



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:48 PM BST

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 PDB ID : 1JFF

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

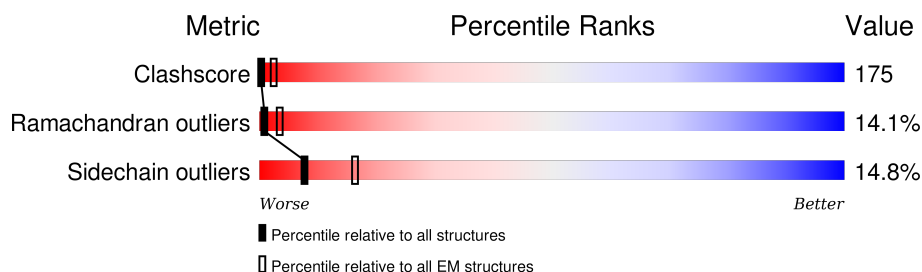
1 Overall quality at a glance

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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	451	
2	B	445	

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
1	A	409	Total	C	N	O	S	0	0
			3210	2034	548	608	20		

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

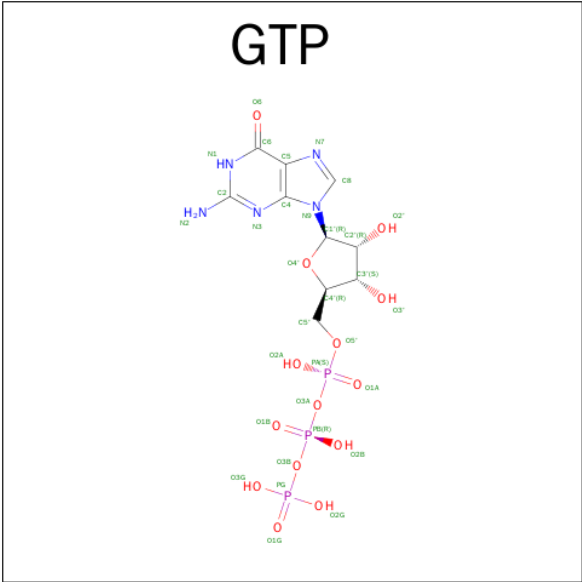
- Molecule 2 is a protein called Tubulin beta chain.

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

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

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

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

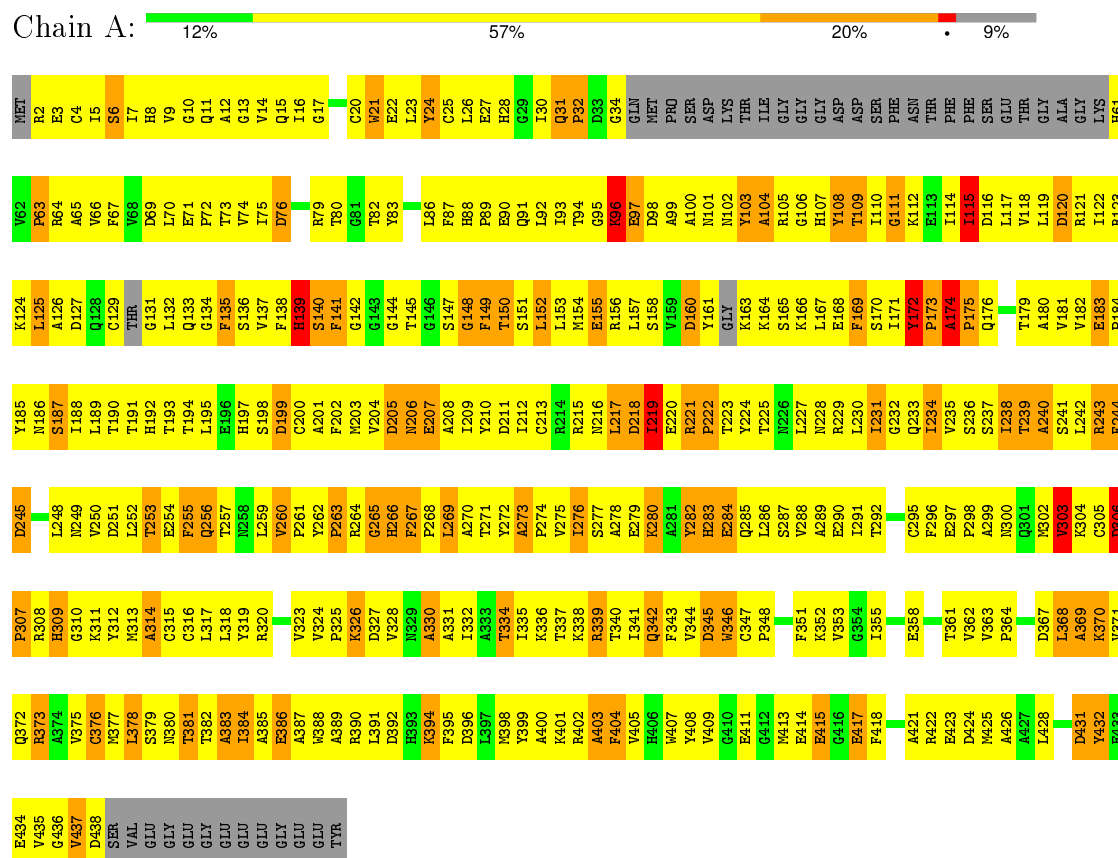


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
4	B	1	Total	C	N	O	P	0
			32	10	5	14	3	

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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



K389	V315	R253	V191
F395	V318	K284	H192
F396	F319	L285	Q193
A397	R320	A286	L194
M398	G321	V287	V195
F399	R322	M289	E196
R400	R323	V260	H197
R401	S324	P261	T198
K402	M325	F262	D199
A403	K326	P263	E200
F404	E327	R264	T201
	V328	L265	Y202
Y408	D329	H266	C203
T409	E330	F267	L204
G410	Q331	F268	D205
E411	M332	M269	N206
G412	L333	P270	E207
M413	M334	G271	A208
D414	V335	F272	L209
	Q336	A273	Y210
E417	N337	P274	D211
F418		L275	C213
T419	Y342	T276	L214
E420	R343	S277	R215
A421	V344	R278	T216
E422	E345	G279	L217
S423	M346	S280	K218
M424	L347	Q281	L219
M425	P348	Q282	
M426	N349	Y283	T223
P427	N350	R284	Y224
L428	V351	A285	G225
V429	K352	L286	D226
S430	T353	T287	L227
E431	A354	V288	N228
Y432	V355	H229	H229
Q433	C356	E290	L230
Q434	D357		V231
Y435	T358		S232
Q436	P359		A233
ASP	P360	Q294	M235
ALA	R369	F296	T234
THR	G370	D297	S236
ALA	L371	A298	G237
ASP		K299	V238
GLU	A375	N300	T239
GLN	T376	M301	T240
GLY	F377	M302	C241
GLU	L378	A303	L242
PHE	G379		R243
GLU	N380	D306	F244
GLU	S381	P307	F245
GLU	T382	R308	G246
GLY	A363	H309	Q247
GLU	L384	G310	L248
GLU	Q386	R311	N249
ASP	E386	Y312	A250
GLU	L387	L313	D251
ALA	F388	T314	L252

4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	320000	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Each Filament	Depositor
Microscope	JEM-2010F	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	40000	Depositor
Image detector	Kodak SO163 Film	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	$\# Z > 2$	RMSZ	$\# Z > 2$
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(°)	Ideal(°)
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(°)	Ideal(°)
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 ⓘ

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:184:PRO:HB3	1:A:394:LYS:CG	1.46	1.44
1:A:169:PHE:CZ	1:A:231:ILE:CG2	1.99	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:192:HIS:CG	2:B:424:ASN:ND2	1.84	1.40
2:B:154:ILE:CD1	2:B:197:ASN:CB	1.97	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:72:PRO:HG3	2:B:47:GLU:CG	1.51	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
2:B:169:PHE:CE2	2:B:235:MET:CB	2.09	1.35
1:A:12:ALA:HB2	4:A:502:GTP:N9	1.38	1.35
2:B:185:TYR:OH	2:B:399:PHE:CA	1.73	1.35
1:A:26:LEU:HD21	1:A:361:THR:CG2	1.54	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:261:PRO:CB	2:B:435:TYR:CD2	2.13	1.32
2:B:194:LEU:CD1	2:B:267:PHE:HZ	1.29	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:206:ASN:ND2	4:B:502:GTP:H1'	1.45	1.28
2:B:169:PHE:CD1	2:B:235:MET:CE	2.16	1.28
2:B:16:ILE:CG1	2:B:228:ASN:CB	2.12	1.28
2:B:346:TRP:CZ3	2:B:435:TYR:HA	1.67	1.27
1:A:12:ALA:HA	4:A:502:GTP:C5	1.68	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
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
1:A:108:TYR:HB3	1:A:411:GLU:O	1.17	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
2:B:185:TYR:CE1	2:B:399:PHE:CD1	1.83	1.25
1:A:9:VAL:CG1	1:A:139:HIS:HB3	1.65	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
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
1:A:184:PRO:HG2	1:A:398: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
2:B:346:TRP:CE3	2:B:435:TYR:O	1.94	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:188:THR:CA	2:B:425:MET:HE3	1.71	1.21
2:B:155:SER:OG	2:B:197:ASN:ND2	1.71	1.21
1:A:296:PHE:CE1	1:A:341:ILE:HD11	1.73	1.20
2:B:185:TYR:CD1	2:B:418:PHE:HD2	1.60	1.19
1:A:189:LEU:CD2	1:A:418:PHE:CE2	2.18	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:210:TYR:CE1	1:A:227:LEU:HD11	1.79	1.17
2:B:385:GLN:HB3	2:B:429:VAL:HG13	1.22	1.17
1:A:150:THR:O	1:A:197:HIS:CE1	1.95	1.17
1:A:392:ASP:CB	1:A:425:MET:HE3	1.73	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
2:B:104:ALA:HB3	2:B:413:MET:HB2	1.21	1.16
1:A:73:THR:HB	2:B:42:LEU:HD13	1.22	1.16
2:B:234:THR:HG21	2:B:270:PRO:HB2	1.23	1.16
1:A:181:VAL:CG2	2:B:352:LYS:HG3	1.74	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
2:B:385:GLN:CB	2:B:429:VAL:HG13	1.74	1.16

