Full wwPDB EM Validation Report (i)

Dec 11, 2022 – 02:52 pm GMT

PDB ID	:	6SMH
EMDB ID	:	EMD-10235
Title	:	Cryo-electron microscopy structure of a RbcL-Raf1 supercomplex from Synechococcus elongatus PCC 7942
Authors	:	Huang, F.; Kong, W.-W.; Sun, Y.; Chen, T.; Dykes, G.F.; Jiang, Y.L.; Liu, L.N.
Deposited on	:	2019-08-21
Resolution	:	4.30 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

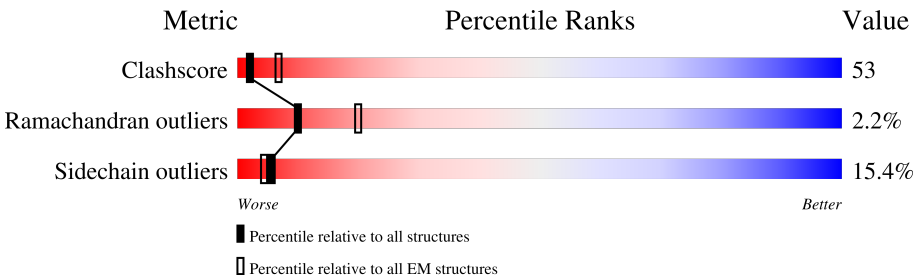
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	447	78% 21%
1	B	447	59% 32% 8%
1	C	447	48% 37% 14%
1	D	447	50% 36% 13%
1	E	447	54% 33% 10%
1	F	447	40% 41% 17%
1	G	447	53% 36% 9%
1	H	447	56% 34% 10%

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Mol	Chain	Length	Quality of chain
2	I	188	74% 70% 23% • 5%
2	J	188	73% 43% 41% 9% 7%
2	K	188	71% 48% 35% 9% • 5%
2	L	188	72% 39% 40% 13% • 5%
2	M	188	69% 49% 36% 7% • •
2	N	188	73% 59% 34% • • •
2	O	188	71% 46% 38% 9% • •
2	P	188	70% 66% 29% • • •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 39744 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Ribulose bisphosphate carboxylase large chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	447	3495	2220	614	644	17	0	0
1	B	447	3495	2220	614	644	17	0	0
1	C	447	3495	2220	614	644	17	0	0
1	D	447	3495	2220	614	644	17	0	0
1	E	447	3495	2220	614	644	17	0	0
1	F	447	3495	2220	614	644	17	0	0
1	G	447	3495	2220	614	644	17	0	0
1	H	447	3495	2220	614	644	17	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	PRO	ASP	conflict	UNP Q31NB3
A	78	ASP	LYS	conflict	UNP Q31NB3
A	100	ASP	TYR	conflict	UNP Q31NB3
B	48	PRO	ASP	conflict	UNP Q31NB3
B	78	ASP	LYS	conflict	UNP Q31NB3
B	100	ASP	TYR	conflict	UNP Q31NB3
C	48	PRO	ASP	conflict	UNP Q31NB3
C	78	ASP	LYS	conflict	UNP Q31NB3
C	100	ASP	TYR	conflict	UNP Q31NB3
D	48	PRO	ASP	conflict	UNP Q31NB3
D	78	ASP	LYS	conflict	UNP Q31NB3
D	100	ASP	TYR	conflict	UNP Q31NB3
E	48	PRO	ASP	conflict	UNP Q31NB3
E	78	ASP	LYS	conflict	UNP Q31NB3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	100	ASP	TYR	conflict	UNP Q31NB3
F	48	PRO	ASP	conflict	UNP Q31NB3
F	78	ASP	LYS	conflict	UNP Q31NB3
F	100	ASP	TYR	conflict	UNP Q31NB3
G	48	PRO	ASP	conflict	UNP Q31NB3
G	78	ASP	LYS	conflict	UNP Q31NB3
G	100	ASP	TYR	conflict	UNP Q31NB3
H	48	PRO	ASP	conflict	UNP Q31NB3
H	78	ASP	LYS	conflict	UNP Q31NB3
H	100	ASP	TYR	conflict	UNP Q31NB3

- Molecule 2 is a protein called Rubisco accumulation factor 1 (RAF1) peptide.

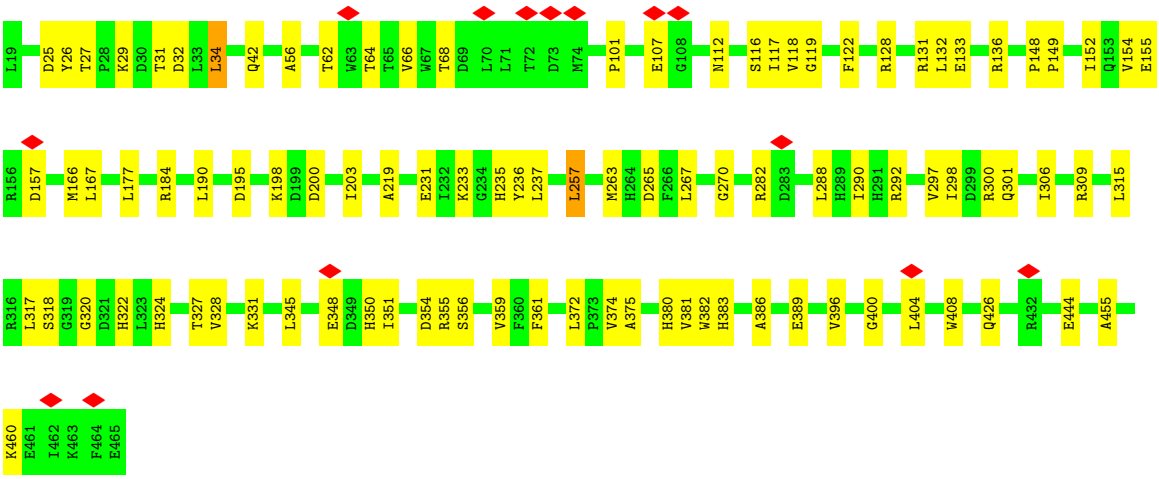
Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	179	Total	C	N	O	S	0	0
			1457	907	275	270	5		
2	J	188	Total	C	N	O	S	0	0
			1523	947	288	283	5		
2	K	179	Total	C	N	O	S	0	0
			1457	907	275	270	5		
2	L	179	Total	C	N	O	S	0	0
			1457	907	275	270	5		
2	M	180	Total	C	N	O	S	0	0
			1465	911	276	273	5		
2	N	181	Total	C	N	O	S	0	0
			1473	917	277	274	5		
2	O	181	Total	C	N	O	S	0	0
			1473	917	277	274	5		
2	P	182	Total	C	N	O	S	0	0
			1479	920	278	276	5		

3 Residue-property plots (i)

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

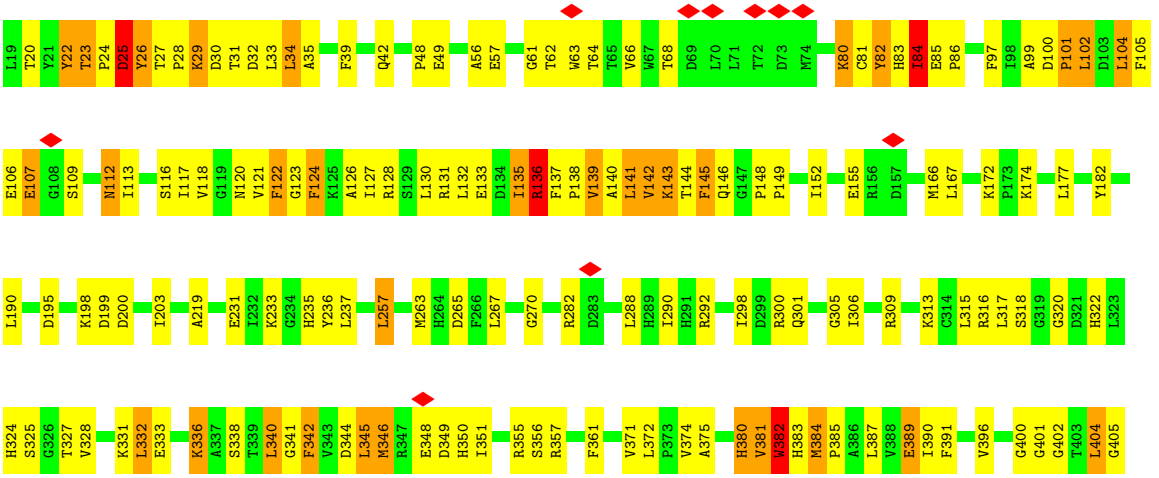
- Molecule 1: Ribulose bisphosphate carboxylase large chain

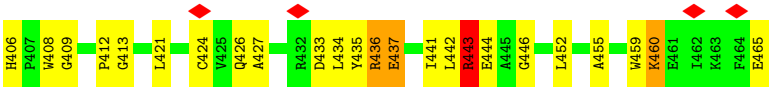
Chain A:



- Molecule 1: Ribulose bisphosphate carboxylase large chain

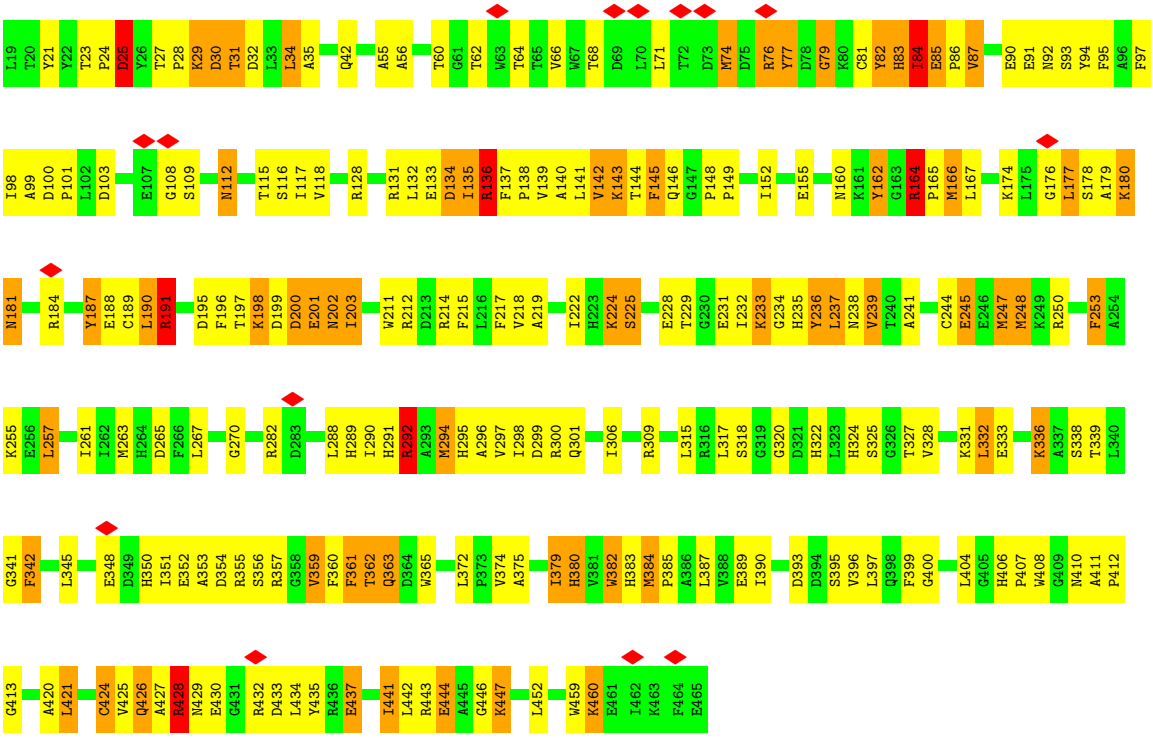
Chain B:





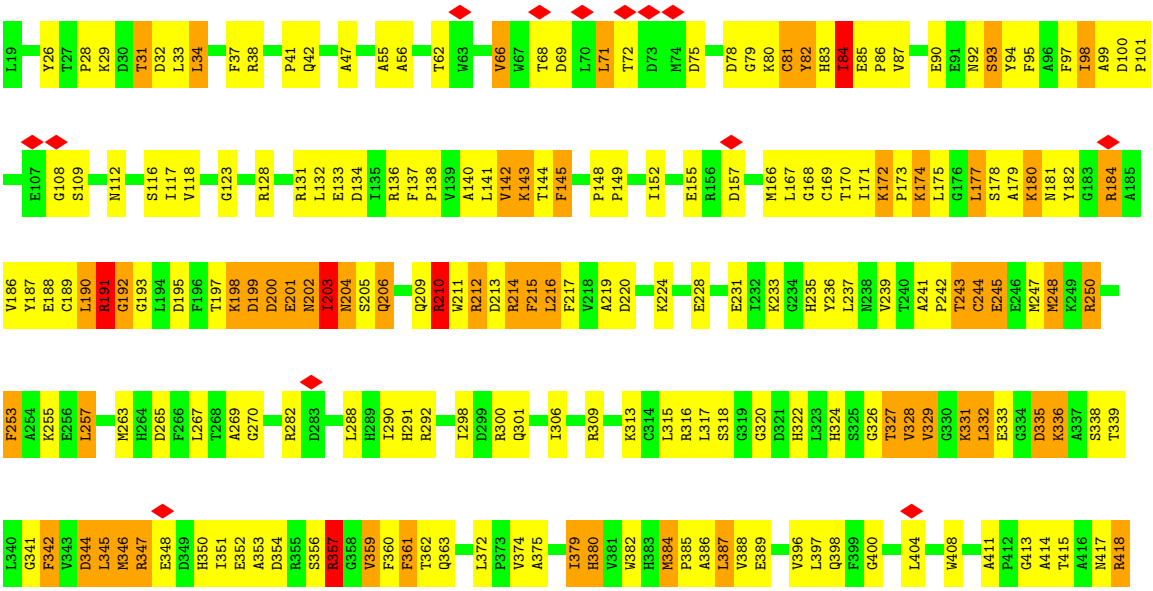
• Molecule 1: Ribulose bisphosphate carboxylase large chain

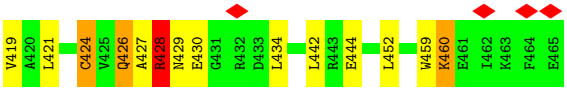
Chain C:



• Molecule 1: Ribulose bisphosphate carboxylase large chain

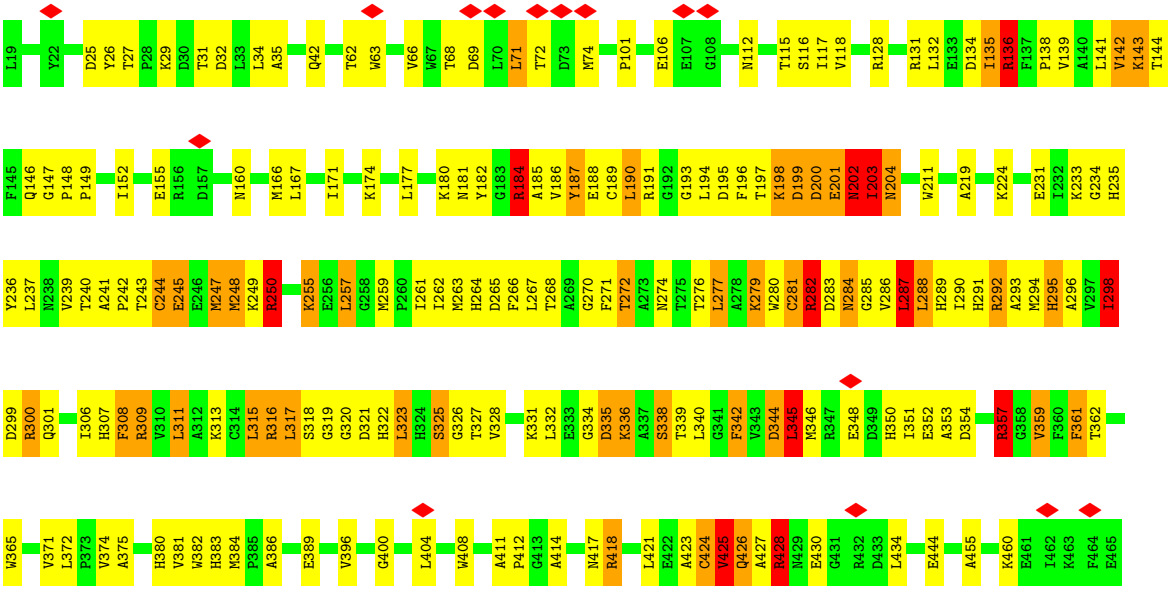
Chain D:





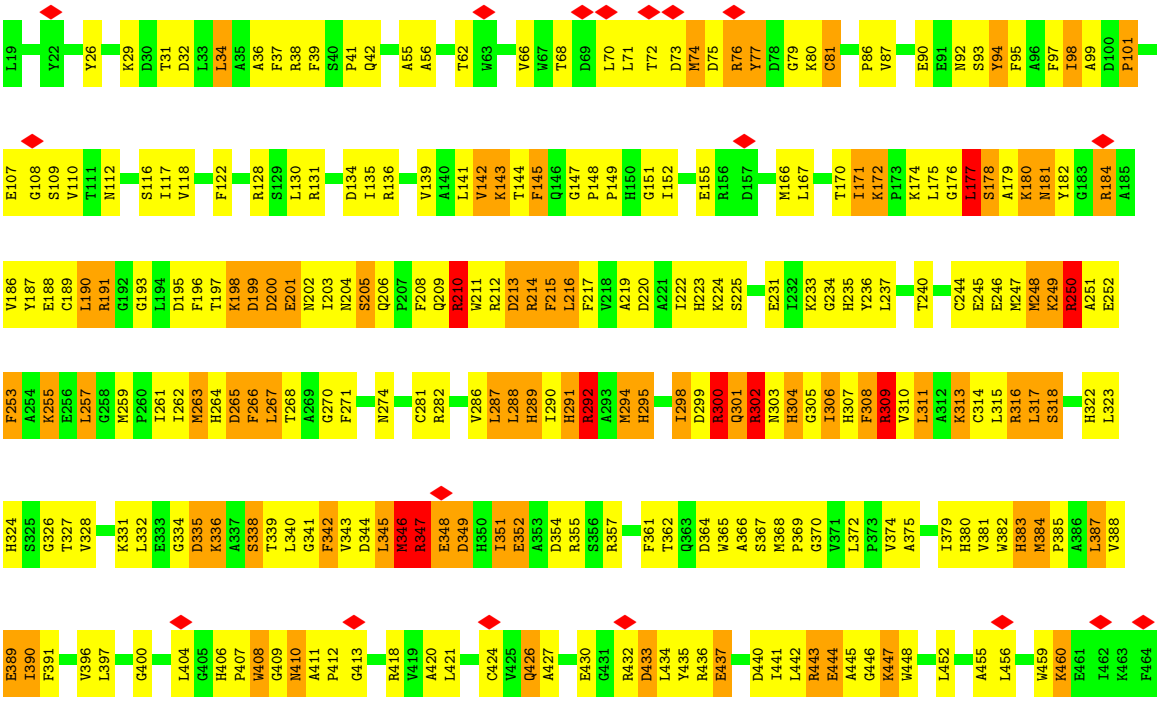
• Molecule 1: Ribulose bisphosphate carboxylase large chain

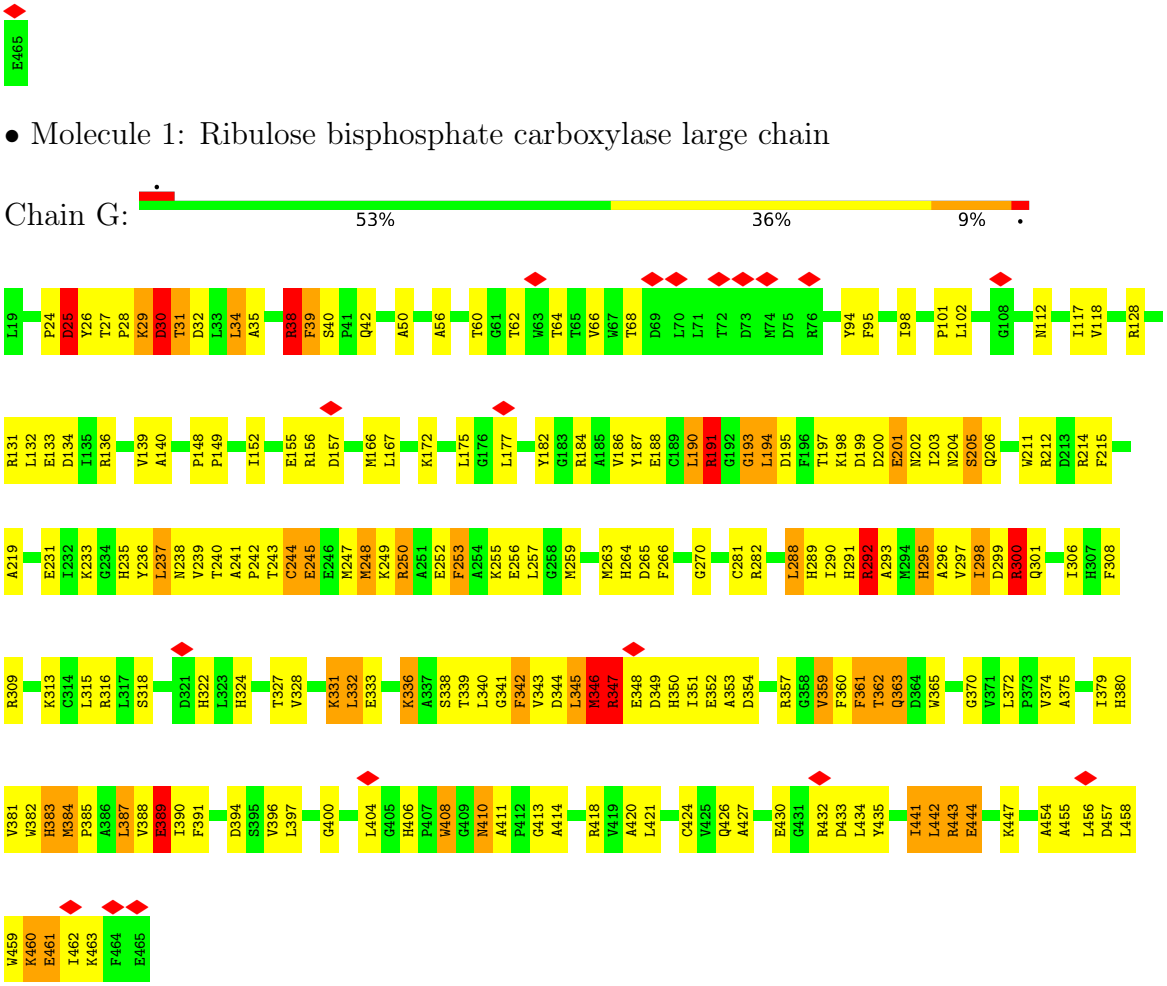
Chain E:

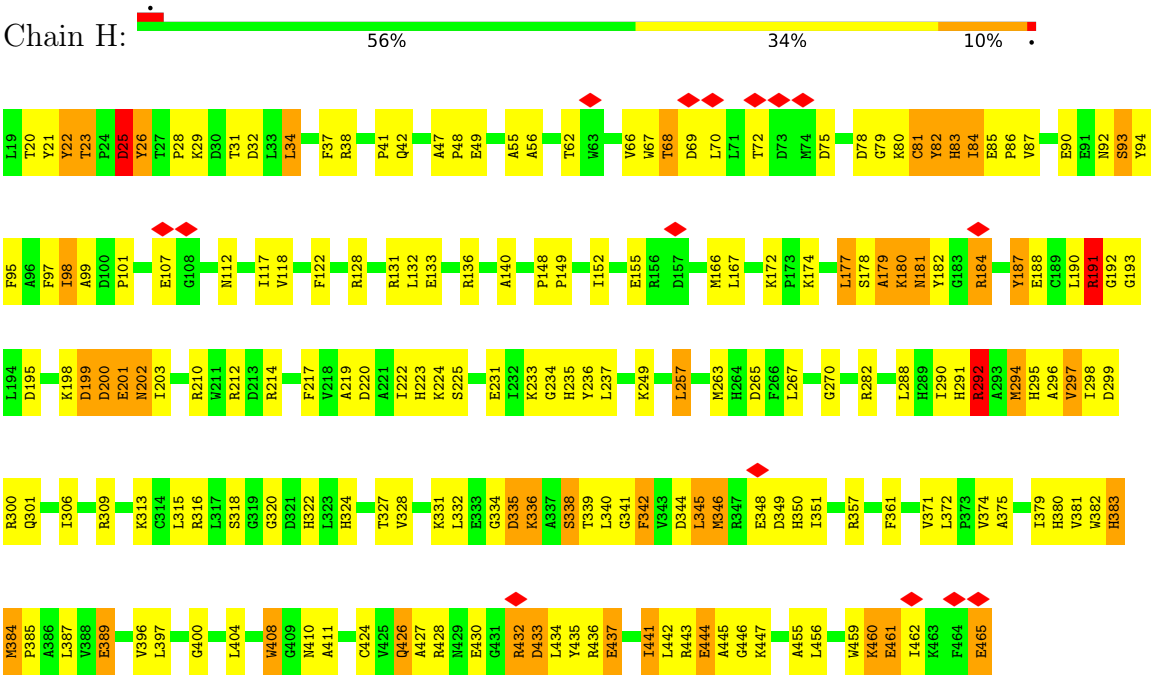


• Molecule 1: Ribulose bisphosphate carboxylase large chain

Chain F:

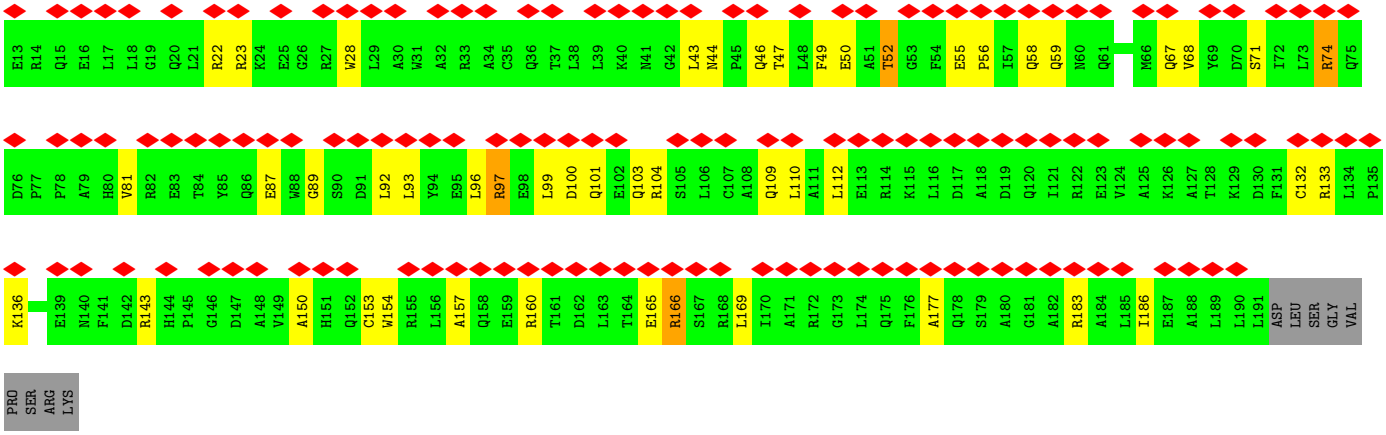



E465
• Molecule 1: Ribulose bisphosphate carboxylase large chain
Chain G:
53%
36%
9%
L19 P24 D25 Y26 T27 P28 K29 D30 T31 D32 L33 L34 A35 R38 F39 S40 P41 Q42 A50 A56 T60 G61 T62 W63 T64 T65 V66 W67 T68 D69 L70 L71 T72 D73 M74 D75 R76 Y94 F95 I98 P101 L102 G108 N112 I117 V118 R128
R131 L132 E133 D134 I135 R136 V139 A140 P148 P149 I152 E155 R156 D157 M166 L167 K172 L175 G176 L177 Y182 G183 R184 A185 V186 Y187 E188 C189 L190 R191 G192 G193 L194 D195 F196 T197 K198 D199 D200 E201 N202 I203 N204 S205 Q206 W211 R212 D213 R214 F215
A219 E231 I232 K233 G234 H235 Y236 L237 N238 V239 T240 A241 P242 T243 C244 E245 E246 M247 M248 K249 R250 A251 E252 F253 A254 K255 E256 L257 G258 M259 M263 H264 D265 F266 G270 C281 R282 L288 H289 I290 H291 R292 A293 M294 H295 A296 V297 I298 D299 R300 Q301 I306 H307 F308
R309 K313 C314 L315 R316 L317 S318 D321 H322 L323 H324 T327 V328 K331 L332 E333 K336 A337 S338 T339 L340 G341 F342 V343 D344 L345 M346 R347 E348 D349 H350 I351 E352 A353 D354 R357 G358 V359 F360 F361 T362 Q363 D364 W365 G370 V371 L372 P373 V374 A375 I379 H380
V381 W382 H383 M384 P385 A386 L387 V388 E389 I390 F391 D394 S395 V396 L397 G400 L404 G405 H406 P407 W408 G409 N410 A411 P412 G413 A414 R418 V419 A420 L421 C424 V425 Q426 A427 E430 G431 R432 D433 L434 Y435 I441 L442 R443 E444 K447 A454 A455 L456 D457 L458
W459 K460 E461 I462 K463 F464 E465


• Molecule 1: Ribulose bisphosphate carboxylase large chain
Chain H:
56%
34%
10%
L19 T20 Y21 Y22 T23 P24 D25 Y26 T27 P28 K29 D30 T31 D32 L33 L34 F37 R38 P41 Q42 A47 P48 E49 A55 A56 T62 W63 V66 W67 T68 D69 L70 L71 T72 D73 M74 D75 D78 G79 K80 C81 Y82 H83 I84 E85 P86 V87 E90 E91 N92 S93 Y94
F95 A96 F97 I98 A99 D100 P101 E107 G108 N112 I117 V118 F122 R128 R131 L132 E133 R136 A140 P148 P149 I152 E155 R156 D157 M166 L167 K172 P173 K174 L177 S178 A179 K180 N181 Y182 G183 R184 Y187 E188 C189 L190 R191 G192 G193
L194 D195 K198 D199 D200 E201 N202 I203 R210 W211 R212 D213 R214 F217 Y218 A219 D220 A221 I222 H223 K224 S225 E231 I232 K233 G234 H235 Y236 L237 K249 L257 M263 H264 D265 F266 L267 G270 R282 L288 H289 I290 H291 R292 A293 M294 H295 A296 V297 I298 D299
R300 Q301 I306 R309 K313 C314 L315 R316 L317 S318 G319 G320 D321 H322 L323 H324 T327 V328 K331 L332 E333 G334 D335 K336 A337 S338 T339 L340 G341 F342 V343 D344 L345 M346 R347 E348 D349 H350 I351 R357 F361 V371 L372 P373 V374 A375 I379 H380 V381 W382 H383
M384 P385 A386 L387 V388 E389 V396 L397 G400 L404 W408 G409 N410 A411 C424 V425 Q426 A427 R428 M429 E430 G431 R432 D433 L434 Y435 R436 E437 I441 L442 R443 E444 A445 G446 K447 A455 L456 W459 K460 E461 I462 K463 F464 E465

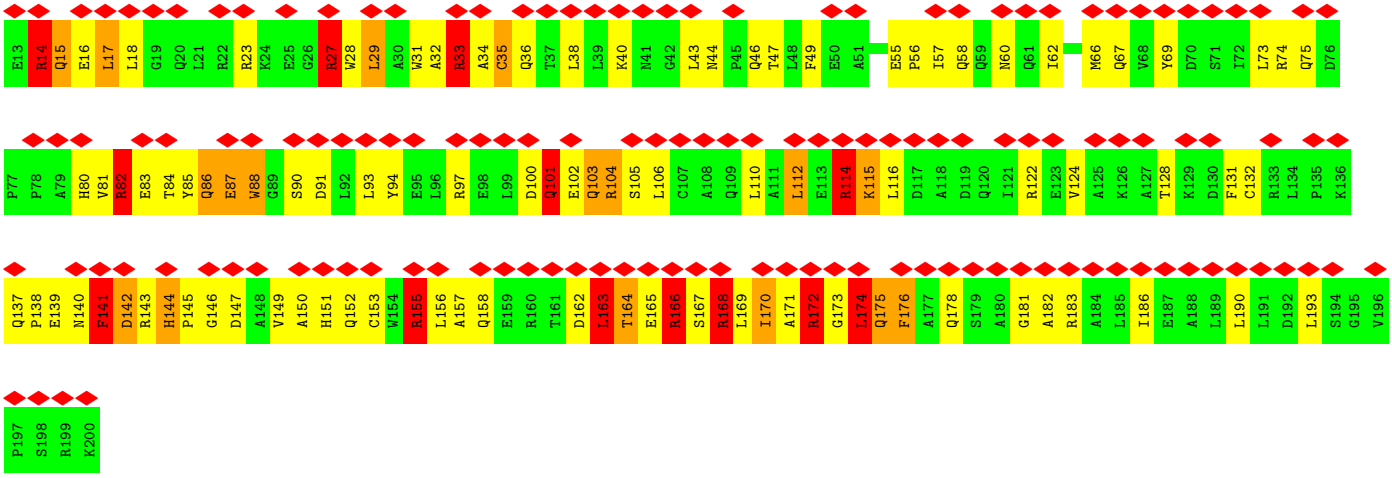
- Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

Chain I:



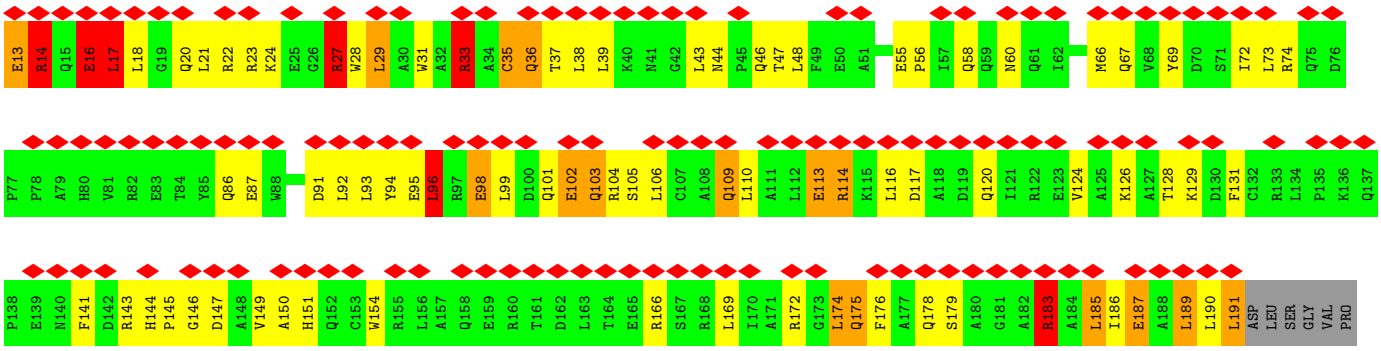
- Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

Chain J:



- Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

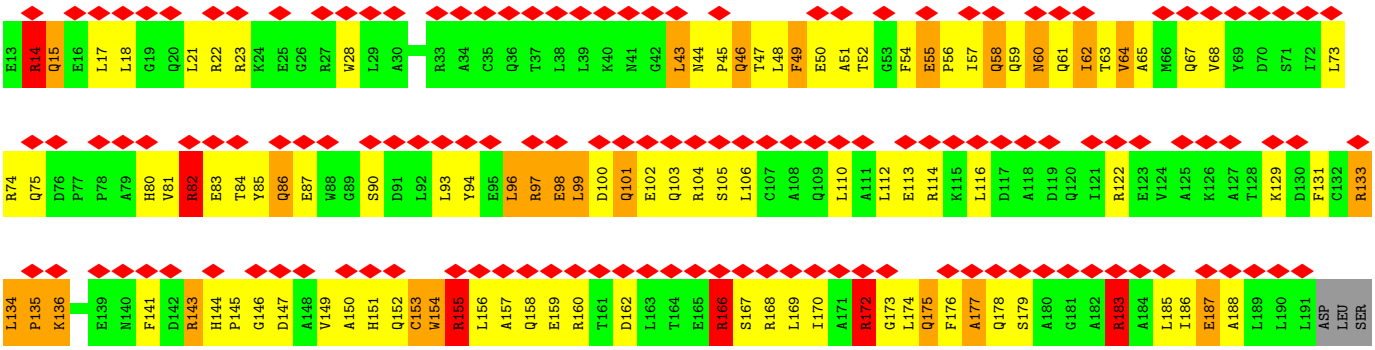
Chain K:



SER ARG LYS

• Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

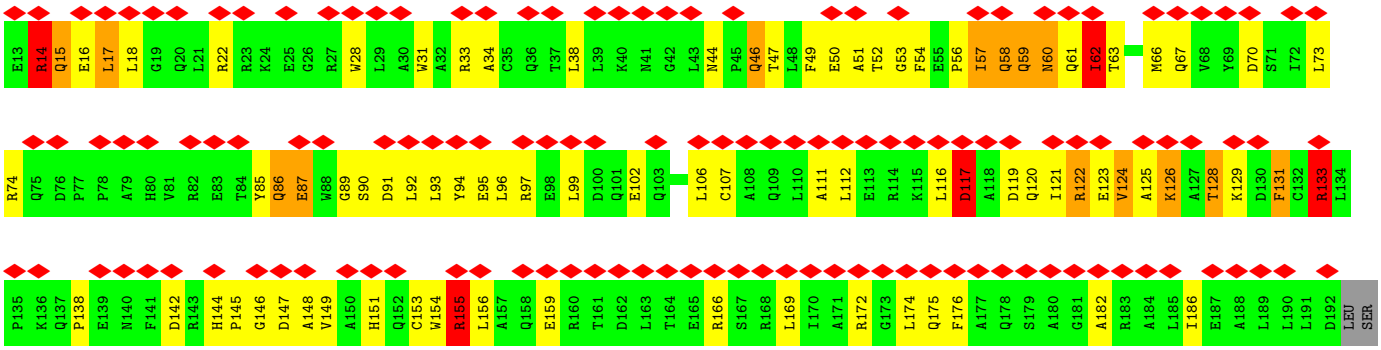
Chain L:



GLY VAL PRO SER ARG LYS

• Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

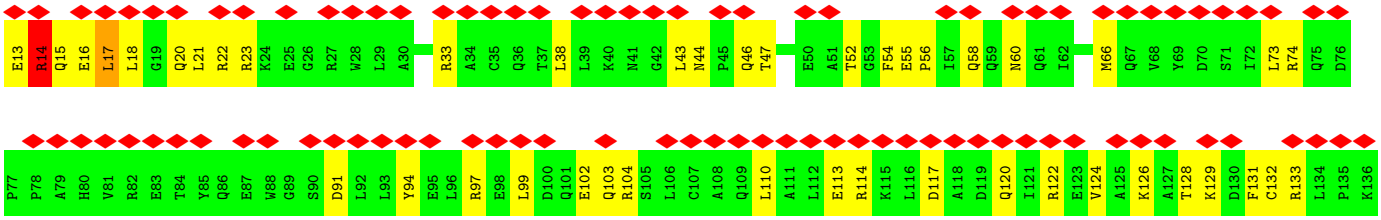
Chain M:

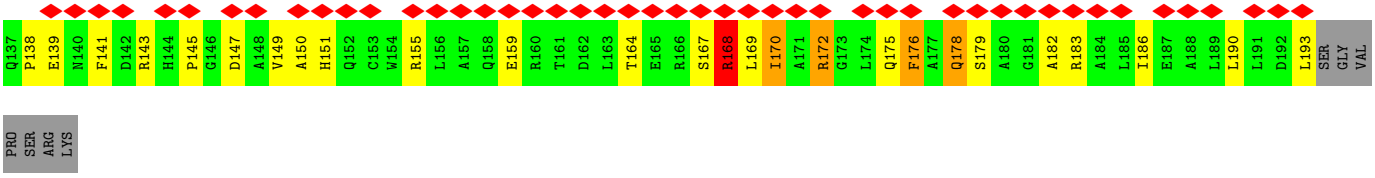


GLY VAL PRO SER ARG LYS

• Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

Chain N:





• Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

Chain O:

• Molecule 2: Rubisco accumulation factor 1 (RAF1) peptide

Chain P:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16022	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.073	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	300.0, 300.0, 300.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.25, 1.25, 1.25	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.37	0/3584	0.62	1/4860 (0.0%)
1	B	0.44	0/3584	0.60	1/4860 (0.0%)
1	C	0.48	0/3584	0.60	1/4860 (0.0%)
1	D	0.47	0/3584	0.60	0/4860
1	E	0.46	0/3584	0.60	0/4860
1	F	0.49	0/3584	0.59	0/4860
1	G	0.45	0/3584	0.59	0/4860
1	H	0.45	0/3584	0.59	1/4860 (0.0%)
2	I	0.37	0/1482	0.76	2/2002 (0.1%)
2	J	0.47	0/1549	0.69	2/2092 (0.1%)
2	K	0.46	0/1482	0.65	1/2002 (0.0%)
2	L	0.49	0/1482	0.65	2/2002 (0.1%)
2	M	0.43	0/1490	0.70	3/2013 (0.1%)
2	N	0.39	0/1498	0.68	1/2024 (0.0%)
2	O	0.46	0/1498	0.68	3/2024 (0.1%)
2	P	0.37	0/1504	0.68	2/2032 (0.1%)
All	All	0.45	0/40657	0.63	20/55071 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	3
1	C	0	8
1	D	0	11
1	E	0	9
1	F	0	12
1	G	0	8
1	H	0	6
2	I	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	J	0	9
2	K	0	6
2	L	0	9
2	M	0	4
2	N	0	2
2	O	0	6
2	P	0	1
All	All	0	98

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	73	LEU	CA-CB-CG	6.58	130.43	115.30
2	O	73	LEU	CA-CB-CG	6.28	129.75	115.30
2	P	73	LEU	CA-CB-CG	6.20	129.56	115.30
2	N	73	LEU	CA-CB-CG	6.19	129.54	115.30
2	K	73	LEU	CA-CB-CG	6.15	129.45	115.30
2	M	96	LEU	CA-CB-CG	6.09	129.31	115.30
2	L	96	LEU	CA-CB-CG	5.98	129.06	115.30
2	M	73	LEU	CA-CB-CG	5.88	128.83	115.30
2	I	43	LEU	CA-CB-CG	5.84	128.74	115.30
2	L	73	LEU	CA-CB-CG	5.76	128.55	115.30
1	H	203	ILE	CG1-CB-CG2	-5.74	98.78	111.40
1	C	203	ILE	CG1-CB-CG2	-5.71	98.83	111.40
1	A	203	ILE	CG1-CB-CG2	-5.71	98.84	111.40
1	B	203	ILE	CG1-CB-CG2	-5.71	98.84	111.40
2	M	17	LEU	CA-CB-CG	5.34	127.58	115.30
2	O	17	LEU	CA-CB-CG	5.33	127.56	115.30
2	J	17	LEU	CA-CB-CG	5.24	127.36	115.30
2	I	110	LEU	CA-CB-CG	5.24	127.35	115.30
2	P	96	LEU	CA-CB-CG	5.18	127.21	115.30
2	O	96	LEU	CA-CB-CG	5.06	126.94	115.30

There are no chirality outliers.

All (98) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	31	THR	Peptide
1	A	318	SER	Peptide
1	B	136	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	318	SER	Peptide
1	B	443	ARG	Sidechain
1	C	136	ARG	Sidechain
1	C	164	ARG	Sidechain
1	C	191	ARG	Sidechain
1	C	292	ARG	Sidechain
1	C	31	THR	Peptide
1	C	318	SER	Peptide
1	C	428	ARG	Sidechain
1	C	76	ARG	Sidechain
1	D	172	LYS	Peptide
1	D	184	ARG	Sidechain
1	D	191	ARG	Sidechain
1	D	210	ARG	Sidechain
1	D	212	ARG	Sidechain
1	D	250	ARG	Sidechain
1	D	31	THR	Peptide
1	D	318	SER	Peptide
1	D	347	ARG	Sidechain
1	D	357	ARG	Sidechain
1	D	428	ARG	Sidechain
1	E	136	ARG	Sidechain
1	E	184	ARG	Sidechain
1	E	250	ARG	Sidechain
1	E	282	ARG	Sidechain
1	E	309	ARG	Sidechain
1	E	31	THR	Peptide
1	E	316	ARG	Sidechain
1	E	357	ARG	Sidechain
1	E	428	ARG	Sidechain
1	F	184	ARG	Sidechain
1	F	191	ARG	Sidechain
1	F	210	ARG	Sidechain
1	F	250	ARG	Sidechain
1	F	292	ARG	Sidechain
1	F	300	ARG	Sidechain
1	F	302	ARG	Sidechain
1	F	309	ARG	Sidechain
1	F	31	THR	Peptide
1	F	316	ARG	Sidechain
1	F	318	SER	Peptide
1	F	347	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	G	191	ARG	Sidechain
1	G	250	ARG	Sidechain
1	G	292	ARG	Sidechain
1	G	300	ARG	Sidechain
1	G	31	THR	Peptide
1	G	318	SER	Peptide
1	G	347	ARG	Sidechain
1	G	38	ARG	Sidechain
1	H	184	ARG	Sidechain
1	H	191	ARG	Sidechain
1	H	292	ARG	Sidechain
1	H	31	THR	Peptide
1	H	318	SER	Peptide
1	H	432	ARG	Sidechain
2	I	136	LYS	Peptide
2	I	52	THR	Peptide
2	J	114	ARG	Sidechain
2	J	14	ARG	Sidechain
2	J	155	ARG	Sidechain
2	J	166	ARG	Sidechain
2	J	168	ARG	Sidechain
2	J	172	ARG	Sidechain
2	J	27	ARG	Sidechain
2	J	33	ARG	Sidechain
2	J	82	ARG	Sidechain
2	K	114	ARG	Sidechain
2	K	14	ARG	Sidechain
2	K	172	ARG	Sidechain
2	K	183	ARG	Sidechain
2	K	27	ARG	Sidechain
2	K	33	ARG	Sidechain
2	L	133	ARG	Sidechain
2	L	14	ARG	Sidechain
2	L	143	ARG	Sidechain
2	L	155	ARG	Sidechain
2	L	168	ARG	Sidechain
2	L	172	ARG	Sidechain
2	L	183	ARG	Sidechain
2	L	82	ARG	Sidechain
2	L	97	ARG	Sidechain
2	M	122	ARG	Sidechain
2	M	133	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	M	14	ARG	Sidechain
2	M	155	ARG	Sidechain
2	N	14	ARG	Sidechain
2	N	168	ARG	Sidechain
2	O	114	ARG	Sidechain
2	O	133	ARG	Sidechain
2	O	14	ARG	Sidechain
2	O	155	ARG	Sidechain
2	O	172	ARG	Sidechain
2	O	183	ARG	Sidechain
2	P	14	ARG	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3495	0	3408	94	0
1	B	3495	0	3405	385	0
1	C	3495	0	3398	554	0
1	D	3495	0	3399	493	0
1	E	3495	0	3402	404	0
1	F	3495	0	3396	586	0
1	G	3495	0	3401	476	0
1	H	3495	0	3404	374	0
2	I	1457	0	1449	58	0
2	J	1523	0	1511	271	0
2	K	1457	0	1446	190	0
2	L	1457	0	1448	247	0
2	M	1465	0	1452	144	0
2	N	1473	0	1464	84	0
2	O	1473	0	1463	139	0
2	P	1479	0	1469	69	0
All	All	39744	0	38915	4195	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 53.

