Full wwPDB EM Validation Report ⓘ

Mar 13, 2024 – 01:06 PM JST

PDB ID	:	3J7I
EMDB ID	:	EMD-2697
Title	:	Structure of alpha- and beta- tubulin in GMPCPP-microtubules
Authors	:	Yajima, H.; Ogura, T.; Nitta, R.; Okada, Y.; Sato, C.; Hirokawa, N.
Deposited on	:	2014-07-01
Resolution	:	8.90 Å(reported)
Based on initial model	:	1JFF

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 ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

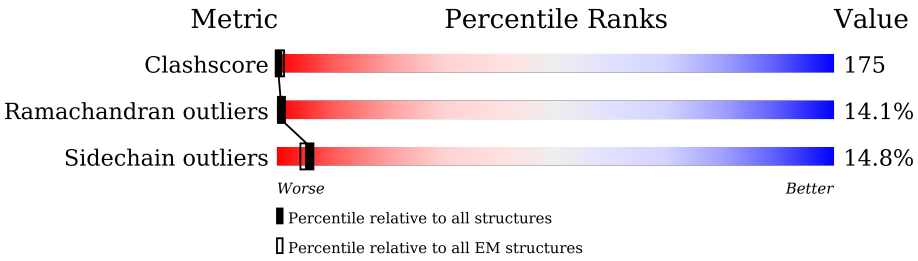
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 8.90 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	451	33% 12% 57% 20% • 9%
2	B	445	32% 19% 55% 15% • 8%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GTP	A	502	-	-	X	-
4	GTP	B	502	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6515 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 Tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	409	3210	2034	548	608	20	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	265	GLY	ALA	SEE REMARK 999	UNP P02550

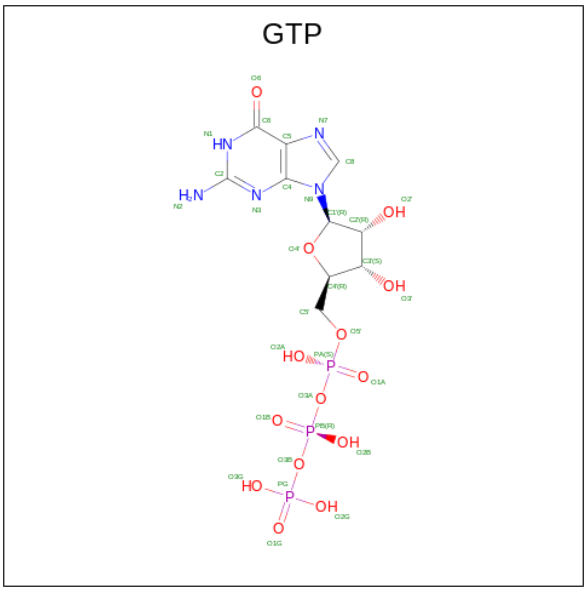
- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	411	3239	2037	558	620	24	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
3	A	1	1	1	0
3	B	1	Total	Mg	0
			1	1	

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

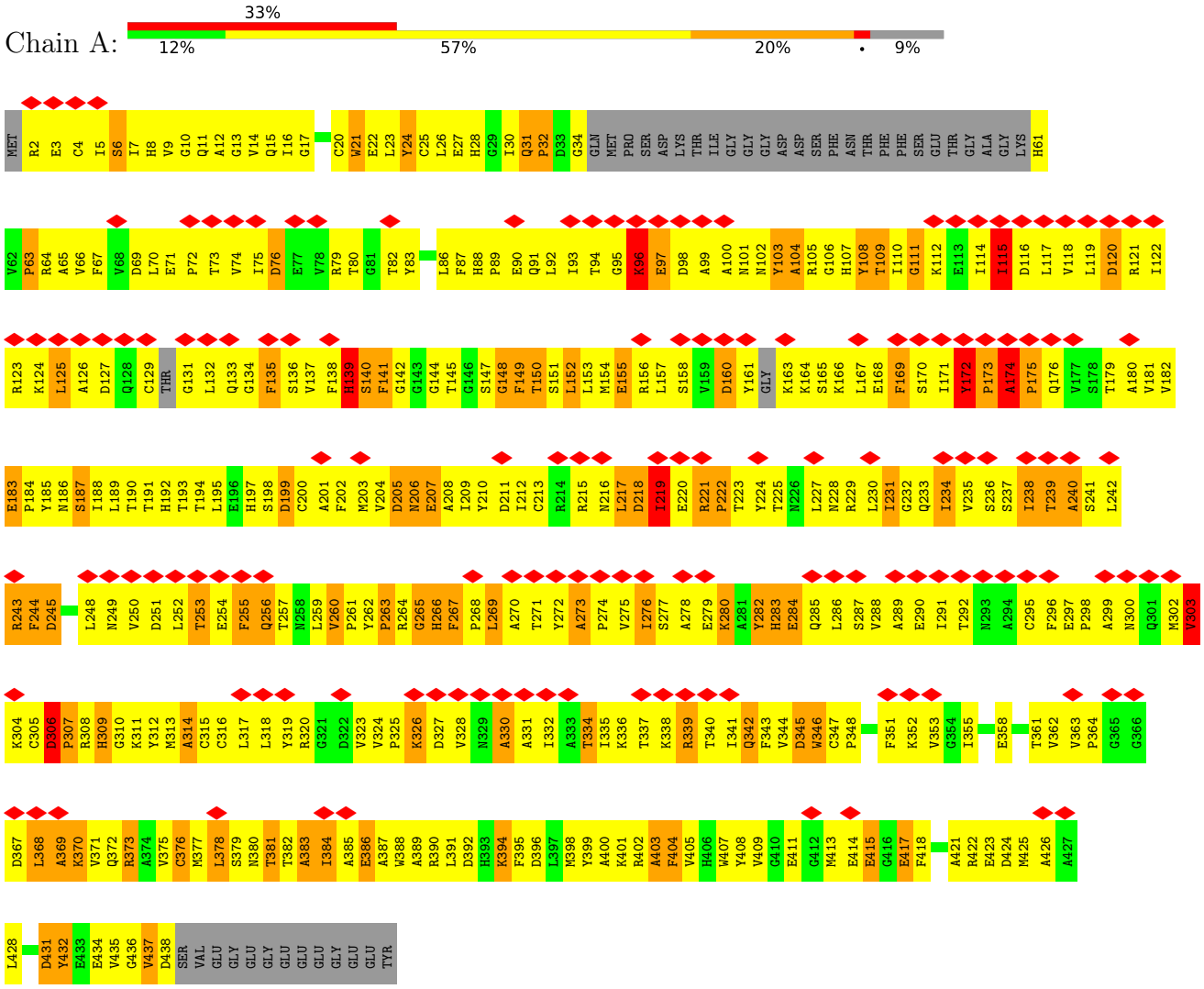


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
4	B	1	Total	C	N	O	P	0
			32	10	5	14	3	

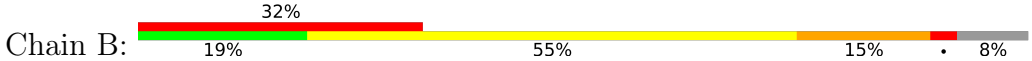
3 Residue-property plots (i)

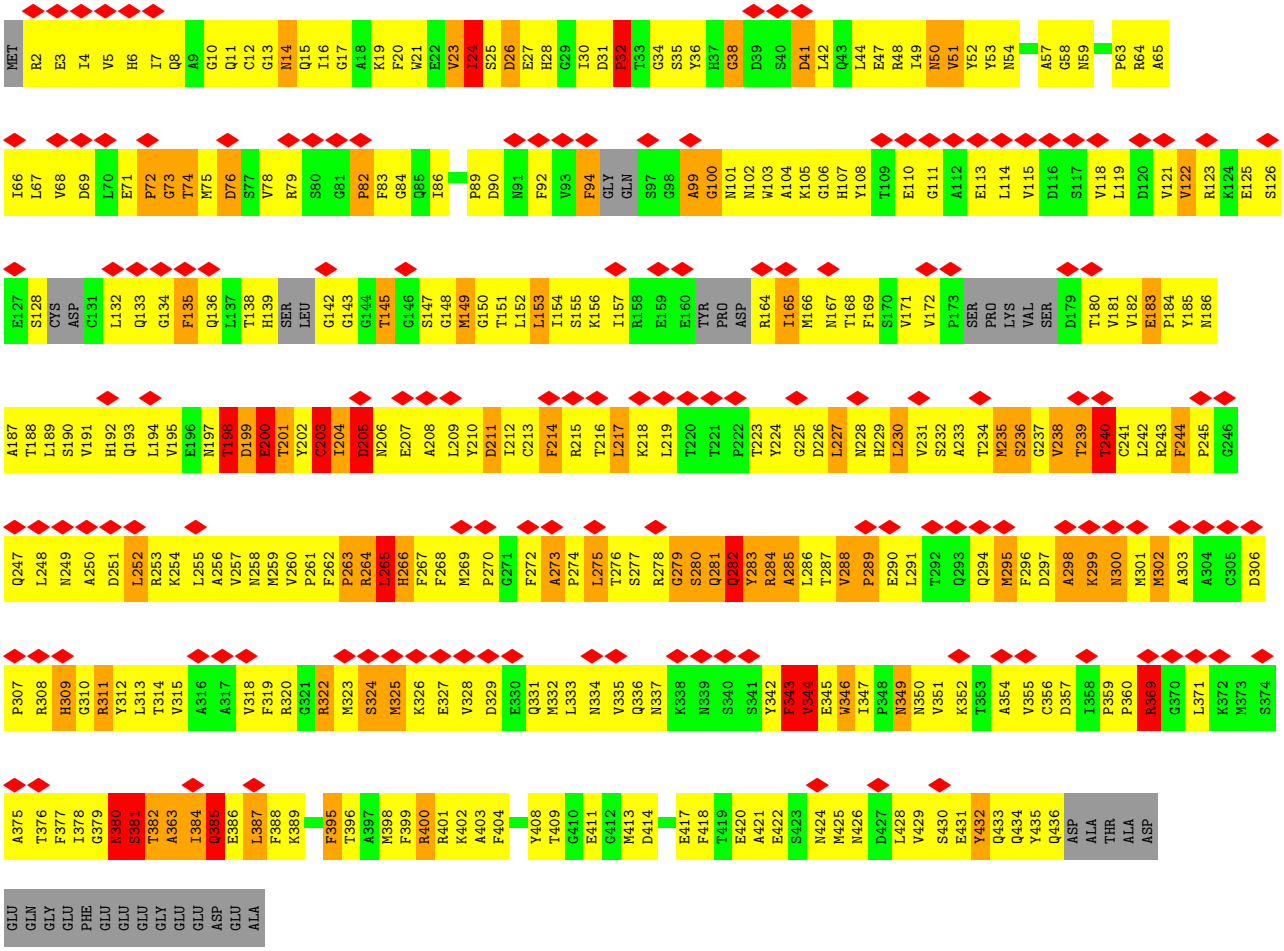
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Tubulin alpha-1A chain



• Molecule 2: Tubulin beta chain




MET R2 E3 I4 V5 H6 I7 Q8 A9 G10 Q11 C12 G13 N14 Q15 I16 G17 A18 K19 F20 W21 E22 V23 I24 S25 D26 E27 H28 G29 I30 D31 P32 T33 G34 S35 Y36 H37 G38 D39 S40 D41 L42 Q43 L44 E47 R48 I49 N50 V51 Y52 Y53 N54 A57 G58 N59 P63 R64 A65
I66 L67 V68 D69 L70 E71 P72 G73 T74 M75 D76 S77 V78 R79 S80 G81 P82 F83 G84 Q85 I86 P89 D90 N91 F92 V93 F94 GLY GLN S97 G98 A99 G100 N101 N102 W103 A104 K105 G106 H107 Y108 T109 E110 G111 A112 E113 L114 V115 D116 S117 V118 L119 D120 V121 V122 R123 K124 E125 S126
E127 S128 CYS ASP C131 L132 Q133 G134 F135 Q136 L137 T138 H139 SER LEU G142 G143 G144 T145 G146 S147 G148 M149 G150 T151 L152 L153 I154 S155 K156 I157 R158 E159 E160 TYR PRO ASP R164 I165 M166 N167 T168 F169 S170 V171 V172 P173 SER PRO LYS VAL SER D179 T180 V181 V182 E183 P184 Y185 N186
A187 T188 L189 S190 V191 H192 Q193 L194 V195 E196 N197 T198 D199 E200 T201 Y202 C203 I204 D205 N206 E207 A208 L209 Y210 D211 I212 C213 F214 R215 T216 L217 K218 L219 T220 T221 P222 T223 Y224 G225 D226 L227 N228 H229 L230 V231 S232 A233 T234 M235 S236 G237 V238 T239 T240 C241 L242 R243 F244 P245 G246
Q247 L248 N249 A250 D251 L252 R253 K254 L255 A256 V257 N258 M259 V260 P261 F262 P263 R264 L265 H266 F267 F268 M269 P270 G271 F272 A273 P274 L275 T276 S277 R278 G279 S280 Q281 Q282 Y283 R284 A285 L286 T287 V288 P289 E290 L291 T292 Q293 Q294 M295 F296 D297 A298 K299 N300 M301 M302 A303 A304 C305 D306
P307 R308 H309 G310 R311 Y312 L313 T314 V315 A316 A317 V318 F319 R320 G321 R322 M323 S324 M325 K326 E327 V328 D329 E330 Q331 M332 L333 N334 V335 Q336 N337 K338 N339 S340 S341 Y342 F343 Y344 E345 W346 I347 P348 N349 N350 V351 K352 T353 A354 V355 C356 D357 I358 P359 P360 R369 G370 L371 K372 M373 S374
A375 T376 F377 I378 G379 N380 S381 T382 A363 I384 Q385 E386 L387 F388 K389 F395 T396 A397 M398 F399 R400 R401 K402 A403 F404 Y408 T409 G410 E411 G412 M413 D414 E417 F418 T419 E420 A421 E422 S423 N424 M425 N426 D427 L428 V429 S430 E431 Y432 Q433 Q434 Y435 Q436 ASP ALA THR ALA ASP
GLU GLN GLY GLU PHE GLU GLU GLU GLY GLU GLU ASP GLU ALA

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	320000	Depositor
Resolution determination method	Not provided	
CTF correction method	Each Filament	Depositor
Microscope	JEOL 2010F	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	10	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	40000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	287.504	Depositor
Minimum map value	-8.307	Depositor
Average map value	26.397	Depositor
Map value standard deviation	58.261	Depositor
Recommended contour level	156.0	Depositor
Map size (Å)	152.5, 157.5, 107.5	wwPDB
Map dimensions	61, 63, 43	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.5, 2.5, 2.5	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.55	2/3281 (0.1%)	0.78	10/4453 (0.2%)
2	B	0.57	3/3306 (0.1%)	0.87	15/4469 (0.3%)
All	All	0.56	5/6587 (0.1%)	0.83	25/8922 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	205	ASP	CB-CG	-9.46	1.31	1.51
2	B	205	ASP	CA-CB	-6.95	1.38	1.53
1	A	173	PRO	N-CD	5.43	1.55	1.47
1	A	307	PRO	N-CD	5.16	1.55	1.47
2	B	205	ASP	CA-C	5.08	1.66	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	205	ASP	CB-CG-OD1	-9.38	109.85	118.30
2	B	205	ASP	CA-CB-CG	-9.22	93.12	113.40
1	A	383	ALA	CA-C-O	-8.86	101.49	120.10
2	B	203	CYS	C-N-CA	8.78	143.65	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	205	ASP	C-N-CA	-8.20	101.19	121.70
1	A	383	ALA	CA-C-N	8.14	135.10	117.20
2	B	385	GLN	C-N-CA	-7.75	102.33	121.70
2	B	205	ASP	N-CA-CB	-7.73	96.69	110.60
2	B	205	ASP	CB-CG-OD1	-7.60	111.46	118.30
2	B	363	ALA	CB-CA-C	-7.54	98.79	110.10
2	B	204	ILE	CA-CB-CG2	-6.89	97.12	110.90
2	B	363	ALA	N-CA-CB	6.57	119.30	110.10
1	A	174	ALA	C-N-CD	6.21	141.44	128.40
1	A	205	ASP	CB-CG-OD2	6.21	123.89	118.30
2	B	205	ASP	N-CA-C	6.13	127.55	111.00
2	B	235	MET	CG-SD-CE	6.10	109.96	100.20
1	A	297	GLU	C-N-CD	6.05	141.10	128.40
2	B	204	ILE	CA-C-O	-5.97	107.56	120.10
1	A	306	ASP	C-N-CD	5.70	140.38	128.40
2	B	384	ILE	N-CA-C	-5.68	95.66	111.00
1	A	205	ASP	CA-CB-CG	-5.61	101.05	113.40
1	A	172	TYR	C-N-CD	5.57	140.09	128.40
2	B	381	SER	C-N-CA	-5.41	108.19	121.70
2	B	217	LEU	N-CA-C	-5.36	96.54	111.00
1	A	381	THR	N-CA-C	-5.21	96.92	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	202	PHE	Mainchain
2	B	380	ASN	Mainchain

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	3210	0	3123	1163	0
2	B	3239	0	3118	1137	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	32	0	12	61	0
4	B	32	0	12	27	0
All	All	6515	0	6265	2233	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 175.