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:GLN:NE2	1:A:256:GLN:OE1	1.79	1.16
2:B:204:ILE:HA	2:B:302:MET:HB3	1.17	1.15
1:A:132:LEU:HG	1:A:164:LYS:HE3	1.26	1.15
1:A:166:LYS:HD2	1:A:197:HIS:O	1.42	1.15
2:B:395:PHE:CD2	2:B:422:GLU:OE1	1.99	1.15
1:A:180:ALA:N	2:B:248:LEU:HD11	1.61	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:262:PHE:HD2	2:B:432:TYR:HA	1.07	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: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
2:B:16:ILE:HA	2:B:228:ASN:HB3	1.15	1.14
1:A:195:LEU:HD22	1:A:424:ASP:C	1.53	1.14
1:A:173:PRO:O	1:A:206:ASN:CB	1.94	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
1:A:181:VAL:HG21	2:B:352:LYS:CG	1.78	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:141:PHE:HE2	1:A:391:LEU:CD2	1.63	1.12
1:A:23:LEU:CD2	1:A:236:SER:HB3	1.62	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:182:VAL:CG1	1:A:404:PHE:CZ	2.33	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:26:LEU:CD2	1:A:361:THR:CG2	2.29	1.10
1:A:141:PHE:CE2	1:A:391:LEU:CD2	2.33	1.10
1:A:402:ARG:O	1:A:405:VAL:HG13	1.51	1.10
1:A:104:ALA:CB	1:A:408:TYR:CA	2.29	1.10
2:B:104:ALA:HB3	2:B:413:MET:CB	1.81	1.10
1:A:101:ASN:HB2	2:B:254:LYS:HD3	1.16	1.10
1:A:26:LEU:HD21	1:A:361:THR:HG22	1.20	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
1:A:104:ALA:CB	1:A:408:TYR:HB3	1.81	1.10
2:B:262:PHE:HB3	2:B:431:GLU:CB	1.80	1.10
2:B:194:LEU:CA	2:B:265:LEU:HD23	1.79	1.10
1:A:189:LEU:HG	1:A:395:PHE:HE2	0.94	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
1:A:191:THR:HA	1:A:194:THR:CG2	1.81	1.10
1:A:12:ALA:CB	4:A:502:GTP:C4	2.35	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
2:B:169:PHE:CD2	2:B:235:MET:HB3	1.88	1.09
1:A:267:PHE:CD2	1:A:388:TRP:HZ2	1.69	1.09
2:B:192:HIS:CG	2:B:424:ASN:CG	2.07	1.08
1:A:108:TYR:CB	1:A:411:GLU:O	2.02	1.08
1:A:26:LEU:HD21	1:A:361:THR:HG21	1.34	1.08
2:B:395:PHE:CD2	2:B:422:GLU:CD	2.26	1.08
1:A:224:TYR:CD2	2:B:322:ARG:NH2	2.22	1.08
1:A:26:LEU:CD2	1:A:361:THR:HG21	1.82	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:185:TYR:HD1	2:B:418:PHE:CD2	1.71	1.07
2:B:169:PHE:CD1	2:B:235:MET:HE2	1.88	1.07
1:A:199:ASP:O	1:A:265:GLY:O	1.69	1.07
1:A:169:PHE:CZ	1:A:231:ILE:HG22	1.86	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:189:LEU:CG	1:A:395:PHE:HE2	1.68	1.06
1:A:135:PHE:CZ	1:A:157:LEU:HD22	1.91	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:266:HIS:CE1	2:B:428:LEU:CD1	2.38	1.06
2:B:195:VAL:HG11	2:B:264:ARG:NH1	1.70	1.06
2:B:182:VAL:HG11	2:B:408:TYR:CE1	1.91	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
2:B:195:VAL:HG21	2:B:264:ARG:CZ	1.86	1.05
1:A:105:ARG:N	1:A:411:GLU:OE1	1.88	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
2:B:172:VAL:O	2:B:205:ASP:HB2	1.55	1.04
2:B:266:HIS:CD2	2:B:428:LEU:HD11	1.92	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
1:A:192:HIS:CD2	1:A:193:THR:N	2.25	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:392:ASP:HB2	1:A:425:MET:CE	1.86	1.04
2:B:204:ILE:HA	2:B:302:MET:CB	1.87	1.04
2:B:105:LYS:CD	2:B:411:GLU:O	2.06	1.04
2:B:267:PHE:CD2	2:B:388:PHE:HZ	1.65	1.04
2:B:102:ASN:CB	2:B:408:TYR:HA	1.76	1.04
1:A:9:VAL:HG13	1:A:139:HIS:HB3	1.40	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
2:B:363:ALA:HB1	2:B:433:GLN:HA	1.11	1.04
1:A:181:VAL:HG21	2:B:258:ASN:HD22	1.23	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
2:B:185:TYR:HB3	2:B:418:PHE:CD2	1.94	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:192:HIS:ND1	2:B:424:ASN:ND2	2.04	1.03
1:A:191:THR:CA	1:A:194:THR:HG22	1.87	1.03
1:A:154:MET:HB3	1:A:197:HIS:O	1.57	1.03
2:B:299:LYS:H	2:B:299:LYS:HD3	1.24	1.03
1:A:161:TYR:HB2	1:A:164:LYS:HG3	1.35	1.03
1:A:23:LEU:HD23	1:A:236:SER:HB3	1.18	1.03
1:A:243:ARG:HH21	1:A:252:LEU:N	1.57	1.03
1:A:108:TYR:CE2	1:A:413:MET:CA	2.42	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:5:ILE:CD1	1:A:125:LEU:HB3	1.87	1.03
1:A:108:TYR:CE2	1:A:413:MET:HA	1.93	1.03
1:A:224:TYR:CD1	4:A:502:GTP:C5	2.47	1.03
2:B:192:HIS:CA	2:B:424:ASN:HD22	1.59	1.03
1:A:296:PHE:CE1	1:A:341:ILE:CD1	2.41	1.03
1:A:407:TRP:HE1	2:B:257:VAL:CG2	1.70	1.02
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
2:B:154:ILE:HD13	2:B:197:ASN:HB3	1.06	1.02
1:A:97:GLU:HB3	1:A:110:ILE:HD11	1.41	1.02
1:A:407:TRP:NE1	2:B:257:VAL:HG21	1.73	1.02
1:A:181:VAL:HG21	2:B:258:ASN:ND2	1.73	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:267:PHE:HD2	2:B:388:PHE:CE1	1.76	1.01
2:B:105:LYS:NZ	2:B:411:GLU:OE1	1.93	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
2:B:184:PRO:HB2	2:B:395:PHE:HB2	1.33	1.01
1:A:181:VAL:HG11	2:B:258:ASN:ND2	1.75	1.01
2:B:262:PHE:HB3	2:B:431:GLU:HB3	1.41	1.01
1:A:195:LEU:CD2	1:A:424:ASP:HB3	1.89	1.00
1:A:173:PRO:C	1:A:206:ASN:CB	2.28	1.00
1:A:200:CYS:HA	1:A:267:PHE:CD2	1.95	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:ASN:HB2	2:B:254:LYS:CD	1.91	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:9:VAL:HG12	1:A:139:HIS:HB3	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:101:ASN:ND2	2:B:143:GLY:HA2	1.76	1.00
2:B:2:ARG:HH21	2:B:48:ARG:NH2	1.58	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:346:TRP:HE3	2:B:435:TYR:C	1.65	0.98
2:B:184:PRO:HB2	2:B:395:PHE:HA	1.41	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:135:PHE:HE1	1:A:157:LEU:HD13	1.24	0.96
1:A:108:TYR:CZ	1:A:413:MET:HG3	1.98	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:142:GLY:O	1:A:172:TYR:CZ	2.19	0.96
1:A:12:ALA:CB	4:A:502:GTP:O4'	2.13	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:191:THR:O	1:A:194:THR:HG22	1.65	0.95
1:A:154:MET:CE	1:A:198:SER:HB2	1.96	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:192:HIS:HA	2:B:424:ASN:ND2	1.81	0.95
2:B:105:LYS:HD3	2:B:411:GLU:O	1.67	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:251:ASP:H	1:A:254:GLU:HG3	1.33	0.93
1:A:72:PRO:HG2	2:B:47:GLU:HG2	1.50	0.93
1:A:195:LEU:HD22	1:A:424:ASP:CB	1.99	0.93
1:A:171:ILE:HG23	1:A:205:ASP:HB3	1.48	0.93
2:B:264:ARG:O	2:B:265:LEU:HB3	1.64	0.93
2:B:262:PHE:CE1	2:B:434:GLN:CB	2.37	0.93
2:B:258:ASN:HD22	2:B:352:LYS:HG3	1.18	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: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:12:ALA:HB1	4:A:502:GTP:C4	2.02	0.92
2:B:267:PHE:CD2	2:B:388:PHE:CE1	2.53	0.92
1:A:237:SER:HB2	1:A:376:CYS:SG	2.08	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:147:SER:HB2	1:A:190:THR:OG1	1.68	0.92
1:A:104:ALA:HB1	1:A:408:TYR:HA	0.93	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: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
1:A:31:GLN:HB3	1:A:32:PRO:HD2	1.51	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: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:12:ALA:HA	4:A:502:GTP:C8	2.05	0.91
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
1:A:98:ASP:HB2	2:B:2:ARG:HD3	1.50	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:405:VAL:CA	1:A:408:TYR:HE2	1.83	0.90
1:A:346:TRP:CZ2	1:A:435:VAL:O	2.25	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: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:73:THR:CB	2:B:42:LEU:HD13	2.01	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: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
2:B:103:TRP:CZ3	2:B:417:GLU:OE2	2.25	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: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
2:B:8:GLN:OE1	2:B:67:LEU:HD22	1.73	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:194:LEU:HD13	2:B:267:PHE:HE1	1.40	0.86
2:B:188:THR:HA	2:B:425:MET:HE3	0.89	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:306:ASP:O	1:A:308:ARG:N	2.07	0.86
2:B:202:TYR:CZ	2:B:238:VAL:CG1	2.58	0.86
2:B:16:ILE:CG1	2:B:228:ASN:HB3	1.93	0.86
2:B:261:PRO:HD3	2:B:432:TYR:CE1	2.01	0.86
2:B:6:HIS:CE1	2:B:8:GLN:HG2	2.10	0.86
1:A:139:HIS:O	1:A:140:SER:OG	1.93	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:195:LEU:HD12	1:A:428:LEU:HD22	1.59	0.84
1:A:5:ILE:HD11	1:A:125:LEU:HB3	1.57	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
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:3:GLU:OE2	1:A:129:CYS:HB2	1.77	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:106:GLY:O	1:A:111:GLY:HA3	1.78	0.83
1:A:28:HIS:CD2	1:A:244:PHE:HB2	2.12	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:346:TRP:HB3	2:B:435:TYR:O	1.78	0.83
2:B:102:ASN:ND2	2:B:408:TYR:O	2.11	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:234:ILE:HG13	1:A:270:ALA:HB1	1.59	0.83
1:A:23:LEU:HD21	1:A:236:SER:HB3	1.60	0.83
1:A:316:CYS:HB3	1:A:378:LEU:CD1	2.08	0.83
1:A:12:ALA:CA	4:A:502:GTP:C5	2.59	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:148:GLY:O	2:B:151:THR:HG22	1.79	0.83
