40	0.53
1:E:274:PHE:CD2	1:E:343:LEU:HD23	2.43	0.53
1:F:203:LEU:HD22	1:F:226:ARG:CG	2.38	0.53
1:F:293:ILE:HG13	1:F:345:CYS:HG	1.72	0.53
1:G:135:LEU:CD1	1:G:136:PHE:N	2.72	0.53
1:G:273:GLN:N	1:G:273:GLN:CD	2.57	0.53
1:H:129:ALA:HA	1:H:132:LYS:HE3	1.90	0.53
1:H:134:VAL:O	1:H:137:SER:HB3	2.08	0.53
1:H:245:GLU:OE1	1:H:245:GLU:C	2.52	0.53
1:A:118:LYS:NZ	1:A:151:MET:O	2.36	0.53
1:B:157:ILE:HB	1:B:218:ASN:OD1	2.08	0.53
1:C:134:VAL:HG11	1:C:268:ALA:CA	2.24	0.53
1:C:229:TYR:CE1	1:C:233:LEU:CD1	2.81	0.53
1:D:203:LEU:HD22	1:D:226:ARG:CB	2.38	0.53
1:D:260:TRP:CD1	2:D:401:CMP:C4	2.96	0.53
1:D:294:LEU:O	1:D:295:GLU:HG3	2.09	0.53
1:E:205:TYR:HD2	1:E:205:TYR:N	2.07	0.53
1:E:273:GLN:HB2	1:E:343:LEU:O	2.09	0.53
1:E:289:GLU:CG	1:E:347:LYS:HZ1	2.22	0.53
1:E:325:ILE:HG12	2:E:402:CMP:P	2.49	0.53
1:F:297:SER:O	1:F:340:ARG:HB2	2.08	0.53
1:F:328:LEU:HD23	1:F:365:LYS:HE3	1.90	0.53
1:G:205:TYR:HD2	1:G:205:TYR:N	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:139:LEU:N	1:H:139:LEU:CD1	2.69	0.53
1:H:144:ARG:O	1:H:145:SER:C	2.51	0.53
1:A:291:PHE:HB2	1:A:322:PHE:CE1	2.44	0.53
1:B:261:GLU:O	1:B:265:VAL:HG23	2.08	0.53
1:C:204:ILE:HG21	1:C:205:TYR:CE2	2.44	0.53
1:D:180:MET:HB2	1:D:192:VAL:HG12	1.91	0.53
1:D:233:LEU:CD1	1:D:233:LEU:N	2.46	0.53
1:D:371:TYR:CZ	2:D:402:CMP:C8	2.91	0.53
1:E:203:LEU:HD13	1:E:226:ARG:CB	2.37	0.53
1:F:203:LEU:CD1	1:F:229:TYR:HD2	2.22	0.53
1:G:116:ILE:HG21	1:G:118:LYS:NZ	2.22	0.53
1:G:294:LEU:HD11	1:G:345:CYS:C	2.34	0.53
1:H:147:ILE:CG1	1:H:148:PHE:N	2.72	0.53
1:H:246:GLU:C	1:H:248:LEU:N	2.59	0.53
1:A:133:ASN:C	1:A:133:ASN:OD1	2.51	0.53
1:A:147:ILE:HG22	1:A:232:ILE:HD13	1.90	0.53
1:A:278:GLN:HG3	1:A:279:LYS:N	2.22	0.53
1:B:291:PHE:CE2	1:B:347:LYS:NZ	2.77	0.53
1:B:315:ARG:C	1:B:316:LEU:HD13	2.34	0.53
1:C:135:LEU:CD1	1:C:136:PHE:H	2.20	0.53
1:C:203:LEU:HD12	1:C:229:TYR:CD2	2.44	0.53
1:C:248:LEU:HD21	1:C:265:VAL:CG1	2.39	0.53
1:C:253:ILE:HG13	1:C:254:LEU:HD23	1.90	0.53
1:C:350:ARG:O	1:C:353:PHE:N	2.42	0.53
1:D:138:HIS:H	1:D:138:HIS:HD1	1.57	0.53
1:D:175:ILE:CD1	1:D:195:GLY:H	2.22	0.53
1:E:329:MET:HA	1:E:329:MET:HE2	1.88	0.53
1:F:113:ARG:NE	1:F:146:ASP:CG	2.67	0.53
1:F:153:PRO:CA	1:F:222:TRP:HZ3	2.21	0.53
1:G:353:PHE:CE1	1:G:357:LEU:HD22	2.44	0.53
1:H:157:ILE:O	1:H:158:ALA:C	2.51	0.53
1:H:300:VAL:O	1:H:312:GLU:HA	2.09	0.53
1:H:313:VAL:CG1	1:H:314:GLY:N	2.71	0.53
1:A:178:GLY:HA3	1:A:219:VAL:CG1	2.17	0.52
1:A:182:VAL:O	1:A:182:VAL:CG2	2.51	0.52
1:A:356:VAL:CG2	1:A:357:LEU:N	2.71	0.52
1:B:161:THR:OG1	1:B:214:LYS:NZ	2.31	0.52
1:B:177:GLN:O	1:B:219:VAL:HB	2.08	0.52
1:C:230:ARG:HG2	1:C:234:MET:HE1	1.91	0.52
1:D:272:VAL:HG22	1:D:273:GLN:H	1.74	0.52
1:F:203:LEU:HD22	1:F:226:ARG:CB	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:254:LEU:HB2	1:F:257:LEU:HD12	1.91	0.52
1:G:196:GLY:HA2	1:G:355:ARG:CZ	2.37	0.52
1:G:280:ILE:HD12	1:G:281:VAL:HG23	1.90	0.52
1:H:111:TYR:HE2	1:H:112:VAL:HG12	1.69	0.52
1:C:120:TYR:CD2	1:C:121:LYS:HA	2.41	0.52
1:C:157:ILE:C	1:C:157:ILE:CD1	2.83	0.52
1:D:139:LEU:N	1:D:139:LEU:CD1	2.65	0.52
1:E:128:LYS:O	1:E:129:ALA:C	2.52	0.52
1:G:122:THR:O	1:G:125:ALA:HB3	2.09	0.52
1:G:171:ASN:H	1:G:209:ARG:HH22	1.58	0.52
1:A:233:LEU:H	1:A:233:LEU:CD1	2.00	0.52
1:A:253:ILE:CG2	1:A:321:TYR:CE2	2.93	0.52
1:B:252:SER:C	1:B:253:ILE:HG12	2.33	0.52
1:C:175:ILE:CD1	1:C:195:GLY:N	2.73	0.52
1:C:284:GLY:HA2	1:C:332:PRO:HB3	1.88	0.52
1:C:352:ARG:HA	1:C:355:ARG:HB2	1.91	0.52
1:D:280:ILE:HD11	1:D:322:PHE:CE2	2.43	0.52
1:E:164:GLN:O	1:E:167:ASP:HB2	2.10	0.52
1:E:243:MET:HE2	1:G:159:GLY:C	2.32	0.52
1:F:280:ILE:HB	1:F:291:PHE:HE2	1.74	0.52
1:F:282:VAL:O	1:F:285:GLU:HG3	2.09	0.52
1:F:290:PHE:C	1:F:291:PHE:CD1	2.79	0.52
1:G:130:ILE:CD1	1:G:151:MET:CE	2.87	0.52
1:A:365:LYS:O	1:A:368:ILE:N	2.32	0.52
1:B:225:ASP:OD1	1:B:225:ASP:N	2.32	0.52
1:B:247:PHE:HE1	1:B:294:LEU:CA	2.12	0.52
1:B:253:ILE:HG13	1:B:254:LEU:CG	2.40	0.52
1:B:328:LEU:HD22	1:B:365:LYS:HE3	1.90	0.52
1:C:121:LYS:O	1:C:122:THR:C	2.52	0.52
1:C:243:MET:HE1	1:E:158:ALA:O	2.10	0.52
1:C:301:LEU:HD12	1:C:336:THR:O	2.10	0.52
1:D:128:LYS:O	1:D:129:ALA:C	2.49	0.52
1:E:253:ILE:CG2	1:E:321:TYR:HE2	2.21	0.52
1:F:262:ARG:HA	1:F:265:VAL:HG21	1.91	0.52
1:G:182:VAL:CG2	1:G:190:THR:O	2.41	0.52
1:G:280:ILE:HD11	1:G:322:PHE:CE2	2.39	0.52
1:H:300:VAL:HG23	1:H:314:GLY:O	2.09	0.52
1:A:154:VAL:CG1	1:A:221:LEU:HB2	2.28	0.52
1:B:316:LEU:HD12	1:B:320:ASP:OD2	2.10	0.52
1:C:229:TYR:HE1	1:C:233:LEU:HD13	1.70	0.52
1:D:246:GLU:O	1:D:248:LEU:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:280:ILE:HD11	1:D:322:PHE:HE2	1.74	0.52
1:E:162:VAL:HG23	1:E:163:ILE:H	1.75	0.52
1:E:233:LEU:O	1:E:234:MET:C	2.51	0.52
1:E:239:ARG:HD3	1:G:157:ILE:HG12	1.91	0.52
1:F:312:GLU:CD	1:F:340:ARG:HH12	2.16	0.52
1:F:348:LEU:HD21	1:F:356:VAL:CG2	2.33	0.52
1:G:211:ASP:OD2	2:G:401:CMP:C5'	2.53	0.52
1:G:318:PRO:O	1:G:319:SER:HB3	2.10	0.52
1:G:357:LEU:HD12	1:G:357:LEU:N	2.16	0.52
1:H:125:ALA:O	1:H:128:LYS:HB3	2.09	0.52
1:A:291:PHE:CD1	1:A:347:LYS:NZ	2.75	0.52
1:B:129:ALA:HA	1:B:132:LYS:HE3	1.92	0.52
1:B:183:TYR:CD1	1:B:188:TRP:CB	2.92	0.52
1:B:198:PHE:CD1	1:B:198:PHE:N	2.71	0.52
1:C:183:TYR:HE1	1:C:188:TRP:HB2	1.72	0.52
1:C:279:LYS:HE3	1:C:282:VAL:HG22	1.91	0.52
1:D:156:PHE:HE2	1:D:162:VAL:HG12	1.61	0.52
1:D:182:VAL:CG2	1:D:190:THR:H	2.22	0.52
1:D:186:ASN:OD1	1:D:186:ASN:N	2.41	0.52
1:F:126:LEU:O	1:F:127:ALA:C	2.51	0.52
1:F:161:THR:CA	1:F:214:LYS:HD2	2.30	0.52
1:G:327:LEU:HD23	1:G:353:PHE:CZ	2.45	0.52
1:H:272:VAL:N	1:H:345:CYS:O	2.42	0.52
1:H:298:ALA:N	1:H:316:LEU:O	2.42	0.52
1:A:204:ILE:HD13	1:A:238:LEU:HD11	1.91	0.52
1:A:247:PHE:CE1	1:A:294:LEU:HB3	2.45	0.52
1:B:252:SER:C	1:B:253:ILE:CG1	2.83	0.52
1:C:138:HIS:O	1:C:139:LEU:C	2.50	0.52
1:E:270:GLU:OE1	1:E:270:GLU:N	2.42	0.52
1:F:112:VAL:CG1	1:F:113:ARG:H	2.00	0.52
1:F:164:GLN:O	1:F:167:ASP:HB2	2.10	0.52
1:G:285:GLU:OE1	1:G:285:GLU:CA	2.53	0.52
1:H:175:ILE:CD1	1:H:195:GLY:N	2.73	0.52
1:A:205:TYR:CD2	1:A:205:TYR:N	2.76	0.52
1:B:180:MET:O	1:B:191:SER:HA	2.10	0.52
1:B:204:ILE:HG22	1:B:205:TYR:HD2	1.74	0.52
1:B:280:ILE:CD1	1:B:337:VAL:HB	2.39	0.52
1:B:322:PHE:N	1:B:322:PHE:CD1	2.76	0.52
1:C:119:ASP:HA	1:D:117:PRO:HA	1.92	0.52
1:C:269:LEU:HB2	1:C:346:VAL:CG2	2.28	0.52
1:C:300:VAL:HG22	1:C:312:GLU:OE2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:GLN:CD	1:C:374:PHE:CB	2.83	0.52
1:D:182:VAL:HG12	1:D:213:VAL:CG2	2.27	0.52
1:D:324:GLU:HB2	1:D:364:LEU:HD13	1.92	0.52
1:E:152:PHE:CD2	1:E:152:PHE:C	2.81	0.52
1:E:176:ASP:O	1:E:194:GLU:HG2	2.09	0.52
1:E:252:SER:O	1:E:255:GLU:HB2	2.10	0.52
1:E:260:TRP:CD2	2:E:401:CMP:N7	2.77	0.52
1:F:248:LEU:HD11	1:F:265:VAL:HG11	1.92	0.52
1:G:205:TYR:CD2	1:G:205:TYR:N	2.78	0.52
1:H:266:ALA:HA	1:H:269:LEU:CD1	2.37	0.52
1:A:182:VAL:CG2	1:A:190:THR:H	2.23	0.52
1:A:327:LEU:HD23	1:A:353:PHE:CD1	2.45	0.52
1:B:173:TYR:HD1	1:B:223:GLY:CA	2.23	0.52
1:C:158:ALA:HA	1:C:217:THR:O	2.09	0.52
1:C:161:THR:CA	1:C:214:LYS:HD2	2.32	0.52
1:C:198:PHE:HD1	1:C:198:PHE:N	2.07	0.52
1:C:204:ILE:HG21	1:C:205:TYR:HE2	1.75	0.52
1:D:366:ARG:O	1:D:369:GLN:HB2	2.09	0.52
1:E:121:LYS:O	1:E:125:ALA:N	2.36	0.52
1:E:153:PRO:CA	1:E:222:TRP:CZ3	2.93	0.52
1:F:130:ILE:HG21	1:F:148:PHE:CE2	2.43	0.52
1:F:253:ILE:HD13	1:F:321:TYR:CD2	2.45	0.52
1:F:272:VAL:CA	1:F:273:GLN:NE2	2.73	0.52
1:F:273:GLN:CB	1:F:344:LYS:HA	2.40	0.52
1:F:283:GLN:HG3	1:F:335:ALA:N	2.25	0.52
1:G:274:PHE:HD2	1:G:343:LEU:HD23	1.75	0.52
1:H:130:ILE:CD1	1:H:151:MET:CE	2.88	0.52
1:H:130:ILE:HD12	1:H:136:PHE:CE2	2.45	0.52
1:H:135:LEU:HD13	1:H:136:PHE:CD1	2.45	0.52
1:H:230:ARG:CZ	1:H:234:MET:CE	2.80	0.52
1:A:175:ILE:HG21	1:A:180:MET:HG3	1.92	0.52
1:A:253:ILE:C	1:A:255:GLU:H	2.16	0.52
1:B:176:ASP:O	1:B:194:GLU:HG2	2.10	0.52
1:B:200:GLU:CG	1:B:201:LEU:HD12	2.36	0.52
1:C:113:ARG:HG2	1:F:112:VAL:HG11	1.88	0.52
1:C:262:ARG:O	1:C:265:VAL:HB	2.11	0.52
1:C:265:VAL:C	1:C:269:LEU:HD11	2.35	0.52
1:D:325:ILE:CD1	1:D:334:ALA:HB3	2.39	0.52
1:E:293:ILE:HG22	1:E:320:ASP:O	2.10	0.52
1:F:325:ILE:HD11	1:F:334:ALA:H	1.75	0.52
1:F:325:ILE:CD1	1:F:334:ALA:CB	2.88	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:175:ILE:HD11	1:H:195:GLY:N	2.25	0.52
1:H:272:VAL:HG22	1:H:273:GLN:H	1.75	0.52
1:H:285:GLU:HB3	1:H:286:PRO:CD	2.39	0.52
1:A:121:LYS:O	1:A:124:ALA:N	2.44	0.51
1:B:139:LEU:HD21	1:B:147:ILE:CD1	2.40	0.51
1:B:151:MET:HA	1:B:224:ILE:HG22	1.91	0.51
1:B:211:ASP:OD2	2:B:401:CMP:O4'	2.27	0.51
1:B:293:ILE:HG21	1:B:317:GLY:C	2.35	0.51
1:B:366:ARG:CG	1:B:367:ASN:N	2.72	0.51
1:C:110:SER:CA	1:F:114:LYS:HZ3	2.24	0.51
1:C:116:ILE:HB	1:C:118:LYS:NZ	2.26	0.51
1:D:112:VAL:HB	1:D:113:ARG:HG3	1.92	0.51
1:D:135:LEU:HD13	1:D:136:PHE:CD1	2.45	0.51
1:D:325:ILE:O	1:D:328:LEU:N	2.43	0.51
1:E:118:LYS:NZ	1:E:151:MET:O	2.43	0.51
1:E:123:MET:HE2	1:F:123:MET:HE3	1.93	0.51
1:E:129:ALA:CB	1:E:222:TRP:HE1	2.23	0.51
1:G:253:ILE:HG13	1:G:254:LEU:N	2.25	0.51
1:H:261:GLU:O	1:H:265:VAL:HG23	2.09	0.51
1:H:324:GLU:HB2	1:H:364:LEU:CD1	2.40	0.51
1:A:174:VAL:HA	1:A:196:GLY:O	2.11	0.51
1:B:118:LYS:CB	1:B:123:MET:HE1	2.40	0.51
1:B:136:PHE:HE1	1:B:233:LEU:CD2	2.23	0.51
1:C:152:PHE:HD2	1:C:152:PHE:H	1.59	0.51
1:C:157:ILE:O	1:C:158:ALA:O	2.28	0.51
1:C:165:GLN:HG2	1:C:166:GLY:N	2.24	0.51
1:C:265:VAL:CG1	1:C:269:LEU:CD2	2.83	0.51
1:C:311:VAL:HG23	1:C:312:GLU:H	1.75	0.51
1:D:113:ARG:HH22	1:D:142:ASN:HD21	1.58	0.51
1:D:119:ASP:O	1:D:120:TYR:C	2.53	0.51
1:D:293:ILE:CG2	1:D:318:PRO:HA	2.40	0.51
1:E:120:TYR:HD2	1:E:121:LYS:HA	1.75	0.51
1:E:161:THR:HA	1:E:214:LYS:CD	2.35	0.51
1:F:173:TYR:CD2	1:F:198:PHE:CZ	2.98	0.51
1:F:327:LEU:HD23	1:F:353:PHE:CE2	2.44	0.51
1:G:154:VAL:O	1:G:221:LEU:N	2.30	0.51
1:G:203:LEU:HD22	1:G:226:ARG:CB	2.39	0.51
1:G:247:PHE:CE1	1:G:294:LEU:CA	2.88	0.51
1:G:371:TYR:CE1	2:G:402:CMP:C8	2.93	0.51
1:A:200:GLU:HG2	1:A:201:LEU:N	2.24	0.51
1:A:366:ARG:CG	1:A:367:ASN:N	2.72	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:GLN:HA	1:B:212:THR:CG2	2.40	0.51
1:B:272:VAL:C	1:B:273:GLN:NE2	2.66	0.51
1:C:162:VAL:CG2	1:C:213:VAL:O	2.58	0.51
1:D:247:PHE:HE1	1:D:294:LEU:CB	2.23	0.51
1:E:262:ARG:HA	1:E:265:VAL:HG21	1.93	0.51
1:F:174:VAL:CG1	1:F:222:TRP:HB2	2.41	0.51
1:F:272:VAL:C	1:F:273:GLN:NE2	2.68	0.51
1:F:291:PHE:CD1	1:F:347:LYS:NZ	2.78	0.51
1:F:310:PHE:O	1:F:311:VAL:CG1	2.58	0.51
1:G:201:LEU:O	1:G:204:ILE:N	2.44	0.51
1:H:352:ARG:O	1:H:353:PHE:C	2.52	0.51
1:A:126:LEU:C	1:A:126:LEU:CD1	2.81	0.51
1:A:135:LEU:CD1	1:A:136:PHE:CG	2.94	0.51
1:A:269:LEU:CB	1:A:346:VAL:CG2	2.80	0.51
1:B:255:GLU:O	1:B:256:SER:C	2.53	0.51
1:B:284:GLY:C	1:B:332:PRO:HB3	2.36	0.51
1:C:114:LYS:HD2	1:C:225:ASP:OD1	2.11	0.51
1:C:135:LEU:HD13	1:C:136:PHE:CG	2.45	0.51
1:C:348:LEU:HD21	1:C:356:VAL:CG2	2.39	0.51
1:E:111:TYR:CD2	1:E:112:VAL:N	2.65	0.51
1:E:275:GLU:O	1:E:278:GLN:HB3	2.10	0.51
1:F:198:PHE:HD1	1:F:198:PHE:O	1.93	0.51
1:G:174:VAL:HG13	1:G:222:TRP:HB2	1.92	0.51
1:G:253:ILE:CD1	1:G:321:TYR:CD2	2.92	0.51
1:G:265:VAL:C	1:G:269:LEU:HD11	2.35	0.51
1:H:294:LEU:O	1:H:295:GLU:CG	2.59	0.51
1:A:135:LEU:HD12	1:A:135:LEU:N	2.24	0.51
1:A:290:PHE:HB2	1:A:327:LEU:HD21	1.92	0.51
1:A:296:GLY:O	1:A:318:PRO:HD3	2.09	0.51
1:A:371:TYR:CD1	2:A:402:CMP:C5	2.98	0.51
1:C:120:TYR:CE1	1:D:148:PHE:CG	2.98	0.51
1:C:130:ILE:HG13	1:C:136:PHE:CG	2.45	0.51
1:C:279:LYS:CB	1:C:337:VAL:O	2.59	0.51
1:E:109:ALA:HB1	1:H:114:LYS:HE2	1.92	0.51
1:E:140:ASP:N	1:E:143:GLU:OE1	2.42	0.51
1:E:196:GLY:HA2	1:E:355:ARG:CZ	2.35	0.51
1:F:226:ARG:HA	1:F:229:TYR:HB3	1.92	0.51
1:G:293:ILE:HG13	1:G:345:CYS:HG	1.69	0.51
1:G:293:ILE:CG2	1:G:318:PRO:HA	2.41	0.51
1:A:309:GLU:CG	1:A:310:PHE:H	2.23	0.51
1:A:371:TYR:CE1	2:A:402:CMP:C5	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:TYR:CD2	1:C:120:TYR:O	2.64	0.51
1:C:157:ILE:O	1:C:158:ALA:C	2.51	0.51
1:C:247:PHE:CE1	1:C:294:LEU:CB	2.93	0.51
1:C:335:ALA:HB3	2:C:402:CMP:H5'1	1.93	0.51
1:D:131:GLU:N	1:D:131:GLU:CD	2.68	0.51
1:E:211:ASP:OD1	1:E:211:ASP:N	2.43	0.51
1:G:342:PRO:O	1:G:342:PRO:HG2	2.10	0.51
1:H:152:PHE:CD2	1:H:152:PHE:C	2.87	0.51
1:H:311:VAL:HG23	1:H:312:GLU:H	1.76	0.51
1:A:285:GLU:OE1	1:A:285:GLU:CA	2.59	0.51
1:B:325:ILE:HG12	2:B:402:CMP:O3'	2.11	0.51
1:B:362:ASP:N	1:B:365:LYS:HZ2	2.08	0.51
1:D:134:VAL:O	1:D:137:SER:HB3	2.11	0.51
1:D:173:TYR:CB	1:D:198:PHE:HE1	2.24	0.51
1:D:324:GLU:HG2	1:D:325:ILE:HG23	1.93	0.51
1:E:152:PHE:HD2	1:E:152:PHE:N	2.02	0.51
1:F:144:ARG:O	1:F:147:ILE:HG12	2.11	0.51
1:F:253:ILE:HD13	1:F:321:TYR:CE2	2.46	0.51
1:F:279:LYS:CB	1:F:279:LYS:HZ2	2.19	0.51
1:F:350:ARG:O	1:F:353:PHE:CB	2.53	0.51
1:G:177:GLN:HA	1:G:194:GLU:CG	2.40	0.51
1:G:249:SER:HA	1:G:262:ARG:HH22	1.73	0.51
1:A:246:GLU:O	1:A:248:LEU:N	2.43	0.51
1:B:130:ILE:CD1	1:B:151:MET:HE3	2.39	0.51
1:B:260:TRP:NE1	2:B:401:CMP:C4	2.78	0.51
1:C:158:ALA:HA	1:C:215:ALA:HB1	1.92	0.51
1:C:235:GLY:O	1:C:238:LEU:N	2.43	0.51
1:C:365:LYS:HA	1:C:368:ILE:HG13	1.93	0.51
1:D:165:GLN:CA	1:D:211:ASP:O	2.56	0.51
1:D:261:GLU:O	1:D:264:THR:N	2.44	0.51
1:D:302:GLN:HG3	1:D:313:VAL:CG1	2.40	0.51
1:E:113:ARG:NH1	1:H:112:VAL:HG23	2.25	0.51
1:E:316:LEU:HA	1:E:320:ASP:OD2	2.10	0.51
1:F:182:VAL:CG2	1:F:190:THR:H	2.23	0.51
1:F:274:PHE:HB2	1:F:343:LEU:HB3	1.93	0.51
1:G:224:ILE:CD1	1:G:224:ILE:H	2.23	0.51
1:G:293:ILE:HA	1:G:345:CYS:SG	2.51	0.51
1:H:173:TYR:HB3	1:H:222:TRP:O	2.11	0.51
1:H:255:GLU:OE1	1:H:255:GLU:CA	2.51	0.51
1:H:293:ILE:CG2	1:H:317:GLY:C	2.84	0.51
1:A:177:GLN:HA	1:A:194:GLU:CG	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:TYR:HD1	1:A:188:TRP:HB2	1.76	0.51
1:A:293:ILE:HG21	1:A:317:GLY:C	2.36	0.51
1:C:110:SER:C	1:F:114:LYS:HZ3	2.19	0.51
1:C:152:PHE:CD2	1:C:152:PHE:N	2.79	0.51
1:C:190:THR:HG22	1:C:191:SER:N	2.11	0.51
1:D:209:ARG:HD2	2:D:401:CMP:O5'	2.10	0.51
1:E:144:ARG:O	1:E:145:SER:C	2.54	0.51
1:E:269:LEU:HB2	1:E:346:VAL:CG2	2.39	0.51
1:E:269:LEU:HB2	1:E:346:VAL:HG21	1.92	0.51
1:E:293:ILE:HG23	1:E:318:PRO:HA	1.91	0.51
1:F:113:ARG:HB3	1:F:146:ASP:OD2	2.11	0.51
1:F:162:VAL:HG23	1:F:163:ILE:H	1.73	0.51
1:G:265:VAL:C	1:G:269:LEU:CD1	2.84	0.51
1:G:300:VAL:HG23	1:G:316:LEU:HD11	1.91	0.51
1:H:118:LYS:HE2	1:H:148:PHE:O	2.10	0.51
1:H:186:ASN:N	1:H:186:ASN:OD1	2.43	0.51
1:H:285:GLU:HB2	1:H:333:ARG:HG3	1.92	0.51
1:A:130:ILE:CD1	1:A:151:MET:HE3	2.40	0.51
1:A:204:ILE:CG2	1:A:205:TYR:CD2	2.92	0.51
1:B:110:SER:O	1:B:111:TYR:HB2	2.10	0.51
1:B:174:VAL:HA	1:B:196:GLY:O	2.10	0.51
1:C:158:ALA:CB	1:C:216:LYS:O	2.55	0.51
1:C:220:LYS:C	1:C:221:LEU:HD23	2.35	0.51
1:C:272:VAL:N	1:C:345:CYS:O	2.44	0.51
1:D:126:LEU:O	1:D:127:ALA:C	2.52	0.51
1:D:157:ILE:HG23	1:F:239:ARG:NH1	2.26	0.51
1:D:253:ILE:C	1:D:255:GLU:H	2.19	0.51
1:E:269:LEU:HD23	1:E:348:LEU:HD13	1.92	0.51
1:F:266:ALA:O	1:F:268:ALA:N	2.44	0.51
1:F:296:GLY:CA	1:F:342:PRO:O	2.58	0.51
1:F:331:ARG:HB3	1:F:332:PRO:HD2	1.91	0.51
1:G:116:ILE:HG13	1:G:152:PHE:HB3	1.93	0.51
1:G:135:LEU:HD12	1:G:135:LEU:N	2.26	0.51
1:G:248:LEU:CB	1:G:262:ARG:HH21	2.24	0.51
1:H:175:ILE:HD11	1:H:194:GLU:C	2.35	0.51
1:H:251:VAL:CG2	1:H:319:SER:O	2.58	0.51
1:H:280:ILE:HB	1:H:291:PHE:CE2	2.40	0.51
1:H:300:VAL:HG23	1:H:314:GLY:N	2.19	0.51
1:A:296:GLY:HA3	1:A:343:LEU:HA	1.93	0.50
1:A:366:ARG:HG2	1:A:367:ASN:H	1.75	0.50
1:B:239:ARG:C	1:B:241:ARG:H	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:SER:HA	1:B:262:ARG:NH2	2.26	0.50
1:C:265:VAL:HG12	1:C:269:LEU:CD2	2.41	0.50
1:F:116:ILE:N	1:F:149:ASP:O	2.36	0.50
1:H:143:GLU:HB3	1:H:232:ILE:HD11	1.92	0.50
1:H:203:LEU:HD12	1:H:229:TYR:HD2	1.71	0.50
1:H:362:ASP:N	1:H:362:ASP:OD1	2.44	0.50
1:A:161:THR:HG23	1:A:214:LYS:HD3	1.93	0.50
1:A:247:PHE:CE1	1:A:294:LEU:CA	2.85	0.50
1:B:162:VAL:HG23	1:B:163:ILE:N	2.25	0.50
1:C:157:ILE:O	1:C:160:GLU:HB2	2.11	0.50
1:C:180:MET:O	1:C:191:SER:HA	2.11	0.50
1:C:260:TRP:CD1	2:C:401:CMP:C4	2.99	0.50
1:D:139:LEU:HD21	1:D:147:ILE:CD1	2.41	0.50
1:D:230:ARG:HG2	1:D:230:ARG:HH11	1.75	0.50
1:D:241:ARG:O	1:D:242:LYS:C	2.52	0.50
1:D:268:ALA:C	1:D:269:LEU:O	2.45	0.50
1:E:130:ILE:HD13	1:E:151:MET:CE	2.41	0.50
1:E:247:PHE:C	1:E:247:PHE:HD2	2.18	0.50
1:F:153:PRO:HA	1:F:222:TRP:CE3	2.46	0.50
1:F:247:PHE:C	1:F:247:PHE:HD2	2.17	0.50
1:F:300:VAL:HG13	1:F:335:ALA:HB1	1.84	0.50
1:G:268:ALA:O	1:G:352:ARG:NH1	2.44	0.50
1:H:357:LEU:N	1:H:357:LEU:HD12	2.19	0.50
1:H:366:ARG:O	1:H:369:GLN:HB2	2.11	0.50
1:A:130:ILE:CG2	1:A:131:GLU:N	2.74	0.50
1:B:171:ASN:HB3	1:B:224:ILE:O	2.10	0.50
1:C:165:GLN:N	1:C:212:THR:CG2	2.50	0.50
1:E:143:GLU:O	1:E:144:ARG:C	2.54	0.50
1:E:158:ALA:HA	1:E:215:ALA:HB1	1.94	0.50
1:E:179:GLU:CG	1:E:216:LYS:HD2	2.42	0.50
1:E:230:ARG:HG2	1:E:230:ARG:HH11	1.76	0.50
1:F:152:PHE:CE2	1:F:223:GLY:CA	2.91	0.50
1:F:226:ARG:O	1:F:227:ASP:C	2.53	0.50
1:F:293:ILE:HG21	1:F:317:GLY:O	2.11	0.50
1:G:175:ILE:HG22	1:G:221:LEU:HD21	1.94	0.50
1:G:371:TYR:CD1	2:G:402:CMP:C6	2.99	0.50
1:H:158:ALA:HB2	1:H:218:ASN:N	2.24	0.50
1:H:185:ASN:N	1:H:185:ASN:OD1	2.45	0.50
1:H:208:PRO:O	1:H:209:ARG:C	2.54	0.50
1:A:293:ILE:HG23	1:A:318:PRO:HA	1.93	0.50
1:B:297:SER:O	1:B:340:ARG:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:362:ASP:HA	1:B:365:LYS:NZ	2.26	0.50
1:D:157:ILE:HD13	1:F:243:MET:CE	2.41	0.50
1:D:200:GLU:CD	1:D:201:LEU:HD12	2.36	0.50
1:D:253:ILE:HG13	1:D:254:LEU:CD1	2.24	0.50
1:E:144:ARG:HG2	1:E:145:SER:N	2.26	0.50
1:E:204:ILE:CG2	1:E:205:TYR:HD2	2.21	0.50
1:E:324:GLU:HB2	1:E:364:LEU:CD1	2.40	0.50
1:F:127:ALA:O	1:F:128:LYS:C	2.52	0.50
1:F:269:LEU:HD22	1:F:346:VAL:CG2	2.41	0.50
1:H:253:ILE:HD13	1:H:321:TYR:CE2	2.46	0.50
1:H:259:LYS:CG	1:H:260:TRP:N	2.62	0.50
1:H:260:TRP:CD1	2:H:401:CMP:C4	2.99	0.50
1:A:164:GLN:O	1:A:167:ASP:HB2	2.12	0.50
1:A:239:ARG:NH2	1:C:156:PHE:HE1	2.09	0.50
1:B:115:VAL:O	1:B:115:VAL:HG23	2.11	0.50
1:B:182:VAL:CG2	1:B:190:THR:O	2.45	0.50
1:B:281:VAL:CG1	1:B:333:ARG:CG	2.90	0.50
1:C:188:TRP:HZ3	1:C:190:THR:C	2.16	0.50
1:C:291:PHE:HB2	1:C:322:PHE:CE1	2.47	0.50
1:C:297:SER:O	1:C:340:ARG:HB2	2.11	0.50
1:D:165:GLN:HG2	1:D:166:GLY:N	2.26	0.50
1:D:173:TYR:CD2	1:D:198:PHE:CE1	2.95	0.50
1:F:248:LEU:HD11	1:F:265:VAL:CG1	2.41	0.50
1:F:260:TRP:CG	2:F:401:CMP:C5	3.00	0.50
1:F:327:LEU:HD23	1:F:353:PHE:CE1	2.46	0.50
1:G:173:TYR:CD2	1:G:198:PHE:HE1	2.28	0.50
1:H:271:PRO:O	1:H:272:VAL:HB	2.12	0.50
1:H:362:ASP:O	1:H:363:ILE:C	2.54	0.50
1:A:120:TYR:HD2	1:A:121:LYS:N	2.07	0.50
1:A:121:LYS:O	1:A:122:THR:C	2.54	0.50
1:B:255:GLU:OE1	1:B:255:GLU:CA	2.45	0.50
1:B:350:ARG:CB	1:B:351:PRO:HD3	2.25	0.50
1:C:153:PRO:CB	1:C:222:TRP:CZ3	2.94	0.50
1:C:173:TYR:CD2	1:C:198:PHE:HE1	2.27	0.50
1:D:157:ILE:HG23	1:F:239:ARG:HH11	1.76	0.50
1:D:269:LEU:CD2	1:D:346:VAL:HG21	2.37	0.50
1:D:280:ILE:CD1	1:D:322:PHE:CZ	2.94	0.50
1:D:285:GLU:OE1	1:D:285:GLU:CA	2.56	0.50
1:D:298:ALA:O	1:D:316:LEU:HD13	2.12	0.50
1:D:300:VAL:HA	1:D:336:THR:O	2.11	0.50
1:F:269:LEU:HD22	1:F:346:VAL:HG21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:356:VAL:CG2	1:G:357:LEU:HD13	2.38	0.50
1:H:324:GLU:O	1:H:328:LEU:CD1	2.58	0.50
1:A:279:LYS:O	1:A:279:LYS:HG2	2.11	0.50
1:B:112:VAL:HG12	1:B:231:ARG:HE	1.72	0.50
1:D:182:VAL:CG2	1:D:190:THR:O	2.41	0.50
1:D:247:PHE:C	1:D:247:PHE:HD2	2.20	0.50
1:D:309:GLU:O	1:D:311:VAL:HG12	2.12	0.50
1:E:205:TYR:CD2	1:E:205:TYR:N	2.79	0.50
1:G:165:GLN:CA	1:G:211:ASP:O	2.57	0.50
1:G:247:PHE:CD2	1:G:247:PHE:O	2.64	0.50
1:G:283:GLN:OE1	1:G:302:GLN:HA	2.12	0.50
1:H:121:LYS:O	1:H:122:THR:C	2.54	0.50
1:H:130:ILE:HD12	1:H:136:PHE:CD2	2.46	0.50
1:H:174:VAL:HG13	1:H:222:TRP:HB2	1.93	0.50
1:A:161:THR:CA	1:A:214:LYS:HD2	2.30	0.50
1:B:201:LEU:HD13	2:B:401:CMP:H2'	1.92	0.50
1:B:300:VAL:HG13	1:B:335:ALA:HB1	1.92	0.50
1:B:366:ARG:HG2	1:B:367:ASN:H	1.75	0.50
1:C:121:LYS:HG3	1:C:122:THR:N	2.26	0.50
1:C:211:ASP:OD1	2:C:401:CMP:H5'1	2.12	0.50
1:D:174:VAL:HA	1:D:196:GLY:O	2.12	0.50
1:D:357:LEU:HD12	1:D:357:LEU:N	2.26	0.50
1:D:365:LYS:O	1:D:368:ILE:CG1	2.43	0.50
1:E:123:MET:C	1:E:125:ALA:N	2.68	0.50
1:E:290:PHE:HB2	1:E:327:LEU:HD21	1.94	0.50
1:E:356:VAL:CG2	1:E:357:LEU:HD13	2.37	0.50
1:F:204:ILE:CG2	1:F:205:TYR:CD2	2.93	0.50
1:F:247:PHE:HE1	1:F:294:LEU:CA	2.16	0.50
1:G:163:ILE:HD12	1:G:213:VAL:HB	1.94	0.50
1:G:272:VAL:HG22	1:G:273:GLN:H	1.77	0.50
1:G:273:GLN:HE21	1:G:273:GLN:H	0.53	0.50
1:G:366:ARG:HG2	1:G:367:ASN:N	2.26	0.50
1:A:262:ARG:HA	1:A:265:VAL:HG21	1.93	0.50
1:B:152:PHE:CD2	1:B:152:PHE:N	2.77	0.50
1:B:290:PHE:HB2	1:B:327:LEU:CD2	2.42	0.50
1:B:331:ARG:NH2	1:B:376:SER:CB	2.73	0.50
1:C:161:THR:HG23	1:C:214:LYS:HD3	1.94	0.50
1:C:253:ILE:O	1:C:255:GLU:N	2.45	0.50
1:D:266:ALA:HA	1:D:269:LEU:CD1	2.41	0.50
1:E:110:SER:OG	1:H:115:VAL:HG23	2.12	0.50
1:F:273:GLN:HB3	1:F:344:LYS:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:120:TYR:O	1:H:121:LYS:C	2.52	0.50
1:A:163:ILE:HD11	1:A:198:PHE:CZ	2.47	0.49
1:A:247:PHE:CE1	1:A:294:LEU:CB	2.95	0.49
1:A:335:ALA:HB3	2:A:402:CMP:O4'	2.12	0.49
1:B:144:ARG:CG	1:B:145:SER:N	2.75	0.49
1:B:253:ILE:HD13	1:B:321:TYR:CE2	2.46	0.49
1:D:278:GLN:HG3	1:D:279:LYS:N	2.23	0.49
1:E:127:ALA:O	1:E:130:ILE:HG22	2.11	0.49
1:E:139:LEU:HD22	1:E:144:ARG:HA	1.93	0.49
1:E:175:ILE:CD1	1:E:193:GLY:O	2.60	0.49
1:G:371:TYR:CD1	2:G:402:CMP:C5	3.00	0.49
1:H:115:VAL:HA	1:H:149:ASP:CB	2.36	0.49
1:A:154:VAL:O	1:A:154:VAL:CG1	2.57	0.49
1:A:348:LEU:HD21	1:A:356:VAL:CG2	2.42	0.49
1:B:157:ILE:O	1:B:160:GLU:HB2	2.11	0.49
1:C:186:ASN:N	1:C:186:ASN:OD1	2.43	0.49
1:C:253:ILE:C	1:C:255:GLU:N	2.68	0.49
1:C:259:LYS:C	1:C:262:ARG:HG3	2.38	0.49
1:C:261:GLU:O	1:C:265:VAL:HG23	2.12	0.49
1:D:161:THR:HG23	1:D:214:LYS:HD3	1.94	0.49
1:D:175:ILE:HD12	1:D:195:GLY:H	1.78	0.49
1:D:279:LYS:O	1:D:279:LYS:CG	2.60	0.49
1:D:300:VAL:O	1:D:313:VAL:HG13	2.11	0.49
1:E:163:ILE:CD1	1:E:213:VAL:HB	2.42	0.49
1:E:260:TRP:O	1:E:263:LEU:HB2	2.12	0.49
1:F:230:ARG:HG2	1:F:234:MET:HE1	1.95	0.49
1:G:294:LEU:N	1:G:294:LEU:CD1	2.45	0.49
1:G:327:LEU:HD23	1:G:353:PHE:CD2	2.46	0.49
1:H:253:ILE:HG13	1:H:254:LEU:CG	2.41	0.49
1:H:324:GLU:OE1	1:H:324:GLU:N	2.45	0.49
1:A:274:PHE:CE2	1:A:280:ILE:HG22	2.48	0.49
1:A:318:PRO:O	1:A:319:SER:HB3	2.11	0.49
1:B:139:LEU:HB3	1:B:143:GLU:HB2	1.95	0.49
1:B:140:ASP:OD1	1:B:140:ASP:O	2.31	0.49
1:B:144:ARG:HG2	1:B:145:SER:N	2.28	0.49
1:C:129:ALA:HB2	1:C:222:TRP:HE1	1.76	0.49
1:C:269:LEU:HD23	1:C:348:LEU:HD11	1.92	0.49
1:C:289:GLU:N	1:C:327:LEU:HD11	2.26	0.49
1:C:333:ARG:NH1	2:C:402:CMP:O1P	2.43	0.49
1:D:144:ARG:O	1:D:147:ILE:N	2.44	0.49
1:D:160:GLU:C	1:D:214:LYS:HE3	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:177:GLN:HA	1:D:194:GLU:CG	2.43	0.49
1:D:251:VAL:O	1:D:254:LEU:CD2	2.58	0.49
1:E:126:LEU:C	1:E:126:LEU:CD1	2.76	0.49
1:E:229:TYR:O	1:E:233:LEU:HD12	2.12	0.49
1:F:162:VAL:CG2	1:F:163:ILE:N	2.75	0.49
1:F:165:GLN:HG2	1:F:166:GLY:N	2.26	0.49
1:G:120:TYR:CE1	1:H:148:PHE:CD1	3.00	0.49
1:G:179:GLU:CG	1:G:216:LYS:HD2	2.42	0.49
1:H:116:ILE:N	1:H:149:ASP:O	2.26	0.49
1:H:129:ALA:HB2	1:H:222:TRP:HE1	1.77	0.49
1:H:144:ARG:O	1:H:147:ILE:N	2.45	0.49
1:H:160:GLU:O	1:H:214:LYS:HA	2.12	0.49
1:B:135:LEU:HD13	1:B:136:PHE:N	2.28	0.49
1:B:157:ILE:HD12	1:B:157:ILE:C	2.36	0.49
1:C:129:ALA:CB	1:C:222:TRP:HE1	2.25	0.49
1:D:356:VAL:HG23	1:D:357:LEU:HD13	1.88	0.49
1:G:175:ILE:HG21	1:G:180:MET:HG3	1.95	0.49
1:G:248:LEU:HB2	1:G:262:ARG:HH21	1.78	0.49
1:H:153:PRO:HA	1:H:222:TRP:CE3	2.46	0.49
1:H:260:TRP:CG	2:H:401:CMP:C8	2.96	0.49
1:B:120:TYR:HE2	1:B:124:ALA:CB	2.26	0.49
1:B:198:PHE:HD1	1:B:198:PHE:N	2.09	0.49
1:B:200:GLU:OE2	1:B:241:ARG:NH2	2.45	0.49
1:C:143:GLU:O	1:C:144:ARG:C	2.54	0.49
1:D:121:LYS:O	1:D:122:THR:C	2.55	0.49
1:D:210:ALA:N	1:D:211:ASP:OD1	2.46	0.49
1:E:112:VAL:HG12	1:E:231:ARG:HE	1.71	0.49
1:E:113:ARG:H	1:H:112:VAL:HG11	1.77	0.49
1:E:224:ILE:HD13	1:E:224:ILE:C	2.36	0.49
1:E:263:LEU:O	1:E:266:ALA:CB	2.57	0.49
1:E:283:GLN:HG3	1:E:335:ALA:N	2.28	0.49
1:F:252:SER:OG	1:F:253:ILE:N	2.42	0.49
1:F:300:VAL:CG1	1:F:335:ALA:CB	2.83	0.49
1:F:366:ARG:O	1:F:369:GLN:HB2	2.12	0.49
1:G:135:LEU:HD13	1:G:136:PHE:CG	2.47	0.49
1:H:260:TRP:CG	2:H:401:CMP:C5	3.01	0.49
1:A:363:ILE:O	1:A:366:ARG:HG2	2.13	0.49
1:B:224:ILE:HD13	1:B:224:ILE:N	2.25	0.49
1:C:177:GLN:HA	1:C:194:GLU:CG	2.42	0.49
1:C:284:GLY:HA2	1:C:332:PRO:CB	2.43	0.49
1:D:116:ILE:CG2	1:D:118:LYS:NZ	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:280:ILE:HD13	1:D:322:PHE:HZ	1.76	0.49
1:D:297:SER:O	1:D:340:ARG:N	2.39	0.49
1:E:121:LYS:O	1:E:122:THR:C	2.55	0.49
1:E:131:GLU:O	1:E:132:LYS:C	2.54	0.49
1:E:153:PRO:CB	1:E:222:TRP:CZ3	2.95	0.49
1:E:253:ILE:HG13	1:E:254:LEU:HG	1.93	0.49
1:E:265:VAL:C	1:E:269:LEU:HG	2.32	0.49
1:F:272:VAL:N	1:F:345:CYS:O	2.41	0.49
1:G:158:ALA:HB1	1:G:216:LYS:O	2.13	0.49
1:H:278:GLN:O	1:H:339:ALA:N	2.32	0.49
1:H:292:ILE:HB	1:H:346:VAL:HG13	1.93	0.49
1:H:325:ILE:HG13	1:H:326:ALA:N	2.27	0.49
1:A:247:PHE:HE1	1:A:294:LEU:CB	2.25	0.49
1:B:173:TYR:HB2	1:B:198:PHE:CE1	2.47	0.49
1:C:173:TYR:CD2	1:C:198:PHE:HZ	2.29	0.49
1:C:230:ARG:HG2	1:C:234:MET:CE	2.42	0.49
1:C:242:LYS:HD3	1:C:242:LYS:N	1.95	0.49
1:D:183:TYR:CD1	1:D:188:TRP:HA	2.45	0.49
1:D:203:LEU:HD12	1:D:229:TYR:CD2	2.47	0.49
1:D:273:GLN:HE21	1:D:273:GLN:CA	2.25	0.49
1:E:281:VAL:HG11	1:E:333:ARG:NE	2.28	0.49
1:F:261:GLU:O	1:F:265:VAL:HG23	2.12	0.49
1:G:116:ILE:HB	1:G:149:ASP:O	2.12	0.49
1:G:360:CYS:O	1:G:364:LEU:HD23	2.13	0.49
1:H:113:ARG:CD	1:H:114:LYS:N	2.71	0.49
1:A:139:LEU:HD21	1:A:147:ILE:CD1	2.42	0.49
1:A:249:SER:HA	1:A:262:ARG:HH22	1.75	0.49
1:B:290:PHE:HB2	1:B:327:LEU:HD21	1.95	0.49
1:C:254:LEU:HD12	1:C:255:GLU:N	2.28	0.49
1:C:265:VAL:HG12	1:C:269:LEU:CG	2.41	0.49
1:C:325:ILE:CD1	1:C:334:ALA:CB	2.90	0.49
1:D:269:LEU:O	1:D:270:GLU:CB	2.59	0.49
1:D:362:ASP:N	1:D:365:LYS:HZ2	2.10	0.49
1:E:287:GLY:HA3	1:E:326:ALA:HB1	1.95	0.49
1:F:121:LYS:O	1:F:122:THR:C	2.55	0.49
1:F:224:ILE:HD12	1:F:224:ILE:H	1.73	0.49
1:F:289:GLU:HG2	1:F:291:PHE:HE1	1.77	0.49
1:G:139:LEU:HD21	1:G:147:ILE:CD1	2.42	0.49
1:A:116:ILE:N	1:A:149:ASP:O	2.43	0.49
1:A:122:THR:O	1:A:125:ALA:HB3	2.12	0.49
1:A:352:ARG:HA	1:A:355:ARG:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:PHE:HE2	1:B:223:GLY:C	2.21	0.49
1:B:253:ILE:HG21	1:B:321:TYR:CE2	2.48	0.49
1:C:120:TYR:HE1	1:D:148:PHE:CG	2.29	0.49
1:C:265:VAL:C	1:C:269:LEU:CD1	2.86	0.49
1:C:280:ILE:HB	1:C:291:PHE:HE2	1.77	0.49
1:C:366:ARG:O	1:C:369:GLN:HB2	2.13	0.49
1:D:120:TYR:HD2	1:D:121:LYS:N	2.11	0.49
1:D:121:LYS:O	1:D:124:ALA:N	2.46	0.49
1:F:118:LYS:CE	1:F:148:PHE:O	2.51	0.49
1:F:135:LEU:HD12	1:F:136:PHE:N	2.27	0.49
1:H:129:ALA:CB	1:H:222:TRP:NE1	2.76	0.49
1:H:139:LEU:HD22	1:H:144:ARG:HA	1.94	0.49
1:H:158:ALA:CB	1:H:217:THR:C	2.74	0.49
1:H:158:ALA:N	1:H:218:ASN:OD1	2.40	0.49
1:A:174:VAL:CG1	1:A:222:TRP:HB2	2.42	0.49
1:A:297:SER:O	1:A:340:ARG:HB2	2.13	0.49
1:A:371:TYR:CD1	2:A:402:CMP:N7	2.80	0.49
1:B:111:TYR:CE2	1:B:112:VAL:O	2.66	0.49
1:B:272:VAL:HA	1:B:273:GLN:HE22	1.75	0.49
1:C:144:ARG:HG2	1:C:145:SER:H	1.74	0.49
1:C:144:ARG:O	1:C:147:ILE:N	2.46	0.49
1:C:153:PRO:CA	1:C:222:TRP:CZ3	2.96	0.49
1:C:211:ASP:OD1	2:C:401:CMP:O2P	2.30	0.49
1:C:315:ARG:HH21	1:C:340:ARG:HH22	1.61	0.49
1:D:183:TYR:HE1	1:D:188:TRP:HB2	1.76	0.49
1:E:201:LEU:HD13	2:E:401:CMP:C2'	2.43	0.49
1:F:230:ARG:HB3	1:F:234:MET:CE	2.41	0.49
1:G:211:ASP:OD2	2:G:401:CMP:N3	2.46	0.49
1:H:196:GLY:CA	1:H:355:ARG:NH2	2.65	0.49
1:H:229:TYR:HD1	1:H:233:LEU:HD11	1.73	0.49
1:A:284:GLY:O	1:A:332:PRO:HB3	2.13	0.48
1:A:296:GLY:CA	1:A:342:PRO:O	2.61	0.48
1:B:154:VAL:O	1:B:221:LEU:N	2.32	0.48
1:B:293:ILE:CG2	1:B:317:GLY:O	2.59	0.48
1:E:249:SER:CA	1:E:262:ARG:NH2	2.70	0.48
1:E:324:GLU:O	1:E:328:LEU:CD1	2.42	0.48
1:E:325:ILE:CD1	1:E:334:ALA:CB	2.92	0.48
1:F:260:TRP:CD2	2:F:401:CMP:C8	2.96	0.48
1:F:291:PHE:CZ	1:F:347:LYS:NZ	2.79	0.48
1:G:153:PRO:HB3	1:G:222:TRP:CH2	2.46	0.48
1:G:256:SER:OG	1:G:363:ILE:HD12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:177:GLN:HA	1:H:194:GLU:CG	2.43	0.48
1:H:235:GLY:O	1:H:238:LEU:N	2.46	0.48
1:H:261:GLU:O	1:H:264:THR:N	2.46	0.48
1:H:262:ARG:HA	1:H:265:VAL:CG2	2.42	0.48
1:H:269:LEU:CD2	1:H:346:VAL:HG21	2.38	0.48
1:H:304:ARG:CB	1:H:308:GLU:CB	2.90	0.48
1:A:130:ILE:HD13	1:A:151:MET:CE	2.38	0.48
1:A:162:VAL:HG22	1:A:213:VAL:O	2.13	0.48
1:A:324:GLU:CG	1:A:325:ILE:H	2.24	0.48
1:B:123:MET:O	1:B:124:ALA:C	2.56	0.48
1:B:175:ILE:HD11	1:B:194:GLU:CA	2.43	0.48
1:C:163:ILE:HD12	1:C:213:VAL:HG21	1.95	0.48
1:C:208:PRO:O	1:C:209:ARG:C	2.52	0.48
1:C:211:ASP:OD2	2:C:401:CMP:C3'	2.56	0.48
1:C:284:GLY:O	1:C:332:PRO:CG	2.61	0.48
1:D:224:ILE:HD13	1:D:224:ILE:C	2.35	0.48
1:D:247:PHE:HE1	1:D:294:LEU:HB3	1.77	0.48
1:E:126:LEU:O	1:E:130:ILE:N	2.44	0.48
1:E:139:LEU:N	1:E:139:LEU:CD1	2.66	0.48
1:F:234:MET:HG3	1:F:238:LEU:CD1	2.41	0.48
1:F:235:GLY:O	1:F:238:LEU:N	2.47	0.48
1:F:273:GLN:HE21	1:F:273:GLN:CA	2.22	0.48
1:F:352:ARG:HA	1:F:355:ARG:HB2	1.95	0.48
1:G:258:ASP:O	1:G:262:ARG:HG2	2.13	0.48
1:G:361:SER:C	1:G:365:LYS:NZ	2.66	0.48
1:A:179:GLU:HG2	1:A:216:LYS:HD3	1.93	0.48
1:C:290:PHE:HB2	1:C:327:LEU:CD2	2.43	0.48
1:D:161:THR:HG23	1:D:214:LYS:HD2	1.95	0.48
1:E:234:MET:HG3	1:E:238:LEU:HD12	1.95	0.48
1:E:281:VAL:HG11	1:E:333:ARG:CD	2.43	0.48
1:F:120:TYR:O	1:F:121:LYS:C	2.51	0.48
1:F:171:ASN:OD1	1:F:225:ASP:HA	2.14	0.48
1:F:249:SER:CB	1:F:262:ARG:HH22	2.26	0.48
1:F:349:ASP:O	1:F:353:PHE:HB2	2.13	0.48
1:G:116:ILE:N	1:G:149:ASP:O	2.41	0.48
1:G:135:LEU:HD13	1:G:136:PHE:CD1	2.49	0.48
1:G:293:ILE:HG21	1:G:317:GLY:C	2.37	0.48
1:G:353:PHE:CE1	1:G:357:LEU:HD23	2.48	0.48
1:H:324:GLU:OE2	1:H:371:TYR:HE2	1.96	0.48
1:A:153:PRO:CA	1:A:222:TRP:HZ3	2.23	0.48
1:B:113:ARG:HG3	1:B:113:ARG:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:TRP:CE2	2:B:401:CMP:H8	2.47	0.48
1:C:260:TRP:CG	2:C:401:CMP:N7	2.81	0.48
1:D:159:GLY:C	1:F:243:MET:HE2	2.37	0.48
1:D:164:GLN:O	1:D:167:ASP:HB2	2.14	0.48
1:D:224:ILE:H	1:D:224:ILE:HD12	1.75	0.48
1:D:296:GLY:HA2	1:D:342:PRO:HG2	1.95	0.48
1:E:134:VAL:O	1:E:137:SER:HB3	2.12	0.48
1:E:243:MET:CE	1:G:158:ALA:O	2.61	0.48
1:E:289:GLU:HG2	1:E:291:PHE:CE1	2.48	0.48
1:F:163:ILE:O	1:F:213:VAL:N	2.43	0.48
1:F:183:TYR:HE1	1:F:188:TRP:HB2	1.78	0.48
1:F:246:GLU:O	1:F:249:SER:N	2.46	0.48
1:F:284:GLY:C	1:F:332:PRO:HB3	2.39	0.48
1:G:116:ILE:HG22	1:G:118:LYS:CG	2.39	0.48
1:G:120:TYR:HD2	1:G:121:LYS:N	2.11	0.48
1:G:247:PHE:CE1	1:G:294:LEU:CB	2.96	0.48
1:H:153:PRO:HB3	1:H:222:TRP:HZ3	1.76	0.48
1:H:163:ILE:O	1:H:212:THR:HG22	2.14	0.48
1:H:165:GLN:N	1:H:212:THR:CG2	2.50	0.48
1:H:183:TYR:HE1	1:H:188:TRP:HB2	1.75	0.48
1:H:260:TRP:CE2	2:H:401:CMP:H8	2.44	0.48
1:H:333:ARG:NH1	2:H:402:CMP:O2P	2.37	0.48
1:A:186:ASN:OD1	1:A:186:ASN:N	2.47	0.48
1:A:309:GLU:HG3	1:A:310:PHE:H	1.79	0.48
1:B:123:MET:C	1:B:125:ALA:N	2.68	0.48
1:C:113:ARG:NE	1:C:146:ASP:OD1	2.41	0.48
1:C:118:LYS:C	1:D:117:PRO:O	2.57	0.48
1:C:188:TRP:CH2	1:C:190:THR:CA	2.94	0.48
1:C:254:LEU:HB2	1:C:257:LEU:HD12	1.94	0.48
1:C:294:LEU:HD13	1:C:345:CYS:HA	1.87	0.48
1:C:318:PRO:O	1:C:319:SER:HB3	2.12	0.48
1:C:325:ILE:HG12	2:C:402:CMP:O3'	2.12	0.48
1:D:290:PHE:C	1:D:291:PHE:CD1	2.83	0.48
1:D:343:LEU:HA	1:D:343:LEU:HD12	1.55	0.48
1:E:226:ARG:O	1:E:227:ASP:C	2.56	0.48
1:E:324:GLU:OE1	1:E:324:GLU:N	2.46	0.48
1:E:325:ILE:HG22	1:E:368:ILE:HG21	1.94	0.48
1:E:353:PHE:CE1	1:E:357:LEU:HD23	2.48	0.48
1:F:280:ILE:HD12	1:F:281:VAL:CG2	2.43	0.48
1:H:115:VAL:O	1:H:115:VAL:CG2	2.54	0.48
1:H:147:ILE:HG13	1:H:148:PHE:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:157:ILE:O	1:H:158:ALA:O	2.31	0.48
1:H:157:ILE:HG13	1:H:160:GLU:OE1	2.14	0.48
1:H:171:ASN:H	1:H:209:ARG:HH22	1.60	0.48
1:H:180:MET:O	1:H:191:SER:HA	2.12	0.48
1:H:204:ILE:CG2	1:H:205:TYR:CE2	2.97	0.48
1:A:113:ARG:CD	1:D:113:ARG:HB3	2.43	0.48
1:B:135:LEU:CD1	1:B:135:LEU:C	2.86	0.48
1:B:298:ALA:HB1	1:B:338:VAL:O	2.14	0.48