All (2233) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:MET:HE2	1:A:197:HIS:CE1	1.22	1.68
2:B:185:TYR:CE1	2:B:399:PHE:HD1	1.02	1.63
1:A:189:LEU:HD21	1:A:418:PHE:CD2	1.12	1.63
2:B:413:MET:HE3	2:B:418:PHE:CE1	1.25	1.62
2:B:169:PHE:CZ	2:B:235:MET:CB	1.83	1.62
2:B:16:ILE:HG12	2:B:228:ASN:CA	1.29	1.60
1:A:182:VAL:HG12	1:A:404:PHE:CE1	1.35	1.59
1:A:23:LEU:CD2	1:A:236:SER:CB	1.81	1.58
2:B:105:LYS:HE2	2:B:110:GLU:CG	1.26	1.58
2:B:262:PHE:CZ	2:B:434:GLN:HB2	1.07	1.57
2:B:413:MET:CE	2:B:418:PHE:CE1	1.85	1.57
2:B:185:TYR:HE1	2:B:399:PHE:CD1	0.93	1.56
2:B:194:LEU:CD1	2:B:267:PHE:CZ	1.86	1.56
2:B:194:LEU:CB	2:B:265:LEU:HD23	1.08	1.54
2:B:267:PHE:HD2	2:B:388:PHE:CZ	1.23	1.53
2:B:105:LYS:CE	2:B:110:GLU:CG	1.86	1.52
2:B:169:PHE:CZ	2:B:235:MET:HB2	1.41	1.52
1:A:189:LEU:CD2	1:A:418:PHE:CD2	1.90	1.50
2:B:194:LEU:HD12	2:B:267:PHE:CZ	1.45	1.48
1:A:72:PRO:CG	2:B:47:GLU:HG2	1.39	1.48
2:B:169:PHE:CE1	2:B:235:MET:HB2	1.46	1.46
2:B:192:HIS:CG	2:B:424:ASN:HD22	1.33	1.46
1:A:169:PHE:CZ	1:A:231:ILE:CG2	1.99	1.44
1:A:184:PRO:HB3	1:A:394:LYS:CG	1.46	1.44
2:B:102:ASN:HA	2:B:408:TYR:CD2	1.50	1.43
1:A:154:MET:CE	1:A:197:HIS:ND1	1.79	1.43
2:B:262:PHE:CZ	2:B:434:GLN:CB	2.01	1.41
2:B:262:PHE:CE1	2:B:434:GLN:HB2	1.56	1.41
2:B:15:GLN:HB2	2:B:228:ASN:ND2	1.21	1.40
2:B:346:TRP:CE3	2:B:435:TYR:HA	1.54	1.40
2:B:15:GLN:CB	2:B:228:ASN:ND2	1.79	1.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:ILE:CD1	2:B:197:ASN:CB	1.97	1.40
2:B:192:HIS:CG	2:B:424:ASN:ND2	1.84	1.40
1:A:72:PRO:HG3	2:B:47:GLU:CG	1.51	1.40
2:B:194:LEU:HD13	2:B:267:PHE:CE1	1.55	1.40
2:B:261:PRO:HD2	2:B:432:TYR:CE1	1.53	1.40
1:A:141:PHE:CE2	1:A:391:LEU:HD21	1.54	1.40
1:A:169:PHE:CE1	1:A:231:ILE:HG21	1.53	1.39
2:B:154:ILE:HD13	2:B:197:ASN:CB	1.52	1.39
1:A:189:LEU:HD21	1:A:418:PHE:CE2	1.56	1.39
1:A:195:LEU:CD2	1:A:424:ASP:C	1.90	1.38
2:B:192:HIS:CB	2:B:424:ASN:HD22	1.37	1.37
1:A:23:LEU:HD23	1:A:236:SER:CB	0.91	1.37
2:B:169:PHE:CE2	2:B:235:MET:HB3	1.60	1.37
1:A:12:ALA:HB2	4:A:502:GTP:C1'	1.51	1.36
2:B:189:LEU:HD23	2:B:421:ALA:CB	1.03	1.35
1:A:12:ALA:HB2	4:A:502:GTP:N9	1.38	1.35
2:B:169:PHE:CE2	2:B:235:MET:CB	2.09	1.35
1:A:26:LEU:HD21	1:A:361:THR:CG2	1.54	1.35
2:B:185:TYR:OH	2:B:399:PHE:CA	1.73	1.35
2:B:267:PHE:CD2	2:B:388:PHE:CZ	2.14	1.34
2:B:154:ILE:CD1	2:B:197:ASN:HB3	1.53	1.34
2:B:192:HIS:CA	2:B:424:ASN:ND2	1.89	1.34
2:B:261:PRO:CB	2:B:435:TYR:HD2	1.39	1.34
1:A:154:MET:HE2	1:A:197:HIS:ND1	1.05	1.33
1:A:173:PRO:C	1:A:206:ASN:HB3	1.46	1.33
2:B:189:LEU:CD2	2:B:421:ALA:CB	1.75	1.33
1:A:185:TYR:HB2	1:A:398:MET:CE	1.55	1.33
2:B:194:LEU:HB3	2:B:265:LEU:CD2	0.86	1.33
2:B:261:PRO:CD	2:B:432:TYR:CE1	2.10	1.33
2:B:194:LEU:CD1	2:B:267:PHE:HZ	1.29	1.32
2:B:261:PRO:CB	2:B:435:TYR:CD2	2.13	1.32
2:B:261:PRO:O	2:B:435:TYR:HE2	1.10	1.32
1:A:24:TYR:CD1	1:A:240:ALA:HB2	1.64	1.31
2:B:169:PHE:CZ	2:B:235:MET:CA	2.11	1.31
1:A:11:GLN:HB3	4:A:502:GTP:O2A	1.20	1.31
1:A:150:THR:C	1:A:197:HIS:CE1	2.04	1.31
2:B:16:ILE:CG1	2:B:228:ASN:HA	1.60	1.31
2:B:409:THR:CA	2:B:413:MET:HG2	1.57	1.31
2:B:408:TYR:CB	2:B:413:MET:SD	2.18	1.31
2:B:194:LEU:O	2:B:265:LEU:CB	1.78	1.30
2:B:169:PHE:CZ	2:B:235:MET:HA	1.67	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:TYR:N	1:A:398:MET:SD	2.03	1.29
2:B:189:LEU:CD2	2:B:421:ALA:HB3	1.34	1.29
2:B:346:TRP:HE3	2:B:435:TYR:O	1.13	1.29
1:A:154:MET:SD	1:A:198:SER:CA	2.21	1.28
4:A:502:GTP:O1A	2:B:245:PRO:HB3	1.28	1.28
1:A:184:PRO:CB	1:A:394:LYS:HG2	1.64	1.28
2:B:169:PHE:CD1	2:B:235:MET:CE	2.16	1.28
2:B:206:ASN:ND2	4:B:502:GTP:H1'	1.45	1.28
2:B:16:ILE:CG1	2:B:228:ASN:CB	2.12	1.28
1:A:12:ALA:HA	4:A:502:GTP:C5	1.68	1.27
2:B:346:TRP:CZ3	2:B:435:TYR:HA	1.67	1.27
2:B:105:LYS:CE	2:B:110:GLU:HG3	1.55	1.27
2:B:195:VAL:HG21	2:B:264:ARG:NH1	1.48	1.27
1:A:195:LEU:HD21	1:A:424:ASP:O	1.31	1.27
2:B:16:ILE:HG13	2:B:228:ASN:CG	1.53	1.26
1:A:108:TYR:HB3	1:A:411:GLU:O	1.17	1.26
2:B:169:PHE:CD1	2:B:235:MET:HE3	1.70	1.26
2:B:192:HIS:C	2:B:424:ASN:ND2	1.89	1.26
2:B:184:PRO:HB2	2:B:395:PHE:CA	1.65	1.25
2:B:206:ASN:ND2	4:B:502:GTP:C1'	1.98	1.25
1:A:188:ILE:HD11	1:A:392:ASP:O	1.32	1.25
1:A:190:THR:O	1:A:194:THR:HB	1.26	1.25
2:B:194:LEU:CB	2:B:265:LEU:CD2	1.78	1.25
1:A:9:VAL:CG1	1:A:139:HIS:HB3	1.65	1.25
2:B:185:TYR:CE1	2:B:399:PHE:CD1	1.83	1.25
1:A:11:GLN:CB	4:A:502:GTP:O2A	1.84	1.24
2:B:346:TRP:CZ3	2:B:435:TYR:HD1	1.55	1.24
2:B:16:ILE:CG1	2:B:228:ASN:CA	2.14	1.24
1:A:104:ALA:HB1	1:A:408:TYR:CA	1.67	1.23
1:A:173:PRO:O	1:A:206:ASN:HB3	1.18	1.23
2:B:189:LEU:HD23	2:B:421:ALA:CA	1.67	1.23
2:B:346:TRP:CH2	2:B:435:TYR:HD1	1.55	1.23
1:A:182:VAL:CG1	1:A:404:PHE:CE1	2.22	1.23
2:B:202:TYR:CZ	2:B:238:VAL:HG11	1.72	1.23
1:A:169:PHE:CE1	1:A:231:ILE:CG2	2.19	1.23
2:B:346:TRP:CE3	2:B:435:TYR:CA	2.20	1.22
1:A:184:PRO:HB3	1:A:394:LYS:CB	1.69	1.22
2:B:16:ILE:CA	2:B:228:ASN:HB3	1.69	1.22
1:A:184:PRO:HG2	1:A:398:MET:SD	1.78	1.22
2:B:16:ILE:HG12	2:B:228:ASN:CB	1.67	1.22
2:B:408:TYR:HB3	2:B:413:MET:SD	1.78	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ILE:CD1	1:A:392:ASP:O	1.88	1.22
2:B:409:THR:HA	2:B:413:MET:CG	1.69	1.22
2:B:346:TRP:CZ3	2:B:435:TYR:CD1	2.27	1.21
2:B:194:LEU:O	2:B:265:LEU:HB2	1.35	1.21
1:A:104:ALA:HB2	1:A:408:TYR:CB	1.69	1.21
1:A:12:ALA:CB	4:A:502:GTP:N9	2.03	1.21
2:B:184:PRO:HB2	2:B:395:PHE:CB	1.70	1.21
2:B:346:TRP:CE3	2:B:435:TYR:O	1.94	1.21
2:B:155:SER:OG	2:B:197:ASN:ND2	1.71	1.21
2:B:188:THR:CA	2:B:425:MET:HE3	1.71	1.21
1:A:296:PHE:CE1	1:A:341:ILE:HD11	1.73	1.20
1:A:189:LEU:CD2	1:A:418:PHE:CE2	2.18	1.19
2:B:185:TYR:CD1	2:B:418:PHE:HD2	1.60	1.19
2:B:395:PHE:CE2	2:B:422:GLU:OE1	1.94	1.19
1:A:108:TYR:OH	1:A:413:MET:HG3	1.43	1.19
1:A:185:TYR:CB	1:A:398:MET:CE	2.20	1.19
1:A:182:VAL:HG12	1:A:404:PHE:CZ	1.76	1.18
1:A:154:MET:CE	1:A:197:HIS:CE1	2.17	1.18
2:B:185:TYR:HB3	2:B:418:PHE:CE2	1.78	1.18
1:A:154:MET:SD	1:A:198:SER:HA	1.80	1.18
2:B:185:TYR:CZ	2:B:399:PHE:HA	1.78	1.18
2:B:206:ASN:CG	4:B:502:GTP:H1'	1.63	1.18
1:A:413:MET:SD	1:A:418:PHE:CE1	2.35	1.17
2:B:103:TRP:CE3	2:B:417:GLU:OE2	1.96	1.17
2:B:258:ASN:ND2	2:B:352:LYS:HG3	1.58	1.17
1:A:150:THR:O	1:A:197:HIS:CE1	1.95	1.17
1:A:210:TYR:CE1	1:A:227:LEU:HD11	1.79	1.17
1:A:392:ASP:CB	1:A:425:MET:HE3	1.73	1.17
2:B:385:GLN:HB3	2:B:429:VAL:HG13	1.22	1.17
2:B:261:PRO:CD	2:B:432:TYR:HE1	1.52	1.17
1:A:189:LEU:HG	1:A:395:PHE:CE2	1.79	1.17
2:B:261:PRO:HB3	2:B:435:TYR:CD2	1.78	1.17
1:A:244:PHE:CE1	1:A:245:ASP:OD1	1.98	1.17
2:B:16:ILE:HG13	2:B:228:ASN:OD1	1.39	1.17
1:A:73:THR:HB	2:B:42:LEU:HD13	1.22	1.16
2:B:104:ALA:HB3	2:B:413:MET:HB2	1.21	1.16
1:A:181:VAL:CG2	2:B:352:LYS:HG3	1.74	1.16
2:B:234:THR:HG21	2:B:270:PRO:HB2	1.23	1.16
2:B:192:HIS:O	2:B:195:VAL:HG12	1.02	1.16
2:B:409:THR:N	2:B:413:MET:SD	2.18	1.16
1:A:133:GLN:NE2	1:A:256:GLN:OE1	1.79	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:385:GLN:CB	2:B:429:VAL:HG13	1.74	1.16
1:A:132:LEU:HG	1:A:164:LYS:HE3	1.26	1.15
2:B:204:ILE:HA	2:B:302:MET:HB3	1.17	1.15
1:A:166:LYS:HD2	1:A:197:HIS:O	1.42	1.15
1:A:180:ALA:N	2:B:248:LEU:HD11	1.61	1.15
2:B:395:PHE:CD2	2:B:422:GLU:OE1	1.99	1.15
1:A:12:ALA:HB2	4:A:502:GTP:O4'	1.42	1.15
1:A:228:ASN:HB3	4:A:502:GTP:N2	1.62	1.15
2:B:102:ASN:ND2	2:B:413:MET:HB3	1.60	1.15
2:B:186:ASN:OD1	2:B:408:TYR:CE2	1.99	1.15
2:B:194:LEU:CD1	2:B:267:PHE:CE1	2.20	1.15
2:B:262:PHE:HD2	2:B:432:TYR:HA	1.07	1.15
2:B:195:VAL:HA	2:B:264:ARG:O	1.45	1.14
1:A:122:ILE:HB	1:A:135:PHE:CE2	1.82	1.14
1:A:243:ARG:NH2	1:A:252:LEU:H	1.45	1.14
2:B:188:THR:HA	2:B:425:MET:CE	1.77	1.14
2:B:204:ILE:HD13	2:B:231:VAL:HG13	1.24	1.14
1:A:195:LEU:HD22	1:A:424:ASP:C	1.53	1.14
2:B:16:ILE:HA	2:B:228:ASN:HB3	1.15	1.14
1:A:173:PRO:O	1:A:206:ASN:CB	1.94	1.13
1:A:181:VAL:HG21	2:B:352:LYS:CG	1.78	1.13
2:B:194:LEU:HB3	2:B:265:LEU:HD21	1.14	1.13
2:B:261:PRO:O	2:B:435:TYR:CE2	1.98	1.13
2:B:262:PHE:CE2	2:B:435:TYR:CD2	2.37	1.13
1:A:392:ASP:HB2	1:A:425:MET:HE3	1.23	1.13
2:B:192:HIS:O	2:B:195:VAL:CG1	1.96	1.13
2:B:102:ASN:HA	2:B:408:TYR:CE2	1.84	1.12
2:B:192:HIS:C	2:B:424:ASN:HD21	1.48	1.12
2:B:346:TRP:CH2	2:B:435:TYR:CD1	2.37	1.12
1:A:185:TYR:OH	1:A:408:TYR:CD2	2.01	1.12
2:B:194:LEU:HD13	2:B:267:PHE:CZ	1.65	1.12
2:B:105:LYS:HE3	2:B:110:GLU:OE2	1.50	1.12
2:B:169:PHE:CE2	2:B:235:MET:CA	2.30	1.12
2:B:185:TYR:CD1	2:B:418:PHE:CD2	2.36	1.12
1:A:23:LEU:CD2	1:A:236:SER:HB3	1.62	1.12
1:A:141:PHE:HE2	1:A:391:LEU:CD2	1.63	1.12
2:B:105:LYS:HD3	2:B:411:GLU:HB3	1.25	1.11
1:A:190:THR:O	1:A:194:THR:CB	1.98	1.11
1:A:191:THR:OG1	1:A:425:MET:SD	2.05	1.11
1:A:26:LEU:CD2	1:A:361:THR:CG2	2.29	1.10
1:A:104:ALA:CB	1:A:408:TYR:HA	1.81	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:ALA:CB	1:A:408:TYR:CA	2.29	1.10
1:A:141:PHE:CE2	1:A:391:LEU:CD2	2.33	1.10
1:A:182:VAL:CG1	1:A:404:PHE:CZ	2.33	1.10
1:A:402:ARG:O	1:A:405:VAL:HG13	1.51	1.10
2:B:104:ALA:HB3	2:B:413:MET:CB	1.81	1.10
1:A:26:LEU:HD21	1:A:361:THR:HG22	1.20	1.10
1:A:101:ASN:HB2	2:B:254:LYS:HD3	1.16	1.10
1:A:104:ALA:CB	1:A:408:TYR:HB3	1.81	1.10
1:A:408:TYR:CD1	1:A:418:PHE:CE1	2.38	1.10
1:A:408:TYR:CD1	1:A:418:PHE:HE1	1.69	1.10
2:B:194:LEU:CA	2:B:265:LEU:HD23	1.79	1.10
2:B:262:PHE:HB3	2:B:431:GLU:CB	1.80	1.10
1:A:12:ALA:CB	4:A:502:GTP:C4	2.35	1.10
1:A:189:LEU:HG	1:A:395:PHE:HE2	0.94	1.10
1:A:191:THR:HA	1:A:194:THR:CG2	1.81	1.10
2:B:195:VAL:CA	2:B:264:ARG:O	1.98	1.10
2:B:408:TYR:HB2	2:B:413:MET:SD	1.90	1.10
2:B:102:ASN:CA	2:B:408:TYR:CD2	2.35	1.09
2:B:102:ASN:HB2	2:B:408:TYR:HA	1.25	1.09
2:B:105:LYS:CE	2:B:110:GLU:HG2	1.68	1.09
2:B:313:LEU:HD12	2:B:432:TYR:CD1	1.88	1.09
1:A:267:PHE:CD2	1:A:388:TRP:HZ2	1.69	1.09
2:B:169:PHE:CD2	2:B:235:MET:HB3	1.88	1.09
2:B:192:HIS:CG	2:B:424:ASN:CG	2.07	1.08
1:A:26:LEU:HD21	1:A:361:THR:HG21	1.34	1.08
1:A:108:TYR:CB	1:A:411:GLU:O	2.02	1.08
2:B:395:PHE:CD2	2:B:422:GLU:CD	2.26	1.08
1:A:26:LEU:CD2	1:A:361:THR:HG21	1.82	1.08
1:A:224:TYR:CD2	2:B:322:ARG:NH2	2.22	1.08
1:A:135:PHE:CE1	1:A:157:LEU:HD13	1.88	1.07
2:B:102:ASN:HD21	2:B:413:MET:CB	1.65	1.07
2:B:169:PHE:CD1	2:B:235:MET:HE2	1.88	1.07
2:B:185:TYR:HD1	2:B:418:PHE:CD2	1.71	1.07
1:A:169:PHE:CZ	1:A:231:ILE:HG22	1.86	1.07
1:A:199:ASP:O	1:A:265:GLY:O	1.69	1.07
2:B:204:ILE:HG21	2:B:231:VAL:CG2	1.84	1.07
1:A:224:TYR:CD1	4:A:502:GTP:C4	2.43	1.07
2:B:184:PRO:CG	2:B:395:PHE:HA	1.84	1.07
1:A:104:ALA:CB	1:A:408:TYR:CB	2.33	1.07
2:B:261:PRO:HB2	2:B:435:TYR:CD2	1.86	1.07
1:A:224:TYR:CE1	4:A:502:GTP:C5	2.43	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:15:GLN:HB3	2:B:228:ASN:HD22	1.18	1.06
1:A:135:PHE:CZ	1:A:157:LEU:HD22	1.91	1.06
1:A:189:LEU:CG	1:A:395:PHE:HE2	1.68	1.06
1:A:407:TRP:HE1	2:B:257:VAL:HG21	1.00	1.06
2:B:184:PRO:CB	2:B:395:PHE:CA	2.33	1.06
2:B:185:TYR:OH	2:B:399:PHE:HA	0.89	1.06
2:B:206:ASN:ND2	4:B:502:GTP:C2'	2.18	1.06
2:B:105:LYS:HE3	2:B:110:GLU:CG	1.77	1.06
1:A:109:THR:OG1	1:A:411:GLU:HG2	1.54	1.06
2:B:182:VAL:HG11	2:B:408:TYR:CE1	1.91	1.06
2:B:195:VAL:HG11	2:B:264:ARG:NH1	1.70	1.06
2:B:266:HIS:CE1	2:B:428:LEU:CD1	2.38	1.06
2:B:195:VAL:HG23	2:B:263:PRO:O	1.55	1.05
2:B:258:ASN:ND2	2:B:352:LYS:CG	2.18	1.05
1:A:105:ARG:N	1:A:411:GLU:OE1	1.88	1.05
2:B:195:VAL:HG21	2:B:264:ARG:CZ	1.86	1.05
1:A:28:HIS:NE2	1:A:244:PHE:HB2	1.70	1.05
2:B:101:ASN:HD21	2:B:143:GLY:HA2	1.15	1.05
1:A:180:ALA:N	2:B:248:LEU:CD1	2.19	1.05
1:A:192:HIS:CD2	1:A:193:THR:N	2.25	1.04
2:B:172:VAL:O	2:B:205:ASP:HB2	1.55	1.04
2:B:184:PRO:CB	2:B:395:PHE:HA	1.86	1.04
2:B:261:PRO:HB2	2:B:435:TYR:HD2	0.94	1.04
2:B:266:HIS:CD2	2:B:428:LEU:HD11	1.92	1.04
1:A:392:ASP:HB2	1:A:425:MET:CE	1.86	1.04
2:B:154:ILE:HD12	2:B:197:ASN:CG	1.78	1.04
2:B:413:MET:HE1	2:B:418:PHE:CE1	1.80	1.04
1:A:9:VAL:HG13	1:A:139:HIS:HB3	1.40	1.04
2:B:102:ASN:CB	2:B:408:TYR:HA	1.76	1.04
2:B:105:LYS:CD	2:B:411:GLU:O	2.06	1.04
2:B:204:ILE:HA	2:B:302:MET:CB	1.87	1.04
2:B:267:PHE:CD2	2:B:388:PHE:HZ	1.65	1.04
2:B:154:ILE:HD12	2:B:197:ASN:CB	1.83	1.04
2:B:205:ASP:OD1	2:B:208:ALA:HB3	1.58	1.04
1:A:181:VAL:HG21	2:B:258:ASN:HD22	1.23	1.04
2:B:363:ALA:HB1	2:B:433:GLN:HA	1.11	1.04
2:B:169:PHE:CE1	2:B:235:MET:HE2	1.93	1.03
2:B:204:ILE:CG2	2:B:231:VAL:HG22	1.86	1.03
1:A:123:ARG:HA	1:A:161:TYR:OH	1.54	1.03
2:B:195:VAL:HG23	2:B:263:PRO:C	1.78	1.03
1:A:154:MET:HB3	1:A:197:HIS:O	1.57	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:THR:CA	1:A:194:THR:HG22	1.87	1.03
2:B:185:TYR:HB3	2:B:418:PHE:CD2	1.94	1.03
2:B:192:HIS:ND1	2:B:424:ASN:ND2	2.04	1.03
2:B:299:LYS:HD3	2:B:299:LYS:H	1.24	1.03
1:A:5:ILE:CD1	1:A:125:LEU:HB3	1.87	1.03
1:A:23:LEU:HD23	1:A:236:SER:HB3	1.18	1.03
1:A:108:TYR:CE2	1:A:413:MET:CA	2.42	1.03
1:A:108:TYR:CE2	1:A:413:MET:HA	1.93	1.03
1:A:161:TYR:HB2	1:A:164:LYS:HG3	1.35	1.03
1:A:224:TYR:CD1	4:A:502:GTP:C5	2.47	1.03
1:A:243:ARG:HH21	1:A:252:LEU:N	1.57	1.03
1:A:296:PHE:CE1	1:A:341:ILE:CD1	2.41	1.03
2:B:192:HIS:CA	2:B:424:ASN:HD22	1.59	1.03
2:B:313:LEU:CD1	2:B:432:TYR:CD1	2.40	1.03
2:B:413:MET:CE	2:B:418:PHE:HE1	1.39	1.03
1:A:12:ALA:CB	4:A:502:GTP:C1'	2.36	1.02
1:A:98:ASP:HB3	1:A:105:ARG:HH21	1.19	1.02
1:A:407:TRP:HE1	2:B:257:VAL:CG2	1.70	1.02
1:A:97:GLU:HB3	1:A:110:ILE:HD11	1.41	1.02
1:A:181:VAL:HG21	2:B:258:ASN:ND2	1.73	1.02
1:A:407:TRP:NE1	2:B:257:VAL:HG21	1.73	1.02
2:B:154:ILE:HD13	2:B:197:ASN:HB3	1.06	1.02
1:A:12:ALA:HA	4:A:502:GTP:N7	1.74	1.02
1:A:267:PHE:CE2	1:A:388:TRP:HZ2	1.77	1.02
1:A:182:VAL:O	1:A:398:MET:SD	2.18	1.02
2:B:105:LYS:HE3	2:B:110:GLU:CD	1.78	1.02
1:A:154:MET:CE	1:A:197:HIS:CG	2.42	1.01
1:A:392:ASP:CG	1:A:425:MET:HE3	1.79	1.01
1:A:26:LEU:CG	1:A:361:THR:HG21	1.90	1.01
1:A:191:THR:C	1:A:194:THR:HG22	1.81	1.01
2:B:105:LYS:NZ	2:B:411:GLU:OE1	1.93	1.01
2:B:267:PHE:HD2	2:B:388:PHE:CE1	1.76	1.01
1:A:169:PHE:CZ	1:A:231:ILE:HG23	1.92	1.01
1:A:244:PHE:HE1	1:A:245:ASP:OD1	1.42	1.01
1:A:132:LEU:HG	1:A:164:LYS:CE	1.91	1.01
1:A:181:VAL:HG11	2:B:258:ASN:ND2	1.75	1.01
2:B:184:PRO:HB2	2:B:395:PHE:HB2	1.33	1.01
2:B:262:PHE:HB3	2:B:431:GLU:HB3	1.41	1.01
1:A:101:ASN:HB2	2:B:254:LYS:CD	1.91	1.00
1:A:173:PRO:C	1:A:206:ASN:CB	2.28	1.00
1:A:195:LEU:CD2	1:A:424:ASP:HB3	1.89	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:CYS:HA	1:A:267:PHE:CD2	1.95	1.00
1:A:9:VAL:HG12	1:A:139:HIS:HB3	1.40	1.00
1:A:150:THR:O	1:A:197:HIS:NE2	1.94	1.00
1:A:185:TYR:OH	1:A:408:TYR:HD2	1.40	1.00
1:A:392:ASP:CB	1:A:425:MET:CE	2.39	1.00
1:A:109:THR:HG22	1:A:110:ILE:N	1.70	1.00
2:B:2:ARG:HH21	2:B:48:ARG:NH2	1.58	1.00
2:B:101:ASN:ND2	2:B:143:GLY:HA2	1.76	1.00
2:B:105:LYS:CD	2:B:411:GLU:HB3	1.90	1.00
2:B:154:ILE:HD13	2:B:197:ASN:HB2	1.39	1.00
1:A:11:GLN:HG3	1:A:74:VAL:HG11	1.43	1.00
1:A:228:ASN:CB	4:A:502:GTP:HN21	1.74	1.00
2:B:236:SER:O	2:B:240:THR:HG23	1.61	1.00
2:B:262:PHE:CD2	2:B:432:TYR:HA	1.96	1.00
1:A:154:MET:SD	1:A:198:SER:CB	2.50	0.99
1:A:23:LEU:CD2	1:A:236:SER:HB2	1.64	0.99
2:B:346:TRP:CZ3	2:B:435:TYR:CA	2.41	0.99
2:B:16:ILE:HG12	2:B:228:ASN:HA	1.03	0.99
2:B:102:ASN:HD21	2:B:413:MET:HB3	1.12	0.99
1:A:199:ASP:C	1:A:265:GLY:O	1.99	0.99
1:A:154:MET:HE2	1:A:197:HIS:CG	1.97	0.99
1:A:195:LEU:HD22	1:A:425:MET:N	1.76	0.99
1:A:108:TYR:CZ	1:A:413:MET:CB	2.46	0.99
1:A:185:TYR:HB2	1:A:398:MET:HE2	0.99	0.99
1:A:23:LEU:HD23	1:A:236:SER:OG	1.62	0.99
2:B:206:ASN:HD21	4:B:502:GTP:C1'	1.64	0.99
2:B:184:PRO:HB2	2:B:395:PHE:HA	1.41	0.98
2:B:346:TRP:HE3	2:B:435:TYR:C	1.65	0.98
2:B:346:TRP:CE3	2:B:435:TYR:C	2.33	0.98
1:A:267:PHE:CE2	1:A:388:TRP:CZ2	2.51	0.98
2:B:186:ASN:OD1	2:B:408:TYR:HE2	1.38	0.98
1:A:27:GLU:HA	1:A:358:GLU:OE2	1.63	0.98
1:A:185:TYR:CB	1:A:398:MET:HE2	1.88	0.98
2:B:385:GLN:HB3	2:B:429:VAL:CG1	1.92	0.98
1:A:154:MET:SD	1:A:198:SER:N	2.36	0.98
2:B:195:VAL:CG2	2:B:264:ARG:NH1	2.26	0.97
2:B:380:ASN:OD1	2:B:432:TYR:OH	1.80	0.97
1:A:184:PRO:HB3	1:A:394:LYS:HG2	0.98	0.97
2:B:185:TYR:HA	2:B:395:PHE:CE1	1.97	0.97
2:B:195:VAL:CG2	2:B:264:ARG:HA	1.94	0.97
2:B:261:PRO:HD3	2:B:432:TYR:HE1	1.24	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:266:HIS:CE1	2:B:428:LEU:HD11	2.00	0.97
1:A:228:ASN:HB3	4:A:502:GTP:HN21	0.83	0.97
2:B:194:LEU:O	2:B:265:LEU:HB3	1.62	0.97
2:B:262:PHE:HZ	2:B:434:GLN:HB2	1.24	0.97
1:A:103:TYR:CD2	1:A:189:LEU:HD13	1.99	0.97
1:A:161:TYR:CB	1:A:164:LYS:HG3	1.95	0.97
2:B:15:GLN:CB	2:B:228:ASN:HD21	1.55	0.96
1:A:108:TYR:CZ	1:A:413:MET:HB2	2.01	0.96
1:A:408:TYR:CE1	1:A:418:PHE:CE1	2.52	0.96
1:A:108:TYR:CZ	1:A:413:MET:HG3	1.98	0.96
1:A:135:PHE:HE1	1:A:157:LEU:HD13	1.24	0.96
2:B:189:LEU:CD2	2:B:421:ALA:HB2	1.64	0.96
1:A:105:ARG:CA	1:A:411:GLU:OE1	2.14	0.96
2:B:189:LEU:CD2	2:B:421:ALA:H	1.79	0.96
1:A:405:VAL:CB	1:A:408:TYR:HE2	1.79	0.96
2:B:104:ALA:HA	2:B:417:GLU:OE2	1.65	0.96
1:A:12:ALA:CB	4:A:502:GTP:O4'	2.13	0.96
1:A:142:GLY:O	1:A:172:TYR:CZ	2.19	0.96
2:B:104:ALA:CB	2:B:413:MET:HB2	1.94	0.96
1:A:72:PRO:CG	2:B:47:GLU:CG	2.21	0.96
1:A:72:PRO:HG3	2:B:47:GLU:CB	1.94	0.96
1:A:185:TYR:HB3	1:A:398:MET:HE1	1.47	0.95
1:A:154:MET:CE	1:A:198:SER:HB2	1.96	0.95
1:A:191:THR:O	1:A:194:THR:HG22	1.65	0.95
1:A:267:PHE:N	1:A:432:TYR:OH	1.98	0.95
2:B:273:ALA:HB3	2:B:274:PRO:HD3	1.48	0.95
1:A:195:LEU:CD2	1:A:424:ASP:CA	2.44	0.95
1:A:405:VAL:CA	1:A:408:TYR:CE2	2.49	0.95
1:A:251:ASP:N	1:A:254:GLU:HG3	1.82	0.95
2:B:105:LYS:HD3	2:B:411:GLU:O	1.67	0.95
2:B:192:HIS:HA	2:B:424:ASN:ND2	1.81	0.95
2:B:313:LEU:HD21	2:B:363:ALA:N	1.82	0.95
2:B:204:ILE:HG21	2:B:231:VAL:HG22	0.96	0.95
1:A:195:LEU:HD21	1:A:424:ASP:C	1.72	0.95
1:A:135:PHE:CE1	1:A:157:LEU:CD1	2.49	0.95
2:B:261:PRO:C	2:B:435:TYR:HE2	1.70	0.94
1:A:135:PHE:CZ	1:A:157:LEU:CD2	2.51	0.94
1:A:199:ASP:HB3	1:A:265:GLY:HA3	1.50	0.94
1:A:28:HIS:CE1	1:A:240:ALA:O	2.21	0.94
1:A:405:VAL:HA	1:A:408:TYR:CE2	2.01	0.94
1:A:259:LEU:HD11	1:A:378:LEU:HD13	1.47	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:ARG:HA	1:A:411:GLU:OE1	1.68	0.94
1:A:228:ASN:HD22	4:A:502:GTP:HN1	1.11	0.94
1:A:404:PHE:HD2	2:B:257:VAL:HG11	1.30	0.94
2:B:2:ARG:HE	2:B:48:ARG:HH22	1.05	0.94
1:A:108:TYR:CZ	1:A:413:MET:CG	2.50	0.94
2:B:195:VAL:HG23	2:B:264:ARG:CA	1.96	0.94
1:A:109:THR:HG22	1:A:110:ILE:H	1.33	0.94
1:A:316:CYS:HB3	1:A:378:LEU:HD11	1.48	0.94
1:A:346:TRP:HZ2	1:A:435:VAL:O	1.51	0.94
1:A:188:ILE:HD11	1:A:392:ASP:C	1.89	0.93
1:A:199:ASP:CA	1:A:265:GLY:HA3	1.97	0.93
1:A:404:PHE:CD2	2:B:257:VAL:CG1	2.50	0.93
1:A:72:PRO:HG2	2:B:47:GLU:HG2	1.50	0.93
1:A:251:ASP:H	1:A:254:GLU:HG3	1.33	0.93
1:A:171:ILE:HG23	1:A:205:ASP:HB3	1.48	0.93
1:A:195:LEU:HD22	1:A:424:ASP:CB	1.99	0.93
2:B:258:ASN:HD22	2:B:352:LYS:HG3	1.18	0.93
2:B:262:PHE:CE1	2:B:434:GLN:CB	2.37	0.93
2:B:264:ARG:O	2:B:265:LEU:HB3	1.64	0.93
2:B:281:GLN:O	2:B:283:TYR:N	2.00	0.93
1:A:104:ALA:HB2	1:A:408:TYR:HB3	0.93	0.93
1:A:224:TYR:HD2	2:B:322:ARG:NH2	1.63	0.93
2:B:395:PHE:HE2	2:B:422:GLU:OE1	1.52	0.93
2:B:102:ASN:ND2	2:B:408:TYR:C	2.20	0.93
2:B:206:ASN:ND2	4:B:502:GTP:O3'	2.01	0.93
1:A:12:ALA:HB1	4:A:502:GTP:C4	2.02	0.92
1:A:150:THR:C	1:A:197:HIS:HE1	1.73	0.92
1:A:184:PRO:CG	1:A:394:LYS:HG2	1.98	0.92
1:A:237:SER:HB2	1:A:376:CYS:SG	2.08	0.92
2:B:267:PHE:CD2	2:B:388:PHE:CE1	2.53	0.92
1:A:199:ASP:HB3	1:A:265:GLY:CA	1.98	0.92
2:B:154:ILE:HD12	2:B:197:ASN:HB3	1.46	0.92
2:B:266:HIS:NE2	2:B:428:LEU:HD11	1.84	0.92
1:A:5:ILE:HG23	1:A:125:LEU:HD13	1.52	0.92
2:B:380:ASN:OD1	2:B:432:TYR:CZ	2.23	0.92
1:A:104:ALA:HB1	1:A:408:TYR:HA	0.93	0.92
1:A:147:SER:HB2	1:A:190:THR:OG1	1.68	0.92
2:B:262:PHE:HB3	2:B:431:GLU:HB2	1.51	0.92
2:B:105:LYS:HD3	2:B:411:GLU:CB	2.00	0.92
1:A:12:ALA:CA	4:A:502:GTP:C8	2.53	0.92
2:B:103:TRP:HE3	2:B:417:GLU:OE2	1.53	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:GLN:HB3	1:A:32:PRO:HD2	1.51	0.92
1:A:346:TRP:HZ2	1:A:435:VAL:HG12	1.35	0.92
2:B:16:ILE:CD1	2:B:228:ASN:HA	2.00	0.92
2:B:363:ALA:HB1	2:B:433:GLN:CA	1.99	0.91
2:B:69:ASP:OD1	2:B:71:GLU:OE1	1.86	0.91
1:A:189:LEU:HD11	1:A:418:PHE:HE2	1.34	0.91
2:B:169:PHE:HZ	2:B:235:MET:HA	1.20	0.91
2:B:261:PRO:HD2	2:B:432:TYR:CD1	2.05	0.91
1:A:154:MET:HB3	1:A:197:HIS:C	1.90	0.91
1:A:122:ILE:HB	1:A:135:PHE:HE2	1.34	0.91
2:B:169:PHE:CE2	2:B:235:MET:HA	1.98	0.91
1:A:189:LEU:HA	1:A:192:HIS:CE1	2.06	0.91
2:B:182:VAL:HG11	2:B:408:TYR:HE1	1.35	0.91
2:B:15:GLN:CB	2:B:228:ASN:HD22	1.61	0.91
1:A:199:ASP:HA	1:A:265:GLY:HA3	1.53	0.91
2:B:105:LYS:HD2	2:B:411:GLU:O	1.69	0.91
1:A:12:ALA:HA	4:A:502:GTP:C8	2.05	0.91
1:A:194:THR:OG1	1:A:198:SER:CB	2.18	0.91
1:A:204:VAL:HG21	1:A:231:ILE:HD12	1.52	0.91
1:A:405:VAL:HB	1:A:408:TYR:CE2	2.06	0.91
1:A:98:ASP:HB2	2:B:2:ARG:HD3	1.50	0.90
2:B:154:ILE:CD1	2:B:197:ASN:ND2	2.35	0.90
2:B:262:PHE:CD2	2:B:432:TYR:CA	2.54	0.90
2:B:132:LEU:HD23	2:B:164:ARG:HG3	1.50	0.90
1:A:191:THR:HA	1:A:194:THR:HG21	1.50	0.90
1:A:404:PHE:CD2	2:B:257:VAL:HG11	2.07	0.90
1:A:346:TRP:CZ2	1:A:435:VAL:O	2.25	0.90
1:A:405:VAL:CA	1:A:408:TYR:HE2	1.83	0.90
2:B:185:TYR:HA	2:B:395:PHE:HE1	1.34	0.90
1:A:10:GLY:HA2	4:A:502:GTP:O2B	1.72	0.90
1:A:73:THR:CB	2:B:42:LEU:HD13	2.01	0.90
1:A:191:THR:HA	1:A:194:THR:HG22	1.47	0.90
1:A:413:MET:SD	1:A:418:PHE:HE1	1.93	0.90
1:A:122:ILE:HD12	1:A:157:LEU:HD21	1.54	0.90
1:A:174:ALA:HB2	1:A:207:GLU:HB2	1.53	0.90
2:B:105:LYS:CE	2:B:110:GLU:CD	2.38	0.90
2:B:262:PHE:HD2	2:B:432:TYR:CA	1.83	0.90
2:B:266:HIS:NE2	2:B:428:LEU:CD1	2.34	0.90
1:A:199:ASP:CB	1:A:265:GLY:HA3	2.01	0.90
2:B:385:GLN:HG3	2:B:388:PHE:HB2	1.54	0.90
1:A:228:ASN:ND2	4:A:502:GTP:HN1	1.70	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:LEU:CD2	1:A:236:SER:OG	2.16	0.89
2:B:103:TRP:CZ3	2:B:417:GLU:OE2	2.25	0.89
2:B:154:ILE:CD1	2:B:197:ASN:HB2	1.95	0.89
2:B:182:VAL:CG1	2:B:408:TYR:HE1	1.85	0.89
1:A:9:VAL:CG1	1:A:139:HIS:CB	2.51	0.89
1:A:296:PHE:HE1	1:A:341:ILE:HD11	1.32	0.89
1:A:343:PHE:CZ	1:A:351:PHE:CE2	2.60	0.89
1:A:119:LEU:HD23	1:A:122:ILE:HD11	1.53	0.89
1:A:174:ALA:HB2	1:A:207:GLU:CB	2.02	0.89
1:A:195:LEU:HD22	1:A:424:ASP:HB3	1.52	0.89
2:B:2:ARG:HH21	2:B:48:ARG:HH21	1.20	0.89
1:A:12:ALA:HA	4:A:502:GTP:C4	2.07	0.89
1:A:225:THR:HA	1:A:228:ASN:ND2	1.88	0.89
2:B:147:SER:O	2:B:151:THR:HB	1.71	0.89
1:A:110:ILE:HG23	1:A:111:GLY:H	1.38	0.89
2:B:15:GLN:HB3	2:B:228:ASN:ND2	1.72	0.89
2:B:205:ASP:HB3	2:B:302:MET:O	1.73	0.89
1:A:108:TYR:CE2	1:A:413:MET:HB2	2.08	0.88
1:A:210:TYR:CZ	1:A:227:LEU:HD11	2.08	0.88
1:A:262:TYR:HE2	1:A:435:VAL:HG13	1.36	0.88
2:B:395:PHE:HD2	2:B:422:GLU:CD	1.76	0.88
1:A:192:HIS:CD2	1:A:193:THR:H	1.90	0.88
2:B:154:ILE:HD11	2:B:197:ASN:HD22	1.37	0.88
1:A:108:TYR:CE2	1:A:413:MET:CB	2.57	0.88
1:A:405:VAL:CB	1:A:408:TYR:CE2	2.57	0.88
1:A:161:TYR:C	1:A:163:LYS:HB3	1.95	0.88
1:A:195:LEU:HD11	1:A:428:LEU:HB2	1.55	0.88
2:B:8:GLN:OE1	2:B:67:LEU:HD22	1.73	0.88
2:B:185:TYR:CB	2:B:418:PHE:CE2	2.56	0.88
2:B:189:LEU:CD2	2:B:421:ALA:N	2.36	0.88
1:A:185:TYR:CB	1:A:398:MET:HE1	1.99	0.88
2:B:205:ASP:CG	2:B:208:ALA:HB3	1.94	0.88
1:A:224:TYR:CE2	2:B:322:ARG:NH2	2.41	0.87
1:A:158:SER:HA	1:A:163:LYS:N	1.89	0.87
1:A:267:PHE:CD2	1:A:388:TRP:CZ2	2.61	0.87
2:B:154:ILE:HD12	2:B:197:ASN:ND2	1.88	0.87
2:B:360:PRO:HG2	2:B:371:LEU:HB3	1.56	0.87
1:A:195:LEU:CD2	1:A:424:ASP:CB	2.52	0.87
2:B:261:PRO:C	2:B:435:TYR:CE2	2.46	0.87
2:B:266:HIS:CE1	2:B:428:LEU:HG	2.09	0.87
1:A:135:PHE:CE1	1:A:157:LEU:HD22	2.10	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:204:ILE:HG12	2:B:302:MET:SD	2.15	0.87
2:B:16:ILE:HG13	2:B:228:ASN:CB	1.87	0.87
1:A:173:PRO:CB	1:A:174:ALA:HB3	2.04	0.86
2:B:311:ARG:HD3	2:B:342:TYR:HA	1.56	0.86
2:B:188:THR:HA	2:B:425:MET:HE3	0.89	0.86
2:B:194:LEU:HD13	2:B:267:PHE:HE1	1.40	0.86
1:A:194:THR:HA	1:A:197:HIS:HB3	1.57	0.86
1:A:224:TYR:HD1	4:A:502:GTP:C4	1.88	0.86
1:A:139:HIS:O	1:A:140:SER:OG	1.93	0.86
1:A:306:ASP:O	1:A:308:ARG:N	2.07	0.86
2:B:6:HIS:CE1	2:B:8:GLN:HG2	2.10	0.86
2:B:16:ILE:CG1	2:B:228:ASN:HB3	1.93	0.86
2:B:202:TYR:CZ	2:B:238:VAL:CG1	2.58	0.86
2:B:261:PRO:HD3	2:B:432:TYR:CE1	2.01	0.86
2:B:189:LEU:HD11	2:B:418:PHE:HA	1.55	0.86
1:A:346:TRP:CZ2	1:A:435:VAL:HG12	2.10	0.86
2:B:276:THR:HB	2:B:281:GLN:HG3	1.56	0.86
1:A:150:THR:HB	1:A:197:HIS:HE1	1.40	0.86
1:A:224:TYR:CE1	4:A:502:GTP:N7	2.43	0.86
2:B:204:ILE:HG22	2:B:205:ASP:H	1.40	0.86
2:B:258:ASN:HB3	2:B:352:LYS:HD2	1.55	0.86
1:A:28:HIS:NE2	1:A:240:ALA:O	2.09	0.85
1:A:154:MET:HE3	1:A:197:HIS:ND1	1.90	0.85
2:B:266:HIS:CG	2:B:428:LEU:HD11	2.11	0.85
1:A:184:PRO:HB3	1:A:394:LYS:HB3	1.57	0.85
2:B:189:LEU:CD2	2:B:417:GLU:O	2.25	0.85
2:B:153:LEU:O	2:B:157:ILE:HG12	1.76	0.85
2:B:262:PHE:CB	2:B:431:GLU:CB	2.54	0.85
2:B:189:LEU:HD22	2:B:421:ALA:HB2	1.58	0.85
2:B:346:TRP:CZ3	2:B:435:TYR:CB	2.59	0.85
1:A:173:PRO:CA	1:A:206:ASN:HB3	2.05	0.84
1:A:12:ALA:CA	4:A:502:GTP:C4	2.60	0.84
2:B:182:VAL:CG1	2:B:408:TYR:CE1	2.58	0.84
1:A:188:ILE:HD12	1:A:392:ASP:O	1.77	0.84
1:A:408:TYR:CG	1:A:418:PHE:CZ	2.65	0.84
1:A:5:ILE:HD11	1:A:125:LEU:HB3	1.57	0.84
1:A:195:LEU:HD12	1:A:428:LEU:HD22	1.59	0.84
2:B:204:ILE:HG22	2:B:209:LEU:HD11	1.60	0.84
2:B:206:ASN:ND2	4:B:502:GTP:C3'	2.40	0.84
1:A:71:GLU:HB2	4:A:502:GTP:O1G	1.77	0.84
1:A:180:ALA:CA	2:B:248:LEU:HD11	2.06	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:324:SER:HB3	2:B:327:GLU:HG2	1.60	0.84
1:A:3:GLU:OE2	1:A:129:CYS:HB2	1.77	0.84
2:B:4:ILE:HD13	2:B:136:GLN:HE21	1.42	0.84
2:B:195:VAL:CG1	2:B:264:ARG:NH1	2.41	0.84
2:B:409:THR:CA	2:B:413:MET:CG	2.40	0.84
1:A:264:ARG:HB2	1:A:266:HIS:CD2	2.13	0.84
2:B:382:THR:O	2:B:385:GLN:HA	1.78	0.84
1:A:188:ILE:CD1	1:A:392:ASP:HA	2.08	0.84
2:B:105:LYS:CE	2:B:110:GLU:OE2	2.24	0.84
1:A:28:HIS:CD2	1:A:244:PHE:HB2	2.12	0.83
1:A:106:GLY:O	1:A:111:GLY:HA3	1.78	0.83
1:A:72:PRO:HG3	2:B:47:GLU:HG2	0.84	0.83
2:B:185:TYR:HD1	2:B:418:PHE:HD2	0.87	0.83
1:A:24:TYR:CE1	1:A:240:ALA:HB2	2.13	0.83
2:B:102:ASN:ND2	2:B:408:TYR:O	2.11	0.83
2:B:346:TRP:HB3	2:B:435:TYR:O	1.78	0.83
1:A:154:MET:HB3	1:A:166:LYS:HD2	1.57	0.83
1:A:199:ASP:O	1:A:265:GLY:C	2.16	0.83
1:A:12:ALA:CA	4:A:502:GTP:C5	2.59	0.83
1:A:23:LEU:HD21	1:A:236:SER:HB3	1.60	0.83
1:A:234:ILE:HG13	1:A:270:ALA:HB1	1.59	0.83
1:A:316:CYS:HB3	1:A:378:LEU:CD1	2.08	0.83
2:B:3:GLU:O	2:B:133:GLN:HB3	1.78	0.83
1:A:103:TYR:HE2	1:A:413:MET:CE	1.92	0.83
1:A:150:THR:CB	1:A:197:HIS:HE1	1.91	0.83
2:B:2:ARG:NE	2:B:48:ARG:HH22	1.75	0.83
2:B:148:GLY:O	2:B:151:THR:HG22	1.79	0.83
1:A:151:SER:HA	1:A:197:HIS:ND1	1.93	0.83
2:B:363:ALA:CB	2:B:436:GLN:HB2	2.09	0.83
1:A:171:ILE:HA	1:A:205:ASP:HB2	1.61	0.83
2:B:234:THR:HG21	2:B:270:PRO:CB	2.06	0.83
1:A:264:ARG:O	1:A:266:HIS:N	2.09	0.82
2:B:181:VAL:O	2:B:398:MET:SD	2.37	0.82
2:B:287:THR:O	2:B:288:VAL:HG23	1.78	0.82
1:A:392:ASP:CG	1:A:425:MET:CE	2.47	0.82
1:A:5:ILE:HD13	1:A:125:LEU:HB3	1.59	0.82
2:B:209:LEU:HB3	2:B:227:LEU:HD22	1.59	0.82
2:B:169:PHE:CG	2:B:235:MET:HE3	2.14	0.82
2:B:242:LEU:HD22	2:B:250:ALA:H	1.42	0.82
1:A:24:TYR:HD1	1:A:240:ALA:HB2	1.39	0.82
1:A:189:LEU:O	1:A:193:THR:HG22	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:194:LEU:O	2:B:265:LEU:CD2	2.28	0.82
2:B:103:TRP:CZ3	2:B:417:GLU:CG	2.62	0.82
1:A:104:ALA:C	1:A:411:GLU:OE1	2.17	0.82
2:B:195:VAL:HG23	2:B:264:ARG:N	1.95	0.82
2:B:105:LYS:CG	2:B:411:GLU:HB3	2.09	0.82
1:A:140:SER:HA	1:A:170:SER:CB	2.09	0.82
2:B:156:LYS:HA	2:B:156:LYS:HE2	1.61	0.82
2:B:206:ASN:OD1	4:B:502:GTP:H1'	1.80	0.82
1:A:12:ALA:HB2	4:A:502:GTP:C8	2.14	0.82
2:B:150:GLY:HA2	2:B:153:LEU:HD22	1.60	0.82
2:B:408:TYR:C	2:B:413:MET:SD	2.57	0.82
1:A:173:PRO:HA	1:A:206:ASN:O	1.79	0.81
2:B:363:ALA:CB	2:B:433:GLN:HA	2.05	0.81
1:A:408:TYR:CD2	1:A:418:PHE:CZ	2.67	0.81
2:B:16:ILE:HG12	2:B:228:ASN:C	2.01	0.81
2:B:169:PHE:CE1	2:B:235:MET:CB	2.33	0.81
2:B:189:LEU:HD23	2:B:421:ALA:N	1.94	0.81
1:A:109:THR:H	1:A:411:GLU:HB3	1.46	0.81
2:B:346:TRP:HZ3	2:B:435:TYR:CD1	1.94	0.81
1:A:103:TYR:CE2	1:A:413:MET:CE	2.64	0.81
1:A:132:LEU:CG	1:A:164:LYS:HE3	2.08	0.81
1:A:201:ALA:H	1:A:267:PHE:HD2	1.29	0.81
1:A:313:MET:HB3	1:A:344:VAL:HG21	1.63	0.81
1:A:310:GLY:HA2	1:A:382:THR:HB	1.63	0.81
2:B:195:VAL:CG2	2:B:263:PRO:O	2.29	0.81
2:B:202:TYR:CE2	2:B:238:VAL:HG11	2.15	0.81
1:A:194:THR:OG1	1:A:198:SER:HB3	1.80	0.81
2:B:20:PHE:CZ	2:B:24:ILE:HD12	2.15	0.81
2:B:110:GLU:O	2:B:113:GLU:HG2	1.79	0.81
2:B:310:GLY:CA	2:B:386:GLU:OE1	2.28	0.81
1:A:9:VAL:HG13	1:A:139:HIS:CB	2.10	0.81
1:A:189:LEU:HD21	1:A:418:PHE:HD2	1.01	0.81
2:B:195:VAL:HG11	2:B:264:ARG:HH11	1.42	0.81
1:A:200:CYS:SG	1:A:268:PRO:HD2	2.20	0.81
1:A:194:THR:OG1	1:A:198:SER:HB2	1.81	0.81
2:B:236:SER:O	2:B:240:THR:CG2	2.29	0.80
2:B:262:PHE:CE2	2:B:435:TYR:CG	2.69	0.80
1:A:6:SER:HB3	1:A:136:SER:OG	1.81	0.80
1:A:27:GLU:OE2	1:A:240:ALA:CB	2.29	0.80
1:A:135:PHE:HZ	1:A:157:LEU:HD22	1.44	0.80
1:A:189:LEU:HD22	1:A:418:PHE:CE2	2.16	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:TYR:HE2	2:B:322:ARG:HH22	1.24	0.80
2:B:2:ARG:NH2	2:B:48:ARG:NH2	2.29	0.80
2:B:189:LEU:HD21	2:B:417:GLU:O	1.81	0.80
2:B:186:ASN:ND2	2:B:408:TYR:OH	2.14	0.80
1:A:405:VAL:O	1:A:408:TYR:CD2	2.34	0.80
2:B:167:ASN:HD21	2:B:252:LEU:CD2	1.95	0.80
1:A:105:ARG:HA	1:A:411:GLU:CD	2.01	0.80
1:A:195:LEU:HD22	1:A:424:ASP:CA	2.08	0.80
1:A:286:LEU:HG	1:A:290:GLU:HB2	1.64	0.80
1:A:248:LEU:HD23	1:A:353:VAL:O	1.81	0.80
2:B:12:CYS:HB2	4:B:502:GTP:C4	2.17	0.80
2:B:147:SER:HB2	2:B:190:SER:HB3	1.60	0.80
2:B:192:HIS:CB	2:B:424:ASN:ND2	2.14	0.80
2:B:258:ASN:HD22	2:B:352:LYS:CG	1.85	0.80
1:A:234:ILE:O	1:A:234:ILE:HD13	1.81	0.80
2:B:204:ILE:CA	2:B:302:MET:HB3	2.07	0.80
1:A:404:PHE:CD2	2:B:257:VAL:HG12	2.16	0.80
2:B:195:VAL:HA	2:B:264:ARG:C	2.01	0.80
1:A:404:PHE:HD2	2:B:257:VAL:CG1	1.90	0.79
2:B:266:HIS:CE1	2:B:428:LEU:CG	2.64	0.79
1:A:132:LEU:HD23	1:A:132:LEU:H	1.46	0.79
2:B:16:ILE:CG1	2:B:228:ASN:OD1	2.26	0.79
2:B:101:ASN:O	2:B:408:TYR:CE2	2.35	0.79
1:A:10:GLY:CA	4:A:502:GTP:O2B	2.29	0.79
1:A:109:THR:CG2	1:A:110:ILE:N	2.44	0.79
1:A:188:ILE:HD11	1:A:395:PHE:H	1.45	0.79
1:A:195:LEU:CD1	1:A:428:LEU:HD22	2.10	0.79
1:A:7:ILE:HG22	1:A:66:VAL:HG22	1.63	0.79
1:A:151:SER:N	1:A:197:HIS:CE1	2.51	0.79
1:A:26:LEU:HG	1:A:361:THR:HG21	1.64	0.79
1:A:140:SER:HA	1:A:170:SER:HB2	1.64	0.79
1:A:190:THR:O	1:A:194:THR:CG2	2.31	0.79
1:A:204:VAL:HB	1:A:209:ILE:HD11	1.63	0.79
2:B:204:ILE:HG23	2:B:302:MET:SD	2.22	0.79
2:B:171:VAL:CG1	2:B:205:ASP:HA	2.13	0.79
2:B:265:LEU:HD12	2:B:265:LEU:O	1.83	0.79
1:A:184:PRO:CB	1:A:394:LYS:CB	2.57	0.79
1:A:192:HIS:C	1:A:421:ALA:HB1	1.96	0.79
1:A:195:LEU:CD2	1:A:424:ASP:O	2.06	0.79
2:B:54:ASN:HD21	2:B:64:ARG:HD3	1.45	0.79
1:A:184:PRO:CG	1:A:398:MET:SD	2.68	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ILE:CD1	1:A:395:PHE:H	1.96	0.79
1:A:402:ARG:HB3	1:A:405:VAL:HG21	1.65	0.79
2:B:154:ILE:CD1	2:B:197:ASN:CG	2.42	0.79
1:A:180:ALA:H	2:B:248:LEU:HD11	1.48	0.78
1:A:189:LEU:HD22	1:A:418:PHE:CD2	2.12	0.78
2:B:172:VAL:O	2:B:205:ASP:CB	2.31	0.78
2:B:206:ASN:ND2	4:B:502:GTP:O2'	2.16	0.78
2:B:409:THR:HA	2:B:413:MET:HG2	0.80	0.78
1:A:11:GLN:HG3	1:A:74:VAL:CG1	2.13	0.78
1:A:71:GLU:HG2	2:B:42:LEU:HD11	1.65	0.78
2:B:15:GLN:HB2	2:B:228:ASN:HD21	0.72	0.78
1:A:187:SER:HB2	1:A:391:LEU:HG	1.64	0.78
1:A:141:PHE:HE2	1:A:391:LEU:HD21	0.70	0.78
1:A:267:PHE:N	1:A:267:PHE:CD1	2.49	0.78
2:B:234:THR:CG2	2:B:270:PRO:HB2	2.11	0.78
2:B:185:TYR:CE2	2:B:398:MET:HG3	2.19	0.78
2:B:203:CYS:HB3	2:B:268:PHE:O	1.84	0.78
1:A:25:CYS:HG	1:A:83:TYR:HE2	1.30	0.78
1:A:231:ILE:HA	1:A:234:ILE:HG22	1.66	0.78
1:A:243:ARG:HH21	1:A:252:LEU:H	0.79	0.78
2:B:12:CYS:HB2	4:B:502:GTP:C5	2.19	0.78
2:B:102:ASN:HD21	2:B:413:MET:CG	1.96	0.78
2:B:413:MET:CE	2:B:418:PHE:CZ	2.63	0.78
1:A:135:PHE:CE1	1:A:157:LEU:CD2	2.65	0.78
1:A:195:LEU:HG	1:A:264:ARG:NH2	1.97	0.78
2:B:258:ASN:CB	2:B:352:LYS:HD2	2.13	0.78
1:A:241:SER:O	1:A:244:PHE:HB3	1.82	0.78
2:B:409:THR:N	2:B:413:MET:HG2	1.99	0.78
1:A:27:GLU:OE1	1:A:241:SER:HB3	1.84	0.77
2:B:184:PRO:C	2:B:395:PHE:HD1	1.87	0.77
2:B:262:PHE:CE2	2:B:434:GLN:HB2	2.10	0.77
1:A:23:LEU:HD23	1:A:236:SER:HB2	0.78	0.77
2:B:35:SER:HB3	2:B:59:ASN:HA	1.65	0.77
2:B:154:ILE:CD1	2:B:197:ASN:HD22	1.95	0.77
2:B:169:PHE:HD1	2:B:235:MET:CE	1.98	0.77
2:B:409:THR:N	2:B:413:MET:CG	2.47	0.77
2:B:204:ILE:HG22	2:B:205:ASP:N	1.96	0.77
2:B:262:PHE:CB	2:B:431:GLU:HB2	2.12	0.77
1:A:200:CYS:HB2	1:A:266:HIS:O	1.85	0.77
1:A:395:PHE:HZ	1:A:418:PHE:HD2	1.33	0.77
2:B:103:TRP:HZ3	2:B:417:GLU:HG3	1.47	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:194:LEU:C	2:B:265:LEU:HD23	2.04	0.77
2:B:204:ILE:CD1	2:B:231:VAL:HG13	2.11	0.77
2:B:171:VAL:HG11	2:B:206:ASN:OD1	1.84	0.76
2:B:310:GLY:HA2	2:B:386:GLU:OE1	1.85	0.76
1:A:283:HIS:CE1	1:A:286:LEU:HD13	2.19	0.76
1:A:224:TYR:HD2	2:B:322:ARG:HH21	1.32	0.76
2:B:185:TYR:CE1	2:B:399:PHE:CG	2.71	0.76
2:B:363:ALA:HB3	2:B:436:GLN:CD	2.05	0.76
2:B:363:ALA:HB3	2:B:436:GLN:OE1	1.86	0.76