2:B:2:ARG:NE	2:B:48:ARG:HH22	1.75	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:189:LEU:O	1:A:193:THR:HG22	1.80	0.82
1:A:24:TYR:HD1	1:A:240:ALA:HB2	1.39	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
2:B:206:ASN:OD1	4:B:502:GTP:H1'	1.80	0.82
1:A:140:SER:HA	1:A:170:SER:CB	2.09	0.82
2:B:156:LYS:HE2	2:B:156:LYS:HA	1.61	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
2:B:169:PHE:CE1	2:B:235:MET:CB	2.33	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: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:110:GLU:O	2:B:113:GLU:HG2	1.79	0.81
2:B:20:PHE:CZ	2:B:24:ILE:HD12	2.15	0.81
2:B:310:GLY:CA	2:B:386:GLU:OE1	2.28	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:9:VAL:HG13	1:A:139:HIS:CB	2.10	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:135:PHE:HZ	1:A:157:LEU:HD22	1.44	0.80
1:A:27:GLU:OE2	1:A:240:ALA:CB	2.29	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)
2:B:189:LEU:HD21	2:B:417:GLU:O	1.81	0.80
2:B:2:ARG:NH2	2:B:48:ARG:NH2	2.29	0.80
1:A:224:TYR:HE2	2:B:322:ARG:HH22	1.24	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
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
1:A:248:LEU:HD23	1:A:353:VAL:O	1.81	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:HD13	1:A:234:ILE:O	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:101:ASN:O	2:B:408:TYR:CE2	2.35	0.79
2:B:16:ILE:CG1	2:B:228:ASN:OD1	2.26	0.79
1:A:109:THR:CG2	1:A:110:ILE:N	2.44	0.79
1:A:195:LEU:CD1	1:A:428:LEU:HD22	2.10	0.79
1:A:188:ILE:HD11	1:A:395:PHE:H	1.45	0.79
1:A:10:GLY:CA	4:A:502:GTP:O2B	2.29	0.79
1:A:151:SER:N	1:A:197:HIS:CE1	2.51	0.79
1:A:7:ILE:HG22	1:A:66:VAL:HG22	1.63	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
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
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: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
1:A:184:PRO:CB	1:A:394:LYS:CB	2.57	0.79
2:B:54:ASN:HD21	2:B:64:ARG:HD3	1.45	0.79
1:A:188:ILE:CD1	1:A:395:PHE:H	1.96	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:PRO:CG	1:A:398:MET:SD	2.68	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: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:180:ALA:H	2:B:248:LEU:HD11	1.48	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:CD1	1:A:267:PHE:N	2.49	0.78
2:B:234:THR:CG2	2:B:270:PRO:HB2	2.11	0.78
2:B:203:CYS:HB3	2:B:268:PHE:O	1.84	0.78
2:B:185:TYR:CE2	2:B:398:MET:HG3	2.19	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
1:A:25:CYS:HG	1:A:83:TYR:HE2	1.30	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
2:B:12:CYS:HB2	4:B:502:GTP:C5	2.19	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
2:B:185:TYR:CE1	2:B:399:PHE:CG	2.71	0.76
1:A:224:TYR:HD2	2:B:322:ARG:HH21	1.32	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
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:362:VAL:HG13	1:A:368:LEU:HD12	1.68	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:250:ALA:HA	2:B:254:LYS:HE2	1.68	0.75
2:B:182:VAL:HG13	2:B:404:PHE:HB2	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
4:A:502:GTP:O1A	2:B:245:PRO:CB	2.24	0.75
1:A:98:ASP:HB3	1:A:105:ARG:NH2	2.01	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:381:THR:OG1	1:A:383:ALA:HB3	1.87	0.75
1:A:11:GLN:HB2	4:A:502:GTP:O2A	1.84	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
1:A:317:LEU:HB3	1:A:319:TYR:HE1	1.52	0.75
1:A:286:LEU:HG	1:A:290:GLU:CB	2.16	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:110:ILE:HG23	1:A:111:GLY:N	1.99	0.74
1:A:5:ILE:CG2	1:A:125:LEU:HD13	2.16	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
2:B:168:THR:HB	2:B:201:THR:HG23	1.68	0.74
1:A:276:ILE:HG23	1:A:369:ALA:CB	2.16	0.74
1:A:189:LEU:CD1	1:A:418:PHE:HE2	2.00	0.74
2:B:209:LEU:HG	2:B:230:LEU:HD22	1.69	0.74
2:B:202:TYR:HE2	2:B:378:ILE:HD13	1.52	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:182:VAL:CG1	1:A:404:PHE:CD1	2.70	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
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: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:139:HIS:CG	1:A:140:SER:H	2.07	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:31:GLN:HB3	1:A:32:PRO:CD	2.18	0.73
1:A:108:TYR:CE1	1:A:413:MET:HB2	2.23	0.73
1:A:69:ASP:O	1:A:94:THR:CA	2.35	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
2:B:262:PHE:CZ	2:B:434:GLN:CA	2.72	0.73
1:A:181:VAL:HG11	2:B:258:ASN:HD21	1.50	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:313:LEU:HD13	2:B:432:TYR:CD1	2.23	0.72
2:B:111:GLY:O	2:B:115:VAL:HG23	1.89	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: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:69:ASP:O	1:A:94:THR:HA	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:171:VAL:HG13	2:B:205:ASP:CA	2.20	0.72
2:B:76:ASP:HA	2:B:79:ARG:HG2	1.71	0.72
2:B:42:LEU:HA	2:B:47:GLU:OE1	1.90	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:181:VAL:CG2	2:B:258:ASN:ND2	2.51	0.71
2:B:346:TRP:HB3	2:B:436:GLN:C	2.11	0.71
1:A:7:ILE:HD11	1:A:137:VAL:HG22	1.71	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:202:TYR:CE2	2:B:238:VAL:CG1	2.74	0.71
2:B:194:LEU:HD12	2:B:267:PHE:HZ	0.55	0.71
1:A:264:ARG:C	1:A:266:HIS:H	1.91	0.71
1:A:181:VAL:CG1	2:B:258:ASN:ND2	2.53	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:259:LEU:HD11	1:A:378:LEU:CD1	2.20	0.70
1:A:188:ILE:CD1	1:A:392:ASP:C	2.52	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:192:HIS:O	2:B:424:ASN:ND2	2.08	0.70
2:B:167:ASN:HD21	2:B:252:LEU:HD22	1.55	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:7:ILE:CG1	1:A:137:VAL:HG22	2.20	0.70
1:A:123:ARG:CA	1:A:161:TYR:OH	2.35	0.70
1:A:266:HIS:CD2	1:A:432:TYR:CE1	2.79	0.70
1:A:184:PRO:CB	1:A:394:LYS:CG	2.37	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
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:296:PHE:CZ	1:A:335:ILE:HG21	2.26	0.70
1:A:151:SER:HB3	1:A:193:THR:HG21	1.72	0.70
1:A:12:ALA:CA	4:A:502:GTP:N9	2.55	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: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
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
2:B:171:VAL:HG12	2:B:206:ASN:N	2.07	0.70
1:A:343:PHE:CZ	1:A:351:PHE:HE2	2.08	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:405:VAL:HA	1:A:408:TYR:CD2	2.26	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:5:ILE:HG22	1:A:6:SER:N	2.07	0.69
2:B:189:LEU:HD13	2:B:417:GLU:HG2	1.74	0.69
2:B:24:ILE:HD11	2:B:52:TYR:CE2	2.28	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: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
2:B:262:PHE:CB	2:B:431:GLU:HB3	2.19	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: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
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
1:A:371:VAL:HG12	1:A:372:GLN:H	1.57	0.69
1:A:88:HIS:C	1:A:90:GLU:H	1.95	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
2:B:395:PHE:HD2	2:B:422:GLU:OE1	1.61	0.69
1:A:282:TYR:O	1:A:284:GLU:N	2.24	0.69
1:A:103:TYR:CE2	1:A:413:MET:HE2	2.26	0.68
1:A:63:PRO:C	1:A:64:ARG:HG2	2.12	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:217:LEU:HD12	1:A:277:SER:HB3	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:408:TYR:CE1	1:A:409:VAL:HG22	2.28	0.68
1:A:72:PRO:HG3	2:B:47:GLU:HB3	1.73	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:402:ARG:HB3	1:A:405:VAL:CG2	2.23	0.68
1:A:262:TYR:CD2	1:A:435:VAL:CG2	2.76	0.68
2:B:194:LEU:C	2:B:265:LEU:CD2	2.62	0.68
2:B:195:VAL:HB	2:B:264:ARG:HA	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:262:PHE:CE1	2:B:435:TYR:CZ	2.81	0.68
2:B:182:VAL:CB	2:B:408:TYR:CE1	2.63	0.68
2:B:103:TRP:CE3	2:B:417:GLU:CD	2.67	0.68
2:B:4:ILE:HG21	2:B:136:GLN:HG2	1.76	0.68
1:A:343:PHE:HZ	1:A:351:PHE:CE2	2.10	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: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:195:VAL:CG2	2:B:264:ARG:CA	2.61	0.67
2:B:194:LEU:C	2:B:265:LEU:HB3	2.14	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:O	2:B:346:TRP:CD2	2.47	0.67
2:B:385:GLN:CA	2:B:429:VAL:HG13	2.24	0.67
2:B:359:PRO:HB2	2:B:360:PRO:HD2	1.74	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:257:VAL:O	2:B:257:VAL:HG12	1.93	0.67
2:B:195:VAL:CG1	2:B:264:ARG:HH11	2.06	0.67
2:B:2:ARG:NH2	2:B:48:ARG:HH21	1.90	0.67
1:A:174:ALA:HB2	1:A:207:GLU:HB3	1.75	0.67
1:A:154:MET:N	1:A:197:HIS:NE2	2.24	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)
2:B:265:LEU:HD12	2:B:265:LEU:C	2.16	0.67
1:A:341:ILE:HG12	1:A:341:ILE:O	1.95	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:191:THR:O	1:A:194:THR:CG2	2.41	0.66
