



Full wwPDB EM Validation Report ⓘ

Dec 12, 2022 – 04:12 PM EST

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

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

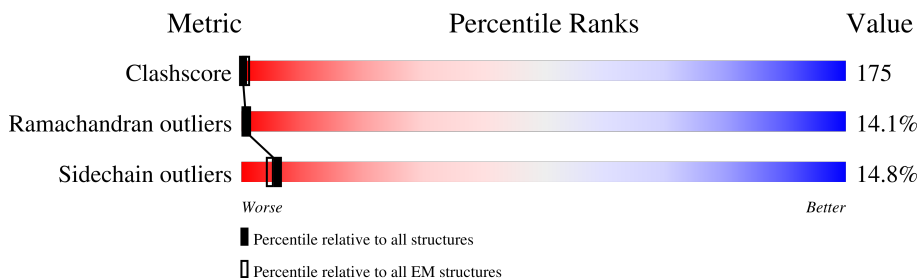
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.90 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	451	
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	A	1	Total	Mg	0
			1	1	
3	B	1	Total	Mg	0
			1	1	

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

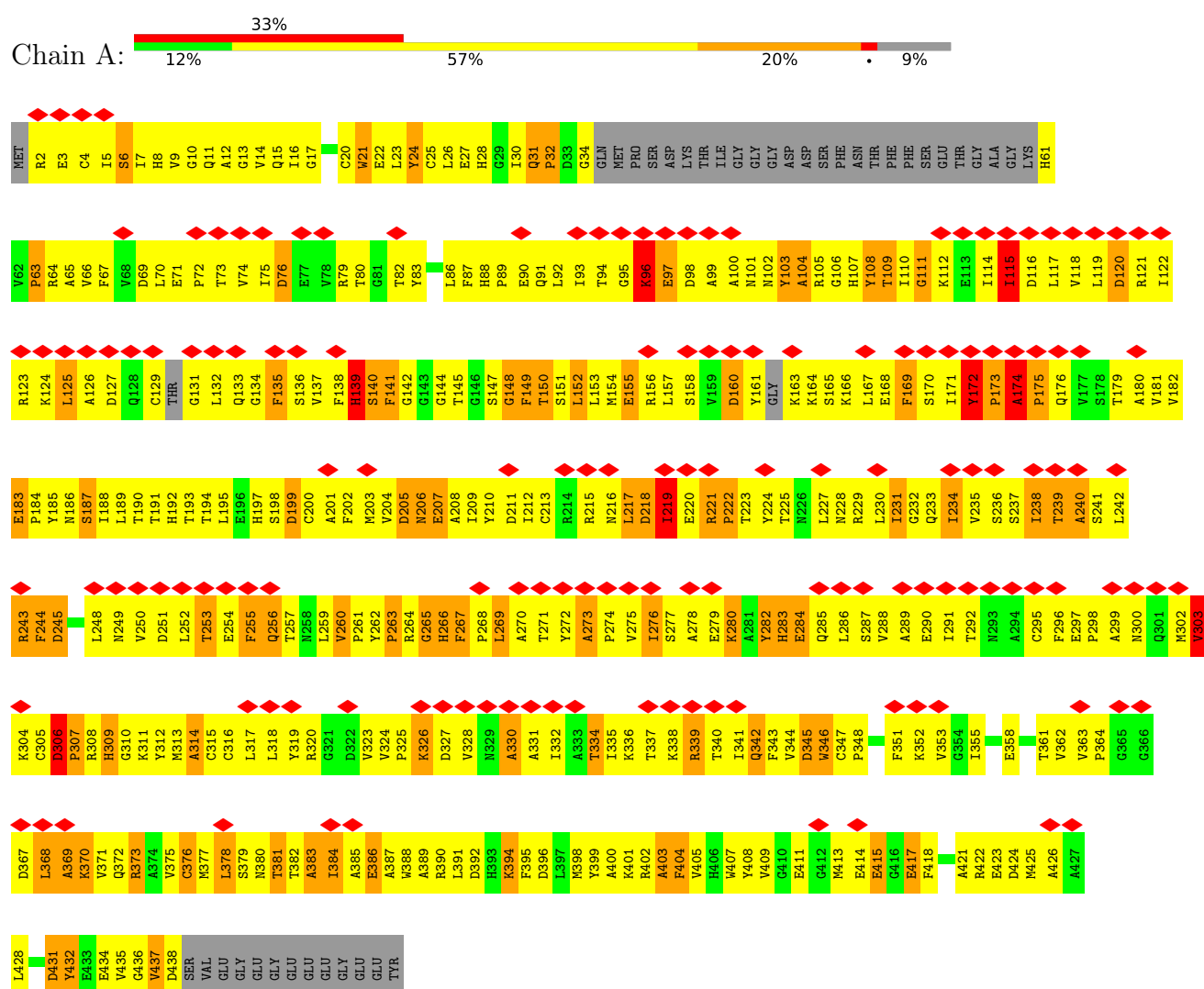


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
4	B	1	Total	C	N	O	P	0
			32	10	5	14	3	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Tubulin alpha-1A chain



