



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:49 AM UTC

PDB ID : 3J7I / pdb_00003j7i
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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

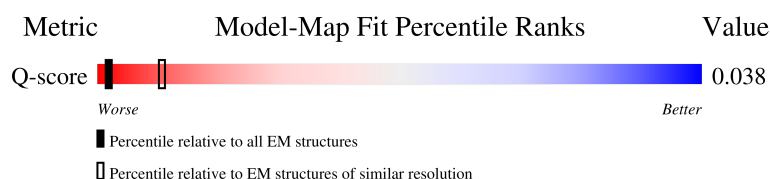
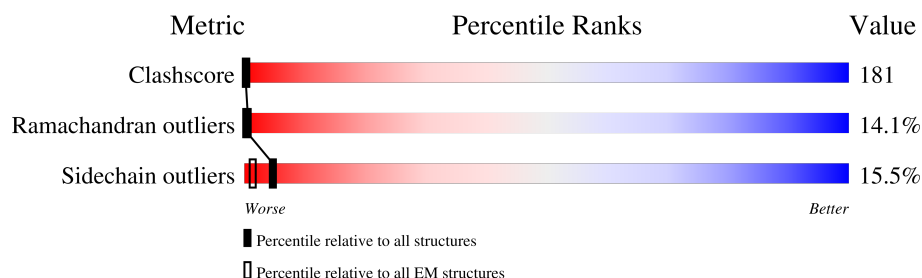
1 Overall quality at a glance

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	258 (8.40 - 9.40)

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 (CCD ID: 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 (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

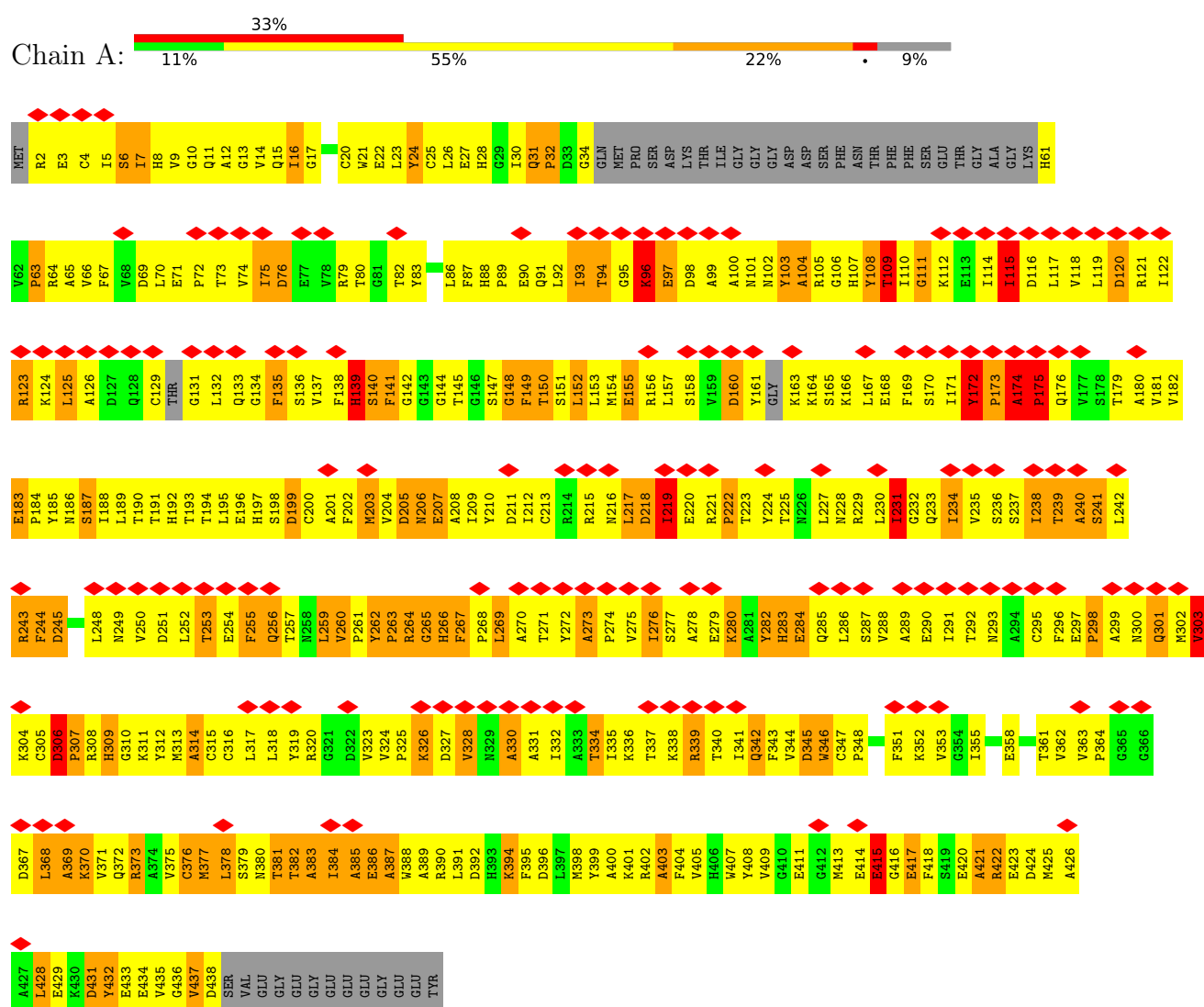


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
4	B	1	Total	C	N	O	P	0
			32	10	5	14	3	

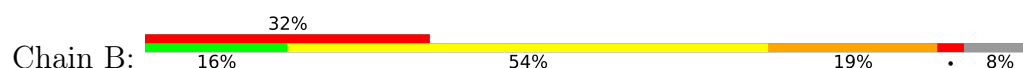
3 Residue-property plots

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



THR	S374	D306	G246	N186	S126	I66	MET
ALA	A375	P307	Q247	A187	E127	L67	R2
GLU	T376	R308	L248	T188	S128	V68	E3
GLN	F377	H309	N249	L189	CYS	D69	I4
GLU	G379	G310	A250	V191	C131	L70	V5
PHE	N380	R311	D251	H192	L132	E71	H6
GLU	S381	L313	L252	L194	Q193	P72	I7
GLU	T382	R253	R253	V195	Q133	G73	Q8
GLU	A363	T314	K254	V195	G134	T74	A9
GLY	T384	V315	L255	E196	F135	M75	G10
GLU	Q386	A316	A256	T197	Q136	D76	Q11
ASP	E386	A317	V257	T198	L137	S77	G12
ASP	F388	V318	N258	D199	T138	V78	G13
GLU	K389	F319	M259	E200	H139	R79	N14
ALA	R390	R320	V260	T201	SER	S90	Q15
	I391	G321	P261	Y202	LEU	G81	I16
		R322	F262	C203	G142	P82	G17
		M323	P263	I204	G143	F83	A18
		S324	R264	D205	G144	G84	K19
		M325	L265	N206	T145	F84	P20
		K326	H266	E207	G146	Q85	W21
		E327	F267	A208	S147	I86	E22
		V328	F268	L209	G148	F87	V23
		D329	M269	Y210	M149	P88	I24
		E330	P270	D211	G150	P89	S25
		Q331	G271	I212	T151	D90	D26
		M332	F272	C213	L152	N91	E27
		L333	A273	F214	L153	F92	H28
		N334	P274	R215	I154	V93	I30
		V335	L275	T216	S155	F94	D31
		Q336	T276	L217	K156	GLY	P32
		N337	S277	K218	I157	GLN	T33
		K338	G279	L219	E158	S97	G34
		N339	S280	T220	E160	G98	Y36
		S340	Q281	T221	TYR	A99	H37
		S341	Q282	T222	ASP	G100	G38
		Y342	Y283	T223	R164	N101	D39
		F343	R284	Y224	I165	N102	S40
		V344	A285	G225	N166	W103	D41
		E345	L286	D226	N167	K105	L42
		W346	T287	L227	T168	G106	L43
		I347	V288	N228	F169	H107	L44
		P348	P289	H229	S170	T109	E47
		N349	E290	L230	V171	E110	R48
		N350	L291	V231	V172	N50	I49
		V351	T292	S232	P173	G111	N50
		K352	Q293	A233	SER	A112	V51
		T353	Q294	T234	PR0	E113	Y52
		A354	M295	M235	LYS	L114	Y53
		V355	F296	S236	VAL	V115	N54
		C356	D297	G237	SER	D116	A57
		D357	A298	V238	D179	S117	G58
		I358	K299	T239	T180	V118	N59
		P359	N300	T240	V181	V118	P63
		R360	M301	C241	V182	L119	R64
		R369	M302	R243	P184	D120	A65
		G370	A303	F244	Y185	V121	
		L371	A304	P245		V122	
		K372	C305			R123	
		M373				K124	
						E125	

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	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	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: MG, GTP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.69	7/3281 (0.2%)	1.13	32/4453 (0.7%)
2	B	0.74	8/3306 (0.2%)	1.28	40/4469 (0.9%)
All	All	0.71	15/6587 (0.2%)	1.21	72/8922 (0.8%)

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 (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	205	ASP	CA-C	9.98	1.66	1.52
2	B	205	ASP	CA-CB	-8.76	1.38	1.53
1	A	383	ALA	C-N	8.57	1.45	1.33
2	B	205	ASP	CB-CG	-8.07	1.31	1.52
1	A	203	MET	CA-C	-7.80	1.44	1.53
2	B	385	GLN	CA-C	-7.08	1.43	1.52
1	A	205	ASP	CA-C	-6.98	1.42	1.52
2	B	205	ASP	C-N	6.64	1.43	1.33
2	B	204	ILE	CA-CB	-6.51	1.45	1.54
2	B	363	ALA	CA-C	-6.42	1.44	1.52
2	B	204	ILE	C-N	6.00	1.42	1.33
1	A	381	THR	N-CA	-5.89	1.38	1.45
1	A	173	PRO	N-CD	5.50	1.55	1.47
1	A	307	PRO	N-CD	5.24	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	298	PRO	N-CD	5.03	1.54	1.47