1:A:93:ILE:HG22	1:A:94:THR:N	2.09	0.66
1:A:103:TYR:HE2	1:A:413:MET:HE2	1.60	0.66
2:B:266:HIS:NE2	2:B:428:LEU:HD12	2.08	0.66
2:B:189:LEU:HD22	2:B:417:GLU:O	1.95	0.66
2:B:194:LEU:CG	2:B:265:LEU:HD21	2.24	0.66
2:B:104:ALA:HB1	2:B:413:MET:HA	1.78	0.66
2:B:44:LEU:HD12	2:B:49:ILE:HD13	1.76	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:413:MET:CE	2:B:418:PHE:CD1	2.71	0.66
2:B:325:MET:HA	2:B:325:MET:HE3	1.76	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:195:VAL:HB	2:B:264:ARG:O	1.95	0.66
2:B:184:PRO:CB	2:B:395:PHE:HB2	2.17	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: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:150:THR:CB	1:A:197:HIS:CE1	2.77	0.66
1:A:16:ILE:HA	1:A:228:ASN:HB2	1.77	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
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:276:ILE:O	1:A:369:ALA:HB2	1.95	0.65
1:A:142:GLY:CA	1:A:172:TYR:CE2	2.79	0.65
2:B:313:LEU:HD12	2:B:432:TYR:CE1	2.30	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
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:185:TYR:CB	2:B:418:PHE:HE2	2.09	0.65
2:B:35:SER:HB3	2:B:59:ASN:CA	2.26	0.65
1:A:225:THR:O	1:A:229:ARG:HG3	1.97	0.65
1:A:69:ASP:O	1:A:94:THR:C	2.35	0.65
2:B:224:TYR:HB3	4:B:502:GTP:O6	1.96	0.65
1:A:217:LEU:HD11	1:A:367:ASP:O	1.97	0.65
1:A:313:MET:HB3	1:A:344:VAL:CG2	2.26	0.65
2:B:266:HIS:CE1	2:B:428:LEU:HD12	2.32	0.65
1:A:372:GLN:O	1:A:373:ARG:HB3	1.96	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:188:THR:O	2:B:425:MET:HB2	1.97	0.65
2:B:16:ILE:CG1	2:B:228:ASN:CG	2.37	0.65
2:B:281:GLN:O	2:B:283:TYR:HB2	1.96	0.65
1:A:154:MET:HB3	1:A:197:HIS:CA	2.27	0.65
1:A:132:LEU:CG	1:A:164:LYS:CE	2.72	0.65
1:A:109:THR:CB	1:A:411:GLU:HG2	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:225:THR:HA	1:A:228:ASN:HD21	1.59	0.64
1:A:27:GLU:OE2	1:A:240:ALA:HB3	1.97	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: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
1:A:23:LEU:HD21	1:A:236:SER:CB	2.11	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: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
1:A:95:GLY:O	1:A:96:LYS:HB3	1.97	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:O	2:B:282:GLN:HG2	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:305:CYS:SG	1:A:383:ALA:C	2.77	0.63
1:A:269:LEU:O	1:A:378:LEU:HA	1.98	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
1:A:220:GLU:C	1:A:222:PRO:HD3	2.19	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: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:24:TYR:OH	1:A:239:THR:HB	1.99	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
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: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
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
2:B:189:LEU:HD11	2:B:418:PHE:CA	2.27	0.63
1:A:275:VAL:HG21	1:A:300:ASN:OD1	1.97	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
1:A:189:LEU:CD2	1:A:395:PHE:CZ	2.81	0.63
1:A:421:ALA:HA	1:A:424:ASP:OD2	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:ASP:OD1	4:A:502:GTP:PG	2.57	0.63
2:B:241:CYS:O	2:B:244:PHE:HB2	1.98	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
1:A:7:ILE:CD1	1:A:137:VAL:HG22	2.29	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:315:VAL:HG13	2:B:377:PHE:CE1	2.34	0.62
2:B:299:LYS:O	2:B:300:ASN:HB2	1.97	0.62
1:A:97:GLU:CB	1:A:110:ILE:HD11	2.23	0.62
1:A:203:MET:O	1:A:206:ASN:ND2	2.31	0.62
1:A:169:PHE:HZ	1:A:231:ILE:CG2	1.93	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
1:A:296:PHE:CE1	1:A:341:ILE:HD12	2.32	0.62
1:A:271:THR:HG23	1:A:300:ASN:O	1.99	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:194:LEU:O	2:B:265:LEU:HD22	2.00	0.62
2:B:171:VAL:C	2:B:205:ASP:HA	2.20	0.62
2:B:115:VAL:HG21	2:B:152:LEU:CD2	2.30	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:HD3	1:A:221:ARG:O	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
2:B:114:LEU:HD23	2:B:149:MET:CE	2.30	0.61
2:B:4:ILE:HG23	2:B:134:GLY:O	2.00	0.61
2:B:185:TYR:CD1	2:B:395:PHE:CE1	2.87	0.61
1:A:273:ALA:HB3	1:A:274:PRO:HD3	1.81	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
2:B:363:ALA:HB2	2:B:436:GLN:HB2	1.81	0.61
1:A:317:LEU:HB3	1:A:319:TYR:CE1	2.33	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:97:GLU:HB3	1:A:110:ILE:CD1	2.26	0.61
2:B:102:ASN:ND2	2:B:413:MET:SD	2.74	0.61
1:A:7:ILE:HG22	1:A:66:VAL:CG2	2.28	0.61
1:A:273:ALA:HB2	1:A:295:CYS:SG	2.41	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
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
2:B:12:CYS:SG	4:B:502:GTP:C2	2.94	0.61
1:A:220:GLU:OE1	1:A:220:GLU:HA	2.01	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
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:362:VAL:HG13	1:A:368:LEU:HB2	1.83	0.61
1:A:205:ASP:OD2	1:A:231:ILE:HD11	2.01	0.60
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
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
1:A:88:HIS:O	1:A:90:GLU:N	2.33	0.60
2:B:204:ILE:HG13	2:B:270:PRO:HG3	1.83	0.60
2:B:185:TYR:CG	2:B:418:PHE:CE2	2.89	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: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: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:158:SER:OG	1:A:166:LYS:NZ	2.33	0.60
1:A:154:MET:CB	1:A:166:LYS:HD2	2.29	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:167:LEU:HG	1:A:200:CYS:HB3	1.82	0.60
1:A:108:TYR:CD2	1:A:413:MET:HB2	2.37	0.60
2:B:202:TYR:OH	2:B:238:VAL:CG1	2.50	0.60
2:B:172:VAL:HG21	2:B:203:CYS:SG	2.42	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
2:B:285:ALA:HB1	2:B:290:GLU:HG2	1.83	0.60
2:B:279:GLY:O	2:B:282:GLN:HB3	2.01	0.60
1:A:435:VAL:HG12	1:A:435:VAL:O	2.02	0.59
2:B:102:ASN:CB	2:B:408:TYR:CD2	2.85	0.59
1:A:115:ILE:HD13	1:A:115:ILE:O	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: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:HB	1:A:408:TYR:CZ	2.38	0.59
1:A:405:VAL:HA	1:A:408:TYR:HE2	1.43	0.59
2:B:102:ASN:HB3	2:B:105:LYS:HB2	1.84	0.59
2:B:49:ILE:O	2:B:51:VAL:N	2.35	0.59
1:A:179:THR:C	2:B:248:LEU:HD22	2.23	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:192:HIS:HD2	2:B:424:ASN:H	1.47	0.59
2:B:54:ASN:ND2	2:B:64:ARG:HD3	2.15	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:142:GLY:HA3	1:A:172:TYR:CE2	2.38	0.59
1:A:199:ASP:OD1	1:A:199:ASP:N	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
1:A:98:ASP:CG	2:B:2:ARG:NH1	2.55	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
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
1:A:278:ALA:HB2	1:A:369:ALA:HA	1.85	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: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
2:B:204:ILE:HG13	2:B:270:PRO:CG	2.31	0.59
2:B:30:ILE:HD13	2:B:53:TYR:CE2	2.38	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:C	2.22	0.58
1:A:173:PRO:HB2	1:A:174:ALA:CB	2.33	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:371:VAL:HG12	1:A:372:GLN:N	2.17	0.58
1:A:315:CYS:HB3	1:A:377:MET:HE2	1.86	0.58
1:A:172:TYR:CD2	1:A:173:PRO:HD2	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:317:LEU:HD11	1:A:351:PHE:CE1	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: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
1:A:63:PRO:HD3	1:A:86:LEU:O	2.04	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
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:369:ALA:O	1:A:370:LYS:HB3	2.03	0.58
1:A:88:HIS:C	1:A:90:GLU:N	2.57	0.58
1:A:6:SER:HA	1:A:136:SER:O	2.02	0.58
2:B:313:LEU:CD1	2:B:432:TYR:CG	2.86	0.58
2:B:184:PRO:HG3	2:B:395:PHE:HA	1.83	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
1:A:12:ALA:N	4:A:502:GTP:C8	2.71	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:179:THR:C	2:B:248:LEU:CD2	2.72	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: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
2:B:30:ILE:HA	2:B:35:SER:O	2.04	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:270:PRO:HA	2:B:377:PHE:O	2.03	0.57
2:B:185:TYR:HA	2:B:395:PHE:CD1	2.37	0.57
2:B:41:ASP:O	2:B:47:GLU:OE2	2.22	0.57
2:B:301:MET:CE	2:B:377:PHE:HE2	2.17	0.57
2:B:401:ARG:HG3	2:B:401:ARG:O	2.04	0.57
1:A:180:ALA:N	2:B:248:LEU:HD13	2.05	0.57
2:B:319:PHE:HA	2:B:375:ALA:HA	1.86	0.57
1:A:220:GLU:O	1:A:222:PRO:HD2	2.04	0.57
2:B:349:ASN:C	2:B:349:ASN:HD22	2.07	0.57
2:B:267:PHE:HB2	2:B:388:PHE:CZ	2.39	0.57
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:PRO:HA	1:A:379:SER: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:139:HIS:C	1:A:140:SER:HG	2.01	0.57
1:A:362:VAL:HG11	1:A:368:LEU:O	2.04	0.57