• Molecule 2: Tubulin beta chain



GLU	A375	P307	Q247	A187	E127	I66	MET
GLN	T376	R308	L248	T188	S128	L67	R2
GLY	F377	H309	N249	L189	CYS	V68	E3
PHE	I378	G310	A250	S190	ASP	I67	I4
GLU	G379	R311	D251	V191	C131	L70	V5
GLU	N380	Y312	L252	H192	L132	E71	H6
GLU	T382	L313	R253	Q193	Q133	P72	I7
GLY	A363	T314	K254	L194	G134	G73	Q8
GLU	I384	V315	L255	V195	F135	T74	A9
ASP	Q385	A316	L256	E196	Q136	M75	G10
GLU	E386	A317	A256	N197	L137	D76	Q11
ALA	L387	V318	V257	T198	S77	G77	C12
	F388	F319	N258	E200	H139	V78	G13
	K389	R320	V260	T201	SER	R79	M14
		G321	P261	Y202	LEU	S90	Q15
		R322	F262	C203	G142	G81	I16
	F395	M323	P263	I204	G143	P82	G17
T396	A397	S324	R264	D205	G144	F83	A18
M398	F399	M325	H266	N206	T145	G84	K19
R400	R401	K326	F267	E207	G146	Q85	F20
K401	K402	E327	F268	A208	S147	I86	W21
A403	A404	V328	M269	L209	G148		E22
F404		D329	P270	Y210	M149		V23
		E330	G271	D211	G150	P89	I24
Y408	Y409	Q331	F272	T212	T151	D90	S25
G410	G411	M332	A273	C213	L152	N91	D26
E411	G412	L333	P274	F214	L153	F92	E27
N413	N414	N334	L275	R215	S154	V93	H28
D414		V335	T276	L216	T155	F94	G29
		Q336	S277	T217	K156	GLY	I30
		K337	R278	K218	R158	GLN	D31
E417	F418	K338	G279	L219	E160		P32
T419	E420	N339	S280	T220	TYR	A99	I33
A421	A422	S340	Q281	T221	ASP	G100	G34
E422	S423	S341	Q282	P222	R164	N101	S35
S423		Y342	Y283	T223	I165	M102	Y36
N424	N425	F343	A285	G225	M166	W103	D39
N426		E345	L286	D226	N167	A104	S40
		W346	T287	L227	T168	G106	D41
		I347	V288	N228	F169	H107	L42
D427	L428	P348	P289	H229	S170	Y108	Q43
V429	S430	N349	E290	L230	V171	T109	L44
S430	E431	N350	L291	V231	V172	E110	E47
Y432	Q433	V351	T292	S232	P173	G111	R48
Q433	Q434	K352	Q293	A233	SER	A112	N50
Y435	Q436	T353	Q294	T234	PRO	E113	V51
		A354	M295	S236	LYS	L114	Y53
ASP		V355	F296	G237	VAL	V115	N54
ALA		C356	D297	V238	SER	D116	A57
THR		D357	A298	T239	D179	S117	G58
ALA		I358	K299	T240	T180	V118	N59
ASP		P359	N300	C241	V181	L119	P63
		P360	M301	L242	V182	D120	R64
		R369	M302	R243	E183	V121	A65
		G370	A303	F244	P184	Y185	
		L371	A304	P245	N186	R123	
		K372	C305	G246	K124	E125	
		M373	D306		S126		

4 Experimental information

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.55	2/3281 (0.1%)	0.78	10/4453 (0.2%)
2	B	0.57	3/3306 (0.1%)	0.87	15/4469 (0.3%)
All	All	0.56	5/6587 (0.1%)	0.83	25/8922 (0.3%)

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

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

All (5) bond length outliers are listed below:

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

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	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:169:PHE:CZ	1:A:231:ILE:CG2	1.99	1.44
1:A:184:PRO:HB3	1:A:394:LYS:CG	1.46	1.44
2:B:102:ASN:HA	2:B:408:TYR:CD2	1.50	1.43
1:A:154:MET:CE	1:A:197:HIS:ND1	1.79	1.43
2:B:262:PHE:CZ	2:B:434:GLN:CB	2.01	1.41
2:B:262:PHE:CE1	2:B:434:GLN:HB2	1.56	1.41
2:B:15:GLN:HB2	2:B:228:ASN:ND2	1.21	1.40
2:B:346:TRP:CE3	2:B:435:TYR:HA	1.54	1.40
2:B:15:GLN:CB	2:B:228:ASN:ND2	1.79	1.40

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

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	4
2	B	399/445 (90%)	262 (66%)	85 (21%)	52 (13%)	0	5
All	All	800/896 (89%)	519 (65%)	168 (21%)	113 (14%)	1	4

All (113) Ramachandran outliers are listed below:

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

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

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Mol	Chain	Res	Type
1	A	239	THR
1	A	245	ASP
1	A	263	PRO
1	A	330	ALA
1	A	336	LYS
1	A	369	ALA
2	B	83	PHE
2	B	99	ALA
2	B	302	MET
1	A	89	PRO
1	A	172	TYR
1	A	256	GLN
1	A	307	PRO
1	A	348	PRO
2	B	34	GLY
2	B	100	GLY
2	B	395	PHE
1	A	139	HIS
1	A	140	SER
1	A	160	ASP
1	A	174	ALA
1	A	284	GLU
1	A	298	PRO
1	A	303	VAL
2	B	57	ALA
2	B	74	THR
2	B	285	ALA
1	A	31	GLN
1	A	273	ALA
2	B	51	VAL
2	B	58	GLY
2	B	145	THR
2	B	400	ARG
1	A	115	ILE
1	A	222	PRO
2	B	72	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	345/377 (92%)	293 (85%)	52 (15%)	3	14
2	B	353/381 (93%)	302 (86%)	51 (14%)	3	16
All	All	698/758 (92%)	595 (85%)	103 (15%)	6	15

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

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

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

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

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

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

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	1.30	4 (15%)	32,54,54	1.10	2 (6%)
4	GTP	B	502	3	26,34,34	1.29	4 (15%)	32,54,54	1.10	2 (6%)

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

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

All (8) bond length outliers are listed below:

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

All (4) bond angle outliers are listed below:

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

There are no chirality outliers.