All (4195) 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:F:236:TYR:CE2	1:F:289:HIS:CE1	1.78	1.67
1:C:408:TRP:CH2	2:J:23:ARG:HD2	1.14	1.64
1:F:236:TYR:CD2	1:F:289:HIS:CE1	1.85	1.64
1:F:219:ALA:HB1	1:F:257:LEU:CD1	1.26	1.64
1:A:122:PHE:CD2	1:H:297:VAL:HG23	1.29	1.62
2:L:149:VAL:HB	2:L:176:PHE:CZ	1.21	1.62
1:G:408:TRP:CH2	2:K:23:ARG:HA	1.14	1.61
1:H:408:TRP:CZ3	2:I:23:ARG:HA	1.18	1.61
1:F:215:PHE:CE1	1:F:237:LEU:HD23	1.11	1.61
1:H:22:TYR:CD2	1:H:48:PRO:HB2	1.27	1.61
1:C:408:TRP:CH2	2:J:23:ARG:CD	1.77	1.60
1:E:328:VAL:HG21	1:E:336:LYS:CE	1.22	1.60
1:F:387:LEU:HD11	1:F:397:LEU:CD2	1.20	1.59
1:C:218:VAL:CG1	1:C:235:HIS:HE1	1.14	1.59
1:G:313:LYS:CE	1:G:345:LEU:CD1	1.79	1.59
2:K:106:LEU:HD23	2:K:144:HIS:CD2	1.34	1.59
1:F:384:MET:CE	1:F:421:LEU:CA	1.76	1.59
1:B:31:THR:HG21	1:B:102:LEU:CB	1.15	1.58
1:D:215:PHE:CE1	1:D:237:LEU:CD2	1.84	1.57
1:F:345:LEU:CD2	1:F:351:ILE:HD12	1.26	1.57
1:H:328:VAL:HG21	1:H:336:LYS:CE	1.18	1.57
1:D:313:LYS:CE	1:D:345:LEU:CD1	1.75	1.57
1:F:198:LYS:CB	1:F:236:TYR:HB2	1.25	1.57
1:C:82:TYR:CE1	1:C:97:PHE:HB3	1.34	1.56
1:F:236:TYR:CE2	1:F:289:HIS:HE1	0.88	1.56
1:G:212:ARG:NH1	1:G:253:PHE:CD1	1.70	1.56
1:F:328:VAL:CB	1:F:336:LYS:NZ	1.68	1.56
1:F:328:VAL:HG21	1:F:336:LYS:CE	1.35	1.56
2:L:149:VAL:HB	2:L:176:PHE:CE1	1.34	1.56
1:D:177:LEU:C	1:D:181:ASN:HD21	1.08	1.56
2:L:149:VAL:CB	2:L:176:PHE:CZ	1.86	1.56
1:C:82:TYR:HE1	1:C:97:PHE:CB	1.14	1.55
1:F:328:VAL:CB	1:F:336:LYS:CE	1.82	1.55
1:G:313:LYS:HE2	1:G:345:LEU:CD1	1.15	1.55
2:K:149:VAL:CB	2:K:176:PHE:HZ	1.16	1.55
1:D:215:PHE:CE1	1:D:237:LEU:HD23	1.06	1.55
2:K:99:LEU:CD1	2:K:104:ARG:HA	1.34	1.55
1:F:328:VAL:HG11	1:F:336:LYS:CE	1.35	1.54
1:B:22:TYR:CD2	1:B:48:PRO:HB2	1.38	1.54
1:E:219:ALA:HB1	1:E:257:LEU:CD1	1.36	1.54
1:F:313:LYS:CE	1:F:345:LEU:CD1	1.78	1.54
1:D:211:TRP:CZ3	1:D:250:ARG:CG	1.88	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:408:TRP:CZ3	2:K:23:ARG:HA	1.37	1.53
1:A:122:PHE:CE2	1:H:297:VAL:HG23	1.42	1.53
1:B:105:PHE:CD1	1:B:113:ILE:HD13	1.39	1.53
1:D:211:TRP:CZ3	1:D:250:ARG:HG2	1.00	1.52
1:G:212:ARG:NH1	1:G:253:PHE:CE1	1.74	1.52
2:M:131:PHE:CZ	2:M:138:PRO:HD2	1.41	1.52
1:D:313:LYS:HE2	1:D:345:LEU:CD1	1.04	1.52
1:F:345:LEU:CD2	1:F:351:ILE:CD1	1.83	1.51
2:N:150:ALA:HB2	2:N:176:PHE:CD2	1.41	1.51
1:F:328:VAL:CG1	1:F:336:LYS:CE	1.85	1.51
1:H:328:VAL:CG2	1:H:336:LYS:CE	1.88	1.50
1:F:215:PHE:CE1	1:F:237:LEU:CD2	1.91	1.50
1:C:408:TRP:CH2	2:J:23:ARG:HB3	1.46	1.49
2:M:95:GLU:CG	2:M:122:ARG:HD3	1.39	1.49
1:G:384:MET:CE	1:G:421:LEU:N	1.70	1.48
1:E:328:VAL:HG21	1:E:336:LYS:NZ	1.24	1.48
2:L:149:VAL:CA	2:L:176:PHE:HZ	1.21	1.48
2:O:134:LEU:HD22	2:O:135:PRO:CD	1.43	1.48
1:F:328:VAL:CG1	1:F:336:LYS:HE3	1.38	1.48
1:D:353:ALA:HA	1:D:359:VAL:CG1	1.44	1.47
1:G:384:MET:HE3	1:G:421:LEU:CA	1.40	1.47
2:J:150:ALA:HB2	2:J:176:PHE:CD2	1.48	1.47
1:C:328:VAL:HG21	1:C:336:LYS:CE	1.36	1.47
1:E:281:CYS:SG	1:E:288:LEU:HD23	1.52	1.47
1:F:215:PHE:HE1	1:F:237:LEU:CD2	1.24	1.47
1:H:22:TYR:HD2	1:H:48:PRO:CB	1.27	1.47
1:C:408:TRP:CZ3	2:J:23:ARG:HA	1.46	1.46
1:B:31:THR:CG2	1:B:102:LEU:HB2	1.42	1.46
1:H:328:VAL:CB	1:H:336:LYS:HE3	1.44	1.45
1:C:408:TRP:CH2	2:J:23:ARG:CB	2.00	1.45
1:D:211:TRP:CH2	1:D:250:ARG:CG	1.99	1.44
1:E:328:VAL:CG2	1:E:336:LYS:CE	1.95	1.44
1:G:241:ALA:N	1:G:247:MET:HE3	1.31	1.44
2:K:93:LEU:O	2:K:96:LEU:CD1	1.64	1.44
1:B:31:THR:CG2	1:B:102:LEU:CB	1.93	1.44
1:D:82:TYR:CE1	1:D:97:PHE:HB3	1.51	1.44
2:P:144:HIS:CD2	2:P:145:PRO:HD2	1.53	1.44
2:K:149:VAL:HB	2:K:176:PHE:CZ	1.50	1.43
2:L:114:ARG:NH1	2:L:172:ARG:HH12	1.15	1.43
1:H:178:SER:H	1:H:181:ASN:ND2	1.14	1.42
1:G:384:MET:SD	1:G:421:LEU:HD12	1.59	1.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:408:TRP:CZ3	2:J:23:ARG:CD	2.00	1.41
1:G:328:VAL:HG21	1:G:336:LYS:NZ	1.09	1.41
2:K:93:LEU:CA	2:K:96:LEU:HD11	1.48	1.41
1:G:408:TRP:CH2	2:K:23:ARG:CA	2.03	1.41
2:M:14:ARG:NH1	2:M:18:LEU:HD23	1.25	1.41
2:M:106:LEU:HD23	2:M:144:HIS:CD2	1.54	1.41
1:B:123:GLY:CA	1:G:300:ARG:HH22	1.35	1.40
1:F:211:TRP:CZ3	1:F:250:ARG:CG	1.88	1.40
1:H:328:VAL:CG2	1:H:336:LYS:NZ	1.80	1.40
1:B:22:TYR:HD2	1:B:48:PRO:CB	1.33	1.39
2:J:28:TRP:CB	2:J:87:GLU:HA	1.49	1.39
2:L:149:VAL:CB	2:L:176:PHE:HZ	1.24	1.39
2:K:99:LEU:HD13	2:K:104:ARG:CA	1.49	1.39
1:F:384:MET:CE	1:F:421:LEU:HA	1.44	1.38
1:A:122:PHE:CE2	1:H:297:VAL:CG2	2.05	1.38
2:L:114:ARG:HH12	2:L:172:ARG:NH1	0.92	1.38
1:C:212:ARG:NH1	1:C:253:PHE:CD1	1.91	1.38
1:C:116:SER:HA	1:F:202:ASN:ND2	1.14	1.38
1:C:218:VAL:CG1	1:C:235:HIS:CE1	2.03	1.38
1:F:387:LEU:CD1	1:F:397:LEU:CD2	1.99	1.38
1:C:355:ARG:CG	2:O:159:GLU:OE2	1.69	1.37
2:L:150:ALA:CB	2:L:176:PHE:CD2	1.88	1.37
1:F:389:GLU:OE1	1:F:435:TYR:CB	1.69	1.37
1:C:218:VAL:HG13	1:C:235:HIS:CE1	1.58	1.37
1:H:178:SER:N	1:H:181:ASN:ND2	1.71	1.37
2:K:93:LEU:C	2:K:96:LEU:HD11	1.39	1.37
1:D:215:PHE:HE1	1:D:237:LEU:CD2	1.27	1.37
1:E:353:ALA:HA	1:E:359:VAL:CG1	1.52	1.37
1:D:34:LEU:CD1	1:D:82:TYR:OH	1.71	1.37
1:F:379:ILE:HA	1:F:383:HIS:CE1	1.59	1.37
1:G:134:ASP:OD2	1:G:360:PHE:CD2	1.78	1.37
1:H:408:TRP:HZ3	2:I:23:ARG:CA	1.37	1.37
1:G:28:PRO:CA	1:G:32:ASP:OD2	1.71	1.36
1:B:35:ALA:HB2	1:B:135:ILE:CD1	1.54	1.36
1:F:387:LEU:CD1	1:F:397:LEU:HD22	1.53	1.36
1:G:384:MET:SD	1:G:421:LEU:CD1	2.13	1.36
1:F:316:ARG:NH1	1:F:346:MET:CA	1.87	1.36
1:F:328:VAL:CB	1:F:336:LYS:HE3	1.40	1.36
1:E:328:VAL:CB	1:E:336:LYS:HE3	1.56	1.35
1:B:34:LEU:CD1	1:B:82:TYR:OH	1.74	1.35
1:F:219:ALA:CB	1:F:257:LEU:HD11	1.54	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:106:LEU:HD23	2:L:144:HIS:CD2	1.62	1.35
1:C:408:TRP:CZ3	2:J:23:ARG:CA	2.07	1.34
1:H:81:CYS:HB3	1:H:98:ILE:CD1	1.56	1.34
1:H:178:SER:N	1:H:181:ASN:HD22	1.20	1.34
1:D:211:TRP:CD2	1:D:250:ARG:HD3	1.61	1.34
1:D:211:TRP:CH2	1:D:250:ARG:HG2	1.54	1.34
1:D:387:LEU:CD1	1:D:397:LEU:HD22	1.57	1.34
1:E:193:GLY:O	1:E:418:ARG:NH1	1.57	1.34
1:G:408:TRP:CH2	2:K:23:ARG:HD3	1.62	1.34
1:C:384:MET:SD	1:C:421:LEU:CD1	2.16	1.34
1:F:219:ALA:CB	1:F:257:LEU:CD1	2.03	1.34
2:L:106:LEU:HD23	2:L:144:HIS:NE2	1.40	1.34
1:C:356:SER:OG	2:O:155:ARG:NH2	1.57	1.33
1:F:384:MET:HE3	1:F:421:LEU:CA	1.41	1.33
1:C:184:ARG:NH1	2:J:56:PRO:CG	1.91	1.33
1:D:188:GLU:HG2	1:D:411:ALA:CB	1.58	1.33
2:K:99:LEU:HD12	2:K:104:ARG:CG	1.57	1.33
2:K:149:VAL:CB	2:K:176:PHE:CZ	2.05	1.33
1:E:384:MET:SD	1:E:421:LEU:HD11	1.68	1.33
1:E:219:ALA:CB	1:E:257:LEU:HD12	1.57	1.33
1:H:408:TRP:CZ3	2:I:23:ARG:CA	2.07	1.33
1:D:211:TRP:CE3	1:D:250:ARG:HD3	1.61	1.32
1:E:352:GLU:O	1:E:359:VAL:CG1	1.75	1.32
2:L:150:ALA:CB	2:L:176:PHE:HD2	1.30	1.32
1:G:28:PRO:HA	1:G:32:ASP:OD2	1.27	1.32
2:L:114:ARG:NH1	2:L:172:ARG:NH1	1.67	1.32
1:D:224:LYS:NZ	2:L:50:GLU:OE2	1.63	1.32
1:E:328:VAL:CG2	1:E:336:LYS:HE3	1.55	1.32
1:G:197:THR:O	1:G:235:HIS:ND1	1.61	1.32
2:O:146:GLY:C	2:O:176:PHE:CD1	2.02	1.32
1:E:241:ALA:N	1:E:247:MET:CE	1.91	1.31
1:H:328:VAL:HG21	1:H:336:LYS:NZ	1.02	1.31
2:N:150:ALA:HB2	2:N:176:PHE:CE2	1.64	1.31
1:D:202:ASN:ND2	1:E:116:SER:HA	1.40	1.31
1:F:355:ARG:CG	2:P:159:GLU:OE2	1.78	1.31
1:B:313:LYS:CE	1:B:345:LEU:HD11	1.58	1.30
1:D:193:GLY:O	1:D:418:ARG:NH1	1.61	1.30
1:E:332:LEU:CB	1:E:335:ASP:OD2	1.79	1.30
1:F:316:ARG:NH2	1:F:370:GLY:HA2	1.43	1.30
2:L:49:PHE:HD1	2:L:54:PHE:C	1.35	1.30
2:L:150:ALA:HB2	2:L:176:PHE:CD2	1.43	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:316:ARG:HH12	1:F:346:MET:CA	1.41	1.30
1:H:332:LEU:CB	1:H:335:ASP:OD2	1.78	1.30
1:B:123:GLY:CA	1:G:300:ARG:NH2	1.91	1.30
2:O:146:GLY:C	2:O:176:PHE:CE1	2.05	1.30
1:B:112:ASN:OD1	1:G:204:ASN:HB2	1.27	1.29
1:C:408:TRP:HZ3	2:J:23:ARG:CA	1.38	1.29
1:H:313:LYS:CE	1:H:345:LEU:HD11	1.59	1.29
1:C:328:VAL:CG2	1:C:336:LYS:CE	2.09	1.29
1:F:236:TYR:CD2	1:F:289:HIS:HE1	1.24	1.29
1:G:384:MET:CE	1:G:421:LEU:CA	2.05	1.29
1:C:408:TRP:CH2	2:J:23:ARG:CG	2.14	1.29
2:M:128:THR:HG23	2:M:148:ALA:CB	1.63	1.29
1:B:31:THR:CB	1:B:102:LEU:HB3	1.60	1.28
1:F:316:ARG:HH22	1:F:370:GLY:CA	1.43	1.28
1:C:197:THR:O	1:C:235:HIS:HB2	1.30	1.28
2:J:157:ALA:CA	2:J:166:ARG:HD3	1.63	1.28
1:C:231:GLU:HB2	1:C:233:LYS:CE	1.64	1.28
1:D:184:ARG:HH12	2:L:56:PRO:CG	1.47	1.28
1:F:313:LYS:HE2	1:F:345:LEU:CD1	1.46	1.28
1:F:387:LEU:HD12	1:F:397:LEU:CD1	1.62	1.28
1:H:174:LYS:CE	1:H:200:ASP:OD1	1.80	1.28
1:B:34:LEU:HD11	1:B:82:TYR:CZ	1.69	1.28
1:C:134:ASP:OD2	1:C:360:PHE:CD2	1.87	1.28
1:C:146:GLN:NE2	1:C:282:ARG:NH1	1.81	1.28
1:C:408:TRP:CZ3	2:J:23:ARG:HD3	1.62	1.28
1:F:211:TRP:CZ3	1:F:250:ARG:HG3	1.25	1.28
1:F:316:ARG:NH1	1:F:346:MET:HA	0.99	1.28
2:K:99:LEU:CD1	2:K:104:ARG:CA	2.07	1.28
2:L:85:TYR:OH	2:L:93:LEU:HD21	1.24	1.28
1:D:353:ALA:CA	1:D:359:VAL:HG12	1.63	1.27
2:L:49:PHE:CD1	2:L:54:PHE:O	1.86	1.27
1:C:435:TYR:CE2	2:O:133:ARG:NH2	2.01	1.27
1:D:137:PHE:CE2	1:D:317:LEU:CD1	2.17	1.27
2:N:167:SER:O	2:N:170:ILE:CD1	1.80	1.27
1:C:389:GLU:OE1	1:C:435:TYR:HB2	1.11	1.27
1:C:384:MET:CE	1:C:421:LEU:CG	2.10	1.27
1:E:211:TRP:CD2	1:E:250:ARG:HD3	1.69	1.27
1:B:34:LEU:HD11	1:B:82:TYR:OH	1.21	1.26
1:D:211:TRP:CZ2	1:D:250:ARG:HG3	1.69	1.26
1:G:299:ASP:CB	1:G:306:ILE:O	1.83	1.26
1:H:328:VAL:CG2	1:H:336:LYS:HE3	1.56	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:TYR:CE1	1:C:97:PHE:CB	2.00	1.26
1:C:384:MET:SD	1:C:421:LEU:HD13	1.73	1.26
1:G:384:MET:CE	1:G:420:ALA:C	2.00	1.26
2:J:14:ARG:NH1	2:J:18:LEU:HD23	1.48	1.26
2:N:167:SER:O	2:N:170:ILE:HD11	1.20	1.26
1:C:184:ARG:NH1	2:J:56:PRO:HG2	0.95	1.26
1:D:177:LEU:C	1:D:181:ASN:ND2	1.89	1.26
1:E:149:PRO:HD3	1:E:319:GLY:O	1.24	1.26
1:G:239:VAL:O	1:G:247:MET:CE	1.83	1.26
1:G:379:ILE:HA	1:G:383:HIS:CE1	1.67	1.26
2:J:150:ALA:HB2	2:J:176:PHE:CE2	1.71	1.26
2:L:134:LEU:CD1	2:L:136:LYS:O	1.83	1.26
2:N:114:ARG:NH1	2:N:175:GLN:NE2	1.84	1.26
1:C:146:GLN:HE22	1:C:282:ARG:CZ	1.48	1.26
1:C:328:VAL:CG2	1:C:336:LYS:HE3	1.62	1.26
2:N:150:ALA:N	2:N:176:PHE:HE2	1.31	1.26
1:F:355:ARG:HG3	2:P:159:GLU:OE2	1.10	1.26
1:H:22:TYR:OH	1:H:49:GLU:CG	1.82	1.26
2:L:28:TRP:CZ2	2:L:62:ILE:HG22	1.71	1.26
1:C:384:MET:HE1	1:C:421:LEU:CG	1.64	1.25
2:L:28:TRP:CB	2:L:87:GLU:HB2	1.65	1.25
1:C:212:ARG:NH1	1:C:253:PHE:CE1	2.04	1.25
1:E:211:TRP:CZ3	1:E:250:ARG:HG2	1.71	1.25
1:C:408:TRP:HH2	2:J:23:ARG:CG	1.49	1.25
1:E:241:ALA:N	1:E:247:MET:HE1	0.95	1.25
2:J:38:LEU:O	2:J:43:LEU:HD21	1.26	1.25
2:J:141:PHE:CE1	2:J:147:ASP:O	1.89	1.25
2:M:131:PHE:CZ	2:M:138:PRO:CD	2.19	1.25
1:D:188:GLU:CG	1:D:411:ALA:HB2	1.67	1.25
1:E:146:GLN:HE21	1:E:282:ARG:NH1	1.32	1.25
1:F:384:MET:HE2	1:F:421:LEU:N	1.51	1.25
1:H:34:LEU:HD11	1:H:82:TYR:OH	1.28	1.25
1:B:116:SER:HA	1:G:202:ASN:ND2	1.52	1.25
1:D:34:LEU:HD11	1:D:82:TYR:CZ	1.72	1.25
1:F:332:LEU:CB	1:F:335:ASP:OD2	1.84	1.25
2:J:85:TYR:OH	2:J:93:LEU:HD21	1.22	1.25
1:G:187:TYR:OH	1:G:191:ARG:HD2	1.21	1.24
1:C:133:GLU:C	1:C:134:ASP:OD1	1.76	1.24
1:E:219:ALA:CB	1:E:257:LEU:CD1	2.12	1.24
1:F:384:MET:CE	1:F:421:LEU:N	2.00	1.24
1:A:356:SER:OG	2:L:155:ARG:NH2	1.68	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:PHE:CD2	1:G:297:VAL:HG21	1.73	1.24
1:E:353:ALA:CA	1:E:359:VAL:HG12	1.64	1.24
2:L:14:ARG:NH1	2:L:18:LEU:HD23	1.53	1.24
1:F:385:PRO:O	1:F:434:LEU:HD22	1.33	1.24
1:G:328:VAL:CG2	1:G:336:LYS:NZ	2.01	1.24
1:D:215:PHE:HE1	1:D:237:LEU:CG	1.48	1.23
1:B:384:MET:SD	1:B:421:LEU:CD1	2.26	1.23
1:C:200:ASP:O	1:C:203:ILE:CD1	1.85	1.23
1:F:224:LYS:NZ	2:M:50:GLU:OE2	1.72	1.23
1:F:198:LYS:HB2	1:F:236:TYR:CB	1.68	1.23
1:G:188:GLU:OE1	1:G:410:ASN:CG	1.75	1.23
1:B:105:PHE:CD1	1:B:113:ILE:CD1	2.19	1.23
1:B:385:PRO:CB	1:B:434:LEU:CD2	2.17	1.23
1:C:167:LEU:CD2	1:C:421:LEU:HD22	1.69	1.22
1:G:328:VAL:CG2	1:G:336:LYS:HZ1	1.52	1.22
1:C:297:VAL:HG22	1:F:122:PHE:CD2	1.73	1.22
1:G:182:TYR:OH	1:G:199:ASP:OD1	1.56	1.22
1:H:408:TRP:CH2	2:I:23:ARG:HA	1.74	1.22
2:M:146:GLY:HA3	2:M:176:PHE:CE1	1.73	1.22
1:C:408:TRP:CZ3	2:J:23:ARG:CB	2.20	1.22
1:D:184:ARG:HH11	2:L:56:PRO:CD	1.53	1.22
1:D:211:TRP:CE3	1:D:250:ARG:CD	2.21	1.21
1:G:239:VAL:O	1:G:247:MET:HE1	1.33	1.21
2:K:149:VAL:CG1	2:K:176:PHE:HZ	1.51	1.21
2:O:146:GLY:CA	2:O:176:PHE:CE1	2.23	1.21
1:B:385:PRO:CB	1:B:434:LEU:HD21	1.68	1.21
1:D:211:TRP:CH2	1:D:250:ARG:HG3	1.70	1.21
2:J:28:TRP:HB2	2:J:87:GLU:CB	1.70	1.21
1:D:137:PHE:CD2	1:D:317:LEU:HD11	1.74	1.20
1:F:87:VAL:HG23	1:F:93:SER:O	1.40	1.20
1:H:174:LYS:HE3	1:H:200:ASP:OD1	1.30	1.20
1:B:22:TYR:CD2	1:B:48:PRO:CB	2.12	1.20
1:E:328:VAL:CG2	1:E:336:LYS:NZ	2.03	1.20
2:J:38:LEU:O	2:J:43:LEU:CD2	1.87	1.20
1:F:313:LYS:NZ	1:F:345:LEU:HD11	1.57	1.20
2:K:149:VAL:CG1	2:K:176:PHE:CZ	2.23	1.20
1:C:382:TRP:HE1	1:C:459:TRP:C	1.44	1.20
2:J:141:PHE:CD1	2:J:147:ASP:OD1	1.94	1.20
1:B:31:THR:OG1	1:B:102:LEU:HD22	1.36	1.19
1:G:313:LYS:CE	1:G:345:LEU:HD11	1.51	1.19
2:M:95:GLU:CD	2:M:122:ARG:CD	2.10	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:34:LEU:HD11	1:C:82:TYR:CZ	1.78	1.19
1:F:387:LEU:CD1	1:F:397:LEU:CD1	2.21	1.19
1:H:174:LYS:CD	1:H:200:ASP:OD1	1.90	1.19
2:L:157:ALA:O	2:L:166:ARG:HD3	1.41	1.19
1:C:328:VAL:HG21	1:C:336:LYS:NZ	1.53	1.19
1:D:137:PHE:CE2	1:D:317:LEU:HD12	1.77	1.19
1:E:240:THR:C	1:E:247:MET:HE1	1.61	1.19
1:E:198:LYS:CB	1:E:236:TYR:HB2	1.71	1.19
1:E:211:TRP:CE3	1:E:250:ARG:HD3	1.78	1.19
2:J:17:LEU:HD12	2:J:38:LEU:HD21	1.21	1.19
2:J:149:VAL:CG1	2:J:172:ARG:HD2	1.71	1.19
1:A:122:PHE:CD2	1:H:297:VAL:CG2	2.25	1.19
1:D:352:GLU:O	1:D:359:VAL:CG1	1.90	1.19
1:G:204:ASN:O	1:G:206:GLN:HG3	1.36	1.19
2:J:28:TRP:CB	2:J:87:GLU:CA	2.21	1.19
2:J:157:ALA:HA	2:J:166:ARG:HD3	1.19	1.19
1:C:116:SER:CA	1:F:202:ASN:ND2	2.05	1.18
1:C:215:PHE:CD1	1:C:237:LEU:HD11	1.71	1.18
1:D:137:PHE:HE2	1:D:317:LEU:CD1	1.54	1.18
1:D:215:PHE:CD1	1:D:237:LEU:HD23	1.77	1.18
1:C:408:TRP:CZ2	2:J:23:ARG:HD2	1.79	1.18
1:F:147:GLY:HA2	1:F:368:MET:CE	1.70	1.18
1:G:384:MET:HE1	1:G:421:LEU:N	1.32	1.18
2:O:146:GLY:HA3	2:O:176:PHE:CE1	1.76	1.18
1:C:218:VAL:HG11	1:C:235:HIS:CE1	1.77	1.18
1:E:198:LYS:HB2	1:E:236:TYR:CB	1.72	1.18
1:F:345:LEU:HD23	1:F:351:ILE:CD1	1.58	1.18
1:F:236:TYR:CZ	1:F:289:HIS:CE1	2.31	1.17
1:C:389:GLU:OE1	1:C:435:TYR:CB	1.91	1.17
1:H:22:TYR:CD2	1:H:48:PRO:CB	2.09	1.17
1:F:316:ARG:HD3	1:F:365:TRP:CZ3	1.80	1.17
2:M:128:THR:HG23	2:M:148:ALA:HB2	1.18	1.17
1:F:379:ILE:CA	1:F:383:HIS:CE1	2.17	1.17
1:B:384:MET:SD	1:B:421:LEU:HD12	1.83	1.17
1:C:87:VAL:HG23	1:C:93:SER:O	1.42	1.17
1:C:239:VAL:O	1:C:247:MET:CE	1.91	1.17
1:D:34:LEU:HD11	1:D:82:TYR:OH	1.02	1.17
1:D:180:LYS:CE	1:D:217:PHE:CZ	2.28	1.17
1:D:184:ARG:NH1	2:L:56:PRO:CD	2.05	1.17
1:F:237:LEU:O	1:F:263:MET:SD	2.02	1.17
1:F:332:LEU:HB3	1:F:335:ASP:OD2	1.00	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:187:TYR:CZ	1:G:191:ARG:CD	2.28	1.17
1:F:236:TYR:CG	1:F:289:HIS:ND1	2.13	1.16
1:H:174:LYS:HA	1:H:200:ASP:OD2	1.43	1.16
1:C:137:PHE:HE2	1:C:317:LEU:HD12	1.08	1.16
1:H:22:TYR:OH	1:H:49:GLU:HG2	0.98	1.16
2:O:146:GLY:CA	2:O:176:PHE:CD1	2.28	1.16
1:D:313:LYS:HE3	1:D:345:LEU:HD12	1.23	1.16
1:D:382:TRP:HE1	1:D:459:TRP:C	1.49	1.16
2:M:95:GLU:CG	2:M:122:ARG:CD	2.24	1.16
1:F:198:LYS:CB	1:F:236:TYR:CB	2.20	1.16
1:G:408:TRP:CZ3	2:K:23:ARG:CA	2.21	1.16
1:H:444:GLU:O	1:H:447:LYS:HG2	1.45	1.16
1:C:146:GLN:NE2	1:C:282:ARG:CZ	2.06	1.15
2:L:28:TRP:NE1	2:L:62:ILE:HG21	1.61	1.15
2:M:131:PHE:CE2	2:M:138:PRO:HD2	1.81	1.15
1:B:137:PHE:HE2	1:B:317:LEU:HD12	1.07	1.15
1:F:328:VAL:CG2	1:F:336:LYS:CE	1.84	1.15
2:J:141:PHE:HE1	2:J:147:ASP:O	1.22	1.15
2:O:147:ASP:N	2:O:176:PHE:CE1	2.13	1.15
1:C:328:VAL:CB	1:C:336:LYS:HE3	1.74	1.15
1:H:345:LEU:HD23	1:H:351:ILE:HD13	1.27	1.15
1:B:313:LYS:HE2	1:B:345:LEU:CD1	1.76	1.15
1:C:236:TYR:CB	1:C:261:ILE:HG23	1.77	1.15
1:D:184:ARG:NH1	2:L:56:PRO:CG	2.08	1.15
2:J:157:ALA:HA	2:J:166:ARG:CD	1.75	1.15
1:D:215:PHE:CD1	1:D:237:LEU:CD2	2.30	1.14
1:E:428:ARG:HE	2:I:97:ARG:CG	1.59	1.14
2:K:106:LEU:CD2	2:K:144:HIS:CD2	2.31	1.14
2:L:59:GLN:O	2:L:63:THR:OG1	1.64	1.14
2:M:146:GLY:HA3	2:M:176:PHE:CD1	1.82	1.14
2:O:106:LEU:HD23	2:O:145:PRO:HD2	1.26	1.14
1:C:435:TYR:CD2	2:O:133:ARG:NH2	2.15	1.14
1:D:81:CYS:HB3	1:D:98:ILE:HD13	1.23	1.14
1:C:239:VAL:O	1:C:247:MET:HE1	1.40	1.14
1:C:355:ARG:HG3	2:O:159:GLU:OE2	0.96	1.14
2:M:95:GLU:CD	2:M:122:ARG:HD3	1.67	1.14
1:B:105:PHE:CE1	1:B:113:ILE:HD13	1.82	1.14
1:B:122:PHE:CE1	1:B:130:LEU:O	2.00	1.14
1:D:184:ARG:HH12	2:L:56:PRO:HG2	0.98	1.14
1:D:211:TRP:CE3	1:D:250:ARG:HG2	1.83	1.14
1:F:180:LYS:HD2	1:F:217:PHE:CE2	1.81	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:86:PRO:HA	1:H:94:TYR:HB3	1.30	1.14
2:L:150:ALA:HB3	2:L:176:PHE:HD2	1.04	1.14
1:C:215:PHE:HD1	1:C:237:LEU:HD11	0.99	1.14
1:D:211:TRP:CE3	1:D:250:ARG:CG	2.30	1.13
1:E:384:MET:SD	1:E:421:LEU:CD1	2.34	1.13
1:F:328:VAL:HB	1:F:336:LYS:HE3	1.30	1.13
1:G:187:TYR:CZ	1:G:191:ARG:HD3	1.80	1.13
1:G:313:LYS:HE3	1:G:345:LEU:HD12	1.27	1.13
2:L:28:TRP:HE1	2:L:62:ILE:CG2	1.61	1.13
1:C:181:ASN:HB3	2:J:55:GLU:OE2	1.46	1.13
1:D:313:LYS:CE	1:D:345:LEU:HD11	1.52	1.13
2:J:170:ILE:CD1	2:J:174:LEU:HD21	1.78	1.13
1:B:82:TYR:CE1	1:B:97:PHE:HB3	1.84	1.13
1:B:146:GLN:NE2	1:B:282:ARG:CZ	2.12	1.13
2:K:149:VAL:HG12	2:K:176:PHE:CZ	1.84	1.13
1:C:384:MET:SD	1:C:421:LEU:HD12	1.84	1.13
2:N:150:ALA:CB	2:N:176:PHE:CD2	2.32	1.12
2:O:106:LEU:CD2	2:O:145:PRO:HD2	1.79	1.13
1:B:123:GLY:HA2	1:G:300:ARG:NH2	1.56	1.12
1:D:329:VAL:CG1	1:D:379:ILE:CG2	2.26	1.12
1:F:215:PHE:HE1	1:F:237:LEU:CG	1.61	1.12
1:G:188:GLU:OE1	1:G:410:ASN:OD1	1.65	1.12
1:C:85:GLU:O	1:C:94:TYR:HB2	1.47	1.12
1:G:187:TYR:OH	1:G:191:ARG:CD	1.97	1.12
2:M:95:GLU:HG2	2:M:122:ARG:CD	1.78	1.12
1:D:180:LYS:HE2	1:D:217:PHE:CE2	1.83	1.12
1:F:210:ARG:NH1	1:G:282:ARG:NH2	1.96	1.12
1:G:241:ALA:N	1:G:247:MET:CE	2.12	1.12
1:C:116:SER:CA	1:F:202:ASN:HD21	1.59	1.12
1:F:198:LYS:HB3	1:F:236:TYR:HB2	1.21	1.12
1:H:328:VAL:HB	1:H:336:LYS:HE3	1.15	1.12
1:E:35:ALA:HB2	1:E:135:ILE:HD13	1.27	1.12
1:E:281:CYS:SG	1:E:288:LEU:CD2	2.36	1.12
1:H:313:LYS:HE2	1:H:345:LEU:CD1	1.79	1.12
1:E:428:ARG:HE	2:I:97:ARG:HG3	1.04	1.11
2:J:17:LEU:HD11	2:J:34:ALA:HB1	1.13	1.11
1:B:122:PHE:HE1	1:B:130:LEU:C	1.52	1.11
1:C:231:GLU:O	1:C:233:LYS:HD3	1.51	1.11
1:C:363:GLN:NE2	1:C:365:TRP:CE2	2.19	1.11
1:G:299:ASP:HB3	1:G:306:ILE:O	1.50	1.11
1:H:174:LYS:HD2	1:H:200:ASP:CG	1.71	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:352:GLU:O	1:D:359:VAL:HG11	0.94	1.11
1:F:382:TRP:HE1	1:F:459:TRP:C	1.52	1.11
1:G:384:MET:HE2	1:G:420:ALA:C	1.65	1.11
1:H:34:LEU:CD1	1:H:82:TYR:OH	1.97	1.11
1:H:82:TYR:HE1	1:H:97:PHE:HB3	1.00	1.11
1:F:384:MET:HE1	1:F:421:LEU:CB	1.52	1.11
1:G:299:ASP:HB2	1:G:306:ILE:O	1.46	1.11
1:A:282:ARG:NH2	1:D:210:ARG:NH1	1.97	1.10
1:C:236:TYR:HB3	1:C:261:ILE:CG2	1.79	1.10
1:E:149:PRO:CD	1:E:319:GLY:O	1.98	1.10
2:K:33:ARG:NH2	2:K:66:MET:HG2	1.65	1.10
1:C:184:ARG:HH11	2:J:56:PRO:CG	1.58	1.10
1:G:353:ALA:HA	1:G:359:VAL:HG12	1.28	1.10
1:G:408:TRP:HZ3	2:K:22:ARG:O	1.34	1.10
1:B:31:THR:HB	1:B:102:LEU:HB3	1.28	1.10
1:G:313:LYS:CE	1:G:345:LEU:HD12	1.73	1.10
2:J:28:TRP:HB3	2:J:87:GLU:CA	1.79	1.10
2:O:134:LEU:CD2	2:O:135:PRO:HD2	1.82	1.10
2:J:28:TRP:HB3	2:J:87:GLU:HA	1.25	1.10
2:K:93:LEU:HA	2:K:96:LEU:HD11	1.19	1.10
1:B:122:PHE:CE1	1:B:130:LEU:C	2.25	1.10
2:N:150:ALA:CB	2:N:176:PHE:CE2	2.34	1.10
1:B:345:LEU:HD23	1:B:351:ILE:HD13	1.28	1.09
1:D:387:LEU:HD12	1:D:397:LEU:HD13	1.33	1.09
1:E:71:LEU:O	2:L:90:SER:OG	1.69	1.09
1:E:427:ALA:CB	1:E:434:LEU:HD12	1.81	1.09
1:B:35:ALA:CB	1:B:135:ILE:HD13	1.83	1.09
1:C:29:LYS:O	1:C:31:THR:N	1.85	1.09
1:F:385:PRO:O	1:F:434:LEU:CD2	1.98	1.09
1:F:389:GLU:CD	1:F:435:TYR:HB2	1.70	1.09
2:J:28:TRP:CG	2:J:87:GLU:HA	1.86	1.09
1:B:137:PHE:CD2	1:B:317:LEU:HD11	1.87	1.09
1:D:87:VAL:HG23	1:D:93:SER:O	1.52	1.09
1:B:31:THR:HA	1:B:138:PRO:HB3	1.29	1.09
1:B:35:ALA:CB	1:B:135:ILE:CD1	2.30	1.09
1:D:178:SER:N	1:D:181:ASN:HD21	1.50	1.09
1:D:387:LEU:CD1	1:D:397:LEU:CD2	2.30	1.09
1:D:387:LEU:HD11	1:D:397:LEU:HD22	1.13	1.09
1:F:387:LEU:CD1	1:F:397:LEU:HD13	1.80	1.09
1:G:408:TRP:CH2	2:K:23:ARG:CD	2.35	1.09
2:J:28:TRP:CE3	2:J:87:GLU:C	2.26	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:LEU:CG	1:C:421:LEU:CD2	2.30	1.08
1:C:215:PHE:CD1	1:C:237:LEU:CD1	2.27	1.08
1:D:313:LYS:CE	1:D:345:LEU:HD12	1.61	1.08
2:K:144:HIS:CG	2:K:145:PRO:HD2	1.88	1.08
2:L:49:PHE:CD1	2:L:54:PHE:C	2.24	1.08
1:B:31:THR:HA	1:B:138:PRO:CB	1.83	1.08
1:B:137:PHE:CE2	1:B:317:LEU:CD1	2.35	1.08
1:C:231:GLU:HB2	1:C:233:LYS:HE3	1.25	1.08
1:D:177:LEU:O	1:D:182:TYR:HB2	1.51	1.08
1:C:353:ALA:HB2	1:C:361:PHE:HA	1.08	1.08
1:E:328:VAL:HB	1:E:336:LYS:HE3	1.28	1.08
1:B:31:THR:O	1:B:33:LEU:N	1.85	1.08
1:D:332:LEU:HB3	1:D:335:ASP:OD2	1.51	1.08
1:H:82:TYR:HE1	1:H:97:PHE:CB	1.67	1.08
1:B:384:MET:CE	1:B:421:LEU:HD12	1.84	1.08
1:E:282:ARG:HH21	1:H:210:ARG:NE	1.52	1.08
2:J:85:TYR:CZ	2:J:93:LEU:HD21	1.87	1.08
1:B:112:ASN:OD1	1:G:204:ASN:CB	2.02	1.07
1:F:219:ALA:CB	1:F:257:LEU:HD12	1.82	1.07
1:H:81:CYS:CB	1:H:98:ILE:HD13	1.83	1.07
2:L:28:TRP:NE1	2:L:62:ILE:CG2	2.17	1.07
1:D:82:TYR:HE1	1:D:97:PHE:CB	1.66	1.07
2:K:33:ARG:NH2	2:K:66:MET:CG	2.17	1.07
1:B:57:GLU:OE2	1:B:120:ASN:ND2	1.87	1.07
1:C:137:PHE:CD2	1:C:317:LEU:HD11	1.88	1.07
1:F:86:PRO:HA	1:F:94:TYR:HB3	1.36	1.07
1:G:384:MET:CE	1:G:421:LEU:HD12	1.83	1.07
1:C:353:ALA:CB	1:C:361:PHE:HA	1.83	1.07
1:F:346:MET:O	1:F:370:GLY:HA3	1.51	1.07
1:G:197:THR:C	1:G:235:HIS:CE1	2.28	1.07
1:H:82:TYR:CE1	1:H:97:PHE:HB3	1.88	1.07
1:B:64:THR:HG21	1:G:172:LYS:HE2	1.36	1.07
1:D:385:PRO:HA	1:D:424:CYS:SG	1.95	1.07
1:F:177:LEU:O	1:F:178:SER:O	1.71	1.07
2:M:106:LEU:HD23	2:M:144:HIS:NE2	1.68	1.07
1:E:332:LEU:HB3	1:E:335:ASP:OD2	0.89	1.06
1:F:236:TYR:CG	1:F:289:HIS:CE1	2.41	1.06
1:H:174:LYS:HD2	1:H:200:ASP:OD2	1.52	1.06
2:M:95:GLU:OE2	2:M:122:ARG:HD2	1.53	1.06
2:N:150:ALA:N	2:N:176:PHE:CE2	2.23	1.06
1:F:345:LEU:HD22	1:F:351:ILE:HD11	1.08	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:ASP:O	1:B:437:GLU:OE1	1.71	1.06
1:E:197:THR:OG1	1:E:235:HIS:CG	2.00	1.06
1:F:147:GLY:HA2	1:F:368:MET:HE2	1.33	1.06
2:L:28:TRP:HE1	2:L:62:ILE:HG21	0.97	1.06
1:B:82:TYR:HE1	1:B:97:PHE:HB3	0.96	1.06
1:D:177:LEU:CA	1:D:181:ASN:HD21	1.69	1.06
2:K:93:LEU:C	2:K:96:LEU:CD1	2.10	1.06
2:M:14:ARG:NH1	2:M:18:LEU:CD2	2.19	1.06
1:C:137:PHE:CE2	1:C:317:LEU:CD1	2.38	1.06
1:C:167:LEU:HD21	1:C:421:LEU:HD22	1.06	1.06
1:C:353:ALA:HA	1:C:359:VAL:HG12	1.37	1.06
1:E:211:TRP:CD2	1:E:250:ARG:CD	2.39	1.06
1:F:313:LYS:CE	1:F:345:LEU:HD11	1.61	1.06
1:G:384:MET:CE	1:G:421:LEU:HA	1.75	1.06
2:J:140:ASN:HB3	2:J:181:GLY:HA3	1.36	1.06
1:B:122:PHE:CD2	1:G:297:VAL:CG2	2.39	1.05
1:B:385:PRO:HB2	1:B:434:LEU:HD23	1.35	1.05
1:B:385:PRO:HB3	1:B:434:LEU:HD21	1.29	1.05
1:F:355:ARG:CB	2:P:159:GLU:OE2	2.05	1.05
1:H:328:VAL:CG2	1:H:336:LYS:HZ1	1.49	1.05
1:H:382:TRP:CZ3	1:H:461:GLU:OE2	2.08	1.05
2:J:28:TRP:HB2	2:J:87:GLU:HB2	1.08	1.05
2:J:85:TYR:OH	2:J:93:LEU:CD2	2.03	1.05
1:E:427:ALA:HB3	1:E:434:LEU:CD1	1.86	1.05
1:F:281:CYS:SG	1:F:288:LEU:HD23	1.97	1.05
2:J:149:VAL:HG13	2:J:172:ARG:HD2	1.37	1.05
2:K:99:LEU:HD12	2:K:104:ARG:CB	1.86	1.05
1:C:146:GLN:HE22	1:C:282:ARG:NH2	1.55	1.05
2:O:106:LEU:HD23	2:O:145:PRO:CD	1.85	1.05
1:C:82:TYR:CE1	1:C:97:PHE:HB2	1.92	1.05
1:C:197:THR:OG1	1:C:235:HIS:CB	2.05	1.05
1:C:408:TRP:HH2	2:J:23:ARG:CB	1.52	1.05
1:D:82:TYR:CE1	1:D:97:PHE:CB	2.39	1.05
1:D:134:ASP:OD2	1:D:360:PHE:CD2	2.10	1.05
1:E:352:GLU:C	1:E:359:VAL:HG11	1.76	1.05
1:G:408:TRP:CZ2	2:K:23:ARG:HD3	1.91	1.05
1:D:137:PHE:HE2	1:D:317:LEU:HD12	0.88	1.04
1:E:155:GLU:OE2	1:E:322:HIS:NE2	1.90	1.04
1:E:211:TRP:CE3	1:E:250:ARG:HG2	1.91	1.04
2:J:28:TRP:CB	2:J:87:GLU:HB2	1.87	1.04
1:E:219:ALA:HB1	1:E:257:LEU:HD11	1.38	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:332:LEU:HB3	1:H:335:ASP:OD2	0.87	1.04
2:J:110:LEU:CD2	2:J:114:ARG:HD3	1.86	1.04
2:K:99:LEU:HD12	2:K:104:ARG:HG2	1.04	1.04
2:K:99:LEU:HB2	2:K:104:ARG:HG3	1.07	1.04
2:L:46:GLN:NE2	2:L:50:GLU:OE1	1.89	1.04
2:O:146:GLY:HA3	2:O:176:PHE:CD1	1.88	1.04
1:B:137:PHE:HE2	1:B:317:LEU:CD1	1.69	1.04
1:D:81:CYS:CB	1:D:98:ILE:HD13	1.86	1.04
1:G:379:ILE:CA	1:G:383:HIS:CE1	2.30	1.04
2:K:99:LEU:CD1	2:K:104:ARG:HG2	1.85	1.04
2:L:28:TRP:CE2	2:L:62:ILE:HG22	1.92	1.04
1:B:384:MET:CE	1:B:421:LEU:CD1	2.35	1.04
1:E:345:LEU:HD23	1:E:351:ILE:HD13	1.31	1.04
1:F:313:LYS:HE3	1:F:345:LEU:CD1	1.60	1.04
1:F:345:LEU:HD21	1:F:351:ILE:HD12	1.39	1.04
1:G:134:ASP:OD2	1:G:360:PHE:HD2	1.18	1.03
2:L:134:LEU:HD12	2:L:136:LYS:O	1.48	1.03
2:L:149:VAL:N	2:L:176:PHE:CZ	2.25	1.03
1:A:157:ASP:HB3	1:D:180:LYS:HD2	1.37	1.03
1:D:244:CYS:N	1:E:276:THR:OG1	1.90	1.03
2:L:28:TRP:HB2	2:L:87:GLU:CB	1.87	1.03
1:A:282:ARG:CZ	1:D:210:ARG:HH11	1.70	1.03
1:D:313:LYS:HE2	1:D:345:LEU:HD13	1.04	1.03
1:F:384:MET:CE	1:F:421:LEU:CB	2.09	1.03
1:H:174:LYS:CE	1:H:200:ASP:CG	2.26	1.03
1:F:210:ARG:NH1	1:G:282:ARG:HH22	1.54	1.03
1:G:313:LYS:HE2	1:G:345:LEU:HD13	1.05	1.03
2:L:114:ARG:NH1	2:L:172:ARG:CZ	2.20	1.03
1:C:87:VAL:HG23	1:C:93:SER:C	1.77	1.02
1:C:167:LEU:HD21	1:C:421:LEU:CD2	1.88	1.02
1:C:231:GLU:C	1:C:233:LYS:HD3	1.78	1.02
2:M:142:ASP:N	2:M:147:ASP:OD2	1.92	1.02
1:C:133:GLU:O	1:C:134:ASP:OD1	1.78	1.02
1:C:164:ARG:HB3	1:C:425:VAL:HG21	1.36	1.02
1:F:316:ARG:HH22	1:F:370:GLY:HA2	0.93	1.02
1:H:433:ASP:N	1:H:437:GLU:OE2	1.91	1.02
2:M:116:LEU:CB	2:M:120:GLN:HE21	1.73	1.02
1:C:164:ARG:CB	1:C:425:VAL:HG21	1.90	1.02
1:F:313:LYS:HE2	1:F:345:LEU:HD13	1.04	1.02
2:J:150:ALA:CB	2:J:176:PHE:CD2	2.43	1.02
2:J:170:ILE:HD13	2:J:174:LEU:HD21	1.39	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:LEU:HG	1:C:421:LEU:CD2	1.87	1.02
1:H:328:VAL:CB	1:H:336:LYS:CE	2.23	1.02
1:C:200:ASP:O	1:C:203:ILE:HD12	1.27	1.02
1:C:406:HIS:HD2	1:C:407:PRO:HD2	1.24	1.02
1:D:184:ARG:HH11	2:L:56:PRO:HD3	1.25	1.02
1:C:353:ALA:HB2	1:C:361:PHE:CA	1.90	1.01
1:G:385:PRO:O	1:G:434:LEU:HD22	1.59	1.01
1:G:389:GLU:OE2	2:M:129:LYS:NZ	1.90	1.01
1:C:134:ASP:OD2	1:C:360:PHE:CE2	2.13	1.01
1:C:137:PHE:HE2	1:C:317:LEU:CD1	1.73	1.01
1:F:210:ARG:HH11	1:G:282:ARG:CZ	1.71	1.01
1:F:215:PHE:CD1	1:F:237:LEU:HD23	1.96	1.01
1:F:313:LYS:HE3	1:F:345:LEU:HD12	1.05	1.01
1:G:408:TRP:CZ2	2:K:23:ARG:CD	2.44	1.01
1:H:22:TYR:CE2	1:H:48:PRO:HG2	1.96	1.01
2:M:95:GLU:CD	2:M:122:ARG:HD2	1.75	1.01
1:C:211:TRP:CZ3	1:C:250:ARG:HG2	1.96	1.01
1:D:215:PHE:CE1	1:D:237:LEU:CG	2.30	1.01
1:F:76:ARG:HB3	1:F:76:ARG:HH11	1.25	1.01
1:G:454:ALA:O	1:G:457:ASP:OD2	1.76	1.01
1:H:382:TRP:HE1	1:H:459:TRP:C	1.63	1.01
2:K:93:LEU:HD13	2:K:96:LEU:HD21	1.42	1.01
2:L:160:ARG:HB2	2:L:166:ARG:HD3	1.42	1.01
1:D:184:ARG:NH1	2:L:56:PRO:HG2	1.74	1.01
1:E:282:ARG:HG2	1:E:282:ARG:HH11	1.25	1.01
1:F:427:ALA:CB	1:F:441:ILE:HD12	1.89	1.01
2:J:157:ALA:CB	2:J:166:ARG:HD3	1.91	1.01
1:B:123:GLY:HA3	1:G:300:ARG:NH2	1.71	1.01
1:B:35:ALA:HB2	1:B:135:ILE:HD11	1.03	1.00
1:E:35:ALA:CB	1:E:135:ILE:HD13	1.89	1.00
1:E:219:ALA:HB1	1:E:257:LEU:HD12	1.11	1.00
1:F:87:VAL:CG2	1:F:93:SER:O	2.09	1.00
1:F:328:VAL:HG11	1:F:336:LYS:HE2	1.03	1.00
1:H:34:LEU:HD11	1:H:82:TYR:CZ	1.95	1.00
1:G:313:LYS:HE2	1:G:345:LEU:HD11	1.11	1.00
1:G:328:VAL:HG21	1:G:336:LYS:HZ3	1.22	1.00
2:M:106:LEU:CD2	2:M:144:HIS:CD2	2.43	1.00
1:B:146:GLN:HE22	1:B:282:ARG:CZ	1.74	1.00
1:C:382:TRP:NE1	1:C:459:TRP:C	2.14	1.00
2:J:80:HIS:HA	2:J:83:GLU:OE2	1.59	1.00
1:D:198:LYS:HB2	1:D:236:TYR:HB2	1.41	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:313:LYS:HE3	1:G:345:LEU:CD1	1.73	1.00
2:L:28:TRP:CB	2:L:87:GLU:CB	2.40	1.00
1:C:188:GLU:HG2	1:C:411:ALA:HB2	1.43	1.00
1:E:146:GLN:NE2	1:E:282:ARG:NH1	2.09	1.00
2:O:134:LEU:CD2	2:O:135:PRO:CD	2.37	1.00
1:C:137:PHE:CE2	1:C:317:LEU:HD12	1.96	0.99
1:G:363:GLN:NE2	1:G:365:TRP:CE2	2.30	0.99
1:C:34:LEU:HD11	1:C:82:TYR:OH	1.62	0.99
1:C:328:VAL:HB	1:C:336:LYS:HE3	1.41	0.99
1:C:384:MET:HE3	1:C:421:LEU:CD1	1.51	0.99
1:D:219:ALA:HB2	1:D:257:LEU:HD13	1.43	0.99
1:B:31:THR:CG2	1:B:102:LEU:HB3	1.70	0.99
1:E:427:ALA:HB1	1:E:434:LEU:HD12	1.40	0.99
1:D:332:LEU:CB	1:D:335:ASP:OD2	2.10	0.99
1:D:211:TRP:CD2	1:D:250:ARG:CD	2.40	0.99
2:J:141:PHE:HD1	2:J:147:ASP:OD1	1.31	0.99
1:F:389:GLU:OE1	1:F:435:TYR:HB2	0.81	0.99
1:G:187:TYR:CZ	1:G:191:ARG:HD2	1.95	0.99
2:K:99:LEU:HB2	2:K:104:ARG:CG	1.92	0.99
1:A:122:PHE:HE2	1:H:297:VAL:CG2	1.55	0.99
1:B:105:PHE:CE1	1:B:113:ILE:CD1	2.39	0.99
1:D:209:GLN:NE2	1:D:214:ARG:HD3	1.77	0.99
1:E:196:PHE:HD1	1:E:234:GLY:O	1.45	0.99
1:E:295:HIS:O	1:E:299:ASP:OD1	1.81	0.99
1:F:131:ARG:NH2	1:F:301:GLN:O	1.95	0.99
2:K:99:LEU:HD13	2:K:104:ARG:N	1.76	0.99
2:K:106:LEU:CD2	2:K:144:HIS:HD2	1.69	0.99
1:B:22:TYR:CE2	1:B:48:PRO:HG2	1.96	0.98
1:C:408:TRP:O	1:C:412:PRO:HG2	1.61	0.98
1:E:421:LEU:O	1:E:425:VAL:HG23	1.61	0.98
2:N:114:ARG:HH11	2:N:175:GLN:NE2	1.58	0.98
1:B:22:TYR:CD2	1:B:48:PRO:CG	2.46	0.98
1:E:35:ALA:HB2	1:E:135:ILE:CD1	1.93	0.98
1:F:219:ALA:HB1	1:F:257:LEU:HD12	1.38	0.98
1:H:87:VAL:HG21	1:H:93:SER:OG	1.63	0.98
1:B:34:LEU:HD11	1:B:82:TYR:CE1	1.98	0.98
1:A:282:ARG:HH22	1:D:210:ARG:NH1	1.58	0.98
1:C:87:VAL:CG2	1:C:93:SER:C	2.31	0.98
1:G:188:GLU:OE1	1:G:410:ASN:ND2	1.97	0.98
1:H:408:TRP:CH2	2:I:23:ARG:HG3	1.98	0.98
1:C:197:THR:OG1	1:C:235:HIS:HB3	1.63	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:VAL:HG11	1:B:336:LYS:HE2	1.46	0.98
1:H:47:ALA:HB1	1:H:94:TYR:OH	1.62	0.98
2:K:99:LEU:CD1	2:K:104:ARG:CG	2.39	0.98
1:H:22:TYR:HH	1:H:49:GLU:HG2	1.16	0.97
1:B:382:TRP:HE1	1:B:459:TRP:C	1.65	0.97
1:E:182:TYR:CE2	1:E:199:ASP:OD1	2.10	0.97
1:G:38:ARG:NH2	1:G:95:PHE:CE1	2.31	0.97
2:L:49:PHE:HD1	2:L:54:PHE:O	1.26	0.97
1:C:146:GLN:HE21	1:C:282:ARG:NH1	1.51	0.97
1:C:384:MET:HE2	1:C:421:LEU:CG	1.84	0.97
1:D:387:LEU:HD13	1:D:397:LEU:CD2	1.91	0.97
1:F:215:PHE:CD1	1:F:237:LEU:CD2	2.47	0.97
2:J:110:LEU:HD22	2:J:114:ARG:HD3	1.46	0.97
1:B:328:VAL:HG11	1:B:336:LYS:CE	1.93	0.97
1:F:263:MET:HA	1:F:289:HIS:HB3	1.44	0.97
1:F:332:LEU:HB3	1:F:335:ASP:CG	1.83	0.97
2:K:102:GLU:HB3	2:K:106:LEU:HD13	1.46	0.97
2:O:144:HIS:CG	2:O:145:PRO:HD2	1.99	0.97
1:B:105:PHE:HE1	1:B:113:ILE:HA	1.26	0.97
1:C:71:LEU:O	2:M:90:SER:OG	1.80	0.97
1:B:385:PRO:CA	1:B:434:LEU:HD21	1.93	0.97
1:C:328:VAL:HG21	1:C:336:LYS:HE2	1.44	0.97
1:G:194:LEU:CD2	1:G:414:ALA:HB1	1.94	0.97
2:K:146:GLY:O	2:K:176:PHE:CD2	2.16	0.97
1:F:432:ARG:C	1:F:437:GLU:OE2	2.03	0.97
2:M:131:PHE:HZ	2:M:138:PRO:HD2	1.21	0.97
1:E:187:TYR:OH	1:E:224:LYS:CD	2.06	0.97
1:H:345:LEU:CD2	1:H:351:ILE:HD13	1.94	0.97
1:C:87:VAL:HG13	1:C:95:PHE:CE2	2.00	0.97
1:B:22:TYR:HD2	1:B:48:PRO:CG	1.76	0.96
1:H:199:ASP:OD1	1:H:214:ARG:HD2	1.65	0.96
1:D:214:ARG:HH11	1:D:214:ARG:HB3	1.28	0.96
1:F:328:VAL:HG23	1:F:336:LYS:NZ	1.32	0.96
2:K:93:LEU:HA	2:K:96:LEU:CD1	1.96	0.96
1:F:408:TRP:O	1:F:412:PRO:HG2	1.65	0.96
1:C:184:ARG:HD2	2:J:49:PHE:CE2	2.00	0.96
1:C:355:ARG:CB	2:O:159:GLU:OE2	2.12	0.96
1:E:352:GLU:O	1:E:359:VAL:HG11	0.79	0.96
1:C:167:LEU:CD2	1:C:421:LEU:CD2	2.41	0.96
1:F:214:ARG:HB3	1:F:214:ARG:HH11	1.30	0.96
2:K:99:LEU:CB	2:K:104:ARG:HG3	1.95	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:328:VAL:CB	1:E:336:LYS:CE	2.35	0.96
1:F:385:PRO:CA	1:F:434:LEU:HD21	1.95	0.96
2:L:106:LEU:CD2	2:L:144:HIS:CD2	2.47	0.96
2:P:144:HIS:CD2	2:P:145:PRO:CD	2.47	0.96
1:H:87:VAL:HG23	1:H:93:SER:O	1.65	0.96
1:E:211:TRP:CE3	1:E:250:ARG:CD	2.49	0.96
1:B:345:LEU:CD2	1:B:351:ILE:HD13	1.95	0.96
1:C:184:ARG:HD2	2:J:49:PHE:CD2	1.99	0.96
1:C:231:GLU:HB2	1:C:233:LYS:HE2	1.48	0.96
2:N:150:ALA:CA	2:N:176:PHE:HE2	1.78	0.96
1:G:239:VAL:O	1:G:247:MET:HE2	1.66	0.95
2:J:150:ALA:HB2	2:J:176:PHE:HD2	1.18	0.95
2:K:106:LEU:HD23	2:K:144:HIS:NE2	1.81	0.95
1:H:328:VAL:HG11	1:H:336:LYS:HE2	1.44	0.95
1:B:137:PHE:CE2	1:B:317:LEU:HD12	1.96	0.95
1:C:212:ARG:HH12	1:C:253:PHE:HD1	1.08	0.95
1:F:316:ARG:HH12	1:F:346:MET:C	1.68	0.95
1:H:81:CYS:CB	1:H:98:ILE:CD1	2.42	0.95
2:P:144:HIS:CG	2:P:145:PRO:HD2	1.99	0.95
1:F:384:MET:HE2	1:F:420:ALA:C	1.86	0.95
1:H:98:ILE:HG23	1:H:99:ALA:H	1.28	0.95
1:C:162:TYR:CE1	2:O:57:ILE:HD13	2.02	0.95
2:L:99:LEU:HD11	2:L:103:GLN:C	1.87	0.95
1:A:122:PHE:HD2	1:H:297:VAL:HG23	1.17	0.95
1:D:352:GLU:C	1:D:359:VAL:HG11	1.86	0.95
1:B:146:GLN:HE22	1:B:282:ARG:NH2	1.64	0.95
1:D:180:LYS:HD2	1:D:217:PHE:CZ	2.02	0.95
1:G:352:GLU:O	1:G:359:VAL:HG11	1.65	0.95
2:O:146:GLY:CA	2:O:176:PHE:HE1	1.75	0.95
1:F:188:GLU:HG2	1:F:411:ALA:HB2	1.46	0.95
1:F:199:ASP:OD2	1:F:235:HIS:NE2	1.99	0.95
1:B:31:THR:OG1	1:B:102:LEU:CD2	2.13	0.95
1:D:313:LYS:HE2	1:D:345:LEU:HD11	1.06	0.95
1:E:283:ASP:OD1	1:H:249:LYS:NZ	2.00	0.95
1:F:352:GLU:O	1:F:362:THR:HA	1.67	0.94
1:H:295:HIS:O	1:H:299:ASP:CG	2.06	0.94
1:E:328:VAL:HG21	1:E:336:LYS:HE2	1.45	0.94
2:J:28:TRP:CB	2:J:87:GLU:CB	2.41	0.94
1:D:382:TRP:NE1	1:D:459:TRP:C	2.19	0.94
2:K:93:LEU:O	2:K:96:LEU:HD13	1.66	0.94
1:B:402:GLY:O	1:B:404:LEU:HD23	1.66	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:174:LYS:CD	1:H:200:ASP:CG	2.31	0.94
2:K:93:LEU:O	2:K:96:LEU:HD12	1.67	0.94
1:D:116:SER:HA	1:E:202:ASN:ND2	1.82	0.94
1:D:180:LYS:HD2	1:D:217:PHE:HZ	1.33	0.94
1:C:167:LEU:CG	1:C:421:LEU:HD22	1.95	0.94
2:M:46:GLN:OE1	2:M:50:GLU:OE1	1.84	0.94
2:O:134:LEU:HD22	2:O:135:PRO:HD3	1.46	0.94
1:B:105:PHE:CE1	1:B:113:ILE:HA	2.01	0.94
1:B:142:VAL:HG22	1:B:317:LEU:HD21	1.47	0.94
2:L:149:VAL:HB	2:L:176:PHE:HE1	1.31	0.94
2:O:190:LEU:O	2:O:193:LEU:N	1.99	0.94
1:E:328:VAL:CG2	1:E:336:LYS:HZ1	1.74	0.94
1:F:205:SER:HB2	1:F:211:TRP:HB3	1.50	0.94
1:D:87:VAL:HG21	1:D:93:SER:OG	1.66	0.94
1:D:219:ALA:CB	1:D:257:LEU:HD13	1.97	0.94
1:C:167:LEU:HG	1:C:421:LEU:HD23	1.47	0.94
2:L:106:LEU:CD2	2:L:144:HIS:NE2	2.30	0.94
1:D:329:VAL:CG1	1:D:379:ILE:HG23	1.98	0.93
1:H:174:LYS:CA	1:H:200:ASP:OD2	2.16	0.93
2:K:102:GLU:CB	2:K:106:LEU:HD13	1.98	0.93
2:L:149:VAL:N	2:L:176:PHE:HZ	1.63	0.93
2:M:144:HIS:CG	2:M:145:PRO:HD2	2.02	0.93
1:B:402:GLY:C	1:B:404:LEU:HD23	1.89	0.93
1:C:184:ARG:CD	2:J:49:PHE:CE2	2.50	0.93
1:F:433:ASP:N	1:F:437:GLU:OE2	2.01	0.93
2:L:99:LEU:HD11	2:L:103:GLN:CB	1.99	0.93
1:F:387:LEU:CD1	1:F:397:LEU:HD21	1.98	0.93
1:B:385:PRO:CB	1:B:434:LEU:HD23	1.92	0.93
1:F:210:ARG:HH11	1:G:282:ARG:NH1	1.65	0.93
1:B:34:LEU:CG	1:B:82:TYR:OH	2.16	0.93
1:C:166:MET:SD	1:C:196:PHE:HE2	1.92	0.93
1:E:428:ARG:NE	2:I:97:ARG:HG3	1.81	0.93
1:F:382:TRP:NE1	1:F:459:TRP:C	2.20	0.93
1:G:39:PHE:CD1	1:G:94:TYR:CE2	2.56	0.93
1:H:82:TYR:CE1	1:H:97:PHE:CB	2.47	0.93
2:K:29:LEU:HB3	2:K:86:GLN:HE21	1.32	0.93
2:N:150:ALA:HB2	2:N:176:PHE:HD2	1.34	0.93
1:C:236:TYR:HB3	1:C:261:ILE:HG23	0.97	0.93
1:D:382:TRP:CD1	1:D:459:TRP:HB2	2.03	0.93
1:H:427:ALA:CB	1:H:441:ILE:HD12	1.99	0.93
1:B:22:TYR:CE2	1:B:49:GLU:N	2.37	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:MET:SD	1:B:421:LEU:HG	2.03	0.93
1:F:313:LYS:HZ1	1:F:345:LEU:HD11	1.18	0.93
2:N:17:LEU:HD22	2:N:20:GLN:OE1	1.69	0.93
1:G:182:TYR:CZ	1:G:199:ASP:OD1	2.22	0.92
2:J:28:TRP:CE3	2:J:87:GLU:CA	2.52	0.92
2:L:28:TRP:HB2	2:L:87:GLU:HB2	0.94	0.92
1:D:313:LYS:HE3	1:D:345:LEU:CD1	1.81	0.92
2:J:149:VAL:CG1	2:J:172:ARG:CD	2.46	0.92
2:M:14:ARG:HH11	2:M:18:LEU:HD23	1.13	0.92
1:B:313:LYS:CE	1:B:345:LEU:CD1	2.43	0.92
1:C:297:VAL:HG22	1:F:122:PHE:HD2	1.33	0.92
1:D:137:PHE:CE2	1:D:317:LEU:HD11	1.94	0.92
1:H:47:ALA:CB	1:H:94:TYR:OH	2.18	0.92
2:L:80:HIS:HA	2:L:83:GLU:OE2	1.69	0.92
1:B:380:HIS:ND1	1:B:459:TRP:CG	2.38	0.92
1:G:444:GLU:O	1:G:447:LYS:HG2	1.69	0.92
2:J:28:TRP:HE3	2:J:87:GLU:CA	1.83	0.92
1:C:87:VAL:HG21	1:C:93:SER:OG	1.69	0.92
1:C:382:TRP:CD1	1:C:459:TRP:HB2	2.05	0.92
1:D:180:LYS:CD	1:D:217:PHE:CZ	2.53	0.92
1:C:21:TYR:O	1:C:81:CYS:SG	2.27	0.92
1:H:98:ILE:HG23	1:H:99:ALA:N	1.82	0.92
2:M:131:PHE:CE1	2:M:138:PRO:HG2	2.04	0.92
1:C:197:THR:C	1:C:235:HIS:HB2	1.90	0.92
1:G:385:PRO:HA	1:G:434:LEU:HD21	1.51	0.92
1:H:328:VAL:HG21	1:H:336:LYS:HE2	1.50	0.92
1:B:22:TYR:CD2	1:B:48:PRO:HG2	2.05	0.92
1:G:197:THR:O	1:G:235:HIS:CE1	2.23	0.92
1:H:69:ASP:OD1	1:H:70:LEU:N	2.03	0.92
2:L:85:TYR:HH	2:L:93:LEU:HD21	1.13	0.92
1:F:134:ASP:OD1	1:F:309:ARG:HD2	1.70	0.91
1:F:198:LYS:HB3	1:F:236:TYR:CB	1.93	0.91
1:G:212:ARG:NH1	1:G:253:PHE:HD1	1.64	0.91
2:K:99:LEU:HD12	2:K:104:ARG:HA	1.50	0.91
1:B:85:GLU:OE2	1:B:86:PRO:O	1.89	0.91
1:C:389:GLU:CD	1:C:435:TYR:HB2	1.90	0.91
1:E:290:ILE:HD13	1:E:315:LEU:HD11	1.52	0.91
1:F:379:ILE:HA	1:F:383:HIS:HE1	1.17	0.91
1:G:197:THR:C	1:G:235:HIS:ND1	2.21	0.91
1:B:122:PHE:HD2	1:G:297:VAL:HG21	1.12	0.91
1:C:181:ASN:CB	2:J:55:GLU:OE2	2.17	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:387:LEU:HD12	1:F:397:LEU:HD13	0.92	0.91
1:G:28:PRO:C	1:G:32:ASP:OD2	2.07	0.91
1:G:211:TRP:CZ3	1:G:250:ARG:HG2	2.06	0.91
1:H:86:PRO:HA	1:H:94:TYR:CB	2.01	0.91
2:K:33:ARG:NH2	2:K:66:MET:SD	2.44	0.91
1:B:385:PRO:HB3	1:B:434:LEU:CD2	1.91	0.91
1:F:108:GLY:C	1:F:145:PHE:CE1	2.44	0.91
1:G:384:MET:HE1	1:G:421:LEU:H	1.35	0.91
1:C:244:CYS:SG	1:C:248:MET:SD	2.69	0.91
1:G:29:LYS:HA	1:G:29:LYS:CE	1.99	0.91
1:G:408:TRP:CZ3	2:K:22:ARG:O	2.23	0.91
1:E:219:ALA:HB2	1:E:257:LEU:HD12	1.51	0.91
2:N:17:LEU:O	2:N:20:GLN:OE1	1.89	0.91
1:C:197:THR:O	1:C:235:HIS:CB	2.18	0.91
1:C:352:GLU:O	1:C:359:VAL:HG11	1.70	0.91
1:D:86:PRO:HA	1:D:94:TYR:HB3	1.52	0.91
1:G:187:TYR:HH	1:G:191:ARG:HD2	1.03	0.91
1:H:177:LEU:O	1:H:182:TYR:HB2	1.71	0.91
1:D:344:ASP:OD2	1:D:357:ARG:NH1	2.04	0.91
1:E:325:SER:OG	1:E:342:PHE:CZ	2.24	0.91
1:F:38:ARG:CZ	1:F:95:PHE:CZ	2.54	0.91
1:G:29:LYS:N	1:G:32:ASP:OD2	2.04	0.91
2:K:93:LEU:CA	2:K:96:LEU:CD1	2.45	0.91
2:K:99:LEU:HD13	2:K:104:ARG:HA	0.92	0.91
2:L:49:PHE:HB2	2:L:54:PHE:O	1.70	0.91
2:N:114:ARG:NH1	2:N:175:GLN:HE21	1.68	0.91
1:C:218:VAL:HG13	1:C:235:HIS:HE1	0.75	0.91
1:C:162:TYR:HE1	2:O:57:ILE:CD1	1.83	0.90
1:G:241:ALA:H	1:G:247:MET:CE	1.77	0.90
1:G:408:TRP:HH2	2:K:23:ARG:HD3	1.22	0.90
1:B:35:ALA:CA	1:B:135:ILE:HD13	2.01	0.90
1:D:180:LYS:CE	1:D:217:PHE:CE2	2.51	0.90
1:D:219:ALA:CB	1:D:257:LEU:CD1	2.50	0.90
1:H:222:ILE:HD11	1:H:235:HIS:N	1.85	0.90
1:H:313:LYS:CE	1:H:345:LEU:CD1	2.45	0.90
2:L:28:TRP:HZ2	2:L:62:ILE:HG22	1.32	0.90
1:C:28:PRO:HB3	1:C:34:LEU:HD23	1.52	0.90
1:D:329:VAL:HG11	1:D:379:ILE:HG23	1.53	0.90
1:F:180:LYS:CD	1:F:217:PHE:CE2	2.55	0.90
1:H:22:TYR:CD2	1:H:48:PRO:CG	2.54	0.90
2:L:85:TYR:OH	2:L:93:LEU:CD2	2.16	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:384:MET:SD	1:B:421:LEU:CG	2.59	0.90
1:B:400:GLY:CA	1:B:404:LEU:HD11	2.00	0.90
1:E:325:SER:OG	1:E:342:PHE:HZ	1.52	0.90
2:J:166:ARG:HA	2:J:166:ARG:CZ	2.02	0.90
1:D:382:TRP:NE1	1:D:460:LYS:N	2.20	0.90
1:E:384:MET:HG2	1:E:421:LEU:HD12	1.53	0.90
1:F:211:TRP:HZ3	1:F:250:ARG:HG3	1.31	0.90
2:O:146:GLY:C	2:O:176:PHE:HD1	1.66	0.90
1:C:166:MET:HA	1:C:195:ASP:OD2	1.69	0.90
1:D:215:PHE:HE1	1:D:237:LEU:CB	1.85	0.90
1:D:177:LEU:CA	1:D:181:ASN:ND2	2.32	0.90
1:E:328:VAL:HG21	1:E:336:LYS:HZ1	1.12	0.90
1:H:41:PRO:HD2	1:H:92:ASN:OD1	1.72	0.90
1:C:174:LYS:HE3	1:C:200:ASP:OD1	1.64	0.90
1:E:211:TRP:CG	1:E:250:ARG:HD3	2.06	0.90
2:J:28:TRP:HE3	2:J:87:GLU:C	1.67	0.90
2:J:150:ALA:CB	2:J:176:PHE:CE2	2.54	0.90
1:E:196:PHE:CD1	1:E:234:GLY:O	2.24	0.90
1:F:240:THR:OG1	1:F:265:ASP:OD1	1.90	0.90
2:K:102:GLU:O	2:K:106:LEU:N	2.05	0.89
1:C:382:TRP:NE1	1:C:460:LYS:N	2.20	0.89
1:D:202:ASN:HD21	1:E:116:SER:HA	1.08	0.89
1:E:198:LYS:HB2	1:E:236:TYR:HB2	0.92	0.89
1:E:427:ALA:CB	1:E:434:LEU:CD1	2.48	0.89
1:G:38:ARG:HH22	1:G:95:PHE:HE1	1.08	0.89
2:J:28:TRP:CD2	2:J:87:GLU:HA	2.06	0.89
1:C:180:LYS:HG2	1:D:157:ASP:CG	1.92	0.89
1:C:328:VAL:HA	1:C:331:LYS:HD2	1.52	0.89
1:D:352:GLU:HA	1:D:362:THR:HG23	1.55	0.89
2:P:155:ARG:HB3	2:P:155:ARG:CZ	1.98	0.89
1:B:82:TYR:HE1	1:B:97:PHE:CB	1.84	0.89
1:B:384:MET:HG2	1:B:424:CYS:SG	2.12	0.89
1:D:137:PHE:HD2	1:D:317:LEU:HD11	1.30	0.89
1:F:147:GLY:CA	1:F:368:MET:CE	2.50	0.89
1:F:387:LEU:CD1	1:F:397:LEU:CG	2.50	0.89
2:K:93:LEU:HD13	2:K:96:LEU:CD2	2.02	0.89
2:O:96:LEU:HD22	2:O:107:CYS:SG	2.12	0.89
1:D:354:ASP:HB3	1:D:357:ARG:HB2	1.53	0.89
1:F:236:TYR:CD1	1:F:289:HIS:ND1	2.40	0.89
1:G:188:GLU:CD	1:G:410:ASN:OD1	2.11	0.89
2:K:33:ARG:HH21	2:K:66:MET:CG	1.82	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:PHE:HD2	1:B:317:LEU:HD11	1.34	0.89
2:O:134:LEU:HD22	2:O:135:PRO:HD2	0.89	0.89
1:H:344:ASP:OD2	2:K:126:LYS:HE3	1.72	0.89
1:C:134:ASP:OD2	1:C:360:PHE:HD2	1.54	0.89
1:F:148:PRO:HG2	1:F:369:PRO:HG2	1.53	0.89
1:G:29:LYS:O	1:G:32:ASP:HB2	1.71	0.89
1:H:81:CYS:HB3	1:H:98:ILE:HD13	0.89	0.89
1:B:123:GLY:HA2	1:G:300:ARG:HH22	0.72	0.88
1:D:138:PRO:HG2	1:D:141:LEU:HB3	1.52	0.88
1:D:239:VAL:O	1:D:247:MET:CE	2.20	0.88
1:E:211:TRP:CE3	1:E:250:ARG:CG	2.55	0.88
2:K:146:GLY:O	2:K:176:PHE:CG	2.25	0.88
1:C:133:GLU:HG3	1:C:134:ASP:OD1	1.73	0.88
1:H:174:LYS:HD2	1:H:200:ASP:OD1	1.63	0.88
2:J:110:LEU:HD21	2:J:114:ARG:CD	2.03	0.88
1:F:210:ARG:NH1	1:G:282:ARG:CZ	2.35	0.88
2:J:28:TRP:CE3	2:J:86:GLN:O	2.27	0.88
2:M:15:GLN:O	2:M:17:LEU:N	2.06	0.88
2:M:95:GLU:HG2	2:M:122:ARG:HD3	0.90	0.88
2:M:133:ARG:HA	2:M:133:ARG:CZ	2.02	0.88
1:D:174:LYS:HE2	1:D:200:ASP:OD2	1.73	0.88
1:D:202:ASN:ND2	1:E:116:SER:CA	2.32	0.88
1:F:70:LEU:HB3	2:J:87:GLU:OE2	1.72	0.88
1:G:454:ALA:HA	1:G:457:ASP:OD2	1.71	0.88
1:E:257:LEU:O	1:E:259:MET:HE3	1.73	0.88
1:E:321:ASP:O	1:E:371:VAL:HG23	1.73	0.88
1:F:204:ASN:O	1:F:206:GLN:N	2.06	0.88
2:J:17:LEU:CD1	2:J:34:ALA:HB1	2.01	0.88
2:O:146:GLY:O	2:O:176:PHE:CD1	2.24	0.88
1:A:282:ARG:CZ	1:D:210:ARG:NH1	2.36	0.88
1:B:31:THR:HG23	1:B:138:PRO:HG3	1.54	0.88
1:D:180:LYS:HB3	1:D:180:LYS:NZ	1.88	0.88
1:E:240:THR:C	1:E:247:MET:CE	2.36	0.88
1:F:108:GLY:CA	1:F:145:PHE:HE1	1.85	0.88
1:G:39:PHE:CD1	1:G:94:TYR:CZ	2.60	0.88
1:H:345:LEU:HD23	1:H:351:ILE:CD1	2.03	0.88
1:B:122:PHE:CB	1:G:297:VAL:CG2	2.52	0.88
1:C:137:PHE:HD2	1:C:317:LEU:HD11	1.32	0.88
1:G:380:HIS:HB2	1:G:459:TRP:CE3	2.09	0.88
2:N:150:ALA:CA	2:N:176:PHE:CE2	2.55	0.88
1:B:345:LEU:HD23	1:B:351:ILE:CD1	2.03	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:VAL:HG21	1:C:336:LYS:HZ1	1.34	0.88
1:C:188:GLU:CG	1:C:411:ALA:HB2	2.04	0.88
1:D:41:PRO:HD2	1:D:92:ASN:OD1	1.73	0.88
1:E:188:GLU:CG	1:E:411:ALA:HB2	2.04	0.88
2:K:174:LEU:CD2	2:K:186:ILE:HG21	2.01	0.88
1:C:328:VAL:CG2	1:C:336:LYS:NZ	2.29	0.87
1:F:41:PRO:HD2	1:F:92:ASN:OD1	1.73	0.87
1:C:211:TRP:CE3	1:C:250:ARG:HG2	2.08	0.87
2:J:166:ARG:O	2:J:169:LEU:CD1	2.22	0.87
1:D:34:LEU:HD11	1:D:82:TYR:HH	1.34	0.87
1:D:180:LYS:HE3	1:D:217:PHE:CZ	2.08	0.87
1:E:146:GLN:HE21	1:E:282:ARG:HH12	1.19	0.87
1:F:211:TRP:CH2	1:F:250:ARG:HA	2.10	0.87
2:L:157:ALA:O	2:L:166:ARG:CD	2.22	0.87
1:A:157:ASP:CB	1:D:180:LYS:HD2	2.03	0.87
1:C:136:ARG:HH11	1:C:136:ARG:HG3	1.37	0.87
1:F:427:ALA:HB1	1:F:441:ILE:HD12	1.55	0.87
1:G:375:ALA:HB2	1:G:391:PHE:CE2	2.09	0.87
1:C:437:GLU:OE1	1:C:437:GLU:N	2.08	0.87
1:E:240:THR:CA	1:E:247:MET:CE	2.52	0.87
1:F:387:LEU:HD11	1:F:397:LEU:HD21	1.48	0.87
2:J:102:GLU:O	2:J:106:LEU:HD13	1.74	0.87
2:J:141:PHE:CD2	2:J:151:HIS:ND1	2.09	0.87
1:D:178:SER:N	1:D:181:ASN:ND2	2.16	0.87
1:F:108:GLY:CA	1:F:145:PHE:CE1	2.58	0.87
1:F:198:LYS:HB3	1:F:236:TYR:CD2	2.10	0.87
1:H:184:ARG:HD3	2:I:49:PHE:CE2	2.10	0.87
2:L:85:TYR:HD1	2:L:112:LEU:HD21	1.39	0.87
1:C:384:MET:HE2	1:C:421:LEU:HA	1.54	0.87
1:D:191:ARG:HG2	1:D:191:ARG:HH11	1.40	0.87
1:F:345:LEU:HD23	1:F:351:ILE:HD12	0.88	0.87
2:L:166:ARG:O	2:L:166:ARG:NH2	2.08	0.87
1:E:328:VAL:HG11	1:E:336:LYS:HE2	1.57	0.87
1:A:282:ARG:NH1	1:D:210:ARG:HH11	1.73	0.86
1:C:382:TRP:CD1	1:C:460:LYS:N	2.42	0.86
1:B:83:HIS:HB3	1:B:97:PHE:HD2	1.40	0.86
1:D:244:CYS:H	1:E:276:THR:HG1	1.23	0.86
1:F:198:LYS:HD2	1:F:236:TYR:HD2	1.40	0.86
1:H:174:LYS:CD	1:H:200:ASP:OD2	2.23	0.86
1:F:98:ILE:HG23	1:F:99:ALA:N	1.88	0.86
1:F:182:TYR:CE2	1:F:214:ARG:HD2	2.10	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:385:PRO:CA	1:G:434:LEU:HD21	2.05	0.86
1:H:68:THR:HG23	1:H:72:THR:OG1	1.73	0.86
1:H:313:LYS:HE2	1:H:345:LEU:HD11	0.86	0.86
2:L:174:LEU:CD2	2:L:186:ILE:HG21	2.04	0.86
2:N:168:ARG:NE	2:N:168:ARG:O	2.08	0.86
1:G:384:MET:HE1	1:G:421:LEU:HD12	1.54	0.86
2:L:99:LEU:CD1	2:L:103:GLN:C	2.43	0.86
1:D:204:ASN:O	1:D:206:GLN:HG2	1.76	0.86
1:E:282:ARG:HH21	1:H:210:ARG:HE	1.24	0.86
1:C:328:VAL:HG12	1:C:331:LYS:HD3	1.57	0.86
1:F:347:ARG:HG3	1:F:347:ARG:NH1	1.91	0.86
1:H:427:ALA:HB1	1:H:441:ILE:HD12	1.54	0.86
2:L:141:PHE:HZ	2:L:185:LEU:HD12	1.39	0.86
2:M:116:LEU:HB2	2:M:120:GLN:HE21	1.40	0.86
2:L:149:VAL:CB	2:L:176:PHE:CE1	2.28	0.86
1:F:175:LEU:HG	1:F:208:PHE:HZ	1.41	0.86
2:J:141:PHE:HD1	2:J:147:ASP:CG	1.79	0.86
1:F:188:GLU:OE2	1:F:411:ALA:N	2.09	0.86
1:F:222:ILE:HD11	1:F:235:HIS:N	1.91	0.86
1:G:211:TRP:CE3	1:G:250:ARG:HG2	2.11	0.86
1:G:375:ALA:HB2	1:G:391:PHE:HE2	1.41	0.86
1:G:384:MET:SD	1:G:421:LEU:CG	2.63	0.86
2:L:150:ALA:HB2	2:L:176:PHE:CG	2.10	0.86
2:O:106:LEU:CD2	2:O:145:PRO:CD	2.48	0.86
1:B:31:THR:HG1	1:B:102:LEU:HD22	1.38	0.85
1:B:106:GLU:OE2	1:G:205:SER:N	2.07	0.85
1:C:164:ARG:HD3	1:C:164:ARG:N	1.91	0.85
1:F:390:ILE:HG22	1:F:391:PHE:N	1.89	0.85
2:M:128:THR:HG23	2:M:148:ALA:HB3	1.55	0.85
1:B:427:ALA:CB	1:B:441:ILE:HD12	2.05	0.85
1:C:197:THR:OG1	1:C:235:HIS:CG	2.28	0.85
2:L:114:ARG:CZ	2:L:175:GLN:NE2	2.39	0.85
2:L:150:ALA:HB3	2:L:176:PHE:CD2	1.84	0.85
2:L:160:ARG:CB	2:L:166:ARG:HG2	2.06	0.85
1:F:109:SER:O	1:F:145:PHE:HZ	1.58	0.85
2:L:144:HIS:CG	2:L:145:PRO:HD2	2.11	0.85
1:C:292:ARG:HE	1:C:324:HIS:HB3	1.42	0.85
1:E:211:TRP:CH2	1:E:250:ARG:HG2	2.10	0.85
1:F:236:TYR:CD2	1:F:289:HIS:ND1	2.35	0.85
1:C:146:GLN:NE2	1:C:146:GLN:O	2.08	0.85
1:C:408:TRP:HZ3	2:J:23:ARG:HA	0.70	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:134:ASP:OD1	1:E:309:ARG:HD2	1.75	0.85
1:G:188:GLU:OE2	1:G:411:ALA:N	2.09	0.85
1:E:146:GLN:HE21	1:E:282:ARG:HH11	1.18	0.85
1:B:402:GLY:O	1:B:404:LEU:CD2	2.25	0.85
1:E:155:GLU:CD	1:E:322:HIS:HE2	1.80	0.85
1:G:353:ALA:HA	1:G:359:VAL:CG1	2.04	0.85
2:L:114:ARG:CZ	2:L:175:GLN:HE22	1.87	0.85
1:F:390:ILE:HG22	1:F:391:PHE:H	1.40	0.85
1:G:241:ALA:H	1:G:247:MET:HE3	0.80	0.85
1:H:334:GLY:O	1:H:338:SER:OG	1.94	0.85
2:L:99:LEU:HD12	2:L:104:ARG:N	1.90	0.85
1:D:180:LYS:HE2	1:D:217:PHE:CZ	2.02	0.85
1:F:219:ALA:HB2	1:F:257:LEU:HD12	1.59	0.85
2:M:85:TYR:OH	2:M:93:LEU:HG	1.77	0.85
2:O:166:ARG:NH1	2:O:189:LEU:HD11	1.91	0.85
1:E:428:ARG:NE	2:I:97:ARG:CG	2.38	0.85
1:G:197:THR:C	1:G:235:HIS:HD1	1.79	0.85
1:G:382:TRP:HD1	1:G:459:TRP:HB2	1.42	0.85
1:G:408:TRP:HH2	2:K:23:ARG:CD	1.78	0.85
1:C:23:THR:CG2	1:C:84:ILE:HG22	2.07	0.84