1:C:129:ALA:CB	1:C:222:TRP:NE1	2.77	0.48
1:C:203:LEU:HD22	1:C:226:ARG:CB	2.38	0.48
1:C:226:ARG:O	1:C:227:ASP:C	2.57	0.48
1:C:278:GLN:O	1:C:339:ALA:N	2.42	0.48
1:C:291:PHE:CD1	1:C:347:LYS:NZ	2.81	0.48
1:D:172:PHE:O	1:D:224:ILE:CD1	2.61	0.48
1:D:200:GLU:HG2	1:D:201:LEU:CG	2.43	0.48
1:D:253:ILE:HD13	1:D:321:TYR:CE2	2.49	0.48
1:F:262:ARG:HA	1:F:265:VAL:HG23	1.94	0.48
1:F:329:MET:HB3	1:F:331:ARG:HG3	1.95	0.48
1:F:352:ARG:O	1:F:353:PHE:C	2.56	0.48
1:G:123:MET:O	1:G:127:ALA:N	2.37	0.48
1:G:211:ASP:OD2	2:G:401:CMP:C4'	2.62	0.48
1:G:233:LEU:CD1	1:G:233:LEU:N	2.53	0.48
1:H:215:ALA:HB1	1:H:217:THR:O	2.13	0.48
1:H:298:ALA:CB	1:H:338:VAL:O	2.62	0.48
1:H:366:ARG:HG2	1:H:367:ASN:N	2.29	0.48
1:B:260:TRP:CZ2	2:B:401:CMP:C8	2.95	0.48
1:B:325:ILE:O	1:B:328:LEU:N	2.46	0.48
1:C:293:ILE:CG2	1:C:317:GLY:C	2.84	0.48
1:C:324:GLU:OE2	1:C:371:TYR:HE2	1.97	0.48
1:D:221:LEU:HD23	1:D:221:LEU:HA	1.46	0.48
1:F:121:LYS:C	1:F:123:MET:N	2.70	0.48
1:F:130:ILE:CG1	1:F:136:PHE:CG	2.95	0.48
1:F:158:ALA:O	1:H:243:MET:HE1	2.14	0.48
1:F:186:ASN:OD1	1:F:186:ASN:N	2.47	0.48
1:F:318:PRO:O	1:F:319:SER:CB	2.58	0.48
1:F:325:ILE:CD1	1:F:334:ALA:HB3	2.44	0.48
1:G:232:ILE:HG23	1:G:233:LEU:HG	1.95	0.48
1:H:158:ALA:HA	1:H:215:ALA:HB3	1.95	0.48
1:H:162:VAL:HG23	1:H:163:ILE:N	2.28	0.48
1:H:198:PHE:CD1	1:H:198:PHE:N	2.78	0.48
1:H:230:ARG:CA	1:H:234:MET:HE2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:247:PHE:CE1	1:H:294:LEU:HB3	2.49	0.48
1:A:135:LEU:CD1	1:A:136:PHE:H	2.07	0.48
1:A:152:PHE:CD2	1:A:152:PHE:N	2.82	0.48
1:A:174:VAL:HG13	1:A:222:TRP:HB2	1.96	0.48
1:A:211:ASP:OD2	2:A:401:CMP:C4'	2.62	0.48
1:A:324:GLU:HB2	1:A:364:LEU:HD11	1.94	0.48
1:A:329:MET:HA	1:A:329:MET:HE2	1.94	0.48
1:B:183:TYR:CE1	1:B:188:TRP:CB	2.95	0.48
1:B:318:PRO:O	1:B:319:SER:HB3	2.14	0.48
1:C:130:ILE:HD12	1:C:136:PHE:CE2	2.48	0.48
1:E:261:GLU:O	1:E:265:VAL:HG23	2.14	0.48
1:G:139:LEU:N	1:G:139:LEU:CD1	2.67	0.48
1:G:229:TYR:O	1:G:233:LEU:HD12	2.14	0.48
1:A:112:VAL:CA	1:A:112:VAL:CG1	2.84	0.48
1:A:296:GLY:HA3	1:A:342:PRO:O	2.13	0.48
1:B:210:ALA:CA	1:B:211:ASP:OD1	2.61	0.48
1:C:266:ALA:N	1:C:269:LEU:CD1	2.77	0.48
1:D:204:ILE:CG2	1:D:205:TYR:CE2	2.96	0.48
1:D:253:ILE:HG13	1:D:254:LEU:H	1.78	0.48
1:D:254:LEU:HB2	1:D:257:LEU:CD1	2.43	0.48
1:E:184:VAL:O	1:E:185:ASN:HB2	2.14	0.48
1:F:259:LYS:HA	1:F:262:ARG:HD3	1.95	0.48
1:G:362:ASP:N	1:G:365:LYS:HZ2	2.09	0.48
1:H:111:TYR:OH	1:H:113:ARG:O	2.20	0.48
1:H:300:VAL:HG11	2:H:402:CMP:H8	1.90	0.48
1:A:115:VAL:HA	1:A:149:ASP:HB3	1.94	0.48
1:A:120:TYR:CE2	1:A:124:ALA:HB2	2.49	0.48
1:A:129:ALA:HA	1:A:132:LYS:HE3	1.95	0.48
1:A:203:LEU:HD22	1:A:226:ARG:CG	2.44	0.48
1:A:253:ILE:C	1:A:255:GLU:N	2.71	0.48
1:A:261:GLU:O	1:A:265:VAL:HG23	2.14	0.48
1:B:200:GLU:HG3	1:B:201:LEU:H	1.74	0.48
1:C:152:PHE:HE2	1:C:223:GLY:CA	2.26	0.48
1:C:266:ALA:O	1:C:268:ALA:N	2.47	0.48
1:D:285:GLU:HB3	1:D:286:PRO:HD2	1.96	0.48
1:E:148:PHE:CD1	1:F:120:TYR:HE1	2.29	0.48
1:E:289:GLU:HG2	1:E:291:PHE:HE1	1.78	0.48
1:E:352:ARG:O	1:E:353:PHE:C	2.55	0.48
1:F:114:LYS:CE	1:F:115:VAL:N	2.77	0.48
1:F:273:GLN:HB2	1:F:343:LEU:O	2.14	0.48
1:H:120:TYR:HD2	1:H:121:LYS:N	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:282:VAL:O	1:H:283:GLN:C	2.56	0.48
1:A:162:VAL:HG23	1:A:163:ILE:N	2.28	0.47
1:A:260:TRP:HB2	2:A:401:CMP:N6	2.28	0.47
1:B:175:ILE:HD12	1:B:175:ILE:C	2.24	0.47
1:B:328:LEU:CD2	1:B:365:LYS:HE3	2.44	0.47
1:B:357:LEU:HA	1:B:357:LEU:HD12	1.58	0.47
1:B:376:SER:CA	1:C:306:GLU:HA	2.44	0.47
1:F:120:TYR:HD2	1:F:121:LYS:HA	1.78	0.47
1:G:226:ARG:NH1	1:G:227:ASP:OD1	2.37	0.47
1:G:269:LEU:CB	1:G:346:VAL:HG21	2.44	0.47
1:G:328:LEU:HD23	1:G:365:LYS:HE3	1.93	0.47
1:H:260:TRP:CD2	2:H:401:CMP:N7	2.82	0.47
1:A:153:PRO:N	1:A:222:TRP:HZ3	2.12	0.47
1:A:204:ILE:HG12	1:A:234:MET:SD	2.54	0.47
1:A:265:VAL:HA	1:A:356:VAL:HG11	1.96	0.47
1:B:224:ILE:N	1:B:224:ILE:HD12	2.29	0.47
1:B:247:PHE:CE1	1:B:294:LEU:CB	2.97	0.47
1:B:309:GLU:OE1	1:B:310:PHE:CE2	2.67	0.47
1:C:158:ALA:CB	1:C:217:THR:C	2.72	0.47
1:C:230:ARG:HB3	1:C:234:MET:HE2	1.96	0.47
1:C:273:GLN:C	1:C:274:PHE:CG	2.91	0.47
1:C:279:LYS:HB2	1:C:337:VAL:O	2.14	0.47
1:C:347:LYS:HE3	1:C:347:LYS:HB3	1.22	0.47
1:D:130:ILE:CD1	1:D:136:PHE:CD2	2.97	0.47
1:D:246:GLU:C	1:D:248:LEU:N	2.66	0.47
1:D:270:GLU:O	1:D:346:VAL:HA	2.14	0.47
1:D:300:VAL:CG1	1:D:314:GLY:H	2.27	0.47
1:D:352:ARG:HA	1:D:355:ARG:HB2	1.96	0.47
1:E:111:TYR:CD1	1:E:112:VAL:N	2.82	0.47
1:E:158:ALA:HB1	1:E:216:LYS:O	2.14	0.47
1:F:295:GLU:O	1:F:344:LYS:N	2.40	0.47
1:G:293:ILE:CG1	1:G:343:LEU:HD11	2.43	0.47
1:H:174:VAL:HG13	1:H:174:VAL:O	2.13	0.47
1:H:190:THR:CG2	1:H:191:SER:N	2.74	0.47
1:H:233:LEU:HD12	1:H:233:LEU:N	2.05	0.47
1:A:123:MET:C	1:A:125:ALA:N	2.71	0.47
1:A:365:LYS:HA	1:A:368:ILE:CD1	2.44	0.47
1:B:152:PHE:CD2	1:B:223:GLY:O	2.68	0.47
1:B:260:TRP:NE1	2:B:401:CMP:C2'	2.72	0.47
1:B:309:GLU:CD	1:B:310:PHE:CD2	2.92	0.47
1:B:356:VAL:HG23	1:B:357:LEU:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:ASP:HB2	1:C:222:TRP:CD1	2.49	0.47
1:C:229:TYR:O	1:C:233:LEU:HD12	2.14	0.47
1:D:160:GLU:O	1:D:214:LYS:HE3	2.15	0.47
1:E:158:ALA:HA	1:E:215:ALA:CB	2.45	0.47
1:F:165:GLN:CB	1:F:211:ASP:O	2.62	0.47
1:F:229:TYR:O	1:F:233:LEU:HD12	2.14	0.47
1:F:266:ALA:C	1:F:268:ALA:N	2.69	0.47
1:F:300:VAL:HG12	1:F:335:ALA:HB1	1.93	0.47
1:H:173:TYR:HB2	1:H:198:PHE:HE1	1.80	0.47
1:H:276:ASP:C	1:H:278:GLN:H	2.22	0.47
1:H:280:ILE:HG12	1:H:337:VAL:HB	1.96	0.47
1:H:301:LEU:O	1:H:302:GLN:CG	2.61	0.47
1:B:251:VAL:C	1:B:252:SER:O	2.56	0.47
1:B:311:VAL:CG1	1:B:312:GLU:H	2.28	0.47
1:C:120:TYR:HB3	1:D:149:ASP:OD1	2.12	0.47
1:C:124:ALA:O	1:C:127:ALA:HB3	2.14	0.47
1:C:280:ILE:HD11	1:C:322:PHE:CE2	2.33	0.47
1:F:171:ASN:H	1:F:209:ARG:HH22	1.61	0.47
1:F:254:LEU:C	1:F:254:LEU:CD1	2.84	0.47
1:F:272:VAL:HA	1:F:273:GLN:HE22	1.79	0.47
1:F:366:ARG:HG2	1:F:367:ASN:H	1.79	0.47
1:G:173:TYR:CD2	1:G:198:PHE:CZ	3.02	0.47
1:H:176:ASP:O	1:H:194:GLU:HG2	2.15	0.47
1:H:289:GLU:N	1:H:327:LEU:HD11	2.30	0.47
1:H:327:LEU:HD23	1:H:353:PHE:CZ	2.48	0.47
1:H:366:ARG:O	1:H:369:GLN:CB	2.63	0.47
1:A:148:PHE:CD1	1:B:120:TYR:CE1	3.02	0.47
1:A:188:TRP:CZ3	1:A:190:THR:O	2.63	0.47
1:A:196:GLY:HA2	1:A:355:ARG:CZ	2.43	0.47
1:A:325:ILE:HD11	1:A:334:ALA:H	1.79	0.47
1:B:175:ILE:HD11	1:B:194:GLU:C	2.40	0.47
1:B:332:PRO:HD3	1:C:332:PRO:HG2	1.97	0.47
1:C:120:TYR:HD2	1:C:121:LYS:N	2.12	0.47
1:C:134:VAL:O	1:C:137:SER:HB3	2.14	0.47
1:E:266:ALA:O	1:E:268:ALA:N	2.47	0.47
1:E:272:VAL:HG22	1:E:273:GLN:N	2.27	0.47
1:E:282:VAL:C	1:E:285:GLU:HG2	2.36	0.47
1:F:199:GLY:H	2:F:401:CMP:H4'	1.79	0.47
1:H:178:GLY:CA	1:H:219:VAL:HG12	2.23	0.47
1:H:234:MET:HG3	1:H:234:MET:O	2.14	0.47
1:H:298:ALA:O	1:H:316:LEU:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:162:VAL:HG23	1:C:163:ILE:N	2.29	0.47
1:C:253:ILE:HG13	1:C:254:LEU:HG	1.96	0.47
1:C:264:THR:O	1:C:265:VAL:C	2.57	0.47
1:C:298:ALA:O	1:C:316:LEU:N	2.46	0.47
1:D:164:GLN:HA	1:D:212:THR:CG2	2.43	0.47
1:D:353:PHE:O	1:D:357:LEU:HB2	2.14	0.47
1:F:248:LEU:CD1	1:F:265:VAL:HG11	2.44	0.47
1:G:230:ARG:HB3	1:G:234:MET:HE2	1.97	0.47
1:H:293:ILE:HA	1:H:345:CYS:SG	2.55	0.47
1:A:110:SER:HB3	1:A:111:TYR:H	1.53	0.47
1:A:139:LEU:HB3	1:A:143:GLU:CB	2.43	0.47
1:A:252:SER:O	1:A:253:ILE:C	2.58	0.47
1:A:321:TYR:C	1:A:321:TYR:HD1	2.18	0.47
1:B:158:ALA:HA	1:B:217:THR:O	2.13	0.47
1:B:183:TYR:HD1	1:B:188:TRP:CA	2.27	0.47
1:B:213:VAL:C	1:B:214:LYS:HG2	2.40	0.47
1:B:279:LYS:CE	1:B:282:VAL:HG22	2.34	0.47
1:C:366:ARG:CG	1:C:367:ASN:N	2.75	0.47
1:D:121:LYS:C	1:D:123:MET:N	2.69	0.47
1:D:124:ALA:O	1:D:127:ALA:HB3	2.14	0.47
1:D:173:TYR:HD2	1:D:198:PHE:CZ	2.32	0.47
1:D:253:ILE:C	1:D:255:GLU:N	2.73	0.47
1:D:259:LYS:O	1:D:260:TRP:C	2.56	0.47
1:D:371:TYR:CE1	2:D:402:CMP:C4	3.03	0.47
1:E:175:ILE:O	1:E:175:ILE:CD1	2.39	0.47
1:E:230:ARG:CB	1:E:234:MET:HE2	2.44	0.47
1:E:294:LEU:HD11	1:E:345:CYS:CA	2.30	0.47
1:F:129:ALA:CB	1:F:222:TRP:NE1	2.76	0.47
1:F:136:PHE:O	1:F:139:LEU:HD11	2.15	0.47
1:F:233:LEU:CD1	1:F:233:LEU:N	2.68	0.47
1:F:276:ASP:C	1:F:278:GLN:H	2.23	0.47
1:F:294:LEU:HD13	1:F:345:CYS:HA	1.92	0.47
1:F:350:ARG:HB3	1:F:351:PRO:HD3	1.97	0.47
1:G:144:ARG:CG	1:G:145:SER:N	2.76	0.47
1:G:148:PHE:CG	1:H:120:TYR:CE1	3.02	0.47
1:G:249:SER:HA	1:G:262:ARG:NH2	2.29	0.47
1:H:118:LYS:HB2	1:H:123:MET:HE1	1.95	0.47
1:H:157:ILE:O	1:H:157:ILE:CD1	2.47	0.47
1:H:253:ILE:C	1:H:255:GLU:N	2.71	0.47
1:H:343:LEU:HD12	1:H:343:LEU:HA	1.74	0.47
1:H:371:TYR:HE1	2:H:402:CMP:C5	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:VAL:HG23	1:A:189:ALA:HB3	1.97	0.47
1:A:245:GLU:OE1	1:A:246:GLU:OE1	2.33	0.47
1:A:329:MET:O	1:A:330:ASN:C	2.58	0.47
1:A:365:LYS:O	1:A:366:ARG:C	2.58	0.47
1:B:127:ALA:O	1:B:130:ILE:HG22	2.15	0.47
1:B:186:ASN:N	1:B:186:ASN:OD1	2.48	0.47
1:B:230:ARG:CA	1:B:234:MET:HE2	2.45	0.47
1:D:127:ALA:O	1:D:128:LYS:C	2.56	0.47
1:D:153:PRO:HA	1:D:222:TRP:CZ3	2.49	0.47
1:D:230:ARG:CB	1:D:234:MET:HE2	2.45	0.47
1:D:311:VAL:O	1:D:311:VAL:HG22	2.14	0.47
1:E:153:PRO:HA	1:E:222:TRP:CE3	2.49	0.47
1:G:204:ILE:CG2	1:G:205:TYR:CE2	2.97	0.47
1:G:248:LEU:C	1:G:262:ARG:NH2	2.73	0.47
1:G:276:ASP:C	1:G:278:GLN:N	2.73	0.47
1:G:279:LYS:O	1:G:279:LYS:HG3	2.14	0.47
1:H:113:ARG:CB	1:H:231:ARG:HH12	2.28	0.47
1:A:260:TRP:CD1	2:A:401:CMP:N7	2.81	0.47
1:B:204:ILE:CG2	1:B:205:TYR:CD2	2.98	0.47
1:C:215:ALA:HB1	1:C:217:THR:O	2.14	0.47
1:C:291:PHE:CD2	1:C:322:PHE:CZ	3.02	0.47
1:C:362:ASP:N	1:C:365:LYS:HZ2	2.07	0.47
1:E:204:ILE:HD13	1:E:238:LEU:HD11	1.96	0.47
1:E:233:LEU:CD1	1:E:233:LEU:N	2.68	0.47
1:E:253:ILE:HG13	1:E:254:LEU:CD2	2.45	0.47
1:E:260:TRP:NE1	2:E:401:CMP:C4	2.82	0.47
1:F:130:ILE:HD12	1:F:136:PHE:CE2	2.50	0.47
1:F:198:PHE:HD1	1:F:198:PHE:H	1.62	0.47
1:F:324:GLU:HB2	1:F:364:LEU:CD1	2.39	0.47
1:G:143:GLU:HB3	1:G:232:ILE:HD11	1.97	0.47
1:G:157:ILE:HG13	1:G:160:GLU:OE1	2.15	0.47
1:G:290:PHE:HB2	1:G:327:LEU:CD2	2.45	0.47
1:A:114:LYS:O	1:A:115:VAL:HG13	2.15	0.47
1:A:308:GLU:O	1:A:309:GLU:HB2	2.15	0.47
1:B:310:PHE:CD2	1:B:310:PHE:N	2.77	0.47
1:C:130:ILE:CD1	1:C:151:MET:CE	2.92	0.47
1:D:251:VAL:HG11	1:D:292:ILE:HD13	1.97	0.47
1:D:281:VAL:HG11	1:D:333:ARG:HD2	1.97	0.47
1:E:251:VAL:CG1	1:E:254:LEU:CD2	2.87	0.47
1:F:296:GLY:HA2	1:F:342:PRO:HG2	1.96	0.47
1:F:325:ILE:HG12	2:F:402:CMP:P	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:244:TYR:O	1:G:245:GLU:C	2.58	0.47
1:G:254:LEU:HB2	1:G:257:LEU:HD12	1.97	0.47
1:H:120:TYR:CD2	1:H:121:LYS:HA	2.46	0.47
1:H:175:ILE:HD12	1:H:175:ILE:C	2.23	0.47
1:H:212:THR:C	1:H:213:VAL:HG23	2.40	0.47
1:H:281:VAL:HG13	1:H:333:ARG:CG	2.45	0.47
1:H:325:ILE:CD1	2:H:402:CMP:O1P	2.61	0.47
1:B:203:LEU:HD22	1:B:226:ARG:CG	2.44	0.46
1:B:266:ALA:O	1:B:269:LEU:N	2.44	0.46
1:C:111:TYR:CG	1:C:112:VAL:N	2.82	0.46
1:C:232:ILE:HG23	1:C:233:LEU:HG	1.96	0.46
1:C:316:LEU:CA	1:C:320:ASP:OD2	2.60	0.46
1:D:158:ALA:N	1:D:218:ASN:OD1	2.41	0.46
1:D:232:ILE:HG23	1:D:233:LEU:CD1	2.45	0.46
1:D:327:LEU:HD23	1:D:353:PHE:CG	2.49	0.46
1:D:347:LYS:HE3	1:D:347:LYS:HB3	1.30	0.46
1:E:183:TYR:HE1	1:E:188:TRP:HB2	1.75	0.46
1:E:186:ASN:N	1:E:186:ASN:OD1	2.47	0.46
1:G:130:ILE:CD1	1:G:136:PHE:CD2	2.98	0.46
1:H:119:ASP:O	1:H:120:TYR:C	2.58	0.46
1:H:138:HIS:O	1:H:139:LEU:C	2.55	0.46
1:H:258:ASP:O	1:H:262:ARG:HG3	2.15	0.46
1:H:301:LEU:HA	1:H:312:GLU:HA	1.97	0.46
1:A:113:ARG:HH22	1:D:114:LYS:C	2.18	0.46
1:A:139:LEU:N	1:A:139:LEU:CD1	2.64	0.46
1:A:260:TRP:CD1	2:A:401:CMP:C4	3.04	0.46
1:A:280:ILE:CD1	1:A:281:VAL:HG23	2.43	0.46
1:B:163:ILE:O	1:B:213:VAL:N	2.39	0.46
1:B:230:ARG:HA	1:B:234:MET:HE2	1.98	0.46
1:B:285:GLU:OE1	1:B:285:GLU:CA	2.63	0.46
1:C:278:GLN:C	1:C:338:VAL:HG22	2.40	0.46
1:C:304:ARG:H	1:C:308:GLU:CB	2.29	0.46
1:D:130:ILE:HD13	1:D:151:MET:HE3	1.97	0.46
1:D:204:ILE:CG2	1:D:205:TYR:HD2	2.23	0.46
1:D:272:VAL:HA	1:D:273:GLN:NE2	2.31	0.46
1:E:116:ILE:HB	1:E:118:LYS:NZ	2.31	0.46
1:F:133:ASN:O	1:F:134:VAL:C	2.58	0.46
1:F:203:LEU:CD1	1:F:226:ARG:HB3	2.38	0.46
1:F:273:GLN:NE2	1:F:273:GLN:H	1.89	0.46
1:F:276:ASP:C	1:F:278:GLN:N	2.72	0.46
1:G:120:TYR:O	1:G:121:LYS:C	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:174:VAL:HA	1:G:196:GLY:O	2.16	0.46
1:H:246:GLU:O	1:H:248:LEU:N	2.47	0.46
1:H:301:LEU:CA	1:H:311:VAL:O	2.63	0.46
1:H:357:LEU:CD1	1:H:357:LEU:N	2.72	0.46
1:A:113:ARG:CG	1:D:113:ARG:CB	2.93	0.46
1:B:126:LEU:C	1:B:126:LEU:CD1	2.79	0.46
1:B:153:PRO:HA	1:B:222:TRP:CZ3	2.46	0.46
1:B:331:ARG:HH21	1:B:376:SER:HB3	1.80	0.46
1:C:145:SER:O	1:C:146:ASP:C	2.56	0.46
1:C:175:ILE:HG22	1:C:221:LEU:HD21	1.97	0.46
1:C:230:ARG:O	1:C:234:MET:CB	2.58	0.46
1:D:201:LEU:HB2	2:D:401:CMP:P	2.55	0.46
1:D:253:ILE:CG2	1:D:321:TYR:CE2	2.98	0.46
1:D:290:PHE:HB2	1:D:327:LEU:CD2	2.45	0.46
1:E:325:ILE:CG1	2:E:402:CMP:O2P	2.62	0.46
1:E:327:LEU:HD23	1:E:353:PHE:CD2	2.51	0.46
1:F:123:MET:O	1:F:124:ALA:C	2.56	0.46
1:F:175:ILE:CD1	1:F:196:GLY:N	2.74	0.46
1:F:292:ILE:HB	1:F:346:VAL:HG13	1.96	0.46
1:F:294:LEU:C	1:F:295:GLU:HG2	2.39	0.46
1:F:366:ARG:O	1:F:369:GLN:CB	2.63	0.46
1:G:266:ALA:N	1:G:269:LEU:HD11	2.30	0.46
1:H:273:GLN:C	1:H:274:PHE:CG	2.93	0.46
1:A:144:ARG:O	1:A:145:SER:C	2.54	0.46
1:A:266:ALA:O	1:A:268:ALA:N	2.49	0.46
1:B:173:TYR:HB3	1:B:222:TRP:O	2.15	0.46
1:B:276:ASP:C	1:B:278:GLN:H	2.24	0.46
1:C:148:PHE:CD1	1:D:120:TYR:CE1	3.03	0.46
1:C:251:VAL:CG2	1:C:319:SER:O	2.63	0.46
1:C:282:VAL:O	1:C:283:GLN:C	2.58	0.46
1:C:371:TYR:OH	2:C:402:CMP:C2'	2.64	0.46
1:D:162:VAL:HG23	1:D:163:ILE:H	1.79	0.46
1:E:152:PHE:CD2	1:E:223:GLY:O	2.69	0.46
1:F:143:GLU:HB3	1:F:232:ILE:HD11	1.98	0.46
1:F:175:ILE:CD1	1:F:194:GLU:HA	2.41	0.46
1:G:179:GLU:HB3	1:G:217:THR:HG23	1.97	0.46
1:G:259:LYS:O	1:G:260:TRP:C	2.59	0.46
1:G:296:GLY:CA	1:G:342:PRO:O	2.63	0.46
1:H:204:ILE:HG21	1:H:238:LEU:HD21	1.97	0.46
1:H:284:GLY:HA2	1:H:332:PRO:HB3	1.97	0.46
1:A:123:MET:HE2	1:A:123:MET:HB2	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:VAL:HG22	1:A:185:ASN:OD1	2.16	0.46
1:B:118:LYS:HB3	1:B:123:MET:HE2	1.98	0.46
1:B:142:ASN:O	1:B:143:GLU:C	2.56	0.46
1:B:253:ILE:HD13	1:B:321:TYR:CD2	2.51	0.46
1:B:327:LEU:HD23	1:B:353:PHE:CG	2.49	0.46
1:B:352:ARG:HA	1:B:355:ARG:HB2	1.97	0.46
1:C:362:ASP:O	1:C:365:LYS:N	2.46	0.46
1:D:325:ILE:CD1	1:D:334:ALA:CB	2.94	0.46
1:E:151:MET:HA	1:E:224:ILE:CG2	2.45	0.46
1:E:160:GLU:C	1:E:214:LYS:HE3	2.41	0.46
1:E:203:LEU:CD1	1:E:229:TYR:HD2	2.28	0.46
1:E:298:ALA:HB1	1:E:338:VAL:O	2.14	0.46
1:E:312:GLU:C	1:E:312:GLU:OE1	2.58	0.46
1:F:234:MET:CG	1:F:238:LEU:HD12	2.45	0.46
1:F:260:TRP:NE1	2:F:401:CMP:N9	2.64	0.46
1:G:130:ILE:HD13	1:G:151:MET:HE3	1.97	0.46
1:G:204:ILE:CG2	1:G:205:TYR:HD2	2.23	0.46
1:H:126:LEU:HD12	1:H:126:LEU:C	2.38	0.46
1:H:151:MET:HA	1:H:224:ILE:HG22	1.96	0.46
1:H:226:ARG:O	1:H:227:ASP:C	2.58	0.46
1:H:262:ARG:O	1:H:265:VAL:CB	2.54	0.46
1:H:276:ASP:HA	1:H:339:ALA:O	2.16	0.46
1:H:356:VAL:HG23	1:H:357:LEU:N	2.29	0.46
1:H:365:LYS:O	1:H:366:ARG:C	2.57	0.46
1:B:118:LYS:HB3	1:B:123:MET:CE	2.46	0.46
1:B:135:LEU:HD13	1:B:136:PHE:CE1	2.51	0.46
1:B:226:ARG:HA	1:B:229:TYR:HB3	1.97	0.46
1:B:325:ILE:HD11	1:B:334:ALA:H	1.79	0.46
1:C:272:VAL:CG2	1:C:273:GLN:H	2.24	0.46
1:D:129:ALA:HB3	1:D:222:TRP:HE1	1.78	0.46
1:D:157:ILE:O	1:D:157:ILE:HD12	2.16	0.46
1:D:266:ALA:C	1:D:268:ALA:N	2.68	0.46
1:D:322:PHE:CD2	1:D:322:PHE:C	2.93	0.46
1:E:133:ASN:C	1:E:133:ASN:OD1	2.59	0.46
1:F:140:ASP:N	1:F:143:GLU:OE1	2.46	0.46
1:F:153:PRO:HA	1:F:222:TRP:CZ3	2.49	0.46
1:F:170:ASP:O	1:F:171:ASN:OD1	2.34	0.46
1:G:210:ALA:C	1:G:211:ASP:OD1	2.59	0.46
1:H:153:PRO:HA	1:H:222:TRP:CZ3	2.51	0.46
1:H:272:VAL:HG22	1:H:273:GLN:N	2.31	0.46
1:A:152:PHE:CE2	1:A:223:GLY:CA	2.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:PHE:HB2	1:A:153:PRO:HD2	1.97	0.46
1:B:131:GLU:O	1:B:133:ASN:N	2.49	0.46
1:B:269:LEU:CB	1:B:346:VAL:CG2	2.73	0.46
1:B:270:GLU:O	1:B:346:VAL:HA	2.15	0.46
1:B:299:ALA:O	1:B:337:VAL:HA	2.15	0.46
1:C:130:ILE:HG13	1:C:136:PHE:CB	2.46	0.46
1:C:362:ASP:O	1:C:363:ILE:C	2.58	0.46
1:D:230:ARG:CA	1:D:234:MET:HE2	2.46	0.46
1:D:366:ARG:HG2	1:D:367:ASN:H	1.80	0.46
1:E:174:VAL:CG1	1:E:222:TRP:HB2	2.46	0.46
1:E:229:TYR:O	1:E:230:ARG:C	2.58	0.46
1:E:279:LYS:O	1:E:279:LYS:HG3	2.15	0.46
1:E:325:ILE:HG12	2:E:402:CMP:O3'	2.16	0.46
1:F:328:LEU:HD11	1:F:364:LEU:HD11	1.96	0.46
1:G:155:SER:O	1:G:156:PHE:CD1	2.69	0.46
1:H:188:TRP:CH2	1:H:190:THR:C	2.93	0.46
1:A:113:ARG:NE	1:D:113:ARG:O	2.49	0.46
1:A:249:SER:CA	1:A:262:ARG:NH2	2.68	0.46
1:A:279:LYS:HB3	1:A:338:VAL:CG2	2.43	0.46
1:B:171:ASN:HB2	1:B:173:TYR:CE1	2.51	0.46
1:B:273:GLN:CB	1:B:343:LEU:O	2.59	0.46
1:B:292:ILE:HB	1:B:346:VAL:CG1	2.45	0.46
1:C:120:TYR:CD2	1:C:121:LYS:N	2.84	0.46
1:C:375:VAL:HG23	1:C:376:SER:N	2.25	0.46
1:E:175:ILE:CD1	1:E:194:GLU:HA	2.41	0.46
1:E:178:GLY:CA	1:E:219:VAL:HG12	2.32	0.46
1:E:209:ARG:HD2	2:E:401:CMP:O5'	2.16	0.46
1:F:152:PHE:HD2	1:F:152:PHE:H	1.63	0.46
1:G:164:GLN:O	1:G:167:ASP:HB2	2.16	0.46
1:G:221:LEU:HA	1:G:221:LEU:HD23	1.42	0.46
1:G:251:VAL:HG12	1:G:254:LEU:HD21	1.90	0.46
1:H:302:GLN:O	1:H:309:GLU:O	2.33	0.46
1:A:111:TYR:O	1:A:112:VAL:CG1	2.64	0.46
1:A:111:TYR:CA	1:D:115:VAL:CG2	2.90	0.46
1:A:133:ASN:O	1:A:135:LEU:HD12	2.16	0.46
1:A:136:PHE:HE1	1:A:233:LEU:CD2	2.28	0.46
1:A:154:VAL:HG12	1:A:221:LEU:CB	2.32	0.46
1:A:247:PHE:HE1	1:A:294:LEU:HB3	1.81	0.46
1:B:260:TRP:CZ2	2:B:401:CMP:H8	2.51	0.46
1:B:302:GLN:O	1:B:310:PHE:CA	2.62	0.46
1:C:176:ASP:N	1:C:220:LYS:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:253:ILE:HD13	1:C:321:TYR:CE2	2.51	0.46
1:C:301:LEU:HD13	1:C:336:THR:HB	1.97	0.46
1:C:328:LEU:HD22	1:C:365:LYS:HE3	1.98	0.46
1:D:348:LEU:HD21	1:D:356:VAL:CG2	2.46	0.46
1:E:116:ILE:HG22	1:E:118:LYS:CG	2.43	0.46
1:E:164:GLN:CA	1:E:212:THR:HG22	2.37	0.46
1:E:363:ILE:O	1:E:366:ARG:HG2	2.16	0.46
1:F:130:ILE:HG13	1:F:136:PHE:CB	2.45	0.46
1:F:274:PHE:N	1:F:343:LEU:O	2.40	0.46
1:G:147:ILE:HD13	1:G:147:ILE:HG21	1.54	0.46
1:G:162:VAL:CG2	1:G:213:VAL:O	2.63	0.46
1:H:158:ALA:HA	1:H:215:ALA:HB1	1.98	0.46
1:H:285:GLU:HB2	1:H:333:ARG:CG	2.46	0.46
1:H:297:SER:HA	1:H:316:LEU:O	2.16	0.46
1:H:313:VAL:HG12	1:H:314:GLY:N	2.31	0.46
1:H:341:GLY:HA3	1:H:342:PRO:HD2	1.67	0.46
1:B:203:LEU:CD1	1:B:229:TYR:HD2	2.28	0.46
1:B:211:ASP:OD1	2:B:401:CMP:O1P	2.34	0.46
1:B:241:ARG:O	1:B:245:GLU:HB2	2.16	0.46
1:C:259:LYS:O	1:C:262:ARG:N	2.49	0.46
1:C:261:GLU:O	1:C:264:THR:N	2.49	0.46
1:C:268:ALA:O	1:C:352:ARG:NH1	2.49	0.46
1:C:343:LEU:HD12	1:C:343:LEU:HA	1.77	0.46
1:D:152:PHE:HE1	1:D:223:GLY:HA3	1.81	0.46
1:E:273:GLN:HE21	1:E:273:GLN:CA	2.20	0.46
1:E:325:ILE:CD1	1:E:334:ALA:HB3	2.46	0.46
1:F:131:GLU:C	1:F:133:ASN:H	2.23	0.46
1:F:232:ILE:HG23	1:F:233:LEU:HG	1.98	0.46
1:F:244:TYR:O	1:F:245:GLU:C	2.59	0.46
1:G:270:GLU:O	1:G:346:VAL:HA	2.15	0.46
1:G:300:VAL:CG2	1:G:316:LEU:HD11	2.46	0.46
1:H:131:GLU:OE1	1:H:131:GLU:CA	2.62	0.46
1:H:164:GLN:O	1:H:167:ASP:HB2	2.16	0.46
1:A:253:ILE:HG13	1:A:254:LEU:HG	1.97	0.45
1:A:343:LEU:HD12	1:A:343:LEU:HA	1.70	0.45
1:B:325:ILE:HD13	1:B:334:ALA:HB3	1.98	0.45
1:C:116:ILE:CG2	1:C:118:LYS:HZ2	2.29	0.45
1:C:158:ALA:HB2	1:C:218:ASN:N	2.29	0.45
1:C:300:VAL:CG2	1:C:312:GLU:OE2	2.64	0.45
1:D:113:ARG:NH1	1:D:146:ASP:OD1	2.49	0.45
1:D:147:ILE:O	1:D:148:PHE:C	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:114:LYS:HD2	1:F:114:LYS:HA	1.33	0.45
1:F:201:LEU:O	1:F:204:ILE:N	2.49	0.45
1:F:221:LEU:HD23	1:F:221:LEU:HA	1.48	0.45
1:G:123:MET:O	1:G:124:ALA:C	2.59	0.45
1:G:152:PHE:HE2	1:G:223:GLY:CA	2.29	0.45
1:G:292:ILE:O	1:G:345:CYS:HB3	2.17	0.45
1:H:188:TRP:HZ3	1:H:190:THR:C	2.22	0.45
1:H:221:LEU:HD23	1:H:221:LEU:HA	1.36	0.45
1:H:281:VAL:HG13	1:H:333:ARG:HG3	1.96	0.45
1:H:325:ILE:HG12	2:H:402:CMP:O3'	2.17	0.45
1:B:121:LYS:O	1:B:122:THR:C	2.59	0.45
1:B:365:LYS:O	1:B:368:ILE:N	2.35	0.45
1:C:144:ARG:NH1	1:C:144:ARG:HB2	2.30	0.45
1:D:234:MET:HG3	1:D:234:MET:O	2.14	0.45
1:D:362:ASP:O	1:D:365:LYS:HG3	2.16	0.45
1:E:230:ARG:NH1	1:E:230:ARG:HG2	2.31	0.45
1:E:255:GLU:OE1	1:E:255:GLU:CA	2.41	0.45
1:E:292:ILE:HB	1:E:346:VAL:CG1	2.38	0.45
1:E:328:LEU:HD11	1:E:364:LEU:HD11	1.98	0.45
1:F:160:GLU:O	1:F:214:LYS:HA	2.16	0.45
1:F:278:GLN:HG2	1:F:279:LYS:H	1.77	0.45
1:G:165:GLN:HG2	1:G:166:GLY:N	2.30	0.45
1:G:198:PHE:HD1	1:G:198:PHE:N	2.14	0.45
1:G:247:PHE:HE1	1:G:294:LEU:CB	2.29	0.45
1:G:265:VAL:C	1:G:269:LEU:CG	2.89	0.45
1:H:188:TRP:CH2	1:H:190:THR:CA	2.97	0.45
1:A:157:ILE:CB	1:A:218:ASN:OD1	2.65	0.45
1:A:280:ILE:HB	1:A:291:PHE:CE2	2.46	0.45
1:B:226:ARG:O	1:B:227:ASP:O	2.35	0.45
1:B:245:GLU:OE1	1:B:246:GLU:OE1	2.35	0.45
1:C:130:ILE:HD12	1:C:136:PHE:CD2	2.51	0.45
1:C:162:VAL:HG22	1:C:213:VAL:O	2.16	0.45
1:C:163:ILE:HD12	1:C:213:VAL:CG2	2.46	0.45
1:C:313:VAL:HG21	2:C:402:CMP:N6	2.32	0.45
1:D:123:MET:O	1:D:126:LEU:N	2.50	0.45
1:D:175:ILE:HD12	1:D:175:ILE:C	2.25	0.45
1:D:274:PHE:HD2	1:D:343:LEU:HD23	1.81	0.45
1:D:366:ARG:CG	1:D:367:ASN:N	2.79	0.45
1:E:175:ILE:HA	1:E:221:LEU:HD23	1.88	0.45
1:E:254:LEU:HB2	1:E:257:LEU:HD12	1.99	0.45
1:F:175:ILE:HG21	1:F:180:MET:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:366:ARG:HG2	1:F:367:ASN:N	2.31	0.45
1:H:371:TYR:CD1	2:H:402:CMP:C6	3.05	0.45
1:A:120:TYR:CD2	1:A:121:LYS:N	2.81	0.45
1:B:162:VAL:HG22	1:B:213:VAL:O	2.15	0.45
1:B:165:GLN:HE22	1:B:185:ASN:HD21	1.64	0.45
1:B:280:ILE:HD12	1:B:281:VAL:HG23	1.98	0.45
1:C:118:LYS:HB2	1:C:123:MET:HE1	1.97	0.45
1:C:154:VAL:O	1:C:221:LEU:N	2.37	0.45
1:D:154:VAL:HG12	1:D:221:LEU:HB2	1.99	0.45
1:D:316:LEU:O	1:D:316:LEU:CD2	2.64	0.45
1:F:153:PRO:HB3	1:F:222:TRP:CH2	2.51	0.45
1:F:325:ILE:CG1	2:F:402:CMP:O1P	2.65	0.45
1:G:325:ILE:O	1:G:328:LEU:N	2.49	0.45
1:G:368:ILE:HA	1:G:371:TYR:HD2	1.81	0.45
1:H:122:THR:C	1:H:125:ALA:HB3	2.39	0.45
1:H:173:TYR:CB	1:H:198:PHE:HE1	2.29	0.45
1:H:254:LEU:O	1:H:257:LEU:HG	2.17	0.45
1:H:260:TRP:HZ2	2:H:401:CMP:O2'	1.98	0.45
1:H:265:VAL:O	1:H:266:ALA:C	2.58	0.45
1:A:157:ILE:O	1:A:160:GLU:HB2	2.16	0.45
1:A:183:TYR:CE1	1:A:188:TRP:HB3	2.51	0.45
1:A:183:TYR:HE1	1:A:188:TRP:CB	2.28	0.45
1:A:221:LEU:HD23	1:A:221:LEU:HA	1.42	0.45
1:B:118:LYS:CE	1:B:148:PHE:O	2.54	0.45
1:B:302:GLN:O	1:B:310:PHE:CB	2.64	0.45
1:C:157:ILE:HB	1:C:218:ASN:OD1	2.17	0.45
1:C:283:GLN:CG	1:C:333:ARG:O	2.64	0.45
1:D:114:LYS:O	1:D:114:LYS:CG	2.62	0.45
1:D:128:LYS:C	1:D:130:ILE:N	2.74	0.45
1:D:174:VAL:HG13	1:D:222:TRP:HB2	1.98	0.45
1:D:358:GLY:C	1:D:360:CYS:H	2.25	0.45
1:E:119:ASP:O	1:E:120:TYR:C	2.59	0.45
1:E:230:ARG:HB3	1:E:234:MET:HE2	1.98	0.45
1:E:239:ARG:HD3	1:G:157:ILE:CG1	2.47	0.45
1:F:139:LEU:N	1:F:139:LEU:CD1	2.67	0.45
1:F:211:ASP:OD2	2:F:401:CMP:C3'	2.63	0.45
1:G:139:LEU:HD21	1:G:147:ILE:HD13	1.99	0.45
1:G:153:PRO:HA	1:G:222:TRP:CE3	2.51	0.45
1:G:183:TYR:HD1	1:G:188:TRP:CA	2.29	0.45
1:G:230:ARG:HG2	1:G:230:ARG:HH11	1.82	0.45
1:G:366:ARG:O	1:G:369:GLN:CB	2.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:371:TYR:OH	2:G:402:CMP:H2'	2.16	0.45
1:H:158:ALA:CA	1:H:217:THR:O	2.65	0.45
1:H:266:ALA:C	1:H:268:ALA:N	2.71	0.45
1:H:283:GLN:CA	1:H:333:ARG:O	2.63	0.45
1:A:230:ARG:CZ	1:A:234:MET:CE	2.94	0.45
1:A:266:ALA:C	1:A:268:ALA:N	2.71	0.45
1:B:259:LYS:CG	1:B:260:TRP:N	2.61	0.45
1:B:262:ARG:HE	1:B:262:ARG:HB3	1.42	0.45
1:C:221:LEU:HD23	1:C:221:LEU:HA	1.43	0.45
1:D:232:ILE:HG23	1:D:233:LEU:CG	2.45	0.45
1:D:254:LEU:HD22	1:D:254:LEU:C	2.41	0.45
1:D:268:ALA:O	1:D:352:ARG:NH1	2.50	0.45
1:D:283:GLN:HG2	1:D:284:GLY:N	2.30	0.45
1:E:194:GLU:O	1:E:355:ARG:HD2	2.17	0.45
1:E:265:VAL:CG1	1:E:269:LEU:CD2	2.65	0.45
1:E:266:ALA:C	1:E:268:ALA:N	2.72	0.45
1:E:293:ILE:CD1	1:E:343:LEU:HD11	2.46	0.45
1:G:269:LEU:HB3	1:G:346:VAL:HG22	1.95	0.45
1:H:352:ARG:HA	1:H:355:ARG:HB2	1.98	0.45
1:A:113:ARG:HH12	1:D:150:ALA:HB2	1.81	0.45
1:B:130:ILE:HD11	1:B:151:MET:CE	2.46	0.45
1:C:153:PRO:HA	1:C:222:TRP:CE3	2.51	0.45
1:C:352:ARG:O	1:C:353:PHE:C	2.58	0.45
1:D:200:GLU:CG	1:D:201:LEU:HD12	2.46	0.45
1:D:273:GLN:N	1:D:273:GLN:CD	2.73	0.45
1:D:300:VAL:HG13	1:D:313:VAL:HG13	1.99	0.45
1:E:118:LYS:CE	1:E:148:PHE:O	2.56	0.45
1:E:270:GLU:O	1:E:346:VAL:HA	2.17	0.45
1:F:130:ILE:HD12	1:F:151:MET:CE	2.47	0.45
1:G:123:MET:HE2	1:G:123:MET:HB2	1.87	0.45
1:G:171:ASN:OD1	1:G:225:ASP:HA	2.16	0.45
1:H:226:ARG:HA	1:H:229:TYR:HB3	1.99	0.45
1:H:254:LEU:HB2	1:H:257:LEU:HD12	1.98	0.45
1:H:262:ARG:HA	1:H:265:VAL:HG21	1.98	0.45
1:H:282:VAL:O	1:H:333:ARG:HB2	2.16	0.45
1:A:253:ILE:HG13	1:A:254:LEU:CG	2.45	0.45
1:A:321:TYR:CD1	1:A:321:TYR:O	2.68	0.45
1:C:120:TYR:CE2	1:C:124:ALA:HB2	2.51	0.45
1:C:188:TRP:CZ3	1:C:190:THR:CA	2.99	0.45
1:C:188:TRP:HZ3	1:C:190:THR:O	2.00	0.45
1:E:126:LEU:O	1:E:127:ALA:C	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:129:ALA:HA	1:F:132:LYS:HE3	1.99	0.45
1:F:209:ARG:HD2	2:F:401:CMP:O5'	2.16	0.45
1:G:175:ILE:HD12	1:G:175:ILE:C	2.24	0.45
1:G:234:MET:O	1:G:238:LEU:HD12	2.17	0.45
1:G:265:VAL:HG12	1:G:269:LEU:CD2	2.41	0.45
1:G:278:GLN:HG3	1:G:279:LYS:H	1.79	0.45
1:H:229:TYR:O	1:H:233:LEU:HD12	2.17	0.45
1:B:262:ARG:HA	1:B:265:VAL:HG21	1.97	0.45
1:C:176:ASP:O	1:C:194:GLU:HG2	2.17	0.45
1:C:188:TRP:CH2	1:C:190:THR:C	2.94	0.45
1:C:190:THR:CG2	1:C:191:SER:N	2.76	0.45
1:C:201:LEU:O	1:C:204:ILE:N	2.50	0.45
1:C:203:LEU:HD22	1:C:226:ARG:CG	2.46	0.45
1:C:293:ILE:CG1	1:C:345:CYS:SG	3.01	0.45
1:D:304:ARG:CB	1:D:308:GLU:CB	2.95	0.45
1:E:110:SER:HB2	1:H:115:VAL:HG22	1.99	0.45
1:E:147:ILE:O	1:E:150:ALA:N	2.50	0.45
1:E:180:MET:O	1:E:191:SER:HA	2.16	0.45
1:E:183:TYR:CD1	1:E:188:TRP:CB	3.00	0.45
1:E:203:LEU:CD1	1:E:229:TYR:CD2	2.95	0.45
1:E:232:ILE:HG23	1:E:233:LEU:HG	1.98	0.45
1:E:239:ARG:HH22	1:G:156:PHE:HD1	1.61	0.45
1:F:301:LEU:HD13	1:F:311:VAL:N	2.32	0.45
1:G:151:MET:HA	1:G:224:ILE:CG2	2.46	0.45
1:G:347:LYS:O	1:G:348:LEU:CD1	2.57	0.45
1:G:350:ARG:O	1:G:353:PHE:CB	2.57	0.45
1:H:302:GLN:O	1:H:310:PHE:CE1	2.69	0.45
1:A:249:SER:HA	1:A:262:ARG:NH2	2.32	0.45
1:B:261:GLU:O	1:B:264:THR:N	2.50	0.45
1:B:357:LEU:O	1:B:360:CYS:HB2	2.17	0.45
1:C:270:GLU:CB	1:C:271:PRO:CD	2.94	0.45
1:C:300:VAL:CG2	1:C:313:VAL:HG12	2.37	0.45
1:C:325:ILE:HG12	2:C:402:CMP:P	2.57	0.45
1:C:328:LEU:HD23	1:C:365:LYS:HE3	1.98	0.45
1:E:234:MET:HG3	1:E:238:LEU:CD1	2.47	0.45
1:E:253:ILE:CG2	1:E:321:TYR:CE2	2.96	0.45
1:E:281:VAL:CG1	1:E:333:ARG:NE	2.80	0.45
1:F:115:VAL:HG12	1:F:149:ASP:HB3	1.99	0.45
1:G:152:PHE:CD2	1:G:152:PHE:N	2.80	0.45
1:G:247:PHE:HE1	1:G:294:LEU:HB3	1.81	0.45
1:A:316:LEU:HB2	1:A:320:ASP:OD2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:LEU:O	1:B:126:LEU:CD1	2.47	0.44
1:D:119:ASP:OD1	1:D:119:ASP:C	2.59	0.44
1:D:237:THR:O	1:D:241:ARG:HG3	2.16	0.44
1:D:300:VAL:HG13	1:D:300:VAL:O	2.16	0.44
1:D:300:VAL:HG23	1:D:335:ALA:HB1	1.96	0.44
1:D:352:ARG:O	1:D:353:PHE:C	2.61	0.44
1:E:116:ILE:HG21	1:E:118:LYS:HZ2	1.82	0.44
1:E:297:SER:O	1:E:340:ARG:HB2	2.17	0.44
1:G:230:ARG:CB	1:G:234:MET:HE2	2.47	0.44
1:H:163:ILE:HD11	1:H:198:PHE:CZ	2.53	0.44
1:A:272:VAL:CG2	1:A:273:GLN:N	2.80	0.44
1:B:300:VAL:CG1	1:B:335:ALA:CB	2.94	0.44
1:C:366:ARG:O	1:C:369:GLN:CB	2.65	0.44
1:D:253:ILE:CD1	1:D:321:TYR:CD2	3.00	0.44
1:E:261:GLU:O	1:E:264:THR:N	2.50	0.44
1:E:278:GLN:O	1:E:338:VAL:HG22	2.18	0.44
1:F:113:ARG:CD	1:F:146:ASP:HA	2.47	0.44
1:F:121:LYS:O	1:F:123:MET:N	2.50	0.44
1:F:280:ILE:HB	1:F:291:PHE:CE2	2.51	0.44
1:G:175:ILE:HA	1:G:221:LEU:HD23	1.92	0.44
1:G:292:ILE:HB	1:G:346:VAL:CG1	2.44	0.44
1:G:295:GLU:CB	1:G:344:LYS:HB3	2.43	0.44
1:H:262:ARG:HE	1:H:262:ARG:HB3	1.48	0.44
1:H:328:LEU:HD12	1:H:328:LEU:H	1.82	0.44
1:A:139:LEU:CD2	1:A:147:ILE:CD1	2.96	0.44
1:A:201:LEU:O	1:A:204:ILE:N	2.51	0.44
1:A:271:PRO:O	1:A:272:VAL:HB	2.18	0.44
1:A:272:VAL:CG2	1:A:273:GLN:H	2.21	0.44
1:B:162:VAL:HG23	1:B:163:ILE:H	1.81	0.44
1:B:173:TYR:CD2	1:B:198:PHE:CZ	2.95	0.44
1:B:269:LEU:CD2	1:B:346:VAL:CG2	2.92	0.44
1:C:183:TYR:HD1	1:C:188:TRP:CA	2.28	0.44
1:C:259:LYS:O	1:C:262:ARG:CG	2.60	0.44
1:D:158:ALA:HB1	1:D:216:LYS:O	2.18	0.44
1:D:183:TYR:CD1	1:D:188:TRP:CB	3.01	0.44
1:E:239:ARG:HH22	1:G:156:PHE:HA	1.82	0.44
1:E:243:MET:HE3	1:G:157:ILE:HD11	1.97	0.44
1:E:302:GLN:NE2	1:E:374:PHE:CB	2.80	0.44
1:F:139:LEU:HD21	1:F:147:ILE:HD13	1.98	0.44
1:G:172:PHE:CE1	1:G:200:GLU:HB3	2.53	0.44
1:G:309:GLU:OE1	1:G:309:GLU:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:GLN:HE21	1:A:273:GLN:CA	2.23	0.44
1:B:124:ALA:O	1:B:127:ALA:HB3	2.17	0.44
1:B:200:GLU:CD	1:B:201:LEU:CD1	2.91	0.44
1:C:111:TYR:CD1	1:C:112:VAL:N	2.85	0.44
1:D:158:ALA:O	1:F:243:MET:HE1	2.16	0.44
1:D:198:PHE:HD1	1:D:198:PHE:H	1.66	0.44
1:D:335:ALA:HB3	2:D:402:CMP:H5'1	2.00	0.44
1:E:259:LYS:O	1:E:262:ARG:N	2.49	0.44
1:E:325:ILE:HD11	1:E:334:ALA:H	1.80	0.44
1:E:352:ARG:HA	1:E:355:ARG:HB2	2.00	0.44
1:F:131:GLU:CD	1:F:131:GLU:H	2.25	0.44
1:F:185:ASN:O	1:F:186:ASN:HB2	2.18	0.44
1:F:300:VAL:HG11	1:F:335:ALA:CB	2.47	0.44
1:G:138:HIS:O	1:G:139:LEU:C	2.57	0.44
1:G:274:PHE:CD2	1:G:343:LEU:HD23	2.52	0.44
1:A:293:ILE:CG1	1:A:343:LEU:HD11	2.48	0.44
1:B:152:PHE:HD2	1:B:152:PHE:N	2.14	0.44
1:B:202:ALA:HB1	1:B:207:THR:O	2.18	0.44
1:B:253:ILE:HG13	1:B:254:LEU:HD23	1.98	0.44
1:B:362:ASP:HA	1:B:365:LYS:HZ3	1.81	0.44
1:E:203:LEU:HD22	1:E:226:ARG:HD3	2.00	0.44
1:F:147:ILE:O	1:F:150:ALA:N	2.51	0.44
1:G:357:LEU:HD12	1:G:357:LEU:HA	1.67	0.44
1:H:126:LEU:O	1:H:127:ALA:C	2.59	0.44
1:H:153:PRO:CB	1:H:222:TRP:HZ3	2.28	0.44
1:A:149:ASP:OD1	1:B:120:TYR:HB2	2.17	0.44
1:A:294:LEU:O	1:A:295:GLU:CG	2.65	0.44
1:B:262:ARG:HA	1:B:265:VAL:HG23	1.99	0.44
1:D:257:LEU:HD21	1:D:360:CYS:SG	2.58	0.44
1:E:266:ALA:N	1:E:269:LEU:HD11	2.33	0.44
1:F:183:TYR:HD1	1:F:188:TRP:CA	2.30	0.44
1:F:220:LYS:C	1:F:221:LEU:HD23	2.42	0.44
1:F:253:ILE:HG13	1:F:254:LEU:N	2.30	0.44
1:F:253:ILE:C	1:F:255:GLU:H	2.25	0.44
1:F:282:VAL:HB	1:F:285:GLU:CD	2.42	0.44
1:G:130:ILE:HG13	1:G:136:PHE:CD2	2.53	0.44
1:G:147:ILE:HG23	1:G:232:ILE:HD13	2.00	0.44
1:H:229:TYR:CD1	1:H:233:LEU:HD12	2.45	0.44
1:H:230:ARG:HB3	1:H:234:MET:CE	2.47	0.44
1:A:144:ARG:HB2	1:A:144:ARG:HH11	1.79	0.44
1:A:238:LEU:O	1:A:241:ARG:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:183:TYR:HE1	1:B:188:TRP:HB2	1.78	0.44
1:C:295:GLU:CG	1:C:318:PRO:HG3	2.48	0.44
1:D:247:PHE:CD2	1:D:247:PHE:O	2.70	0.44
1:D:278:GLN:HG2	1:D:279:LYS:N	2.32	0.44
1:D:280:ILE:HB	1:D:291:PHE:HE2	1.82	0.44
1:D:316:LEU:CD2	1:D:316:LEU:C	2.91	0.44
1:E:175:ILE:HD13	1:E:194:GLU:CA	2.43	0.44
1:E:357:LEU:HD12	1:E:357:LEU:N	2.28	0.44
1:E:366:ARG:O	1:E:369:GLN:HB2	2.18	0.44
1:F:113:ARG:NE	1:F:146:ASP:OD1	2.51	0.44
1:F:153:PRO:N	1:F:222:TRP:HZ3	2.16	0.44
1:F:178:GLY:N	1:F:194:GLU:HG3	2.30	0.44
1:F:185:ASN:OD1	1:F:185:ASN:N	2.46	0.44
1:G:157:ILE:CA	1:G:218:ASN:OD1	2.66	0.44
1:H:147:ILE:O	1:H:150:ALA:N	2.51	0.44
1:H:273:GLN:HB3	1:H:343:LEU:O	2.17	0.44
1:A:115:VAL:HG12	1:A:149:ASP:HB3	2.00	0.44
1:A:130:ILE:HG23	1:A:131:GLU:N	2.33	0.44
1:A:247:PHE:C	1:A:247:PHE:HD2	2.26	0.44
1:B:164:GLN:O	1:B:167:ASP:HB2	2.18	0.44
1:C:130:ILE:O	1:C:131:GLU:C	2.60	0.44
1:C:130:ILE:CG1	1:C:136:PHE:CD2	3.01	0.44
1:C:151:MET:HA	1:C:224:ILE:CG2	2.48	0.44
1:C:175:ILE:HD11	1:C:195:GLY:N	2.33	0.44
1:C:353:PHE:CD1	1:C:357:LEU:HD22	2.53	0.44
1:D:230:ARG:HG2	1:D:234:MET:HE1	1.99	0.44
1:D:348:LEU:HD23	1:D:353:PHE:HA	1.99	0.44
1:F:147:ILE:O	1:F:148:PHE:C	2.60	0.44
1:F:152:PHE:CE2	1:F:223:GLY:C	2.96	0.44
1:F:278:GLN:HG2	1:F:279:LYS:N	2.27	0.44
1:F:331:ARG:HB3	1:F:332:PRO:CD	2.48	0.44
1:G:247:PHE:C	1:G:247:PHE:HD2	2.21	0.44
1:G:253:ILE:HG13	1:G:254:LEU:HD23	1.99	0.44
1:G:352:ARG:HA	1:G:355:ARG:HB2	1.99	0.44
1:G:357:LEU:CD1	1:G:357:LEU:N	2.74	0.44
1:H:126:LEU:HD11	1:H:151:MET:HE3	1.99	0.44
1:H:165:GLN:CG	1:H:166:GLY:N	2.81	0.44
1:H:172:PHE:HB3	1:H:224:ILE:HD13	1.94	0.44
1:A:120:TYR:CD1	1:B:148:PHE:CB	2.97	0.44
1:A:152:PHE:HD2	1:A:152:PHE:H	1.65	0.44