All (6) torsion outliers are listed below:

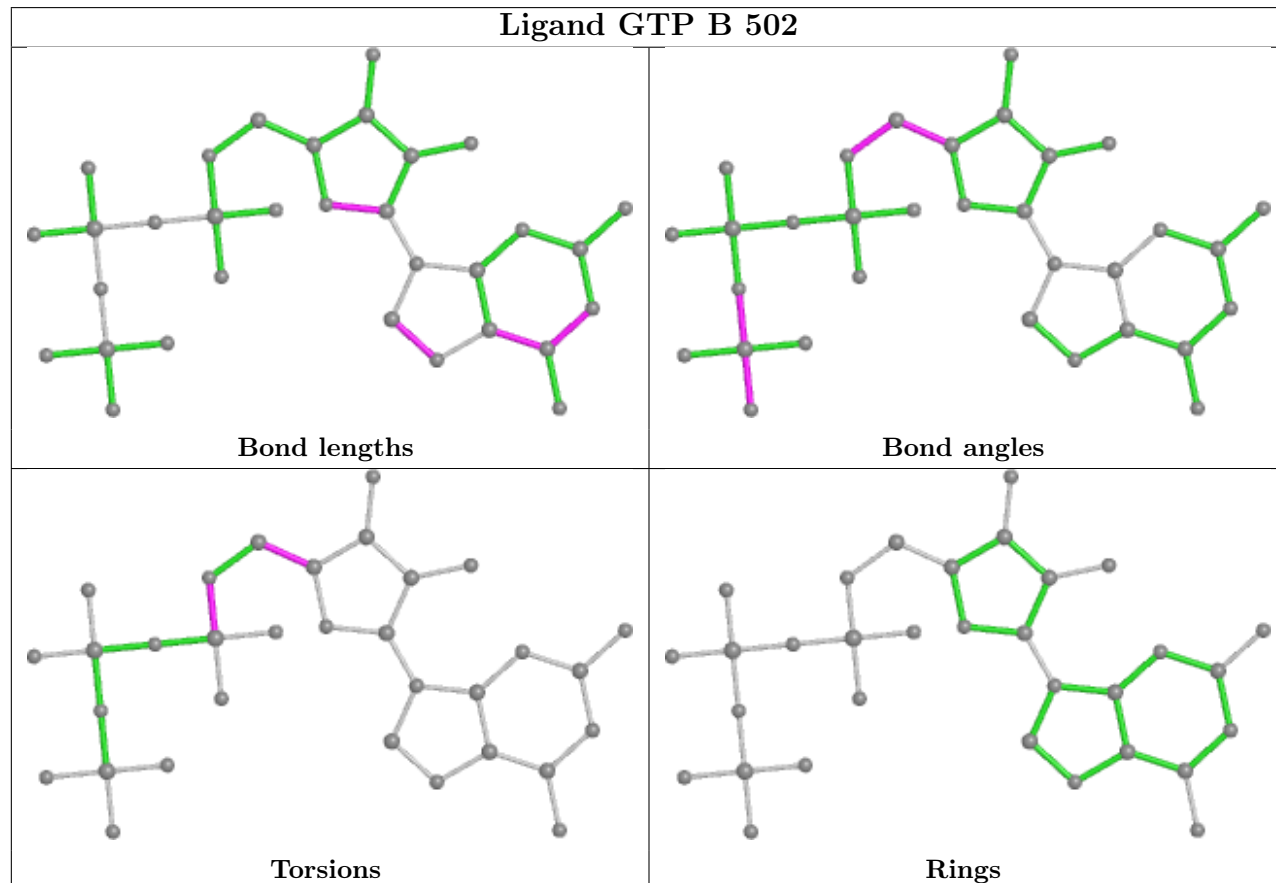
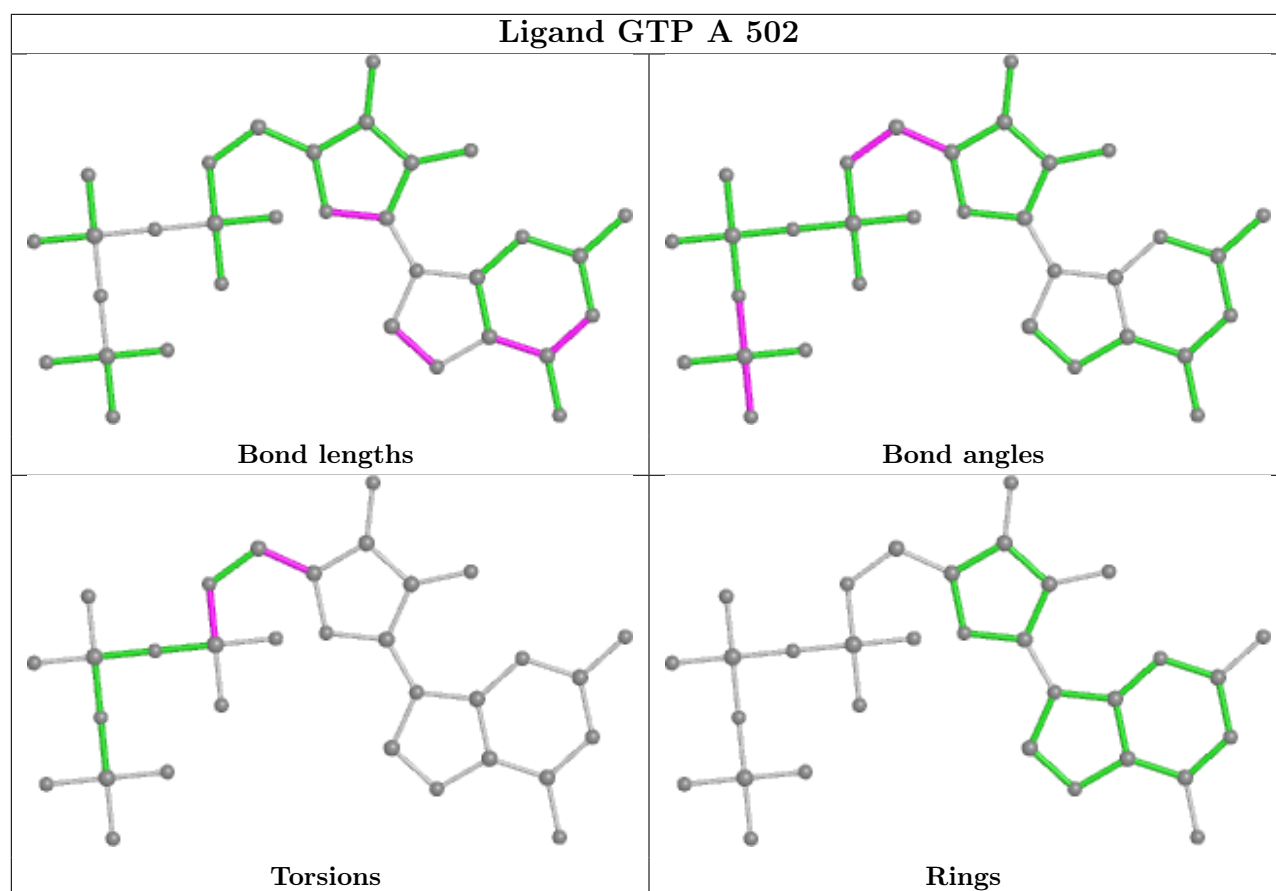
Mol	Chain	Res	Type	Atoms
4	A	502	GTP	C3'-C4'-C5'-O5'
4	B	502	GTP	C3'-C4'-C5'-O5'
4	A	502	GTP	O4'-C4'-C5'-O5'
4	B	502	GTP	O4'-C4'-C5'-O5'
4	A	502	GTP	C5'-O5'-PA-O1A
4	B	502	GTP	C5'-O5'-PA-O1A