1:A:11:GLN:HB3	4:A:502:GTP:PA	2.26	0.76
1:A:244:PHE:CD1	1:A:245:ASP:OD1	2.38	0.76
1:A:362:VAL:HG13	1:A:368:LEU:HD12	1.68	0.76
2:B:16:ILE:CB	2:B:228:ASN:HB3	2.16	0.76
2:B:259:MET:HA	2:B:314:THR:HG21	1.65	0.76
1:A:184:PRO:HA	1:A:187:SER:OG	1.86	0.76
1:A:404:PHE:CE2	2:B:257:VAL:HG12	2.20	0.76
2:B:204:ILE:CG2	2:B:209:LEU:HD11	2.16	0.76
2:B:259:MET:HG2	2:B:314:THR:HG21	1.67	0.76
1:A:154:MET:SD	1:A:198:SER:HB2	2.23	0.76
1:A:154:MET:SD	1:A:197:HIS:C	2.64	0.76
1:A:224:TYR:HE1	4:A:502:GTP:C5	2.01	0.76
1:A:344:VAL:HG11	1:A:346:TRP:CE2	2.21	0.75
2:B:182:VAL:HG13	2:B:404:PHE:HB2	1.68	0.75
2:B:250:ALA:HA	2:B:254:LYS:HE2	1.68	0.75
1:A:189:LEU:CD1	1:A:418:PHE:CE2	2.69	0.75
1:A:331:ALA:O	1:A:335:ILE:HG12	1.86	0.75
1:A:195:LEU:HD23	1:A:424:ASP:HB3	1.69	0.75
2:B:103:TRP:HZ3	2:B:417:GLU:CG	2.00	0.75
2:B:185:TYR:CB	2:B:418:PHE:CD2	2.69	0.75
2:B:262:PHE:CZ	2:B:435:TYR:CD2	2.74	0.75
1:A:182:VAL:HB	1:A:398:MET:HE1	1.67	0.75
1:A:98:ASP:HB3	1:A:105:ARG:NH2	2.01	0.75
4:A:502:GTP:O1A	2:B:245:PRO:CB	2.24	0.75
2:B:194:LEU:CA	2:B:265:LEU:CD2	2.50	0.75
2:B:346:TRP:HZ3	2:B:435:TYR:CB	1.98	0.75
1:A:11:GLN:HB2	4:A:502:GTP:O2A	1.84	0.75
1:A:286:LEU:HG	1:A:290:GLU:CB	2.16	0.75
1:A:317:LEU:HB3	1:A:319:TYR:HE1	1.52	0.75
1:A:381:THR:OG1	1:A:383:ALA:HB3	1.87	0.75
2:B:195:VAL:CB	2:B:264:ARG:O	2.34	0.75
2:B:396:THR:HG23	2:B:422:GLU:OE2	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:LEU:HD21	1:A:384:ILE:HG12	1.69	0.75
1:A:154:MET:H	1:A:197:HIS:HE2	1.34	0.75
1:A:5:ILE:CG2	1:A:125:LEU:HD13	2.16	0.74
1:A:110:ILE:HG23	1:A:111:GLY:N	1.99	0.74
1:A:180:ALA:H	2:B:248:LEU:CD1	1.96	0.74
2:B:8:GLN:CD	2:B:67:LEU:HD22	2.08	0.74
1:A:276:ILE:HG23	1:A:369:ALA:CB	2.16	0.74
2:B:168:THR:HB	2:B:201:THR:HG23	1.68	0.74
1:A:189:LEU:CD1	1:A:418:PHE:HE2	2.00	0.74
2:B:202:TYR:HE2	2:B:378:ILE:HD13	1.52	0.74
2:B:209:LEU:HG	2:B:230:LEU:HD22	1.69	0.74
1:A:192:HIS:HD2	1:A:193:THR:N	1.81	0.74
2:B:203:CYS:C	2:B:270:PRO:HD2	2.08	0.74
2:B:217:LEU:C	2:B:219:LEU:H	1.91	0.74
2:B:205:ASP:OD1	2:B:209:LEU:HD13	1.88	0.74
2:B:165:ILE:HG13	2:B:252:LEU:HD12	1.67	0.74
2:B:242:LEU:HD13	2:B:250:ALA:C	2.08	0.74
2:B:155:SER:HA	2:B:197:ASN:OD1	1.88	0.74
1:A:63:PRO:O	1:A:64:ARG:HG2	1.88	0.73
1:A:69:ASP:OD1	4:A:502:GTP:O3B	2.06	0.73
2:B:274:PRO:HG2	2:B:371:LEU:HD21	1.69	0.73
1:A:93:ILE:HD12	1:A:93:ILE:N	2.03	0.73
1:A:181:VAL:HG21	2:B:352:LYS:HG3	0.85	0.73
1:A:182:VAL:CG1	1:A:404:PHE:CD1	2.70	0.73
2:B:102:ASN:HA	2:B:408:TYR:HD2	1.45	0.73
1:A:108:TYR:HE2	1:A:413:MET:HA	1.51	0.73
2:B:184:PRO:CB	2:B:395:PHE:N	2.51	0.73
1:A:139:HIS:CG	1:A:140:SER:H	2.07	0.73
1:A:173:PRO:CA	1:A:174:ALA:HB3	2.18	0.73
1:A:242:LEU:HG	1:A:250:VAL:O	1.88	0.73
2:B:104:ALA:CA	2:B:417:GLU:OE2	2.37	0.73
1:A:31:GLN:HB3	1:A:32:PRO:CD	2.18	0.73
1:A:142:GLY:O	1:A:172:TYR:CE2	2.41	0.73
1:A:184:PRO:CB	1:A:394:LYS:HB3	2.18	0.73
2:B:6:HIS:HE1	2:B:8:GLN:HG2	1.52	0.73
1:A:69:ASP:O	1:A:94:THR:CA	2.35	0.73
1:A:108:TYR:CE1	1:A:413:MET:HB2	2.23	0.73
2:B:194:LEU:HB2	2:B:265:LEU:HD23	1.56	0.73
1:A:25:CYS:HB2	1:A:30:ILE:O	1.89	0.73
1:A:181:VAL:HG11	2:B:258:ASN:HD21	1.50	0.73
2:B:262:PHE:CZ	2:B:434:GLN:CA	2.72	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:GLU:OE2	1:A:129:CYS:CB	2.37	0.73
1:A:27:GLU:OE2	1:A:240:ALA:HB1	1.89	0.73
2:B:189:LEU:HD23	2:B:421:ALA:HB3	0.73	0.72
2:B:217:LEU:O	2:B:219:LEU:N	2.22	0.72
2:B:262:PHE:CD2	2:B:435:TYR:CD2	2.76	0.72
1:A:105:ARG:O	1:A:110:ILE:HG22	1.89	0.72
2:B:16:ILE:HA	2:B:228:ASN:CB	2.08	0.72
2:B:111:GLY:O	2:B:115:VAL:HG23	1.89	0.72
2:B:313:LEU:HD13	2:B:432:TYR:CD1	2.23	0.72
2:B:346:TRP:CZ3	2:B:435:TYR:CG	2.76	0.72
2:B:356:CYS:SG	2:B:357:ASP:N	2.62	0.72
1:A:305:CYS:SG	1:A:383:ALA:HB1	2.29	0.72
1:A:392:ASP:HA	1:A:425:MET:HE1	1.69	0.72
2:B:195:VAL:HG11	2:B:264:ARG:HH12	1.52	0.72
1:A:408:TYR:CG	1:A:418:PHE:CE1	2.76	0.72
1:A:112:LYS:O	1:A:115:ILE:HG22	1.89	0.72
1:A:242:LEU:HD21	1:A:250:VAL:HB	1.71	0.72
2:B:243:ARG:NH2	2:B:252:LEU:HG	2.05	0.72
1:A:69:ASP:O	1:A:94:THR:HA	1.90	0.72
1:A:169:PHE:HZ	1:A:231:ILE:HG23	1.48	0.72
1:A:312:TYR:O	1:A:344:VAL:HG23	1.90	0.72
1:A:188:ILE:CD1	1:A:392:ASP:CA	2.67	0.72
2:B:10:GLY:O	2:B:14:ASN:HB2	1.90	0.72
2:B:76:ASP:HA	2:B:79:ARG:HG2	1.71	0.72
2:B:171:VAL:HG13	2:B:205:ASP:CA	2.20	0.72
2:B:42:LEU:HA	2:B:47:GLU:OE1	1.90	0.71
1:A:181:VAL:CG2	2:B:258:ASN:ND2	2.51	0.71
1:A:188:ILE:HD13	1:A:392:ASP:HA	1.71	0.71
2:B:262:PHE:HZ	2:B:434:GLN:C	1.93	0.71
1:A:7:ILE:HD11	1:A:137:VAL:HG22	1.71	0.71
2:B:346:TRP:HB3	2:B:436:GLN:C	2.11	0.71
2:B:16:ILE:HG12	2:B:228:ASN:HB3	1.62	0.71
2:B:155:SER:HG	2:B:197:ASN:ND2	1.88	0.71
2:B:194:LEU:HD12	2:B:267:PHE:HZ	0.55	0.71
2:B:202:TYR:CE2	2:B:238:VAL:CG1	2.74	0.71
1:A:181:VAL:CG1	2:B:258:ASN:ND2	2.53	0.71
1:A:264:ARG:C	1:A:266:HIS:H	1.91	0.71
2:B:299:LYS:HD3	2:B:299:LYS:N	2.04	0.71
1:A:173:PRO:HB2	1:A:174:ALA:HB3	1.73	0.71
2:B:346:TRP:HZ3	2:B:435:TYR:CG	2.09	0.71
2:B:105:LYS:CD	2:B:110:GLU:HG2	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:TYR:CE2	1:A:435:VAL:HG13	2.22	0.71
2:B:237:GLY:O	2:B:241:CYS:HB3	1.91	0.71
1:A:193:THR:N	1:A:421:ALA:HB1	2.05	0.71
2:B:262:PHE:CZ	2:B:435:TYR:CG	2.79	0.71
1:A:210:TYR:CE1	1:A:227:LEU:CD1	2.70	0.70
1:A:244:PHE:HD1	1:A:245:ASP:N	1.89	0.70
2:B:194:LEU:CG	2:B:265:LEU:CD2	2.69	0.70
2:B:311:ARG:HB2	2:B:436:GLN:NE2	2.06	0.70
1:A:188:ILE:CD1	1:A:392:ASP:C	2.52	0.70
1:A:259:LEU:HD11	1:A:378:LEU:CD1	2.20	0.70
2:B:105:LYS:HE3	2:B:110:GLU:HG2	1.53	0.70
2:B:171:VAL:CG1	2:B:205:ASP:C	2.59	0.70
2:B:167:ASN:HD21	2:B:252:LEU:HD22	1.55	0.70
2:B:192:HIS:O	2:B:424:ASN:ND2	2.08	0.70
1:A:7:ILE:CG1	1:A:137:VAL:HG22	2.20	0.70
1:A:195:LEU:HD23	1:A:424:ASP:CA	2.19	0.70
2:B:255:LEU:O	2:B:259:MET:HG3	1.91	0.70
1:A:123:ARG:CA	1:A:161:TYR:OH	2.35	0.70
1:A:184:PRO:CB	1:A:394:LYS:CG	2.37	0.70
1:A:266:HIS:CD2	1:A:432:TYR:CE1	2.79	0.70
1:A:189:LEU:HD11	1:A:418:PHE:CE2	2.21	0.70
2:B:291:LEU:O	2:B:295:MET:HG3	1.91	0.70
1:A:296:PHE:CZ	1:A:335:ILE:HG21	2.26	0.70
2:B:171:VAL:HG13	2:B:205:ASP:C	2.12	0.70
2:B:385:GLN:HB3	2:B:429:VAL:HG22	1.72	0.70
1:A:12:ALA:CA	4:A:502:GTP:N9	2.55	0.70
1:A:151:SER:HB3	1:A:193:THR:HG21	1.72	0.70
1:A:237:SER:CB	1:A:376:CYS:SG	2.80	0.70
1:A:317:LEU:HD12	1:A:351:PHE:HD1	1.55	0.70
2:B:180:THR:HG22	2:B:181:VAL:N	2.07	0.70
2:B:413:MET:HE1	2:B:418:PHE:CZ	2.24	0.70
1:A:173:PRO:HB2	1:A:174:ALA:O	1.90	0.70
2:B:8:GLN:NE2	2:B:17:GLY:HA3	2.06	0.70
2:B:195:VAL:CB	2:B:264:ARG:HA	2.21	0.70
1:A:343:PHE:CZ	1:A:351:PHE:HE2	2.08	0.70
2:B:171:VAL:HG12	2:B:206:ASN:N	2.07	0.70
1:A:182:VAL:HG12	1:A:404:PHE:CD1	2.17	0.69
1:A:12:ALA:CB	4:A:502:GTP:C8	2.71	0.69
1:A:123:ARG:CG	1:A:161:TYR:OH	2.40	0.69
2:B:185:TYR:CD1	2:B:399:PHE:CD1	2.72	0.69
1:A:5:ILE:HG22	1:A:6:SER:N	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:HIS:CG	1:A:432:TYR:HE1	2.11	0.69
1:A:405:VAL:HA	1:A:408:TYR:CD2	2.26	0.69
2:B:24:ILE:HD11	2:B:52:TYR:CE2	2.28	0.69
2:B:189:LEU:HD13	2:B:417:GLU:HG2	1.74	0.69
1:A:123:ARG:HG2	1:A:161:TYR:OH	1.92	0.69
1:A:189:LEU:CG	1:A:395:PHE:CE2	2.56	0.69
2:B:262:PHE:CB	2:B:431:GLU:HB3	2.19	0.69
2:B:313:LEU:HD21	2:B:363:ALA:H	1.55	0.69
2:B:382:THR:CG2	2:B:386:GLU:HB2	2.23	0.69
1:A:205:ASP:CG	1:A:209:ILE:HD12	2.13	0.69
1:A:243:ARG:NH2	1:A:252:LEU:N	2.28	0.69
2:B:19:LYS:HE3	2:B:225:GLY:CA	2.23	0.69
1:A:88:HIS:C	1:A:90:GLU:H	1.95	0.69
1:A:148:GLY:O	1:A:151:SER:HB2	1.91	0.69
1:A:346:TRP:CZ2	1:A:435:VAL:CG1	2.75	0.69
1:A:371:VAL:HG12	1:A:372:GLN:H	1.57	0.69
2:B:209:LEU:HD23	2:B:227:LEU:HB3	1.75	0.69
2:B:395:PHE:HD2	2:B:422:GLU:OE2	1.76	0.69
2:B:234:THR:O	2:B:238:VAL:HG23	1.92	0.69
2:B:267:PHE:CG	2:B:388:PHE:HZ	2.10	0.69
1:A:234:ILE:HG21	1:A:302:MET:HE3	1.75	0.69
1:A:282:TYR:O	1:A:284:GLU:N	2.24	0.69
2:B:395:PHE:HD2	2:B:422:GLU:OE1	1.61	0.69
1:A:63:PRO:C	1:A:64:ARG:HG2	2.12	0.68
1:A:103:TYR:CE2	1:A:413:MET:HE2	2.26	0.68
1:A:217:LEU:HD12	1:A:277:SER:HB3	1.75	0.68
2:B:206:ASN:HD22	4:B:502:GTP:C3'	2.03	0.68
2:B:384:ILE:HG13	2:B:386:GLU:HG3	1.75	0.68
1:A:154:MET:CB	1:A:197:HIS:C	2.61	0.68
2:B:16:ILE:CA	2:B:228:ASN:CB	2.61	0.68
2:B:206:ASN:OD1	4:B:502:GTP:N3	2.27	0.68
1:A:72:PRO:HG3	2:B:47:GLU:HB3	1.73	0.68
1:A:408:TYR:CE1	1:A:409:VAL:HG22	2.28	0.68
2:B:101:ASN:O	2:B:408:TYR:CZ	2.45	0.68
2:B:395:PHE:CD2	2:B:422:GLU:OE2	2.47	0.68
1:A:115:ILE:CD1	1:A:119:LEU:HG	2.23	0.68
2:B:242:LEU:CD2	2:B:250:ALA:H	2.07	0.68
1:A:262:TYR:CD2	1:A:435:VAL:CG2	2.76	0.68
1:A:402:ARG:HB3	1:A:405:VAL:CG2	2.23	0.68
2:B:194:LEU:C	2:B:265:LEU:CD2	2.62	0.68
1:A:343:PHE:HZ	1:A:351:PHE:CE2	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:ILE:HG21	2:B:136:GLN:HG2	1.76	0.68
2:B:103:TRP:CE3	2:B:417:GLU:CD	2.67	0.68
2:B:182:VAL:CB	2:B:408:TYR:CE1	2.63	0.68
2:B:195:VAL:HB	2:B:264:ARG:HA	1.75	0.68
2:B:262:PHE:CE1	2:B:435:TYR:CZ	2.81	0.68
1:A:27:GLU:OE2	1:A:236:SER:OG	2.11	0.68
1:A:296:PHE:CE2	1:A:335:ILE:HG21	2.29	0.68
1:A:72:PRO:HG2	2:B:47:GLU:CG	2.15	0.68
2:B:250:ALA:HB1	2:B:254:LYS:HB2	1.76	0.68
2:B:262:PHE:HZ	2:B:434:GLN:CB	1.86	0.68
1:A:72:PRO:CG	2:B:47:GLU:CB	2.64	0.67
2:B:15:GLN:HG3	4:B:502:GTP:O6	1.94	0.67
2:B:194:LEU:C	2:B:265:LEU:HB3	2.14	0.67
2:B:195:VAL:CG2	2:B:264:ARG:CA	2.61	0.67
2:B:251:ASP:O	2:B:253:ARG:N	2.26	0.67
2:B:262:PHE:CZ	2:B:434:GLN:C	2.67	0.67
2:B:328:VAL:O	2:B:332:MET:HG2	1.94	0.67
1:A:142:GLY:HA3	1:A:172:TYR:HE2	1.60	0.67
2:B:256:ALA:O	2:B:260:VAL:HG22	1.94	0.67
2:B:346:TRP:CD2	2:B:346:TRP:O	2.47	0.67
2:B:359:PRO:HB2	2:B:360:PRO:HD2	1.74	0.67
2:B:385:GLN:CA	2:B:429:VAL:HG13	2.24	0.67
1:A:73:THR:HB	2:B:42:LEU:CD1	2.14	0.67
2:B:104:ALA:CB	2:B:413:MET:CB	2.62	0.67
2:B:189:LEU:HD22	2:B:421:ALA:H	1.55	0.67
1:A:251:ASP:O	1:A:254:GLU:HB2	1.95	0.67
2:B:66:ILE:C	2:B:67:LEU:HD23	2.15	0.67
1:A:171:ILE:HG23	1:A:205:ASP:CB	2.21	0.67
2:B:103:TRP:CZ3	2:B:108:TYR:HE1	2.11	0.67
2:B:195:VAL:CB	2:B:264:ARG:NH1	2.57	0.67
1:A:109:THR:OG1	1:A:411:GLU:CG	2.38	0.67
2:B:2:ARG:NH2	2:B:48:ARG:HH21	1.90	0.67
2:B:195:VAL:CG1	2:B:264:ARG:HH11	2.06	0.67
2:B:257:VAL:HG12	2:B:257:VAL:O	1.93	0.67
1:A:154:MET:N	1:A:197:HIS:NE2	2.24	0.67
1:A:174:ALA:HB2	1:A:207:GLU:HB3	1.75	0.67
2:B:107:HIS:CD2	2:B:151:THR:CG2	2.77	0.67
2:B:165:ILE:HG13	2:B:252:LEU:CD1	2.25	0.67
2:B:182:VAL:HG23	2:B:186:ASN:HD21	1.60	0.67
2:B:384:ILE:HG22	2:B:433:GLN:OE1	1.94	0.67
1:A:262:TYR:CD2	1:A:435:VAL:HG22	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:ILE:O	1:A:341:ILE:HG12	1.95	0.67
2:B:265:LEU:HD12	2:B:265:LEU:C	2.16	0.67
2:B:325:MET:CE	2:B:355:VAL:HG21	2.24	0.67
1:A:133:GLN:NE2	1:A:256:GLN:CD	2.46	0.67
2:B:243:ARG:HH22	2:B:252:LEU:HG	1.59	0.67
2:B:185:TYR:CG	2:B:418:PHE:CD2	2.83	0.67
1:A:5:ILE:HD13	1:A:125:LEU:CB	2.25	0.66
1:A:71:GLU:CG	2:B:42:LEU:HD11	2.25	0.66
1:A:93:ILE:HG22	1:A:94:THR:N	2.09	0.66
1:A:191:THR:O	1:A:194:THR:CG2	2.41	0.66
1:A:103:TYR:HE2	1:A:413:MET:HE2	1.60	0.66
2:B:189:LEU:HD22	2:B:417:GLU:O	1.95	0.66
2:B:266:HIS:NE2	2:B:428:LEU:HD12	2.08	0.66
2:B:44:LEU:HD12	2:B:49:ILE:HD13	1.76	0.66
2:B:104:ALA:HB1	2:B:413:MET:HA	1.78	0.66
2:B:194:LEU:CG	2:B:265:LEU:HD21	2.24	0.66
2:B:230:LEU:HD23	2:B:231:VAL:N	2.10	0.66
2:B:310:GLY:HA3	2:B:386:GLU:OE1	1.95	0.66
2:B:325:MET:HA	2:B:325:MET:HE3	1.76	0.66
2:B:413:MET:CE	2:B:418:PHE:CD1	2.71	0.66
1:A:151:SER:HB3	1:A:193:THR:CG2	2.25	0.66
2:B:385:GLN:HB3	2:B:429:VAL:CG2	2.26	0.66
2:B:184:PRO:CB	2:B:395:PHE:HB2	2.17	0.66
2:B:195:VAL:HB	2:B:264:ARG:O	1.95	0.66
1:A:308:ARG:O	1:A:309:HIS:HB3	1.96	0.66
2:B:242:LEU:CD1	2:B:255:LEU:HD11	2.26	0.66
1:A:16:ILE:HA	1:A:228:ASN:HB2	1.77	0.66
1:A:150:THR:CB	1:A:197:HIS:CE1	2.77	0.66
1:A:152:LEU:HA	1:A:155:GLU:HB2	1.76	0.66
1:A:191:THR:CA	1:A:194:THR:CG2	2.55	0.66
1:A:185:TYR:CA	1:A:398:MET:SD	2.84	0.66
2:B:202:TYR:OH	2:B:238:VAL:HG11	1.95	0.66
1:A:188:ILE:O	1:A:191:THR:HG22	1.96	0.65
1:A:276:ILE:O	1:A:369:ALA:HB2	1.95	0.65
2:B:276:THR:HB	2:B:281:GLN:CG	2.25	0.65
2:B:332:MET:HE3	2:B:351:VAL:HG11	1.77	0.65
1:A:142:GLY:CA	1:A:172:TYR:CE2	2.79	0.65
1:A:317:LEU:HD12	1:A:351:PHE:CD1	2.32	0.65
1:A:396:ASP:O	1:A:400:ALA:HB2	1.95	0.65
2:B:313:LEU:HD12	2:B:432:TYR:CE1	2.30	0.65
1:A:100:ALA:CB	1:A:105:ARG:HD3	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:35:SER:HB3	2:B:59:ASN:CA	2.26	0.65
2:B:185:TYR:CB	2:B:418:PHE:HE2	2.09	0.65
1:A:69:ASP:O	1:A:94:THR:C	2.35	0.65
1:A:217:LEU:HD11	1:A:367:ASP:O	1.97	0.65
1:A:225:THR:O	1:A:229:ARG:HG3	1.97	0.65
2:B:224:TYR:HB3	4:B:502:GTP:O6	1.96	0.65
1:A:313:MET:HB3	1:A:344:VAL:CG2	2.26	0.65
1:A:372:GLN:O	1:A:373:ARG:HB3	1.96	0.65
2:B:266:HIS:CE1	2:B:428:LEU:HD12	2.32	0.65
1:A:195:LEU:HD23	1:A:424:ASP:CB	2.24	0.65
1:A:185:TYR:CZ	1:A:189:LEU:HD11	2.31	0.65
1:A:408:TYR:CG	1:A:418:PHE:HZ	2.13	0.65
2:B:16:ILE:CG1	2:B:228:ASN:CG	2.37	0.65
2:B:188:THR:O	2:B:425:MET:HB2	1.97	0.65
2:B:281:GLN:O	2:B:283:TYR:HB2	1.96	0.65
1:A:109:THR:CB	1:A:411:GLU:HG2	2.27	0.65
1:A:132:LEU:CG	1:A:164:LYS:CE	2.72	0.65
1:A:154:MET:HB3	1:A:197:HIS:CA	2.27	0.65
2:B:258:ASN:HB2	2:B:352:LYS:HZ2	1.62	0.65
2:B:262:PHE:O	2:B:266:HIS:NE2	2.30	0.65
1:A:209:ILE:CG2	1:A:227:LEU:HD22	2.27	0.65
2:B:182:VAL:HG11	2:B:408:TYR:CD1	2.32	0.65
2:B:185:TYR:CZ	2:B:399:PHE:CA	2.60	0.65
1:A:402:ARG:O	1:A:403:ALA:C	2.36	0.64
1:A:27:GLU:OE2	1:A:240:ALA:HB3	1.97	0.64
1:A:225:THR:HA	1:A:228:ASN:HD21	1.59	0.64
2:B:242:LEU:HD12	2:B:255:LEU:HD11	1.78	0.64
2:B:258:ASN:ND2	2:B:352:LYS:CD	2.60	0.64
1:A:402:ARG:O	1:A:405:VAL:CG1	2.37	0.64
2:B:186:ASN:OD1	2:B:408:TYR:CZ	2.48	0.64
1:A:189:LEU:CD2	1:A:395:PHE:CE2	2.79	0.64
1:A:344:VAL:HG12	1:A:345:ASP:N	2.12	0.64
1:A:204:VAL:O	1:A:206:ASN:OD1	2.15	0.64
1:A:209:ILE:HG23	1:A:230:LEU:HD23	1.79	0.64
2:B:205:ASP:O	2:B:209:LEU:HD22	1.97	0.64
2:B:243:ARG:HH21	2:B:252:LEU:H	1.45	0.64
2:B:266:HIS:HA	2:B:388:PHE:HE2	1.61	0.64
2:B:133:GLN:HG3	2:B:165:ILE:HD11	1.80	0.64
1:A:23:LEU:HD21	1:A:236:SER:CB	2.11	0.64
1:A:115:ILE:HG23	1:A:116:ASP:N	2.12	0.64
1:A:205:ASP:CA	1:A:209:ILE:HD12	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:395:PHE:CE2	2:B:422:GLU:CD	2.63	0.64
1:A:209:ILE:HG22	1:A:227:LEU:HD22	1.80	0.64
2:B:185:TYR:OH	2:B:399:PHE:N	2.30	0.64
1:A:392:ASP:CB	1:A:425:MET:HE1	2.28	0.64
2:B:102:ASN:CA	2:B:408:TYR:HD2	2.01	0.64
1:A:95:GLY:O	1:A:96:LYS:HB3	1.97	0.63
1:A:103:TYR:CE2	1:A:413:MET:HE1	2.32	0.63
1:A:413:MET:HG2	1:A:414:GLU:H	1.63	0.63
2:B:114:LEU:O	2:B:118:VAL:HG23	1.98	0.63
2:B:184:PRO:C	2:B:395:PHE:CD1	2.70	0.63
2:B:282:GLN:HG2	2:B:282:GLN:O	1.97	0.63
1:A:234:ILE:HD13	1:A:234:ILE:C	2.18	0.63
1:A:386:GLU:O	1:A:389:ALA:N	2.31	0.63
1:A:189:LEU:HA	1:A:192:HIS:ND1	2.13	0.63
1:A:220:GLU:C	1:A:222:PRO:HD3	2.19	0.63
1:A:269:LEU:O	1:A:378:LEU:HA	1.98	0.63
1:A:305:CYS:SG	1:A:383:ALA:C	2.77	0.63
2:B:284:ARG:O	2:B:286:LEU:N	2.31	0.63
2:B:318:VAL:HA	2:B:354:ALA:HB3	1.81	0.63
2:B:180:THR:CG2	2:B:181:VAL:N	2.61	0.63
2:B:205:ASP:H	2:B:209:LEU:CD1	2.12	0.63
2:B:262:PHE:CZ	2:B:435:TYR:CE2	2.86	0.63
1:A:24:TYR:OH	1:A:239:THR:HB	1.99	0.63
1:A:123:ARG:HA	1:A:161:TYR:HH	1.63	0.63
1:A:154:MET:HE1	1:A:198:SER:HB2	1.81	0.63
1:A:191:THR:HG21	1:A:425:MET:CE	2.27	0.63
1:A:150:THR:HG22	1:A:197:HIS:CE1	2.34	0.63
1:A:266:HIS:CG	1:A:432:TYR:CE1	2.86	0.63
1:A:276:ILE:HG23	1:A:369:ALA:HB2	1.80	0.63
1:A:315:CYS:HB3	1:A:377:MET:CE	2.29	0.63
2:B:4:ILE:HA	2:B:134:GLY:O	1.98	0.63
2:B:105:LYS:HD3	2:B:411:GLU:CA	2.29	0.63
2:B:261:PRO:CA	2:B:435:TYR:CD2	2.80	0.63
1:A:151:SER:O	1:A:155:GLU:HB2	1.98	0.63
1:A:185:TYR:HB2	1:A:398:MET:SD	2.38	0.63
1:A:275:VAL:HG21	1:A:300:ASN:OD1	1.97	0.63
2:B:189:LEU:HD11	2:B:418:PHE:CA	2.27	0.63
1:A:69:ASP:OD1	4:A:502:GTP:PG	2.57	0.63
1:A:189:LEU:CD2	1:A:395:PHE:CZ	2.81	0.63
1:A:200:CYS:SG	1:A:268:PRO:CD	2.80	0.63
1:A:205:ASP:N	1:A:209:ILE:HD12	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:ALA:HA	1:A:424:ASP:OD2	1.99	0.63
2:B:241:CYS:O	2:B:244:PHE:HB2	1.98	0.63
1:A:7:ILE:CD1	1:A:137:VAL:HG22	2.29	0.63
1:A:135:PHE:CZ	1:A:157:LEU:HD21	2.31	0.63
1:A:152:LEU:HD12	1:A:153:LEU:N	2.14	0.63
1:A:185:TYR:CB	1:A:398:MET:SD	2.87	0.63
2:B:63:PRO:HD2	2:B:86:ILE:HG12	1.80	0.63
1:A:191:THR:CB	1:A:425:MET:SD	2.87	0.62
2:B:185:TYR:CE1	2:B:399:PHE:HA	2.33	0.62
1:A:102:ASN:OD1	1:A:105:ARG:HB3	1.99	0.62
2:B:299:LYS:O	2:B:300:ASN:HB2	1.97	0.62
2:B:315:VAL:HG13	2:B:377:PHE:CE1	2.34	0.62
1:A:97:GLU:CB	1:A:110:ILE:HD11	2.23	0.62
1:A:169:PHE:HZ	1:A:231:ILE:CG2	1.93	0.62
1:A:203:MET:O	1:A:206:ASN:ND2	2.31	0.62
1:A:271:THR:HG23	1:A:300:ASN:O	1.99	0.62
1:A:296:PHE:CE1	1:A:341:ILE:HD12	2.32	0.62
2:B:262:PHE:CE1	2:B:435:TYR:CE2	2.87	0.62
2:B:266:HIS:ND1	2:B:428:LEU:HD11	2.14	0.62
2:B:325:MET:HE2	2:B:355:VAL:HG21	1.79	0.62
2:B:193:GLN:HG3	2:B:197:ASN:ND2	2.14	0.62
2:B:431:GLU:HA	2:B:434:GLN:CG	2.29	0.62
1:A:200:CYS:HA	1:A:267:PHE:CG	2.34	0.62
2:B:103:TRP:CZ3	2:B:417:GLU:HG3	2.28	0.62
1:A:102:ASN:HD22	1:A:407:TRP:HB3	1.65	0.62
1:A:189:LEU:N	1:A:395:PHE:CD2	2.67	0.62
1:A:236:SER:O	1:A:240:ALA:HB3	1.99	0.62
1:A:317:LEU:HD11	1:A:351:PHE:HE1	1.63	0.62
1:A:102:ASN:ND2	1:A:407:TRP:HB3	2.15	0.62
2:B:115:VAL:HG21	2:B:152:LEU:CD2	2.30	0.62
2:B:171:VAL:C	2:B:205:ASP:HA	2.20	0.62
2:B:194:LEU:O	2:B:265:LEU:HD22	2.00	0.62
1:A:264:ARG:CG	1:A:431:ASP:OD2	2.48	0.62
1:A:151:SER:CA	1:A:197:HIS:ND1	2.61	0.62
1:A:221:ARG:O	1:A:221:ARG:HD3	2.00	0.62
1:A:206:ASN:O	1:A:207:GLU:HB2	1.99	0.62
1:A:223:THR:HB	1:A:225:THR:HG22	1.82	0.62
2:B:211:ASP:OD1	2:B:212:ILE:N	2.33	0.62
2:B:253:ARG:O	2:B:256:ALA:N	2.33	0.62
2:B:313:LEU:HD21	2:B:363:ALA:CA	2.29	0.62
2:B:382:THR:HG21	2:B:386:GLU:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:105:LYS:HE2	2:B:110:GLU:HG3	0.63	0.61
2:B:324:SER:C	2:B:326:LYS:H	2.03	0.61
1:A:184:PRO:HB2	1:A:394:LYS:C	2.21	0.61
1:A:273:ALA:HB3	1:A:274:PRO:HD3	1.81	0.61
2:B:4:ILE:HG23	2:B:134:GLY:O	2.00	0.61
2:B:114:LEU:HD23	2:B:149:MET:CE	2.30	0.61
2:B:185:TYR:CD1	2:B:395:PHE:CE1	2.87	0.61
1:A:267:PHE:HD1	1:A:267:PHE:H	1.47	0.61
1:A:269:LEU:HD22	1:A:384:ILE:HD11	1.83	0.61
2:B:324:SER:CB	2:B:327:GLU:HG2	2.30	0.61
1:A:317:LEU:HB3	1:A:319:TYR:CE1	2.33	0.61
2:B:363:ALA:HB2	2:B:436:GLN:HB2	1.81	0.61
1:A:115:ILE:HG13	1:A:152:LEU:HD13	1.81	0.61
2:B:105:LYS:HD3	2:B:411:GLU:C	2.21	0.61
1:A:7:ILE:HG22	1:A:66:VAL:CG2	2.28	0.61
1:A:97:GLU:HB3	1:A:110:ILE:CD1	2.26	0.61
1:A:273:ALA:HB2	1:A:295:CYS:SG	2.41	0.61
2:B:102:ASN:ND2	2:B:413:MET:SD	2.74	0.61
1:A:118:VAL:HG11	1:A:149:PHE:HZ	1.65	0.61
1:A:195:LEU:CG	1:A:264:ARG:NH2	2.64	0.61
1:A:220:GLU:OE1	1:A:220:GLU:HA	2.01	0.61
2:B:12:CYS:SG	4:B:502:GTP:C2	2.94	0.61
2:B:191:VAL:HG23	2:B:267:PHE:HE2	1.64	0.61
2:B:408:TYR:CA	2:B:413:MET:SD	2.88	0.61
1:A:344:VAL:HG11	1:A:346:TRP:NE1	2.16	0.61
2:B:385:GLN:N	2:B:429:VAL:HG13	2.16	0.61
2:B:385:GLN:O	2:B:389:LYS:HB2	2.00	0.61
1:A:11:GLN:HE21	1:A:74:VAL:HG22	1.66	0.61
1:A:119:LEU:CD2	1:A:122:ILE:HD11	2.28	0.61
1:A:229:ARG:NH1	1:A:363:VAL:HG21	2.16	0.61
1:A:362:VAL:HG13	1:A:368:LEU:HB2	1.83	0.61
2:B:230:LEU:O	2:B:233:ALA:HB3	2.00	0.61
2:B:346:TRP:HH2	2:B:435:TYR:CD1	2.14	0.61
1:A:12:ALA:HB1	4:A:502:GTP:N3	2.15	0.60
1:A:71:GLU:OE1	2:B:42:LEU:HD21	2.01	0.60
1:A:88:HIS:O	1:A:90:GLU:N	2.33	0.60
1:A:205:ASP:OD2	1:A:231:ILE:HD11	2.01	0.60
2:B:171:VAL:HG13	2:B:205:ASP:HA	1.81	0.60
2:B:195:VAL:CB	2:B:264:ARG:HH11	2.14	0.60
2:B:185:TYR:CG	2:B:418:PHE:CE2	2.89	0.60
2:B:204:ILE:HG13	2:B:270:PRO:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:THR:HG23	1:A:192:HIS:N	2.13	0.60
1:A:262:TYR:CE2	1:A:435:VAL:HG22	2.36	0.60
1:A:104:ALA:HB2	1:A:408:TYR:CA	2.15	0.60
1:A:267:PHE:HD1	1:A:432:TYR:OH	1.85	0.60
2:B:182:VAL:HG11	2:B:404:PHE:O	2.00	0.60
2:B:198:THR:O	2:B:199:ASP:HB3	2.01	0.60
2:B:258:ASN:ND2	2:B:352:LYS:CB	2.63	0.60
2:B:107:HIS:HD2	2:B:151:THR:CG2	2.12	0.60
2:B:217:LEU:C	2:B:219:LEU:N	2.55	0.60
1:A:139:HIS:HE1	1:A:168:GLU:HB2	1.66	0.60
1:A:284:GLU:O	1:A:286:LEU:N	2.34	0.60
1:A:345:ASP:C	1:A:347:CYS:H	2.04	0.60
1:A:392:ASP:CA	1:A:425:MET:HE1	2.32	0.60
2:B:380:ASN:OD1	2:B:432:TYR:CE1	2.54	0.60
1:A:154:MET:CB	1:A:166:LYS:HD2	2.29	0.60
1:A:158:SER:OG	1:A:166:LYS:NZ	2.33	0.60
1:A:167:LEU:HA	1:A:200:CYS:O	2.01	0.60
1:A:189:LEU:N	1:A:395:PHE:CE2	2.69	0.60
2:B:182:VAL:CG1	2:B:404:PHE:O	2.49	0.60
2:B:408:TYR:CG	2:B:418:PHE:HZ	2.20	0.60
1:A:108:TYR:CD2	1:A:413:MET:HB2	2.37	0.60
1:A:167:LEU:HG	1:A:200:CYS:HB3	1.82	0.60
2:B:172:VAL:HG21	2:B:203:CYS:SG	2.42	0.60
2:B:202:TYR:OH	2:B:238:VAL:CG1	2.50	0.60
2:B:279:GLY:O	2:B:282:GLN:HB3	2.01	0.60
2:B:285:ALA:HB1	2:B:290:GLU:HG2	1.83	0.60
2:B:313:LEU:CD2	2:B:363:ALA:HB2	2.32	0.60
2:B:324:SER:O	2:B:328:VAL:HG23	2.01	0.60
1:A:435:VAL:O	1:A:435:VAL:HG12	2.02	0.59
2:B:102:ASN:CB	2:B:408:TYR:CD2	2.85	0.59
1:A:115:ILE:O	1:A:115:ILE:HD13	2.02	0.59
1:A:311:LYS:HE3	1:A:342:GLN:CD	2.22	0.59
1:A:172:TYR:CD2	1:A:173:PRO:CD	2.86	0.59
1:A:179:THR:C	2:B:248:LEU:HD22	2.23	0.59
1:A:205:ASP:OD1	1:A:209:ILE:HD12	2.03	0.59
1:A:264:ARG:HG2	1:A:431:ASP:OD2	2.02	0.59
1:A:405:VAL:HA	1:A:408:TYR:HE2	1.43	0.59
1:A:405:VAL:HB	1:A:408:TYR:CZ	2.38	0.59
2:B:49:ILE:O	2:B:51:VAL:N	2.35	0.59
2:B:102:ASN:HB3	2:B:105:LYS:HB2	1.84	0.59
1:A:154:MET:HA	1:A:166:LYS:HD3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:ARG:HE	2:B:48:ARG:NH2	1.88	0.59
2:B:54:ASN:ND2	2:B:64:ARG:HD3	2.15	0.59
2:B:192:HIS:HD2	2:B:424:ASN:H	1.47	0.59
1:A:119:LEU:O	1:A:122:ILE:HG12	2.02	0.59
1:A:166:LYS:CD	1:A:197:HIS:O	2.35	0.59
1:A:248:LEU:CD2	1:A:353:VAL:O	2.49	0.59
1:A:135:PHE:HE1	1:A:157:LEU:CD1	2.00	0.59
1:A:228:ASN:OD1	1:A:229:ARG:N	2.36	0.59
2:B:167:ASN:HD21	2:B:252:LEU:HD21	1.65	0.59
2:B:258:ASN:HD22	2:B:352:LYS:CD	2.14	0.59
1:A:98:ASP:CG	2:B:2:ARG:NH1	2.55	0.59
1:A:142:GLY:HA3	1:A:172:TYR:CE2	2.38	0.59
1:A:199:ASP:N	1:A:199:ASP:OD1	2.35	0.59
1:A:266:HIS:HA	1:A:432:TYR:OH	2.02	0.59
2:B:102:ASN:ND2	2:B:408:TYR:CA	2.51	0.59
2:B:332:MET:CE	2:B:351:VAL:HG11	2.32	0.59
1:A:199:ASP:HB3	1:A:265:GLY:HA2	1.84	0.59
1:A:203:MET:HB3	1:A:206:ASN:HD21	1.66	0.59
1:A:278:ALA:HB2	1:A:369:ALA:HA	1.85	0.59
2:B:184:PRO:CG	2:B:395:PHE:CA	2.68	0.59
2:B:431:GLU:HA	2:B:434:GLN:HG3	1.83	0.59
2:B:30:ILE:HD13	2:B:53:TYR:CE2	2.38	0.59
2:B:183:GLU:HB3	2:B:184:PRO:CD	2.33	0.59
2:B:204:ILE:HG23	2:B:302:MET:HB3	1.83	0.59
2:B:204:ILE:HG13	2:B:270:PRO:CG	2.31	0.59
2:B:224:TYR:HB3	4:B:502:GTP:C6	2.37	0.59
2:B:267:PHE:CB	2:B:388:PHE:HZ	2.16	0.59
1:A:184:PRO:HB2	1:A:394:LYS:O	2.03	0.58
2:B:151:THR:OG1	2:B:193:GLN:HB3	2.03	0.58
1:A:173:PRO:HB2	1:A:174:ALA:CB	2.33	0.58
1:A:173:PRO:HB2	1:A:174:ALA:C	2.22	0.58
1:A:315:CYS:HB3	1:A:377:MET:HE2	1.86	0.58
1:A:371:VAL:HG12	1:A:372:GLN:N	2.17	0.58
2:B:103:TRP:HE3	2:B:417:GLU:CD	2.05	0.58
2:B:189:LEU:CD1	2:B:418:PHE:HA	2.31	0.58
1:A:172:TYR:CD2	1:A:173:PRO:HD2	2.38	0.58
1:A:317:LEU:HD11	1:A:351:PHE:CE1	2.38	0.58
1:A:382:THR:O	1:A:385:ALA:HB2	2.03	0.58
1:A:413:MET:O	1:A:414:GLU:HG3	2.02	0.58
2:B:89:PRO:HA	2:B:92:PHE:CD2	2.38	0.58
1:A:228:ASN:HB3	4:A:502:GTP:C2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:195:VAL:N	2:B:264:ARG:O	2.37	0.58
2:B:307:PRO:HB3	2:B:312:TYR:OH	2.04	0.58
1:A:63:PRO:HD3	1:A:86:LEU:O	2.04	0.58
1:A:172:TYR:CG	1:A:173:PRO:CD	2.87	0.58
1:A:189:LEU:CA	1:A:192:HIS:CE1	2.86	0.58
2:B:184:PRO:HB3	2:B:395:PHE:N	2.18	0.58
2:B:299:LYS:O	2:B:300:ASN:CB	2.51	0.58
1:A:88:HIS:C	1:A:90:GLU:N	2.57	0.58
1:A:369:ALA:O	1:A:370:LYS:HB3	2.03	0.58
2:B:19:LYS:HG3	2:B:229:HIS:HB2	1.85	0.58
2:B:184:PRO:O	2:B:395:PHE:CD1	2.57	0.58
1:A:6:SER:HA	1:A:136:SER:O	2.02	0.58
2:B:103:TRP:CE3	2:B:417:GLU:CG	2.86	0.58
2:B:115:VAL:HG21	2:B:152:LEU:HD23	1.84	0.58
2:B:184:PRO:HG3	2:B:395:PHE:HA	1.83	0.58
2:B:313:LEU:CD1	2:B:432:TYR:CG	2.86	0.58
1:A:12:ALA:N	4:A:502:GTP:C8	2.71	0.58
1:A:179:THR:C	2:B:248:LEU:CD2	2.72	0.58
2:B:180:THR:CG2	2:B:181:VAL:H	2.17	0.58
2:B:192:HIS:ND1	2:B:424:ASN:CG	2.41	0.58
2:B:194:LEU:O	2:B:265:LEU:CG	2.51	0.58
1:A:117:LEU:HD11	1:A:121:ARG:HH22	1.69	0.57
1:A:154:MET:CB	1:A:197:HIS:O	2.43	0.57
2:B:30:ILE:HA	2:B:35:SER:O	2.04	0.57
2:B:103:TRP:HZ3	2:B:108:TYR:HE1	1.52	0.57
2:B:258:ASN:OD1	2:B:258:ASN:O	2.22	0.57
1:A:172:TYR:HB3	1:A:173:PRO:HD2	1.85	0.57
1:A:189:LEU:HD23	1:A:395:PHE:CZ	2.39	0.57
1:A:192:HIS:CG	1:A:193:THR:N	2.73	0.57
2:B:41:ASP:O	2:B:47:GLU:OE2	2.22	0.57
2:B:185:TYR:HA	2:B:395:PHE:CD1	2.37	0.57
2:B:270:PRO:HA	2:B:377:PHE:O	2.03	0.57
1:A:180:ALA:N	2:B:248:LEU:HD13	2.05	0.57
1:A:220:GLU:O	1:A:222:PRO:HD2	2.04	0.57
2:B:301:MET:CE	2:B:377:PHE:HE2	2.17	0.57
2:B:319:PHE:HA	2:B:375:ALA:HA	1.86	0.57
2:B:349:ASN:C	2:B:349:ASN:HD22	2.07	0.57
2:B:401:ARG:HG3	2:B:401:ARG:O	2.04	0.57
2:B:267:PHE:HB2	2:B:388:PHE:CZ	2.39	0.57
1:A:139:HIS:C	1:A:140:SER:HG	2.01	0.57
1:A:145:THR:O	1:A:145:THR:HG22	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:LEU:HA	1:A:155:GLU:CB	2.35	0.57
1:A:173:PRO:HB2	1:A:174:ALA:CA	2.35	0.57
1:A:268:PRO:HA	1:A:379:SER:O	2.04	0.57
1:A:362:VAL:HG11	1:A:368:LEU:O	2.04	0.57
2:B:194:LEU:CD1	2:B:267:PHE:HE1	1.98	0.57
2:B:346:TRP:CZ3	2:B:435:TYR:HB3	2.39	0.57
2:B:346:TRP:HZ3	2:B:435:TYR:HB3	1.68	0.57
1:A:135:PHE:CD1	1:A:157:LEU:HD13	2.39	0.57
1:A:181:VAL:CG1	2:B:258:ASN:HD21	2.16	0.57
1:A:218:ASP:O	1:A:219:ILE:HG23	2.04	0.57
2:B:320:ARG:O	2:B:359:PRO:HA	2.04	0.57
2:B:182:VAL:HG23	2:B:186:ASN:ND2	2.20	0.57
1:A:2:ARG:N	1:A:131:GLY:O	2.37	0.57
2:B:103:TRP:HB2	2:B:186:ASN:HA	1.86	0.57
1:A:70:LEU:HD23	1:A:94:THR:O	2.05	0.57
1:A:172:TYR:HB3	1:A:173:PRO:CD	2.35	0.57
1:A:173:PRO:HA	1:A:174:ALA:HB3	1.85	0.57
1:A:313:MET:O	1:A:314:ALA:HB2	2.04	0.57
2:B:346:TRP:CB	2:B:435:TYR:O	2.52	0.57
1:A:16:ILE:CB	1:A:228:ASN:HB2	2.35	0.57
1:A:179:THR:C	2:B:248:LEU:CD1	2.73	0.57
1:A:345:ASP:O	1:A:347:CYS:N	2.38	0.57
2:B:205:ASP:O	2:B:209:LEU:HB2	2.05	0.57
2:B:253:ARG:O	2:B:254:LYS:C	2.42	0.57
2:B:274:PRO:CG	2:B:371:LEU:HD21	2.34	0.57
1:A:283:HIS:CE1	1:A:286:LEU:CD1	2.87	0.56
2:B:19:LYS:HG3	2:B:225:GLY:O	2.05	0.56
2:B:149:MET:O	2:B:153:LEU:HD13	2.04	0.56
2:B:189:LEU:HD22	2:B:421:ALA:CB	2.10	0.56
1:A:224:TYR:HD1	4:A:502:GTP:C5	2.08	0.56
1:A:362:VAL:CG1	1:A:368:LEU:HB2	2.35	0.56
2:B:14:ASN:OD1	2:B:75:MET:HG2	2.05	0.56
2:B:385:GLN:HB3	2:B:429:VAL:CB	2.34	0.56
1:A:71:GLU:CB	4:A:502:GTP:O1G	2.52	0.56
1:A:331:ALA:O	1:A:334:THR:HG22	2.05	0.56
1:A:388:TRP:HA	1:A:388:TRP:CE3	2.41	0.56
1:A:395:PHE:CZ	1:A:418:PHE:HD2	2.18	0.56
2:B:5:VAL:CG2	2:B:135:PHE:HD2	2.18	0.56
2:B:105:LYS:O	2:B:110:GLU:HB2	2.06	0.56
2:B:313:LEU:HD11	2:B:363:ALA:HA	1.87	0.56
2:B:346:TRP:O	2:B:346:TRP:CG	2.58	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:TYR:CE1	4:A:502:GTP:C6	2.92	0.56
2:B:171:VAL:HG12	2:B:205:ASP:HA	1.86	0.56
2:B:258:ASN:HB2	2:B:352:LYS:NZ	2.19	0.56
2:B:319:PHE:CD2	2:B:375:ALA:HB2	2.40	0.56
2:B:15:GLN:OE1	2:B:224:TYR:HB2	2.06	0.56
2:B:151:THR:OG1	2:B:193:GLN:CB	2.54	0.56
2:B:185:TYR:N	2:B:395:PHE:HD1	2.02	0.56
1:A:2:ARG:O	1:A:243:ARG:NH1	2.34	0.56
2:B:6:HIS:HB3	2:B:65:ALA:HB2	1.86	0.56
2:B:16:ILE:HD11	2:B:228:ASN:HA	1.82	0.56
2:B:50:ASN:O	2:B:64:ARG:NH2	2.38	0.56
2:B:139:HIS:HE1	2:B:168:THR:HG23	1.70	0.56
2:B:185:TYR:CD1	2:B:418:PHE:CE2	2.93	0.56
2:B:283:TYR:C	2:B:284:ARG:HG2	2.25	0.56
1:A:154:MET:SD	1:A:197:HIS:CG	2.99	0.56
1:A:163:LYS:O	1:A:163:LYS:HG2	2.04	0.56
2:B:165:ILE:HD13	2:B:165:ILE:H	1.71	0.56
2:B:206:ASN:HD22	4:B:502:GTP:C2'	2.12	0.56
2:B:206:ASN:CB	4:B:502:GTP:O2'	2.54	0.56
2:B:216:THR:O	2:B:217:LEU:HD12	2.05	0.56
2:B:312:TYR:O	2:B:344:VAL:HB	2.05	0.56
2:B:313:LEU:HD13	2:B:432:TYR:HD1	1.69	0.56
1:A:15:GLN:HG3	4:A:502:GTP:N7	2.21	0.56
1:A:242:LEU:C	1:A:244:PHE:H	2.09	0.56
1:A:436:GLY:C	1:A:438:ASP:H	2.08	0.56
2:B:261:PRO:CD	2:B:432:TYR:CD1	2.78	0.56
2:B:311:ARG:HG2	2:B:311:ARG:HH11	1.71	0.56
1:A:11:GLN:CG	1:A:74:VAL:HG11	2.28	0.56
1:A:26:LEU:CD2	1:A:361:THR:HG22	2.09	0.56
1:A:73:THR:CB	2:B:42:LEU:CD1	2.79	0.56
1:A:192:HIS:CD2	1:A:193:THR:HB	2.41	0.56
1:A:224:TYR:HE1	4:A:502:GTP:N7	2.01	0.56
2:B:31:ASP:O	2:B:32:PRO:C	2.44	0.56
2:B:203:CYS:O	2:B:270:PRO:HD2	2.06	0.56
2:B:382:THR:HG23	2:B:386:GLU:HB2	1.88	0.56
1:A:16:ILE:HD12	1:A:171:ILE:HD11	1.87	0.55
1:A:253:THR:O	1:A:256:GLN:HG2	2.06	0.55
2:B:19:LYS:O	2:B:23:VAL:HG23	2.06	0.55
2:B:273:ALA:HB3	2:B:274:PRO:CD	2.29	0.55
1:A:169:PHE:CE2	1:A:231:ILE:HG22	2.39	0.55
2:B:67:LEU:HD23	2:B:67:LEU:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:205:ASP:CB	2:B:302:MET:O	2.52	0.55
2:B:258:ASN:HD22	2:B:352:LYS:HZ2	1.52	0.55
2:B:261:PRO:CA	2:B:435:TYR:CE2	2.89	0.55
1:A:70:LEU:HB2	4:A:502:GTP:O2G	2.05	0.55
1:A:173:PRO:O	1:A:206:ASN:CG	2.44	0.55
1:A:216:ASN:O	1:A:217:LEU:HB2	2.05	0.55
1:A:382:THR:HG21	1:A:437:VAL:HG23	1.87	0.55
2:B:119:LEU:O	2:B:123:ARG:HG3	2.06	0.55
2:B:324:SER:C	2:B:326:LYS:N	2.59	0.55
1:A:141:PHE:CE2	1:A:391:LEU:HD22	2.39	0.55
1:A:181:VAL:CG2	2:B:352:LYS:CG	2.60	0.55
1:A:186:ASN:O	1:A:190:THR:OG1	2.20	0.55
1:A:194:THR:HG1	1:A:198:SER:HB3	1.70	0.55
1:A:409:VAL:C	1:A:411:GLU:H	2.09	0.55
2:B:12:CYS:HA	4:B:502:GTP:C6	2.42	0.55
2:B:185:TYR:HE2	2:B:398:MET:HG3	1.67	0.55
2:B:311:ARG:HD2	2:B:344:VAL:H	1.71	0.55
1:A:10:GLY:HA2	4:A:502:GTP:PB	2.45	0.55
1:A:224:TYR:CE1	4:A:502:GTP:C8	2.94	0.55
2:B:384:ILE:HG13	2:B:386:GLU:CG	2.36	0.55
1:A:150:THR:O	1:A:153:LEU:N	2.39	0.55
1:A:175:PRO:HD2	1:A:176:GLN:H	1.71	0.55
1:A:234:ILE:HB	1:A:302:MET:HE1	1.89	0.55
1:A:405:VAL:O	1:A:408:TYR:CE2	2.60	0.55
2:B:169:PHE:HD1	2:B:235:MET:HE3	1.52	0.55
2:B:205:ASP:O	2:B:209:LEU:HD13	2.06	0.55
2:B:313:LEU:HD21	2:B:363:ALA:CB	2.37	0.55
1:A:5:ILE:CD1	1:A:125:LEU:CB	2.74	0.55
1:A:408:TYR:O	1:A:411:GLU:N	2.39	0.55
2:B:103:TRP:CZ3	2:B:417:GLU:CD	2.80	0.55
2:B:147:SER:O	2:B:151:THR:CB	2.51	0.55
2:B:195:VAL:HG11	2:B:424:ASN:OD1	2.07	0.55
2:B:205:ASP:H	2:B:209:LEU:HD13	1.71	0.55
2:B:346:TRP:CD2	2:B:435:TYR:O	2.57	0.55
2:B:385:GLN:CB	2:B:429:VAL:HG22	2.36	0.55
1:A:6:SER:O	1:A:65:ALA:HB1	2.07	0.55
1:A:402:ARG:O	1:A:405:VAL:HG22	2.06	0.55
2:B:223:THR:HG22	2:B:224:TYR:N	2.21	0.55
2:B:253:ARG:O	2:B:257:VAL:N	2.33	0.55
2:B:262:PHE:O	2:B:266:HIS:CD2	2.59	0.55
1:A:157:LEU:HD12	1:A:166:LYS:HG2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:TYR:HB3	1:A:164:LYS:HG3	1.83	0.55
1:A:184:PRO:HG2	1:A:398:MET:CG	2.37	0.55
2:B:5:VAL:HG22	2:B:135:PHE:CD2	2.42	0.55
2:B:239:THR:HG22	2:B:240:THR:N	2.22	0.55
2:B:266:HIS:CB	2:B:432:TYR:OH	2.54	0.55
1:A:118:VAL:HG21	1:A:149:PHE:CZ	2.42	0.54
1:A:139:HIS:CG	1:A:140:SER:N	2.74	0.54
1:A:150:THR:CA	1:A:197:HIS:CE1	2.89	0.54
1:A:126:ALA:HB1	1:A:132:LEU:HD22	1.90	0.54
2:B:169:PHE:CD1	2:B:235:MET:HB2	2.31	0.54
2:B:184:PRO:HG2	2:B:395:PHE:HA	1.83	0.54
1:A:231:ILE:HA	1:A:234:ILE:CG2	2.36	0.54
1:A:262:TYR:CD2	1:A:435:VAL:HG21	2.42	0.54
2:B:262:PHE:CE2	2:B:435:TYR:N	2.76	0.54
2:B:325:MET:O	2:B:329:ASP:HB2	2.08	0.54
1:A:182:VAL:CG1	1:A:404:PHE:CE2	2.90	0.54
1:A:204:VAL:HG21	1:A:231:ILE:CD1	2.33	0.54
1:A:210:TYR:CD1	1:A:227:LEU:HD21	2.42	0.54
1:A:402:ARG:C	1:A:405:VAL:HG13	2.24	0.54
2:B:103:TRP:CE3	2:B:189:LEU:HD13	2.42	0.54
2:B:323:MET:HG3	2:B:328:VAL:HG21	1.90	0.54
1:A:110:ILE:O	1:A:112:LYS:N	2.41	0.54
1:A:150:THR:HG22	1:A:197:HIS:NE2	2.23	0.54
1:A:154:MET:HE3	1:A:197:HIS:CG	2.34	0.54
2:B:44:LEU:O	2:B:49:ILE:HG12	2.07	0.54
2:B:227:LEU:CB	4:B:502:GTP:N2	2.70	0.54
2:B:239:THR:O	2:B:241:CYS:N	2.41	0.54
1:A:17:GLY:O	1:A:21:TRP:HB2	2.08	0.54
2:B:259:MET:HG2	2:B:314:THR:CG2	2.38	0.54
2:B:261:PRO:CG	2:B:432:TYR:CE1	2.90	0.54
1:A:98:ASP:O	1:A:110:ILE:HD13	2.08	0.54
1:A:154:MET:HE2	1:A:197:HIS:CD2	2.43	0.54
1:A:184:PRO:HA	1:A:187:SER:HG	1.73	0.54
1:A:324:VAL:O	1:A:327:ASP:HB2	2.08	0.54
1:A:338:LYS:O	1:A:340:THR:N	2.34	0.54
2:B:272:PHE:HB3	2:B:275:LEU:HD22	1.88	0.54
1:A:154:MET:HG2	1:A:166:LYS:HG2	1.90	0.54
1:A:175:PRO:CD	1:A:176:GLN:H	2.21	0.54
2:B:20:PHE:CE1	2:B:24:ILE:HD12	2.42	0.54
2:B:126:SER:CB	2:B:132:LEU:HD22	2.38	0.54
2:B:258:ASN:ND2	2:B:352:LYS:HB2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:ARG:NE	2:B:48:ARG:NH2	2.53	0.54
2:B:4:ILE:CG2	2:B:136:GLN:HG2	2.38	0.54
2:B:250:ALA:CA	2:B:254:LYS:HE2	2.35	0.54
2:B:331:GLN:O	2:B:335:VAL:HG23	2.08	0.54
2:B:343:PHE:O	2:B:344:VAL:O	2.26	0.54
1:A:172:TYR:CB	1:A:173:PRO:CD	2.86	0.53
2:B:31:ASP:HB3	2:B:32:PRO:HD2	1.89	0.53
1:A:154:MET:HG2	1:A:166:LYS:CG	2.38	0.53
1:A:184:PRO:HD3	1:A:394:LYS:CD	2.38	0.53
1:A:282:TYR:O	1:A:284:GLU:HG3	2.09	0.53
2:B:132:LEU:CD2	2:B:164:ARG:HG3	2.32	0.53
2:B:385:GLN:CG	2:B:388:PHE:HB2	2.33	0.53
2:B:422:GLU:O	2:B:426:ASN:HB2	2.08	0.53
1:A:5:ILE:O	1:A:135:PHE:HA	2.08	0.53
1:A:182:VAL:O	1:A:184:PRO:N	2.42	0.53
1:A:243:ARG:CZ	1:A:252:LEU:HG	2.39	0.53
2:B:36:TYR:CZ	2:B:38:GLY:HA3	2.43	0.53