1:E:240:THR:CA	1:E:247:MET:HE2	2.04	0.84
1:E:332:LEU:HB3	1:E:335:ASP:CG	1.95	0.84
1:G:212:ARG:NH1	1:G:253:PHE:HE1	1.71	0.84
1:G:408:TRP:CZ2	2:K:23:ARG:HD2	2.12	0.84
1:C:384:MET:HE3	1:C:421:LEU:HD12	1.19	0.84
1:F:315:LEU:CD2	1:F:323:LEU:HD13	2.06	0.84
1:H:382:TRP:NE1	1:H:459:TRP:C	2.29	0.84
2:M:14:ARG:HH11	2:M:18:LEU:CD2	1.86	0.84
1:B:433:ASP:O	1:B:437:GLU:CD	2.15	0.84
1:G:379:ILE:HA	1:G:383:HIS:HE1	1.42	0.84
1:G:384:MET:SD	1:G:421:LEU:HG	2.17	0.84
1:H:332:LEU:HB3	1:H:335:ASP:CG	1.96	0.84
2:J:110:LEU:CD2	2:J:114:ARG:CD	2.54	0.84
1:C:211:TRP:CZ3	1:C:250:ARG:CG	2.59	0.84
1:C:239:VAL:O	1:C:247:MET:HE2	1.76	0.84
1:D:214:ARG:HH11	1:D:214:ARG:CB	1.89	0.84
1:D:239:VAL:O	1:D:247:MET:HE1	1.77	0.84
1:D:269:ALA:O	1:E:272:THR:OG1	1.96	0.84
1:E:424:CYS:O	1:E:427:ALA:N	2.10	0.84
1:F:108:GLY:N	1:F:145:PHE:HE1	1.74	0.84
1:G:384:MET:HE3	1:G:421:LEU:HA	0.86	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:384:MET:SD	1:G:421:LEU:HD11	2.17	0.84
1:C:211:TRP:CE3	1:C:250:ARG:CG	2.60	0.84
1:F:143:LYS:HD2	1:F:143:LYS:O	1.77	0.84
1:F:198:LYS:HB2	1:F:236:TYR:HB2	0.84	0.84
1:B:313:LYS:HE2	1:B:345:LEU:HD11	0.84	0.84
1:G:28:PRO:CB	1:G:32:ASP:OD2	2.26	0.84
1:B:35:ALA:HA	1:B:135:ILE:HD13	1.59	0.84
1:B:122:PHE:CG	1:G:297:VAL:CG2	2.61	0.84
1:D:353:ALA:CA	1:D:359:VAL:CG1	2.37	0.84
1:E:241:ALA:CA	1:E:247:MET:HE1	2.07	0.84
1:G:182:TYR:CE2	1:G:199:ASP:OD1	2.31	0.84
1:C:382:TRP:HD1	1:C:459:TRP:CB	1.90	0.84
1:F:214:ARG:HH11	1:F:214:ARG:CB	1.90	0.84
2:N:149:VAL:HB	2:N:176:PHE:HZ	1.42	0.84
1:A:355:ARG:HG3	2:L:159:GLU:OE2	1.78	0.84
1:F:406:HIS:ND1	1:F:413:GLY:CA	2.41	0.84
2:L:14:ARG:NH1	2:L:18:LEU:CD2	2.40	0.84
1:E:384:MET:CG	1:E:421:LEU:HD12	2.07	0.83
2:L:14:ARG:CZ	2:L:18:LEU:HD23	2.07	0.83
1:E:174:LYS:HE3	1:E:200:ASP:HB3	1.59	0.83
1:B:116:SER:HA	1:G:202:ASN:HD22	1.39	0.83
1:B:137:PHE:CE2	1:B:317:LEU:HD11	2.06	0.83
1:H:180:LYS:HB2	2:I:55:GLU:OE2	1.78	0.83
2:J:28:TRP:CH2	2:J:90:SER:HA	2.13	0.83
1:F:177:LEU:CA	1:F:181:ASN:HB2	2.08	0.83
1:H:98:ILE:CG2	1:H:99:ALA:N	2.42	0.83
2:O:170:ILE:O	2:O:170:ILE:HD12	1.79	0.83
1:D:387:LEU:CD1	1:D:397:LEU:HD13	2.09	0.83
1:B:402:GLY:C	1:B:404:LEU:CD2	2.46	0.83
1:C:222:ILE:HG12	1:C:234:GLY:HA2	1.60	0.83
1:E:282:ARG:NH2	1:H:210:ARG:NE	2.26	0.83
1:H:428:ARG:HB2	1:H:434:LEU:HD12	1.60	0.83
1:B:427:ALA:HB1	1:B:441:ILE:HD12	1.59	0.83
1:C:382:TRP:HD1	1:C:459:TRP:HB2	1.42	0.83
1:F:108:GLY:C	1:F:145:PHE:HE1	1.82	0.83
1:G:38:ARG:NH1	1:G:95:PHE:CZ	2.46	0.83
1:G:408:TRP:HH2	2:K:23:ARG:CA	1.66	0.83
1:C:191:ARG:HG2	1:C:191:ARG:NH1	1.93	0.83
1:D:354:ASP:OD2	1:D:357:ARG:HG3	1.78	0.83
1:F:382:TRP:CD1	1:F:459:TRP:HB2	2.13	0.83
2:L:28:TRP:CE2	2:L:62:ILE:CG2	2.61	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:28:TRP:CE3	2:J:87:GLU:HA	2.14	0.83
1:C:138:PRO:HG2	1:C:141:LEU:HB3	1.61	0.83
1:F:295:HIS:CG	1:F:299:ASP:OD2	2.15	0.83
1:B:385:PRO:CA	1:B:434:LEU:CD2	2.53	0.82
1:D:82:TYR:CD1	1:D:97:PHE:O	2.32	0.82
1:E:148:PRO:HA	1:E:319:GLY:CA	2.09	0.82
1:F:147:GLY:CA	1:F:368:MET:HE2	2.07	0.82
1:F:211:TRP:CH2	1:F:250:ARG:CG	2.49	0.82
1:D:215:PHE:CE1	1:D:237:LEU:HB3	2.14	0.82
1:E:255:LYS:O	1:E:255:LYS:HD2	1.78	0.82
2:L:154:TRP:HZ2	2:L:185:LEU:HB3	1.43	0.82
2:L:160:ARG:HB2	2:L:166:ARG:CD	2.08	0.82
1:D:81:CYS:CB	1:D:98:ILE:CD1	2.56	0.82
1:D:382:TRP:HD1	1:D:459:TRP:HB2	1.43	0.82
1:E:295:HIS:O	1:E:299:ASP:CG	2.17	0.82
1:F:38:ARG:CZ	1:F:95:PHE:HZ	1.92	0.82
1:H:296:ALA:HA	1:H:299:ASP:OD1	1.78	0.82
1:B:122:PHE:HE1	1:B:130:LEU:CB	1.92	0.82
1:C:87:VAL:CG2	1:C:93:SER:O	2.26	0.82
1:D:211:TRP:CE2	1:D:250:ARG:HG3	2.14	0.82
1:F:281:CYS:SG	1:F:288:LEU:CD2	2.68	0.82
1:F:432:ARG:CB	1:F:437:GLU:OE2	2.27	0.82
2:O:146:GLY:CA	2:O:176:PHE:HD1	1.85	0.82
1:D:382:TRP:HD1	1:D:459:TRP:CB	1.93	0.82
1:F:176:GLY:O	1:F:178:SER:N	2.11	0.82
1:H:432:ARG:C	1:H:437:GLU:OE2	2.18	0.82
2:J:33:ARG:NH2	2:J:66:MET:SD	2.52	0.82
2:M:116:LEU:HB3	2:M:120:GLN:HE21	1.43	0.82
1:H:295:HIS:O	1:H:299:ASP:OD1	1.97	0.82
1:H:437:GLU:OE1	1:H:437:GLU:N	2.11	0.82
2:K:93:LEU:O	2:K:96:LEU:HD11	1.48	0.82
1:A:122:PHE:HE2	1:H:297:VAL:HG22	1.43	0.82
2:J:144:HIS:CG	2:J:145:PRO:HD2	2.14	0.82
2:J:157:ALA:CB	2:J:166:ARG:CD	2.56	0.82
1:D:188:GLU:CG	1:D:411:ALA:CB	2.39	0.82
1:F:255:LYS:HD2	1:F:255:LYS:C	1.99	0.82
2:J:69:TYR:CE1	2:J:85:TYR:HE2	1.97	0.82
2:J:74:ARG:HH12	2:J:102:GLU:HA	1.45	0.82
2:K:146:GLY:O	2:K:176:PHE:CE2	2.31	0.82
2:K:149:VAL:HB	2:K:176:PHE:CE1	2.15	0.82
2:M:106:LEU:HD23	2:M:144:HIS:HD2	1.33	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:332:LEU:CA	1:F:335:ASP:OD2	2.28	0.81
1:G:191:ARG:NH1	1:G:191:ARG:HB3	1.95	0.81
1:C:363:GLN:NE2	1:C:365:TRP:NE1	2.26	0.81
2:J:17:LEU:HD11	2:J:34:ALA:CB	2.06	0.81
2:L:28:TRP:HB3	2:L:87:GLU:CB	2.10	0.81
2:M:28:TRP:HE1	2:M:62:ILE:HG22	1.45	0.81
2:N:167:SER:O	2:N:170:ILE:HD13	1.75	0.81
1:B:136:ARG:HG3	1:B:136:ARG:HH11	1.43	0.81
1:B:380:HIS:CE1	1:B:459:TRP:CG	2.68	0.81
1:E:281:CYS:HG	1:E:288:LEU:HD23	1.42	0.81
1:E:430:GLU:O	2:I:67:GLN:OE1	1.98	0.81
1:G:194:LEU:HD21	1:G:414:ALA:HB1	1.60	0.81
1:H:408:TRP:CZ3	2:I:23:ARG:C	2.54	0.81
2:L:114:ARG:NH1	2:L:172:ARG:NH2	2.28	0.81
2:M:86:GLN:HA	2:M:86:GLN:NE2	1.93	0.81
1:B:385:PRO:HA	1:B:434:LEU:HD21	1.62	0.81
1:C:137:PHE:CE2	1:C:317:LEU:HD11	2.11	0.81
1:E:138:PRO:HG2	1:E:141:LEU:HB3	1.60	0.81
1:E:345:LEU:CD2	1:E:351:ILE:HD13	2.10	0.81
2:J:86:GLN:HA	2:J:86:GLN:NE2	1.95	0.81
2:L:160:ARG:HB3	2:L:166:ARG:HG2	1.62	0.81
1:B:122:PHE:HZ	1:B:131:ARG:HA	1.46	0.81
1:B:382:TRP:NE1	1:B:460:LYS:N	2.29	0.81
1:F:177:LEU:C	1:F:181:ASN:HB2	2.01	0.81
1:F:210:ARG:CZ	1:G:282:ARG:NH2	2.43	0.81
1:F:328:VAL:HG21	1:F:336:LYS:CD	2.09	0.81
1:H:177:LEU:C	1:H:181:ASN:HD22	1.83	0.81
1:E:292:ARG:CG	1:E:295:HIS:HD2	1.76	0.81
1:F:316:ARG:HD3	1:F:365:TRP:CH2	2.15	0.81
2:L:49:PHE:CG	2:L:54:PHE:O	2.33	0.81
1:B:82:TYR:CE1	1:B:97:PHE:CB	2.61	0.81
1:E:292:ARG:HD3	1:E:308:PHE:CE2	2.15	0.81
1:F:215:PHE:CE1	1:F:237:LEU:CG	2.46	0.81
1:G:188:GLU:OE2	1:G:411:ALA:HB2	1.79	0.81
1:G:292:ARG:O	1:G:295:HIS:CD2	2.33	0.81
2:J:28:TRP:HB2	2:J:87:GLU:CA	1.96	0.81
2:L:99:LEU:HD12	2:L:104:ARG:CA	2.11	0.81
1:C:87:VAL:HG22	1:C:94:TYR:HA	1.61	0.81
1:H:182:TYR:CE2	1:H:199:ASP:OD1	2.23	0.81
1:H:382:TRP:CE3	1:H:461:GLU:CG	2.64	0.81
1:B:380:HIS:HE1	1:B:459:TRP:HB3	1.45	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:81:CYS:HB2	1:F:98:ILE:HD11	1.60	0.81
2:K:38:LEU:O	2:K:43:LEU:HD21	1.80	0.81
1:F:383:HIS:H	1:F:383:HIS:CD2	1.99	0.81
1:G:408:TRP:CH2	2:K:23:ARG:CB	2.63	0.81
2:J:155:ARG:HB3	2:J:155:ARG:CZ	2.09	0.81
2:M:131:PHE:CZ	2:M:138:PRO:CG	2.64	0.81
2:N:17:LEU:HD22	2:N:17:LEU:O	1.80	0.81
1:C:295:HIS:O	1:C:299:ASP:CG	2.18	0.80
1:C:328:VAL:CB	1:C:336:LYS:CE	2.52	0.80
1:B:116:SER:HA	1:G:202:ASN:HD21	1.43	0.80
1:C:231:GLU:CB	1:C:233:LYS:CE	2.54	0.80
1:E:219:ALA:CB	1:E:257:LEU:HD11	1.98	0.80
1:F:427:ALA:HB1	1:F:441:ILE:CD1	2.11	0.80
2:O:14:ARG:NE	2:O:14:ARG:O	2.15	0.80
1:D:81:CYS:HB3	1:D:98:ILE:CD1	2.09	0.80
1:D:382:TRP:CD1	1:D:459:TRP:CB	2.64	0.80
1:G:219:ALA:CB	1:G:257:LEU:HD13	2.10	0.80
2:L:99:LEU:CD1	2:L:104:ARG:N	2.45	0.80
1:C:167:LEU:CG	1:C:421:LEU:HD23	2.07	0.80
1:D:345:LEU:HD22	1:D:351:ILE:HD13	1.62	0.80
1:G:454:ALA:HA	1:G:457:ASP:CG	2.00	0.80
2:M:149:VAL:HG13	2:M:172:ARG:HH11	1.44	0.80
1:C:384:MET:CE	1:C:421:LEU:HD13	1.31	0.80
1:B:122:PHE:CE1	1:B:130:LEU:HG	2.16	0.80
1:D:87:VAL:HG22	1:D:95:PHE:CE2	2.17	0.80
1:F:98:ILE:HG23	1:F:99:ALA:H	1.45	0.80
1:F:267:LEU:O	1:F:294:MET:HE1	1.80	0.80
1:G:328:VAL:HG21	1:G:336:LYS:CE	2.11	0.80
2:P:106:LEU:HD23	2:P:144:HIS:CD2	2.17	0.80
1:B:382:TRP:HE1	1:B:460:LYS:N	1.79	0.80
1:F:385:PRO:C	1:F:434:LEU:CD2	2.49	0.80
1:F:434:LEU:HD23	1:F:434:LEU:O	1.81	0.80
1:D:177:LEU:HA	1:D:181:ASN:ND2	1.96	0.80
1:G:35:ALA:O	1:G:98:ILE:HG22	1.82	0.80
1:G:197:THR:HG1	1:G:235:HIS:CG	1.99	0.80
1:G:408:TRP:HZ2	2:K:23:ARG:HD2	1.46	0.80
2:M:89:GLY:HA3	2:M:93:LEU:HD23	1.64	0.80
1:B:137:PHE:CD2	1:B:317:LEU:CD1	2.62	0.80
1:E:136:ARG:HH11	1:E:136:ARG:HG3	1.46	0.80
1:G:29:LYS:HA	1:G:29:LYS:HE3	1.64	0.80
2:K:17:LEU:O	2:K:21:LEU:HD23	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:29:LEU:HB3	2:K:86:GLN:NE2	1.97	0.80
1:F:148:PRO:CG	1:F:369:PRO:HG2	2.11	0.79
1:F:182:TYR:CD2	1:F:214:ARG:HD2	2.16	0.79
1:C:184:ARG:HD3	2:J:49:PHE:CE2	2.17	0.79
1:C:428:ARG:HD2	1:C:428:ARG:C	2.01	0.79
1:D:313:LYS:NZ	1:D:345:LEU:HD11	1.96	0.79
1:E:174:LYS:HE3	1:E:200:ASP:CB	2.13	0.79
1:G:29:LYS:H	1:G:32:ASP:CG	1.84	0.79
2:L:166:ARG:HB3	2:L:166:ARG:HH21	1.45	0.79
1:B:31:THR:CB	1:B:102:LEU:CB	2.41	0.79
1:B:105:PHE:HD1	1:B:113:ILE:HD13	1.03	0.79
1:D:329:VAL:HG13	1:D:379:ILE:CG2	2.13	0.79
1:D:428:ARG:HD2	1:D:428:ARG:C	2.02	0.79
2:K:102:GLU:HB3	2:K:106:LEU:CD1	2.12	0.79
1:C:176:GLY:HA2	1:F:77:TYR:OH	1.82	0.79
1:F:250:ARG:HB2	1:F:250:ARG:HH11	1.47	0.79
1:H:295:HIS:O	1:H:299:ASP:OD2	2.01	0.79
2:J:170:ILE:CD1	2:J:174:LEU:CD2	2.58	0.79
1:C:385:PRO:HA	1:C:424:CYS:SG	2.23	0.79
1:F:108:GLY:N	1:F:145:PHE:CE1	2.50	0.79
1:F:390:ILE:CG2	1:F:391:PHE:N	2.45	0.79
1:B:31:THR:CG2	1:B:138:PRO:HG3	2.13	0.79
1:B:122:PHE:CE1	1:B:130:LEU:CB	2.66	0.79
1:C:162:TYR:HE1	2:O:57:ILE:HD13	1.43	0.79
1:D:184:ARG:HH11	2:L:56:PRO:HD2	1.47	0.79
2:L:43:LEU:O	2:L:43:LEU:HD23	1.83	0.79
1:G:29:LYS:C	1:G:31:THR:H	1.84	0.79
1:H:444:GLU:O	1:H:447:LYS:CG	2.29	0.79
1:D:341:GLY:HA3	1:D:357:ARG:O	1.83	0.79
1:G:290:ILE:HG21	1:G:315:LEU:HD21	1.64	0.79
2:M:149:VAL:CG1	2:M:172:ARG:HH11	1.96	0.79
1:B:345:LEU:HA	1:B:351:ILE:HD13	1.65	0.79
1:C:34:LEU:CD1	1:C:82:TYR:OH	2.31	0.79
1:F:345:LEU:CD2	1:F:351:ILE:HD11	1.73	0.79
1:B:122:PHE:HB3	1:G:297:VAL:CG2	2.12	0.79
1:B:138:PRO:HD2	1:B:141:LEU:HB3	1.63	0.79
1:G:427:ALA:CB	1:G:441:ILE:HD12	2.13	0.79
2:K:38:LEU:O	2:K:38:LEU:HD13	1.83	0.79
2:M:116:LEU:HB2	2:M:120:GLN:NE2	1.98	0.79
2:O:147:ASP:N	2:O:176:PHE:HE1	1.65	0.79
1:B:146:GLN:NE2	1:B:282:ARG:NH1	2.31	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:302:ARG:O	1:F:302:ARG:HD3	1.83	0.78
1:G:194:LEU:HD21	1:G:414:ALA:CB	2.13	0.78
1:G:380:HIS:CB	1:G:459:TRP:CE3	2.66	0.78
1:H:222:ILE:HD13	1:H:234:GLY:HA2	1.63	0.78
2:O:137:GLN:OE1	2:O:143:ARG:HG3	1.82	0.78
1:C:184:ARG:HH12	2:J:56:PRO:HG2	0.98	0.78
1:C:353:ALA:HA	1:C:359:VAL:CG1	2.13	0.78
1:D:199:ASP:OD2	1:D:235:HIS:NE2	2.15	0.78
1:B:83:HIS:CB	1:B:97:PHE:HD2	1.96	0.78
1:D:177:LEU:HD13	1:D:181:ASN:HD22	1.47	0.78
1:F:328:VAL:HB	1:F:336:LYS:CE	1.89	0.78
1:F:385:PRO:HA	1:F:434:LEU:HD21	1.62	0.78
1:B:22:TYR:CE2	1:B:48:PRO:C	2.56	0.78
1:D:326:GLY:O	1:D:375:ALA:CB	2.31	0.78
1:E:187:TYR:OH	1:E:224:LYS:HD3	1.82	0.78
1:C:146:GLN:NE2	1:C:282:ARG:HH12	1.81	0.78
1:D:382:TRP:CD1	1:D:460:LYS:N	2.52	0.78
1:E:241:ALA:H	1:E:247:MET:HE1	0.98	0.78
1:G:383:HIS:H	1:G:383:HIS:CD2	1.98	0.78
1:B:146:GLN:HE21	1:B:282:ARG:CZ	1.96	0.78
1:C:382:TRP:CD1	1:C:459:TRP:CB	2.66	0.78
1:F:334:GLY:O	1:F:338:SER:OG	2.02	0.78
1:G:39:PHE:HD1	1:G:94:TYR:CE2	1.97	0.78
2:K:17:LEU:O	2:K:17:LEU:HD22	1.84	0.78
1:D:182:TYR:CE2	1:D:214:ARG:HD2	2.18	0.78
1:F:382:TRP:NE1	1:F:460:LYS:N	2.31	0.78
2:J:150:ALA:N	2:J:176:PHE:HE2	1.81	0.78
1:B:122:PHE:HZ	1:B:131:ARG:CA	1.97	0.78
1:D:34:LEU:CG	1:D:82:TYR:OH	2.32	0.78
1:E:241:ALA:HB3	1:E:247:MET:HB2	1.65	0.78
1:G:434:LEU:HD23	1:G:434:LEU:O	1.83	0.78
1:H:433:ASP:HB3	1:H:436:ARG:HB3	1.66	0.78
1:D:384:MET:SD	1:D:421:LEU:N	2.57	0.78
2:L:176:PHE:O	2:L:178:GLN:N	2.17	0.78
1:D:87:VAL:CG2	1:D:93:SER:O	2.30	0.78
1:F:81:CYS:HA	1:F:98:ILE:HD13	1.65	0.78
1:G:204:ASN:O	1:G:206:GLN:CG	2.28	0.78
1:A:282:ARG:NH2	1:D:210:ARG:CZ	2.47	0.77
1:H:178:SER:H	1:H:181:ASN:HD21	1.28	0.77
1:H:382:TRP:CD2	1:H:461:GLU:HG3	2.19	0.77
1:F:81:CYS:CA	1:F:98:ILE:CD1	2.62	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:198:LYS:HB3	1:F:236:TYR:CG	2.18	0.77
1:H:380:HIS:CE1	1:H:382:TRP:HB2	2.19	0.77
1:B:64:THR:HG21	1:G:172:LYS:CE	2.14	0.77
1:C:295:HIS:O	1:C:299:ASP:OD1	2.00	0.77
1:F:38:ARG:NH1	1:F:95:PHE:CZ	2.52	0.77
1:C:244:CYS:O	1:C:248:MET:SD	2.43	0.77
1:C:384:MET:HE1	1:C:421:LEU:HD13	0.92	0.77
1:D:211:TRP:CZ2	1:D:250:ARG:CG	2.47	0.77
1:H:66:VAL:HG13	1:H:68:THR:H	1.50	0.77
1:B:141:LEU:HD12	1:B:141:LEU:O	1.85	0.77
1:B:384:MET:SD	1:B:421:LEU:HD11	2.24	0.77
1:H:328:VAL:HG21	1:H:336:LYS:HZ1	0.95	0.77
2:K:144:HIS:CD2	2:K:145:PRO:HD2	2.19	0.77
2:L:133:ARG:NE	2:L:133:ARG:O	2.18	0.77
2:N:149:VAL:HB	2:N:176:PHE:CZ	2.18	0.77
1:A:154:VAL:HG13	1:D:213:ASP:OD2	1.84	0.77
1:B:380:HIS:ND1	1:B:459:TRP:CD2	2.52	0.77
2:J:150:ALA:CB	2:J:176:PHE:HD2	1.91	0.77
1:H:292:ARG:HE	1:H:324:HIS:HB3	1.47	0.77
2:K:154:TRP:CZ2	2:K:185:LEU:HB3	2.19	0.77
2:P:106:LEU:HD23	2:P:144:HIS:NE2	1.98	0.77
1:D:387:LEU:HD12	1:D:397:LEU:CD1	2.13	0.77
1:G:387:LEU:HD13	1:G:397:LEU:HD22	1.65	0.77
1:C:411:ALA:HB3	1:C:412:PRO:HD3	1.67	0.77
1:E:188:GLU:HG3	1:E:411:ALA:HB2	1.65	0.77
1:E:334:GLY:O	1:E:338:SER:OG	2.02	0.77
2:M:146:GLY:CA	2:M:176:PHE:CD1	2.65	0.77
1:B:122:PHE:CG	1:G:297:VAL:HG22	2.19	0.77
1:F:222:ILE:HD13	1:F:234:GLY:HA2	1.65	0.77
2:L:85:TYR:CZ	2:L:93:LEU:HD21	2.20	0.77
1:B:122:PHE:CZ	1:B:130:LEU:O	2.37	0.76
2:O:178:GLN:OE1	2:O:178:GLN:HA	1.83	0.76
1:E:290:ILE:HD13	1:E:315:LEU:CD1	2.14	0.76
1:G:454:ALA:CA	1:G:457:ASP:OD2	2.33	0.76
1:H:178:SER:CA	1:H:181:ASN:ND2	2.48	0.76
2:K:38:LEU:HD13	2:K:43:LEU:HD21	1.67	0.76
1:B:34:LEU:HG	1:B:82:TYR:OH	1.84	0.76
1:C:406:HIS:CD2	1:C:407:PRO:HD2	2.16	0.76
1:F:81:CYS:HA	1:F:98:ILE:CD1	2.14	0.76
1:H:328:VAL:CG1	1:H:336:LYS:HE2	2.14	0.76
2:L:44:ASN:HB3	2:L:45:PRO:CD	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:85:TYR:OH	2:M:93:LEU:CG	2.34	0.76
2:M:146:GLY:CA	2:M:176:PHE:CE1	2.64	0.76
2:K:17:LEU:O	2:K:21:LEU:CD2	2.34	0.76
2:M:131:PHE:CE2	2:M:138:PRO:CD	2.55	0.76
1:D:38:ARG:CZ	1:D:95:PHE:CZ	2.68	0.76
2:M:14:ARG:CZ	2:M:18:LEU:HD23	2.12	0.76
1:B:380:HIS:CE1	1:B:459:TRP:HB3	2.21	0.76
1:C:408:TRP:CZ3	2:J:23:ARG:CG	2.53	0.76
1:F:81:CYS:HB2	1:F:98:ILE:CD1	2.16	0.76
2:L:174:LEU:HD21	2:L:186:ILE:HG21	1.62	0.76
1:G:380:HIS:CE1	1:G:382:TRP:HB2	2.21	0.76
2:J:17:LEU:HD12	2:J:38:LEU:CD2	2.08	0.76
1:B:380:HIS:CE1	1:B:459:TRP:CB	2.69	0.76
1:C:87:VAL:HG22	1:C:94:TYR:CA	2.16	0.76
1:D:171:ILE:HD13	1:D:171:ILE:N	2.01	0.76
1:E:384:MET:SD	1:E:421:LEU:HD12	2.25	0.76
1:F:245:GLU:O	1:F:249:LYS:HB2	1.84	0.76
1:G:39:PHE:CE1	1:G:94:TYR:OH	2.38	0.76
1:F:255:LYS:HD2	1:F:255:LYS:O	1.86	0.76
1:G:38:ARG:NH2	1:G:95:PHE:HE1	1.77	0.76
2:K:74:ARG:HH12	2:K:102:GLU:CB	1.98	0.76
2:N:14:ARG:HH21	2:N:16:GLU:HA	1.51	0.76
1:B:404:LEU:HD23	1:B:404:LEU:N	2.01	0.76
1:C:87:VAL:CG1	1:C:95:PHE:CE2	2.68	0.76
1:G:198:LYS:N	1:G:235:HIS:HE1	1.84	0.76
2:P:18:LEU:O	2:P:21:LEU:N	2.17	0.76
1:G:408:TRP:HH2	2:K:23:ARG:CB	1.98	0.75
1:H:22:TYR:CE2	1:H:48:PRO:CG	2.69	0.75
1:F:219:ALA:HB1	1:F:257:LEU:HD11	0.76	0.75
2:L:98:GLU:OE1	2:L:129:LYS:HD2	1.86	0.75
2:L:166:ARG:HH21	2:L:166:ARG:CB	1.99	0.75
1:A:122:PHE:CE2	1:H:297:VAL:HG22	2.19	0.75
1:C:167:LEU:HD11	1:C:421:LEU:CD2	2.16	0.75
1:D:82:TYR:HE1	1:D:97:PHE:HB3	0.73	0.75
1:D:386:ALA:O	1:D:389:GLU:HB3	1.86	0.75
1:F:87:VAL:HG23	1:F:93:SER:C	2.06	0.75
1:H:87:VAL:HG23	1:H:93:SER:C	2.06	0.75
1:H:202:ASN:OD1	1:H:202:ASN:N	2.20	0.75
1:H:408:TRP:CH2	2:I:23:ARG:CA	2.54	0.75
1:B:39:PHE:CZ	1:B:127:ILE:HG21	2.21	0.75
1:B:122:PHE:CE1	1:B:130:LEU:HB3	2.21	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:LEU:CD1	1:C:421:LEU:CD2	2.64	0.75
1:D:413:GLY:O	1:D:417:ASN:ND2	2.19	0.75
1:H:22:TYR:CE2	1:H:48:PRO:C	2.60	0.75
1:B:146:GLN:HE21	1:B:282:ARG:NH1	1.84	0.75
1:D:348:GLU:OE1	2:J:122:ARG:NH1	2.20	0.75
1:F:328:VAL:HG22	1:F:336:LYS:HZ3	0.62	0.75
2:J:157:ALA:CB	2:J:166:ARG:NE	2.49	0.75
1:E:263:MET:CB	1:E:289:HIS:HB3	2.17	0.75
1:F:175:LEU:HG	1:F:208:PHE:CZ	2.22	0.75
1:F:389:GLU:OE1	1:F:435:TYR:CA	2.33	0.75
2:J:28:TRP:CZ2	2:J:90:SER:HA	2.21	0.75
2:L:153:CYS:SG	2:L:173:GLY:O	2.44	0.75
1:B:105:PHE:CE1	1:B:113:ILE:HD12	2.21	0.75
1:D:34:LEU:HD11	1:D:82:TYR:CE1	2.22	0.75
1:D:47:ALA:CB	1:D:94:TYR:OH	2.35	0.75
1:G:197:THR:OG1	1:G:235:HIS:ND1	2.17	0.75
1:A:356:SER:HG	2:L:155:ARG:NH2	1.84	0.75
1:F:316:ARG:HH11	1:F:346:MET:HA	0.93	0.75
1:F:348:GLU:HB3	2:P:122:ARG:HH11	1.50	0.75
1:H:22:TYR:HE2	1:H:48:PRO:HG2	1.43	0.75
1:H:382:TRP:NE1	1:H:460:LYS:N	2.35	0.75
2:K:14:ARG:HH21	2:K:14:ARG:HG3	1.52	0.75
2:K:175:GLN:HA	2:K:175:GLN:NE2	2.02	0.75
1:B:328:VAL:CG1	1:B:336:LYS:CE	2.49	0.75
1:D:55:ALA:HB2	1:D:98:ILE:HD11	1.67	0.75
1:D:202:ASN:HD22	1:E:116:SER:HA	1.49	0.75
1:F:345:LEU:HD22	1:F:351:ILE:CD1	1.69	0.75
1:C:354:ASP:N	1:C:359:VAL:O	2.20	0.74
1:F:316:ARG:NH2	1:F:370:GLY:CA	2.18	0.74
1:F:352:GLU:O	1:F:362:THR:CA	2.34	0.74
1:H:22:TYR:CE2	1:H:49:GLU:N	2.54	0.74
2:J:81:VAL:HG22	2:J:112:LEU:HD21	1.68	0.74
1:C:184:ARG:HH12	2:J:56:PRO:CG	1.80	0.74
1:C:432:ARG:HB3	1:C:437:GLU:OE2	1.87	0.74
1:D:180:LYS:CD	1:D:217:PHE:CE2	2.71	0.74
1:E:426:GLN:CA	1:E:426:GLN:HE21	2.00	0.74
1:F:382:TRP:CD1	1:F:460:LYS:N	2.55	0.74
1:H:182:TYR:CE2	1:H:214:ARG:HD2	2.22	0.74
1:B:143:LYS:O	1:B:143:LYS:HD2	1.87	0.74
1:B:389:GLU:O	2:N:129:LYS:NZ	2.15	0.74
1:D:215:PHE:CD1	1:D:237:LEU:HD21	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:380:HIS:CE1	1:F:382:TRP:HB2	2.21	0.74
1:G:236:TYR:HB3	1:G:263:MET:HG2	1.67	0.74
2:M:85:TYR:HD1	2:M:112:LEU:HD21	1.52	0.74
1:E:257:LEU:O	1:E:259:MET:CE	2.35	0.74
1:E:282:ARG:NH2	1:H:210:ARG:CZ	2.50	0.74
1:F:37:PHE:O	1:F:95:PHE:HA	1.88	0.74
2:K:36:GLN:OE1	2:K:36:GLN:HA	1.86	0.74
2:M:128:THR:CG2	2:M:148:ALA:HB2	2.10	0.74
2:N:170:ILE:HD13	2:N:170:ILE:N	2.03	0.74
1:B:22:TYR:HE2	1:B:48:PRO:HG2	1.53	0.74
1:H:345:LEU:CD2	1:H:351:ILE:CD1	2.62	0.74
1:B:22:TYR:CZ	1:B:49:GLU:HA	2.22	0.74
1:B:345:LEU:CD2	1:B:351:ILE:CD1	2.62	0.74
1:F:76:ARG:HB3	1:F:76:ARG:NH1	2.03	0.74
1:F:177:LEU:HA	1:F:181:ASN:HD22	1.52	0.74
1:F:90:GLU:CG	1:F:93:SER:HB3	2.18	0.74
1:F:210:ARG:NH1	1:G:282:ARG:NH1	2.35	0.74
2:K:106:LEU:HD23	2:K:144:HIS:HD2	0.91	0.74
1:C:140:ALA:HA	1:G:140:ALA:HA	1.70	0.74
1:H:188:GLU:HG2	1:H:411:ALA:HB2	1.70	0.74
2:L:99:LEU:HD11	2:L:103:GLN:HB3	1.69	0.74
1:C:426:GLN:HE22	2:O:67:GLN:HE22	1.35	0.74
1:D:329:VAL:HG12	1:D:379:ILE:CG2	2.17	0.74
1:H:385:PRO:HA	1:H:434:LEU:HD21	1.70	0.74
2:J:157:ALA:HB1	2:J:166:ARG:HD3	1.66	0.74
2:J:175:GLN:NE2	2:J:175:GLN:O	2.20	0.74
2:K:141:PHE:HZ	2:K:185:LEU:HD12	1.51	0.74
2:M:155:ARG:CZ	2:M:155:ARG:HB2	2.18	0.74
1:D:209:GLN:O	1:D:210:ARG:O	2.05	0.74
1:E:240:THR:HA	1:E:247:MET:HE2	1.70	0.74
1:F:134:ASP:OD1	1:F:309:ARG:CD	2.36	0.74
1:F:432:ARG:HB3	1:F:437:GLU:OE2	1.88	0.74
2:L:135:PRO:O	2:L:136:LYS:CB	2.36	0.74
1:E:190:LEU:CD2	1:E:197:THR:HG23	2.18	0.73
1:G:29:LYS:O	1:G:31:THR:N	2.21	0.73
1:H:328:VAL:CG1	1:H:336:LYS:CE	2.64	0.73
2:L:176:PHE:C	2:L:178:GLN:H	1.90	0.73
1:B:437:GLU:OE1	1:B:437:GLU:N	2.17	0.73
1:C:211:TRP:CE3	1:C:250:ARG:HD3	2.23	0.73
1:D:239:VAL:O	1:D:247:MET:HE2	1.88	0.73
1:F:38:ARG:NH2	1:F:95:PHE:HZ	1.86	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:96:LEU:HD12	2:K:96:LEU:N	2.03	0.73
2:L:134:LEU:HD13	2:L:136:LYS:O	1.85	0.73
1:D:173:PRO:CD	1:D:177:LEU:HG	2.19	0.73
1:F:345:LEU:HD21	1:F:351:ILE:CD1	2.03	0.73
1:G:241:ALA:HB3	1:G:247:MET:HB2	1.69	0.73
2:J:33:ARG:NH2	2:J:66:MET:CG	2.52	0.73
2:J:69:TYR:CE1	2:J:85:TYR:CE2	2.76	0.73
2:M:60:ASN:O	2:M:63:THR:HB	1.88	0.73
1:B:31:THR:CA	1:B:138:PRO:HB3	2.15	0.73
1:C:180:LYS:CE	1:C:180:LYS:HA	2.17	0.73
1:C:211:TRP:CD2	1:C:250:ARG:HD3	2.24	0.73
1:E:292:ARG:HD3	1:E:308:PHE:CZ	2.22	0.73
1:F:147:GLY:HA2	1:F:368:MET:HE3	1.68	0.73
1:F:171:ILE:HD13	1:F:171:ILE:N	2.03	0.73
1:H:22:TYR:CD2	1:H:48:PRO:HG2	2.22	0.73
2:N:178:GLN:HA	2:N:178:GLN:HE21	1.51	0.73
1:B:443:ARG:NH2	1:B:443:ARG:HG3	2.03	0.73
1:D:81:CYS:CA	1:D:98:ILE:HD12	2.17	0.73
1:E:141:LEU:HD12	1:E:141:LEU:O	1.89	0.73
2:L:49:PHE:CB	2:L:54:PHE:O	2.35	0.73
2:O:146:GLY:O	2:O:176:PHE:HD1	1.64	0.73
1:C:116:SER:HA	1:F:202:ASN:HD22	1.43	0.73
1:C:165:PRO:HB3	1:C:395:SER:O	1.88	0.73
1:E:171:ILE:HG13	1:E:186:VAL:HG23	1.69	0.73
1:H:382:TRP:CD1	1:H:460:LYS:N	2.57	0.73
1:C:86:PRO:HA	1:C:94:TYR:HB3	1.71	0.73
1:C:352:GLU:O	1:C:359:VAL:CG1	2.37	0.73
1:E:309:ARG:HH11	1:E:309:ARG:HB2	1.53	0.73
2:M:128:THR:CG2	2:M:148:ALA:CB	2.56	0.73
1:C:201:GLU:OE1	1:C:201:GLU:N	2.20	0.73
1:F:90:GLU:HG2	1:F:93:SER:HB3	1.69	0.73
2:L:64:VAL:O	2:L:67:GLN:N	2.21	0.73
2:O:166:ARG:CZ	2:O:189:LEU:HD11	2.19	0.73
1:E:351:ILE:HG22	1:E:359:VAL:HG21	1.69	0.73
1:H:328:VAL:HG11	1:H:336:LYS:CE	2.19	0.73
1:C:187:TYR:HE2	1:C:191:ARG:HD3	1.54	0.73
1:F:148:PRO:HG3	1:F:369:PRO:O	1.89	0.73
1:G:30:ASP:OD1	1:G:30:ASP:N	2.22	0.73
1:B:328:VAL:CG1	1:B:336:LYS:HE3	2.00	0.72
1:B:344:ASP:OD2	2:N:126:LYS:HE3	1.88	0.72
1:C:83:HIS:HB2	1:C:97:PHE:HB2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:141:LEU:HD12	1:C:141:LEU:O	1.88	0.72
1:D:201:GLU:OE1	1:D:201:GLU:N	2.21	0.72
1:D:219:ALA:HB2	1:D:257:LEU:CD1	2.16	0.72
1:H:201:GLU:OE1	1:H:201:GLU:N	2.22	0.72
2:J:85:TYR:OH	2:J:93:LEU:HD11	1.88	0.72
1:C:270:GLY:HA3	1:F:270:GLY:HA3	1.70	0.72
1:D:34:LEU:CD1	1:D:82:TYR:HH	1.95	0.72
1:E:292:ARG:CD	1:E:308:PHE:CE2	2.72	0.72
1:E:411:ALA:HB3	1:E:412:PRO:HD3	1.69	0.72
1:F:348:GLU:HB3	2:P:122:ARG:NH1	2.04	0.72
1:H:408:TRP:CH2	2:I:23:ARG:CG	2.71	0.72
1:B:346:MET:CE	1:B:371:VAL:HG13	2.19	0.72
1:E:199:ASP:HB3	1:E:203:ILE:HD13	1.69	0.72
1:G:212:ARG:CZ	1:G:253:PHE:CE1	2.70	0.72
1:D:241:ALA:H	1:D:247:MET:HE3	1.55	0.72
1:E:211:TRP:CD2	1:E:250:ARG:CG	2.72	0.72
1:F:98:ILE:CG2	1:F:99:ALA:N	2.51	0.72
1:G:188:GLU:OE2	1:G:411:ALA:CB	2.37	0.72
1:H:82:TYR:CE1	1:H:97:PHE:HB2	2.24	0.72
1:H:434:LEU:O	1:H:434:LEU:HD23	1.89	0.72
2:O:144:HIS:CD2	2:O:145:PRO:HD2	2.24	0.72
1:F:328:VAL:HG22	1:F:336:LYS:NZ	1.15	0.72
1:F:384:MET:HE3	1:F:421:LEU:HA	0.73	0.72
1:G:385:PRO:CA	1:G:434:LEU:CD2	2.67	0.72
1:G:454:ALA:C	1:G:457:ASP:OD2	2.26	0.72
2:J:17:LEU:CD1	2:J:38:LEU:HD21	2.12	0.72
2:J:168:ARG:HA	2:J:168:ARG:HH21	1.54	0.72
1:D:316:ARG:NH1	1:D:346:MET:HA	2.04	0.72
1:H:427:ALA:HB1	1:H:441:ILE:CD1	2.19	0.72
2:L:144:HIS:ND1	2:L:145:PRO:HD2	2.05	0.72
2:L:166:ARG:NH2	2:L:166:ARG:HB3	2.04	0.72
1:D:387:LEU:HD13	1:D:397:LEU:HD21	1.72	0.72
1:C:83:HIS:CB	1:C:97:PHE:HD2	2.02	0.72
1:C:297:VAL:HG22	1:F:122:PHE:CE2	2.23	0.72
1:C:384:MET:CE	1:C:421:LEU:HD11	1.23	0.72
1:D:81:CYS:CA	1:D:98:ILE:CD1	2.68	0.72
1:E:188:GLU:HG2	1:E:411:ALA:HB2	1.70	0.72
1:G:211:TRP:CD2	1:G:250:ARG:HD3	2.25	0.72
2:L:160:ARG:HB2	2:L:166:ARG:CG	2.19	0.72
1:B:34:LEU:HD11	1:B:82:TYR:HH	1.52	0.72
1:D:387:LEU:CD1	1:D:397:LEU:CD1	2.67	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:237:LEU:O	1:F:263:MET:CG	2.37	0.72
1:F:257:LEU:HD13	1:F:259:MET:CE	2.19	0.72
1:H:408:TRP:CZ3	2:I:23:ARG:O	2.43	0.72
2:J:14:ARG:HH11	2:J:18:LEU:HD23	1.51	0.72
2:L:114:ARG:HH11	2:L:172:ARG:NH2	1.86	0.72
1:C:162:TYR:CE1	2:O:57:ILE:CD1	2.66	0.72
1:C:179:ALA:HB1	1:C:217:PHE:HD2	1.55	0.72
1:C:408:TRP:CZ3	2:J:23:ARG:HB3	2.03	0.72
1:D:38:ARG:CZ	1:D:95:PHE:HZ	2.03	0.72
1:F:188:GLU:CG	1:F:411:ALA:HB2	2.20	0.72
1:F:265:ASP:OD1	1:F:265:ASP:N	2.21	0.72
1:H:385:PRO:O	1:H:434:LEU:HD22	1.89	0.72
2:L:174:LEU:HD21	2:L:186:ILE:CB	2.19	0.72
1:B:122:PHE:HE1	1:B:130:LEU:CA	2.03	0.71
1:C:180:LYS:HG2	1:D:157:ASP:CB	2.19	0.71
1:D:181:ASN:HA	2:L:55:GLU:OE1	1.90	0.71
1:E:316:ARG:NE	1:E:365:TRP:CH2	2.58	0.71
1:E:323:LEU:HG	1:E:323:LEU:O	1.88	0.71
1:G:25:ASP:N	1:G:25:ASP:OD1	2.23	0.71
1:G:313:LYS:NZ	1:G:345:LEU:HD11	2.05	0.71
2:K:74:ARG:HH12	2:K:102:GLU:CA	2.02	0.71
1:D:109:SER:O	1:D:145:PHE:HZ	1.72	0.71
1:D:190:LEU:HD11	1:D:233:LYS:HD2	1.72	0.71
1:D:244:CYS:HB3	1:E:276:THR:HG21	1.73	0.71
1:E:240:THR:HA	1:E:247:MET:CE	2.20	0.71
1:F:90:GLU:HG2	1:F:93:SER:CB	2.20	0.71
1:F:209:GLN:O	1:F:210:ARG:O	2.08	0.71
2:J:170:ILE:HD12	2:J:174:LEU:CD2	2.20	0.71
2:L:134:LEU:HD13	2:L:134:LEU:O	1.90	0.71
1:B:124:PHE:HD1	1:B:124:PHE:H	1.36	0.71
1:C:83:HIS:CG	1:C:97:PHE:HD2	2.08	0.71
1:G:384:MET:CE	1:G:421:LEU:CD1	2.62	0.71
1:G:408:TRP:HH2	2:K:23:ARG:CG	2.03	0.71
1:G:427:ALA:HB1	1:G:441:ILE:HD12	1.71	0.71
2:K:99:LEU:HD12	2:K:104:ARG:CA	1.95	0.71
2:L:44:ASN:HB3	2:L:45:PRO:HD2	1.71	0.71
1:F:224:LYS:HZ2	2:M:50:GLU:CD	1.88	0.71
2:M:28:TRP:NE1	2:M:62:ILE:HG22	2.04	0.71
2:M:149:VAL:HG13	2:M:172:ARG:NH1	2.04	0.71
1:G:385:PRO:O	1:G:434:LEU:CD2	2.38	0.71
1:H:328:VAL:HG23	1:H:336:LYS:NZ	1.97	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:LEU:CD1	1:B:82:TYR:HH	2.02	0.71
1:E:353:ALA:CA	1:E:359:VAL:CG1	2.42	0.71
1:F:79:GLY:HA2	1:F:99:ALA:O	1.90	0.71
2:J:157:ALA:HA	2:J:166:ARG:HD2	1.72	0.71
2:L:99:LEU:HD12	2:L:104:ARG:HA	1.73	0.71
2:M:116:LEU:O	2:M:117:ASP:O	2.07	0.71
1:B:424:CYS:SG	1:B:442:LEU:HD21	2.30	0.71
1:C:28:PRO:HD3	1:C:82:TYR:CE2	2.26	0.71
1:C:82:TYR:CD1	1:C:97:PHE:HB2	2.24	0.71
1:G:328:VAL:CG2	1:G:336:LYS:CE	2.68	0.71
1:G:353:ALA:HB2	1:G:361:PHE:HA	1.71	0.71
1:G:353:ALA:HB2	1:G:362:THR:H	1.54	0.71
2:L:17:LEU:O	2:L:17:LEU:HD22	1.91	0.71
1:A:282:ARG:NH1	1:D:210:ARG:NH1	2.38	0.71
1:C:82:TYR:CD1	1:C:97:PHE:CB	2.72	0.71
1:C:241:ALA:H	1:C:247:MET:HE3	1.56	0.71
1:E:63:TRP:HZ3	1:E:74:MET:HB3	1.54	0.71
1:F:109:SER:N	1:F:145:PHE:CE1	2.59	0.71
1:H:178:SER:CB	1:H:181:ASN:HD21	2.04	0.71
1:H:345:LEU:HA	1:H:351:ILE:HD13	1.73	0.71
2:K:74:ARG:HH12	2:K:102:GLU:HA	1.54	0.71
2:K:154:TRP:CH2	2:K:185:LEU:HB3	2.25	0.71
2:M:121:ILE:HA	2:M:124:VAL:HG13	1.73	0.71
1:C:215:PHE:HA	1:C:237:LEU:HD11	1.71	0.71
1:F:38:ARG:NH2	1:F:95:PHE:CZ	2.59	0.71
1:F:87:VAL:HG21	1:F:93:SER:OG	1.91	0.71
1:H:22:TYR:HD2	1:H:48:PRO:CG	1.93	0.71
2:P:156:LEU:O	2:P:160:ARG:HG2	1.91	0.71
1:C:87:VAL:HG21	1:C:93:SER:CB	2.21	0.71
1:D:38:ARG:NH1	1:D:95:PHE:CZ	2.59	0.71
1:E:241:ALA:H	1:E:247:MET:CE	1.78	0.71
2:O:114:ARG:O	2:O:114:ARG:HD2	1.91	0.71
1:D:329:VAL:CG1	1:D:379:ILE:HG21	2.20	0.70
1:F:382:TRP:CD1	1:F:459:TRP:CB	2.74	0.70
1:H:382:TRP:CD1	1:H:459:TRP:HB2	2.25	0.70
1:B:402:GLY:N	1:B:404:LEU:HD21	2.06	0.70
1:C:64:THR:HG21	1:F:172:LYS:HG3	1.71	0.70
1:E:148:PRO:HA	1:E:319:GLY:HA2	1.71	0.70
1:E:292:ARG:CG	1:E:295:HIS:CD2	2.52	0.70
2:L:46:GLN:HE21	2:L:46:GLN:C	1.94	0.70
2:L:85:TYR:HD1	2:L:112:LEU:CD2	2.04	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:GLU:OE2	1:E:143:LYS:HE2	1.91	0.70
1:B:400:GLY:H	1:B:404:LEU:CD1	2.03	0.70
1:C:295:HIS:O	1:C:299:ASP:OD2	2.09	0.70
1:D:354:ASP:OD2	2:J:155:ARG:NH1	2.24	0.70
1:F:76:ARG:HH11	1:F:76:ARG:CB	2.02	0.70
1:F:244:CYS:C	1:F:248:MET:CE	2.60	0.70
2:K:93:LEU:HA	2:K:96:LEU:HD21	1.71	0.70
1:C:429:ASN:OD1	2:O:64:VAL:HG23	1.91	0.70
1:F:72:THR:HB	1:F:74:MET:HE2	1.72	0.70
1:G:408:TRP:HH2	2:K:23:ARG:HA	1.06	0.70
2:L:183:ARG:NH2	2:L:183:ARG:HG3	2.05	0.70
1:D:173:PRO:HD2	1:D:177:LEU:HG	1.73	0.70
1:H:87:VAL:CG2	1:H:93:SER:OG	2.38	0.70
1:B:384:MET:HE1	1:B:421:LEU:HD12	1.71	0.70
1:C:363:GLN:NE2	1:C:365:TRP:CD2	2.59	0.70
1:D:211:TRP:CH2	1:D:250:ARG:HA	2.26	0.70
1:E:241:ALA:HB2	1:E:247:MET:HE3	1.72	0.70
2:J:166:ARG:HA	2:J:166:ARG:NE	2.05	0.70
2:N:114:ARG:HH12	2:N:175:GLN:HE21	1.39	0.70
2:P:155:ARG:HB3	2:P:155:ARG:NH1	2.06	0.70
1:C:109:SER:O	1:C:145:PHE:HZ	1.72	0.70
1:C:176:GLY:CA	1:F:77:TYR:OH	2.39	0.70
1:C:184:ARG:HG3	2:J:56:PRO:HD2	1.74	0.70
1:C:384:MET:SD	1:C:421:LEU:HA	2.31	0.70
1:D:108:GLY:N	1:D:145:PHE:HE1	1.89	0.70
1:F:432:ARG:CA	1:F:437:GLU:OE2	2.39	0.70
1:H:28:PRO:HB3	1:H:82:TYR:CE2	2.26	0.70
1:F:236:TYR:CE1	1:F:289:HIS:CE1	2.79	0.70
1:F:244:CYS:C	1:F:248:MET:HE3	2.11	0.70
1:C:342:PHE:HA	1:C:345:LEU:HD12	1.73	0.70
1:G:191:ARG:HB3	1:G:191:ARG:CZ	2.22	0.70
1:H:47:ALA:HB1	1:H:94:TYR:CZ	2.26	0.70
2:K:144:HIS:ND1	2:K:145:PRO:HD2	2.05	0.70
1:C:34:LEU:HD11	1:C:82:TYR:CE1	2.26	0.69
1:D:179:ALA:O	1:D:217:PHE:HD2	1.75	0.69
1:D:201:GLU:CD	1:D:201:GLU:H	1.94	0.69
1:E:188:GLU:OE2	1:E:411:ALA:N	2.24	0.69
1:E:198:LYS:CB	1:E:236:TYR:CD2	2.75	0.69
1:F:387:LEU:CD1	1:F:397:LEU:HD11	2.21	0.69
1:D:66:VAL:HG13	1:D:68:THR:H	1.57	0.69
1:E:201:GLU:H	1:E:201:GLU:CD	1.94	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:240:THR:CA	1:E:247:MET:HE1	2.19	0.69
1:C:201:GLU:H	1:C:201:GLU:CD	1.95	0.69
1:C:428:ARG:HD2	1:C:428:ARG:O	1.92	0.69
1:E:316:ARG:NH2	1:E:365:TRP:CG	2.59	0.69
1:F:446:GLY:C	1:F:448:TRP:H	1.96	0.69
1:G:408:TRP:CZ3	2:K:23:ARG:C	2.65	0.69
1:B:105:PHE:HE1	1:B:113:ILE:CA	2.01	0.69
1:D:172:LYS:NZ	1:D:400:GLY:O	2.25	0.69
1:D:198:LYS:HB2	1:D:236:TYR:CB	2.21	0.69
1:E:428:ARG:HE	2:I:97:ARG:HG2	1.54	0.69
1:F:147:GLY:CA	1:F:368:MET:HE3	2.21	0.69
1:F:263:MET:HA	1:F:289:HIS:CB	2.20	0.69
1:F:292:ARG:NH2	1:F:326:GLY:N	2.39	0.69
1:G:382:TRP:CD1	1:G:459:TRP:HB2	2.25	0.69
2:K:13:GLU:OE2	2:K:37:THR:O	2.10	0.69
2:K:17:LEU:HD23	2:K:20:GLN:OE1	1.92	0.69
1:D:178:SER:N	1:D:181:ASN:OD1	2.25	0.69
1:D:211:TRP:CD2	1:D:250:ARG:CG	2.71	0.69
1:G:382:TRP:HB3	1:G:461:GLU:HG3	1.75	0.69
1:G:404:LEU:HB2	1:G:459:TRP:CH2	2.27	0.69
2:J:166:ARG:O	2:J:169:LEU:HD12	1.91	0.69
2:N:14:ARG:NH1	2:N:18:LEU:HD23	2.07	0.69
1:B:105:PHE:CE1	1:B:113:ILE:HG23	2.28	0.69
1:C:164:ARG:HD3	1:C:164:ARG:H	1.55	0.69
1:D:199:ASP:OD2	1:D:199:ASP:N	2.26	0.69
1:F:385:PRO:HG3	1:F:442:LEU:HD11	1.75	0.69
1:G:194:LEU:N	1:G:194:LEU:HD23	2.07	0.69
1:C:167:LEU:CD1	1:C:421:LEU:HD22	2.21	0.69
1:G:345:LEU:HD22	1:G:351:ILE:HD13	1.74	0.69
1:H:387:LEU:HD13	1:H:397:LEU:HD22	1.72	0.69
2:M:131:PHE:CZ	2:M:138:PRO:HG2	2.27	0.69
1:B:22:TYR:CG	1:B:48:PRO:HB2	2.18	0.69
1:C:28:PRO:HB3	1:C:34:LEU:CD2	2.23	0.69
1:C:166:MET:CA	1:C:195:ASP:OD2	2.40	0.69
1:C:200:ASP:O	1:C:203:ILE:HD13	1.80	0.69
1:D:87:VAL:HG23	1:D:93:SER:C	2.13	0.69
1:D:215:PHE:CE1	1:D:237:LEU:HG	2.26	0.69
1:D:345:LEU:CD2	1:D:351:ILE:HD13	2.23	0.69
1:G:292:ARG:O	1:G:295:HIS:HD2	1.74	0.69
2:J:168:ARG:HA	2:J:168:ARG:NE	2.08	0.69
2:K:99:LEU:HB3	2:K:103:GLN:HB3	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:49:PHE:CE1	2:L:55:GLU:HA	2.28	0.69
2:L:174:LEU:HD21	2:L:186:ILE:CG2	2.22	0.69
2:O:134:LEU:CD2	2:O:135:PRO:HD3	2.15	0.69
2:P:17:LEU:HD11	2:P:34:ALA:CB	2.23	0.69
1:A:355:ARG:CG	2:L:159:GLU:OE2	2.40	0.69
1:B:122:PHE:CD1	1:B:130:LEU:HB3	2.27	0.69
1:F:201:GLU:CD	1:F:201:GLU:H	1.96	0.69
1:F:302:ARG:HH11	1:F:302:ARG:CG	2.05	0.69
2:J:104:ARG:HD2	2:J:104:ARG:C	2.14	0.69
1:F:355:ARG:H	2:P:159:GLU:CD	1.96	0.69
1:G:194:LEU:HD21	1:G:414:ALA:CA	2.23	0.69
1:D:87:VAL:CG2	1:D:93:SER:OG	2.41	0.68
1:E:351:ILE:CG2	1:E:359:VAL:HG21	2.22	0.68
1:F:387:LEU:HD13	1:F:397:LEU:CD1	2.23	0.68
1:H:380:HIS:CD2	1:H:383:HIS:HE2	2.11	0.68
1:D:140:ALA:HB1	1:F:139:VAL:O	1.91	0.68
1:D:209:GLN:HE21	1:D:214:ARG:HD3	1.56	0.68
1:G:454:ALA:HA	1:G:457:ASP:OD1	1.93	0.68
2:L:94:TYR:CZ	2:L:97:ARG:NH1	2.62	0.68
1:C:137:PHE:CD2	1:C:317:LEU:CD1	2.63	0.68
1:C:231:GLU:CB	1:C:233:LYS:HE2	2.22	0.68
1:D:179:ALA:C	1:D:217:PHE:HD2	1.96	0.68
1:E:283:ASP:CG	1:H:249:LYS:NZ	2.47	0.68
2:M:156:LEU:O	2:M:159:GLU:HB3	1.92	0.68
1:C:134:ASP:OD1	1:C:134:ASP:N	2.25	0.68
1:G:316:ARG:NH1	1:G:346:MET:HA	2.08	0.68
2:J:141:PHE:O	2:J:142:ASP:O	2.11	0.68
1:C:180:LYS:HD2	1:C:217:PHE:CE2	2.29	0.68
1:D:219:ALA:CB	1:D:257:LEU:HD11	2.24	0.68
1:E:241:ALA:CB	1:E:247:MET:CE	2.71	0.68
1:F:346:MET:O	1:F:370:GLY:CA	2.34	0.68
2:K:110:LEU:O	2:K:110:LEU:HD13	1.93	0.68
2:L:100:ASP:O	2:L:103:GLN:N	2.26	0.68
1:C:184:ARG:HH11	2:J:56:PRO:HG2	0.87	0.68
1:C:355:ARG:HB2	2:O:159:GLU:OE2	1.94	0.68
1:F:267:LEU:O	1:F:294:MET:CE	2.42	0.68
1:F:315:LEU:HD22	1:F:323:LEU:HD13	1.76	0.68
1:F:347:ARG:HG3	1:F:347:ARG:HH11	1.58	0.68
1:G:29:LYS:N	1:G:32:ASP:CG	2.45	0.68
1:G:240:THR:HA	1:G:247:MET:HE1	1.76	0.68
2:K:146:GLY:O	2:K:176:PHE:CD1	2.45	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:ARG:HH11	2:J:56:PRO:CD	2.07	0.68
1:C:202:ASN:OD1	1:C:202:ASN:N	2.26	0.68
1:D:167:LEU:HD11	1:D:418:ARG:HA	1.75	0.68
1:E:197:THR:OG1	1:E:235:HIS:CD2	2.45	0.68
1:F:355:ARG:HB2	2:P:159:GLU:OE2	1.92	0.68
1:F:427:ALA:CB	1:F:441:ILE:CD1	2.66	0.68
1:G:198:LYS:N	1:G:235:HIS:CE1	2.62	0.68
2:L:160:ARG:HB2	2:L:166:ARG:HG2	1.75	0.68
1:D:81:CYS:HA	1:D:98:ILE:HD12	1.74	0.68
2:L:134:LEU:HD22	2:L:135:PRO:HD2	1.74	0.68
2:O:110:LEU:O	2:O:110:LEU:HD22	1.94	0.68
1:D:241:ALA:HB3	1:D:247:MET:HB2	1.75	0.68
1:E:427:ALA:HB3	1:E:434:LEU:HD11	1.73	0.68
1:H:328:VAL:CG2	1:H:336:LYS:HZ2	1.99	0.68
1:C:162:TYR:HE1	2:O:57:ILE:HD11	1.57	0.67
1:C:177:LEU:HD13	1:C:181:ASN:HB2	1.75	0.67
1:H:382:TRP:CE3	1:H:461:GLU:OE2	2.46	0.67
1:B:116:SER:CA	1:G:202:ASN:ND2	2.45	0.67
1:C:384:MET:HE1	1:C:421:LEU:HD11	0.76	0.67
1:D:184:ARG:NH1	2:L:56:PRO:HD2	2.07	0.67
1:E:263:MET:HA	1:E:289:HIS:O	1.94	0.67
1:F:266:PHE:CZ	1:F:311:LEU:HD13	2.29	0.67
2:M:106:LEU:CD2	2:M:144:HIS:HD2	1.94	0.67
1:C:23:THR:HG21	1:C:84:ILE:HG22	1.75	0.67
2:I:56:PRO:HA	2:I:59:GLN:HG2	1.76	0.67
1:A:355:ARG:HB2	2:L:159:GLU:OE2	1.95	0.67
1:D:211:TRP:CE2	1:D:250:ARG:CG	2.76	0.67
1:E:68:THR:HG22	1:E:72:THR:OG1	1.94	0.67
1:F:179:ALA:HB2	1:F:213:ASP:OD2	1.95	0.67
1:H:22:TYR:CE2	1:H:48:PRO:CB	2.76	0.67
2:N:190:LEU:O	2:N:193:LEU:HB3	1.93	0.67
1:C:197:THR:H	1:C:235:HIS:CB	2.07	0.67
1:C:328:VAL:HG12	1:C:331:LYS:CD	2.23	0.67
1:D:380:HIS:H	1:D:380:HIS:CD2	2.13	0.67
2:K:110:LEU:O	2:K:110:LEU:HD22	1.93	0.67
1:D:329:VAL:HG13	1:D:379:ILE:HG21	1.74	0.67
2:J:157:ALA:HB2	2:J:166:ARG:NE	2.09	0.67
2:M:14:ARG:HG3	2:M:14:ARG:O	1.92	0.67
1:C:134:ASP:CG	1:C:360:PHE:CD2	2.68	0.67
1:G:363:GLN:NE2	1:G:365:TRP:CD2	2.61	0.67
2:J:74:ARG:NH1	2:J:101:GLN:O	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:142:VAL:HG22	1:E:317:LEU:CD2	2.24	0.67
2:J:15:GLN:HE21	2:J:15:GLN:H	1.41	0.67
2:M:92:LEU:HD11	2:M:121:ILE:HD11	1.77	0.67
1:C:85:GLU:O	1:C:94:TYR:CB	2.35	0.67
1:F:211:TRP:CD1	1:F:250:ARG:NE	2.61	0.67
1:F:384:MET:HE1	1:F:421:LEU:CA	1.79	0.67
1:H:34:LEU:CG	1:H:82:TYR:OH	2.42	0.67
1:H:87:VAL:CG2	1:H:93:SER:O	2.40	0.67
2:L:162:ASP:O	2:L:166:ARG:HB2	1.95	0.67
1:C:23:THR:CG2	1:C:84:ILE:CG2	2.73	0.67
1:C:184:ARG:HG3	2:J:56:PRO:CD	2.25	0.67
1:D:316:ARG:HH11	1:D:346:MET:HA	1.59	0.67
1:G:241:ALA:CB	1:G:247:MET:HE2	2.25	0.67
1:H:187:TYR:HE2	1:H:191:ARG:HD3	1.60	0.67
1:H:382:TRP:CE3	1:H:461:GLU:HG2	2.30	0.67
2:J:170:ILE:HD12	2:J:174:LEU:HD21	1.74	0.67
2:M:61:GLN:HA	2:M:94:TYR:CE1	2.30	0.67
2:M:85:TYR:OH	2:M:93:LEU:CD2	2.43	0.67
1:A:157:ASP:HA	1:D:180:LYS:CD	2.25	0.66
1:C:238:ASN:OD1	1:C:239:VAL:N	2.28	0.66
1:D:68:THR:HG22	1:D:72:THR:OG1	1.94	0.66
1:D:211:TRP:CG	1:D:250:ARG:HD3	2.29	0.66
1:E:198:LYS:HB3	1:E:236:TYR:CD2	2.30	0.66
1:E:211:TRP:CG	1:E:250:ARG:CD	2.74	0.66
1:G:197:THR:HG1	1:G:235:HIS:CE1	2.13	0.66
2:L:169:LEU:HB3	2:L:173:GLY:HA3	1.77	0.66
2:M:144:HIS:CD2	2:M:145:PRO:HD2	2.29	0.66
1:B:122:PHE:CE1	1:B:130:LEU:CG	2.78	0.66
1:B:122:PHE:HB3	1:G:297:VAL:HG23	1.77	0.66
1:C:160:ASN:HA	1:C:162:TYR:CE2	2.31	0.66
1:C:167:LEU:HD11	1:C:421:LEU:HD22	1.77	0.66
1:E:146:GLN:NE2	1:E:282:ARG:HH12	1.86	0.66
1:H:188:GLU:OE1	1:H:410:ASN:ND2	2.26	0.66
1:H:430:GLU:OE1	1:H:432:ARG:HD3	1.95	0.66
2:J:171:ALA:HA	2:J:175:GLN:HB3	1.77	0.66
2:L:114:ARG:NH1	2:L:172:ARG:HH22	1.94	0.66
1:A:157:ASP:HA	1:D:180:LYS:HD3	1.76	0.66
1:B:400:GLY:N	1:B:404:LEU:HD11	2.09	0.66
1:D:184:ARG:NH1	2:L:56:PRO:HD3	1.90	0.66
1:E:134:ASP:OD1	1:E:309:ARG:CD	2.43	0.66
1:H:34:LEU:HD11	1:H:82:TYR:CE1	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:157:ALA:HB1	2:J:166:ARG:CD	2.23	0.66
1:D:216:LEU:C	1:D:216:LEU:HD12	2.16	0.66
1:E:136:ARG:HD3	1:E:136:ARG:C	2.15	0.66
1:E:201:GLU:OE1	1:E:201:GLU:N	2.25	0.66
1:F:141:LEU:O	1:F:141:LEU:HD12	1.95	0.66
1:G:239:VAL:C	1:G:247:MET:HE1	2.16	0.66
1:G:263:MET:HA	1:G:289:HIS:O	1.96	0.66
1:B:122:PHE:CD2	1:G:297:VAL:HG22	2.29	0.66
1:E:155:GLU:OE2	1:E:322:HIS:CE1	2.47	0.66
1:F:244:CYS:O	1:F:248:MET:CE	2.44	0.66
1:G:384:MET:HE2	1:G:420:ALA:CB	2.25	0.66
1:C:353:ALA:CB	1:C:361:PHE:CA	2.63	0.66
1:D:329:VAL:CG1	1:D:379:ILE:HG22	2.25	0.66
1:E:292:ARG:HG3	1:E:292:ARG:O	1.95	0.66
1:F:406:HIS:ND1	1:F:413:GLY:N	2.43	0.66
1:G:351:ILE:HG22	1:G:362:THR:HG23	1.76	0.66
2:J:110:LEU:HD21	2:J:114:ARG:NE	2.11	0.66
1:D:332:LEU:CA	1:D:335:ASP:OD2	2.43	0.66
1:H:34:LEU:HD11	1:H:82:TYR:HH	1.55	0.66
1:A:157:ASP:CA	1:D:180:LYS:HD2	2.25	0.66
1:B:433:ASP:O	1:B:437:GLU:OE2	2.14	0.66
1:C:167:LEU:CD1	1:C:421:LEU:HD23	2.23	0.66
1:C:236:TYR:CA	1:C:261:ILE:HG23	2.24	0.66
1:C:385:PRO:HG3	1:C:442:LEU:HD11	1.78	0.66
1:D:332:LEU:HB3	1:D:335:ASP:CG	2.16	0.66
1:F:215:PHE:HE1	1:F:237:LEU:CB	2.09	0.66
2:L:141:PHE:CZ	2:L:185:LEU:HD12	2.28	0.66
1:B:34:LEU:HD21	1:B:82:TYR:CZ	2.31	0.66
1:E:236:TYR:HB3	1:E:263:MET:HG2	1.78	0.66
1:E:282:ARG:NH1	1:E:282:ARG:HG2	2.00	0.66
1:F:292:ARG:O	1:F:292:ARG:HG2	1.93	0.66
2:J:85:TYR:OH	2:J:93:LEU:CG	2.44	0.66
2:L:114:ARG:CZ	2:L:172:ARG:HH12	2.02	0.66
2:O:190:LEU:O	2:O:192:ASP:N	2.28	0.66
1:B:104:LEU:HD11	1:G:175:LEU:HD22	1.78	0.66
1:C:408:TRP:CZ3	2:J:23:ARG:HD2	1.84	0.66
1:D:188:GLU:HG2	1:D:411:ALA:HB2	0.74	0.66
1:D:214:ARG:HB3	1:D:214:ARG:NH1	2.08	0.66
1:E:266:PHE:CE2	1:E:311:LEU:HD13	2.31	0.66
1:H:201:GLU:H	1:H:201:GLU:CD	1.95	0.66
2:P:17:LEU:O	2:P:17:LEU:HD13	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:216:LEU:C	1:F:216:LEU:HD12	2.17	0.65
2:O:186:ILE:HD12	2:O:186:ILE:O	1.96	0.65
1:C:197:THR:CA	1:C:235:HIS:HB2	2.25	0.65
1:D:191:ARG:HD2	1:D:228:GLU:OE1	1.95	0.65
1:G:131:ARG:NH2	1:G:301:GLN:O	2.29	0.65
1:G:460:LYS:H	1:G:460:LYS:HD2	1.61	0.65
2:J:168:ARG:HA	2:J:168:ARG:NH2	2.12	0.65
2:N:175:GLN:HG3	2:N:175:GLN:O	1.96	0.65
1:D:191:ARG:HG2	1:D:191:ARG:NH1	2.02	0.65
1:C:356:SER:CB	2:O:155:ARG:NH2	2.58	0.65
1:H:174:LYS:HE2	1:H:200:ASP:CG	2.15	0.65
1:H:178:SER:OG	1:H:181:ASN:ND2	2.25	0.65
1:B:123:GLY:CA	1:G:300:ARG:HH21	2.04	0.65
1:C:23:THR:HG21	1:C:84:ILE:CG2	2.26	0.65
1:C:198:LYS:HB2	1:C:236:TYR:HE2	1.60	0.65
1:C:384:MET:SD	1:C:421:LEU:CA	2.85	0.65
1:H:384:MET:HG2	1:H:424:CYS:SG	2.36	0.65
2:L:155:ARG:HB2	2:L:155:ARG:CZ	2.26	0.65
1:B:345:LEU:O	1:B:345:LEU:HD22	1.97	0.65
1:E:263:MET:HA	1:E:289:HIS:HB3	1.78	0.65
1:F:180:LYS:HD3	1:F:217:PHE:CZ	2.32	0.65
1:H:345:LEU:O	1:H:345:LEU:HD22	1.97	0.65
2:J:146:GLY:O	2:J:176:PHE:CZ	2.50	0.65
1:B:136:ARG:O	1:B:136:ARG:HD3	1.96	0.65
1:E:421:LEU:O	1:E:425:VAL:CG2	2.39	0.65
1:F:38:ARG:CZ	1:F:95:PHE:CE1	2.79	0.65
1:C:166:MET:SD	1:C:196:PHE:CE2	2.84	0.65
1:D:209:GLN:HE22	1:D:214:ARG:HD3	1.60	0.65
1:D:329:VAL:HG11	1:D:379:ILE:CG2	2.12	0.65
1:F:316:ARG:HD3	1:F:365:TRP:CE3	2.30	0.65
2:N:169:LEU:HD12	2:N:169:LEU:N	2.12	0.65
2:P:74:ARG:HH12	2:P:102:GLU:HA	1.62	0.65
1:C:384:MET:CE	1:C:421:LEU:CD1	0.73	0.65
1:D:215:PHE:CE1	1:D:237:LEU:CB	2.67	0.65
1:F:263:MET:CA	1:F:289:HIS:HB3	2.22	0.65
1:H:174:LYS:CB	1:H:200:ASP:OD2	2.45	0.65
1:B:31:THR:HG23	1:B:138:PRO:CG	2.26	0.64
1:B:345:LEU:O	1:B:345:LEU:HD13	1.97	0.64
1:C:345:LEU:HD21	1:C:359:VAL:HG22	1.78	0.64
1:E:328:VAL:CG1	1:E:336:LYS:HE2	2.27	0.64
1:E:344:ASP:OD2	1:E:357:ARG:NH1	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:157:ALA:HB2	2:L:169:LEU:HD22	1.79	0.64
1:B:104:LEU:HD11	1:G:175:LEU:CD2	2.27	0.64
1:C:85:GLU:HG2	1:C:86:PRO:HD2	1.79	0.64
1:E:428:ARG:NE	2:I:97:ARG:HG2	2.12	0.64
1:F:215:PHE:CD1	1:F:237:LEU:HD21	2.30	0.64
1:F:244:CYS:O	1:F:248:MET:HG3	1.97	0.64
1:G:204:ASN:O	1:G:206:GLN:N	2.30	0.64
1:G:316:ARG:HH11	1:G:346:MET:HA	1.63	0.64
2:K:74:ARG:NH1	2:K:102:GLU:HA	2.12	0.64
2:M:74:ARG:HH12	2:M:102:GLU:HA	1.63	0.64
2:M:95:GLU:OE2	2:M:122:ARG:CD	2.30	0.64
2:N:164:THR:O	2:N:168:ARG:HB2	1.98	0.64
1:E:426:GLN:HE21	1:E:426:GLN:HA	1.61	0.64
1:F:81:CYS:CB	1:F:98:ILE:CD1	2.75	0.64
1:F:355:ARG:N	2:P:159:GLU:OE2	2.30	0.64
1:H:345:LEU:O	1:H:345:LEU:HD13	1.97	0.64
2:J:114:ARG:O	2:J:116:LEU:N	2.31	0.64
2:L:149:VAL:N	2:L:176:PHE:CE2	2.65	0.64
1:B:22:TYR:CD2	1:B:48:PRO:C	2.71	0.64
1:C:296:ALA:HA	1:C:299:ASP:OD1	1.98	0.64
1:D:199:ASP:HB3	1:D:203:ILE:HD13	1.79	0.64
2:P:17:LEU:O	2:P:17:LEU:HD22	1.97	0.64
1:C:290:ILE:HG21	1:C:315:LEU:HD21	1.80	0.64
1:C:353:ALA:HB1	1:C:360:PHE:C	2.18	0.64
1:G:201:GLU:CD	1:G:201:GLU:H	2.00	0.64
2:L:134:LEU:HD13	2:L:134:LEU:C	2.17	0.64
1:B:22:TYR:HD2	1:B:48:PRO:HB2	0.73	0.64
1:B:400:GLY:CA	1:B:404:LEU:CD1	2.75	0.64
1:C:435:TYR:CE2	2:O:133:ARG:CZ	2.79	0.64
1:D:38:ARG:NH1	1:D:95:PHE:HZ	1.94	0.64
1:D:47:ALA:HB1	1:D:94:TYR:CZ	2.33	0.64
1:D:142:VAL:HG22	1:D:317:LEU:HD21	1.80	0.64
1:G:134:ASP:CG	1:G:360:PHE:HD2	1.97	0.64
1:H:222:ILE:CD1	1:H:235:HIS:N	2.58	0.64
1:B:138:PRO:C	1:B:140:ALA:H	2.01	0.64
1:D:86:PRO:HA	1:D:94:TYR:CB	2.27	0.64
1:D:178:SER:N	1:D:181:ASN:CG	2.51	0.64
1:D:290:ILE:HG21	1:D:315:LEU:HD21	1.80	0.64
1:E:68:THR:HG22	1:E:72:THR:HG1	1.63	0.64
1:F:430:GLU:OE1	1:F:432:ARG:HD3	1.97	0.64
1:G:241:ALA:HA	1:G:250:ARG:HH12	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:257:LEU:O	1:G:259:MET:HE3	1.97	0.64
2:J:163:LEU:C	2:J:163:LEU:HD23	2.18	0.64
2:J:176:PHE:O	2:J:183:ARG:HD3	1.97	0.64
2:M:56:PRO:HA	2:M:59:GLN:HB3	1.79	0.64
1:E:263:MET:HB3	1:E:289:HIS:HB3	1.80	0.64
1:F:214:ARG:HB3	1:F:214:ARG:NH1	2.10	0.64
2:J:171:ALA:HB1	2:J:175:GLN:OE1	1.98	0.64
2:L:15:GLN:HE21	2:L:15:GLN:H	1.44	0.64
1:C:180:LYS:HG2	1:D:157:ASP:OD1	1.95	0.64
1:D:353:ALA:HA	1:D:359:VAL:HG12	0.68	0.64
1:F:286:VAL:O	1:F:287:LEU:O	2.16	0.64
1:G:408:TRP:HE3	1:G:408:TRP:O	1.80	0.64
2:O:169:LEU:HB3	2:O:173:GLY:HA3	1.79	0.64
1:B:382:TRP:CE3	1:B:382:TRP:HA	2.32	0.64
1:C:241:ALA:HB3	1:C:247:MET:HB2	1.80	0.64
1:C:384:MET:CE	1:C:421:LEU:HD12	0.44	0.64
1:G:182:TYR:OH	1:G:199:ASP:CG	2.35	0.64
1:G:197:THR:OG1	1:G:235:HIS:CE1	2.51	0.64
1:H:174:LYS:HE3	1:H:200:ASP:CG	2.07	0.64
1:H:385:PRO:CB	1:H:434:LEU:CD2	2.76	0.64
1:B:122:PHE:CZ	1:B:131:ARG:HA	2.29	0.63
1:D:85:GLU:OE1	1:D:86:PRO:O	2.17	0.63
1:D:137:PHE:CD2	1:D:317:LEU:CD1	2.52	0.63
1:F:385:PRO:C	1:F:434:LEU:HD21	2.16	0.63
2:J:85:TYR:CZ	2:J:93:LEU:CD2	2.73	0.63
2:L:131:PHE:HE2	2:L:143:ARG:HA	1.63	0.63
2:O:174:LEU:HD21	2:O:186:ILE:HG22	1.80	0.63
1:E:332:LEU:CA	1:E:335:ASP:OD2	2.43	0.63
1:F:151:GLY:HA2	1:F:369:PRO:HB2	1.80	0.63
1:F:257:LEU:CD1	1:F:259:MET:CE	2.76	0.63
1:F:328:VAL:CG2	1:F:336:LYS:NZ	0.48	0.63
1:F:387:LEU:HD13	1:F:397:LEU:HD11	1.81	0.63
2:K:183:ARG:NH2	2:K:183:ARG:HG3	2.14	0.63
1:B:290:ILE:HG21	1:B:315:LEU:HD21	1.80	0.63
1:C:184:ARG:HB3	2:J:49:PHE:CZ	2.33	0.63
1:C:384:MET:SD	1:C:421:LEU:N	2.71	0.63
1:D:140:ALA:CB	1:F:139:VAL:O	2.46	0.63
1:D:219:ALA:HB3	1:D:257:LEU:HD11	1.81	0.63
1:E:241:ALA:HB3	1:E:247:MET:CB	2.28	0.63
1:F:309:ARG:HB2	1:F:309:ARG:HH11	1.63	0.63
1:G:301:GLN:OE1	1:G:301:GLN:HA	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:290:ILE:HG21	1:H:315:LEU:HD21	1.80	0.63
2:L:99:LEU:CD1	2:L:103:GLN:CB	2.76	0.63
2:M:28:TRP:HE1	2:M:62:ILE:CG2	2.12	0.63
2:N:15:GLN:OE1	2:N:15:GLN:N	2.31	0.63
1:A:66:VAL:HG13	1:A:68:THR:H	1.63	0.63
1:F:316:ARG:CD	1:F:365:TRP:CH2	2.80	0.63
1:H:190:LEU:HD13	1:H:190:LEU:C	2.19	0.63
1:B:375:ALA:HB2	1:B:391:PHE:HE2	1.63	0.63
1:D:178:SER:O	1:D:182:TYR:N	2.28	0.63
1:E:295:HIS:O	1:E:299:ASP:OD2	2.16	0.63
1:F:302:ARG:HH11	1:F:302:ARG:CB	2.11	0.63
2:L:85:TYR:CE1	2:L:112:LEU:HD11	2.33	0.63
1:C:222:ILE:CG1	1:C:234:GLY:HA2	2.28	0.63
1:F:201:GLU:N	1:F:201:GLU:OE1	2.31	0.63
1:G:66:VAL:HG13	1:G:68:THR:H	1.63	0.63
1:H:433:ASP:CA	1:H:437:GLU:OE2	2.39	0.63
2:M:15:GLN:C	2:M:17:LEU:H	2.01	0.63
2:M:116:LEU:CB	2:M:120:GLN:NE2	2.53	0.63
1:B:122:PHE:CZ	1:B:130:LEU:C	2.72	0.63
1:C:427:ALA:CB	1:C:441:ILE:HD12	2.28	0.63
1:D:55:ALA:HB1	1:D:79:GLY:O	1.98	0.63
1:F:387:LEU:HD13	1:F:397:LEU:HD21	1.79	0.63
2:O:146:GLY:C	2:O:176:PHE:HE1	1.74	0.63
1:B:34:LEU:CD1	1:B:82:TYR:CZ	2.56	0.63
1:C:145:PHE:CD2	1:C:317:LEU:HB3	2.34	0.63
1:C:241:ALA:N	1:C:247:MET:HE3	2.14	0.63
1:E:190:LEU:HD22	1:E:197:THR:CG2	2.29	0.63
1:E:241:ALA:CB	1:E:247:MET:HE3	2.28	0.63
1:F:87:VAL:HG23	1:F:94:TYR:HA	1.79	0.63
1:G:382:TRP:HD1	1:G:459:TRP:CB	2.12	0.63
2:K:29:LEU:CB	2:K:86:GLN:NE2	2.61	0.63
1:B:381:VAL:HG21	1:B:455:ALA:HB1	1.80	0.63
1:B:427:ALA:HB1	1:B:441:ILE:CD1	2.28	0.63
1:C:292:ARG:HG3	1:C:292:ARG:O	1.99	0.63
1:E:184:ARG:HD3	2:P:49:PHE:CE2	2.33	0.63
1:F:131:ARG:HH11	1:F:307:HIS:HD2	1.47	0.63
1:F:237:LEU:O	1:F:263:MET:HG3	1.98	0.63
1:G:187:TYR:CE2	1:G:191:ARG:HD3	2.31	0.63
2:K:110:LEU:CD1	2:K:116:LEU:HD11	2.29	0.63
1:A:290:ILE:HG21	1:A:315:LEU:HD21	1.80	0.62
1:F:81:CYS:CA	1:F:98:ILE:HD13	2.27	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:290:ILE:HD13	1:F:315:LEU:HD11	1.81	0.62
1:H:379:ILE:HD12	1:H:387:LEU:HD11	1.79	0.62
2:J:171:ALA:HA	2:J:175:GLN:CB	2.14	0.62
2:N:16:GLU:O	2:N:16:GLU:HG2	1.98	0.62
1:F:135:ILE:HG22	1:F:310:VAL:HG22	1.81	0.62
1:F:316:ARG:CD	1:F:365:TRP:CZ3	2.72	0.62
1:G:187:TYR:CE1	1:G:191:ARG:CD	2.82	0.62
1:H:292:ARG:HE	1:H:324:HIS:CB	2.11	0.62
2:J:18:LEU:HD21	2:J:38:LEU:CD1	2.28	0.62
2:O:96:LEU:CD2	2:O:107:CYS:SG	2.86	0.62
1:C:174:LYS:HA	1:C:200:ASP:OD2	1.99	0.62
1:D:141:LEU:HD12	1:D:141:LEU:O	1.97	0.62
1:E:261:ILE:HD12	1:E:287:LEU:HD12	1.81	0.62
1:G:39:PHE:HZ	1:G:50:ALA:CB	2.13	0.62
1:G:197:THR:C	1:G:235:HIS:HE1	1.93	0.62
1:H:385:PRO:CA	1:H:434:LEU:CD2	2.76	0.62
2:M:85:TYR:OH	2:M:93:LEU:HD21	2.00	0.62
1:A:157:ASP:CA	1:D:180:LYS:CD	2.78	0.62
1:B:22:TYR:CZ	1:B:49:GLU:CA	2.82	0.62
1:B:25:ASP:O	1:B:26:TYR:HB3	1.99	0.62
1:F:198:LYS:HD2	1:F:236:TYR:CD2	2.27	0.62
1:C:191:ARG:HG2	1:C:191:ARG:HH11	1.63	0.62
1:G:29:LYS:C	1:G:31:THR:N	2.53	0.62
1:G:236:TYR:HB3	1:G:263:MET:CG	2.30	0.62
1:G:382:TRP:CE3	1:G:461:GLU:HG3	2.34	0.62
1:H:131:ARG:NH2	1:H:301:GLN:O	2.32	0.62
2:K:38:LEU:CD1	2:K:43:LEU:HD11	2.29	0.62
2:K:110:LEU:HA	2:K:113:GLU:HG3	1.81	0.62
2:P:157:ALA:O	2:P:166:ARG:NH2	2.33	0.62
1:B:29:LYS:HZ3	1:B:29:LYS:HB2	1.65	0.62
1:B:131:ARG:NH2	1:B:301:GLN:O	2.32	0.62
1:C:179:ALA:HB1	1:C:217:PHE:CD2	2.33	0.62
1:H:38:ARG:CZ	1:H:95:PHE:CZ	2.83	0.62
1:H:332:LEU:CA	1:H:335:ASP:OD2	2.45	0.62
2:L:18:LEU:HD12	2:L:52:THR:HG21	1.81	0.62
2:O:110:LEU:CD1	2:O:116:LEU:HD11	2.29	0.62
2:P:17:LEU:HD11	2:P:34:ALA:HA	1.82	0.62
1:B:66:VAL:HG13	1:B:68:THR:H	1.63	0.62
1:C:236:TYR:HD1	1:C:261:ILE:HD13	1.63	0.62
1:C:353:ALA:HB1	1:C:360:PHE:O	1.99	0.62
1:D:329:VAL:HG12	1:D:379:ILE:HG22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:338:SER:HA	1:E:357:ARG:O	2.00	0.62
1:E:345:LEU:HD23	1:E:351:ILE:CD1	2.18	0.62
1:F:109:SER:O	1:F:145:PHE:CZ	2.49	0.62
1:F:290:ILE:HG21	1:F:315:LEU:HD11	1.81	0.62
1:H:408:TRP:CH2	2:I:23:ARG:CB	2.83	0.62
1:A:131:ARG:NH2	1:A:301:GLN:O	2.32	0.62
1:C:29:LYS:O	1:C:32:ASP:HB2	1.99	0.62