There are no ring outliers.

2 monomers are involved in 88 short contacts:

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

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

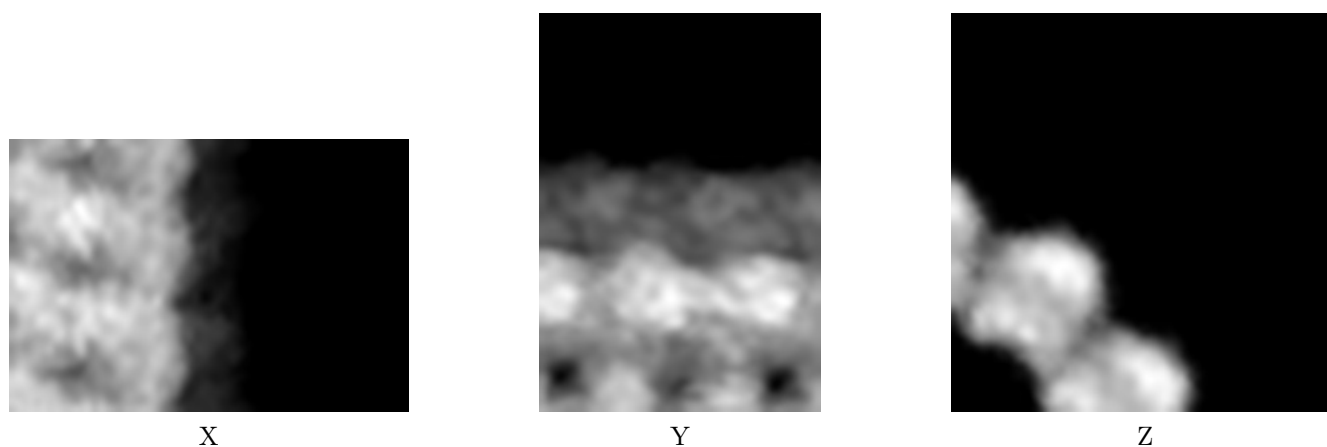
6 Map visualisation [i](#)