1:A:145:THR:O	1:A:145:THR:HG22	2.03	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
2:B:320:ARG:O	2:B:359:PRO:HA	2.04	0.57
1:A:218:ASP:O	1:A:219:ILE:HG23	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: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
1:A:70:LEU:HD23	1:A:94:THR:O	2.05	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: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
1:A:179:THR:C	2:B:248:LEU:CD1	2.73	0.57
2:B:274:PRO:CG	2:B:371:LEU:HD21	2.34	0.57
2:B:149:MET:O	2:B:153:LEU:HD13	2.04	0.56
2:B:19:LYS:HG3	2:B:225:GLY:O	2.05	0.56
2:B:189:LEU:HD22	2:B:421:ALA:CB	2.10	0.56
1:A:283:HIS:CE1	1:A:286:LEU:CD1	2.87	0.56
1:A:224:TYR:HD1	4:A:502:GTP:C5	2.08	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:362:VAL:CG1	1:A:368:LEU:HB2	2.35	0.56
1:A:395:PHE:CZ	1:A:418:PHE:HD2	2.18	0.56
2:B:105:LYS:O	2:B:110:GLU:HB2	2.06	0.56
1:A:388:TRP:HA	1:A:388:TRP:CE3	2.41	0.56
1:A:71:GLU:CB	4:A:502:GTP:O1G	2.52	0.56
2:B:5:VAL:CG2	2:B:135:PHE:HD2	2.18	0.56
2:B:346:TRP:O	2:B:346:TRP:CG	2.58	0.56
2:B:313:LEU:HD11	2:B:363:ALA:HA	1.87	0.56
1:A:331:ALA:O	1:A:334:THR:HG22	2.05	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: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: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:6:HIS:HB3	2:B:65:ALA:HB2	1.86	0.56
2:B:283:TYR:C	2:B:284:ARG:HG2	2.25	0.56
1:A:163:LYS:O	1:A:163:LYS:HG2	2.04	0.56
1:A:154:MET:SD	1:A:197:HIS:CG	2.99	0.56
2:B:165:ILE:H	2:B:165:ILE:HD13	1.71	0.56
2:B:206:ASN:HD22	4:B:502:GTP:C2'	2.12	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
2:B:206:ASN:CB	4:B:502:GTP:O2'	2.54	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
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:436:GLY:C	1:A:438:ASP:H	2.08	0.56
1:A:192:HIS:CD2	1:A:193:THR:HB	2.41	0.56
1:A:26:LEU:CD2	1:A:361:THR:HG22	2.09	0.56
1:A:224:TYR:HE1	4:A:502:GTP:N7	2.01	0.56
1:A:73:THR:CB	2:B:42:LEU:CD1	2.79	0.56
1:A:11:GLN:CG	1:A:74:VAL:HG11	2.28	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
2:B:31:ASP:O	2:B:32:PRO:C	2.44	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:205:ASP:CB	2:B:302:MET:O	2.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:261:PRO:CA	2:B:435:TYR:CE2	2.89	0.55
2:B:67:LEU:HD23	2:B:67:LEU:N	2.22	0.55
2:B:258:ASN:HD22	2:B:352:LYS:HZ2	1.52	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:382:THR:HG21	1:A:437:VAL:HG23	1.87	0.55
2:B:324:SER:C	2:B:326:LYS:N	2.59	0.55
1:A:216:ASN:O	1:A:217:LEU:HB2	2.05	0.55
2:B:119:LEU:O	2:B:123:ARG:HG3	2.06	0.55
1:A:141:PHE:CE2	1:A:391:LEU:HD22	2.39	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: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
2:B:12:CYS:HA	4:B:502:GTP:C6	2.42	0.55
1:A:181:VAL:CG2	2:B:352:LYS:CG	2.60	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: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:205:ASP:O	2:B:209:LEU:HD13	2.06	0.55
2:B:169:PHE:HD1	2:B:235:MET:HE3	1.52	0.55
2:B:313:LEU:HD21	2:B:363:ALA:CB	2.37	0.55
1:A:175:PRO:HD2	1:A:176:GLN:H	1.71	0.55
1:A:408:TYR:O	1:A:411:GLU:N	2.39	0.55
1:A:5:ILE:CD1	1:A:125:LEU:CB	2.74	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:205:ASP:H	2:B:209:LEU:HD13	1.71	0.55
2:B:195:VAL:HG11	2:B:424:ASN:OD1	2.07	0.55
2:B:385:GLN:CB	2:B:429:VAL:HG22	2.36	0.55
2:B:346:TRP:CD2	2:B:435:TYR:O	2.57	0.55
1:A:402:ARG:O	1:A:405:VAL:HG22	2.06	0.55
1:A:6:SER:O	1:A:65:ALA:HB1	2.07	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:161:TYR:HB3	1:A:164:LYS:HG3	1.83	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:LEU:HD12	1:A:166:LYS:HG2	1.88	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:150:THR:CA	1:A:197:HIS:CE1	2.89	0.54
1:A:139:HIS:CG	1:A:140:SER:N	2.74	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:154:MET:HE3	1:A:197:HIS:CG	2.34	0.54
1:A:150:THR:HG22	1:A:197:HIS:NE2	2.23	0.54
2:B:227:LEU:CB	4:B:502:GTP:N2	2.70	0.54
2:B:44:LEU:O	2:B:49:ILE:HG12	2.07	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
2:B:20:PHE:CE1	2:B:24:ILE:HD12	2.42	0.54
2:B:258:ASN:ND2	2:B:352:LYS:HB2	2.23	0.54
2:B:126:SER:CB	2:B:132:LEU:HD22	2.38	0.54
1:A:175:PRO:CD	1:A:176:GLN:H	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:250:ALA:CA	2:B:254:LYS:HE2	2.35	0.54
2:B:2:ARG:NE	2:B:48:ARG:NH2	2.53	0.54
2:B:343:PHE:O	2:B:344:VAL:O	2.26	0.54
2:B:4:ILE:CG2	2:B:136:GLN:HG2	2.38	0.54
2:B:331:GLN:O	2:B:335:VAL:HG23	2.08	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
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
2:B:132:LEU:CD2	2:B:164:ARG:HG3	2.32	0.53
1:A:282:TYR:O	1:A:284:GLU:HG3	2.09	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: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
2:B:36:TYR:CZ	2:B:38:GLY:HA3	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:262:PHE:CZ	2:B:435:TYR:CD1	2.96	0.53
2:B:259:MET:CG	2:B:314:THR:HG21	2.36	0.53
1:A:173:PRO:CA	1:A:174:ALA:CB	2.85	0.53
1:A:172:TYR:CG	1:A:173:PRO:HD3	2.43	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:O	2:B:5:VAL:HG23	2.09	0.53
1:A:231:ILE:CA	1:A:234:ILE:HG22	2.38	0.53
1:A:5:ILE:O	1:A:136:SER:N	2.40	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:ND1	2:B:229:HIS:C	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
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:291:ILE:HD12	1:A:375:VAL:HG23	1.89	0.52
2:B:322:ARG:HG3	2:B:322:ARG:HH11	1.74	0.52
1:A:73:THR:HG21	2:B:42:LEU:HB2	1.90	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:213:CYS:SG	2:B:219:LEU:HD23	2.48	0.52
2:B:169:PHE:CD1	2:B:235:MET:CB	2.92	0.52
2:B:259:MET:CA	2:B:314:THR:HG21	2.35	0.52
2:B:27:GLU:HG2	2:B:27:GLU:O	2.08	0.52
1:A:172:TYR:CD2	1:A:173:PRO:HD3	2.44	0.52
1:A:4:CYS:HB2	1:A:252:LEU:HD13	1.91	0.52
1:A:115:ILE:C	1:A:115:ILE:HD13	2.28	0.52
1:A:8:HIS:HB3	1:A:13:GLY:O	2.10	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: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
1:A:4:CYS:HA	1:A:134:GLY:O	2.10	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:O	2:B:346:TRP:CE3	2.63	0.52
2:B:49:ILE:O	2:B:50:ASN:C	2.48	0.52
2:B:21:TRP:CZ2	2:B:65:ALA:HB2	2.44	0.52
1:A:119:LEU:HD11	1:A:156:ARG:CD	2.40	0.52
1:A:109:THR:CB	1:A:411:GLU:CG	2.87	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:344:VAL:HG12	1:A:345:ASP:H	1.74	0.52
1:A:184:PRO:CD	1:A:394:LYS:HG2	2.39	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:215:ARG:C	1:A:216:ASN:HD22	2.12	0.52
2:B:149:MET:O	2:B:153:LEU:HD22	2.10	0.52
2:B:16:ILE:N	2:B:228:ASN:HB3	2.20	0.52
2:B:384:ILE:O	2:B:386:GLU:HG2	2.09	0.52
2:B:188:THR:CB	2:B:425:MET:HE3	2.35	0.52
1:A:283:HIS:ND1	1:A:286:LEU:HD13	2.24	0.52
1:A:191:THR:CG2	1:A:192:HIS:N	2.73	0.51
1:A:174:ALA:CB	1:A:207:GLU:HB2	2.31	0.51
1:A:244:PHE:C	1:A:244:PHE:CD1	2.83	0.51
1:A:109:THR:HG1	1:A:411:GLU:HG2	1.67	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:384:ILE:HG13	2:B:384:ILE:O	2.11	0.51
2:B:277:SER:OG	2:B:281:GLN:HB2	2.10	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
1:A:23:LEU:CG	1:A:236:SER:OG	2.58	0.51
2:B:251:ASP:O	2:B:252:LEU:C	2.49	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
2:B:258:ASN:CG	2:B:352:LYS:HD2	2.31	0.51
1:A:231:ILE:HD13	1:A:231:ILE:N	2.24	0.51
1:A:24:TYR:HE1	1:A:236:SER:HA	1.75	0.51
2:B:205:ASP:CG	2:B:208:ALA:CB	2.72	0.51
2:B:21:TRP:HZ2	2:B:65:ALA:HB2	1.76	0.51
2:B:16:ILE:N	2:B:228:ASN:ND2	2.59	0.51
1:A:220:GLU:C	1:A:222:PRO:CD	2.79	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:HG23	2:B:260:VAL:O	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:150:THR:CA	1:A:197:HIS:HE1	2.23	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
1:A:191:THR:HG21	1:A:425:MET:SD	2.51	0.51
1:A:93:ILE:CG2	1:A:94:THR:N	2.73	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: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
1:A:69:ASP:O	1:A:94:THR:O	2.29	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:205:ASP:HA	1:A:209:ILE:HD12	1.92	0.50
1:A:93:ILE:HG22	1:A:94:THR:H	1.76	0.50
2:B:226:ASP:O	2:B:227:LEU:C	2.46	0.50
2:B:185:TYR:CA	2:B:395:PHE:CE1	2.86	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: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:3:GLU:HA	2:B:51:VAL:HA	1.93	0.50
2:B:385:GLN:HB2	2:B:429:VAL:HG13	1.84	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: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:320:ARG:HA	2:B:356:CYS:HB3	1.92	0.50
2:B:280:SER:O	2:B:282:GLN:N	2.45	0.50
1:A:328:VAL:C	1:A:330:ALA:H	2.15	0.50
1:A:67:PHE:HE2	1:A:87:PHE:CE2	2.29	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:HG2	2:B:149:MET:O	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:149:PHE:HE1	1:A:153:LEU:HD22	1.77	0.50