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	205	ASP	CA-CB-CG	-19.48	93.12	112.60
1	A	383	ALA	CA-C-O	-18.14	101.49	120.90
2	B	203	CYS	CA-C-N	12.04	143.65	121.97
2	B	203	CYS	C-N-CA	12.04	143.65	121.97
1	A	205	ASP	CA-CB-CG	-11.55	101.05	112.60
2	B	205	ASP	CA-C-N	-11.46	101.19	120.68
2	B	205	ASP	C-N-CA	-11.46	101.19	120.68
2	B	204	ILE	CA-C-O	-10.58	107.56	120.78
2	B	385	GLN	CA-C-N	-10.46	102.33	122.61
2	B	385	GLN	C-N-CA	-10.46	102.33	122.61
1	A	382	THR	N-CA-C	-10.24	99.93	111.71
2	B	262	PHE	CA-C-N	9.97	132.31	119.84
2	B	262	PHE	C-N-CA	9.97	132.31	119.84
1	A	381	THR	N-CA-C	-8.99	96.92	110.14
2	B	381	SER	CA-C-N	-8.86	108.19	122.36
2	B	381	SER	C-N-CA	-8.86	108.19	122.36
1	A	382	THR	CA-C-N	8.56	132.09	120.54
1	A	382	THR	C-N-CA	8.56	132.09	120.54
2	B	205	ASP	N-CA-CB	-8.17	96.69	110.49
2	B	77	SER	N-CA-C	-7.87	104.28	114.04
2	B	204	ILE	CA-CB-CG2	-7.87	97.12	110.50
2	B	205	ASP	N-CA-C	7.87	127.55	110.80
2	B	159	GLU	N-CA-C	-7.81	104.23	114.31
2	B	313	LEU	N-CA-C	-7.76	103.78	113.55
1	A	428	LEU	N-CA-C	-7.57	104.28	113.97
2	B	208	ALA	N-CA-C	-7.48	102.81	112.23
2	B	293	GLN	N-CA-C	-7.41	102.90	110.97
2	B	399	PHE	N-CA-C	-7.01	103.57	111.07
2	B	388	PHE	N-CA-C	-7.00	104.00	112.54
2	B	22	GLU	N-CA-C	-6.96	103.39	110.97
1	A	422	ARG	N-CA-C	-6.85	103.05	111.40
1	A	385	ALA	N-CA-C	-6.83	103.06	111.33
2	B	389	LYS	N-CA-C	-6.71	103.66	110.97
2	B	384	ILE	N-CA-C	-6.58	95.66	109.34
1	A	123	ARG	N-CA-C	-6.51	105.91	114.31
2	B	363	ALA	CB-CA-C	-6.51	98.79	110.70
2	B	202	TYR	CA-C-N	6.43	133.82	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	202	TYR	C-N-CA	6.43	133.82	121.54
2	B	217	LEU	N-CA-C	-6.40	96.54	107.23
2	B	27	GLU	N-CA-C	-6.21	106.06	113.21
1	A	380	ASN	CA-C-N	-6.17	112.00	123.05
1	A	380	ASN	C-N-CA	-6.17	112.00	123.05
2	B	363	ALA	N-CA-CB	6.11	119.30	110.20
2	B	181	VAL	N-CA-C	6.09	116.83	111.90
2	B	88	ARG	N-CA-C	-5.96	102.26	109.83
2	B	382	THR	CA-C-N	5.96	130.77	120.58
2	B	382	THR	C-N-CA	5.96	130.77	120.58
2	B	243	ARG	N-CA-C	-5.95	106.67	112.97
2	B	247	GLN	N-CA-C	-5.93	104.81	111.28
1	A	301	GLN	N-CA-C	5.93	121.49	112.54
1	A	264	ARG	N-CA-C	-5.92	101.54	110.24
1	A	231	ILE	N-CA-C	-5.85	103.95	110.62
2	B	296	PHE	N-CA-C	5.83	120.09	113.15
1	A	415	GLU	N-CA-C	-5.56	105.60	112.38
1	A	262	TYR	CA-C-N	5.55	126.78	119.84
1	A	262	TYR	C-N-CA	5.55	126.78	119.84
1	A	75	ILE	N-CA-C	-5.48	104.24	111.09
1	A	306	ASP	CA-C-N	-5.42	113.06	119.84
1	A	306	ASP	C-N-CA	-5.42	113.06	119.84
2	B	59	ASN	N-CA-C	-5.40	105.72	114.09
1	A	259	LEU	N-CA-C	5.39	120.87	113.97
1	A	172	TYR	CA-C-N	-5.34	113.17	119.84
1	A	172	TYR	C-N-CA	-5.34	113.17	119.84
1	A	297	GLU	CA-C-N	-5.22	113.31	119.84
1	A	297	GLU	C-N-CA	-5.22	113.31	119.84
1	A	429	GLU	N-CA-C	-5.21	106.08	112.90
1	A	241	SER	N-CA-C	5.12	116.86	111.28
1	A	175	PRO	CA-N-CD	-5.11	104.84	112.00
1	A	421	ALA	N-CA-C	-5.09	107.10	113.72
2	B	289	PRO	N-CA-C	-5.09	107.22	113.84
1	A	174	ALA	CA-C-N	-5.01	113.58	119.84
1	A	174	ALA	C-N-CA	-5.01	113.58	119.84

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	1190	0
2	B	3239	0	3118	1186	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	32	0	12	61	0
4	B	32	0	12	27	0
All	All	6515	0	6265	2308	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 181.