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

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

6.1 Orthogonal projections [i](#)

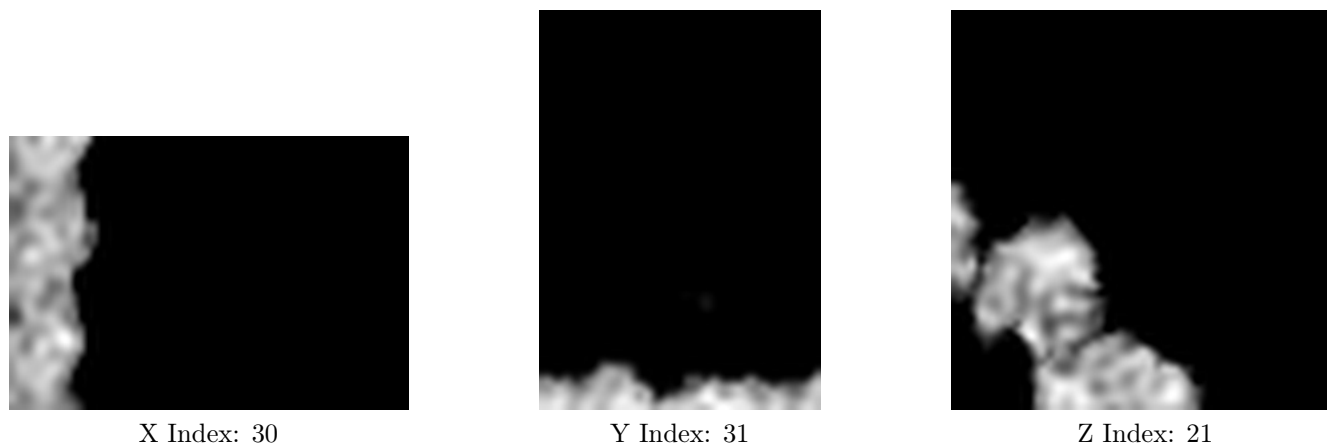
6.1.1 Primary map



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

6.2 Central slices [i](#)

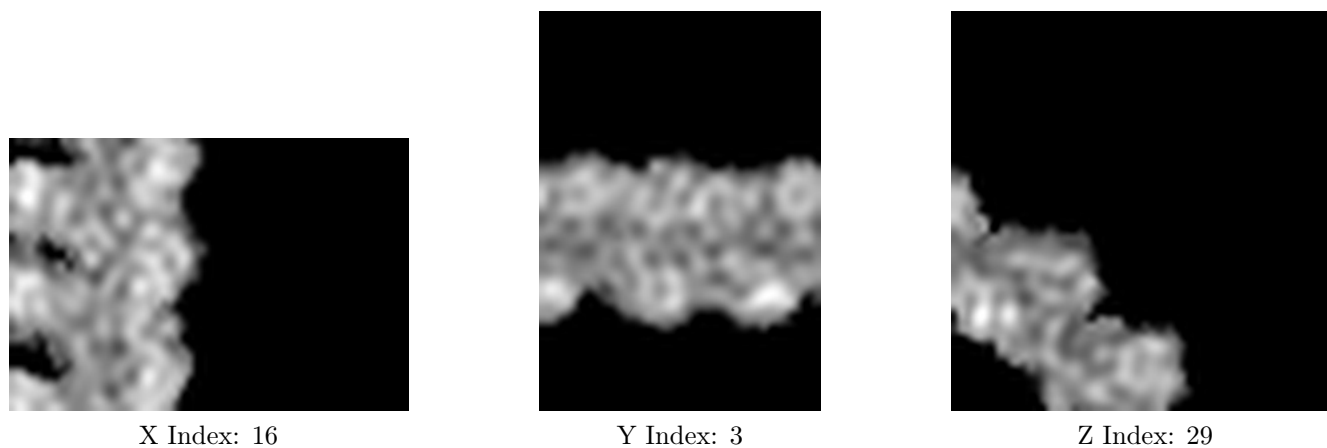
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

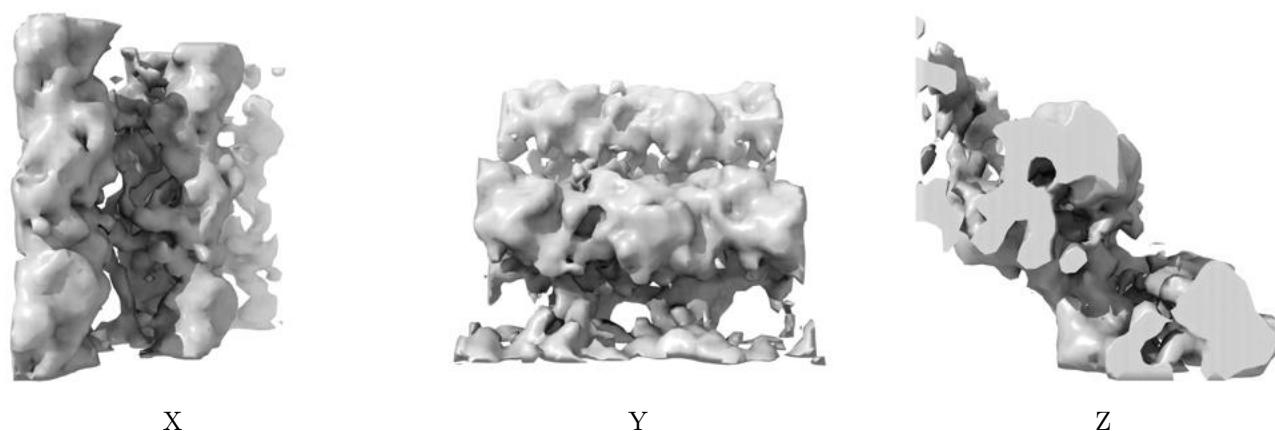
6.3.1 Primary map



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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