2:B:107:HIS:HD2	2:B:151:THR:HG22	1.72	0.53
2:B:168:THR:CB	2:B:201:THR:HG23	2.38	0.53
2:B:206:ASN:CG	4:B:502:GTP:O2'	2.46	0.53
2:B:388:PHE:CD2	2:B:428:LEU:HD23	2.43	0.53
1:A:5:ILE:CG2	1:A:6:SER:N	2.70	0.53
2:B:169:PHE:CE2	2:B:235:MET:N	2.76	0.53
2:B:189:LEU:CD2	2:B:421:ALA:CA	2.51	0.53
2:B:259:MET:CG	2:B:314:THR:HG21	2.36	0.53
2:B:262:PHE:CZ	2:B:435:TYR:CD1	2.96	0.53
1:A:172:TYR:CG	1:A:173:PRO:HD3	2.43	0.53
1:A:173:PRO:CA	1:A:174:ALA:CB	2.85	0.53
2:B:264:ARG:HD2	2:B:424:ASN:O	2.08	0.53
2:B:325:MET:CE	2:B:355:VAL:HG11	2.38	0.53
1:A:228:ASN:ND2	4:A:502:GTP:N1	2.36	0.53
1:A:248:LEU:HB3	1:A:355:ILE:H	1.73	0.53
1:A:150:THR:O	1:A:151:SER:C	2.47	0.53
2:B:8:GLN:OE1	2:B:14:ASN:ND2	2.42	0.53
1:A:101:ASN:CG	2:B:254:LYS:HZ3	2.10	0.53
2:B:5:VAL:HG23	2:B:5:VAL:O	2.09	0.53
1:A:5:ILE:O	1:A:136:SER:N	2.40	0.53
1:A:231:ILE:CA	1:A:234:ILE:HG22	2.38	0.53
2:B:102:ASN:HB3	2:B:105:LYS:CB	2.39	0.53
2:B:263:PRO:HG2	2:B:431:GLU:OE1	2.09	0.53
1:A:151:SER:CA	1:A:197:HIS:CE1	2.92	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:PHE:CE1	1:A:231:ILE:HG23	2.25	0.53
1:A:264:ARG:HG3	1:A:431:ASP:OD2	2.09	0.53
1:A:266:HIS:CA	1:A:432:TYR:OH	2.57	0.53
2:B:182:VAL:O	2:B:185:TYR:HD2	1.91	0.53
2:B:212:ILE:O	2:B:216:THR:HB	2.09	0.53
2:B:229:HIS:C	2:B:229:HIS:ND1	2.62	0.53
2:B:297:ASP:OD1	2:B:298:ALA:N	2.39	0.53
1:A:121:ARG:O	1:A:125:LEU:HB2	2.08	0.52
1:A:195:LEU:CG	1:A:264:ARG:HH21	2.22	0.52
1:A:291:ILE:HD12	1:A:375:VAL:HG23	1.89	0.52
2:B:209:LEU:O	2:B:210:TYR:C	2.48	0.52
2:B:226:ASP:O	2:B:229:HIS:N	2.42	0.52
1:A:73:THR:HG21	2:B:42:LEU:HB2	1.90	0.52
2:B:322:ARG:HH11	2:B:322:ARG:HG3	1.74	0.52
1:A:16:ILE:CA	1:A:228:ASN:HB2	2.40	0.52
1:A:251:ASP:OD1	1:A:252:LEU:N	2.43	0.52
1:A:262:TYR:HD2	1:A:435:VAL:HG21	1.74	0.52
2:B:27:GLU:O	2:B:27:GLU:HG2	2.08	0.52
2:B:169:PHE:CD1	2:B:235:MET:CB	2.92	0.52
2:B:213:CYS:SG	2:B:219:LEU:HD23	2.48	0.52
2:B:259:MET:CA	2:B:314:THR:HG21	2.35	0.52
1:A:4:CYS:HB2	1:A:252:LEU:HD13	1.91	0.52
1:A:172:TYR:CD2	1:A:173:PRO:HD3	2.44	0.52
1:A:8:HIS:HB3	1:A:13:GLY:O	2.10	0.52
1:A:115:ILE:HD13	1:A:115:ILE:C	2.28	0.52
1:A:339:ARG:C	1:A:341:ILE:H	2.11	0.52
1:A:154:MET:HG2	1:A:166:LYS:HB3	1.91	0.52
2:B:194:LEU:HD22	2:B:265:LEU:HD21	1.92	0.52
2:B:295:MET:SD	2:B:375:ALA:O	2.68	0.52
1:A:4:CYS:HA	1:A:134:GLY:O	2.10	0.52
1:A:109:THR:HB	1:A:411:GLU:CD	2.30	0.52
1:A:264:ARG:HB2	1:A:266:HIS:HD2	1.67	0.52
2:B:21:TRP:CZ2	2:B:65:ALA:HB2	2.44	0.52
2:B:49:ILE:O	2:B:50:ASN:C	2.48	0.52
2:B:114:LEU:HD23	2:B:149:MET:HE1	1.91	0.52
2:B:169:PHE:CG	2:B:235:MET:HB3	2.42	0.52
2:B:346:TRP:CE3	2:B:346:TRP:O	2.63	0.52
1:A:109:THR:CB	1:A:411:GLU:CG	2.87	0.52
1:A:119:LEU:HD11	1:A:156:ARG:CD	2.40	0.52
2:B:314:THR:CG2	2:B:315:VAL:N	2.73	0.52
1:A:142:GLY:O	1:A:172:TYR:OH	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:PHE:HE1	1:A:204:VAL:CG2	2.22	0.52
1:A:184:PRO:CD	1:A:394:LYS:HG2	2.39	0.52
1:A:215:ARG:C	1:A:216:ASN:HD22	2.12	0.52
1:A:344:VAL:HG12	1:A:345:ASP:H	1.74	0.52
2:B:262:PHE:CE1	2:B:434:GLN:CG	2.93	0.52
2:B:345:GLU:C	2:B:347:ILE:H	2.12	0.52
1:A:283:HIS:ND1	1:A:286:LEU:HD13	2.24	0.52
2:B:16:ILE:N	2:B:228:ASN:HB3	2.20	0.52
2:B:149:MET:O	2:B:153:LEU:HD22	2.10	0.52
2:B:188:THR:CB	2:B:425:MET:HE3	2.35	0.52
2:B:384:ILE:O	2:B:386:GLU:HG2	2.09	0.52
1:A:109:THR:HG1	1:A:411:GLU:HG2	1.67	0.51
1:A:174:ALA:CB	1:A:207:GLU:HB2	2.31	0.51
1:A:191:THR:CG2	1:A:192:HIS:N	2.73	0.51
1:A:244:PHE:CD1	1:A:244:PHE:C	2.83	0.51
1:A:243:ARG:NH2	1:A:251:ASP:OD1	2.44	0.51
1:A:310:GLY:CA	1:A:382:THR:HB	2.39	0.51
1:A:408:TYR:CZ	1:A:418:PHE:CE1	2.98	0.51
2:B:4:ILE:HD13	2:B:136:GLN:NE2	2.18	0.51
1:A:122:ILE:HB	1:A:135:PHE:CD2	2.41	0.51
2:B:107:HIS:CD2	2:B:151:THR:HG22	2.45	0.51
2:B:277:SER:OG	2:B:281:GLN:HB2	2.10	0.51
2:B:384:ILE:HG13	2:B:384:ILE:O	2.11	0.51
1:A:23:LEU:CG	1:A:236:SER:OG	2.58	0.51
1:A:110:ILE:CG2	1:A:111:GLY:H	2.15	0.51
1:A:154:MET:CB	1:A:197:HIS:CA	2.84	0.51
2:B:251:ASP:O	2:B:252:LEU:C	2.49	0.51
2:B:258:ASN:CG	2:B:352:LYS:HD2	2.31	0.51
2:B:313:LEU:HD21	2:B:363:ALA:HB2	1.92	0.51
2:B:382:THR:HG23	2:B:386:GLU:H	1.75	0.51
2:B:363:ALA:HB3	2:B:436:GLN:HB2	1.90	0.51
1:A:24:TYR:HE1	1:A:236:SER:HA	1.75	0.51
1:A:220:GLU:C	1:A:222:PRO:CD	2.79	0.51
1:A:231:ILE:HD13	1:A:231:ILE:N	2.24	0.51
2:B:16:ILE:N	2:B:228:ASN:ND2	2.59	0.51
2:B:21:TRP:HZ2	2:B:65:ALA:HB2	1.76	0.51
2:B:205:ASP:CG	2:B:208:ALA:CB	2.72	0.51
1:A:108:TYR:CZ	1:A:413:MET:HA	2.43	0.51
2:B:206:ASN:HD21	4:B:502:GTP:H1'	1.32	0.51
1:A:392:ASP:OD2	1:A:425:MET:HE3	2.08	0.51
2:B:5:VAL:CG2	2:B:135:PHE:CD2	2.94	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:227:LEU:HB2	4:B:502:GTP:N2	2.26	0.51
2:B:262:PHE:CD1	2:B:435:TYR:CE2	2.99	0.51
1:A:266:HIS:NE2	1:A:431:ASP:OD1	2.40	0.51
2:B:19:LYS:CB	2:B:229:HIS:HA	2.41	0.51
2:B:260:VAL:O	2:B:260:VAL:HG23	2.11	0.51
2:B:323:MET:HG3	2:B:328:VAL:CG2	2.41	0.51
1:A:122:ILE:CD1	1:A:157:LEU:HD21	2.35	0.51
1:A:239:THR:O	1:A:240:ALA:C	2.48	0.51
2:B:171:VAL:HG12	2:B:205:ASP:C	2.30	0.51
1:A:93:ILE:CG2	1:A:94:THR:N	2.73	0.51
1:A:150:THR:CA	1:A:197:HIS:HE1	2.23	0.51
1:A:191:THR:HG21	1:A:425:MET:SD	2.51	0.51
1:A:201:ALA:O	1:A:203:MET:HG3	2.11	0.51
1:A:261:PRO:HB2	1:A:262:TYR:CD2	2.46	0.51
2:B:103:TRP:CE3	2:B:417:GLU:HG2	2.46	0.51
2:B:171:VAL:CA	2:B:205:ASP:HA	2.41	0.51
1:A:69:ASP:O	1:A:94:THR:O	2.29	0.50
1:A:209:ILE:HG22	1:A:227:LEU:CD2	2.41	0.50
1:A:382:THR:HG21	1:A:437:VAL:CG2	2.41	0.50
2:B:192:HIS:HA	2:B:424:ASN:CG	2.32	0.50
2:B:265:LEU:O	2:B:266:HIS:O	2.29	0.50
1:A:93:ILE:HG22	1:A:94:THR:H	1.76	0.50
1:A:205:ASP:HA	1:A:209:ILE:HD12	1.92	0.50
2:B:185:TYR:CA	2:B:395:PHE:CE1	2.86	0.50
2:B:226:ASP:O	2:B:227:LEU:C	2.46	0.50
2:B:298:ALA:O	2:B:299:LYS:C	2.50	0.50
1:A:171:ILE:O	1:A:171:ILE:HG22	2.10	0.50
1:A:182:VAL:HG11	1:A:404:PHE:CD1	2.44	0.50
2:B:3:GLU:HA	2:B:51:VAL:HA	1.93	0.50
2:B:189:LEU:HD21	2:B:418:PHE:CA	2.41	0.50
2:B:261:PRO:HB3	2:B:435:TYR:CG	2.40	0.50
2:B:385:GLN:HB2	2:B:429:VAL:HG13	1.84	0.50
1:A:67:PHE:HE2	1:A:87:PHE:CE2	2.29	0.50
1:A:142:GLY:C	1:A:172:TYR:CE2	2.84	0.50
1:A:238:ILE:O	1:A:242:LEU:HB2	2.11	0.50
1:A:328:VAL:C	1:A:330:ALA:H	2.15	0.50
1:A:417:GLU:OE1	1:A:417:GLU:HA	2.10	0.50
2:B:195:VAL:CB	2:B:264:ARG:CA	2.90	0.50
2:B:262:PHE:CE2	2:B:435:TYR:CE2	2.95	0.50
2:B:280:SER:O	2:B:282:GLN:N	2.45	0.50
2:B:320:ARG:HA	2:B:356:CYS:HB3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:ILE:HG23	1:A:17:GLY:N	2.26	0.50
1:A:195:LEU:HG	1:A:264:ARG:HH21	1.72	0.50
1:A:269:LEU:CD2	1:A:384:ILE:HD11	2.41	0.50
2:B:149:MET:O	2:B:149:MET:HG2	2.10	0.50
2:B:227:LEU:HB2	4:B:502:GTP:HN21	1.77	0.50
2:B:385:GLN:CB	2:B:429:VAL:CG1	2.64	0.50
1:A:11:GLN:O	1:A:14:VAL:HB	2.12	0.50
1:A:149:PHE:HE1	1:A:153:LEU:HD22	1.77	0.50
1:A:194:THR:O	1:A:198:SER:N	2.44	0.50
1:A:224:TYR:CD1	4:A:502:GTP:C6	2.98	0.50
1:A:408:TYR:CD1	1:A:409:VAL:N	2.80	0.50
2:B:4:ILE:HG22	2:B:5:VAL:N	2.27	0.50
2:B:296:PHE:CZ	2:B:315:VAL:HG11	2.46	0.50
1:A:70:LEU:CD2	1:A:95:GLY:HA3	2.40	0.50
1:A:413:MET:HG2	1:A:414:GLU:N	2.24	0.50
2:B:205:ASP:N	2:B:209:LEU:HD13	2.26	0.50
1:A:200:CYS:CB	1:A:266:HIS:O	2.59	0.50
1:A:264:ARG:HE	1:A:428:LEU:HD13	1.76	0.50
2:B:19:LYS:HE3	2:B:225:GLY:HA3	1.93	0.50
2:B:240:THR:HG23	2:B:241:CYS:H	1.76	0.50
2:B:265:LEU:HD12	2:B:266:HIS:O	2.12	0.50
2:B:333:LEU:O	2:B:336:GLN:N	2.44	0.50
2:B:336:GLN:HE22	2:B:349:ASN:ND2	2.10	0.50
1:A:119:LEU:HA	1:A:122:ILE:HG12	1.93	0.50
1:A:402:ARG:O	1:A:403:ALA:O	2.29	0.50
1:A:150:THR:HB	1:A:197:HIS:CE1	2.32	0.49
1:A:267:PHE:H	1:A:432:TYR:HH	1.51	0.49
1:A:305:CYS:SG	1:A:383:ALA:O	2.70	0.49
1:A:413:MET:SD	1:A:418:PHE:CZ	3.00	0.49
2:B:103:TRP:CZ3	2:B:417:GLU:HG2	2.46	0.49
2:B:113:GLU:HG3	2:B:114:LEU:N	2.26	0.49
1:A:184:PRO:HD3	1:A:394:LYS:HD3	1.94	0.49
1:A:305:CYS:O	1:A:306:ASP:C	2.51	0.49
2:B:19:LYS:HB2	2:B:229:HIS:HA	1.92	0.49
2:B:20:PHE:HB2	2:B:232:SER:HB3	1.94	0.49
2:B:171:VAL:CG1	2:B:206:ASN:N	2.75	0.49
2:B:266:HIS:HA	2:B:428:LEU:HD21	1.93	0.49
2:B:369:ARG:HD2	2:B:369:ARG:C	2.32	0.49
2:B:399:PHE:O	2:B:402:LYS:N	2.29	0.49
1:A:108:TYR:OH	1:A:417:GLU:HG3	2.12	0.49
1:A:244:PHE:CD1	1:A:245:ASP:N	2.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:GLN:HB3	2:B:14:ASN:HA	1.94	0.49
1:A:414:GLU:N	1:A:414:GLU:OE1	2.46	0.49
2:B:104:ALA:CB	2:B:413:MET:HA	2.42	0.49
2:B:168:THR:O	2:B:201:THR:HA	2.12	0.49
2:B:262:PHE:O	2:B:264:ARG:N	2.46	0.49
2:B:266:HIS:HA	2:B:388:PHE:CE2	2.46	0.49
2:B:363:ALA:C	2:B:385:GLN:N	2.66	0.49
1:A:115:ILE:CG2	1:A:116:ASP:N	2.75	0.49
1:A:115:ILE:HD11	1:A:119:LEU:HG	1.93	0.49
1:A:150:THR:CG2	1:A:197:HIS:CE1	2.94	0.49
1:A:194:THR:HG1	1:A:198:SER:CB	2.21	0.49
2:B:194:LEU:CD2	2:B:198:THR:CB	2.91	0.49
2:B:308:ARG:HG3	2:B:342:TYR:OH	2.13	0.49
2:B:345:GLU:O	2:B:347:ILE:N	2.45	0.49
1:A:24:TYR:CZ	1:A:239:THR:HB	2.48	0.49
1:A:133:GLN:CD	1:A:256:GLN:HE22	2.15	0.49
1:A:231:ILE:O	1:A:235:VAL:HG23	2.12	0.49
1:A:269:LEU:HD21	1:A:384:ILE:CG1	2.40	0.49
1:A:395:PHE:HZ	1:A:418:PHE:CD2	2.22	0.49
2:B:24:ILE:HG22	2:B:25:SER:N	2.27	0.49
2:B:103:TRP:HD1	2:B:147:SER:OG	1.96	0.49
2:B:104:ALA:HB3	2:B:413:MET:HB3	1.83	0.49
2:B:167:ASN:HA	2:B:200:GLU:HB3	1.95	0.49
2:B:189:LEU:HD21	2:B:418:PHE:C	2.33	0.49
2:B:230:LEU:HD21	2:B:302:MET:HE2	1.94	0.49
1:A:15:GLN:CG	4:A:502:GTP:N7	2.76	0.49
1:A:118:VAL:HG21	1:A:149:PHE:CE2	2.48	0.49
1:A:266:HIS:ND1	1:A:432:TYR:HE1	2.10	0.49
1:A:398:MET:HE3	1:A:404:PHE:CE1	2.48	0.49
2:B:385:GLN:H	2:B:429:VAL:HG13	1.75	0.49
1:A:26:LEU:CD1	1:A:361:THR:HG21	2.42	0.49
1:A:104:ALA:CB	1:A:408:TYR:N	2.74	0.49
1:A:173:PRO:CA	1:A:206:ASN:CB	2.86	0.49
1:A:267:PHE:N	1:A:432:TYR:HH	2.07	0.49
2:B:385:GLN:HB2	2:B:429:VAL:HA	1.95	0.49
1:A:73:THR:OG1	2:B:42:LEU:HA	2.13	0.49
1:A:105:ARG:HH11	1:A:105:ARG:HG3	1.78	0.49
1:A:195:LEU:CD1	1:A:425:MET:HA	2.43	0.49
2:B:267:PHE:HB2	2:B:388:PHE:HZ	1.78	0.49
2:B:296:PHE:HZ	2:B:315:VAL:HG11	1.78	0.49
2:B:387:LEU:HD23	2:B:388:PHE:CD1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:16:ILE:N	2:B:228:ASN:CG	2.66	0.48
2:B:142:GLY:HA3	2:B:183:GLU:OE2	2.13	0.48
2:B:269:MET:HB3	2:B:303:ALA:HB2	1.94	0.48
2:B:385:GLN:CG	2:B:429:VAL:HG22	2.42	0.48
1:A:189:LEU:CG	1:A:418:PHE:CE2	2.93	0.48
1:A:242:LEU:C	1:A:244:PHE:N	2.66	0.48
2:B:49:ILE:HG13	2:B:50:ASN:H	1.76	0.48
2:B:262:PHE:CE1	2:B:431:GLU:O	2.59	0.48
2:B:262:PHE:HE2	2:B:435:TYR:N	2.11	0.48
1:A:195:LEU:CD2	1:A:264:ARG:NH2	2.76	0.48
1:A:264:ARG:HG3	1:A:431:ASP:CG	2.34	0.48
1:A:317:LEU:CD1	1:A:351:PHE:CD1	2.96	0.48
2:B:299:LYS:H	2:B:299:LYS:CD	2.07	0.48
1:A:274:PRO:CB	1:A:371:VAL:HG21	2.43	0.48
1:A:396:ASP:O	1:A:400:ALA:CB	2.59	0.48
2:B:205:ASP:H	2:B:209:LEU:HD11	1.78	0.48
1:A:189:LEU:CD2	1:A:395:PHE:HZ	2.25	0.48
1:A:286:LEU:HG	1:A:290:GLU:HB3	1.96	0.48
1:A:362:VAL:HG13	1:A:368:LEU:CD1	2.38	0.48
2:B:2:ARG:CZ	2:B:48:ARG:NH2	2.76	0.48
2:B:258:ASN:ND2	2:B:352:LYS:HD2	2.28	0.48
2:B:389:LYS:HG3	2:B:429:VAL:HG11	1.95	0.48
1:A:369:ALA:O	1:A:370:LYS:CB	2.62	0.48
1:A:96:LYS:HD2	1:A:96:LYS:O	2.12	0.48
1:A:200:CYS:HB2	1:A:265:GLY:O	2.12	0.48
2:B:181:VAL:O	2:B:398:MET:CE	2.62	0.48
2:B:191:VAL:HG13	2:B:192:HIS:N	2.28	0.48
2:B:273:ALA:CB	2:B:274:PRO:HD3	2.30	0.48
1:A:115:ILE:O	1:A:116:ASP:C	2.51	0.48
1:A:126:ALA:CB	1:A:132:LEU:HD13	2.43	0.48
1:A:224:TYR:HE1	4:A:502:GTP:C6	2.31	0.48
2:B:360:PRO:HG2	2:B:371:LEU:CB	2.38	0.48
2:B:399:PHE:O	2:B:400:ARG:C	2.52	0.48
1:A:98:ASP:OD1	1:A:99:ALA:N	2.47	0.48
1:A:169:PHE:HE1	1:A:204:VAL:HG21	1.79	0.48
1:A:217:LEU:CD1	1:A:277:SER:HA	2.44	0.48
1:A:405:VAL:C	1:A:408:TYR:CE2	2.86	0.48
2:B:209:LEU:CD2	2:B:227:LEU:HD13	2.44	0.48
2:B:242:LEU:HD22	2:B:250:ALA:N	2.19	0.48
2:B:266:HIS:HB2	2:B:432:TYR:OH	2.14	0.48
1:A:126:ALA:HB1	1:A:132:LEU:CD2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:GLY:O	1:A:151:SER:CB	2.61	0.48
2:B:287:THR:O	2:B:288:VAL:CG2	2.58	0.48
2:B:363:ALA:O	2:B:433:GLN:HB2	2.14	0.48
1:A:107:HIS:CE1	1:A:152:LEU:HB3	2.49	0.47
1:A:182:VAL:O	1:A:398:MET:CE	2.62	0.47
2:B:209:LEU:O	2:B:213:CYS:N	2.47	0.47
2:B:237:GLY:O	2:B:241:CYS:CB	2.61	0.47
1:A:99:ALA:O	1:A:100:ALA:HB3	2.14	0.47
1:A:266:HIS:CE1	1:A:432:TYR:HE1	2.32	0.47
2:B:313:LEU:HD22	2:B:363:ALA:HB2	1.95	0.47
1:A:105:ARG:CA	1:A:411:GLU:CD	2.72	0.47
1:A:262:TYR:CE2	1:A:435:VAL:CG1	2.96	0.47
1:A:384:ILE:HG22	1:A:388:TRP:CD1	2.49	0.47
1:A:386:GLU:O	1:A:388:TRP:N	2.47	0.47
2:B:156:LYS:HA	2:B:156:LYS:CE	2.38	0.47
2:B:185:TYR:CE1	2:B:399:PHE:CB	2.97	0.47
2:B:307:PRO:HB3	2:B:312:TYR:CZ	2.49	0.47
1:A:6:SER:OG	1:A:65:ALA:HB2	2.14	0.47
1:A:101:ASN:CB	2:B:254:LYS:NZ	2.77	0.47
1:A:135:PHE:CD1	1:A:157:LEU:CD1	2.97	0.47
1:A:288:VAL:HA	1:A:291:ILE:HG12	1.94	0.47
2:B:115:VAL:CG2	2:B:152:LEU:HD23	2.44	0.47
2:B:194:LEU:CD2	2:B:265:LEU:CD2	2.92	0.47
2:B:195:VAL:HB	2:B:264:ARG:CA	2.42	0.47
2:B:242:LEU:CD1	2:B:250:ALA:HB3	2.45	0.47
1:A:339:ARG:C	1:A:341:ILE:N	2.68	0.47
2:B:211:ASP:OD1	2:B:212:ILE:HG13	2.13	0.47
2:B:227:LEU:HB3	4:B:502:GTP:N2	2.29	0.47
2:B:243:ARG:N	2:B:243:ARG:HD3	2.26	0.47
2:B:262:PHE:CZ	2:B:435:TYR:CZ	3.02	0.47
2:B:313:LEU:HD12	2:B:432:TYR:CG	2.42	0.47
1:A:109:THR:HB	1:A:411:GLU:CG	2.45	0.47
1:A:154:MET:HA	1:A:157:LEU:HD12	1.96	0.47
1:A:154:MET:CA	1:A:166:LYS:HD3	2.44	0.47
1:A:241:SER:HB3	1:A:320:ARG:NH2	2.29	0.47
1:A:345:ASP:C	1:A:347:CYS:N	2.68	0.47
2:B:35:SER:CB	2:B:59:ASN:HA	2.42	0.47
1:A:183:GLU:HB3	1:A:184:PRO:CD	2.45	0.47
1:A:205:ASP:H	1:A:209:ILE:CD1	2.28	0.47
1:A:234:ILE:CG1	1:A:270:ALA:HB1	2.38	0.47
1:A:256:GLN:O	1:A:260:VAL:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:TYR:C	1:A:284:GLU:H	2.15	0.47
2:B:49:ILE:HG13	2:B:50:ASN:N	2.29	0.47
2:B:171:VAL:HA	2:B:204:ILE:C	2.35	0.47
2:B:185:TYR:OH	2:B:398:MET:O	2.33	0.47
2:B:188:THR:CA	2:B:425:MET:CE	2.58	0.47
2:B:202:TYR:CE2	2:B:378:ILE:HD13	2.42	0.47
2:B:204:ILE:HG23	2:B:302:MET:CG	2.45	0.47
1:A:120:ASP:O	1:A:124:LYS:HB2	2.15	0.47
1:A:256:GLN:HA	1:A:260:VAL:HG13	1.97	0.47
1:A:315:CYS:HB3	1:A:377:MET:HE1	1.97	0.47
1:A:344:VAL:CG1	1:A:345:ASP:N	2.78	0.47
1:A:405:VAL:CG1	1:A:408:TYR:HE2	2.27	0.47
1:A:16:ILE:HG13	1:A:228:ASN:HB2	1.97	0.47
1:A:34:GLY:C	1:A:61:HIS:N	2.68	0.47
1:A:384:ILE:HG22	1:A:384:ILE:O	2.15	0.47
2:B:134:GLY:HA3	2:B:165:ILE:HG12	1.97	0.47
2:B:185:TYR:OH	2:B:398:MET:C	2.53	0.47
1:A:119:LEU:HD11	1:A:156:ARG:HD2	1.97	0.47
1:A:173:PRO:CB	1:A:174:ALA:CB	2.85	0.47
1:A:201:ALA:N	1:A:267:PHE:HD2	2.06	0.47
1:A:253:THR:O	1:A:254:GLU:C	2.52	0.47
1:A:288:VAL:HG23	1:A:373:ARG:HH11	1.79	0.47
1:A:404:PHE:CD1	1:A:404:PHE:N	2.83	0.47
2:B:204:ILE:HA	2:B:302:MET:HB2	1.87	0.47
2:B:242:LEU:HA	2:B:242:LEU:HD23	1.76	0.47
2:B:242:LEU:HD11	2:B:250:ALA:HB3	1.97	0.47
2:B:262:PHE:CG	2:B:431:GLU:HB3	2.50	0.47
2:B:297:ASP:OD2	2:B:299:LYS:HE2	2.15	0.47
1:A:4:CYS:HB2	1:A:252:LEU:CD1	2.45	0.46
1:A:154:MET:HA	1:A:166:LYS:CD	2.45	0.46
1:A:243:ARG:NH2	1:A:252:LEU:CB	2.78	0.46
2:B:20:PHE:O	2:B:24:ILE:HB	2.14	0.46
2:B:113:GLU:CG	2:B:114:LEU:N	2.78	0.46
2:B:194:LEU:HD11	2:B:267:PHE:CE1	2.40	0.46
2:B:224:TYR:O	2:B:225:GLY:C	2.53	0.46
1:A:108:TYR:CD1	1:A:413:MET:HB2	2.50	0.46
1:A:150:THR:HG22	1:A:154:MET:HG3	1.98	0.46
1:A:255:PHE:O	1:A:256:GLN:C	2.53	0.46
1:A:265:GLY:O	1:A:266:HIS:O	2.33	0.46
1:A:434:GLU:C	1:A:436:GLY:H	2.18	0.46
2:B:133:GLN:O	2:B:165:ILE:CD1	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:169:PHE:HD2	2:B:204:ILE:CD1	2.28	0.46
2:B:287:THR:N	2:B:290:GLU:OE1	2.48	0.46
1:A:70:LEU:HD22	1:A:95:GLY:HA3	1.97	0.46
1:A:115:ILE:HG23	1:A:116:ASP:H	1.79	0.46
1:A:407:TRP:CH2	2:B:253:ARG:HD3	2.49	0.46
2:B:226:ASP:O	2:B:229:HIS:HB3	2.14	0.46
2:B:431:GLU:HA	2:B:434:GLN:HG2	1.96	0.46
1:A:215:ARG:CZ	1:A:299:ALA:HB1	2.45	0.46
1:A:335:ILE:O	1:A:337:THR:N	2.47	0.46
1:A:413:MET:C	1:A:414:GLU:HG3	2.36	0.46
2:B:185:TYR:CE1	2:B:399:PHE:CE1	2.81	0.46
2:B:324:SER:OG	2:B:326:LYS:HB3	2.16	0.46
1:A:23:LEU:HG	1:A:236:SER:OG	2.16	0.46
1:A:27:GLU:O	1:A:244:PHE:CD2	2.68	0.46
2:B:15:GLN:CA	2:B:228:ASN:ND2	2.72	0.46
2:B:126:SER:HB2	2:B:132:LEU:HD22	1.97	0.46
2:B:169:PHE:HD2	2:B:204:ILE:HD11	1.80	0.46
2:B:307:PRO:C	2:B:309:HIS:H	2.18	0.46
2:B:359:PRO:CB	2:B:360:PRO:HD2	2.45	0.46
1:A:383:ALA:C	1:A:385:ALA:N	2.69	0.46
1:A:388:TRP:HA	1:A:388:TRP:HE3	1.79	0.46
1:A:423:GLU:O	1:A:426:ALA:HB3	2.16	0.46
1:A:436:GLY:O	1:A:438:ASP:N	2.49	0.46
2:B:203:CYS:N	2:B:270:PRO:CD	2.79	0.46
2:B:204:ILE:HG23	2:B:302:MET:CB	2.46	0.46
2:B:208:ALA:O	2:B:212:ILE:HG13	2.16	0.46
1:A:10:GLY:O	1:A:11:GLN:C	2.54	0.46
1:A:115:ILE:CG1	1:A:152:LEU:HD13	2.45	0.46
1:A:190:THR:O	1:A:194:THR:HG22	2.11	0.46
1:A:241:SER:C	1:A:244:PHE:HB3	2.36	0.46
1:A:408:TYR:CD1	1:A:413:MET:SD	3.09	0.46
2:B:11:GLN:O	2:B:14:ASN:HB3	2.16	0.46
2:B:194:LEU:CD2	2:B:265:LEU:HD21	2.44	0.46
2:B:202:TYR:CD2	2:B:238:VAL:HG21	2.51	0.46
1:A:220:GLU:O	1:A:222:PRO:CD	2.64	0.46
1:A:260:VAL:CG2	1:A:260:VAL:O	2.63	0.46
1:A:392:ASP:OD1	1:A:422:ARG:NE	2.48	0.46
2:B:199:ASP:HA	2:B:265:LEU:HD13	1.98	0.46
1:A:191:THR:CG2	1:A:425:MET:SD	3.04	0.46
1:A:395:PHE:CE1	1:A:399:TYR:HB2	2.51	0.46
1:A:408:TYR:HD1	1:A:413:MET:HB3	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:250:ALA:HB1	2:B:254:LYS:CB	2.44	0.46
2:B:360:PRO:O	2:B:369:ARG:C	2.54	0.46
1:A:154:MET:CB	1:A:166:LYS:CD	2.93	0.46
1:A:189:LEU:HD23	1:A:395:PHE:CE2	2.49	0.46
1:A:276:ILE:HG12	1:A:277:SER:N	2.31	0.46
2:B:194:LEU:HD22	2:B:198:THR:CB	2.46	0.46
2:B:237:GLY:HA3	2:B:376:THR:OG1	2.15	0.46
2:B:262:PHE:CG	2:B:431:GLU:CB	2.99	0.46
2:B:387:LEU:O	2:B:387:LEU:HG	2.14	0.46
2:B:408:TYR:O	2:B:411:GLU:HB2	2.16	0.46
1:A:181:VAL:HG11	2:B:258:ASN:CG	2.32	0.45
1:A:195:LEU:HB2	1:A:424:ASP:HB3	1.98	0.45
1:A:243:ARG:NH2	1:A:252:LEU:HB2	2.31	0.45
2:B:6:HIS:HB3	2:B:21:TRP:HZ2	1.81	0.45
2:B:23:VAL:O	2:B:25:SER:N	2.50	0.45
2:B:135:PHE:N	2:B:135:PHE:CD1	2.84	0.45
1:A:122:ILE:CB	1:A:135:PHE:CE2	2.76	0.45
1:A:205:ASP:N	1:A:209:ILE:CD1	2.78	0.45
1:A:334:THR:CG2	1:A:335:ILE:N	2.79	0.45
1:A:392:ASP:OD1	1:A:422:ARG:CZ	2.65	0.45
2:B:24:ILE:CD1	2:B:52:TYR:CE2	2.97	0.45
2:B:204:ILE:CG2	2:B:302:MET:HB3	2.47	0.45
2:B:204:ILE:CG2	2:B:302:MET:SD	3.00	0.45
1:A:5:ILE:HG22	1:A:6:SER:H	1.78	0.45
1:A:317:LEU:CD1	1:A:351:PHE:CE1	2.99	0.45
2:B:133:GLN:HE21	2:B:243:ARG:HH12	1.63	0.45
2:B:209:LEU:HD23	2:B:227:LEU:HD13	1.98	0.45
2:B:288:VAL:N	2:B:289:PRO:CD	2.80	0.45
2:B:309:HIS:O	2:B:386:GLU:OE1	2.35	0.45
1:A:117:LEU:HD12	1:A:121:ARG:HH12	1.80	0.45
1:A:181:VAL:CB	2:B:258:ASN:ND2	2.80	0.45
1:A:228:ASN:O	1:A:232:GLY:N	2.39	0.45
2:B:72:PRO:O	2:B:74:THR:N	2.50	0.45
2:B:274:PRO:HG2	2:B:371:LEU:CD2	2.43	0.45
2:B:311:ARG:O	2:B:382:THR:HG22	2.16	0.45
1:A:114:ILE:O	1:A:118:VAL:HG23	2.16	0.45
1:A:151:SER:CB	1:A:193:THR:HG21	2.42	0.45
1:A:268:PRO:CA	1:A:379:SER:O	2.65	0.45
1:A:274:PRO:HB2	1:A:371:VAL:HG21	1.98	0.45
2:B:8:GLN:CG	2:B:67:LEU:HD22	2.46	0.45
2:B:106:GLY:O	2:B:149:MET:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:258:ASN:HD21	2:B:352:LYS:HG3	1.67	0.45
2:B:312:TYR:HA	2:B:381:SER:O	2.16	0.45
1:A:72:PRO:CB	2:B:47:GLU:HG2	2.33	0.45
1:A:231:ILE:HD13	1:A:231:ILE:H	1.82	0.45
1:A:271:THR:O	1:A:376:CYS:HA	2.17	0.45
1:A:303:VAL:O	1:A:303:VAL:CG1	2.64	0.45
2:B:94:PHE:N	2:B:94:PHE:CD1	2.84	0.45
2:B:154:ILE:HD12	2:B:155:SER:N	2.31	0.45
2:B:168:THR:N	2:B:200:GLU:O	2.45	0.45
2:B:273:ALA:CB	2:B:274:PRO:CD	2.93	0.45
2:B:323:MET:CE	2:B:328:VAL:HG22	2.46	0.45
2:B:324:SER:O	2:B:326:LYS:N	2.50	0.45
1:A:22:GLU:O	1:A:23:LEU:C	2.54	0.45
1:A:103:TYR:CD1	1:A:148:GLY:HA2	2.52	0.45
1:A:173:PRO:HA	1:A:206:ASN:C	2.37	0.45
1:A:175:PRO:CG	1:A:176:GLN:H	2.29	0.45
2:B:185:TYR:CA	2:B:395:PHE:CD1	3.00	0.45
2:B:189:LEU:HD21	2:B:418:PHE:HA	1.97	0.45
2:B:313:LEU:O	2:B:347:ILE:HD12	2.16	0.45
1:A:63:PRO:C	1:A:64:ARG:CG	2.83	0.45
1:A:173:PRO:HA	1:A:174:ALA:CB	2.47	0.45
1:A:182:VAL:O	1:A:184:PRO:CD	2.65	0.45
1:A:184:PRO:HG3	1:A:394:LYS:HG2	1.91	0.45
1:A:204:VAL:CB	1:A:209:ILE:HD11	2.40	0.45
1:A:209:ILE:CD1	1:A:231:ILE:HD11	2.47	0.45
1:A:278:ALA:HB2	1:A:369:ALA:CA	2.45	0.45
2:B:171:VAL:CG1	2:B:206:ASN:OD1	2.61	0.45
1:A:148:GLY:O	1:A:149:PHE:C	2.55	0.45
1:A:203:MET:CB	1:A:206:ASN:HD21	2.30	0.45
1:A:383:ALA:C	1:A:385:ALA:H	2.20	0.45
2:B:82:PRO:C	2:B:84:GLY:H	2.20	0.45
2:B:195:VAL:CB	2:B:264:ARG:C	2.85	0.45
1:A:11:GLN:NE2	1:A:74:VAL:HG22	2.30	0.45
1:A:153:LEU:O	1:A:157:LEU:HG	2.17	0.45
1:A:157:LEU:HD12	1:A:166:LYS:CG	2.47	0.45
1:A:165:SER:HA	1:A:199:ASP:OD2	2.17	0.45
1:A:203:MET:HB3	1:A:206:ASN:ND2	2.32	0.45
1:A:288:VAL:HG21	1:A:323:VAL:HG13	1.99	0.45
2:B:288:VAL:N	2:B:289:PRO:HD2	2.32	0.45
1:A:7:ILE:HG13	1:A:137:VAL:HG22	1.98	0.44
1:A:93:ILE:CG2	1:A:94:THR:H	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:SER:CB	1:A:193:THR:CG2	2.94	0.44
1:A:192:HIS:CG	1:A:193:THR:H	2.32	0.44
1:A:343:PHE:CE1	1:A:351:PHE:HE2	2.36	0.44
1:A:408:TYR:CE2	1:A:418:PHE:CZ	3.04	0.44
1:A:117:LEU:HD11	1:A:121:ARG:NH2	2.30	0.44
1:A:154:MET:HG2	1:A:166:LYS:CB	2.48	0.44
1:A:161:TYR:O	1:A:163:LYS:HD3	2.17	0.44
1:A:229:ARG:NH1	1:A:229:ARG:HG2	2.31	0.44
1:A:362:VAL:HG13	1:A:368:LEU:CG	2.47	0.44
1:A:189:LEU:HD23	1:A:192:HIS:HE1	1.81	0.44
1:A:398:MET:HE3	1:A:404:PHE:HE1	1.81	0.44
2:B:67:LEU:HD12	2:B:92:PHE:CD1	2.52	0.44
2:B:169:PHE:HZ	2:B:235:MET:CA	1.86	0.44
2:B:195:VAL:CG1	2:B:264:ARG:HH12	2.20	0.44
1:A:63:PRO:HG2	1:A:91:GLN:OE1	2.18	0.44
1:A:172:TYR:CE2	1:A:183:GLU:OE2	2.70	0.44
1:A:182:VAL:HG13	1:A:404:PHE:CZ	2.42	0.44
2:B:194:LEU:HD13	2:B:265:LEU:HD21	1.99	0.44
2:B:242:LEU:C	2:B:244:PHE:H	2.19	0.44
2:B:430:SER:O	2:B:434:GLN:HG2	2.17	0.44
1:A:21:TRP:HE1	1:A:63:PRO:HB3	1.83	0.44
1:A:154:MET:HB3	1:A:166:LYS:CD	2.38	0.44
2:B:194:LEU:HB3	2:B:265:LEU:HD23	0.53	0.44
2:B:413:MET:HE3	2:B:418:PHE:HE1	0.46	0.44
1:A:286:LEU:HD12	1:A:286:LEU:HA	1.84	0.44
2:B:67:LEU:HD12	2:B:92:PHE:CE1	2.53	0.44
2:B:180:THR:HG22	2:B:181:VAL:H	1.81	0.44
1:A:72:PRO:HG2	1:A:73:THR:H	1.83	0.44
1:A:218:ASP:C	1:A:219:ILE:HG12	2.37	0.44
2:B:115:VAL:HG21	2:B:152:LEU:HD21	1.98	0.44
2:B:193:GLN:O	2:B:197:ASN:HB2	2.17	0.44
2:B:212:ILE:O	2:B:212:ILE:HG22	2.17	0.44
2:B:262:PHE:CD1	2:B:431:GLU:HB3	2.52	0.44
2:B:288:VAL:C	2:B:290:GLU:N	2.70	0.44
1:A:132:LEU:CD2	1:A:164:LYS:CE	2.96	0.44
1:A:149:PHE:O	1:A:150:THR:C	2.56	0.44
1:A:152:LEU:HD12	1:A:152:LEU:C	2.38	0.44
2:B:182:VAL:O	2:B:185:TYR:CD2	2.71	0.44
2:B:203:CYS:N	2:B:270:PRO:HD3	2.33	0.44
1:A:189:LEU:CD2	1:A:192:HIS:HE1	2.30	0.44
1:A:402:ARG:O	1:A:405:VAL:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:VAL:HB	1:A:408:TYR:OH	2.18	0.44
2:B:14:ASN:O	2:B:17:GLY:N	2.50	0.44
1:A:191:THR:HG1	1:A:425:MET:CG	2.16	0.43
1:A:212:ILE:HD11	1:A:302:MET:H	1.81	0.43
2:B:295:MET:SD	2:B:375:ALA:HB3	2.57	0.43
1:A:8:HIS:HA	1:A:138:PHE:HB2	2.00	0.43
1:A:266:HIS:CE1	1:A:432:TYR:CE1	3.06	0.43
1:A:404:PHE:CE2	2:B:257:VAL:O	2.71	0.43
2:B:24:ILE:CG2	2:B:25:SER:N	2.80	0.43
2:B:409:THR:C	2:B:411:GLU:H	2.22	0.43
1:A:161:TYR:O	1:A:163:LYS:HB3	2.17	0.43
1:A:252:LEU:O	1:A:253:THR:C	2.56	0.43
2:B:72:PRO:HG2	2:B:73:GLY:H	1.83	0.43
2:B:105:LYS:HG2	2:B:411:GLU:HB3	1.94	0.43
2:B:194:LEU:HD22	2:B:265:LEU:CD2	2.47	0.43
2:B:301:MET:O	2:B:303:ALA:N	2.51	0.43
1:A:5:ILE:HG23	1:A:125:LEU:CD1	2.37	0.43
1:A:13:GLY:C	1:A:16:ILE:HG22	2.38	0.43
1:A:133:GLN:CD	1:A:256:GLN:NE2	2.72	0.43
1:A:161:TYR:CD1	1:A:161:TYR:N	2.86	0.43
1:A:263:PRO:O	1:A:264:ARG:C	2.56	0.43
1:A:304:LYS:HG3	1:A:304:LYS:O	2.19	0.43
1:A:409:VAL:C	1:A:411:GLU:N	2.71	0.43
2:B:104:ALA:CB	2:B:413:MET:CA	2.96	0.43
2:B:192:HIS:CD2	2:B:424:ASN:H	2.30	0.43
2:B:240:THR:HG23	2:B:241:CYS:N	2.33	0.43
1:A:192:HIS:HA	1:A:424:ASP:HB2	2.00	0.43
1:A:272:TYR:CE2	1:A:274:PRO:HD2	2.53	0.43
1:A:343:PHE:HZ	1:A:351:PHE:CZ	2.36	0.43
2:B:6:HIS:HB3	2:B:65:ALA:CB	2.48	0.43
2:B:7:ILE:N	2:B:136:GLN:O	2.51	0.43
2:B:191:VAL:HG23	2:B:267:PHE:CE2	2.50	0.43
1:A:23:LEU:O	1:A:26:LEU:HB3	2.17	0.43
1:A:328:VAL:O	1:A:330:ALA:N	2.38	0.43
2:B:103:TRP:CE2	2:B:189:LEU:HB3	2.53	0.43
2:B:243:ARG:HH21	2:B:252:LEU:N	2.12	0.43
1:A:115:ILE:CG2	1:A:116:ASP:H	2.32	0.43
1:A:154:MET:SD	1:A:197:HIS:O	2.75	0.43
1:A:175:PRO:CD	1:A:176:GLN:N	2.81	0.43
1:A:185:TYR:CE1	1:A:189:LEU:HD11	2.53	0.43
1:A:195:LEU:HD21	1:A:264:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:VAL:CG1	1:A:364:PRO:HD2	2.48	0.43
2:B:185:TYR:CG	2:B:418:PHE:HE2	2.35	0.43
2:B:239:THR:O	2:B:240:THR:C	2.56	0.43
2:B:307:PRO:C	2:B:309:HIS:N	2.70	0.43
1:A:121:ARG:HG2	1:A:121:ARG:HH11	1.83	0.43
1:A:192:HIS:HD2	1:A:193:THR:CA	2.31	0.43
1:A:390:ARG:HG3	1:A:390:ARG:HH11	1.83	0.43
2:B:153:LEU:HD13	2:B:153:LEU:N	2.34	0.43
1:A:93:ILE:N	1:A:93:ILE:CD1	2.73	0.43
1:A:193:THR:O	1:A:197:HIS:HB3	2.19	0.43
1:A:209:ILE:CD1	1:A:231:ILE:CD1	2.97	0.43
1:A:255:PHE:O	1:A:259:LEU:N	2.50	0.43
1:A:405:VAL:CA	1:A:408:TYR:CD2	2.95	0.43
1:A:408:TYR:CG	1:A:409:VAL:N	2.86	0.43
2:B:262:PHE:CD2	2:B:435:TYR:CE2	3.07	0.43
1:A:110:ILE:O	1:A:111:GLY:C	2.57	0.43
1:A:141:PHE:CZ	1:A:391:LEU:CD2	2.97	0.43
1:A:205:ASP:H	1:A:209:ILE:HG13	1.83	0.43
1:A:238:ILE:O	1:A:242:LEU:CB	2.67	0.43
2:B:72:PRO:O	2:B:73:GLY:C	2.58	0.43
2:B:105:LYS:CB	2:B:411:GLU:HB3	2.48	0.43
2:B:242:LEU:HD22	2:B:250:ALA:O	2.18	0.43
1:A:11:GLN:HE21	1:A:74:VAL:CG2	2.29	0.42
1:A:101:ASN:OD1	2:B:249:ASN:O	2.37	0.42
1:A:115:ILE:CD1	1:A:115:ILE:C	2.87	0.42
1:A:123:ARG:CB	1:A:161:TYR:OH	2.67	0.42
1:A:154:MET:CG	1:A:197:HIS:CE1	2.77	0.42
1:A:184:PRO:CB	1:A:394:LYS:C	2.86	0.42
1:A:264:ARG:C	1:A:266:HIS:N	2.60	0.42
2:B:15:GLN:C	2:B:228:ASN:ND2	2.73	0.42
2:B:26:ASP:C	2:B:28:HIS:H	2.21	0.42
2:B:168:THR:CG2	2:B:201:THR:HG23	2.48	0.42
2:B:182:VAL:O	2:B:183:GLU:C	2.56	0.42
2:B:395:PHE:CE2	2:B:422:GLU:HB2	2.54	0.42
2:B:41:ASP:O	2:B:47:GLU:CD	2.57	0.42
1:A:5:ILE:CG2	1:A:6:SER:H	2.29	0.42
1:A:7:ILE:HD11	1:A:137:VAL:CG2	2.44	0.42
1:A:12:ALA:HB3	4:A:502:GTP:O4'	2.15	0.42
1:A:132:LEU:H	1:A:132:LEU:CD2	2.23	0.42
1:A:436:GLY:C	1:A:438:ASP:N	2.72	0.42
2:B:20:PHE:HB2	2:B:232:SER:CB	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:138:THR:O	2:B:139:HIS:HB3	2.20	0.42
2:B:181:VAL:O	2:B:398:MET:HE1	2.18	0.42
2:B:401:ARG:O	2:B:401:ARG:CG	2.67	0.42
1:A:16:ILE:CG2	1:A:17:GLY:N	2.82	0.42
1:A:25:CYS:SG	1:A:26:LEU:N	2.92	0.42
1:A:121:ARG:HG2	1:A:121:ARG:NH1	2.33	0.42
1:A:378:LEU:O	1:A:378:LEU:HD12	2.19	0.42
2:B:206:ASN:CG	4:B:502:GTP:C1'	2.52	0.42
2:B:210:TYR:O	2:B:214:PHE:N	2.52	0.42
2:B:250:ALA:CB	2:B:254:LYS:HE2	2.50	0.42
1:A:208:ALA:HA	1:A:211:ASP:OD2	2.18	0.42
1:A:251:ASP:CA	1:A:254:GLU:HG3	2.48	0.42
2:B:118:VAL:O	2:B:122:VAL:HG13	2.20	0.42
1:A:328:VAL:C	1:A:330:ALA:N	2.73	0.42
2:B:19:LYS:HE3	2:B:225:GLY:C	2.39	0.42
2:B:171:VAL:CG1	2:B:205:ASP:CA	2.81	0.42
2:B:191:VAL:HG21	2:B:425:MET:HG2	1.46	0.42
2:B:343:PHE:CD1	2:B:350:ASN:ND2	2.88	0.42
1:A:2:ARG:HG2	1:A:243:ARG:HH12	1.84	0.42
1:A:187:SER:CB	1:A:391:LEU:HG	2.40	0.42
1:A:213:CYS:O	1:A:219:ILE:HG13	2.20	0.42
1:A:224:TYR:HD1	4:A:502:GTP:N3	2.14	0.42
1:A:238:ILE:HD11	1:A:378:LEU:HD23	2.01	0.42
1:A:267:PHE:HD1	1:A:432:TYR:CZ	2.36	0.42
1:A:363:VAL:HG13	1:A:364:PRO:HD2	2.02	0.42
1:A:399:TYR:OH	1:A:415:GLU:HG2	2.19	0.42
2:B:307:PRO:O	2:B:309:HIS:N	2.53	0.42
1:A:76:ASP:O	1:A:79:ARG:N	2.52	0.42
1:A:132:LEU:HD21	1:A:161:TYR:CD2	2.54	0.42
1:A:137:VAL:HG12	1:A:139:HIS:CE1	2.55	0.42
1:A:147:SER:HB2	1:A:186:ASN:O	2.19	0.42
1:A:158:SER:CA	1:A:163:LYS:N	2.71	0.42
1:A:291:ILE:HG13	1:A:292:THR:N	2.35	0.42
1:A:377:MET:O	1:A:377:MET:HG3	2.18	0.42
1:A:404:PHE:HE2	2:B:257:VAL:O	2.02	0.42
1:A:103:TYR:O	1:A:104:ALA:C	2.57	0.42
1:A:160:ASP:HB3	1:A:161:TYR:CD1	2.54	0.42
1:A:204:VAL:C	1:A:206:ASN:H	2.23	0.42
1:A:230:LEU:O	1:A:231:ILE:C	2.57	0.42
1:A:255:PHE:O	1:A:257:THR:N	2.53	0.42
1:A:335:ILE:C	1:A:337:THR:N	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:16:ILE:N	2:B:228:ASN:CB	2.79	0.42
2:B:262:PHE:CZ	2:B:435:TYR:CE1	3.07	0.42
1:A:103:TYR:CG	1:A:189:LEU:HD13	2.51	0.42
1:A:195:LEU:CB	1:A:424:ASP:HB3	2.50	0.42
1:A:200:CYS:SG	1:A:266:HIS:O	2.77	0.42
1:A:242:LEU:HD11	1:A:250:VAL:HG23	2.02	0.42
2:B:25:SER:O	2:B:28:HIS:N	2.53	0.42
2:B:147:SER:HB2	2:B:190:SER:CB	2.41	0.42
2:B:187:ALA:O	2:B:188:THR:C	2.57	0.42
1:A:224:TYR:O	4:A:502:GTP:N2	2.53	0.41
2:B:210:TYR:O	2:B:211:ASP:C	2.57	0.41
2:B:261:PRO:HB2	2:B:262:PHE:CD2	2.54	0.41
2:B:431:GLU:O	2:B:434:GLN:CG	2.68	0.41
1:A:8:HIS:CD2	1:A:138:PHE:CD2	3.07	0.41
1:A:100:ALA:O	1:A:144:GLY:HA3	2.20	0.41
1:A:381:THR:C	1:A:383:ALA:N	2.72	0.41
2:B:171:VAL:HA	2:B:205:ASP:N	2.35	0.41
2:B:189:LEU:HD21	2:B:418:PHE:O	2.19	0.41
2:B:363:ALA:HB3	2:B:436:GLN:CB	2.50	0.41
1:A:76:ASP:O	1:A:80:THR:N	2.53	0.41
1:A:204:VAL:HG23	1:A:205:ASP:N	2.28	0.41
1:A:231:ILE:C	1:A:233:GLN:N	2.73	0.41
1:A:242:LEU:HD12	1:A:242:LEU:HA	1.87	0.41
1:A:262:TYR:HB3	1:A:263:PRO:HD2	2.00	0.41
1:A:287:SER:C	1:A:289:ALA:N	2.73	0.41
1:A:332:ILE:CD1	1:A:353:VAL:HG22	2.51	0.41
1:A:404:PHE:CE2	2:B:257:VAL:CG1	2.92	0.41
1:A:408:TYR:CD2	1:A:418:PHE:HZ	2.24	0.41
2:B:194:LEU:CD1	2:B:265:LEU:HD21	2.50	0.41
2:B:202:TYR:CE2	2:B:238:VAL:HG13	2.54	0.41
1:A:132:LEU:HD21	1:A:164:LYS:HE2	2.03	0.41
1:A:224:TYR:HD1	4:A:502:GTP:C2	2.38	0.41
1:A:408:TYR:CE1	1:A:409:VAL:CG2	3.01	0.41
1:A:434:GLU:C	1:A:436:GLY:N	2.74	0.41
2:B:12:CYS:C	2:B:14:ASN:N	2.71	0.41
2:B:106:GLY:O	2:B:149:MET:CA	2.68	0.41
2:B:194:LEU:CA	2:B:265:LEU:HD22	2.44	0.41
2:B:333:LEU:O	2:B:334:ASN:C	2.58	0.41
2:B:399:PHE:O	2:B:401:ARG:N	2.53	0.41
1:A:100:ALA:HB2	1:A:105:ARG:HD3	2.03	0.41
1:A:152:LEU:C	1:A:152:LEU:CD1	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ILE:HD13	4:A:502:GTP:HN22	1.86	0.41
1:A:384:ILE:O	1:A:385:ALA:C	2.59	0.41
2:B:155:SER:HA	2:B:197:ASN:CG	2.39	0.41
2:B:325:MET:HE2	2:B:355:VAL:CG2	2.47	0.41
2:B:333:LEU:HD11	2:B:337:ASN:HD21	1.85	0.41
1:A:195:LEU:CD2	1:A:425:MET:N	2.51	0.41
1:A:273:ALA:HB2	1:A:375:VAL:HB	2.03	0.41
1:A:282:TYR:CD1	1:A:284:GLU:OE2	2.74	0.41
4:A:502:GTP:O3'	2:B:247:GLN:HA	2.19	0.41
2:B:133:GLN:CG	2:B:165:ILE:HD11	2.49	0.41
1:A:154:MET:HE3	1:A:198:SER:HB2	1.90	0.41
1:A:217:LEU:HD12	1:A:277:SER:CB	2.49	0.41
1:A:296:PHE:CD1	1:A:341:ILE:CD1	2.98	0.41
1:A:308:ARG:O	1:A:308:ARG:HG2	2.20	0.41
1:A:100:ALA:C	1:A:102:ASN:H	2.24	0.41
1:A:179:THR:O	2:B:248:LEU:HD22	2.21	0.41
1:A:273:ALA:O	1:A:275:VAL:N	2.54	0.41
1:A:324:VAL:HG12	1:A:326:LYS:H	1.85	0.41
2:B:242:LEU:HB3	2:B:250:ALA:O	2.20	0.41
2:B:281:GLN:C	2:B:283:TYR:N	2.67	0.41
1:A:67:PHE:CE2	1:A:87:PHE:CE2	3.08	0.41
1:A:108:TYR:CZ	1:A:413:MET:CA	2.91	0.41
1:A:149:PHE:CD1	1:A:150:THR:N	2.89	0.41
1:A:172:TYR:HE2	1:A:183:GLU:OE2	2.03	0.41
1:A:230:LEU:O	1:A:233:GLN:N	2.35	0.41
1:A:287:SER:O	1:A:289:ALA:N	2.53	0.41
1:A:318:LEU:HB2	1:A:376:CYS:SG	2.61	0.41
1:A:428:LEU:HD12	1:A:428:LEU:HA	1.79	0.41
2:B:12:CYS:O	2:B:13:GLY:C	2.59	0.41
2:B:105:LYS:HB2	2:B:411:GLU:HB3	2.03	0.41
2:B:189:LEU:CG	2:B:418:PHE:HA	2.51	0.41
2:B:202:TYR:C	2:B:270:PRO:HG3	2.40	0.41
2:B:239:THR:CG2	2:B:240:THR:N	2.80	0.41
2:B:262:PHE:CE1	2:B:434:GLN:HG3	2.56	0.41
2:B:409:THR:C	2:B:411:GLU:N	2.73	0.41
1:A:5:ILE:HD11	1:A:125:LEU:C	2.42	0.41
2:B:19:LYS:CE	2:B:225:GLY:CA	2.97	0.41
2:B:23:VAL:O	2:B:24:ILE:C	2.59	0.41
2:B:103:TRP:HZ3	2:B:108:TYR:CE1	2.37	0.41
2:B:187:ALA:O	2:B:190:SER:N	2.54	0.41
2:B:273:ALA:HB1	2:B:291:LEU:HG	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:417:GLU:O	2:B:420:GLU:HB3	2.21	0.41
1:A:119:LEU:HD11	1:A:156:ARG:HD3	2.01	0.40
1:A:132:LEU:CD2	1:A:164:LYS:HE2	2.51	0.40
1:A:139:HIS:N	1:A:139:HIS:ND1	2.69	0.40
1:A:147:SER:OG	1:A:148:GLY:N	2.54	0.40
2:B:118:VAL:O	2:B:121:VAL:N	2.54	0.40
2:B:135:PHE:CD1	2:B:166:MET:SD	3.14	0.40
2:B:182:VAL:O	2:B:184:PRO:N	2.54	0.40
2:B:264:ARG:HA	2:B:264:ARG:HD3	1.78	0.40
1:A:14:VAL:HG11	1:A:75:ILE:HD13	2.04	0.40
1:A:192:HIS:CD2	1:A:193:THR:CA	3.01	0.40
1:A:243:ARG:NH2	1:A:252:LEU:HG	2.35	0.40
1:A:244:PHE:HD1	1:A:244:PHE:C	2.24	0.40
1:A:401:LYS:C	1:A:403:ALA:H	2.24	0.40
2:B:78:VAL:O	2:B:84:GLY:HA3	2.21	0.40
2:B:125:GLU:O	2:B:128:SER:HB3	2.22	0.40
2:B:268:PHE:HA	2:B:379:GLY:O	2.22	0.40
2:B:408:TYR:C	2:B:413:MET:CG	2.90	0.40
1:A:67:PHE:HB2	1:A:92:LEU:HD23	2.02	0.40
1:A:234:ILE:C	1:A:234:ILE:CD1	2.86	0.40
2:B:12:CYS:O	2:B:14:ASN:N	2.55	0.40
2:B:188:THR:O	2:B:191:VAL:HG12	2.21	0.40
1:A:25:CYS:SG	1:A:83:TYR:HE2	2.38	0.40
2:B:99:ALA:O	2:B:100:GLY:C	2.60	0.40
2:B:199:ASP:O	2:B:200:GLU:HB2	2.21	0.40
2:B:282:GLN:HB3	2:B:282:GLN:HE21	1.50	0.40
1:A:13:GLY:HA2	1:A:16:ILE:CG2	2.50	0.40
1:A:185:TYR:OH	1:A:418:PHE:CZ	2.72	0.40
2:B:186:ASN:OD1	2:B:408:TYR:OH	2.40	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	401/451 (89%)	257 (64%)	83 (21%)	61 (15%)	0 4
2	B	399/445 (90%)	262 (66%)	85 (21%)	52 (13%)	0 5
All	All	800/896 (89%)	519 (65%)	168 (21%)	113 (14%)	1 4