1:A:11:GLN:O	1:A:14:VAL:HB	2.12	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:296:PHE:CZ	2:B:315:VAL:HG11	2.46	0.50
2:B:4:ILE:HG22	2:B:5:VAL:N	2.27	0.50
1:A:413:MET:HG2	1:A:414:GLU:N	2.24	0.50
1:A:70:LEU:CD2	1:A:95:GLY:HA3	2.40	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:305:CYS:O	1:A:306:ASP:C	2.51	0.49
1:A:184:PRO:HD3	1:A:394:LYS:HD3	1.94	0.49
2:B:19:LYS:HB2	2:B:229:HIS:HA	1.92	0.49
2:B:171:VAL:CG1	2:B:206:ASN:N	2.75	0.49
2:B:20:PHE:HB2	2:B:232:SER:HB3	1.94	0.49
2:B:399:PHE:O	2:B:402:LYS:N	2.29	0.49
2:B:266:HIS:HA	2:B:428:LEU:HD21	1.93	0.49
2:B:369:ARG:C	2:B:369:ARG:HD2	2.32	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:OE1	1:A:414:GLU:N	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: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:24:TYR:CZ	1:A:239:THR:HB	2.48	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:104:ALA:HB3	2:B:413:MET:HB3	1.83	0.49
2:B:103:TRP:HD1	2:B:147:SER:OG	1.96	0.49
2:B:167:ASN:HA	2:B:200:GLU:HB3	1.95	0.49
2:B:24:ILE:HG22	2:B:25:SER:N	2.27	0.49
2:B:230:LEU:HD21	2:B:302:MET:HE2	1.94	0.49
2:B:189:LEU:HD21	2:B:418:PHE:C	2.33	0.49
1:A:118:VAL:HG21	1:A:149:PHE:CE2	2.48	0.49
1:A:15:GLN:CG	4:A:502:GTP:N7	2.76	0.49
1:A:398:MET:HE3	1:A:404:PHE:CE1	2.48	0.49
1:A:266:HIS:ND1	1:A:432:TYR:HE1	2.10	0.49
2:B:385:GLN:H	2:B:429:VAL:HG13	1.75	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
1:A:26:LEU:CD1	1:A:361:THR:HG21	2.42	0.49
2:B:385:GLN:HB2	2:B:429:VAL:HA	1.95	0.49
1:A:105:ARG:HG3	1:A:105:ARG:HH11	1.78	0.49
1:A:195:LEU:CD1	1:A:425:MET:HA	2.43	0.49
1:A:73:THR:OG1	2:B:42:LEU:HA	2.13	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:142:GLY:HA3	2:B:183:GLU:OE2	2.13	0.48
2:B:16:ILE:N	2:B:228:ASN:CG	2.66	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:242:LEU:C	1:A:244:PHE:N	2.66	0.48
1:A:189:LEU:CG	1:A:418:PHE:CE2	2.93	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
2:B:49:ILE:HG13	2:B:50:ASN:H	1.76	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
2:B:299:LYS:CD	2:B:299:LYS:H	2.07	0.48
1:A:317:LEU:CD1	1:A:351:PHE:CD1	2.96	0.48
2:B:205:ASP:H	2:B:209:LEU:HD11	1.78	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
1:A:189:LEU:CD2	1:A:395:PHE:HZ	2.25	0.48
2:B:389:LYS:HG3	2:B:429:VAL:HG11	1.95	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
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
1:A:369:ALA:O	1:A:370:LYS:CB	2.62	0.48
1:A:200:CYS:HB2	1:A:265:GLY:O	2.12	0.48
1:A:96:LYS:O	1:A:96:LYS:HD2	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:399:PHE:O	2:B:400:ARG:C	2.52	0.48
2:B:360:PRO:HG2	2:B:371:LEU:CB	2.38	0.48
1:A:169:PHE:HE1	1:A:204:VAL:HG21	1.79	0.48
1:A:405:VAL:C	1:A:408:TYR:CE2	2.86	0.48
1:A:98:ASP:OD1	1:A:99:ALA:N	2.47	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:217:LEU:CD1	1:A:277:SER:HA	2.44	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:363:ALA:O	2:B:433:GLN:HB2	2.14	0.48
2:B:287:THR:O	2:B:288:VAL:CG2	2.58	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:266:HIS:CE1	1:A:432:TYR:HE1	2.32	0.47
1:A:99:ALA:O	1:A:100:ALA:HB3	2.14	0.47
2:B:313:LEU:HD22	2:B:363:ALA:HB2	1.95	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
1:A:105:ARG:CA	1:A:411:GLU:CD	2.72	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
2:B:156:LYS:CE	2:B:156:LYS:HA	2.38	0.47
1:A:135:PHE:CD1	1:A:157:LEU:CD1	2.97	0.47
1:A:6:SER:OG	1:A:65:ALA:HB2	2.14	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:101:ASN:CB	2:B:254:LYS:NZ	2.77	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: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:HD3	2:B:243:ARG:N	2.26	0.47
2:B:313:LEU:HD12	2:B:432:TYR:CG	2.42	0.47
2:B:262:PHE:CZ	2:B:435:TYR:CZ	3.02	0.47
1:A:339:ARG:C	1:A:341:ILE:N	2.68	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:234:ILE:CG1	1:A:270:ALA:HB1	2.38	0.47
2:B:171:VAL:HA	2:B:204:ILE:C	2.35	0.47
2:B:188:THR:CA	2:B:425:MET:CE	2.58	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:202:TYR:CE2	2:B:378:ILE:HD13	2.42	0.47
2:B:49:ILE:HG13	2:B:50:ASN:N	2.29	0.47
1:A:205:ASP:H	1:A:209:ILE:CD1	2.28	0.47
1:A:256:GLN:O	1:A:260:VAL:HG13	2.15	0.47
2:B:204:ILE:HG23	2:B:302:MET:CG	2.45	0.47
2:B:185:TYR:OH	2:B:398:MET:O	2.33	0.47
1:A:282:TYR:C	1:A:284:GLU:H	2.15	0.47
1:A:256:GLN:HA	1:A:260:VAL:HG13	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:315:CYS:HB3	1:A:377:MET:HE1	1.97	0.47
1:A:120:ASP:O	1:A:124:LYS:HB2	2.15	0.47
1:A:16:ILE:HG13	1:A:228:ASN:HB2	1.97	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:34:GLY:C	1:A:61:HIS:N	2.68	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:253:THR:O	1:A:254:GLU:C	2.52	0.47
1:A:201:ALA:N	1:A:267:PHE:HD2	2.06	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:288:VAL:HG23	1:A:373:ARG:HH11	1.79	0.47
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
1:A:4:CYS:HB2	1:A:252:LEU:CD1	2.45	0.46
2:B:113:GLU:CG	2:B:114:LEU:N	2.78	0.46
2:B:224:TYR:O	2:B:225:GLY:C	2.53	0.46
2:B:20:PHE:O	2:B:24:ILE:HB	2.14	0.46
2:B:194:LEU:HD11	2:B:267:PHE:CE1	2.40	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
2:B:133:GLN:O	2:B:165:ILE:CD1	2.64	0.46
2:B:169:PHE:HD2	2:B:204:ILE:CD1	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:287:THR:N	2:B:290:GLU:OE1	2.48	0.46
1:A:434:GLU:C	1:A:436:GLY:H	2.18	0.46
1:A:115:ILE:HG23	1:A:116:ASP:H	1.79	0.46
1:A:70:LEU:HD22	1:A:95:GLY:HA3	1.97	0.46
2:B:226:ASP:O	2:B:229:HIS:HB3	2.14	0.46
1:A:407:TRP:CH2	2:B:253:ARG:HD3	2.49	0.46
2:B:431:GLU:HA	2:B:434:GLN:HG2	1.96	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
1:A:335:ILE:O	1:A:337:THR:N	2.47	0.46
2:B:324:SER:OG	2:B:326:LYS:HB3	2.16	0.46
1:A:215:ARG:CZ	1:A:299:ALA:HB1	2.45	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:169:PHE:HD2	2:B:204:ILE:HD11	1.80	0.46
2:B:15:GLN:CA	2:B:228:ASN:ND2	2.72	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
2:B:126:SER:HB2	2:B:132:LEU:HD22	1.97	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
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:436:GLY:O	1:A:438:ASP:N	2.49	0.46
1:A:423:GLU:O	1:A:426:ALA:HB3	2.16	0.46
1:A:115:ILE:CG1	1:A:152:LEU:HD13	2.45	0.46
1:A:10:GLY:O	1:A:11:GLN:C	2.54	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:202:TYR:CD2	2:B:238:VAL:HG21	2.51	0.46
2:B:194:LEU:CD2	2:B:265:LEU:HD21	2.44	0.46
1:A:260:VAL:O	1:A:260:VAL:CG2	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:220:GLU:O	1:A:222:PRO:CD	2.64	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
1:A:191:THR:CG2	1:A:425:MET:SD	3.04	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
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: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
2:B:262:PHE:CG	2:B:431:GLU:CB	2.99	0.46
1:A:276:ILE:HG12	1:A:277:SER:N	2.31	0.46
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:135:PHE:CD1	2:B:135:PHE:N	2.84	0.45
2:B:23:VAL:O	2:B:25:SER:N	2.50	0.45
2:B:6:HIS:HB3	2:B:21:TRP:HZ2	1.81	0.45
1:A:181:VAL:HG11	2:B:258:ASN:CG	2.32	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:392:ASP:OD1	1:A:422:ARG:CZ	2.65	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
2:B:24:ILE:CD1	2:B:52:TYR:CE2	2.97	0.45
1:A:334:THR:CG2	1:A:335:ILE:N	2.79	0.45
1:A:5:ILE:HG22	1:A:6:SER:H	1.78	0.45
2:B:209:LEU:HD23	2:B:227:LEU:HD13	1.98	0.45
2:B:133:GLN:HE21	2:B:243:ARG:HH12	1.63	0.45
2:B:309:HIS:O	2:B:386:GLU:OE1	2.35	0.45
1:A:317:LEU:CD1	1:A:351:PHE:CE1	2.99	0.45
2:B:288:VAL:N	2:B:289:PRO:CD	2.80	0.45
1:A:117:LEU:HD12	1:A:121:ARG:HH12	1.80	0.45
1:A:228:ASN:O	1:A:232:GLY:N	2.39	0.45
2:B:311:ARG:O	2:B:382:THR:HG22	2.16	0.45
1:A:181:VAL:CB	2:B:258:ASN:ND2	2.80	0.45
2:B:274:PRO:HG2	2:B:371:LEU:CD2	2.43	0.45
2:B:72:PRO:O	2:B:74:THR:N	2.50	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
2:B:106:GLY:O	2:B:149:MET:HB2	2.17	0.45
2:B:312:TYR:HA	2:B:381:SER:O	2.16	0.45
2:B:8:GLN:CG	2:B:67:LEU:HD22	2.46	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
1:A:274:PRO:HB2	1:A:371:VAL:HG21	1.98	0.45
1:A:231:ILE:H	1:A:231:ILE:HD13	1.82	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
1:A:72:PRO:CB	2:B:47:GLU:HG2	2.33	0.45
2:B:273:ALA:CB	2:B:274:PRO:CD	2.93	0.45
1:A:271:THR:O	1:A:376:CYS:HA	2.17	0.45
2:B:324:SER:O	2:B:326:LYS:N	2.50	0.45
2:B:323:MET:CE	2:B:328:VAL:HG22	2.46	0.45
1:A:303:VAL:CG1	1:A:303:VAL:O	2.64	0.45
2:B:94:PHE:N	2:B:94:PHE:CD1	2.84	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:22:GLU:O	1:A:23:LEU:C	2.54	0.45
2:B:313:LEU:O	2:B:347:ILE:HD12	2.16	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
1:A:175:PRO:CG	1:A:176:GLN:H	2.29	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: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:184:PRO:HG3	1:A:394:LYS:HG2	1.91	0.45