1:A:294:LEU:O	1:A:318:PRO:HB3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:GLY:O	1:A:320:ASP:HB2	2.18	0.44
1:B:175:ILE:HA	1:B:221:LEU:HD23	1.90	0.44
1:B:209:ARG:HD3	2:B:401:CMP:O2P	2.17	0.44
1:B:234:MET:HG3	1:B:238:LEU:CD1	2.42	0.44
1:B:263:LEU:O	1:B:266:ALA:CB	2.58	0.44
1:C:126:LEU:O	1:C:127:ALA:C	2.60	0.44
1:C:127:ALA:O	1:C:130:ILE:HG22	2.18	0.44
1:C:173:TYR:HB2	1:C:198:PHE:HE1	1.83	0.44
1:C:203:LEU:HD12	1:C:229:TYR:HD2	1.83	0.44
1:C:260:TRP:HA	1:C:263:LEU:HD23	1.99	0.44
1:D:121:LYS:O	1:D:123:MET:N	2.50	0.44
1:D:126:LEU:C	1:D:126:LEU:CD1	2.68	0.44
1:D:323:GLY:O	1:D:324:GLU:O	2.36	0.44
1:E:131:GLU:C	1:E:133:ASN:N	2.74	0.44
1:E:144:ARG:O	1:E:147:ILE:HG12	2.18	0.44
1:E:157:ILE:CB	1:E:218:ASN:OD1	2.66	0.44
1:E:163:ILE:O	1:E:213:VAL:N	2.39	0.44
1:E:276:ASP:C	1:E:278:GLN:H	2.25	0.44
1:F:119:ASP:O	1:F:120:TYR:C	2.60	0.44
1:F:126:LEU:C	1:F:126:LEU:CD1	2.81	0.44
1:F:269:LEU:CB	1:F:346:VAL:HG21	2.40	0.44
1:G:253:ILE:C	1:G:255:GLU:H	2.25	0.44
1:H:138:HIS:HD1	1:H:138:HIS:H	1.65	0.44
1:H:173:TYR:O	1:H:197:SER:HA	2.17	0.44
1:H:283:GLN:OE1	1:H:302:GLN:HG2	2.18	0.44
1:H:360:CYS:O	1:H:364:LEU:HD23	2.18	0.44
1:A:118:LYS:CB	1:A:123:MET:HE1	2.48	0.43
1:A:183:TYR:HE1	1:A:188:TRP:HB2	1.79	0.43
1:A:325:ILE:O	1:A:328:LEU:N	2.51	0.43
1:B:294:LEU:N	1:B:294:LEU:CD1	2.52	0.43
1:C:245:GLU:OE1	1:C:245:GLU:C	2.61	0.43
1:C:325:ILE:HD11	1:C:334:ALA:HB3	1.99	0.43
1:D:126:LEU:CB	1:D:222:TRP:CZ2	2.91	0.43
1:D:226:ARG:HA	1:D:229:TYR:HB3	1.99	0.43
1:D:230:ARG:NH1	1:D:230:ARG:HG2	2.33	0.43
1:D:325:ILE:O	1:D:326:ALA:C	2.62	0.43
1:E:123:MET:HE2	1:E:123:MET:HB2	1.77	0.43
1:E:238:LEU:HD23	1:E:238:LEU:HA	1.71	0.43
1:E:252:SER:OG	1:E:253:ILE:N	2.41	0.43
1:E:284:GLY:C	1:E:332:PRO:HB3	2.43	0.43
1:E:293:ILE:HD12	1:E:343:LEU:HD11	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:324:GLU:OE2	1:E:371:TYR:HE2	2.00	0.43
1:F:114:LYS:CE	1:F:115:VAL:CG2	2.96	0.43
1:F:157:ILE:O	1:H:243:MET:HE1	2.18	0.43
1:F:278:GLN:O	1:F:279:LYS:HB3	2.18	0.43
1:F:300:VAL:HG13	1:F:336:THR:O	2.18	0.43
1:F:348:LEU:CD2	1:F:356:VAL:CG2	2.96	0.43
1:G:180:MET:O	1:G:191:SER:HA	2.18	0.43
1:G:203:LEU:HD22	1:G:226:ARG:CG	2.48	0.43
1:G:283:GLN:N	1:G:336:THR:OG1	2.39	0.43
1:H:123:MET:HE2	1:H:123:MET:HB2	1.74	0.43
1:H:146:ASP:O	1:H:147:ILE:C	2.60	0.43
1:H:158:ALA:HA	1:H:217:THR:O	2.16	0.43
1:H:173:TYR:HD1	1:H:223:GLY:HA3	1.83	0.43
1:A:210:ALA:C	1:A:211:ASP:OD1	2.61	0.43
1:A:322:PHE:CD2	1:A:337:VAL:HG21	2.53	0.43
1:A:362:ASP:HA	1:A:365:LYS:HZ3	1.83	0.43
1:B:115:VAL:HA	1:B:149:ASP:HB3	2.00	0.43
1:B:171:ASN:OD1	1:B:225:ASP:HA	2.18	0.43
1:B:262:ARG:O	1:B:265:VAL:CB	2.58	0.43
1:B:276:ASP:C	1:B:278:GLN:N	2.75	0.43
1:B:365:LYS:O	1:B:368:ILE:CG1	2.54	0.43
1:C:173:TYR:CB	1:C:198:PHE:HE1	2.31	0.43
1:C:243:MET:HE3	1:C:243:MET:HB2	1.76	0.43
1:D:175:ILE:HG22	1:D:221:LEU:CD2	2.48	0.43
1:D:204:ILE:HG22	1:D:205:TYR:CE2	2.51	0.43
1:D:299:ALA:N	1:D:338:VAL:O	2.42	0.43
1:D:349:ASP:C	1:D:349:ASP:OD1	2.58	0.43
1:E:152:PHE:CE2	1:E:223:GLY:CA	2.96	0.43
1:F:203:LEU:CD1	1:F:229:TYR:CD2	2.96	0.43
1:H:131:GLU:C	1:H:133:ASN:H	2.24	0.43
1:H:291:PHE:CD1	1:H:347:LYS:NZ	2.86	0.43
1:A:119:ASP:O	1:A:120:TYR:C	2.61	0.43
1:A:157:ILE:HD12	1:A:157:ILE:C	2.38	0.43
1:A:173:TYR:HD1	1:A:223:GLY:CA	2.32	0.43
1:A:209:ARG:HA	2:A:401:CMP:O2P	2.18	0.43
1:A:309:GLU:CD	1:A:310:PHE:H	2.26	0.43
1:A:325:ILE:CD1	1:A:334:ALA:HB2	2.48	0.43
1:B:244:TYR:O	1:B:245:GLU:C	2.61	0.43
1:C:111:TYR:O	1:C:112:VAL:HG12	2.13	0.43
1:C:122:THR:C	1:C:125:ALA:HB3	2.42	0.43
1:C:163:ILE:HD11	1:C:198:PHE:CZ	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:262:ARG:HA	1:C:265:VAL:CG2	2.47	0.43
1:C:266:ALA:C	1:C:268:ALA:N	2.72	0.43
1:C:287:GLY:HA3	1:C:326:ALA:HB3	1.97	0.43
1:D:254:LEU:HB2	1:D:257:LEU:HD12	2.00	0.43
1:D:323:GLY:HA2	2:D:402:CMP:O2P	2.18	0.43
1:E:198:PHE:C	1:E:198:PHE:HD1	2.13	0.43
1:F:139:LEU:HD21	1:F:147:ILE:CD1	2.48	0.43
1:F:151:MET:HA	1:F:224:ILE:CG2	2.48	0.43
1:F:161:THR:HA	1:F:214:LYS:CD	2.34	0.43
1:F:247:PHE:CE2	1:F:292:ILE:HG21	2.53	0.43
1:G:204:ILE:HG22	1:G:205:TYR:CE2	2.52	0.43
1:H:135:LEU:CD1	1:H:136:PHE:N	2.78	0.43
1:H:303:ARG:N	1:H:310:PHE:CE1	2.85	0.43
1:A:112:VAL:O	1:A:231:ARG:NH2	2.51	0.43
1:A:135:LEU:CD1	1:A:136:PHE:CD2	3.02	0.43
1:A:226:ARG:O	1:A:227:ASP:O	2.37	0.43
1:B:139:LEU:CD2	1:B:147:ILE:CD1	2.95	0.43
1:B:153:PRO:CA	1:B:222:TRP:HZ3	2.27	0.43
1:B:276:ASP:OD2	1:B:341:GLY:N	2.39	0.43
1:B:362:ASP:CG	1:B:363:ILE:HG13	2.43	0.43
1:C:280:ILE:HB	1:C:291:PHE:CE2	2.52	0.43
1:C:285:GLU:HB2	1:C:333:ARG:CG	2.48	0.43
1:D:201:LEU:O	1:D:205:TYR:N	2.49	0.43
1:E:135:LEU:CD1	1:E:135:LEU:C	2.90	0.43
1:E:249:SER:H	1:E:262:ARG:HH22	1.57	0.43
1:E:305:SER:O	1:E:306:GLU:C	2.60	0.43
2:E:402:CMP:N3	2:E:402:CMP:H2'	2.32	0.43
1:F:152:PHE:CD2	1:F:152:PHE:N	2.83	0.43
1:F:258:ASP:O	1:F:259:LYS:C	2.61	0.43
1:G:120:TYR:CD2	1:G:120:TYR:O	2.72	0.43
1:G:129:ALA:CB	1:G:222:TRP:HE1	2.30	0.43
1:H:130:ILE:CD1	1:H:136:PHE:CE2	3.02	0.43
1:H:157:ILE:C	1:H:157:ILE:CD1	2.92	0.43
1:B:115:VAL:O	1:B:115:VAL:CG2	2.65	0.43
1:C:148:PHE:CE1	1:D:120:TYR:CE1	3.06	0.43
1:C:322:PHE:CD1	1:C:322:PHE:N	2.85	0.43
1:D:285:GLU:HB3	1:D:286:PRO:CD	2.48	0.43
1:D:333:ARG:HA	2:D:402:CMP:O1P	2.19	0.43
1:D:371:TYR:OH	2:D:402:CMP:C8	2.66	0.43
1:E:120:TYR:O	1:E:121:LYS:C	2.56	0.43
1:E:138:HIS:O	1:E:139:LEU:C	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:178:GLY:N	1:E:194:GLU:HG3	2.29	0.43
1:E:253:ILE:C	1:E:255:GLU:H	2.26	0.43
1:G:253:ILE:H	1:G:253:ILE:HG12	1.49	0.43
1:G:283:GLN:HG2	1:G:284:GLY:N	2.32	0.43
1:G:365:LYS:O	1:G:368:ILE:N	2.42	0.43
1:H:204:ILE:HG21	1:H:205:TYR:CE2	2.54	0.43
1:H:258:ASP:O	1:H:262:ARG:CG	2.66	0.43
1:A:196:GLY:HA2	1:A:355:ARG:HH21	1.74	0.43
1:A:204:ILE:CG2	1:A:205:TYR:HD2	2.28	0.43
1:B:157:ILE:CA	1:B:218:ASN:OD1	2.66	0.43
1:B:234:MET:O	1:B:238:LEU:HD12	2.19	0.43
1:B:289:GLU:HG2	1:B:333:ARG:HH22	1.83	0.43
1:B:317:GLY:O	1:B:320:ASP:HB2	2.19	0.43
1:B:349:ASP:C	1:B:349:ASP:OD1	2.61	0.43
1:C:162:VAL:HG23	1:C:213:VAL:O	2.18	0.43
1:C:276:ASP:C	1:C:278:GLN:N	2.77	0.43
1:D:357:LEU:O	1:D:358:GLY:C	2.61	0.43
1:E:113:ARG:O	1:H:112:VAL:CG1	2.67	0.43
1:E:160:GLU:O	1:E:214:LYS:HD2	2.19	0.43
1:E:200:GLU:HG2	1:E:201:LEU:N	2.33	0.43
1:E:224:ILE:HD12	1:E:224:ILE:H	1.78	0.43
1:E:269:LEU:CB	1:E:346:VAL:HG23	2.47	0.43
1:E:294:LEU:C	1:E:295:GLU:HG2	2.43	0.43
1:E:300:VAL:HG13	1:E:336:THR:O	2.17	0.43
1:E:324:GLU:HG2	1:E:325:ILE:N	2.34	0.43
1:F:183:TYR:CD1	1:F:188:TRP:CB	3.01	0.43
1:G:152:PHE:HD2	1:G:152:PHE:H	1.66	0.43
1:H:251:VAL:CG1	1:H:254:LEU:CD2	2.87	0.43
1:H:254:LEU:C	1:H:254:LEU:HD12	2.43	0.43
1:A:114:LYS:HB3	1:A:114:LYS:HE2	1.69	0.43
1:B:153:PRO:CA	1:B:222:TRP:CE3	2.98	0.43
1:B:188:TRP:CD1	1:B:188:TRP:C	2.93	0.43
1:B:220:LYS:O	1:B:221:LEU:HD23	2.19	0.43
1:B:316:LEU:HD12	1:B:316:LEU:HA	1.42	0.43
1:D:133:ASN:OD1	1:D:133:ASN:C	2.62	0.43
1:D:244:TYR:O	1:D:245:GLU:C	2.59	0.43
1:D:294:LEU:HD13	1:D:344:LYS:C	2.43	0.43
1:E:127:ALA:O	1:E:128:LYS:C	2.61	0.43
1:E:152:PHE:CE2	1:E:223:GLY:HA3	2.42	0.43
1:E:160:GLU:O	1:E:214:LYS:HA	2.18	0.43
1:E:165:GLN:CB	1:E:211:ASP:O	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:144:ARG:HG2	1:F:145:SER:H	1.82	0.43
1:F:184:VAL:O	1:F:185:ASN:HB2	2.19	0.43
1:F:233:LEU:O	1:F:234:MET:C	2.60	0.43
1:F:324:GLU:HG2	1:F:325:ILE:N	2.33	0.43
1:G:211:ASP:OD1	2:G:401:CMP:H5'1	2.14	0.43
1:G:269:LEU:HB2	1:G:346:VAL:HG21	1.99	0.43
1:G:350:ARG:O	1:G:353:PHE:N	2.51	0.43
1:A:281:VAL:CG1	1:A:333:ARG:CG	2.92	0.43
1:B:118:LYS:NZ	1:B:151:MET:O	2.41	0.43
1:B:230:ARG:CB	1:B:234:MET:HE2	2.49	0.43
1:B:238:LEU:HD23	1:B:238:LEU:HA	1.76	0.43
1:B:283:GLN:HG2	1:B:284:GLY:N	2.33	0.43
1:B:365:LYS:O	1:B:366:ARG:C	2.62	0.43
1:C:241:ARG:NH2	1:C:263:LEU:HB3	2.32	0.43
1:C:280:ILE:HD11	1:C:337:VAL:CB	2.43	0.43
1:C:288:ASP:C	1:C:327:LEU:HD11	2.43	0.43
1:D:262:ARG:HA	1:D:265:VAL:HG23	2.00	0.43
1:E:158:ALA:HB2	1:E:218:ASN:N	2.34	0.43
1:E:201:LEU:H	1:E:201:LEU:HD12	1.83	0.43
1:F:131:GLU:N	1:F:131:GLU:CD	2.76	0.43
1:F:204:ILE:CG2	1:F:238:LEU:HD11	2.49	0.43
1:F:230:ARG:CB	1:F:234:MET:CE	2.96	0.43
1:F:243:MET:HE3	1:F:243:MET:HB2	1.74	0.43
1:F:289:GLU:HG2	1:F:291:PHE:CE1	2.53	0.43
1:G:123:MET:HE2	1:H:123:MET:HE3	2.00	0.43
1:H:174:VAL:HG23	1:H:196:GLY:O	2.19	0.43
1:H:303:ARG:CB	1:H:308:GLU:H	2.32	0.43
1:H:366:ARG:CG	1:H:367:ASN:N	2.81	0.43
1:A:203:LEU:CD1	1:A:229:TYR:HD2	2.32	0.43
1:B:123:MET:O	1:B:125:ALA:N	2.52	0.43
1:C:139:LEU:HD22	1:C:144:ARG:CA	2.49	0.43
1:C:148:PHE:CD1	1:D:120:TYR:HD1	2.34	0.43
1:D:220:LYS:C	1:D:221:LEU:HD23	2.43	0.43
1:D:301:LEU:HD21	1:D:310:PHE:CG	2.52	0.43
1:D:328:LEU:H	1:D:328:LEU:HD12	1.83	0.43
1:E:173:TYR:HD1	1:E:223:GLY:CA	2.32	0.43
1:E:297:SER:O	1:E:340:ARG:N	2.46	0.43
1:F:204:ILE:CG2	1:F:205:TYR:CE2	3.02	0.43
1:F:229:TYR:HE1	1:F:233:LEU:HD13	1.78	0.43
1:F:342:PRO:O	1:F:342:PRO:CG	2.67	0.43
1:G:130:ILE:HD13	1:G:151:MET:CE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:152:PHE:HD2	1:G:152:PHE:N	2.15	0.43
1:G:220:LYS:O	1:G:221:LEU:HD23	2.19	0.43
1:A:254:LEU:HB2	1:A:257:LEU:HD12	2.00	0.43
1:A:273:GLN:CB	1:A:343:LEU:O	2.57	0.43
1:B:358:GLY:C	1:B:360:CYS:H	2.27	0.43
1:C:111:TYR:CE1	1:F:111:TYR:CD2	2.88	0.43
1:D:157:ILE:HD11	1:F:243:MET:HE3	2.01	0.43
1:G:300:VAL:HG13	1:G:335:ALA:HB1	1.99	0.43
1:H:172:PHE:HE1	1:H:200:GLU:HB3	1.84	0.43
1:H:260:TRP:CD1	2:H:401:CMP:C8	3.02	0.43
1:A:120:TYR:HE2	1:A:124:ALA:HB2	1.84	0.42
1:A:131:GLU:H	1:A:131:GLU:CD	2.22	0.42
1:A:147:ILE:O	1:A:148:PHE:C	2.59	0.42
1:A:158:ALA:CB	1:A:216:LYS:O	2.60	0.42
1:A:175:ILE:HG21	1:A:180:MET:CG	2.49	0.42
1:A:230:ARG:HG2	1:A:234:MET:CE	2.49	0.42
1:A:232:ILE:HG23	1:A:233:LEU:HG	2.01	0.42
1:A:352:ARG:O	1:A:353:PHE:C	2.58	0.42
1:B:173:TYR:CB	1:B:198:PHE:HE1	2.32	0.42
1:B:178:GLY:HA3	1:B:219:VAL:HB	2.00	0.42
1:B:201:LEU:HB2	2:B:401:CMP:O3'	2.18	0.42
1:B:224:ILE:HD13	1:B:224:ILE:C	2.38	0.42
1:B:248:LEU:HD23	1:B:248:LEU:HA	1.72	0.42
1:B:263:LEU:HD23	1:B:263:LEU:HA	1.61	0.42
1:C:139:LEU:HB3	1:C:143:GLU:HB2	2.00	0.42
1:C:182:VAL:HG23	1:C:190:THR:H	1.81	0.42
1:E:110:SER:OG	1:H:115:VAL:CG2	2.67	0.42
1:E:131:GLU:OE1	1:E:132:LYS:N	2.51	0.42
1:E:230:ARG:CA	1:E:234:MET:HE2	2.49	0.42
1:E:273:GLN:NE2	1:E:273:GLN:H	1.88	0.42
1:F:113:ARG:CD	1:F:146:ASP:OD2	2.64	0.42
1:F:122:THR:C	1:F:125:ALA:HB3	2.44	0.42
1:F:347:LYS:HB3	1:F:347:LYS:HE3	1.16	0.42
1:F:368:ILE:O	1:F:371:TYR:HB2	2.19	0.42
1:G:112:VAL:HG12	1:G:231:ARG:NE	2.34	0.42
1:G:138:HIS:H	1:G:138:HIS:HD1	1.65	0.42
1:G:173:TYR:O	1:G:197:SER:HA	2.19	0.42
1:G:265:VAL:HG12	1:G:269:LEU:CG	2.48	0.42
1:H:170:ASP:H	1:H:209:ARG:CZ	2.32	0.42
1:A:111:TYR:C	1:A:112:VAL:CB	2.92	0.42
1:A:120:TYR:HD2	1:A:121:LYS:CA	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:GLY:O	1:A:324:GLU:C	2.62	0.42
1:A:357:LEU:HB2	1:A:360:CYS:HB2	2.01	0.42
1:B:203:LEU:HD22	1:B:226:ARG:CB	2.47	0.42
1:C:113:ARG:CD	1:F:112:VAL:HB	2.27	0.42
1:C:130:ILE:HD13	1:C:151:MET:HE3	2.01	0.42
1:C:230:ARG:CZ	1:C:234:MET:CE	2.91	0.42
1:D:362:ASP:O	1:D:365:LYS:N	2.52	0.42
1:E:203:LEU:HD22	1:E:226:ARG:CD	2.49	0.42
1:E:285:GLU:OE1	1:E:285:GLU:CA	2.66	0.42
1:E:308:GLU:O	1:E:309:GLU:HG2	2.19	0.42
1:E:325:ILE:CG1	2:E:402:CMP:P	3.07	0.42
1:E:329:MET:HB2	1:E:331:ARG:HG2	2.01	0.42
1:E:366:ARG:HH11	1:E:366:ARG:HD3	1.51	0.42
1:F:129:ALA:HB2	1:F:222:TRP:HE1	1.83	0.42
1:H:118:LYS:O	1:H:119:ASP:C	2.62	0.42
1:H:260:TRP:NE1	2:H:401:CMP:C8	2.81	0.42
1:A:115:VAL:CG2	1:D:112:VAL:N	2.61	0.42
1:A:204:ILE:CG2	1:A:238:LEU:HD11	2.49	0.42
1:A:226:ARG:HA	1:A:229:TYR:HB3	2.01	0.42
1:A:239:ARG:NH2	1:C:156:PHE:CD1	2.66	0.42
1:A:293:ILE:CG2	1:A:317:GLY:O	2.66	0.42
1:A:360:CYS:O	1:A:364:LEU:HD23	2.18	0.42
1:A:365:LYS:HA	1:A:368:ILE:HD11	2.01	0.42
1:B:260:TRP:CD1	2:B:401:CMP:N7	2.85	0.42
1:C:246:GLU:HA	1:C:249:SER:OG	2.18	0.42
1:C:368:ILE:HG13	1:C:368:ILE:H	1.66	0.42
1:D:143:GLU:O	1:D:146:ASP:HB2	2.19	0.42
1:D:182:VAL:HG23	1:D:189:ALA:HB3	2.01	0.42
1:D:254:LEU:CD2	1:D:255:GLU:N	2.80	0.42
1:D:296:GLY:HA2	1:D:342:PRO:O	2.17	0.42
1:D:318:PRO:O	1:D:319:SER:CB	2.66	0.42
1:E:185:ASN:N	1:E:185:ASN:OD1	2.48	0.42
1:E:199:GLY:H	2:E:401:CMP:H4'	1.85	0.42
1:E:353:PHE:O	1:E:357:LEU:HB2	2.19	0.42
1:F:130:ILE:CD1	1:F:136:PHE:CE2	3.02	0.42
1:F:175:ILE:CD1	1:F:193:GLY:O	2.67	0.42
1:F:211:ASP:OD1	2:F:401:CMP:H5'1	2.18	0.42
1:G:148:PHE:CG	1:H:120:TYR:HE1	2.35	0.42
1:G:152:PHE:HD2	1:G:152:PHE:C	2.19	0.42
1:G:241:ARG:O	1:G:242:LYS:C	2.60	0.42
1:H:116:ILE:HD13	1:H:116:ILE:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:284:GLY:H	1:H:333:ARG:C	2.22	0.42
1:A:224:ILE:HD13	1:A:224:ILE:N	2.30	0.42
1:B:118:LYS:CB	1:B:123:MET:CE	2.98	0.42
1:B:283:GLN:HG3	1:B:333:ARG:O	2.18	0.42
1:B:329:MET:HA	1:B:329:MET:HE2	2.00	0.42
1:B:329:MET:HB2	1:B:331:ARG:HG2	2.00	0.42
1:C:121:LYS:C	1:C:123:MET:N	2.74	0.42
1:C:291:PHE:CZ	1:C:347:LYS:NZ	2.86	0.42
1:D:165:GLN:CG	1:D:166:GLY:N	2.81	0.42
1:D:269:LEU:CB	1:D:346:VAL:CG2	2.89	0.42
1:E:111:TYR:C	1:E:112:VAL:CG2	2.92	0.42
1:F:253:ILE:CG2	1:F:321:TYR:HE2	2.32	0.42
1:G:185:ASN:O	1:G:186:ASN:HB2	2.18	0.42
1:G:252:SER:OG	1:G:253:ILE:HG23	2.19	0.42
1:H:135:LEU:HD13	1:H:136:PHE:CE1	2.54	0.42
1:H:151:MET:HA	1:H:224:ILE:CG2	2.49	0.42
1:H:204:ILE:HG21	1:H:205:TYR:HE2	1.84	0.42
1:H:321:TYR:C	1:H:321:TYR:HD1	2.26	0.42
1:H:350:ARG:O	1:H:353:PHE:N	2.52	0.42
1:A:134:VAL:HG13	1:A:135:LEU:N	2.34	0.42
1:A:235:GLY:O	1:A:238:LEU:N	2.53	0.42
1:A:272:VAL:CG2	1:A:273:GLN:NE2	2.83	0.42
1:A:278:GLN:O	1:A:279:LYS:HB3	2.18	0.42
1:C:276:ASP:C	1:C:278:GLN:H	2.26	0.42
1:D:200:GLU:CD	1:D:201:LEU:CD1	2.92	0.42
1:D:263:LEU:O	1:D:266:ALA:CB	2.67	0.42
1:D:290:PHE:HB2	1:D:327:LEU:HD22	2.02	0.42
1:D:293:ILE:HD11	1:D:343:LEU:HD13	1.91	0.42
1:F:138:HIS:O	1:F:139:LEU:C	2.60	0.42
1:F:204:ILE:HD13	1:F:238:LEU:CD1	2.45	0.42
1:F:247:PHE:CE1	1:F:294:LEU:HB3	2.54	0.42
1:G:192:VAL:O	1:G:192:VAL:HG12	2.18	0.42
1:A:171:ASN:OD1	1:A:225:ASP:HA	2.20	0.42
1:A:309:GLU:HG3	1:A:310:PHE:O	2.19	0.42
1:A:325:ILE:HG13	2:A:402:CMP:O2P	2.18	0.42
1:A:368:ILE:O	1:A:371:TYR:HB2	2.19	0.42
1:B:274:PHE:CE2	1:B:280:ILE:HG22	2.55	0.42
1:D:262:ARG:HG3	1:D:263:LEU:N	2.35	0.42
1:D:315:ARG:NH1	1:D:340:ARG:HH22	2.17	0.42
1:E:148:PHE:CE1	1:F:120:TYR:HE1	2.38	0.42
1:E:200:GLU:HG2	1:E:201:LEU:HG	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:239:ARG:HH11	1:F:239:ARG:HD2	1.63	0.42
1:F:266:ALA:HA	1:F:269:LEU:CD1	2.46	0.42
1:G:163:ILE:O	1:G:212:THR:HG22	2.19	0.42
1:G:184:VAL:O	1:G:185:ASN:HB2	2.19	0.42
1:G:260:TRP:NE1	2:G:401:CMP:C2'	2.76	0.42
1:G:263:LEU:O	1:G:266:ALA:N	2.53	0.42
1:G:358:GLY:C	1:G:360:CYS:H	2.27	0.42
1:H:139:LEU:CB	1:H:143:GLU:HB2	2.50	0.42
1:H:158:ALA:CB	1:H:217:THR:O	2.65	0.42
1:A:144:ARG:NH1	1:A:144:ARG:CB	2.80	0.42
1:A:263:LEU:O	1:A:266:ALA:N	2.53	0.42
1:A:302:GLN:O	1:A:310:PHE:HA	2.19	0.42
1:A:348:LEU:CD2	1:A:356:VAL:HG21	2.47	0.42
1:B:139:LEU:HB3	1:B:143:GLU:CB	2.49	0.42
1:B:154:VAL:O	1:B:154:VAL:CG1	2.62	0.42
1:B:199:GLY:H	2:B:401:CMP:H4'	1.84	0.42
1:C:110:SER:C	1:F:114:LYS:CE	2.93	0.42
1:C:158:ALA:HA	1:C:215:ALA:HB3	2.01	0.42
1:C:260:TRP:NE1	2:C:401:CMP:C2'	2.80	0.42
1:D:251:VAL:C	1:D:252:SER:O	2.60	0.42
1:D:342:PRO:O	1:D:342:PRO:HG2	2.20	0.42
1:E:130:ILE:CG2	1:E:131:GLU:N	2.83	0.42
1:E:135:LEU:HD13	1:E:136:PHE:CG	2.55	0.42
1:E:147:ILE:HD13	1:E:147:ILE:HG21	1.40	0.42
1:E:253:ILE:HG13	1:E:254:LEU:N	2.33	0.42
1:E:327:LEU:HD23	1:E:353:PHE:CZ	2.55	0.42
1:F:116:ILE:O	1:F:118:LYS:HG3	2.19	0.42
1:G:172:PHE:O	1:G:224:ILE:CD1	2.67	0.42
1:G:188:TRP:CH2	1:G:190:THR:CA	3.03	0.42
1:H:295:GLU:O	1:H:344:LYS:N	2.53	0.42
1:A:153:PRO:CA	1:A:222:TRP:CE3	3.01	0.42
1:A:203:LEU:CD1	1:A:229:TYR:CD2	3.00	0.42
1:A:247:PHE:CD2	1:A:247:PHE:O	2.73	0.42
1:A:363:ILE:H	1:A:363:ILE:HG13	1.51	0.42
1:B:134:VAL:O	1:B:134:VAL:CG2	2.64	0.42
1:B:211:ASP:OD2	2:B:401:CMP:N3	2.52	0.42
1:B:322:PHE:CE2	1:B:337:VAL:HG21	2.54	0.42
1:B:327:LEU:HD23	1:B:353:PHE:CE1	2.55	0.42
1:C:110:SER:CB	1:F:114:LYS:HZ3	2.32	0.42
1:C:123:MET:HE2	1:C:123:MET:HB2	1.78	0.42
1:D:135:LEU:HD13	1:D:136:PHE:CG	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:242:LYS:HD2	1:D:242:LYS:HA	1.66	0.42
1:D:260:TRP:CA	1:D:263:LEU:HD12	2.44	0.42
1:D:305:SER:O	1:D:306:GLU:C	2.61	0.42
1:E:136:PHE:O	1:E:139:LEU:HD11	2.20	0.42
1:E:171:ASN:H	1:E:209:ARG:HH22	1.67	0.42
1:F:111:TYR:CD2	1:F:112:VAL:N	2.87	0.42
1:F:162:VAL:HG22	1:F:213:VAL:O	2.19	0.42
1:F:173:TYR:HD1	1:F:223:GLY:CA	2.33	0.42
1:F:203:LEU:HD22	1:F:226:ARG:HD3	2.01	0.42
1:F:253:ILE:HG13	1:F:254:LEU:HG	2.02	0.42
1:F:321:TYR:HD1	1:F:322:PHE:N	2.16	0.42
1:G:183:TYR:CD1	1:G:188:TRP:CB	3.03	0.42
1:G:266:ALA:O	1:G:269:LEU:N	2.51	0.42
1:H:116:ILE:HA	1:H:117:PRO:HD3	1.77	0.42
1:H:174:VAL:O	1:H:174:VAL:CG1	2.67	0.42
1:A:259:LYS:O	1:A:260:TRP:C	2.63	0.42
1:B:116:ILE:HA	1:B:117:PRO:HD3	1.78	0.42
1:B:126:LEU:O	1:B:129:ALA:HB3	2.20	0.42
1:C:111:TYR:C	1:C:112:VAL:CG1	2.90	0.42
1:C:245:GLU:OE1	1:C:246:GLU:N	2.53	0.42
1:D:163:ILE:CD1	1:D:213:VAL:HB	2.39	0.42
1:D:175:ILE:HG21	1:D:180:MET:CG	2.49	0.42
1:D:183:TYR:HA	1:D:188:TRP:HA	2.02	0.42
1:D:368:ILE:HD13	1:D:368:ILE:HG21	1.84	0.42
1:E:111:TYR:CD2	1:H:111:TYR:OH	2.73	0.42
1:E:133:ASN:ND2	1:E:174:VAL:HG21	2.35	0.42
1:E:163:ILE:HD11	1:E:198:PHE:CE2	2.54	0.42
1:E:348:LEU:HD23	1:E:353:PHE:HA	2.01	0.42
1:F:329:MET:CB	1:F:331:ARG:CG	2.91	0.42
1:H:163:ILE:HD12	1:H:213:VAL:HB	2.02	0.42
1:H:211:ASP:OD1	1:H:211:ASP:N	2.52	0.42
1:H:235:GLY:O	1:H:236:SER:C	2.61	0.42
1:H:294:LEU:CG	1:H:295:GLU:H	2.32	0.42
1:A:204:ILE:CG2	1:A:205:TYR:CE2	3.03	0.42
1:A:253:ILE:HG23	1:A:321:TYR:HE2	1.85	0.42
1:B:268:ALA:C	1:B:269:LEU:O	2.54	0.42
1:B:371:TYR:CZ	2:B:402:CMP:C8	3.00	0.42
1:C:148:PHE:O	1:C:149:ASP:C	2.61	0.42
1:E:294:LEU:HD13	1:E:344:LYS:C	2.45	0.42
1:F:114:LYS:CE	1:F:115:VAL:HG22	2.49	0.42
1:F:135:LEU:CD1	1:F:136:PHE:N	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:201:LEU:H	1:F:201:LEU:HD12	1.85	0.42
1:G:149:ASP:OD1	1:H:120:TYR:HB3	2.17	0.42
1:H:120:TYR:CD2	1:H:121:LYS:N	2.87	0.42
1:H:162:VAL:HG21	1:H:213:VAL:HG12	2.02	0.42
1:H:183:TYR:CD1	1:H:188:TRP:CB	3.02	0.42
1:H:253:ILE:H	1:H:253:ILE:HG12	1.46	0.42
1:A:247:PHE:CZ	1:A:294:LEU:HA	2.53	0.41
1:A:264:THR:O	1:A:265:VAL:C	2.62	0.41
1:B:158:ALA:HB2	1:B:217:THR:CA	2.45	0.41
1:B:175:ILE:CG2	1:B:221:LEU:HD21	2.44	0.41
1:B:301:LEU:N	1:B:336:THR:O	2.51	0.41
1:C:135:LEU:HD13	1:C:136:PHE:CE1	2.55	0.41
1:C:154:VAL:O	1:C:154:VAL:CG1	2.63	0.41
1:C:172:PHE:CB	1:C:224:ILE:HD11	2.33	0.41
1:C:248:LEU:C	1:C:262:ARG:NH2	2.78	0.41
1:C:254:LEU:O	1:C:257:LEU:HG	2.20	0.41
1:C:333:ARG:C	1:C:335:ALA:H	2.27	0.41
1:E:342:PRO:HG2	1:E:342:PRO:O	2.19	0.41
1:E:366:ARG:O	1:E:369:GLN:CB	2.68	0.41
1:F:135:LEU:HD13	1:F:136:PHE:CD1	2.55	0.41
1:F:253:ILE:H	1:F:253:ILE:HG12	1.52	0.41
1:H:124:ALA:O	1:H:127:ALA:HB3	2.20	0.41
1:H:165:GLN:CA	1:H:211:ASP:O	2.67	0.41
1:H:174:VAL:CG1	1:H:222:TRP:HB2	2.50	0.41
1:H:244:TYR:O	1:H:245:GLU:C	2.61	0.41
1:H:285:GLU:HB3	1:H:286:PRO:HD2	2.01	0.41
1:H:294:LEU:CG	1:H:295:GLU:N	2.82	0.41
1:H:321:TYR:CD1	1:H:321:TYR:O	2.73	0.41
1:A:158:ALA:HA	1:A:215:ALA:HB1	2.02	0.41
1:A:230:ARG:HH12	1:A:234:MET:CE	2.12	0.41
1:A:269:LEU:CG	1:A:346:VAL:HG21	2.49	0.41
1:A:352:ARG:O	1:A:355:ARG:HB2	2.21	0.41
1:B:116:ILE:HA	1:B:116:ILE:HD13	1.63	0.41
1:B:158:ALA:HA	1:B:215:ALA:CB	2.50	0.41
1:B:201:LEU:HD13	2:B:401:CMP:C2'	2.50	0.41
1:B:263:LEU:H	1:B:263:LEU:HG	1.61	0.41
1:D:144:ARG:CZ	1:D:144:ARG:CB	2.98	0.41
1:D:251:VAL:HG11	1:D:292:ILE:CD1	2.50	0.41
1:D:263:LEU:HA	1:D:263:LEU:HD23	1.74	0.41
1:D:269:LEU:CD2	1:D:346:VAL:CG2	2.86	0.41
1:D:362:ASP:HA	1:D:365:LYS:NZ	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:121:LYS:C	1:E:123:MET:N	2.77	0.41
1:F:129:ALA:CB	1:F:222:TRP:CD1	3.03	0.41
1:F:325:ILE:CG1	1:F:326:ALA:N	2.79	0.41
1:G:260:TRP:CG	2:G:401:CMP:N7	2.88	0.41
1:G:272:VAL:HG22	1:G:273:GLN:N	2.34	0.41
1:G:273:GLN:HB2	1:G:343:LEU:O	2.19	0.41
1:G:283:GLN:CB	1:G:336:THR:OG1	2.67	0.41
1:H:130:ILE:HG13	1:H:136:PHE:CD2	2.55	0.41
1:H:153:PRO:CA	1:H:222:TRP:HZ3	2.32	0.41
1:B:112:VAL:HG12	1:B:231:ARG:CZ	2.48	0.41
1:B:269:LEU:HD23	1:B:348:LEU:HD13	2.02	0.41
1:C:175:ILE:CA	1:C:221:LEU:CD2	2.81	0.41
1:D:133:ASN:O	1:D:134:VAL:C	2.62	0.41
1:E:249:SER:HA	1:E:262:ARG:NH2	2.35	0.41
1:E:260:TRP:NE1	2:E:401:CMP:C2'	2.79	0.41
1:E:262:ARG:HA	1:E:265:VAL:HG23	2.02	0.41
1:F:164:GLN:CA	1:F:212:THR:HG22	2.40	0.41
1:F:253:ILE:C	1:F:255:GLU:N	2.78	0.41
1:F:265:VAL:HG12	1:F:269:LEU:HD11	2.03	0.41
1:F:329:MET:HA	1:F:329:MET:HE2	2.02	0.41
1:H:147:ILE:HD13	1:H:147:ILE:HG21	1.48	0.41
1:A:138:HIS:O	1:A:139:LEU:C	2.63	0.41
1:A:156:PHE:HD1	1:A:156:PHE:HA	1.71	0.41
1:A:156:PHE:HE2	1:A:162:VAL:HG12	1.72	0.41
1:A:287:GLY:HA3	1:A:326:ALA:HB1	2.00	0.41
1:A:293:ILE:CG1	1:A:345:CYS:SG	2.96	0.41
1:B:157:ILE:O	1:B:158:ALA:C	2.63	0.41
1:B:298:ALA:C	1:B:316:LEU:HB2	2.44	0.41
1:C:262:ARG:HA	1:C:265:VAL:HG21	2.02	0.41
1:D:131:GLU:O	1:D:132:LYS:C	2.62	0.41
1:D:133:ASN:O	1:D:135:LEU:HD12	2.21	0.41
1:E:116:ILE:HG22	1:E:118:LYS:NZ	2.35	0.41
1:E:183:TYR:CD1	1:E:188:TRP:HA	2.51	0.41
1:E:221:LEU:HD23	1:E:221:LEU:HA	1.34	0.41
1:E:353:PHE:CD1	1:E:357:LEU:HD22	2.54	0.41
1:F:112:VAL:CG1	1:F:113:ARG:N	2.65	0.41
1:F:211:ASP:OD1	2:F:401:CMP:O1P	2.39	0.41
1:G:324:GLU:HB2	1:G:364:LEU:HD11	2.01	0.41
1:H:343:LEU:HG	1:H:344:LYS:N	2.34	0.41
1:A:113:ARG:HE	1:D:113:ARG:CA	2.32	0.41
1:A:347:LYS:HE3	1:A:347:LYS:HB3	1.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:TYR:HB2	1:B:198:PHE:HE1	1.86	0.41
1:B:285:GLU:O	1:B:332:PRO:HA	2.20	0.41
1:B:322:PHE:N	1:B:322:PHE:HD1	2.18	0.41
1:C:120:TYR:O	1:C:123:MET:HB3	2.20	0.41
1:D:157:ILE:CD1	1:F:243:MET:HE3	2.46	0.41
1:D:183:TYR:HD1	1:D:188:TRP:CA	2.30	0.41
1:D:297:SER:O	1:D:340:ARG:HB2	2.20	0.41
1:E:116:ILE:O	1:E:118:LYS:HG3	2.21	0.41
1:E:312:GLU:OE1	1:E:313:VAL:N	2.54	0.41
1:F:157:ILE:HG13	1:F:157:ILE:H	1.81	0.41
1:F:224:ILE:CD1	1:F:224:ILE:C	2.94	0.41
1:F:260:TRP:NE1	2:F:401:CMP:C4	2.88	0.41
1:G:341:GLY:HA3	1:G:342:PRO:HD2	1.70	0.41
1:H:259:LYS:O	1:H:260:TRP:C	2.63	0.41
1:H:283:GLN:HG2	1:H:333:ARG:O	2.20	0.41
1:A:254:LEU:C	1:A:254:LEU:CD1	2.81	0.41
1:A:263:LEU:HD23	1:A:263:LEU:HA	1.74	0.41
1:A:321:TYR:HD1	1:A:322:PHE:N	2.18	0.41
1:B:261:GLU:OE2	1:B:359:PRO:HG2	2.20	0.41
1:B:262:ARG:O	1:B:263:LEU:C	2.64	0.41
1:C:197:SER:O	1:C:198:PHE:HB3	2.21	0.41
1:C:290:PHE:CE2	1:C:357:LEU:HD21	2.56	0.41
1:D:153:PRO:HB3	1:D:222:TRP:CH2	2.49	0.41
1:D:157:ILE:CA	1:D:218:ASN:OD1	2.68	0.41
1:D:163:ILE:HD12	1:D:213:VAL:CB	2.39	0.41
1:D:200:GLU:CG	1:D:201:LEU:N	2.51	0.41
1:D:263:LEU:O	1:D:267:ASP:N	2.43	0.41
1:D:269:LEU:CG	1:D:346:VAL:HG21	2.50	0.41
1:E:260:TRP:NE1	2:E:401:CMP:N9	2.68	0.41
1:E:362:ASP:O	1:E:365:LYS:N	2.50	0.41
1:F:316:LEU:HD22	1:F:320:ASP:HB3	2.02	0.41
1:F:325:ILE:HD13	1:F:334:ALA:HB3	2.03	0.41
1:H:163:ILE:HD11	1:H:198:PHE:CE2	2.55	0.41
1:A:255:GLU:O	1:A:256:SER:C	2.63	0.41
1:B:230:ARG:HG2	1:B:230:ARG:HH11	1.86	0.41
1:B:289:GLU:HG3	1:B:347:LYS:HZ3	1.86	0.41
1:B:313:VAL:CG2	2:B:402:CMP:HN61	2.22	0.41
1:C:162:VAL:CG2	1:C:163:ILE:HG13	2.49	0.41
1:C:183:TYR:CD1	1:C:188:TRP:CB	3.04	0.41
1:C:253:ILE:HG13	1:C:254:LEU:CG	2.50	0.41
1:C:290:PHE:HB2	1:C:327:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:154:VAL:HG12	1:D:154:VAL:O	2.20	0.41
1:D:201:LEU:HB2	2:D:401:CMP:O3'	2.19	0.41
1:D:313:VAL:HG21	2:D:402:CMP:N6	2.36	0.41
1:E:130:ILE:CD1	1:E:151:MET:HE3	2.46	0.41
1:E:316:LEU:HD22	1:E:320:ASP:HB3	2.03	0.41
1:E:347:LYS:O	1:E:348:LEU:CD1	2.65	0.41
1:F:147:ILE:HD13	1:F:147:ILE:HG21	1.68	0.41
1:F:160:GLU:C	1:F:214:LYS:HE3	2.45	0.41
1:F:229:TYR:O	1:F:230:ARG:C	2.63	0.41
1:F:268:ALA:O	1:F:269:LEU:C	2.61	0.41
1:F:329:MET:HB3	1:F:331:ARG:CG	2.50	0.41
1:F:343:LEU:HD12	1:F:343:LEU:HA	1.73	0.41
1:G:202:ALA:HB1	1:G:207:THR:O	2.20	0.41
1:H:283:GLN:HG3	1:H:333:ARG:O	2.21	0.41
1:H:300:VAL:H	1:H:312:GLU:HB2	1.84	0.41
1:H:357:LEU:HD12	1:H:357:LEU:HA	1.49	0.41
1:A:113:ARG:CZ	1:D:114:LYS:CA	2.99	0.41
1:A:209:ARG:HD3	2:A:401:CMP:O1P	2.21	0.41
1:B:325:ILE:HG12	2:B:402:CMP:P	2.60	0.41
1:C:299:ALA:HA	1:C:314:GLY:O	2.21	0.41
1:D:140:ASP:C	1:D:140:ASP:OD1	2.63	0.41
1:D:269:LEU:CB	1:D:346:VAL:HG21	2.47	0.41
1:D:325:ILE:HD11	1:D:334:ALA:H	1.86	0.41
1:E:352:ARG:O	1:E:355:ARG:HB2	2.20	0.41
1:F:158:ALA:HB2	1:F:218:ASN:N	2.35	0.41
1:F:263:LEU:O	1:F:266:ALA:CB	2.56	0.41
1:G:162:VAL:HG23	1:G:163:ILE:H	1.84	0.41
1:G:176:ASP:O	1:G:194:GLU:HG2	2.20	0.41
1:G:233:LEU:O	1:G:234:MET:C	2.62	0.41
1:G:235:GLY:O	1:G:238:LEU:N	2.54	0.41
1:H:304:ARG:N	1:H:308:GLU:CB	2.75	0.41
1:A:116:ILE:HA	1:A:117:PRO:HD3	1.69	0.41
1:A:120:TYR:HE2	1:A:124:ALA:CB	2.33	0.41
1:A:144:ARG:CB	1:A:144:ARG:CZ	2.98	0.41
1:A:147:ILE:HD13	1:A:147:ILE:HG21	1.74	0.41
1:A:183:TYR:CD1	1:A:188:TRP:CA	3.03	0.41
1:A:260:TRP:HE1	2:A:401:CMP:C2'	2.31	0.41
1:A:276:ASP:C	1:A:278:GLN:H	2.29	0.41
1:A:350:ARG:CB	1:A:351:PRO:HD3	2.37	0.41
1:A:353:PHE:O	1:A:357:LEU:CD1	2.69	0.41
1:B:119:ASP:O	1:B:120:TYR:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:TYR:CD2	1:B:198:PHE:HE1	2.39	0.41
1:B:203:LEU:CD1	1:B:226:ARG:HB3	2.43	0.41
1:B:230:ARG:HA	1:B:234:MET:HB2	2.03	0.41
1:B:239:ARG:O	1:B:243:MET:HB3	2.21	0.41
1:B:295:GLU:HA	1:B:318:PRO:HG3	2.02	0.41
1:C:110:SER:O	1:F:114:LYS:CD	2.64	0.41
1:C:132:LYS:HG3	1:C:133:ASN:N	2.36	0.41
1:C:260:TRP:NE1	2:C:401:CMP:C8	2.84	0.41
1:C:272:VAL:O	1:C:345:CYS:N	2.51	0.41
1:C:342:PRO:HG2	1:C:342:PRO:O	2.21	0.41
1:D:208:PRO:O	1:D:209:ARG:C	2.64	0.41
1:D:262:ARG:HA	1:D:265:VAL:HG21	2.03	0.41
1:D:343:LEU:HG	1:D:344:LYS:N	2.35	0.41
1:E:113:ARG:N	1:H:112:VAL:HG11	2.36	0.41
1:E:133:ASN:HD22	1:E:174:VAL:HG21	1.86	0.41
1:E:155:SER:HA	1:E:220:LYS:HA	2.03	0.41
1:E:174:VAL:HG13	1:E:222:TRP:HB2	2.02	0.41
1:E:181:ASP:OD1	1:E:191:SER:HB3	2.21	0.41
1:E:247:PHE:CE1	1:E:294:LEU:CA	2.97	0.41
1:E:261:GLU:OE2	1:E:359:PRO:HG2	2.21	0.41
1:E:321:TYR:HD1	1:E:322:PHE:N	2.18	0.41
1:F:143:GLU:O	1:F:144:ARG:C	2.64	0.41
1:F:212:THR:C	1:F:213:VAL:HG23	2.46	0.41
1:G:126:LEU:O	1:G:127:ALA:C	2.62	0.41
1:G:147:ILE:O	1:G:148:PHE:C	2.62	0.41
1:G:173:TYR:HB2	1:G:198:PHE:CZ	2.52	0.41
1:G:173:TYR:HD1	1:G:223:GLY:CA	2.34	0.41
1:G:188:TRP:HZ3	1:G:190:THR:C	2.23	0.41
1:G:343:LEU:HA	1:G:343:LEU:HD12	1.71	0.41
1:G:362:ASP:O	1:G:365:LYS:N	2.53	0.41
1:H:253:ILE:CD1	1:H:254:LEU:HD23	2.51	0.41
1:H:284:GLY:HA2	1:H:332:PRO:CB	2.51	0.41
1:H:328:LEU:HD12	1:H:328:LEU:N	2.35	0.41
1:A:117:PRO:HG2	1:D:110:SER:HB2	2.00	0.41
1:B:126:LEU:HD11	1:B:130:ILE:HD13	2.03	0.41
1:B:129:ALA:O	1:B:130:ILE:C	2.62	0.41
1:B:175:ILE:CG1	1:B:193:GLY:O	2.69	0.41
1:B:230:ARG:HG2	1:B:234:MET:CE	2.51	0.41
1:C:156:PHE:CD2	1:C:162:VAL:HG13	2.52	0.41
1:C:170:ASP:H	1:C:209:ARG:CZ	2.32	0.41
1:C:175:ILE:HG21	1:C:180:MET:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:MET:O	1:C:238:LEU:CD1	2.61	0.41
1:D:243:MET:HB2	1:D:243:MET:HE3	1.73	0.41
1:D:270:GLU:HA	1:D:271:PRO:HD3	1.57	0.41
1:E:139:LEU:HD22	1:E:144:ARG:CA	2.51	0.41
1:E:201:LEU:HD12	2:E:401:CMP:O2'	2.20	0.41
1:E:261:GLU:O	1:E:262:ARG:C	2.64	0.41
1:F:181:ASP:OD1	1:F:191:SER:HB3	2.21	0.41
1:F:200:GLU:HG2	1:F:201:LEU:N	2.35	0.41
1:F:247:PHE:CE1	1:F:294:LEU:CA	2.94	0.41
1:F:270:GLU:HB2	1:F:271:PRO:CD	2.50	0.41
1:F:365:LYS:O	1:F:368:ILE:CG1	2.58	0.41
1:G:174:VAL:HG13	1:G:174:VAL:O	2.20	0.41
1:G:290:PHE:C	1:G:291:PHE:CD1	2.88	0.41
1:G:365:LYS:HA	1:G:368:ILE:CD1	2.51	0.41
1:H:130:ILE:HG23	1:H:131:GLU:N	2.36	0.41
1:H:162:VAL:CG2	1:H:213:VAL:HG12	2.51	0.41
1:H:243:MET:HE3	1:H:243:MET:HB2	1.83	0.41
1:H:342:PRO:HG2	1:H:342:PRO:O	2.21	0.41
1:B:147:ILE:HD13	1:B:147:ILE:HG21	1.70	0.40
1:B:207:THR:OG1	1:B:208:PRO:O	2.32	0.40
1:B:280:ILE:CG1	1:B:337:VAL:HB	2.51	0.40
1:D:301:LEU:CD2	1:D:310:PHE:CB	2.81	0.40
1:F:175:ILE:HG22	1:F:221:LEU:CD2	2.49	0.40
1:F:353:PHE:O	1:F:357:LEU:HB2	2.21	0.40
1:F:365:LYS:O	1:F:368:ILE:N	2.38	0.40
1:G:245:GLU:OE1	1:G:246:GLU:N	2.54	0.40
1:G:301:LEU:HD13	1:G:310:PHE:CG	2.55	0.40
1:H:171:ASN:OD1	1:H:225:ASP:HA	2.21	0.40
1:A:280:ILE:CD1	1:A:337:VAL:HB	2.46	0.40
1:A:282:VAL:HA	1:A:336:THR:HG23	2.02	0.40
1:A:316:LEU:HD12	1:A:316:LEU:O	2.19	0.40
1:B:252:SER:O	1:B:254:LEU:N	2.54	0.40
1:C:111:TYR:HD1	1:F:111:TYR:CE2	2.36	0.40
1:C:130:ILE:HD13	1:C:151:MET:CE	2.51	0.40
1:C:157:ILE:CA	1:C:218:ASN:OD1	2.68	0.40
1:C:258:ASP:O	1:C:259:LYS:C	2.64	0.40
1:C:270:GLU:HB3	1:C:271:PRO:CD	2.51	0.40
1:C:271:PRO:O	1:C:272:VAL:HB	2.20	0.40
1:C:279:LYS:HD2	1:C:336:THR:CG2	2.50	0.40
1:D:180:MET:HB2	1:D:192:VAL:CG1	2.51	0.40
1:E:129:ALA:CB	1:E:222:TRP:NE1	2.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:132:LYS:HG3	1:E:133:ASN:N	2.36	0.40
1:E:230:ARG:O	1:E:234:MET:HB2	2.20	0.40
1:E:268:ALA:O	1:E:352:ARG:NH1	2.54	0.40
1:E:282:VAL:HB	1:E:285:GLU:CG	2.51	0.40
1:E:365:LYS:O	1:E:368:ILE:N	2.40	0.40
1:G:197:SER:O	1:G:198:PHE:HB3	2.22	0.40
1:H:181:ASP:OD1	1:H:191:SER:HB3	2.21	0.40
1:H:198:PHE:HD1	1:H:198:PHE:N	2.17	0.40
1:A:153:PRO:N	1:A:222:TRP:CZ3	2.90	0.40
1:A:204:ILE:HG23	1:A:238:LEU:HD11	2.03	0.40
1:A:241:ARG:O	1:A:245:GLU:N	2.54	0.40
1:A:244:TYR:O	1:A:245:GLU:C	2.64	0.40
1:B:116:ILE:HD12	1:B:116:ILE:HG23	1.86	0.40
1:B:139:LEU:N	1:B:139:LEU:CD1	2.62	0.40
1:B:204:ILE:HG12	1:B:234:MET:SD	2.61	0.40
1:B:266:ALA:C	1:B:268:ALA:N	2.76	0.40
1:B:274:PHE:N	1:B:343:LEU:O	2.41	0.40
1:B:371:TYR:CD1	2:B:402:CMP:C5	3.08	0.40
1:C:247:PHE:CE1	1:C:294:LEU:CA	2.91	0.40
1:D:157:ILE:HD12	1:D:157:ILE:C	2.46	0.40
1:D:253:ILE:CD1	1:D:254:LEU:HD13	2.50	0.40
1:D:266:ALA:O	1:D:268:ALA:N	2.54	0.40
1:D:325:ILE:HG13	2:D:402:CMP:O1P	2.21	0.40
1:E:253:ILE:C	1:E:255:GLU:N	2.79	0.40
1:E:271:PRO:O	1:E:272:VAL:HB	2.21	0.40
1:F:174:VAL:O	1:F:222:TRP:HB2	2.21	0.40
1:F:182:VAL:HG23	1:F:189:ALA:HB3	2.04	0.40
1:F:298:ALA:N	1:F:316:LEU:O	2.40	0.40
1:G:230:ARG:HA	1:G:234:MET:HB2	2.02	0.40
1:G:342:PRO:O	1:G:342:PRO:CG	2.70	0.40
1:H:131:GLU:O	1:H:132:LYS:C	2.64	0.40
1:A:325:ILE:CG1	1:A:326:ALA:N	2.80	0.40
1:B:130:ILE:HD12	1:B:130:ILE:HA	1.80	0.40
1:B:264:THR:O	1:B:265:VAL:C	2.64	0.40
1:B:301:LEU:HD13	1:B:310:PHE:CB	2.37	0.40
1:B:329:MET:HA	1:B:329:MET:HE3	2.04	0.40
1:C:173:TYR:HD1	1:C:223:GLY:CA	2.33	0.40
1:C:259:LYS:O	1:C:261:GLU:N	2.54	0.40
1:C:352:ARG:O	1:C:355:ARG:HB2	2.21	0.40
1:D:175:ILE:H	1:D:175:ILE:HG13	1.59	0.40
1:D:230:ARG:HB3	1:D:234:MET:HE2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:260:TRP:CG	2:D:401:CMP:N7	2.89	0.40
1:E:160:GLU:H	1:E:215:ALA:HB3	1.86	0.40
1:E:248:LEU:C	1:E:262:ARG:NH2	2.77	0.40
1:E:248:LEU:HB2	1:E:262:ARG:HH21	1.84	0.40
1:H:157:ILE:HB	1:H:218:ASN:OD1	2.21	0.40
1:A:157:ILE:O	1:A:158:ALA:C	2.64	0.40
1:A:162:VAL:HG23	1:A:163:ILE:H	1.86	0.40
1:B:139:LEU:HD22	1:B:144:ARG:HA	2.04	0.40
1:C:172:PHE:HE1	1:C:200:GLU:HG3	1.86	0.40
1:D:238:LEU:HD23	1:D:238:LEU:HA	1.96	0.40
1:E:165:GLN:HG3	1:E:211:ASP:N	2.36	0.40
1:E:201:LEU:O	1:E:204:ILE:N	2.55	0.40
1:E:243:MET:HE3	1:E:243:MET:HB2	1.73	0.40
1:E:263:LEU:O	1:E:266:ALA:N	2.53	0.40
1:E:347:LYS:HB3	1:E:347:LYS:HE3	1.14	0.40
1:F:121:LYS:O	1:F:124:ALA:N	2.54	0.40
1:F:290:PHE:HB2	1:F:327:LEU:HD22	2.03	0.40
1:G:174:VAL:HG23	1:G:196:GLY:O	2.20	0.40
1:H:242:LYS:HD2	1:H:242:LYS:HA	1.60	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	266/269 (99%)	225 (85%)	32 (12%)	9 (3%)	3	21
1	B	266/269 (99%)	218 (82%)	40 (15%)	8 (3%)	3	23
1	C	266/269 (99%)	221 (83%)	34 (13%)	11 (4%)	2	18
1	D	264/269 (98%)	226 (86%)	31 (12%)	7 (3%)	4	26
1	E	266/269 (99%)	219 (82%)	41 (15%)	6 (2%)	5	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	266/269 (99%)	224 (84%)	37 (14%)	5 (2%)	6	32
1	G	266/269 (99%)	224 (84%)	31 (12%)	11 (4%)	2	18
1	H	266/269 (99%)	225 (85%)	35 (13%)	6 (2%)	5	29
All	All	2126/2152 (99%)	1782 (84%)	281 (13%)	63 (3%)	3	23

