



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:08 PM UTC

PDB ID : 2XRP / pdb_00002xrp
EMDB ID : EMD-1788
Title : Human Doublecortin N-DC Repeat (1MJD) and Mammalian Tubulin (1JFF and 3HKE) Docked into the 8-Angstrom Cryo-EM Map of Doublecortin- Stabilised Microtubules
Authors : Fourniol, F.J.; Sindelar, C.V.; Amigues, B.; Clare, D.K.; Thomas, G.; Perderiset, M.; Francis, F.; Houdusse, A.; Moores, C.A.
Deposited on : 2010-09-18
Resolution : 8.20 Å(reported)
Based on initial models : 1MJD, 3HKE, 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:

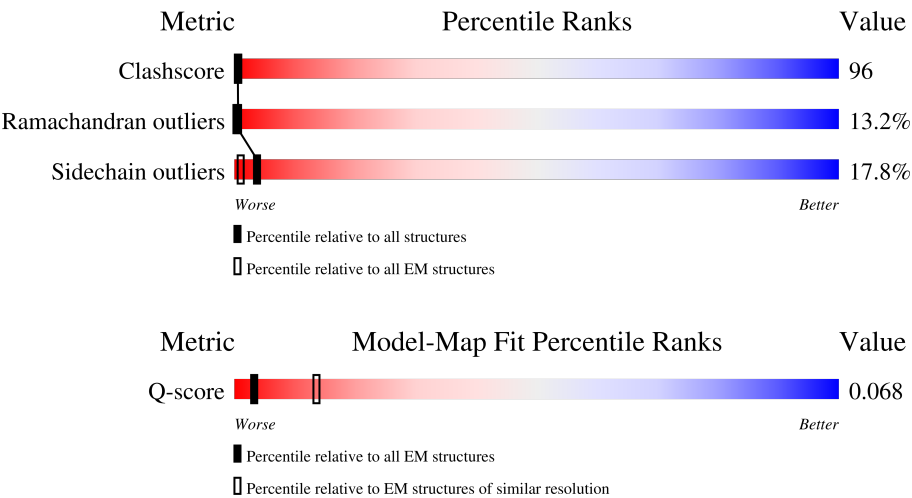
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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)

1 Overall quality at a glance i

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

The reported resolution of this entry is 8.20 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	337 (7.70 - 8.70)

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	445	81% 17% 55% 22% • •
1	C	445	17% 55% 22% • •
1	E	445	82% 17% 55% 22% • •

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Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
1	G	445	25%15%56%22%••
2	B	452	21%14%56%21%•5%
2	D	452	81%15%56%21%•5%
2	F	452	20%15%56%21%•5%
2	H	452	81%16%56%20%•5%
3	I	95	47%29%56%15%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 28352 atoms, of which 596 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 BETA-2B CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	426	Total	C	N	O	S	0	0
			3351	2105	575	646	25		
1	C	426	Total	C	N	O	S	0	0
			3351	2105	575	646	25		
1	E	426	Total	C	N	O	S	0	0
			3351	2105	575	646	25		
1	G	426	Total	C	N	O	S	0	0
			3351	2105	575	646	25		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	172	VAL	MET	conflict	UNP Q6B856
A	318	VAL	ILE	conflict	UNP Q6B856
C	172	VAL	MET	conflict	UNP Q6B856
C	318	VAL	ILE	conflict	UNP Q6B856
E	172	VAL	MET	conflict	UNP Q6B856
E	318	VAL	ILE	conflict	UNP Q6B856
G	172	VAL	MET	conflict	UNP Q6B856
G	318	VAL	ILE	conflict	UNP Q6B856

- Molecule 2 is a protein called TUBULIN ALPHA-1D CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	429	Total	C	N	O	S	0	0
			3334	2114	569	630	21		
2	D	429	Total	C	N	O	S	0	0
			3334	2114	569	630	21		
2	F	429	Total	C	N	O	S	0	0
			3334	2114	569	630	21		
2	H	429	Total	C	N	O	S	0	0
			3334	2114	569	630	21		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	7	ILE	VAL	conflict	UNP Q2HJ86
B	114	ILE	LEU	conflict	UNP Q2HJ86
B	136	SER	LEU	conflict	UNP Q2HJ86
B	358	GLU	GLN	conflict	UNP Q2HJ86
B	437	VAL	MET	conflict	UNP Q2HJ86
B	450	GLU	ASP	conflict	UNP Q2HJ86
D	7	ILE	VAL	conflict	UNP Q2HJ86
D	114	ILE	LEU	conflict	UNP Q2HJ86
D	136	SER	LEU	conflict	UNP Q2HJ86
D	358	GLU	GLN	conflict	UNP Q2HJ86
D	437	VAL	MET	conflict	UNP Q2HJ86
D	450	GLU	ASP	conflict	UNP Q2HJ86
F	7	ILE	VAL	conflict	UNP Q2HJ86
F	114	ILE	LEU	conflict	UNP Q2HJ86
F	136	SER	LEU	conflict	UNP Q2HJ86
F	358	GLU	GLN	conflict	UNP Q2HJ86
F	437	VAL	MET	conflict	UNP Q2HJ86
F	450	GLU	ASP	conflict	UNP Q2HJ86
H	7	ILE	VAL	conflict	UNP Q2HJ86
H	114	ILE	LEU	conflict	UNP Q2HJ86
H	136	SER	LEU	conflict	UNP Q2HJ86
H	358	GLU	GLN	conflict	UNP Q2HJ86
H	437	VAL	MET	conflict	UNP Q2HJ86
H	450	GLU	ASP	conflict	UNP Q2HJ86

- Molecule 3 is a protein called NEURONAL MIGRATION PROTEIN DOUBLECORTIN.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	I	95	Total	C	H	N	O	S	0	0
			1372	490	596	134	150	2		

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

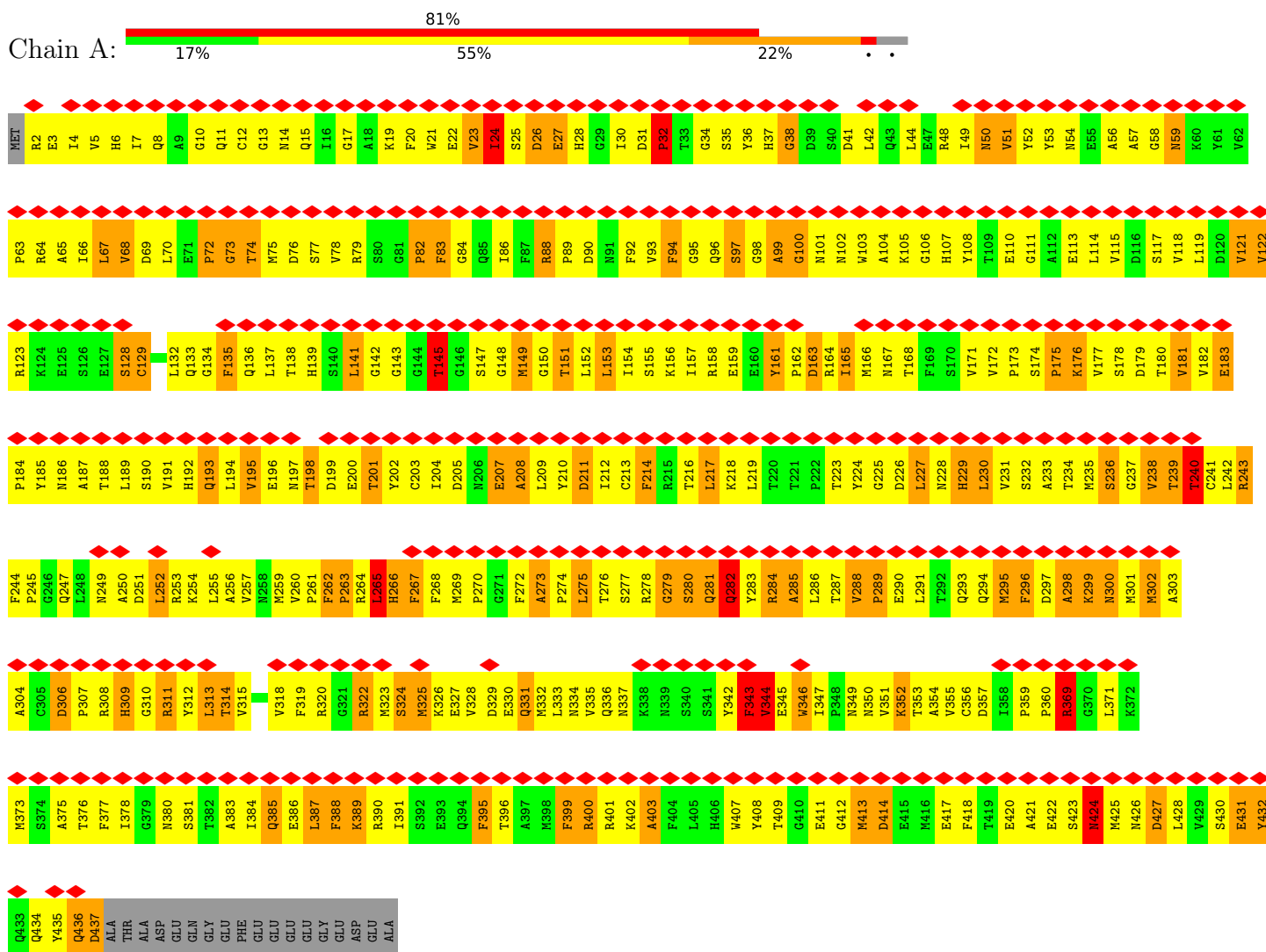


Mol	Chain	Residues	Atoms					AltConf
5	B	1	Total 32	C 10	N 5	O 14	P 3	0
5	D	1	Total 32	C 10	N 5	O 14	P 3	0
5	F	1	Total 32	C 10	N 5	O 14	P 3	0
5	H	1	Total 32	C 10	N 5	O 14	P 3	0

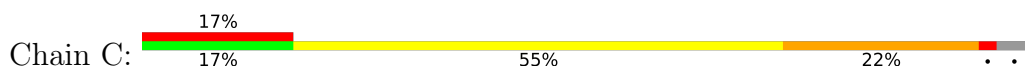
3 Residue-property plots

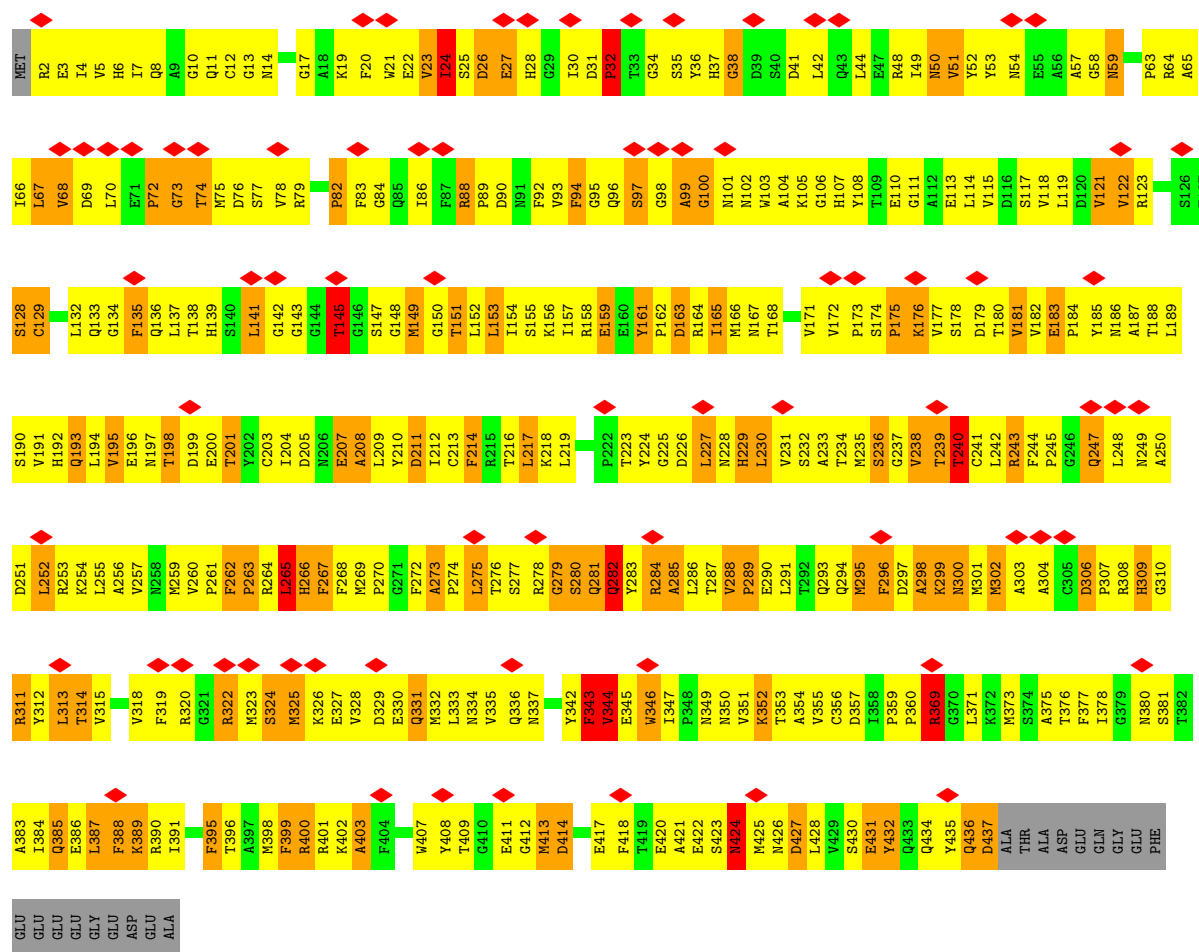
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 BETA-2B CHAIN

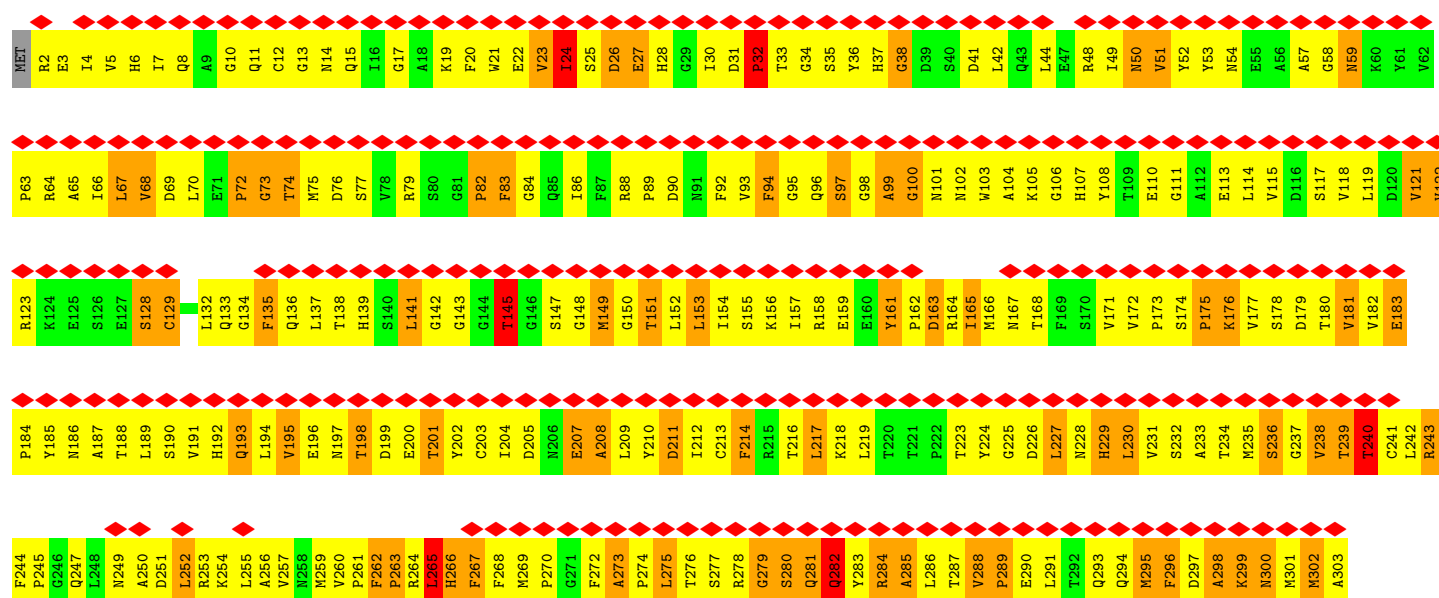
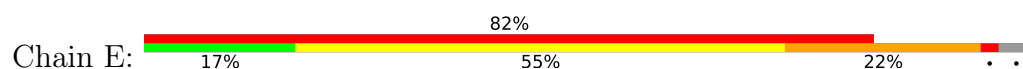


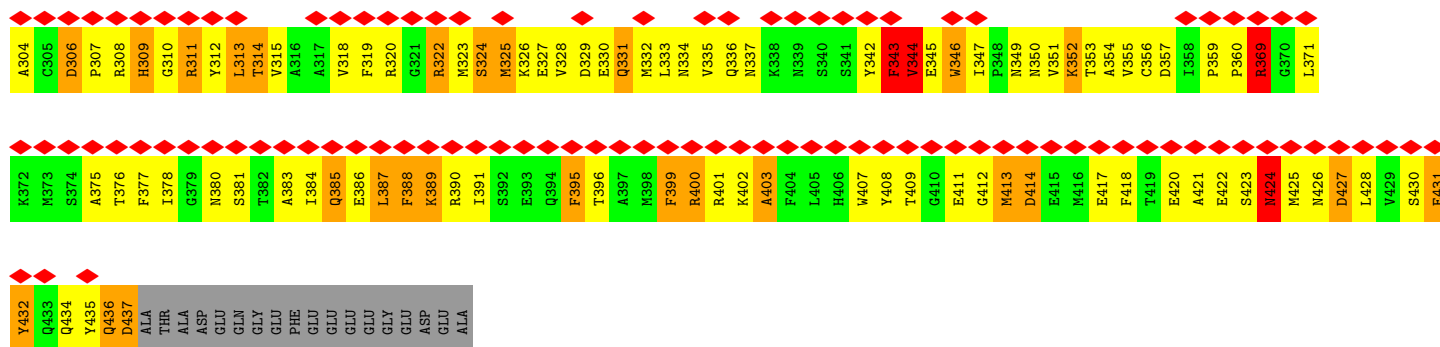
• Molecule 1: TUBULIN BETA-2B CHAIN

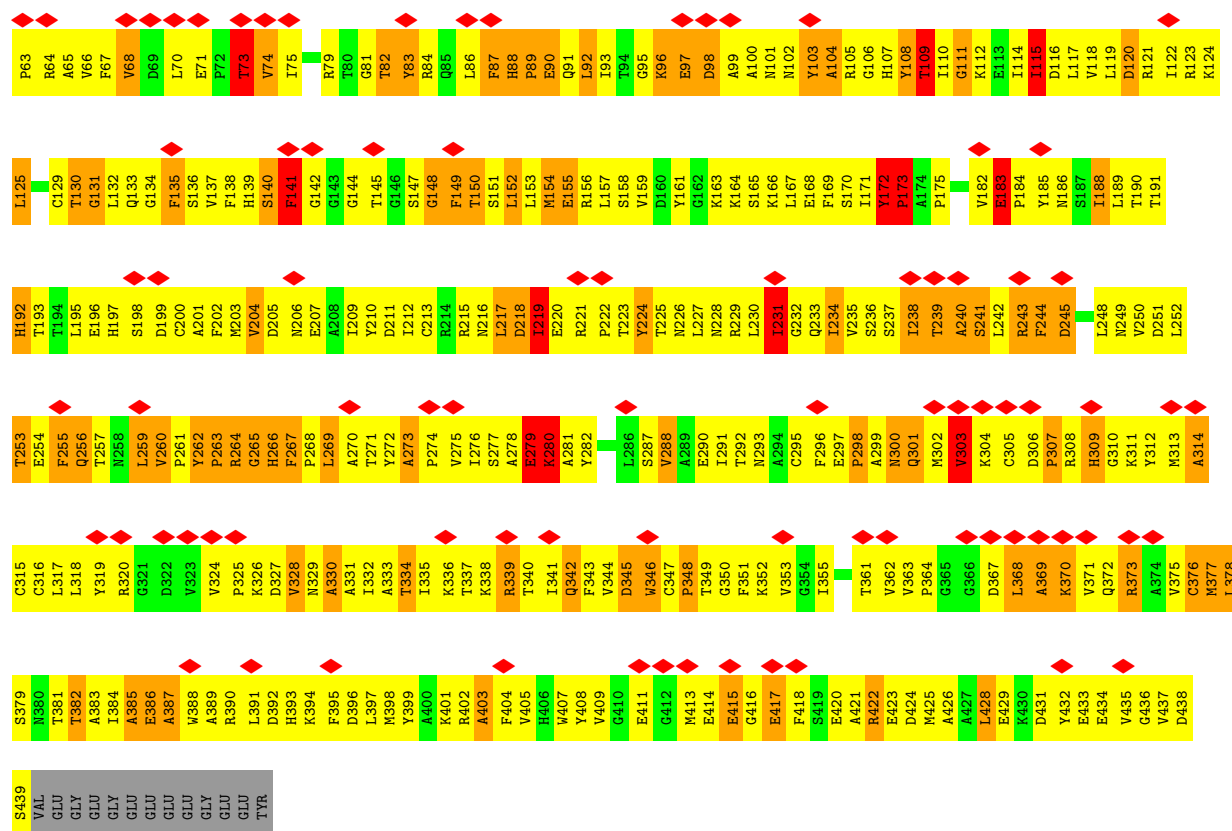




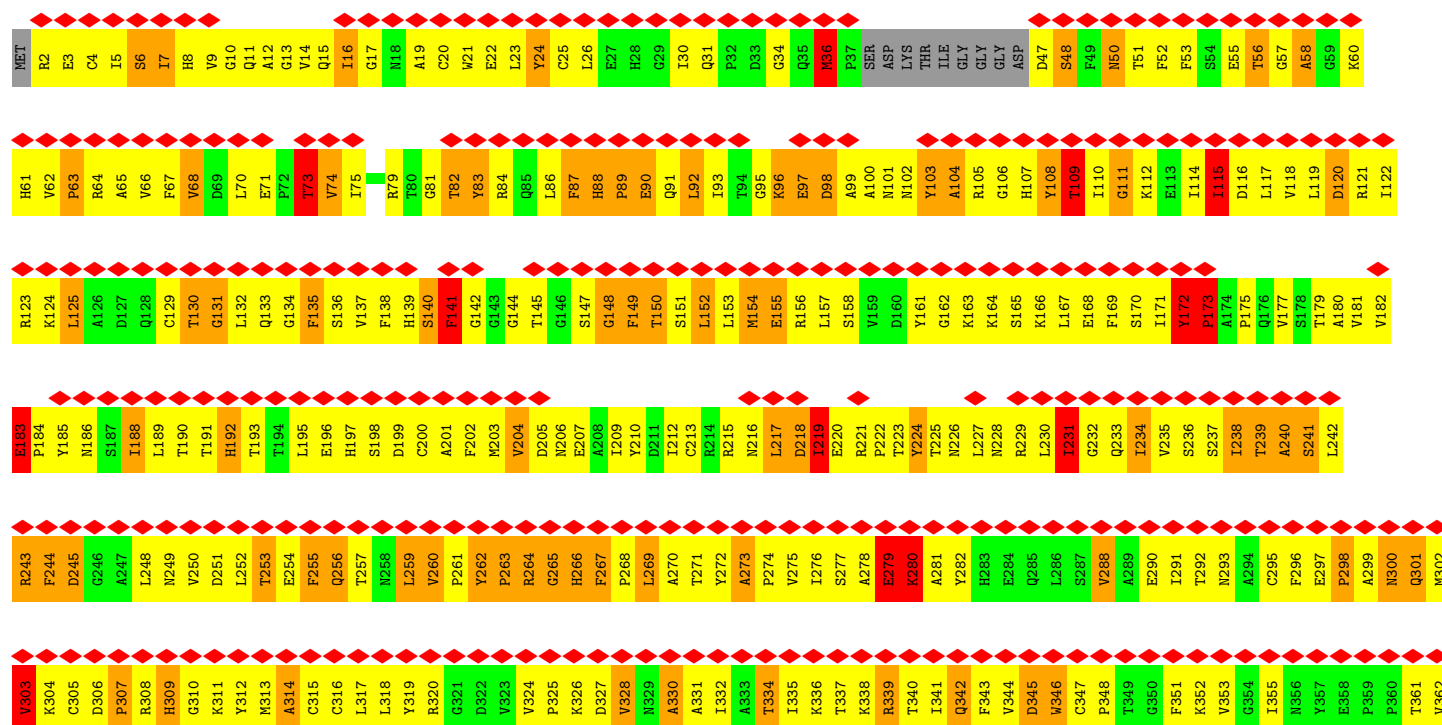
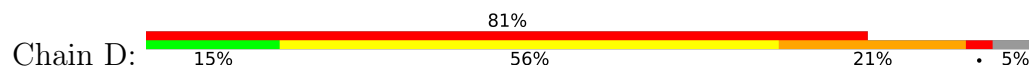
• Molecule 1: TUBULIN BETA-2B CHAIN

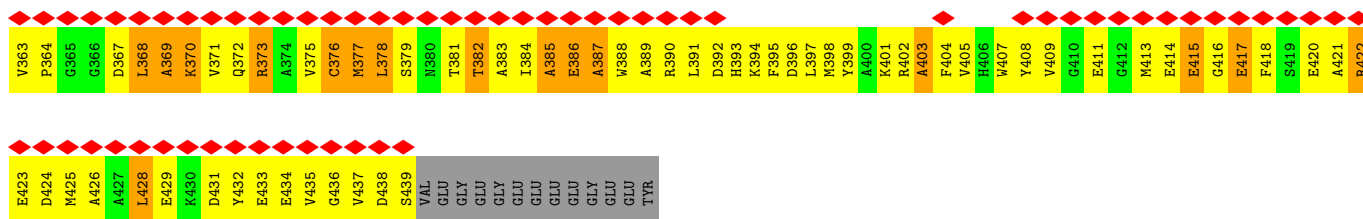




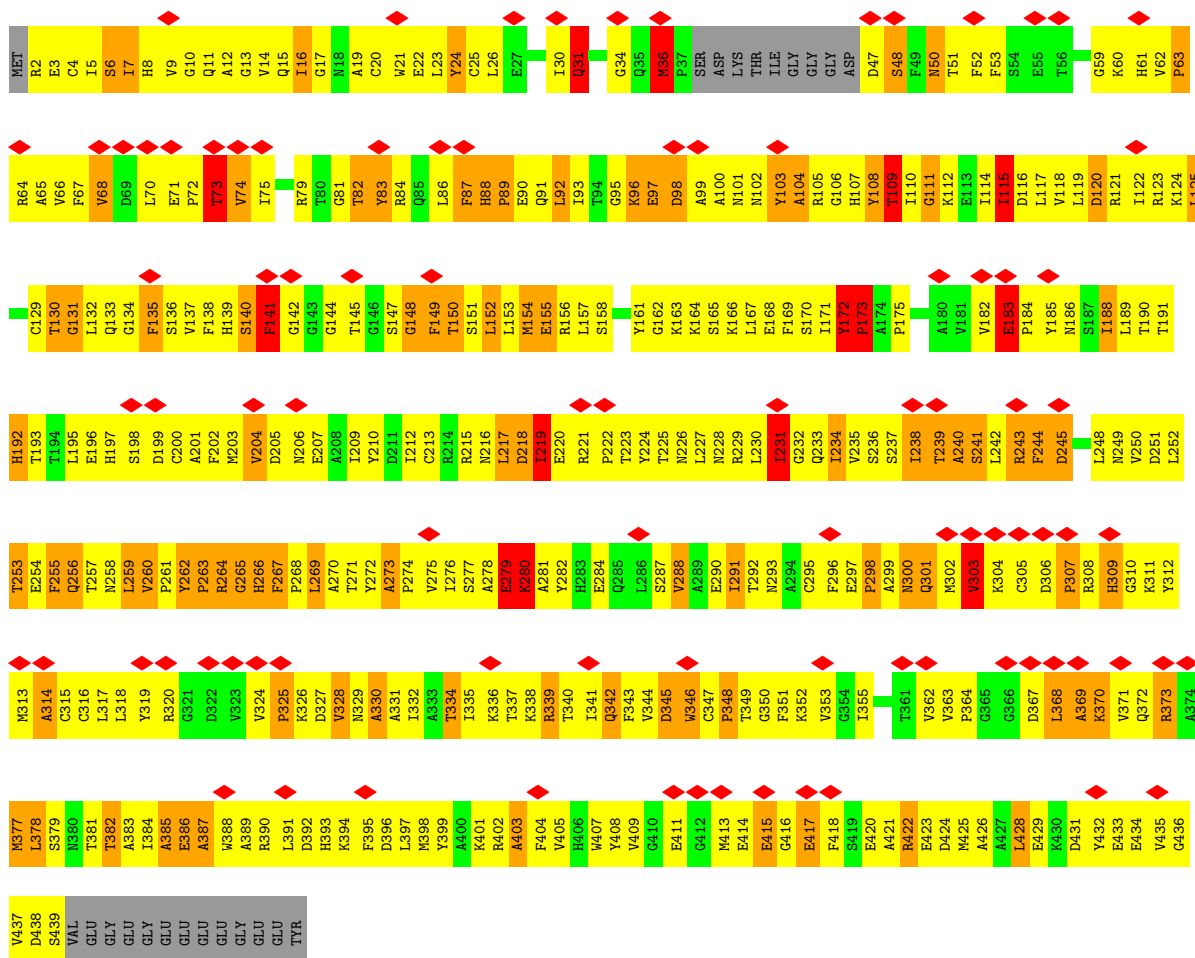
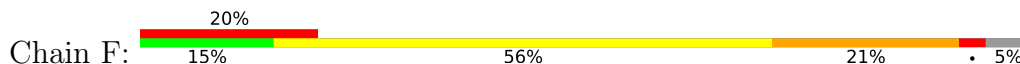


Molecule 2: TUBULIN ALPHA-1D CHAIN

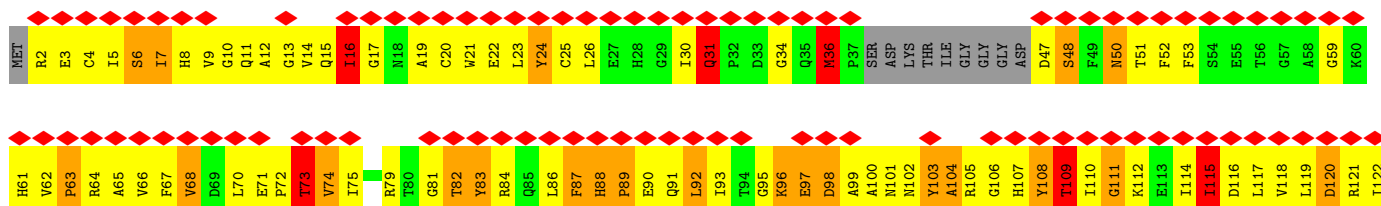
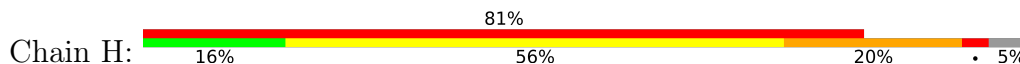


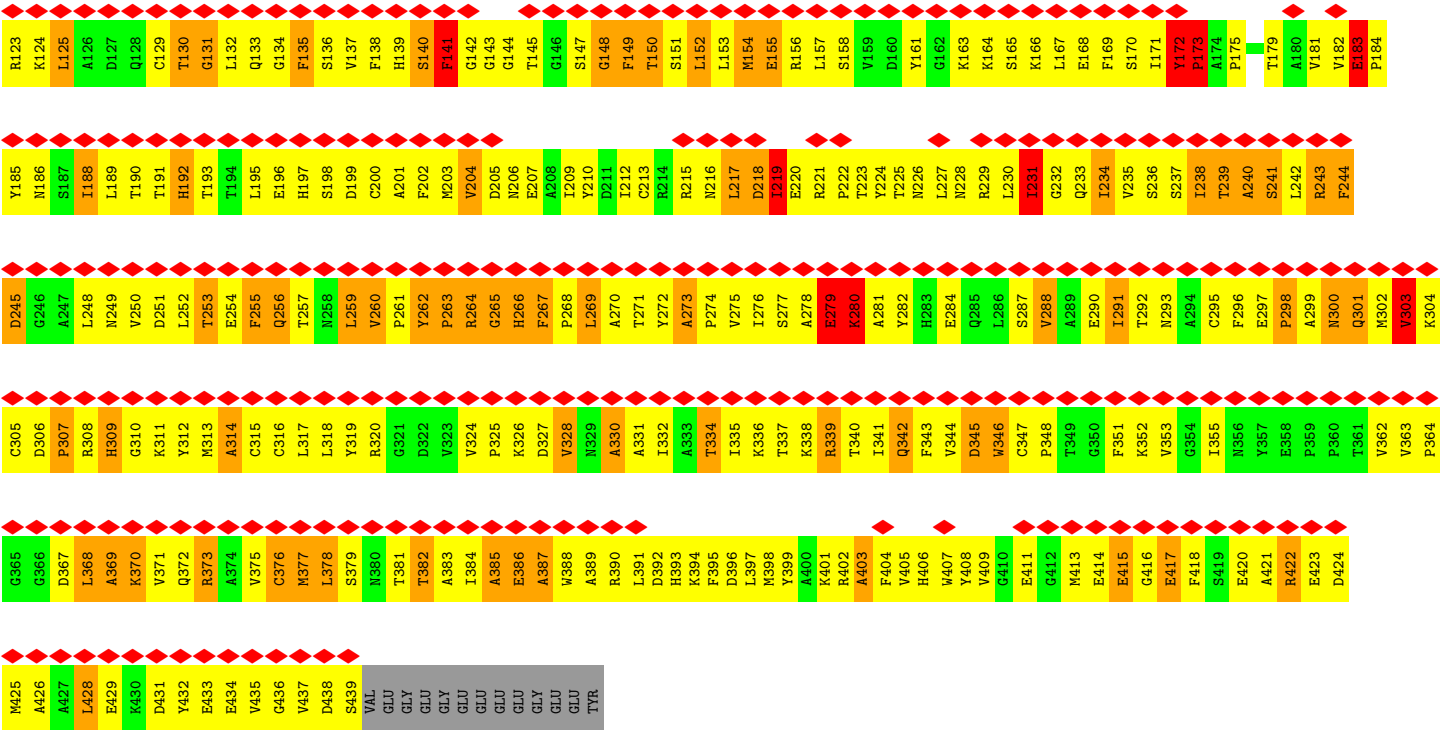


• Molecule 2: TUBULIN ALPHA-1D CHAIN

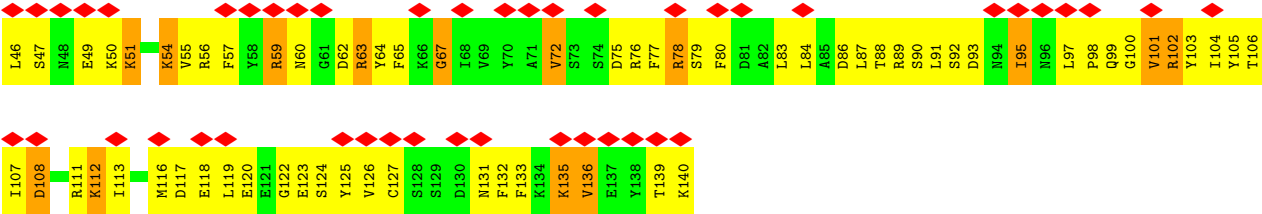


• Molecule 2: TUBULIN ALPHA-1D CHAIN





● Molecule 3: NEURONAL MIGRATION PROTEIN DOUBLECORTIN



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of particles used	168000	Depositor
Resolution determination method	Not provided	
CTF correction method	DONE IN FREALIGN	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	760	Depositor
Maximum defocus (nm)	2900	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	5.698	Depositor
Minimum map value	-4.734	Depositor
Average map value	0.106	Depositor
Map value standard deviation	0.755	Depositor
Recommended contour level	0.92	Depositor
Map size (Å)	95.2, 140, 137.2	wwPDB
Map dimensions	34, 50, 49	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.8, 2.8, 2.8	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, 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	0.63	0/3426	1.11	22/4642 (0.5%)
1	C	0.63	0/3426	1.11	22/4642 (0.5%)
1	E	0.63	0/3426	1.11	23/4642 (0.5%)
1	G	0.63	0/3426	1.11	23/4642 (0.5%)
2	B	1.33	4/3410 (0.1%)	1.12	23/4629 (0.5%)
2	D	1.33	4/3410 (0.1%)	1.12	23/4629 (0.5%)
2	F	1.33	4/3410 (0.1%)	1.13	23/4629 (0.5%)
2	H	1.33	4/3410 (0.1%)	1.13	24/4629 (0.5%)
3	I	0.32	0/789	0.58	0/1055
All	All	1.03	16/28133 (0.1%)	1.11	183/38139 (0.5%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	92	LEU	C-N	52.10	1.98	1.33
2	B	92	LEU	C-N	52.05	1.98	1.33
2	H	92	LEU	C-N	52.04	1.98	1.33
2	F	92	LEU	C-N	52.03	1.98	1.33
2	F	298	PRO	C-N	35.33	1.73	1.33
2	H	298	PRO	C-N	35.30	1.73	1.33
2	B	298	PRO	C-N	35.28	1.73	1.33
2	D	298	PRO	C-N	35.26	1.73	1.33
2	D	68	VAL	C-N	24.48	1.67	1.33
2	B	68	VAL	C-N	24.43	1.67	1.33
2	H	68	VAL	C-N	24.43	1.67	1.33
2	F	68	VAL	C-N	24.38	1.67	1.33
2	D	36	MET	SD-CE	7.64	1.98	1.79
2	H	36	MET	SD-CE	7.63	1.98	1.79
2	F	36	MET	SD-CE	7.63	1.98	1.79
2	B	36	MET	SD-CE	7.62	1.98	1.79

All (183) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	68	VAL	O-C-N	-10.95	111.27	122.99
2	B	68	VAL	O-C-N	-10.92	111.31	122.99
2	F	68	VAL	O-C-N	-10.92	111.31	122.99
2	H	68	VAL	O-C-N	-10.89	111.34	122.99
2	F	172	TYR	CA-C-N	10.73	133.25	119.84
2	F	172	TYR	C-N-CA	10.73	133.25	119.84
2	H	172	TYR	CA-C-N	10.71	133.23	119.84
2	H	172	TYR	C-N-CA	10.71	133.23	119.84
2	D	172	TYR	CA-C-N	10.71	133.22	119.84
2	D	172	TYR	C-N-CA	10.71	133.22	119.84
2	B	172	TYR	CA-C-N	10.69	133.20	119.84
2	B	172	TYR	C-N-CA	10.69	133.20	119.84
1	G	262	PHE	CA-C-N	9.99	132.32	119.84
1	G	262	PHE	C-N-CA	9.99	132.32	119.84
1	A	262	PHE	CA-C-N	9.97	132.30	119.84
1	A	262	PHE	C-N-CA	9.97	132.30	119.84
1	C	262	PHE	CA-C-N	9.97	132.30	119.84
1	C	262	PHE	C-N-CA	9.97	132.30	119.84
1	E	262	PHE	CA-C-N	9.96	132.29	119.84
1	E	262	PHE	C-N-CA	9.96	132.29	119.84
2	D	298	PRO	O-C-N	-7.94	111.93	122.64
2	F	298	PRO	O-C-N	-7.94	111.93	122.64
1	C	77	SER	N-CA-C	-7.93	104.21	114.04
2	H	298	PRO	O-C-N	-7.92	111.95	122.64
1	A	77	SER	N-CA-C	-7.91	104.23	114.04
1	G	77	SER	N-CA-C	-7.91	104.24	114.04
1	E	77	SER	N-CA-C	-7.90	104.24	114.04
2	B	298	PRO	O-C-N	-7.90	111.97	122.64
1	A	159	GLU	N-CA-C	-7.81	104.23	114.31
1	G	159	GLU	N-CA-C	-7.80	104.24	114.31
1	E	159	GLU	N-CA-C	-7.80	104.25	114.31
1	C	159	GLU	N-CA-C	-7.79	104.26	114.31
1	G	313	LEU	N-CA-C	-7.69	103.86	113.55
1	E	313	LEU	N-CA-C	-7.68	103.87	113.55
1	A	313	LEU	N-CA-C	-7.68	103.88	113.55
1	C	313	LEU	N-CA-C	-7.66	103.90	113.55
2	H	428	LEU	N-CA-C	-7.56	104.29	113.97
2	B	428	LEU	N-CA-C	-7.55	104.30	113.97
2	D	428	LEU	N-CA-C	-7.55	104.31	113.97
2	F	428	LEU	N-CA-C	-7.54	104.31	113.97
1	G	208	ALA	N-CA-C	-7.48	102.80	112.23
1	A	208	ALA	N-CA-C	-7.48	102.81	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	208	ALA	N-CA-C	-7.47	102.81	112.23
1	E	208	ALA	N-CA-C	-7.46	102.83	112.23
1	E	293	GLN	N-CA-C	-7.42	102.88	110.97
1	G	293	GLN	N-CA-C	-7.41	102.89	110.97
1	A	293	GLN	N-CA-C	-7.39	102.92	110.97
1	C	293	GLN	N-CA-C	-7.35	102.96	110.97
1	G	385	GLN	N-CA-C	-7.09	103.48	111.14
1	C	385	GLN	N-CA-C	-7.09	103.49	111.14
1	A	385	GLN	N-CA-C	-7.08	103.49	111.14
1	E	385	GLN	N-CA-C	-7.07	103.51	111.14
2	H	301	GLN	N-CA-C	7.01	121.52	112.41
2	F	301	GLN	N-CA-C	7.00	121.51	112.41
1	A	22	GLU	N-CA-C	-6.99	103.36	110.97
1	C	22	GLU	N-CA-C	-6.99	103.36	110.97
2	D	301	GLN	N-CA-C	6.99	121.49	112.41
1	C	388	PHE	N-CA-C	-6.98	104.02	112.54
1	A	388	PHE	N-CA-C	-6.97	104.03	112.54
1	G	388	PHE	N-CA-C	-6.97	104.03	112.54
2	B	301	GLN	N-CA-C	6.96	121.46	112.41
1	E	22	GLU	N-CA-C	-6.96	103.38	110.97
1	E	399	PHE	N-CA-C	-6.96	103.62	111.07
1	G	22	GLU	N-CA-C	-6.96	103.38	110.97
1	G	399	PHE	N-CA-C	-6.96	103.62	111.07
1	A	399	PHE	N-CA-C	-6.96	103.63	111.07
1	E	388	PHE	N-CA-C	-6.96	104.06	112.54
1	C	399	PHE	N-CA-C	-6.95	103.63	111.07
2	H	422	ARG	N-CA-C	-6.86	103.03	111.40
1	A	389	LYS	N-CA-C	-6.85	103.50	110.97
2	F	422	ARG	N-CA-C	-6.85	103.04	111.40
1	G	389	LYS	N-CA-C	-6.84	103.52	110.97
1	C	389	LYS	N-CA-C	-6.82	103.54	110.97
1	E	389	LYS	N-CA-C	-6.82	103.54	110.97
2	H	385	ALA	N-CA-C	-6.82	103.08	111.33
2	B	422	ARG	N-CA-C	-6.81	103.09	111.40
2	F	385	ALA	N-CA-C	-6.80	103.10	111.33
2	D	422	ARG	N-CA-C	-6.77	103.14	111.40
2	D	385	ALA	N-CA-C	-6.75	103.16	111.33
2	F	188	ILE	N-CA-C	-6.74	103.12	113.16
2	H	188	ILE	N-CA-C	-6.74	103.12	113.16
2	B	385	ALA	N-CA-C	-6.71	103.20	111.33
2	B	188	ILE	N-CA-C	-6.71	103.17	113.16
2	D	188	ILE	N-CA-C	-6.68	103.21	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	92	LEU	O-C-N	6.66	129.70	122.64
2	F	92	LEU	O-C-N	6.63	129.66	122.64
2	D	92	LEU	O-C-N	6.60	129.64	122.64
2	B	92	LEU	O-C-N	6.55	129.59	122.64
2	F	123	ARG	N-CA-C	-6.54	105.88	114.31
2	H	123	ARG	N-CA-C	-6.52	105.90	114.31
2	B	123	ARG	N-CA-C	-6.49	105.94	114.31
2	D	123	ARG	N-CA-C	-6.48	105.95	114.31
1	E	217	LEU	N-CA-C	-6.47	96.43	107.23
1	G	217	LEU	N-CA-C	-6.46	96.44	107.23
1	A	217	LEU	N-CA-C	-6.45	96.46	107.23
1	C	217	LEU	N-CA-C	-6.45	96.47	107.23
1	C	27	GLU	N-CA-C	-6.24	106.03	113.21
1	E	27	GLU	N-CA-C	-6.23	106.05	113.21
1	G	27	GLU	N-CA-C	-6.23	106.05	113.21
1	A	27	GLU	N-CA-C	-6.22	106.06	113.21
1	A	181	VAL	N-CA-C	6.07	116.82	111.90
1	E	181	VAL	N-CA-C	6.02	116.78	111.90
1	A	88	ARG	N-CA-C	-6.01	102.19	109.83
1	A	243	ARG	N-CA-C	-6.01	106.60	112.97
1	G	181	VAL	N-CA-C	6.01	116.77	111.90
1	E	88	ARG	N-CA-C	-6.00	102.21	109.83
1	G	243	ARG	N-CA-C	-6.00	106.62	112.97
1	G	88	ARG	N-CA-C	-5.98	102.23	109.83
1	E	243	ARG	N-CA-C	-5.98	106.64	112.97
1	C	88	ARG	N-CA-C	-5.98	102.24	109.83
1	C	181	VAL	N-CA-C	5.96	116.73	111.90
1	C	243	ARG	N-CA-C	-5.96	106.66	112.97
2	H	264	ARG	N-CA-C	-5.90	101.57	110.24
2	F	264	ARG	N-CA-C	-5.89	101.58	110.24
2	D	264	ARG	N-CA-C	-5.89	101.58	110.24
2	B	264	ARG	N-CA-C	-5.88	101.60	110.24
2	H	231	ILE	N-CA-C	-5.87	103.93	110.62
2	B	231	ILE	N-CA-C	-5.86	103.94	110.62
2	D	231	ILE	N-CA-C	-5.85	103.95	110.62
2	F	231	ILE	N-CA-C	-5.85	103.95	110.62
1	C	296	PHE	N-CA-C	5.78	119.95	113.02
1	G	296	PHE	N-CA-C	5.78	119.95	113.02
1	A	296	PHE	N-CA-C	5.75	119.92	113.02
1	E	296	PHE	N-CA-C	5.74	119.98	113.15
1	A	247	GLN	N-CA-C	-5.74	105.03	111.28
1	G	247	GLN	N-CA-C	-5.71	105.05	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	247	GLN	N-CA-C	-5.71	105.06	111.28
1	E	247	GLN	N-CA-C	-5.69	105.08	111.28
2	D	415	GLU	N-CA-C	-5.60	105.54	112.38
2	B	415	GLU	N-CA-C	-5.59	105.56	112.38
2	H	415	GLU	N-CA-C	-5.55	105.60	112.38
2	F	415	GLU	N-CA-C	-5.55	105.61	112.38
2	F	262	TYR	CA-C-N	5.54	126.77	119.84
2	F	262	TYR	C-N-CA	5.54	126.77	119.84
2	B	262	TYR	CA-C-N	5.54	126.77	119.84
2	B	262	TYR	C-N-CA	5.54	126.77	119.84
2	D	262	TYR	CA-C-N	5.54	126.77	119.84
2	D	262	TYR	C-N-CA	5.54	126.77	119.84
2	H	262	TYR	CA-C-N	5.54	126.76	119.84
2	H	262	TYR	C-N-CA	5.54	126.76	119.84
1	C	59	ASN	N-CA-C	-5.49	105.59	114.09
1	A	59	ASN	N-CA-C	-5.49	105.59	114.09
2	B	259	LEU	N-CA-C	5.47	120.98	113.97
2	F	259	LEU	N-CA-C	5.46	120.96	113.97
1	E	59	ASN	N-CA-C	-5.45	105.64	114.09
2	H	259	LEU	N-CA-C	5.45	120.95	113.97
1	G	59	ASN	N-CA-C	-5.45	105.64	114.09
2	D	259	LEU	N-CA-C	5.44	120.94	113.97
1	C	436	GLN	N-CA-C	-5.44	106.34	112.87
2	B	280	LYS	N-CA-C	-5.41	106.18	112.89
1	E	436	GLN	N-CA-C	-5.39	106.40	112.87
1	A	436	GLN	N-CA-C	-5.39	106.40	112.87
2	D	280	LYS	N-CA-C	-5.38	106.21	112.89
1	G	436	GLN	N-CA-C	-5.37	106.43	112.87
2	F	280	LYS	N-CA-C	-5.36	106.24	112.89
2	F	429	GLU	N-CA-C	-5.35	105.89	112.90
2	H	280	LYS	N-CA-C	-5.35	106.26	112.89
2	H	429	GLU	N-CA-C	-5.35	105.89	112.90
2	D	429	GLU	N-CA-C	-5.32	105.94	112.90
2	B	429	GLU	N-CA-C	-5.31	105.95	112.90
1	E	289	PRO	N-CA-C	-5.19	107.09	113.84
1	G	289	PRO	N-CA-C	-5.19	107.09	113.84
1	A	289	PRO	N-CA-C	-5.18	107.10	113.84
1	C	289	PRO	N-CA-C	-5.17	107.11	113.84
2	F	421	ALA	N-CA-C	-5.12	107.06	113.72
2	H	421	ALA	N-CA-C	-5.12	107.07	113.72
2	B	421	ALA	N-CA-C	-5.11	107.08	113.72
2	F	140	SER	N-CA-C	5.11	116.36	109.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	140	SER	N-CA-C	5.11	116.36	109.11
2	H	89	PRO	N-CA-C	-5.10	106.41	113.81
2	B	89	PRO	N-CA-C	-5.09	106.42	113.81
2	D	421	ALA	N-CA-C	-5.09	107.10	113.72
2	D	89	PRO	N-CA-C	-5.09	106.43	113.81
2	F	89	PRO	N-CA-C	-5.09	106.43	113.81
2	D	140	SER	N-CA-C	5.08	116.32	109.11
2	H	241	SER	N-CA-C	5.07	116.81	111.28
2	F	241	SER	N-CA-C	5.07	116.81	111.28
2	B	140	SER	N-CA-C	5.04	116.27	109.11
2	D	241	SER	N-CA-C	5.03	116.77	111.28
2	B	241	SER	N-CA-C	5.03	116.76	111.28
1	G	33	THR	N-CA-C	-5.01	107.20	113.72
2	H	16	ILE	N-CA-C	-5.01	105.51	110.62
1	E	33	THR	N-CA-C	-5.00	107.21	113.72

There are no chirality outliers.