All (113) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	LYS
1	A	108	TYR
1	A	109	THR
1	A	175	PRO
1	A	183	GLU
1	A	207	GLU
1	A	217	LEU
1	A	240	ALA
1	A	249	ASN
1	A	255	PHE
1	A	266	HIS
1	A	280	LYS
1	A	283	HIS
1	A	285	GLN
1	A	309	HIS
1	A	346	TRP
1	A	370	LYS
1	A	387	ALA
1	A	403	ALA
1	A	437	VAL
2	B	23	VAL
2	B	24	ILE
2	B	32	PRO
2	B	50	ASN
2	B	82	PRO
2	B	183	GLU
2	B	199	ASP
2	B	200	GLU
2	B	218	LYS
2	B	238	VAL
2	B	239	THR
2	B	240	THR
2	B	252	LEU
2	B	263	PRO
2	B	266	HIS

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Mol	Chain	Res	Type
2	B	273	ALA
2	B	278	ARG
2	B	280	SER
2	B	281	GLN
2	B	282	GLN
2	B	288	VAL
2	B	294	GLN
2	B	295	MET
2	B	343	PHE
2	B	344	VAL
2	B	346	TRP
2	B	369	ARG
2	B	381	SER
2	B	385	GLN
2	B	403	ALA
1	A	24	TYR
1	A	63	PRO
1	A	103	TYR
1	A	111	GLY
1	A	218	ASP
1	A	219	ILE
1	A	238	ILE
1	A	265	GLY
1	A	279	GLU
1	A	314	ALA
1	A	339	ARG
1	A	342	GLN
1	A	373	ARG
1	A	384	ILE
1	A	386	GLU
2	B	38	GLY
2	B	73	GLY
2	B	198	THR
2	B	265	LEU
2	B	279	GLY
2	B	298	ALA
2	B	300	ASN
2	B	311	ARG
1	A	104	ALA
1	A	141	PHE
1	A	148	GLY
1	A	149	PHE