1:C:66:VAL:HG13	1:C:68:THR:H	1.63	0.62
1:C:211:TRP:CE3	1:C:250:ARG:CD	2.83	0.62
1:E:131:ARG:NH2	1:E:301:GLN:O	2.32	0.62
1:E:292:ARG:HH22	1:E:326:GLY:N	1.97	0.62
1:F:72:THR:HB	1:F:74:MET:CE	2.30	0.62
1:F:246:GLU:OE2	1:F:250:ARG:NE	2.32	0.62
1:F:385:PRO:HD3	1:F:442:LEU:HD11	1.81	0.62
1:G:375:ALA:CB	1:G:391:PHE:HE2	2.13	0.62
2:K:38:LEU:O	2:K:43:LEU:CD2	2.48	0.62
1:B:123:GLY:C	1:G:300:ARG:NH2	2.52	0.62
1:C:131:ARG:NH2	1:C:301:GLN:O	2.32	0.62
1:E:261:ILE:HD12	1:E:287:LEU:CD1	2.30	0.62
1:F:66:VAL:HG13	1:F:68:THR:H	1.63	0.62
1:G:24:PRO:C	1:G:25:ASP:OD1	2.38	0.62
1:G:328:VAL:HA	1:G:331:LYS:HD2	1.82	0.62
1:G:382:TRP:CE3	1:G:461:GLU:OE2	2.53	0.62
1:G:408:TRP:HZ3	2:K:22:ARG:C	2.01	0.62
1:D:131:ARG:NH2	1:D:301:GLN:O	2.32	0.62
1:F:199:ASP:OD2	1:F:199:ASP:N	2.32	0.62
1:F:257:LEU:HD13	1:F:259:MET:HE3	1.82	0.62
1:F:385:PRO:O	1:F:434:LEU:HD21	1.96	0.62
1:H:68:THR:CG2	1:H:72:THR:OG1	2.47	0.62
1:H:90:GLU:CG	1:H:93:SER:HB3	2.30	0.62
1:H:462:ILE:HG22	1:H:462:ILE:O	2.00	0.62
2:K:16:GLU:C	2:K:18:LEU:H	2.03	0.62
2:K:92:LEU:O	2:K:96:LEU:HG	1.99	0.62
2:L:157:ALA:O	2:L:160:ARG:HB2	2.00	0.62
1:B:31:THR:C	1:B:33:LEU:H	1.96	0.61
1:C:345:LEU:HD21	1:C:359:VAL:CG2	2.30	0.61
1:D:179:ALA:C	1:D:217:PHE:CD2	2.73	0.61
1:H:87:VAL:HG22	1:H:95:PHE:CE2	2.34	0.61
2:J:163:LEU:HD23	2:J:163:LEU:O	2.00	0.61
2:J:167:SER:C	2:J:169:LEU:H	2.03	0.61
1:C:435:TYR:CZ	2:O:133:ARG:NH1	2.67	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:84:ILE:HD13	1:D:84:ILE:O	2.00	0.61
1:F:38:ARG:NH1	1:F:95:PHE:HZ	1.92	0.61
1:F:177:LEU:HA	1:F:181:ASN:ND2	2.15	0.61
1:F:385:PRO:CD	1:F:442:LEU:HD11	2.30	0.61
2:L:86:GLN:NE2	2:L:86:GLN:HA	2.15	0.61
2:L:99:LEU:HD11	2:L:103:GLN:CA	2.30	0.61
2:L:152:GLN:HG2	2:L:156:LEU:HD12	1.82	0.61
1:A:157:ASP:OD1	1:D:180:LYS:HG3	2.01	0.61
1:B:381:VAL:CG2	1:B:455:ALA:HB1	2.31	0.61
1:C:115:THR:CG2	1:F:201:GLU:HB2	2.30	0.61
1:D:397:LEU:HD12	1:D:421:LEU:HD21	1.80	0.61
1:F:306:ILE:O	1:F:306:ILE:HG12	1.99	0.61
1:F:328:VAL:CG1	1:F:336:LYS:HE2	1.86	0.61
1:G:201:GLU:OE1	1:G:201:GLU:N	2.33	0.61
2:O:105:SER:O	2:O:109:GLN:HG2	2.00	0.61
1:C:116:SER:CA	1:F:202:ASN:HD22	2.06	0.61
1:D:47:ALA:HB1	1:D:94:TYR:OH	2.00	0.61
1:E:63:TRP:CZ3	1:E:74:MET:HB3	2.34	0.61
1:F:109:SER:N	1:F:145:PHE:HE1	1.95	0.61
1:F:236:TYR:CD1	1:F:289:HIS:CE1	2.83	0.61
1:G:443:ARG:HG2	1:G:456:LEU:HD13	1.82	0.61
2:L:114:ARG:NH2	2:L:175:GLN:NE2	2.47	0.61
1:B:23:THR:O	1:B:23:THR:OG1	2.16	0.61
1:C:328:VAL:HG11	1:C:336:LYS:HE2	1.82	0.61
1:H:90:GLU:HG2	1:H:93:SER:HB3	1.81	0.61
1:H:292:ARG:HG3	1:H:292:ARG:O	2.00	0.61
2:L:85:TYR:CE1	2:L:112:LEU:CD1	2.83	0.61
2:L:87:GLU:O	2:L:87:GLU:HG2	2.01	0.61
2:L:114:ARG:NH2	2:L:175:GLN:HE21	1.99	0.61
2:L:135:PRO:O	2:L:136:LYS:HB3	2.01	0.61
2:L:177:ALA:HA	2:L:183:ARG:NH2	2.15	0.61
1:B:136:ARG:HD3	1:B:136:ARG:C	2.19	0.61
1:C:325:SER:OG	1:C:342:PHE:CZ	2.53	0.61
1:D:116:SER:HA	1:E:202:ASN:HD21	1.62	0.61
1:F:382:TRP:CZ2	1:F:456:LEU:HA	2.36	0.61
1:G:203:ILE:O	1:G:203:ILE:HG22	2.00	0.61
1:C:82:TYR:HE1	1:C:97:PHE:HB3	0.46	0.61
1:C:82:TYR:CD1	1:C:97:PHE:O	2.53	0.61
1:C:363:GLN:NE2	1:C:365:TRP:CD1	2.68	0.61
1:C:384:MET:HE2	1:C:421:LEU:CA	2.27	0.61
1:G:430:GLU:O	2:M:67:GLN:NE2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:38:ARG:NH2	1:H:95:PHE:HZ	1.97	0.61
1:E:328:VAL:CG1	1:E:336:LYS:CE	2.78	0.61
1:F:237:LEU:C	1:F:263:MET:CG	2.65	0.61
1:G:462:ILE:O	1:G:462:ILE:HG22	2.01	0.61
1:C:28:PRO:HD3	1:C:82:TYR:HE2	1.65	0.61
1:D:28:PRO:HB3	1:D:82:TYR:CE2	2.35	0.61
1:E:136:ARG:HD3	1:E:136:ARG:O	2.01	0.61
1:G:359:VAL:HG12	1:G:359:VAL:O	2.01	0.61
2:J:149:VAL:HG11	2:J:172:ARG:CD	2.31	0.61
1:A:122:PHE:CE2	1:H:297:VAL:HG21	2.29	0.61
1:A:355:ARG:CB	2:L:159:GLU:OE2	2.48	0.61
1:B:24:PRO:O	1:B:26:TYR:N	2.34	0.61
1:D:168:GLY:O	1:D:398:GLN:HA	2.01	0.61
1:F:177:LEU:HB3	1:F:181:ASN:HB2	1.82	0.61
1:F:181:ASN:OD1	1:F:181:ASN:N	2.34	0.61
1:F:290:ILE:O	1:F:290:ILE:HG22	2.01	0.61
1:G:240:THR:CA	1:G:247:MET:HE1	2.31	0.61
1:H:28:PRO:HG3	1:H:82:TYR:CE2	2.36	0.61
2:I:68:VAL:HA	2:I:71:SER:HB3	1.82	0.61
2:J:144:HIS:ND1	2:J:145:PRO:HD2	2.15	0.61
2:J:166:ARG:O	2:J:166:ARG:NH2	2.34	0.61
2:K:146:GLY:O	2:K:176:PHE:CZ	2.53	0.61
2:L:146:GLY:HA2	2:L:176:PHE:CD1	2.36	0.61
2:P:190:LEU:O	2:P:193:LEU:HB3	2.00	0.61
1:B:102:LEU:O	1:B:102:LEU:HD12	2.01	0.60
1:C:197:THR:H	1:C:235:HIS:HB2	1.66	0.60
1:C:384:MET:CE	1:C:421:LEU:HA	2.16	0.60
1:D:201:GLU:OE2	1:D:291:HIS:CE1	2.54	0.60
1:D:326:GLY:O	1:D:375:ALA:HB1	2.00	0.60
1:F:352:GLU:OE1	1:F:352:GLU:N	2.33	0.60
1:F:379:ILE:CB	1:F:383:HIS:CE1	2.84	0.60
1:G:133:GLU:CG	1:G:360:PHE:HE2	2.14	0.60
1:G:134:ASP:OD2	1:G:360:PHE:CE2	2.48	0.60
1:G:299:ASP:OD2	1:G:308:PHE:N	2.34	0.60
2:M:61:GLN:NE2	2:M:90:SER:HB2	2.15	0.60
2:P:56:PRO:HA	2:P:59:GLN:HG2	1.83	0.60
1:C:359:VAL:HG12	1:C:359:VAL:O	2.01	0.60
1:F:244:CYS:O	1:F:248:MET:HE2	2.01	0.60
1:E:219:ALA:HB1	1:E:257:LEU:HD13	1.66	0.60
1:E:255:LYS:HD3	1:E:284:ASN:OD1	2.02	0.60
1:E:384:MET:CE	1:E:421:LEU:CD1	2.79	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:257:LEU:HD13	1:F:259:MET:HE2	1.81	0.60
1:F:446:GLY:O	1:F:448:TRP:N	2.35	0.60
2:K:17:LEU:HA	2:K:20:GLN:OE1	2.00	0.60
2:L:85:TYR:CD1	2:L:112:LEU:HD21	2.28	0.60
2:L:149:VAL:CG1	2:L:176:PHE:CZ	2.79	0.60
2:L:186:ILE:HG23	2:L:186:ILE:O	2.01	0.60
1:B:313:LYS:HE3	1:B:345:LEU:CD1	2.31	0.60
1:C:430:GLU:HG3	2:O:67:GLN:NE2	2.16	0.60
1:E:190:LEU:HD22	1:E:197:THR:HG23	1.83	0.60
1:F:175:LEU:N	1:F:175:LEU:HD12	2.16	0.60
1:F:203:ILE:O	1:F:203:ILE:HG22	2.00	0.60
1:F:250:ARG:HH11	1:F:250:ARG:CB	2.13	0.60
1:F:385:PRO:CB	1:F:434:LEU:HD21	2.30	0.60
1:G:182:TYR:OH	1:G:199:ASP:HA	2.01	0.60
1:E:143:LYS:O	1:E:143:LYS:HD2	2.00	0.60
1:H:28:PRO:HG3	1:H:82:TYR:HE2	1.66	0.60
1:C:136:ARG:HG2	1:C:363:GLN:HB2	1.84	0.60
1:E:190:LEU:CD2	1:E:197:THR:CG2	2.79	0.60
1:F:266:PHE:HZ	1:F:311:LEU:HD13	1.66	0.60
1:G:328:VAL:HG11	1:G:336:LYS:HZ3	1.67	0.60
2:L:81:VAL:O	2:L:81:VAL:HG12	2.02	0.60
1:D:243:THR:HG21	1:E:279:LYS:HE3	1.83	0.60
1:D:359:VAL:HG12	1:D:359:VAL:O	2.01	0.60
1:E:187:TYR:OH	1:E:224:LYS:HD2	2.01	0.60
1:G:427:ALA:HB1	1:G:441:ILE:CD1	2.30	0.60
2:J:110:LEU:O	2:J:114:ARG:HB2	2.01	0.60
2:K:186:ILE:O	2:K:186:ILE:HG23	2.01	0.60
2:O:110:LEU:HD13	2:O:110:LEU:C	2.22	0.60
1:C:212:ARG:NH1	1:C:253:PHE:HE1	1.93	0.60
1:C:384:MET:HE3	1:C:421:LEU:HD11	1.32	0.60
1:F:328:VAL:CG1	1:F:336:LYS:NZ	2.35	0.60
1:H:382:TRP:HD1	1:H:459:TRP:HB2	1.65	0.60
2:K:93:LEU:HA	2:K:96:LEU:CD2	2.32	0.60
2:L:114:ARG:HH11	2:L:172:ARG:CZ	2.03	0.60
1:B:85:GLU:CD	1:B:86:PRO:O	2.39	0.60
1:C:222:ILE:O	1:C:225:SER:OG	2.19	0.60
1:E:134:ASP:HB3	1:E:361:PHE:CE2	2.37	0.60
1:E:309:ARG:HB2	1:E:309:ARG:NH1	2.16	0.60
1:F:180:LYS:CD	1:F:217:PHE:CZ	2.84	0.60
1:H:28:PRO:CB	1:H:82:TYR:HE2	2.15	0.60
2:K:183:ARG:HA	2:K:186:ILE:HG22	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:157:ALA:O	2:P:166:ARG:HD2	2.02	0.60
1:A:157:ASP:HB3	1:D:180:LYS:CD	2.23	0.60
1:A:157:ASP:CB	1:D:180:LYS:CD	2.78	0.60
1:C:116:SER:CB	1:F:202:ASN:HD22	2.13	0.60
1:D:33:LEU:HD21	1:D:141:LEU:HD23	1.83	0.60
1:D:384:MET:SD	1:D:421:LEU:CA	2.71	0.60
1:E:359:VAL:HG12	1:E:359:VAL:O	2.01	0.60
1:F:332:LEU:C	1:F:335:ASP:OD2	2.40	0.60
1:A:184:ARG:HH11	2:N:56:PRO:HG2	1.67	0.59
1:G:194:LEU:HD21	1:G:414:ALA:HA	1.84	0.59
1:B:106:GLU:CD	1:G:204:ASN:C	2.54	0.59
1:B:155:GLU:OE2	1:B:322:HIS:NE2	2.35	0.59
1:D:180:LYS:HB3	1:D:180:LYS:HZ3	1.65	0.59
1:F:198:LYS:CD	1:F:236:TYR:HD2	2.11	0.59
1:G:190:LEU:HD11	1:G:233:LYS:HD2	1.83	0.59
1:G:384:MET:HE3	1:G:421:LEU:N	1.65	0.59
1:H:292:ARG:NE	1:H:324:HIS:C	2.55	0.59
2:J:18:LEU:CD2	2:J:38:LEU:HD11	2.32	0.59
2:L:154:TRP:CZ2	2:L:185:LEU:HB3	2.33	0.59
2:O:56:PRO:HA	2:O:59:GLN:HG2	1.85	0.59
1:B:116:SER:CA	1:G:202:ASN:HD22	2.12	0.59
1:D:90:GLU:CG	1:D:93:SER:HB3	2.32	0.59
1:E:292:ARG:HD3	1:E:308:PHE:HE2	1.64	0.59
1:G:38:ARG:NH2	1:G:95:PHE:CZ	2.66	0.59
1:G:384:MET:HE1	1:G:421:LEU:CD1	2.27	0.59
1:H:155:GLU:OE2	1:H:322:HIS:NE2	2.36	0.59
1:H:180:LYS:CB	2:I:55:GLU:OE2	2.49	0.59
2:J:81:VAL:O	2:J:81:VAL:HG12	2.02	0.59
2:K:99:LEU:CG	2:K:104:ARG:HG2	2.31	0.59
1:E:142:VAL:HG22	1:E:317:LEU:HD21	1.84	0.59
1:E:263:MET:CA	1:E:289:HIS:HB3	2.32	0.59
1:G:211:TRP:CE3	1:G:250:ARG:CG	2.83	0.59
2:J:141:PHE:CD1	2:J:147:ASP:O	2.49	0.59
1:B:109:SER:O	1:B:145:PHE:HZ	1.84	0.59
1:C:155:GLU:OE2	1:C:322:HIS:NE2	2.35	0.59
1:C:435:TYR:CZ	2:O:133:ARG:NH2	2.67	0.59
1:D:90:GLU:HG2	1:D:93:SER:HB3	1.83	0.59
1:D:216:LEU:HD12	1:D:216:LEU:O	2.02	0.59
1:D:384:MET:N	1:D:385:PRO:HD2	2.17	0.59
2:I:97:ARG:HA	2:I:104:ARG:HD3	1.84	0.59
2:J:36:GLN:HA	2:J:36:GLN:OE1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:VAL:O	1:F:139:VAL:HG12	2.03	0.59
1:G:28:PRO:HB3	1:G:32:ASP:OD2	2.01	0.59
2:L:14:ARG:HD2	2:L:14:ARG:C	2.22	0.59
1:B:346:MET:HE2	1:B:371:VAL:HG13	1.84	0.59
1:B:381:VAL:O	1:B:381:VAL:HG23	2.01	0.59
1:C:160:ASN:HA	1:C:162:TYR:HE2	1.67	0.59
1:D:143:LYS:HE2	1:F:107:GLU:OE2	2.03	0.59
1:E:292:ARG:HG3	1:E:295:HIS:CD2	2.38	0.59
1:F:177:LEU:CB	1:F:181:ASN:HB2	2.32	0.59
1:F:302:ARG:HH11	1:F:302:ARG:HG2	1.66	0.59
1:H:313:LYS:HE3	1:H:345:LEU:CD1	2.32	0.59
1:B:106:GLU:OE1	1:G:204:ASN:O	2.21	0.59
1:C:60:THR:H	1:F:174:LYS:NZ	1.99	0.59
1:C:82:TYR:HD1	1:C:97:PHE:O	1.84	0.59
1:C:146:GLN:HE21	1:C:282:ARG:HH12	1.43	0.59
1:D:82:TYR:HD1	1:D:97:PHE:O	1.80	0.59
2:J:80:HIS:CA	2:J:83:GLU:OE2	2.44	0.59
2:M:120:GLN:N	2:M:120:GLN:OE1	2.35	0.59
1:C:348:GLU:HG3	1:C:350:HIS:H	1.68	0.59
1:E:348:GLU:HG3	1:E:350:HIS:H	1.68	0.59
1:G:241:ALA:HB2	1:G:247:MET:HE2	1.85	0.59
1:G:253:PHE:HE2	1:G:257:LEU:HD12	1.67	0.59
1:G:332:LEU:HD22	1:G:333:GLU:H	1.68	0.59
1:H:384:MET:N	1:H:385:PRO:HD2	2.18	0.59
2:I:166:ARG:NH2	2:I:169:LEU:O	2.36	0.59
2:L:99:LEU:CD1	2:L:103:GLN:HB2	2.33	0.59
2:O:144:HIS:ND1	2:O:145:PRO:HD2	2.18	0.59
2:P:14:ARG:HH21	2:P:16:GLU:HA	1.67	0.59
1:C:384:MET:HE2	1:C:421:LEU:HD12	0.59	0.59
1:F:352:GLU:HA	1:F:362:THR:HG23	1.83	0.59
1:G:404:LEU:HB2	1:G:459:TRP:HH2	1.68	0.59
2:J:114:ARG:O	2:J:116:LEU:HG	2.03	0.59
2:J:140:ASN:HB3	2:J:181:GLY:CA	2.24	0.59
2:K:102:GLU:O	2:K:106:LEU:HB2	2.03	0.59
2:K:149:VAL:CA	2:K:176:PHE:CZ	2.65	0.59
2:M:155:ARG:HG3	2:M:155:ARG:O	2.02	0.59
1:B:400:GLY:C	1:B:404:LEU:HD11	2.22	0.58
1:D:108:GLY:N	1:D:145:PHE:CE1	2.70	0.58
1:D:173:PRO:CG	1:D:177:LEU:HG	2.33	0.58
1:D:348:GLU:HG3	1:D:350:HIS:H	1.67	0.58
1:G:352:GLU:O	1:G:359:VAL:CG1	2.45	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:444:GLU:O	1:G:447:LYS:CG	2.47	0.58
2:J:14:ARG:NH1	2:J:18:LEU:CD2	2.44	0.58
2:J:44:ASN:O	2:J:47:THR:OG1	2.21	0.58
2:L:100:ASP:O	2:L:102:GLU:N	2.36	0.58
2:N:44:ASN:O	2:N:47:THR:OG1	2.20	0.58
2:P:44:ASN:O	2:P:47:THR:OG1	2.21	0.58
1:B:443:ARG:HG3	1:B:443:ARG:HH21	1.67	0.58
1:H:90:GLU:HG2	1:H:93:SER:CB	2.32	0.58
1:B:142:VAL:CG2	1:B:317:LEU:HD21	2.29	0.58
1:B:400:GLY:HA2	1:B:404:LEU:CD1	2.33	0.58
1:E:148:PRO:CA	1:E:319:GLY:HA2	2.33	0.58
1:F:190:LEU:HD11	1:F:233:LYS:HB3	1.83	0.58
1:F:316:ARG:HH22	1:F:370:GLY:N	1.98	0.58
1:G:241:ALA:CB	1:G:247:MET:CE	2.80	0.58
1:G:328:VAL:HG12	1:G:331:LYS:HD3	1.85	0.58
1:G:385:PRO:CB	1:G:434:LEU:CD2	2.82	0.58
2:J:168:ARG:HG3	2:J:168:ARG:O	2.03	0.58
1:D:215:PHE:CZ	1:D:237:LEU:HB3	2.38	0.58
1:F:257:LEU:CD1	1:F:259:MET:HE3	2.33	0.58
1:F:264:HIS:N	1:F:289:HIS:O	2.36	0.58
1:G:155:GLU:OE2	1:G:322:HIS:NE2	2.35	0.58
1:G:384:MET:CE	1:G:420:ALA:O	2.49	0.58
2:I:74:ARG:NH1	2:I:101:GLN:OE1	2.36	0.58
1:B:83:HIS:CB	1:B:97:PHE:CD2	2.84	0.58
1:B:348:GLU:HG3	1:B:350:HIS:H	1.68	0.58
1:C:427:ALA:HB1	1:C:441:ILE:HD12	1.83	0.58
1:E:328:VAL:HG11	1:E:336:LYS:CE	2.31	0.58
1:H:348:GLU:HG3	1:H:350:HIS:H	1.68	0.58
1:H:462:ILE:HD12	1:H:462:ILE:N	2.18	0.58
2:M:166:ARG:NH2	2:M:169:LEU:O	2.37	0.58
1:D:201:GLU:HB2	1:E:115:THR:HG22	1.84	0.58
1:F:215:PHE:CE1	1:F:237:LEU:HB3	2.39	0.58
1:G:348:GLU:HG3	1:G:350:HIS:H	1.68	0.58
1:G:384:MET:CE	1:G:421:LEU:CB	2.81	0.58
1:H:385:PRO:CA	1:H:434:LEU:HD21	2.31	0.58
2:L:183:ARG:HA	2:L:186:ILE:HG22	1.86	0.58
1:A:155:GLU:OE2	1:A:322:HIS:NE2	2.35	0.58
1:B:384:MET:N	1:B:385:PRO:HD2	2.19	0.58
1:D:83:HIS:HB2	1:D:97:PHE:HB2	1.86	0.58
1:F:210:ARG:NH1	1:G:282:ARG:HH12	2.01	0.58
1:F:215:PHE:CE1	1:F:237:LEU:HG	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:384:MET:N	1:F:385:PRO:HD2	2.18	0.58
2:L:21:LEU:HD12	2:L:54:PHE:CE2	2.37	0.58
2:M:22:ARG:NH1	2:M:52:THR:O	2.36	0.58
2:O:110:LEU:HD11	2:O:116:LEU:HD11	1.86	0.58
1:B:122:PHE:HB3	1:G:297:VAL:HG22	1.85	0.58
1:D:68:THR:HG22	1:D:68:THR:O	2.03	0.58
1:D:428:ARG:HD2	1:D:428:ARG:O	2.02	0.58
1:F:435:TYR:CE2	2:P:133:ARG:NH1	2.66	0.58
2:J:32:ALA:HB2	2:J:62:ILE:HB	1.84	0.58
2:K:93:LEU:HA	2:K:96:LEU:CG	2.33	0.58
2:L:84:THR:O	2:L:84:THR:HG22	2.04	0.58
2:P:66:MET:HE3	2:P:67:GLN:HB2	1.86	0.58
1:B:139:VAL:O	1:B:139:VAL:HG12	2.04	0.58
1:D:85:GLU:OE2	1:D:86:PRO:O	2.21	0.58
1:D:90:GLU:HG2	1:D:93:SER:CB	2.34	0.58
1:D:427:ALA:HB3	1:D:434:LEU:CD1	2.34	0.58
1:E:290:ILE:HD12	1:E:320:GLY:HA3	1.85	0.58
1:F:433:ASP:N	1:F:437:GLU:CD	2.56	0.58
1:G:384:MET:CE	1:G:421:LEU:CG	2.81	0.58
2:I:28:TRP:HB3	2:I:87:GLU:HA	1.85	0.58
2:J:84:THR:O	2:J:84:THR:HG22	2.03	0.58
1:B:219:ALA:HB1	1:B:257:LEU:HD22	1.86	0.58
1:C:116:SER:CB	1:F:202:ASN:ND2	2.66	0.58
2:J:28:TRP:HB3	2:J:87:GLU:N	2.18	0.58
2:J:85:TYR:OH	2:J:93:LEU:CD1	2.51	0.58
2:J:157:ALA:CA	2:J:166:ARG:CD	2.45	0.58
2:O:157:ALA:O	2:O:160:ARG:HB2	2.03	0.58
1:C:164:ARG:CB	1:C:425:VAL:CG2	2.75	0.57
1:C:232:ILE:O	1:C:233:LYS:HD2	2.03	0.57
1:E:66:VAL:HG13	1:E:68:THR:H	1.69	0.57
1:G:39:PHE:CD1	1:G:94:TYR:OH	2.57	0.57
2:L:14:ARG:HH11	2:L:18:LEU:HD23	1.63	0.57
2:L:15:GLN:H	2:L:15:GLN:NE2	2.01	0.57
2:L:131:PHE:CE2	2:L:143:ARG:HA	2.39	0.57
1:A:348:GLU:HG3	1:A:350:HIS:H	1.68	0.57
1:B:433:ASP:N	1:B:437:GLU:OE2	2.36	0.57
1:C:87:VAL:CG2	1:C:93:SER:CB	2.83	0.57
1:C:219:ALA:HB1	1:C:257:LEU:HD22	1.86	0.57
1:D:214:ARG:HH11	1:D:214:ARG:CG	2.16	0.57
1:E:211:TRP:CG	1:E:250:ARG:NE	2.72	0.57
1:F:177:LEU:CA	1:F:181:ASN:CB	2.81	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:222:ILE:CD1	1:F:235:HIS:N	2.66	0.57
1:F:387:LEU:HD11	1:F:397:LEU:HD22	0.59	0.57
1:G:297:VAL:HG12	1:G:297:VAL:O	2.02	0.57
1:B:145:PHE:CD2	1:B:317:LEU:HB3	2.39	0.57
1:D:241:ALA:HA	1:D:250:ARG:HH12	1.70	0.57
1:E:198:LYS:HB2	1:E:236:TYR:CG	2.38	0.57
1:F:197:THR:O	1:F:197:THR:OG1	2.22	0.57
2:J:28:TRP:CE3	2:J:88:TRP:N	2.73	0.57
1:D:201:GLU:HB2	1:E:115:THR:CG2	2.33	0.57
1:E:361:PHE:N	1:E:361:PHE:CD2	2.73	0.57
1:G:211:TRP:CG	1:G:250:ARG:HD3	2.39	0.57
1:G:363:GLN:NE2	1:G:365:TRP:NE1	2.46	0.57
2:J:166:ARG:O	2:J:169:LEU:HD11	2.04	0.57
2:K:102:GLU:CA	2:K:106:LEU:HD13	2.33	0.57
1:B:122:PHE:CB	1:G:297:VAL:HG22	2.34	0.57
1:C:83:HIS:CG	1:C:97:PHE:CD2	2.91	0.57
1:C:162:TYR:CD2	1:C:162:TYR:N	2.73	0.57
1:C:184:ARG:CD	2:J:49:PHE:CD2	2.81	0.57
1:E:292:ARG:CD	1:E:308:PHE:CZ	2.87	0.57
1:E:354:ASP:OD2	1:E:357:ARG:HG3	2.03	0.57
1:H:188:GLU:CG	1:H:411:ALA:HB2	2.33	0.57
2:M:182:ALA:O	2:M:186:ILE:HB	2.04	0.57
1:A:119:GLY:O	1:H:294:MET:N	2.33	0.57
1:B:106:GLU:OE2	1:G:205:SER:HB3	1.98	0.57
1:B:400:GLY:HA2	1:B:404:LEU:HD11	1.84	0.57
1:D:380:HIS:CD2	1:D:380:HIS:N	2.73	0.57
1:E:199:ASP:OD2	1:E:199:ASP:N	2.38	0.57
1:E:255:LYS:HD2	1:E:255:LYS:C	2.25	0.57
2:I:44:ASN:O	2:I:47:THR:OG1	2.21	0.57
2:L:17:LEU:O	2:L:17:LEU:HD13	2.04	0.57
2:O:14:ARG:HG2	2:O:38:LEU:CD2	2.35	0.57
2:P:18:LEU:HD12	2:P:21:LEU:HB2	1.86	0.57
2:P:186:ILE:HD12	2:P:189:LEU:HD12	1.86	0.57
1:B:346:MET:CE	1:B:371:VAL:CG1	2.83	0.57
1:C:35:ALA:HA	1:C:135:ILE:HA	1.87	0.57
1:C:145:PHE:HD2	1:C:317:LEU:HB3	1.68	0.57
1:C:384:MET:N	1:C:385:PRO:HD2	2.19	0.57
1:D:155:GLU:OE2	1:D:322:HIS:NE2	2.35	0.57
1:E:194:LEU:HG	1:E:414:ALA:HB1	1.86	0.57
1:G:385:PRO:C	1:G:434:LEU:CD2	2.73	0.57
1:H:23:THR:O	1:H:23:THR:OG1	2.15	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:85:TYR:CD1	2:L:112:LEU:HD11	2.40	0.57
2:M:60:ASN:O	2:M:63:THR:CB	2.53	0.57
2:O:94:TYR:O	2:O:97:ARG:NH1	2.38	0.57
1:A:219:ALA:HB1	1:A:257:LEU:HD22	1.86	0.57
1:C:408:TRP:CE3	2:J:23:ARG:HA	2.27	0.57
1:F:155:GLU:OE2	1:F:322:HIS:NE2	2.35	0.57
1:F:237:LEU:C	1:F:263:MET:HG3	2.25	0.57
1:F:316:ARG:HH11	1:F:346:MET:CA	1.86	0.57
1:G:197:THR:CB	1:G:235:HIS:CE1	2.88	0.57
2:M:155:ARG:HB2	2:M:155:ARG:NH1	2.20	0.57
1:C:79:GLY:HA2	1:C:99:ALA:O	2.05	0.57
1:C:87:VAL:H	1:C:94:TYR:HA	1.69	0.57
1:F:81:CYS:CB	1:F:98:ILE:HD13	2.35	0.57
1:F:205:SER:CB	1:F:211:TRP:HB3	2.31	0.57
2:L:134:LEU:HD22	2:L:135:PRO:CD	2.35	0.57
1:C:87:VAL:HG22	1:C:94:TYR:N	2.20	0.57
1:C:231:GLU:O	1:C:233:LYS:CD	2.40	0.57
1:C:332:LEU:HD22	1:C:333:GLU:H	1.69	0.57
1:C:382:TRP:HD1	1:C:459:TRP:HB3	1.70	0.57
1:C:389:GLU:OE1	1:C:435:TYR:CG	2.58	0.57
1:E:68:THR:HG22	1:E:68:THR:O	2.05	0.57
1:E:282:ARG:HH21	1:H:210:ARG:CZ	2.09	0.57
1:F:177:LEU:C	1:F:178:SER:O	2.40	0.57
1:F:315:LEU:HD23	1:F:323:LEU:HD22	1.87	0.57
1:G:291:HIS:CE1	1:G:293:ALA:HB2	2.40	0.57
1:G:384:MET:N	1:G:385:PRO:HD2	2.20	0.57
1:H:292:ARG:HE	1:H:324:HIS:C	2.08	0.57
1:D:68:THR:HA	1:D:71:LEU:HD12	1.87	0.56
1:E:424:CYS:O	1:E:426:GLN:N	2.38	0.56
1:F:177:LEU:HA	1:F:181:ASN:CB	2.35	0.56
1:F:214:ARG:HH11	1:F:214:ARG:CG	2.18	0.56
1:F:385:PRO:CG	1:F:442:LEU:HD11	2.34	0.56
1:G:204:ASN:O	1:G:205:SER:C	2.43	0.56
1:G:461:GLU:CD	1:G:461:GLU:H	2.06	0.56
2:M:133:ARG:O	2:M:133:ARG:NE	2.38	0.56
1:B:380:HIS:CD2	1:B:380:HIS:H	2.23	0.56
1:B:433:ASP:C	1:B:437:GLU:OE1	2.42	0.56
1:C:382:TRP:HA	1:C:382:TRP:CE3	2.40	0.56
1:D:209:GLN:O	1:D:209:GLN:HG2	2.05	0.56
1:F:382:TRP:HD1	1:F:459:TRP:CB	2.18	0.56
1:G:194:LEU:HD23	1:G:414:ALA:HB1	1.82	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:382:TRP:HD1	1:H:459:TRP:CB	2.18	0.56
1:H:408:TRP:HH2	2:I:23:ARG:HG3	1.62	0.56
2:K:33:ARG:HH21	2:K:66:MET:HG3	1.68	0.56
2:K:105:SER:O	2:K:109:GLN:NE2	2.37	0.56
2:O:175:GLN:O	2:O:175:GLN:HG3	2.03	0.56
1:C:25:ASP:OD1	1:C:25:ASP:N	2.36	0.56
1:C:134:ASP:CG	1:C:360:PHE:CE2	2.78	0.56
1:C:181:ASN:OD1	1:C:181:ASN:N	2.38	0.56
1:C:328:VAL:CG2	1:C:336:LYS:HZ1	2.05	0.56
1:C:380:HIS:N	1:C:380:HIS:CD2	2.73	0.56
1:D:361:PHE:CD2	1:D:361:PHE:N	2.73	0.56
1:E:147:GLY:O	1:E:319:GLY:HA3	2.05	0.56
1:E:354:ASP:HB3	1:E:357:ARG:HB2	1.88	0.56
1:G:197:THR:OG1	1:G:235:HIS:CG	2.57	0.56
1:G:263:MET:HA	1:G:289:HIS:HB3	1.88	0.56
1:G:353:ALA:CB	1:G:361:PHE:HA	2.34	0.56
1:H:382:TRP:CD1	1:H:459:TRP:CB	2.87	0.56
1:H:382:TRP:CH2	1:H:461:GLU:OE2	2.59	0.56
2:J:28:TRP:CH2	2:J:90:SER:CA	2.87	0.56
2:K:74:ARG:HH22	2:K:102:GLU:HG3	1.70	0.56
2:L:85:TYR:CD1	2:L:112:LEU:CD2	2.86	0.56
2:O:174:LEU:HD21	2:O:186:ILE:CG2	2.35	0.56
1:B:122:PHE:CE2	1:B:305:GLY:O	2.59	0.56
1:C:136:ARG:C	1:C:136:ARG:HD3	2.26	0.56
1:E:241:ALA:HB2	1:E:247:MET:HA	1.87	0.56
1:G:385:PRO:CB	1:G:434:LEU:HD21	2.34	0.56
2:J:157:ALA:C	2:J:166:ARG:HD3	2.26	0.56
2:N:149:VAL:HG12	2:N:176:PHE:CE2	2.41	0.56
2:O:177:ALA:HA	2:O:183:ARG:NH2	2.20	0.56
1:A:270:GLY:HA3	1:H:270:GLY:HA3	1.87	0.56
1:C:164:ARG:HB3	1:C:425:VAL:CG2	2.24	0.56
1:F:70:LEU:O	2:J:87:GLU:OE2	2.24	0.56
1:H:445:ALA:O	1:H:447:LYS:N	2.38	0.56
2:J:149:VAL:HG12	2:J:172:ARG:HD2	1.78	0.56
2:K:91:ASP:HA	2:K:94:TYR:HB3	1.88	0.56
1:D:82:TYR:CE1	1:D:97:PHE:O	2.58	0.56
1:D:108:GLY:C	1:D:145:PHE:CE1	2.79	0.56
1:D:174:LYS:O	1:D:175:LEU:HD12	2.06	0.56
1:E:294:MET:O	1:E:294:MET:HG2	2.05	0.56
1:F:216:LEU:HD12	1:F:216:LEU:O	2.05	0.56
1:F:446:GLY:C	1:F:448:TRP:N	2.59	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:361:PHE:CD2	1:G:361:PHE:N	2.73	0.56
1:G:404:LEU:HA	1:G:459:TRP:HZ2	1.71	0.56
2:P:14:ARG:HD2	2:P:14:ARG:C	2.26	0.56
1:C:77:TYR:N	1:C:77:TYR:CD2	2.73	0.56
1:D:178:SER:O	1:D:182:TYR:HB3	2.06	0.56
1:E:241:ALA:CB	1:E:247:MET:HA	2.36	0.56
1:E:354:ASP:N	1:E:359:VAL:O	2.39	0.56
1:F:77:TYR:N	1:F:77:TYR:CD2	2.73	0.56
1:G:430:GLU:OE1	1:G:432:ARG:HD3	2.05	0.56
2:K:74:ARG:HH22	2:K:102:GLU:CG	2.19	0.56
1:B:33:LEU:HD21	1:B:141:LEU:HD23	1.87	0.56
1:B:138:PRO:CD	1:B:141:LEU:HB3	2.34	0.56
1:D:85:GLU:CD	1:D:86:PRO:O	2.44	0.56
1:D:382:TRP:HD1	1:D:459:TRP:HB3	1.69	0.56
1:F:71:LEU:HD23	2:J:87:GLU:HG2	1.87	0.56
1:H:385:PRO:HA	1:H:434:LEU:CD2	2.33	0.56
2:P:28:TRP:HE1	2:P:62:ILE:HG22	1.71	0.56
1:D:38:ARG:NH2	1:D:95:PHE:HZ	2.04	0.56
1:D:211:TRP:HH2	1:D:250:ARG:HA	1.69	0.56
1:E:149:PRO:HD3	1:E:319:GLY:C	2.17	0.56
1:E:351:ILE:O	1:E:362:THR:HG23	2.05	0.56
1:F:406:HIS:ND1	1:F:413:GLY:HA2	2.19	0.56
1:G:39:PHE:CZ	1:G:50:ALA:CB	2.88	0.56
1:G:380:HIS:CE1	1:G:459:TRP:HB3	2.41	0.56
1:B:400:GLY:N	1:B:404:LEU:CD1	2.66	0.56
1:E:35:ALA:CA	1:E:135:ILE:HD13	2.35	0.56
1:E:190:LEU:HD11	1:E:233:LYS:HD2	1.88	0.56
1:F:177:LEU:HD23	1:F:177:LEU:H	1.71	0.56
2:P:94:TYR:O	2:P:97:ARG:NH1	2.39	0.56
1:A:348:GLU:OE1	2:L:122:ARG:NH2	2.31	0.55
1:C:361:PHE:N	1:C:361:PHE:CD2	2.73	0.55
1:D:143:LYS:CE	1:F:107:GLU:OE2	2.55	0.55
1:D:327:THR:HB	1:D:375:ALA:HB1	1.88	0.55
1:D:351:ILE:O	1:D:362:THR:HG23	2.06	0.55
1:E:131:ARG:HH11	1:E:307:HIS:CD2	2.24	0.55
1:H:222:ILE:HD11	1:H:234:GLY:C	2.26	0.55
2:K:17:LEU:HD13	2:K:21:LEU:HD21	1.86	0.55
2:M:144:HIS:ND1	2:M:145:PRO:HD2	2.22	0.55
2:N:14:ARG:C	2:N:14:ARG:HD2	2.26	0.55
2:N:150:ALA:CB	2:N:176:PHE:HD2	2.00	0.55
1:D:201:GLU:CD	1:D:291:HIS:CE1	2.80	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:241:ALA:CA	1:E:247:MET:CE	2.78	0.55
1:F:198:LYS:HA	1:F:235:HIS:CE1	2.41	0.55
2:J:110:LEU:HD21	2:J:114:ARG:HE	1.71	0.55
2:K:16:GLU:O	2:K:18:LEU:N	2.39	0.55
2:P:156:LEU:HB3	2:P:169:LEU:HD22	1.87	0.55
1:C:380:HIS:CE1	1:C:459:TRP:CG	2.94	0.55
1:D:108:GLY:CA	1:D:145:PHE:HE1	2.20	0.55
1:F:384:MET:HE3	1:F:421:LEU:CB	1.94	0.55
1:F:387:LEU:HD13	1:F:397:LEU:CD2	2.22	0.55
2:J:38:LEU:O	2:J:43:LEU:HD22	1.98	0.55
2:K:146:GLY:O	2:K:176:PHE:CE1	2.59	0.55
2:O:190:LEU:O	2:O:191:LEU:C	2.44	0.55
1:B:382:TRP:CD1	1:B:459:TRP:HB2	2.42	0.55
1:C:345:LEU:HD23	1:C:351:ILE:HD13	1.88	0.55
1:D:87:VAL:HG21	1:D:93:SER:HG	1.68	0.55
1:D:171:ILE:HD11	1:D:197:THR:HB	1.88	0.55
1:F:217:PHE:CZ	1:G:157:ASP:HB3	2.41	0.55
1:G:341:GLY:HA3	1:G:357:ARG:HB3	1.87	0.55
1:G:388:VAL:HG21	1:G:424:CYS:HB3	1.89	0.55
2:I:153:CYS:O	2:I:157:ALA:HB3	2.06	0.55
2:J:28:TRP:HE3	2:J:88:TRP:N	2.04	0.55
2:K:29:LEU:CB	2:K:86:GLN:HE21	2.11	0.55
2:M:133:ARG:O	2:M:133:ARG:NH1	2.40	0.55
2:O:150:ALA:HB1	2:O:182:ALA:HB1	1.88	0.55
2:P:17:LEU:HD11	2:P:34:ALA:CA	2.37	0.55
1:C:238:ASN:ND2	1:C:263:MET:SD	2.80	0.55
1:E:316:ARG:NH2	1:E:365:TRP:CD1	2.74	0.55
1:F:382:TRP:HE1	1:F:459:TRP:CA	2.20	0.55
1:G:400:GLY:H	1:G:404:LEU:HD11	1.72	0.55
2:J:18:LEU:HD21	2:J:38:LEU:HD11	1.88	0.55
2:M:60:ASN:O	2:M:60:ASN:ND2	2.35	0.55
2:N:94:TYR:O	2:N:97:ARG:NH1	2.40	0.55
1:A:400:GLY:H	1:A:404:LEU:HD11	1.72	0.55
1:B:84:ILE:O	1:B:84:ILE:HD13	2.05	0.55
1:F:87:VAL:CB	1:F:93:SER:O	2.54	0.55
1:F:205:SER:O	1:F:205:SER:OG	2.16	0.55
1:G:240:THR:HA	1:G:247:MET:CE	2.35	0.55
2:J:131:PHE:HE2	2:J:143:ARG:HA	1.70	0.55
2:K:27:ARG:N	2:K:27:ARG:HD2	2.21	0.55
2:L:134:LEU:HD11	2:L:136:LYS:O	1.97	0.55
1:C:197:THR:N	1:C:235:HIS:HB2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:LYS:CB	1:D:236:TYR:HD2	2.20	0.55
1:D:430:GLU:HA	2:J:67:GLN:NE2	2.22	0.55
1:E:292:ARG:HG3	1:E:295:HIS:HD2	1.66	0.55
1:G:328:VAL:CB	1:G:336:LYS:HZ3	2.20	0.55
1:H:38:ARG:CZ	1:H:95:PHE:HZ	2.19	0.55
1:H:426:GLN:OE1	2:K:67:GLN:NE2	2.37	0.55
2:N:17:LEU:C	2:N:17:LEU:HD13	2.27	0.55
2:O:44:ASN:O	2:O:47:THR:OG1	2.21	0.55
1:E:266:PHE:CZ	1:E:311:LEU:HD13	2.42	0.55
1:F:188:GLU:OE1	1:F:410:ASN:ND2	2.38	0.55
2:K:38:LEU:HD13	2:K:43:LEU:CD2	2.36	0.55
1:A:157:ASP:HB3	1:D:217:PHE:CZ	2.42	0.55
1:A:345:LEU:HD23	1:A:351:ILE:HD13	1.88	0.55
1:B:375:ALA:HB2	1:B:391:PHE:CE2	2.42	0.55
1:F:177:LEU:HD23	1:F:177:LEU:N	2.22	0.55
1:G:460:LYS:HD2	1:G:460:LYS:N	2.22	0.55
2:I:153:CYS:O	2:I:157:ALA:CB	2.55	0.55
2:K:17:LEU:CD2	2:K:20:GLN:OE1	2.55	0.55
2:L:176:PHE:C	2:L:178:GLN:N	2.58	0.55
2:N:114:ARG:NH1	2:N:175:GLN:CD	2.55	0.55
2:O:147:ASP:H	2:O:176:PHE:HE1	1.50	0.55
1:B:80:LYS:O	1:B:99:ALA:N	2.40	0.55
1:D:180:LYS:HB3	1:D:180:LYS:HZ2	1.71	0.55
1:G:257:LEU:O	1:G:259:MET:CE	2.54	0.55
2:J:14:ARG:HH12	2:J:18:LEU:HD23	1.61	0.55
2:J:124:VAL:O	2:J:128:THR:OG1	2.23	0.55
2:M:44:ASN:O	2:M:47:THR:OG1	2.22	0.55
1:C:222:ILE:HA	1:C:225:SER:OG	2.07	0.54
1:E:255:LYS:CD	1:E:284:ASN:OD1	2.56	0.54
1:E:328:VAL:HG23	1:E:336:LYS:NZ	2.15	0.54
1:F:177:LEU:O	1:F:181:ASN:HB2	2.07	0.54
1:F:261:ILE:HD12	1:F:287:LEU:HD12	1.89	0.54
1:H:219:ALA:HB1	1:H:257:LEU:HD22	1.89	0.54
1:H:400:GLY:H	1:H:404:LEU:HD11	1.72	0.54
2:J:110:LEU:HD22	2:J:114:ARG:HB2	1.88	0.54
2:K:166:ARG:NH2	2:K:169:LEU:O	2.41	0.54
2:L:146:GLY:CA	2:L:176:PHE:CD1	2.88	0.54
1:B:122:PHE:CB	1:G:297:VAL:HG23	2.31	0.54
1:E:353:ALA:HA	1:E:359:VAL:HG12	0.67	0.54
1:F:131:ARG:HH11	1:F:307:HIS:CD2	2.25	0.54
1:G:182:TYR:HE2	1:G:199:ASP:OD1	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:33:ARG:NH2	2:J:66:MET:HG2	2.21	0.54
2:M:89:GLY:O	2:M:93:LEU:HB2	2.07	0.54
1:D:400:GLY:H	1:D:404:LEU:HD11	1.72	0.54
1:F:400:GLY:H	1:F:404:LEU:HD11	1.72	0.54
1:G:240:THR:CA	1:G:247:MET:CE	2.85	0.54
2:K:44:ASN:O	2:K:47:THR:OG1	2.23	0.54
2:O:106:LEU:HD22	2:O:145:PRO:CD	2.35	0.54
1:C:87:VAL:CG2	1:C:94:TYR:N	2.69	0.54
1:C:387:LEU:HD13	1:C:397:LEU:HD22	1.89	0.54
1:C:443:ARG:HG3	1:C:443:ARG:NH2	2.23	0.54
1:F:406:HIS:CE1	1:F:413:GLY:N	2.75	0.54
1:G:328:VAL:CG2	1:G:336:LYS:HZ3	1.93	0.54
1:G:353:ALA:HB2	1:G:362:THR:N	2.21	0.54
2:O:15:GLN:N	2:O:15:GLN:HE21	2.05	0.54
2:O:106:LEU:HD23	2:O:145:PRO:CG	2.35	0.54
1:B:35:ALA:CA	1:B:135:ILE:CD1	2.75	0.54
1:C:400:GLY:H	1:C:404:LEU:HD11	1.72	0.54
1:D:253:PHE:HE2	1:D:257:LEU:HD12	1.73	0.54
1:E:283:ASP:CG	1:H:249:LYS:HZ3	2.06	0.54
1:E:345:LEU:HA	1:E:351:ILE:HD13	1.90	0.54
1:G:38:ARG:HB3	1:G:131:ARG:HB3	1.90	0.54
1:G:300:ARG:HD2	1:G:300:ARG:O	2.07	0.54
2:L:74:ARG:HH22	2:L:102:GLU:HA	1.72	0.54
2:N:117:ASP:H	2:N:120:GLN:HE22	1.55	0.54
1:B:83:HIS:HB3	1:B:97:PHE:CD2	2.32	0.54
1:E:286:VAL:O	1:E:287:LEU:O	2.24	0.54
1:E:400:GLY:H	1:E:404:LEU:HD11	1.72	0.54
1:H:382:TRP:CE3	1:H:461:GLU:HG3	2.39	0.54
2:J:15:GLN:HE21	2:J:15:GLN:N	2.04	0.54
2:L:149:VAL:CG1	2:L:176:PHE:CE1	2.91	0.54
2:P:116:LEU:HD13	2:P:121:ILE:HG21	1.88	0.54
1:B:29:LYS:HB2	1:B:29:LYS:NZ	2.21	0.54
1:C:443:ARG:HG3	1:C:443:ARG:HH21	1.72	0.54
1:D:177:LEU:O	1:D:182:TYR:CB	2.41	0.54
1:D:270:GLY:HA3	1:E:270:GLY:HA3	1.89	0.54
2:K:74:ARG:HH12	2:K:102:GLU:HB3	1.72	0.54
1:C:382:TRP:CD1	1:C:459:TRP:C	2.76	0.54
1:D:143:LYS:HD2	1:D:143:LYS:O	2.07	0.54
1:E:321:ASP:O	1:E:371:VAL:CG2	2.52	0.54
1:G:191:ARG:CZ	1:G:191:ARG:CB	2.86	0.54
1:D:170:THR:OG1	1:D:198:LYS:NZ	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:352:GLU:HA	1:E:362:THR:HG23	1.90	0.54
1:G:184:ARG:HH11	2:K:56:PRO:HG2	1.73	0.54
2:L:75:GLN:NE2	2:L:105:SER:OG	2.41	0.54
1:C:211:TRP:CZ3	1:C:250:ARG:HG3	2.41	0.54
1:D:332:LEU:O	1:D:335:ASP:OD2	2.27	0.54
1:E:146:GLN:NE2	1:E:282:ARG:HH11	1.92	0.54
1:F:309:ARG:HB2	1:F:309:ARG:NH1	2.22	0.54
2:O:74:ARG:HH12	2:O:102:GLU:HA	1.73	0.54
1:B:118:VAL:HG11	1:B:122:PHE:HD2	1.72	0.53
1:B:346:MET:HE3	1:B:371:VAL:CG1	2.38	0.53
1:B:385:PRO:HA	1:B:434:LEU:CD2	2.30	0.53
1:C:133:GLU:CG	1:C:134:ASP:OD1	2.52	0.53
1:C:211:TRP:CD2	1:C:250:ARG:CD	2.90	0.53
1:C:384:MET:HE1	1:C:421:LEU:CD1	0.37	0.53
1:C:389:GLU:OE1	1:C:435:TYR:CD1	2.62	0.53
1:F:301:GLN:OE1	1:F:301:GLN:HA	2.05	0.53
1:F:328:VAL:HG11	1:F:336:LYS:HE3	1.20	0.53
2:J:14:ARG:HG3	2:J:14:ARG:O	2.08	0.53
2:K:38:LEU:HD11	2:K:43:LEU:CD1	2.37	0.53
2:M:94:TYR:O	2:M:97:ARG:NH1	2.41	0.53
2:N:149:VAL:CB	2:N:176:PHE:CZ	2.91	0.53
2:O:174:LEU:CD2	2:O:186:ILE:HG21	2.38	0.53
1:E:428:ARG:O	1:E:428:ARG:HD2	2.08	0.53
1:H:22:TYR:CD2	1:H:48:PRO:C	2.82	0.53
1:H:328:VAL:HB	1:H:336:LYS:CE	2.08	0.53
2:K:144:HIS:CE1	2:K:145:PRO:HD2	2.43	0.53
2:L:98:GLU:OE1	2:L:129:LYS:CD	2.55	0.53
1:C:87:VAL:HG13	1:C:95:PHE:CD2	2.43	0.53
1:E:292:ARG:CD	1:E:308:PHE:HE2	2.16	0.53
1:F:315:LEU:HD21	1:F:323:LEU:HD13	1.88	0.53
1:G:187:TYR:CE1	1:G:191:ARG:HD3	2.41	0.53
1:H:382:TRP:CD2	1:H:461:GLU:CG	2.89	0.53
2:K:99:LEU:CB	2:K:104:ARG:CG	2.69	0.53
1:B:435:TYR:CZ	2:N:133:ARG:NH1	2.75	0.53
1:D:81:CYS:N	1:D:98:ILE:CD1	2.71	0.53
1:D:99:ALA:O	1:D:100:ASP:OD1	2.27	0.53
1:D:385:PRO:CA	1:D:424:CYS:SG	2.84	0.53
2:J:114:ARG:O	2:J:115:LYS:C	2.46	0.53
2:J:150:ALA:CA	2:J:176:PHE:HE2	2.20	0.53
2:J:163:LEU:HD22	2:J:163:LEU:H	1.72	0.53
2:J:168:ARG:HA	2:J:168:ARG:CZ	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:244:CYS:SG	1:C:248:MET:CE	2.97	0.53
1:C:297:VAL:O	1:C:297:VAL:HG12	2.07	0.53
1:D:202:ASN:HD21	1:E:116:SER:CA	2.00	0.53
1:D:205:SER:HB3	1:E:106:GLU:CD	2.28	0.53
1:G:211:TRP:CZ3	1:G:250:ARG:CG	2.88	0.53
1:G:240:THR:C	1:G:247:MET:CE	2.75	0.53
1:H:28:PRO:CB	1:H:82:TYR:CE2	2.89	0.53
2:L:64:VAL:CG1	2:L:65:ALA:N	2.72	0.53
1:F:175:LEU:CG	1:F:208:PHE:CZ	2.90	0.53
1:G:265:ASP:N	1:G:265:ASP:OD1	2.42	0.53
2:K:99:LEU:CG	2:K:104:ARG:CG	2.87	0.53
1:B:124:PHE:CE1	1:B:126:ALA:HB3	2.44	0.53
1:B:138:PRO:HG2	1:B:141:LEU:CB	2.38	0.53
1:B:265:ASP:OD1	1:B:265:ASP:N	2.42	0.53
1:C:180:LYS:CG	1:D:157:ASP:OD1	2.56	0.53
1:D:81:CYS:HA	1:D:98:ILE:HA	1.90	0.53
1:E:264:HIS:N	1:E:289:HIS:O	2.35	0.53
1:F:264:HIS:O	1:F:290:ILE:HA	2.09	0.53
1:H:265:ASP:OD1	1:H:265:ASP:N	2.42	0.53
2:N:114:ARG:HH11	2:N:175:GLN:HE22	1.51	0.53
1:A:42:GLN:OE1	1:A:128:ARG:NH2	2.42	0.53
1:C:179:ALA:CB	1:C:217:PHE:HD2	2.22	0.53
1:D:108:GLY:CA	1:D:145:PHE:CE1	2.91	0.53
1:E:148:PRO:HA	1:E:319:GLY:C	2.28	0.53
1:F:134:ASP:OD1	1:F:309:ARG:NE	2.42	0.53
1:F:409:GLY:C	1:F:412:PRO:HD2	2.29	0.53
1:H:408:TRP:HH2	2:I:23:ARG:CB	2.21	0.53
2:I:81:VAL:HG21	2:I:109:GLN:HA	1.91	0.53
2:K:93:LEU:C	2:K:96:LEU:HD12	2.19	0.53
1:A:265:ASP:N	1:A:265:ASP:OD1	2.42	0.53
1:D:109:SER:O	1:D:145:PHE:CZ	2.57	0.53
1:D:430:GLU:HA	2:J:67:GLN:HE21	1.74	0.53
1:E:344:ASP:C	1:E:346:MET:H	2.12	0.53
1:G:384:MET:HE2	1:G:420:ALA:CA	2.36	0.53
1:H:383:HIS:CD2	1:H:383:HIS:H	2.27	0.53
2:I:154:TRP:HZ2	2:I:186:ILE:HA	1.73	0.53
2:K:147:ASP:O	2:K:151:HIS:N	2.42	0.53
2:M:33:ARG:HH22	2:M:66:MET:HG2	1.74	0.53
1:B:328:VAL:HG11	1:B:336:LYS:HE3	1.71	0.53
1:C:389:GLU:OE1	1:C:435:TYR:CA	2.56	0.53
1:G:42:GLN:OE1	1:G:128:ARG:NH2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:443:ARG:HH21	1:H:443:ARG:HG3	1.74	0.53
2:J:82:ARG:HG2	2:J:82:ARG:O	2.09	0.53
2:L:134:LEU:O	2:L:136:LYS:N	2.42	0.53
2:M:128:THR:CG2	2:M:148:ALA:HB3	2.33	0.53
1:C:143:LYS:NZ	1:G:102:LEU:HD21	2.24	0.52
1:C:166:MET:HG3	1:C:396:VAL:HG22	1.90	0.52
1:C:199:ASP:OD1	1:C:214:ARG:HD2	2.09	0.52
1:C:380:HIS:CD2	1:C:380:HIS:H	2.26	0.52
1:D:34:LEU:HD21	1:D:82:TYR:CZ	2.44	0.52
1:E:282:ARG:HH11	1:E:282:ARG:CG	2.07	0.52
1:F:177:LEU:HD13	1:F:181:ASN:HB3	1.91	0.52
1:F:184:ARG:NH1	2:M:56:PRO:HG2	2.23	0.52
1:G:281:CYS:SG	1:G:288:LEU:HD23	2.49	0.52
1:G:328:VAL:CG2	1:G:336:LYS:HE2	2.38	0.52
1:H:445:ALA:C	1:H:447:LYS:H	2.12	0.52
2:K:99:LEU:CD1	2:K:104:ARG:CB	2.58	0.52
2:L:103:GLN:HA	2:L:106:LEU:HB2	1.91	0.52
1:B:105:PHE:HE1	1:B:113:ILE:HG23	1.73	0.52
1:C:380:HIS:CE1	1:C:459:TRP:CB	2.93	0.52
1:D:427:ALA:CB	1:D:434:LEU:HD12	2.40	0.52
1:H:69:ASP:OD1	1:H:70:LEU:HG	2.08	0.52
1:H:184:ARG:CD	2:I:49:PHE:CD2	2.92	0.52
2:I:150:ALA:HB2	2:I:177:ALA:HA	1.91	0.52
2:K:38:LEU:HD11	2:K:43:LEU:HD11	1.90	0.52
2:N:103:GLN:HG3	2:N:145:PRO:HD3	1.91	0.52
1:B:31:THR:HA	1:B:138:PRO:CG	2.40	0.52
1:B:235:HIS:HD2	1:B:237:LEU:HD12	1.75	0.52
1:C:42:GLN:OE1	1:C:128:ARG:NH2	2.42	0.52
1:C:164:ARG:HB2	1:C:165:PRO:CD	2.40	0.52
1:C:348:GLU:OE1	2:O:122:ARG:NH1	2.29	0.52
1:C:382:TRP:NE1	1:C:460:LYS:CA	2.72	0.52
1:D:235:HIS:HD2	1:D:237:LEU:HD12	1.75	0.52
1:D:243:THR:HB	1:E:276:THR:OG1	2.09	0.52
1:D:387:LEU:CD1	1:D:397:LEU:CG	2.88	0.52
1:E:42:GLN:OE1	1:E:128:ARG:NH2	2.42	0.52
1:F:235:HIS:HD2	1:F:237:LEU:HD12	1.75	0.52
2:L:58:GLN:HA	2:L:61:GLN:HB2	1.91	0.52
2:L:100:ASP:HB3	2:L:103:GLN:NE2	2.24	0.52
2:O:124:VAL:O	2:O:128:THR:OG1	2.22	0.52
1:B:145:PHE:HD2	1:B:317:LEU:HB3	1.75	0.52
1:C:224:LYS:O	1:C:224:LYS:HD3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:MET:O	1:C:294:MET:HG2	2.09	0.52
1:F:316:ARG:NH2	1:F:370:GLY:N	2.57	0.52
1:G:241:ALA:CA	1:G:247:MET:HE3	2.30	0.52
1:H:235:HIS:HD2	1:H:237:LEU:HD12	1.75	0.52
1:H:465:GLU:O	1:H:465:GLU:HG2	2.09	0.52
2:N:33:ARG:NH2	2:N:66:MET:SD	2.83	0.52
2:O:176:PHE:HD2	2:O:176:PHE:O	1.91	0.52
1:A:235:HIS:HD2	1:A:237:LEU:HD12	1.75	0.52
1:B:22:TYR:CE2	1:B:48:PRO:CB	2.88	0.52
1:C:167:LEU:HD11	1:C:421:LEU:HB2	1.92	0.52
1:E:345:LEU:CD2	1:E:351:ILE:CD1	2.82	0.52
1:F:74:MET:CE	1:F:74:MET:N	2.73	0.52
1:F:261:ILE:HD12	1:F:287:LEU:CD1	2.40	0.52
1:F:309:ARG:NH1	1:F:309:ARG:CB	2.73	0.52
2:M:155:ARG:CZ	2:M:155:ARG:CB	2.86	0.52
2:O:142:ASP:N	2:O:147:ASP:OD2	2.25	0.52
1:B:42:GLN:OE1	1:B:128:ARG:NH2	2.42	0.52
1:B:356:SER:OG	2:N:155:ARG:NH2	2.43	0.52
1:C:84:ILE:O	1:C:84:ILE:HD13	2.09	0.52
1:C:384:MET:HE2	1:C:421:LEU:CD1	1.24	0.52
1:F:42:GLN:OE1	1:F:128:ARG:NH2	2.42	0.52
2:J:14:ARG:CZ	2:J:18:LEU:HD23	2.34	0.52
2:M:155:ARG:NH1	2:M:155:ARG:CB	2.73	0.52
1:B:231:GLU:HB2	1:B:233:LYS:HE2	1.92	0.52
1:B:433:ASP:C	1:B:437:GLU:OE2	2.48	0.52
1:D:180:LYS:CD	1:D:217:PHE:HZ	2.01	0.52
1:D:198:LYS:HB2	1:D:236:TYR:CD2	2.45	0.52
1:D:215:PHE:HD1	1:D:237:LEU:HD21	1.73	0.52
1:E:198:LYS:CA	1:E:236:TYR:HB2	2.38	0.52
1:E:203:ILE:O	1:E:204:ASN:O	2.26	0.52
1:F:385:PRO:CA	1:F:434:LEU:CD2	2.75	0.52
1:G:382:TRP:CZ2	1:G:456:LEU:HA	2.44	0.52
1:H:38:ARG:NH2	1:H:95:PHE:CZ	2.77	0.52
1:H:231:GLU:HB2	1:H:233:LYS:HE2	1.91	0.52
1:H:297:VAL:HG12	1:H:298:ILE:HG13	1.92	0.52
2:J:94:TYR:O	2:J:97:ARG:NH1	2.42	0.52
1:C:29:LYS:C	1:C:30:ASP:OD1	2.48	0.52
1:C:181:ASN:OD1	2:J:57:ILE:HG13	2.10	0.52
1:D:42:GLN:OE1	1:D:128:ARG:NH2	2.42	0.52
1:D:81:CYS:SG	1:D:98:ILE:HD13	2.50	0.52
1:D:231:GLU:HB2	1:D:233:LYS:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:231:GLU:HB2	1:F:233:LYS:HE2	1.92	0.52
1:F:354:ASP:HA	2:P:159:GLU:OE1	2.10	0.52
1:G:166:MET:HB2	1:G:396:VAL:HG22	1.92	0.52
1:G:354:ASP:N	1:G:359:VAL:O	2.43	0.52
1:H:42:GLN:OE1	1:H:128:ARG:NH2	2.42	0.52
2:O:133:ARG:NE	2:O:133:ARG:HA	2.23	0.52
1:A:166:MET:HB2	1:A:396:VAL:HG22	1.92	0.52
1:B:341:GLY:HA3	1:B:357:ARG:HB3	1.92	0.52
1:B:401:GLY:N	1:B:404:LEU:HD11	2.25	0.52
1:F:214:ARG:NH1	1:F:214:ARG:CG	2.73	0.52
1:G:443:ARG:HA	1:G:456:LEU:HD11	1.92	0.52
1:H:75:ASP:HA	1:H:78:ASP:OD2	2.09	0.52
2:J:163:LEU:N	2:J:163:LEU:CD2	2.73	0.52
1:C:79:GLY:HA3	1:C:100:ASP:OD1	2.10	0.52
1:C:116:SER:HA	1:F:202:ASN:HD21	0.69	0.52
1:F:175:LEU:N	1:F:175:LEU:CD1	2.73	0.52
1:F:313:LYS:CE	1:F:345:LEU:HD12	1.72	0.52
2:J:168:ARG:NE	2:J:168:ARG:CA	2.73	0.52
2:K:16:GLU:C	2:K:18:LEU:N	2.63	0.52
2:K:27:ARG:N	2:K:27:ARG:CD	2.73	0.52
2:L:155:ARG:NH1	2:L:155:ARG:CB	2.73	0.52
2:M:106:LEU:CD2	2:M:144:HIS:NE2	2.59	0.52
1:A:354:ASP:CG	2:L:155:ARG:HH21	2.13	0.51
1:B:122:PHE:CZ	1:B:131:ARG:CA	2.85	0.51
1:B:380:HIS:CE1	1:B:459:TRP:CD1	2.98	0.51
1:B:404:LEU:CD2	1:B:404:LEU:N	2.73	0.51
1:D:38:ARG:NH2	1:D:95:PHE:CZ	2.78	0.51
1:E:245:GLU:HA	1:E:245:GLU:OE2	2.11	0.51
1:F:177:LEU:N	1:F:177:LEU:CD2	2.73	0.51
1:H:85:GLU:O	1:H:94:TYR:HB2	2.10	0.51
2:L:155:ARG:HB2	2:L:155:ARG:NH1	2.25	0.51
2:P:69:TYR:HA	2:P:72:ILE:HG13	1.92	0.51
1:B:402:GLY:N	1:B:404:LEU:CD2	2.73	0.51
1:B:443:ARG:HH21	1:B:443:ARG:CG	2.23	0.51
1:C:137:PHE:HB3	1:C:142:VAL:HG23	1.92	0.51
1:C:384:MET:CE	1:C:421:LEU:CA	2.84	0.51
1:D:191:ARG:O	1:D:193:GLY:N	2.42	0.51
1:D:265:ASP:N	1:D:265:ASP:OD1	2.42	0.51
1:E:134:ASP:OD1	1:E:309:ARG:NE	2.43	0.51
1:E:414:ALA:HA	1:E:417:ASN:HD22	1.74	0.51
1:G:194:LEU:CD2	1:G:194:LEU:N	2.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:158:GLN:OE1	2:J:158:GLN:HA	2.09	0.51
2:K:55:GLU:OE1	2:K:58:GLN:NE2	2.43	0.51
1:C:112:ASN:OD1	1:F:204:ASN:HB2	2.11	0.51
1:C:232:ILE:C	1:C:233:LYS:CD	2.77	0.51
1:E:231:GLU:HB2	1:E:233:LYS:HE2	1.92	0.51
1:E:384:MET:CE	1:E:421:LEU:HD11	2.39	0.51
1:F:166:MET:HB2	1:F:396:VAL:HG22	1.92	0.51
1:F:266:PHE:CZ	1:F:267:LEU:HD22	2.46	0.51
1:G:382:TRP:CB	1:G:461:GLU:HG3	2.40	0.51
1:H:294:MET:O	1:H:294:MET:HG2	2.09	0.51
1:H:408:TRP:HZ3	2:I:23:ARG:C	1.97	0.51
2:L:44:ASN:CB	2:L:45:PRO:CD	2.84	0.51
2:L:85:TYR:HE1	2:L:112:LEU:CD1	2.21	0.51
2:L:183:ARG:NH2	2:L:183:ARG:CG	2.73	0.51
2:M:133:ARG:HA	2:M:133:ARG:NE	2.23	0.51
1:A:29:LYS:N	1:A:32:ASP:OD2	2.42	0.51
1:C:180:LYS:CA	1:C:180:LYS:HE2	2.40	0.51
1:D:166:MET:HB2	1:D:396:VAL:HG22	1.92	0.51
1:D:180:LYS:HD2	1:D:217:PHE:CE2	2.42	0.51
1:E:283:ASP:OD1	1:H:249:LYS:CE	2.58	0.51
1:E:309:ARG:HH11	1:E:309:ARG:CB	2.23	0.51
1:G:266:PHE:HE1	1:G:292:ARG:HA	1.76	0.51
1:G:347:ARG:NH1	1:G:347:ARG:HG3	2.25	0.51
1:H:28:PRO:CG	1:H:82:TYR:HE2	2.22	0.51
2:K:144:HIS:CG	2:K:145:PRO:CD	2.79	0.51
1:C:143:LYS:HZ2	1:G:102:LEU:HD21	1.75	0.51
1:F:198:LYS:HB3	1:F:236:TYR:HD2	1.71	0.51
1:F:250:ARG:CB	1:F:250:ARG:NH1	2.73	0.51
1:F:294:MET:O	1:F:294:MET:HG2	2.10	0.51
1:G:199:ASP:OD2	1:G:214:ARG:HD2	2.10	0.51
1:G:328:VAL:CB	1:G:336:LYS:NZ	2.72	0.51
1:H:346:MET:CE	1:H:371:VAL:HG13	2.40	0.51
2:K:141:PHE:CZ	2:K:185:LEU:HD12	2.39	0.51
2:L:166:ARG:HH21	2:L:166:ARG:C	2.13	0.51
2:M:85:TYR:CD1	2:M:112:LEU:HD21	2.39	0.51
1:A:231:GLU:HB2	1:A:233:LYS:HE2	1.92	0.51
1:A:354:ASP:OD1	2:L:155:ARG:NH2	2.44	0.51
1:A:356:SER:CB	2:L:155:ARG:HH22	2.24	0.51
1:C:211:TRP:CH2	1:C:250:ARG:HG3	2.45	0.51
1:E:380:HIS:H	1:E:383:HIS:HD2	1.58	0.51
1:F:292:ARG:HD2	1:F:324:HIS:CB	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:355:ARG:CA	2:P:159:GLU:OE2	2.58	0.51
1:G:231:GLU:HB2	1:G:233:LYS:HE2	1.92	0.51
1:H:86:PRO:CA	1:H:94:TYR:HB3	2.19	0.51
2:J:87:GLU:HG2	2:J:87:GLU:O	2.09	0.51
2:O:59:GLN:O	2:O:63:THR:OG1	2.24	0.51
1:A:282:ARG:HH12	1:D:210:ARG:NH1	2.06	0.51
1:B:198:LYS:HB3	1:B:236:TYR:HD2	1.75	0.51
1:C:379:ILE:HG22	1:C:383:HIS:CD2	2.46	0.51
1:C:430:GLU:O	2:O:71:SER:OG	2.27	0.51
1:D:37:PHE:O	1:D:95:PHE:HA	2.11	0.51
1:G:351:ILE:CG2	1:G:362:THR:HG23	2.41	0.51
1:D:414:ALA:HA	1:D:417:ASN:HD22	1.76	0.51
1:F:110:VAL:HG11	1:F:314:CYS:HB3	1.92	0.51
1:F:148:PRO:HG2	1:F:369:PRO:CG	2.34	0.51
1:G:29:LYS:HE3	1:G:29:LYS:CA	2.38	0.51
1:G:443:ARG:HA	1:G:456:LEU:CD1	2.41	0.51
1:H:316:ARG:NH1	1:H:346:MET:HA	2.26	0.51
1:H:380:HIS:CE1	1:H:383:HIS:HE2	2.27	0.51
2:K:183:ARG:NH2	2:K:183:ARG:CG	2.73	0.51
2:L:46:GLN:CD	2:L:50:GLU:OE1	2.48	0.51
1:A:345:LEU:HA	1:A:351:ILE:HD13	1.93	0.51
1:B:149:PRO:HA	1:B:282:ARG:HE	1.76	0.51
1:B:316:ARG:HH11	1:B:346:MET:HA	1.75	0.51
1:B:316:ARG:NH1	1:B:346:MET:HA	2.26	0.51
1:C:181:ASN:HB3	2:J:55:GLU:CD	2.28	0.51
1:D:87:VAL:HG22	1:D:95:PHE:CD2	2.45	0.51
1:E:180:LYS:HE3	1:E:184:ARG:HH11	1.76	0.51
1:E:309:ARG:NH1	1:E:309:ARG:CB	2.73	0.51
1:F:171:ILE:N	1:F:171:ILE:CD1	2.73	0.51
1:F:177:LEU:O	1:F:182:TYR:N	2.43	0.51
1:G:29:LYS:HA	1:G:29:LYS:NZ	2.25	0.51
1:H:29:LYS:N	1:H:32:ASP:OD2	2.42	0.51
1:H:184:ARG:HD3	2:I:49:PHE:CD2	2.46	0.51
2:J:75:GLN:HG2	2:J:105:SER:OG	2.10	0.51
2:J:103:GLN:HA	2:J:106:LEU:HB2	1.93	0.51
2:J:103:GLN:OE1	2:J:132:CYS:SG	2.69	0.51
2:J:131:PHE:CE1	2:J:138:PRO:HD2	2.46	0.51
2:J:163:LEU:HD22	2:J:163:LEU:N	2.25	0.51
2:J:165:GLU:OE1	2:J:165:GLU:HA	2.11	0.51
2:P:151:HIS:HA	2:P:154:TRP:CE3	2.46	0.51
1:B:402:GLY:O	1:B:404:LEU:HD21	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:209:GLN:C	1:D:210:ARG:O	2.49	0.51
1:E:386:ALA:O	1:E:389:GLU:HB3	2.12	0.51
1:H:149:PRO:HA	1:H:282:ARG:HE	1.76	0.51
1:H:179:ALA:HB1	1:H:217:PHE:CE2	2.46	0.51
1:H:428:ARG:HB2	1:H:434:LEU:CD1	2.38	0.51
2:N:124:VAL:O	2:N:128:THR:OG1	2.23	0.51
1:B:22:TYR:CE2	1:B:48:PRO:CG	2.74	0.50
1:B:166:MET:HB2	1:B:396:VAL:HG22	1.92	0.50
1:B:325:SER:HG	1:B:342:PHE:HZ	1.54	0.50
1:C:345:LEU:HA	1:C:351:ILE:HD13	1.93	0.50
1:D:177:LEU:HD13	1:D:181:ASN:ND2	2.22	0.50
1:F:244:CYS:C	1:F:248:MET:HE2	2.27	0.50
2:I:89:GLY:HA2	2:I:92:LEU:HB3	1.92	0.50
2:M:133:ARG:NE	2:M:133:ARG:CA	2.73	0.50
1:A:380:HIS:H	1:A:383:HIS:HD2	1.58	0.50
1:C:140:ALA:HB1	1:G:139:VAL:HG12	1.94	0.50
1:C:184:ARG:HH11	1:C:184:ARG:HG3	1.76	0.50
1:C:244:CYS:HG	1:C:248:MET:CE	2.22	0.50
1:C:444:GLU:O	1:C:444:GLU:HG2	2.10	0.50
1:D:180:LYS:HG2	1:D:217:PHE:HE2	1.77	0.50
1:D:191:ARG:NH1	1:D:191:ARG:CG	2.73	0.50
1:D:241:ALA:N	1:D:247:MET:HE3	2.26	0.50
1:D:332:LEU:HD22	1:D:333:GLU:H	1.75	0.50
1:F:387:LEU:HD12	1:F:397:LEU:CG	2.27	0.50
1:G:291:HIS:ND1	1:G:293:ALA:N	2.59	0.50
2:K:146:GLY:HA2	2:K:176:PHE:CE1	2.46	0.50
1:A:149:PRO:HA	1:A:282:ARG:HE	1.76	0.50
1:B:138:PRO:C	1:B:140:ALA:N	2.64	0.50
2:M:121:ILE:HG22	2:M:124:VAL:HG21	1.93	0.50
1:B:316:ARG:NH1	1:B:346:MET:O	2.44	0.50
1:B:325:SER:OG	1:B:342:PHE:CZ	2.65	0.50
1:D:33:LEU:HD22	1:D:138:PRO:HG3	1.93	0.50
1:D:351:ILE:HG22	1:D:359:VAL:HG21	1.92	0.50
1:E:198:LYS:CB	1:E:236:TYR:CG	2.94	0.50
1:E:283:ASP:CG	1:H:249:LYS:HZ1	2.10	0.50
1:F:200:ASP:H	1:F:203:ILE:HD13	1.76	0.50
1:F:308:PHE:HD1	1:F:308:PHE:O	1.95	0.50
1:G:460:LYS:N	1:G:460:LYS:CD	2.74	0.50
1:H:166:MET:HB2	1:H:396:VAL:HG22	1.92	0.50
1:H:222:ILE:HD13	1:H:234:GLY:CA	2.37	0.50
1:H:316:ARG:HH11	1:H:346:MET:HA	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:49:PHE:CD1	2:L:55:GLU:N	2.77	0.50
2:N:14:ARG:HD3	2:N:17:LEU:H	1.76	0.50
2:O:174:LEU:CD2	2:O:186:ILE:CG2	2.90	0.50
1:B:143:LYS:HE2	1:H:107:GLU:OE2	2.12	0.50
1:B:436:ARG:HB2	1:B:465:GLU:OE2	2.11	0.50
1:C:149:PRO:HA	1:C:282:ARG:HE	1.76	0.50
1:C:197:THR:N	1:C:235:HIS:CB	2.75	0.50
1:E:190:LEU:CD1	1:E:233:LYS:HD2	2.42	0.50
1:F:316:ARG:NH1	1:F:346:MET:O	2.40	0.50
1:G:133:GLU:HG2	1:G:360:PHE:HE2	1.75	0.50
1:G:149:PRO:HA	1:G:282:ARG:HE	1.76	0.50
1:H:341:GLY:HA3	1:H:357:ARG:HB3	1.93	0.50
1:B:382:TRP:NE1	1:B:460:LYS:CA	2.74	0.50
1:C:184:ARG:HD3	2:J:49:PHE:HE2	1.75	0.50
1:D:34:LEU:HG	1:D:82:TYR:OH	2.11	0.50
1:F:74:MET:HE2	1:F:74:MET:N	2.27	0.50
1:G:408:TRP:CZ3	2:K:23:ARG:O	2.65	0.50
2:J:18:LEU:HD21	2:J:38:LEU:HD12	1.92	0.50
2:J:166:ARG:NH1	2:J:169:LEU:HD21	2.22	0.50
2:M:116:LEU:C	2:M:117:ASP:O	2.50	0.50
1:A:198:LYS:HB3	1:A:236:TYR:HD2	1.75	0.50
1:A:386:ALA:O	1:A:389:GLU:HB3	2.11	0.50
1:B:22:TYR:CD2	1:B:48:PRO:CA	2.91	0.50
1:D:345:LEU:HA	1:D:351:ILE:HD13	1.94	0.50
1:E:166:MET:HB2	1:E:396:VAL:HG22	1.92	0.50
1:B:406:HIS:ND1	1:B:413:GLY:CA	2.75	0.50
1:C:140:ALA:CB	1:G:139:VAL:HG12	2.41	0.50
1:D:171:ILE:N	1:D:171:ILE:CD1	2.73	0.50
1:F:80:LYS:O	1:F:80:LYS:HG2	2.11	0.50
1:F:142:VAL:HG13	1:F:142:VAL:O	2.12	0.50
1:G:408:TRP:HZ2	2:K:23:ARG:CD	2.00	0.50
2:L:28:TRP:CZ2	2:L:62:ILE:CG2	2.66	0.50
1:D:214:ARG:NH1	1:D:214:ARG:CG	2.73	0.50
1:E:426:GLN:CA	1:E:426:GLN:NE2	2.73	0.50
2:I:99:LEU:O	2:I:104:ARG:NE	2.41	0.50
2:J:150:ALA:CB	2:J:176:PHE:HE2	2.16	0.50
2:K:117:ASP:H	2:K:120:GLN:HE22	1.59	0.50
2:L:135:PRO:O	2:L:136:LYS:HB2	2.10	0.50
2:N:14:ARG:O	2:N:14:ARG:HG3	2.11	0.50
2:N:17:LEU:CD2	2:N:20:GLN:OE1	2.51	0.50
2:P:154:TRP:CH2	2:P:189:LEU:HD21	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:162:TYR:CD1	2:O:57:ILE:HD13	2.44	0.49
1:C:180:LYS:HG2	1:D:157:ASP:HB3	1.91	0.49
1:C:342:PHE:C	1:C:342:PHE:CD2	2.86	0.49
1:D:253:PHE:C	1:D:253:PHE:CD2	2.86	0.49
2:I:160:ARG:HD2	2:I:165:GLU:HB3	1.94	0.49
2:J:27:ARG:CD	2:J:27:ARG:N	2.75	0.49
2:J:29:LEU:CB	2:J:86:GLN:NE2	2.75	0.49
2:K:124:VAL:O	2:K:128:THR:OG1	2.25	0.49
2:L:15:GLN:NE2	2:L:15:GLN:N	2.60	0.49
2:M:95:GLU:HG2	2:M:122:ARG:CG	2.39	0.49
2:O:156:LEU:O	2:O:160:ARG:HG2	2.12	0.49
1:E:292:ARG:CB	1:E:295:HIS:HD2	2.24	0.49
1:F:384:MET:HE1	1:F:421:LEU:N	1.97	0.49
1:G:290:ILE:HD13	1:G:315:LEU:HD11	1.93	0.49
1:G:381:VAL:O	1:G:384:MET:HB3	2.12	0.49
1:H:20:THR:O	1:H:20:THR:OG1	2.25	0.49
2:K:174:LEU:CD2	2:K:186:ILE:CG2	2.62	0.49
2:K:189:LEU:N	2:K:189:LEU:HD23	2.27	0.49
2:L:56:PRO:HA	2:L:59:GLN:HB3	1.93	0.49
2:L:156:LEU:O	2:L:160:ARG:HG2	2.11	0.49
1:B:29:LYS:NZ	1:B:29:LYS:CB	2.73	0.49
1:C:384:MET:HE2	1:C:421:LEU:CB	2.42	0.49
1:D:244:CYS:SG	1:D:248:MET:SD	3.10	0.49
1:E:171:ILE:CG1	1:E:186:VAL:HG23	2.40	0.49
1:E:182:TYR:HE2	1:E:199:ASP:OD1	1.85	0.49
1:E:265:ASP:OD1	1:E:265:ASP:N	2.42	0.49
1:H:383:HIS:CD2	1:H:383:HIS:N	2.80	0.49
2:O:116:LEU:HD13	2:O:121:ILE:HG21	1.95	0.49
2:O:154:TRP:HA	2:O:158:GLN:HB3	1.94	0.49
1:B:146:GLN:NE2	1:B:282:ARG:NH2	2.39	0.49
1:C:253:PHE:C	1:C:253:PHE:CD2	2.86	0.49
1:F:257:LEU:CD1	1:F:259:MET:HE2	2.39	0.49
1:G:382:TRP:CZ3	1:G:461:GLU:OE2	2.65	0.49
1:H:342:PHE:C	1:H:342:PHE:CD2	2.86	0.49
2:J:15:GLN:N	2:J:15:GLN:NE2	2.60	0.49
1:C:380:HIS:O	1:C:399:PHE:HE1	1.96	0.49
1:D:75:ASP:HA	1:D:78:ASP:OD2	2.13	0.49
1:D:149:PRO:HA	1:D:282:ARG:HE	1.76	0.49
1:D:387:LEU:HD13	1:D:397:LEU:CD1	2.41	0.49
1:E:167:LEU:HD11	1:E:418:ARG:HA	1.95	0.49
1:F:149:PRO:HA	1:F:282:ARG:HE	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:188:GLU:OE2	1:G:411:ALA:CA	2.59	0.49
1:G:380:HIS:HB2	1:G:459:TRP:CZ3	2.48	0.49
1:H:177:LEU:HD13	1:H:181:ASN:C	2.32	0.49
2:L:94:TYR:CE1	2:L:97:ARG:NH1	2.81	0.49
1:B:342:PHE:CD2	1:B:342:PHE:C	2.86	0.49
1:C:420:ALA:O	1:C:424:CYS:HB2	2.13	0.49
1:D:81:CYS:N	1:D:98:ILE:HD12	2.27	0.49
1:E:136:ARG:HG3	1:E:136:ARG:NH1	2.24	0.49
1:E:198:LYS:CB	1:E:236:TYR:HD2	2.24	0.49
1:E:342:PHE:C	1:E:342:PHE:CD2	2.85	0.49
1:F:190:LEU:HD11	1:F:233:LYS:HD2	1.95	0.49
1:F:385:PRO:CB	1:F:434:LEU:CD2	2.91	0.49
1:G:38:ARG:CZ	1:G:95:PHE:CZ	2.95	0.49
1:H:26:TYR:C	1:H:26:TYR:CD2	2.86	0.49
1:H:184:ARG:CD	2:I:49:PHE:CE2	2.91	0.49
2:J:166:ARG:NE	2:J:166:ARG:CA	2.73	0.49
2:L:60:ASN:HA	2:L:63:THR:HB	1.95	0.49
1:C:148:PRO:O	1:C:282:ARG:NH1	2.42	0.49
1:F:266:PHE:C	1:F:266:PHE:CD2	2.86	0.49
1:F:433:ASP:HB3	1:F:436:ARG:HB3	1.94	0.49
1:F:443:ARG:HG2	1:F:456:LEU:HD13	1.94	0.49
1:G:328:VAL:HG12	1:G:331:LYS:CD	2.42	0.49
1:G:346:MET:O	1:G:370:GLY:HA3	2.12	0.49
1:G:382:TRP:CD1	1:G:459:TRP:CB	2.91	0.49
2:L:85:TYR:CD1	2:L:112:LEU:CD1	2.95	0.49
1:E:290:ILE:CD1	1:E:320:GLY:HA3	2.42	0.49
1:E:292:ARG:HH22	1:E:325:SER:C	2.14	0.49
1:F:253:PHE:C	1:F:253:PHE:CD2	2.86	0.49
2:N:21:LEU:HB3	2:N:54:PHE:HE2	1.78	0.49
2:O:14:ARG:HH21	2:O:16:GLU:HA	1.77	0.49
2:O:107:CYS:SG	2:O:108:ALA:N	2.86	0.49
2:P:14:ARG:HG3	2:P:14:ARG:O	2.12	0.49
1:F:316:ARG:CZ	1:F:370:GLY:HA2	2.30	0.49
1:F:384:MET:HE1	1:F:421:LEU:HB2	1.75	0.49
2:J:146:GLY:C	2:J:176:PHE:CZ	2.87	0.49
2:L:166:ARG:HH21	2:L:166:ARG:CA	2.25	0.49
2:O:15:GLN:N	2:O:15:GLN:NE2	2.60	0.49
1:E:241:ALA:CB	1:E:247:MET:CA	2.91	0.49
1:F:94:TYR:N	1:F:94:TYR:CD1	2.81	0.49
1:F:222:ILE:HD13	1:F:234:GLY:CA	2.41	0.49