All (2308) 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)
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: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
2:B:169:PHE:CD1	2:B:235:MET:HE3	1.31	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:413:MET:CE	2:B:418:PHE:CE1	1.85	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:185:TYR:HE1	2:B:399:PHE:CD1	0.93	1.56
2:B:413:MET:HE1	2:B:418:PHE:CE1	1.39	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:195:LEU:CD2	1:A:424:ASP:C	1.90	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
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:173:PRO:C	1:A:206:ASN:HB3	1.46	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:154:MET:HE3	1:A:197:HIS:ND1	1.10	1.36
1:A:12:ALA:HB2	4:A:502:GTP:C1'	1.51	1.36
1:A:150:THR:C	1:A:197:HIS:CE1	2.04	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
1:A:154:MET:HE3	1:A:197:HIS:CG	1.61	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:16:ILE:HG13	2:B:228:ASN:CG	1.53	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:192:HIS:C	2:B:424:ASN:ND2	1.89	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
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:HE2	1:A:197:HIS:CE1	1.66	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
1:A:154:MET:CE	1:A:197:HIS:CE1	2.17	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
1:A:108:TYR:HB3	1:A:411:GLU:O	1.17	1.26
2:B:184:PRO:HB2	2:B:395:PHE:CA	1.65	1.25
2:B:206:ASN:ND2	4:B:502:GTP:C1'	1.98	1.25
1:A:188:ILE:HD11	1:A:392:ASP:O	1.32	1.25
1:A:190:THR:O	1:A:194:THR:HB	1.26	1.25
2:B:194:LEU:CB	2:B:265:LEU:CD2	1.78	1.25
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:206:ASN:CG	4:B:502:GTP:H1'	1.63	1.22
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
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
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:103:TYR:CE2	1:A:413:MET:HE1	1.76	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:195:LEU:HD22	1:A:424:ASP:C	1.53	1.18
1:A:182:VAL:HG12	1:A:404:PHE:CZ	1.76	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
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
2:B:385:GLN:HB3	2:B:429:VAL:HG13	1.22	1.17
2:B:192:HIS:C	2:B:424:ASN:HD21	1.48	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:413:MET:HE1	2:B:418:PHE:CZ	1.80	1.15
2:B:195:VAL:HA	2:B:264:ARG:O	1.45	1.14
1:A:122:ILE:HB	1:A:135:PHE:CE2	1.82	1.14
1:A:243:ARG:NH2	1:A:252:LEU:H	1.45	1.14
2:B:188:THR:HA	2:B:425:MET:CE	1.77	1.14
2:B:204:ILE:HD13	2:B:231:VAL:HG13	1.24	1.14
2:B:16:ILE:HA	2:B:228:ASN:HB3	1.15	1.14
1:A: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:188:THR:CA	2:B:425:MET:HE3	1.78	1.13
2:B:192:HIS:CG	2:B:424:ASN:CG	2.07	1.13
2:B:262:PHE:CE2	2:B:435:TYR:CD2	2.37	1.13
2:B:192:HIS:O	2:B:195:VAL:CG1	1.96	1.13
2:B:395:PHE:CD2	2:B:422:GLU:CD	2.26	1.13
2:B:102:ASN:HA	2:B:408:TYR:CE2	1.84	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:413:MET:HE3	2:B:418:PHE:CE1	1.65	1.09
2:B:105:LYS:CE	2:B:110:GLU:HG2	1.68	1.09
2:B:154:ILE:HD12	2:B:197:ASN:CG	1.78	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
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:195:VAL:HG23	2:B:263:PRO:C	1.78	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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:154:MET:HE1	1:A:198:SER:HB2	1.32	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:105:LYS:HE3	2:B:110:GLU:CD	1.78	1.06
1:A:392:ASP:CB	1:A:425:MET:HE3	1.86	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
1:A:173:PRO:C	1:A:206:ASN:CB	2.28	1.05
1:A:392:ASP:CG	1:A:425:MET:HE3	1.81	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:392:ASP:HB2	1:A:425:MET:CE	1.86	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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
1:A:191:THR:C	1:A:194:THR:HG22	1.81	1.04
1:A:199:ASP:C	1:A:265:GLY:O	1.99	1.04
2:B:363:ALA:HB1	2:B:433:GLN:HA	1.11	1.04
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
1:A:154:MET:HB3	1:A:197:HIS:O	1.57	1.03
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
2:B:346:TRP:CE3	2:B:435:TYR:C	2.33	1.03
2:B:346:TRP:HE3	2:B:435:TYR:C	1.65	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:413:MET:HE3	2:B:418:PHE:HE1	0.86	1.02
1:A:182:VAL:O	1:A:398:MET:SD	2.18	1.02
1:A:26:LEU:CG	1:A:361:THR:HG21	1.90	1.01
2:B:105:LYS:NZ	2:B:411:GLU:OE1	1.93	1.01
2:B:169:PHE:CG	2:B:235:MET:HE3	1.95	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:195:LEU:CD2	1:A:424:ASP:HB3	1.89	1.00
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:HB2	1:A:425:MET:HE3	1.38	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:154:ILE:HD12	2:B:197:ASN:CB	1.83	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
2:B:261:PRO:C	2:B:435:TYR:HE2	1.70	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:184:PRO:HB2	2:B:395:PHE:HA	1.41	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:188:ILE:HD11	1:A:392:ASP:C	1.89	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:188:THR:HA	2:B:425:MET:HE3	1.01	0.97
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
2:B:102:ASN:ND2	2:B:408:TYR:C	2.20	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
2:B:332:MET:HE3	2:B:351:VAL:HG11	1.45	0.97
2:B:266:HIS:CE1	2:B:428:LEU:HD11	2.00	0.97
1:A:150:THR:C	1:A:197:HIS:HE1	1.73	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:154:MET:HB3	1:A:197:HIS:C	1.90	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:135:PHE:CE1	1:A:157:LEU:CD1	2.49	0.95
2:B:105:LYS:CE	2:B:110:GLU:CD	2.38	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
1:A:105:ARG:HA	1:A:411:GLU:OE1	1.68	0.94
1:A:154:MET:CE	1:A:198:SER:HB2	1.96	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
1:A:195:LEU:HD21	1:A:424:ASP:C	1.72	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:161:TYR:C	1:A:163:LYS:HB3	1.95	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:205:ASP:CG	2:B:208:ALA:HB3	1.94	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
1:A:31:GLN:HB3	1:A:32:PRO:HD2	1.51	0.92
1:A:103:TYR:HE2	1:A:413:MET:HE1	1.23	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
2:B:261:PRO:C	2:B:435:TYR:CE2	2.46	0.91
1:A:122:ILE:HB	1:A:135:PHE:HE2	1.34	0.91
2:B:16:ILE:CG1	2:B:228:ASN:CG	2.37	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:395:PHE:HD2	2:B:422:GLU:CD	1.76	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: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
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
2:B:323:MET:HE2	2:B:328:VAL:HG22	1.54	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:199:ASP:O	1:A:265:GLY:C	2.16	0.88
1:A:405:VAL:CB	1:A:408:TYR:CE2	2.57	0.88
1:A:104:ALA:C	1:A:411:GLU:OE1	2.17	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
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
1:A:392:ASP:CG	1:A:425:MET:CE	2.47	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
2:B:204:ILE:HG12	2:B:302:MET:SD	2.15	0.87
2:B:16:ILE:HG13	2:B:228:ASN:CB	1.87	0.87
1:A:173:PRO:CB	1:A:174:ALA:HB3	2.04	0.86
2:B:311:ARG:HD3	2:B:342:TYR:HA	1.56	0.86
2:B:194:LEU:HD13	2:B:267:PHE:HE1	1.40	0.86
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
2:B:408:TYR:C	2:B:413:MET:SD	2.57	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:16:ILE:HG12	2:B:228:ASN:C	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:105:ARG:HA	1:A:411:GLU:CD	2.01	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
2:B:195:VAL:HA	2:B:264:ARG:C	2.01	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
2:B:169:PHE:HD1	2:B:235:MET:HE3	1.35	0.84
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:154:ILE:CD1	2:B:197:ASN:CG	2.42	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
1:A:192:HIS:C	1:A:421:ALA:HB1	1.96	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:MET:HB3	1:A:166:LYS:HD2	1.57	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: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: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
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
2:B:184:PRO:C	2:B:395:PHE:HD1	1.87	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
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: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
2:B:194:LEU:C	2:B:265:LEU:HD23	2.04	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:132:LEU:CG	1:A:164:LYS:HE3	2.08	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:363:ALA:HB3	2:B:436:GLN:CD	2.05	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
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
1:A:154:MET:SD	1:A:197:HIS:C	2.64	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: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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:8:GLN:CD	2:B:67:LEU:HD22	2.08	0.79
2:B:169:PHE:CE1	2:B:235:MET:HE3	2.16	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
1:A:392:ASP:HA	1:A:425:MET:HE1	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
2:B:54:ASN:HD21	2:B:64:ARG:HD3	1.45	0.79
2:B:203:CYS:C	2:B:270:PRO:HD2	2.08	0.79
1:A:184:PRO:CG	1:A:398:MET:SD	2.68	0.79
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
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:242:LEU:HD13	2:B:250:ALA:C	2.08	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:392:ASP:CB	1:A:425:MET:HE1	2.14	0.77
1:A:27:GLU:OE1	1:A:241:SER:HB3	1.84	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
1:A:154:MET:CE	1:A:197:HIS:CG	2.42	0.77
2:B:154:ILE:CD1	2:B:197:ASN:HD22	1.95	0.77
2:B:409:THR:N	2:B:413:MET:CG	2.47	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
2:B:204:ILE:HG22	2:B:205:ASP:N	1.96	0.77
2:B:204:ILE:CD1	2:B:231:VAL:HG13	2.11	0.77
2:B:171:VAL:HG11	2:B:206:ASN:OD1	1.84	0.76
2:B:310:GLY:HA2	2:B:386:GLU:OE1	1.85	0.76
1:A:283:HIS:CE1	1:A:286:LEU:HD13	2.19	0.76
2:B:169:PHE:CE1	2:B:235:MET:CE	2.68	0.76
2:B:325:MET:HE1	2:B:355:VAL:HG11	1.67	0.76
1:A:224:TYR:HD2	2:B:322:ARG:HH21	1.32	0.76
1:A:264:ARG:C	1:A:266:HIS:H	1.91	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:OE1	1.86	0.76
1:A:11:GLN:HB3	4:A:502:GTP:PA	2.26	0.76
2:B:262:PHE:HZ	2:B:434:GLN:C	1.93	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:346:TRP:HB3	2:B:436:GLN:C	2.11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:TYR:CE2	1:A:413:MET:CE	2.64	0.76
1:A:154:MET:SD	1:A:198:SER:HB2	2.23	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:217:LEU:C	2:B:219:LEU:H	1.91	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:188:ILE:CD1	1:A:392:ASP:C	2.52	0.75
2:B:171:VAL:CG1	2:B:205:ASP:C	2.59	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
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
2:B:171:VAL:HG13	2:B:205:ASP:C	2.12	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
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:154:MET:CB	1:A:197:HIS:C	2.61	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:205:ASP:OD1	2:B:209:LEU:HD13	1.88	0.74
1:A:205:ASP:CG	1:A:209:ILE:HD12	2.13	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:165:ILE:HG13	2:B:252:LEU:HD12	1.67	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:88:HIS:C	1:A:90:GLU:H	1.95	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:63:PRO:C	1:A:64:ARG:HG2	2.12	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
1:A:195:LEU:CD2	1:A:424:ASP:O	2.06	0.73
2:B:262:PHE:CZ	2:B:434:GLN:CA	2.72	0.73
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:194:LEU:C	2:B:265:LEU:CD2	2.62	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
2:B:103:TRP:CE3	2:B:417:GLU:CD	2.67	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:194:LEU:C	2:B:265:LEU:HB3	2.14	0.72
2:B:346:TRP:CZ3	2:B:435:TYR:CG	2.76	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:195:VAL:HG11	2:B:264:ARG:HH12	1.52	0.72
2:B:262:PHE:CZ	2:B:434:GLN:C	2.67	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:133:GLN:NE2	1:A:256:GLN:CD	2.46	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
2:B:66:ILE:C	2:B:67:LEU:HD23	2.15	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
1:A:234:ILE:HG21	1:A:302:MET:HE1	1.73	0.71
1:A:7:ILE:HD11	1:A:137:VAL:HG22	1.71	0.71
2:B:16:ILE:HG12	2:B:228:ASN:HB3	1.62	0.71
2:B: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
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
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
1:A:392:ASP:CA	1:A:425:MET:HE1	2.20	0.71
2:B:262:PHE:CZ	2:B:435:TYR:CG	2.79	0.71
1:A:210:TYR:CE1	1:A:227:LEU:CD1	2.70	0.70
1:A:244:PHE:HD1	1:A:245:ASP:N	1.89	0.70
2:B:194:LEU:CG	2:B:265:LEU:CD2	2.69	0.70
2:B:311:ARG:HB2	2:B:436:GLN:NE2	2.06	0.70
1:A:259:LEU:HD11	1:A:378:LEU:CD1	2.20	0.70
2:B:105:LYS:HE3	2:B:110:GLU:HG2	1.53	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:167:ASN:HD21	2:B:252:LEU:HD22	1.55	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
2:B:265:LEU:HD12	2:B:265:LEU:C	2.16	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: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
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: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:180:THR:HG22	2:B:181:VAL:N	2.07	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
1:A:402:ARG:O	1:A:403:ALA:C	2.36	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:69:ASP:O	1:A:94:THR:C	2.35	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
2:B:155:SER:HG	2:B:197:ASN:ND2	1.91	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: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:325:MET:HA	2:B:325:MET:HE3	1.73	0.69
2:B:395:PHE:HD2	2:B:422:GLU:OE2	1.76	0.69