There are no planarity outliers.

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	3351	0	3229	588	0
1	C	3351	0	3229	662	0
1	E	3351	0	3229	585	0
1	G	3351	0	3229	790	0
2	B	3334	0	3223	720	0
2	D	3334	0	3223	691	0
2	F	3334	0	3223	759	0
2	H	3334	0	3223	747	0
3	I	776	596	764	63	0
4	A	28	0	12	1	0
4	C	28	0	12	1	0
4	E	28	0	12	1	0
4	G	28	0	12	4	0
5	B	32	0	12	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	32	0	12	4	0
5	F	32	0	12	5	0
5	H	32	0	12	5	0
All	All	27756	596	26668	5248	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 96.

All (5248) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:257:VAL:HG21	2:H:407:TRP:CG	1.28	1.63
2:D:296:PHE:CE2	2:D:341:ILE:HD11	1.32	1.59
2:B:296:PHE:CE2	2:B:341:ILE:HD11	1.32	1.59
2:F:296:PHE:CE2	2:F:341:ILE:HD11	1.32	1.57
2:H:296:PHE:CE2	2:H:341:ILE:HD11	1.32	1.57
1:G:352:LYS:CD	2:H:181:VAL:HG23	1.43	1.47
2:F:298:PRO:C	2:F:299:ALA:N	1.73	1.47
2:H:298:PRO:C	2:H:299:ALA:N	1.73	1.46
2:F:326:LYS:CB	1:G:222:PRO:HG2	1.42	1.45
2:B:298:PRO:C	2:B:299:ALA:N	1.73	1.45
2:F:261:PRO:HA	1:G:404:PHE:CD2	1.47	1.45
2:F:349:THR:HG21	1:G:178:SER:CA	1.46	1.45
2:F:349:THR:CB	1:G:178:SER:HB2	1.45	1.45
2:D:298:PRO:C	2:D:299:ALA:N	1.73	1.44
2:B:5:ILE:HG12	2:B:64:ARG:NH1	1.27	1.43
1:G:250:ALA:CB	1:G:254:LYS:HD3	1.44	1.42
1:G:253:ARG:HB3	2:H:407:TRP:CH2	1.53	1.41
1:G:248:LEU:HD22	2:H:179:THR:CG2	1.49	1.38
1:A:88:ARG:HD2	1:E:283:TYR:CE1	1.58	1.37
1:G:257:VAL:CG2	2:H:407:TRP:CG	2.06	1.36
1:G:257:VAL:HG23	2:H:407:TRP:CB	1.57	1.34
1:G:257:VAL:CG2	2:H:407:TRP:CB	2.02	1.34
2:F:3:GLU:CG	2:F:51:THR:HA	1.57	1.33
2:D:296:PHE:CE2	2:D:341:ILE:CD1	2.11	1.33
2:H:3:GLU:CG	2:H:51:THR:HA	1.57	1.33
1:G:257:VAL:CG2	2:H:407:TRP:HB2	1.59	1.33
2:D:3:GLU:CG	2:D:51:THR:HA	1.57	1.32
2:F:3:GLU:HG2	2:F:51:THR:CA	1.60	1.32
2:H:3:GLU:HG2	2:H:51:THR:CA	1.60	1.32
2:B:3:GLU:HG2	2:B:51:THR:CA	1.60	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3:GLU:CG	2:B:51:THR:HA	1.57	1.32
2:F:296:PHE:CE2	2:F:341:ILE:CD1	2.11	1.32
2:B:296:PHE:CE2	2:B:341:ILE:CD1	2.11	1.32
2:D:3:GLU:HG2	2:D:51:THR:CA	1.60	1.31
2:H:296:PHE:CE2	2:H:341:ILE:CD1	2.11	1.31
2:F:329:ASN:HB3	1:G:210:TYR:CE1	1.66	1.31
2:D:57:GLY:HA3	2:D:58:ALA:CB	1.45	1.29
2:B:63:PRO:HG2	2:B:91:GLN:OE1	1.29	1.29
1:G:352:LYS:HD3	2:H:181:VAL:CG2	1.60	1.29
2:D:57:GLY:CA	2:D:58:ALA:HB2	1.63	1.29
2:B:57:GLY:CA	2:B:58:ALA:HB2	1.63	1.28
2:B:348:PRO:CD	1:C:398:MET:HE3	1.65	1.27
2:B:57:GLY:HA3	2:B:58:ALA:CB	1.45	1.26
2:B:62:VAL:CG1	2:B:63:PRO:HD2	1.67	1.25
2:F:349:THR:CG2	1:G:178:SER:HB2	1.65	1.25
2:F:349:THR:HG21	1:G:178:SER:N	1.50	1.25
2:F:326:LYS:HB2	1:G:222:PRO:CG	1.66	1.24
2:F:329:ASN:CG	1:G:210:TYR:HE1	1.44	1.24
2:B:348:PRO:CD	1:C:398:MET:CE	2.18	1.22
2:F:324:VAL:CG2	1:G:221:THR:HB	1.70	1.21
1:G:257:VAL:HB	2:H:407:TRP:CE3	1.73	1.21
2:B:92:LEU:C	2:B:93:ILE:N	1.98	1.20
2:D:92:LEU:C	2:D:93:ILE:N	1.98	1.20
2:H:92:LEU:C	2:H:93:ILE:N	1.98	1.20
2:F:92:LEU:C	2:F:93:ILE:N	1.98	1.20
2:F:326:LYS:CB	1:G:222:PRO:CG	2.18	1.20
2:F:324:VAL:HG21	1:G:221:THR:CB	1.70	1.19
2:D:217:LEU:HD12	2:D:277:SER:CB	1.72	1.19
2:B:5:ILE:CG1	2:B:64:ARG:NH1	2.05	1.18
2:B:217:LEU:HD12	2:B:277:SER:CB	1.72	1.18
2:F:329:ASN:CB	1:G:210:TYR:CE1	2.26	1.18
2:F:217:LEU:HD12	2:F:277:SER:CB	1.72	1.18
2:H:217:LEU:HD12	2:H:277:SER:CB	1.72	1.18
2:D:30:ILE:HG12	2:D:36:MET:HB3	1.19	1.18
1:G:2:ARG:CZ	2:H:98:ASP:HB3	1.73	1.18
1:C:88:ARG:HD2	1:G:283:TYR:CZ	1.79	1.17
2:F:349:THR:HG21	1:G:178:SER:CB	1.73	1.17
1:G:254:LYS:CE	1:G:352:LYS:HE3	1.73	1.16
2:F:262:TYR:OH	1:G:403:ALA:HA	1.46	1.16
2:B:30:ILE:HG12	2:B:36:MET:HB3	1.19	1.15
2:B:348:PRO:HD2	1:C:398:MET:CE	1.73	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:88:ARG:HD2	1:G:283:TYR:OH	1.43	1.15
2:F:261:PRO:HB3	1:G:404:PHE:CE2	1.81	1.15
2:F:349:THR:HB	1:G:178:SER:HB2	1.16	1.15
2:F:30:ILE:HG12	2:F:36:MET:HB3	1.17	1.15
2:D:56:THR:O	2:H:284:GLU:HB3	1.46	1.15
1:C:88:ARG:HD3	1:G:283:TYR:HE1	1.01	1.14
2:B:5:ILE:CD1	2:B:64:ARG:HH12	1.57	1.14
2:H:30:ILE:HG12	2:H:36:MET:HB3	1.17	1.14
2:B:243:ARG:NH2	2:B:252:LEU:H	1.45	1.14
2:D:243:ARG:NH2	2:D:252:LEU:H	1.45	1.14
2:B:62:VAL:HG12	2:B:63:PRO:CD	1.76	1.14
2:F:243:ARG:NH2	2:F:252:LEU:H	1.45	1.14
1:G:93:VAL:HG11	1:G:118:VAL:HG22	1.30	1.14
2:H:243:ARG:NH2	2:H:252:LEU:H	1.45	1.14
1:C:88:ARG:HD3	1:G:283:TYR:CE1	1.83	1.13
1:G:258:ASN:HA	2:H:404:PHE:CD2	1.84	1.13
2:B:296:PHE:CE1	2:B:335:ILE:HG21	1.84	1.13
1:C:257:VAL:HG13	2:D:407:TRP:CG	1.83	1.13
2:D:296:PHE:CE1	2:D:335:ILE:HG21	1.84	1.13
2:H:296:PHE:CE1	2:H:335:ILE:HG21	1.84	1.13
1:A:88:ARG:CD	1:E:283:TYR:CE1	2.31	1.13
2:B:439:SER:C	1:C:401:ARG:HH21	1.58	1.12
2:F:296:PHE:CE1	2:F:335:ILE:HG21	1.84	1.12
1:E:93:VAL:HG11	1:E:118:VAL:HG22	1.30	1.12
1:A:234:THR:HG21	1:A:270:PRO:HB2	1.23	1.12
2:B:348:PRO:CG	1:C:398:MET:HE3	1.77	1.12
2:F:261:PRO:CB	1:G:404:PHE:CE2	2.32	1.12
2:F:261:PRO:CA	1:G:404:PHE:CD2	2.32	1.12
1:A:88:ARG:CD	1:E:283:TYR:HE1	1.63	1.12
1:E:234:THR:HG21	1:E:270:PRO:HB2	1.23	1.11
2:F:70:LEU:HD13	2:F:145:THR:OG1	1.49	1.11
1:G:352:LYS:CD	2:H:181:VAL:CG2	2.20	1.11
2:H:70:LEU:HD13	2:H:145:THR:OG1	1.49	1.11
2:B:274:PRO:C	2:B:275:VAL:N	2.09	1.11
2:D:274:PRO:C	2:D:275:VAL:N	2.09	1.11
2:D:67:PHE:HE1	2:D:87:PHE:CE1	1.68	1.10
2:F:67:PHE:HE1	2:F:87:PHE:CE1	1.69	1.10
2:H:274:PRO:C	2:H:275:VAL:N	2.09	1.10
2:B:67:PHE:HE1	2:B:87:PHE:CE1	1.68	1.10
2:B:70:LEU:HD13	2:B:145:THR:OG1	1.49	1.10
1:C:88:ARG:CD	1:G:283:TYR:CE1	2.34	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:THR:HG21	1:C:270:PRO:HB2	1.23	1.10
2:H:67:PHE:HE1	2:H:87:PHE:CE1	1.68	1.10
2:F:274:PRO:C	2:F:275:VAL:N	2.09	1.10
2:D:70:LEU:HD13	2:D:145:THR:OG1	1.49	1.10
2:F:349:THR:CG2	1:G:178:SER:H	1.65	1.09
1:G:234:THR:HG21	1:G:270:PRO:HB2	1.23	1.09
1:G:258:ASN:ND2	1:G:352:LYS:HE2	1.67	1.09
1:A:93:VAL:HG11	1:A:118:VAL:HG22	1.30	1.08
2:D:56:THR:O	2:D:58:ALA:HB3	1.54	1.08
1:C:93:VAL:HG11	1:C:118:VAL:HG22	1.30	1.07
2:F:329:ASN:CB	1:G:210:TYR:HE1	1.66	1.07
1:A:56:ALA:CB	1:E:283:TYR:CE2	2.37	1.06
1:G:352:LYS:HD2	2:H:181:VAL:HG23	1.24	1.06
2:B:11:GLN:HG3	2:B:74:VAL:HG11	1.34	1.06
2:B:109:THR:HG22	2:B:110:ILE:N	1.71	1.06
2:B:350:GLY:CA	1:C:181:VAL:HG13	1.86	1.05
2:F:109:THR:HG22	2:F:110:ILE:N	1.71	1.05
2:F:326:LYS:HG3	1:G:222:PRO:HG3	1.30	1.05
2:F:329:ASN:CG	1:G:210:TYR:CE1	2.34	1.05
2:D:5:ILE:HG21	2:D:135:PHE:HD2	1.18	1.05
2:D:109:THR:HG22	2:D:110:ILE:N	1.70	1.05
2:D:217:LEU:CD1	2:D:277:SER:HB3	1.87	1.05
2:H:109:THR:HG22	2:H:110:ILE:N	1.70	1.05
2:H:11:GLN:HG3	2:H:74:VAL:HG11	1.34	1.05
2:B:5:ILE:CG1	2:B:64:ARG:HH12	1.67	1.05
2:B:217:LEU:CD1	2:B:277:SER:HB3	1.87	1.05
2:B:298:PRO:HB3	2:B:307:PRO:HD2	1.36	1.05
2:B:350:GLY:HA2	1:C:181:VAL:CG1	1.86	1.05
2:D:296:PHE:CD2	2:D:341:ILE:CD1	2.40	1.05
2:F:5:ILE:HG21	2:F:135:PHE:HD2	1.18	1.05
2:F:11:GLN:HG3	2:F:74:VAL:HG11	1.34	1.05
2:B:296:PHE:CD2	2:B:341:ILE:CD1	2.40	1.04
1:G:257:VAL:HG21	2:H:407:TRP:CD1	1.91	1.04
2:H:5:ILE:HG21	2:H:135:PHE:HD2	1.17	1.04
2:D:11:GLN:HG3	2:D:74:VAL:HG11	1.34	1.04
2:D:67:PHE:CE1	2:D:87:PHE:CE1	2.45	1.04
2:F:296:PHE:CD2	2:F:341:ILE:CD1	2.40	1.04
2:F:349:THR:CG2	1:G:178:SER:CB	2.32	1.04
2:H:296:PHE:CD2	2:H:341:ILE:CD1	2.40	1.04
2:B:67:PHE:CE1	2:B:87:PHE:CE1	2.45	1.04
1:G:250:ALA:HB1	1:G:254:LYS:HD3	1.39	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ARG:HD2	1:E:283:TYR:CZ	1.91	1.04
2:F:67:PHE:CE1	2:F:87:PHE:CE1	2.45	1.04
2:F:217:LEU:CD1	2:F:277:SER:HB3	1.86	1.04
1:G:250:ALA:HB2	1:G:254:LYS:CD	1.88	1.04
1:G:352:LYS:HD3	2:H:181:VAL:HG23	1.07	1.04
2:H:217:LEU:CD1	2:H:277:SER:HB3	1.87	1.04
2:H:67:PHE:CE1	2:H:87:PHE:CE1	2.45	1.03
2:H:298:PRO:HB3	2:H:307:PRO:HD2	1.36	1.03
2:F:298:PRO:HB3	2:F:307:PRO:HD2	1.36	1.03
2:F:349:THR:CG2	1:G:178:SER:N	2.21	1.03
1:G:2:ARG:NH2	2:H:98:ASP:HB3	1.74	1.03
2:D:298:PRO:HB3	2:D:307:PRO:HD2	1.36	1.02
2:D:243:ARG:HH21	2:D:252:LEU:N	1.57	1.02
2:H:243:ARG:HH21	2:H:252:LEU:N	1.58	1.02
2:B:63:PRO:HG2	2:B:91:GLN:CD	1.84	1.02
2:B:243:ARG:HH21	2:B:252:LEU:N	1.57	1.02
2:F:243:ARG:HH21	2:F:252:LEU:N	1.58	1.02
1:G:250:ALA:CB	1:G:254:LYS:CD	2.38	1.02
2:F:325:PRO:HD2	1:G:223:THR:HA	1.40	1.02
1:C:172:VAL:HG11	1:C:387:LEU:HD21	1.37	1.02
1:A:56:ALA:HB2	1:E:283:TYR:HE2	1.25	1.01
2:F:326:LYS:CG	1:G:222:PRO:CG	2.38	1.01
2:B:88:HIS:HB2	2:B:91:GLN:HE21	1.22	1.01
1:G:248:LEU:CD2	2:H:179:THR:CG2	2.37	1.01
1:A:172:VAL:HG11	1:A:387:LEU:HD21	1.37	1.01
1:E:236:SER:O	1:E:240:THR:HG23	1.61	1.01
1:G:254:LYS:HE2	1:G:352:LYS:CE	1.90	1.01
1:G:236:SER:O	1:G:240:THR:HG23	1.61	1.00
2:D:88:HIS:HB2	2:D:91:GLN:HE21	1.22	1.00
1:E:172:VAL:HG11	1:E:387:LEU:HD21	1.37	1.00
1:G:253:ARG:CB	2:H:407:TRP:CH2	2.43	1.00
1:A:88:ARG:NH1	1:E:283:TYR:CE1	2.29	1.00
2:B:5:ILE:HG12	2:B:64:ARG:CZ	1.90	1.00
2:B:350:GLY:HA2	1:C:181:VAL:HG13	1.03	1.00
1:G:172:VAL:HG11	1:G:387:LEU:HD21	1.37	1.00
1:G:258:ASN:O	2:H:404:PHE:HE2	1.42	1.00
1:G:257:VAL:HG21	2:H:407:TRP:CB	1.77	1.00
1:A:236:SER:O	1:A:240:THR:HG23	1.61	1.00
2:B:30:ILE:HD11	2:B:61:HIS:CE1	1.97	1.00
2:H:88:HIS:HB2	2:H:91:GLN:HE21	1.22	1.00
1:C:236:SER:O	1:C:240:THR:HG23	1.61	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:56:THR:O	2:B:58:ALA:HB3	1.59	0.99
1:G:253:ARG:CB	2:H:407:TRP:HH2	1.75	0.99
2:D:56:THR:CB	2:H:284:GLU:CD	2.34	0.99
2:F:349:THR:CB	1:G:178:SER:CB	2.40	0.99
2:F:88:HIS:HB2	2:F:91:GLN:HE21	1.22	0.99
1:C:329:ASP:HB3	2:D:177:VAL:CG1	1.93	0.98
1:G:250:ALA:HB2	1:G:254:LYS:HD3	1.01	0.98
1:C:299:LYS:H	1:C:299:LYS:HD3	1.24	0.98
1:G:352:LYS:HA	2:H:181:VAL:HG22	1.44	0.98
1:G:248:LEU:HD22	2:H:179:THR:HG22	1.43	0.98
2:B:52:PHE:HZ	2:B:239:THR:HG21	1.27	0.98
2:H:276:ILE:HG23	2:H:369:ALA:HB2	1.43	0.98
1:A:299:LYS:HD3	1:A:299:LYS:H	1.24	0.97
1:C:332:MET:HE3	1:C:351:VAL:HG11	1.45	0.97
1:G:248:LEU:HD22	2:H:179:THR:HG21	1.46	0.97
2:B:276:ILE:HG23	2:B:369:ALA:HB2	1.43	0.97
2:F:276:ILE:HG23	2:F:369:ALA:HB2	1.43	0.97
2:D:276:ILE:HG23	2:D:369:ALA:HB2	1.43	0.97
2:F:349:THR:CG2	1:G:178:SER:CA	2.42	0.97
1:G:254:LYS:HE2	1:G:352:LYS:HE3	0.97	0.97
1:E:299:LYS:H	1:E:299:LYS:HD3	1.24	0.96
2:D:259:LEU:HD11	2:D:378:LEU:HD13	1.47	0.96
2:F:259:LEU:HD11	2:F:378:LEU:HD13	1.47	0.96
2:F:326:LYS:HG3	1:G:222:PRO:CG	1.96	0.96
2:B:62:VAL:HG12	2:B:63:PRO:HD2	0.97	0.96
2:B:278:ALA:O	2:B:279:GLU:HB3	1.66	0.96
2:F:326:LYS:CG	1:G:222:PRO:HG3	1.94	0.96
2:H:259:LEU:HD11	2:H:378:LEU:HD13	1.47	0.96
1:G:299:LYS:HD3	1:G:299:LYS:H	1.24	0.96
2:D:278:ALA:O	2:D:279:GLU:HB3	1.66	0.96
1:A:56:ALA:HB2	1:E:283:TYR:CE2	2.00	0.96
1:A:332:MET:HE3	1:A:351:VAL:HG11	1.45	0.96
2:H:98:ASP:HB2	2:H:105:ARG:HH21	1.31	0.96
2:F:324:VAL:HG21	1:G:221:THR:HB	0.97	0.96
2:B:98:ASP:HB2	2:B:105:ARG:HH21	1.31	0.95
2:B:259:LEU:HD11	2:B:378:LEU:HD13	1.47	0.95
1:C:273:ALA:HB3	1:C:274:PRO:HD3	1.48	0.95
2:F:98:ASP:HB2	2:F:105:ARG:HH21	1.31	0.95
2:B:251:ASP:N	2:B:254:GLU:HG3	1.82	0.95
2:D:98:ASP:HB2	2:D:105:ARG:HH21	1.31	0.95
2:H:5:ILE:CG2	2:H:135:PHE:HD2	1.78	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:257:VAL:HB	2:H:407:TRP:CD2	2.01	0.95
2:D:251:ASP:N	2:D:254:GLU:HG3	1.82	0.95
2:F:5:ILE:CG2	2:F:135:PHE:HD2	1.78	0.95
1:A:273:ALA:HB3	1:A:274:PRO:HD3	1.48	0.95
2:D:5:ILE:CG2	2:D:135:PHE:HD2	1.78	0.95
2:H:251:ASP:N	2:H:254:GLU:HG3	1.82	0.95
2:F:251:ASP:N	2:F:254:GLU:HG3	1.82	0.95
1:G:332:MET:HE3	1:G:351:VAL:HG11	1.45	0.95
1:C:248:LEU:HD22	2:D:179:THR:HG21	1.47	0.95
2:D:52:PHE:CZ	2:D:239:THR:HB	2.02	0.94
2:D:217:LEU:HD12	2:D:277:SER:HB3	0.95	0.94
1:E:332:MET:HE3	1:E:351:VAL:HG11	1.45	0.94
1:G:273:ALA:HB3	1:G:274:PRO:HD3	1.48	0.94
2:H:278:ALA:O	2:H:279:GLU:HB3	1.66	0.94
1:C:88:ARG:CD	1:G:283:TYR:OH	2.13	0.94
2:F:278:ALA:O	2:F:279:GLU:HB3	1.66	0.94
2:B:217:LEU:HD12	2:B:277:SER:HB3	0.95	0.94
1:C:346:TRP:CD1	2:D:401:LYS:HZ2	1.86	0.94
2:F:30:ILE:CG1	2:F:36:MET:HB3	1.96	0.94
2:H:30:ILE:CG1	2:H:36:MET:HB3	1.96	0.94
2:H:251:ASP:H	2:H:254:GLU:HG3	1.33	0.94
2:B:316:CYS:HB3	2:B:378:LEU:HD11	1.49	0.94
1:E:273:ALA:HB3	1:E:274:PRO:HD3	1.48	0.94
2:F:251:ASP:H	2:F:254:GLU:HG3	1.33	0.94
2:H:217:LEU:HD12	2:H:277:SER:HB3	0.95	0.94
2:D:109:THR:HG22	2:D:110:ILE:H	1.33	0.94
1:A:70:LEU:H	1:A:145:THR:HG21	1.33	0.93
1:C:70:LEU:H	1:C:145:THR:HG21	1.33	0.93
2:F:217:LEU:HD12	2:F:277:SER:HB3	0.95	0.93
2:F:151:SER:HB3	2:F:193:THR:HG21	1.51	0.93
2:D:237:SER:HB2	2:D:376:CYS:SG	2.08	0.93
1:E:281:GLN:O	1:E:283:TYR:N	2.00	0.93
2:F:109:THR:HG22	2:F:110:ILE:H	1.33	0.93
2:H:151:SER:HB3	2:H:193:THR:HG21	1.51	0.93
2:D:62:VAL:HG21	2:D:88:HIS:CE1	2.04	0.93
1:A:132:LEU:HD23	1:A:164:ARG:HG3	1.50	0.93
2:B:237:SER:HB2	2:B:376:CYS:SG	2.08	0.93
1:G:264:ARG:O	1:G:265:LEU:HB3	1.69	0.93
2:H:316:CYS:HB3	2:H:378:LEU:HD11	1.48	0.93
2:B:151:SER:HB3	2:B:193:THR:HG21	1.51	0.93
1:E:264:ARG:O	1:E:265:LEU:HB3	1.69	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:281:GLN:O	1:G:283:TYR:N	2.00	0.93
1:C:88:ARG:HD2	1:G:283:TYR:CE1	2.02	0.93
1:C:132:LEU:HD23	1:C:164:ARG:HG3	1.50	0.93
1:C:281:GLN:O	1:C:283:TYR:N	2.00	0.93
1:E:132:LEU:HD23	1:E:164:ARG:HG3	1.50	0.93
2:F:316:CYS:HB3	2:F:378:LEU:HD11	1.48	0.93
2:B:109:THR:HG22	2:B:110:ILE:H	1.33	0.93
2:D:316:CYS:HB3	2:D:378:LEU:HD11	1.49	0.93
2:F:62:VAL:HG21	2:F:88:HIS:CE1	2.03	0.93
2:H:109:THR:HG22	2:H:110:ILE:H	1.33	0.93
1:A:281:GLN:O	1:A:283:TYR:N	2.00	0.93
2:F:237:SER:HB2	2:F:376:CYS:SG	2.08	0.93
2:H:237:SER:HB2	2:H:376:CYS:SG	2.08	0.93
1:G:132:LEU:HD23	1:G:164:ARG:HG3	1.50	0.92
2:H:52:PHE:CZ	2:H:239:THR:HB	2.04	0.92
2:H:62:VAL:HG21	2:H:88:HIS:CE1	2.04	0.92
2:D:151:SER:HB3	2:D:193:THR:HG21	1.51	0.92
2:B:439:SER:C	1:C:401:ARG:NH2	2.28	0.92
1:A:264:ARG:O	1:A:265:LEU:HB3	1.69	0.92
1:C:264:ARG:O	1:C:265:LEU:HB3	1.69	0.92
2:B:251:ASP:H	2:B:254:GLU:HG3	1.33	0.92
2:F:52:PHE:CZ	2:F:239:THR:HB	2.05	0.92
2:H:52:PHE:HZ	2:H:239:THR:HG21	1.35	0.92
1:E:70:LEU:H	1:E:145:THR:HG21	1.33	0.91
2:B:30:ILE:CD1	2:B:61:HIS:ND1	2.34	0.91
1:C:88:ARG:CD	1:G:283:TYR:HE1	1.73	0.91
1:G:70:LEU:H	1:G:145:THR:HG21	1.33	0.91
2:B:57:GLY:CA	2:B:58:ALA:CB	2.30	0.91
1:C:88:ARG:CD	1:G:283:TYR:CZ	2.52	0.91
2:D:251:ASP:H	2:D:254:GLU:HG3	1.33	0.91
2:F:52:PHE:HZ	2:F:239:THR:HG21	1.35	0.91
2:F:296:PHE:CD2	2:F:341:ILE:HD11	2.03	0.91
2:F:337:THR:HG22	3:I:99:GLN:OE1	1.69	0.91
2:H:296:PHE:CD2	2:H:341:ILE:HD11	2.03	0.91
1:G:254:LYS:CE	1:G:352:LYS:CE	2.49	0.91
2:H:296:PHE:HE2	2:H:341:ILE:HD11	1.21	0.91
2:B:55:GLU:O	2:B:57:GLY:N	2.04	0.91
1:A:88:ARG:HH11	1:E:283:TYR:HE1	1.09	0.90
2:F:261:PRO:HG3	1:G:404:PHE:HE2	1.35	0.90
2:D:5:ILE:CG2	2:D:135:PHE:CD2	2.54	0.90
2:D:70:LEU:CD1	2:D:145:THR:OG1	2.18	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:352:LYS:HB2	2:H:181:VAL:HG21	1.52	0.90
2:B:70:LEU:CD1	2:B:145:THR:OG1	2.18	0.90
2:D:119:LEU:HD23	2:D:122:ILE:HD11	1.53	0.90
2:D:52:PHE:HZ	2:D:239:THR:HG21	1.34	0.90
1:E:147:SER:O	1:E:151:THR:HB	1.71	0.90
1:G:253:ARG:HB3	2:H:407:TRP:HH2	1.10	0.90
2:F:70:LEU:CD1	2:F:145:THR:OG1	2.18	0.90
2:F:296:PHE:HE2	2:F:341:ILE:HD11	1.21	0.90
2:H:5:ILE:CG2	2:H:135:PHE:CD2	2.54	0.90
2:B:119:LEU:HD23	2:B:122:ILE:HD11	1.53	0.89
2:D:56:THR:C	2:H:284:GLU:CB	2.44	0.89
2:F:119:LEU:HD23	2:F:122:ILE:HD11	1.53	0.89
2:F:262:TYR:CE2	1:G:403:ALA:O	2.24	0.89
1:G:257:VAL:HG21	2:H:407:TRP:CD2	2.08	0.89
2:D:296:PHE:HE2	2:D:341:ILE:HD11	1.21	0.89
1:E:323:MET:HE2	1:E:328:VAL:HG22	1.54	0.89
2:F:5:ILE:CG2	2:F:135:PHE:CD2	2.54	0.89
1:G:147:SER:O	1:G:151:THR:HB	1.71	0.89
2:H:119:LEU:HD23	2:H:122:ILE:HD11	1.53	0.89
1:A:323:MET:HE2	1:A:328:VAL:HG22	1.54	0.89
1:A:8:GLN:OE1	1:A:67:LEU:HD22	1.72	0.89
1:A:102:ASN:HD21	1:A:408:TYR:HA	1.38	0.89
1:C:8:GLN:OE1	1:C:67:LEU:HD22	1.73	0.89
1:C:102:ASN:HD21	1:C:408:TYR:HA	1.38	0.89
2:H:70:LEU:CD1	2:H:145:THR:OG1	2.18	0.89
1:A:93:VAL:HG11	1:A:118:VAL:CG2	2.03	0.89
1:A:147:SER:O	1:A:151:THR:HB	1.71	0.89
1:E:102:ASN:HD21	1:E:408:TYR:HA	1.38	0.89
1:G:93:VAL:HG11	1:G:118:VAL:CG2	2.03	0.89
1:G:102:ASN:HD21	1:G:408:TYR:HA	1.38	0.89
1:G:264:ARG:HB2	1:G:266:HIS:CD2	2.08	0.89
1:E:93:VAL:HG11	1:E:118:VAL:CG2	2.03	0.89
1:E:264:ARG:HB2	1:E:266:HIS:CD2	2.08	0.89
2:B:52:PHE:CE1	2:B:239:THR:HB	2.07	0.89
1:C:93:VAL:HG11	1:C:118:VAL:CG2	2.03	0.89
2:D:56:THR:O	2:H:284:GLU:CB	2.21	0.89
1:G:258:ASN:HA	2:H:404:PHE:CE2	2.08	0.89
1:G:323:MET:HE2	1:G:328:VAL:HG22	1.54	0.89
2:B:296:PHE:HE2	2:B:341:ILE:HD11	1.21	0.89
1:C:264:ARG:HB2	1:C:266:HIS:CD2	2.08	0.89
2:F:257:THR:HG21	1:G:101:ASN:HB3	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:343:PHE:CZ	2:B:351:PHE:CE1	2.61	0.88
1:C:323:MET:HE2	1:C:328:VAL:HG22	1.54	0.88
1:A:101:ASN:HD21	1:A:143:GLY:HA2	1.38	0.88
1:A:264:ARG:HB2	1:A:266:HIS:CD2	2.08	0.88
2:B:110:ILE:HG23	2:B:111:GLY:H	1.38	0.88
2:B:63:PRO:CD	2:B:87:PHE:HA	2.03	0.88
1:C:147:SER:O	1:C:151:THR:HB	1.71	0.88
2:D:343:PHE:CZ	2:D:351:PHE:CE1	2.61	0.88
2:F:343:PHE:CZ	2:F:351:PHE:CE1	2.60	0.88
2:H:343:PHE:CZ	2:H:351:PHE:CE1	2.60	0.88
2:D:122:ILE:HD12	2:D:157:LEU:HD21	1.54	0.88
2:F:110:ILE:HG23	2:F:111:GLY:H	1.38	0.88
2:F:261:PRO:HA	1:G:404:PHE:HD2	0.87	0.88
1:C:101:ASN:HD21	1:C:143:GLY:HA2	1.38	0.88
2:H:110:ILE:HG23	2:H:111:GLY:H	1.38	0.88
2:B:349:THR:HG21	1:C:178:SER:OG	1.74	0.88
1:C:311:ARG:HD3	1:C:342:TYR:HA	1.56	0.88
2:F:296:PHE:CD2	2:F:341:ILE:HD12	2.08	0.88
2:F:349:THR:HG21	1:G:178:SER:C	1.98	0.88
2:F:349:THR:HB	1:G:178:SER:CB	2.02	0.88
1:G:8:GLN:OE1	1:G:67:LEU:HD22	1.73	0.88
1:E:8:GLN:OE1	1:E:67:LEU:HD22	1.73	0.88
2:F:261:PRO:CA	1:G:404:PHE:CE2	2.56	0.88
1:G:10:GLY:HA2	1:G:145:THR:HB	1.55	0.88
1:A:311:ARG:HD3	1:A:342:TYR:HA	1.56	0.88
2:D:110:ILE:HG23	2:D:111:GLY:H	1.38	0.88
2:B:296:PHE:CD2	2:B:341:ILE:HD12	2.08	0.87
2:D:30:ILE:CG1	2:D:36:MET:HB3	2.02	0.87
1:G:2:ARG:CZ	2:H:98:ASP:CB	2.52	0.87
1:G:248:LEU:CD2	2:H:179:THR:HG22	2.03	0.87
1:A:10:GLY:HA2	1:A:145:THR:HB	1.55	0.87
1:E:10:GLY:HA2	1:E:145:THR:HB	1.55	0.87
2:H:296:PHE:CD2	2:H:341:ILE:HD12	2.08	0.87
1:C:346:TRP:HB2	2:D:401:LYS:HD2	1.56	0.87
2:F:147:SER:HB2	2:F:190:THR:OG1	1.73	0.87
2:H:147:SER:HB2	2:H:190:THR:OG1	1.73	0.87
2:B:30:ILE:CD1	2:B:61:HIS:CE1	2.57	0.87
2:B:122:ILE:HD12	2:B:157:LEU:HD21	1.54	0.87
2:D:52:PHE:HZ	2:D:239:THR:CG2	1.88	0.87
1:E:311:ARG:HD3	1:E:342:TYR:HA	1.56	0.87
1:G:311:ARG:HD3	1:G:342:TYR:HA	1.56	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:30:ILE:CG1	2:B:36:MET:HB3	2.02	0.87
2:D:147:SER:HB2	2:D:190:THR:OG1	1.73	0.87
1:G:360:PRO:HG2	1:G:371:LEU:HB3	1.56	0.87
1:E:360:PRO:HG2	1:E:371:LEU:HB3	1.56	0.87
2:D:5:ILE:HG21	2:D:135:PHE:CD2	2.08	0.87
2:F:122:ILE:HD12	2:F:157:LEU:HD21	1.54	0.87
2:H:122:ILE:HD12	2:H:157:LEU:HD21	1.54	0.87
2:D:57:GLY:CA	2:D:58:ALA:CB	2.30	0.86
2:H:52:PHE:HZ	2:H:239:THR:CG2	1.88	0.86
1:A:360:PRO:HG2	1:A:371:LEU:HB3	1.56	0.86
1:C:10:GLY:HA2	1:C:145:THR:HB	1.55	0.86
1:E:6:HIS:CE1	1:E:8:GLN:HG2	2.10	0.86
1:G:257:VAL:CB	2:H:407:TRP:CD2	2.57	0.86
1:G:153:LEU:O	1:G:157:ILE:HG12	1.76	0.86
1:G:248:LEU:HD22	2:H:179:THR:HG23	1.56	0.86
2:B:63:PRO:CG	2:B:91:GLN:OE1	2.19	0.86
1:C:19:LYS:HG3	1:C:228:ASN:HB3	1.57	0.86
1:G:6:HIS:CE1	1:G:8:GLN:HG2	2.10	0.86
1:A:6:HIS:CE1	1:A:8:GLN:HG2	2.10	0.86
1:A:153:LEU:O	1:A:157:ILE:HG12	1.75	0.86
2:B:147:SER:HB2	2:B:190:THR:OG1	1.73	0.86
1:E:153:LEU:O	1:E:157:ILE:HG12	1.75	0.86
1:E:195:VAL:HG13	1:E:196:GLU:HG2	1.57	0.86
2:H:102:ASN:CG	2:H:407:TRP:HE1	1.83	0.86
1:A:276:THR:HB	1:A:281:GLN:HG3	1.56	0.86
2:B:333:ALA:HA	1:C:177:VAL:CG2	2.05	0.86
2:F:52:PHE:HZ	2:F:239:THR:CG2	1.89	0.86
1:G:276:THR:HB	1:G:281:GLN:HG3	1.56	0.86
2:B:63:PRO:HD3	2:B:87:PHE:HA	1.56	0.86
2:D:296:PHE:CD2	2:D:341:ILE:HD12	2.08	0.86
1:G:19:LYS:HG3	1:G:228:ASN:HB3	1.57	0.86
1:C:360:PRO:HG2	1:C:371:LEU:HB3	1.56	0.86
2:F:324:VAL:HG11	1:G:221:THR:CA	2.06	0.86
1:C:276:THR:HB	1:C:281:GLN:HG3	1.56	0.86
1:C:6:HIS:CE1	1:C:8:GLN:HG2	2.10	0.85
1:E:276:THR:HB	1:E:281:GLN:HG3	1.56	0.85
1:A:19:LYS:HG3	1:A:228:ASN:HB3	1.57	0.85
1:C:153:LEU:O	1:C:157:ILE:HG12	1.75	0.85
1:E:19:LYS:HG3	1:E:228:ASN:HB3	1.57	0.85
1:E:101:ASN:HD21	1:E:143:GLY:HA2	1.38	0.85
1:C:346:TRP:CG	2:D:401:LYS:HZ2	1.94	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:101:ASN:HD21	1:G:143:GLY:HA2	1.38	0.85
1:G:195:VAL:HG13	1:G:196:GLU:HG2	1.57	0.85
2:F:5:ILE:HG21	2:F:135:PHE:CD2	2.08	0.85
2:H:5:ILE:HG21	2:H:135:PHE:CD2	2.08	0.85
1:C:257:VAL:HG13	2:D:407:TRP:CD2	2.11	0.85
2:D:220:GLU:C	2:D:222:PRO:HD3	2.02	0.85
1:G:257:VAL:CG2	2:H:407:TRP:CD2	2.59	0.85
2:F:261:PRO:CG	1:G:404:PHE:HE2	1.88	0.85
1:G:352:LYS:HA	2:H:181:VAL:CG2	2.06	0.85
1:A:195:VAL:HG13	1:A:196:GLU:HG2	1.57	0.85
2:D:234:ILE:HG13	2:D:270:ALA:HB1	1.59	0.85
2:B:220:GLU:C	2:B:222:PRO:HD3	2.02	0.85
2:B:234:ILE:HG13	2:B:270:ALA:HB1	1.59	0.85
1:C:195:VAL:HG13	1:C:196:GLU:HG2	1.57	0.85
2:D:204:VAL:HG11	2:D:231:ILE:HD12	1.59	0.85
2:F:220:GLU:C	2:F:222:PRO:HD3	2.02	0.84
2:F:234:ILE:HG13	2:F:270:ALA:HB1	1.59	0.84
2:F:264:ARG:O	2:F:266:HIS:N	2.09	0.84
2:H:264:ARG:O	2:H:266:HIS:N	2.09	0.84
1:E:234:THR:HG21	1:E:270:PRO:CB	2.06	0.84
2:F:204:VAL:HG11	2:F:231:ILE:HD12	1.59	0.84
1:G:179:ASP:HB2	4:G:600:GDP:H3'	1.58	0.84
2:H:234:ILE:HG13	2:H:270:ALA:HB1	1.59	0.84
2:D:52:PHE:CZ	2:D:239:THR:CB	2.60	0.84
2:F:263:PRO:HD3	1:G:406:HIS:CD2	2.12	0.84
2:H:220:GLU:C	2:H:222:PRO:HD3	2.02	0.84
2:B:204:VAL:HG11	2:B:231:ILE:HD12	1.59	0.84
1:C:209:LEU:HB3	1:C:227:LEU:HD22	1.59	0.84
2:B:52:PHE:CZ	2:B:239:THR:HG21	2.11	0.84
1:C:150:GLY:HA2	1:C:153:LEU:HD22	1.60	0.84
1:C:242:LEU:HD22	1:C:250:ALA:H	1.41	0.84
2:H:204:VAL:HG11	2:H:231:ILE:HD12	1.59	0.84
1:A:150:GLY:HA2	1:A:153:LEU:HD22	1.60	0.84
2:B:264:ARG:O	2:B:266:HIS:N	2.09	0.84
2:D:106:GLY:O	2:D:111:GLY:HA3	1.78	0.84
2:D:264:ARG:HB2	2:D:266:HIS:CD2	2.13	0.84
2:F:324:VAL:HG21	1:G:221:THR:CG2	2.06	0.84
1:G:209:LEU:HB3	1:G:227:LEU:HD22	1.59	0.84
1:G:234:THR:HG21	1:G:270:PRO:CB	2.06	0.84
2:B:106:GLY:O	2:B:111:GLY:HA3	1.78	0.84
1:G:242:LEU:HD22	1:G:250:ALA:H	1.41	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:PHE:CD2	1:A:235:MET:SD	2.71	0.84
1:A:56:ALA:HB1	1:E:283:TYR:CD2	2.13	0.84
1:A:242:LEU:HD22	1:A:250:ALA:H	1.41	0.84
1:C:3:GLU:O	1:C:133:GLN:HB3	1.78	0.84
1:C:248:LEU:CD2	2:D:179:THR:HG21	2.08	0.84
2:D:52:PHE:CE1	2:D:239:THR:HB	2.12	0.84
2:D:264:ARG:O	2:D:266:HIS:N	2.09	0.84
2:F:316:CYS:HB3	2:F:378:LEU:CD1	2.08	0.84
1:G:150:GLY:HA2	1:G:153:LEU:HD22	1.60	0.84
1:A:4:ILE:HD13	1:A:136:GLN:HE21	1.42	0.84
1:A:209:LEU:HB3	1:A:227:LEU:HD22	1.59	0.84
1:C:191:VAL:HG11	1:C:425:MET:HG3	1.60	0.84
1:E:3:GLU:O	1:E:133:GLN:HB3	1.78	0.84
1:E:4:ILE:HD13	1:E:136:GLN:HE21	1.42	0.84
1:G:3:GLU:O	1:G:133:GLN:HB3	1.78	0.84
1:G:4:ILE:HD13	1:G:136:GLN:HE21	1.42	0.84
2:H:217:LEU:CD1	2:H:277:SER:CA	2.56	0.84
1:A:324:SER:HB3	1:A:327:GLU:HG2	1.60	0.83
1:C:20:PHE:CD2	1:C:235:MET:SD	2.71	0.83
2:D:316:CYS:HB3	2:D:378:LEU:CD1	2.08	0.83
2:B:264:ARG:HB2	2:B:266:HIS:CD2	2.13	0.83
1:E:20:PHE:CD2	1:E:235:MET:SD	2.71	0.83
2:F:217:LEU:CD1	2:F:277:SER:CA	2.56	0.83
2:H:316:CYS:HB3	2:H:378:LEU:CD1	2.08	0.83
1:A:3:GLU:O	1:A:133:GLN:HB3	1.78	0.83
1:C:4:ILE:HD13	1:C:136:GLN:HE21	1.42	0.83
2:D:56:THR:CB	2:H:284:GLU:CG	2.56	0.83
1:A:191:VAL:HG11	1:A:425:MET:HG3	1.60	0.83
2:B:151:SER:CB	2:B:193:THR:HG21	2.09	0.83
1:E:150:GLY:HA2	1:E:153:LEU:HD22	1.60	0.83
1:E:209:LEU:HB3	1:E:227:LEU:HD22	1.59	0.83
2:F:151:SER:CB	2:F:193:THR:HG21	2.09	0.83
1:G:20:PHE:CD2	1:G:235:MET:SD	2.71	0.83
2:H:102:ASN:CG	2:H:407:TRP:NE1	2.36	0.83
1:C:324:SER:HB3	1:C:327:GLU:HG2	1.60	0.83
2:F:106:GLY:O	2:F:111:GLY:HA3	1.78	0.83