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	VAL
1	A	252	SER
1	A	253	ILE
1	B	112	VAL
1	B	252	SER
1	C	361	SER
1	C	362	ASP
1	D	252	SER
1	D	324	GLU
1	E	112	VAL
1	F	112	VAL
1	G	113	ARG
1	G	252	SER
1	H	306	GLU
1	A	115	VAL
1	B	111	TYR
1	B	253	ILE
1	C	113	ARG
1	C	311	VAL
1	D	253	ILE
1	D	325	ILE
1	F	252	SER
1	G	114	LYS
1	G	375	VAL
1	H	272	VAL
1	B	304	ARG
1	C	131	GLU
1	C	252	SER
1	D	254	LEU
1	E	252	SER
1	F	304	ARG
1	G	118	LYS
1	G	325	ILE

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Mol	Chain	Res	Type
1	H	252	SER
1	A	111	TYR
1	A	254	LEU
1	B	130	ILE
1	C	272	VAL
1	C	300	VAL
1	D	201	LEU
1	F	272	VAL
1	H	112	VAL
1	B	254	LEU
1	C	111	TYR
1	E	123	MET
1	G	117	PRO
1	G	247	PHE
1	H	119	ASP
1	H	304	ARG
1	A	304	ARG
1	C	201	LEU
1	F	201	LEU
1	G	112	VAL
1	G	123	MET
1	G	350	ARG
1	A	325	ILE
1	B	272	VAL
1	C	130	ILE
1	E	130	ILE
1	E	318	PRO
1	A	272	VAL
1	E	272	VAL
1	D	272	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	222/229 (97%)	164 (74%)	58 (26%)	0 4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	222/229 (97%)	159 (72%)	63 (28%)	0	2
1	C	222/229 (97%)	152 (68%)	70 (32%)	0	2
1	D	220/229 (96%)	154 (70%)	66 (30%)	0	2
1	E	222/229 (97%)	165 (74%)	57 (26%)	0	4
1	F	222/229 (97%)	161 (72%)	61 (28%)	0	3
1	G	222/229 (97%)	169 (76%)	53 (24%)	1	5
1	H	222/229 (97%)	159 (72%)	63 (28%)	0	2
All	All	1774/1832 (97%)	1283 (72%)	491 (28%)	0	3