1:A:234:ILE:HD13	1:A:234:ILE:C	2.18	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
2:B:301:MET:HE1	2:B:377:PHE:HE2	1.58	0.69
1:A:282:TYR:O	1:A:284:GLU:N	2.24	0.69
2:B:230:LEU:HD21	2:B:302:MET:HE2	1.74	0.69
2:B:395:PHE:HD2	2:B:422:GLU:OE1	1.61	0.69
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
2:B:395:PHE:CE2	2:B:422:GLU:CD	2.63	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:184:PRO:C	2:B:395:PHE:CD1	2.70	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
1:A:220:GLU:C	1:A:222:PRO:HD3	2.19	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
1:A:343:PHE:HZ	1:A:351:PHE:CE2	2.10	0.68
2:B:4:ILE:HG21	2:B:136:GLN:HG2	1.76	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:A:305:CYS:SG	1:A:383:ALA:C	2.77	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
1:A:6:SER:HB3	1:A:136:SER:HG	1.59	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
2:B:325:MET:CE	2:B:355:VAL:HG21	2.24	0.67
2:B:171:VAL:C	2:B:205:ASP:HA	2.20	0.67
2:B:243:ARG:HH22	2:B:252:LEU:HG	1.59	0.67
1:A:234:ILE:CB	1:A:302:MET:HE1	2.24	0.67
2:B:185:TYR:CG	2:B:418:PHE:CD2	2.83	0.67
2:B:324:SER:C	2:B:326:LYS:H	2.03	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:315:CYS:HB3	1:A:377:MET:HE1	1.78	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:105:LYS:HD3	2:B:411:GLU:C	2.21	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
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:341:ILE:O	1:A:341:ILE:HG12	1.95	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
1:A:184:PRO:HB2	1:A:394:LYS:C	2.21	0.65
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: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:188:THR:O	2:B:425:MET:HB2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:345:ASP:C	1:A:347:CYS:H	2.04	0.65
2:B:262:PHE:O	2:B:266:HIS:NE2	2.30	0.65
1:A:98:ASP:CG	2:B:2:ARG:NH1	2.55	0.65
1:A:123:ARG:HA	1:A:161:TYR:HH	1.61	0.65
1:A:209:ILE:CG2	1:A:227:LEU:HD22	2.27	0.65
2:B:169:PHE:HD1	2:B:235:MET:CE	1.98	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:173:PRO:HB2	1:A:174:ALA:C	2.22	0.64
1:A:234:ILE:CG2	1:A:302:MET:HE1	2.27	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
1:A:179:THR:C	2:B:248:LEU:HD22	2.23	0.64
1:A:311:LYS:HE3	1:A:342:GLN:CD	2.22	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
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: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:282:GLN:HG2	2:B:282:GLN:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:269:LEU:O	1:A:378:LEU:HA	1.98	0.63
2:B:284:ARG:O	2:B:286:LEU:N	2.31	0.63
2:B:318:VAL:HA	2:B:354:ALA:HB3	1.81	0.63
2:B:103:TRP:HE3	2:B:417:GLU:CD	2.05	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: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
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
1:A:179:THR:C	2:B:248:LEU:CD2	2.72	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:192:HIS:ND1	2:B:424:ASN:CG	2.41	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: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
2:B:188:THR:CB	2:B:425:MET:HE3	2.29	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:402:ARG:C	1:A:405:VAL:HG13	2.24	0.62
2:B:349:ASN:C	2:B:349:ASN:HD22	2.07	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:194:LEU:O	2:B:265:LEU:HD22	2.00	0.62
1:A:88:HIS:C	1:A:90:GLU:N	2.57	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
2:B:105:LYS:HE2	2:B:110:GLU:HG3	0.63	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
2:B:205:ASP:CG	2:B:208:ALA:CB	2.72	0.61
1:A:179:THR:C	2:B:248:LEU:CD1	2.73	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:253:ARG:O	2:B:254:LYS:C	2.42	0.61
2:B:324:SER:CB	2:B:327:GLU:HG2	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:242:LEU:C	1:A:244:PHE:H	2.09	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
2:B:283:TYR:C	2:B:284:ARG:HG2	2.25	0.60
1:A:262:TYR:CE2	1:A:435:VAL:HG22	2.36	0.60
1:A:436:GLY:C	1:A:438:ASP:H	2.08	0.60
1:A:104:ALA:HB2	1:A:408:TYR:CA	2.15	0.60
1:A:191:THR:HG23	1:A:192:HIS:N	2.13	0.60
2:B:31:ASP:O	2:B:32:PRO:C	2.44	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:HIS:HD2	2:B:151:THR:CG2	2.12	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
2:B:206:ASN:CG	4:B:502:GTP:C1'	2.52	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:173:PRO:O	1:A:206:ASN:CG	2.44	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:324:SER:C	2:B:326:LYS:N	2.59	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:409:VAL:C	1:A:411:GLU:H	2.09	0.59
2:B:230:LEU:CD2	2:B:302:MET:HE2	2.32	0.59
1:A:392:ASP:OD2	1:A:425:MET:HE3	2.02	0.59
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
2:B:103:TRP:CZ3	2:B:417:GLU:CD	2.80	0.59
1:A:115:ILE:O	1:A:115:ILE:HD13	2.02	0.59
1:A:172:TYR:CD2	1:A:173:PRO:CD	2.86	0.59
1:A:205:ASP:OD1	1:A:209:ILE:HD12	2.03	0.59
1:A:264:ARG:HG2	1:A:431:ASP:OD2	2.02	0.59
1:A:405:VAL: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
1:A:234:ILE:HB	1:A:302:MET:HE1	1.85	0.59
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:LYS:CD	1:A:197:HIS:O	2.35	0.59
1:A:248:LEU:CD2	1:A:353:VAL:O	2.49	0.59
1:A:135:PHE:HE1	1:A:157:LEU:CD1	2.00	0.59
1:A:228:ASN:OD1	1:A:229:ARG:N	2.36	0.59
2:B:167:ASN:HD21	2:B:252:LEU:HD21	1.65	0.59
2:B:258:ASN:HD22	2:B:352:LYS:CD	2.14	0.59
1:A:142:GLY:HA3	1:A:172:TYR:CE2	2.38	0.59
1:A:199:ASP: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
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:371:VAL:HG12	1:A:372:GLN:N	2.17	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:339:ARG:C	1:A:341:ILE:H	2.11	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
2:B:114:LEU:HD23	2:B:149:MET:HE1	1.85	0.58
1:A:101:ASN:CG	2:B:254:LYS:HZ3	2.09	0.58
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:206:ASN:CG	4:B:502:GTP:O2'	2.46	0.58
2:B:299:LYS:O	2:B:300:ASN:CB	2.51	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
2:B:180:THR:CG2	2:B:181:VAL:H	2.17	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:150:THR:O	1:A:151:SER:C	2.47	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:319:PHE:HA	2:B:375:ALA:HA	1.86	0.57
2:B:401:ARG:HG3	2:B:401:ARG:O	2.04	0.57
2:B:229:HIS:C	2:B:229:HIS:ND1	2.62	0.57
2:B:267:PHE:HB2	2:B:388:PHE:CZ	2.39	0.57
1:A:152:LEU:HA	1:A:155:GLU:CB	2.35	0.57
1:A:173:PRO:HB2	1:A:174:ALA:CA	2.35	0.57
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:209:LEU:O	2:B:210:TYR:C	2.48	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ASP:O	1:A:219:ILE:HG23	2.04	0.57
2:B:217:LEU:C	2:B:219:LEU:N	2.55	0.57
2:B:320:ARG:O	2:B:359:PRO:HA	2.04	0.57
1:A:145:THR:O	1:A:145:THR:HG22	2.03	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
1:A:115:ILE:HD13	1:A:115:ILE:C	2.28	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: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: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:49:ILE:O	2:B:50:ASN:C	2.48	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
2:B:301:MET:CE	2:B:377:PHE:HE2	2.17	0.56
1:A:109:THR:HB	1:A:411:GLU:CD	2.30	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:215:ARG:C	1:A:216:ASN:HD22	2.12	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
1:A:224:TYR:CE1	4:A:502:GTP:C6	2.92	0.56
1:A:244:PHE:CD1	1:A:244:PHE:C	2.83	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:319:PHE:CD2	2:B:375:ALA:HB2	2.40	0.56
2:B:345:GLU:C	2:B:347:ILE:H	2.12	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
1:A:105:ARG:CA	1:A:411:GLU:CD	2.72	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
1:A:154:MET:SD	1:A:197:HIS:CG	2.99	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:251:ASP:O	2:B:252:LEU:C	2.49	0.56
2:B:258:ASN:CG	2:B:352:LYS:HD2	2.31	0.56
1:A:220:GLU:C	1:A:222:PRO:CD	2.79	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:163:LYS:O	1:A:163:LYS:HG2	2.04	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: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
1:A:239:THR:O	1:A:240:ALA:C	2.48	0.55
2:B:67:LEU:HD23	2:B:67:LEU:N	2.22	0.55
2:B:205:ASP:CB	2:B:302:MET:O	2.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B: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
2:B:171:VAL:HG12	2:B:205:ASP:C	2.30	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:192:HIS:HA	2:B:424:ASN:CG	2.32	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
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:226:ASP:O	2:B:227:LEU:C	2.46	0.55
2:B:298:ALA:O	2:B:299:LYS:C	2.50	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:328:VAL:C	1:A:330:ALA:H	2.15	0.55
1:A:405:VAL:O	1:A:408:TYR:CE2	2.60	0.55
2:B:205:ASP:O	2:B:209:LEU:HD13	2.06	0.55
2:B: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:142:GLY:C	1:A:172:TYR:CE2	2.84	0.55
1:A:408:TYR:O	1:A:411:GLU:N	2.39	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
1:A:161:TYR:HB3	1:A:164:LYS:HG3	1.83	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A: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:305:CYS:O	1:A:306:ASP:C	2.51	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
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:369:ARG:HD2	2:B:369:ARG:C	2.32	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
2:B:363:ALA:C	2:B:385:GLN:N	2.66	0.54
1:A:98:ASP:O	1:A:110:ILE:HD13	2.08	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:133:GLN:CD	1:A:256:GLN:HE22	2.15	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
2:B:2:ARG:NE	2:B:48:ARG:NH2	2.53	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:188:THR:CA	2:B:425:MET:CE	2.58	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:169:PHE:CE1	2:B:235:MET:HE2	2.42	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:181:VAL:HG11	2:B:258:ASN:CG	2.32	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:16:ILE:N	2:B:228:ASN:CG	2.66	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: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
2:B:301:MET:HE1	2:B:377:PHE:CE2	2.43	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
1:A:264:ARG:HG3	1:A:431:ASP:CG	2.34	0.53
2:B:264:ARG:HD2	2:B:424:ASN:O	2.08	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:242:LEU:C	1:A:244:PHE:N	2.66	0.53
2:B:8:GLN:OE1	2:B:14:ASN:ND2	2.42	0.53
1:A:184:PRO:HA	1:A:187:SER:HG	1.72	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:115:ILE:O	1:A:116:ASP:C	2.51	0.53
1:A:151:SER:CA	1:A:197:HIS:CE1	2.92	0.53
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:297:ASP:OD1	2:B:298:ALA:N	2.39	0.53
2:B:399:PHE:O	2:B:400:ARG:C	2.52	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
1:A:405:VAL:C	1:A:408:TYR:CE2	2.86	0.52
2:B:189:LEU:HD21	2:B:418:PHE:C	2.33	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:192:HIS:O	2:B:424:ASN:ND2	2.08	0.52
2:B:322:ARG:HH11	2:B:322:ARG:HG3	1.74	0.52
2:B:325:MET:CE	2:B:355:VAL:HG11	2.38	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:188:THR:OG1	2:B:425:MET:HE3	2.10	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: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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:282:TYR:C	1:A:284:GLU:H	2.15	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:288:VAL:HG22	2:B:323:MET:HE3	1.90	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:171:VAL:HA	2:B:204:ILE:C	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:345:ASP:C	1:A:347:CYS:N	2.68	0.51
2:B:181:VAL:O	2:B:398:MET:HE1	2.11	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
2:B:185:TYR:OH	2:B:398:MET:C	2.53	0.51
1:A:34:GLY:C	1:A:61:HIS:N	2.68	0.51
1:A:122:ILE:HB	1:A:135:PHE:CD2	2.41	0.51
1:A:253:THR:O	1:A:254:GLU:C	2.52	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:224:TYR:O	2:B:225:GLY:C	2.53	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:231:ILE:HD13	1:A:231:ILE:N	2.24	0.51
1:A:255:PHE:O	1:A:256:GLN:C	2.53	0.51
2:B:16:ILE:N	2:B:228:ASN:ND2	2.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:TRP:HZ2	2:B:65:ALA:HB2	1.76	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
2:B:5:VAL:CG2	2:B:135:PHE:CD2	2.94	0.51
2:B:169:PHE:CD1	2:B:235:MET:HE2	2.34	0.51
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:288:VAL:CG2	2:B:323:MET:HE3	2.40	0.51
2:B:307:PRO:C	2:B:309:HIS:H	2.18	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:10:GLY:O	1:A:11:GLN:C	2.54	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:241:SER:C	1:A:244:PHE:HB3	2.36	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
1:A:434:GLU:C	1:A:436:GLY:H	2.18	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
1:A:383:ALA:C	1:A:385:ALA:N	2.69	0.50
2:B:185:TYR:CA	2:B:395:PHE:CE1	2.86	0.50
2:B:360:PRO:O	2:B:369:ARG:C	2.54	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:260:VAL:O	2:B:260:VAL:HG23	2.11	0.50
2:B:261:PRO:HB3	2:B:435:TYR:CG	2.40	0.50
2:B:281:GLN:C	2:B:283:TYR:N	2.67	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ILE:O	1:A:242:LEU:HB2	2.11	0.50
1:A:417:GLU:OE1	1:A:417:GLU:HA	2.10	0.50
2:B:195:VAL:CB	2:B:264:ARG:CA	2.90	0.50
2:B:262:PHE:CE2	2:B:435:TYR:CE2	2.95	0.50
2:B: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
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:339:ARG:C	1:A:341:ILE:N	2.68	0.50
1:A:408:TYR:CD1	1:A:409:VAL:N	2.80	0.50
1:A:413:MET:C	1:A:414:GLU:HG3	2.36	0.50
2:B:4:ILE:HG22	2:B:5:VAL:N	2.27	0.50
2:B:82:PRO:C	2:B:84:GLY:H	2.20	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:383:ALA:C	1:A:385:ALA:H	2.20	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:173:PRO:HA	1:A:206:ASN:C	2.37	0.50
1:A:402:ARG:O	1:A:403:ALA:O	2.29	0.50
1:A:22:GLU:O	1:A:23:LEU:C	2.54	0.49