1:F:309:ARG:CZ	1:F:309:ARG:HB3	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:363:GLN:NE2	1:G:365:TRP:CD1	2.81	0.49
1:H:385:PRO:CB	1:H:434:LEU:HD23	2.43	0.49
2:I:55:GLU:H	2:I:58:GLN:HE21	1.61	0.49
2:J:81:VAL:HG22	2:J:112:LEU:CD2	2.42	0.49
2:K:28:TRP:HB3	2:K:87:GLU:HA	1.94	0.49
2:L:85:TYR:HH	2:L:93:LEU:CD2	2.04	0.49
2:L:93:LEU:HD13	2:L:96:LEU:HD21	1.94	0.49
2:M:60:ASN:HD22	2:M:63:THR:HB	1.78	0.49
2:N:91:ASP:HA	2:N:94:TYR:HB3	1.94	0.49
1:B:105:PHE:HD1	1:B:113:ILE:CD1	1.92	0.48
1:C:55:ALA:HB1	1:C:79:GLY:O	2.13	0.48
1:C:133:GLU:OE2	1:C:309:ARG:NH2	2.46	0.48
1:C:446:GLY:CA	1:C:452:LEU:HD23	2.43	0.48
1:F:268:THR:HB	1:F:294:MET:HE2	1.95	0.48
1:G:39:PHE:HZ	1:G:50:ALA:HB1	1.78	0.48
1:G:186:VAL:O	1:G:190:LEU:HB2	2.12	0.48
2:K:96:LEU:HD13	2:K:96:LEU:O	2.13	0.48
2:P:34:ALA:O	2:P:38:LEU:HB2	2.13	0.48
1:A:116:SER:HA	1:H:202:ASN:HD22	1.77	0.48
1:A:267:LEU:HD21	1:A:298:ILE:HD12	1.95	0.48
1:B:82:TYR:N	1:B:82:TYR:CD1	2.80	0.48
1:C:164:ARG:HB2	1:C:425:VAL:HG21	1.85	0.48
1:C:222:ILE:HD13	1:C:234:GLY:CA	2.43	0.48
1:C:267:LEU:HD21	1:C:298:ILE:HD12	1.95	0.48
1:F:262:ILE:O	1:F:289:HIS:N	2.40	0.48
1:F:309:ARG:HH11	1:F:309:ARG:CB	2.26	0.48
1:F:406:HIS:HD2	1:F:407:PRO:HD2	1.77	0.48
1:G:191:ARG:NH1	1:G:191:ARG:CB	2.73	0.48
1:G:328:VAL:CG1	1:G:336:LYS:HZ3	2.25	0.48
1:G:382:TRP:CE3	1:G:461:GLU:CG	2.96	0.48
1:H:34:LEU:HD21	1:H:82:TYR:CZ	2.48	0.48
1:H:380:HIS:ND1	1:H:382:TRP:HB2	2.27	0.48
2:J:149:VAL:CG1	2:J:172:ARG:HD3	2.42	0.48
2:K:35:CYS:SG	2:K:48:LEU:CD2	3.01	0.48
2:M:131:PHE:C	2:M:131:PHE:CD2	2.86	0.48
2:N:169:LEU:N	2:N:169:LEU:CD1	2.76	0.48
2:O:167:SER:O	2:O:170:ILE:HG22	2.13	0.48
1:A:116:SER:HA	1:H:202:ASN:ND2	2.27	0.48
1:B:20:THR:O	1:B:20:THR:OG1	2.30	0.48
1:E:268:THR:HB	1:E:294:MET:HE2	1.96	0.48
1:E:321:ASP:C	1:E:371:VAL:HG23	2.33	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:187:GLU:HA	2:K:190:LEU:CD1	2.43	0.48
2:L:15:GLN:HE21	2:L:15:GLN:N	2.10	0.48
1:D:180:LYS:CG	1:D:217:PHE:HE2	2.26	0.48
1:H:133:GLU:OE2	1:H:309:ARG:NH2	2.46	0.48
1:H:182:TYR:CD2	1:H:214:ARG:HG3	2.48	0.48
2:K:131:PHE:HE2	2:K:143:ARG:HG2	1.78	0.48
2:K:174:LEU:HD22	2:K:186:ILE:HG21	1.91	0.48
2:L:99:LEU:HD22	2:L:100:ASP:H	1.77	0.48
1:B:133:GLU:OE2	1:B:309:ARG:NH2	2.46	0.48
1:B:409:GLY:C	1:B:412:PRO:HD2	2.33	0.48
1:C:83:HIS:HB3	1:C:97:PHE:HD2	1.77	0.48
1:C:265:ASP:OD1	1:C:265:ASP:N	2.42	0.48
1:C:385:PRO:CG	1:C:442:LEU:HD11	2.42	0.48
1:C:435:TYR:CZ	2:O:133:ARG:CZ	2.97	0.48
1:C:435:TYR:OH	2:O:133:ARG:NH1	2.46	0.48
1:D:326:GLY:O	1:D:375:ALA:HA	2.14	0.48
1:G:352:GLU:O	1:G:362:THR:HG23	2.13	0.48
1:H:187:TYR:C	1:H:187:TYR:CD2	2.86	0.48
2:L:147:ASP:O	2:L:176:PHE:CE2	2.67	0.48
2:M:60:ASN:HD22	2:M:60:ASN:C	2.09	0.48
1:C:83:HIS:CB	1:C:97:PHE:CD2	2.91	0.48
1:D:28:PRO:CB	1:D:82:TYR:CE2	2.96	0.48
1:D:385:PRO:HD3	1:D:442:LEU:HD11	1.95	0.48
1:G:219:ALA:HB2	1:G:257:LEU:HD13	1.95	0.48
1:G:241:ALA:HB3	1:G:247:MET:CB	2.39	0.48
1:H:34:LEU:HG	1:H:82:TYR:OH	2.14	0.48
2:N:55:GLU:OE1	2:N:58:GLN:NE2	2.42	0.48
2:N:132:CYS:SG	2:N:143:ARG:NH2	2.87	0.48
2:O:81:VAL:O	2:O:112:LEU:HD22	2.13	0.48
1:C:406:HIS:ND1	1:C:413:GLY:CA	2.77	0.48
1:D:29:LYS:N	1:D:32:ASP:OD2	2.42	0.48
1:D:351:ILE:O	1:D:362:THR:CG2	2.61	0.48
1:F:29:LYS:N	1:F:32:ASP:OD2	2.42	0.48
1:F:190:LEU:CD1	1:F:233:LYS:HD2	2.44	0.48
1:G:133:GLU:OE2	1:G:309:ARG:NH2	2.46	0.48
1:G:188:GLU:O	1:G:411:ALA:HB2	2.14	0.48
1:H:83:HIS:HB2	1:H:97:PHE:HB2	1.94	0.48
1:H:382:TRP:CG	1:H:461:GLU:HG3	2.47	0.48
2:I:93:LEU:HA	2:I:96:LEU:HG	1.95	0.48
2:I:100:ASP:HA	2:I:104:ARG:HH21	1.78	0.48
1:C:180:LYS:HA	1:C:180:LYS:HE2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:GLU:OE2	1:D:309:ARG:NH2	2.46	0.48
1:D:345:LEU:HD22	1:D:351:ILE:CD1	2.40	0.48
1:F:151:GLY:HA2	1:F:369:PRO:CB	2.42	0.48
1:G:263:MET:CB	1:G:289:HIS:HB3	2.44	0.48
1:H:178:SER:H	1:H:181:ASN:HD22	0.77	0.48
2:J:150:ALA:CA	2:J:176:PHE:CE2	2.96	0.48
2:K:174:LEU:HD23	2:K:186:ILE:HG21	1.92	0.48
2:O:137:GLN:OE1	2:O:143:ARG:CG	2.57	0.48
2:P:14:ARG:NH2	2:P:16:GLU:HA	2.29	0.48
2:P:59:GLN:O	2:P:63:THR:OG1	2.25	0.48
1:B:267:LEU:HD21	1:B:298:ILE:HD12	1.95	0.48
1:C:325:SER:HG	1:C:342:PHE:HZ	1.49	0.48
1:D:316:ARG:CZ	1:D:346:MET:O	2.62	0.48
1:E:68:THR:HA	1:E:71:LEU:CD1	2.44	0.48
1:E:131:ARG:HH11	1:E:307:HIS:HD2	1.62	0.48
1:H:267:LEU:HD21	1:H:298:ILE:HD12	1.95	0.48
2:O:151:HIS:HA	2:O:154:TRP:CE3	2.49	0.48
1:A:133:GLU:OE2	1:A:309:ARG:NH2	2.46	0.48
1:A:157:ASP:OD1	1:D:180:LYS:CG	2.61	0.48
1:A:345:LEU:HD11	1:A:359:VAL:HG22	1.96	0.48
1:B:33:LEU:HG	1:B:105:PHE:CE2	2.49	0.48
1:B:384:MET:CG	1:B:424:CYS:SG	2.94	0.48
1:D:66:VAL:HG13	1:D:68:THR:N	2.29	0.48
1:E:29:LYS:N	1:E:32:ASP:OD2	2.42	0.48
1:E:384:MET:CE	1:E:421:LEU:HG	2.44	0.48
1:E:424:CYS:O	1:E:425:VAL:C	2.53	0.48
1:G:245:GLU:OE2	1:G:245:GLU:HA	2.14	0.48
1:H:316:ARG:NH1	1:H:346:MET:O	2.47	0.48
2:J:28:TRP:HB2	2:J:87:GLU:HA	1.54	0.48
2:J:149:VAL:HG12	2:J:172:ARG:CD	2.35	0.48
2:L:63:THR:O	2:L:63:THR:HG22	2.14	0.48
2:O:91:ASP:HA	2:O:94:TYR:HB3	1.96	0.48
2:O:132:CYS:HB3	2:O:143:ARG:HH22	1.79	0.48
1:C:29:LYS:HD2	1:C:29:LYS:HA	1.46	0.47
1:C:115:THR:HG22	1:F:201:GLU:HB2	1.95	0.47
1:C:430:GLU:HG3	2:O:67:GLN:HE22	1.79	0.47
1:D:173:PRO:HG2	1:D:177:LEU:HB2	1.94	0.47
1:D:267:LEU:HD21	1:D:298:ILE:HD12	1.95	0.47
1:F:444:GLU:O	1:F:444:GLU:HG2	2.08	0.47
1:H:184:ARG:HD2	2:I:49:PHE:CD2	2.49	0.47
2:J:28:TRP:CE3	2:J:87:GLU:O	2.65	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:61:GLN:C	2:M:63:THR:H	2.17	0.47
2:N:182:ALA:O	2:N:186:ILE:HB	2.14	0.47
2:P:17:LEU:HD22	2:P:17:LEU:C	2.34	0.47
2:P:162:ASP:O	2:P:166:ARG:N	2.47	0.47
1:C:427:ALA:HB2	1:C:441:ILE:HD12	1.96	0.47
1:D:202:ASN:HD22	1:E:116:SER:CA	2.17	0.47
1:D:205:SER:HB2	1:D:211:TRP:HB3	1.95	0.47
1:D:328:VAL:HA	1:D:331:LYS:CD	2.44	0.47
1:E:296:ALA:O	1:E:300:ARG:HB2	2.14	0.47
1:G:380:HIS:CE1	1:G:459:TRP:CB	2.96	0.47
1:H:81:CYS:CA	1:H:98:ILE:CD1	2.92	0.47
1:B:382:TRP:NE1	1:B:459:TRP:C	2.48	0.47
1:D:174:LYS:C	1:D:175:LEU:HD12	2.34	0.47
1:E:68:THR:HA	1:E:71:LEU:HD12	1.95	0.47
1:F:266:PHE:HD1	1:F:290:ILE:CG2	2.27	0.47
1:G:39:PHE:CZ	1:G:50:ALA:HB3	2.49	0.47
1:G:354:ASP:OD2	2:M:155:ARG:NE	2.47	0.47
2:L:86:GLN:NE2	2:L:86:GLN:CA	2.73	0.47
1:C:139:VAL:O	1:G:140:ALA:HB1	2.13	0.47
1:C:231:GLU:CB	1:C:233:LYS:HE3	2.18	0.47
1:C:292:ARG:HD2	1:C:295:HIS:CE1	2.50	0.47
1:D:34:LEU:CD1	1:D:82:TYR:CZ	2.64	0.47
1:F:74:MET:CE	1:F:74:MET:CA	2.92	0.47
1:F:291:HIS:HD1	1:F:291:HIS:C	2.17	0.47
1:G:253:PHE:C	1:G:253:PHE:CD2	2.88	0.47
1:G:384:MET:HE2	1:G:420:ALA:HB1	1.94	0.47
2:L:61:GLN:HA	2:L:94:TYR:CD1	2.50	0.47
2:M:95:GLU:CG	2:M:122:ARG:CG	2.91	0.47
1:A:148:PRO:O	1:A:282:ARG:NH1	2.42	0.47
1:B:124:PHE:CD1	1:B:124:PHE:N	2.81	0.47
1:C:108:GLY:C	1:C:145:PHE:HE1	2.18	0.47
1:C:385:PRO:HD3	1:C:442:LEU:HD11	1.96	0.47
1:C:427:ALA:HB3	1:C:434:LEU:CD1	2.45	0.47
1:D:28:PRO:HB3	1:D:82:TYR:CD2	2.49	0.47
1:F:209:GLN:C	1:F:210:ARG:O	2.51	0.47
1:G:328:VAL:HG21	1:G:336:LYS:HZ1	0.66	0.47
1:H:188:GLU:OE2	1:H:411:ALA:N	2.47	0.47
1:H:345:LEU:HD22	1:H:345:LEU:C	2.32	0.47
2:J:33:ARG:HH21	2:J:66:MET:CG	2.25	0.47
1:C:82:TYR:CD1	1:C:82:TYR:C	2.86	0.47
1:D:354:ASP:CB	1:D:357:ARG:HB2	2.36	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:85:TYR:CE1	2:L:112:LEU:HD13	2.48	0.47
2:O:69:TYR:HA	2:O:72:ILE:HG13	1.95	0.47
1:A:297:VAL:HA	1:H:122:PHE:HD2	1.80	0.47
1:B:100:ASP:O	1:B:101:PRO:O	2.32	0.47
1:B:148:PRO:O	1:B:282:ARG:NH1	2.42	0.47
1:B:380:HIS:CD2	1:B:380:HIS:N	2.82	0.47
1:C:385:PRO:CD	1:C:442:LEU:HD11	2.45	0.47
1:D:83:HIS:CB	1:D:97:PHE:HB2	2.45	0.47
1:E:134:ASP:HB3	1:E:361:PHE:HE2	1.80	0.47
1:E:247:MET:HG2	1:E:277:LEU:CD1	2.45	0.47
1:F:311:LEU:HD23	1:F:311:LEU:HA	1.71	0.47
1:G:382:TRP:HB3	1:G:461:GLU:CG	2.43	0.47
1:G:384:MET:HE2	1:G:420:ALA:O	2.09	0.47
1:H:187:TYR:C	1:H:187:TYR:HD2	2.17	0.47
2:J:86:GLN:NE2	2:J:86:GLN:CA	2.73	0.47
2:K:14:ARG:HD3	2:K:18:LEU:CD2	2.45	0.47
2:K:99:LEU:HD11	2:K:104:ARG:HA	1.68	0.47
2:L:22:ARG:CZ	2:L:52:THR:O	2.62	0.47
2:M:126:LYS:HA	2:M:129:LYS:HB3	1.97	0.47
2:N:149:VAL:CG1	2:N:176:PHE:CZ	2.97	0.47
2:N:170:ILE:CD1	2:N:170:ILE:N	2.73	0.47
1:C:108:GLY:C	1:C:145:PHE:CE1	2.88	0.47
1:C:215:PHE:HD1	1:C:237:LEU:CD1	1.79	0.47
1:C:215:PHE:HZ	1:C:238:ASN:O	1.97	0.47
1:D:28:PRO:HG3	1:D:82:TYR:CE2	2.49	0.47
1:F:109:SER:C	1:F:145:PHE:HZ	2.17	0.47
1:F:236:TYR:CE1	1:F:289:HIS:ND1	2.81	0.47
1:F:380:HIS:CE1	1:F:382:TRP:HD1	2.33	0.47
1:G:384:MET:HG2	1:G:424:CYS:SG	2.54	0.47
2:J:146:GLY:O	2:J:176:PHE:CE1	2.68	0.47
2:K:24:LYS:HB2	2:K:24:LYS:HE2	1.67	0.47
2:K:175:GLN:NE2	2:K:175:GLN:CA	2.73	0.47
2:O:65:ALA:HA	2:O:68:VAL:HB	1.96	0.47
2:O:157:ALA:HB1	2:O:166:ARG:CZ	2.44	0.47
1:B:138:PRO:O	1:B:140:ALA:N	2.47	0.47
1:B:382:TRP:CD1	1:B:460:LYS:N	2.83	0.47
1:C:384:MET:HE1	1:C:421:LEU:CD2	2.39	0.47
1:D:148:PRO:O	1:D:282:ARG:NH1	2.42	0.47
1:E:295:HIS:C	1:E:295:HIS:HD1	2.17	0.47
1:E:327:THR:HB	1:E:375:ALA:HB1	1.97	0.47
1:E:426:GLN:HA	1:E:426:GLN:NE2	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:316:ARG:CZ	1:G:346:MET:O	2.62	0.47
1:H:56:ALA:HB1	1:H:62:THR:H	1.80	0.47
1:H:85:GLU:C	1:H:94:TYR:HB2	2.35	0.47
1:H:424:CYS:SG	1:H:442:LEU:HD21	2.55	0.47
2:I:99:LEU:HD21	2:I:103:GLN:HB2	1.97	0.47
2:M:34:ALA:O	2:M:38:LEU:HB2	2.14	0.47
2:P:156:LEU:HD13	2:P:169:LEU:CD2	2.45	0.47
1:B:124:PHE:CZ	1:B:126:ALA:HB3	2.50	0.47
1:B:380:HIS:H	1:B:380:HIS:HD2	1.62	0.47
1:B:382:TRP:HA	1:B:382:TRP:HE3	1.78	0.47
1:B:446:GLY:CA	1:B:452:LEU:HD23	2.45	0.47
1:C:327:THR:HB	1:C:375:ALA:HB1	1.97	0.47
1:D:34:LEU:O	1:D:361:PHE:CE1	2.67	0.47
1:D:83:HIS:CE1	1:D:85:GLU:HB2	2.50	0.47
1:D:382:TRP:NE1	1:D:460:LYS:CA	2.78	0.47
1:E:219:ALA:HB3	1:E:257:LEU:HD11	1.91	0.47
1:F:56:ALA:HB1	1:F:62:THR:H	1.80	0.47
1:F:148:PRO:O	1:F:282:ARG:NH1	2.42	0.47
1:H:148:PRO:O	1:H:282:ARG:NH1	2.42	0.47
1:B:328:VAL:HG12	1:B:331:LYS:HD3	1.96	0.46
1:C:74:MET:SD	1:C:74:MET:C	2.94	0.46
1:D:56:ALA:HB1	1:D:62:THR:H	1.80	0.46
1:E:261:ILE:HD12	1:E:287:LEU:HB3	1.97	0.46
1:F:110:VAL:CG1	1:F:314:CYS:HB3	2.46	0.46
1:F:388:VAL:HG11	1:F:424:CYS:HB3	1.96	0.46
1:G:194:LEU:CD2	1:G:414:ALA:CB	2.74	0.46
2:L:49:PHE:CD1	2:L:55:GLU:HA	2.50	0.46
2:N:138:PRO:HG2	2:N:141:PHE:CB	2.44	0.46
2:N:169:LEU:HB3	2:N:172:ARG:HB3	1.96	0.46
1:B:118:VAL:HG11	1:B:122:PHE:CD2	2.50	0.46
1:C:86:PRO:HA	1:C:94:TYR:CB	2.42	0.46
1:C:134:ASP:CG	1:C:360:PHE:HD2	2.10	0.46
1:D:68:THR:HA	1:D:71:LEU:CD1	2.45	0.46
1:D:427:ALA:HB3	1:D:434:LEU:HD11	1.97	0.46
1:E:271:PHE:HA	1:E:274:ASN:HB3	1.98	0.46
1:F:210:ARG:HD2	1:F:210:ARG:HA	1.53	0.46
1:H:327:THR:HB	1:H:375:ALA:HB1	1.97	0.46
2:P:75:GLN:NE2	2:P:105:SER:OG	2.43	0.46
1:A:327:THR:HB	1:A:375:ALA:HB1	1.98	0.46
1:B:104:LEU:CD1	1:G:175:LEU:CD2	2.94	0.46
1:B:123:GLY:HA3	1:G:300:ARG:HH21	1.66	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:THR:HB	1:B:375:ALA:HB1	1.97	0.46
1:B:345:LEU:HD22	1:B:345:LEU:C	2.32	0.46
1:C:56:ALA:HB1	1:C:62:THR:H	1.80	0.46
1:D:116:SER:HA	1:E:202:ASN:HD22	1.73	0.46
1:F:382:TRP:NE1	1:F:459:TRP:HB2	2.30	0.46
1:G:327:THR:HB	1:G:375:ALA:HB1	1.97	0.46
1:H:328:VAL:HG12	1:H:331:LYS:HD3	1.96	0.46
2:J:69:TYR:CZ	2:J:85:TYR:CE2	3.03	0.46
2:J:131:PHE:CZ	2:J:138:PRO:HD2	2.50	0.46
2:O:124:VAL:O	2:O:128:THR:CB	2.63	0.46
2:O:134:LEU:HD23	2:O:134:LEU:HA	1.79	0.46
2:P:17:LEU:CD1	2:P:34:ALA:HB1	2.44	0.46
1:A:328:VAL:HG12	1:A:331:LYS:HD3	1.96	0.46
1:C:60:THR:H	1:F:174:LYS:HZ1	1.61	0.46
1:C:79:GLY:CA	1:C:100:ASP:OD1	2.64	0.46
1:C:222:ILE:CD1	1:C:234:GLY:HA2	2.45	0.46
1:D:354:ASP:N	1:D:359:VAL:O	2.48	0.46
1:E:141:LEU:O	1:E:144:THR:HG22	2.16	0.46
1:E:211:TRP:CB	1:E:250:ARG:HD3	2.45	0.46
1:E:282:ARG:NH2	1:H:210:ARG:NH1	2.64	0.46
1:E:328:VAL:HG12	1:E:331:LYS:HD3	1.96	0.46
1:E:424:CYS:C	1:E:426:GLN:N	2.69	0.46
1:E:428:ARG:CZ	2:I:97:ARG:HG3	2.41	0.46
1:F:90:GLU:HG3	1:F:93:SER:HB3	1.94	0.46
1:F:426:GLN:OE1	2:P:67:GLN:NE2	2.45	0.46
1:G:132:LEU:HB3	1:G:306:ILE:HG22	1.98	0.46
1:H:25:ASP:OD1	1:H:25:ASP:N	2.47	0.46
1:H:38:ARG:NH1	1:H:95:PHE:CZ	2.84	0.46
1:H:190:LEU:HD12	1:H:225:SER:HB2	1.96	0.46
2:L:46:GLN:HE21	2:L:46:GLN:CA	2.25	0.46
2:M:14:ARG:HD3	2:M:38:LEU:HD21	1.96	0.46
2:M:128:THR:HA	2:M:148:ALA:HB1	1.96	0.46
2:O:185:LEU:N	2:O:185:LEU:HD23	2.30	0.46
2:P:106:LEU:CD2	2:P:144:HIS:CD2	2.95	0.46
1:A:132:LEU:HB3	1:A:306:ILE:HG22	1.98	0.46
1:C:180:LYS:HD2	1:C:217:PHE:CZ	2.50	0.46
1:D:384:MET:HE2	1:D:421:LEU:HA	1.43	0.46
1:E:66:VAL:HG12	1:E:69:ASP:HB3	1.97	0.46
1:E:408:TRP:HZ3	2:P:23:ARG:HB3	1.80	0.46
1:F:327:THR:HB	1:F:375:ALA:HB1	1.97	0.46
1:G:404:LEU:HA	1:G:459:TRP:CZ2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:460:LYS:HB2	1:G:462:ILE:HD12	1.97	0.46
2:J:29:LEU:HB3	2:J:86:GLN:NE2	2.31	0.46
2:J:166:ARG:CZ	2:J:166:ARG:CA	2.86	0.46
2:L:146:GLY:O	2:L:176:PHE:CZ	2.47	0.46
1:C:245:GLU:OE2	1:C:245:GLU:HA	2.13	0.46
1:C:325:SER:OG	1:C:342:PHE:HZ	1.96	0.46
1:D:28:PRO:CB	1:D:82:TYR:HE2	2.29	0.46
1:D:180:LYS:N	1:D:217:PHE:CE2	2.84	0.46
1:D:426:GLN:OE1	1:D:426:GLN:HA	2.16	0.46
1:F:211:TRP:CH2	1:F:250:ARG:CA	2.93	0.46
1:F:267:LEU:C	1:F:294:MET:CE	2.84	0.46
1:F:341:GLY:HA3	1:F:357:ARG:HB3	1.96	0.46
1:G:148:PRO:O	1:G:282:ARG:NH1	2.42	0.46
1:G:345:LEU:CD2	1:G:351:ILE:HD13	2.43	0.46
2:O:176:PHE:CE2	2:O:179:SER:OG	2.69	0.46
1:B:332:LEU:HD22	1:B:333:GLU:H	1.80	0.46
1:B:424:CYS:SG	1:B:442:LEU:CD2	3.02	0.46
1:C:180:LYS:HA	1:C:180:LYS:HE3	1.97	0.46
1:C:328:VAL:HB	1:C:336:LYS:CE	2.28	0.46
1:D:202:ASN:HD22	1:E:116:SER:CB	2.27	0.46
1:E:198:LYS:CB	1:E:236:TYR:CB	2.57	0.46
1:E:211:TRP:CE2	1:E:250:ARG:CG	2.98	0.46
1:G:264:HIS:N	1:G:289:HIS:O	2.43	0.46
2:L:155:ARG:CZ	2:L:155:ARG:CB	2.92	0.46
2:N:138:PRO:HG2	2:N:141:PHE:HB2	1.96	0.46
1:A:324:HIS:HD2	1:A:374:VAL:HG13	1.81	0.46
1:B:25:ASP:OD1	1:B:25:ASP:N	2.48	0.46
1:B:132:LEU:HB3	1:B:306:ILE:HG22	1.98	0.46
1:B:198:LYS:NZ	1:B:200:ASP:OD1	2.49	0.46
1:B:270:GLY:HA3	1:G:270:GLY:HA3	1.97	0.46
1:B:324:HIS:HD2	1:B:374:VAL:HG13	1.81	0.46
1:C:222:ILE:CA	1:C:225:SER:OG	2.63	0.46
1:C:406:HIS:ND1	1:C:413:GLY:N	2.64	0.46
1:D:316:ARG:NH1	1:D:346:MET:CA	2.77	0.46
1:D:328:VAL:CG1	1:D:336:LYS:HA	2.46	0.46
1:D:385:PRO:HA	1:D:424:CYS:HG	1.77	0.46
1:E:142:VAL:HG13	1:E:142:VAL:O	2.16	0.46
1:E:283:ASP:OD2	1:H:249:LYS:NZ	2.49	0.46
1:F:193:GLY:O	1:F:418:ARG:NH1	2.48	0.46
1:H:68:THR:HG23	1:H:68:THR:O	2.16	0.46
2:I:81:VAL:HG23	2:I:112:LEU:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:TYR:N	1:B:82:TYR:HD1	2.13	0.46
1:C:385:PRO:HA	1:C:434:LEU:HD21	1.97	0.46
1:D:55:ALA:CB	1:D:98:ILE:HD11	2.42	0.46
1:D:198:LYS:HB2	1:D:236:TYR:HD2	1.79	0.46
1:D:211:TRP:CE2	1:D:250:ARG:CD	2.98	0.46
1:D:351:ILE:CG2	1:D:359:VAL:HG21	2.46	0.46
1:F:204:ASN:C	1:F:206:GLN:N	2.69	0.46
1:G:244:CYS:SG	1:G:248:MET:SD	3.10	0.46
1:G:324:HIS:HD2	1:G:374:VAL:HG13	1.81	0.46
1:H:324:HIS:HD2	1:H:374:VAL:HG13	1.81	0.46
2:P:156:LEU:HD13	2:P:169:LEU:HD21	1.96	0.46
1:A:64:THR:HG21	1:H:172:LYS:HE2	1.97	0.46
1:A:198:LYS:NZ	1:A:200:ASP:OD1	2.49	0.46
2:K:69:TYR:HA	2:K:72:ILE:HG13	1.97	0.46
2:K:98:GLU:HB2	2:K:129:LYS:HD2	1.97	0.46
2:M:67:GLN:HA	2:M:70:ASP:HB2	1.98	0.46
1:A:408:TRP:HZ3	2:N:23:ARG:HB3	1.81	0.45
1:B:56:ALA:HB1	1:B:62:THR:HA	1.98	0.45
1:B:152:ILE:HG12	1:B:372:LEU:HG	1.98	0.45
1:F:39:PHE:HB3	1:F:94:TYR:O	2.16	0.45
1:F:328:VAL:HG12	1:F:331:LYS:HD3	1.96	0.45
1:F:427:ALA:HB2	1:F:441:ILE:HD12	1.90	0.45
1:G:266:PHE:CE1	1:G:292:ARG:HA	2.51	0.45
1:H:132:LEU:HB3	1:H:306:ILE:HG22	1.98	0.45
1:H:387:LEU:HD23	1:H:387:LEU:HA	1.78	0.45
2:J:27:ARG:N	2:J:27:ARG:HD2	2.31	0.45
2:O:110:LEU:HA	2:O:113:GLU:HG2	1.98	0.45
2:P:144:HIS:CG	2:P:145:PRO:CD	2.87	0.45
1:C:117:ILE:HG22	1:C:118:VAL:HG23	1.98	0.45
1:C:292:ARG:HG2	1:C:324:HIS:HB2	1.97	0.45
1:E:160:ASN:HD21	1:H:180:LYS:NZ	2.13	0.45
1:F:108:GLY:CA	1:F:145:PHE:CD1	2.98	0.45
1:G:39:PHE:CZ	1:G:50:ALA:HB1	2.52	0.45
1:G:56:ALA:HB1	1:G:62:THR:H	1.80	0.45
1:G:152:ILE:HG12	1:G:372:LEU:HG	1.98	0.45
1:G:193:GLY:O	1:G:418:ARG:NH1	2.48	0.45
1:G:384:MET:HE1	1:G:421:LEU:CA	2.00	0.45
1:H:380:HIS:CE1	1:H:383:HIS:NE2	2.84	0.45
2:M:15:GLN:C	2:M:17:LEU:N	2.61	0.45
1:C:427:ALA:CB	1:C:434:LEU:HD12	2.46	0.45
1:E:117:ILE:HG22	1:E:118:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:244:CYS:SG	1:E:248:MET:SD	3.10	0.45
1:F:179:ALA:CB	1:F:213:ASP:OD2	2.64	0.45
1:F:349:ASP:OD1	1:F:349:ASP:N	2.47	0.45
1:H:427:ALA:CB	1:H:441:ILE:CD1	2.81	0.45
2:J:162:ASP:O	2:J:164:THR:N	2.46	0.45
2:L:114:ARG:HH12	2:L:172:ARG:HH12	0.46	0.45
2:O:34:ALA:O	2:O:38:LEU:HB2	2.16	0.45
1:A:152:ILE:HG12	1:A:372:LEU:HG	1.98	0.45
1:B:345:LEU:HD22	1:B:351:ILE:CD1	2.45	0.45
1:D:241:ALA:O	1:E:272:THR:HG23	2.16	0.45
1:G:198:LYS:CA	1:G:235:HIS:CE1	2.99	0.45
1:G:211:TRP:CD2	1:G:250:ARG:CD	2.97	0.45
1:G:382:TRP:CD2	1:G:461:GLU:HG3	2.52	0.45
1:H:117:ILE:HG22	1:H:118:VAL:HG23	1.98	0.45
1:H:152:ILE:HG12	1:H:372:LEU:HG	1.98	0.45
1:H:385:PRO:HD3	1:H:442:LEU:HD11	1.98	0.45
2:L:14:ARG:HG3	2:L:14:ARG:O	2.15	0.45
1:B:34:LEU:HD21	1:B:82:TYR:CE2	2.52	0.45
1:B:182:TYR:OH	1:B:199:ASP:OD1	2.29	0.45
1:C:188:GLU:OE2	1:C:410:ASN:CB	2.62	0.45
1:C:211:TRP:CG	1:C:250:ARG:HD3	2.52	0.45
1:D:328:VAL:HA	1:D:331:LYS:HD2	1.98	0.45
1:E:280:TRP:CE3	1:E:280:TRP:C	2.90	0.45
1:F:222:ILE:O	1:F:225:SER:OG	2.20	0.45
1:F:286:VAL:C	1:F:287:LEU:O	2.53	0.45
1:H:443:ARG:HA	1:H:456:LEU:CD2	2.47	0.45
1:H:460:LYS:HB2	1:H:462:ILE:CD1	2.46	0.45
2:L:100:ASP:O	2:L:101:GLN:C	2.54	0.45
2:P:151:HIS:HA	2:P:154:TRP:HE3	1.80	0.45
1:A:56:ALA:HB1	1:A:62:THR:H	1.80	0.45
1:C:77:TYR:HD1	1:C:103:ASP:HB2	1.81	0.45
1:C:164:ARG:HB2	1:C:425:VAL:CG2	2.44	0.45
1:C:197:THR:OG1	1:C:235:HIS:HB2	2.10	0.45
1:C:222:ILE:C	1:C:225:SER:OG	2.54	0.45
1:C:354:ASP:H	1:C:359:VAL:HG12	1.82	0.45
1:C:421:LEU:HD12	1:C:421:LEU:HA	1.77	0.45
1:D:66:VAL:HG12	1:D:69:ASP:HB3	1.99	0.45
1:D:123:GLY:HA2	1:E:300:ARG:NH2	2.32	0.45
1:D:132:LEU:HB3	1:D:306:ILE:HG22	1.98	0.45
1:E:149:PRO:HD2	1:E:319:GLY:O	2.05	0.45
1:F:117:ILE:HG22	1:F:118:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:224:LYS:CE	2:M:50:GLU:OE2	2.59	0.45
1:F:406:HIS:CE1	1:F:413:GLY:HA2	2.52	0.45
1:G:117:ILE:HG22	1:G:118:VAL:HG23	1.98	0.45
1:H:182:TYR:HE2	1:H:199:ASP:OD1	1.94	0.45
2:L:106:LEU:CD2	2:L:144:HIS:HD2	2.20	0.45
1:B:117:ILE:HG22	1:B:118:VAL:HG23	1.98	0.45
1:B:172:LYS:HE2	1:G:64:THR:HG21	1.98	0.45
1:C:411:ALA:HB3	1:C:412:PRO:CD	2.44	0.45
1:D:108:GLY:C	1:D:145:PHE:HE1	2.19	0.45
1:D:199:ASP:OD2	1:D:235:HIS:CE1	2.70	0.45
1:D:380:HIS:CE1	1:D:459:TRP:CG	3.05	0.45
1:E:180:LYS:O	1:E:184:ARG:HB2	2.16	0.45
1:G:133:GLU:HG2	1:G:360:PHE:CE2	2.52	0.45
1:H:187:TYR:CE2	1:H:191:ARG:HD3	2.47	0.45
2:K:124:VAL:O	2:K:128:THR:CB	2.65	0.45
1:B:31:THR:HG21	1:B:102:LEU:HB2	0.47	0.45
1:C:31:THR:HA	1:C:138:PRO:HB3	1.99	0.45
1:C:132:LEU:HB3	1:C:306:ILE:HG22	1.98	0.45
1:D:117:ILE:HG22	1:D:118:VAL:HG23	1.98	0.45
1:D:203:ILE:HG23	1:D:203:ILE:O	2.16	0.45
1:E:66:VAL:HG13	1:E:68:THR:N	2.32	0.45
1:E:132:LEU:HB3	1:E:306:ILE:HG22	1.98	0.45
1:F:139:VAL:HG13	1:F:366:ALA:HB2	1.98	0.45
1:F:210:ARG:CZ	1:G:282:ARG:HH22	2.12	0.45
1:G:34:LEU:O	1:G:361:PHE:CE1	2.70	0.45
1:H:443:ARG:HG3	1:H:443:ARG:NH2	2.32	0.45
2:J:28:TRP:CD1	2:J:28:TRP:O	2.70	0.45
2:O:190:LEU:C	2:O:192:ASP:N	2.70	0.45
2:P:155:ARG:H	2:P:155:ARG:HG2	1.62	0.45
1:B:139:VAL:O	1:H:140:ALA:CB	2.64	0.45
1:C:139:VAL:O	1:G:140:ALA:CB	2.65	0.45
1:D:382:TRP:HA	1:D:382:TRP:CE3	2.52	0.45
1:F:139:VAL:CG2	1:F:364:ASP:HB3	2.47	0.45
1:F:342:PHE:CD2	1:F:342:PHE:O	2.70	0.45
1:G:264:HIS:O	1:G:290:ILE:HA	2.17	0.45
1:H:34:LEU:CD1	1:H:82:TYR:HH	2.21	0.45
2:L:114:ARG:HG3	2:L:116:LEU:HG	1.99	0.45
2:M:67:GLN:HG3	2:M:70:ASP:HB2	1.99	0.45
2:M:86:GLN:NE2	2:M:86:GLN:CA	2.73	0.45
1:B:25:ASP:O	1:B:26:TYR:CB	2.64	0.45
1:B:57:GLU:HB3	1:B:121:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:34:LEU:C	1:C:135:ILE:HD12	2.35	0.45
1:C:177:LEU:CD1	1:C:181:ASN:HB2	2.43	0.45
1:C:353:ALA:HB2	1:C:362:THR:H	1.82	0.45
1:C:384:MET:CE	1:C:421:LEU:CB	2.89	0.45
1:D:142:VAL:O	1:D:142:VAL:HG13	2.15	0.45
1:D:211:TRP:CE3	1:D:211:TRP:O	2.70	0.45
1:F:98:ILE:HD13	1:F:98:ILE:HA	1.69	0.45
1:F:290:ILE:CD1	1:F:315:LEU:HD11	2.46	0.45
1:F:409:GLY:O	1:F:412:PRO:HD2	2.17	0.45
1:G:340:LEU:HD23	1:G:340:LEU:HA	1.85	0.45
1:H:224:LYS:NZ	2:I:50:GLU:OE1	2.50	0.45
2:J:131:PHE:CE2	2:J:143:ARG:HA	2.52	0.45
2:J:170:ILE:HD13	2:J:170:ILE:HA	1.69	0.45
2:J:172:ARG:HD3	2:J:172:ARG:HA	1.70	0.45
2:K:22:ARG:O	2:K:24:LYS:NZ	2.38	0.45
2:L:157:ALA:C	2:L:166:ARG:HD3	2.28	0.45
2:M:95:GLU:HG2	2:M:122:ARG:HB2	1.99	0.45
2:O:176:PHE:O	2:O:176:PHE:CD2	2.70	0.45
1:A:117:ILE:HG22	1:A:118:VAL:HG23	1.98	0.44
1:B:349:ASP:OD1	1:B:349:ASP:N	2.50	0.44
1:D:133:GLU:HG2	1:D:360:PHE:HE2	1.82	0.44
1:D:210:ARG:HD2	1:D:210:ARG:HA	1.38	0.44
1:D:243:THR:CB	1:E:276:THR:OG1	2.65	0.44
1:F:180:LYS:HD2	1:F:180:LYS:HA	1.71	0.44
1:F:382:TRP:HD1	1:F:459:TRP:HB3	1.82	0.44
1:F:406:HIS:CE1	1:F:413:GLY:CA	3.00	0.44
1:G:435:TYR:CD2	1:G:435:TYR:O	2.71	0.44
1:H:21:TYR:O	1:H:81:CYS:SG	2.74	0.44
1:H:178:SER:O	1:H:179:ALA:O	2.35	0.44
1:H:349:ASP:OD1	1:H:349:ASP:N	2.50	0.44
2:J:110:LEU:CD2	2:J:114:ARG:CG	2.95	0.44
2:J:110:LEU:HD21	2:J:114:ARG:CG	2.46	0.44
2:J:110:LEU:HD13	2:J:114:ARG:CB	2.47	0.44
2:L:49:PHE:O	2:L:49:PHE:CD2	2.70	0.44
2:L:151:HIS:CD2	2:L:151:HIS:O	2.70	0.44
2:L:166:ARG:HA	2:L:166:ARG:HD2	1.79	0.44
2:M:49:PHE:CD1	2:M:49:PHE:O	2.70	0.44
2:O:106:LEU:CD2	2:O:145:PRO:HD3	2.44	0.44
2:O:144:HIS:CE1	2:O:145:PRO:HD2	2.51	0.44
1:B:57:GLU:HG2	1:B:121:VAL:HA	1.98	0.44
1:B:435:TYR:O	1:B:435:TYR:CG	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:324:HIS:HD2	1:C:374:VAL:HG13	1.81	0.44
1:D:109:SER:N	1:D:145:PHE:CE1	2.85	0.44
1:D:177:LEU:HA	1:D:177:LEU:HD22	1.86	0.44
1:D:342:PHE:O	1:D:342:PHE:CD2	2.70	0.44
1:F:211:TRP:HH2	1:F:250:ARG:HA	1.74	0.44
1:G:133:GLU:HG3	1:G:360:PHE:HE2	1.82	0.44
1:H:435:TYR:O	1:H:435:TYR:CD2	2.70	0.44
2:J:29:LEU:HB2	2:J:86:GLN:NE2	2.32	0.44
2:J:182:ALA:O	2:J:186:ILE:HB	2.17	0.44
2:L:114:ARG:NH1	2:L:175:GLN:NE2	2.63	0.44
2:P:14:ARG:C	2:P:14:ARG:CD	2.86	0.44
1:B:138:PRO:HG2	1:B:141:LEU:HB3	1.99	0.44
1:C:292:ARG:HE	1:C:324:HIS:CB	2.22	0.44
1:D:31:THR:HA	1:D:138:PRO:HB3	1.99	0.44
1:D:134:ASP:HB2	1:D:360:PHE:HD2	1.83	0.44
1:D:209:GLN:NE2	1:D:214:ARG:CD	2.65	0.44
1:D:324:HIS:HD2	1:D:374:VAL:HG13	1.81	0.44
1:F:324:HIS:HD2	1:F:374:VAL:HG13	1.81	0.44
1:F:380:HIS:ND1	1:F:382:TRP:HB2	2.32	0.44
1:G:313:LYS:CE	1:G:345:LEU:HD13	1.95	0.44
1:H:435:TYR:O	1:H:435:TYR:CG	2.70	0.44
2:J:69:TYR:HE1	2:J:93:LEU:HG	1.81	0.44
2:J:190:LEU:O	2:J:193:LEU:HB3	2.17	0.44
2:O:106:LEU:HD22	2:O:145:PRO:HD2	1.86	0.44
1:B:139:VAL:O	1:H:140:ALA:HB1	2.18	0.44
1:D:134:ASP:HB3	1:D:361:PHE:CE2	2.53	0.44
1:D:326:GLY:O	1:D:375:ALA:CA	2.66	0.44
1:E:199:ASP:CB	1:E:203:ILE:HD13	2.45	0.44
1:E:342:PHE:CD2	1:E:342:PHE:O	2.70	0.44
1:F:211:TRP:CE3	1:F:211:TRP:O	2.71	0.44
1:G:342:PHE:CD2	1:G:342:PHE:O	2.70	0.44
1:G:410:ASN:O	1:G:413:GLY:N	2.51	0.44
1:H:87:VAL:HG22	1:H:95:PHE:CD2	2.52	0.44
1:H:184:ARG:HG3	2:I:55:GLU:HG3	1.99	0.44
2:K:110:LEU:HD12	2:K:116:LEU:HD11	1.99	0.44
2:O:151:HIS:HA	2:O:154:TRP:CZ3	2.52	0.44
2:P:152:GLN:HG2	2:P:152:GLN:O	2.18	0.44
1:A:157:ASP:CG	1:D:180:LYS:HG2	2.37	0.44
1:B:22:TYR:CE2	1:B:49:GLU:CA	3.01	0.44
1:B:355:ARG:NH2	2:N:159:GLU:HG3	2.32	0.44
1:E:211:TRP:CH2	1:E:250:ARG:CG	2.93	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:55:ALA:HB2	1:F:98:ILE:HD11	1.99	0.44
1:F:216:LEU:C	1:F:216:LEU:CD1	2.86	0.44
1:F:249:LYS:HE2	1:F:249:LYS:HB3	1.53	0.44
1:F:266:PHE:CE2	1:F:311:LEU:HD13	2.51	0.44
1:F:443:ARG:HG3	1:F:443:ARG:NH2	2.31	0.44
1:H:190:LEU:C	1:H:190:LEU:CD1	2.86	0.44
2:J:110:LEU:HD22	2:J:114:ARG:CD	2.27	0.44
2:J:151:HIS:CD2	2:J:151:HIS:O	2.70	0.44
2:J:157:ALA:HB1	2:J:166:ARG:NE	2.28	0.44
2:L:65:ALA:HA	2:L:68:VAL:HB	2.00	0.44
1:B:34:LEU:CG	1:B:82:TYR:CZ	2.98	0.44
1:E:63:TRP:CD1	1:E:63:TRP:O	2.71	0.44
1:E:63:TRP:O	1:E:63:TRP:CG	2.70	0.44
1:E:282:ARG:O	1:E:282:ARG:HD3	2.17	0.44
1:F:74:MET:CE	1:F:74:MET:HA	2.47	0.44
1:G:241:ALA:CB	1:G:247:MET:HA	2.48	0.44
1:G:384:MET:HE1	1:G:421:LEU:CB	2.44	0.44
1:G:435:TYR:O	1:G:435:TYR:CG	2.70	0.44
1:H:385:PRO:CB	1:H:434:LEU:HD21	2.47	0.44
2:J:104:ARG:HD2	2:J:105:SER:N	2.32	0.44
2:N:117:ASP:N	2:N:120:GLN:HE22	2.15	0.44
1:B:106:GLU:OE2	1:G:204:ASN:C	2.53	0.44
1:C:28:PRO:HD3	1:C:82:TYR:CD2	2.52	0.44
1:C:136:ARG:C	1:C:136:ARG:CD	2.85	0.44
1:E:293:ALA:O	1:E:294:MET:HB3	2.17	0.44
1:F:108:GLY:HA2	1:F:145:PHE:CD1	2.53	0.44
1:F:109:SER:C	1:F:145:PHE:CZ	2.91	0.44
1:F:328:VAL:HG11	1:F:336:LYS:HA	1.98	0.44
1:F:406:HIS:ND1	1:F:413:GLY:HA3	2.29	0.44
1:G:349:ASP:OD1	1:G:349:ASP:N	2.50	0.44
2:J:170:ILE:CD1	2:J:174:LEU:HD11	2.47	0.44
2:M:85:TYR:CD2	2:M:85:TYR:O	2.71	0.44
2:N:74:ARG:HH12	2:N:102:GLU:HG3	1.83	0.44
2:O:28:TRP:HE1	2:O:62:ILE:HG22	1.82	0.44
2:O:131:PHE:O	2:O:131:PHE:CD2	2.70	0.44
1:A:288:LEU:HD12	1:A:320:GLY:HA2	2.00	0.44
1:C:236:TYR:CZ	1:C:289:HIS:ND1	2.85	0.44
1:E:181:ASN:O	1:E:185:ALA:HB2	2.17	0.44
1:E:266:PHE:HE2	1:E:311:LEU:HD13	1.76	0.44
1:E:285:GLY:HA3	1:H:212:ARG:HD3	1.99	0.44
1:G:253:PHE:CD2	1:G:253:PHE:O	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:380:HIS:HE1	1:G:382:TRP:HB2	1.80	0.44
1:G:384:MET:HE3	1:G:420:ALA:O	2.13	0.44
2:J:15:GLN:H	2:J:15:GLN:NE2	2.09	0.44
2:J:151:HIS:O	2:J:151:HIS:CG	2.71	0.44
2:J:166:ARG:HH12	2:J:169:LEU:HD21	1.82	0.44
2:M:99:LEU:HD11	2:M:125:ALA:HB1	1.99	0.44
2:M:151:HIS:CD2	2:M:151:HIS:O	2.70	0.44
2:P:17:LEU:CD1	2:P:34:ALA:CB	2.92	0.44
1:B:435:TYR:O	1:B:435:TYR:CD2	2.70	0.44
1:C:152:ILE:HG12	1:C:372:LEU:HG	1.98	0.44
1:C:435:TYR:CE2	2:O:133:ARG:NH1	2.85	0.44
1:C:447:LYS:HD3	1:C:447:LYS:HA	1.68	0.44
1:D:328:VAL:HG11	1:D:336:LYS:HA	1.99	0.44
1:E:142:VAL:HG22	1:E:317:LEU:HD23	1.97	0.44
1:E:180:LYS:NZ	1:E:184:ARG:NH1	2.65	0.44
1:E:187:TYR:C	1:E:187:TYR:CD2	2.91	0.44
1:H:26:TYR:HE2	1:H:28:PRO:HA	1.83	0.44
1:H:26:TYR:O	1:H:26:TYR:CG	2.70	0.44
1:H:288:LEU:HD12	1:H:320:GLY:HA2	2.00	0.44
2:J:176:PHE:O	2:J:183:ARG:CG	2.66	0.44
2:M:131:PHE:CE2	2:M:138:PRO:HD3	2.49	0.44
2:N:14:ARG:C	2:N:14:ARG:CD	2.85	0.44
2:N:17:LEU:HD22	2:N:17:LEU:C	2.38	0.44
1:D:180:LYS:CG	1:D:217:PHE:CE2	3.01	0.43
1:D:182:TYR:CD2	1:D:182:TYR:O	2.70	0.43
1:D:198:LYS:CB	1:D:236:TYR:CD2	3.00	0.43
1:D:288:LEU:HD12	1:D:320:GLY:HA2	2.00	0.43
1:D:316:ARG:NH1	1:D:346:MET:O	2.51	0.43
1:E:35:ALA:HB2	1:E:135:ILE:HD11	1.90	0.43
1:E:152:ILE:HG12	1:E:372:LEU:HG	1.98	0.43
1:E:280:TRP:CD2	1:E:280:TRP:O	2.70	0.43
1:E:426:GLN:HE21	1:E:426:GLN:C	2.21	0.43
1:F:81:CYS:HA	1:F:98:ILE:HD12	1.99	0.43
1:F:266:PHE:CD2	1:F:271:PHE:HE1	2.36	0.43
1:G:241:ALA:HB3	1:G:247:MET:CE	2.48	0.43
1:G:380:HIS:ND1	1:G:382:TRP:HB2	2.31	0.43
2:L:49:PHE:CD2	2:L:49:PHE:C	2.91	0.43
2:M:149:VAL:CG1	2:M:172:ARG:NH1	2.71	0.43
2:N:99:LEU:HD13	2:N:103:GLN:HB3	1.98	0.43
2:O:99:LEU:HD13	2:O:103:GLN:HB3	2.00	0.43
1:B:112:ASN:HA	1:G:204:ASN:ND2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:LEU:HD12	1:B:320:GLY:HA2	2.00	0.43
1:C:136:ARG:HD3	1:C:136:ARG:O	2.19	0.43
1:C:288:LEU:HD12	1:C:320:GLY:HA2	2.00	0.43
1:C:297:VAL:HG12	1:F:298:ILE:HG21	1.99	0.43
1:D:152:ILE:HG12	1:D:372:LEU:HG	1.98	0.43
1:D:180:LYS:N	1:D:217:PHE:HE2	2.16	0.43
1:D:216:LEU:C	1:D:216:LEU:CD1	2.86	0.43
1:F:87:VAL:HG22	1:F:95:PHE:CE2	2.53	0.43
1:F:145:PHE:HB3	1:F:317:LEU:HD13	1.90	0.43
1:F:152:ILE:HG12	1:F:372:LEU:HG	1.98	0.43
1:G:353:ALA:HB2	1:G:361:PHE:CA	2.44	0.43
1:H:389:GLU:O	1:H:389:GLU:HG3	2.18	0.43
2:J:176:PHE:O	2:J:183:ARG:CD	2.66	0.43
2:K:147:ASP:HA	2:K:150:ALA:HB3	2.00	0.43
2:L:172:ARG:HD3	2:L:172:ARG:HA	1.65	0.43
1:A:282:ARG:HH22	1:D:210:ARG:CZ	2.15	0.43
1:B:380:HIS:ND1	1:B:459:TRP:CB	2.74	0.43
1:C:430:GLU:CG	2:O:67:GLN:NE2	2.80	0.43
1:D:424:CYS:SG	1:D:434:LEU:HD21	2.59	0.43
1:E:247:MET:HG2	1:E:277:LEU:HD13	2.00	0.43
1:E:257:LEU:HD13	1:E:259:MET:CE	2.48	0.43
1:E:308:PHE:O	1:E:308:PHE:HD1	2.01	0.43
1:E:423:ALA:O	1:E:426:GLN:HB2	2.18	0.43
1:F:250:ARG:HB2	1:F:250:ARG:NH1	2.22	0.43
1:F:292:ARG:HD2	1:F:324:HIS:HB2	1.99	0.43
1:G:387:LEU:HD23	1:G:387:LEU:HA	1.72	0.43
1:G:389:GLU:OE2	2:M:129:LYS:CE	2.64	0.43
1:H:328:VAL:HG23	1:H:336:LYS:HZ2	1.71	0.43
2:J:33:ARG:HA	2:J:33:ARG:HD3	1.34	0.43
2:J:152:GLN:HG2	2:J:156:LEU:HD12	1.99	0.43
2:J:166:ARG:O	2:J:169:LEU:CG	2.66	0.43
2:M:49:PHE:O	2:M:49:PHE:CG	2.70	0.43
2:O:14:ARG:HD3	2:O:18:LEU:CD2	2.48	0.43
2:O:15:GLN:NE2	2:O:15:GLN:H	2.16	0.43
2:O:151:HIS:O	2:O:151:HIS:CD2	2.70	0.43
2:O:170:ILE:HD12	2:O:170:ILE:C	2.30	0.43
1:A:122:PHE:HD2	1:H:297:VAL:CG2	1.95	0.43
1:C:353:ALA:HB2	1:C:362:THR:N	2.33	0.43
1:D:245:GLU:OE2	1:D:245:GLU:HA	2.17	0.43
1:E:171:ILE:CD1	1:E:186:VAL:HG23	2.48	0.43
1:E:257:LEU:HD22	1:E:257:LEU:HA	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:288:LEU:HD22	1:G:288:LEU:HA	1.76	0.43
1:G:380:HIS:CB	1:G:459:TRP:CZ3	3.02	0.43
2:N:74:ARG:HH12	2:N:102:GLU:HA	1.83	0.43
1:C:74:MET:HG3	1:C:74:MET:O	2.19	0.43
1:C:81:CYS:HA	1:C:98:ILE:HD12	2.00	0.43
1:C:197:THR:OG1	1:C:235:HIS:CD2	2.70	0.43
1:C:292:ARG:HD2	1:C:295:HIS:NE2	2.33	0.43
1:C:379:ILE:HG22	1:C:383:HIS:CG	2.54	0.43
1:D:219:ALA:HB1	1:D:257:LEU:HD22	2.01	0.43
1:E:180:LYS:CE	1:E:184:ARG:NH1	2.82	0.43
1:F:145:PHE:HD1	1:F:145:PHE:HA	1.71	0.43
1:F:240:THR:HG1	1:F:265:ASP:CG	2.19	0.43
1:F:266:PHE:HB2	1:F:274:ASN:HD22	1.82	0.43
1:G:316:ARG:NH1	1:G:346:MET:CA	2.79	0.43
1:H:344:ASP:OD2	2:K:126:LYS:CE	2.57	0.43
2:J:74:ARG:CZ	2:J:101:GLN:O	2.67	0.43
2:L:147:ASP:C	2:L:176:PHE:CE2	2.92	0.43
2:N:38:LEU:HD13	2:N:43:LEU:HD21	2.00	0.43
1:C:202:ASN:HD22	1:F:116:SER:HA	1.83	0.43
1:C:384:MET:SD	1:C:420:ALA:C	2.97	0.43
1:D:82:TYR:CD1	1:D:97:PHE:CB	2.99	0.43
1:D:427:ALA:HB3	1:D:434:LEU:HD12	1.98	0.43
1:E:353:ALA:HA	1:E:359:VAL:O	2.18	0.43
1:F:77:TYR:HA	1:F:101:PRO:HG3	1.99	0.43
1:F:215:PHE:CE1	1:F:237:LEU:CB	2.90	0.43
1:F:294:MET:HE2	1:F:294:MET:HB3	1.67	0.43
1:G:406:HIS:ND1	1:G:413:GLY:CA	2.82	0.43
1:H:87:VAL:HG23	1:H:94:TYR:HA	2.01	0.43
1:H:292:ARG:HG2	1:H:324:HIS:HB2	2.01	0.43
1:H:345:LEU:HD22	1:H:351:ILE:CD1	2.46	0.43
2:J:167:SER:C	2:J:169:LEU:N	2.71	0.43
2:J:174:LEU:HB2	2:J:175:GLN:H	1.55	0.43
2:L:49:PHE:CG	2:L:49:PHE:O	2.70	0.43
2:L:157:ALA:O	2:L:166:ARG:NE	2.52	0.43
1:E:198:LYS:HB2	1:E:236:TYR:CD2	2.50	0.43
1:F:267:LEU:HB3	1:F:294:MET:HE3	2.00	0.43
1:G:385:PRO:HB2	1:G:434:LEU:HD23	2.01	0.43
1:H:222:ILE:CD1	1:H:234:GLY:HA2	2.43	0.43
2:J:35:CYS:HA	2:J:38:LEU:HB2	2.01	0.43
2:K:106:LEU:CD2	2:K:144:HIS:NE2	2.63	0.43
2:K:117:ASP:N	2:K:120:GLN:HE22	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:146:GLY:HA2	2:L:176:PHE:CE1	2.54	0.43
1:A:157:ASP:CG	1:D:180:LYS:CG	2.87	0.43
1:B:433:ASP:CA	1:B:437:GLU:OE2	2.66	0.43
1:E:136:ARG:HH11	1:E:136:ARG:CG	2.26	0.43
1:E:280:TRP:CE3	1:E:280:TRP:O	2.72	0.43
1:E:298:ILE:O	1:E:298:ILE:HG23	2.18	0.43
1:F:292:ARG:HD2	1:F:324:HIS:HB3	2.00	0.43
1:F:380:HIS:CE1	1:F:382:TRP:CD1	3.06	0.43
1:G:241:ALA:CA	1:G:247:MET:CE	2.96	0.43
1:G:384:MET:HE3	1:G:420:ALA:C	1.99	0.43
1:H:22:TYR:CZ	1:H:49:GLU:HA	2.54	0.43
1:H:346:MET:HE2	1:H:371:VAL:HG13	2.01	0.43
2:I:183:ARG:HA	2:I:186:ILE:HB	2.01	0.43
2:L:85:TYR:HE1	2:L:112:LEU:HD11	1.80	0.43
2:P:91:ASP:HA	2:P:94:TYR:HB3	2.01	0.43
1:E:317:LEU:HD22	1:E:317:LEU:HA	1.84	0.43
1:E:357:ARG:HE	1:E:357:ARG:HB3	1.57	0.43
1:F:345:LEU:HA	1:F:351:ILE:CD1	2.47	0.43
2:M:61:GLN:HA	2:M:94:TYR:CD1	2.53	0.43
2:P:151:HIS:CD2	2:P:151:HIS:O	2.70	0.43
1:B:138:PRO:CG	1:B:141:LEU:HB3	2.48	0.43
1:E:380:HIS:CE1	1:E:382:TRP:HB2	2.54	0.43
1:F:180:LYS:HG2	1:G:157:ASP:OD1	2.18	0.43
1:G:211:TRP:CE3	1:G:250:ARG:HD3	2.54	0.43
1:G:341:GLY:CA	1:G:357:ARG:HB3	2.48	0.43
1:G:385:PRO:HA	1:G:434:LEU:CD2	2.32	0.43
1:H:294:MET:HE3	1:H:294:MET:HB3	1.88	0.43
1:H:408:TRP:HH2	2:I:23:ARG:CG	2.23	0.43
2:K:110:LEU:CD1	2:K:116:LEU:CD1	2.97	0.43
2:M:85:TYR:HD1	2:M:112:LEU:CD2	2.27	0.43
1:B:28:PRO:HG3	1:B:82:TYR:HE2	1.84	0.42
1:D:33:LEU:HD21	1:D:141:LEU:CD2	2.49	0.42
1:D:357:ARG:HE	1:D:357:ARG:HB3	1.45	0.42
1:D:387:LEU:HD23	1:D:387:LEU:HA	1.85	0.42
1:E:292:ARG:HD3	1:E:308:PHE:HZ	1.80	0.42
1:E:295:HIS:C	1:E:295:HIS:ND1	2.73	0.42
1:E:428:ARG:HD2	1:E:428:ARG:C	2.39	0.42
1:F:261:ILE:CB	1:F:287:LEU:HB2	2.48	0.42
1:G:316:ARG:HD2	1:G:346:MET:HA	2.01	0.42
1:G:332:LEU:HD23	1:G:332:LEU:HA	1.86	0.42
2:J:69:TYR:HE1	2:J:85:TYR:CE2	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:35:CYS:SG	2:K:48:LEU:HD21	2.59	0.42
2:O:151:HIS:O	2:O:151:HIS:CG	2.72	0.42
1:A:34:LEU:HD12	1:A:361:PHE:CE1	2.54	0.42
1:B:107:GLU:H	1:B:107:GLU:HG3	1.31	0.42
1:B:305:GLY:HA2	1:G:297:VAL:HG13	2.00	0.42
1:F:217:PHE:HZ	1:G:157:ASP:HB3	1.84	0.42
1:G:34:LEU:O	1:G:361:PHE:CZ	2.72	0.42
1:G:240:THR:OG1	1:G:265:ASP:OD1	2.36	0.42
1:H:98:ILE:HD13	1:H:98:ILE:HA	1.74	0.42
1:H:167:LEU:H	1:H:195:ASP:HB2	1.85	0.42
2:K:93:LEU:HD13	2:K:96:LEU:HD22	1.91	0.42
2:M:131:PHE:CD2	2:M:131:PHE:O	2.71	0.42
2:O:139:GLU:HG2	2:O:140:ASN:N	2.27	0.42
1:B:167:LEU:H	1:B:195:ASP:HB2	1.85	0.42
1:B:332:LEU:HD23	1:B:332:LEU:HA	1.77	0.42
1:C:29:LYS:C	1:C:31:THR:N	2.68	0.42
1:C:198:LYS:O	1:C:198:LYS:HG2	2.18	0.42
1:C:235:HIS:CG	1:C:235:HIS:O	2.72	0.42
1:C:380:HIS:CE1	1:C:459:TRP:HB3	2.55	0.42
1:C:380:HIS:HE1	1:C:459:TRP:HB3	1.83	0.42
1:D:38:ARG:CZ	1:D:95:PHE:CE1	3.03	0.42
1:D:241:ALA:N	1:D:247:MET:CE	2.82	0.42
1:E:139:VAL:O	1:E:139:VAL:HG12	2.19	0.42
1:E:291:HIS:ND1	1:E:291:HIS:C	2.73	0.42
1:F:352:GLU:N	1:F:352:GLU:CD	2.73	0.42
1:F:430:GLU:OE1	1:F:432:ARG:CD	2.65	0.42
2:N:147:ASP:O	2:N:151:HIS:N	2.53	0.42
1:C:24:PRO:C	1:C:25:ASP:OD1	2.58	0.42
1:C:389:GLU:O	1:C:389:GLU:HG3	2.18	0.42
1:D:382:TRP:CD1	1:D:459:TRP:C	2.90	0.42
1:E:267:LEU:HD23	1:E:294:MET:O	2.20	0.42
1:E:286:VAL:C	1:E:287:LEU:O	2.58	0.42
1:F:34:LEU:HD12	1:F:361:PHE:CE1	2.54	0.42
1:G:263:MET:CA	1:G:289:HIS:HB3	2.48	0.42
1:G:461:GLU:CD	1:G:461:GLU:N	2.73	0.42
1:H:291:HIS:ND1	1:H:291:HIS:C	2.73	0.42
2:J:27:ARG:CD	2:J:27:ARG:H	2.31	0.42
2:K:55:GLU:HA	2:K:56:PRO:HD3	1.83	0.42
1:B:146:GLN:NE2	1:B:146:GLN:O	2.52	0.42
1:C:136:ARG:HG3	1:C:136:ARG:NH1	2.14	0.42
1:C:363:GLN:NE2	1:C:365:TRP:CG	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:316:ARG:NE	1:E:365:TRP:CZ2	2.78	0.42
1:F:196:PHE:O	1:F:197:THR:HG22	2.20	0.42
1:F:309:ARG:CB	1:F:309:ARG:CZ	2.98	0.42
1:G:256:GLU:O	1:G:256:GLU:HG2	2.19	0.42
1:G:384:MET:CE	1:G:420:ALA:CB	2.96	0.42
1:G:442:LEU:H	1:G:442:LEU:HG	1.57	0.42
2:J:85:TYR:HH	2:J:93:LEU:HD11	1.83	0.42
2:J:166:ARG:O	2:J:169:LEU:HG	2.19	0.42
2:J:176:PHE:HD1	2:J:176:PHE:HA	1.73	0.42
2:L:134:LEU:HD22	2:L:135:PRO:N	2.34	0.42
2:O:133:ARG:HA	2:O:133:ARG:HD2	1.89	0.42
1:B:142:VAL:HG13	1:B:142:VAL:O	2.19	0.42
1:B:434:LEU:HA	1:B:437:GLU:OE1	2.20	0.42
1:C:336:LYS:NZ	1:C:390:ILE:HD12	2.34	0.42
1:D:199:ASP:CB	1:D:203:ILE:HD13	2.49	0.42
1:D:419:VAL:HG12	1:D:452:LEU:HD22	2.00	0.42
1:E:167:LEU:H	1:E:195:ASP:HB2	1.85	0.42
1:E:381:VAL:HG21	1:E:455:ALA:HB1	2.02	0.42
1:F:445:ALA:HB3	1:F:452:LEU:HD21	2.01	0.42
1:H:82:TYR:N	1:H:82:TYR:CD1	2.88	0.42
1:H:328:VAL:HG11	1:H:336:LYS:HA	2.02	0.42
2:J:110:LEU:HD11	2:J:114:ARG:HG2	2.02	0.42
2:M:60:ASN:ND2	2:M:60:ASN:C	2.73	0.42
2:O:18:LEU:O	2:O:22:ARG:N	2.52	0.42
1:A:122:PHE:HD2	1:H:297:VAL:HA	1.85	0.42
1:A:167:LEU:H	1:A:195:ASP:HB2	1.85	0.42
1:B:34:LEU:HD12	1:B:361:PHE:CE1	2.54	0.42
1:B:105:PHE:HE1	1:B:113:ILE:CB	2.32	0.42
1:B:106:GLU:OE2	1:G:205:SER:CB	2.60	0.42
1:C:109:SER:N	1:C:145:PHE:HE1	2.17	0.42
1:C:222:ILE:CD1	1:C:234:GLY:CA	2.98	0.42
1:D:198:LYS:CB	1:D:236:TYR:HB2	2.30	0.42
1:D:198:LYS:HE3	1:D:324:HIS:HE1	1.85	0.42
1:E:203:ILE:O	1:E:203:ILE:HG23	2.20	0.42
1:F:381:VAL:HG21	1:F:455:ALA:HB1	2.02	0.42
1:G:167:LEU:H	1:G:195:ASP:HB2	1.85	0.42
1:H:22:TYR:HD2	1:H:48:PRO:HB2	0.52	0.42
1:H:382:TRP:CE3	1:H:461:GLU:CD	2.92	0.42
2:L:110:LEU:HA	2:L:113:GLU:HG2	2.01	0.42
2:L:187:GLU:HG2	2:L:188:ALA:N	2.34	0.42
2:O:14:ARG:HD2	2:O:17:LEU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:HIS:CE1	1:A:382:TRP:HB2	2.54	0.42
1:B:34:LEU:HD12	1:B:82:TYR:OH	2.00	0.42
1:B:143:LYS:CE	1:H:107:GLU:OE2	2.67	0.42
1:B:340:LEU:HD13	2:N:126:LYS:NZ	2.35	0.42
1:E:187:TYR:C	1:E:187:TYR:HD2	2.23	0.42
1:E:384:MET:HE2	1:E:421:LEU:HG	2.01	0.42
1:F:152:ILE:HG13	1:F:370:GLY:O	2.19	0.42
1:F:219:ALA:HB3	1:F:257:LEU:HD11	1.78	0.42
1:G:345:LEU:HD22	1:G:345:LEU:HA	1.75	0.42
1:H:408:TRP:CE3	2:I:23:ARG:O	2.73	0.42
1:C:82:TYR:CE1	1:C:97:PHE:CG	2.98	0.42
1:C:291:HIS:ND1	1:C:291:HIS:C	2.73	0.42
1:C:380:HIS:CE1	1:C:382:TRP:HB2	2.54	0.42
1:D:167:LEU:CD1	1:D:418:ARG:HA	2.47	0.42
1:D:178:SER:O	1:D:182:TYR:CB	2.67	0.42
1:D:236:TYR:HB3	1:D:263:MET:HB3	2.01	0.42
1:E:255:LYS:CE	1:E:284:ASN:OD1	2.68	0.42
1:E:262:ILE:O	1:E:289:HIS:N	2.47	0.42
1:F:109:SER:N	1:F:145:PHE:CZ	2.87	0.42
1:F:380:HIS:HE1	1:F:382:TRP:HB2	1.81	0.42
1:G:28:PRO:HB3	1:G:34:LEU:HD23	2.01	0.42
1:H:22:TYR:OH	1:H:49:GLU:HG3	2.01	0.42
1:H:55:ALA:HB1	1:H:79:GLY:O	2.20	0.42
2:M:58:GLN:HA	2:M:61:GLN:HB3	2.02	0.42
2:M:151:HIS:O	2:M:151:HIS:CG	2.73	0.42
2:O:154:TRP:HA	2:O:158:GLN:CB	2.49	0.42
1:A:236:TYR:HB3	1:A:263:MET:HB3	2.01	0.42
1:B:34:LEU:CD2	1:B:82:TYR:CZ	3.03	0.42
1:B:105:PHE:HE1	1:B:113:ILE:CG2	2.33	0.42
1:B:122:PHE:O	1:G:296:ALA:HB1	2.19	0.42
1:B:142:VAL:HG22	1:B:317:LEU:CD2	2.35	0.42
1:B:435:TYR:OH	2:N:133:ARG:NH1	2.53	0.42
1:C:408:TRP:CZ3	2:J:23:ARG:C	2.89	0.42
1:D:167:LEU:H	1:D:195:ASP:HB2	1.85	0.42
1:D:190:LEU:CD1	1:D:190:LEU:C	2.89	0.42
1:D:204:ASN:O	1:D:206:GLN:CG	2.59	0.42
1:E:257:LEU:HD13	1:E:259:MET:HE3	2.02	0.42
1:F:382:TRP:HA	1:F:382:TRP:CE3	2.55	0.42
1:G:381:VAL:HG21	1:G:455:ALA:HB1	2.02	0.42
1:H:34:LEU:HD12	1:H:361:PHE:CE1	2.54	0.42
1:H:380:HIS:HE1	1:H:382:TRP:HB2	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:132:CYS:HA	2:I:143:ARG:HH12	1.85	0.42
2:I:150:ALA:HB1	2:I:154:TRP:HZ3	1.85	0.42
2:K:31:TRP:CD1	2:K:31:TRP:N	2.88	0.42
2:M:53:GLY:O	2:M:54:PHE:CD2	2.73	0.42
2:P:18:LEU:O	2:P:21:LEU:HB2	2.20	0.42
1:B:316:ARG:CZ	1:B:346:MET:O	2.68	0.41
1:E:266:PHE:CG	1:E:315:LEU:HD21	2.55	0.41
1:E:352:GLU:C	1:E:359:VAL:CG1	2.60	0.41
1:F:167:LEU:H	1:F:195:ASP:HB2	1.85	0.41
1:F:247:MET:O	1:F:251:ALA:HB3	2.20	0.41
1:H:184:ARG:HB3	2:I:49:PHE:CZ	2.55	0.41
2:I:22:ARG:HB2	2:I:52:THR:HB	2.01	0.41
2:L:82:ARG:O	2:L:82:ARG:HG2	2.20	0.41
2:L:160:ARG:CB	2:L:166:ARG:CG	2.80	0.41
1:B:325:SER:OG	1:B:342:PHE:HZ	2.02	0.41
1:D:145:PHE:HD1	1:D:145:PHE:HA	1.73	0.41
1:D:317:LEU:HD23	1:D:317:LEU:HA	1.89	0.41
1:E:338:SER:H	1:E:338:SER:HG	1.50	0.41
1:E:384:MET:CG	1:E:421:LEU:CD1	2.78	0.41
1:H:236:TYR:HB3	1:H:263:MET:HB3	2.01	0.41
1:H:381:VAL:HG21	1:H:455:ALA:HB1	2.02	0.41
2:J:169:LEU:HB3	2:J:173:GLY:H	1.85	0.41
2:L:28:TRP:CE3	2:L:87:GLU:HA	2.55	0.41
2:N:176:PHE:O	2:N:183:ARG:HD3	2.20	0.41
2:O:129:LYS:C	2:O:131:PHE:H	2.23	0.41
1:A:381:VAL:HG21	1:A:455:ALA:HB1	2.02	0.41
1:D:332:LEU:C	1:D:335:ASP:OD2	2.58	0.41
1:E:328:VAL:CG2	1:E:336:LYS:HZ2	2.21	0.41
1:F:80:LYS:O	1:F:81:CYS:O	2.38	0.41
1:F:302:ARG:HG2	1:F:302:ARG:NH1	2.34	0.41
1:G:198:LYS:CA	1:G:235:HIS:HE1	2.31	0.41
1:G:291:HIS:ND1	1:G:291:HIS:C	2.73	0.41
1:G:295:HIS:C	1:G:295:HIS:ND1	2.73	0.41
1:G:404:LEU:CB	1:G:459:TRP:CH2	3.01	0.41
2:I:132:CYS:SG	2:I:133:ARG:NH2	2.93	0.41
2:K:187:GLU:O	2:K:187:GLU:HG2	2.17	0.41
2:L:28:TRP:HB3	2:L:87:GLU:CA	2.50	0.41
2:L:62:ILE:C	2:L:62:ILE:CD1	2.89	0.41
2:M:15:GLN:HE21	2:M:15:GLN:N	2.18	0.41
1:B:236:TYR:HB3	1:B:263:MET:HB3	2.01	0.41
1:B:328:VAL:HB	1:B:336:LYS:HE3	1.30	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:ALA:CB	1:D:94:TYR:CZ	3.00	0.41
1:E:236:TYR:HB3	1:E:263:MET:CG	2.48	0.41
1:F:130:LEU:O	1:F:304:HIS:HA	2.21	0.41
1:F:291:HIS:C	1:F:291:HIS:ND1	2.73	0.41
1:H:81:CYS:CA	1:H:98:ILE:HD12	2.50	0.41
2:K:110:LEU:HD22	2:K:113:GLU:HG3	2.02	0.41
1:B:122:PHE:CZ	1:B:131:ARG:N	2.88	0.41
1:C:385:PRO:CA	1:C:424:CYS:SG	3.02	0.41
1:C:426:GLN:HE21	1:C:426:GLN:C	2.24	0.41
1:D:82:TYR:CD1	1:D:82:TYR:N	2.86	0.41
1:E:292:ARG:HD2	1:E:308:PHE:CE2	2.52	0.41
1:F:80:LYS:O	1:F:81:CYS:C	2.58	0.41
1:G:443:ARG:HA	1:G:456:LEU:CD2	2.50	0.41
1:H:22:TYR:CD2	1:H:48:PRO:CA	2.95	0.41
2:J:55:GLU:OE1	2:J:58:GLN:NE2	2.48	0.41
2:J:104:ARG:C	2:J:104:ARG:CD	2.87	0.41
2:J:141:PHE:CE1	2:J:147:ASP:OD1	2.63	0.41
1:B:145:PHE:HD1	1:B:145:PHE:HA	1.70	0.41
1:B:342:PHE:CD2	1:B:342:PHE:O	2.74	0.41
1:B:348:GLU:OE1	2:N:122:ARG:NH1	2.36	0.41
1:B:400:GLY:H	1:B:404:LEU:HD12	1.83	0.41
1:D:219:ALA:HB1	1:D:257:LEU:CD2	2.50	0.41
1:E:149:PRO:HA	1:E:282:ARG:HB2	2.02	0.41
1:E:171:ILE:HD11	1:E:186:VAL:HG22	2.03	0.41
1:F:304:HIS:ND1	1:F:304:HIS:C	2.73	0.41
1:G:347:ARG:HG3	1:G:347:ARG:HH11	1.86	0.41
2:M:121:ILE:HA	2:M:124:VAL:CG1	2.48	0.41
1:B:31:THR:O	1:B:33:LEU:HD22	2.20	0.41
1:B:138:PRO:HG2	1:B:141:LEU:HB2	2.02	0.41
1:B:433:ASP:C	1:B:437:GLU:CD	2.77	0.41
1:C:356:SER:CB	2:O:155:ARG:HH22	2.32	0.41
1:C:433:ASP:O	1:C:437:GLU:OE1	2.38	0.41
1:E:25:ASP:O	1:E:27:THR:N	2.54	0.41
1:E:211:TRP:HB2	1:E:250:ARG:HD3	2.02	0.41
1:E:328:VAL:HG11	1:E:336:LYS:HA	2.02	0.41
1:F:263:MET:SD	1:F:263:MET:O	2.79	0.41
2:J:28:TRP:CH2	2:J:90:SER:N	2.89	0.41
2:K:187:GLU:HA	2:K:190:LEU:HG	2.03	0.41
2:K:191:LEU:O	2:K:191:LEU:HD23	2.21	0.41
2:M:57:ILE:HD12	2:M:57:ILE:HA	1.85	0.41
1:C:317:LEU:HD23	1:C:317:LEU:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:ALA:HB2	1:D:94:TYR:OH	2.19	0.41
1:F:222:ILE:HD11	1:F:234:GLY:C	2.39	0.41
1:H:190:LEU:HD13	1:H:190:LEU:O	2.20	0.41
2:K:27:ARG:CD	2:K:27:ARG:H	2.33	0.41
2:M:91:ASP:HA	2:M:94:TYR:HB3	2.02	0.41
2:N:131:PHE:HE2	2:N:143:ARG:HA	1.85	0.41
2:O:106:LEU:HD22	2:O:145:PRO:HD3	2.02	0.41
1:A:25:ASP:O	1:A:27:THR:N	2.54	0.41
1:A:190:LEU:HD11	1:A:233:LYS:HB3	2.03	0.41
1:B:63:TRP:CG	1:B:63:TRP:O	2.70	0.41
1:B:190:LEU:HD11	1:B:233:LYS:HB3	2.03	0.41
1:C:164:ARG:HB2	1:C:165:PRO:HD2	2.01	0.41
1:C:184:ARG:HD3	1:C:184:ARG:HA	1.90	0.41
1:C:328:VAL:CG1	1:C:336:LYS:HE2	2.49	0.41
1:C:341:GLY:HA3	1:C:357:ARG:HB3	2.01	0.41
1:C:361:PHE:HD2	1:C:361:PHE:O	2.04	0.41
1:C:437:GLU:H	1:C:437:GLU:CD	2.08	0.41
1:D:137:PHE:HB2	1:D:363:GLN:NE2	2.36	0.41
1:F:36:ALA:HB2	1:F:97:PHE:CD1	2.56	0.41
1:F:196:PHE:C	1:F:197:THR:CG2	2.89	0.41
1:F:267:LEU:HD21	1:F:311:LEU:CD1	2.51	0.41
1:F:315:LEU:O	1:F:318:SER:O	2.39	0.41
1:H:297:VAL:HG13	1:H:297:VAL:O	2.19	0.41
2:J:91:ASP:HA	2:J:94:TYR:HB3	2.02	0.41
2:L:85:TYR:CD2	2:L:85:TYR:O	2.74	0.41
2:M:174:LEU:HB3	2:M:175:GLN:H	1.69	0.41
2:N:99:LEU:O	2:N:104:ARG:NE	2.54	0.41
2:P:81:VAL:HA	2:P:112:LEU:HD22	2.02	0.41
2:P:110:LEU:HA	2:P:113:GLU:HG2	2.03	0.41
1:B:174:LYS:HB2	1:G:60:THR:HG22	2.03	0.41
1:C:71:LEU:HD11	2:M:31:TRP:HZ3	1.86	0.41
1:C:379:ILE:HD13	1:C:387:LEU:HD11	2.03	0.41
1:D:191:ARG:O	1:D:192:GLY:C	2.60	0.41
1:D:191:ARG:C	1:D:193:GLY:N	2.74	0.41
1:F:211:TRP:CZ3	1:F:250:ARG:HA	2.54	0.41
1:G:215:PHE:CD2	1:G:237:LEU:CD2	2.86	0.41
1:H:179:ALA:HB1	1:H:217:PHE:HE2	1.83	0.41
2:J:18:LEU:HD22	2:J:38:LEU:HD11	2.00	0.41
2:J:85:TYR:CE1	2:J:93:LEU:HD21	2.48	0.41
2:M:56:PRO:HA	2:M:59:GLN:HE21	1.84	0.41
2:N:22:ARG:NH1	2:N:52:THR:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:157:ALA:O	2:P:166:ARG:CZ	2.69	0.41
1:C:177:LEU:HD22	1:C:177:LEU:HA	1.77	0.40
1:D:224:LYS:CE	2:L:50:GLU:OE2	2.59	0.40
1:D:408:TRP:HZ3	2:L:23:ARG:HB3	1.86	0.40
1:E:311:LEU:HD23	1:E:311:LEU:HA	1.85	0.40
1:G:28:PRO:HG3	1:G:34:LEU:HD21	2.03	0.40
1:H:37:PHE:O	1:H:95:PHE:HA	2.22	0.40
2:K:22:ARG:HH21	2:K:24:LYS:NZ	2.19	0.40
2:K:99:LEU:CD1	2:K:104:ARG:N	2.58	0.40
2:M:58:GLN:H	2:M:58:GLN:HG2	1.57	0.40
1:A:157:ASP:HB3	1:D:217:PHE:HZ	1.86	0.40
1:C:406:HIS:NE2	1:C:408:TRP:HB2	2.37	0.40
1:C:429:ASN:OD1	2:O:64:VAL:CG2	2.67	0.40
1:D:82:TYR:HD1	1:D:82:TYR:N	2.19	0.40
1:D:345:LEU:HD22	1:D:345:LEU:HA	1.77	0.40
1:D:345:LEU:HD23	1:D:351:ILE:HG21	2.04	0.40
1:E:135:ILE:O	1:E:135:ILE:HG23	2.20	0.40
1:E:374:VAL:HB	1:E:396:VAL:HB	2.03	0.40
1:F:261:ILE:HD12	1:F:287:LEU:HB3	2.03	0.40
1:H:178:SER:O	1:H:179:ALA:C	2.59	0.40
1:H:191:ARG:O	1:H:193:GLY:N	2.55	0.40
1:H:424:CYS:SG	1:H:442:LEU:CD2	3.09	0.40
2:J:28:TRP:CE3	2:J:86:GLN:C	2.93	0.40
1:C:34:LEU:O	1:C:361:PHE:CZ	2.74	0.40
1:C:374:VAL:HB	1:C:396:VAL:HB	2.03	0.40
1:C:382:TRP:NE1	1:C:459:TRP:O	2.34	0.40
1:D:326:GLY:O	1:D:375:ALA:HB2	2.15	0.40
1:F:131:ARG:HG3	1:F:305:GLY:O	2.21	0.40
1:G:385:PRO:CB	1:G:434:LEU:HD23	2.50	0.40
1:H:316:ARG:CZ	1:H:346:MET:O	2.69	0.40
1:H:342:PHE:CD2	1:H:342:PHE:O	2.75	0.40
2:J:169:LEU:O	2:J:174:LEU:HG	2.22	0.40
2:M:92:LEU:HD21	2:M:111:ALA:HB1	2.03	0.40
2:M:107:CYS:SG	2:M:121:ILE:HD12	2.60	0.40
2:N:110:LEU:HA	2:N:113:GLU:HG2	2.03	0.40
1:A:317:LEU:HD23	1:A:317:LEU:HA	1.89	0.40
1:C:231:GLU:OE1	1:C:233:LYS:HE2	2.22	0.40
1:C:382:TRP:HA	1:C:382:TRP:HE3	1.86	0.40
1:E:342:PHE:CE2	1:E:346:MET:HE2	2.56	0.40
1:F:87:VAL:HG23	1:F:94:TYR:CA	2.49	0.40
1:F:222:ILE:HD11	1:F:235:HIS:CB	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:156:ARG:HH21	1:G:394:ASP:HA	1.87	0.40
1:G:390:ILE:N	1:G:390:ILE:CD1	2.83	0.40
2:N:55:GLU:HA	2:N:56:PRO:HD3	1.84	0.40
1:B:355:ARG:CZ	2:N:159:GLU:HG3	2.52	0.40
1:C:83:HIS:ND1	1:C:97:PHE:CD2	2.89	0.40
1:C:165:PRO:HG3	1:C:393:ASP:O	2.22	0.40
1:C:166:MET:CB	1:C:195:ASP:OD2	2.69	0.40
1:C:190:LEU:HD11	1:C:233:LYS:HB2	2.04	0.40
1:D:31:THR:O	1:D:138:PRO:HB3	2.22	0.40
1:E:261:ILE:HB	1:E:287:LEU:HB2	2.03	0.40
1:F:200:ASP:N	1:F:203:ILE:HD13	2.36	0.40
1:H:222:ILE:HD11	1:H:235:HIS:CB	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	445/447 (100%)	402 (90%)	41 (9%)	2 (0%)	34	72
1	B	445/447 (100%)	389 (87%)	44 (10%)	12 (3%)	5	34
1	C	445/447 (100%)	384 (86%)	50 (11%)	11 (2%)	5	35
1	D	445/447 (100%)	379 (85%)	56 (13%)	10 (2%)	6	38
1	E	445/447 (100%)	388 (87%)	45 (10%)	12 (3%)	5	34
1	F	445/447 (100%)	362 (81%)	69 (16%)	14 (3%)	4	31
1	G	445/447 (100%)	383 (86%)	49 (11%)	13 (3%)	4	32
1	H	445/447 (100%)	387 (87%)	50 (11%)	8 (2%)	8	42
2	I	177/188 (94%)	146 (82%)	31 (18%)	0	100	100
2	J	186/188 (99%)	147 (79%)	30 (16%)	9 (5%)	2	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	177/188 (94%)	155 (88%)	17 (10%)	5 (3%)	5	33
2	L	177/188 (94%)	143 (81%)	27 (15%)	7 (4%)	3	26
2	M	178/188 (95%)	147 (83%)	26 (15%)	5 (3%)	5	33
2	N	179/188 (95%)	159 (89%)	20 (11%)	0	100	100
2	O	179/188 (95%)	153 (86%)	24 (13%)	2 (1%)	14	52
2	P	180/188 (96%)	162 (90%)	18 (10%)	0	100	100
All	All	4993/5080 (98%)	4286 (86%)	597 (12%)	110 (2%)	10	38