2:H:106:GLY:O	2:H:111:GLY:HA3	1.78	0.83
2:H:151:SER:CB	2:H:193:THR:HG21	2.09	0.83
1:A:148:GLY:O	1:A:151:THR:HG22	1.79	0.83
2:B:217:LEU:CD1	2:B:277:SER:CA	2.56	0.83
2:B:316:CYS:HB3	2:B:378:LEU:CD1	2.08	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:67:PHE:CE1	2:F:87:PHE:HE1	1.96	0.83
1:G:148:GLY:O	1:G:151:THR:HG22	1.79	0.83
2:D:151:SER:CB	2:D:193:THR:HG21	2.09	0.83
2:H:67:PHE:CE1	2:H:87:PHE:HE1	1.96	0.83
2:H:264:ARG:HB2	2:H:266:HIS:CD2	2.13	0.83
1:A:234:THR:HG21	1:A:270:PRO:CB	2.06	0.83
2:D:217:LEU:CD1	2:D:277:SER:CA	2.56	0.83
1:E:242:LEU:HD22	1:E:250:ALA:H	1.41	0.83
1:A:287:THR:O	1:A:288:VAL:HG23	1.78	0.83
1:C:148:GLY:O	1:C:151:THR:HG22	1.79	0.83
1:C:234:THR:HG21	1:C:270:PRO:CB	2.06	0.83
1:C:287:THR:O	1:C:288:VAL:HG23	1.78	0.83
2:F:264:ARG:HB2	2:F:266:HIS:CD2	2.13	0.83
2:H:52:PHE:CZ	2:H:239:THR:CB	2.62	0.83
1:E:110:GLU:O	1:E:113:GLU:HG2	1.79	0.83
1:E:148:GLY:O	1:E:151:THR:HG22	1.79	0.83
1:E:324:SER:HB3	1:E:327:GLU:HG2	1.60	0.82
2:F:346:TRP:O	1:G:398:MET:HE2	1.79	0.82
1:G:110:GLU:O	1:G:113:GLU:HG2	1.79	0.82
2:H:52:PHE:CE1	2:H:239:THR:HB	2.13	0.82
1:C:110:GLU:O	1:C:113:GLU:HG2	1.79	0.82
1:G:324:SER:HB3	1:G:327:GLU:HG2	1.60	0.82
1:A:110:GLU:O	1:A:113:GLU:HG2	1.80	0.82
1:G:287:THR:O	1:G:288:VAL:HG23	1.78	0.82
2:F:52:PHE:CE1	2:F:239:THR:HB	2.14	0.82
2:B:172:TYR:C	2:B:172:TYR:HD1	1.87	0.82
2:F:52:PHE:CZ	2:F:239:THR:CB	2.62	0.82
1:G:101:ASN:ND2	1:G:143:GLY:HA2	1.94	0.82
1:E:287:THR:O	1:E:288:VAL:HG23	1.79	0.82
2:D:67:PHE:CE1	2:D:87:PHE:HE1	1.96	0.82
2:D:172:TYR:HD1	2:D:172:TYR:C	1.87	0.82
1:G:346:TRP:HB2	2:H:401:LYS:HG3	1.61	0.82
1:E:257:VAL:HG13	2:F:407:TRP:CG	2.15	0.82
1:E:191:VAL:HG11	1:E:425:MET:HG3	1.60	0.82
2:F:172:TYR:HD1	2:F:172:TYR:C	1.87	0.82
1:A:88:ARG:NH1	1:E:283:TYR:HE1	1.71	0.81
1:E:101:ASN:ND2	1:E:143:GLY:HA2	1.94	0.81
1:E:147:SER:HB2	1:E:190:SER:HB3	1.60	0.81
1:A:147:SER:HB2	1:A:190:SER:HB3	1.60	0.81
1:C:101:ASN:ND2	1:C:143:GLY:HA2	1.94	0.81
2:H:172:TYR:C	2:H:172:TYR:HD1	1.87	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:ASN:ND2	1:A:143:GLY:HA2	1.94	0.81
1:C:20:PHE:CZ	1:C:24:ILE:HD12	2.15	0.81
1:C:147:SER:HB2	1:C:190:SER:HB3	1.60	0.81
2:F:52:PHE:CZ	2:F:239:THR:HG21	2.15	0.81
1:G:191:VAL:HG11	1:G:425:MET:HG3	1.60	0.81
2:H:52:PHE:CZ	2:H:239:THR:HG21	2.15	0.81
2:B:67:PHE:CE1	2:B:87:PHE:HE1	1.96	0.81
2:B:23:LEU:HD23	2:B:236:SER:HB2	1.60	0.81
2:F:324:VAL:HG11	1:G:221:THR:C	2.05	0.81
2:H:52:PHE:CZ	2:H:239:THR:CG2	2.64	0.81
2:D:23:LEU:HD23	2:D:236:SER:HB2	1.61	0.81
2:D:52:PHE:CZ	2:D:239:THR:CG2	2.64	0.81
2:F:313:MET:HB3	2:F:344:VAL:HG21	1.63	0.81
2:F:326:LYS:CG	1:G:222:PRO:HG2	2.05	0.81
1:G:156:LYS:HA	1:G:156:LYS:HE2	1.61	0.81
2:H:313:MET:HB3	2:H:344:VAL:HG21	1.63	0.81
2:F:23:LEU:HD23	2:F:236:SER:HB2	1.61	0.81
1:G:20:PHE:CZ	1:G:24:ILE:HD12	2.15	0.81
1:G:352:LYS:HD3	2:H:181:VAL:HG21	1.61	0.81
2:H:267:PHE:N	2:H:267:PHE:CD1	2.49	0.81
2:H:276:ILE:HG23	2:H:369:ALA:CB	2.10	0.81
1:A:20:PHE:CZ	1:A:24:ILE:HD12	2.15	0.81
1:E:20:PHE:CZ	1:E:24:ILE:HD12	2.15	0.81
2:F:52:PHE:CZ	2:F:239:THR:CG2	2.64	0.81
2:F:267:PHE:N	2:F:267:PHE:CD1	2.49	0.81
2:F:276:ILE:HG23	2:F:369:ALA:CB	2.10	0.81
2:B:6:SER:HB3	2:B:136:SER:OG	1.81	0.81
2:F:6:SER:HB3	2:F:136:SER:OG	1.81	0.81
1:G:2:ARG:NH2	2:H:98:ASP:CB	2.44	0.81
1:G:147:SER:HB2	1:G:190:SER:HB3	1.60	0.81
2:H:6:SER:HB3	2:H:136:SER:OG	1.81	0.81
2:H:23:LEU:HD23	2:H:236:SER:HB2	1.61	0.81
2:B:52:PHE:CZ	2:B:239:THR:HB	2.14	0.81
2:B:109:THR:CG2	2:B:110:ILE:N	2.44	0.81
2:B:313:MET:HB3	2:B:344:VAL:HG21	1.63	0.81
1:C:156:LYS:HE2	1:C:156:LYS:HA	1.61	0.81
1:G:257:VAL:HG22	1:G:257:VAL:O	1.78	0.81
2:H:109:THR:CG2	2:H:110:ILE:N	2.44	0.81
2:H:248:LEU:HD23	2:H:353:VAL:O	1.80	0.81
2:D:248:LEU:HD23	2:D:353:VAL:O	1.80	0.80
1:E:156:LYS:HE2	1:E:156:LYS:HA	1.61	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:7:ILE:HG22	2:F:66:VAL:HG22	1.63	0.80
2:F:109:THR:CG2	2:F:110:ILE:N	2.44	0.80
2:H:7:ILE:HG22	2:H:66:VAL:HG22	1.63	0.80
2:H:132:LEU:HD23	2:H:132:LEU:H	1.46	0.80
2:B:248:LEU:HD23	2:B:353:VAL:O	1.80	0.80
2:B:267:PHE:N	2:B:267:PHE:CD1	2.49	0.80
2:D:52:PHE:CZ	2:D:239:THR:HG21	2.15	0.80
2:D:267:PHE:N	2:D:267:PHE:CD1	2.49	0.80
2:B:52:PHE:HZ	2:B:239:THR:CG2	1.94	0.80
2:D:6:SER:HB3	2:D:136:SER:OG	1.81	0.80
2:F:248:LEU:HD23	2:F:353:VAL:O	1.80	0.80
1:A:234:THR:CG2	1:A:270:PRO:HB2	2.11	0.80
2:B:7:ILE:HG22	2:B:66:VAL:HG22	1.63	0.80
2:D:109:THR:CG2	2:D:110:ILE:N	2.44	0.80
2:D:313:MET:HB3	2:D:344:VAL:HG21	1.63	0.80
1:A:413:MET:HG3	1:A:414:ASP:H	1.47	0.80
2:F:132:LEU:HD23	2:F:132:LEU:H	1.46	0.80
2:F:241:SER:O	2:F:244:PHE:HB3	1.82	0.80
2:B:70:LEU:CD1	2:B:145:THR:HG23	2.12	0.80
2:D:56:THR:O	2:D:58:ALA:CB	2.30	0.80
2:H:241:SER:O	2:H:244:PHE:HB3	1.82	0.80
1:E:234:THR:CG2	1:E:270:PRO:HB2	2.11	0.80
1:E:413:MET:HG3	1:E:414:ASP:H	1.47	0.80
1:G:413:MET:HG3	1:G:414:ASP:H	1.47	0.80
2:D:70:LEU:CD1	2:D:145:THR:HG23	2.12	0.80
2:D:276:ILE:HG23	2:D:369:ALA:CB	2.10	0.80
1:G:236:SER:O	1:G:240:THR:CG2	2.29	0.80
2:B:276:ILE:HG23	2:B:369:ALA:CB	2.10	0.80
1:G:254:LYS:HE3	1:G:352:LYS:NZ	1.97	0.80
1:A:217:LEU:C	1:A:219:LEU:H	1.91	0.79
2:B:67:PHE:HE1	2:B:87:PHE:CD1	2.00	0.79
2:B:241:SER:O	2:B:244:PHE:HB3	1.82	0.79
1:C:217:LEU:C	1:C:219:LEU:H	1.91	0.79
1:C:413:MET:HG3	1:C:414:ASP:H	1.47	0.79
1:A:156:LYS:HE2	1:A:156:LYS:HA	1.61	0.79
1:C:54:ASN:HD21	1:C:64:ARG:HD3	1.46	0.79
1:C:329:ASP:HB3	2:D:177:VAL:HG12	1.61	0.79
1:A:236:SER:O	1:A:240:THR:CG2	2.29	0.79
2:B:184:PRO:HG2	2:B:398:MET:HE1	1.64	0.79
2:D:7:ILE:HG22	2:D:66:VAL:HG22	1.63	0.79
1:E:54:ASN:HD21	1:E:64:ARG:HD3	1.46	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:67:PHE:HE1	2:F:87:PHE:CD1	1.99	0.79
2:D:67:PHE:HE1	2:D:87:PHE:CD1	2.00	0.79
1:E:236:SER:O	1:E:240:THR:CG2	2.29	0.79
2:F:234:ILE:O	2:F:234:ILE:HD13	1.81	0.79
2:H:234:ILE:O	2:H:234:ILE:HD13	1.81	0.79
1:A:54:ASN:HD21	1:A:64:ARG:HD3	1.46	0.79
1:A:68:VAL:HG12	1:A:149:MET:SD	2.22	0.79
1:C:236:SER:O	1:C:240:THR:CG2	2.29	0.79
1:G:54:ASN:HD21	1:G:64:ARG:HD3	1.46	0.79
2:H:67:PHE:HE1	2:H:87:PHE:CD1	1.99	0.79
1:C:68:VAL:HG12	1:C:149:MET:SD	2.22	0.79
1:C:264:ARG:HB2	1:C:266:HIS:HD2	1.45	0.79
1:C:265:LEU:HD12	1:C:265:LEU:O	1.83	0.79
2:D:234:ILE:HD13	2:D:234:ILE:O	1.81	0.79
2:D:11:GLN:HE21	2:D:74:VAL:HG22	1.47	0.79
2:D:241:SER:O	2:D:244:PHE:HB3	1.82	0.79
2:F:184:PRO:HG2	2:F:398:MET:HE1	1.64	0.79
2:H:11:GLN:HE21	2:H:74:VAL:HG22	1.47	0.79
2:H:184:PRO:HG2	2:H:398:MET:HE1	1.64	0.79
2:D:132:LEU:HD23	2:D:132:LEU:H	1.46	0.79
2:F:11:GLN:HE21	2:F:74:VAL:HG22	1.47	0.79
2:H:70:LEU:CD1	2:H:145:THR:HG23	2.12	0.79
2:H:264:ARG:C	2:H:266:HIS:H	1.91	0.79
1:A:265:LEU:O	1:A:265:LEU:HD12	1.83	0.79
2:B:243:ARG:HH21	2:B:252:LEU:H	0.79	0.79
1:E:264:ARG:HB2	1:E:266:HIS:HD2	1.45	0.79
2:F:70:LEU:CD1	2:F:145:THR:HG23	2.12	0.79
2:F:264:ARG:C	2:F:266:HIS:H	1.91	0.79
1:G:264:ARG:HB2	1:G:266:HIS:HD2	1.45	0.79
1:A:264:ARG:HB2	1:A:266:HIS:HD2	1.45	0.79
2:B:56:THR:O	2:B:58:ALA:CB	2.30	0.79
2:B:264:ARG:C	2:B:266:HIS:H	1.91	0.79
2:D:184:PRO:HG2	2:D:398:MET:HE1	1.64	0.79
2:D:264:ARG:C	2:D:266:HIS:H	1.91	0.79
1:E:68:VAL:HG12	1:E:149:MET:SD	2.22	0.79
1:G:8:GLN:CD	1:G:67:LEU:HD22	2.08	0.79
2:H:217:LEU:CD1	2:H:277:SER:HA	2.13	0.78
2:H:296:PHE:CZ	2:H:335:ILE:HG21	2.18	0.78
2:B:234:ILE:O	2:B:234:ILE:HD13	1.81	0.78
2:D:217:LEU:CD1	2:D:277:SER:HA	2.13	0.78
1:E:8:GLN:CD	1:E:67:LEU:HD22	2.08	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:217:LEU:CD1	2:F:277:SER:HA	2.13	0.78
2:F:243:ARG:HH21	2:F:252:LEU:H	0.79	0.78
2:F:296:PHE:CZ	2:F:335:ILE:HG21	2.18	0.78
1:G:68:VAL:HG12	1:G:149:MET:SD	2.22	0.78
2:H:199:ASP:HB3	2:H:256:GLN:NE2	1.99	0.78
2:B:3:GLU:HG2	2:B:51:THR:HA	0.80	0.78
1:C:257:VAL:HA	2:D:407:TRP:CE2	2.18	0.78
1:G:352:LYS:CB	2:H:181:VAL:HG21	2.13	0.78
2:H:3:GLU:HG2	2:H:51:THR:HA	0.80	0.78
1:A:205:ASP:OD1	1:A:304:ALA:HB2	1.84	0.78
2:B:132:LEU:HD23	2:B:132:LEU:H	1.46	0.78
2:B:199:ASP:HB3	2:B:256:GLN:NE2	1.99	0.78
1:C:259:MET:HA	1:C:314:THR:HG21	1.65	0.78
2:D:243:ARG:HH21	2:D:252:LEU:H	0.79	0.78
2:F:3:GLU:HG2	2:F:51:THR:HA	0.80	0.78
2:F:199:ASP:HB3	2:F:256:GLN:NE2	1.99	0.78
2:F:346:TRP:HZ3	1:G:404:PHE:CZ	2.01	0.78
1:G:205:ASP:OD1	1:G:304:ALA:HB2	1.84	0.78
2:H:102:ASN:ND2	2:H:407:TRP:CD1	2.51	0.78
2:H:243:ARG:HH21	2:H:252:LEU:H	0.79	0.78
2:B:11:GLN:HE21	2:B:74:VAL:HG22	1.47	0.78
2:B:52:PHE:CZ	2:B:239:THR:CB	2.67	0.78
2:B:217:LEU:CD1	2:B:277:SER:HA	2.13	0.78
1:C:205:ASP:OD1	1:C:304:ALA:HB2	1.84	0.78
2:D:172:TYR:C	2:D:172:TYR:CD1	2.61	0.78
2:D:199:ASP:HB3	2:D:256:GLN:NE2	1.98	0.78
2:D:276:ILE:O	2:D:369:ALA:HB2	1.84	0.78
1:E:205:ASP:OD1	1:E:304:ALA:HB2	1.84	0.78
2:F:276:ILE:O	2:F:369:ALA:HB2	1.83	0.78
2:H:30:ILE:HG12	2:H:36:MET:CB	2.09	0.78
1:A:8:GLN:CD	1:A:67:LEU:HD22	2.08	0.78
2:B:204:VAL:HG13	2:B:209:ILE:HD11	1.66	0.78
1:C:346:TRP:CB	2:D:401:LYS:HD2	2.13	0.78
2:D:3:GLU:HG2	2:D:51:THR:HA	0.80	0.78
2:F:172:TYR:C	2:F:172:TYR:CD1	2.61	0.78
2:H:172:TYR:C	2:H:172:TYR:CD1	2.61	0.78
2:H:204:VAL:HG13	2:H:209:ILE:HD11	1.65	0.78
2:H:276:ILE:O	2:H:369:ALA:HB2	1.84	0.78
1:C:8:GLN:CD	1:C:67:LEU:HD22	2.07	0.78
2:D:55:GLU:O	2:D:57:GLY:N	2.17	0.78
2:F:67:PHE:HD1	2:F:92:LEU:HD23	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:5:ILE:CG1	2:B:64:ARG:CZ	2.56	0.78
2:B:172:TYR:C	2:B:172:TYR:CD1	2.61	0.78
1:C:325:MET:HG2	2:D:224:TYR:CE1	2.18	0.78
2:D:231:ILE:HA	2:D:234:ILE:HG22	1.66	0.78
2:F:231:ILE:HA	2:F:234:ILE:HG22	1.66	0.78
2:H:67:PHE:HD1	2:H:92:LEU:HD23	1.49	0.78
2:H:231:ILE:HA	2:H:234:ILE:HG22	1.66	0.78
1:A:242:LEU:HD13	1:A:250:ALA:C	2.08	0.78
2:B:231:ILE:HA	2:B:234:ILE:HG22	1.66	0.78
2:D:296:PHE:CD2	2:D:341:ILE:HD11	2.03	0.78
2:F:204:VAL:HG13	2:F:209:ILE:HD11	1.66	0.78
1:A:259:MET:HA	1:A:314:THR:HG21	1.65	0.78
1:A:396:THR:HG23	1:A:422:GLU:OE2	1.83	0.78
1:G:258:ASN:C	2:H:404:PHE:HE2	1.90	0.78
2:D:296:PHE:CZ	2:D:335:ILE:HG21	2.18	0.77
1:E:35:SER:HB3	1:E:59:ASN:HA	1.65	0.77
2:F:30:ILE:HG12	2:F:36:MET:CB	2.09	0.77
2:B:223:THR:HB	2:B:225:THR:HG22	1.67	0.77
1:C:242:LEU:HD13	1:C:250:ALA:C	2.08	0.77
2:D:155:GLU:HA	2:D:197:HIS:ND1	1.99	0.77
1:E:265:LEU:HD12	1:E:265:LEU:O	1.83	0.77
2:B:52:PHE:CZ	2:B:239:THR:CG2	2.66	0.77
2:B:276:ILE:O	2:B:369:ALA:HB2	1.84	0.77
2:B:296:PHE:CZ	2:B:335:ILE:HG21	2.18	0.77
2:B:348:PRO:HD3	1:C:398:MET:CE	2.12	0.77
2:D:223:THR:HB	2:D:225:THR:HG22	1.67	0.77
1:E:259:MET:HA	1:E:314:THR:HG21	1.65	0.77
1:G:35:SER:HB3	1:G:59:ASN:HA	1.65	0.77
2:D:204:VAL:HG13	2:D:209:ILE:HD11	1.66	0.77
2:D:67:PHE:HD1	2:D:92:LEU:HD23	1.49	0.77
2:F:5:ILE:HG23	2:F:135:PHE:HB3	1.66	0.77
2:H:155:GLU:HA	2:H:197:HIS:ND1	1.99	0.77
2:F:155:GLU:HA	2:F:197:HIS:ND1	1.99	0.77
2:B:155:GLU:HA	2:B:197:HIS:ND1	1.99	0.77
1:E:396:THR:HG23	1:E:422:GLU:OE2	1.83	0.77
2:F:223:THR:HB	2:F:225:THR:HG22	1.67	0.77
1:G:242:LEU:HD13	1:G:250:ALA:C	2.08	0.77
1:G:259:MET:HA	1:G:314:THR:HG21	1.65	0.77
1:G:265:LEU:HD12	1:G:265:LEU:O	1.83	0.77
1:G:396:THR:HG23	1:G:422:GLU:OE2	1.83	0.77
2:F:261:PRO:CA	1:G:404:PHE:HD2	1.82	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:5:ILE:HG23	2:H:135:PHE:HB3	1.66	0.77
2:H:223:THR:HB	2:H:225:THR:HG22	1.67	0.77
1:C:396:THR:HG23	1:C:422:GLU:OE2	1.83	0.77
2:F:298:PRO:HB3	2:F:307:PRO:CD	2.15	0.77
2:H:298:PRO:HB3	2:H:307:PRO:CD	2.15	0.77
2:B:67:PHE:HD1	2:B:92:LEU:HD23	1.49	0.77
1:C:35:SER:HB3	1:C:59:ASN:HA	1.65	0.77
2:D:62:VAL:HG21	2:D:88:HIS:HE1	1.48	0.77
1:E:192:HIS:ND1	1:E:424:ASN:OD1	2.18	0.77
1:A:35:SER:HB3	1:A:59:ASN:HA	1.65	0.76
1:C:247:GLN:HB3	2:D:224:TYR:HD1	1.50	0.76
2:F:63:PRO:HD3	2:F:86:LEU:O	1.85	0.76
2:H:63:PRO:HD3	2:H:86:LEU:O	1.85	0.76
1:A:192:HIS:ND1	1:A:424:ASN:OD1	2.18	0.76
2:F:70:LEU:CD1	2:F:145:THR:CG2	2.64	0.76
2:F:225:THR:O	2:F:229:ARG:HG3	1.86	0.76
2:F:344:VAL:HG11	2:F:346:TRP:CE2	2.21	0.76
2:H:70:LEU:CD1	2:H:145:THR:CG2	2.64	0.76
2:B:70:LEU:CD1	2:B:145:THR:CG2	2.64	0.76
1:E:242:LEU:HD13	1:E:250:ALA:C	2.08	0.76
2:F:62:VAL:HG21	2:F:88:HIS:HE1	1.48	0.76
1:G:192:HIS:ND1	1:G:424:ASN:OD1	2.18	0.76
2:H:225:THR:O	2:H:229:ARG:HG3	1.86	0.76
2:D:362:VAL:HG13	2:D:368:LEU:HD12	1.68	0.76
1:G:217:LEU:C	1:G:219:LEU:H	1.91	0.76
2:H:344:VAL:HG11	2:H:346:TRP:CE2	2.21	0.76
2:B:298:PRO:HB3	2:B:307:PRO:CD	2.15	0.76
2:D:63:PRO:HD3	2:D:86:LEU:O	1.85	0.76
1:E:217:LEU:C	1:E:219:LEU:H	1.91	0.76
2:H:163:LYS:O	2:H:164:LYS:HG2	1.86	0.76
1:C:192:HIS:ND1	1:C:424:ASN:OD1	2.18	0.76
2:F:163:LYS:O	2:F:164:LYS:HG2	1.86	0.76
2:F:331:ALA:O	2:F:335:ILE:HG12	1.86	0.76
1:C:198:THR:O	1:C:265:LEU:HD22	1.85	0.76
2:D:5:ILE:HG23	2:D:135:PHE:HB3	1.66	0.76
2:F:362:VAL:HG13	2:F:368:LEU:HD12	1.68	0.76
1:G:198:THR:O	1:G:265:LEU:HD22	1.85	0.76
2:B:296:PHE:CD2	2:B:341:ILE:HD11	2.03	0.76
1:E:259:MET:HG2	1:E:314:THR:HG21	1.67	0.76
2:H:331:ALA:O	2:H:335:ILE:HG12	1.86	0.76
2:D:163:LYS:O	2:D:164:LYS:HG2	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:298:PRO:HB3	2:D:307:PRO:CD	2.15	0.75
2:H:7:ILE:HD12	2:H:153:LEU:HD21	1.68	0.75
2:B:344:VAL:HG11	2:B:346:TRP:CE2	2.21	0.75
2:D:11:GLN:HG3	2:D:74:VAL:CG1	2.15	0.75
2:D:56:THR:C	2:H:284:GLU:HB3	2.11	0.75
2:D:221:ARG:HD3	2:D:221:ARG:O	1.85	0.75
1:E:19:LYS:HG3	1:E:228:ASN:CB	2.17	0.75
2:F:7:ILE:HD12	2:F:153:LEU:HD21	1.68	0.75
2:H:62:VAL:HG21	2:H:88:HIS:HE1	1.48	0.75
1:A:198:THR:O	1:A:265:LEU:HD22	1.85	0.75
2:B:30:ILE:HD13	2:B:61:HIS:CG	2.20	0.75
2:D:70:LEU:CD1	2:D:145:THR:CG2	2.64	0.75
2:D:172:TYR:OH	2:D:387:ALA:HB1	1.87	0.75
1:E:198:THR:O	1:E:265:LEU:HD22	1.85	0.75
1:G:19:LYS:HG3	1:G:228:ASN:CB	2.17	0.75
2:H:362:VAL:HG13	2:H:368:LEU:HD12	1.68	0.75
2:B:221:ARG:O	2:B:221:ARG:HD3	1.85	0.75
2:B:348:PRO:CD	1:C:398:MET:HE2	2.16	0.75
2:B:362:VAL:HG13	2:B:368:LEU:HD12	1.68	0.75
2:D:7:ILE:HD12	2:D:153:LEU:HD21	1.68	0.75
2:D:331:ALA:O	2:D:335:ILE:HG12	1.86	0.75
2:B:11:GLN:HG3	2:B:74:VAL:CG1	2.15	0.75
2:B:225:THR:O	2:B:229:ARG:HG3	1.86	0.75
1:C:168:THR:HB	1:C:201:THR:HG23	1.68	0.75
1:C:325:MET:HE1	1:C:355:VAL:HG11	1.67	0.75
2:D:225:THR:O	2:D:229:ARG:HG3	1.86	0.75
2:F:172:TYR:OH	2:F:387:ALA:HB1	1.87	0.75
2:H:172:TYR:OH	2:H:387:ALA:HB1	1.87	0.75
1:A:6:HIS:HE1	1:A:8:GLN:HG2	1.52	0.75
2:B:348:PRO:HD3	1:C:398:MET:HE3	1.68	0.75
2:D:344:VAL:HG11	2:D:346:TRP:CE2	2.21	0.75
1:E:325:MET:HE1	1:E:355:VAL:HG11	1.67	0.75
1:G:176:LYS:HE3	1:G:207:GLU:HG3	1.68	0.75
1:G:259:MET:HG2	1:G:314:THR:HG21	1.67	0.75
1:A:325:MET:HE1	1:A:355:VAL:HG11	1.67	0.75
2:B:172:TYR:OH	2:B:387:ALA:HB1	1.87	0.75
2:B:331:ALA:O	2:B:335:ILE:HG12	1.86	0.75
1:C:19:LYS:HG3	1:C:228:ASN:CB	2.17	0.75
1:A:19:LYS:HG3	1:A:228:ASN:CB	2.17	0.75
1:A:168:THR:HB	1:A:201:THR:HG23	1.68	0.75
2:D:167:LEU:HG	2:D:200:CYS:HB3	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:348:PRO:HD3	1:G:398:MET:HE3	1.68	0.75
2:F:257:THR:CG2	1:G:101:ASN:HB3	2.16	0.75
2:F:317:LEU:HB3	2:F:319:TYR:HE1	1.52	0.75
1:A:103:TRP:CZ3	1:A:108:TYR:HE1	2.05	0.74
1:A:259:MET:HG2	1:A:314:THR:HG21	1.67	0.74
2:B:163:LYS:O	2:B:164:LYS:HG2	1.86	0.74
2:B:167:LEU:HG	2:B:200:CYS:HB3	1.69	0.74
2:D:110:ILE:HG23	2:D:111:GLY:N	1.99	0.74
2:D:317:LEU:HB3	2:D:319:TYR:HE1	1.52	0.74
1:E:250:ALA:HA	1:E:254:LYS:HE2	1.68	0.74
1:G:2:ARG:NH2	2:H:98:ASP:CA	2.49	0.74
1:A:176:LYS:HE3	1:A:207:GLU:HG3	1.68	0.74
2:B:317:LEU:HB3	2:B:319:TYR:HE1	1.52	0.74
2:B:349:THR:CB	1:C:178:SER:HB2	2.17	0.74
2:D:205:ASP:CB	2:D:303:VAL:HA	2.17	0.74
2:F:221:ARG:O	2:F:221:ARG:HD3	1.85	0.74
1:G:103:TRP:CZ3	1:G:108:TYR:HE1	2.05	0.74
2:H:70:LEU:HD11	2:H:145:THR:HG23	1.70	0.74
1:C:6:HIS:HE1	1:C:8:GLN:HG2	1.52	0.74
1:C:250:ALA:HA	1:C:254:LYS:HE2	1.68	0.74
1:E:176:LYS:HE3	1:E:207:GLU:HG3	1.68	0.74
2:F:70:LEU:HD11	2:F:145:THR:HG23	1.70	0.74
2:F:329:ASN:OD1	1:G:210:TYR:HE1	1.70	0.74
2:B:7:ILE:HD12	2:B:153:LEU:HD21	1.68	0.74
1:C:103:TRP:CZ3	1:C:108:TYR:HE1	2.05	0.74
1:E:168:THR:HB	1:E:201:THR:HG23	1.68	0.74
1:G:325:MET:HE1	1:G:355:VAL:HG11	1.67	0.74
2:H:317:LEU:HB3	2:H:319:TYR:HE1	1.52	0.74
1:C:176:LYS:HE3	1:C:207:GLU:HG3	1.68	0.74
1:E:103:TRP:CZ3	1:E:108:TYR:HE1	2.05	0.74
1:G:234:THR:CG2	1:G:270:PRO:HB2	2.11	0.74
2:H:167:LEU:HG	2:H:200:CYS:HB3	1.69	0.74
2:H:221:ARG:O	2:H:221:ARG:HD3	1.85	0.74
1:C:259:MET:HG2	1:C:314:THR:HG21	1.67	0.74
2:F:167:LEU:HG	2:F:200:CYS:HB3	1.69	0.74
2:F:205:ASP:CB	2:F:303:VAL:HA	2.17	0.74
1:G:168:THR:HB	1:G:201:THR:HG23	1.68	0.74
2:H:4:CYS:SG	2:H:252:LEU:HD11	2.27	0.74
2:B:56:THR:O	2:F:284:GLU:HB3	1.87	0.74
2:B:104:ALA:CB	2:B:413:MET:HG3	2.18	0.74
2:B:381:THR:C	2:B:383:ALA:H	1.95	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:6:HIS:HE1	1:G:8:GLN:HG2	1.52	0.74
2:H:104:ALA:CB	2:H:413:MET:HG3	2.18	0.74
2:B:110:ILE:HG23	2:B:111:GLY:N	1.99	0.74
2:B:205:ASP:CB	2:B:303:VAL:HA	2.17	0.74
1:C:254:LYS:HZ3	2:D:101:ASN:HD21	1.34	0.74
1:C:257:VAL:HG13	2:D:407:TRP:CD1	2.22	0.74
1:E:6:HIS:HE1	1:E:8:GLN:HG2	1.52	0.74
2:D:4:CYS:SG	2:D:252:LEU:HD11	2.27	0.74
2:D:56:THR:CB	2:H:284:GLU:HG3	2.16	0.74
2:F:4:CYS:SG	2:F:252:LEU:HD11	2.27	0.74
2:F:104:ALA:CB	2:F:413:MET:HG3	2.18	0.74
2:F:110:ILE:HG23	2:F:111:GLY:N	1.99	0.74
2:H:205:ASP:CB	2:H:303:VAL:HA	2.17	0.74
1:A:250:ALA:HA	1:A:254:LYS:HE2	1.68	0.74
2:B:4:CYS:SG	2:B:252:LEU:HD11	2.27	0.74
2:D:70:LEU:HD11	2:D:145:THR:HG23	1.70	0.74
2:D:104:ALA:CB	2:D:413:MET:HG3	2.18	0.74
2:B:62:VAL:CG1	2:B:63:PRO:CD	2.50	0.73
1:A:209:LEU:HG	1:A:230:LEU:HD22	1.69	0.73
2:D:381:THR:C	2:D:383:ALA:H	1.95	0.73
1:E:274:PRO:HG2	1:E:371:LEU:HD21	1.70	0.73
2:H:110:ILE:HG23	2:H:111:GLY:N	1.99	0.73
2:D:103:TYR:CD2	2:D:189:LEU:HD13	2.24	0.73
2:F:154:MET:HE1	2:F:166:LYS:HB3	1.71	0.73
2:H:102:ASN:CB	2:H:407:TRP:CD1	2.71	0.73
2:H:154:MET:HE1	2:H:166:LYS:HB3	1.71	0.73
1:A:274:PRO:HG2	1:A:371:LEU:HD21	1.70	0.73
2:B:242:LEU:HG	2:B:250:VAL:O	1.88	0.73
1:E:217:LEU:O	1:E:219:LEU:N	2.22	0.73
1:G:217:LEU:O	1:G:219:LEU:N	2.22	0.73
2:H:11:GLN:HG3	2:H:74:VAL:CG1	2.15	0.73
2:B:70:LEU:HD11	2:B:145:THR:HG23	1.70	0.73
2:B:348:PRO:HD2	1:C:398:MET:HE1	1.68	0.73
2:F:103:TYR:CD2	2:F:189:LEU:HD13	2.24	0.73
1:G:257:VAL:HG23	2:H:407:TRP:HB2	0.77	0.73
2:D:242:LEU:HG	2:D:250:VAL:O	1.88	0.73
2:F:62:VAL:HG11	2:F:88:HIS:ND1	2.04	0.73
2:F:381:THR:C	2:F:383:ALA:H	1.95	0.73
2:H:103:TYR:CD2	2:H:189:LEU:HD13	2.24	0.73
2:B:103:TYR:CD2	2:B:189:LEU:HD13	2.24	0.73
2:D:306:ASP:O	2:D:308:ARG:N	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:2:ARG:NH1	2:H:98:ASP:HB3	2.04	0.73
2:H:242:LEU:HG	2:H:250:VAL:O	1.88	0.73
2:H:381:THR:C	2:H:383:ALA:H	1.95	0.73
1:A:76:ASP:HA	1:A:79:ARG:HG2	1.71	0.73
1:E:76:ASP:HA	1:E:79:ARG:HG2	1.71	0.73
2:F:242:LEU:HG	2:F:250:VAL:O	1.88	0.73
1:C:257:VAL:HA	2:D:407:TRP:NE1	2.04	0.73
1:G:258:ASN:CA	2:H:404:PHE:CE2	2.71	0.73
1:G:274:PRO:HG2	1:G:371:LEU:HD21	1.70	0.73
2:H:62:VAL:HG11	2:H:88:HIS:ND1	2.04	0.73
2:B:104:ALA:HB2	2:B:413:MET:HG3	1.71	0.73
1:C:209:LEU:HG	1:C:230:LEU:HD22	1.69	0.73
2:D:217:LEU:CD1	2:D:277:SER:CB	2.54	0.73
1:E:209:LEU:HG	1:E:230:LEU:HD22	1.69	0.73
2:F:11:GLN:HG3	2:F:74:VAL:CG1	2.15	0.73
1:G:76:ASP:HA	1:G:79:ARG:HG2	1.71	0.73
1:G:356:CYS:SG	1:G:357:ASP:N	2.62	0.73
2:H:104:ALA:HB2	2:H:413:MET:HG3	1.71	0.73
1:A:217:LEU:O	1:A:219:LEU:N	2.22	0.72
1:C:217:LEU:O	1:C:219:LEU:N	2.22	0.72
1:C:274:PRO:HG2	1:C:371:LEU:HD21	1.70	0.72
2:D:154:MET:HE1	2:D:166:LYS:HB3	1.70	0.72
1:A:108:TYR:CD1	1:A:413:MET:HE1	2.24	0.72
1:A:356:CYS:SG	1:A:357:ASP:N	2.62	0.72
1:C:88:ARG:CG	1:G:283:TYR:OH	2.36	0.72
2:D:105:ARG:O	2:D:110:ILE:HG22	1.89	0.72
2:F:112:LYS:O	2:F:115:ILE:HG22	1.89	0.72
2:F:324:VAL:HG11	1:G:221:THR:HA	1.70	0.72
2:H:112:LYS:O	2:H:115:ILE:HG22	1.89	0.72
2:B:105:ARG:O	2:B:110:ILE:HG22	1.89	0.72
1:C:76:ASP:HA	1:C:79:ARG:HG2	1.71	0.72
1:E:191:VAL:CG1	1:E:425:MET:HG3	2.19	0.72
2:F:337:THR:CG2	3:I:99:GLN:OE1	2.37	0.72
1:G:209:LEU:HG	1:G:230:LEU:HD22	1.69	0.72
1:A:299:LYS:HD3	1:A:299:LYS:N	2.04	0.72
2:B:154:MET:HE1	2:B:166:LYS:HB3	1.70	0.72
1:C:70:LEU:HG	1:C:145:THR:CG2	2.20	0.72
1:C:234:THR:CG2	1:C:270:PRO:HB2	2.11	0.72
2:D:296:PHE:CE2	2:D:341:ILE:HD12	2.20	0.72
2:F:30:ILE:HD13	2:F:61:HIS:CD2	2.24	0.72
2:F:104:ALA:HB2	2:F:413:MET:HG3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:108:TYR:CD1	1:G:413:MET:HE1	2.24	0.72
1:G:111:GLY:O	1:G:115:VAL:HG23	1.89	0.72
1:A:191:VAL:CG1	1:A:425:MET:HG3	2.19	0.72
1:C:108:TYR:CD1	1:C:413:MET:HE1	2.24	0.72
1:E:108:TYR:CD1	1:E:413:MET:HE1	2.24	0.72
2:F:3:GLU:HG2	2:F:51:THR:C	2.14	0.72
1:G:191:VAL:CG1	1:G:425:MET:HG3	2.19	0.72
1:A:70:LEU:HG	1:A:145:THR:CG2	2.20	0.72
1:C:299:LYS:HD3	1:C:299:LYS:N	2.04	0.72
2:D:56:THR:C	2:H:284:GLU:HB2	2.14	0.72
2:D:242:LEU:HD21	2:D:250:VAL:HB	1.71	0.72
2:F:263:PRO:HD3	1:G:406:HIS:CG	2.24	0.72
2:B:7:ILE:CG1	2:B:137:VAL:HG22	2.20	0.72
2:B:166:LYS:HE3	2:B:199:ASP:OD1	1.90	0.72
2:B:306:ASP:O	2:B:308:ARG:N	2.20	0.72
1:C:191:VAL:CG1	1:C:425:MET:HG3	2.19	0.72
1:E:70:LEU:HG	1:E:145:THR:CG2	2.20	0.72
1:E:243:ARG:NH2	1:E:252:LEU:HG	2.05	0.72
2:F:346:TRP:CZ3	1:G:404:PHE:CZ	2.76	0.72
2:H:306:ASP:O	2:H:308:ARG:N	2.20	0.72
1:C:356:CYS:SG	1:C:357:ASP:N	2.62	0.72
2:D:3:GLU:HG2	2:D:51:THR:C	2.15	0.72
2:D:7:ILE:CG1	2:D:137:VAL:HG22	2.20	0.72
2:D:104:ALA:HB2	2:D:413:MET:HG3	1.71	0.72
2:F:7:ILE:CG1	2:F:137:VAL:HG22	2.20	0.72
2:F:166:LYS:HE3	2:F:199:ASP:OD1	1.89	0.72
1:G:243:ARG:NH2	1:G:252:LEU:HG	2.05	0.72
1:G:258:ASN:O	2:H:404:PHE:CE2	2.35	0.72
2:D:7:ILE:HD11	2:D:137:VAL:HG22	1.71	0.72
2:F:261:PRO:HA	1:G:404:PHE:CE2	2.15	0.72
2:F:306:ASP:O	2:F:308:ARG:N	2.20	0.72
2:H:3:GLU:HG2	2:H:51:THR:C	2.14	0.72
2:H:7:ILE:CG1	2:H:137:VAL:HG22	2.20	0.72
2:B:3:GLU:HG2	2:B:51:THR:C	2.15	0.72
2:D:62:VAL:HG11	2:D:88:HIS:ND1	2.05	0.72
1:E:66:ILE:C	1:E:67:LEU:HD23	2.15	0.72
1:E:111:GLY:O	1:E:115:VAL:HG23	1.89	0.72
1:G:70:LEU:HG	1:G:145:THR:CG2	2.20	0.72
2:H:166:LYS:HE3	2:H:199:ASP:OD1	1.90	0.72
2:H:296:PHE:CE2	2:H:341:ILE:HD12	2.20	0.72
3:I:55:VAL:HG21	3:I:57:PHE:CE1	2.25	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:57:PHE:CE2	3:I:87:LEU:HD11	2.25	0.72
2:B:296:PHE:CE2	2:B:341:ILE:HD12	2.20	0.71
2:F:7:ILE:HD11	2:F:137:VAL:HG22	1.71	0.71
1:G:66:ILE:C	1:G:67:LEU:HD23	2.15	0.71
1:A:66:ILE:C	1:A:67:LEU:HD23	2.15	0.71
1:A:111:GLY:O	1:A:115:VAL:HG23	1.89	0.71
1:C:111:GLY:O	1:C:115:VAL:HG23	1.89	0.71
2:D:166:LYS:HE3	2:D:199:ASP:OD1	1.90	0.71
1:G:48:ARG:HG2	1:G:243:ARG:O	1.90	0.71
1:A:201:THR:OG1	1:A:265:LEU:HD11	1.90	0.71
1:C:201:THR:OG1	1:C:265:LEU:HD11	1.90	0.71
2:H:11:GLN:HE21	2:H:74:VAL:CG2	2.03	0.71
2:B:112:LYS:O	2:B:115:ILE:HG22	1.89	0.71
2:B:242:LEU:HD21	2:B:250:VAL:HB	1.71	0.71
2:D:112:LYS:O	2:D:115:ILE:HG22	1.89	0.71
1:E:325:MET:HA	1:E:325:MET:HE3	1.72	0.71
2:F:105:ARG:O	2:F:110:ILE:HG22	1.89	0.71
2:H:105:ARG:O	2:H:110:ILE:HG22	1.89	0.71
1:A:291:LEU:O	1:A:295:MET:HG3	1.91	0.71
1:C:431:GLU:OE1	1:C:432:TYR:HA	1.91	0.71
1:E:48:ARG:HG2	1:E:243:ARG:O	1.90	0.71
2:H:7:ILE:HD11	2:H:137:VAL:HG22	1.71	0.71
1:A:431:GLU:OE1	1:A:432:TYR:HA	1.91	0.71
2:B:7:ILE:HD11	2:B:137:VAL:HG22	1.71	0.71
1:C:88:ARG:HG3	1:G:283:TYR:OH	1.90	0.71
1:C:265:LEU:HD12	1:C:265:LEU:C	2.16	0.71
2:D:234:ILE:HG21	2:D:302:MET:HE1	1.72	0.71
1:E:10:GLY:O	1:E:14:ASN:HB2	1.90	0.71
1:E:431:GLU:OE1	1:E:432:TYR:HA	1.91	0.71
2:F:11:GLN:HE21	2:F:74:VAL:CG2	2.03	0.71
2:F:326:LYS:HB3	1:G:222:PRO:HD2	1.72	0.71
1:G:291:LEU:O	1:G:295:MET:HG3	1.91	0.71
1:A:56:ALA:HB1	1:E:283:TYR:CE2	2.25	0.71
2:B:11:GLN:HE21	2:B:74:VAL:CG2	2.03	0.71
1:C:8:GLN:NE2	1:C:17:GLY:HA3	2.06	0.71
1:C:269:MET:HE2	1:C:381:SER:OG	1.91	0.71
1:C:291:LEU:O	1:C:295:MET:HG3	1.91	0.71