All (491) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	ARG
1	A	114	LYS
1	A	115	VAL
1	A	116	ILE
1	A	119	ASP
1	A	120	TYR
1	A	121	LYS
1	A	122	THR
1	A	126	LEU
1	A	128	LYS
1	A	131	GLU
1	A	135	LEU
1	A	139	LEU
1	A	144	ARG
1	A	145	SER
1	A	151	MET
1	A	152	PHE
1	A	154	VAL
1	A	156	PHE
1	A	168	GLU
1	A	177	GLN
1	A	186	ASN
1	A	188	TRP
1	A	198	PHE
1	A	205	TYR
1	A	207	THR
1	A	211	ASP
1	A	212	THR

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Mol	Chain	Res	Type
1	A	222	TRP
1	A	224	ILE
1	A	226	ARG
1	A	233	LEU
1	A	236	SER
1	A	242	LYS
1	A	246	GLU
1	A	254	LEU
1	A	255	GLU
1	A	256	SER
1	A	262	ARG
1	A	264	THR
1	A	270	GLU
1	A	273	GLN
1	A	279	LYS
1	A	291	PHE
1	A	292	ILE
1	A	293	ILE
1	A	294	LEU
1	A	310	PHE
1	A	311	VAL
1	A	313	VAL
1	A	329	MET
1	A	338	VAL
1	A	346	VAL
1	A	348	LEU
1	A	357	LEU
1	A	364	LEU
1	A	368	ILE
1	A	372	ASN
1	B	112	VAL
1	B	115	VAL
1	B	120	TYR
1	B	121	LYS
1	B	122	THR
1	B	126	LEU
1	B	128	LYS
1	B	134	VAL
1	B	135	LEU
1	B	139	LEU
1	B	144	ARG
1	B	145	SER