1:A:150:THR:HB	1:A:197:HIS:CE1	2.32	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:218:ASP:C	1:A:219:ILE:HG12	2.37	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
1:A:63:PRO:C	1:A:64:ARG:CG	2.83	0.49
1:A:148:GLY:O	1:A:149:PHE:C	2.55	0.49
2:B:195:VAL:CB	2:B:264:ARG:C	2.85	0.49
2:B:266:HIS:HA	2:B:428:LEU:HD21	1.93	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
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
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:154:MET:HE1	1:A:194:THR:OG1	2.13	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: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:325:MET:HE2	2:B:355:VAL:HG21	1.92	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:242:LEU:C	2:B:244:PHE:H	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:332:MET:HE3	2:B:351:VAL:CG1	2.32	0.49
2:B:387:LEU:HD23	2:B:388:PHE:CD1	2.47	0.49
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:149:PHE:O	1:A:150:THR:C	2.56	0.48
1:A:189:LEU:CG	1:A:418:PHE:CE2	2.93	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
2:B:288:VAL:C	2:B:290:GLU:N	2.70	0.48
1:A:152:LEU:HD12	1:A:152:LEU:C	2.38	0.48
1:A:195:LEU:CD2	1:A:264:ARG:NH2	2.76	0.48
1:A:317:LEU:CD1	1:A:351:PHE:CD1	2.96	0.48
2:B:195:VAL:CG2	2:B:263:PRO:C	2.70	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:252:LEU:O	1:A:253:THR:C	2.56	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
2:B:409:THR:C	2:B:411:GLU:H	2.22	0.48
1:A:13:GLY:C	1:A:16:ILE:HG22	2.38	0.48
1:A:133:GLN:CD	1:A:256:GLN:NE2	2.72	0.48
1:A:184:PRO:CB	1:A:394:LYS:C	2.86	0.48
1:A:369:ALA:O	1:A:370:LYS:CB	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:332:MET:CE	2:B:351:VAL:HG11	2.32	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
1:A:263:PRO:O	1:A:264:ARG:C	2.56	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: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
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
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
1:A:148:GLY:O	1:A:151:SER:CB	2.61	0.48
2:B:239:THR:O	2:B:240:THR:C	2.56	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
2:B:307:PRO:C	2:B:309:HIS:N	2.70	0.47
2:B:382:THR:C	2:B:385:GLN:HA	2.39	0.47
1:A:110:ILE:O	1:A:111:GLY:C	2.57	0.47
1:A:115:ILE:CD1	1:A:115:ILE:C	2.87	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: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:72:PRO:O	2:B:73:GLY:C	2.58	0.47
2:B:156:LYS:HA	2:B:156:LYS:CE	2.38	0.47
2:B:182:VAL:O	2:B:183:GLU:C	2.56	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:15:GLN:C	2:B:228:ASN:ND2	2.73	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
2:B:26:ASP:C	2:B:28:HIS:H	2.21	0.47
2:B:41:ASP:O	2:B:47:GLU:CD	2.57	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:436:GLY:C	1:A:438:ASP:N	2.72	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
2:B:49:ILE:HG13	2:B:50:ASN:N	2.29	0.47
2:B:155:SER:HA	2:B:197:ASN:CG	2.39	0.47
2:B:185:TYR:OH	2:B:398:MET:O	2.33	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
2:B:259:MET:HE1	2:B:378:ILE:CG2	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:328:VAL:C	1:A:330:ALA:N	2.73	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
2:B:19:LYS:HE3	2:B:225:GLY:C	2.39	0.47
1:A:16:ILE:HG13	1:A:228:ASN:HB2	1.97	0.47
2:B:134:GLY:HA3	2:B:165:ILE:HG12	1.97	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:VAL:C	1:A:206:ASN:H	2.23	0.47
1:A:288:VAL:HG23	1:A:373:ARG:HH11	1.79	0.47
1:A:384:ILE:HG22	1:A:384:ILE:O	2.15	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:99:ALA:O	1:A:100:ALA:HB3	2.14	0.46
1:A:103:TYR:O	1:A:104:ALA:C	2.57	0.46
1:A:154:MET:HA	1:A:166:LYS:CD	2.45	0.46
1:A:230:LEU:O	1:A:231:ILE:C	2.57	0.46
1:A:243:ARG:NH2	1:A:252:LEU:CB	2.78	0.46
1:A:335:ILE:C	1:A:337:THR:N	2.73	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:346:TRP:CB	2:B:436:GLN:C	2.85	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:265:GLY:O	1:A:266:HIS:O	2.33	0.46
2:B:133:GLN:O	2:B:165:ILE:CD1	2.64	0.46
2:B:138:THR:HG22	2:B:235:MET:HE1	1.96	0.46
2:B:169:PHE:HD2	2:B:204:ILE:CD1	2.28	0.46
2:B:187:ALA:O	2:B:188:THR:C	2.57	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:401:LYS:C	1:A:403:ALA:H	2.24	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
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
1:A:287:SER:C	1:A:289:ALA:N	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:CYS:C	2:B:14:ASN:N	2.71	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:202:TYR:C	2:B:270:PRO:HG3	2.40	0.46
2:B:359:PRO:CB	2:B:360:PRO:HD2	2.45	0.46
1:A:381:THR:C	1:A:383:ALA:N	2.72	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:434:GLU:C	1:A:436:GLY:N	2.74	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
2:B:333:LEU:O	2:B:334:ASN:C	2.58	0.46
1:A:115:ILE:CG1	1:A:152:LEU:HD13	2.45	0.46
1:A:152:LEU:C	1:A:152:LEU:CD1	2.89	0.46
1:A:190:THR:O	1:A:194:THR:HG22	2.11	0.46
1:A:384:ILE:O	1:A:385:ALA:C	2.59	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:O	1:A:260:VAL:CG2	2.63	0.46
1:A:392:ASP:OD1	1:A:422:ARG:NE	2.48	0.46
2:B:199:ASP:HA	2:B:265:LEU:HD13	1.98	0.46
1:A:25:CYS:SG	1:A:83:TYR:HE2	2.38	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
2:B:250:ALA:HB1	2:B:254:LYS:CB	2.44	0.46
2:B:409:THR:C	2:B:411:GLU:N	2.73	0.46
1:A:100:ALA:C	1:A:102:ASN:H	2.24	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:210:TYR:O	2:B:211:ASP:C	2.57	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
2:B:259:MET:HE1	2:B:378:ILE:HG21	1.98	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:12:CYS:O	2:B:13:GLY:C	2.59	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:HD11	1:A:125:LEU:C	2.42	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:23:VAL:O	2:B:24:ILE:C	2.59	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
1:A:234:ILE:C	1:A:234:ILE:CD1	2.86	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:244:PHE:HD1	1:A:244:PHE:C	2.24	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
2:B:186:ASN:CG	2:B:408:TYR:OH	2.59	0.45
2:B:230:LEU:CG	2:B:302:MET:HE2	2.46	0.45
2:B:258:ASN:HD21	2:B:352:LYS:HG3	1.67	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:312:TYR:HA	2:B:381:SER:O	2.16	0.45
2:B:408:TYR:C	2:B:413:MET:CG	2.90	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:324:SER:O	2:B:326:LYS:N	2.50	0.45
1:A:103:TYR:CD1	1:A:148:GLY:HA2	2.52	0.45
1:A:175:PRO:CG	1:A:176:GLN:H	2.29	0.45
2:B:99:ALA:O	2:B:100:GLY:C	2.60	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: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:231:ILE:C	1:A:233:GLN:N	2.73	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:71:GLU:CD	2:B:42:LEU:HD11	2.42	0.45
1:A:203:MET:CB	1:A:206:ASN:HD21	2.30	0.45
1:A:399:TYR:C	1:A:401:LYS:N	2.74	0.45
1:A:414:GLU:C	1:A:416:GLY:N	2.74	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:42:LEU:C	2:B:44:LEU:H	2.25	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
1:A:151:SER:CB	1:A:193:THR:CG2	2.94	0.44
1:A:192:HIS:CG	1:A:193:THR:H	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A: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:413:MET:C	1:A:414:GLU:CG	2.89	0.44
2:B:380:ASN:C	2:B:380:ASN:HD22	2.24	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
2:B:325:MET:HE1	2:B:355:VAL:HG21	1.99	0.44
1:A:189:LEU:HD23	1:A:192:HIS:HE1	1.81	0.44
1:A:264:ARG:C	1:A:266:HIS:N	2.60	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:98:GLY:C	2:B:100:GLY:H	2.25	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: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
1:A:286:LEU:HD12	1:A:286:LEU:HA	1.84	0.44
1:A:425:MET:O	1:A:426:ALA:C	2.60	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
2:B:269:MET:HB2	2:B:301:MET:HE3	2.00	0.44
1:A:72:PRO:HG2	1:A:73:THR:H	1.83	0.44
1:A:282:TYR:C	1:A:284:GLU:N	2.73	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:319:PHE:CD2	2:B:323:MET:HE1	2.52	0.44
1:A:12:ALA:C	1:A:14:VAL:N	2.75	0.44
1:A:132:LEU:CD2	1:A:164:LYS:CE	2.96	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:390:ARG:O	2:B:391:ILE:C	2.61	0.44
2:B:402:LYS:O	2:B:403:ALA:C	2.61	0.44
1:A:189:LEU:CD2	1:A:192:HIS:HE1	2.30	0.44
1:A:293:ASN:C	1:A:295:CYS:H	2.26	0.44
1:A:402:ARG:O	1:A:405:VAL:N	2.49	0.44
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:119:LEU:O	1:A:120:ASP:C	2.60	0.43
1:A:182:VAL:O	1:A:183:GLU:C	2.60	0.43
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:301:GLN:O	1:A:302:MET:C	2.61	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:384:ILE:C	2:B:389:LYS:HZ3	2.26	0.43
1:A:161:TYR:O	1:A:163:LYS:HB3	2.17	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:161:TYR:CD1	1:A:161:TYR:N	2.86	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:195:VAL:CA	2:B:264:ARG:C	2.75	0.43
2:B:240:THR:HG23	2:B:241:CYS:N	2.33	0.43
1:A:191:THR:HG21	1:A:425:MET:HE2	1.99	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:37:HIS:O	2:B:38:GLY:C	2.60	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:92:LEU:C	1:A:93:ILE:HD12	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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
2:B:262:PHE:CB	2:B:431:GLU:C	2.79	0.43
1:A:93:ILE:N	1:A:93:ILE:CD1	2.73	0.43
1:A:184:PRO:O	1:A:185:TYR:C	2.62	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:268:PRO:C	1:A:269:LEU:HD23	2.44	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
2:B:330:GLU:O	2:B:331:GLN:C	2.61	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
1:A:265:GLY:O	1:A:266:HIS:C	2.62	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:108:TYR:O	1:A:109:THR:C	2.61	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:384:ILE:C	1:A:386:GLU:N	2.72	0.42
2:B:121:VAL:C	2:B:123:ARG:N	2.76	0.42
2:B:168:THR:CG2	2:B:201:THR:HG23	2.48	0.42
2:B:263:PRO:O	2:B:264:ARG:C	2.61	0.42
2:B:395:PHE:CE2	2:B:422:GLU:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:MET:HE3	1:A:381:THR:C	2.44	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
2:B:20:PHE:HB2	2:B:232:SER:CB	2.48	0.42
2:B:138:THR:O	2:B:139:HIS:HB3	2.20	0.42
2:B:345:GLU:C	2:B:347:ILE:N	2.76	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: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
2:B:254:LYS:C	2:B:352:LYS:HE2	2.44	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:119:LEU:C	2.62	0.42
2:B:118:VAL:O	2:B:122:VAL:HG13	2.20	0.42
2:B:349:ASN:C	2:B:349:ASN:ND2	2.77	0.42
2:B:191:VAL:HG21	2:B:425:MET:HG2	1.46	0.42
2:B:297:ASP:CG	2:B:299:LYS:HE2	2.45	0.42
2:B:343:PHE:CD1	2:B:350:ASN:ND2	2.88	0.42
2:B:389:LYS:O	2:B:390:ARG:C	2.62	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:301:MET:C	2:B:303:ALA:N	2.77	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:160:ASP:HB3	1:A:161:TYR:CD1	2.54	0.42
1:A:255:PHE:O	1:A:257:THR:N	2.53	0.42
2:B:16:ILE:N	2:B:228:ASN:CB	2.79	0.42
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
1:A:386:GLU:O	1:A:387:ALA:C	2.63	0.42
2:B:11:GLN:O	2:B:12:CYS:C	2.63	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
1:A:224:TYR:O	4:A:502:GTP:N2	2.53	0.41
2:B:202:TYR:C	2:B:270:PRO:CD	2.93	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:421:ALA:HA	1:A:424:ASP:CG	2.45	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: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:332:ILE:CD1	1:A:353:VAL:HG22	2.51	0.41
1:A:335:ILE:C	1:A:337:THR:H	2.28	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:203:MET:C	1:A:206:ASN:HD21	2.29	0.41
1:A:224:TYR:HD1	4:A:502:GTP:C2	2.38	0.41
1:A:408:TYR:CE1	1:A:409:VAL:CG2	3.01	0.41
2:B:106:GLY:O	2:B:149:MET:CA	2.68	0.41
2:B:194:LEU:CA	2:B:265:LEU:HD22	2.44	0.41
2:B:399:PHE:O	2:B:401:ARG:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ALA:HB2	1:A:105:ARG:HD3	2.03	0.41
1:A:171:ILE:HD13	4:A:502:GTP:HN22	1.86	0.41
2:B:202:TYR:C	2:B:270:PRO:HD3	2.46	0.41
2:B:333:LEU:HD11	2:B:337:ASN:HD21	1.85	0.41
1:A:133:GLN:C	1:A:164:LYS:HD3	2.46	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: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
2:B:82:PRO:C	2:B:84:GLY:N	2.78	0.41
2:B:259:MET:HE3	2:B:268:PHE:CZ	2.56	0.41
1:A:179:THR:O	2:B:248:LEU:HD22	2.21	0.41
1:A:231:ILE:C	1:A:233:GLN:H	2.28	0.41
1:A:273:ALA:O	1:A:275:VAL:N	2.54	0.41
1:A:276:ILE:C	1:A:369:ALA:HB2	2.45	0.41
1:A:324:VAL:HG12	1:A:326:LYS:H	1.85	0.41
2:B:14:ASN:O	2:B:15:GLN:C	2.64	0.41
2:B:26:ASP:C	2:B:26:ASP:OD1	2.64	0.41
2:B:242:LEU:HB3	2:B:250:ALA:O	2.20	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:408:TYR:O	1:A:409:VAL:C	2.63	0.41
1:A:428:LEU:HD12	1:A:428:LEU:HA	1.79	0.41
2:B:15:GLN:C	2:B:228:ASN:HD22	2.29	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:239:THR:CG2	2:B:240:THR:N	2.80	0.41
2:B:262:PHE:CE1	2:B:434:GLN:HG3	2.56	0.41
1:A:308:ARG:O	1:A:308:ARG:HG2	2.20	0.41
2:B:19:LYS:CE	2:B:225:GLY:CA	2.97	0.41
2:B:52:TYR:C	2:B:53:TYR:CD1	2.99	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:273:ALA:HB1	2:B:291:LEU:HG	2.01	0.41
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
1:A:267:PHE:N	1:A:432:TYR:HH	2.12	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:195:VAL:HB	2:B:264:ARG:C	2.45	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:199:ASP:C	1:A:265:GLY:C	2.74	0.40
1:A:243:ARG:NH2	1:A:252:LEU:HG	2.35	0.40
1:A:287:SER:C	1:A:289:ALA:H	2.30	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:380:ASN:C	2:B:380:ASN:ND2	2.79	0.40
1:A:28:HIS:CE1	1:A:240:ALA:C	2.96	0.40
1:A:67:PHE:HB2	1:A:92:LEU:HD23	2.02	0.40
1:A:132:LEU:C	1:A:164:LYS:HE3	2.46	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:24:TYR:O	1:A:25:CYS:C	2.63	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	3
2	B	399/445 (90%)	262 (66%)	85 (21%)	52 (13%)	0	4
All	All	800/896 (89%)	519 (65%)	168 (21%)	113 (14%)	0	3