2:D:11:GLN:HE21	2:D:74:VAL:CG2	2.03	0.71
1:E:291:LEU:O	1:E:295:MET:HG3	1.91	0.71
2:F:259:LEU:HD11	2:F:378:LEU:CD1	2.20	0.71
1:G:325:MET:HA	1:G:325:MET:HE3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:431:GLU:OE1	1:G:432:TYR:HA	1.91	0.71
1:A:8:GLN:NE2	1:A:17:GLY:HA3	2.06	0.71
1:A:265:LEU:HD12	1:A:265:LEU:C	2.16	0.71
1:C:245:PRO:HA	2:D:73:THR:CG2	2.21	0.71
1:E:237:GLY:O	1:E:241:CYS:HB3	1.90	0.71
2:F:242:LEU:HD21	2:F:250:VAL:HB	1.71	0.71
1:G:10:GLY:O	1:G:14:ASN:HB2	1.90	0.71
1:G:258:ASN:HA	2:H:404:PHE:HD2	1.52	0.71
1:G:265:LEU:HD12	1:G:265:LEU:C	2.16	0.71
2:H:242:LEU:HD21	2:H:250:VAL:HB	1.71	0.71
2:H:259:LEU:HD11	2:H:378:LEU:CD1	2.20	0.71
2:B:259:LEU:HD11	2:B:378:LEU:CD1	2.20	0.71
1:C:325:MET:HE3	1:C:325:MET:HA	1.73	0.71
2:D:259:LEU:HD11	2:D:378:LEU:CD1	2.20	0.71
2:F:12:ALA:HB3	2:F:140:SER:OG	1.91	0.71
2:F:217:LEU:CD1	2:F:277:SER:CB	2.54	0.71
2:F:296:PHE:CE2	2:F:341:ILE:HD12	2.20	0.71
2:F:317:LEU:HD12	2:F:351:PHE:HD2	1.56	0.71
2:H:12:ALA:HB3	2:H:140:SER:OG	1.91	0.71
2:H:317:LEU:HD12	2:H:351:PHE:HD2	1.56	0.71
1:A:10:GLY:O	1:A:14:ASN:HB2	1.90	0.71
1:A:175:PRO:HD2	1:A:207:GLU:OE2	1.91	0.71
1:A:325:MET:HA	1:A:325:MET:HE3	1.72	0.71
1:C:237:GLY:O	1:C:241:CYS:HB3	1.90	0.71
2:F:234:ILE:HG21	2:F:302:MET:HE1	1.72	0.71
1:G:175:PRO:HD2	1:G:207:GLU:OE2	1.91	0.71
1:A:48:ARG:HG2	1:A:243:ARG:O	1.90	0.70
1:A:243:ARG:NH2	1:A:252:LEU:HG	2.05	0.70
1:A:269:MET:HE2	1:A:381:SER:OG	1.91	0.70
2:B:234:ILE:HG21	2:B:302:MET:HE1	1.72	0.70
2:B:343:PHE:CZ	2:B:351:PHE:HE1	2.08	0.70
1:C:66:ILE:C	1:C:67:LEU:HD23	2.15	0.70
2:F:148:GLY:O	2:F:151:SER:HB2	1.90	0.70
1:C:48:ARG:HG2	1:C:243:ARG:O	1.90	0.70
1:E:175:PRO:HD2	1:E:207:GLU:OE2	1.91	0.70
1:E:265:LEU:HD12	1:E:265:LEU:C	2.16	0.70
1:G:269:MET:HE2	1:G:381:SER:OG	1.91	0.70
2:H:148:GLY:O	2:H:151:SER:HB2	1.91	0.70
2:H:217:LEU:CD1	2:H:277:SER:CB	2.54	0.70
2:H:234:ILE:HG21	2:H:302:MET:HE1	1.72	0.70
2:B:312:TYR:O	2:B:344:VAL:HG23	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:30:ILE:HD13	2:D:61:HIS:CD2	2.27	0.70
2:D:312:TYR:O	2:D:344:VAL:HG23	1.90	0.70
1:A:237:GLY:O	1:A:241:CYS:HB3	1.90	0.70
2:B:5:ILE:CD1	2:B:64:ARG:NH1	2.38	0.70
2:D:148:GLY:O	2:D:151:SER:HB2	1.91	0.70
2:D:343:PHE:CZ	2:D:351:PHE:HE1	2.08	0.70
1:E:269:MET:HE2	1:E:381:SER:OG	1.90	0.70
1:G:237:GLY:O	1:G:241:CYS:HB3	1.90	0.70
1:G:352:LYS:CB	2:H:181:VAL:CG2	2.69	0.70
2:H:67:PHE:CD1	2:H:92:LEU:HD23	2.26	0.70
3:I:107:ILE:HD13	3:I:124:SER:HB3	1.73	0.70
2:B:348:PRO:HG2	1:C:398:MET:HE3	1.72	0.70
1:E:8:GLN:NE2	1:E:17:GLY:HA3	2.06	0.70
1:E:201:THR:OG1	1:E:265:LEU:HD11	1.90	0.70
2:F:312:TYR:O	2:F:344:VAL:HG23	1.90	0.70
1:G:8:GLN:NE2	1:G:17:GLY:HA3	2.06	0.70
1:C:175:PRO:HD2	1:C:207:GLU:OE2	1.91	0.70
1:C:243:ARG:NH2	1:C:252:LEU:HG	2.05	0.70
2:F:51:THR:O	2:F:52:PHE:CD1	2.44	0.70
2:F:67:PHE:CD1	2:F:92:LEU:HD23	2.26	0.70
1:G:179:ASP:HB2	4:G:600:GDP:C3'	2.21	0.70
1:G:234:THR:O	1:G:238:VAL:HG23	1.92	0.70
2:H:51:THR:O	2:H:52:PHE:CD1	2.44	0.70
2:H:312:TYR:O	2:H:344:VAL:HG23	1.90	0.70
2:B:199:ASP:HB3	2:B:256:GLN:HE21	1.57	0.70
2:D:317:LEU:HD12	2:D:351:PHE:HD2	1.55	0.70
1:E:234:THR:O	1:E:238:VAL:HG23	1.92	0.70
1:G:306:ASP:OD2	3:I:95:ILE:HD13	1.91	0.70
1:C:10:GLY:O	1:C:14:ASN:HB2	1.90	0.70
2:D:12:ALA:HB3	2:D:140:SER:OG	1.91	0.70
2:D:67:PHE:CD1	2:D:92:LEU:HD23	2.26	0.70
1:E:356:CYS:SG	1:E:357:ASP:N	2.62	0.70
2:D:51:THR:O	2:D:52:PHE:CD1	2.45	0.70
2:F:343:PHE:CZ	2:F:351:PHE:HE1	2.08	0.70
1:A:234:THR:O	1:A:238:VAL:HG23	1.92	0.70
2:B:67:PHE:CD1	2:B:92:LEU:HD23	2.26	0.70
2:B:217:LEU:CD1	2:B:277:SER:CB	2.55	0.70
2:B:371:VAL:HG12	2:B:372:GLN:H	1.57	0.70
1:C:254:LYS:HZ2	2:D:101:ASN:CG	1.99	0.70
2:D:199:ASP:HB3	2:D:256:GLN:HE21	1.57	0.70
2:D:371:VAL:HG12	2:D:372:GLN:H	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:237:SER:CB	2:F:376:CYS:SG	2.80	0.70
2:H:237:SER:CB	2:H:376:CYS:SG	2.80	0.70
2:B:5:ILE:HG22	2:B:6:SER:N	2.07	0.69
2:B:12:ALA:HB3	2:B:140:SER:OG	1.91	0.69
2:B:148:GLY:O	2:B:151:SER:HB2	1.91	0.69
2:D:237:SER:CB	2:D:376:CYS:SG	2.80	0.69
1:G:201:THR:OG1	1:G:265:LEU:HD11	1.90	0.69
2:B:317:LEU:HD12	2:B:351:PHE:HD2	1.55	0.69
1:C:255:LEU:O	1:C:259:MET:HG3	1.91	0.69
2:D:244:PHE:HD2	2:D:245:ASP:N	1.89	0.69
1:G:255:LEU:O	1:G:259:MET:HG3	1.91	0.69
1:A:255:LEU:O	1:A:259:MET:HG3	1.91	0.69
1:C:70:LEU:HG	1:C:145:THR:HG23	1.74	0.69
1:E:180:THR:HG22	1:E:181:VAL:N	2.07	0.69
2:F:349:THR:CG2	1:G:178:SER:O	2.40	0.69
2:B:243:ARG:NH2	2:B:252:LEU:N	2.29	0.69
2:F:244:PHE:HD2	2:F:245:ASP:N	1.89	0.69
2:H:6:SER:HB3	2:H:136:SER:HG	1.56	0.69
1:A:70:LEU:HG	1:A:145:THR:HG23	1.74	0.69
1:C:301:MET:HE1	1:C:377:PHE:HE2	1.58	0.69
2:H:244:PHE:HD2	2:H:245:ASP:N	1.89	0.69
1:A:180:THR:HG22	1:A:181:VAL:N	2.07	0.69
1:A:260:VAL:HG23	2:B:407:TRP:HE1	1.57	0.69
1:A:301:MET:HE1	1:A:377:PHE:HE2	1.58	0.69
2:B:237:SER:CB	2:B:376:CYS:SG	2.80	0.69
1:C:24:ILE:HD11	1:C:52:TYR:CE1	2.28	0.69
1:C:234:THR:O	1:C:238:VAL:HG23	1.92	0.69
2:D:56:THR:CA	2:H:284:GLU:HG3	2.22	0.69
1:A:24:ILE:HD11	1:A:52:TYR:CE1	2.28	0.69
1:A:230:LEU:HD21	1:A:302:MET:HE2	1.74	0.69
2:B:115:ILE:CD1	2:B:119:LEU:HG	2.23	0.69
2:B:205:ASP:HB3	2:B:303:VAL:HA	1.73	0.69
2:B:333:ALA:CA	1:C:177:VAL:HG21	2.23	0.69
1:C:180:THR:HG22	1:C:181:VAL:N	2.07	0.69
1:E:255:LEU:O	1:E:259:MET:HG3	1.91	0.69
1:E:346:TRP:CD1	2:F:401:LYS:HZ2	2.11	0.69
2:F:205:ASP:HB3	2:F:303:VAL:HA	1.73	0.69
2:F:261:PRO:CG	1:G:404:PHE:CE2	2.69	0.69
1:G:180:THR:HG22	1:G:181:VAL:N	2.07	0.69
1:G:253:ARG:CG	2:H:407:TRP:HH2	2.06	0.69
1:G:301:MET:HE1	1:G:377:PHE:HE2	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:205:ASP:HB3	2:H:303:VAL:HA	1.73	0.69
2:H:343:PHE:CZ	2:H:351:PHE:HE1	2.08	0.69
2:H:343:PHE:HZ	2:H:351:PHE:CE1	2.10	0.69
2:H:371:VAL:HG12	2:H:372:GLN:H	1.57	0.69
1:A:359:PRO:HB2	1:A:360:PRO:HD2	1.74	0.69
2:B:244:PHE:HD2	2:B:245:ASP:N	1.90	0.69
2:B:343:PHE:HZ	2:B:351:PHE:CE1	2.10	0.69
2:D:205:ASP:HB3	2:D:303:VAL:HA	1.73	0.69
1:E:24:ILE:HD11	1:E:52:TYR:CE1	2.28	0.69
1:E:257:VAL:O	1:E:257:VAL:HG12	1.93	0.69
1:E:301:MET:HE1	1:E:377:PHE:HE2	1.58	0.69
2:F:343:PHE:HZ	2:F:351:PHE:CE1	2.10	0.69
2:H:276:ILE:O	2:H:369:ALA:N	2.25	0.69
2:D:115:ILE:CD1	2:D:119:LEU:HG	2.23	0.69
1:E:70:LEU:HG	1:E:145:THR:HG23	1.74	0.69
1:E:230:LEU:HD21	1:E:302:MET:HE2	1.73	0.69
1:C:230:LEU:HD21	1:C:302:MET:HE2	1.74	0.68
1:E:242:LEU:CD2	1:E:250:ALA:H	2.06	0.68
2:F:115:ILE:CD1	2:F:119:LEU:HG	2.23	0.68
2:F:276:ILE:O	2:F:369:ALA:N	2.25	0.68
2:F:371:VAL:HG12	2:F:372:GLN:H	1.57	0.68
1:G:242:LEU:CD2	1:G:250:ALA:H	2.07	0.68
1:A:242:LEU:CD2	1:A:250:ALA:H	2.06	0.68
1:C:242:LEU:CD2	1:C:250:ALA:H	2.06	0.68
1:E:251:ASP:O	1:E:253:ARG:N	2.26	0.68
1:G:24:ILE:HD11	1:G:52:TYR:CE1	2.28	0.68
2:H:402:ARG:O	2:H:403:ALA:C	2.36	0.68
2:B:141:PHE:O	2:B:147:SER:HB3	1.94	0.68
2:D:6:SER:HB3	2:D:136:SER:HG	1.57	0.68
2:D:343:PHE:HZ	2:D:351:PHE:CE1	2.10	0.68
2:F:402:ARG:O	2:F:403:ALA:C	2.36	0.68
1:G:209:LEU:HD23	1:G:227:LEU:HB3	1.75	0.68
1:G:243:ARG:HH22	1:G:252:LEU:HG	1.59	0.68
1:G:251:ASP:O	1:G:253:ARG:N	2.26	0.68
2:H:115:ILE:CD1	2:H:119:LEU:HG	2.23	0.68
1:A:256:ALA:O	1:A:260:VAL:HG22	1.94	0.68
2:B:349:THR:HB	1:C:178:SER:HB2	1.75	0.68
2:D:102:ASN:HB2	2:D:408:TYR:CE2	2.29	0.68
1:E:243:ARG:HH22	1:E:252:LEU:HG	1.59	0.68
1:E:250:ALA:HB1	1:E:254:LYS:HB2	1.75	0.68
1:E:256:ALA:O	1:E:260:VAL:HG22	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:217:LEU:HD12	2:F:277:SER:CA	2.23	0.68
2:B:102:ASN:HB2	2:B:408:TYR:CE2	2.29	0.68
2:D:221:ARG:N	2:D:222:PRO:HD3	2.09	0.68
1:E:209:LEU:HD23	1:E:227:LEU:HB3	1.75	0.68
1:G:70:LEU:HG	1:G:145:THR:HG23	1.74	0.68
1:G:230:LEU:HD21	1:G:302:MET:HE2	1.74	0.68
1:G:256:ALA:O	1:G:260:VAL:HG22	1.94	0.68
2:H:141:PHE:O	2:H:147:SER:HB3	1.94	0.68
2:H:217:LEU:HD12	2:H:277:SER:CA	2.23	0.68
1:A:250:ALA:HB1	1:A:254:LYS:HB2	1.75	0.68
2:D:141:PHE:O	2:D:147:SER:HB3	1.94	0.68
1:A:257:VAL:O	1:A:257:VAL:HG12	1.93	0.68
2:D:234:ILE:HD13	2:D:234:ILE:C	2.18	0.68
2:F:141:PHE:O	2:F:147:SER:HB3	1.94	0.68
1:G:2:ARG:NH2	2:H:98:ASP:HA	2.09	0.68
1:G:325:MET:CE	1:G:355:VAL:HG21	2.24	0.68
1:A:251:ASP:O	1:A:253:ARG:N	2.26	0.68
1:A:325:MET:CE	1:A:355:VAL:HG21	2.24	0.68
2:B:234:ILE:CB	2:B:302:MET:HE1	2.24	0.68
2:D:234:ILE:CB	2:D:302:MET:HE1	2.24	0.68
1:E:44:LEU:HD12	1:E:49:ILE:HD13	1.76	0.68
1:E:325:MET:CE	1:E:355:VAL:HG21	2.24	0.68
1:A:209:LEU:HD23	1:A:227:LEU:HB3	1.75	0.68
2:B:70:LEU:HD12	2:B:145:THR:CG2	2.24	0.68
2:B:234:ILE:HD13	2:B:234:ILE:C	2.18	0.68
1:C:256:ALA:O	1:C:260:VAL:HG22	1.94	0.68
1:C:359:PRO:HB2	1:C:360:PRO:HD2	1.74	0.68
1:E:267:PHE:CD1	1:E:267:PHE:N	2.62	0.68
1:E:359:PRO:HB2	1:E:360:PRO:HD2	1.74	0.68
2:F:261:PRO:HG3	1:G:404:PHE:CE2	2.23	0.68
2:F:284:GLU:O	2:F:284:GLU:HG2	1.93	0.68
1:G:359:PRO:HB2	1:G:360:PRO:HD2	1.74	0.68
2:H:102:ASN:HB2	2:H:408:TYR:CE2	2.29	0.68
2:B:133:GLN:HG2	2:B:243:ARG:HH22	1.57	0.68
2:B:221:ARG:N	2:B:222:PRO:HD3	2.09	0.68
1:C:209:LEU:HD23	1:C:227:LEU:HB3	1.75	0.68
1:C:257:VAL:O	1:C:257:VAL:HG12	1.93	0.68
2:F:102:ASN:HB2	2:F:408:TYR:CE2	2.29	0.68
1:G:44:LEU:HD12	1:G:49:ILE:HD13	1.76	0.68
1:G:267:PHE:N	1:G:267:PHE:CD1	2.62	0.68
2:H:70:LEU:HD12	2:H:145:THR:CG2	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:PHE:CE1	2:B:61:HIS:HE1	2.12	0.67
2:B:296:PHE:CE1	2:B:335:ILE:CG2	2.73	0.67
1:C:251:ASP:O	1:C:253:ARG:N	2.26	0.67
1:C:325:MET:CE	1:C:355:VAL:HG21	2.24	0.67
2:D:70:LEU:HD12	2:D:145:THR:CG2	2.24	0.67
2:D:133:GLN:HG2	2:D:243:ARG:HH22	1.57	0.67
2:D:276:ILE:O	2:D:369:ALA:N	2.25	0.67
1:G:107:HIS:CD2	1:G:151:THR:CG2	2.77	0.67
2:H:284:GLU:HG2	2:H:284:GLU:O	1.93	0.67
3:I:97:LEU:HD22	3:I:100:GLY:O	1.94	0.67
1:A:267:PHE:N	1:A:267:PHE:CD1	2.62	0.67
1:C:250:ALA:HB1	1:C:254:LYS:HB2	1.75	0.67
1:C:328:VAL:O	1:C:332:MET:HG2	1.94	0.67
2:D:152:LEU:HA	2:D:155:GLU:HB2	1.77	0.67
2:D:243:ARG:NH2	2:D:252:LEU:N	2.29	0.67
2:F:70:LEU:HD12	2:F:145:THR:CG2	2.24	0.67
2:F:133:GLN:HG2	2:F:243:ARG:HH22	1.57	0.67
2:F:152:LEU:HA	2:F:155:GLU:HB2	1.77	0.67
2:H:7:ILE:HD12	2:H:153:LEU:CD2	2.24	0.67
2:H:133:GLN:HG2	2:H:243:ARG:HH22	1.57	0.67
1:E:107:HIS:CD2	1:E:151:THR:CG2	2.77	0.67
2:F:251:ASP:O	2:F:254:GLU:HB2	1.94	0.67
1:G:258:ASN:CA	2:H:404:PHE:CD2	2.70	0.67
2:H:152:LEU:HA	2:H:155:GLU:HB2	1.77	0.67
3:I:84:LEU:HD13	3:I:102:ARG:O	1.93	0.67
1:A:4:ILE:HG21	1:A:136:GLN:HG2	1.76	0.67
2:B:166:LYS:H	2:B:199:ASP:CG	2.03	0.67
2:B:276:ILE:O	2:B:369:ALA:N	2.25	0.67
2:F:7:ILE:HD12	2:F:153:LEU:CD2	2.24	0.67
2:H:221:ARG:N	2:H:222:PRO:HD3	2.09	0.67
2:B:175:PRO:HG3	2:B:304:LYS:HG2	1.76	0.67
1:C:310:GLY:HA3	1:C:436:GLN:HE21	1.59	0.67
2:F:234:ILE:CB	2:F:302:MET:HE1	2.24	0.67
1:G:258:ASN:C	2:H:404:PHE:CE2	2.72	0.67
2:H:95:GLY:O	2:H:97:GLU:N	2.27	0.67
2:H:251:ASP:O	2:H:254:GLU:HB2	1.94	0.67
3:I:97:LEU:HD13	3:I:100:GLY:O	1.94	0.67
1:A:328:VAL:O	1:A:332:MET:HG2	1.94	0.67
2:B:251:ASP:O	2:B:254:GLU:HB2	1.94	0.67
1:C:44:LEU:HD12	1:C:49:ILE:HD13	1.76	0.67
2:D:7:ILE:HD12	2:D:153:LEU:CD2	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4:ILE:HG21	1:E:136:GLN:HG2	1.76	0.67
2:F:221:ARG:N	2:F:222:PRO:HD3	2.09	0.67
2:F:326:LYS:HB2	1:G:222:PRO:HG2	0.71	0.67
1:G:4:ILE:HG21	1:G:136:GLN:HG2	1.76	0.67
1:A:107:HIS:CD2	1:A:151:THR:CG2	2.77	0.67
1:A:230:LEU:HD23	1:A:231:VAL:N	2.10	0.67
2:D:166:LYS:H	2:D:199:ASP:CG	2.03	0.67
2:F:95:GLY:O	2:F:97:GLU:N	2.27	0.67
2:F:166:LYS:H	2:F:199:ASP:CG	2.03	0.67
1:G:328:VAL:O	1:G:332:MET:HG2	1.95	0.67
2:H:234:ILE:HD13	2:H:234:ILE:C	2.18	0.67
2:B:7:ILE:HD12	2:B:153:LEU:CD2	2.24	0.67
2:B:152:LEU:HA	2:B:155:GLU:HB2	1.77	0.67
2:B:333:ALA:CA	1:C:177:VAL:CG2	2.73	0.67
1:C:230:LEU:HD23	1:C:231:VAL:N	2.10	0.67
1:E:328:VAL:O	1:E:332:MET:HG2	1.95	0.67
2:H:166:LYS:H	2:H:199:ASP:CG	2.03	0.67
2:H:199:ASP:HB3	2:H:256:GLN:HE21	1.57	0.67
2:H:234:ILE:CB	2:H:302:MET:HE1	2.24	0.67
1:A:44:LEU:HD12	1:A:49:ILE:HD13	1.76	0.67
1:A:310:GLY:HA3	1:A:436:GLN:HE21	1.59	0.67
1:C:4:ILE:HG21	1:C:136:GLN:HG2	1.76	0.67
2:D:251:ASP:O	2:D:254:GLU:HB2	1.94	0.67
2:F:6:SER:HB3	2:F:136:SER:HG	1.58	0.67
2:F:175:PRO:HG3	2:F:304:LYS:HG2	1.76	0.67
1:G:204:ILE:HD13	1:G:231:VAL:HG22	1.76	0.67
1:G:260:VAL:HG23	2:H:406:HIS:CE1	2.29	0.67
2:H:22:GLU:HG3	2:H:83:TYR:OH	1.95	0.67
2:D:95:GLY:O	2:D:97:GLU:N	2.27	0.67
2:F:199:ASP:HB3	2:F:256:GLN:HE21	1.57	0.67
2:F:234:ILE:HD13	2:F:234:ILE:C	2.18	0.67
2:F:243:ARG:NH2	2:F:252:LEU:N	2.29	0.67
2:B:95:GLY:O	2:B:97:GLU:N	2.27	0.66
1:C:242:LEU:CD1	1:C:255:LEU:HD11	2.25	0.66
2:D:175:PRO:HG3	2:D:304:LYS:HG2	1.76	0.66
2:D:402:ARG:O	2:D:403:ALA:C	2.36	0.66
1:E:204:ILE:HD13	1:E:231:VAL:HG22	1.76	0.66
2:F:22:GLU:HG3	2:F:83:TYR:OH	1.95	0.66
2:H:172:TYR:HD1	2:H:173:PRO:N	1.93	0.66
2:H:175:PRO:HG3	2:H:304:LYS:HG2	1.76	0.66
2:H:341:ILE:O	2:H:341:ILE:HG12	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:HIS:CD2	1:C:151:THR:CG2	2.77	0.66
2:F:341:ILE:O	2:F:341:ILE:HG12	1.95	0.66
1:A:243:ARG:HH22	1:A:252:LEU:HG	1.59	0.66
2:B:172:TYR:HD1	2:B:173:PRO:N	1.93	0.66
2:B:402:ARG:O	2:B:403:ALA:C	2.36	0.66
1:C:204:ILE:HD13	1:C:231:VAL:HG22	1.76	0.66
2:D:22:GLU:HG3	2:D:83:TYR:OH	1.95	0.66
1:E:230:LEU:HD23	1:E:231:VAL:N	2.10	0.66
2:F:172:TYR:HD1	2:F:173:PRO:N	1.93	0.66
1:A:242:LEU:CD1	1:A:255:LEU:HD11	2.25	0.66
2:B:67:PHE:CD1	2:B:92:LEU:CD2	2.79	0.66
2:B:100:ALA:CB	2:B:105:ARG:HD3	2.26	0.66
2:D:172:TYR:HD1	2:D:173:PRO:N	1.93	0.66
2:F:67:PHE:CD1	2:F:92:LEU:CD2	2.79	0.66
1:G:230:LEU:HD23	1:G:231:VAL:N	2.10	0.66
1:G:310:GLY:HA3	1:G:436:GLN:HE21	1.59	0.66
2:H:100:ALA:CB	2:H:105:ARG:HD3	2.26	0.66
1:A:204:ILE:HD13	1:A:231:VAL:HG22	1.76	0.66
1:C:242:LEU:HD12	1:C:255:LEU:HD11	1.77	0.66
2:D:67:PHE:CD1	2:D:92:LEU:CD2	2.79	0.66
2:D:68:VAL:HG11	2:D:149:PHE:CZ	2.30	0.66
1:E:310:GLY:HA3	1:E:436:GLN:HE21	1.59	0.66
2:F:100:ALA:CB	2:F:105:ARG:HD3	2.26	0.66
1:G:242:LEU:CD1	1:G:255:LEU:HD11	2.25	0.66
1:G:352:LYS:CA	2:H:181:VAL:CG2	2.73	0.66
1:G:413:MET:HG2	1:G:418:PHE:HE1	1.61	0.66
2:H:67:PHE:CD1	2:H:92:LEU:CD2	2.79	0.66
1:E:413:MET:HG2	1:E:418:PHE:HE1	1.61	0.66
2:F:68:VAL:HG11	2:F:149:PHE:CZ	2.30	0.66
2:H:68:VAL:HG11	2:H:149:PHE:CZ	2.30	0.66
1:A:413:MET:HG2	1:A:418:PHE:HE1	1.61	0.66
2:B:313:MET:HB3	2:B:344:VAL:CG2	2.26	0.66
1:C:245:PRO:HA	2:D:73:THR:HG21	1.77	0.66
1:E:242:LEU:CD1	1:E:255:LEU:HD11	2.25	0.66
1:E:324:SER:C	1:E:326:LYS:H	2.03	0.66
2:H:313:MET:HB3	2:H:344:VAL:CG2	2.26	0.66
1:A:242:LEU:HD12	1:A:255:LEU:HD11	1.77	0.66
2:B:22:GLU:HG3	2:B:83:TYR:OH	1.95	0.66
2:B:49:PHE:CE1	2:B:61:HIS:CE1	2.84	0.66
2:B:68:VAL:HG11	2:B:149:PHE:CZ	2.30	0.66
1:C:172:VAL:HG11	1:C:387:LEU:CD2	2.22	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:100:ALA:CB	2:D:105:ARG:HD3	2.26	0.66
2:D:313:MET:HB3	2:D:344:VAL:CG2	2.26	0.66
1:E:182:VAL:HG23	1:E:186:ASN:HD21	1.60	0.66
2:F:30:ILE:CD1	2:F:61:HIS:CD2	2.78	0.66
2:F:313:MET:HB3	2:F:344:VAL:CG2	2.26	0.66
2:F:326:LYS:HE2	1:G:214:PHE:CB	2.26	0.66
2:H:243:ARG:NH2	2:H:252:LEU:N	2.29	0.66
1:A:182:VAL:HG23	1:A:186:ASN:HD21	1.60	0.66
1:C:413:MET:HG2	1:C:418:PHE:HE1	1.61	0.66
2:F:315:CYS:HB3	2:F:377:MET:HE1	1.78	0.66
1:G:299:LYS:HD3	1:G:299:LYS:N	2.04	0.66
1:A:88:ARG:HD2	1:E:283:TYR:OH	1.96	0.66
2:B:372:GLN:O	2:B:373:ARG:HB3	1.96	0.66
1:C:182:VAL:HG23	1:C:186:ASN:HD21	1.60	0.66
1:C:243:ARG:HH22	1:C:252:LEU:HG	1.59	0.66
1:C:267:PHE:N	1:C:267:PHE:CD1	2.62	0.66
1:C:281:GLN:O	1:C:283:TYR:HB2	1.96	0.66
2:D:315:CYS:HB3	2:D:377:MET:HE1	1.78	0.66
1:E:281:GLN:O	1:E:283:TYR:HB2	1.96	0.66
1:G:242:LEU:HD12	1:G:255:LEU:HD11	1.78	0.66
1:G:324:SER:C	1:G:326:LYS:H	2.03	0.66
2:H:315:CYS:HB3	2:H:377:MET:HE1	1.78	0.66
1:A:35:SER:HB3	1:A:59:ASN:CA	2.26	0.65
1:A:281:GLN:O	1:A:283:TYR:HB2	1.96	0.65
2:B:206:ASN:OD1	2:B:227:LEU:HD13	1.96	0.65
2:B:348:PRO:HD2	1:C:398:MET:HE2	1.75	0.65
1:C:35:SER:HB3	1:C:59:ASN:CA	2.26	0.65
1:C:103:TRP:HZ3	1:C:108:TYR:HE1	1.42	0.65
1:E:242:LEU:HD12	1:E:255:LEU:HD11	1.77	0.65
1:G:248:LEU:HD13	2:H:179:THR:HG21	1.76	0.65
1:A:66:ILE:CD1	1:A:122:VAL:HG12	2.26	0.65
2:B:63:PRO:CG	2:B:87:PHE:HA	2.26	0.65
2:B:296:PHE:CZ	2:B:341:ILE:HD11	2.22	0.65
2:B:439:SER:CA	1:C:401:ARG:NH2	2.59	0.65
1:C:66:ILE:CD1	1:C:122:VAL:HG12	2.26	0.65
2:D:234:ILE:CG2	2:D:302:MET:HE1	2.27	0.65
2:B:315:CYS:HB3	2:B:377:MET:HE1	1.78	0.65
2:B:317:LEU:HD12	2:B:351:PHE:CD2	2.32	0.65
2:B:345:ASP:C	2:B:347:CYS:H	2.04	0.65
1:C:352:LYS:HZ3	2:D:180:ALA:HA	1.61	0.65
1:C:352:LYS:NZ	2:D:180:ALA:HA	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:66:ILE:CD1	1:E:122:VAL:HG12	2.26	0.65
2:F:234:ILE:CG2	2:F:302:MET:HE1	2.27	0.65
1:G:182:VAL:HG23	1:G:186:ASN:HD21	1.60	0.65
2:H:102:ASN:HB3	2:H:407:TRP:CD1	2.31	0.65
1:A:103:TRP:HZ3	1:A:108:TYR:HE1	1.42	0.65
2:B:234:ILE:CG2	2:B:302:MET:HE1	2.27	0.65
1:C:324:SER:C	1:C:326:LYS:H	2.03	0.65
2:D:317:LEU:HD12	2:D:351:PHE:CD2	2.32	0.65
1:G:66:ILE:CD1	1:G:122:VAL:HG12	2.26	0.65
1:G:281:GLN:O	1:G:283:TYR:HB2	1.96	0.65
2:H:317:LEU:HD12	2:H:351:PHE:CD2	2.32	0.65
2:D:217:LEU:HD11	2:D:367:ASP:O	1.96	0.65
2:D:372:GLN:O	2:D:373:ARG:HB3	1.96	0.65
2:F:261:PRO:CB	1:G:404:PHE:HE2	1.95	0.65
2:F:317:LEU:HD12	2:F:351:PHE:CD2	2.32	0.65
1:G:250:ALA:HB1	1:G:254:LYS:HB3	1.78	0.65
1:G:306:ASP:OD2	3:I:95:ILE:CD1	2.44	0.65
2:H:206:ASN:OD1	2:H:227:LEU:HD13	1.97	0.65
2:D:206:ASN:OD1	2:D:227:LEU:HD13	1.97	0.65
2:F:206:ASN:OD1	2:F:227:LEU:HD13	1.96	0.65
2:D:341:ILE:HG12	2:D:341:ILE:O	1.95	0.65
1:E:299:LYS:HD3	1:E:299:LYS:N	2.04	0.65
1:E:431:GLU:O	1:E:434:GLN:HG2	1.97	0.65
1:G:431:GLU:O	1:G:434:GLN:HG2	1.97	0.65
2:B:271:THR:HG23	2:B:300:ASN:O	1.97	0.65
2:B:293:ASN:OD1	2:B:338:LYS:NZ	2.30	0.65
2:B:311:LYS:HE3	2:B:342:GLN:CD	2.22	0.65
2:B:341:ILE:O	2:B:341:ILE:HG12	1.95	0.65
2:D:3:GLU:HA	2:D:51:THR:CB	2.27	0.65
2:F:115:ILE:HG23	2:F:116:ASP:N	2.12	0.65
2:F:296:PHE:CZ	2:F:341:ILE:HD11	2.22	0.65
2:F:345:ASP:C	2:F:347:CYS:H	2.04	0.65
2:F:349:THR:HG23	1:G:178:SER:H	1.58	0.65
2:H:102:ASN:CG	2:H:407:TRP:CD1	2.75	0.65
1:C:282:GLN:O	1:C:282:GLN:HG2	1.97	0.65
1:E:241:CYS:O	1:E:244:PHE:HB2	1.97	0.65
2:H:234:ILE:CG2	2:H:302:MET:HE1	2.27	0.65
1:A:324:SER:C	1:A:326:LYS:H	2.03	0.65
2:B:3:GLU:HA	2:B:51:THR:CB	2.27	0.65
2:B:217:LEU:HD11	2:B:367:ASP:O	1.97	0.65
2:D:293:ASN:OD1	2:D:338:LYS:NZ	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:217:LEU:HD11	2:F:367:ASP:O	1.96	0.65
1:G:35:SER:HB3	1:G:59:ASN:CA	2.26	0.65
1:G:241:CYS:O	1:G:244:PHE:HB2	1.97	0.65
1:G:276:THR:HB	1:G:281:GLN:CG	2.25	0.65
2:H:296:PHE:CZ	2:H:341:ILE:HD11	2.22	0.65
2:H:345:ASP:C	2:H:347:CYS:H	2.04	0.65
1:A:282:GLN:HG2	1:A:282:GLN:O	1.97	0.64
2:D:271:THR:HG23	2:D:300:ASN:O	1.97	0.64
2:D:305:CYS:SG	2:D:384:ILE:HD13	2.37	0.64
2:D:345:ASP:C	2:D:347:CYS:H	2.04	0.64
1:E:35:SER:HB3	1:E:59:ASN:CA	2.26	0.64
1:E:103:TRP:HZ3	1:E:108:TYR:HE1	1.42	0.64
1:E:282:GLN:O	1:E:282:GLN:HG2	1.97	0.64
2:F:3:GLU:HA	2:F:51:THR:CB	2.27	0.64
2:F:349:THR:O	1:G:181:VAL:HA	1.96	0.64
1:G:158:ARG:NE	1:G:197:ASN:O	2.30	0.64
2:H:3:GLU:HA	2:H:51:THR:CB	2.27	0.64
2:H:217:LEU:HD11	2:H:367:ASP:O	1.96	0.64
2:H:311:LYS:HE3	2:H:342:GLN:CD	2.22	0.64
1:A:241:CYS:O	1:A:244:PHE:HB2	1.97	0.64
1:A:431:GLU:O	1:A:434:GLN:HG2	1.97	0.64
2:D:296:PHE:CZ	2:D:341:ILE:HD11	2.22	0.64
2:F:311:LYS:HE3	2:F:342:GLN:CD	2.22	0.64
1:G:70:LEU:N	1:G:145:THR:HG21	2.11	0.64
1:G:282:GLN:HG2	1:G:282:GLN:O	1.97	0.64
2:H:209:ILE:HG23	2:H:230:LEU:HD23	1.79	0.64
2:H:271:THR:HG23	2:H:300:ASN:O	1.97	0.64
1:A:114:LEU:O	1:A:118:VAL:HG23	1.97	0.64
1:A:276:THR:HB	1:A:281:GLN:CG	2.25	0.64
1:C:114:LEU:O	1:C:118:VAL:HG23	1.97	0.64
1:C:241:CYS:O	1:C:244:PHE:HB2	1.98	0.64
1:E:180:THR:CG2	1:E:181:VAL:N	2.61	0.64
1:E:422:GLU:O	1:E:426:ASN:HB2	1.97	0.64
2:F:388:TRP:CE3	2:F:425:MET:HE1	2.32	0.64
2:H:115:ILE:HG23	2:H:116:ASP:N	2.12	0.64
2:H:388:TRP:CE3	2:H:425:MET:HE1	2.32	0.64
1:A:66:ILE:HD13	1:A:122:VAL:HG12	1.79	0.64
1:A:158:ARG:NE	1:A:197:ASN:O	2.30	0.64
2:B:388:TRP:CE3	2:B:425:MET:HE1	2.32	0.64
1:C:70:LEU:N	1:C:145:THR:HG21	2.11	0.64
1:C:158:ARG:NE	1:C:197:ASN:O	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:161:TYR:C	1:C:163:ASP:H	2.05	0.64
2:D:311:LYS:HE3	2:D:342:GLN:CD	2.22	0.64
1:E:161:TYR:C	1:E:163:ASP:H	2.05	0.64
2:F:271:THR:HG23	2:F:300:ASN:O	1.97	0.64
2:F:305:CYS:SG	2:F:384:ILE:HD13	2.37	0.64
2:F:372:GLN:O	2:F:373:ARG:HB3	1.96	0.64
2:B:305:CYS:SG	2:B:384:ILE:HD13	2.37	0.64
2:B:344:VAL:HG12	2:B:345:ASP:N	2.12	0.64
1:C:66:ILE:HD13	1:C:122:VAL:HG12	1.79	0.64
1:C:276:THR:HB	1:C:281:GLN:CG	2.25	0.64
1:C:427:ASP:O	1:C:430:SER:HB3	1.97	0.64
1:C:431:GLU:O	1:C:434:GLN:HG2	1.97	0.64
1:E:276:THR:HB	1:E:281:GLN:CG	2.25	0.64
2:F:209:ILE:HG23	2:F:230:LEU:HD23	1.79	0.64
2:F:262:TYR:HH	1:G:403:ALA:HA	1.61	0.64
1:G:427:ASP:O	1:G:430:SER:HB3	1.97	0.64
1:A:70:LEU:N	1:A:145:THR:HG21	2.11	0.64
2:B:56:THR:CB	2:F:284:GLU:CG	2.76	0.64
2:B:63:PRO:HG3	2:B:87:PHE:HA	1.79	0.64
1:E:158:ARG:NE	1:E:197:ASN:O	2.30	0.64
1:G:103:TRP:HZ3	1:G:108:TYR:HE1	1.42	0.64
1:G:180:THR:CG2	1:G:181:VAL:N	2.61	0.64
2:H:305:CYS:SG	2:H:384:ILE:HD13	2.37	0.64
1:C:192:HIS:O	1:C:195:VAL:HG12	1.98	0.64
1:C:422:GLU:O	1:C:426:ASN:HB2	1.97	0.64
2:D:388:TRP:CE3	2:D:425:MET:HE1	2.32	0.64
2:H:372:GLN:O	2:H:373:ARG:HB3	1.96	0.64
1:A:284:ARG:O	1:A:286:LEU:N	2.31	0.64
1:A:422:GLU:O	1:A:426:ASN:HB2	1.97	0.64
2:D:115:ILE:HG23	2:D:116:ASP:N	2.12	0.64
2:D:209:ILE:HG23	2:D:230:LEU:HD23	1.79	0.64
2:D:344:VAL:HG12	2:D:345:ASP:N	2.12	0.64
1:E:70:LEU:N	1:E:145:THR:HG21	2.11	0.64
1:G:161:TYR:C	1:G:163:ASP:H	2.05	0.64
1:G:284:ARG:O	1:G:286:LEU:N	2.31	0.64
1:G:422:GLU:O	1:G:426:ASN:HB2	1.97	0.64
1:A:427:ASP:O	1:A:430:SER:HB3	1.97	0.64
2:B:25:CYS:HB2	2:B:30:ILE:O	1.98	0.64
1:C:133:GLN:HG3	1:C:165:ILE:HD11	1.80	0.64
1:C:284:ARG:O	1:C:286:LEU:N	2.31	0.64
1:E:66:ILE:HD13	1:E:122:VAL:HG12	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:175:PRO:HG2	2:F:207:GLU:OE1	1.98	0.64
2:H:175:PRO:HG2	2:H:207:GLU:OE1	1.98	0.64
2:B:209:ILE:HG23	2:B:230:LEU:HD23	1.79	0.64
2:D:30:ILE:CD1	2:D:61:HIS:CD2	2.81	0.64
1:E:284:ARG:O	1:E:286:LEU:N	2.31	0.64
1:G:299:LYS:H	1:G:299:LYS:CD	2.07	0.64
1:A:133:GLN:HG3	1:A:165:ILE:HD11	1.80	0.63
1:A:192:HIS:O	1:A:195:VAL:HG12	1.98	0.63
2:D:317:LEU:HB3	2:D:319:TYR:CE1	2.33	0.63
1:E:137:LEU:HD22	1:E:154:ILE:CG2	2.28	0.63
2:F:151:SER:O	2:F:155:GLU:HB2	1.98	0.63
2:F:293:ASN:OD1	2:F:338:LYS:NZ	2.30	0.63
1:G:105:LYS:O	1:G:110:GLU:HB2	1.97	0.63
1:G:137:LEU:HD22	1:G:154:ILE:CG2	2.28	0.63
1:A:161:TYR:C	1:A:163:ASP:H	2.05	0.63
2:B:115:ILE:HG23	2:B:116:ASP:N	2.12	0.63
2:B:381:THR:C	2:B:383:ALA:N	2.56	0.63
1:E:63:PRO:HD2	1:E:86:ILE:HG12	1.80	0.63
1:E:427:ASP:O	1:E:430:SER:HB3	1.97	0.63
2:F:284:GLU:OE1	2:F:284:GLU:N	2.30	0.63
1:G:66:ILE:HD13	1:G:122:VAL:HG12	1.79	0.63
1:G:349:ASN:C	1:G:349:ASN:HD22	2.06	0.63
2:H:151:SER:O	2:H:155:GLU:HB2	1.98	0.63
2:H:284:GLU:OE1	2:H:284:GLU:N	2.30	0.63
1:A:63:PRO:HD2	1:A:86:ILE:HG12	1.80	0.63
1:A:70:LEU:C	1:A:99:ALA:HB2	2.24	0.63
1:A:107:HIS:HD2	1:A:151:THR:CG2	2.12	0.63
1:C:70:LEU:C	1:C:99:ALA:HB2	2.24	0.63
1:C:137:LEU:HD22	1:C:154:ILE:CG2	2.28	0.63
1:E:105:LYS:O	1:E:110:GLU:HB2	1.97	0.63
1:E:349:ASN:C	1:E:349:ASN:HD22	2.07	0.63
1:G:70:LEU:C	1:G:99:ALA:HB2	2.24	0.63
2:H:7:ILE:HG22	2:H:66:VAL:CG2	2.28	0.63
1:A:137:LEU:HD22	1:A:154:ILE:CG2	2.28	0.63
2:B:386:GLU:O	2:B:389:ALA:N	2.31	0.63
2:D:25:CYS:HB2	2:D:30:ILE:O	1.98	0.63
2:D:175:PRO:HG2	2:D:207:GLU:OE1	1.98	0.63
2:D:381:THR:C	2:D:383:ALA:N	2.56	0.63
2:D:386:GLU:O	2:D:389:ALA:N	2.31	0.63
1:E:299:LYS:H	1:E:299:LYS:CD	2.07	0.63