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Mol	Chain	Res	Type
1	B	151	MET
1	B	152	PHE
1	B	154	VAL
1	B	156	PHE
1	B	168	GLU
1	B	170	ASP
1	B	177	GLN
1	B	186	ASN
1	B	188	TRP
1	B	191	SER
1	B	198	PHE
1	B	200	GLU
1	B	201	LEU
1	B	205	TYR
1	B	207	THR
1	B	211	ASP
1	B	212	THR
1	B	219	VAL
1	B	222	TRP
1	B	224	ILE
1	B	226	ARG
1	B	233	LEU
1	B	234	MET
1	B	236	SER
1	B	242	LYS
1	B	243	MET
1	B	246	GLU
1	B	250	LYS
1	B	251	VAL
1	B	254	LEU
1	B	262	ARG
1	B	264	THR
1	B	273	GLN
1	B	279	LYS
1	B	289	GLU
1	B	291	PHE
1	B	292	ILE
1	B	293	ILE
1	B	294	LEU
1	B	301	LEU
1	B	310	PHE
1	B	312	GLU

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Mol	Chain	Res	Type
1	B	313	VAL
1	B	315	ARG
1	B	316	LEU
1	B	329	MET
1	B	338	VAL
1	B	346	VAL
1	B	348	LEU
1	B	364	LEU
1	B	375	VAL
1	C	110	SER
1	C	113	ARG
1	C	115	VAL
1	C	116	ILE
1	C	121	LYS
1	C	122	THR
1	C	126	LEU
1	C	128	LYS
1	C	131	GLU
1	C	134	VAL
1	C	135	LEU
1	C	139	LEU
1	C	144	ARG
1	C	145	SER
1	C	151	MET
1	C	152	PHE
1	C	154	VAL
1	C	156	PHE
1	C	161	THR
1	C	162	VAL
1	C	177	GLN
1	C	186	ASN
1	C	188	TRP
1	C	198	PHE
1	C	200	GLU
1	C	205	TYR
1	C	207	THR
1	C	211	ASP
1	C	212	THR
1	C	213	VAL
1	C	222	TRP
1	C	224	ILE
1	C	226	ARG

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Mol	Chain	Res	Type
1	C	233	LEU
1	C	234	MET
1	C	236	SER
1	C	242	LYS
1	C	246	GLU
1	C	247	PHE
1	C	248	LEU
1	C	249	SER
1	C	251	VAL
1	C	254	LEU
1	C	262	ARG
1	C	263	LEU
1	C	264	THR
1	C	269	LEU
1	C	270	GLU
1	C	273	GLN
1	C	279	LYS
1	C	289	GLU
1	C	291	PHE
1	C	292	ILE
1	C	293	ILE
1	C	294	LEU
1	C	297	SER
1	C	301	LEU
1	C	309	GLU
1	C	312	GLU
1	C	313	VAL
1	C	315	ARG
1	C	316	LEU
1	C	329	MET
1	C	332	PRO
1	C	338	VAL
1	C	348	LEU
1	C	364	LEU
1	C	365	LYS
1	C	366	ARG
1	C	368	ILE
1	D	112	VAL
1	D	114	LYS
1	D	116	ILE
1	D	121	LYS
1	D	122	THR

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Mol	Chain	Res	Type
1	D	126	LEU
1	D	128	LYS
1	D	131	GLU
1	D	134	VAL
1	D	135	LEU
1	D	139	LEU
1	D	144	ARG
1	D	145	SER
1	D	147	ILE
1	D	151	MET
1	D	152	PHE
1	D	154	VAL
1	D	157	ILE
1	D	161	THR
1	D	168	GLU
1	D	177	GLN
1	D	186	ASN
1	D	188	TRP
1	D	191	SER
1	D	192	VAL
1	D	198	PHE
1	D	201	LEU
1	D	205	TYR
1	D	207	THR
1	D	211	ASP
1	D	212	THR
1	D	222	TRP
1	D	224	ILE
1	D	226	ARG
1	D	233	LEU
1	D	234	MET
1	D	236	SER
1	D	242	LYS
1	D	246	GLU
1	D	247	PHE
1	D	249	SER
1	D	250	LYS
1	D	251	VAL
1	D	254	LEU
1	D	256	SER
1	D	264	THR
1	D	270	GLU

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Mol	Chain	Res	Type
1	D	273	GLN
1	D	279	LYS
1	D	291	PHE
1	D	292	ILE
1	D	293	ILE
1	D	294	LEU
1	D	301	LEU
1	D	309	GLU
1	D	311	VAL
1	D	312	GLU
1	D	313	VAL
1	D	316	LEU
1	D	325	ILE
1	D	329	MET
1	D	336	THR
1	D	338	VAL
1	D	362	ASP
1	D	364	LEU
1	D	368	ILE
1	E	110	SER
1	E	112	VAL
1	E	115	VAL
1	E	116	ILE
1	E	121	LYS
1	E	122	THR
1	E	126	LEU
1	E	131	GLU
1	E	134	VAL
1	E	135	LEU
1	E	139	LEU
1	E	144	ARG
1	E	145	SER
1	E	151	MET
1	E	152	PHE
1	E	154	VAL
1	E	156	PHE
1	E	157	ILE
1	E	168	GLU
1	E	177	GLN
1	E	188	TRP
1	E	198	PHE
1	E	205	TYR

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Mol	Chain	Res	Type
1	E	207	THR
1	E	211	ASP
1	E	212	THR
1	E	222	TRP
1	E	224	ILE
1	E	226	ARG
1	E	233	LEU
1	E	236	SER
1	E	242	LYS
1	E	243	MET
1	E	246	GLU
1	E	249	SER
1	E	250	LYS
1	E	254	LEU
1	E	262	ARG
1	E	264	THR
1	E	269	LEU
1	E	270	GLU
1	E	273	GLN
1	E	279	LYS
1	E	281	VAL
1	E	291	PHE
1	E	294	LEU
1	E	301	LEU
1	E	309	GLU
1	E	312	GLU
1	E	329	MET
1	E	338	VAL
1	E	344	LYS
1	E	346	VAL
1	E	364	LEU
1	E	366	ARG
1	E	368	ILE
1	E	375	VAL
1	F	113	ARG
1	F	114	LYS
1	F	115	VAL
1	F	116	ILE
1	F	121	LYS
1	F	122	THR
1	F	126	LEU
1	F	128	LYS

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Mol	Chain	Res	Type
1	F	130	ILE
1	F	131	GLU
1	F	134	VAL
1	F	135	LEU
1	F	139	LEU
1	F	144	ARG
1	F	145	SER
1	F	146	ASP
1	F	151	MET
1	F	152	PHE
1	F	154	VAL
1	F	156	PHE
1	F	157	ILE
1	F	168	GLU
1	F	177	GLN
1	F	186	ASN
1	F	188	TRP
1	F	190	THR
1	F	191	SER
1	F	198	PHE
1	F	205	TYR
1	F	207	THR
1	F	211	ASP
1	F	212	THR
1	F	222	TRP
1	F	224	ILE
1	F	226	ARG
1	F	233	LEU
1	F	236	SER
1	F	242	LYS
1	F	243	MET
1	F	246	GLU
1	F	247	PHE
1	F	249	SER
1	F	250	LYS
1	F	251	VAL
1	F	254	LEU
1	F	255	GLU
1	F	262	ARG
1	F	264	THR
1	F	273	GLN
1	F	279	LYS

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Mol	Chain	Res	Type
1	F	291	PHE
1	F	293	ILE
1	F	294	LEU
1	F	301	LEU
1	F	302	GLN
1	F	329	MET
1	F	338	VAL
1	F	344	LYS
1	F	346	VAL
1	F	364	LEU
1	F	368	ILE
1	G	112	VAL
1	G	116	ILE
1	G	120	TYR
1	G	122	THR
1	G	126	LEU
1	G	131	GLU
1	G	134	VAL
1	G	135	LEU
1	G	139	LEU
1	G	144	ARG
1	G	151	MET
1	G	152	PHE
1	G	154	VAL
1	G	161	THR
1	G	177	GLN
1	G	188	TRP
1	G	191	SER
1	G	198	PHE
1	G	205	TYR
1	G	207	THR
1	G	211	ASP
1	G	212	THR
1	G	224	ILE
1	G	226	ARG
1	G	233	LEU
1	G	234	MET
1	G	236	SER
1	G	242	LYS
1	G	246	GLU
1	G	249	SER
1	G	250	LYS

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Mol	Chain	Res	Type
1	G	251	VAL
1	G	254	LEU
1	G	256	SER
1	G	262	ARG
1	G	264	THR
1	G	269	LEU
1	G	273	GLN
1	G	279	LYS
1	G	291	PHE
1	G	292	ILE
1	G	293	ILE
1	G	294	LEU
1	G	309	GLU
1	G	311	VAL
1	G	313	VAL
1	G	329	MET
1	G	338	VAL
1	G	346	VAL
1	G	348	LEU
1	G	364	LEU
1	G	368	ILE
1	G	375	VAL
1	H	110	SER
1	H	113	ARG
1	H	114	LYS
1	H	116	ILE
1	H	121	LYS
1	H	122	THR
1	H	126	LEU
1	H	128	LYS
1	H	131	GLU
1	H	134	VAL
1	H	135	LEU
1	H	139	LEU
1	H	144	ARG
1	H	145	SER
1	H	147	ILE
1	H	151	MET
1	H	152	PHE
1	H	154	VAL
1	H	156	PHE
1	H	168	GLU

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Mol	Chain	Res	Type
1	H	177	GLN
1	H	186	ASN
1	H	188	TRP
1	H	198	PHE
1	H	205	TYR
1	H	207	THR
1	H	211	ASP
1	H	212	THR
1	H	222	TRP
1	H	224	ILE
1	H	226	ARG
1	H	233	LEU
1	H	234	MET
1	H	236	SER
1	H	242	LYS
1	H	246	GLU
1	H	247	PHE
1	H	249	SER
1	H	250	LYS
1	H	251	VAL
1	H	254	LEU
1	H	256	SER
1	H	262	ARG
1	H	264	THR
1	H	270	GLU
1	H	273	GLN
1	H	279	LYS
1	H	285	GLU
1	H	289	GLU
1	H	291	PHE
1	H	292	ILE
1	H	293	ILE
1	H	300	VAL
1	H	301	LEU
1	H	309	GLU
1	H	311	VAL
1	H	313	VAL
1	H	329	MET
1	H	331	ARG
1	H	332	PRO
1	H	338	VAL
1	H	364	LEU

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Mol	Chain	Res	Type
1	H	376	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	273	GLN
1	A	370	GLN
1	A	372	ASN
1	B	185	ASN
1	B	273	GLN
1	B	370	GLN
1	B	372	ASN
1	C	273	GLN
1	D	142	ASN
1	D	273	GLN
1	D	372	ASN
1	E	142	ASN
1	E	273	GLN
1	E	302	GLN
1	E	372	ASN
1	F	273	GLN
1	F	302	GLN
1	F	372	ASN
1	G	273	GLN
1	G	372	ASN
1	H	273	GLN
1	H	302	GLN
1	H	367	ASN
1	H	372	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	CMP	D	402	-	25,25,25	2.04	8 (32%)	37,39,39	2.34	12 (32%)
2	CMP	C	401	-	25,25,25	1.95	5 (20%)	37,39,39	2.87	13 (35%)
2	CMP	D	401	-	25,25,25	2.10	5 (20%)	37,39,39	2.55	12 (32%)
2	CMP	E	401	-	25,25,25	2.13	9 (36%)	37,39,39	2.53	13 (35%)
2	CMP	F	402	-	25,25,25	2.18	5 (20%)	37,39,39	2.31	10 (27%)
2	CMP	H	402	-	25,25,25	2.03	8 (32%)	37,39,39	2.21	11 (29%)
2	CMP	A	402	-	25,25,25	2.21	8 (32%)	37,39,39	3.11	13 (35%)
2	CMP	C	402	-	25,25,25	2.12	8 (32%)	37,39,39	2.66	10 (27%)
2	CMP	G	401	-	25,25,25	2.20	6 (24%)	37,39,39	2.30	11 (29%)
2	CMP	B	402	-	25,25,25	2.33	6 (24%)	37,39,39	2.55	12 (32%)
2	CMP	E	402	-	25,25,25	2.18	5 (20%)	37,39,39	2.15	10 (27%)
2	CMP	G	402	-	25,25,25	1.94	8 (32%)	37,39,39	2.80	12 (32%)
2	CMP	A	401	-	25,25,25	1.88	5 (20%)	37,39,39	2.65	13 (35%)
2	CMP	H	401	-	25,25,25	2.38	6 (24%)	37,39,39	3.27	14 (37%)
2	CMP	B	401	-	25,25,25	1.96	6 (24%)	37,39,39	2.89	14 (37%)
2	CMP	F	401	-	25,25,25	2.11	9 (36%)	37,39,39	2.27	13 (35%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CMP	D	402	-	-	0/4/31/31	0/4/4/4
2	CMP	C	401	-	-	0/4/31/31	0/4/4/4
2	CMP	D	401	-	-	0/4/31/31	0/4/4/4
2	CMP	E	401	-	-	0/4/31/31	0/4/4/4
2	CMP	F	402	-	-	3/4/31/31	0/4/4/4
2	CMP	H	402	-	-	3/4/31/31	0/4/4/4
2	CMP	A	402	-	-	1/4/31/31	0/4/4/4
2	CMP	C	402	-	-	0/4/31/31	0/4/4/4
2	CMP	G	401	-	-	1/4/31/31	0/4/4/4
2	CMP	B	402	-	-	0/4/31/31	0/4/4/4
2	CMP	E	402	-	-	2/4/31/31	0/4/4/4
2	CMP	G	402	-	-	1/4/31/31	0/4/4/4
2	CMP	A	401	-	-	0/4/31/31	0/4/4/4
2	CMP	H	401	-	-	1/4/31/31	0/4/4/4
2	CMP	B	401	-	-	0/4/31/31	0/4/4/4
2	CMP	F	401	-	-	0/4/31/31	0/4/4/4

All (107) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	402	CMP	P-O3'	6.88	1.69	1.57
2	H	401	CMP	P-O3'	6.86	1.69	1.57
2	G	401	CMP	C5-C4	6.12	1.50	1.39
2	D	401	CMP	P-O3'	5.93	1.67	1.57
2	E	402	CMP	C5-C4	5.67	1.49	1.39
2	F	402	CMP	C5-C4	5.61	1.49	1.39
2	H	401	CMP	C5-C4	5.52	1.48	1.39
2	G	402	CMP	C5-C4	5.49	1.48	1.39
2	A	402	CMP	P-O5'	5.43	1.63	1.57
2	A	401	CMP	P-O3'	5.41	1.66	1.57
2	B	401	CMP	P-O3'	5.40	1.66	1.57
2	C	402	CMP	C5-C4	5.38	1.48	1.39
2	B	402	CMP	P-O5'	5.32	1.63	1.57
2	G	401	CMP	P-O3'	5.24	1.66	1.57
2	D	401	CMP	C5-C4	5.08	1.48	1.39
2	F	402	CMP	P-O5'	5.06	1.63	1.57
2	C	401	CMP	C5-C4	4.96	1.47	1.39
2	H	402	CMP	P-O5'	4.96	1.63	1.57
2	A	402	CMP	C5-C4	4.92	1.47	1.39
2	E	402	CMP	P-O5'	4.88	1.63	1.57
2	E	402	CMP	P-O3'	4.87	1.65	1.57
2	F	401	CMP	P-O3'	4.85	1.65	1.57
2	C	401	CMP	P-O3'	4.83	1.65	1.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	402	CMP	P-O3'	4.82	1.65	1.57
2	D	402	CMP	P-O3'	4.81	1.65	1.57
2	H	401	CMP	C5-C6	4.55	1.53	1.41
2	H	402	CMP	P-O3'	4.53	1.65	1.57
2	H	402	CMP	C5-C4	4.52	1.47	1.39
2	D	402	CMP	C5-C4	4.48	1.47	1.39
2	F	402	CMP	P-O3'	4.44	1.65	1.57
2	E	401	CMP	P-O3'	4.23	1.64	1.57
2	F	402	CMP	C5-C6	4.22	1.52	1.41
2	B	401	CMP	C5-C4	4.20	1.46	1.39
2	B	402	CMP	C5-C4	4.18	1.46	1.39
2	C	402	CMP	P-O5'	4.15	1.62	1.57
2	E	401	CMP	C5-C4	4.07	1.46	1.39
2	A	401	CMP	C5-C4	3.99	1.46	1.39
2	C	402	CMP	P-O3'	3.95	1.64	1.57
2	F	401	CMP	C4-N9	-3.79	1.29	1.37
2	F	401	CMP	C5-C4	3.75	1.45	1.39
2	E	402	CMP	C5-C6	3.63	1.51	1.41
2	E	401	CMP	C5-C6	3.55	1.50	1.41
2	G	401	CMP	C5-C6	3.49	1.50	1.41
2	B	402	CMP	C5-N7	-3.43	1.32	1.39
2	C	401	CMP	C5-C6	3.43	1.50	1.41
2	E	401	CMP	C4-N9	-3.38	1.30	1.37
2	D	401	CMP	P-O5'	3.33	1.61	1.57
2	D	402	CMP	C5-C6	3.30	1.50	1.41
2	D	401	CMP	C5-C6	3.26	1.50	1.41
2	G	402	CMP	P-O3'	3.26	1.63	1.57
2	F	401	CMP	O5'-C5'	-3.24	1.41	1.46
2	E	401	CMP	C8-N9	-3.24	1.32	1.37
2	G	401	CMP	P-O5'	3.23	1.61	1.57
2	A	402	CMP	C5-C6	3.22	1.50	1.41
2	F	401	CMP	C8-N9	-3.19	1.32	1.37
2	E	401	CMP	O5'-C5'	-3.15	1.41	1.46
2	C	402	CMP	C5-C6	3.11	1.49	1.41
2	G	402	CMP	O3'-C3'	-3.01	1.40	1.44
2	E	401	CMP	O3'-C3'	-3.00	1.40	1.44
2	H	401	CMP	C8-N7	2.95	1.37	1.31
2	F	401	CMP	O3'-C3'	-2.92	1.40	1.44
2	C	402	CMP	C8-N7	2.92	1.37	1.31
2	D	402	CMP	P-O5'	2.89	1.61	1.57
2	B	401	CMP	O5'-C5'	-2.85	1.42	1.46
2	D	402	CMP	O3'-C3'	-2.85	1.40	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	401	CMP	O3'-C3'	-2.80	1.40	1.44
2	A	401	CMP	C5-N7	-2.78	1.34	1.39
2	A	401	CMP	O5'-C5'	-2.76	1.42	1.46
2	F	401	CMP	C5-N7	-2.76	1.34	1.39
2	H	401	CMP	O5'-C5'	-2.74	1.42	1.46
2	C	401	CMP	O3'-C3'	-2.64	1.40	1.44
2	E	402	CMP	C8-N7	2.61	1.36	1.31
2	H	402	CMP	C5-C6	2.54	1.48	1.41
2	G	402	CMP	C5'-C4'	-2.52	1.47	1.51
2	C	402	CMP	C5-N7	-2.49	1.34	1.39
2	G	401	CMP	O5'-C5'	-2.48	1.42	1.46
2	F	402	CMP	C8-N7	2.47	1.36	1.31
2	G	402	CMP	C5-N7	-2.46	1.34	1.39
2	H	402	CMP	O3'-C3'	-2.42	1.40	1.44
2	C	402	CMP	O5'-C5'	-2.40	1.42	1.46
2	B	401	CMP	C8-N7	2.40	1.36	1.31
2	D	401	CMP	C5-N7	-2.37	1.34	1.39
2	C	401	CMP	C5-N7	-2.36	1.34	1.39
2	A	402	CMP	C8-N7	2.34	1.36	1.31
2	G	402	CMP	C5-C6	2.34	1.47	1.41
2	G	402	CMP	O5'-C5'	-2.32	1.42	1.46
2	C	402	CMP	O3'-C3'	-2.30	1.41	1.44
2	H	402	CMP	O5'-C5'	-2.24	1.43	1.46
2	B	402	CMP	C5-C6	2.24	1.47	1.41
2	F	401	CMP	C5-C6	2.23	1.47	1.41
2	A	402	CMP	C4-N3	2.22	1.38	1.34
2	D	402	CMP	C8-N9	-2.18	1.33	1.37
2	A	402	CMP	C5-N7	-2.18	1.35	1.39
2	G	402	CMP	P-O5'	2.16	1.60	1.57
2	F	401	CMP	C8-N7	2.16	1.35	1.31
2	H	402	CMP	C8-N7	2.15	1.35	1.31
2	A	401	CMP	P-O5'	2.14	1.60	1.57
2	E	401	CMP	C8-N7	2.14	1.35	1.31
2	D	402	CMP	O5'-C5'	-2.12	1.43	1.46
2	E	401	CMP	P-O5'	2.12	1.60	1.57
2	H	402	CMP	C5-N7	-2.09	1.35	1.39
2	A	402	CMP	O5'-C5'	-2.09	1.43	1.46
2	B	401	CMP	C4-N3	2.08	1.38	1.34
2	B	401	CMP	O3'-C3'	-2.07	1.41	1.44
2	D	402	CMP	C8-N7	2.05	1.35	1.31
2	H	401	CMP	O3'-C3'	-2.03	1.41	1.44
2	B	402	CMP	C5'-C4'	-2.02	1.48	1.51

All (193) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	401	CMP	C5-C4-N3	-11.41	111.01	126.72
2	A	402	CMP	C5-C4-N3	-9.75	113.30	126.72
2	C	401	CMP	C5-C4-N3	-9.67	113.41	126.72
2	D	401	CMP	C5-C4-N3	-8.50	115.02	126.72
2	C	402	CMP	C5-C4-N3	-8.28	115.32	126.72
2	G	402	CMP	C1'-N9-C8	-8.17	108.96	127.09
2	B	402	CMP	C5-C4-N3	-8.01	115.69	126.72
2	H	401	CMP	C4-C5-N7	-7.58	101.92	110.58
2	A	402	CMP	N3-C4-N9	7.29	139.57	127.17
2	G	401	CMP	C5-C4-N3	-7.19	116.82	126.72
2	F	402	CMP	C5-C4-N3	-6.74	117.44	126.72
2	G	402	CMP	C4-N9-C1'	6.47	141.76	126.63
2	D	401	CMP	N3-C4-N9	6.47	138.17	127.17
2	A	402	CMP	O3'-P-O1P	-6.46	96.56	110.39
2	E	402	CMP	C5-C4-N3	-6.44	117.85	126.72
2	A	401	CMP	N3-C4-N9	6.42	138.08	127.17
2	E	401	CMP	C4-C5-N7	-6.39	103.28	110.58
2	D	402	CMP	C5-C4-N3	-6.37	117.94	126.72
2	C	401	CMP	N3-C4-N9	6.37	138.00	127.17
2	H	401	CMP	N3-C4-N9	6.36	137.99	127.17
2	B	401	CMP	N3-C4-N9	6.35	137.96	127.17
2	B	401	CMP	N3-C2-N1	-6.33	119.01	128.58
2	A	401	CMP	C5-C4-N3	-6.27	118.09	126.72
2	A	401	CMP	N3-C2-N1	-6.18	119.22	128.58
2	G	402	CMP	C5-C4-N3	-6.18	118.21	126.72
2	G	402	CMP	N3-C4-N9	6.17	137.67	127.17
2	B	402	CMP	N3-C4-N9	6.10	137.54	127.17
2	H	402	CMP	C5-C4-N3	-6.01	118.45	126.72
2	E	401	CMP	C5-C4-N3	-5.99	118.46	126.72
2	H	402	CMP	O5'-P-O3'	5.87	113.56	105.70
2	A	402	CMP	C2-N3-C4	5.82	126.04	111.83
2	C	402	CMP	N3-C4-N9	5.81	137.05	127.17
2	C	402	CMP	O5'-P-O3'	5.73	113.37	105.70
2	B	401	CMP	C5-C4-N3	-5.71	118.85	126.72
2	G	401	CMP	N3-C4-N9	5.67	136.82	127.17
2	C	402	CMP	O3'-P-O1P	-5.52	98.57	110.39
2	D	402	CMP	N3-C4-N9	5.41	136.36	127.17
2	H	401	CMP	C2-N3-C4	5.41	125.03	111.83
2	F	401	CMP	C5-C4-N3	-5.35	119.35	126.72
2	B	401	CMP	C4-N9-C8	5.29	111.29	105.74
2	C	401	CMP	C4-C5-N7	-5.26	104.56	110.58
2	C	402	CMP	C2-N3-C4	5.23	124.61	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	CMP	C2-N3-C4	5.12	124.33	111.83
2	F	401	CMP	C4-C5-N7	-4.92	104.95	110.58
2	A	401	CMP	C2-N3-C4	4.92	123.84	111.83
2	F	402	CMP	O3'-P-O1P	-4.90	99.90	110.39
2	B	401	CMP	C5-C6-N6	-4.87	111.22	123.29
2	F	402	CMP	N3-C4-N9	4.84	135.40	127.17
2	E	401	CMP	C4-N9-C8	4.82	110.80	105.74
2	B	402	CMP	O2P-P-O3'	-4.80	95.85	107.04
2	H	401	CMP	C5-C4-N9	4.75	110.99	105.81
2	C	401	CMP	C2-N3-C4	4.73	123.39	111.83
2	D	401	CMP	C2-N3-C4	4.71	123.34	111.83
2	E	402	CMP	N3-C4-N9	4.66	135.09	127.17
2	B	401	CMP	O3'-P-O1P	-4.66	100.42	110.39
2	H	402	CMP	N3-C4-N9	4.64	135.06	127.17
2	F	402	CMP	C4-C5-N7	-4.64	105.28	110.58
2	C	401	CMP	C1'-N9-C8	-4.62	116.84	127.09
2	G	402	CMP	O3'-P-O1P	-4.58	100.57	110.39
2	F	401	CMP	C4-N9-C8	4.58	110.55	105.74
2	C	401	CMP	C4-N9-C1'	4.39	136.90	126.63
2	B	402	CMP	C2-N3-C4	4.38	122.54	111.83
2	A	402	CMP	O5'-P-O3'	4.33	111.50	105.70
2	B	401	CMP	N6-C6-N1	4.29	127.94	118.38
2	E	402	CMP	C4-C5-N7	-4.29	105.68	110.58
2	H	401	CMP	C5-N7-C8	4.24	110.11	103.45
2	E	401	CMP	C5-N7-C8	4.21	110.06	103.45
2	F	402	CMP	C2-N3-C4	4.20	122.09	111.83
2	G	401	CMP	C1'-N9-C8	-4.18	117.81	127.09
2	D	402	CMP	C4-N9-C8	4.16	110.11	105.74
2	D	402	CMP	C2-N3-C4	4.11	121.86	111.83
2	A	402	CMP	N3-C2-N1	-4.04	122.47	128.58
2	D	402	CMP	C4-C5-N7	-4.01	106.00	110.58
2	E	401	CMP	N3-C4-N9	4.01	133.98	127.17
2	E	401	CMP	N9-C8-N7	-3.99	108.27	113.94
2	D	401	CMP	C4-C5-N7	-3.98	106.03	110.58
2	A	402	CMP	C4-N9-C1'	3.95	135.86	126.63
2	D	402	CMP	O2P-P-O3'	-3.94	97.86	107.04
2	E	402	CMP	C2-N3-C4	3.92	121.41	111.83
2	F	401	CMP	N3-C4-N9	3.89	133.78	127.17
2	A	402	CMP	C1'-N9-C8	-3.88	118.47	127.09
2	A	401	CMP	C5-C6-N6	-3.80	113.88	123.29
2	A	402	CMP	C4-C5-N7	-3.79	106.24	110.58
2	G	402	CMP	O2P-P-O1P	3.79	120.22	108.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	CMP	N6-C6-N1	3.78	126.79	118.38
2	C	402	CMP	N3-C2-N1	-3.76	122.90	128.58
2	B	402	CMP	O5'-P-O3'	3.74	110.70	105.70
2	D	401	CMP	C1'-N9-C8	-3.70	118.88	127.09
2	G	401	CMP	C4-C5-N7	-3.63	106.44	110.58
2	E	401	CMP	C2-N3-C4	3.61	120.66	111.83
2	G	401	CMP	C2-N3-C4	3.61	120.65	111.83
2	F	401	CMP	O2P-P-O1P	3.61	119.66	108.56
2	A	401	CMP	C1'-N9-C8	-3.56	119.19	127.09
2	G	401	CMP	O2P-P-O1P	3.55	119.46	108.56
2	H	401	CMP	C4-N9-C1'	3.54	134.91	126.63
2	H	402	CMP	C2-N3-C4	3.53	120.46	111.83
2	G	402	CMP	C2-N3-C4	3.49	120.36	111.83
2	F	401	CMP	N9-C8-N7	-3.47	109.01	113.94
2	E	401	CMP	C6-C5-N7	3.47	138.77	132.09
2	E	401	CMP	O2P-P-O1P	3.45	119.15	108.56
2	G	401	CMP	O3'-C3'-C4'	-3.39	108.15	110.71
2	B	402	CMP	O3'-C3'-C4'	-3.35	108.18	110.71
2	D	402	CMP	N3-C2-N1	-3.27	123.63	128.58
2	F	401	CMP	C2-N3-C4	3.27	119.82	111.83
2	C	401	CMP	O2P-P-O1P	3.27	118.60	108.56
2	F	401	CMP	C5-N7-C8	3.25	108.56	103.45
2	B	401	CMP	O2P-P-O1P	3.23	118.49	108.56
2	C	401	CMP	C5-N7-C8	3.22	108.51	103.45
2	D	402	CMP	O2P-P-O1P	3.22	118.46	108.56
2	E	402	CMP	O2P-P-O1P	3.22	118.45	108.56
2	C	402	CMP	O2P-P-O1P	3.22	118.44	108.56
2	E	401	CMP	O3'-P-O1P	-3.21	103.51	110.39
2	H	401	CMP	C1'-N9-C8	-3.20	119.99	127.09
2	H	402	CMP	O2P-P-O1P	3.19	118.35	108.56
2	D	401	CMP	O2P-P-O1P	3.17	118.31	108.56
2	F	402	CMP	O2P-P-O1P	3.17	118.31	108.56
2	A	402	CMP	O2P-P-O1P	3.17	118.30	108.56
2	A	401	CMP	O2P-P-O1P	3.16	118.27	108.56
2	E	402	CMP	O2P-P-O3'	-3.12	99.77	107.04
2	C	401	CMP	O3'-P-O1P	-3.12	103.70	110.39
2	H	401	CMP	O2P-P-O1P	3.12	118.13	108.56
2	D	401	CMP	C4-N9-C1'	3.11	133.89	126.63
2	H	401	CMP	N6-C6-N1	-3.10	111.47	118.38
2	A	401	CMP	C4-N9-C8	3.09	108.98	105.74
2	F	402	CMP	C6-C5-N7	3.03	137.94	132.09
2	H	402	CMP	C4-C5-N7	-3.03	107.12	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	402	CMP	N3-C2-N1	-2.98	124.06	128.58
2	D	402	CMP	C5-N7-C8	2.98	108.13	103.45
2	B	402	CMP	O2P-P-O1P	2.98	117.72	108.56
2	G	402	CMP	N3-C2-N1	-2.97	124.08	128.58
2	D	401	CMP	C5-N7-C8	2.91	108.02	103.45
2	B	402	CMP	N3-C2-N1	-2.89	124.20	128.58
2	B	402	CMP	C4-C5-N7	-2.89	107.28	110.58
2	G	401	CMP	C4-N9-C1'	2.86	133.33	126.63
2	A	401	CMP	C2-N1-C6	2.84	123.40	118.73
2	H	401	CMP	C6-C5-N7	2.84	137.56	132.09
2	H	402	CMP	O3'-P-O1P	-2.83	104.33	110.39
2	G	402	CMP	C4-N9-C8	2.76	108.64	105.74
2	F	402	CMP	C5-N7-C8	2.76	107.78	103.45
2	G	401	CMP	O4'-C1'-N9	2.74	113.35	108.09
2	B	402	CMP	O3'-C3'-C2'	-2.73	112.93	115.61
2	A	402	CMP	O3'-C3'-C4'	2.72	112.76	110.71
2	D	402	CMP	N9-C8-N7	-2.72	110.08	113.94
2	A	402	CMP	C5-N7-C8	2.72	107.72	103.45
2	F	402	CMP	N3-C2-N1	-2.71	124.48	128.58
2	G	401	CMP	O3'-P-O1P	-2.70	104.60	110.39
2	F	401	CMP	C6-C5-N7	2.68	137.25	132.09
2	F	401	CMP	N3-C2-N1	-2.67	124.55	128.58
2	B	401	CMP	N9-C8-N7	-2.66	110.16	113.94
2	H	402	CMP	O2P-P-O3'	-2.65	100.86	107.04
2	D	401	CMP	N3-C2-N1	-2.64	124.58	128.58
2	E	402	CMP	C5-N7-C8	2.62	107.57	103.45
2	C	402	CMP	C4-C5-N7	-2.62	107.58	110.58
2	C	402	CMP	C4-N9-C1'	2.61	132.74	126.63
2	C	401	CMP	C5-C4-N9	2.54	108.58	105.81
2	E	402	CMP	C6-C5-N7	2.52	136.95	132.09
2	H	402	CMP	N3-C2-N1	-2.47	124.85	128.58
2	H	401	CMP	C6-C5-C4	2.45	120.52	117.18
2	F	401	CMP	O4'-C4'-C3'	-2.43	99.79	104.92
2	B	401	CMP	C5-C4-N9	-2.43	103.17	105.81
2	B	401	CMP	O3'-C3'-C2'	2.42	117.98	115.61
2	B	402	CMP	C1'-N9-C8	-2.42	121.73	127.09
2	A	401	CMP	O3'-P-O1P	-2.42	105.22	110.39
2	D	402	CMP	C6-C5-N7	2.41	136.74	132.09
2	G	402	CMP	N6-C6-N1	2.34	123.59	118.38
2	E	401	CMP	O5'-P-O3'	2.34	108.83	105.70
2	G	402	CMP	O3'-C3'-C4'	-2.32	108.96	110.71
2	H	401	CMP	O3'-C3'-C2'	2.32	117.88	115.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	402	CMP	C4-N9-C1'	2.31	132.04	126.63
2	A	401	CMP	O3'-C3'-C2'	2.31	117.87	115.61
2	C	401	CMP	O5'-C5'-C4'	2.30	111.07	105.71
2	D	401	CMP	O5'-P-O3'	-2.28	102.65	105.70
2	D	401	CMP	O3'-C3'-C2'	2.24	117.80	115.61
2	B	401	CMP	O4'-C4'-C3'	-2.24	100.20	104.92
2	H	401	CMP	C5-C6-N6	2.20	128.74	123.29
2	F	401	CMP	O2P-P-O3'	-2.20	101.92	107.04
2	E	402	CMP	O3'-C3'-C4'	2.20	112.37	110.71
2	G	401	CMP	C5-N7-C8	2.19	106.90	103.45
2	G	402	CMP	C2-N1-C6	2.17	122.29	118.73
2	E	401	CMP	N3-C2-N1	-2.16	125.31	128.58
2	E	401	CMP	O4'-C4'-C3'	-2.16	100.36	104.92
2	B	401	CMP	C2-N1-C6	2.15	122.25	118.73
2	C	401	CMP	O4'-C1'-N9	2.13	112.18	108.09
2	A	401	CMP	O4'-C4'-C3'	-2.13	100.43	104.92
2	F	401	CMP	C4'-O4'-C1'	-2.12	104.78	109.47
2	D	402	CMP	C4'-O4'-C1'	-2.12	104.78	109.47
2	D	401	CMP	O5'-C5'-C4'	2.11	110.62	105.71
2	F	402	CMP	C4-N9-C8	2.08	107.93	105.74
2	A	402	CMP	C5-C6-N6	-2.07	118.15	123.29
2	H	402	CMP	C4-N9-C8	2.04	107.88	105.74
2	C	401	CMP	O4'-C4'-C3'	-2.04	100.62	104.92
2	H	402	CMP	C5-N7-C8	2.02	106.62	103.45
2	C	402	CMP	C1'-N9-C8	-2.02	122.62	127.09

There are no chirality outliers.