1:A:63:PRO:C	1:A:64:ARG:CG	2.83	0.45
2:B:171:VAL:CG1	2:B:206:ASN:OD1	2.61	0.45
1:A:278:ALA:HB2	1:A:369:ALA:CA	2.45	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:195:VAL:CB	2:B:264:ARG:C	2.85	0.45
2:B:82:PRO:C	2:B:84:GLY:H	2.20	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:11:GLN:NE2	1:A:74:VAL:HG22	2.30	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:TYR:CE2	1:A:418:PHE:CZ	3.04	0.44
1:A:93:ILE:CG2	1:A:94:THR:H	2.30	0.44
1:A:7:ILE:HG13	1:A:137:VAL:HG22	1.98	0.44
1:A:343:PHE:CE1	1:A:351:PHE:HE2	2.36	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:HG2	1:A:229:ARG:NH1	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: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
2:B:67:LEU:HD12	2:B:92:PHE:CD1	2.52	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
1:A:63:PRO:HG2	1:A:91:GLN:OE1	2.18	0.44
2:B:242:LEU:C	2:B:244:PHE:H	2.19	0.44
2:B:194:LEU:HD13	2:B:265:LEU:HD21	1.99	0.44
2:B:430:SER:O	2:B:434:GLN:HG2	2.17	0.44
1:A:154:MET:HB3	1:A:166:LYS:CD	2.38	0.44
1:A:21:TRP:HE1	1:A:63:PRO:HB3	1.83	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
2:B:180:THR:HG22	2:B:181:VAL:H	1.81	0.44
2:B:67:LEU:HD12	2:B:92:PHE:CE1	2.53	0.44
1:A:286:LEU:HD12	1:A:286:LEU:HA	1.84	0.44
1:A:72:PRO:HG2	1:A:73:THR:H	1.83	0.44
2:B:193:GLN:O	2:B:197:ASN:HB2	2.17	0.44
2:B:212:ILE:HG22	2:B:212:ILE:O	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
2:B:115:VAL:HG21	2:B:152:LEU:HD21	1.98	0.44
1:A:218:ASP:C	1:A:219:ILE:HG12	2.37	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: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
2:B:105:LYS:HG2	2:B:411:GLU:HB3	1.94	0.43
2:B:72:PRO:HG2	2:B:73:GLY:H	1.83	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:13:GLY:C	1:A:16:ILE:HG22	2.38	0.43
1:A:263:PRO:O	1:A:264:ARG:C	2.56	0.43
1:A:409:VAL:C	1:A:411:GLU:N	2.71	0.43
1:A:5:ILE:HG23	1:A:125:LEU:CD1	2.37	0.43
2:B:240:THR:HG23	2:B:241:CYS:N	2.33	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
1:A:304:LYS:HG3	1:A:304:LYS:O	2.19	0.43
1:A:192:HIS:HA	1:A:424:ASP:HB2	2.00	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
2:B:6:HIS:HB3	2:B:65:ALA:CB	2.48	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
1:A:23:LEU:O	1:A:26:LEU:HB3	2.17	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:328:VAL:O	1:A:330:ALA:N	2.38	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: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
1:A:363:VAL:CG1	1:A:364:PRO:HD2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:185:TYR:CG	2:B:418:PHE:HE2	2.35	0.43
1:A:175:PRO:CD	1:A:176:GLN:N	2.81	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
2:B:153:LEU:HD13	2:B:153:LEU:N	2.34	0.43
1:A:390:ARG:HG3	1:A:390:ARG:HH11	1.83	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
1:A:93:ILE:N	1:A:93:ILE:CD1	2.73	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: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
1:A:141:PHE:CZ	1:A:391:LEU:CD2	2.97	0.43
2:B:242:LEU:HD22	2:B:250:ALA:O	2.18	0.43
2:B:105:LYS:CB	2:B:411:GLU:HB3	2.48	0.43
2:B:72:PRO:O	2:B:73:GLY:C	2.58	0.43
1:A:115:ILE:C	1:A:115:ILE:CD1	2.87	0.42
1:A:11:GLN:HE21	1:A:74:VAL:CG2	2.29	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:264:ARG:C	1:A:266:HIS:N	2.60	0.42
1:A:184:PRO:CB	1:A:394:LYS:C	2.86	0.42
2:B:182:VAL:O	2:B:183:GLU:C	2.56	0.42
2:B:168:THR:CG2	2:B:201:THR:HG23	2.48	0.42
2:B:15:GLN:C	2:B:228:ASN:ND2	2.73	0.42
1:A:101:ASN:OD1	2:B:249:ASN:O	2.37	0.42
2:B:26:ASP:C	2:B:28:HIS:H	2.21	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:132:LEU:CD2	1:A:132:LEU:H	2.23	0.42
1:A:12:ALA:HB3	4:A:502:GTP:O4'	2.15	0.42
1:A:5:ILE:CG2	1:A:6:SER:H	2.29	0.42
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: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:401:ARG:CG	2:B:401:ARG:O	2.67	0.42
1:A:7:ILE:HD11	1:A:137:VAL:CG2	2.44	0.42
1:A:436:GLY:C	1:A:438:ASP:N	2.72	0.42
1:A:121:ARG:NH1	1:A:121:ARG:HG2	2.33	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:378:LEU:HD12	1:A:378:LEU:O	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: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:208:ALA:HA	1:A:211:ASP:OD2	2.18	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:19:LYS:HE3	2:B:225:GLY:C	2.39	0.42
2:B:343:PHE:CD1	2:B:350:ASN:ND2	2.88	0.42
1:A:328:VAL:C	1:A:330:ALA:N	2.73	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:2:ARG:HG2	1:A:243:ARG:HH12	1.84	0.42
1:A:363:VAL:HG13	1:A:364:PRO:HD2	2.02	0.42
1:A:187:SER:CB	1:A:391:LEU:HG	2.40	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:213:CYS:O	1:A:219:ILE:HG13	2.20	0.42
1:A:132:LEU:HD21	1:A:161:TYR:CD2	2.54	0.42
1:A:158:SER:CA	1:A:163:LYS:N	2.71	0.42
1:A:147:SER:HB2	1:A:186:ASN:O	2.19	0.42
1:A:404:PHE:HE2	2:B:257:VAL:O	2.02	0.42
1:A:137:VAL:HG12	1:A:139:HIS:CE1	2.55	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:76:ASP:O	1:A:79:ARG:N	2.52	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
2:B:16:ILE:N	2:B:228:ASN:CB	2.79	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:262:PHE:CZ	2:B:435:TYR:CE1	3.07	0.42
1:A:335:ILE:C	1:A:337:THR:N	2.73	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: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
2:B:25:SER:O	2:B:28:HIS:N	2.53	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:100:ALA:O	1:A:144:GLY:HA3	2.20	0.41
1:A:8:HIS:CD2	1:A:138:PHE:CD2	3.07	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: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:HA	1:A:242:LEU:HD12	1.87	0.41
1:A:262:TYR:HB3	1:A:263:PRO:HD2	2.00	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:202:TYR:CE2	2:B:238:VAL:HG13	2.54	0.41
2:B:194:LEU:CD1	2:B:265:LEU:HD21	2.50	0.41
1:A:332:ILE:CD1	1:A:353:VAL:HG22	2.51	0.41
1:A:76:ASP:O	1:A:80:THR:N	2.53	0.41
1:A:287:SER:C	1:A:289:ALA:N	2.73	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
2:B:106:GLY:O	2:B:149:MET:CA	2.68	0.41
2:B:12:CYS:C	2:B:14:ASN:N	2.71	0.41
2:B:194:LEU:CA	2:B:265:LEU:HD22	2.44	0.41
2:B:399:PHE:O	2:B:401:ARG:N	2.53	0.41
2:B:333:LEU:O	2:B:334:ASN:C	2.58	0.41
1:A:434:GLU:C	1:A:436:GLY:N	2.74	0.41
1:A:100:ALA:HB2	1:A:105:ARG:HD3	2.03	0.41
1:A:152:LEU:CD1	1:A:152:LEU:C	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:ILE:O	1:A:385:ALA:C	2.59	0.41
1:A:171:ILE:HD13	4:A:502:GTP:HN22	1.86	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
2:B:133:GLN:CG	2:B:165:ILE:HD11	2.49	0.41
4:A:502:GTP:O3'	2:B:247:GLN:HA	2.19	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
1:A:154:MET:HE3	1:A:198:SER:HB2	1.90	0.41
1:A:308:ARG:HG2	1:A:308:ARG:O	2.20	0.41
1:A:296:PHE:CD1	1:A:341:ILE:CD1	2.98	0.41
1:A:217:LEU:HD12	1:A:277:SER:CB	2.49	0.41
1:A:100:ALA:C	1:A:102:ASN:H	2.24	0.41
2:B:242:LEU:HB3	2:B:250:ALA:O	2.20	0.41
1:A:179:THR:O	2:B:248:LEU:HD22	2.21	0.41
2:B:281:GLN:C	2:B:283:TYR:N	2.67	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
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:230:LEU:O	1:A:233:GLN:N	2.35	0.41
1:A:428:LEU:HA	1:A:428:LEU:HD12	1.79	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
1:A:172:TYR:HE2	1:A:183:GLU:OE2	2.03	0.41
2:B:105:LYS:HB2	2:B:411:GLU:HB3	2.03	0.41
2:B:12:CYS:O	2:B:13:GLY:C	2.59	0.41
2:B:189:LEU:CG	2:B:418:PHE:HA	2.51	0.41
2:B:409:THR:C	2:B:411:GLU:N	2.73	0.41
1:A:318:LEU:HB2	1:A:376:CYS:SG	2.61	0.41
1:A:67:PHE:CE2	1:A:87:PHE:CE2	3.08	0.41
1:A:287:SER:O	1:A:289:ALA:N	2.53	0.41
1:A:5:ILE:HD11	1:A:125:LEU:C	2.42	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: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:417:GLU:O	2:B:420:GLU:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:273:ALA:HB1	2:B:291:LEU:HG	2.01	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: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:HD3	2:B:264:ARG:HA	1.78	0.40
1:A:139:HIS:ND1	1:A:139:HIS:N	2.69	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:C	1:A:244:PHE:HD1	2.24	0.40
1:A:401:LYS:C	1:A:403:ALA:H	2.24	0.40
1:A:14:VAL:HG11	1:A:75:ILE:HD13	2.04	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
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
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:67:PHE:HB2	1:A:92:LEU:HD23	2.02	0.40
1:A:25:CYS:SG	1:A:83:TYR:HE2	2.38	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
2:B:99:ALA:O	2:B:100:GLY:C	2.60	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 ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	5
2	B	399/445 (90%)	262 (66%)	85 (21%)	52 (13%)	0	7
All	All	800/896 (89%)	519 (65%)	168 (21%)	113 (14%)	1	6