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

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Mol	Chain	Res	Type
2	B	240	THR
2	B	252	LEU
2	B	263	PRO
2	B	266	HIS
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

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Mol	Chain	Res	Type
1	A	104	ALA
1	A	141	PHE
1	A	148	GLY
1	A	149	PHE
1	A	239	THR
1	A	245	ASP
1	A	263	PRO
1	A	330	ALA
1	A	336	LYS
1	A	369	ALA
2	B	83	PHE
2	B	99	ALA
2	B	302	MET
1	A	89	PRO
1	A	172	TYR
1	A	256	GLN
1	A	307	PRO
1	A	348	PRO
2	B	34	GLY
2	B	100	GLY
2	B	395	PHE
1	A	139	HIS
1	A	140	SER
1	A	160	ASP
1	A	174	ALA
1	A	284	GLU
1	A	298	PRO
1	A	303	VAL
2	B	57	ALA
2	B	74	THR
2	B	285	ALA
1	A	31	GLN
1	A	273	ALA
2	B	51	VAL
2	B	58	GLY
2	B	145	THR
2	B	400	ARG
1	A	115	ILE
1	A	222	PRO
2	B	72	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	345/377 (92%)	289 (84%)	56 (16%)	2	11
2	B	353/381 (93%)	301 (85%)	52 (15%)	3	13
All	All	698/758 (92%)	590 (84%)	108 (16%)	5	12

All (108) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	SER
1	A	7	ILE
1	A	16	ILE
1	A	20	CYS
1	A	32	PRO
1	A	76	ASP
1	A	82	THR
1	A	93	ILE
1	A	94	THR
1	A	96	LYS
1	A	97	GLU
1	A	109	THR
1	A	115	ILE
1	A	120	ASP
1	A	125	LEU
1	A	135	PHE
1	A	139	HIS
1	A	150	THR
1	A	152	LEU
1	A	155	GLU
1	A	172	TYR
1	A	187	SER
1	A	196	GLU
1	A	199	ASP
1	A	206	ASN
1	A	219	ILE
1	A	231	ILE

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Mol	Chain	Res	Type
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
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	328	VAL
1	A	334	THR
1	A	345	ASP
1	A	352	LYS
1	A	368	LEU
1	A	376	CYS
1	A	377	MET
1	A	378	LEU
1	A	394	LYS
1	A	415	GLU
1	A	417	GLU
1	A	420	GLU
1	A	431	ASP
1	A	432	TYR
1	A	433	GLU
2	B	24	ILE
2	B	26	ASP
2	B	32	PRO
2	B	41	ASP
2	B	67	LEU
2	B	68	VAL
2	B	90	ASP
2	B	94	PHE
2	B	121	VAL
2	B	122	VAL
2	B	135	PHE
2	B	145	THR
2	B	149	MET

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Mol	Chain	Res	Type
2	B	151	THR
2	B	153	LEU
2	B	158	ARG
2	B	165	ILE
2	B	193	GLN
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
2	B	227	LEU
2	B	229	HIS
2	B	230	LEU
2	B	232	SER
2	B	236	SER
2	B	240	THR
2	B	265	LEU
2	B	275	LEU
2	B	282	GLN
2	B	284	ARG
2	B	299	LYS
2	B	306	ASP
2	B	309	HIS
2	B	314	THR
2	B	322	ARG
2	B	324	SER
2	B	325	MET
2	B	331	GLN
2	B	343	PHE
2	B	344	VAL
2	B	353	THR
2	B	369	ARG
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 (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	11	GLN
1	A	15	GLN
1	A	107	HIS
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	256	GLN
1	A	283	HIS
1	A	309	HIS
2	B	14	ASN
2	B	43	GLN
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	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	336	GLN
2	B	337	ASN
2	B	349	ASN
2	B	406	HIS
2	B	424	ASN
2	B	434	GLN

5.3.3 RNA ⓘ

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 oligosaccharides 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	33,34,34	1.87	3 (9%)	50,54,54	0.91	2 (4%)
4	GTP	B	502	3	33,34,34	1.87	3 (9%)	50,54,54	0.91	2 (4%)

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	-	4/22/38/38	0/3/3/3
4	GTP	B	502	3	-	4/22/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	502	GTP	PA-O3A	-5.94	1.53	1.59
4	A	502	GTP	PA-O3A	-5.93	1.53	1.59
4	A	502	GTP	PB-O3A	-5.70	1.53	1.59
4	B	502	GTP	PB-O3A	-5.58	1.53	1.59
4	B	502	GTP	PB-O3B	5.34	1.65	1.59
4	A	502	GTP	PB-O3B	5.23	1.65	1.59

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'	2.09	116.12	108.99
4	B	502	GTP	O5'-C5'-C4'	2.09	116.12	108.99

There are no chirality outliers.

All (8) torsion outliers are listed below:

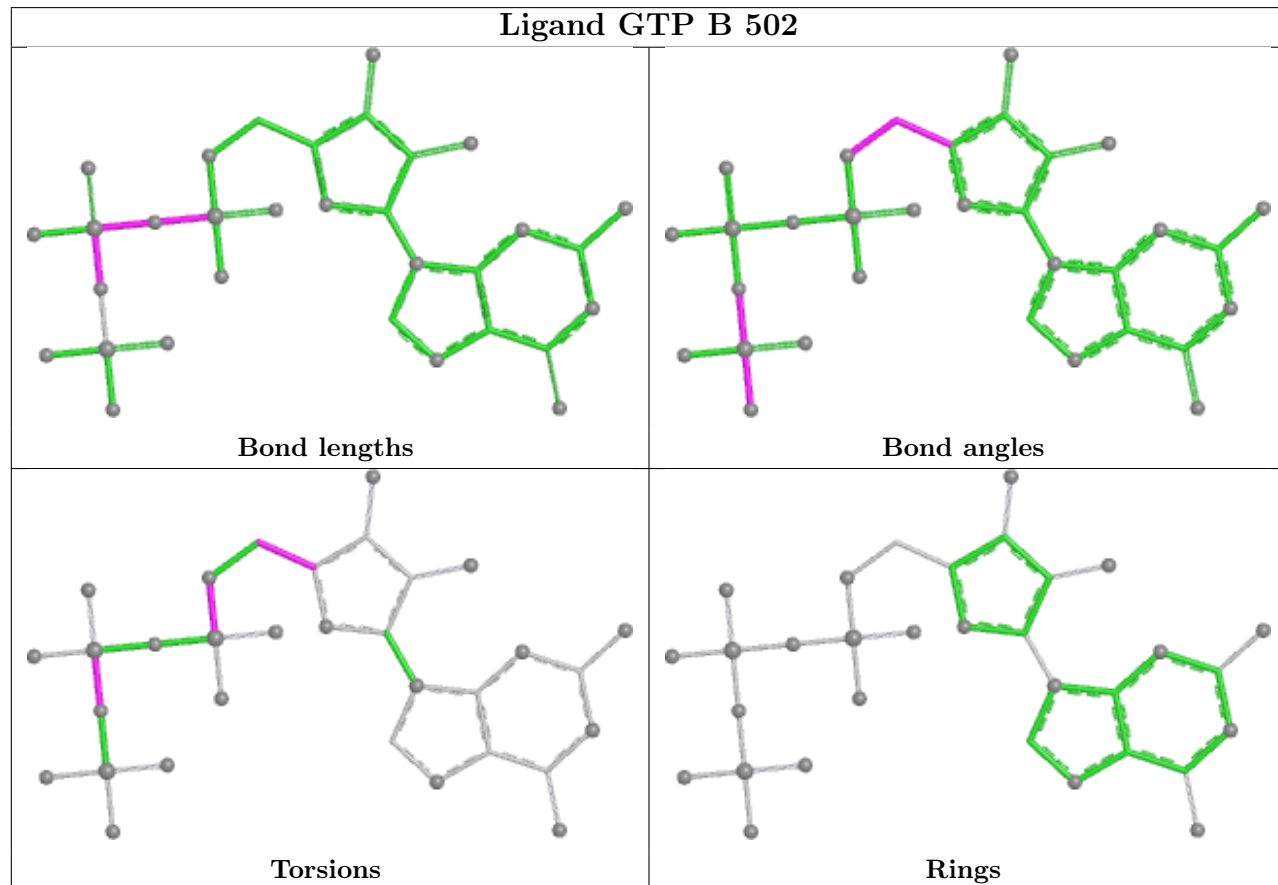
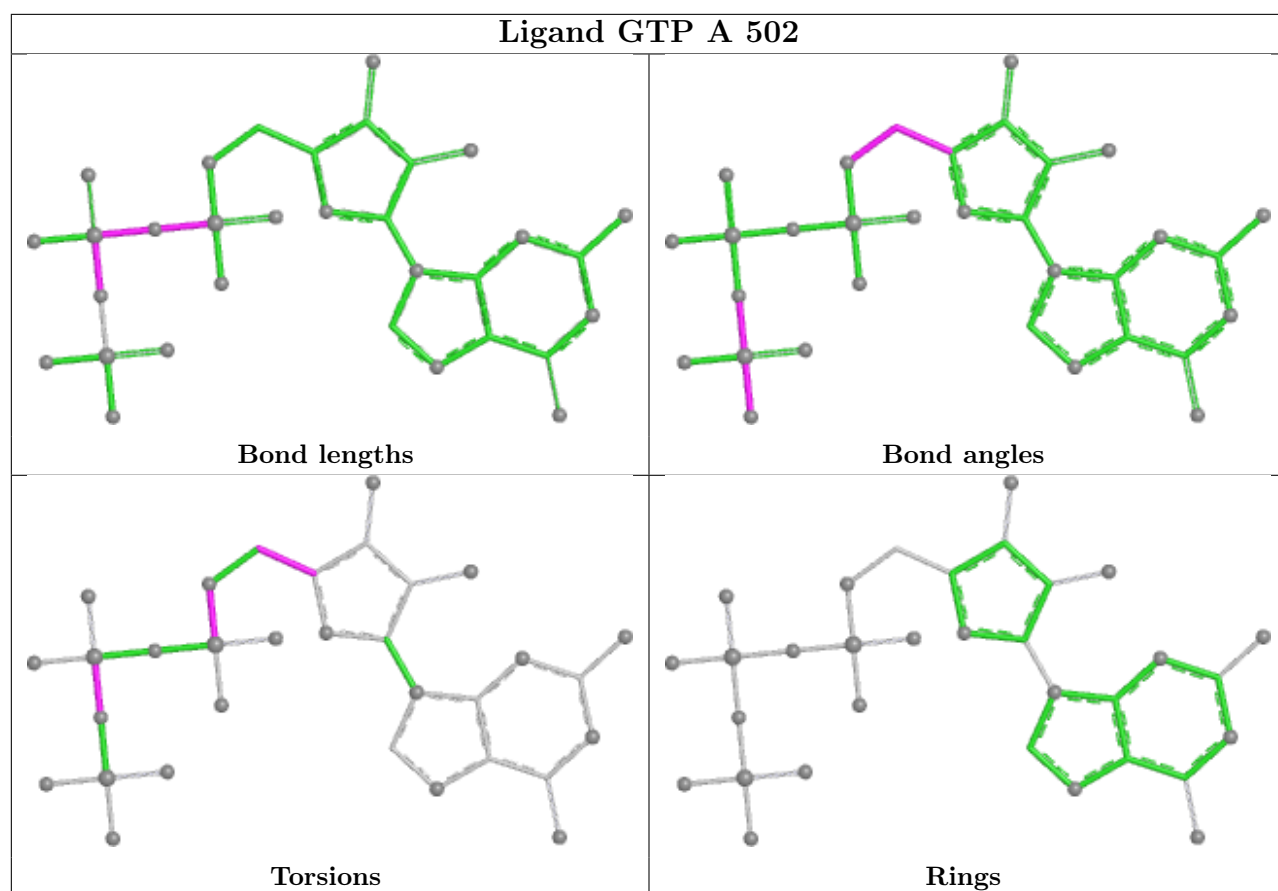
Mol	Chain	Res	Type	Atoms
4	A	502	GTP	C3'-C4'-C5'-O5'
4	B	502	GTP	C3'-C4'-C5'-O5'
4	A	502	GTP	C5'-O5'-PA-O1A
4	B	502	GTP	C5'-O5'-PA-O1A
4	A	502	GTP	O4'-C4'-C5'-O5'
4	B	502	GTP	O4'-C4'-C5'-O5'
4	A	502	GTP	PG-O3B-PB-O2B
4	B	502	GTP	PG-O3B-PB-O2B

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.