All (12) torsion outliers are listed below:

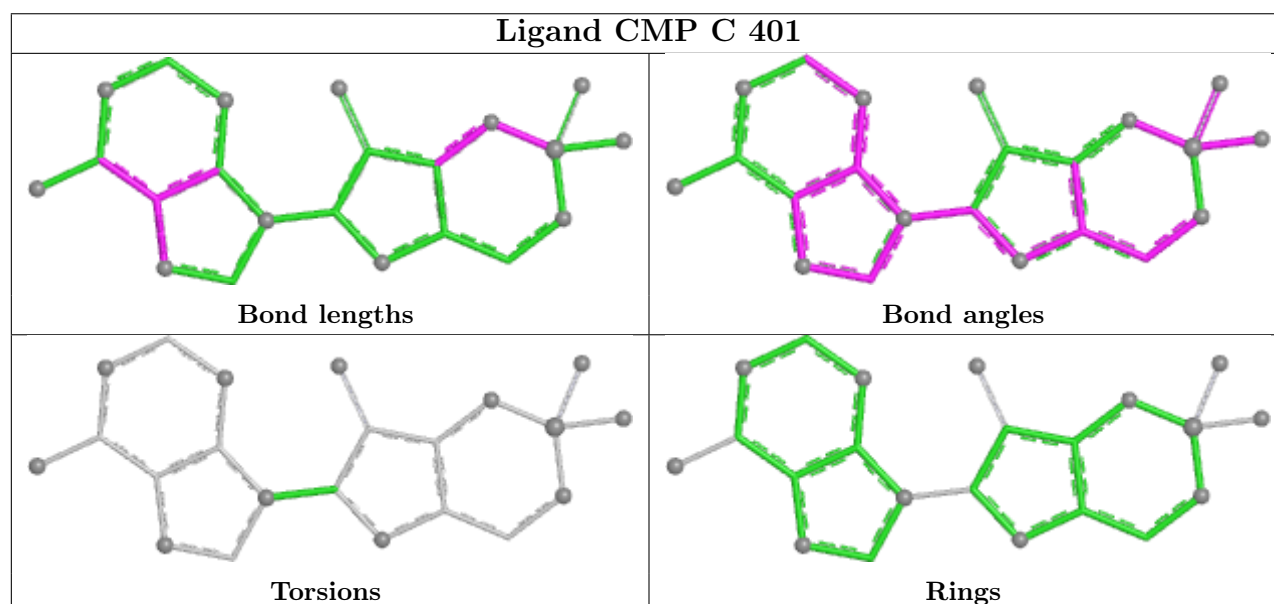
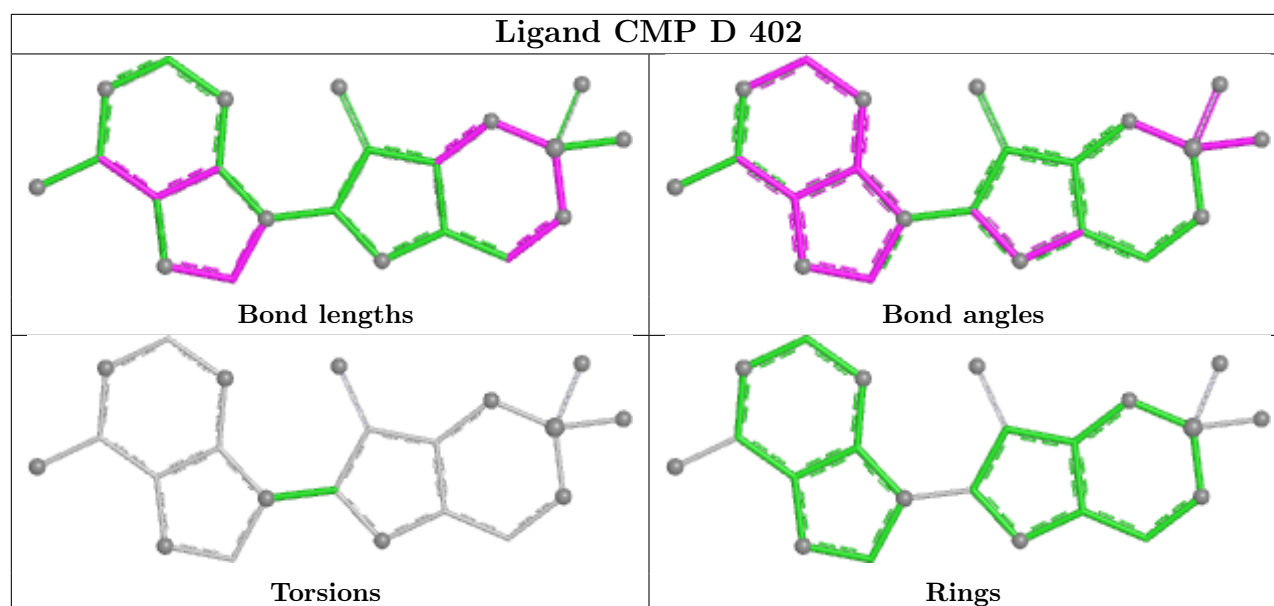
Mol	Chain	Res	Type	Atoms
2	E	402	CMP	C2'-C1'-N9-C4
2	F	402	CMP	C2'-C1'-N9-C4
2	E	402	CMP	C2'-C1'-N9-C8
2	F	402	CMP	C2'-C1'-N9-C8
2	H	402	CMP	C2'-C1'-N9-C8
2	F	402	CMP	O4'-C1'-N9-C8
2	H	402	CMP	O4'-C1'-N9-C8
2	G	401	CMP	C2'-C1'-N9-C4
2	H	402	CMP	C2'-C1'-N9-C4
2	A	402	CMP	O4'-C1'-N9-C8
2	G	402	CMP	O4'-C1'-N9-C8
2	H	401	CMP	O4'-C1'-N9-C8

There are no ring outliers.

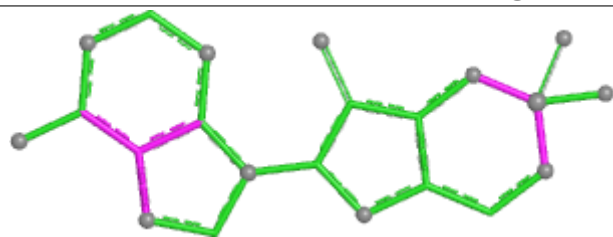
16 monomers are involved in 300 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	402	CMP	21	0
2	C	401	CMP	17	0
2	D	401	CMP	16	0
2	E	401	CMP	24	0
2	F	402	CMP	7	0
2	H	402	CMP	16	0
2	A	402	CMP	15	0
2	C	402	CMP	19	0
2	G	401	CMP	19	0
2	B	402	CMP	21	0
2	E	402	CMP	11	0
2	G	402	CMP	11	0
2	A	401	CMP	25	0
2	H	401	CMP	22	0
2	B	401	CMP	34	0
2	F	401	CMP	22	0

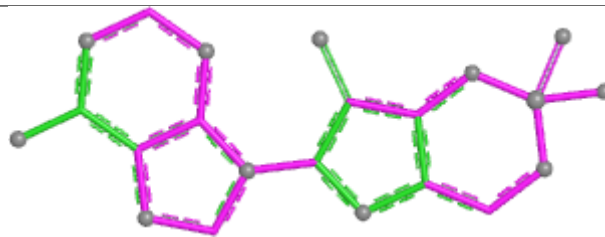
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



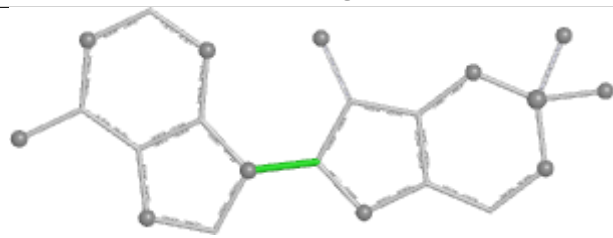
Ligand CMP D 401



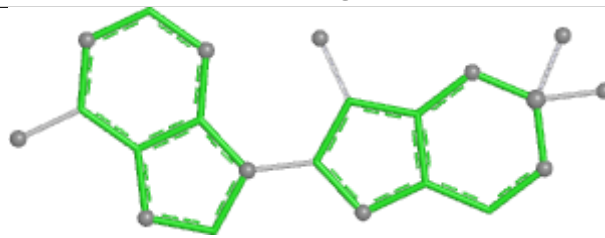
Bond lengths



Bond angles

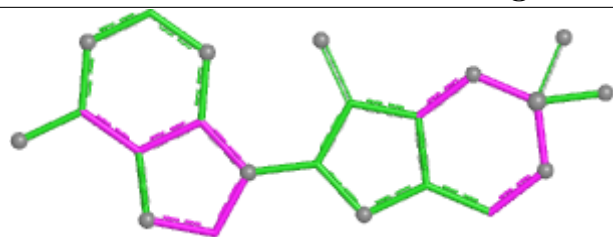


Torsions

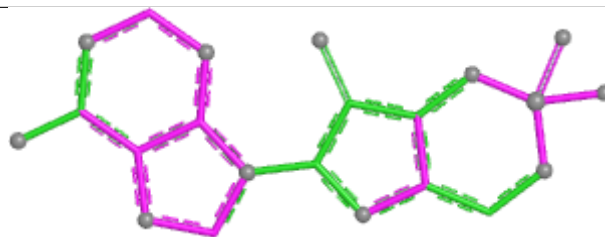


Rings

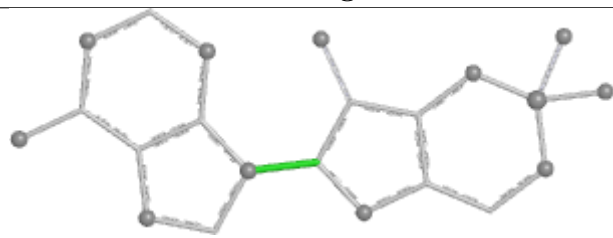
Ligand CMP E 401



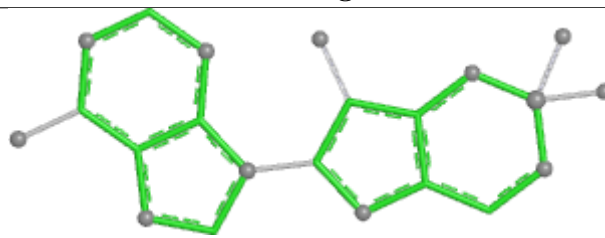
Bond lengths



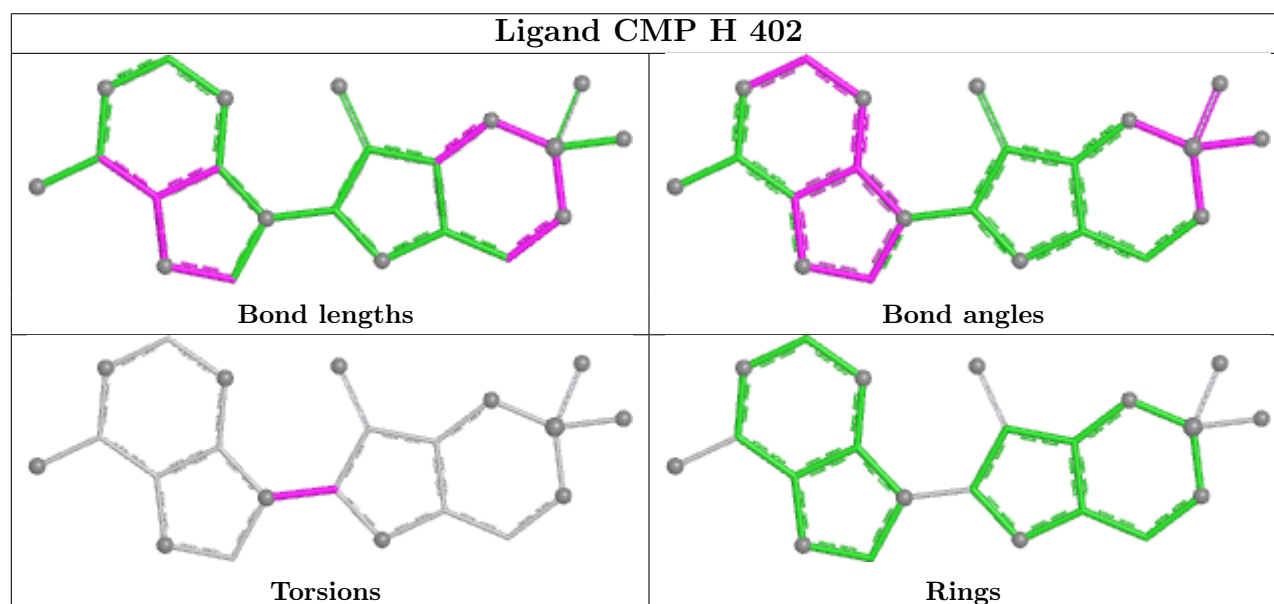
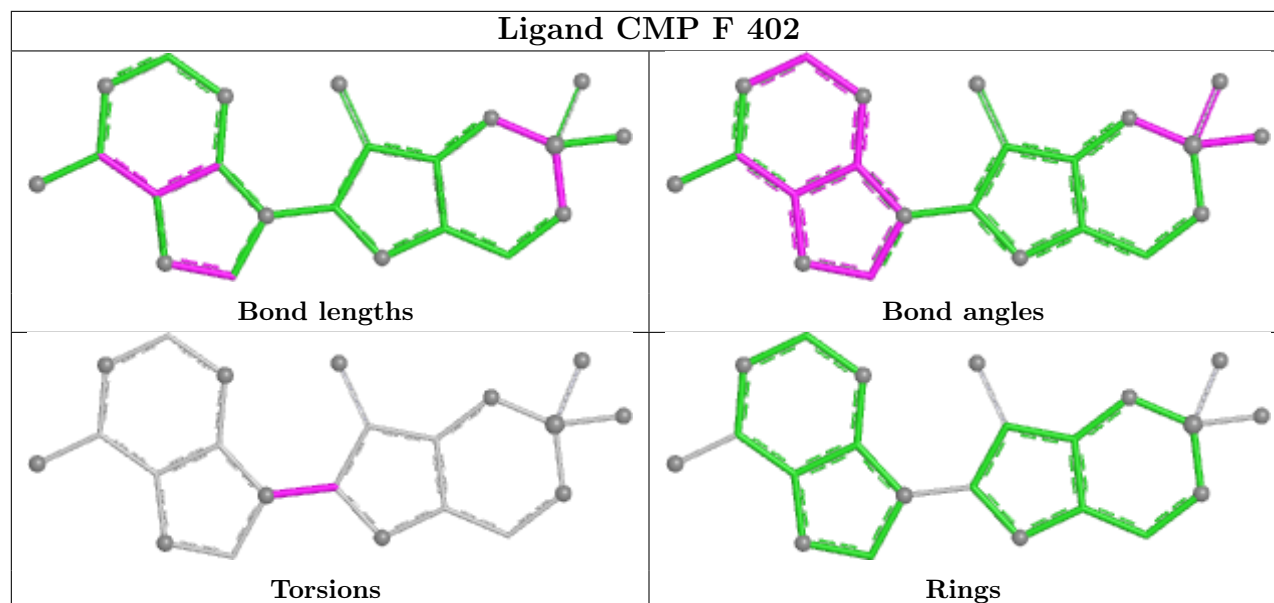
Bond angles



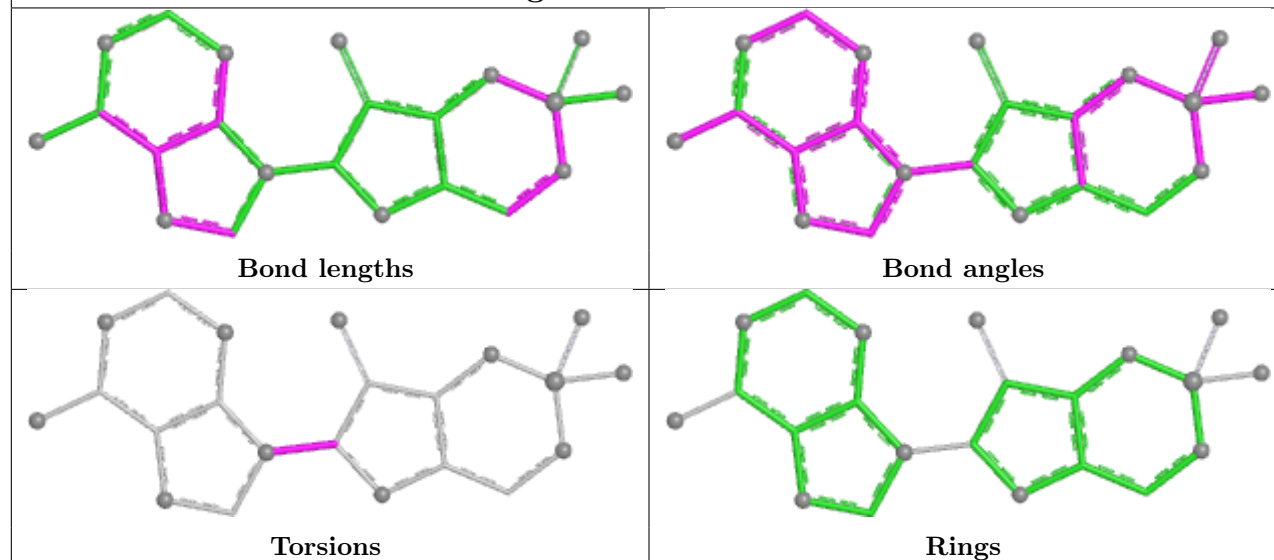
Torsions



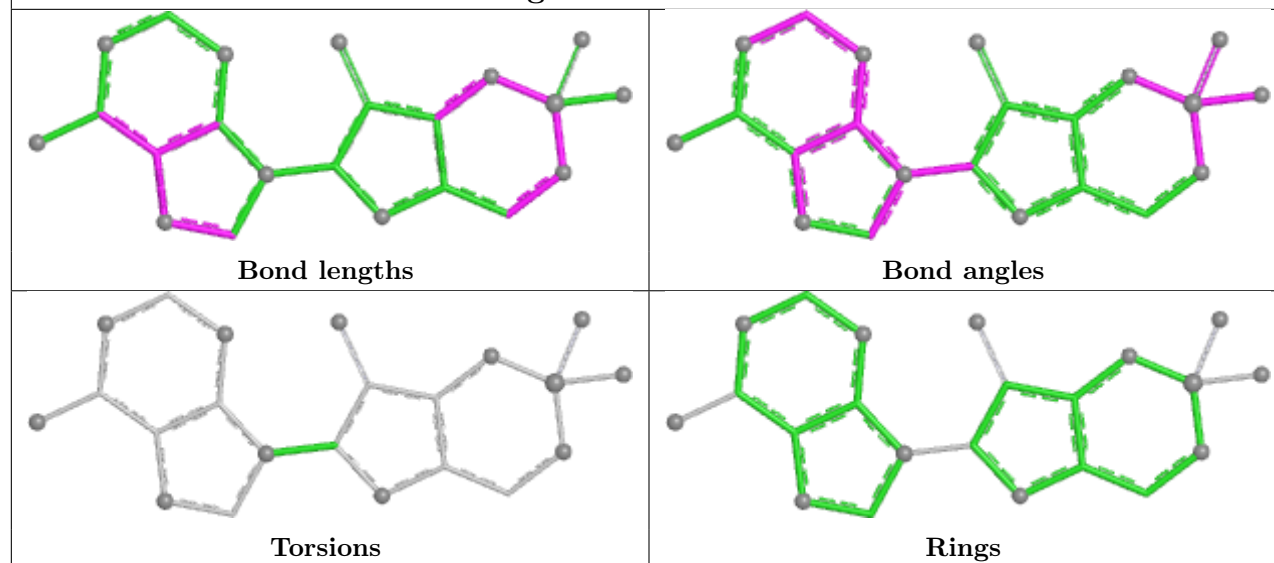
Rings

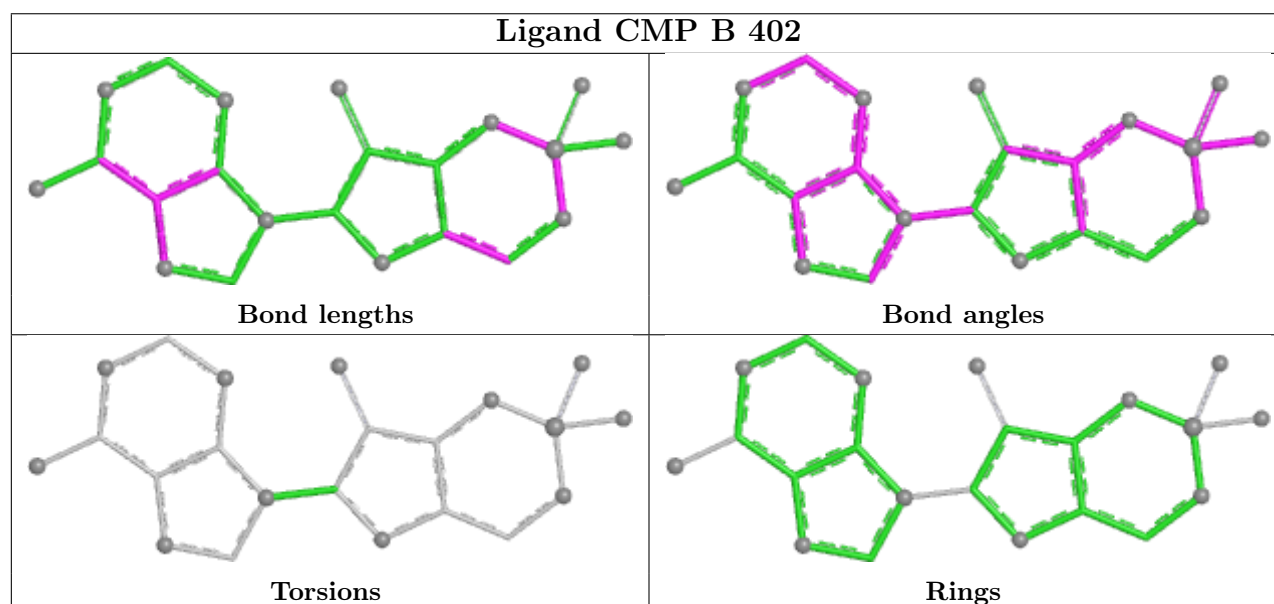
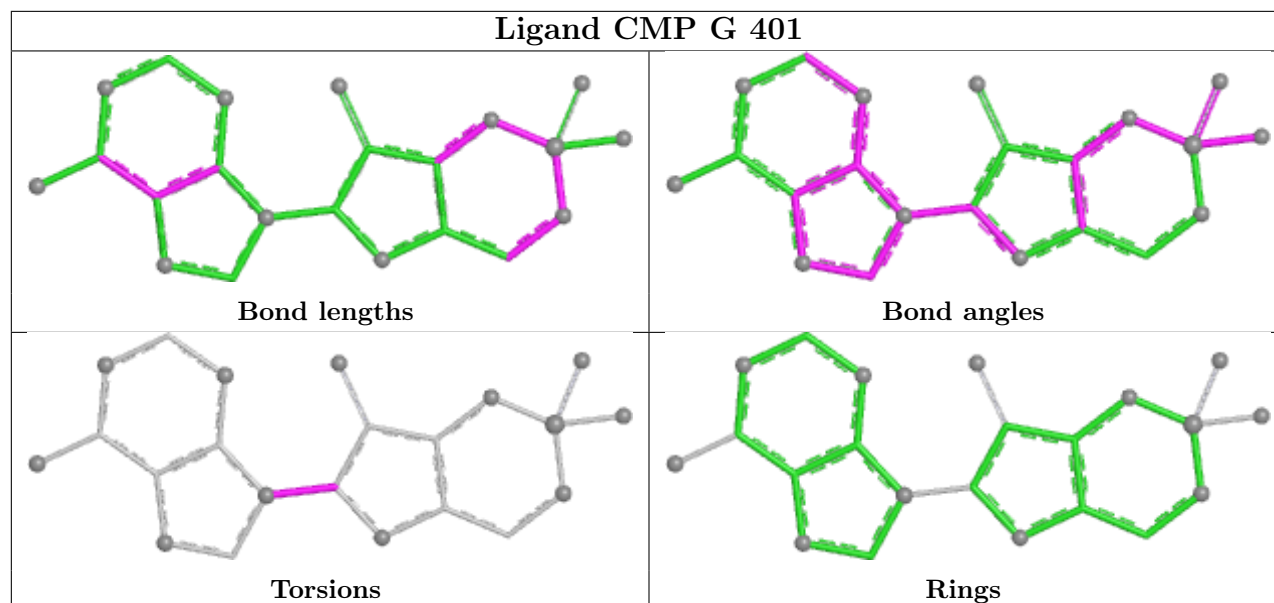


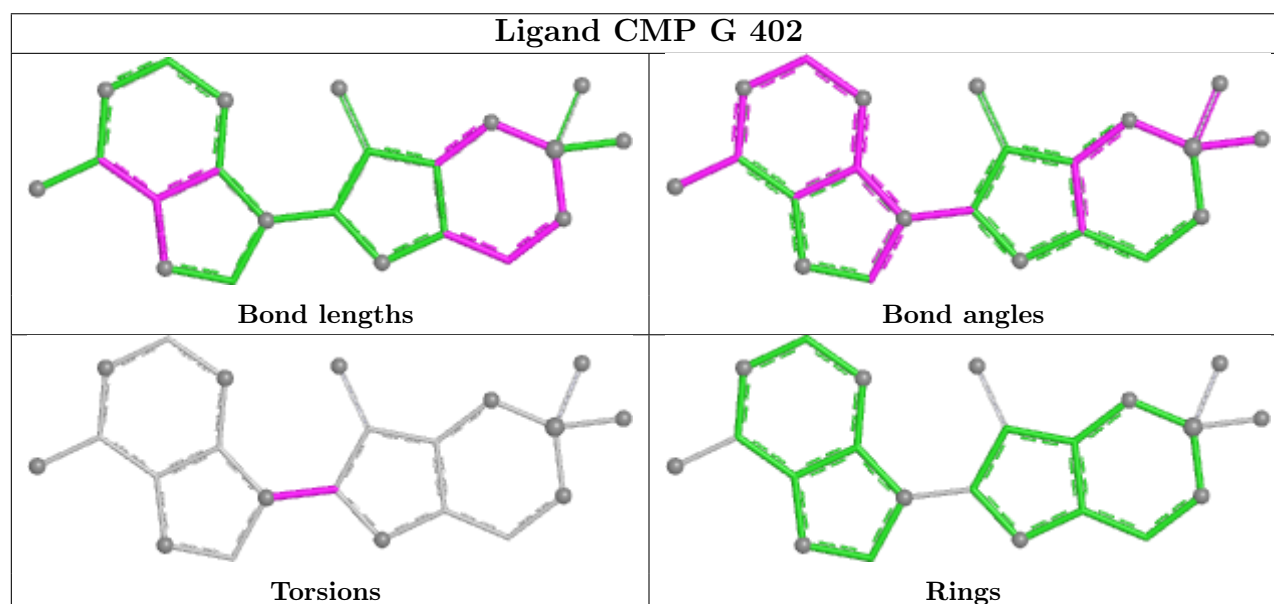
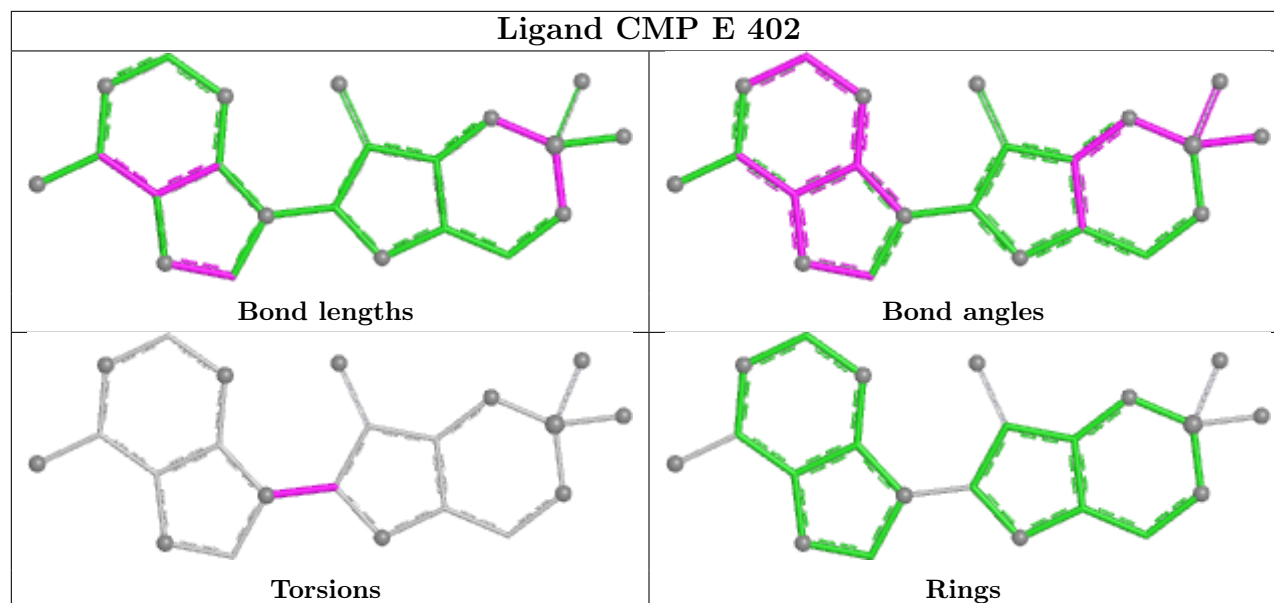
Ligand CMP A 402

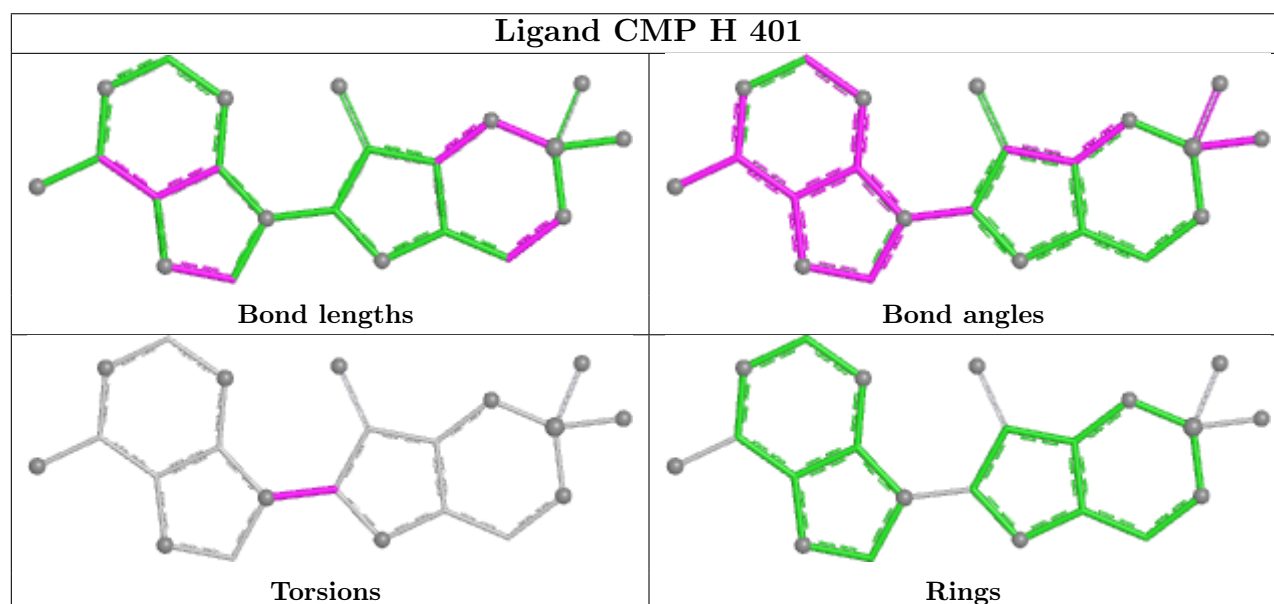
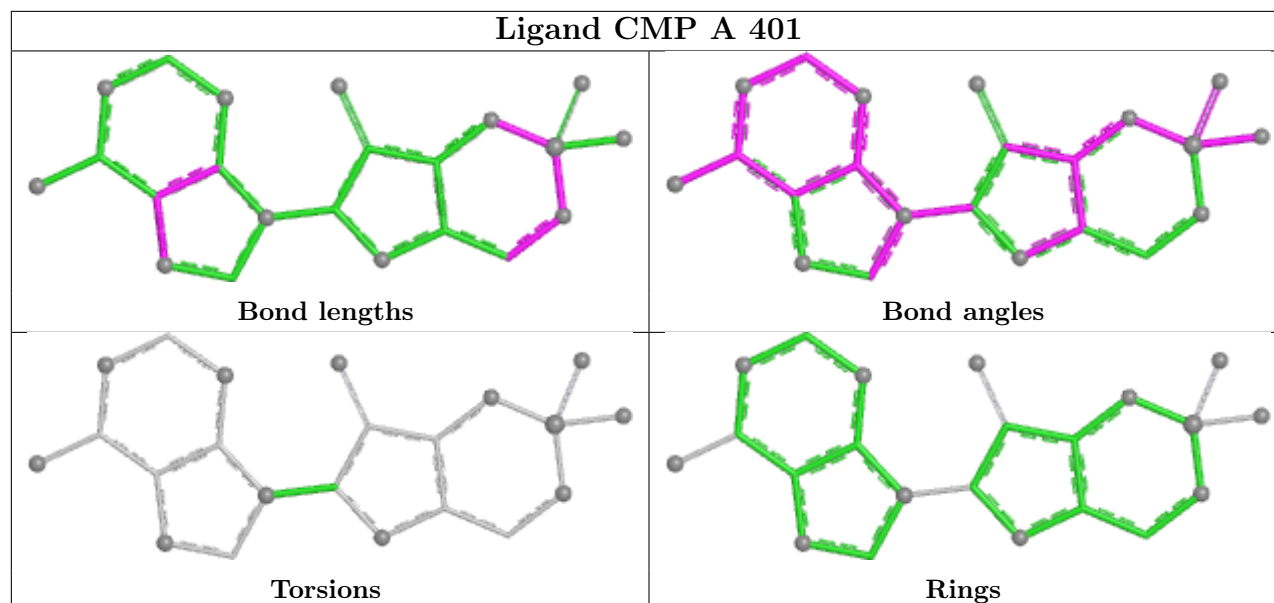