2:F:386:GLU:O	2:F:389:ALA:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:114:LEU:O	1:G:118:VAL:HG23	1.97	0.63
1:G:133:GLN:HG3	1:G:165:ILE:HD11	1.80	0.63
1:G:318:VAL:HA	1:G:354:ALA:HB3	1.81	0.63
1:A:180:THR:CG2	1:A:181:VAL:N	2.61	0.63
1:A:318:VAL:HA	1:A:354:ALA:HB3	1.81	0.63
2:B:175:PRO:HG2	2:B:207:GLU:OE1	1.98	0.63
1:C:107:HIS:HD2	1:C:151:THR:CG2	2.12	0.63
1:C:180:THR:CG2	1:C:181:VAL:N	2.61	0.63
1:C:318:VAL:HA	1:C:354:ALA:HB3	1.81	0.63
1:C:346:TRP:CD1	2:D:401:LYS:NZ	2.65	0.63
1:E:70:LEU:C	1:E:99:ALA:HB2	2.24	0.63
2:F:7:ILE:HG22	2:F:66:VAL:CG2	2.28	0.63
2:F:296:PHE:CE1	2:F:335:ILE:CG2	2.73	0.63
1:G:192:HIS:O	1:G:195:VAL:HG12	1.98	0.63
1:G:352:LYS:CA	2:H:181:VAL:HG22	2.24	0.63
2:H:293:ASN:OD1	2:H:338:LYS:NZ	2.30	0.63
2:H:296:PHE:CE1	2:H:335:ILE:CG2	2.73	0.63
2:H:386:GLU:O	2:H:389:ALA:N	2.31	0.63
1:A:349:ASN:C	1:A:349:ASN:HD22	2.07	0.63
1:C:105:LYS:O	1:C:110:GLU:HB2	1.97	0.63
1:C:349:ASN:HD22	1:C:349:ASN:C	2.07	0.63
2:D:88:HIS:HB2	2:D:91:GLN:NE2	2.06	0.63
1:E:114:LEU:O	1:E:118:VAL:HG23	1.97	0.63
1:E:192:HIS:O	1:E:195:VAL:HG12	1.98	0.63
2:F:278:ALA:O	2:F:279:GLU:CB	2.43	0.63
1:G:63:PRO:HD2	1:G:86:ILE:HG12	1.80	0.63
2:H:88:HIS:HB2	2:H:91:GLN:NE2	2.06	0.63
2:B:151:SER:O	2:B:155:GLU:HB2	1.98	0.63
2:B:152:LEU:HD12	2:B:153:LEU:N	2.14	0.63
2:B:317:LEU:HB3	2:B:319:TYR:CE1	2.33	0.63
1:C:315:VAL:HG13	1:C:377:PHE:CE1	2.34	0.63
1:E:318:VAL:HA	1:E:354:ALA:HB3	1.81	0.63
2:F:88:HIS:HB2	2:F:91:GLN:NE2	2.06	0.63
2:F:317:LEU:HB3	2:F:319:TYR:CE1	2.33	0.63
2:H:278:ALA:O	2:H:279:GLU:CB	2.43	0.63
2:H:317:LEU:HB3	2:H:319:TYR:CE1	2.33	0.63
2:H:344:VAL:HG12	2:H:345:ASP:N	2.12	0.63
1:A:315:VAL:HG13	1:A:377:PHE:CE1	2.34	0.63
2:B:159:VAL:CG1	3:I:78:ARG:HG3	2.29	0.63
1:C:243:ARG:HH21	1:C:252:LEU:H	1.45	0.63
1:C:247:GLN:HB3	2:D:224:TYR:CD1	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:7:ILE:HG22	2:D:66:VAL:CG2	2.28	0.63
2:D:102:ASN:OD1	2:D:105:ARG:HB3	1.99	0.63
1:E:172:VAL:HG11	1:E:387:LEU:CD2	2.22	0.63
1:E:299:LYS:O	1:E:300:ASN:HB2	1.97	0.63
2:B:102:ASN:OD1	2:B:105:ARG:HB3	1.99	0.63
1:C:299:LYS:O	1:C:300:ASN:HB2	1.97	0.63
2:D:7:ILE:CD1	2:D:137:VAL:HG22	2.29	0.63
1:E:133:GLN:HG3	1:E:165:ILE:HD11	1.80	0.63
2:F:344:VAL:HG12	2:F:345:ASP:N	2.12	0.63
1:G:245:PRO:HB3	2:H:73:THR:CG2	2.29	0.63
1:G:258:ASN:OD1	2:H:181:VAL:HB	1.99	0.63
1:A:105:LYS:O	1:A:110:GLU:HB2	1.97	0.62
1:C:205:ASP:OD1	1:C:304:ALA:N	2.32	0.62
2:D:155:GLU:HA	2:D:197:HIS:HD1	1.63	0.62
1:G:107:HIS:HD2	1:G:151:THR:CG2	2.12	0.62
1:G:154:ILE:HG22	1:G:166:MET:HE2	1.81	0.62
1:G:172:VAL:HG11	1:G:387:LEU:CD2	2.22	0.62
1:C:63:PRO:HD2	1:C:86:ILE:HG12	1.80	0.62
2:D:151:SER:O	2:D:155:GLU:HB2	1.98	0.62
1:E:154:ILE:HG22	1:E:166:MET:HE2	1.81	0.62
2:H:267:PHE:H	2:H:267:PHE:HD1	1.47	0.62
1:A:299:LYS:H	1:A:299:LYS:CD	2.07	0.62
2:B:7:ILE:CD1	2:B:137:VAL:HG22	2.29	0.62
2:D:267:PHE:HD1	2:D:267:PHE:H	1.47	0.62
2:F:152:LEU:HD12	2:F:153:LEU:N	2.14	0.62
1:G:243:ARG:HH21	1:G:252:LEU:H	1.45	0.62
1:G:250:ALA:HB1	1:G:254:LYS:CD	2.17	0.62
2:H:152:LEU:HD12	2:H:153:LEU:N	2.14	0.62
2:H:269:LEU:O	2:H:378:LEU:HA	1.99	0.62
2:H:381:THR:C	2:H:383:ALA:N	2.56	0.62
1:A:243:ARG:HH21	1:A:252:LEU:H	1.45	0.62
1:C:4:ILE:HA	1:C:134:GLY:O	1.99	0.62
2:D:152:LEU:HD12	2:D:153:LEU:N	2.14	0.62
2:D:315:CYS:HB3	2:D:377:MET:CE	2.29	0.62
2:F:115:ILE:HG13	2:F:152:LEU:HD13	1.81	0.62
2:F:273:ALA:HB3	2:F:274:PRO:HD3	1.81	0.62
2:F:315:CYS:HB3	2:F:377:MET:CE	2.29	0.62
2:F:381:THR:C	2:F:383:ALA:N	2.56	0.62
1:G:299:LYS:O	1:G:300:ASN:HB2	1.98	0.62
2:H:70:LEU:O	2:H:95:GLY:O	2.17	0.62
1:A:56:ALA:CB	1:E:283:TYR:CD2	2.76	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ILE:HG22	1:A:166:MET:HE2	1.81	0.62
1:A:205:ASP:OD1	1:A:304:ALA:N	2.32	0.62
1:A:253:ARG:O	1:A:256:ALA:N	2.33	0.62
2:B:205:ASP:HB2	2:B:303:VAL:HA	1.82	0.62
1:E:315:VAL:HG13	1:E:377:PHE:CE1	2.34	0.62
2:F:62:VAL:CG1	2:F:91:GLN:HE22	2.13	0.62
2:F:102:ASN:OD1	2:F:105:ARG:HB3	1.99	0.62
2:H:115:ILE:HG13	2:H:152:LEU:HD13	1.81	0.62
2:H:236:SER:O	2:H:240:ALA:HB3	1.99	0.62
2:H:273:ALA:HB3	2:H:274:PRO:HD3	1.81	0.62
2:B:7:ILE:HG22	2:B:66:VAL:CG2	2.28	0.62
1:C:70:LEU:CG	1:C:145:THR:HG23	2.30	0.62
1:C:253:ARG:O	1:C:256:ALA:N	2.33	0.62
2:D:115:ILE:HG13	2:D:152:LEU:HD13	1.81	0.62
2:D:205:ASP:HB2	2:D:303:VAL:HA	1.82	0.62
2:D:236:SER:O	2:D:240:ALA:HB3	1.99	0.62
1:E:243:ARG:HH21	1:E:252:LEU:H	1.45	0.62
1:G:4:ILE:HG23	1:G:134:GLY:O	2.00	0.62
2:H:62:VAL:CG1	2:H:91:GLN:HE22	2.13	0.62
2:H:315:CYS:HB3	2:H:377:MET:CE	2.29	0.62
1:A:211:ASP:OD1	1:A:212:ILE:N	2.33	0.62
1:A:299:LYS:O	1:A:300:ASN:HB2	1.98	0.62
2:B:267:PHE:H	2:B:267:PHE:HD1	1.47	0.62
2:B:317:LEU:HD11	2:B:351:PHE:HE2	1.63	0.62
1:C:211:ASP:OD1	1:C:212:ILE:N	2.33	0.62
1:C:254:LYS:NZ	2:D:101:ASN:ND2	2.47	0.62
1:E:70:LEU:CG	1:E:145:THR:HG23	2.30	0.62
1:E:107:HIS:HD2	1:E:151:THR:CG2	2.12	0.62
1:E:253:ARG:O	1:E:256:ALA:N	2.33	0.62
2:F:7:ILE:CD1	2:F:137:VAL:HG22	2.29	0.62
2:F:70:LEU:O	2:F:95:GLY:O	2.18	0.62
2:F:269:LEU:O	2:F:378:LEU:HA	1.99	0.62
1:G:205:ASP:OD1	1:G:304:ALA:N	2.32	0.62
1:G:230:LEU:O	1:G:233:ALA:HB3	2.00	0.62
1:G:315:VAL:HG13	1:G:377:PHE:CE1	2.34	0.62
2:H:102:ASN:OD1	2:H:105:ARG:HB3	1.99	0.62
1:A:115:VAL:HG21	1:A:152:LEU:CD2	2.30	0.62
2:B:115:ILE:HG13	2:B:152:LEU:HD13	1.81	0.62
2:B:118:VAL:HG11	2:B:149:PHE:HZ	1.65	0.62
2:B:236:SER:O	2:B:240:ALA:HB3	1.99	0.62
2:B:269:LEU:O	2:B:378:LEU:HA	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:315:CYS:HB3	2:B:377:MET:CE	2.29	0.62
1:C:249:ASN:OD1	2:D:71:GLU:OE1	2.17	0.62
2:D:118:VAL:HG11	2:D:149:PHE:HZ	1.65	0.62
1:E:4:ILE:HA	1:E:134:GLY:O	1.99	0.62
1:E:205:ASP:OD1	1:E:304:ALA:N	2.32	0.62
2:F:326:LYS:CB	1:G:222:PRO:CD	2.77	0.62
2:H:7:ILE:CD1	2:H:137:VAL:HG22	2.29	0.62
2:H:155:GLU:HA	2:H:197:HIS:HD1	1.63	0.62
2:B:155:GLU:HA	2:B:197:HIS:HD1	1.63	0.62
1:C:93:VAL:CG1	1:C:118:VAL:HG22	2.19	0.62
1:E:4:ILE:HG23	1:E:134:GLY:O	2.00	0.62
2:F:236:SER:O	2:F:240:ALA:HB3	1.99	0.62
1:G:70:LEU:CG	1:G:145:THR:HG23	2.30	0.62
1:G:115:VAL:HG21	1:G:152:LEU:CD2	2.30	0.62
1:A:4:ILE:HA	1:A:134:GLY:O	1.99	0.62
1:A:70:LEU:CG	1:A:145:THR:HG23	2.30	0.62
2:B:62:VAL:HG11	2:B:88:HIS:ND1	2.15	0.62
2:B:159:VAL:HG13	3:I:78:ARG:HG2	1.81	0.62
2:B:296:PHE:CZ	2:B:341:ILE:CD1	2.79	0.62
2:B:436:GLY:C	2:B:438:ASP:H	2.08	0.62
1:C:115:VAL:HG21	1:C:152:LEU:CD2	2.30	0.62
2:D:317:LEU:HD11	2:D:351:PHE:HE2	1.63	0.62
2:D:436:GLY:C	2:D:438:ASP:H	2.08	0.62
1:E:115:VAL:HG21	1:E:152:LEU:CD2	2.30	0.62
1:E:230:LEU:O	1:E:233:ALA:HB3	2.00	0.62
2:F:155:GLU:HA	2:F:197:HIS:HD1	1.63	0.62
2:F:277:SER:HA	2:F:367:ASP:O	2.00	0.62
1:G:4:ILE:HA	1:G:134:GLY:O	1.99	0.62
1:G:248:LEU:CD2	2:H:179:THR:HG21	2.21	0.62
2:D:62:VAL:CG1	2:D:91:GLN:HE22	2.13	0.61
2:D:269:LEU:O	2:D:378:LEU:HA	1.99	0.61
2:D:277:SER:HA	2:D:367:ASP:O	2.00	0.61
2:D:70:LEU:O	2:D:95:GLY:O	2.17	0.61
1:E:253:ARG:O	1:E:254:LYS:C	2.42	0.61
2:F:205:ASP:HB2	2:F:303:VAL:HA	1.82	0.61
2:F:296:PHE:CZ	2:F:341:ILE:CD1	2.79	0.61
2:F:436:GLY:C	2:F:438:ASP:H	2.08	0.61
1:G:253:ARG:O	1:G:256:ALA:N	2.33	0.61
2:H:277:SER:HA	2:H:367:ASP:O	2.00	0.61
2:H:436:GLY:C	2:H:438:ASP:H	2.08	0.61
2:B:70:LEU:O	2:B:95:GLY:O	2.17	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:88:HIS:HB2	2:B:91:GLN:NE2	2.06	0.61
1:C:299:LYS:H	1:C:299:LYS:CD	2.07	0.61
2:D:23:LEU:HD22	2:D:232:GLY:O	1.99	0.61
2:D:30:ILE:HG12	2:D:36:MET:CB	2.12	0.61
2:F:23:LEU:HD22	2:F:232:GLY:O	1.99	0.61
1:G:211:ASP:OD1	1:G:212:ILE:N	2.33	0.61
2:H:205:ASP:HB2	2:H:303:VAL:HA	1.82	0.61
1:A:4:ILE:HG23	1:A:134:GLY:O	2.00	0.61
1:A:70:LEU:H	1:A:145:THR:CG2	2.10	0.61
2:B:62:VAL:HG13	2:B:63:PRO:HD2	1.78	0.61
2:B:217:LEU:HD11	2:B:277:SER:HA	1.83	0.61
2:B:277:SER:HA	2:B:367:ASP:O	2.00	0.61
1:C:70:LEU:H	1:C:145:THR:CG2	2.10	0.61
1:C:154:ILE:HG22	1:C:166:MET:HE2	1.81	0.61
1:C:324:SER:CB	1:C:327:GLU:HG2	2.30	0.61
1:E:204:ILE:CD1	1:E:231:VAL:HG13	2.30	0.61
2:F:118:VAL:HG11	2:F:149:PHE:HZ	1.65	0.61
2:F:168:GLU:OE1	2:F:198:SER:HB2	2.00	0.61
1:G:253:ARG:O	1:G:254:LYS:C	2.42	0.61
2:H:118:VAL:HG11	2:H:149:PHE:HZ	1.65	0.61
1:A:93:VAL:CG1	1:A:118:VAL:HG22	2.19	0.61
2:B:5:ILE:HD11	2:B:64:ARG:HH22	1.65	0.61
2:B:23:LEU:HD22	2:B:232:GLY:O	1.99	0.61
2:B:168:GLU:OE1	2:B:198:SER:HB2	2.00	0.61
2:B:273:ALA:HB3	2:B:274:PRO:HD3	1.81	0.61
1:C:114:LEU:HD23	1:C:149:MET:CE	2.30	0.61
2:D:217:LEU:HD11	2:D:277:SER:HA	1.82	0.61
2:F:317:LEU:HD11	2:F:351:PHE:HE2	1.63	0.61
1:G:114:LEU:HD23	1:G:149:MET:CE	2.30	0.61
2:H:23:LEU:HD22	2:H:232:GLY:O	1.99	0.61
2:H:168:GLU:OE1	2:H:198:SER:HB2	2.01	0.61
1:A:88:ARG:HD3	1:E:283:TYR:CE1	2.34	0.61
2:B:30:ILE:CD1	2:B:61:HIS:CG	2.82	0.61
2:D:119:LEU:CD2	2:D:122:ILE:HD11	2.28	0.61
2:F:242:LEU:C	2:F:244:PHE:H	2.09	0.61
1:G:204:ILE:CD1	1:G:231:VAL:HG13	2.30	0.61
1:A:230:LEU:O	1:A:233:ALA:HB3	2.00	0.61
2:D:273:ALA:HB3	2:D:274:PRO:HD3	1.81	0.61
2:D:409:VAL:C	2:D:411:GLU:H	2.09	0.61
1:E:211:ASP:OD1	1:E:212:ILE:N	2.33	0.61
1:E:283:TYR:C	1:E:284:ARG:HG2	2.24	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:242:LEU:C	2:H:244:PHE:H	2.09	0.61
2:H:296:PHE:CZ	2:H:341:ILE:CD1	2.79	0.61
2:H:409:VAL:C	2:H:411:GLU:H	2.09	0.61
1:A:324:SER:CB	1:A:327:GLU:HG2	2.30	0.61
2:B:169:PHE:CE1	2:B:235:VAL:HG22	2.36	0.61
2:B:229:ARG:NH1	2:B:363:VAL:HG21	2.16	0.61
2:B:242:LEU:C	2:B:244:PHE:H	2.09	0.61
1:C:4:ILE:HG23	1:C:134:GLY:O	2.00	0.61
1:C:54:ASN:ND2	1:C:64:ARG:HD3	2.15	0.61
1:C:248:LEU:HD22	2:D:179:THR:CG2	2.27	0.61
2:D:168:GLU:OE1	2:D:198:SER:HB2	2.00	0.61
1:E:424:ASN:HD22	1:E:424:ASN:C	2.09	0.61
2:F:346:TRP:HZ3	1:G:404:PHE:HZ	1.47	0.61
2:F:409:VAL:C	2:F:411:GLU:H	2.09	0.61
1:A:114:LEU:HD23	1:A:149:MET:CE	2.30	0.61
1:C:424:ASN:HD22	1:C:424:ASN:C	2.09	0.61
2:D:248:LEU:CD2	2:D:353:VAL:O	2.49	0.61
2:D:296:PHE:CZ	2:D:341:ILE:CD1	2.79	0.61
2:H:317:LEU:HD11	2:H:351:PHE:HE2	1.63	0.61
1:A:424:ASN:C	1:A:424:ASN:HD22	2.09	0.61
1:C:230:LEU:O	1:C:233:ALA:HB3	2.00	0.61
2:D:229:ARG:NH1	2:D:363:VAL:HG21	2.16	0.61
1:E:324:SER:C	1:E:326:LYS:N	2.59	0.61
2:F:119:LEU:CD2	2:F:122:ILE:HD11	2.28	0.61
2:F:191:THR:HG21	2:F:425:MET:SD	2.41	0.61
1:G:93:VAL:CG1	1:G:118:VAL:HG22	2.19	0.61
1:G:245:PRO:HA	2:H:73:THR:HG21	1.83	0.61
1:G:424:ASN:C	1:G:424:ASN:HD22	2.09	0.61
2:H:119:LEU:CD2	2:H:122:ILE:HD11	2.28	0.61
2:H:169:PHE:CE1	2:H:235:VAL:HG22	2.36	0.61
2:H:191:THR:HG21	2:H:425:MET:SD	2.41	0.61
1:A:54:ASN:ND2	1:A:64:ARG:HD3	2.15	0.60
1:A:283:TYR:C	1:A:284:ARG:HG2	2.24	0.60
2:B:5:ILE:HD13	2:B:64:ARG:HH12	1.59	0.60
2:B:409:VAL:C	2:B:411:GLU:H	2.09	0.60
1:E:114:LEU:HD23	1:E:149:MET:CE	2.30	0.60
2:F:87:PHE:CD2	2:F:87:PHE:N	2.69	0.60
2:F:169:PHE:CE1	2:F:235:VAL:HG22	2.36	0.60
2:H:87:PHE:N	2:H:87:PHE:CD2	2.69	0.60
2:H:362:VAL:HG13	2:H:368:LEU:HB2	1.83	0.60
2:B:30:ILE:HG12	2:B:36:MET:CB	2.12	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:56:THR:CB	2:F:284:GLU:CD	2.74	0.60
2:D:169:PHE:CE1	2:D:235:VAL:HG22	2.36	0.60
1:E:93:VAL:CG1	1:E:118:VAL:HG22	2.19	0.60
2:F:267:PHE:HD1	2:F:267:PHE:H	1.47	0.60
2:F:329:ASN:CB	1:G:210:TYR:CZ	2.81	0.60
2:F:348:PRO:CD	1:G:398:MET:HE3	2.31	0.60
3:I:63:ARG:HB3	3:I:136:VAL:HG11	1.83	0.60
1:A:188:THR:HA	1:A:425:MET:HE2	1.83	0.60
1:A:204:ILE:HG21	1:A:231:VAL:HG22	1.84	0.60
2:B:88:HIS:CE1	2:F:284:GLU:OE2	2.54	0.60
2:B:119:LEU:CD2	2:B:122:ILE:HD11	2.28	0.60
2:B:191:THR:HG21	2:B:425:MET:SD	2.41	0.60
1:C:115:VAL:HG21	1:C:152:LEU:HD23	1.84	0.60
1:C:273:ALA:HB3	1:C:274:PRO:CD	2.29	0.60
1:C:285:ALA:HB1	1:C:290:GLU:HG2	1.82	0.60
1:G:283:TYR:C	1:G:284:ARG:HG2	2.24	0.60
1:A:172:VAL:HG11	1:A:387:LEU:CD2	2.22	0.60
1:A:273:ALA:HB3	1:A:274:PRO:CD	2.29	0.60
2:B:6:SER:HB3	2:B:136:SER:HG	1.67	0.60
1:C:204:ILE:CD1	1:C:231:VAL:HG13	2.30	0.60
1:E:204:ILE:HG21	1:E:231:VAL:HG22	1.84	0.60
1:A:115:VAL:HG21	1:A:152:LEU:HD23	1.84	0.60
1:A:204:ILE:CD1	1:A:231:VAL:HG13	2.30	0.60
1:C:188:THR:HA	1:C:425:MET:HE2	1.83	0.60
1:C:283:TYR:C	1:C:284:ARG:HG2	2.24	0.60
2:D:191:THR:HG21	2:D:425:MET:SD	2.41	0.60
2:D:242:LEU:C	2:D:244:PHE:H	2.09	0.60
1:E:188:THR:HA	1:E:425:MET:HE2	1.83	0.60
2:F:362:VAL:HG13	2:F:368:LEU:HB2	1.83	0.60
1:A:49:ILE:O	1:A:51:VAL:N	2.35	0.60
2:B:87:PHE:N	2:B:87:PHE:CD2	2.69	0.60
1:C:31:ASP:O	1:C:32:PRO:C	2.44	0.60
1:C:230:LEU:CD2	1:C:302:MET:HE2	2.31	0.60
1:C:253:ARG:O	1:C:254:LYS:C	2.42	0.60
2:D:362:VAL:HG13	2:D:368:LEU:HB2	1.83	0.60
2:F:63:PRO:CD	2:F:87:PHE:HA	2.32	0.60
1:C:141:LEU:N	1:C:141:LEU:CD1	2.65	0.60
1:C:204:ILE:HG21	1:C:231:VAL:HG22	1.84	0.60
2:D:3:GLU:HG3	2:D:51:THR:HA	1.75	0.60
2:D:57:GLY:HA3	2:D:58:ALA:HB2	0.66	0.60
2:D:87:PHE:CD2	2:D:87:PHE:N	2.69	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:371:VAL:HG12	2:F:372:GLN:N	2.17	0.60
1:G:2:ARG:HH21	2:H:98:ASP:HA	1.64	0.60
1:G:49:ILE:O	1:G:51:VAL:N	2.35	0.60
1:G:204:ILE:HG21	1:G:231:VAL:HG22	1.84	0.60
1:C:254:LYS:HZ3	2:D:101:ASN:ND2	2.00	0.60
2:D:344:VAL:HG11	2:D:346:TRP:NE1	2.16	0.60
1:E:115:VAL:HG21	1:E:152:LEU:HD23	1.84	0.60
1:E:273:ALA:HB3	1:E:274:PRO:CD	2.29	0.60
1:G:188:THR:HA	1:G:425:MET:HE2	1.83	0.60
2:H:63:PRO:CD	2:H:87:PHE:HA	2.32	0.60
2:H:229:ARG:NH1	2:H:363:VAL:HG21	2.16	0.60
2:H:371:VAL:HG12	2:H:372:GLN:N	2.17	0.60
2:B:362:VAL:HG13	2:B:368:LEU:HB2	1.83	0.60
1:C:49:ILE:O	1:C:51:VAL:N	2.35	0.60
1:C:254:LYS:NZ	2:D:101:ASN:HD21	1.98	0.60
2:F:229:ARG:NH1	2:F:363:VAL:HG21	2.16	0.60
2:F:344:VAL:HG11	2:F:346:TRP:NE1	2.16	0.60
1:G:115:VAL:HG21	1:G:152:LEU:HD23	1.84	0.60
1:A:141:LEU:N	1:A:141:LEU:CD1	2.65	0.60
1:A:285:ALA:HB1	1:A:290:GLU:HG2	1.82	0.60
1:E:49:ILE:O	1:E:51:VAL:N	2.35	0.60
1:E:285:ALA:HB1	1:E:290:GLU:HG2	1.82	0.60
2:F:3:GLU:HG3	2:F:51:THR:HA	1.74	0.60
2:F:217:LEU:HD11	2:F:277:SER:HA	1.82	0.60
1:G:102:ASN:ND2	1:G:407:TRP:O	2.35	0.60
1:G:408:TYR:CG	1:G:418:PHE:HZ	2.20	0.60
2:H:167:LEU:HA	2:H:200:CYS:O	2.01	0.60
2:H:248:LEU:CD2	2:H:353:VAL:O	2.49	0.60
2:H:344:VAL:HG11	2:H:346:TRP:NE1	2.16	0.60
1:A:102:ASN:ND2	1:A:407:TRP:O	2.35	0.59
1:C:102:ASN:ND2	1:C:407:TRP:O	2.35	0.59
1:C:279:GLY:O	1:C:282:GLN:HB3	2.01	0.59
1:E:102:ASN:ND2	1:E:407:TRP:O	2.35	0.59
2:F:407:TRP:O	2:F:411:GLU:HG2	2.02	0.59
1:G:279:GLY:O	1:G:282:GLN:HB3	2.01	0.59
1:A:253:ARG:O	1:A:254:LYS:C	2.42	0.59
2:B:276:ILE:HD11	2:B:280:LYS:HD2	1.85	0.59
2:B:371:VAL:HG12	2:B:372:GLN:N	2.17	0.59
2:B:435:VAL:O	2:B:435:VAL:HG12	2.02	0.59
1:E:324:SER:O	1:E:328:VAL:HG23	2.02	0.59
1:G:285:ALA:HB1	1:G:290:GLU:HG2	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:324:SER:O	1:G:328:VAL:HG23	2.01	0.59
2:H:407:TRP:O	2:H:411:GLU:HG2	2.02	0.59
3:I:91:LEU:HD12	3:I:127:CYS:SG	2.42	0.59
2:B:57:GLY:HA3	2:B:58:ALA:HB2	0.66	0.59
1:C:30:ILE:HD13	1:C:53:TYR:CE2	2.38	0.59
2:D:63:PRO:CD	2:D:87:PHE:HA	2.32	0.59
1:E:408:TYR:CG	1:E:418:PHE:HZ	2.20	0.59
2:F:167:LEU:HA	2:F:200:CYS:O	2.01	0.59
2:F:324:VAL:CG1	1:G:221:THR:C	2.74	0.59
1:A:30:ILE:HD13	1:A:53:TYR:CE2	2.38	0.59
1:A:31:ASP:O	1:A:32:PRO:C	2.44	0.59
1:A:230:LEU:CD2	1:A:302:MET:HE2	2.32	0.59
2:B:344:VAL:HG11	2:B:346:TRP:NE1	2.16	0.59
1:C:114:LEU:HD23	1:C:149:MET:HE1	1.85	0.59
2:D:276:ILE:HD11	2:D:280:LYS:HD2	1.85	0.59
2:D:407:TRP:O	2:D:411:GLU:HG2	2.02	0.59
2:D:413:MET:O	2:D:414:GLU:HG3	2.02	0.59
1:E:30:ILE:HD13	1:E:53:TYR:CE2	2.38	0.59
1:E:114:LEU:HD23	1:E:149:MET:HE1	1.85	0.59
1:E:172:VAL:CG1	1:E:387:LEU:HD21	2.24	0.59
2:F:248:LEU:CD2	2:F:353:VAL:O	2.49	0.59
2:F:435:VAL:O	2:F:435:VAL:HG12	2.02	0.59
1:G:30:ILE:HD13	1:G:53:TYR:CE2	2.38	0.59
1:G:70:LEU:H	1:G:145:THR:CG2	2.10	0.59
2:H:217:LEU:HD11	2:H:277:SER:HA	1.82	0.59
2:H:435:VAL:HG12	2:H:435:VAL:O	2.02	0.59
2:D:371:VAL:HG12	2:D:372:GLN:N	2.17	0.59
2:D:435:VAL:O	2:D:435:VAL:HG12	2.02	0.59
1:E:19:LYS:CG	1:E:228:ASN:HB3	2.31	0.59
1:E:70:LEU:H	1:E:145:THR:CG2	2.10	0.59
1:E:205:ASP:OD1	1:E:304:ALA:CB	2.50	0.59
2:F:369:ALA:O	2:F:370:LYS:HB3	2.03	0.59
1:G:172:VAL:CG1	1:G:387:LEU:HD21	2.24	0.59
1:G:230:LEU:CD2	1:G:302:MET:HE2	2.31	0.59
1:G:273:ALA:HB3	1:G:274:PRO:CD	2.29	0.59
3:I:72:VAL:HG13	3:I:83:LEU:HD13	1.84	0.59
1:A:114:LEU:HD23	1:A:149:MET:HE1	1.85	0.59
1:A:205:ASP:OD1	1:A:304:ALA:CB	2.50	0.59
2:B:369:ALA:O	2:B:370:LYS:HB3	2.03	0.59
1:C:19:LYS:CG	1:C:228:ASN:HB3	2.31	0.59
1:C:408:TYR:CG	1:C:418:PHE:HZ	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:296:PHE:CE1	2:D:335:ILE:CG2	2.73	0.59
2:D:339:ARG:C	2:D:341:ILE:H	2.11	0.59
2:D:369:ALA:O	2:D:370:LYS:HB3	2.03	0.59
1:E:279:GLY:O	1:E:282:GLN:HB3	2.01	0.59
2:H:369:ALA:O	2:H:370:LYS:HB3	2.03	0.59
1:A:324:SER:O	1:A:328:VAL:HG23	2.01	0.59
1:A:408:TYR:CG	1:A:418:PHE:HZ	2.20	0.59
1:C:205:ASP:OD1	1:C:304:ALA:CB	2.50	0.59
1:C:324:SER:O	1:C:328:VAL:HG23	2.01	0.59
1:G:19:LYS:CG	1:G:228:ASN:HB3	2.31	0.59
1:G:114:LEU:HD23	1:G:149:MET:HE1	1.85	0.59
1:G:254:LYS:HE3	1:G:352:LYS:CE	2.27	0.59
2:H:115:ILE:O	2:H:115:ILE:HD13	2.02	0.59
1:A:279:GLY:O	1:A:282:GLN:HB3	2.01	0.59
2:B:339:ARG:C	2:B:341:ILE:H	2.11	0.59
2:D:115:ILE:O	2:D:115:ILE:HD13	2.02	0.59
2:D:167:LEU:HA	2:D:200:CYS:O	2.01	0.59
1:E:230:LEU:CD2	1:E:302:MET:HE2	2.31	0.59
2:F:115:ILE:O	2:F:115:ILE:HD13	2.02	0.59
2:H:276:ILE:HD11	2:H:280:LYS:HD2	1.85	0.59
2:B:167:LEU:HA	2:B:200:CYS:O	2.01	0.59
2:B:234:ILE:HB	2:B:302:MET:HE1	1.85	0.59
2:B:407:TRP:O	2:B:411:GLU:HG2	2.02	0.59
1:C:194:LEU:C	1:C:196:GLU:H	2.11	0.59
2:D:234:ILE:HB	2:D:302:MET:HE1	1.85	0.59
2:F:276:ILE:HD11	2:F:280:LYS:HD2	1.85	0.59
2:F:413:MET:O	2:F:414:GLU:HG3	2.02	0.59
1:G:324:SER:CB	1:G:327:GLU:HG2	2.30	0.59
2:H:3:GLU:HG3	2:H:51:THR:HA	1.75	0.59
2:H:413:MET:O	2:H:414:GLU:HG3	2.02	0.59
2:B:61:HIS:C	2:B:62:VAL:HG23	2.28	0.59
2:B:413:MET:O	2:B:414:GLU:HG3	2.02	0.59
1:C:151:THR:OG1	1:C:193:GLN:HB3	2.03	0.59
2:D:119:LEU:O	2:D:122:ILE:HG12	2.02	0.59
1:E:141:LEU:CD1	1:E:141:LEU:N	2.65	0.59
2:F:339:ARG:C	2:F:341:ILE:H	2.11	0.59
2:H:115:ILE:HD13	2:H:115:ILE:C	2.28	0.59
3:I:113:ILE:HD12	3:I:118:GLU:HB3	1.85	0.59
1:A:19:LYS:CG	1:A:228:ASN:HB3	2.31	0.58
1:A:324:SER:C	1:A:326:LYS:N	2.59	0.58
2:B:3:GLU:HG3	2:B:51:THR:HA	1.75	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:349:ASN:O	2:D:181:VAL:HG13	2.03	0.58
2:D:6:SER:HA	2:D:136:SER:O	2.03	0.58
2:F:115:ILE:HD13	2:F:115:ILE:C	2.28	0.58
1:G:2:ARG:NH2	2:H:99:ALA:H	2.00	0.58
1:G:31:ASP:O	1:G:32:PRO:C	2.44	0.58
1:G:68:VAL:CG1	1:G:149:MET:SD	2.90	0.58
1:G:141:LEU:N	1:G:141:LEU:CD1	2.65	0.58
1:G:205:ASP:OD1	1:G:304:ALA:CB	2.50	0.58
2:H:202:PHE:CE2	2:H:378:LEU:HD22	2.38	0.58
1:A:151:THR:OG1	1:A:193:GLN:HB3	2.03	0.58
1:A:194:LEU:C	1:A:196:GLU:H	2.11	0.58
1:A:307:PRO:HB3	1:A:312:TYR:OH	2.04	0.58
2:B:115:ILE:HD13	2:B:115:ILE:C	2.28	0.58
1:C:68:VAL:CG1	1:C:149:MET:SD	2.90	0.58
1:C:254:LYS:NZ	2:D:101:ASN:OD1	2.26	0.58
1:E:31:ASP:O	1:E:32:PRO:C	2.44	0.58
2:F:6:SER:HA	2:F:136:SER:O	2.03	0.58
2:F:202:PHE:CE2	2:F:378:LEU:HD22	2.38	0.58
2:H:339:ARG:C	2:H:341:ILE:H	2.11	0.58
3:I:100:GLY:O	3:I:101:VAL:HG23	2.02	0.58
1:A:88:ARG:CZ	1:E:283:TYR:HE1	2.16	0.58
1:A:89:PRO:HA	1:A:92:PHE:CD1	2.38	0.58
1:A:229:HIS:C	1:A:229:HIS:ND1	2.62	0.58
2:B:6:SER:HA	2:B:136:SER:O	2.03	0.58
2:B:119:LEU:O	2:B:122:ILE:HG12	2.02	0.58
2:B:202:PHE:CE2	2:B:378:LEU:HD22	2.38	0.58
2:B:317:LEU:HD11	2:B:351:PHE:CE2	2.38	0.58
1:C:307:PRO:HB3	1:C:312:TYR:OH	2.04	0.58
1:C:325:MET:HG2	2:D:224:TYR:CD1	2.37	0.58
2:D:317:LEU:HD11	2:D:351:PHE:CE2	2.38	0.58
1:E:89:PRO:HA	1:E:92:PHE:CD1	2.38	0.58
1:E:194:LEU:C	1:E:196:GLU:H	2.11	0.58
1:E:324:SER:CB	1:E:327:GLU:HG2	2.30	0.58
2:F:215:ARG:C	2:F:216:ASN:HD22	2.12	0.58
2:F:326:LYS:HB3	1:G:222:PRO:CD	2.33	0.58
1:G:151:THR:OG1	1:G:193:GLN:HB3	2.03	0.58
1:G:194:LEU:C	1:G:196:GLU:H	2.11	0.58
2:B:5:ILE:HD11	2:B:64:ARG:HH12	1.59	0.58
2:B:115:ILE:HD13	2:B:115:ILE:O	2.02	0.58
2:D:202:PHE:CE2	2:D:378:LEU:HD22	2.38	0.58
2:F:2:ARG:N	2:F:131:GLY:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:119:LEU:O	2:F:122:ILE:HG12	2.02	0.58
1:G:258:ASN:ND2	1:G:352:LYS:CE	2.55	0.58
2:H:215:ARG:C	2:H:216:ASN:HD22	2.12	0.58
1:A:319:PHE:HA	1:A:375:ALA:HA	1.86	0.58
1:C:89:PRO:HA	1:C:92:PHE:CD1	2.38	0.58
2:D:115:ILE:HD13	2:D:115:ILE:C	2.28	0.58
2:D:215:ARG:C	2:D:216:ASN:HD22	2.12	0.58
2:D:264:ARG:HB2	2:D:266:HIS:HD2	1.67	0.58
1:E:198:THR:HG22	1:E:265:LEU:HD22	1.86	0.58
2:F:67:PHE:CZ	2:F:87:PHE:CE1	2.92	0.58
2:F:264:ARG:C	2:F:266:HIS:N	2.60	0.58
1:G:253:ARG:O	1:G:257:VAL:N	2.33	0.58
1:C:229:HIS:ND1	1:C:229:HIS:C	2.62	0.58
1:C:319:PHE:HA	1:C:375:ALA:HA	1.86	0.58
2:D:5:ILE:HD12	2:D:64:ARG:HH12	1.69	0.58
1:E:68:VAL:CG1	1:E:149:MET:SD	2.90	0.58
1:E:151:THR:OG1	1:E:193:GLN:HB3	2.03	0.58
1:G:273:ALA:CB	1:G:274:PRO:HD3	2.30	0.58
2:H:2:ARG:N	2:H:131:GLY:O	2.36	0.58
2:H:6:SER:HA	2:H:136:SER:O	2.03	0.58
2:H:67:PHE:CZ	2:H:87:PHE:CE1	2.92	0.58
2:B:51:THR:O	2:B:52:PHE:CD1	2.57	0.58
2:B:218:ASP:O	2:B:219:ILE:HG23	2.04	0.58
1:C:324:SER:C	1:C:326:LYS:N	2.59	0.58
2:D:2:ARG:N	2:D:131:GLY:O	2.36	0.58
2:D:67:PHE:CZ	2:D:87:PHE:CE1	2.92	0.58
1:E:229:HIS:C	1:E:229:HIS:ND1	2.62	0.58
2:F:5:ILE:HD12	2:F:64:ARG:HH12	1.68	0.58
2:F:30:ILE:HD13	2:F:61:HIS:CG	2.38	0.58
2:F:234:ILE:HB	2:F:302:MET:HE1	1.85	0.58
2:F:293:ASN:HD21	2:F:338:LYS:HZ1	1.51	0.58
1:G:89:PRO:HA	1:G:92:PHE:CD1	2.38	0.58
1:A:128:SER:OG	1:A:129:CYS:N	2.34	0.58
2:B:67:PHE:CZ	2:B:87:PHE:CE1	2.92	0.58
1:C:183:GLU:HB3	1:C:184:PRO:CD	2.33	0.58
2:D:150:THR:O	2:D:151:SER:C	2.47	0.58
1:G:229:HIS:C	1:G:229:HIS:ND1	2.62	0.58
2:H:5:ILE:HD12	2:H:64:ARG:HH12	1.69	0.58
2:H:119:LEU:O	2:H:122:ILE:HG12	2.02	0.58
2:H:268:PRO:HA	2:H:379:SER:O	2.04	0.58
2:B:215:ARG:C	2:B:216:ASN:HD22	2.12	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:299:LYS:O	1:C:300:ASN:CB	2.51	0.58
2:D:110:ILE:CG2	2:D:111:GLY:H	2.15	0.58
2:D:218:ASP:O	2:D:219:ILE:HG23	2.04	0.58
2:F:218:ASP:O	2:F:219:ILE:HG23	2.04	0.58
2:F:268:PRO:HA	2:F:379:SER:O	2.04	0.58
1:G:198:THR:HG22	1:G:265:LEU:HD22	1.86	0.58
2:H:218:ASP:O	2:H:219:ILE:HG23	2.04	0.58
2:H:264:ARG:C	2:H:266:HIS:N	2.60	0.58
2:H:317:LEU:HD11	2:H:351:PHE:CE2	2.38	0.58
1:A:68:VAL:CG1	1:A:149:MET:SD	2.90	0.58
1:A:226:ASP:O	1:A:227:LEU:C	2.46	0.58
2:B:63:PRO:HG3	2:B:87:PHE:CB	2.34	0.58
2:B:150:THR:O	2:B:151:SER:C	2.47	0.58
2:B:159:VAL:HG13	3:I:78:ARG:CG	2.33	0.58
2:B:165:SER:HA	2:B:199:ASP:OD2	2.04	0.58
2:B:260:VAL:HG22	1:C:407:TRP:HE1	1.68	0.58
2:D:268:PRO:HA	2:D:379:SER:O	2.04	0.58
1:E:226:ASP:O	1:E:227:LEU:C	2.46	0.58
1:E:274:PRO:CG	1:E:371:LEU:HD21	2.34	0.58
1:E:307:PRO:HB3	1:E:312:TYR:OH	2.04	0.58
2:F:317:LEU:HD11	2:F:351:PHE:CE2	2.38	0.58
1:G:307:PRO:HB3	1:G:312:TYR:OH	2.04	0.58
2:H:234:ILE:HB	2:H:302:MET:HE1	1.85	0.58
2:B:248:LEU:CD2	2:B:353:VAL:O	2.49	0.57
1:C:422:GLU:O	1:C:426:ASN:N	2.37	0.57
1:E:54:ASN:ND2	1:E:64:ARG:HD3	2.15	0.57
1:E:253:ARG:O	1:E:257:VAL:N	2.33	0.57
1:G:226:ASP:O	1:G:227:LEU:C	2.46	0.57
1:G:274:PRO:CG	1:G:371:LEU:HD21	2.34	0.57
1:A:5:VAL:CG2	1:A:135:PHE:HD2	2.18	0.57
1:A:274:PRO:CG	1:A:371:LEU:HD21	2.34	0.57
1:A:299:LYS:O	1:A:300:ASN:CB	2.51	0.57
2:B:345:ASP:O	2:B:347:CYS:N	2.37	0.57
1:C:274:PRO:CG	1:C:371:LEU:HD21	2.34	0.57
1:C:301:MET:CE	1:C:377:PHE:HE2	2.17	0.57
2:F:196:GLU:C	2:F:197:HIS:CD2	2.82	0.57
1:G:5:VAL:CG2	1:G:135:PHE:HD2	2.18	0.57
1:G:149:MET:O	1:G:153:LEU:HD13	2.05	0.57
2:H:150:THR:O	2:H:151:SER:C	2.47	0.57
2:H:196:GLU:C	2:H:197:HIS:CD2	2.82	0.57
3:I:55:VAL:HG21	3:I:57:PHE:CZ	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:GLU:HB3	1:A:184:PRO:CD	2.33	0.57
1:A:198:THR:HG22	1:A:265:LEU:HD22	1.85	0.57
2:B:313:MET:O	2:B:314:ALA:HB2	2.04	0.57