All (110) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	32	ASP
1	B	84	ILE
1	C	30	ASP
1	C	84	ILE
1	D	84	ILE
1	D	204	ASN
1	D	210	ARG
1	E	204	ASN
1	E	287	LEU
1	F	177	LEU
1	F	178	SER
1	F	205	SER
1	F	210	ARG
1	F	287	LEU
1	G	30	ASP
1	G	205	SER
1	H	84	ILE
1	H	179	ALA
2	J	115	LYS
2	J	142	ASP
2	L	136	LYS
2	L	177	ALA
2	M	16	GLU
2	M	117	ASP
2	O	191	LEU
1	B	25	ASP
1	B	61	GLY
1	B	101	PRO
1	B	139	VAL

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Mol	Chain	Res	Type
1	B	381	VAL
1	C	79	GLY
1	C	292	ARG
1	D	359	VAL
1	E	203	ILE
1	E	298	ILE
1	E	359	VAL
1	E	425	VAL
1	F	81	CYS
1	F	291	HIS
1	F	447	LYS
1	G	238	ASN
1	G	298	ILE
1	G	359	VAL
1	H	292	ARG
1	H	446	GLY
2	J	174	LEU
2	K	17	LEU
2	K	96	LEU
2	L	101	GLN
1	A	26	TYR
1	A	101	PRO
1	C	101	PRO
1	C	359	VAL
1	D	26	TYR
1	D	101	PRO
1	D	192	GLY
1	D	203	ILE
1	E	26	TYR
1	E	101	PRO
1	E	292	ARG
1	F	26	TYR
1	F	101	PRO
1	F	346	MET
1	G	101	PRO
1	G	389	GLU
1	H	101	PRO
2	J	27	ARG
2	J	101	GLN
2	J	163	LEU
2	K	27	ARG
2	L	82	ARG