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

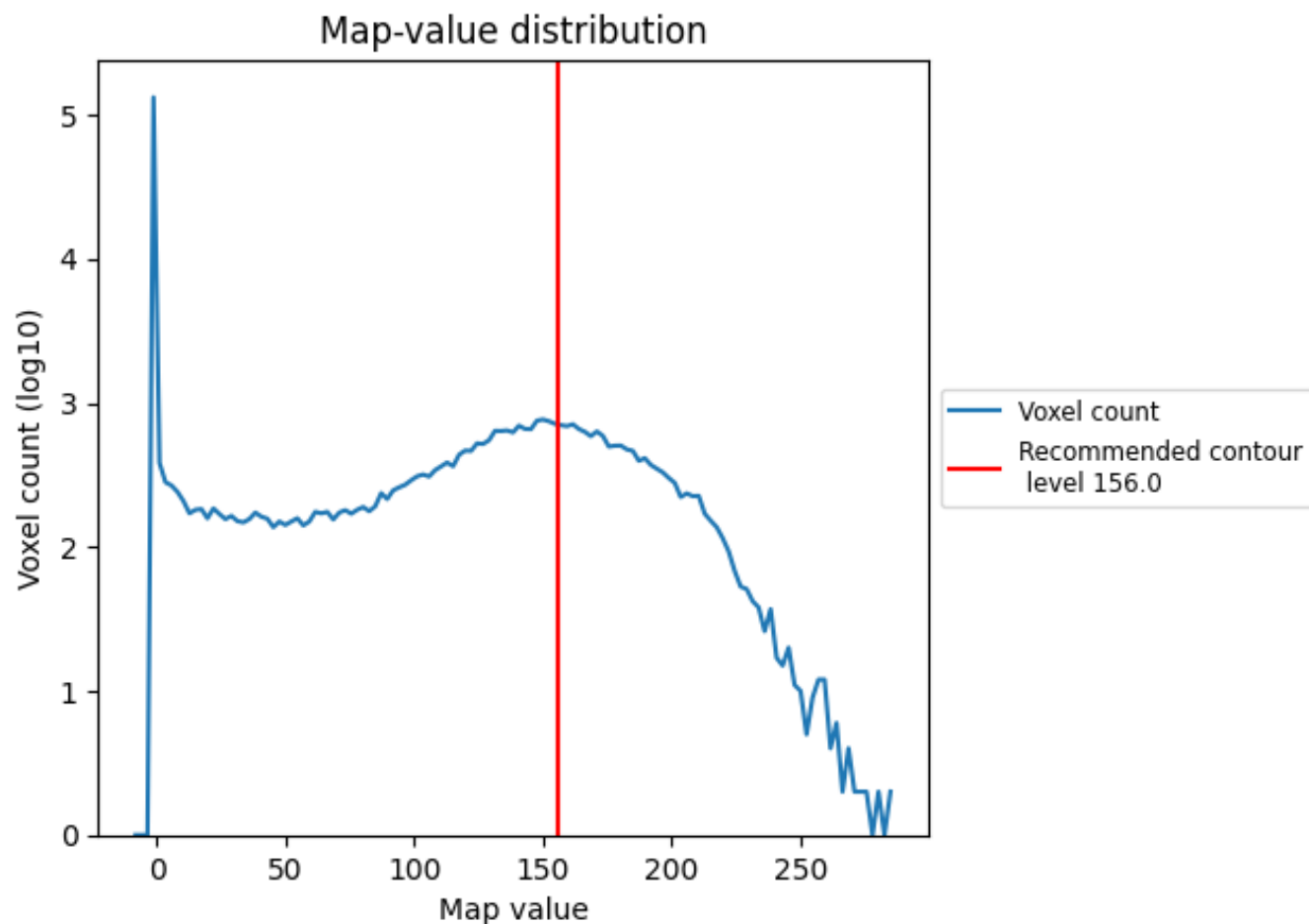
6.5 Mask visualisation

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

7 Map analysis [i](#)

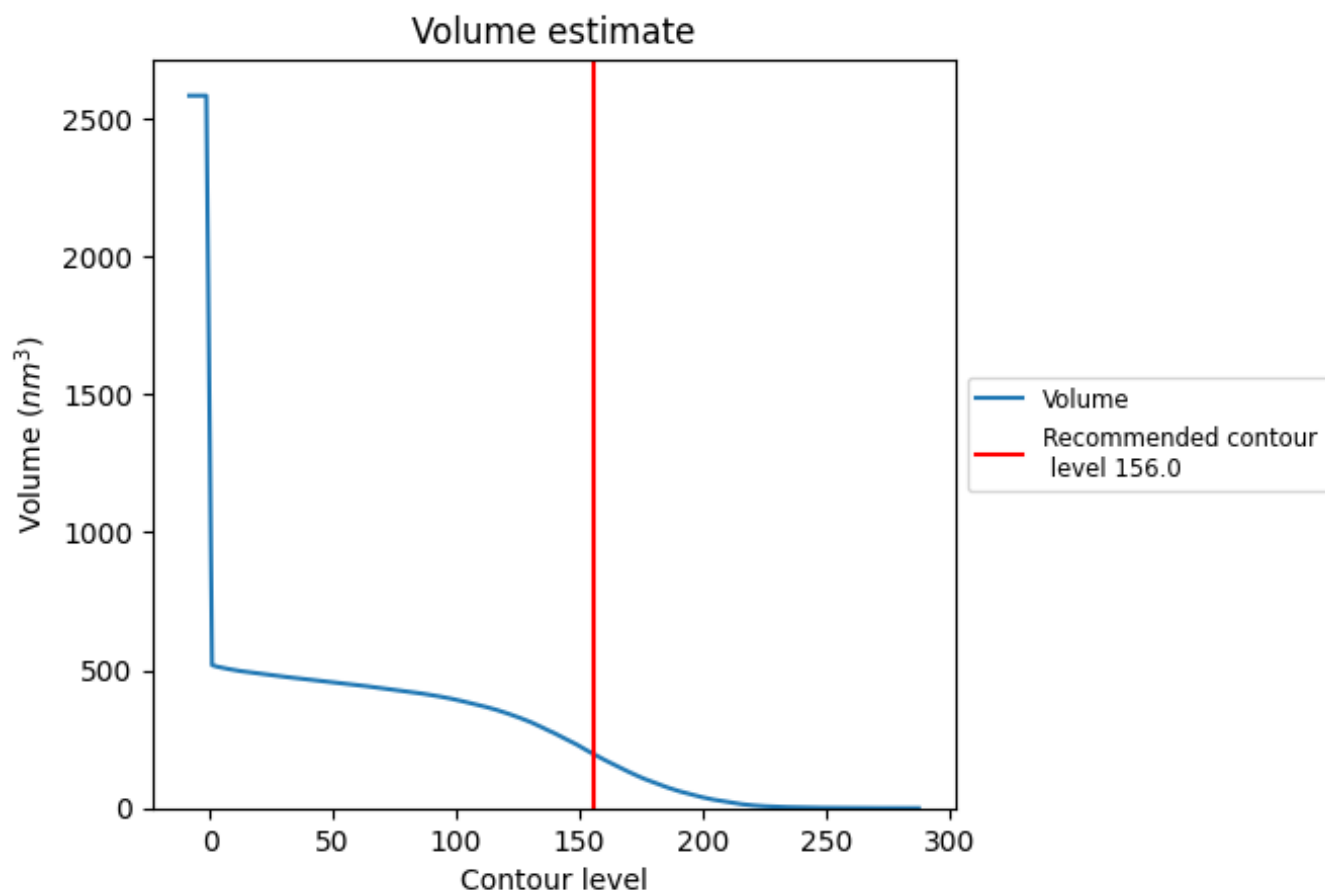
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 194 nm³; this corresponds to an approximate mass of 175 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