1:C:128:SER:OG	1:C:129:CYS:N	2.34	0.57
1:C:149:MET:O	1:C:153:LEU:HD13	2.05	0.57
1:C:180:THR:CG2	1:C:181:VAL:H	2.17	0.57
2:D:196:GLU:C	2:D:197:HIS:CD2	2.82	0.57
1:E:5:VAL:CG2	1:E:135:PHE:HD2	2.18	0.57
2:F:165:SER:HA	2:F:199:ASP:OD2	2.04	0.57
2:F:166:LYS:HD2	2:F:197:HIS:O	2.04	0.57
2:H:165:SER:HA	2:H:199:ASP:OD2	2.04	0.57
2:H:345:ASP:O	2:H:347:CYS:N	2.37	0.57
1:A:301:MET:CE	1:A:377:PHE:HE2	2.17	0.57
2:B:2:ARG:N	2:B:131:GLY:O	2.36	0.57
2:B:110:ILE:CG2	2:B:111:GLY:H	2.15	0.57
1:C:5:VAL:CG2	1:C:135:PHE:HD2	2.18	0.57
1:C:6:HIS:HB3	1:C:65:ALA:HB2	1.87	0.57
1:C:254:LYS:NZ	2:D:101:ASN:CG	2.62	0.57
2:D:165:SER:HA	2:D:199:ASP:OD2	2.04	0.57
2:D:345:ASP:O	2:D:347:CYS:N	2.37	0.57
1:E:273:ALA:CB	1:E:274:PRO:HD3	2.30	0.57
1:E:320:ARG:O	1:E:359:PRO:HA	2.04	0.57
1:G:324:SER:C	1:G:326:LYS:N	2.59	0.57
1:G:424:ASN:C	1:G:424:ASN:ND2	2.61	0.57
1:A:180:THR:CG2	1:A:181:VAL:H	2.17	0.57
1:A:320:ARG:O	1:A:359:PRO:HA	2.04	0.57
1:A:424:ASN:C	1:A:424:ASN:ND2	2.61	0.57
2:B:196:GLU:C	2:B:197:HIS:CD2	2.82	0.57
2:B:216:ASN:O	2:B:217:LEU:HB2	2.05	0.57
1:C:424:ASN:C	1:C:424:ASN:ND2	2.61	0.57
1:E:149:MET:O	1:E:153:LEU:HD13	2.05	0.57
1:E:301:MET:CE	1:E:377:PHE:HE2	2.17	0.57
2:F:345:ASP:O	2:F:347:CYS:N	2.37	0.57
1:G:301:MET:CE	1:G:377:PHE:HE2	2.17	0.57
1:A:149:MET:O	1:A:153:LEU:HD13	2.05	0.57
1:A:209:LEU:O	1:A:210:TYR:C	2.48	0.57
2:B:117:LEU:HD11	2:B:121:ARG:HH22	1.69	0.57
2:B:264:ARG:HB2	2:B:266:HIS:HD2	1.67	0.57
2:B:268:PRO:HA	2:B:379:SER:O	2.04	0.57
1:C:270:PRO:HA	1:C:377:PHE:O	2.04	0.57
2:D:152:LEU:HA	2:D:155:GLU:CB	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:216:ASN:O	2:D:217:LEU:HB2	2.05	0.57
1:E:6:HIS:HB3	1:E:65:ALA:HB2	1.87	0.57
1:G:6:HIS:HB3	1:G:65:ALA:HB2	1.87	0.57
1:G:299:LYS:O	1:G:300:ASN:CB	2.51	0.57
1:G:320:ARG:O	1:G:359:PRO:HA	2.04	0.57
1:A:6:HIS:HB3	1:A:65:ALA:HB2	1.87	0.57
1:A:70:LEU:CD1	1:A:145:THR:HG23	2.35	0.57
2:B:152:LEU:HA	2:B:155:GLU:CB	2.35	0.57
2:B:209:ILE:CG2	2:B:227:LEU:HD22	2.35	0.57
2:B:264:ARG:C	2:B:266:HIS:N	2.60	0.57
1:C:30:ILE:HA	1:C:35:SER:O	2.04	0.57
1:C:198:THR:HG22	1:C:265:LEU:HD22	1.86	0.57
1:C:209:LEU:O	1:C:210:TYR:C	2.48	0.57
1:C:319:PHE:CD2	1:C:375:ALA:HB2	2.40	0.57
2:D:313:MET:O	2:D:314:ALA:HB2	2.04	0.57
1:E:70:LEU:CD1	1:E:145:THR:HG23	2.35	0.57
1:E:209:LEU:O	1:E:210:TYR:C	2.48	0.57
2:F:117:LEU:HD11	2:F:121:ARG:HH22	1.69	0.57
2:F:152:LEU:HA	2:F:155:GLU:CB	2.35	0.57
1:G:270:PRO:HA	1:G:377:PHE:O	2.04	0.57
1:G:319:PHE:HA	1:G:375:ALA:HA	1.86	0.57
2:H:152:LEU:HA	2:H:155:GLU:CB	2.35	0.57
2:H:166:LYS:HD2	2:H:197:HIS:O	2.04	0.57
2:H:362:VAL:CG1	2:H:368:LEU:HB2	2.35	0.57
2:B:278:ALA:O	2:B:279:GLU:CB	2.43	0.57
2:B:349:THR:O	1:C:181:VAL:HG13	2.05	0.57
1:C:226:ASP:O	1:C:227:LEU:C	2.46	0.57
2:D:63:PRO:HG2	2:D:87:PHE:HA	1.86	0.57
2:D:117:LEU:HD11	2:D:121:ARG:HH22	1.69	0.57
2:D:209:ILE:CG2	2:D:227:LEU:HD22	2.35	0.57
1:E:14:ASN:OD1	1:E:75:MET:HG2	2.05	0.57
1:E:183:GLU:HB3	1:E:184:PRO:CD	2.33	0.57
1:G:54:ASN:ND2	1:G:64:ARG:HD3	2.15	0.57
1:G:70:LEU:CD1	1:G:145:THR:HG23	2.35	0.57
1:G:345:GLU:C	1:G:347:ILE:H	2.13	0.57
2:H:209:ILE:CG2	2:H:227:LEU:HD22	2.35	0.57
1:A:319:PHE:CD2	1:A:375:ALA:HB2	2.40	0.57
1:C:70:LEU:CD1	1:C:145:THR:HG23	2.35	0.57
1:C:320:ARG:O	1:C:359:PRO:HA	2.04	0.57
2:D:139:HIS:CE1	2:D:170:SER:HB3	2.40	0.57
1:E:180:THR:CG2	1:E:181:VAL:H	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:270:PRO:HA	1:E:377:PHE:O	2.04	0.57
1:E:345:GLU:C	1:E:347:ILE:H	2.13	0.57
2:F:209:ILE:CG2	2:F:227:LEU:HD22	2.35	0.57
2:F:216:ASN:O	2:F:217:LEU:HB2	2.05	0.57
2:F:276:ILE:CG2	2:F:369:ALA:HB2	2.26	0.57
2:F:329:ASN:HB3	1:G:210:TYR:CZ	2.35	0.57
1:G:2:ARG:HH21	2:H:99:ALA:H	1.50	0.57
2:H:293:ASN:HD21	2:H:338:LYS:HZ1	1.52	0.57
1:A:30:ILE:HA	1:A:35:SER:O	2.04	0.57
1:A:270:PRO:HA	1:A:377:PHE:O	2.04	0.57
2:B:139:HIS:CE1	2:B:170:SER:HB3	2.40	0.57
2:B:166:LYS:HD2	2:B:197:HIS:O	2.04	0.57
2:D:210:TYR:CE2	2:D:227:LEU:HD11	2.40	0.57
2:F:139:HIS:CE1	2:F:170:SER:HB3	2.40	0.57
2:F:175:PRO:HG3	2:F:304:LYS:CG	2.35	0.57
2:F:362:VAL:CG1	2:F:368:LEU:HB2	2.35	0.57
1:G:257:VAL:O	2:H:404:PHE:HD2	1.88	0.57
1:G:319:PHE:CD2	1:G:375:ALA:HB2	2.40	0.57
2:H:63:PRO:HG2	2:H:87:PHE:HA	1.86	0.57
2:H:117:LEU:HD11	2:H:121:ARG:HH22	1.69	0.57
2:H:175:PRO:HG3	2:H:304:LYS:CG	2.35	0.57
2:H:216:ASN:O	2:H:217:LEU:HB2	2.05	0.57
1:A:50:ASN:O	1:A:64:ARG:NH2	2.38	0.56
1:C:50:ASN:O	1:C:64:ARG:NH2	2.38	0.56
1:C:248:LEU:CD2	2:D:179:THR:CG2	2.82	0.56
1:C:345:GLU:C	1:C:347:ILE:H	2.13	0.56
2:D:166:LYS:HD2	2:D:197:HIS:O	2.04	0.56
1:E:50:ASN:O	1:E:64:ARG:NH2	2.38	0.56
1:E:299:LYS:O	1:E:300:ASN:CB	2.51	0.56
1:E:319:PHE:HA	1:E:375:ALA:HA	1.86	0.56
1:E:424:ASN:C	1:E:424:ASN:ND2	2.61	0.56
1:G:4:ILE:HD13	1:G:136:GLN:NE2	2.18	0.56
1:G:180:THR:CG2	1:G:181:VAL:H	2.17	0.56
2:H:102:ASN:ND2	2:H:407:TRP:NE1	2.52	0.56
1:A:345:GLU:C	1:A:347:ILE:H	2.13	0.56
2:B:210:TYR:CE2	2:B:227:LEU:HD11	2.40	0.56
2:B:362:VAL:CG1	2:B:368:LEU:HB2	2.35	0.56
2:D:362:VAL:CG1	2:D:368:LEU:HB2	2.35	0.56
1:E:251:ASP:O	1:E:252:LEU:C	2.49	0.56
1:E:319:PHE:CD2	1:E:375:ALA:HB2	2.40	0.56
2:F:63:PRO:HG2	2:F:87:PHE:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:183:GLU:HB3	1:G:184:PRO:CD	2.33	0.56
1:G:209:LEU:O	1:G:210:TYR:C	2.48	0.56
1:G:245:PRO:HG3	2:H:73:THR:HG23	1.87	0.56
2:H:276:ILE:CG2	2:H:369:ALA:HB2	2.26	0.56
2:B:239:THR:O	2:B:240:ALA:C	2.48	0.56
2:B:362:VAL:HG11	2:B:368:LEU:O	2.04	0.56
2:B:382:THR:O	2:B:382:THR:HG22	2.05	0.56
2:D:276:ILE:O	2:D:369:ALA:CB	2.53	0.56
2:F:210:TYR:CE2	2:F:227:LEU:HD11	2.40	0.56
2:F:239:THR:O	2:F:240:ALA:C	2.48	0.56
2:F:362:VAL:HG11	2:F:368:LEU:O	2.04	0.56
1:G:14:ASN:OD1	1:G:75:MET:HG2	2.05	0.56
1:G:30:ILE:HA	1:G:35:SER:O	2.04	0.56
1:G:50:ASN:O	1:G:64:ARG:NH2	2.38	0.56
1:G:251:ASP:O	1:G:252:LEU:C	2.49	0.56
2:H:139:HIS:CE1	2:H:170:SER:HB3	2.40	0.56
2:H:210:TYR:CE2	2:H:227:LEU:HD11	2.40	0.56
2:H:239:THR:O	2:H:240:ALA:C	2.48	0.56
1:A:216:THR:O	1:A:217:LEU:HD12	2.05	0.56
1:C:223:THR:HG22	1:C:224:TYR:N	2.21	0.56
1:E:4:ILE:HD13	1:E:136:GLN:NE2	2.18	0.56
1:E:223:THR:HG22	1:E:224:TYR:N	2.21	0.56
1:G:108:TYR:CE1	1:G:413:MET:HE1	2.40	0.56
1:G:223:THR:HG22	1:G:224:TYR:N	2.21	0.56
2:H:313:MET:O	2:H:314:ALA:HB2	2.04	0.56
2:H:362:VAL:HG11	2:H:368:LEU:O	2.04	0.56
1:A:108:TYR:CE1	1:A:413:MET:HE1	2.40	0.56
1:C:132:LEU:CD2	1:C:164:ARG:HG3	2.32	0.56
1:C:250:ALA:CA	1:C:254:LYS:HE2	2.35	0.56
2:D:239:THR:O	2:D:240:ALA:C	2.48	0.56
2:D:362:VAL:HG11	2:D:368:LEU:O	2.04	0.56
1:E:312:TYR:O	1:E:344:VAL:HB	2.05	0.56
2:F:150:THR:O	2:F:151:SER:C	2.47	0.56
1:A:223:THR:HG22	1:A:224:TYR:N	2.21	0.56
1:A:311:ARG:HG2	1:A:311:ARG:HH11	1.71	0.56
2:B:56:THR:CB	2:F:284:GLU:HG3	2.35	0.56
1:C:216:THR:O	1:C:217:LEU:HD12	2.05	0.56
1:C:311:ARG:HG2	1:C:311:ARG:HH11	1.71	0.56
2:D:382:THR:O	2:D:382:THR:HG22	2.05	0.56
1:E:30:ILE:HA	1:E:35:SER:O	2.05	0.56
1:E:108:TYR:CE1	1:E:413:MET:HE1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:313:MET:O	2:F:314:ALA:HB2	2.04	0.56
2:F:382:THR:HG22	2:F:382:THR:O	2.06	0.56
1:G:312:TYR:O	1:G:344:VAL:HB	2.05	0.56
1:A:132:LEU:CD2	1:A:164:ARG:HG3	2.32	0.56
1:A:151:THR:OG1	1:A:193:GLN:CB	2.54	0.56
2:B:19:ALA:CB	2:B:228:ASN:HB3	2.35	0.56
1:C:19:LYS:O	1:C:23:VAL:HG23	2.06	0.56
1:C:108:TYR:CE1	1:C:413:MET:HE1	2.40	0.56
1:C:312:TYR:O	1:C:344:VAL:HB	2.05	0.56
1:E:311:ARG:HD2	1:E:344:VAL:H	1.71	0.56
2:H:382:THR:O	2:H:382:THR:HG22	2.06	0.56
1:A:251:ASP:O	1:A:252:LEU:C	2.49	0.56
1:A:297:ASP:OD1	1:A:298:ALA:N	2.39	0.56
2:B:277:SER:O	2:B:280:LYS:HB2	2.06	0.56
1:C:151:THR:OG1	1:C:193:GLN:CB	2.54	0.56
1:C:251:ASP:O	1:C:252:LEU:C	2.49	0.56
2:D:175:PRO:HG3	2:D:304:LYS:CG	2.35	0.56
2:D:253:THR:O	2:D:256:GLN:HG2	2.06	0.56
1:E:19:LYS:O	1:E:23:VAL:HG23	2.06	0.56
1:E:311:ARG:HG2	1:E:311:ARG:HH11	1.71	0.56
2:F:172:TYR:OH	2:F:387:ALA:O	2.24	0.56
2:F:331:ALA:O	2:F:334:THR:HG22	2.05	0.56
1:G:139:HIS:HE1	1:G:168:THR:HG23	1.71	0.56
1:A:139:HIS:HE1	1:A:168:THR:HG23	1.71	0.56
1:A:250:ALA:CA	1:A:254:LYS:HE2	2.35	0.56
1:C:14:ASN:OD1	1:C:75:MET:HG2	2.05	0.56
1:C:165:ILE:HD13	1:C:165:ILE:H	1.71	0.56
1:E:139:HIS:HE1	1:E:168:THR:HG23	1.71	0.56
1:E:204:ILE:HG21	1:E:231:VAL:CG2	2.36	0.56
2:F:253:THR:O	2:F:256:GLN:HG2	2.06	0.56
1:G:19:LYS:O	1:G:23:VAL:HG23	2.06	0.56
1:G:216:THR:O	1:G:217:LEU:HD12	2.05	0.56
1:G:311:ARG:HG2	1:G:311:ARG:HH11	1.71	0.56
1:G:311:ARG:HD2	1:G:344:VAL:H	1.71	0.56
2:H:16:ILE:HD12	2:H:171:ILE:HD11	1.87	0.56
2:H:276:ILE:O	2:H:369:ALA:CB	2.53	0.56
1:A:19:LYS:O	1:A:23:VAL:HG23	2.06	0.56
1:A:311:ARG:HD2	1:A:344:VAL:H	1.71	0.56
2:B:175:PRO:HG3	2:B:304:LYS:CG	2.35	0.56
2:B:276:ILE:O	2:B:369:ALA:CB	2.53	0.56
2:B:329:ASN:HB3	1:C:210:TYR:HE1	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:408:TYR:CD1	2:B:418:PHE:HZ	2.24	0.56
1:C:139:HIS:HE1	1:C:168:THR:HG23	1.71	0.56
1:C:272:PHE:HB3	1:C:275:LEU:HD22	1.88	0.56
2:D:19:ALA:CB	2:D:228:ASN:HB3	2.35	0.56
2:D:388:TRP:CE3	2:D:388:TRP:HA	2.41	0.56
1:E:182:VAL:HG23	1:E:186:ASN:ND2	2.20	0.56
2:F:305:CYS:O	2:F:306:ASP:C	2.49	0.56
1:G:191:VAL:HA	1:G:194:LEU:HD12	1.88	0.56
1:G:352:LYS:HD2	2:H:181:VAL:CG2	2.11	0.56
2:H:305:CYS:O	2:H:306:ASP:C	2.49	0.56
1:A:182:VAL:HG23	1:A:186:ASN:ND2	2.20	0.55
1:C:182:VAL:HG23	1:C:186:ASN:ND2	2.20	0.55
1:C:297:ASP:OD1	1:C:298:ALA:N	2.39	0.55
1:C:311:ARG:HD2	1:C:344:VAL:H	1.71	0.55
2:F:5:ILE:HG22	2:F:135:PHE:CD2	2.40	0.55
2:F:276:ILE:O	2:F:369:ALA:CB	2.52	0.55
1:G:2:ARG:NH2	2:H:99:ALA:N	2.54	0.55
1:G:151:THR:OG1	1:G:193:GLN:CB	2.54	0.55
1:G:204:ILE:HG21	1:G:231:VAL:CG2	2.36	0.55
2:H:253:THR:O	2:H:256:GLN:HG2	2.06	0.55
2:H:277:SER:O	2:H:280:LYS:HB2	2.06	0.55
2:H:331:ALA:O	2:H:334:THR:HG22	2.05	0.55
1:A:190:SER:O	1:A:194:LEU:HG	2.06	0.55
1:A:204:ILE:HG21	1:A:231:VAL:CG2	2.36	0.55
1:A:312:TYR:O	1:A:344:VAL:HB	2.05	0.55
2:B:388:TRP:CE3	2:B:388:TRP:HA	2.41	0.55
1:E:191:VAL:HA	1:E:194:LEU:HD12	1.88	0.55
1:G:182:VAL:HG23	1:G:186:ASN:ND2	2.20	0.55
2:H:19:ALA:CB	2:H:228:ASN:HB3	2.35	0.55
2:H:30:ILE:HG23	2:H:34:GLY:O	2.07	0.55
1:A:14:ASN:OD1	1:A:75:MET:HG2	2.05	0.55
1:A:272:PHE:HB3	1:A:275:LEU:HD22	1.88	0.55
2:B:63:PRO:CG	2:B:91:GLN:CD	2.71	0.55
1:C:191:VAL:HA	1:C:194:LEU:HD12	1.88	0.55
2:D:278:ALA:O	2:D:279:GLU:CB	2.43	0.55
1:E:49:ILE:O	1:E:50:ASN:C	2.48	0.55
1:E:216:THR:O	1:E:217:LEU:HD12	2.05	0.55
2:F:16:ILE:HD12	2:F:171:ILE:HD11	1.88	0.55
2:F:260:VAL:CG2	1:G:407:TRP:HE1	2.20	0.55
2:F:277:SER:O	2:F:280:LYS:HB2	2.06	0.55
2:H:5:ILE:HG22	2:H:135:PHE:CD2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:150:THR:O	2:H:153:LEU:N	2.40	0.55
2:H:264:ARG:HB2	2:H:266:HIS:HD2	1.67	0.55
3:I:113:ILE:HG23	3:I:118:GLU:HB2	1.88	0.55
1:A:49:ILE:O	1:A:50:ASN:C	2.48	0.55
1:A:165:ILE:H	1:A:165:ILE:HD13	1.71	0.55
2:B:209:ILE:HG22	2:B:227:LEU:HD22	1.88	0.55
2:B:253:THR:O	2:B:256:GLN:HG2	2.06	0.55
2:B:276:ILE:CG2	2:B:369:ALA:HB2	2.26	0.55
2:B:331:ALA:O	2:B:334:THR:HG22	2.05	0.55
2:B:346:TRP:HB3	1:C:401:ARG:CG	2.36	0.55
1:C:310:GLY:CA	1:C:436:GLN:HE21	2.19	0.55
2:D:5:ILE:HG22	2:D:135:PHE:CD2	2.40	0.55
2:D:244:PHE:C	2:D:244:PHE:CD2	2.84	0.55
2:D:305:CYS:O	2:D:306:ASP:C	2.49	0.55
2:D:331:ALA:O	2:D:334:THR:HG22	2.05	0.55
1:E:132:LEU:CD2	1:E:164:ARG:HG3	2.32	0.55
2:F:30:ILE:HG23	2:F:34:GLY:O	2.07	0.55
2:F:150:THR:O	2:F:153:LEU:N	2.40	0.55
1:G:119:LEU:O	1:G:123:ARG:HG3	2.06	0.55
1:G:239:THR:HG22	1:G:240:THR:N	2.22	0.55
2:B:150:THR:O	2:B:153:LEU:N	2.40	0.55
2:B:260:VAL:HG22	1:C:407:TRP:NE1	2.22	0.55
1:C:204:ILE:HG21	1:C:231:VAL:CG2	2.36	0.55
2:D:150:THR:O	2:D:153:LEU:N	2.40	0.55
2:D:277:SER:O	2:D:280:LYS:HB2	2.06	0.55
1:E:369:ARG:HD2	1:E:369:ARG:C	2.32	0.55
2:H:209:ILE:HG22	2:H:227:LEU:HD22	1.88	0.55
1:A:191:VAL:HA	1:A:194:LEU:HD12	1.88	0.55
1:A:310:GLY:CA	1:A:436:GLN:HE21	2.19	0.55
1:C:298:ALA:O	1:C:299:LYS:C	2.50	0.55
2:D:209:ILE:HG22	2:D:227:LEU:HD22	1.88	0.55
1:E:151:THR:OG1	1:E:193:GLN:CB	2.54	0.55
1:E:239:THR:HG22	1:E:240:THR:N	2.22	0.55
1:E:272:PHE:HB3	1:E:275:LEU:HD22	1.88	0.55
1:E:310:GLY:CA	1:E:436:GLN:HE21	2.19	0.55
2:F:19:ALA:CB	2:F:228:ASN:HB3	2.35	0.55
2:F:349:THR:HG21	1:G:178:SER:O	2.05	0.55
1:G:49:ILE:O	1:G:50:ASN:C	2.48	0.55
1:A:210:TYR:HD2	1:A:227:LEU:HD21	1.71	0.55
2:B:5:ILE:CG2	2:B:6:SER:N	2.70	0.55
1:C:49:ILE:O	1:C:50:ASN:C	2.48	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:SER:O	1:C:194:LEU:HG	2.06	0.55
2:F:6:SER:O	2:F:65:ALA:HB1	2.07	0.55
2:F:209:ILE:HG22	2:F:227:LEU:HD22	1.88	0.55
2:F:264:ARG:HB2	2:F:266:HIS:HD2	1.67	0.55
1:G:107:HIS:HD2	1:G:151:THR:HG22	1.72	0.55
1:G:310:GLY:CA	1:G:436:GLN:HE21	2.19	0.55
2:D:6:SER:O	2:D:65:ALA:HB1	2.07	0.55
2:D:30:ILE:HD13	2:D:61:HIS:CG	2.41	0.55
1:E:119:LEU:O	1:E:123:ARG:HG3	2.06	0.55
1:E:190:SER:O	1:E:194:LEU:HG	2.06	0.55
2:F:231:ILE:HA	2:F:234:ILE:CG2	2.36	0.55
2:F:388:TRP:CE3	2:F:388:TRP:HA	2.41	0.55
1:G:190:SER:O	1:G:194:LEU:HG	2.06	0.55
1:G:369:ARG:HD2	1:G:369:ARG:C	2.32	0.55
1:G:383:ALA:C	1:G:385:GLN:H	2.15	0.55
2:H:102:ASN:HD22	2:H:407:TRP:CD1	2.25	0.55
1:A:239:THR:HG22	1:A:240:THR:N	2.22	0.55
1:C:67:LEU:HD23	1:C:67:LEU:N	2.22	0.55
2:D:408:TYR:CD1	2:D:418:PHE:HZ	2.24	0.55
1:E:67:LEU:HD23	1:E:67:LEU:N	2.22	0.55
1:G:5:VAL:HG22	1:G:135:PHE:CD2	2.42	0.55
1:A:5:VAL:HG22	1:A:135:PHE:CD2	2.42	0.55
1:A:119:LEU:O	1:A:123:ARG:HG3	2.06	0.55
1:A:172:VAL:CG1	1:A:387:LEU:HD21	2.24	0.55
1:A:298:ALA:O	1:A:299:LYS:C	2.50	0.55
1:A:369:ARG:HD2	1:A:369:ARG:C	2.32	0.55
2:B:6:SER:O	2:B:65:ALA:HB1	2.07	0.55
2:B:288:VAL:HG22	2:B:373:ARG:NH1	2.22	0.55
2:B:305:CYS:O	2:B:306:ASP:C	2.49	0.55
1:C:5:VAL:HG22	1:C:135:PHE:CD2	2.42	0.55
1:E:5:VAL:HG22	1:E:135:PHE:CD2	2.42	0.55
1:E:107:HIS:HD2	1:E:151:THR:HG22	1.72	0.55
1:E:210:TYR:HD2	1:E:227:LEU:HD21	1.71	0.55
2:F:30:ILE:O	2:F:30:ILE:HG22	2.07	0.55
2:F:408:TYR:CD1	2:F:418:PHE:HZ	2.24	0.55
1:G:67:LEU:HD23	1:G:67:LEU:N	2.22	0.55
1:G:166:MET:HB3	1:G:198:THR:OG1	2.06	0.55
1:G:210:TYR:HD2	1:G:227:LEU:HD21	1.71	0.55
1:G:342:TYR:HD2	3:I:64:TYR:HH	1.47	0.55
2:H:6:SER:O	2:H:65:ALA:HB1	2.07	0.55
2:H:231:ILE:HA	2:H:234:ILE:CG2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:388:TRP:CE3	2:H:388:TRP:HA	2.41	0.55
2:H:408:TYR:CD1	2:H:418:PHE:HZ	2.24	0.55
2:B:24:TYR:OH	2:B:239:THR:OG1	2.24	0.54
2:B:30:ILE:HG23	2:B:34:GLY:O	2.07	0.54
2:B:231:ILE:HA	2:B:234:ILE:CG2	2.36	0.54
1:C:204:ILE:HD13	1:C:231:VAL:HG13	1.89	0.54
1:C:210:TYR:HD2	1:C:227:LEU:HD21	1.71	0.54
1:C:369:ARG:HD2	1:C:369:ARG:C	2.32	0.54
2:D:231:ILE:HA	2:D:234:ILE:CG2	2.36	0.54
2:D:288:VAL:HG22	2:D:373:ARG:NH1	2.23	0.54
1:E:166:MET:HB3	1:E:198:THR:OG1	2.06	0.54
1:E:383:ALA:C	1:E:385:GLN:H	2.15	0.54
1:G:165:ILE:H	1:G:165:ILE:HD13	1.71	0.54
1:G:272:PHE:HB3	1:G:275:LEU:HD22	1.88	0.54
2:H:244:PHE:C	2:H:244:PHE:CD2	2.83	0.54
2:B:346:TRP:HB3	1:C:401:ARG:HG3	1.89	0.54
2:B:381:THR:OG1	2:B:383:ALA:HB3	2.07	0.54
1:C:4:ILE:HD13	1:C:136:GLN:NE2	2.18	0.54
1:C:119:LEU:O	1:C:123:ARG:HG3	2.06	0.54
1:C:239:THR:HG22	1:C:240:THR:N	2.22	0.54
2:D:110:ILE:O	2:D:112:LYS:N	2.41	0.54
1:G:132:LEU:CD2	1:G:164:ARG:HG3	2.32	0.54
3:I:55:VAL:CG2	3:I:57:PHE:CE1	2.90	0.54
1:A:204:ILE:HD13	1:A:231:VAL:HG13	1.89	0.54
2:B:56:THR:O	2:F:284:GLU:CB	2.53	0.54
1:C:239:THR:O	1:C:241:CYS:N	2.41	0.54
2:D:381:THR:OG1	2:D:383:ALA:HB3	2.07	0.54
1:E:250:ALA:CA	1:E:254:LYS:HE2	2.36	0.54
1:E:298:ALA:O	1:E:299:LYS:C	2.50	0.54
2:F:64:ARG:HG3	2:F:64:ARG:O	2.06	0.54
2:F:244:PHE:C	2:F:244:PHE:CD2	2.83	0.54
2:F:248:LEU:HB3	2:F:355:ILE:H	1.73	0.54
2:F:258:ASN:OD1	1:G:180:THR:HG23	2.06	0.54
2:F:288:VAL:HG22	2:F:373:ARG:NH1	2.22	0.54
1:G:298:ALA:O	1:G:299:LYS:C	2.50	0.54
2:H:248:LEU:HB3	2:H:355:ILE:H	1.73	0.54
2:H:288:VAL:HG22	2:H:373:ARG:NH1	2.23	0.54
1:A:166:MET:HB3	1:A:198:THR:OG1	2.06	0.54
2:B:16:ILE:HD12	2:B:171:ILE:HD11	1.87	0.54
1:C:427:ASP:OD1	1:C:428:LEU:N	2.41	0.54
2:D:16:ILE:HD12	2:D:171:ILE:HD11	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:64:ARG:HG3	2:D:64:ARG:O	2.07	0.54
1:E:44:LEU:O	1:E:49:ILE:HG12	2.07	0.54
1:E:165:ILE:HD13	1:E:165:ILE:H	1.71	0.54
1:E:239:THR:O	1:E:241:CYS:N	2.40	0.54
1:E:297:ASP:OD1	1:E:298:ALA:N	2.39	0.54
1:E:325:MET:O	1:E:329:ASP:HB2	2.07	0.54
2:F:261:PRO:CB	1:G:404:PHE:CD2	2.78	0.54
2:F:381:THR:OG1	2:F:383:ALA:HB3	2.07	0.54
1:G:239:THR:O	1:G:241:CYS:N	2.41	0.54
2:H:64:ARG:HG3	2:H:64:ARG:O	2.07	0.54
2:H:102:ASN:CB	2:H:407:TRP:NE1	2.71	0.54
3:I:113:ILE:HG13	3:I:125:TYR:CE1	2.42	0.54
1:A:239:THR:O	1:A:241:CYS:N	2.41	0.54
2:B:17:GLY:O	2:B:21:TRP:HB2	2.08	0.54
2:B:110:ILE:O	2:B:112:LYS:N	2.41	0.54
2:D:17:GLY:O	2:D:21:TRP:HB2	2.08	0.54
2:D:118:VAL:HG21	2:D:149:PHE:CZ	2.42	0.54
1:E:249:ASN:OD1	2:F:71:GLU:OE1	2.25	0.54
1:E:259:MET:CA	1:E:314:THR:HG21	2.35	0.54
2:F:23:LEU:HD23	2:F:236:SER:CB	2.37	0.54
2:F:118:VAL:HG21	2:F:149:PHE:CZ	2.42	0.54
2:F:163:LYS:O	2:F:163:LYS:HG2	2.08	0.54
1:G:68:VAL:HG12	1:G:149:MET:CE	2.38	0.54
1:G:259:MET:CA	1:G:314:THR:HG21	2.35	0.54
2:H:9:VAL:CG1	2:H:139:HIS:HB3	2.38	0.54
2:H:30:ILE:HG22	2:H:30:ILE:O	2.07	0.54
1:A:331:GLN:O	1:A:335:VAL:HG23	2.08	0.54
2:B:64:ARG:HG3	2:B:64:ARG:O	2.07	0.54
2:B:110:ILE:CG2	2:B:111:GLY:N	2.71	0.54
2:B:244:PHE:C	2:B:244:PHE:CD2	2.84	0.54
1:C:2:ARG:NH2	2:D:98:ASP:HA	2.22	0.54
1:C:166:MET:HB3	1:C:198:THR:OG1	2.06	0.54
1:C:253:ARG:O	1:C:257:VAL:N	2.33	0.54
1:C:323:MET:HG3	1:C:328:VAL:HG21	1.90	0.54
1:C:325:MET:O	1:C:329:ASP:HB2	2.07	0.54
2:D:5:ILE:HG23	2:D:135:PHE:CB	2.38	0.54
1:E:213:CYS:SG	1:E:219:LEU:HD23	2.48	0.54
1:E:257:VAL:HA	2:F:407:TRP:CE2	2.42	0.54
1:G:297:ASP:OD1	1:G:298:ALA:N	2.39	0.54
2:H:23:LEU:HD23	2:H:236:SER:CB	2.37	0.54
2:H:163:LYS:O	2:H:163:LYS:HG2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:381:THR:OG1	2:H:383:ALA:HB3	2.07	0.54
1:A:133:GLN:HE21	1:A:252:LEU:HB2	1.73	0.54
1:A:343:PHE:O	1:A:344:VAL:O	2.26	0.54
1:A:383:ALA:C	1:A:385:GLN:H	2.15	0.54
1:A:427:ASP:OD1	1:A:428:LEU:N	2.41	0.54
2:B:55:GLU:O	2:B:56:THR:C	2.50	0.54
2:B:328:VAL:C	2:B:330:ALA:H	2.16	0.54
1:C:343:PHE:O	1:C:344:VAL:O	2.26	0.54
2:D:62:VAL:CG1	2:D:88:HIS:ND1	2.71	0.54
2:F:9:VAL:CG1	2:F:139:HIS:HB3	2.38	0.54
2:F:17:GLY:O	2:F:21:TRP:HB2	2.08	0.54
1:G:44:LEU:O	1:G:49:ILE:HG12	2.07	0.54
1:G:323:MET:HG3	1:G:328:VAL:HG21	1.90	0.54
1:G:343:PHE:O	1:G:344:VAL:O	2.26	0.54
2:H:98:ASP:O	2:H:110:ILE:HD13	2.08	0.54
1:A:323:MET:HG3	1:A:328:VAL:HG21	1.90	0.54
1:A:325:MET:O	1:A:329:ASP:HB2	2.07	0.54
2:B:98:ASP:O	2:B:110:ILE:HD13	2.08	0.54
2:B:115:ILE:O	2:B:116:ASP:C	2.51	0.54
2:D:9:VAL:CG1	2:D:139:HIS:HB3	2.38	0.54
2:D:30:ILE:HG23	2:D:34:GLY:O	2.08	0.54
2:D:115:ILE:O	2:D:116:ASP:C	2.51	0.54
2:D:328:VAL:C	2:D:330:ALA:H	2.16	0.54
1:E:343:PHE:O	1:E:344:VAL:O	2.26	0.54
2:F:182:VAL:O	2:F:184:PRO:N	2.41	0.54
2:F:257:THR:HG21	1:G:101:ASN:CB	2.32	0.54
1:G:213:CYS:SG	1:G:219:LEU:HD23	2.48	0.54
1:G:322:ARG:HH11	1:G:322:ARG:HG3	1.73	0.54
2:H:98:ASP:CB	2:H:105:ARG:HH21	2.14	0.54
2:H:118:VAL:HG21	2:H:149:PHE:CZ	2.42	0.54
2:H:182:VAL:O	2:H:184:PRO:N	2.41	0.54
1:A:44:LEU:O	1:A:49:ILE:HG12	2.07	0.54
1:A:213:CYS:SG	1:A:219:LEU:HD23	2.48	0.54
1:A:253:ARG:O	1:A:257:VAL:N	2.33	0.54
2:B:118:VAL:HG21	2:B:149:PHE:CZ	2.42	0.54
2:B:439:SER:O	1:C:401:ARG:NH2	2.33	0.54
1:C:2:ARG:HH22	2:D:99:ALA:H	1.54	0.54
1:C:31:ASP:HB3	1:C:32:PRO:HD2	1.89	0.54
2:D:24:TYR:OH	2:D:239:THR:OG1	2.24	0.54
1:E:322:ARG:HH11	1:E:322:ARG:HG3	1.73	0.54
2:F:98:ASP:O	2:F:110:ILE:HD13	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:5:ILE:HG23	2:H:135:PHE:CB	2.38	0.54
2:H:17:GLY:O	2:H:21:TRP:HB2	2.08	0.54
1:A:4:ILE:HD13	1:A:136:GLN:NE2	2.18	0.54
1:A:191:VAL:HG11	1:A:425:MET:HE2	1.89	0.54
2:B:9:VAL:CG1	2:B:139:HIS:HB3	2.38	0.54
1:C:68:VAL:HG12	1:C:149:MET:CE	2.38	0.54
1:C:133:GLN:HE21	1:C:252:LEU:HB2	1.73	0.54
1:C:331:GLN:O	1:C:335:VAL:HG23	2.08	0.54
2:D:98:ASP:O	2:D:110:ILE:HD13	2.08	0.54
2:D:173:PRO:HB2	2:D:391:LEU:CD1	2.38	0.54
1:E:4:ILE:CG2	1:E:136:GLN:HG2	2.38	0.54
2:F:110:ILE:O	2:F:112:LYS:N	2.41	0.54
2:H:110:ILE:O	2:H:112:LYS:N	2.41	0.54
2:B:163:LYS:O	2:B:163:LYS:HG2	2.08	0.53
1:C:213:CYS:SG	1:C:219:LEU:HD23	2.48	0.53
1:C:259:MET:CA	1:C:314:THR:HG21	2.35	0.53
1:C:431:GLU:O	1:C:434:GLN:CG	2.56	0.53
1:E:323:MET:HG3	1:E:328:VAL:HG21	1.90	0.53
2:F:5:ILE:HG23	2:F:135:PHE:CB	2.38	0.53
2:F:328:VAL:C	2:F:330:ALA:H	2.16	0.53
2:F:329:ASN:OD1	1:G:210:TYR:CE1	2.53	0.53
1:G:4:ILE:CG2	1:G:136:GLN:HG2	2.38	0.53
1:G:204:ILE:HD13	1:G:231:VAL:HG13	1.89	0.53
2:H:328:VAL:C	2:H:330:ALA:H	2.16	0.53
2:D:5:ILE:O	2:D:135:PHE:HA	2.09	0.53
2:D:276:ILE:CG2	2:D:369:ALA:HB2	2.27	0.53
1:E:5:VAL:HG23	1:E:5:VAL:O	2.09	0.53
1:E:431:GLU:O	1:E:434:GLN:CG	2.56	0.53
1:G:31:ASP:HB3	1:G:32:PRO:HD2	1.89	0.53
2:H:5:ILE:O	2:H:135:PHE:HA	2.08	0.53
1:A:107:HIS:HD2	1:A:151:THR:HG22	1.72	0.53
2:B:159:VAL:CG1	3:I:78:ARG:CG	2.86	0.53
1:C:44:LEU:O	1:C:49:ILE:HG12	2.07	0.53
1:C:147:SER:O	1:C:151:THR:CB	2.51	0.53
2:D:163:LYS:O	2:D:163:LYS:HG2	2.08	0.53
1:E:31:ASP:HB3	1:E:32:PRO:HD2	1.89	0.53
2:F:5:ILE:O	2:F:135:PHE:HA	2.08	0.53
2:F:98:ASP:CB	2:F:105:ARG:HH21	2.14	0.53
2:F:115:ILE:O	2:F:116:ASP:C	2.51	0.53
2:F:173:PRO:HB2	2:F:391:LEU:CD1	2.38	0.53
2:F:332:ILE:CG2	1:G:177:VAL:HG11	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:408:TYR:O	2:F:411:GLU:N	2.39	0.53
1:G:431:GLU:O	1:G:434:GLN:CG	2.56	0.53
2:H:101:ASN:ND2	5:H:500:GTP:O3G	2.42	0.53
1:A:68:VAL:HG12	1:A:149:MET:CE	2.38	0.53
1:A:259:MET:CG	1:A:314:THR:HG21	2.37	0.53
2:B:173:PRO:HB2	2:B:391:LEU:CD1	2.39	0.53
1:C:172:VAL:CG1	1:C:387:LEU:HD21	2.24	0.53
1:C:281:GLN:C	1:C:283:TYR:N	2.67	0.53
2:D:98:ASP:CB	2:D:105:ARG:HH21	2.14	0.53
1:E:204:ILE:HD13	1:E:231:VAL:HG13	1.89	0.53
2:F:101:ASN:ND2	5:F:500:GTP:O3G	2.42	0.53
2:F:121:ARG:O	2:F:125:LEU:HB2	2.08	0.53
1:G:254:LYS:HE3	1:G:352:LYS:HZ2	1.71	0.53
1:G:427:ASP:OD1	1:G:428:LEU:N	2.41	0.53
2:H:115:ILE:O	2:H:116:ASP:C	2.51	0.53
2:H:173:PRO:HB2	2:H:391:LEU:CD1	2.38	0.53
2:B:88:HIS:HE1	2:F:284:GLU:OE2	1.92	0.53
2:B:349:THR:HG21	1:C:178:SER:CB	2.38	0.53
2:B:408:TYR:O	2:B:411:GLU:N	2.39	0.53
1:C:191:VAL:HG11	1:C:425:MET:HE2	1.89	0.53
1:C:383:ALA:C	1:C:385:GLN:H	2.15	0.53
1:E:331:GLN:O	1:E:335:VAL:HG23	2.08	0.53
1:G:5:VAL:HG23	1:G:5:VAL:O	2.09	0.53
2:H:67:PHE:CZ	2:H:87:PHE:HE1	2.27	0.53
2:H:121:ARG:O	2:H:125:LEU:HB2	2.08	0.53
2:H:408:TYR:O	2:H:411:GLU:N	2.39	0.53
1:A:31:ASP:HB3	1:A:32:PRO:HD2	1.89	0.53
2:B:5:ILE:O	2:B:135:PHE:HA	2.09	0.53
2:B:182:VAL:O	2:B:184:PRO:N	2.41	0.53
2:B:231:ILE:CA	2:B:234:ILE:HG22	2.38	0.53
1:C:4:ILE:CG2	1:C:136:GLN:HG2	2.38	0.53
1:C:36:TYR:CZ	1:C:38:GLY:HA3	2.43	0.53
1:C:259:MET:CG	1:C:314:THR:HG21	2.36	0.53
1:E:20:PHE:CE2	1:E:24:ILE:HD12	2.43	0.53
1:E:168:THR:CB	1:E:201:THR:HG23	2.38	0.53
1:E:191:VAL:HG11	1:E:425:MET:HE2	1.89	0.53
2:F:67:PHE:CZ	2:F:87:PHE:HE1	2.27	0.53
1:G:8:GLN:OE1	1:G:14:ASN:ND2	2.42	0.53
1:G:331:GLN:O	1:G:335:VAL:HG23	2.08	0.53
1:A:67:LEU:HD23	1:A:67:LEU:N	2.22	0.53
1:A:281:GLN:C	1:A:283:TYR:N	2.67	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:ARG:HG3	1:A:322:ARG:HH11	1.73	0.53
2:B:121:ARG:O	2:B:125:LEU:HB2	2.08	0.53
1:C:107:HIS:HD2	1:C:151:THR:HG22	1.72	0.53
1:C:259:MET:HG2	1:C:314:THR:CG2	2.38	0.53
2:D:101:ASN:ND2	5:D:500:GTP:O3G	2.42	0.53
2:D:231:ILE:CA	2:D:234:ILE:HG22	2.38	0.53
1:E:8:GLN:OE1	1:E:14:ASN:ND2	2.42	0.53
1:E:427:ASP:OD1	1:E:428:LEU:N	2.41	0.53
2:F:231:ILE:CA	2:F:234:ILE:HG22	2.38	0.53
2:F:243:ARG:CZ	2:F:252:LEU:HG	2.39	0.53
1:G:27:GLU:HG2	1:G:27:GLU:O	2.08	0.53
1:A:259:MET:HG2	1:A:314:THR:CG2	2.38	0.53