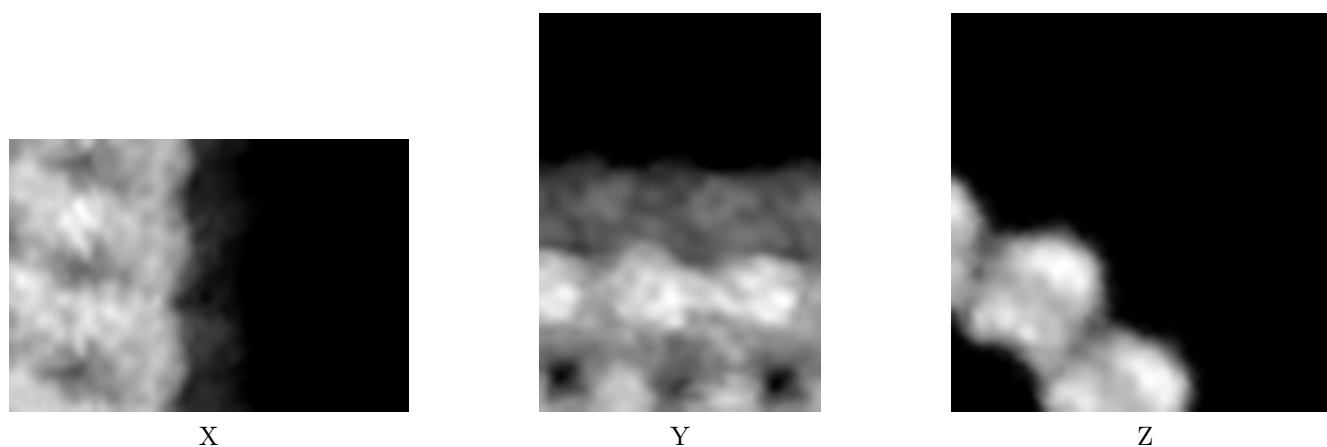
6 Map visualisation [i](#)

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](#)

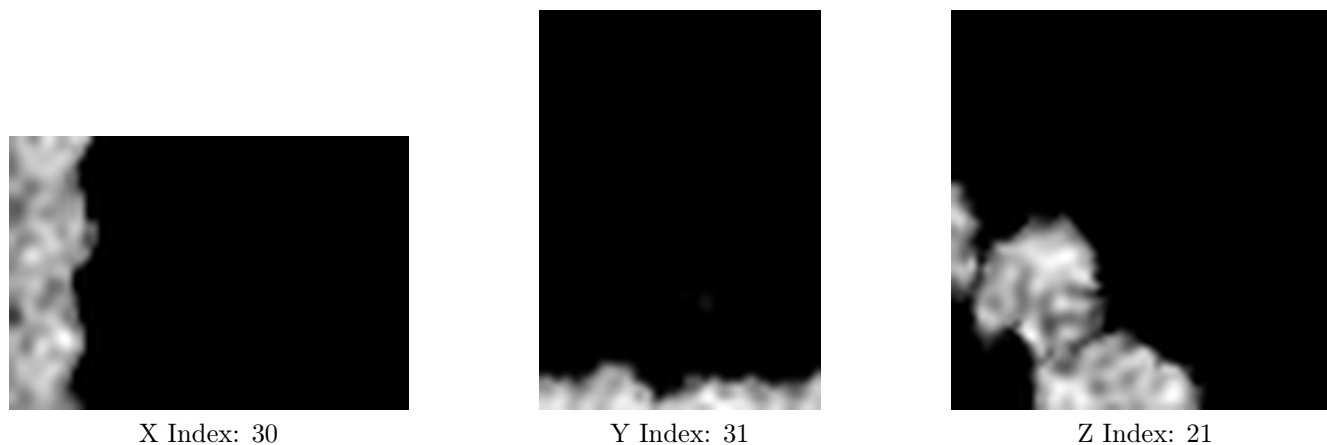
6.1.1 Primary map



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

6.2 Central slices [i](#)

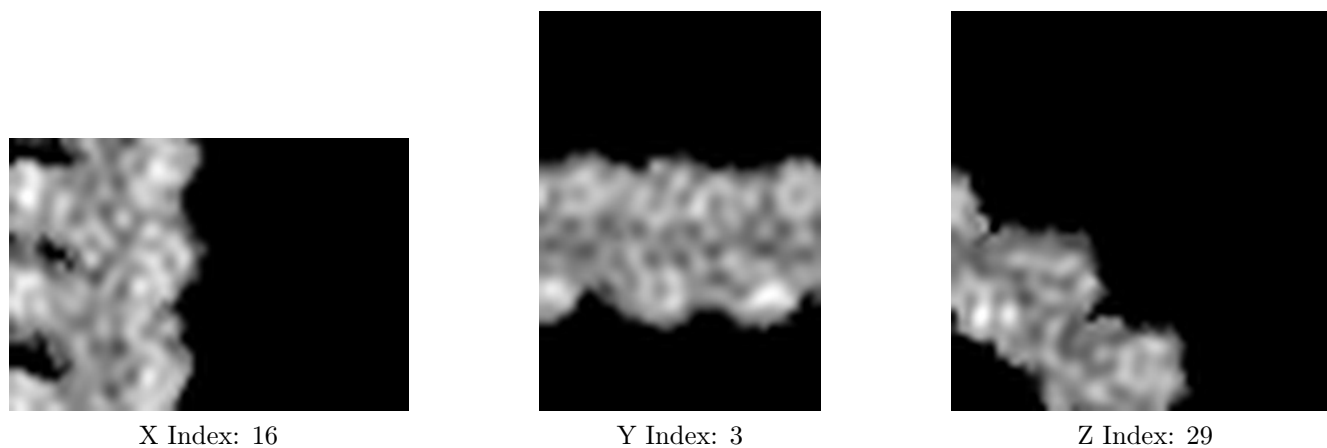
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

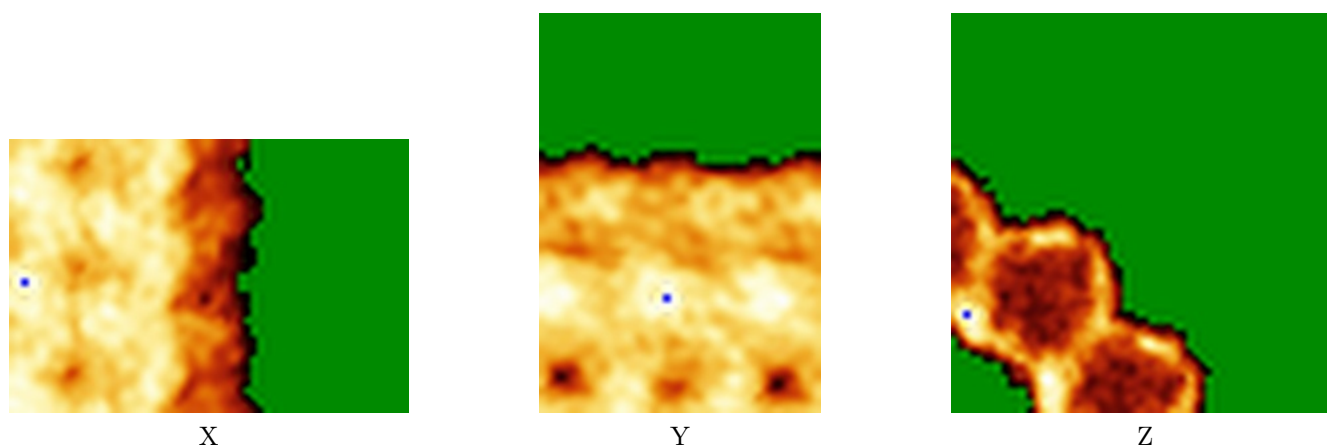
6.3.1 Primary map



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

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

6.4.1 Primary map



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

6.5 Orthogonal surface views

This section was not generated.