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Mol	Chain	Res	Type
1	A	239	THR
1	A	245	ASP
1	A	263	PRO
1	A	330	ALA
1	A	336	LYS
1	A	369	ALA
2	B	83	PHE
2	B	99	ALA
2	B	302	MET
1	A	89	PRO
1	A	172	TYR
1	A	256	GLN
1	A	307	PRO
1	A	348	PRO
2	B	34	GLY
2	B	100	GLY
2	B	395	PHE
1	A	139	HIS
1	A	140	SER
1	A	160	ASP
1	A	174	ALA
1	A	284	GLU
1	A	298	PRO
1	A	303	VAL
2	B	57	ALA
2	B	74	THR
2	B	285	ALA
1	A	31	GLN
1	A	273	ALA
2	B	51	VAL
2	B	58	GLY
2	B	145	THR
2	B	400	ARG
1	A	115	ILE
1	A	222	PRO
2	B	72	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	345/377 (92%)	293 (85%)	52 (15%)	3 14
2	B	353/381 (93%)	302 (86%)	51 (14%)	3 16
All	All	698/758 (92%)	595 (85%)	103 (15%)	6 15

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	SER
1	A	20	CYS
1	A	21	TRP
1	A	32	PRO
1	A	76	ASP
1	A	82	THR
1	A	96	LYS
1	A	97	GLU
1	A	115	ILE
1	A	120	ASP
1	A	125	LEU
1	A	127	ASP
1	A	135	PHE
1	A	139	HIS
1	A	150	THR
1	A	152	LEU
1	A	155	GLU
1	A	169	PHE
1	A	172	TYR
1	A	187	SER
1	A	199	ASP
1	A	206	ASN
1	A	219	ILE
1	A	221	ARG
1	A	231	ILE
1	A	234	ILE
1	A	243	ARG
1	A	244	PHE
1	A	253	THR
1	A	260	VAL
1	A	267	PHE
1	A	269	LEU
1	A	276	ILE