1:A:259:MET:CA	1:A:314:THR:HG21	2.35	0.53
1:A:263:PRO:O	1:A:264:ARG:C	2.52	0.53
1:A:431:GLU:O	1:A:434:GLN:CG	2.56	0.53
2:B:30:ILE:HD12	2:B:61:HIS:ND1	2.22	0.53
1:C:21:TRP:CZ2	1:C:65:ALA:HB2	2.44	0.53
1:C:210:TYR:CD2	1:C:227:LEU:HD21	2.44	0.53
2:D:88:HIS:O	2:D:89:PRO:C	2.52	0.53
2:D:121:ARG:O	2:D:125:LEU:HB2	2.08	0.53
1:E:21:TRP:CZ2	1:E:65:ALA:HB2	2.44	0.53
1:E:36:TYR:CZ	1:E:38:GLY:HA3	2.43	0.53
1:E:263:PRO:O	1:E:264:ARG:C	2.52	0.53
1:G:191:VAL:HG11	1:G:425:MET:HE2	1.89	0.53
1:G:281:GLN:C	1:G:283:TYR:N	2.67	0.53
2:H:231:ILE:CA	2:H:234:ILE:HG22	2.38	0.53
1:A:70:LEU:HD12	1:A:145:THR:HG23	1.91	0.53
2:B:101:ASN:ND2	5:B:500:GTP:O3G	2.42	0.53
2:B:122:ILE:CD1	2:B:157:LEU:HD21	2.35	0.53
1:C:263:PRO:O	1:C:264:ARG:C	2.52	0.53
2:D:163:LYS:C	2:D:164:LYS:HG2	2.33	0.53
1:E:198:THR:HG22	1:E:265:LEU:CD2	2.39	0.53
2:F:242:LEU:C	2:F:244:PHE:N	2.66	0.53
1:G:20:PHE:CE2	1:G:24:ILE:HD12	2.42	0.53
1:G:399:PHE:O	1:G:400:ARG:C	2.52	0.53
2:H:102:ASN:HB3	2:H:407:TRP:NE1	2.24	0.53
2:H:243:ARG:CZ	2:H:252:LEU:HG	2.39	0.53
1:A:168:THR:CB	1:A:201:THR:HG23	2.38	0.53
1:A:179:ASP:HB2	4:A:600:GDP:H3'	1.90	0.53
1:A:288:VAL:HG22	1:A:323:MET:HE3	1.90	0.53
1:A:325:MET:CE	1:A:355:VAL:HG11	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:253:THR:O	2:B:254:GLU:C	2.52	0.53
1:C:5:VAL:O	1:C:5:VAL:HG23	2.09	0.53
1:C:264:ARG:HA	1:C:264:ARG:HE	1.75	0.53
1:E:27:GLU:O	1:E:27:GLU:HG2	2.08	0.53
1:E:68:VAL:HG12	1:E:149:MET:CE	2.38	0.53
1:E:212:ILE:O	1:E:216:THR:HB	2.09	0.53
2:F:11:GLN:NE2	2:F:74:VAL:HG22	2.22	0.53
1:G:21:TRP:CZ2	1:G:65:ALA:HB2	2.44	0.53
1:G:36:TYR:CZ	1:G:38:GLY:HA3	2.43	0.53
1:G:133:GLN:HE21	1:G:252:LEU:HB2	1.73	0.53
1:G:168:THR:CB	1:G:201:THR:HG23	2.38	0.53
1:G:212:ILE:O	1:G:216:THR:HB	2.09	0.53
1:G:425:MET:O	1:G:428:LEU:HB3	2.09	0.53
1:G:431:GLU:OE1	1:G:432:TYR:CA	2.57	0.53
1:A:4:ILE:CG2	1:A:136:GLN:HG2	2.38	0.52
1:A:5:VAL:HG23	1:A:5:VAL:O	2.09	0.52
1:A:21:TRP:CZ2	1:A:65:ALA:HB2	2.44	0.52
1:A:36:TYR:CZ	1:A:38:GLY:HA3	2.43	0.52
1:A:210:TYR:CD2	1:A:227:LEU:HD21	2.44	0.52
1:A:425:MET:O	1:A:428:LEU:HB3	2.09	0.52
2:B:172:TYR:OH	2:B:387:ALA:O	2.24	0.52
1:C:27:GLU:O	1:C:27:GLU:HG2	2.08	0.52
1:C:325:MET:CE	1:C:355:VAL:HG11	2.38	0.52
1:C:425:MET:O	1:C:428:LEU:HB3	2.09	0.52
2:D:67:PHE:CZ	2:D:87:PHE:HE1	2.27	0.52
2:D:182:VAL:O	2:D:184:PRO:N	2.41	0.52
2:D:324:VAL:O	2:D:327:ASP:HB2	2.08	0.52
1:E:288:VAL:HG22	1:E:323:MET:HE3	1.90	0.52
1:E:425:MET:O	1:E:428:LEU:HB3	2.09	0.52
1:E:431:GLU:OE1	1:E:432:TYR:CA	2.57	0.52
2:F:206:ASN:OD1	2:F:227:LEU:CD1	2.58	0.52
2:F:326:LYS:HE2	1:G:214:PHE:HB3	1.91	0.52
2:F:332:ILE:HG22	1:G:177:VAL:HG21	1.89	0.52
2:F:348:PRO:HD3	1:G:398:MET:CE	2.38	0.52
1:G:210:TYR:CD2	1:G:227:LEU:HD21	2.44	0.52
1:G:288:VAL:HG22	1:G:323:MET:HE3	1.90	0.52
2:H:206:ASN:OD1	2:H:227:LEU:CD1	2.58	0.52
1:A:264:ARG:HA	1:A:264:ARG:HE	1.75	0.52
2:B:8:HIS:HB3	2:B:13:GLY:O	2.10	0.52
2:B:67:PHE:CZ	2:B:87:PHE:HE1	2.27	0.52
2:B:88:HIS:O	2:B:89:PRO:C	2.52	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:PHE:CE2	1:C:24:ILE:HD12	2.43	0.52
1:C:141:LEU:HA	1:C:147:SER:HB3	1.91	0.52
1:C:168:THR:CB	1:C:201:THR:HG23	2.38	0.52
1:C:322:ARG:HH11	1:C:322:ARG:HG3	1.73	0.52
2:D:8:HIS:HB3	2:D:13:GLY:O	2.10	0.52
2:D:151:SER:HB3	2:D:193:THR:CG2	2.34	0.52
2:D:173:PRO:HB2	2:D:391:LEU:HD11	1.92	0.52
2:D:248:LEU:HB3	2:D:355:ILE:H	1.73	0.52
1:E:210:TYR:CD2	1:E:227:LEU:HD21	2.44	0.52
1:E:399:PHE:O	1:E:400:ARG:C	2.52	0.52
2:F:88:HIS:O	2:F:89:PRO:C	2.52	0.52
2:F:163:LYS:C	2:F:164:LYS:HG2	2.33	0.52
2:F:173:PRO:HB2	2:F:391:LEU:HD11	1.92	0.52
1:G:259:MET:HG2	1:G:314:THR:CG2	2.38	0.52
1:G:259:MET:CG	1:G:314:THR:HG21	2.36	0.52
2:H:242:LEU:C	2:H:244:PHE:N	2.66	0.52
1:A:27:GLU:HG2	1:A:27:GLU:O	2.08	0.52
1:A:149:MET:O	1:A:149:MET:HG2	2.10	0.52
1:A:431:GLU:OE1	1:A:432:TYR:CA	2.57	0.52
2:B:147:SER:CB	2:B:190:THR:OG1	2.52	0.52
1:C:149:MET:O	1:C:149:MET:HG2	2.10	0.52
1:C:176:LYS:CE	1:C:207:GLU:HG3	2.39	0.52
1:C:288:VAL:HG22	1:C:323:MET:HE3	1.90	0.52
1:C:320:ARG:HA	1:C:356:CYS:HB3	1.92	0.52
1:E:133:GLN:HE21	1:E:252:LEU:HB2	1.73	0.52
1:E:179:ASP:HB2	4:E:600:GDP:H3'	1.90	0.52
1:G:198:THR:HG22	1:G:265:LEU:CD2	2.39	0.52
2:H:11:GLN:NE2	2:H:74:VAL:HG22	2.22	0.52
2:H:25:CYS:HB2	2:H:30:ILE:O	2.10	0.52
2:H:88:HIS:O	2:H:89:PRO:C	2.52	0.52
2:H:173:PRO:HB2	2:H:391:LEU:HD11	1.92	0.52
3:I:100:GLY:O	3:I:101:VAL:CG2	2.57	0.52
1:A:8:GLN:OE1	1:A:14:ASN:ND2	2.42	0.52
1:A:176:LYS:CE	1:A:207:GLU:HG3	2.39	0.52
1:A:320:ARG:HA	1:A:356:CYS:HB3	1.92	0.52
2:B:98:ASP:CB	2:B:105:ARG:HH21	2.14	0.52
2:B:231:ILE:HD13	2:B:231:ILE:N	2.25	0.52
2:B:242:LEU:C	2:B:244:PHE:N	2.66	0.52
2:B:348:PRO:HD3	1:C:398:MET:HE2	1.83	0.52
2:D:172:TYR:OH	2:D:387:ALA:O	2.24	0.52
1:E:141:LEU:HA	1:E:147:SER:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:226:ASP:O	1:E:229:HIS:N	2.42	0.52
2:F:4:CYS:HA	2:F:134:GLY:O	2.10	0.52
2:F:25:CYS:HB2	2:F:30:ILE:O	2.10	0.52
1:G:103:TRP:CE2	1:G:189:LEU:HB3	2.45	0.52
1:G:141:LEU:HA	1:G:147:SER:HB3	1.91	0.52
1:G:226:ASP:O	1:G:229:HIS:N	2.42	0.52
2:H:110:ILE:CG2	2:H:111:GLY:N	2.71	0.52
2:H:163:LYS:C	2:H:164:LYS:HG2	2.33	0.52
1:A:20:PHE:CE2	1:A:24:ILE:HD12	2.43	0.52
1:A:103:TRP:CE2	1:A:189:LEU:HB3	2.45	0.52
1:A:141:LEU:HA	1:A:147:SER:HB3	1.91	0.52
1:A:212:ILE:O	1:A:216:THR:HB	2.09	0.52
2:B:5:ILE:O	2:B:136:SER:N	2.40	0.52
2:B:173:PRO:HB2	2:B:391:LEU:HD11	1.92	0.52
2:B:248:LEU:HB3	2:B:355:ILE:H	1.73	0.52
2:B:349:THR:O	1:C:181:VAL:HA	2.09	0.52
1:C:70:LEU:HD12	1:C:145:THR:HG23	1.91	0.52
1:C:103:TRP:CE2	1:C:189:LEU:HB3	2.45	0.52
1:C:399:PHE:O	1:C:400:ARG:C	2.52	0.52
2:D:253:THR:O	2:D:254:GLU:C	2.52	0.52
2:F:110:ILE:CG2	2:F:111:GLY:H	2.15	0.52
2:H:4:CYS:HA	2:H:134:GLY:O	2.10	0.52
2:H:62:VAL:CG1	2:H:88:HIS:ND1	2.71	0.52
2:H:172:TYR:OH	2:H:387:ALA:O	2.24	0.52
1:A:226:ASP:O	1:A:229:HIS:N	2.42	0.52
2:B:163:LYS:C	2:B:164:LYS:HG2	2.33	0.52
2:B:324:VAL:O	2:B:327:ASP:HB2	2.08	0.52
1:C:226:ASP:O	1:C:229:HIS:N	2.42	0.52
2:D:24:TYR:CE2	2:D:240:ALA:HB2	2.45	0.52
1:E:103:TRP:CE2	1:E:189:LEU:HB3	2.45	0.52
1:E:320:ARG:HA	1:E:356:CYS:HB3	1.92	0.52
2:F:62:VAL:CG1	2:F:88:HIS:ND1	2.71	0.52
2:F:231:ILE:N	2:F:231:ILE:HD13	2.25	0.52
2:F:345:ASP:OD2	2:F:439:SER:HB3	2.10	0.52
2:F:348:PRO:HG3	1:G:394:GLN:HB3	1.91	0.52
2:H:110:ILE:CG2	2:H:111:GLY:H	2.15	0.52
2:H:253:THR:O	2:H:254:GLU:C	2.52	0.52
2:H:345:ASP:OD2	2:H:439:SER:HB3	2.09	0.52
1:A:147:SER:O	1:A:151:THR:CB	2.51	0.52
2:B:243:ARG:CZ	2:B:252:LEU:HG	2.39	0.52
1:C:107:HIS:CD2	1:C:151:THR:HG22	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:231:ILE:HD13	2:D:231:ILE:N	2.25	0.52
1:E:259:MET:HG2	1:E:314:THR:CG2	2.38	0.52
1:E:259:MET:CG	1:E:314:THR:HG21	2.37	0.52
1:E:288:VAL:CG2	1:E:323:MET:HE3	2.40	0.52
2:F:8:HIS:HB3	2:F:13:GLY:O	2.10	0.52
1:G:70:LEU:HD12	1:G:145:THR:HG23	1.91	0.52
1:G:175:PRO:O	1:G:176:LYS:C	2.52	0.52
1:G:422:GLU:O	1:G:426:ASN:N	2.37	0.52
1:A:277:SER:OG	1:A:281:GLN:HB2	2.10	0.52
1:A:288:VAL:CG2	1:A:323:MET:HE3	2.40	0.52
2:B:4:CYS:HA	2:B:134:GLY:O	2.10	0.52
2:B:345:ASP:OD2	2:B:439:SER:HB3	2.10	0.52
1:C:212:ILE:O	1:C:216:THR:HB	2.09	0.52
1:C:288:VAL:CG2	1:C:323:MET:HE3	2.40	0.52
1:C:431:GLU:OE1	1:C:432:TYR:CA	2.57	0.52
2:D:206:ASN:OD1	2:D:227:LEU:CD1	2.58	0.52
2:D:243:ARG:CZ	2:D:252:LEU:HG	2.39	0.52
2:D:345:ASP:OD2	2:D:439:SER:HB3	2.09	0.52
2:D:408:TYR:O	2:D:411:GLU:N	2.39	0.52
1:E:70:LEU:HD12	1:E:145:THR:HG23	1.91	0.52
1:E:147:SER:O	1:E:151:THR:CB	2.51	0.52
1:E:175:PRO:O	1:E:176:LYS:C	2.52	0.52
1:E:295:MET:SD	1:E:375:ALA:O	2.68	0.52
1:G:320:ARG:HA	1:G:356:CYS:HB3	1.92	0.52
2:H:231:ILE:HD13	2:H:231:ILE:N	2.25	0.52
2:H:234:ILE:CG1	2:H:270:ALA:HB1	2.38	0.52
1:A:399:PHE:O	1:A:400:ARG:C	2.52	0.52
2:B:119:LEU:HD11	2:B:156:ARG:CD	2.40	0.52
2:B:244:PHE:CD2	2:B:245:ASP:N	2.76	0.52
2:B:333:ALA:N	1:C:177:VAL:HG21	2.25	0.52
1:C:8:GLN:OE1	1:C:14:ASN:ND2	2.42	0.52
2:D:4:CYS:HA	2:D:134:GLY:O	2.10	0.52
2:F:253:THR:O	2:F:254:GLU:C	2.52	0.52
2:H:8:HIS:HB3	2:H:13:GLY:O	2.10	0.52
2:H:251:ASP:OD1	2:H:252:LEU:N	2.43	0.52
1:A:198:THR:HG22	1:A:265:LEU:CD2	2.39	0.52
1:A:307:PRO:C	1:A:309:HIS:H	2.18	0.52
2:B:24:TYR:CE2	2:B:240:ALA:HB2	2.45	0.52
2:B:201:ALA:O	2:B:267:PHE:HA	2.10	0.52
2:D:201:ALA:O	2:D:267:PHE:HA	2.10	0.52
2:D:244:PHE:CD2	2:D:245:ASP:N	2.76	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:149:MET:O	1:E:149:MET:HG2	2.10	0.52
1:E:149:MET:O	1:E:153:LEU:HD22	2.10	0.52
1:E:188:THR:HA	1:E:425:MET:CE	2.40	0.52
1:E:325:MET:HE2	1:E:355:VAL:HG21	1.92	0.52
2:F:350:GLY:HA2	1:G:181:VAL:HG22	1.90	0.52
1:G:200:GLU:N	1:G:265:LEU:HD13	2.25	0.52
1:G:288:VAL:CG2	1:G:323:MET:HE3	2.40	0.52
1:A:175:PRO:O	1:A:176:LYS:C	2.52	0.51
2:B:9:VAL:HG21	2:B:149:PHE:CD1	2.46	0.51
2:B:63:PRO:HG3	2:B:87:PHE:CA	2.40	0.51
2:B:243:ARG:NH2	2:B:251:ASP:OD1	2.44	0.51
1:C:277:SER:OG	1:C:281:GLN:HB2	2.10	0.51
1:C:295:MET:SD	1:C:375:ALA:O	2.68	0.51
1:C:325:MET:HE2	1:C:355:VAL:HG21	1.92	0.51
1:C:346:TRP:CD1	1:C:346:TRP:H	2.27	0.51
2:D:147:SER:CB	2:D:190:THR:OG1	2.52	0.51
2:D:242:LEU:C	2:D:244:PHE:N	2.66	0.51
1:E:200:GLU:N	1:E:265:LEU:HD13	2.25	0.51
2:F:24:TYR:CE2	2:F:240:ALA:HB2	2.45	0.51
2:F:63:PRO:CG	2:F:87:PHE:HA	2.40	0.51
2:F:147:SER:CB	2:F:190:THR:OG1	2.52	0.51
2:F:251:ASP:OD1	2:F:252:LEU:N	2.43	0.51
1:G:147:SER:O	1:G:151:THR:CB	2.51	0.51
1:G:188:THR:HA	1:G:425:MET:CE	2.40	0.51
1:G:260:VAL:HG23	1:G:260:VAL:O	2.10	0.51
1:G:295:MET:SD	1:G:375:ALA:O	2.68	0.51
2:H:63:PRO:CG	2:H:87:PHE:HA	2.40	0.51
1:A:107:HIS:CD2	1:A:151:THR:HG22	2.45	0.51
1:A:188:THR:HA	1:A:425:MET:CE	2.40	0.51
1:A:295:MET:SD	1:A:375:ALA:O	2.68	0.51
2:B:206:ASN:OD1	2:B:227:LEU:CD1	2.57	0.51
1:C:175:PRO:O	1:C:176:LYS:C	2.52	0.51
1:C:198:THR:HG22	1:C:265:LEU:CD2	2.39	0.51
1:C:200:GLU:N	1:C:265:LEU:HD13	2.25	0.51
2:D:5:ILE:O	2:D:136:SER:N	2.40	0.51
2:D:9:VAL:HG21	2:D:149:PHE:CD1	2.46	0.51
2:D:417:GLU:HA	2:D:417:GLU:OE1	2.10	0.51
1:E:260:VAL:O	1:E:260:VAL:HG23	2.10	0.51
1:E:264:ARG:HA	1:E:264:ARG:HE	1.75	0.51
1:E:422:GLU:O	1:E:426:ASN:N	2.37	0.51
2:F:234:ILE:CG1	2:F:270:ALA:HB1	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:324:VAL:O	2:F:327:ASP:HB2	2.08	0.51
1:G:176:LYS:HG3	1:G:177:VAL:H	1.76	0.51
1:G:325:MET:HE2	1:G:355:VAL:HG21	1.92	0.51
2:H:24:TYR:CE2	2:H:240:ALA:HB2	2.45	0.51
2:H:147:SER:CB	2:H:190:THR:OG1	2.52	0.51
2:H:324:VAL:O	2:H:327:ASP:HB2	2.08	0.51
2:B:11:GLN:NE2	2:B:74:VAL:HG22	2.22	0.51
2:B:14:VAL:HG11	2:B:75:ILE:HD13	1.93	0.51
1:C:175:PRO:HD2	1:C:207:GLU:CD	2.35	0.51
2:D:14:VAL:HG11	2:D:75:ILE:HD13	1.93	0.51
2:D:55:GLU:O	2:D:56:THR:C	2.52	0.51
1:E:21:TRP:HZ2	1:E:65:ALA:HB2	1.76	0.51
1:E:307:PRO:C	1:E:309:HIS:H	2.18	0.51
1:G:149:MET:O	1:G:153:LEU:HD22	2.10	0.51
1:G:264:ARG:HA	1:G:264:ARG:HE	1.75	0.51
2:H:191:THR:HG23	2:H:192:HIS:N	2.25	0.51
1:A:200:GLU:N	1:A:265:LEU:HD13	2.25	0.51
1:A:260:VAL:HG23	1:A:260:VAL:O	2.10	0.51
1:C:5:VAL:CG2	1:C:135:PHE:CD2	2.94	0.51
1:C:260:VAL:HG23	1:C:260:VAL:O	2.10	0.51
1:C:307:PRO:C	1:C:309:HIS:H	2.18	0.51
2:D:243:ARG:NH2	2:D:251:ASP:OD1	2.44	0.51
2:D:434:GLU:C	2:D:436:GLY:H	2.18	0.51
1:E:257:VAL:HA	2:F:407:TRP:NE1	2.24	0.51
2:F:119:LEU:HD11	2:F:156:ARG:CD	2.40	0.51
2:F:191:THR:HG23	2:F:192:HIS:N	2.25	0.51
2:F:434:GLU:C	2:F:436:GLY:H	2.18	0.51
1:G:21:TRP:HZ2	1:G:65:ALA:HB2	1.76	0.51
1:G:149:MET:O	1:G:149:MET:HG2	2.10	0.51
1:G:257:VAL:CB	2:H:407:TRP:CE3	2.65	0.51
1:G:346:TRP:CD1	1:G:346:TRP:H	2.27	0.51
1:A:149:MET:O	1:A:153:LEU:HD22	2.10	0.51
1:C:188:THR:HA	1:C:425:MET:CE	2.40	0.51
2:D:119:LEU:HD11	2:D:156:ARG:CD	2.40	0.51
1:E:277:SER:OG	1:E:281:GLN:HB2	2.10	0.51
1:E:325:MET:CE	1:E:355:VAL:HG11	2.38	0.51
1:G:5:VAL:CG2	1:G:135:PHE:CD2	2.94	0.51
1:G:224:TYR:O	1:G:225:GLY:C	2.53	0.51
1:G:307:PRO:C	1:G:309:HIS:H	2.18	0.51
2:H:14:VAL:HG11	2:H:75:ILE:HD13	1.93	0.51
2:H:22:GLU:O	2:H:23:LEU:C	2.54	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:119:LEU:HD11	2:H:156:ARG:CD	2.40	0.51
2:H:201:ALA:O	2:H:267:PHE:HA	2.10	0.51
1:A:5:VAL:CG2	1:A:135:PHE:CD2	2.94	0.51
1:A:240:THR:HG23	1:A:241:CYS:H	1.76	0.51
1:A:314:THR:CG2	1:A:315:VAL:N	2.73	0.51
2:B:56:THR:C	2:F:284:GLU:CB	2.83	0.51
2:B:87:PHE:H	2:B:87:PHE:HD2	1.59	0.51
2:D:22:GLU:O	2:D:23:LEU:C	2.54	0.51
2:D:63:PRO:CG	2:D:87:PHE:HA	2.40	0.51
2:D:191:THR:HG23	2:D:192:HIS:N	2.25	0.51
2:D:251:ASP:OD1	2:D:252:LEU:N	2.43	0.51
2:D:255:PHE:O	2:D:256:GLN:C	2.53	0.51
2:D:338:LYS:O	2:D:340:THR:N	2.34	0.51
2:D:402:ARG:O	2:D:403:ALA:O	2.29	0.51
2:F:14:VAL:HG11	2:F:75:ILE:HD13	1.93	0.51
2:F:22:GLU:O	2:F:23:LEU:C	2.54	0.51
2:F:201:ALA:O	2:F:267:PHE:HA	2.10	0.51
1:G:107:HIS:CD2	1:G:151:THR:HG22	2.45	0.51
1:G:277:SER:OG	1:G:281:GLN:HB2	2.10	0.51
2:H:9:VAL:HG21	2:H:149:PHE:CD1	2.46	0.51
3:I:84:LEU:CD2	3:I:101:VAL:HG12	2.41	0.51
2:B:191:THR:HG23	2:B:192:HIS:N	2.25	0.51
2:B:251:ASP:OD1	2:B:252:LEU:N	2.43	0.51
1:E:107:HIS:CD2	1:E:151:THR:HG22	2.45	0.51
1:E:240:THR:HG23	1:E:241:CYS:H	1.76	0.51
2:F:9:VAL:HG21	2:F:149:PHE:CD1	2.46	0.51
2:F:263:PRO:HD3	1:G:406:HIS:CE1	2.45	0.51
1:G:314:THR:CG2	1:G:315:VAL:N	2.73	0.51
2:H:3:GLU:CD	2:H:50:ASN:O	2.54	0.51
2:H:243:ARG:NH2	2:H:251:ASP:OD1	2.44	0.51
2:H:434:GLU:C	2:H:436:GLY:H	2.18	0.51
3:I:84:LEU:HD22	3:I:101:VAL:HG12	1.92	0.51
1:A:325:MET:HE2	1:A:355:VAL:HG21	1.92	0.51
1:A:346:TRP:CD1	1:A:346:TRP:H	2.27	0.51
2:B:171:ILE:O	2:B:171:ILE:HG22	2.10	0.51
2:B:255:PHE:O	2:B:256:GLN:C	2.53	0.51
1:C:240:THR:HG23	1:C:241:CYS:H	1.76	0.51
2:D:11:GLN:NE2	2:D:74:VAL:HG22	2.22	0.51
2:D:87:PHE:H	2:D:87:PHE:HD2	1.59	0.51
2:D:238:ILE:O	2:D:242:LEU:HB2	2.11	0.51
1:E:113:GLU:HG3	1:E:114:LEU:N	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:224:TYR:O	1:E:225:GLY:C	2.53	0.51
1:E:346:TRP:CD1	1:E:346:TRP:H	2.27	0.51
2:F:3:GLU:CD	2:F:50:ASN:O	2.54	0.51
2:F:87:PHE:H	2:F:87:PHE:HD2	1.59	0.51
2:F:243:ARG:NH2	2:F:251:ASP:OD1	2.44	0.51
2:F:260:VAL:HG22	1:G:407:TRP:HE1	1.76	0.51
2:F:338:LYS:O	2:F:340:THR:N	2.34	0.51
1:G:240:THR:HG23	1:G:241:CYS:H	1.76	0.51
2:H:362:VAL:HG13	2:H:368:LEU:CD1	2.38	0.51
1:A:175:PRO:HD2	1:A:207:GLU:CD	2.36	0.51
2:B:22:GLU:O	2:B:23:LEU:C	2.54	0.51
2:B:362:VAL:HG13	2:B:368:LEU:CD1	2.38	0.51
1:C:224:TYR:O	1:C:225:GLY:C	2.53	0.51
1:C:314:THR:CG2	1:C:315:VAL:N	2.73	0.51
2:D:132:LEU:CD2	2:D:164:LYS:HE3	2.41	0.51
1:E:5:VAL:CG2	1:E:135:PHE:CD2	2.94	0.51
2:F:133:GLN:CB	2:F:243:ARG:HH12	2.24	0.51
2:F:238:ILE:O	2:F:242:LEU:HB2	2.11	0.51
2:F:332:ILE:HG21	1:G:177:VAL:HG11	1.91	0.51
1:G:113:GLU:HG3	1:G:114:LEU:N	2.26	0.51
1:G:342:TYR:CD2	3:I:64:TYR:OH	2.63	0.51
2:H:87:PHE:H	2:H:87:PHE:HD2	1.59	0.51
2:H:171:ILE:HG22	2:H:171:ILE:O	2.10	0.51
2:H:238:ILE:O	2:H:242:LEU:HB2	2.11	0.51
1:A:422:GLU:O	1:A:426:ASN:N	2.37	0.51
2:B:402:ARG:O	2:B:403:ALA:O	2.29	0.51
1:E:49:ILE:HG13	1:E:50:ASN:H	1.76	0.51
1:E:314:THR:CG2	1:E:315:VAL:N	2.73	0.51
2:F:133:GLN:HB3	2:F:243:ARG:HH12	1.76	0.51
2:F:196:GLU:O	2:F:197:HIS:CD2	2.64	0.51
2:F:362:VAL:HG13	2:F:368:LEU:CD1	2.38	0.51
1:G:265:LEU:O	1:G:266:HIS:O	2.29	0.51
1:G:323:MET:HG3	1:G:328:VAL:CG2	2.41	0.51
1:G:348:PRO:HD3	2:H:397:LEU:HB3	1.92	0.51
2:H:132:LEU:CD2	2:H:164:LYS:HE3	2.41	0.51
2:H:133:GLN:HB3	2:H:243:ARG:HH12	1.76	0.51
2:H:151:SER:HB3	2:H:193:THR:CG2	2.34	0.51
1:A:265:LEU:O	1:A:266:HIS:O	2.29	0.50
2:B:119:LEU:HA	2:B:122:ILE:HG12	1.93	0.50
1:C:149:MET:O	1:C:153:LEU:HD22	2.10	0.50
1:E:323:MET:HG3	1:E:328:VAL:CG2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:132:LEU:CD2	2:F:164:LYS:HE3	2.41	0.50
2:F:140:SER:O	2:F:142:GLY:N	2.44	0.50
2:F:171:ILE:HG22	2:F:171:ILE:O	2.10	0.50
1:G:325:MET:CE	1:G:355:VAL:HG11	2.38	0.50
2:H:102:ASN:CB	2:H:407:TRP:HD1	2.23	0.50
2:H:133:GLN:CB	2:H:243:ARG:HH12	2.24	0.50
2:H:140:SER:O	2:H:142:GLY:N	2.44	0.50
2:H:196:GLU:O	2:H:197:HIS:CD2	2.64	0.50
2:H:338:LYS:O	2:H:340:THR:N	2.34	0.50
2:B:3:GLU:CD	2:B:50:ASN:O	2.54	0.50
2:B:70:LEU:CD1	2:B:145:THR:CB	2.89	0.50
2:B:132:LEU:CD2	2:B:164:LYS:HE3	2.42	0.50
2:B:417:GLU:OE1	2:B:417:GLU:HA	2.10	0.50
2:D:133:GLN:CB	2:D:243:ARG:HH12	2.24	0.50
2:D:133:GLN:HB3	2:D:243:ARG:HH12	1.76	0.50
2:F:119:LEU:HA	2:F:122:ILE:HG12	1.93	0.50
2:F:151:SER:HB3	2:F:193:THR:CG2	2.34	0.50
2:H:70:LEU:CD1	2:H:145:THR:CB	2.89	0.50
1:A:242:LEU:C	1:A:244:PHE:H	2.20	0.50
2:B:133:GLN:CB	2:B:243:ARG:HH12	2.24	0.50
2:B:144:GLY:H	5:B:500:GTP:PG	2.33	0.50
2:B:196:GLU:O	2:B:197:HIS:CD2	2.64	0.50
2:B:434:GLU:C	2:B:436:GLY:H	2.18	0.50
2:D:119:LEU:HA	2:D:122:ILE:HG12	1.93	0.50
2:D:148:GLY:O	2:D:149:PHE:C	2.55	0.50
2:D:362:VAL:HG13	2:D:368:LEU:CD1	2.38	0.50
1:E:24:ILE:HG22	1:E:25:SER:N	2.27	0.50
1:E:265:LEU:O	1:E:266:HIS:O	2.29	0.50
1:E:346:TRP:CG	2:F:401:LYS:HZ2	2.29	0.50
1:E:360:PRO:O	1:E:369:ARG:C	2.54	0.50
2:H:119:LEU:HA	2:H:122:ILE:HG12	1.93	0.50
1:A:265:LEU:HD12	1:A:266:HIS:O	2.12	0.50
1:A:360:PRO:O	1:A:369:ARG:C	2.54	0.50
2:B:148:GLY:O	2:B:149:PHE:C	2.55	0.50
2:B:238:ILE:O	2:B:242:LEU:HB2	2.11	0.50
2:D:171:ILE:O	2:D:171:ILE:HG22	2.10	0.50
2:D:310:GLY:HA3	2:D:383:ALA:N	2.26	0.50
2:D:339:ARG:C	2:D:341:ILE:N	2.68	0.50
1:E:242:LEU:C	1:E:244:PHE:H	2.19	0.50
2:F:70:LEU:CD1	2:F:145:THR:CB	2.89	0.50
2:F:148:GLY:O	2:F:149:PHE:C	2.55	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:49:ILE:HG13	1:G:50:ASN:H	1.76	0.50
1:G:257:VAL:CG2	1:G:257:VAL:O	2.50	0.50
2:H:148:GLY:O	2:H:149:PHE:C	2.55	0.50
2:H:417:GLU:OE1	2:H:417:GLU:HA	2.10	0.50
3:I:80:PHE:HE1	3:I:119:LEU:HD21	1.76	0.50
1:A:224:TYR:O	1:A:225:GLY:C	2.53	0.50
1:A:387:LEU:HD23	1:A:388:PHE:CD2	2.47	0.50
2:B:133:GLN:HB3	2:B:243:ARG:HH12	1.76	0.50
2:B:339:ARG:C	2:B:341:ILE:N	2.68	0.50
1:C:242:LEU:C	1:C:244:PHE:H	2.20	0.50
1:C:265:LEU:HD12	1:C:266:HIS:O	2.12	0.50
2:D:11:GLN:O	2:D:14:VAL:HB	2.12	0.50
2:D:16:ILE:HG23	2:D:17:GLY:N	2.26	0.50
2:D:70:LEU:CD1	2:D:145:THR:CB	2.89	0.50
1:E:3:GLU:HA	1:E:51:VAL:HA	1.93	0.50
2:F:255:PHE:O	2:F:256:GLN:C	2.53	0.50
2:F:339:ARG:C	2:F:341:ILE:N	2.67	0.50
2:F:413:MET:C	2:F:414:GLU:HG3	2.36	0.50
2:F:417:GLU:OE1	2:F:417:GLU:HA	2.10	0.50
1:G:175:PRO:HD2	1:G:207:GLU:CD	2.35	0.50
1:G:242:LEU:C	1:G:244:PHE:H	2.19	0.50
1:G:257:VAL:O	2:H:404:PHE:CD2	2.64	0.50
1:G:280:SER:O	1:G:282:GLN:N	2.45	0.50
1:G:333:LEU:O	1:G:336:GLN:N	2.45	0.50
1:G:360:PRO:O	1:G:369:ARG:C	2.54	0.50
2:H:16:ILE:HG23	2:H:17:GLY:N	2.26	0.50
1:A:262:PHE:O	1:A:264:ARG:N	2.45	0.50
1:A:323:MET:HG3	1:A:328:VAL:CG2	2.41	0.50
2:B:11:GLN:O	2:B:14:VAL:HB	2.12	0.50
2:B:63:PRO:HD3	2:B:86:LEU:O	2.11	0.50
1:C:323:MET:HG3	1:C:328:VAL:CG2	2.41	0.50
1:C:387:LEU:HD23	1:C:388:PHE:CD2	2.47	0.50
2:D:95:GLY:C	2:D:97:GLU:N	2.69	0.50
2:D:396:ASP:O	2:D:397:LEU:C	2.53	0.50
1:E:281:GLN:C	1:E:283:TYR:N	2.67	0.50
1:E:333:LEU:O	1:E:336:GLN:N	2.45	0.50
1:E:345:GLU:O	1:E:347:ILE:N	2.45	0.50
2:F:16:ILE:HG23	2:F:17:GLY:N	2.26	0.50
2:F:241:SER:C	2:F:244:PHE:HB3	2.36	0.50
1:G:253:ARG:CD	2:H:407:TRP:HH2	2.24	0.50
1:G:269:MET:HB3	1:G:303:ALA:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:241:SER:C	2:H:244:PHE:HB3	2.36	0.50
2:H:344:VAL:HG12	2:H:345:ASP:H	1.74	0.50
1:A:82:PRO:C	1:A:84:GLY:H	2.20	0.50
2:B:140:SER:O	2:B:142:GLY:N	2.44	0.50
1:C:265:LEU:O	1:C:266:HIS:O	2.29	0.50
1:C:273:ALA:CB	1:C:274:PRO:HD3	2.30	0.50
1:C:336:GLN:HE22	1:C:349:ASN:ND2	2.10	0.50
2:D:5:ILE:HG12	2:D:6:SER:N	2.26	0.50
1:E:4:ILE:HG22	1:E:5:VAL:N	2.27	0.50
1:E:168:THR:O	1:E:201:THR:HA	2.12	0.50
1:E:245:PRO:HA	2:F:73:THR:CG2	2.42	0.50
1:E:262:PHE:O	1:E:264:ARG:N	2.45	0.50
1:E:269:MET:HB3	1:E:303:ALA:HB2	1.94	0.50
1:E:280:SER:O	1:E:282:GLN:N	2.45	0.50
2:F:12:ALA:CB	2:F:140:SER:OG	2.60	0.50
1:G:3:GLU:HA	1:G:51:VAL:HA	1.93	0.50
1:G:4:ILE:HG22	1:G:5:VAL:N	2.27	0.50
1:G:262:PHE:O	1:G:264:ARG:N	2.45	0.50
2:H:12:ALA:CB	2:H:140:SER:OG	2.59	0.50
2:H:413:MET:C	2:H:414:GLU:HG3	2.37	0.50
1:A:4:ILE:HD12	1:A:239:THR:CG2	2.42	0.50
1:A:173:PRO:HB3	1:A:183:GLU:CG	2.42	0.50
1:A:332:MET:HE3	1:A:351:VAL:CG1	2.32	0.50
1:A:431:GLU:HA	1:A:434:GLN:CG	2.42	0.50
2:B:218:ASP:C	2:B:219:ILE:HG12	2.37	0.50
2:B:261:PRO:HB2	2:B:262:TYR:CD1	2.46	0.50
2:B:310:GLY:HA3	2:B:383:ALA:N	2.26	0.50
2:B:396:ASP:O	2:B:397:LEU:C	2.53	0.50
1:C:82:PRO:C	1:C:84:GLY:H	2.20	0.50
1:C:345:GLU:O	1:C:347:ILE:N	2.45	0.50
2:D:218:ASP:C	2:D:219:ILE:HG12	2.37	0.50
2:D:413:MET:C	2:D:414:GLU:HG3	2.36	0.50
1:E:173:PRO:HB3	1:E:183:GLU:CG	2.42	0.50
1:E:175:PRO:HD2	1:E:207:GLU:CD	2.36	0.50
1:E:336:GLN:HE22	1:E:349:ASN:ND2	2.10	0.50
2:F:344:VAL:HG12	2:F:345:ASP:H	1.74	0.50
1:G:345:GLU:O	1:G:347:ILE:N	2.45	0.50
1:G:387:LEU:HD23	1:G:388:PHE:CD2	2.47	0.50
2:H:218:ASP:C	2:H:219:ILE:HG12	2.37	0.50
2:H:255:PHE:O	2:H:256:GLN:C	2.53	0.50
2:H:261:PRO:HB2	2:H:262:TYR:CD1	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:310:GLY:HA3	2:H:383:ALA:N	2.26	0.50
1:A:49:ILE:HG13	1:A:50:ASN:H	1.76	0.50
1:A:333:LEU:O	1:A:336:GLN:N	2.45	0.50
1:A:336:GLN:HE22	1:A:349:ASN:ND2	2.10	0.50
1:A:345:GLU:O	1:A:347:ILE:N	2.45	0.50
2:B:149:PHE:HE1	2:B:153:LEU:HD22	1.77	0.50
1:C:4:ILE:HD12	1:C:239:THR:CG2	2.42	0.50
1:C:262:PHE:O	1:C:264:ARG:N	2.45	0.50
1:C:269:MET:HB3	1:C:303:ALA:HB2	1.94	0.50
1:C:332:MET:CE	1:C:351:VAL:HG11	2.32	0.50
1:C:360:PRO:O	1:C:369:ARG:C	2.54	0.50
1:C:431:GLU:HA	1:C:434:GLN:CG	2.42	0.50
2:D:3:GLU:CD	2:D:50:ASN:O	2.54	0.50
2:D:62:VAL:CG2	2:D:88:HIS:CE1	2.87	0.50
2:D:140:SER:O	2:D:142:GLY:N	2.44	0.50
2:D:196:GLU:O	2:D:197:HIS:CD2	2.64	0.50
1:E:387:LEU:HD23	1:E:388:PHE:CD2	2.47	0.50
2:F:218:ASP:C	2:F:219:ILE:HG12	2.37	0.50
2:F:261:PRO:HB2	2:F:262:TYR:CD1	2.46	0.50
1:G:4:ILE:HD12	1:G:239:THR:CG2	2.42	0.50
1:A:88:ARG:NE	1:E:283:TYR:HE1	2.09	0.49
1:A:133:GLN:NE2	1:A:252:LEU:HB2	2.27	0.49
1:A:273:ALA:CB	1:A:274:PRO:HD3	2.30	0.49
1:A:296:PHE:CZ	1:A:315:VAL:HG11	2.46	0.49
1:A:301:MET:HE1	1:A:377:PHE:CE2	2.43	0.49
2:B:10:GLY:O	2:B:11:GLN:C	2.53	0.49
2:B:12:ALA:CB	2:B:140:SER:OG	2.59	0.49
1:C:49:ILE:HG13	1:C:50:ASN:H	1.76	0.49
2:D:115:ILE:CG2	2:D:116:ASP:N	2.75	0.49
2:D:227:LEU:O	2:D:231:ILE:HG12	2.12	0.49
1:E:4:ILE:HD12	1:E:239:THR:CG2	2.42	0.49
1:E:301:MET:HE1	1:E:377:PHE:CE2	2.43	0.49
2:F:95:GLY:C	2:F:97:GLU:N	2.69	0.49
1:G:133:GLN:NE2	1:G:252:LEU:HB2	2.27	0.49
1:G:173:PRO:HB3	1:G:183:GLU:CG	2.42	0.49
1:G:245:PRO:CB	2:H:73:THR:CG2	2.89	0.49
1:G:263:PRO:O	1:G:264:ARG:C	2.52	0.49
2:H:2:ARG:NH1	2:H:47:ASP:CB	2.75	0.49
1:A:4:ILE:HG22	1:A:5:VAL:N	2.27	0.49
1:A:168:THR:O	1:A:201:THR:HA	2.12	0.49
1:A:280:SER:O	1:A:282:GLN:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95:GLY:C	2:B:97:GLU:N	2.69	0.49
2:B:115:ILE:CG2	2:B:116:ASP:N	2.75	0.49
1:C:4:ILE:HG22	1:C:5:VAL:N	2.27	0.49
1:C:24:ILE:HG22	1:C:25:SER:N	2.27	0.49
1:C:173:PRO:HB3	1:C:183:GLU:CG	2.42	0.49
1:C:296:PHE:CZ	1:C:315:VAL:HG11	2.46	0.49
2:D:62:VAL:O	2:D:63:PRO:O	2.30	0.49
2:D:414:GLU:OE1	2:D:414:GLU:N	2.46	0.49
1:E:431:GLU:HA	1:E:434:GLN:CG	2.42	0.49
2:F:2:ARG:NH1	2:F:47:ASP:CB	2.75	0.49
2:F:5:ILE:HG12	2:F:6:SER:N	2.26	0.49
2:F:149:PHE:HE1	2:F:153:LEU:HD22	1.77	0.49
2:F:263:PRO:HD3	1:G:406:HIS:NE2	2.27	0.49
2:F:402:ARG:O	2:F:403:ALA:O	2.29	0.49
1:G:82:PRO:C	1:G:84:GLY:H	2.20	0.49
1:G:168:THR:O	1:G:201:THR:HA	2.12	0.49
1:G:336:GLN:HE22	1:G:349:ASN:ND2	2.10	0.49
2:H:402:ARG:O	2:H:403:ALA:O	2.29	0.49
2:B:345:ASP:C	2:B:347:CYS:N	2.68	0.49
2:B:414:GLU:OE1	2:B:414:GLU:N	2.46	0.49
1:C:133:GLN:NE2	1:C:252:LEU:HB2	2.28	0.49
1:C:168:THR:O	1:C:201:THR:HA	2.12	0.49
2:D:56:THR:HA	2:H:284:GLU:HG3	1.92	0.49
2:D:241:SER:C	2:D:244:PHE:HB3	2.36	0.49
2:D:261:PRO:HB2	2:D:262:TYR:CD1	2.46	0.49