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

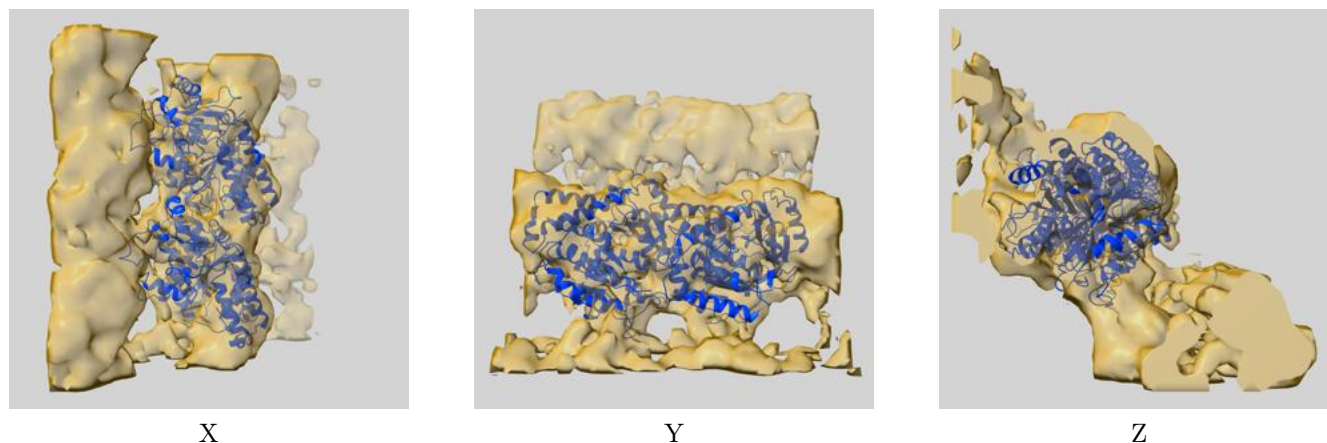
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

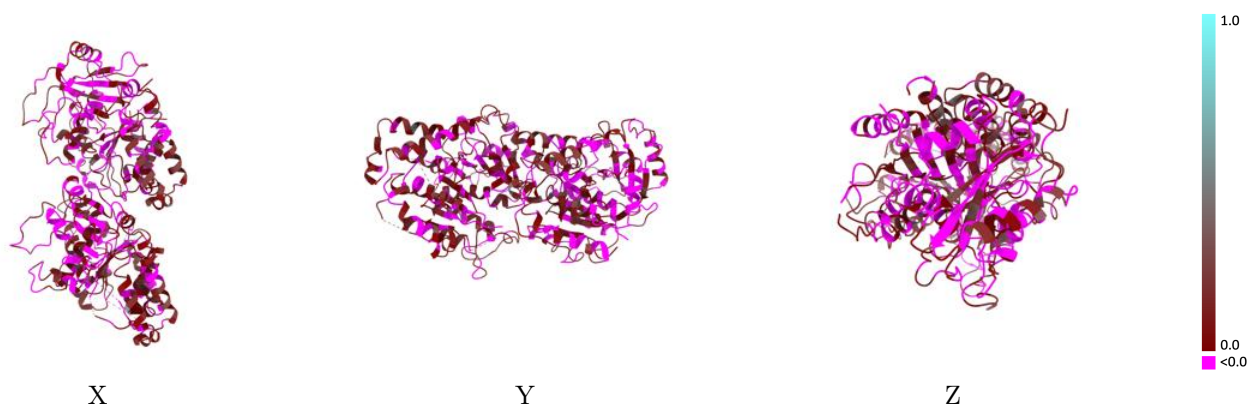
This section contains information regarding the fit between EMDB map EMD-2697 and PDB model 3J7I. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