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Mol	Chain	Res	Type
2	L	135	PRO
2	L	166	ARG
1	B	22	TYR
1	B	382	TRP
1	C	25	ASP
1	C	27	THR
1	C	228	GLU
1	D	242	PRO
1	E	345	LEU
1	F	352	GLU
1	G	25	ASP
1	G	27	THR
1	G	193	GLY
1	H	22	TYR
1	H	25	ASP
2	J	82	ARG
2	J	141	PHE
2	K	16	GLU
2	K	101	GLN
2	M	87	GLU
2	O	178	GLN
1	B	26	TYR
1	B	27	THR
1	B	405	GLY
1	E	202	ASN
1	F	300	ARG
1	F	303	ASN
2	J	100	ASP
2	M	51	ALA
1	C	92	ASN
1	G	292	ARG
1	G	346	MET
2	L	51	ALA
1	H	192	GLY
1	G	242	PRO
2	M	62	ILE
1	C	239	VAL
1	D	66	VAL
1	E	242	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	363/363 (100%)	353 (97%)	10 (3%)	43	65
1	B	363/363 (100%)	315 (87%)	48 (13%)	4	20
1	C	363/363 (100%)	292 (80%)	71 (20%)	1	9
1	D	363/363 (100%)	288 (79%)	75 (21%)	1	7
1	E	363/363 (100%)	296 (82%)	67 (18%)	1	11
1	F	363/363 (100%)	269 (74%)	94 (26%)	0	4
1	G	363/363 (100%)	303 (84%)	60 (16%)	2	14
1	H	363/363 (100%)	312 (86%)	51 (14%)	3	19
2	I	151/159 (95%)	147 (97%)	4 (3%)	46	67
2	J	159/159 (100%)	124 (78%)	35 (22%)	1	6
2	K	151/159 (95%)	122 (81%)	29 (19%)	1	9
2	L	151/159 (95%)	122 (81%)	29 (19%)	1	9
2	M	152/159 (96%)	131 (86%)	21 (14%)	3	20
2	N	153/159 (96%)	141 (92%)	12 (8%)	12	38
2	O	153/159 (96%)	130 (85%)	23 (15%)	3	17
2	P	154/159 (97%)	147 (96%)	7 (4%)	27	54
All	All	4128/4176 (99%)	3492 (85%)	636 (15%)	6	16