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 ⓘ

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	23
2	B	353/381 (93%)	302 (86%)	51 (14%)	4	25
All	All	698/758 (92%)	595 (85%)	103 (15%)	8	24

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

Some 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 carbohydrates 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	A	502	3	26,34,34	1.36	2 (7%)	29,54,54	2.30	4 (13%)
4	GTP	B	502	3	26,34,34	1.35	1 (3%)	29,54,54	2.29	4 (13%)

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	A	502	3	-	0/18/38/38	0/3/3/3
4	GTP	B	502	3	-	0/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	502	GTP	O4'-C1'	2.01	1.44	1.41
4	B	502	GTP	C6-N1	4.81	1.41	1.33
4	A	502	GTP	C6-N1	4.82	1.41	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	502	GTP	C5-C6-N1	-7.81	113.31	123.52
4	B	502	GTP	C5-C6-N1	-7.80	113.33	123.52
4	A	502	GTP	N3-C2-N1	-3.59	122.67	127.56
4	B	502	GTP	N3-C2-N1	-3.49	122.81	127.56
4	B	502	GTP	C6-C5-C4	-2.14	118.41	120.86
4	A	502	GTP	C6-C5-C4	-2.13	118.43	120.86
4	B	502	GTP	C6-N1-C2	7.53	124.70	115.88
4	A	502	GTP	C6-N1-C2	7.56	124.73	115.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 88 short contacts:

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

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.