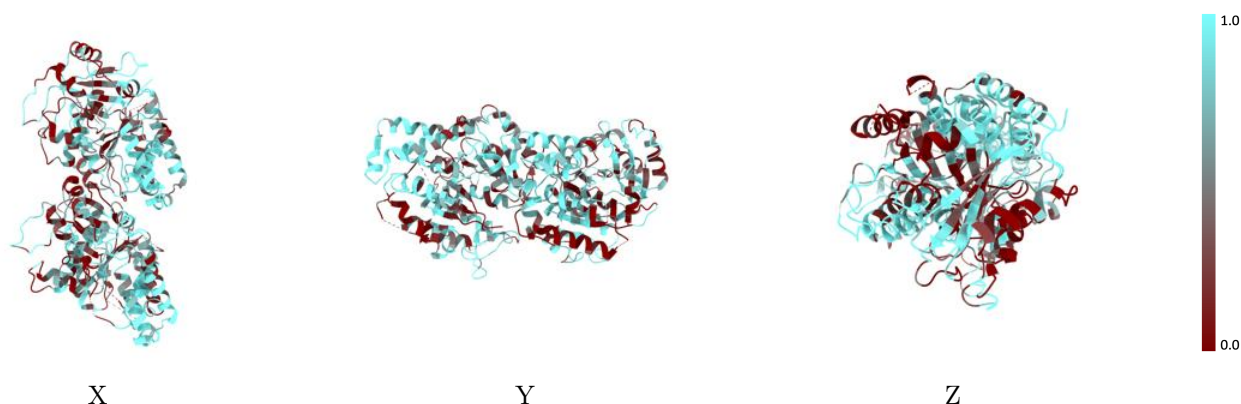
The images above show the 3D surface view of the map at the recommended contour level 156.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



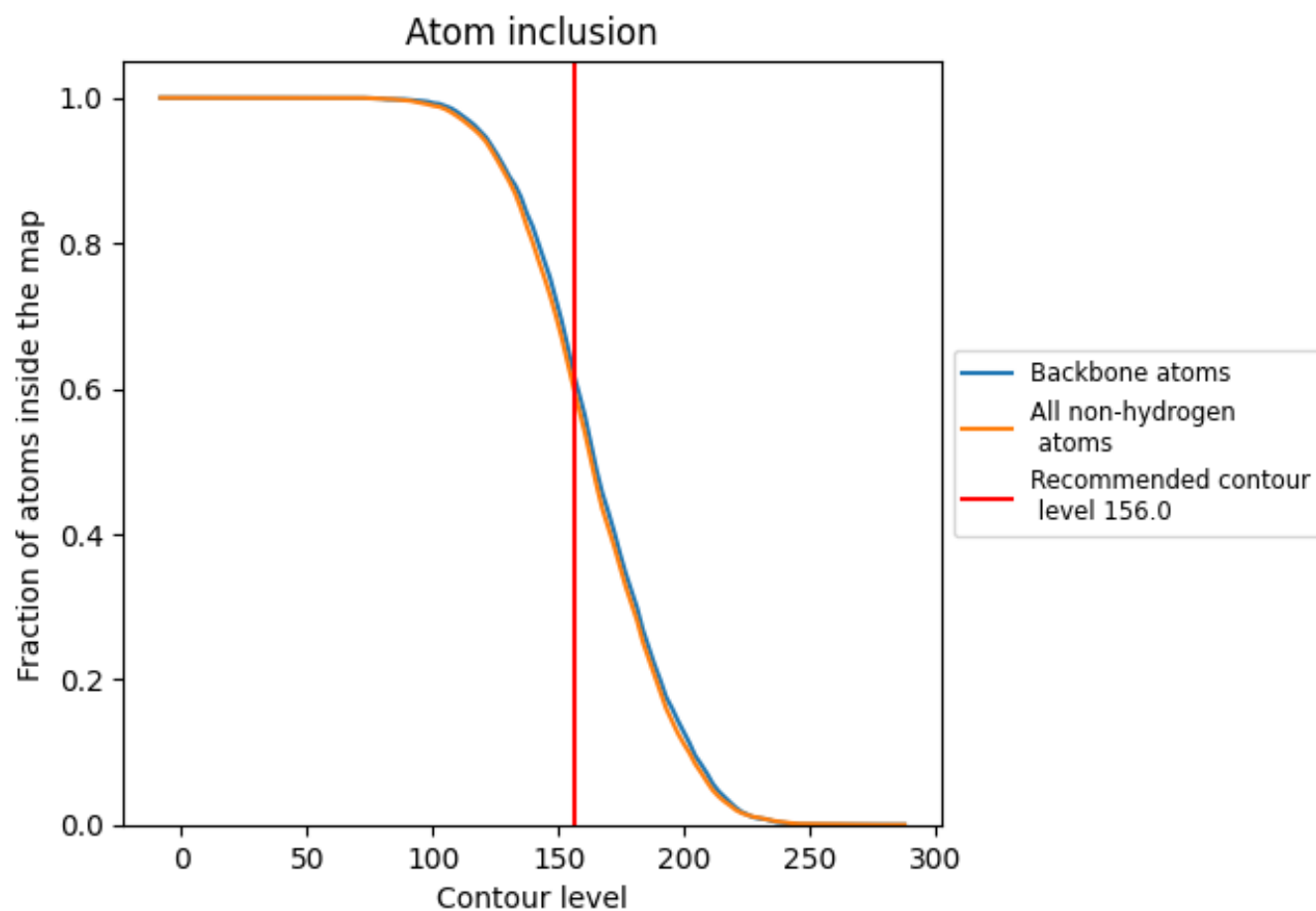
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (156.0).

9.4 Atom inclusion [i](#)



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

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	<div></div> 0.5999	<div></div> 0.0380
A	<div></div> 0.5917	<div></div> 0.0340
B	<div></div> 0.6080	<div></div> 0.0420