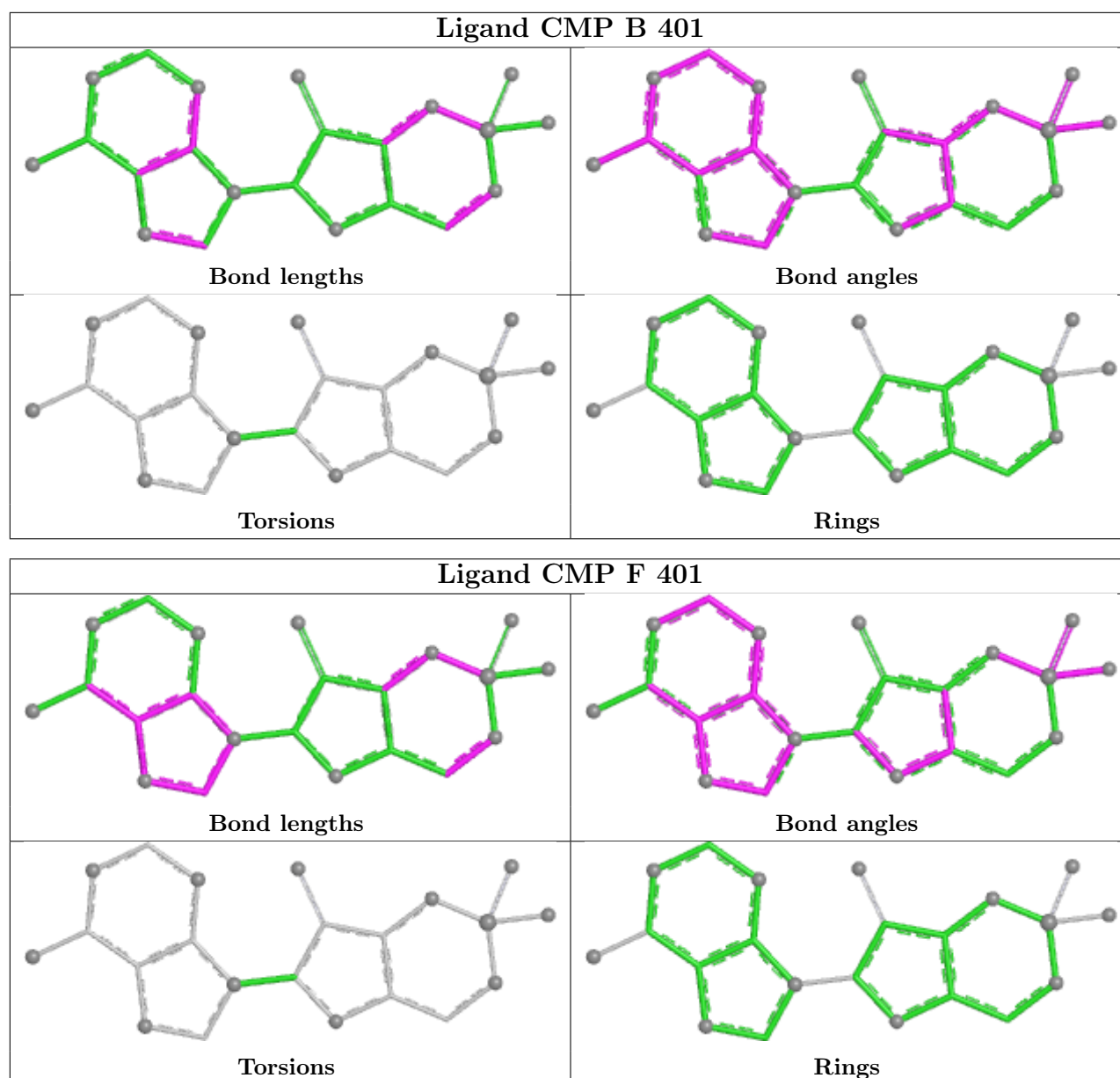
Ligand CMP C 402











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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	268/269 (99%)	-0.69	5 (1%) 66 51	70, 133, 202, 260	0
1	B	268/269 (99%)	-0.74	4 (1%) 72 56	70, 133, 202, 266	0
1	C	268/269 (99%)	-0.72	2 (0%) 84 70	71, 131, 201, 286	0
1	D	266/269 (98%)	-0.73	2 (0%) 82 68	75, 133, 194, 246	0
1	E	268/269 (99%)	-0.75	0 100 100	75, 139, 215, 259	0
1	F	268/269 (99%)	-0.69	1 (0%) 88 76	75, 138, 212, 261	0
1	G	268/269 (99%)	-0.70	1 (0%) 88 76	77, 135, 201, 268	0
1	H	268/269 (99%)	-0.70	3 (1%) 78 62	71, 132, 199, 274	0
All	All	2142/2152 (99%)	-0.72	18 (0%) 82 68	70, 134, 205, 286	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	166	GLY	4.2
1	F	185	ASN	3.6
1	H	169	GLY	3.2
1	D	166	GLY	2.7
1	A	168	GLU	2.6
1	C	305	SER	2.5
1	A	185	ASN	2.4
1	B	179	GLU	2.4
1	B	306	GLU	2.4
1	H	308	GLU	2.4
1	H	164	GLN	2.3
1	A	307	ASN	2.2
1	B	168	GLU	2.2
1	A	179	GLU	2.2
1	A	306	GLU	2.2
1	B	178	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	286	PRO	2.0
1	C	169	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

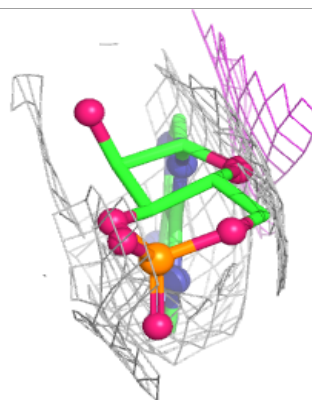
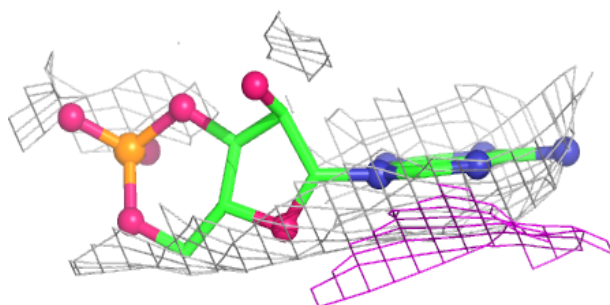
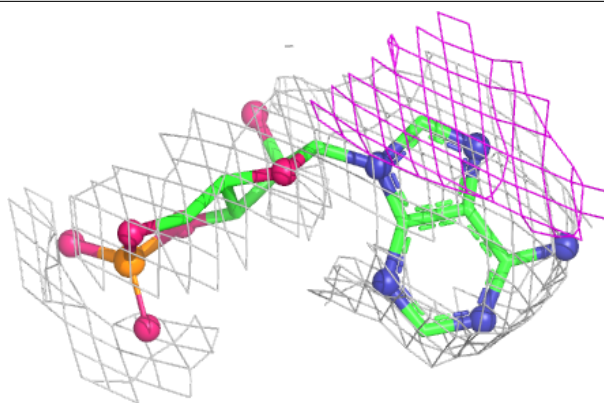
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CMP	A	401	22/22	0.99	0.05	77,102,123,128	0
2	CMP	A	402	22/22	0.99	0.06	79,151,186,198	0
2	CMP	B	401	22/22	0.99	0.04	70,102,127,132	0
2	CMP	C	401	22/22	0.99	0.05	77,107,140,155	0
2	CMP	C	402	22/22	0.99	0.03	79,130,177,213	0
2	CMP	D	401	22/22	0.99	0.05	84,111,128,131	0
2	CMP	E	401	22/22	0.99	0.04	73,108,130,140	0
2	CMP	E	402	22/22	0.99	0.04	118,201,228,242	0
2	CMP	F	401	22/22	0.99	0.04	69,96,132,143	0
2	CMP	F	402	22/22	0.99	0.04	137,185,218,227	0
2	CMP	G	401	22/22	0.99	0.04	79,112,144,145	0
2	CMP	H	401	22/22	0.99	0.05	74,105,125,133	0
2	CMP	H	402	22/22	0.99	0.04	81,139,165,200	0
2	CMP	G	402	22/22	1.00	0.04	101,148,200,208	0
2	CMP	D	402	22/22	1.00	0.04	112,143,193,210	0
2	CMP	B	402	22/22	1.00	0.04	86,150,175,194	0

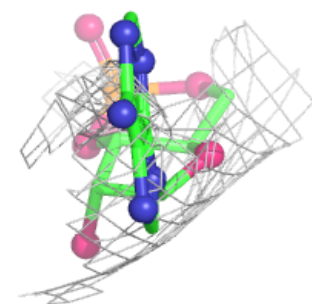
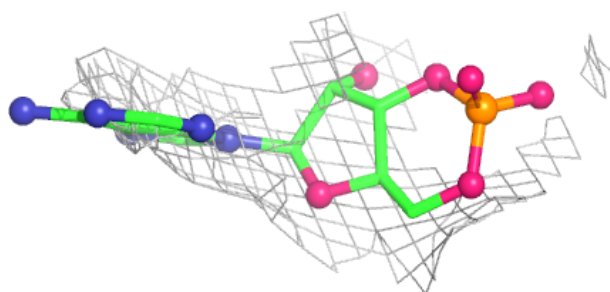
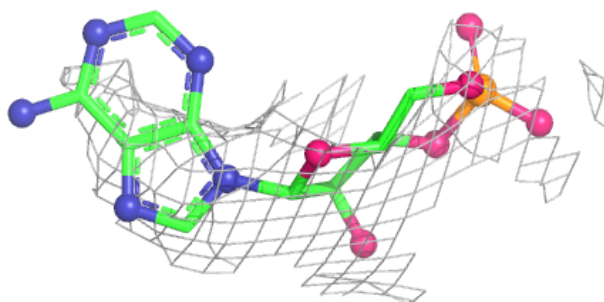
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around CMP A 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

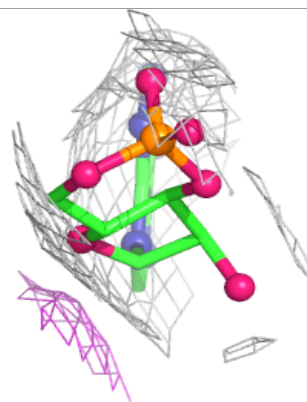
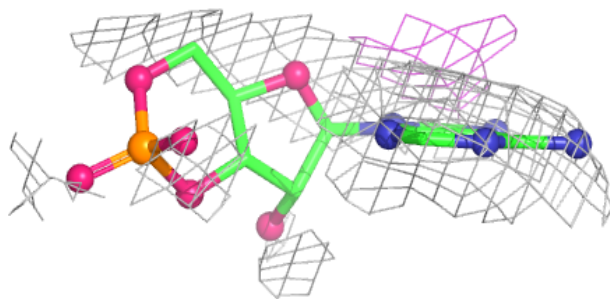
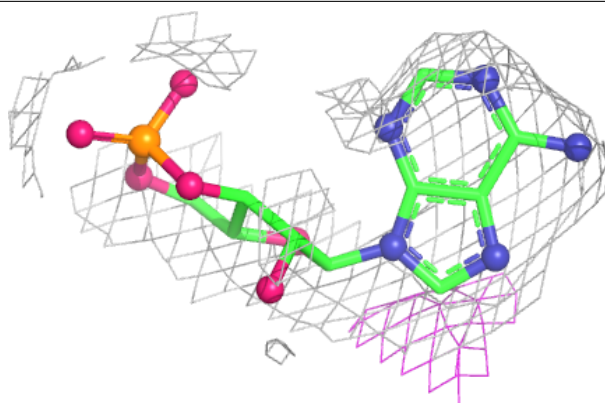
**Electron density around CMP A 402:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

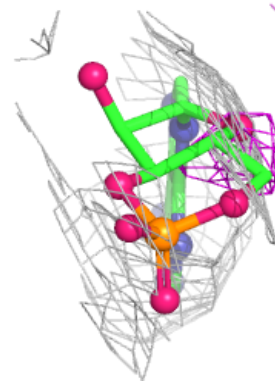
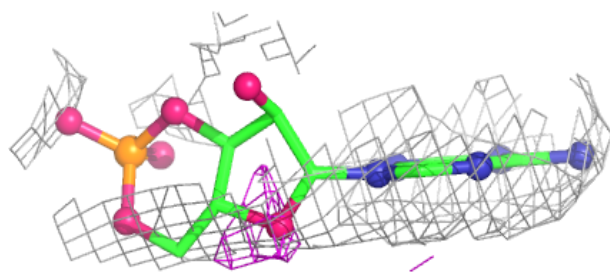
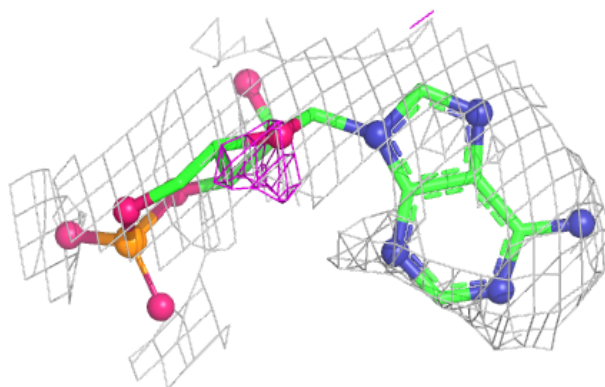


Electron density around CMP B 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

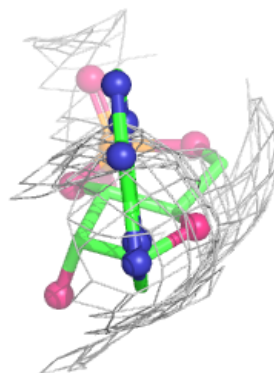
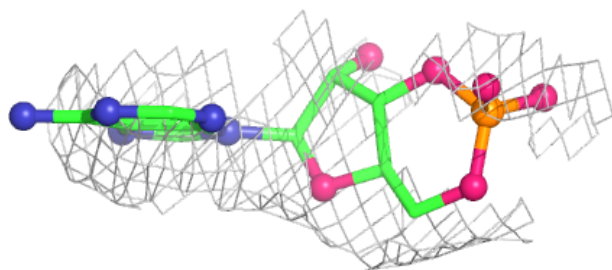
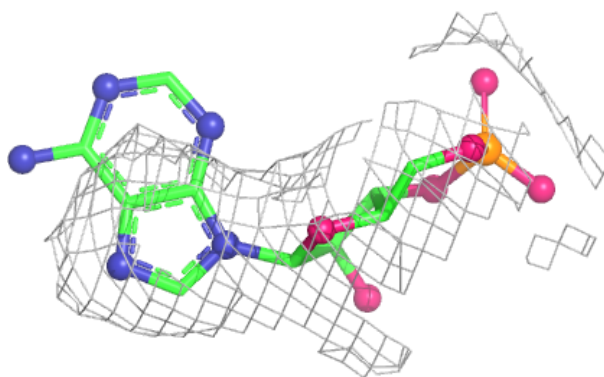
**Electron density around CMP C 401:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

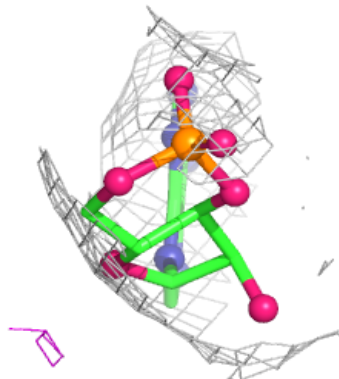
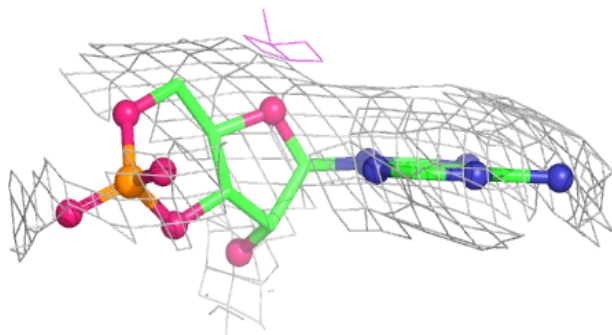
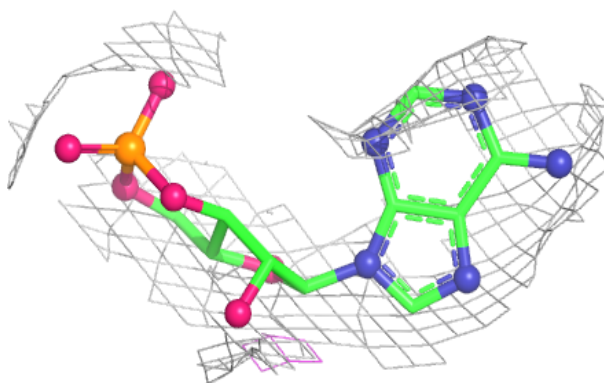


Electron density around CMP C 402:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

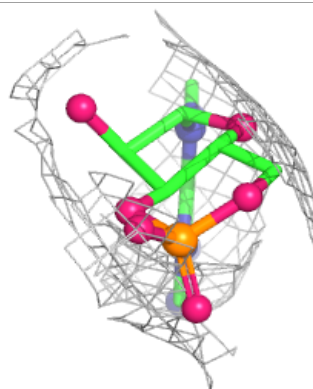
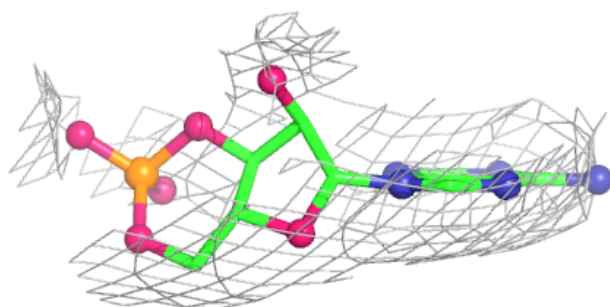
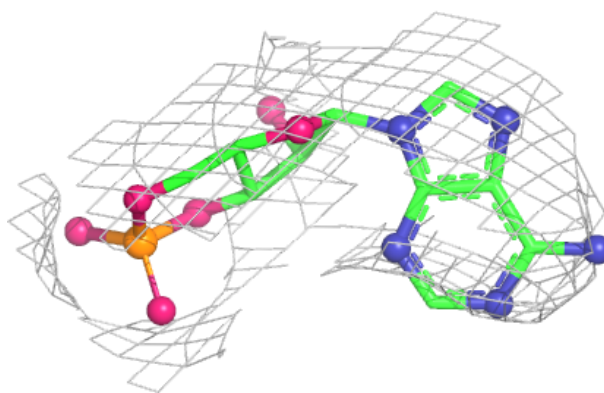
**Electron density around CMP D 401:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

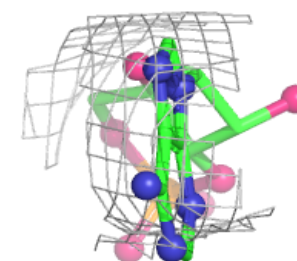
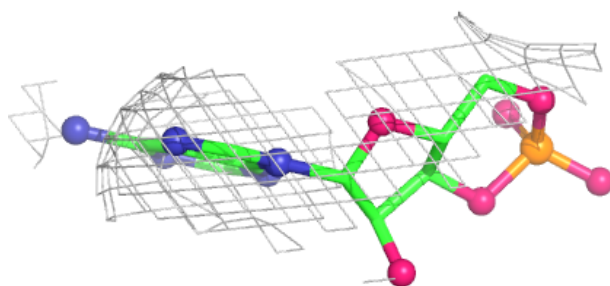
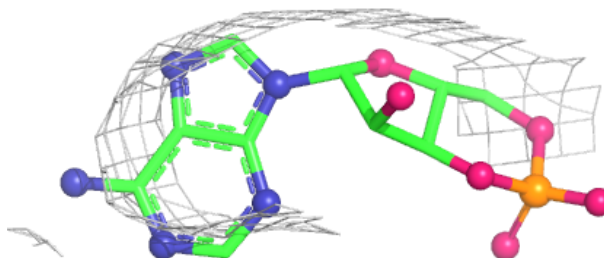


Electron density around CMP E 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

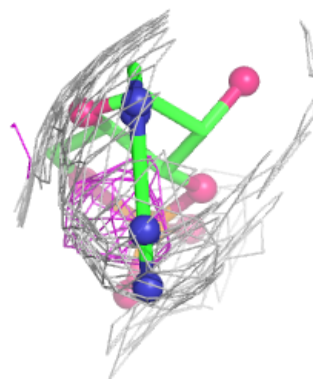
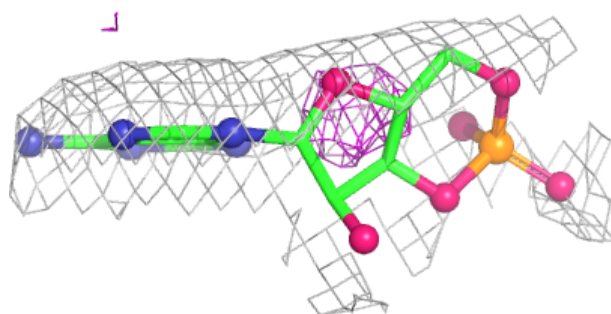
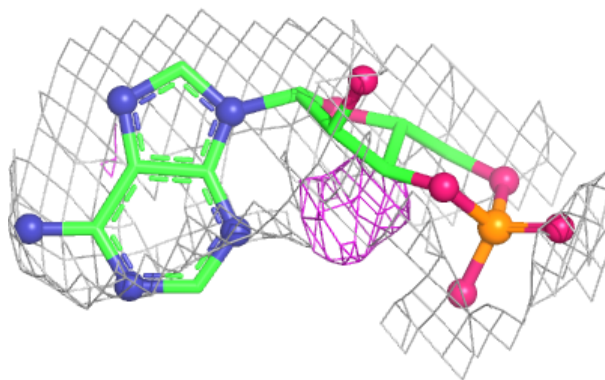
**Electron density around CMP E 402:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

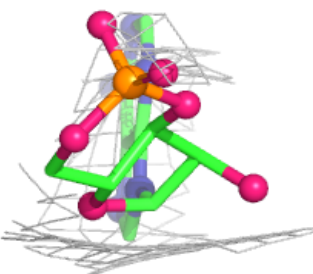
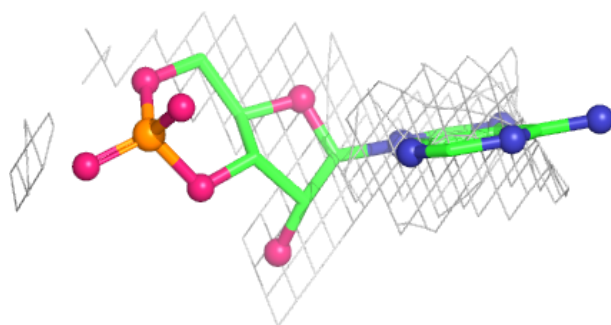
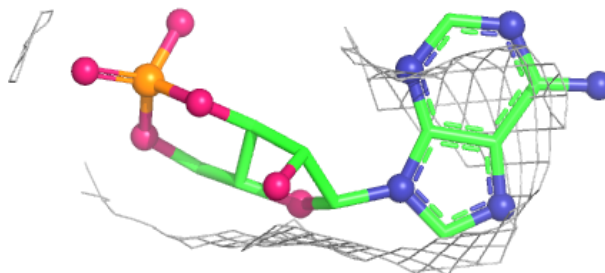


Electron density around CMP F 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

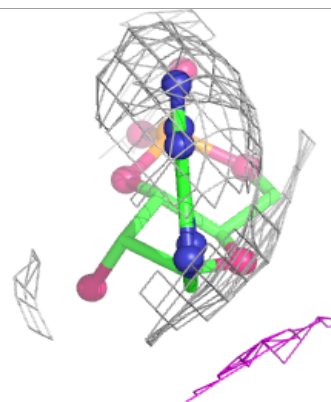
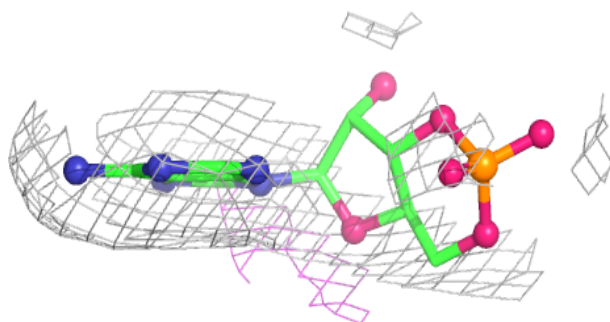
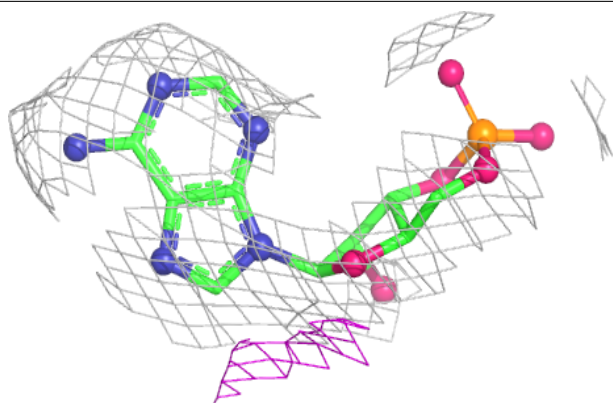
**Electron density around CMP F 402:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

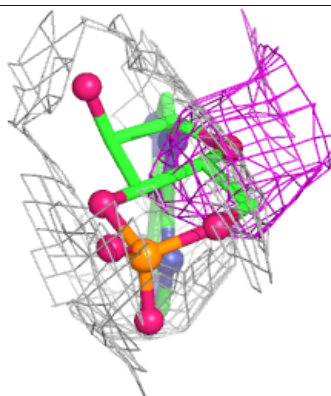
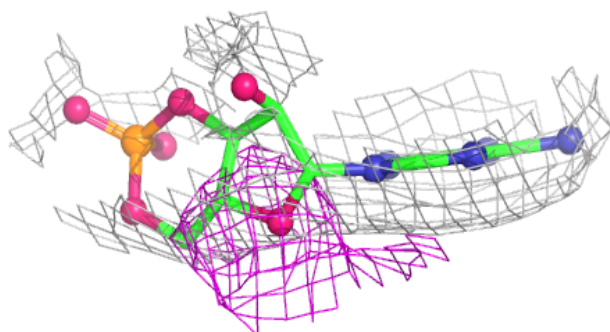
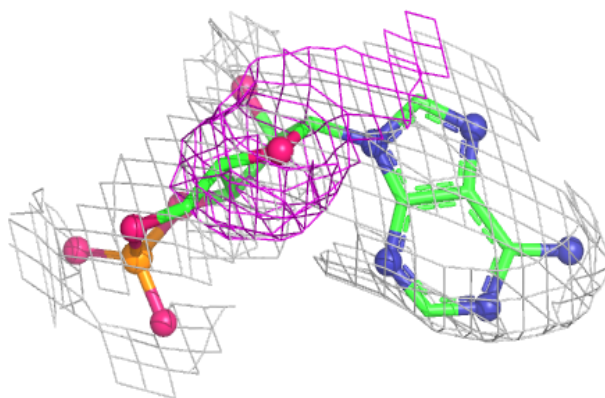


Electron density around CMP G 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

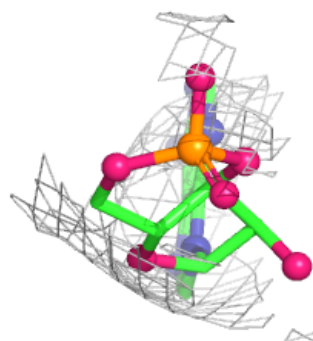
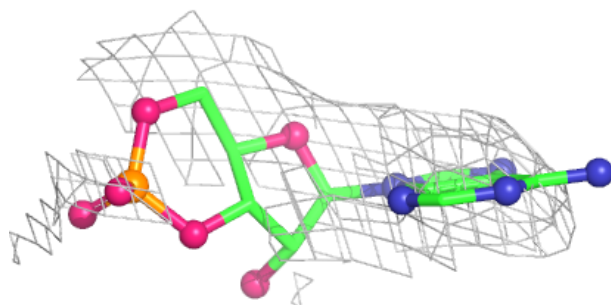
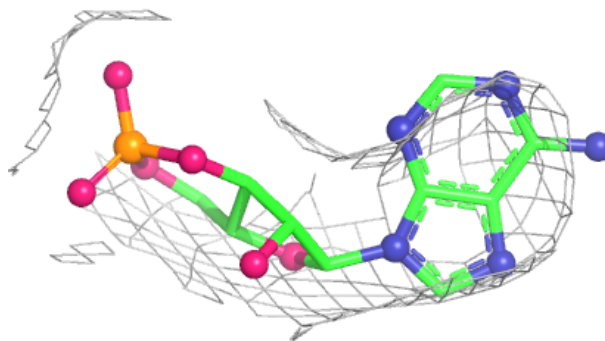
**Electron density around CMP H 401:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

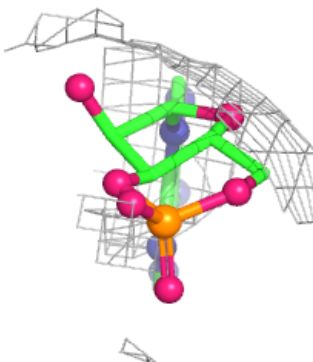
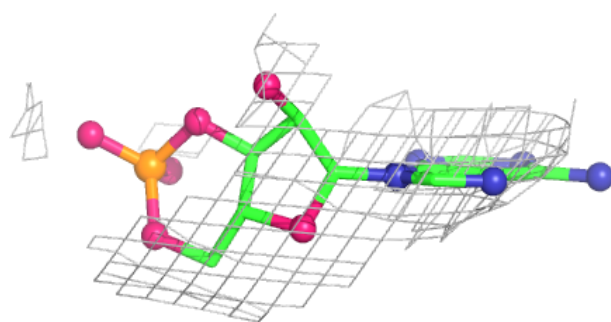
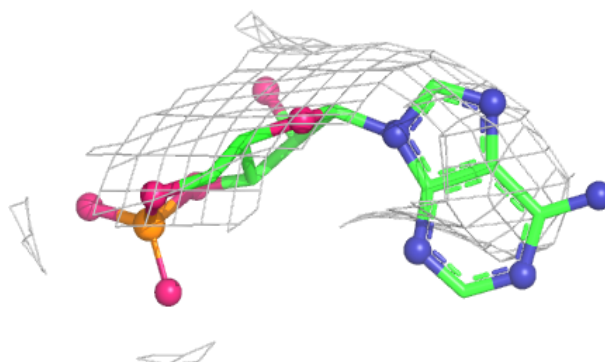


Electron density around CMP H 402:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

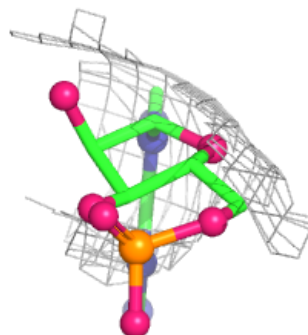
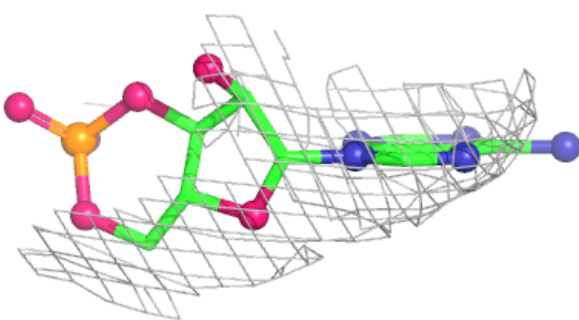
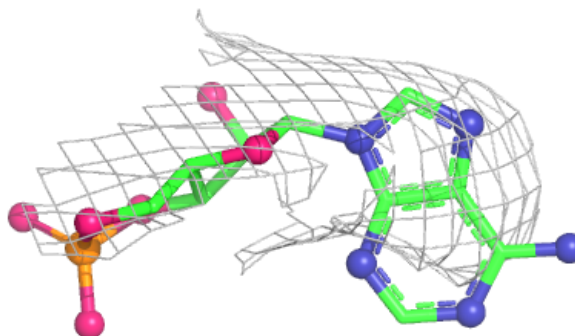
**Electron density around CMP G 402:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

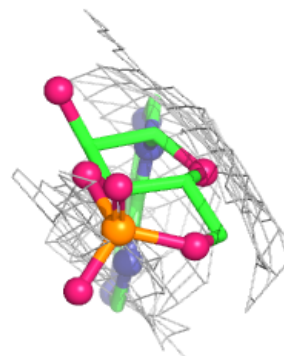
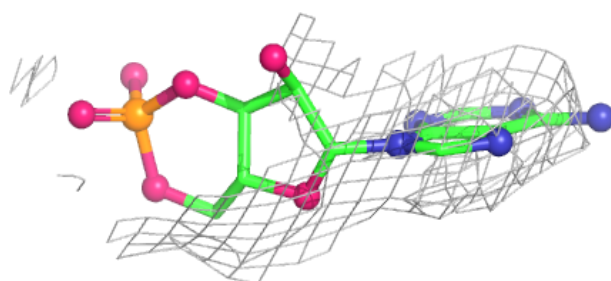
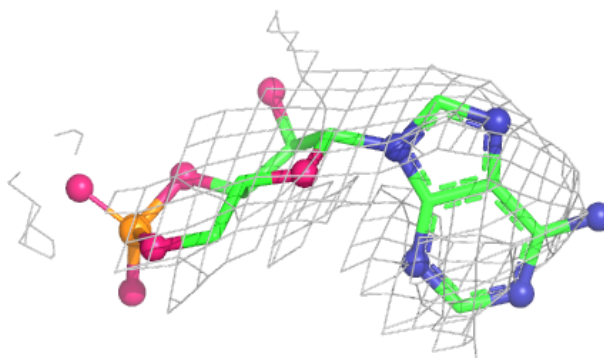


Electron density around CMP D 402:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around CMP B 402:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.