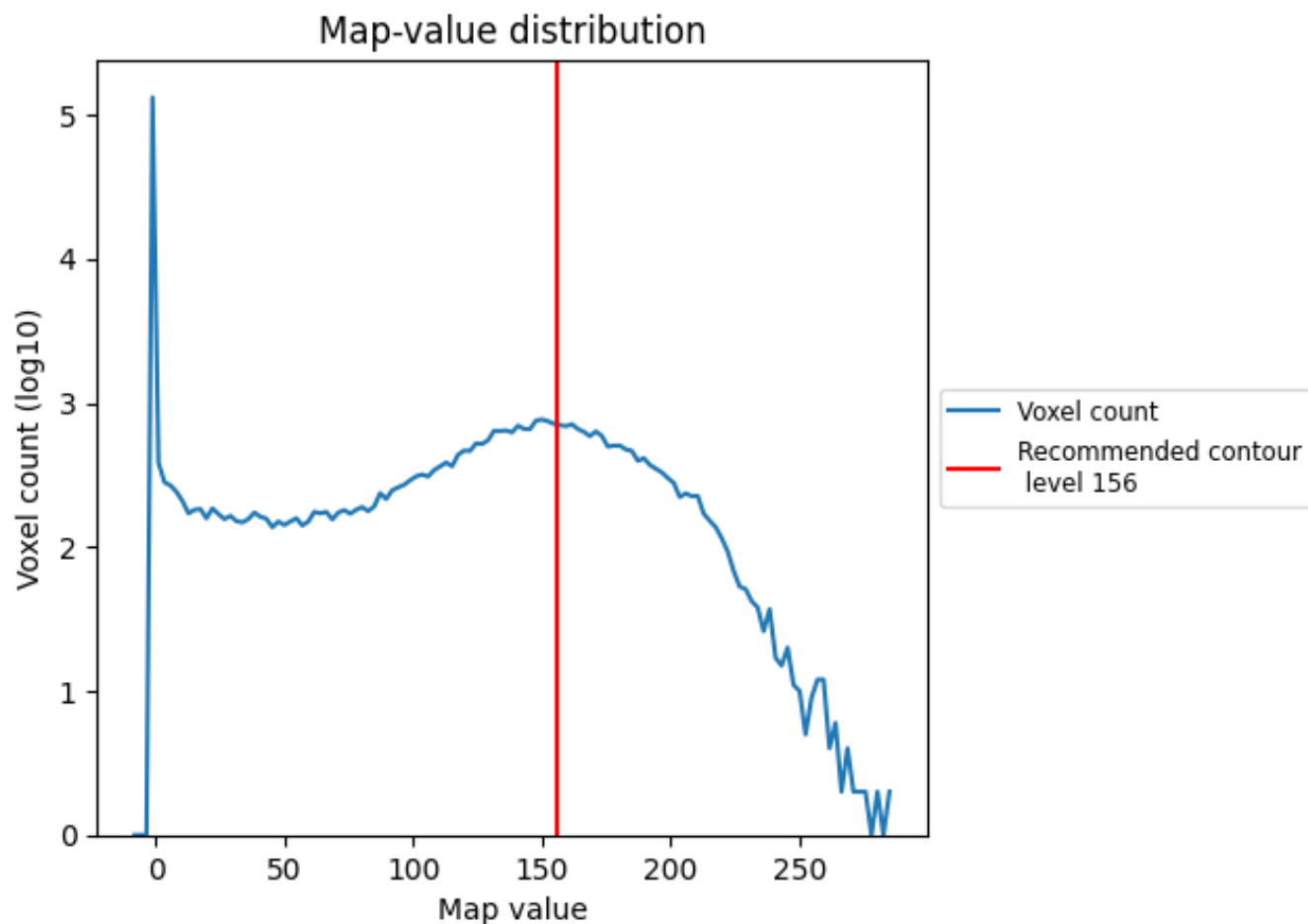
6.6 Mask visualisation

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

7 Map analysis [i](#)

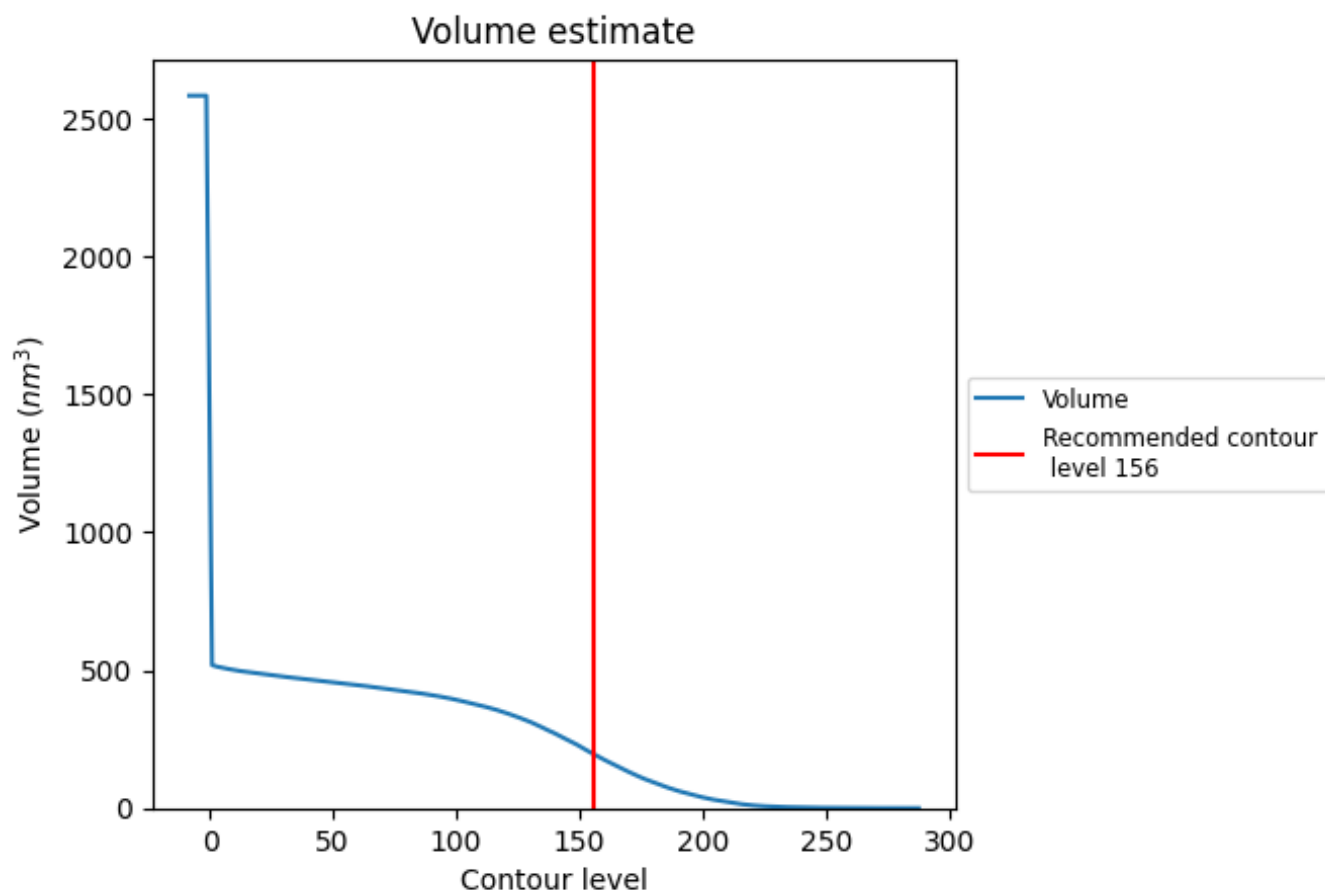
This section contains the results of statistical analysis of the map.

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 nm^3 ; this corresponds to an approximate mass of 175 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

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

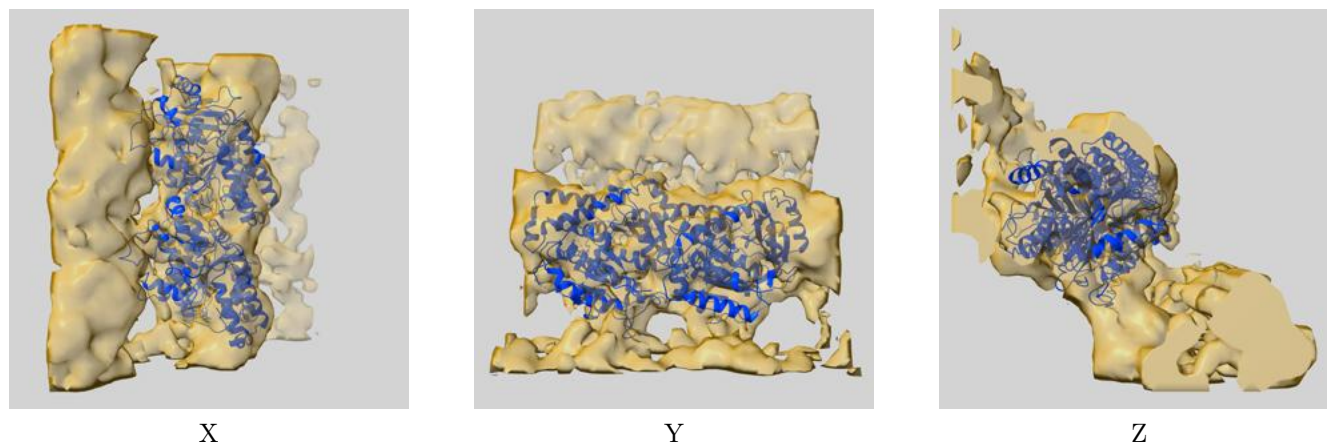
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

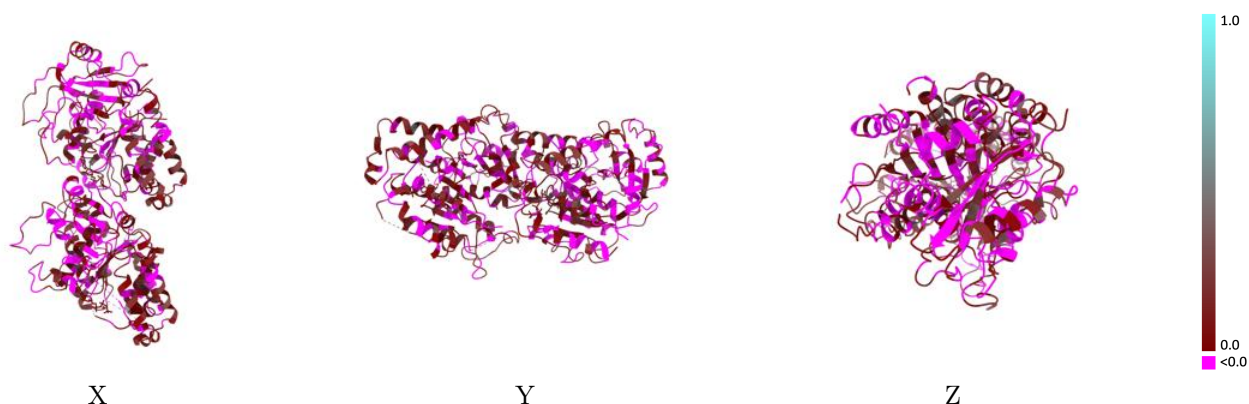
This section contains information regarding the fit between EMDB map EMD-2697 and PDB model 3J7I. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



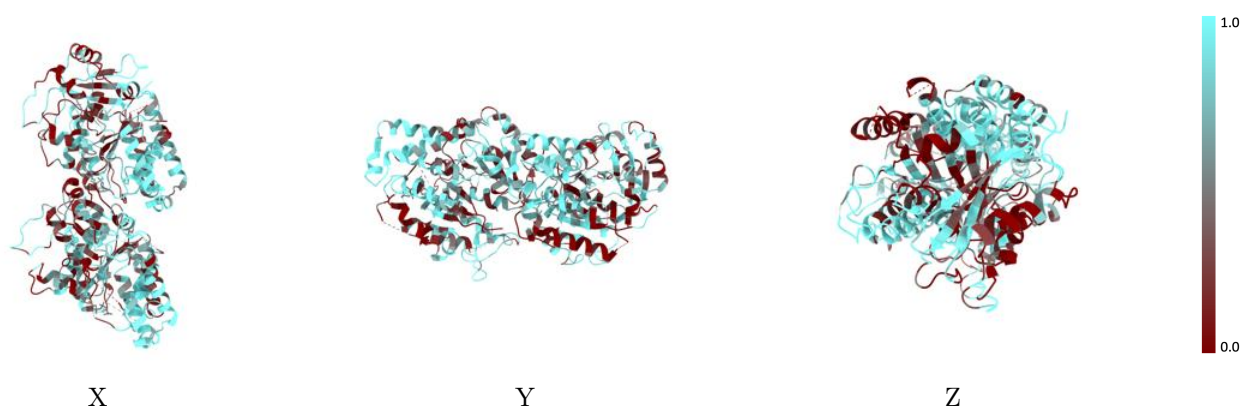
The images above show the 3D surface view of the map at the recommended contour level 156.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



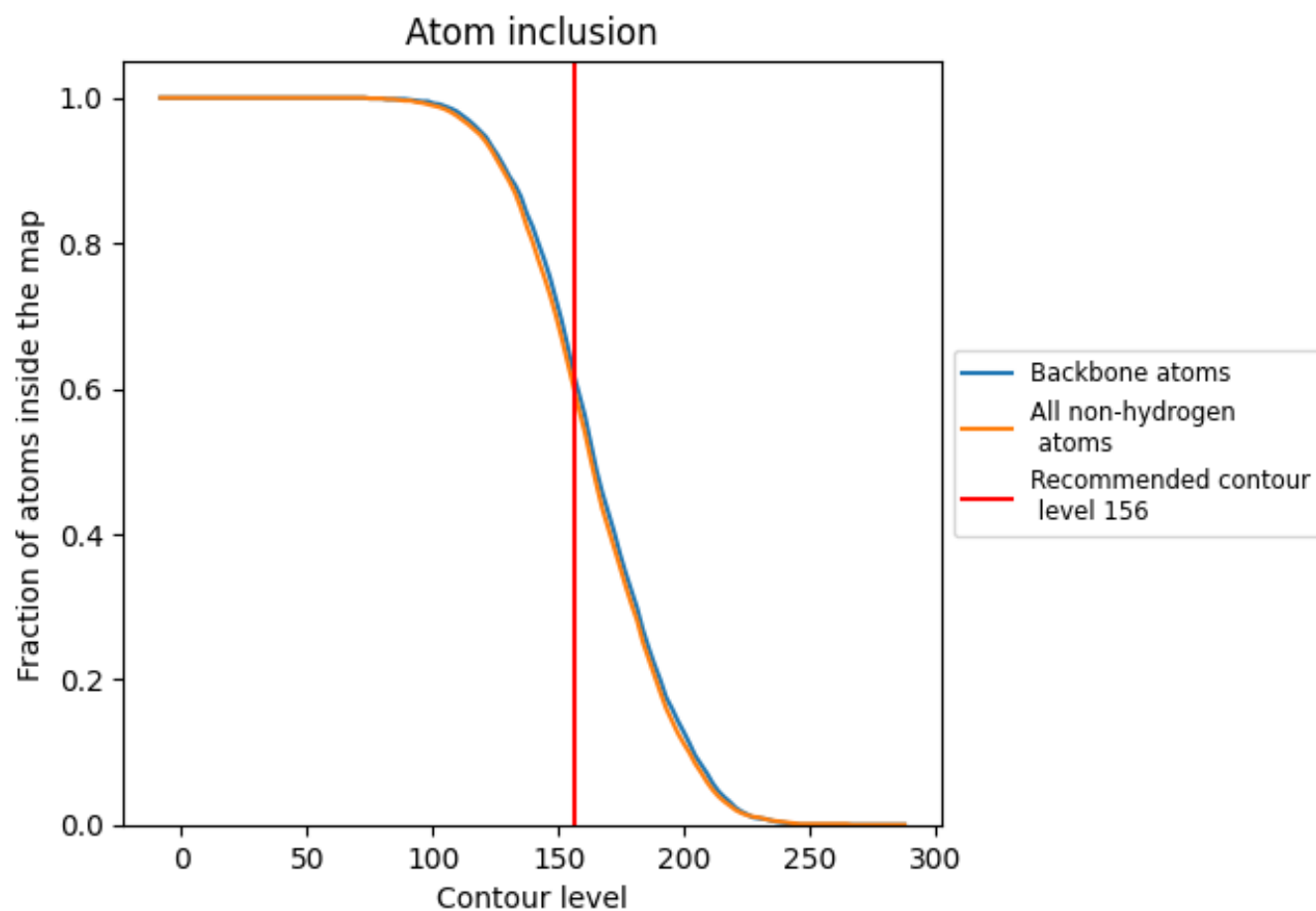
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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).

9.4 Atom inclusion ⓘ



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) and Q-score for the entire model and for each chain.

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