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Mol	Chain	Res	Type
1	A	280	LYS
1	A	282	TYR
1	A	303	VAL
1	A	306	ASP
1	A	325	PRO
1	A	326	LYS
1	A	334	THR
1	A	345	ASP
1	A	352	LYS
1	A	368	LEU
1	A	376	CYS
1	A	378	LEU
1	A	380	ASN
1	A	394	LYS
1	A	404	PHE
1	A	415	GLU
1	A	417	GLU
1	A	431	ASP
1	A	432	TYR
2	B	14	ASN
2	B	24	ILE
2	B	26	ASP
2	B	32	PRO
2	B	41	ASP
2	B	68	VAL
2	B	76	ASP
2	B	90	ASP
2	B	94	PHE
2	B	122	VAL
2	B	135	PHE
2	B	145	THR
2	B	149	MET
2	B	153	LEU
2	B	165	ILE
2	B	198	THR
2	B	200	GLU
2	B	201	THR
2	B	203	CYS
2	B	205	ASP
2	B	207	GLU
2	B	211	ASP
2	B	214	PHE

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Mol	Chain	Res	Type
2	B	215	ARG
2	B	227	LEU
2	B	230	LEU
2	B	236	SER
2	B	240	THR
2	B	244	PHE
2	B	264	ARG
2	B	265	LEU
2	B	275	LEU
2	B	282	GLN
2	B	283	TYR
2	B	284	ARG
2	B	289	PRO
2	B	299	LYS
2	B	306	ASP
2	B	309	HIS
2	B	322	ARG
2	B	324	SER
2	B	325	MET
2	B	343	PHE
2	B	344	VAL
2	B	349	ASN
2	B	369	ARG
2	B	380	ASN
2	B	382	THR
2	B	387	LEU
2	B	414	ASP
2	B	432	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	15	GLN
1	A	128	GLN
1	A	133	GLN
1	A	192	HIS
1	A	197	HIS
1	A	216	ASN
1	A	228	ASN
1	A	233	GLN
1	A	256	GLN

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Mol	Chain	Res	Type
1	A	283	HIS
1	A	380	ASN
2	B	14	ASN
2	B	91	ASN
2	B	101	ASN
2	B	102	ASN
2	B	107	HIS
2	B	133	GLN
2	B	136	GLN
2	B	139	HIS
2	B	167	ASN
2	B	186	ASN
2	B	192	HIS
2	B	197	ASN
2	B	206	ASN
2	B	258	ASN
2	B	282	GLN
2	B	331	GLN
2	B	334	ASN
2	B	337	ASN
2	B	349	ASN
2	B	406	HIS
2	B	424	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	GTP	B	502	3	26,34,34	1.29	4 (15%)	32,54,54	1.10	2 (6%)
4	GTP	A	502	3	26,34,34	1.30	4 (15%)	32,54,54	1.10	2 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GTP	B	502	3	-	3/18/38/38	0/3/3/3
4	GTP	A	502	3	-	3/18/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	502	GTP	C5-C6	-3.66	1.40	1.47
4	B	502	GTP	C5-C6	-3.66	1.40	1.47
4	A	502	GTP	C6-N1	2.59	1.41	1.37
4	B	502	GTP	C6-N1	2.58	1.41	1.37
4	A	502	GTP	C8-N7	-2.45	1.30	1.35
4	B	502	GTP	C8-N7	-2.38	1.31	1.35
4	A	502	GTP	O4'-C1'	2.18	1.44	1.41
4	B	502	GTP	O4'-C1'	2.15	1.44	1.41

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	502	GTP	O2G-PG-O3B	2.66	113.54	104.64
4	A	502	GTP	O2G-PG-O3B	2.64	113.49	104.64
4	A	502	GTP	O5'-C5'-C4'	2.07	116.12	108.99
4	B	502	GTP	O5'-C5'-C4'	2.07	116.12	108.99

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	502	GTP	C3'-C4'-C5'-O5'
4	B	502	GTP	C3'-C4'-C5'-O5'
4	A	502	GTP	O4'-C4'-C5'-O5'
4	B	502	GTP	O4'-C4'-C5'-O5'
4	A	502	GTP	C5'-O5'-PA-O1A
4	B	502	GTP	C5'-O5'-PA-O1A

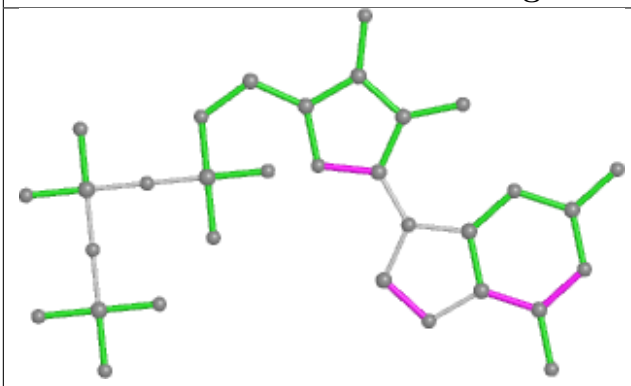
There are no ring outliers.