All (636) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LEU
1	A	112	ASN
1	A	136	ARG
1	A	177	LEU
1	A	257	LEU
1	A	292	ARG
1	A	300	ARG
1	A	426	GLN

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Mol	Chain	Res	Type
1	A	444	GLU
1	A	460	LYS
1	B	23	THR
1	B	25	ASP
1	B	29	LYS
1	B	30	ASP
1	B	34	LEU
1	B	80	LYS
1	B	81	CYS
1	B	82	TYR
1	B	84	ILE
1	B	102	LEU
1	B	104	LEU
1	B	107	GLU
1	B	112	ASN
1	B	122	PHE
1	B	124	PHE
1	B	135	ILE
1	B	136	ARG
1	B	141	LEU
1	B	142	VAL
1	B	143	LYS
1	B	144	THR
1	B	145	PHE
1	B	177	LEU
1	B	257	LEU
1	B	292	ARG
1	B	300	ARG
1	B	332	LEU
1	B	336	LYS
1	B	338	SER
1	B	340	LEU
1	B	342	PHE
1	B	345	LEU
1	B	346	MET
1	B	380	HIS
1	B	382	TRP
1	B	383	HIS
1	B	384	MET
1	B	387	LEU
1	B	389	GLU
1	B	390	ILE

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Mol	Chain	Res	Type
1	B	404	LEU
1	B	408	TRP
1	B	426	GLN
1	B	436	ARG
1	B	437	GLU
1	B	443	ARG
1	B	444	GLU
1	B	460	LYS
1	C	25	ASP
1	C	29	LYS
1	C	34	LEU
1	C	74	MET
1	C	76	ARG
1	C	77	TYR
1	C	82	TYR
1	C	83	HIS
1	C	84	ILE
1	C	85	GLU
1	C	87	VAL
1	C	90	GLU
1	C	91	GLU
1	C	112	ASN
1	C	134	ASP
1	C	135	ILE
1	C	136	ARG
1	C	142	VAL
1	C	143	LYS
1	C	144	THR
1	C	145	PHE
1	C	162	TYR
1	C	164	ARG
1	C	166	MET
1	C	177	LEU
1	C	178	SER
1	C	180	LYS
1	C	181	ASN
1	C	187	TYR
1	C	189	CYS
1	C	190	LEU
1	C	191	ARG
1	C	198	LYS
1	C	200	ASP

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Mol	Chain	Res	Type
1	C	201	GLU
1	C	202	ASN
1	C	224	LYS
1	C	225	SER
1	C	229	THR
1	C	233	LYS
1	C	236	TYR
1	C	237	LEU
1	C	245	GLU
1	C	247	MET
1	C	248	MET
1	C	253	PHE
1	C	255	LYS
1	C	257	LEU
1	C	294	MET
1	C	300	ARG
1	C	332	LEU
1	C	336	LYS
1	C	338	SER
1	C	339	THR
1	C	342	PHE
1	C	361	PHE
1	C	362	THR
1	C	363	GLN
1	C	379	ILE
1	C	380	HIS
1	C	382	TRP
1	C	384	MET
1	C	421	LEU
1	C	424	CYS
1	C	426	GLN
1	C	428	ARG
1	C	437	GLU
1	C	441	ILE
1	C	444	GLU
1	C	447	LYS
1	C	460	LYS
1	D	34	LEU
1	D	71	LEU
1	D	80	LYS
1	D	81	CYS
1	D	82	TYR

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Mol	Chain	Res	Type
1	D	84	ILE
1	D	93	SER
1	D	98	ILE
1	D	112	ASN
1	D	136	ARG
1	D	142	VAL
1	D	143	LYS
1	D	144	THR
1	D	145	PHE
1	D	169	CYS
1	D	174	LYS
1	D	177	LEU
1	D	180	LYS
1	D	186	VAL
1	D	187	TYR
1	D	189	CYS
1	D	190	LEU
1	D	191	ARG
1	D	198	LYS
1	D	199	ASP
1	D	200	ASP
1	D	201	GLU
1	D	202	ASN
1	D	203	ILE
1	D	206	GLN
1	D	210	ARG
1	D	212	ARG
1	D	214	ARG
1	D	215	PHE
1	D	216	LEU
1	D	220	ASP
1	D	243	THR
1	D	244	CYS
1	D	245	GLU
1	D	248	MET
1	D	253	PHE
1	D	255	LYS
1	D	257	LEU
1	D	292	ARG
1	D	300	ARG
1	D	327	THR
1	D	328	VAL

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Mol	Chain	Res	Type
1	D	329	VAL
1	D	331	LYS
1	D	332	LEU
1	D	335	ASP
1	D	336	LYS
1	D	338	SER
1	D	339	THR
1	D	342	PHE
1	D	344	ASP
1	D	345	LEU
1	D	346	MET
1	D	347	ARG
1	D	356	SER
1	D	357	ARG
1	D	361	PHE
1	D	379	ILE
1	D	380	HIS
1	D	384	MET
1	D	387	LEU
1	D	388	VAL
1	D	415	THR
1	D	418	ARG
1	D	424	CYS
1	D	426	GLN
1	D	428	ARG
1	D	429	ASN
1	D	444	GLU
1	D	460	LYS
1	E	34	LEU
1	E	62	THR
1	E	71	LEU
1	E	112	ASN
1	E	135	ILE
1	E	136	ARG
1	E	142	VAL
1	E	143	LYS
1	E	177	LEU
1	E	184	ARG
1	E	187	TYR
1	E	189	CYS
1	E	190	LEU
1	E	191	ARG

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Mol	Chain	Res	Type
1	E	198	LYS
1	E	199	ASP
1	E	200	ASP
1	E	201	GLU
1	E	202	ASN
1	E	203	ILE
1	E	237	LEU
1	E	239	VAL
1	E	243	THR
1	E	244	CYS
1	E	245	GLU
1	E	247	MET
1	E	248	MET
1	E	249	LYS
1	E	250	ARG
1	E	255	LYS
1	E	257	LEU
1	E	272	THR
1	E	277	LEU
1	E	279	LYS
1	E	281	CYS
1	E	282	ARG
1	E	284	ASN
1	E	287	LEU
1	E	288	LEU
1	E	295	HIS
1	E	298	ILE
1	E	300	ARG
1	E	308	PHE
1	E	311	LEU
1	E	313	LYS
1	E	315	LEU
1	E	317	LEU
1	E	318	SER
1	E	323	LEU
1	E	325	SER
1	E	335	ASP
1	E	336	LYS
1	E	338	SER
1	E	339	THR
1	E	340	LEU
1	E	342	PHE

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Mol	Chain	Res	Type
1	E	344	ASP
1	E	345	LEU
1	E	357	ARG
1	E	361	PHE
1	E	418	ARG
1	E	424	CYS
1	E	425	VAL
1	E	426	GLN
1	E	428	ARG
1	E	444	GLU
1	E	460	LYS
1	F	34	LEU
1	F	73	ASP
1	F	74	MET
1	F	75	ASP
1	F	76	ARG
1	F	77	TYR
1	F	94	TYR
1	F	98	ILE
1	F	112	ASN
1	F	136	ARG
1	F	142	VAL
1	F	143	LYS
1	F	144	THR
1	F	145	PHE
1	F	170	THR
1	F	171	ILE
1	F	172	LYS
1	F	177	LEU
1	F	180	LYS
1	F	181	ASN
1	F	186	VAL
1	F	187	TYR
1	F	189	CYS
1	F	190	LEU
1	F	191	ARG
1	F	198	LYS
1	F	199	ASP
1	F	200	ASP
1	F	201	GLU
1	F	210	ARG
1	F	212	ARG

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Mol	Chain	Res	Type
1	F	213	ASP
1	F	214	ARG
1	F	215	PHE
1	F	216	LEU
1	F	220	ASP
1	F	223	HIS
1	F	248	MET
1	F	249	LYS
1	F	250	ARG
1	F	252	GLU
1	F	253	PHE
1	F	255	LYS
1	F	257	LEU
1	F	263	MET
1	F	265	ASP
1	F	266	PHE
1	F	267	LEU
1	F	288	LEU
1	F	289	HIS
1	F	292	ARG
1	F	294	MET
1	F	295	HIS
1	F	298	ILE
1	F	300	ARG
1	F	301	GLN
1	F	302	ARG
1	F	304	HIS
1	F	306	ILE
1	F	308	PHE
1	F	309	ARG
1	F	311	LEU
1	F	313	LYS
1	F	317	LEU
1	F	335	ASP
1	F	336	LYS
1	F	338	SER
1	F	339	THR
1	F	340	LEU
1	F	342	PHE
1	F	343	VAL
1	F	344	ASP
1	F	345	LEU

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Mol	Chain	Res	Type
1	F	346	MET
1	F	347	ARG
1	F	348	GLU
1	F	349	ASP
1	F	351	ILE
1	F	367	SER
1	F	383	HIS
1	F	384	MET
1	F	387	LEU
1	F	389	GLU
1	F	390	ILE
1	F	408	TRP
1	F	410	ASN
1	F	426	GLN
1	F	433	ASP
1	F	437	GLU
1	F	440	ASP
1	F	443	ARG
1	F	444	GLU
1	F	447	LYS
1	F	460	LYS
1	G	25	ASP
1	G	26	TYR
1	G	29	LYS
1	G	30	ASP
1	G	34	LEU
1	G	38	ARG
1	G	39	PHE
1	G	40	SER
1	G	112	ASN
1	G	136	ARG
1	G	177	LEU
1	G	190	LEU
1	G	191	ARG
1	G	194	LEU
1	G	200	ASP
1	G	201	GLU
1	G	237	LEU
1	G	243	THR
1	G	244	CYS
1	G	245	GLU
1	G	248	MET

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Mol	Chain	Res	Type
1	G	249	LYS
1	G	252	GLU
1	G	253	PHE
1	G	255	LYS
1	G	288	LEU
1	G	292	ARG
1	G	295	HIS
1	G	298	ILE
1	G	300	ARG
1	G	331	LYS
1	G	332	LEU
1	G	336	LYS
1	G	338	SER
1	G	339	THR
1	G	342	PHE
1	G	343	VAL
1	G	344	ASP
1	G	345	LEU
1	G	346	MET
1	G	347	ARG
1	G	361	PHE
1	G	362	THR
1	G	363	GLN
1	G	383	HIS
1	G	384	MET
1	G	387	LEU
1	G	389	GLU
1	G	408	TRP
1	G	410	ASN
1	G	426	GLN
1	G	433	ASP
1	G	441	ILE
1	G	442	LEU
1	G	443	ARG
1	G	444	GLU
1	G	458	LEU
1	G	460	LYS
1	G	461	GLU
1	G	463	LYS
1	H	23	THR
1	H	25	ASP
1	H	26	TYR

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Mol	Chain	Res	Type
1	H	34	LEU
1	H	67	TRP
1	H	68	THR
1	H	80	LYS
1	H	81	CYS
1	H	82	TYR
1	H	83	HIS
1	H	84	ILE
1	H	93	SER
1	H	98	ILE
1	H	112	ASN
1	H	136	ARG
1	H	177	LEU
1	H	180	LYS
1	H	181	ASN
1	H	187	TYR
1	H	191	ARG
1	H	198	LYS
1	H	199	ASP
1	H	200	ASP
1	H	201	GLU
1	H	202	ASN
1	H	220	ASP
1	H	223	HIS
1	H	257	LEU
1	H	294	MET
1	H	297	VAL
1	H	300	ARG
1	H	335	ASP
1	H	336	LYS
1	H	338	SER
1	H	339	THR
1	H	340	LEU
1	H	342	PHE
1	H	345	LEU
1	H	346	MET
1	H	383	HIS
1	H	384	MET
1	H	389	GLU
1	H	408	TRP
1	H	426	GLN
1	H	433	ASP

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Mol	Chain	Res	Type
1	H	437	GLU
1	H	441	ILE
1	H	444	GLU
1	H	460	LYS
1	H	461	GLU
1	H	465	GLU
2	I	46	GLN
2	I	74	ARG
2	I	97	ARG
2	I	166	ARG
2	J	14	ARG
2	J	15	GLN
2	J	16	GLU
2	J	27	ARG
2	J	29	LEU
2	J	31	TRP
2	J	33	ARG
2	J	35	CYS
2	J	40	LYS
2	J	46	GLN
2	J	60	ASN
2	J	86	GLN
2	J	87	GLU
2	J	88	TRP
2	J	101	GLN
2	J	103	GLN
2	J	104	ARG
2	J	112	LEU
2	J	114	ARG
2	J	137	GLN
2	J	139	GLU
2	J	141	PHE
2	J	144	HIS
2	J	153	CYS
2	J	155	ARG
2	J	163	LEU
2	J	164	THR
2	J	166	ARG
2	J	168	ARG
2	J	170	ILE
2	J	172	ARG
2	J	174	LEU

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Mol	Chain	Res	Type
2	J	175	GLN
2	J	176	PHE
2	J	178	GLN
2	K	13	GLU
2	K	14	ARG
2	K	16	GLU
2	K	17	LEU
2	K	27	ARG
2	K	29	LEU
2	K	33	ARG
2	K	35	CYS
2	K	36	GLN
2	K	39	LEU
2	K	46	GLN
2	K	60	ASN
2	K	95	GLU
2	K	96	LEU
2	K	98	GLU
2	K	102	GLU
2	K	103	GLN
2	K	109	GLN
2	K	113	GLU
2	K	114	ARG
2	K	174	LEU
2	K	175	GLN
2	K	178	GLN
2	K	179	SER
2	K	183	ARG
2	K	185	LEU
2	K	187	GLU
2	K	189	LEU
2	K	191	LEU
2	L	14	ARG
2	L	15	GLN
2	L	43	LEU
2	L	46	GLN
2	L	47	THR
2	L	48	LEU
2	L	49	PHE
2	L	55	GLU
2	L	57	ILE
2	L	58	GLN

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Mol	Chain	Res	Type
2	L	60	ASN
2	L	62	ILE
2	L	64	VAL
2	L	86	GLN
2	L	98	GLU
2	L	99	LEU
2	L	134	LEU
2	L	153	CYS
2	L	154	TRP
2	L	155	ARG
2	L	158	GLN
2	L	166	ARG
2	L	167	SER
2	L	170	ILE
2	L	172	ARG
2	L	175	GLN
2	L	179	SER
2	L	183	ARG
2	L	187	GLU
2	M	14	ARG
2	M	15	GLN
2	M	46	GLN
2	M	57	ILE
2	M	58	GLN
2	M	59	GLN
2	M	60	ASN
2	M	62	ILE
2	M	86	GLN
2	M	87	GLU
2	M	117	ASP
2	M	119	ASP
2	M	123	GLU
2	M	124	VAL
2	M	126	LYS
2	M	128	THR
2	M	131	PHE
2	M	133	ARG
2	M	153	CYS
2	M	154	TRP
2	M	155	ARG
2	N	13	GLU
2	N	14	ARG

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Mol	Chain	Res	Type
2	N	17	LEU
2	N	46	GLN
2	N	60	ASN
2	N	139	GLU
2	N	168	ARG
2	N	170	ILE
2	N	172	ARG
2	N	176	PHE
2	N	178	GLN
2	N	179	SER
2	O	14	ARG
2	O	15	GLN
2	O	16	GLU
2	O	46	GLN
2	O	60	ASN
2	O	106	LEU
2	O	109	GLN
2	O	110	LEU
2	O	114	ARG
2	O	132	CYS
2	O	133	ARG
2	O	134	LEU
2	O	137	GLN
2	O	139	GLU
2	O	155	ARG
2	O	170	ILE
2	O	172	ARG
2	O	178	GLN
2	O	179	SER
2	O	183	ARG
2	O	185	LEU
2	O	186	ILE
2	O	187	GLU
2	P	14	ARG
2	P	15	GLN
2	P	17	LEU
2	P	18	LEU
2	P	46	GLN
2	P	60	ASN
2	P	155	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	HIS
1	A	146	GLN
1	A	181	ASN
1	A	324	HIS
1	A	383	HIS
1	B	146	GLN
1	B	160	ASN
1	B	324	HIS
1	C	146	GLN
1	C	160	ASN
1	C	235	HIS
1	C	324	HIS
1	C	380	HIS
1	C	426	GLN
1	D	83	HIS
1	D	146	GLN
1	D	209	GLN
1	D	264	HIS
1	D	289	HIS
1	D	324	HIS
1	D	380	HIS
1	D	417	ASN
1	E	83	HIS
1	E	146	GLN
1	E	160	ASN
1	E	181	ASN
1	E	383	HIS
1	E	417	ASN
1	E	426	GLN
1	F	83	HIS
1	F	146	GLN
1	F	202	ASN
1	F	204	ASN
1	F	274	ASN
1	F	289	HIS
1	F	324	HIS
1	G	83	HIS
1	G	146	GLN
1	G	181	ASN
1	G	324	HIS
1	H	146	GLN
1	H	160	ASN
1	H	181	ASN

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Mol	Chain	Res	Type
1	H	324	HIS
2	I	58	GLN
2	I	67	GLN
2	I	144	HIS
2	J	15	GLN
2	J	60	ASN
2	J	86	GLN
2	K	60	ASN
2	K	86	GLN
2	K	175	GLN
2	L	15	GLN
2	L	46	GLN
2	L	59	GLN
2	L	61	GLN
2	L	75	GLN
2	L	86	GLN
2	L	103	GLN
2	L	151	HIS
2	L	175	GLN
2	M	15	GLN
2	M	46	GLN
2	M	59	GLN
2	M	60	ASN
2	M	86	GLN
2	M	144	HIS
2	M	151	HIS
2	N	60	ASN
2	N	86	GLN
2	N	175	GLN
2	N	178	GLN
2	O	15	GLN
2	O	60	ASN
2	O	67	GLN
2	O	86	GLN
2	O	151	HIS
2	P	15	GLN
2	P	60	ASN
2	P	86	GLN
2	P	144	HIS
2	P	151	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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.

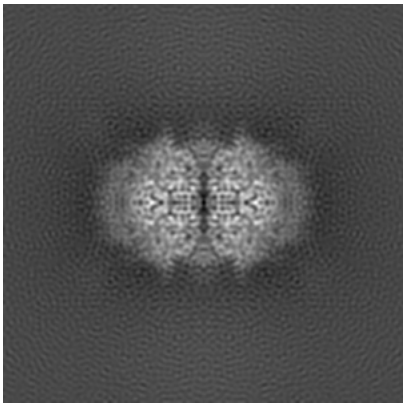
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-10235. These allow visual inspection of the internal detail of the map and identification of artifacts.

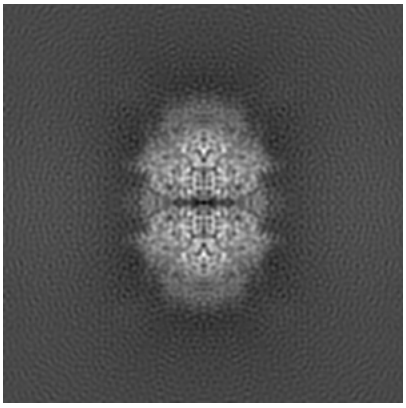
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

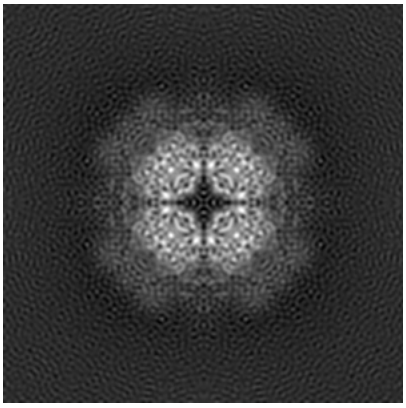
6.1.1 Primary map



X



Y

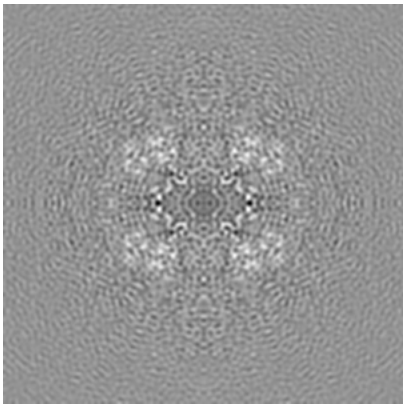


Z

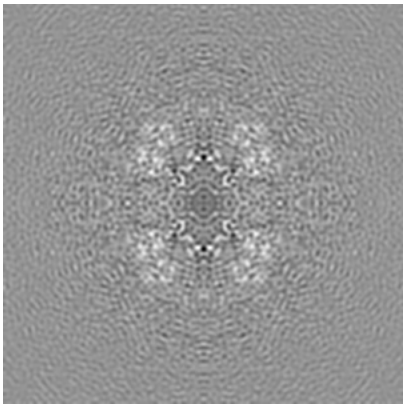
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

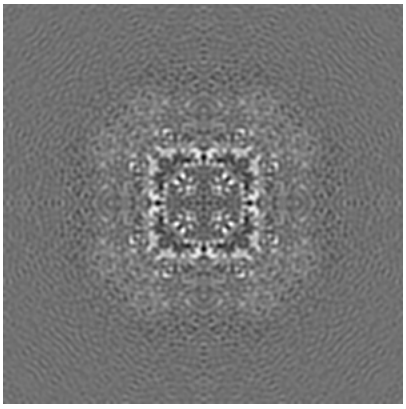
6.2.1 Primary map



X Index: 120



Y Index: 120

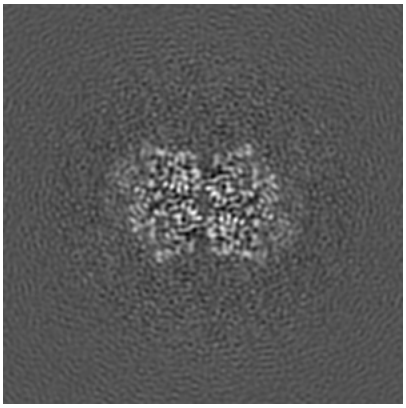


Z Index: 120

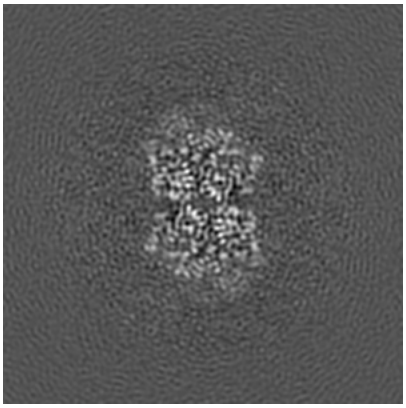
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

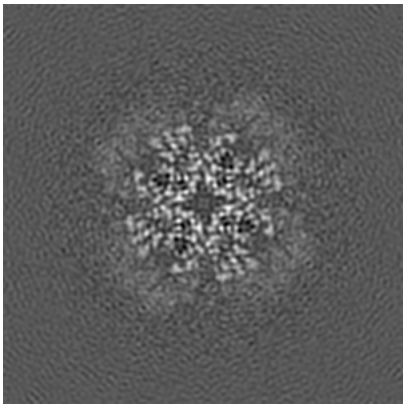
6.3.1 Primary map



X Index: 105



Y Index: 135



Z Index: 129

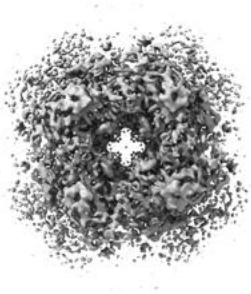
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

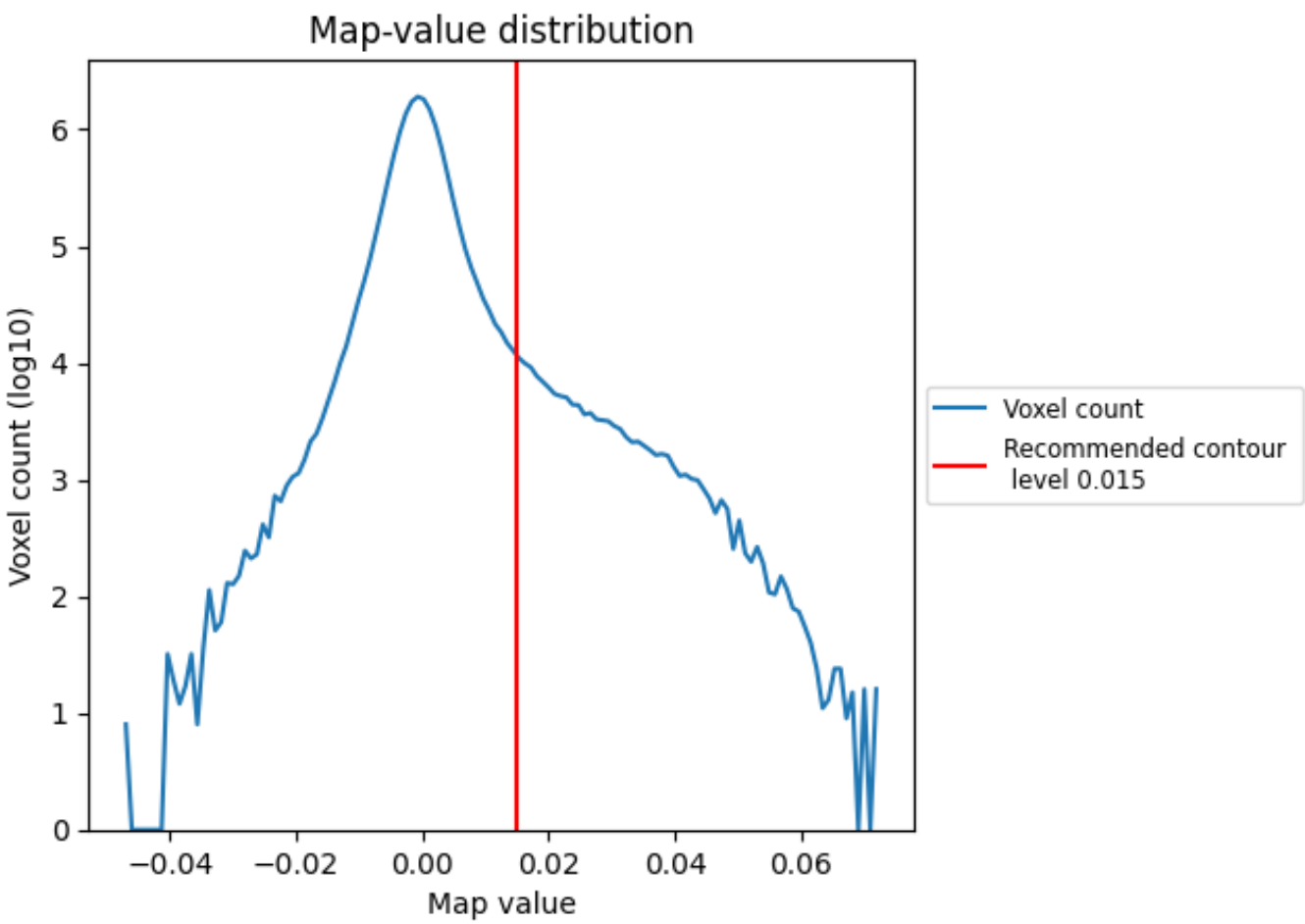
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

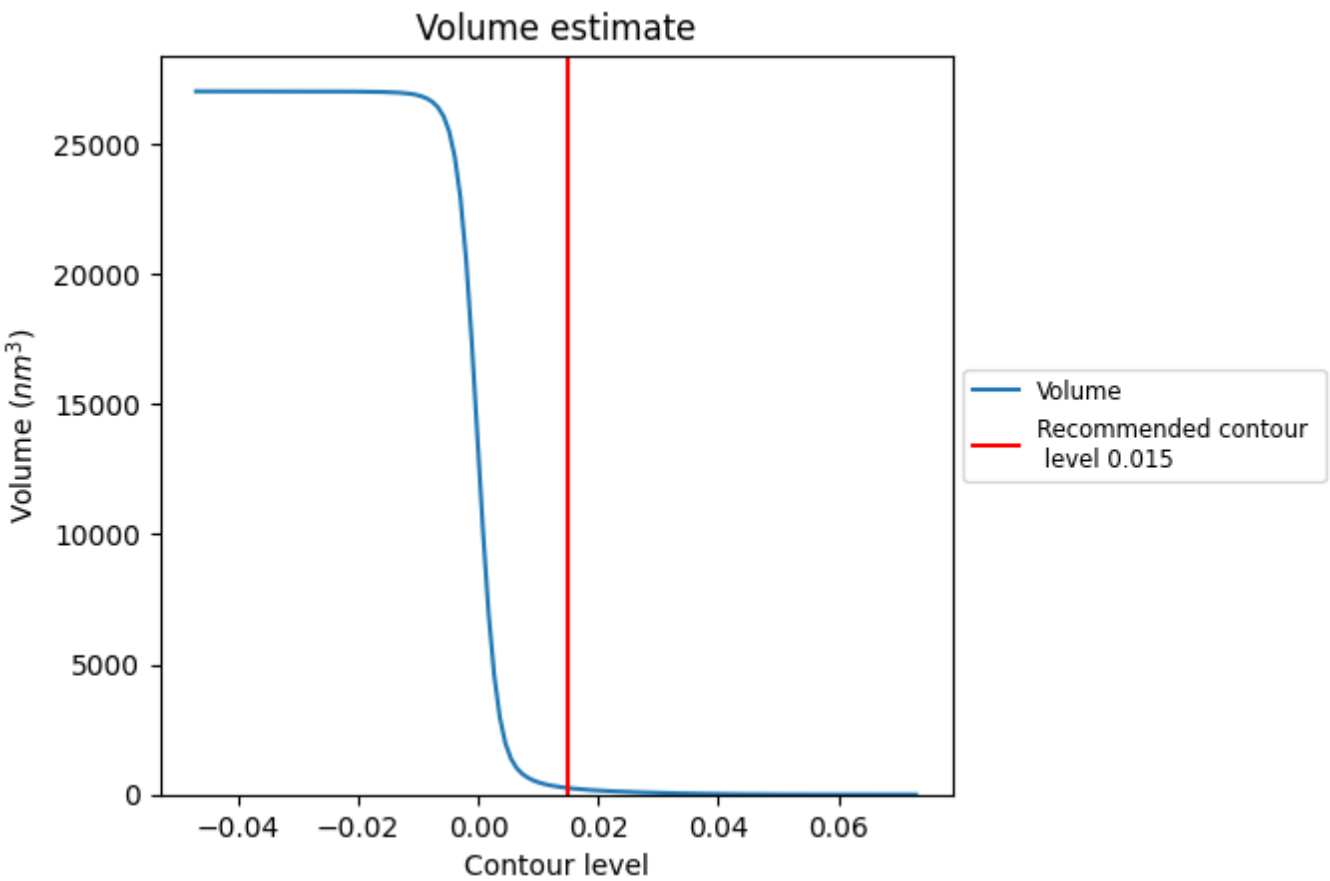
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

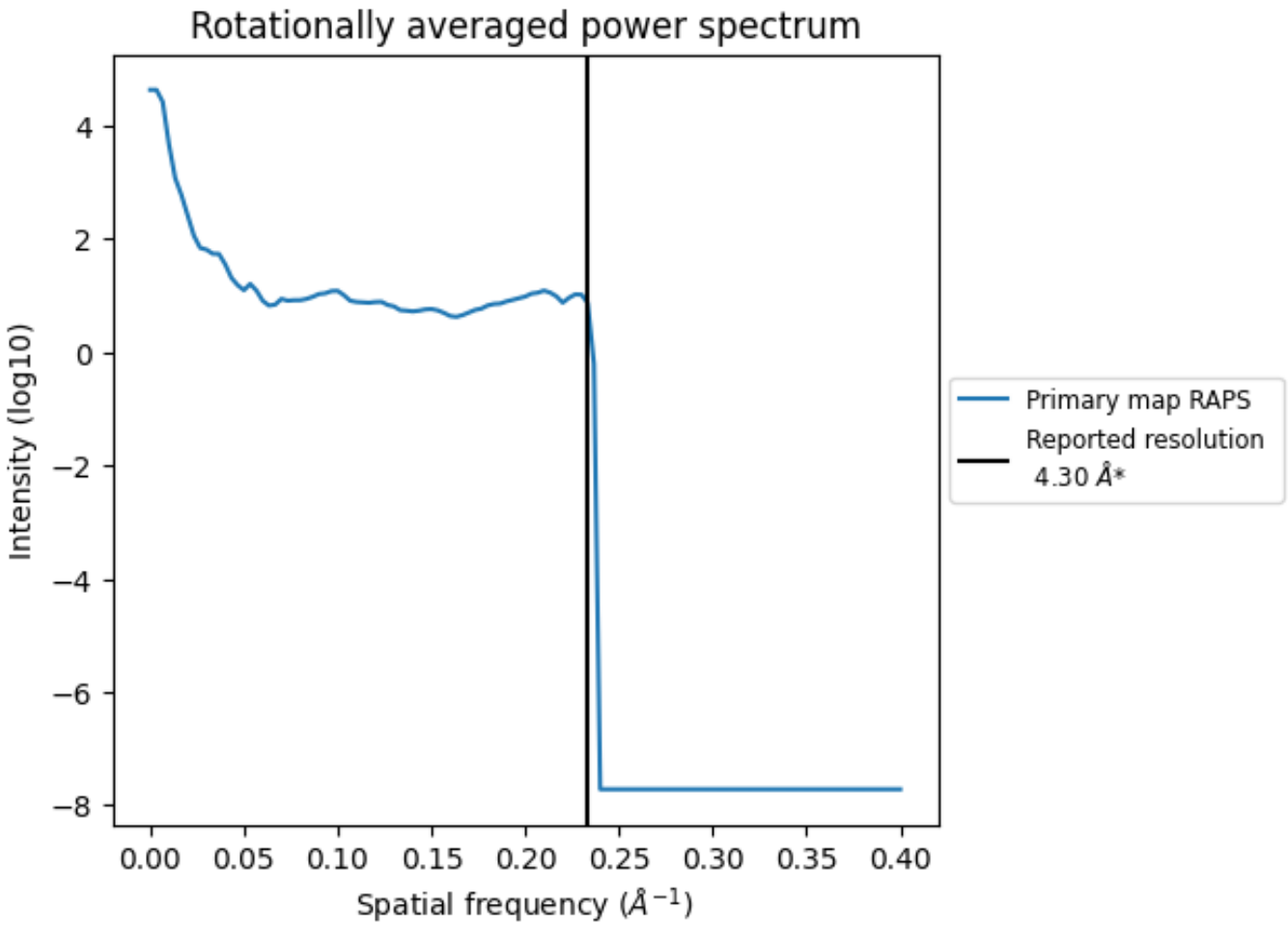
7.2 Volume estimate (i)



The volume at the recommended contour level is 252 nm^3; this corresponds to an approximate mass of 227 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

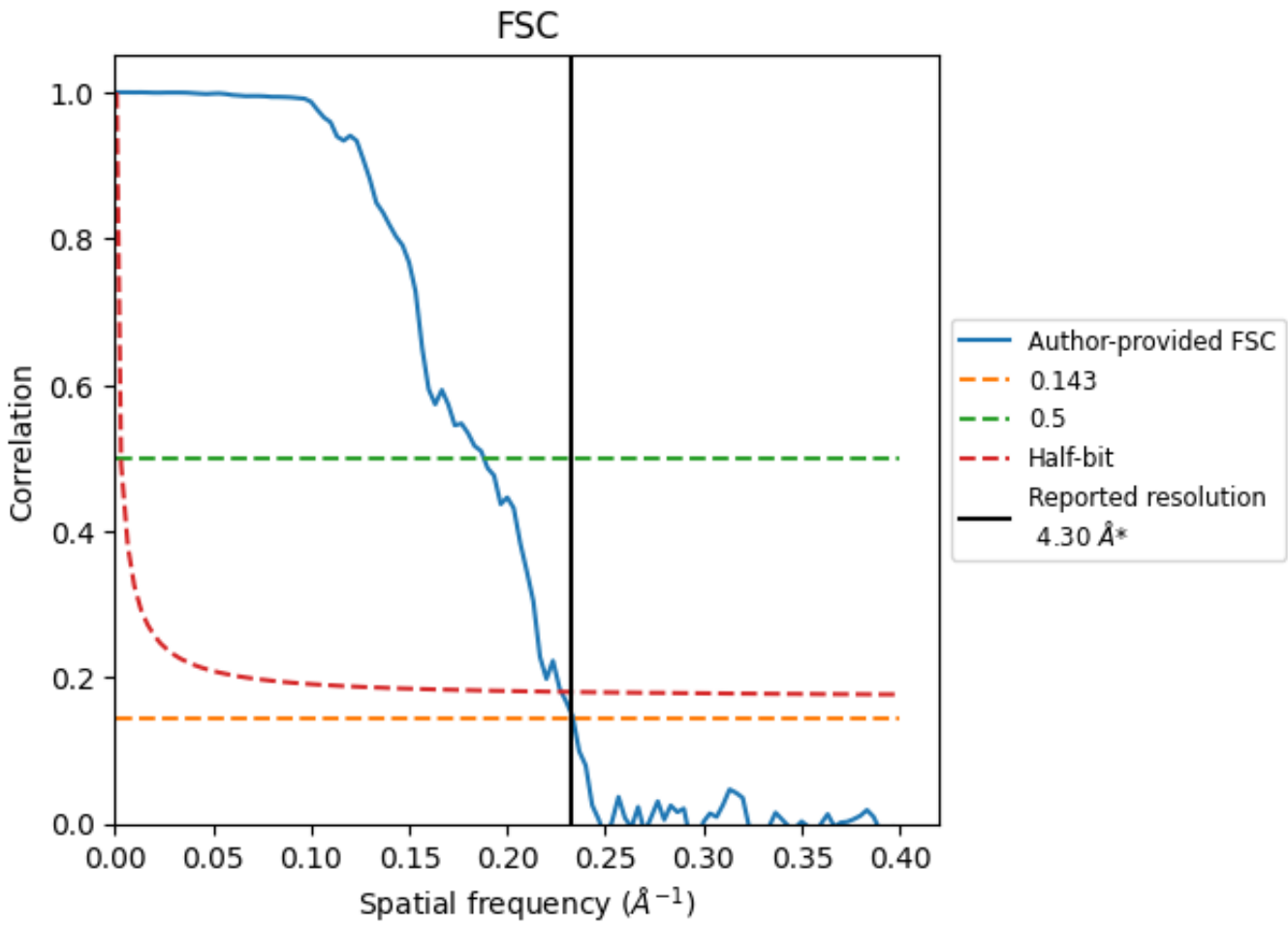


*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

8.2 Resolution estimates (i)

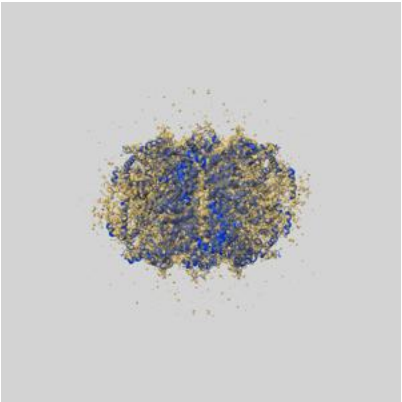
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.28	5.32	4.40
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

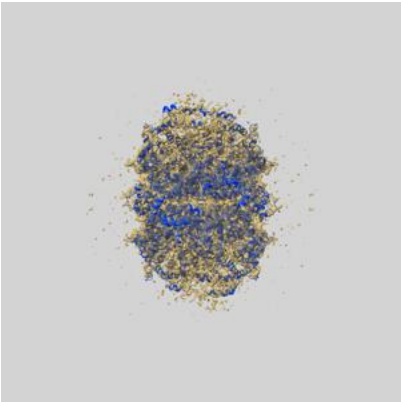
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-10235 and PDB model 6SMH. Per-residue inclusion information can be found in section 3 on page 6.

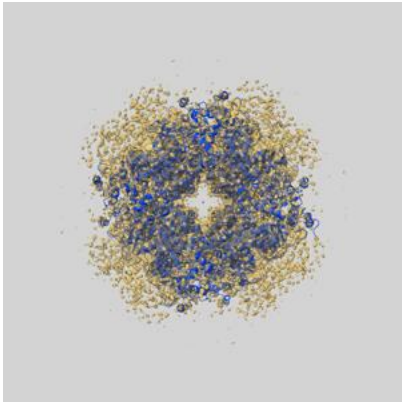
9.1 Map-model overlay (i)



X



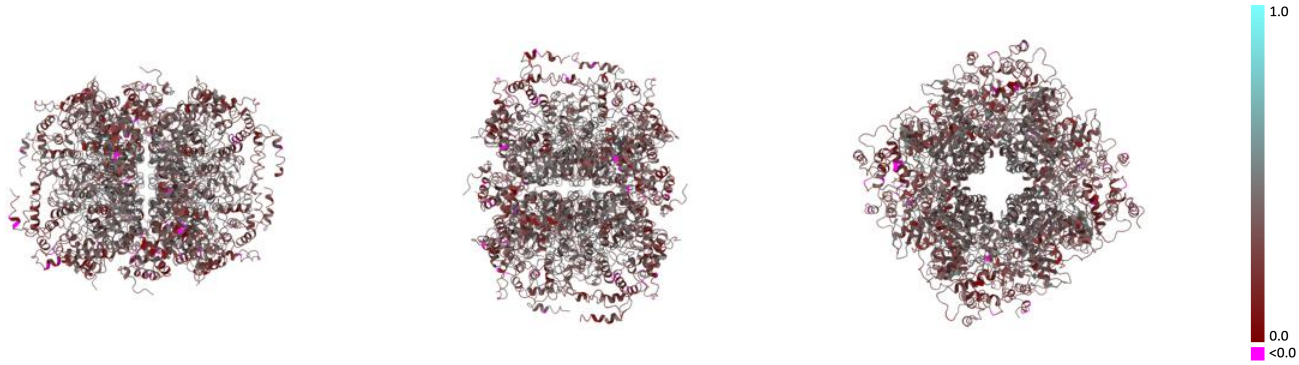
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

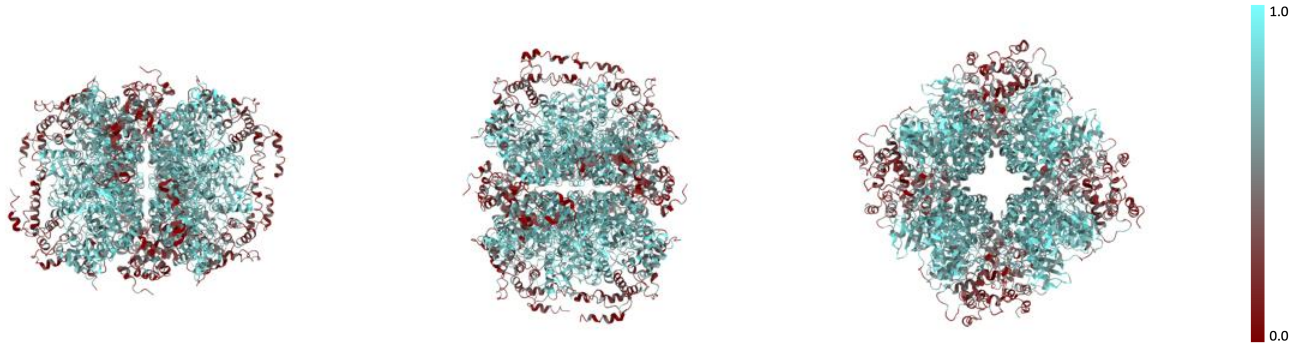
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

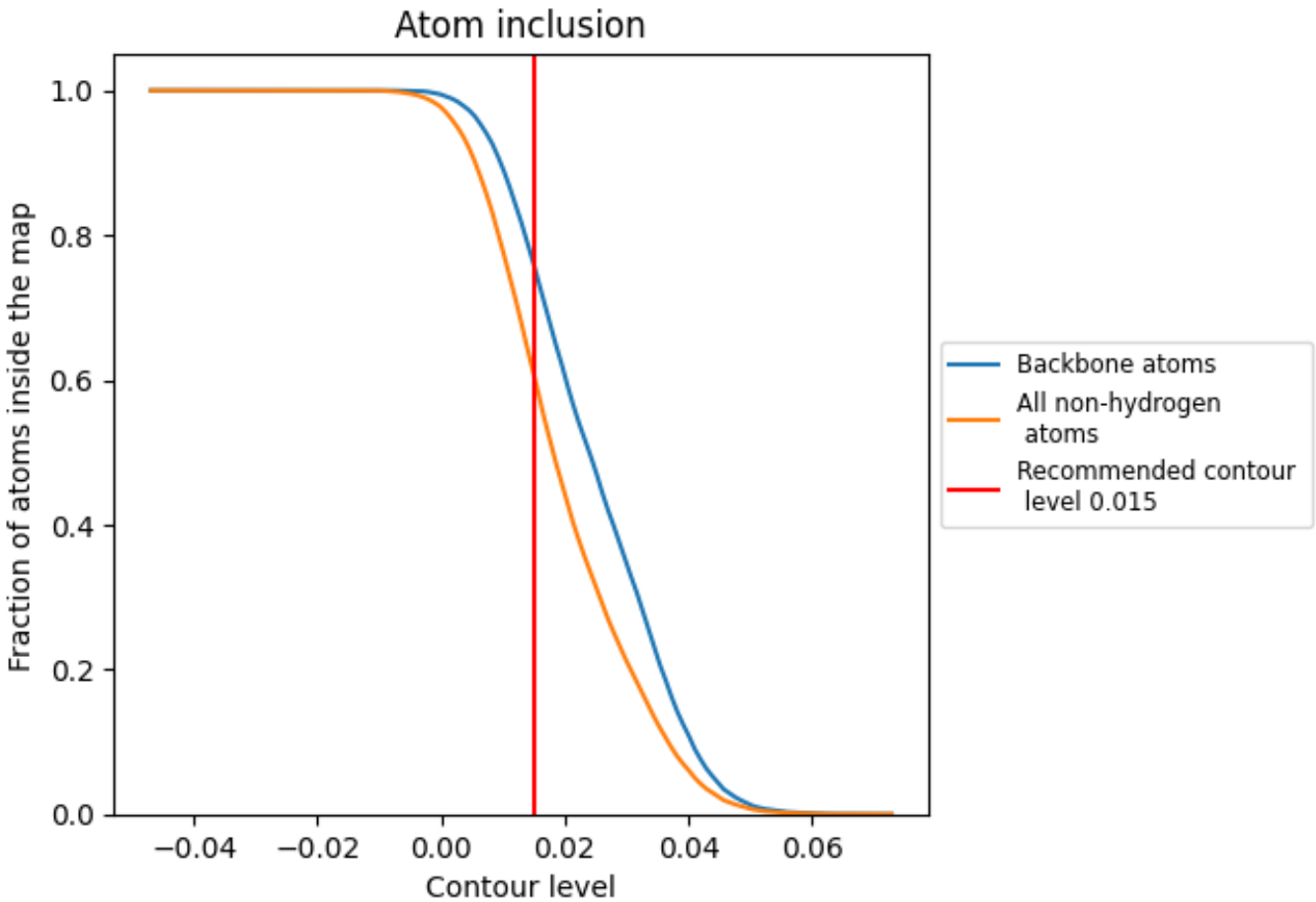
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6084	0.3540
A	0.7331	0.3700
B	0.7419	0.3830
C	0.7559	0.3890
D	0.7515	0.3890
E	0.7530	0.3880
F	0.7510	0.3880
G	0.7565	0.3880
H	0.7507	0.3870
I	0.2578	0.2460
J	0.2724	0.2960
K	0.2684	0.2870
L	0.2812	0.3100
M	0.2803	0.2930
N	0.2661	0.2700
O	0.2794	0.2870
P	0.2629	0.2640