2 monomers are involved in 88 short contacts:

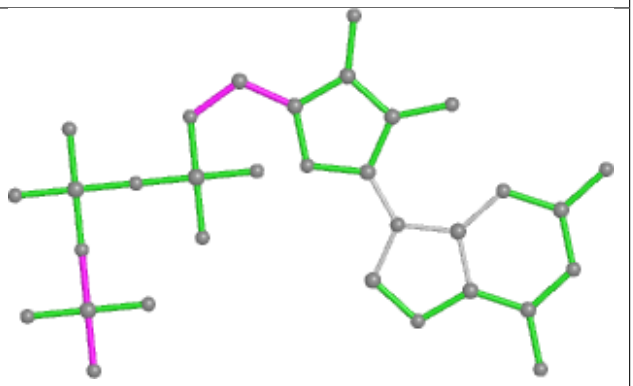
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	502	GTP	27	0
4	A	502	GTP	61	0

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

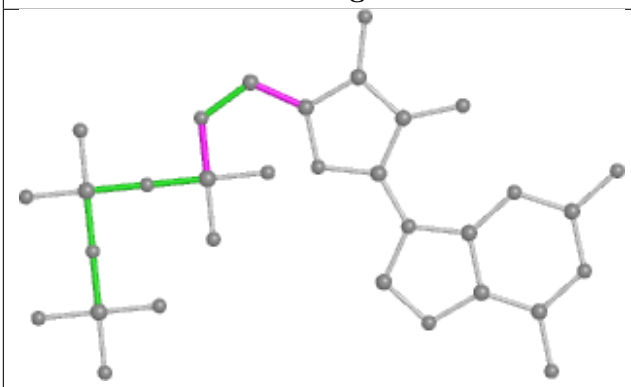
Ligand GTP B 502



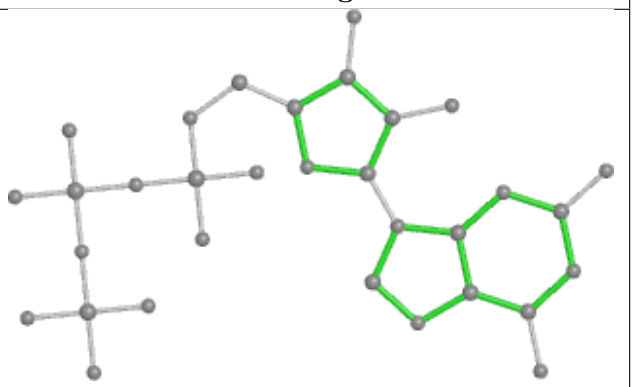
Bond lengths



Bond angles

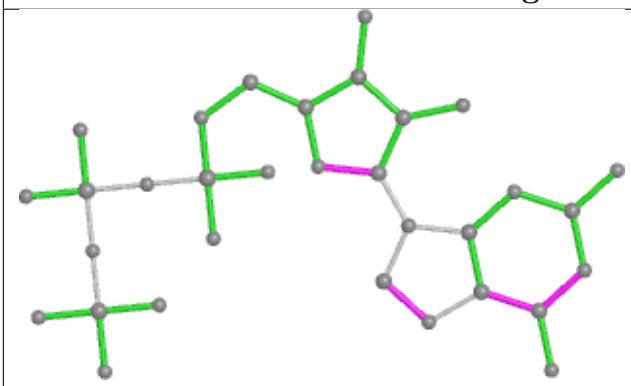


Torsions

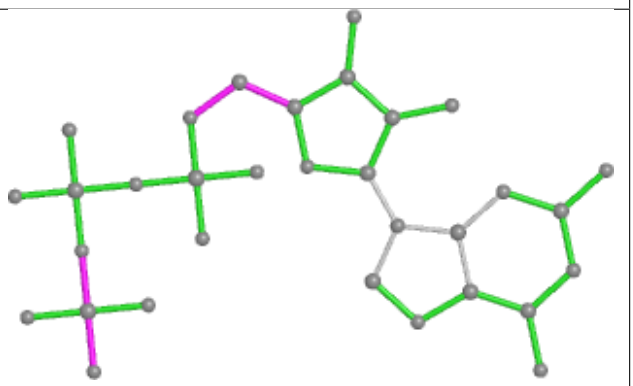


Rings

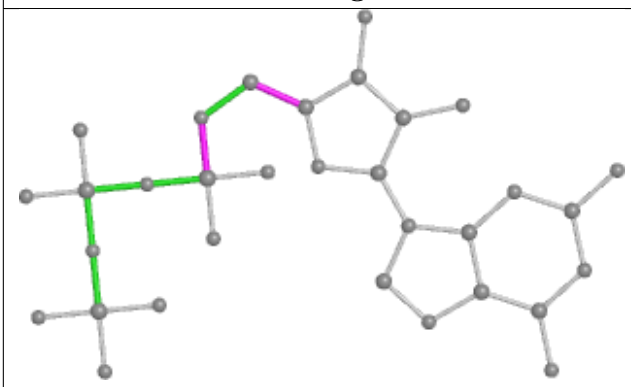
Ligand GTP A 502



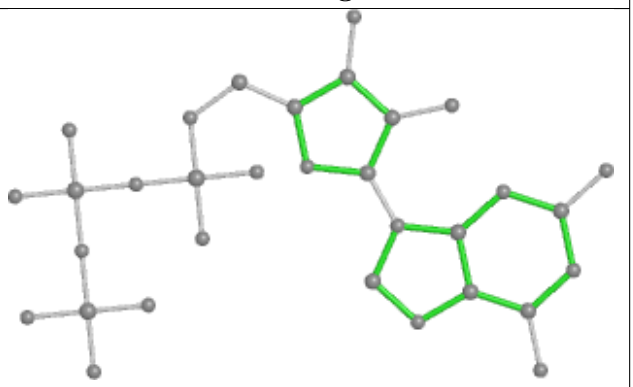
Bond lengths



Bond angles



Torsions



Rings

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.

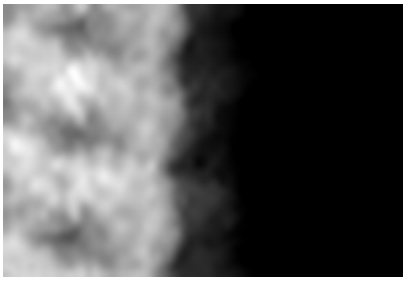
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-2697. These allow visual inspection of the internal detail of the map and identification of artifacts.

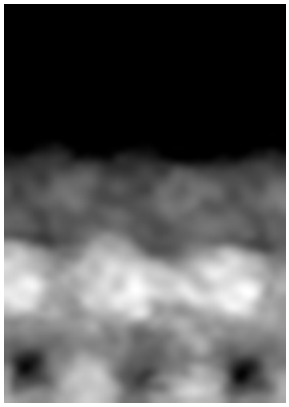
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

6.1.1 Primary map



X



Y

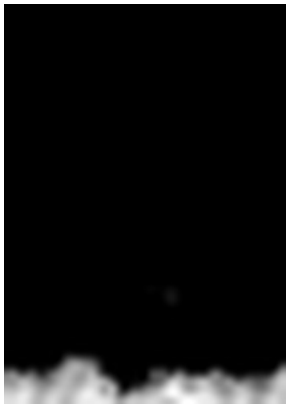
Z

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

6.2 Central slices

6.2.1 Primary map

X Index: 30



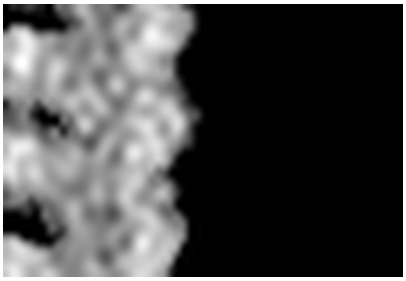
Y Index: 31

Z Index: 21

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: 16

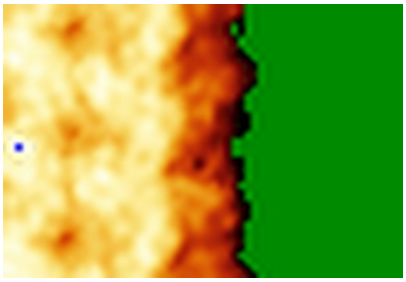
Y Index: 3

Z Index: 29

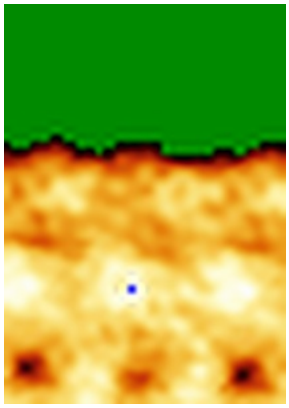
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

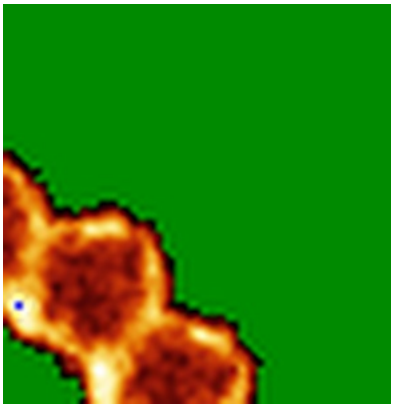
6.4.1 Primary map



X



Y

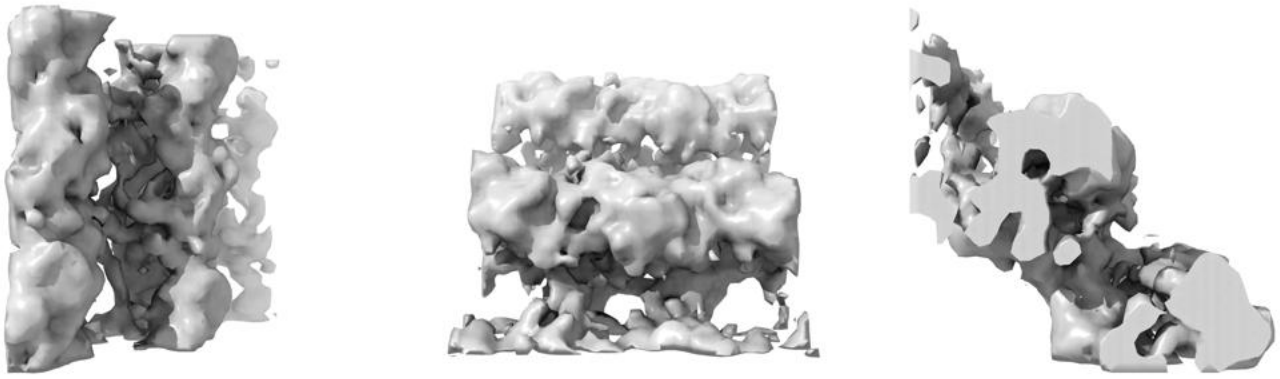


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 156.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

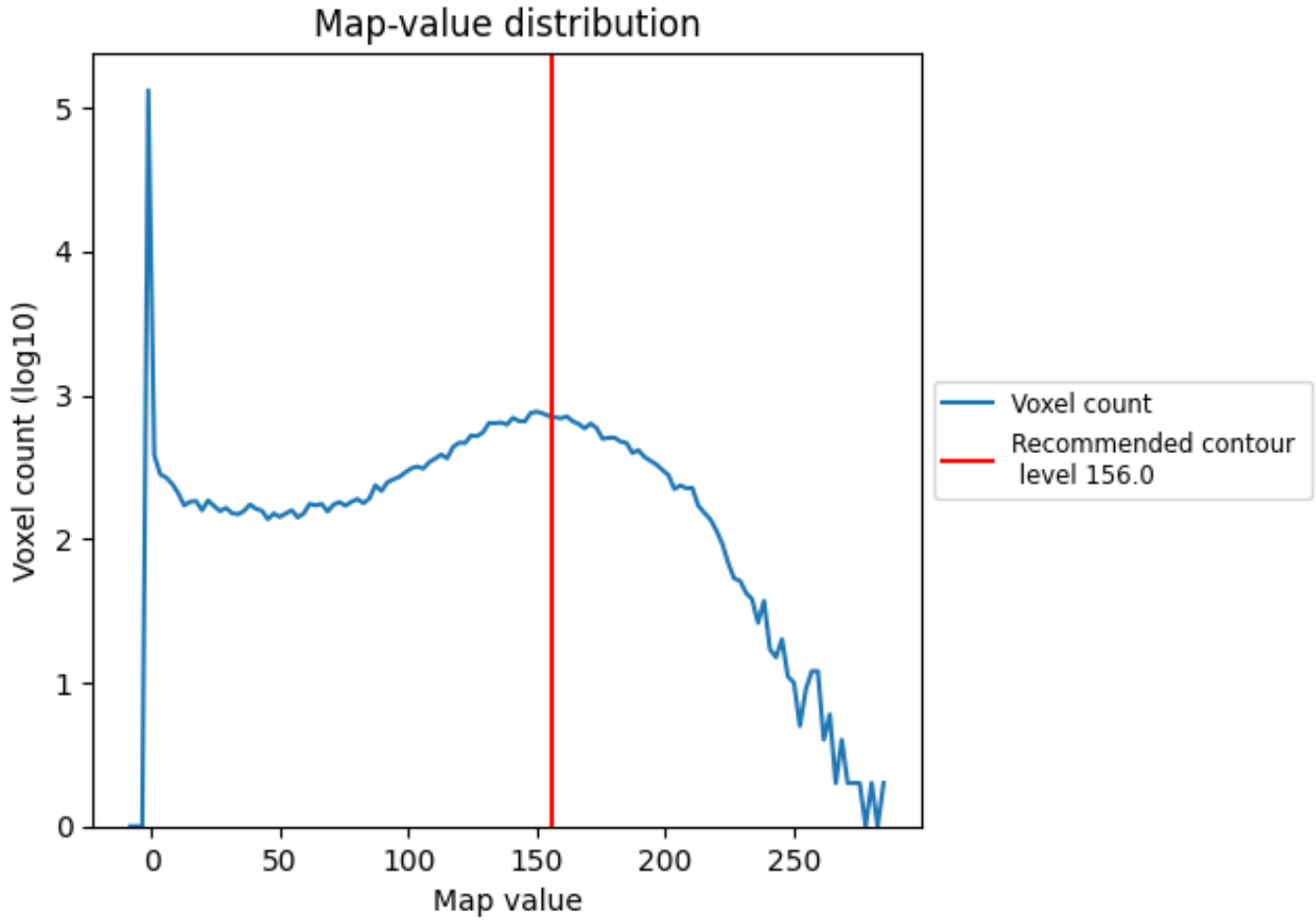
6.6 Mask visualisation (i)

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

7 Map analysis

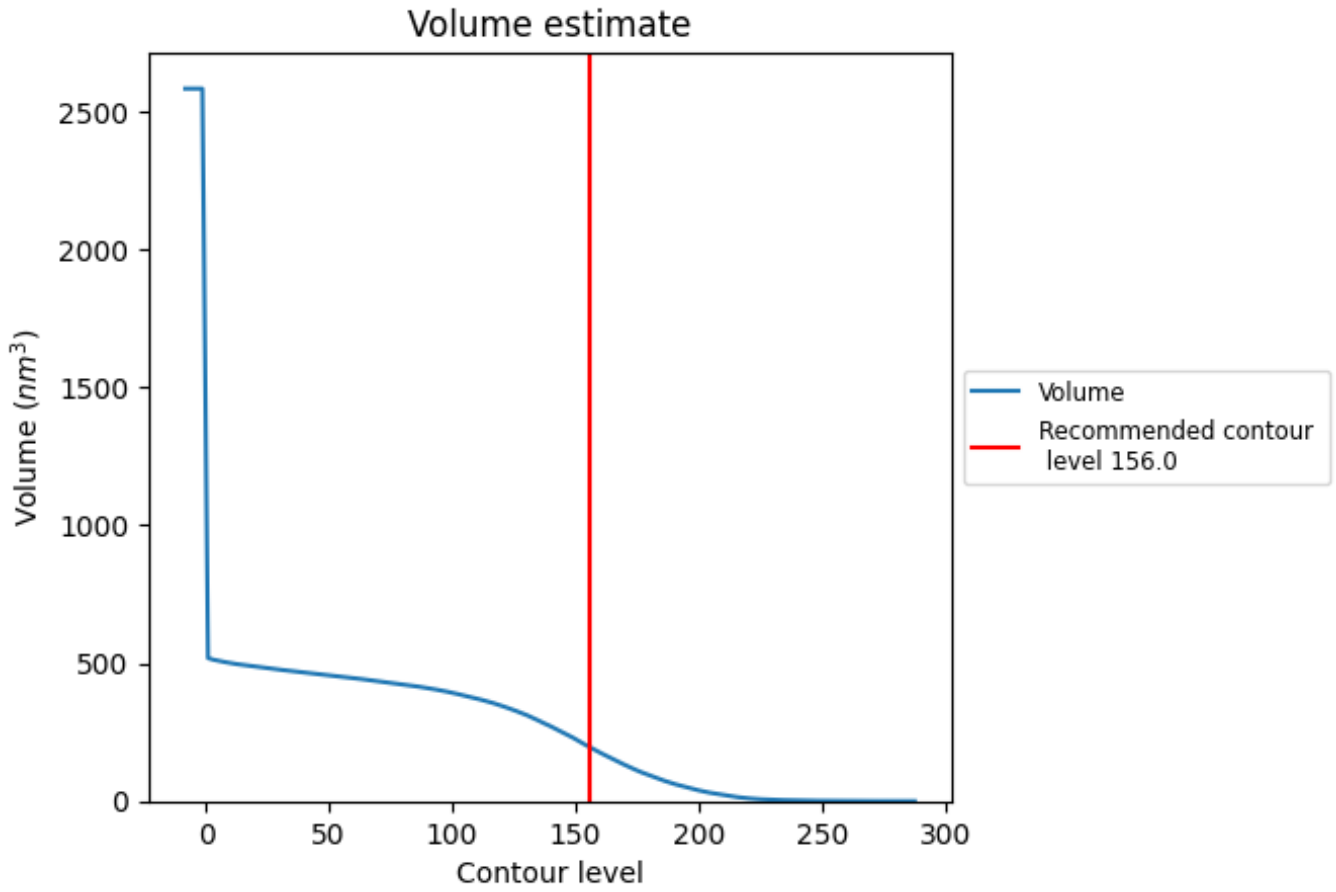
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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



The volume at the recommended contour level is 194 nm^3; this corresponds to an approximate mass of 175 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

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

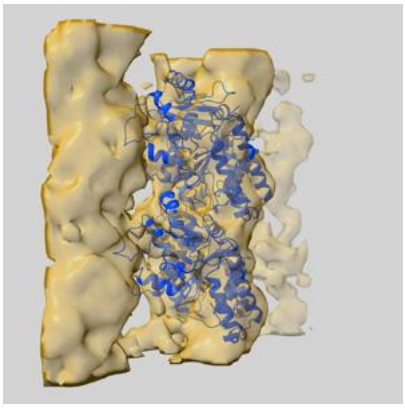
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

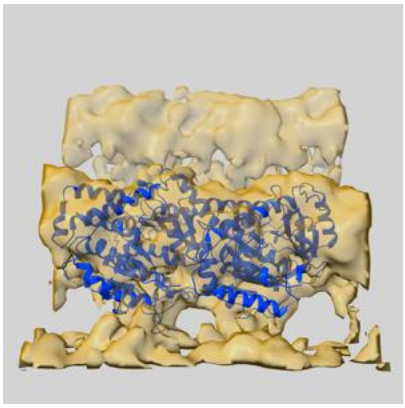
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-2697 and PDB model 3J7I. Per-residue inclusion information can be found in section 3 on page 5.

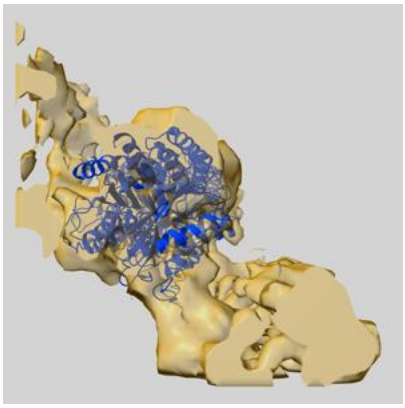
9.1 Map-model overlay



X



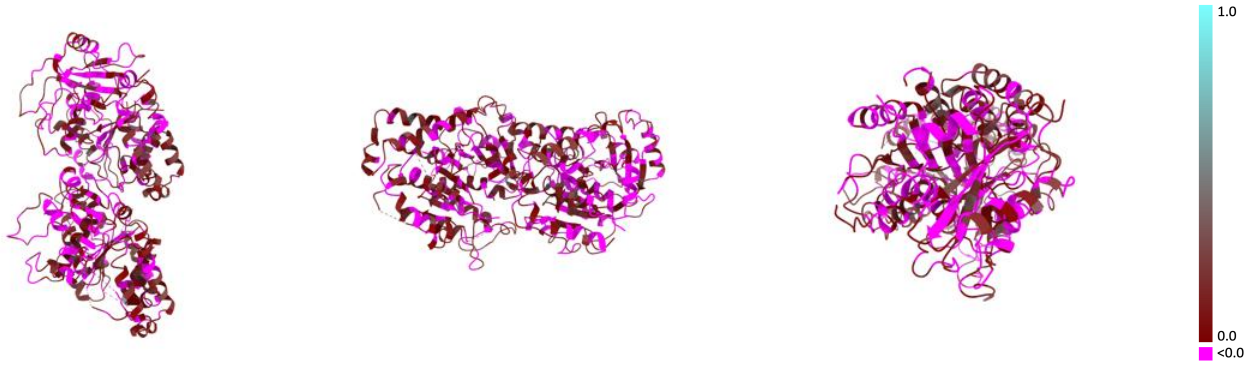
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 156.0 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.

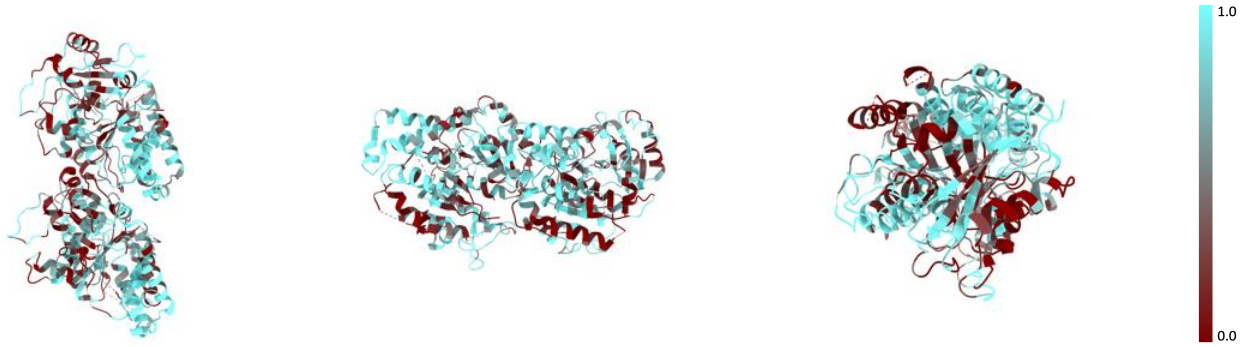
9.2 Q-score mapped to coordinate model



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.

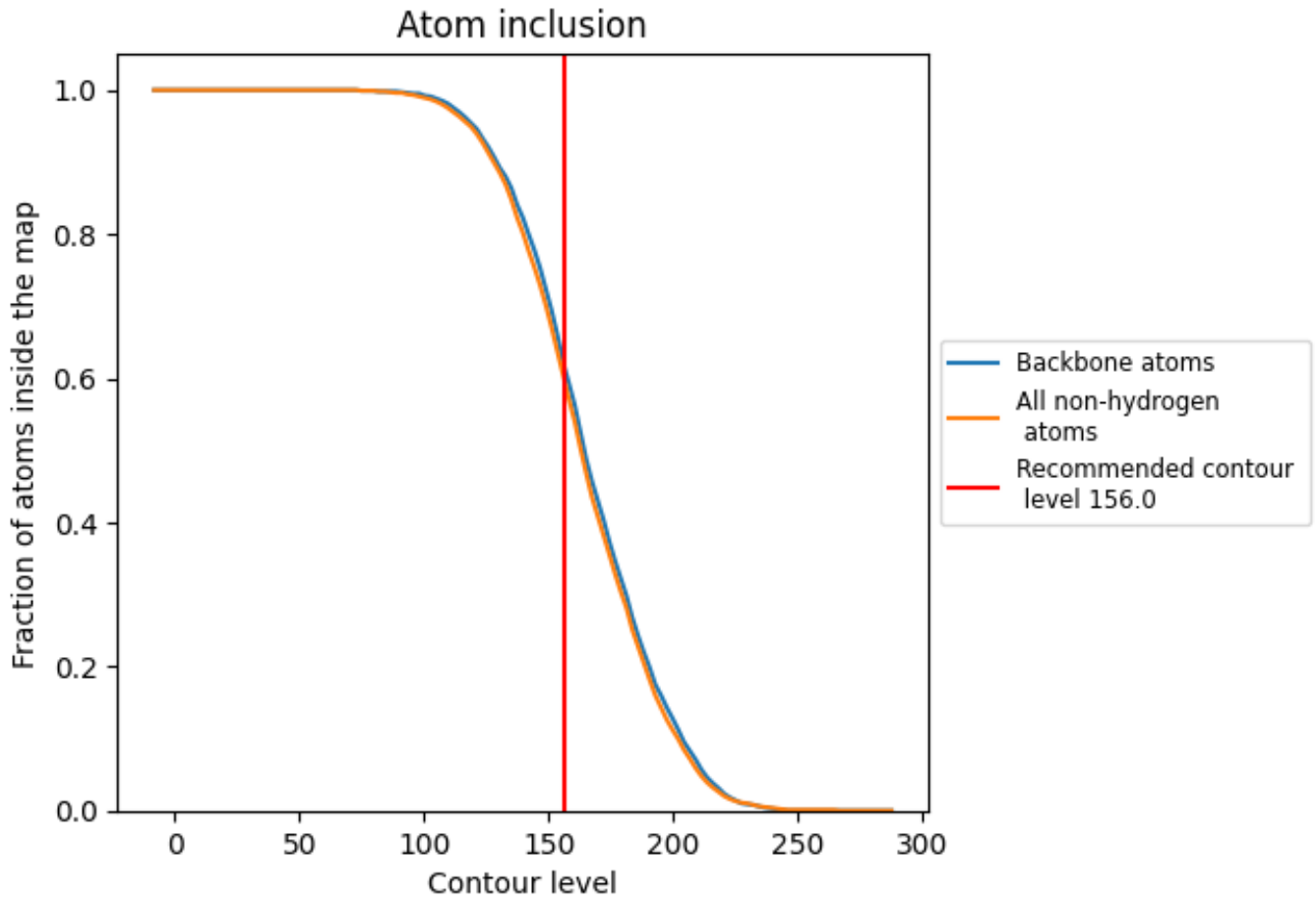
9.3 Atom inclusion mapped to coordinate model



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 (156.0).

9.4 Atom inclusion (i)



At the recommended contour level, 62% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (156.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6000	0.0380
A	0.5920	0.0340
B	0.6080	0.0420