2:D:293:ASN:HD21	2:D:338:LYS:NZ	2.11	0.49
1:E:82:PRO:C	1:E:84:GLY:H	2.20	0.49
2:F:11:GLN:O	2:F:14:VAL:HB	2.12	0.49
2:F:293:ASN:HD21	2:F:338:LYS:NZ	2.10	0.49
2:F:310:GLY:HA3	2:F:383:ALA:N	2.26	0.49
1:G:24:ILE:HG22	1:G:25:SER:N	2.26	0.49
1:G:352:LYS:CD	2:H:181:VAL:HG21	2.26	0.49
1:G:431:GLU:HA	1:G:434:GLN:CG	2.42	0.49
2:H:11:GLN:O	2:H:14:VAL:HB	2.12	0.49
1:A:21:TRP:HZ2	1:A:65:ALA:HB2	1.76	0.49
1:A:332:MET:CE	1:A:351:VAL:HG11	2.32	0.49
2:B:5:ILE:CG1	2:B:64:ARG:NH2	2.75	0.49
2:B:152:LEU:HD12	2:B:152:LEU:C	2.38	0.49
2:B:338:LYS:O	2:B:340:THR:N	2.34	0.49
2:B:413:MET:C	2:B:414:GLU:HG3	2.36	0.49
1:C:280:SER:O	1:C:282:GLN:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:133:GLN:NE2	1:E:252:LEU:HB2	2.28	0.49
1:E:257:VAL:HG13	2:F:407:TRP:CD2	2.48	0.49
1:E:265:LEU:HD12	1:E:266:HIS:O	2.12	0.49
2:F:234:ILE:C	2:F:234:ILE:CD1	2.86	0.49
1:G:258:ASN:HD21	1:G:352:LYS:HE2	1.69	0.49
1:G:265:LEU:HD12	1:G:266:HIS:O	2.12	0.49
1:G:301:MET:HE1	1:G:377:PHE:CE2	2.43	0.49
2:H:5:ILE:HG12	2:H:6:SER:N	2.26	0.49
2:H:62:VAL:O	2:H:63:PRO:O	2.30	0.49
2:H:149:PHE:HE1	2:H:153:LEU:HD22	1.77	0.49
2:B:241:SER:C	2:B:244:PHE:HB3	2.36	0.49
2:B:293:ASN:HD21	2:B:338:LYS:NZ	2.11	0.49
1:C:21:TRP:HZ2	1:C:65:ALA:HB2	1.76	0.49
2:D:12:ALA:CB	2:D:140:SER:OG	2.59	0.49
2:D:152:LEU:HD12	2:D:152:LEU:C	2.38	0.49
2:D:184:PRO:HG2	2:D:398:MET:CE	2.40	0.49
2:D:274:PRO:CB	2:D:371:VAL:HG21	2.43	0.49
1:E:173:PRO:HB3	1:E:183:GLU:HG2	1.93	0.49
2:F:105:ARG:HH11	2:F:105:ARG:HG3	1.78	0.49
2:F:192:HIS:CD2	2:F:424:ASP:OD2	2.66	0.49
2:F:297:GLU:HG3	2:F:299:ALA:N	2.28	0.49
2:F:414:GLU:N	2:F:414:GLU:OE1	2.46	0.49
1:G:137:LEU:HD22	1:G:154:ILE:HG21	1.94	0.49
2:H:105:ARG:HG3	2:H:105:ARG:HH11	1.78	0.49
2:H:234:ILE:C	2:H:234:ILE:CD1	2.86	0.49
2:H:293:ASN:HD21	2:H:338:LYS:NZ	2.11	0.49
2:H:297:GLU:HG3	2:H:299:ALA:N	2.28	0.49
1:A:269:MET:HB3	1:A:303:ALA:HB2	1.94	0.49
2:B:16:ILE:HG23	2:B:17:GLY:N	2.26	0.49
2:B:118:VAL:HG21	2:B:149:PHE:CE2	2.48	0.49
2:B:192:HIS:CD2	2:B:424:ASP:OD2	2.66	0.49
2:B:230:LEU:O	2:B:233:GLN:N	2.35	0.49
1:C:333:LEU:O	1:C:336:GLN:N	2.45	0.49
2:D:149:PHE:HE1	2:D:153:LEU:HD22	1.77	0.49
2:D:192:HIS:CD2	2:D:424:ASP:OD2	2.66	0.49
2:D:252:LEU:O	2:D:253:THR:C	2.56	0.49
2:D:392:ASP:O	2:D:395:PHE:HB3	2.13	0.49
2:F:62:VAL:CG2	2:F:88:HIS:CE1	2.87	0.49
2:F:152:LEU:HD12	2:F:152:LEU:C	2.38	0.49
2:F:203:MET:SD	2:F:267:PHE:HB3	2.53	0.49
2:F:396:ASP:O	2:F:397:LEU:C	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:296:PHE:CZ	1:G:315:VAL:HG11	2.46	0.49
2:H:95:GLY:C	2:H:97:GLU:N	2.69	0.49
2:H:152:LEU:HD12	2:H:152:LEU:C	2.38	0.49
2:H:192:HIS:CD2	2:H:424:ASP:OD2	2.66	0.49
2:H:396:ASP:O	2:H:397:LEU:C	2.53	0.49
3:I:72:VAL:HG11	3:I:116:MET:SD	2.52	0.49
1:A:3:GLU:HA	1:A:51:VAL:HA	1.93	0.49
1:A:8:GLN:HB3	1:A:14:ASN:HA	1.94	0.49
2:B:188:ILE:O	2:B:191:THR:HG22	2.13	0.49
2:B:227:LEU:O	2:B:231:ILE:HG12	2.12	0.49
2:B:260:VAL:HG22	1:C:407:TRP:CZ2	2.48	0.49
2:B:274:PRO:CB	2:B:371:VAL:HG21	2.43	0.49
2:B:392:ASP:O	2:B:395:PHE:HB3	2.13	0.49
1:C:194:LEU:C	1:C:196:GLU:N	2.70	0.49
1:C:431:GLU:OE1	1:C:432:TYR:N	2.46	0.49
2:D:2:ARG:NH1	2:D:47:ASP:CB	2.75	0.49
2:D:158:SER:OG	2:D:197:HIS:HB3	2.13	0.49
2:D:230:LEU:O	2:D:233:GLN:N	2.35	0.49
1:E:103:TRP:HZ3	1:E:108:TYR:CE1	2.27	0.49
2:F:62:VAL:O	2:F:63:PRO:O	2.30	0.49
1:G:258:ASN:CG	1:G:352:LYS:HE2	2.35	0.49
2:H:70:LEU:HD12	2:H:70:LEU:N	2.28	0.49
2:H:203:MET:SD	2:H:267:PHE:HB3	2.53	0.49
2:H:414:GLU:OE1	2:H:414:GLU:N	2.46	0.49
1:A:69:ASP:HA	1:A:145:THR:HG21	1.95	0.49
2:B:158:SER:OG	2:B:197:HIS:HB3	2.13	0.49
2:B:184:PRO:HG2	2:B:398:MET:CE	2.40	0.49
2:B:297:GLU:HG3	2:B:299:ALA:N	2.28	0.49
1:C:8:GLN:HB3	1:C:14:ASN:HA	1.94	0.49
2:D:23:LEU:HD23	2:D:236:SER:CB	2.37	0.49
2:D:70:LEU:HD12	2:D:70:LEU:N	2.28	0.49
2:D:115:ILE:HD11	2:D:119:LEU:HG	1.92	0.49
2:D:118:VAL:HG21	2:D:149:PHE:CE2	2.48	0.49
2:D:297:GLU:HG3	2:D:299:ALA:N	2.28	0.49
2:D:344:VAL:HG12	2:D:345:ASP:H	1.74	0.49
1:E:175:PRO:CD	1:E:207:GLU:OE1	2.61	0.49
1:E:199:ASP:O	1:E:200:GLU:HG3	2.13	0.49
2:F:70:LEU:HD12	2:F:70:LEU:N	2.28	0.49
2:F:118:VAL:HG21	2:F:149:PHE:CE2	2.48	0.49
1:G:175:PRO:CD	1:G:207:GLU:OE1	2.61	0.49
1:G:199:ASP:O	1:G:200:GLU:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:431:GLU:OE1	1:G:432:TYR:N	2.46	0.49
3:I:113:ILE:HG21	3:I:119:LEU:HD21	1.95	0.49
1:A:239:THR:O	1:A:240:THR:C	2.56	0.49
1:A:431:GLU:OE1	1:A:432:TYR:N	2.46	0.49
2:B:252:LEU:O	2:B:253:THR:C	2.56	0.49
1:C:301:MET:HE1	1:C:377:PHE:CE2	2.43	0.49
2:D:203:MET:SD	2:D:267:PHE:HB3	2.53	0.49
1:E:128:SER:OG	1:E:129:CYS:N	2.34	0.49
1:E:137:LEU:HD22	1:E:154:ILE:HG21	1.95	0.49
1:E:211:ASP:OD1	1:E:212:ILE:HG13	2.13	0.49
1:E:296:PHE:CZ	1:E:315:VAL:HG11	2.46	0.49
2:F:151:SER:OG	2:F:193:THR:HG21	2.13	0.49
1:G:211:ASP:OD1	1:G:212:ILE:HG13	2.13	0.49
2:H:115:ILE:HD11	2:H:119:LEU:HG	1.92	0.49
2:H:118:VAL:HG21	2:H:149:PHE:CE2	2.48	0.49
1:A:113:GLU:HG3	1:A:114:LEU:N	2.26	0.49
1:A:192:HIS:HD1	1:A:424:ASN:CG	2.20	0.49
1:A:260:VAL:HG23	2:B:407:TRP:NE1	2.25	0.49
2:B:2:ARG:NH1	2:B:47:ASP:CB	2.76	0.49
2:B:105:ARG:HH11	2:B:105:ARG:HG3	1.78	0.49
2:B:203:MET:SD	2:B:267:PHE:HB3	2.53	0.49
1:C:3:GLU:HA	1:C:51:VAL:HA	1.93	0.49
1:C:113:GLU:HG3	1:C:114:LEU:N	2.26	0.49
1:C:217:LEU:C	1:C:219:LEU:N	2.55	0.49
2:D:10:GLY:O	2:D:11:GLN:C	2.53	0.49
1:E:431:GLU:OE1	1:E:432:TYR:N	2.46	0.49
2:F:115:ILE:HD11	2:F:119:LEU:HG	1.93	0.49
2:F:155:GLU:OE1	2:F:197:HIS:HE1	1.96	0.49
2:F:158:SER:OG	2:F:197:HIS:HB3	2.13	0.49
1:G:8:GLN:HB3	1:G:14:ASN:HA	1.94	0.49
1:G:102:ASN:HB3	1:G:105:LYS:HB2	1.95	0.49
1:G:173:PRO:HB3	1:G:183:GLU:HG2	1.93	0.49
1:G:179:ASP:CB	4:G:600:GDP:H3'	2.36	0.49
2:H:115:ILE:CG2	2:H:116:ASP:N	2.75	0.49
2:B:70:LEU:HD12	2:B:70:LEU:N	2.28	0.48
2:B:115:ILE:HD11	2:B:119:LEU:HG	1.92	0.48
2:B:344:VAL:HG12	2:B:345:ASP:H	1.75	0.48
1:C:142:GLY:HA3	1:C:183:GLU:OE2	2.13	0.48
1:C:173:PRO:HB3	1:C:183:GLU:HG2	1.93	0.48
1:C:175:PRO:CD	1:C:207:GLU:OE1	2.61	0.48
2:D:50:ASN:ND2	2:D:53:PHE:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:151:SER:OG	2:D:193:THR:HG21	2.13	0.48
2:D:188:ILE:O	2:D:191:THR:HG22	2.13	0.48
1:E:69:ASP:HA	1:E:145:THR:HG21	1.95	0.48
2:F:13:GLY:C	2:F:16:ILE:HG22	2.38	0.48
2:F:188:ILE:O	2:F:191:THR:HG22	2.13	0.48
2:F:196:GLU:C	2:F:197:HIS:HD2	2.19	0.48
1:G:191:VAL:HG13	1:G:192:HIS:N	2.28	0.48
2:H:151:SER:OG	2:H:193:THR:HG21	2.13	0.48
2:H:155:GLU:OE1	2:H:197:HIS:HE1	1.96	0.48
2:H:158:SER:OG	2:H:197:HIS:HB3	2.13	0.48
1:A:137:LEU:HD22	1:A:154:ILE:HG21	1.95	0.48
1:A:142:GLY:HA3	1:A:183:GLU:OE2	2.13	0.48
1:A:154:ILE:HG22	1:A:166:MET:CE	2.44	0.48
1:A:194:LEU:C	1:A:196:GLU:N	2.70	0.48
2:B:13:GLY:C	2:B:16:ILE:HG22	2.38	0.48
2:B:96:LYS:O	2:B:97:GLU:O	2.31	0.48
2:B:149:PHE:O	2:B:150:THR:C	2.56	0.48
2:B:231:ILE:O	2:B:235:VAL:HG23	2.12	0.48
1:C:239:THR:O	1:C:240:THR:C	2.56	0.48
2:D:13:GLY:C	2:D:16:ILE:HG22	2.38	0.48
2:D:155:GLU:OE1	2:D:197:HIS:HE1	1.96	0.48
2:D:231:ILE:O	2:D:235:VAL:HG23	2.12	0.48
1:E:176:LYS:HG3	1:E:177:VAL:H	1.78	0.48
1:E:257:VAL:HG13	2:F:407:TRP:CD1	2.48	0.48
2:F:50:ASN:ND2	2:F:53:PHE:O	2.46	0.48
2:F:104:ALA:CB	2:F:408:TYR:HD2	2.26	0.48
1:G:103:TRP:HZ3	1:G:108:TYR:CE1	2.27	0.48
2:H:13:GLY:C	2:H:16:ILE:HG22	2.38	0.48
2:H:50:ASN:ND2	2:H:53:PHE:O	2.46	0.48
2:H:96:LYS:O	2:H:97:GLU:O	2.31	0.48
2:H:188:ILE:O	2:H:191:THR:HG22	2.13	0.48
2:H:263:PRO:O	2:H:264:ARG:C	2.56	0.48
2:H:274:PRO:CB	2:H:371:VAL:HG21	2.43	0.48
1:A:173:PRO:HB3	1:A:183:GLU:HG2	1.93	0.48
1:A:413:MET:HG3	1:A:414:ASP:N	2.22	0.48
1:C:69:ASP:HA	1:C:145:THR:HG21	1.95	0.48
1:C:103:TRP:HZ3	1:C:108:TYR:CE1	2.27	0.48
1:C:154:ILE:HG22	1:C:166:MET:CE	2.44	0.48
1:E:8:GLN:HB3	1:E:14:ASN:HA	1.94	0.48
1:E:20:PHE:CG	1:E:235:MET:SD	3.07	0.48
1:E:191:VAL:HG13	1:E:192:HIS:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:24:TYR:OH	2:F:239:THR:OG1	2.24	0.48
2:F:115:ILE:CG2	2:F:116:ASP:N	2.75	0.48
2:F:263:PRO:O	2:F:264:ARG:C	2.56	0.48
2:F:274:PRO:CB	2:F:371:VAL:HG21	2.43	0.48
1:G:26:ASP:C	1:G:28:HIS:H	2.21	0.48
1:G:176:LYS:CE	1:G:207:GLU:HG3	2.39	0.48
1:G:307:PRO:C	1:G:309:HIS:N	2.71	0.48
2:H:231:ILE:O	2:H:235:VAL:HG23	2.12	0.48
3:I:55:VAL:HG12	3:I:123:GLU:HB2	1.94	0.48
1:A:24:ILE:HG22	1:A:25:SER:N	2.27	0.48
2:B:151:SER:OG	2:B:193:THR:HG21	2.13	0.48
2:B:409:VAL:C	2:B:411:GLU:N	2.71	0.48
1:C:2:ARG:NH1	1:C:251:ASP:OD2	2.46	0.48
1:C:137:LEU:HD22	1:C:154:ILE:HG21	1.94	0.48
1:C:307:PRO:C	1:C:309:HIS:N	2.71	0.48
1:C:308:ARG:HG3	1:C:342:TYR:OH	2.13	0.48
2:D:9:VAL:HG11	2:D:150:THR:OG1	2.13	0.48
2:D:196:GLU:C	2:D:197:HIS:HD2	2.19	0.48
1:E:264:ARG:HA	1:E:264:ARG:NE	2.29	0.48
2:F:5:ILE:O	2:F:136:SER:N	2.40	0.48
2:F:96:LYS:O	2:F:97:GLU:O	2.31	0.48
2:F:230:LEU:O	2:F:233:GLN:N	2.35	0.48
2:F:231:ILE:O	2:F:235:VAL:HG23	2.12	0.48
2:F:260:VAL:HG21	1:G:407:TRP:HZ2	1.77	0.48
1:G:69:ASP:HA	1:G:145:THR:HG21	1.95	0.48
1:G:248:LEU:CD1	2:H:179:THR:HG21	2.41	0.48
1:G:264:ARG:HA	1:G:264:ARG:NE	2.29	0.48
2:H:10:GLY:O	2:H:11:GLN:C	2.53	0.48
2:H:24:TYR:OH	2:H:239:THR:OG1	2.24	0.48
2:H:104:ALA:CB	2:H:408:TYR:HD2	2.26	0.48
2:H:392:ASP:O	2:H:395:PHE:HB3	2.13	0.48
2:H:436:GLY:C	2:H:438:ASP:N	2.72	0.48
2:B:155:GLU:OE1	2:B:197:HIS:HE1	1.96	0.48
1:C:102:ASN:HB3	1:C:105:LYS:HB2	1.95	0.48
1:C:179:ASP:HB3	4:C:600:GDP:H3'	1.95	0.48
1:C:237:GLY:O	1:C:241:CYS:CB	2.61	0.48
2:D:96:LYS:O	2:D:97:GLU:O	2.31	0.48
2:D:99:ALA:O	2:D:100:ALA:HB3	2.14	0.48
2:D:104:ALA:CB	2:D:408:TYR:HD2	2.26	0.48
2:D:384:ILE:HG22	2:D:388:TRP:CD1	2.49	0.48
2:D:436:GLY:C	2:D:438:ASP:N	2.72	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:26:ASP:C	1:E:28:HIS:H	2.21	0.48
1:E:49:ILE:HG13	1:E:50:ASN:N	2.28	0.48
1:E:102:ASN:HB3	1:E:105:LYS:HB2	1.95	0.48
1:E:142:GLY:HA3	1:E:183:GLU:OE2	2.13	0.48
1:E:154:ILE:HG22	1:E:166:MET:CE	2.44	0.48
2:F:436:GLY:C	2:F:438:ASP:N	2.72	0.48
1:G:49:ILE:HG13	1:G:50:ASN:N	2.28	0.48
1:G:154:ILE:HG22	1:G:166:MET:CE	2.44	0.48
1:G:192:HIS:HD1	1:G:424:ASN:CG	2.20	0.48
2:H:62:VAL:CG2	2:H:88:HIS:CE1	2.87	0.48
2:H:196:GLU:C	2:H:197:HIS:HD2	2.19	0.48
1:A:2:ARG:NH1	1:A:251:ASP:OD2	2.46	0.48
1:A:102:ASN:HB3	1:A:105:LYS:HB2	1.95	0.48
1:A:161:TYR:C	1:A:163:ASP:N	2.71	0.48
1:A:191:VAL:HG13	1:A:192:HIS:N	2.28	0.48
1:A:199:ASP:O	1:A:200:GLU:HG3	2.13	0.48
1:A:211:ASP:OD1	1:A:212:ILE:HG13	2.13	0.48
1:A:237:GLY:O	1:A:241:CYS:CB	2.61	0.48
2:B:104:ALA:CB	2:B:408:TYR:HD2	2.26	0.48
1:C:115:VAL:CG2	1:C:152:LEU:HD23	2.44	0.48
1:C:346:TRP:HB3	2:D:401:LYS:NZ	2.28	0.48
2:D:409:VAL:C	2:D:411:GLU:N	2.71	0.48
1:E:307:PRO:C	1:E:309:HIS:N	2.71	0.48
2:F:227:LEU:O	2:F:231:ILE:HG12	2.12	0.48
2:F:252:LEU:O	2:F:253:THR:C	2.56	0.48
1:G:128:SER:OG	1:G:129:CYS:N	2.34	0.48
1:G:209:LEU:CD2	1:G:227:LEU:HD13	2.44	0.48
2:H:227:LEU:O	2:H:231:ILE:HG12	2.12	0.48
1:A:20:PHE:CG	1:A:235:MET:SD	3.07	0.48
1:A:103:TRP:HZ3	1:A:108:TYR:CE1	2.27	0.48
1:A:175:PRO:CD	1:A:207:GLU:OE1	2.61	0.48
2:B:50:ASN:ND2	2:B:53:PHE:O	2.46	0.48
2:B:62:VAL:HG12	2:B:63:PRO:N	2.25	0.48
2:B:99:ALA:O	2:B:100:ALA:HB3	2.14	0.48
2:B:386:GLU:O	2:B:388:TRP:N	2.47	0.48
1:C:156:LYS:HA	1:C:156:LYS:CE	2.38	0.48
1:C:191:VAL:HG13	1:C:192:HIS:N	2.28	0.48
2:D:105:ARG:HH11	2:D:105:ARG:HG3	1.78	0.48
1:E:209:LEU:O	1:E:213:CYS:N	2.47	0.48
1:E:239:THR:O	1:E:240:THR:C	2.56	0.48
2:F:392:ASP:O	2:F:395:PHE:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:20:PHE:CG	1:G:235:MET:SD	3.07	0.48
1:G:142:GLY:HA3	1:G:183:GLU:OE2	2.13	0.48
1:G:239:THR:O	1:G:240:THR:C	2.56	0.48
1:G:409:THR:C	1:G:411:GLU:H	2.22	0.48
2:H:62:VAL:HG12	2:H:91:GLN:HE22	1.77	0.48
2:H:99:ALA:O	2:H:100:ALA:HB3	2.13	0.48
2:H:230:LEU:O	2:H:233:GLN:N	2.35	0.48
1:A:115:VAL:CG2	1:A:152:LEU:HD23	2.44	0.48
1:A:308:ARG:HG3	1:A:342:TYR:OH	2.13	0.48
2:B:67:PHE:CE1	2:B:87:PHE:CD1	2.89	0.48
1:C:211:ASP:OD1	1:C:212:ILE:HG13	2.13	0.48
2:D:386:GLU:O	2:D:388:TRP:N	2.47	0.48
1:E:413:MET:HG3	1:E:414:ASP:N	2.22	0.48
2:F:10:GLY:O	2:F:11:GLN:C	2.54	0.48
2:F:155:GLU:HG2	2:F:197:HIS:CE1	2.49	0.48
2:F:261:PRO:HB3	1:G:404:PHE:CD2	2.40	0.48
2:F:386:GLU:O	2:F:388:TRP:N	2.47	0.48
2:F:409:VAL:C	2:F:411:GLU:N	2.71	0.48
1:G:209:LEU:O	1:G:213:CYS:N	2.47	0.48
1:G:253:ARG:HB3	2:H:407:TRP:CZ3	2.34	0.48
1:G:287:THR:O	1:G:288:VAL:CG2	2.58	0.48
1:G:413:MET:HG3	1:G:414:ASP:N	2.22	0.48
2:H:155:GLU:HG2	2:H:197:HIS:CE1	2.49	0.48
2:H:252:LEU:O	2:H:253:THR:C	2.56	0.48
2:H:409:VAL:C	2:H:411:GLU:N	2.71	0.48
3:I:113:ILE:HG21	3:I:119:LEU:CD2	2.44	0.48
2:B:6:SER:OG	2:B:65:ALA:HB2	2.14	0.48
2:B:23:LEU:HD23	2:B:236:SER:CB	2.37	0.48
2:B:230:LEU:O	2:B:231:ILE:C	2.57	0.48
2:B:348:PRO:CG	1:C:398:MET:CE	2.67	0.48
2:B:384:ILE:HG22	2:B:388:TRP:CD1	2.49	0.48
1:C:199:ASP:O	1:C:200:GLU:HG3	2.13	0.48
1:C:209:LEU:CD2	1:C:227:LEU:HD13	2.44	0.48
1:C:409:THR:C	1:C:411:GLU:H	2.22	0.48
2:D:6:SER:OG	2:D:65:ALA:HB2	2.14	0.48
2:D:149:PHE:O	2:D:150:THR:C	2.56	0.48
1:E:2:ARG:NH1	1:E:251:ASP:OD2	2.46	0.48
1:E:182:VAL:O	1:E:183:GLU:C	2.56	0.48
1:E:296:PHE:HZ	1:E:315:VAL:HG11	1.78	0.48
2:F:99:ALA:O	2:F:100:ALA:HB3	2.13	0.48
2:F:107:HIS:CE1	2:F:152:LEU:HB3	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:261:PRO:HB3	1:G:404:PHE:CZ	2.45	0.48
1:G:182:VAL:O	1:G:183:GLU:C	2.56	0.48
1:G:226:ASP:O	1:G:229:HIS:HB3	2.14	0.48
2:H:386:GLU:O	2:H:388:TRP:N	2.47	0.48
1:A:307:PRO:C	1:A:309:HIS:N	2.71	0.48
2:B:5:ILE:HG22	2:B:6:SER:H	1.78	0.48
2:B:9:VAL:HG11	2:B:150:THR:OG1	2.13	0.48
2:B:436:GLY:C	2:B:438:ASP:N	2.72	0.48
1:C:20:PHE:CG	1:C:235:MET:SD	3.07	0.48
1:C:49:ILE:HG13	1:C:50:ASN:N	2.28	0.48
1:C:242:LEU:HD22	1:C:250:ALA:N	2.19	0.48
2:D:70:LEU:HD12	2:D:145:THR:HG21	1.95	0.48
1:E:176:LYS:CE	1:E:207:GLU:HG3	2.39	0.48
1:E:226:ASP:O	1:E:229:HIS:HB3	2.14	0.48
2:F:9:VAL:HG11	2:F:150:THR:OG1	2.13	0.48
2:F:70:LEU:HD12	2:F:145:THR:HG21	1.95	0.48
2:F:191:THR:CG2	2:F:192:HIS:N	2.76	0.48
1:G:217:LEU:C	1:G:219:LEU:N	2.55	0.48
1:G:296:PHE:HZ	1:G:315:VAL:HG11	1.78	0.48
1:G:308:ARG:HG3	1:G:342:TYR:OH	2.13	0.48
2:H:5:ILE:O	2:H:136:SER:N	2.40	0.48
2:H:147:SER:O	2:H:190:THR:HG23	2.14	0.48
1:A:209:LEU:CD2	1:A:227:LEU:HD13	2.44	0.47
1:A:409:THR:C	1:A:411:GLU:H	2.22	0.47
2:B:196:GLU:C	2:B:197:HIS:HD2	2.19	0.47
2:D:52:PHE:O	2:D:64:ARG:HB3	2.14	0.47
2:D:115:ILE:HG23	2:D:116:ASP:H	1.79	0.47
2:D:147:SER:O	2:D:190:THR:HG23	2.14	0.47
1:E:209:LEU:CD2	1:E:227:LEU:HD13	2.44	0.47
1:E:217:LEU:C	1:E:219:LEU:N	2.55	0.47
1:E:308:ARG:HG3	1:E:342:TYR:OH	2.13	0.47
2:F:147:SER:O	2:F:190:THR:HG23	2.14	0.47
1:G:2:ARG:NH1	1:G:251:ASP:OD2	2.46	0.47
1:G:187:ALA:O	1:G:188:THR:C	2.57	0.47
2:H:107:HIS:CE1	2:H:152:LEU:HB3	2.49	0.47
1:A:26:ASP:C	1:A:28:HIS:H	2.21	0.47
1:A:49:ILE:HG13	1:A:50:ASN:N	2.28	0.47
1:A:288:VAL:C	1:A:290:GLU:N	2.70	0.47
2:B:56:THR:C	2:F:284:GLU:HB2	2.40	0.47
2:B:260:VAL:O	2:B:260:VAL:CG2	2.62	0.47
2:D:335:ILE:O	2:D:337:THR:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:192:HIS:HD1	1:E:424:ASN:CG	2.20	0.47
1:G:115:VAL:CG2	1:G:152:LEU:HD23	2.44	0.47
1:G:288:VAL:C	1:G:290:GLU:N	2.70	0.47
2:H:9:VAL:HG11	2:H:150:THR:OG1	2.13	0.47
2:H:97:GLU:HB2	2:H:110:ILE:HD11	1.96	0.47
2:H:122:ILE:CD1	2:H:157:LEU:HD21	2.35	0.47
2:H:191:THR:CG2	2:H:192:HIS:N	2.76	0.47
2:H:339:ARG:C	2:H:341:ILE:N	2.68	0.47
1:A:20:PHE:O	1:A:24:ILE:HB	2.14	0.47
1:A:217:LEU:C	1:A:219:LEU:N	2.55	0.47
1:A:387:LEU:O	1:A:387:LEU:HG	2.14	0.47
2:B:115:ILE:HG23	2:B:116:ASP:H	1.79	0.47
2:B:145:THR:H	5:B:500:GTP:PG	2.37	0.47
2:B:204:VAL:CG1	2:B:209:ILE:HD11	2.42	0.47
1:C:210:TYR:O	1:C:211:ASP:C	2.57	0.47
2:D:115:ILE:CD1	2:D:115:ILE:C	2.87	0.47
2:D:191:THR:CG2	2:D:192:HIS:N	2.76	0.47
2:D:260:VAL:O	2:D:260:VAL:CG2	2.63	0.47
2:F:241:SER:HB3	2:F:320:ARG:NH2	2.29	0.47
2:F:335:ILE:O	2:F:337:THR:N	2.47	0.47
1:G:20:PHE:O	1:G:24:ILE:HB	2.14	0.47
2:H:70:LEU:HD12	2:H:145:THR:HG21	1.95	0.47
2:H:154:MET:HA	2:H:157:LEU:HD12	1.96	0.47
2:H:335:ILE:O	2:H:337:THR:N	2.47	0.47
2:H:384:ILE:HG22	2:H:388:TRP:CD1	2.49	0.47
1:A:264:ARG:HA	1:A:264:ARG:NE	2.29	0.47
1:A:296:PHE:HZ	1:A:315:VAL:HG11	1.78	0.47
2:B:107:HIS:CE1	2:B:152:LEU:HB3	2.49	0.47
2:B:117:LEU:HD12	2:B:121:ARG:HH12	1.80	0.47
2:B:147:SER:O	2:B:190:THR:HG23	2.14	0.47
2:B:154:MET:HA	2:B:157:LEU:HD12	1.97	0.47
1:C:26:ASP:C	1:C:28:HIS:H	2.21	0.47
1:C:209:LEU:O	1:C:213:CYS:N	2.47	0.47
1:C:242:LEU:CD1	1:C:250:ALA:HB3	2.45	0.47
1:C:274:PRO:HG2	1:C:371:LEU:CD2	2.43	0.47
2:D:97:GLU:HB2	2:D:110:ILE:HD11	1.96	0.47
2:D:154:MET:HA	2:D:157:LEU:HD12	1.96	0.47
2:D:155:GLU:HA	2:D:197:HIS:CE1	2.49	0.47
2:D:264:ARG:C	2:D:266:HIS:N	2.60	0.47
2:D:317:LEU:CD1	2:D:351:PHE:CD2	2.97	0.47
2:D:388:TRP:HA	2:D:388:TRP:HE3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:185:TYR:HD2	1:E:395:PHE:CE1	2.33	0.47
1:E:243:ARG:HA	1:E:243:ARG:HD3	1.62	0.47
1:E:287:THR:O	1:E:288:VAL:CG2	2.58	0.47
2:F:6:SER:OG	2:F:65:ALA:HB2	2.14	0.47
2:F:122:ILE:CD1	2:F:157:LEU:HD21	2.35	0.47
2:F:154:MET:HA	2:F:157:LEU:HD12	1.97	0.47
2:F:260:VAL:CG2	2:F:260:VAL:O	2.63	0.47
2:F:369:ALA:O	2:F:370:LYS:CB	2.62	0.47
2:H:5:ILE:CG2	2:H:135:PHE:HB3	2.41	0.47
2:H:6:SER:OG	2:H:65:ALA:HB2	2.14	0.47
2:H:241:SER:HB3	2:H:320:ARG:NH2	2.29	0.47
1:A:185:TYR:HD2	1:A:395:PHE:CE1	2.33	0.47
1:A:187:ALA:O	1:A:188:THR:C	2.57	0.47
1:A:274:PRO:HG2	1:A:371:LEU:CD2	2.43	0.47
2:B:115:ILE:CD1	2:B:115:ILE:C	2.87	0.47
2:B:175:PRO:HD2	2:B:207:GLU:HB3	1.96	0.47
2:B:185:TYR:OH	2:B:399:TYR:HA	2.15	0.47
1:C:20:PHE:O	1:C:24:ILE:HB	2.14	0.47
1:C:182:VAL:O	1:C:183:GLU:C	2.56	0.47
1:C:387:LEU:O	1:C:387:LEU:HG	2.14	0.47
2:D:107:HIS:CE1	2:D:152:LEU:HB3	2.49	0.47
2:D:117:LEU:HD12	2:D:121:ARG:HH12	1.80	0.47
2:D:230:LEU:O	2:D:231:ILE:C	2.57	0.47
2:D:407:TRP:O	2:D:411:GLU:CG	2.63	0.47
1:E:20:PHE:O	1:E:24:ILE:HB	2.14	0.47
1:E:307:PRO:HB3	1:E:312:TYR:CZ	2.49	0.47
1:E:384:ILE:O	1:E:384:ILE:HG23	2.14	0.47
2:F:97:GLU:HB2	2:F:110:ILE:HD11	1.96	0.47
2:F:117:LEU:HD12	2:F:121:ARG:HH12	1.80	0.47
2:F:175:PRO:HD2	2:F:207:GLU:HB3	1.97	0.47
2:F:384:ILE:HG22	2:F:388:TRP:CD1	2.49	0.47
1:G:210:TYR:O	1:G:211:ASP:C	2.57	0.47
1:G:260:VAL:HG23	2:H:406:HIS:HE1	1.79	0.47
2:H:317:LEU:CD1	2:H:351:PHE:CD2	2.97	0.47
2:H:369:ALA:O	2:H:370:LYS:CB	2.62	0.47
1:A:176:LYS:HG3	1:A:177:VAL:H	1.78	0.47
1:A:242:LEU:HD22	1:A:250:ALA:N	2.19	0.47
1:A:384:ILE:O	1:A:384:ILE:HG23	2.14	0.47
2:B:407:TRP:O	2:B:411:GLU:CG	2.63	0.47
1:C:176:LYS:HG3	1:C:177:VAL:H	1.78	0.47
1:C:296:PHE:HZ	1:C:315:VAL:HG11	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:384:ILE:O	1:C:384:ILE:HG23	2.14	0.47
2:D:57:GLY:N	2:H:284:GLU:HB2	2.30	0.47
2:D:62:VAL:HG12	2:D:91:GLN:HE22	1.78	0.47
2:D:210:TYR:CE2	2:D:227:LEU:HD21	2.49	0.47
1:E:70:LEU:O	1:E:99:ALA:HB2	2.15	0.47
1:E:101:ASN:ND2	1:E:101:ASN:O	2.48	0.47
1:E:387:LEU:O	1:E:387:LEU:HG	2.14	0.47
2:F:62:VAL:HG12	2:F:91:GLN:HE22	1.77	0.47
2:F:120:ASP:O	2:F:124:LYS:HB2	2.15	0.47
2:F:210:TYR:CE2	2:F:227:LEU:HD21	2.49	0.47
2:F:317:LEU:CD1	2:F:351:PHE:CD2	2.97	0.47
1:G:101:ASN:ND2	1:G:101:ASN:O	2.48	0.47
1:G:185:TYR:HD2	1:G:395:PHE:CE1	2.33	0.47
1:G:253:ARG:CG	2:H:407:TRP:CH2	2.92	0.47
2:H:175:PRO:HD2	2:H:207:GLU:HB3	1.97	0.47
2:H:210:TYR:CE2	2:H:227:LEU:HD21	2.49	0.47
2:H:260:VAL:O	2:H:260:VAL:CG2	2.63	0.47
1:A:82:PRO:HB2	1:A:83:PHE:H	1.56	0.47
1:A:101:ASN:ND2	1:A:101:ASN:O	2.48	0.47
1:A:168:THR:N	1:A:200:GLU:O	2.43	0.47
1:A:242:LEU:CD1	1:A:250:ALA:HB3	2.45	0.47
1:A:259:MET:HE1	1:A:378:ILE:CG2	2.45	0.47
1:A:360:PRO:HG2	1:A:371:LEU:CB	2.38	0.47
2:B:70:LEU:HD12	2:B:145:THR:HG21	1.95	0.47
2:B:97:GLU:HB2	2:B:110:ILE:HD11	1.96	0.47
2:B:155:GLU:HG2	2:B:197:HIS:CE1	2.49	0.47
2:B:191:THR:O	2:B:195:LEU:HB2	2.15	0.47
2:B:263:PRO:O	2:B:264:ARG:C	2.56	0.47
2:B:328:VAL:O	2:B:330:ALA:N	2.38	0.47
2:B:335:ILE:O	2:B:337:THR:N	2.47	0.47
2:B:388:TRP:HA	2:B:388:TRP:HE3	1.79	0.47
1:C:185:TYR:HD2	1:C:395:PHE:CE1	2.33	0.47
1:C:187:ALA:O	1:C:188:THR:C	2.57	0.47
1:C:226:ASP:O	1:C:229:HIS:HB3	2.14	0.47
1:C:259:MET:HE1	1:C:378:ILE:CG2	2.45	0.47
1:C:264:ARG:HA	1:C:264:ARG:NE	2.29	0.47
1:C:288:VAL:C	1:C:290:GLU:N	2.70	0.47
2:D:9:VAL:HG21	2:D:149:PHE:HD1	1.80	0.47
2:D:120:ASP:O	2:D:124:LYS:HB2	2.15	0.47
2:D:132:LEU:HD21	2:D:164:LYS:HE3	1.96	0.47
2:D:148:GLY:O	2:D:151:SER:CB	2.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:172:TYR:CD1	2:D:173:PRO:N	2.80	0.47
2:D:263:PRO:O	2:D:264:ARG:C	2.56	0.47
1:E:242:LEU:HD11	1:E:250:ALA:HB3	1.97	0.47
1:E:259:MET:HE1	1:E:378:ILE:CG2	2.45	0.47
1:E:409:THR:C	1:E:411:GLU:H	2.22	0.47
2:F:5:ILE:CG2	2:F:135:PHE:HB3	2.41	0.47
2:F:9:VAL:HG21	2:F:149:PHE:HD1	1.80	0.47
2:F:115:ILE:CD1	2:F:115:ILE:C	2.87	0.47
2:F:115:ILE:HG23	2:F:116:ASP:H	1.79	0.47
2:F:132:LEU:HD21	2:F:164:LYS:HE3	1.96	0.47
2:F:256:GLN:O	2:F:260:VAL:HG13	2.15	0.47
2:F:407:TRP:O	2:F:411:GLU:CG	2.63	0.47
1:G:12:CYS:C	1:G:14:ASN:N	2.71	0.47
1:G:70:LEU:O	1:G:99:ALA:HB2	2.15	0.47
1:G:168:THR:N	1:G:200:GLU:O	2.43	0.47
1:G:242:LEU:CD1	1:G:250:ALA:HB3	2.45	0.47
1:G:242:LEU:HD11	1:G:250:ALA:HB3	1.97	0.47
1:G:259:MET:HE1	1:G:378:ILE:CG2	2.45	0.47
1:G:274:PRO:HG2	1:G:371:LEU:CD2	2.43	0.47
1:G:387:LEU:O	1:G:387:LEU:HG	2.14	0.47
2:H:9:VAL:HG21	2:H:149:PHE:HD1	1.80	0.47
2:H:102:ASN:CB	2:H:407:TRP:HE1	2.25	0.47
2:H:115:ILE:CD1	2:H:115:ILE:C	2.87	0.47
2:H:115:ILE:HG23	2:H:116:ASP:H	1.79	0.47
2:H:117:LEU:HD12	2:H:121:ARG:HH12	1.80	0.47
2:H:120:ASP:O	2:H:124:LYS:HB2	2.15	0.47
2:H:132:LEU:HD21	2:H:164:LYS:HE3	1.96	0.47
2:H:256:GLN:O	2:H:260:VAL:HG13	2.15	0.47
2:H:407:TRP:O	2:H:411:GLU:CG	2.63	0.47
1:A:156:LYS:HA	1:A:156:LYS:CE	2.38	0.47
1:A:182:VAL:O	1:A:183:GLU:C	2.56	0.47
1:A:209:LEU:O	1:A:213:CYS:N	2.47	0.47
2:B:120:ASP:O	2:B:124:LYS:HB2	2.15	0.47
2:B:191:THR:CG2	2:B:192:HIS:N	2.76	0.47
2:B:210:TYR:CE2	2:B:227:LEU:HD21	2.49	0.47
2:B:369:ALA:O	2:B:370:LYS:CB	2.62	0.47
2:B:392:ASP:OD2	2:B:422:ARG:NE	2.48	0.47
1:C:2:ARG:NH1	1:C:251:ASP:CG	2.73	0.47
1:C:101:ASN:ND2	1:C:101:ASN:O	2.47	0.47
1:C:198:THR:HG23	1:C:200:GLU:H	1.79	0.47
2:D:155:GLU:HG2	2:D:197:HIS:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:185:TYR:OH	2:D:399:TYR:HA	2.15	0.47
2:D:241:SER:HB3	2:D:320:ARG:NH2	2.29	0.47
2:D:265:GLY:O	2:D:266:HIS:O	2.33	0.47
2:D:369:ALA:O	2:D:370:LYS:CB	2.62	0.47
1:E:24:ILE:CD1	1:E:52:TYR:CE1	2.97	0.47
2:F:149:PHE:O	2:F:150:THR:C	2.56	0.47
2:F:262:TYR:HE2	1:G:403:ALA:O	1.91	0.47
2:F:346:TRP:CZ3	1:G:404:PHE:HZ	2.27	0.47
2:H:148:GLY:O	2:H:151:SER:CB	2.61	0.47
1:A:226:ASP:O	1:A:229:HIS:HB3	2.14	0.47
1:A:242:LEU:HD11	1:A:250:ALA:HB3	1.97	0.47
2:B:103:TYR:O	2:B:104:ALA:C	2.57	0.47
2:B:243:ARG:NH2	2:B:252:LEU:CB	2.78	0.47
1:C:257:VAL:CG1	2:D:407:TRP:CG	2.76	0.47
1:C:287:THR:N	1:C:290:GLU:OE1	2.48	0.47
1:C:307:PRO:HB3	1:C:312:TYR:CZ	2.49	0.47
2:D:5:ILE:CG2	2:D:135:PHE:HB3	2.41	0.47
2:D:175:PRO:HD2	2:D:207:GLU:HB3	1.96	0.47
2:D:204:VAL:CG1	2:D:209:ILE:HD11	2.42	0.47
2:D:256:GLN:HA	2:D:260:VAL:HG13	1.97	0.47
2:D:392:ASP:OD2	2:D:422:ARG:NE	2.48	0.47
2:D:436:GLY:O	2:D:438:ASP:N	2.48	0.47
1:E:2:ARG:NH1	1:E:251:ASP:CG	2.73	0.47
1:E:103:TRP:CE3	1:E:189:LEU:HD13	2.50	0.47
1:E:194:LEU:C	1:E:196:GLU:N	2.70	0.47
1:E:198:THR:HG23	1:E:200:GLU:H	1.79	0.47
1:E:237:GLY:HA3	1:E:376:THR:OG1	2.15	0.47
1:E:297:ASP:OD2	1:E:299:LYS:HE2	2.14	0.47
2:F:148:GLY:O	2:F:151:SER:CB	2.61	0.47
2:F:348:PRO:CD	1:G:398:MET:CE	2.92	0.47
1:G:103:TRP:CE3	1:G:189:LEU:HD13	2.50	0.47
1:G:243:ARG:HA	1:G:243:ARG:HD3	1.62	0.47
1:G:307:PRO:HB3	1:G:312:TYR:CZ	2.49	0.47
1:G:427:ASP:OD1	1:G:427:ASP:C	2.57	0.47
2:H:231:ILE:C	2:H:233:GLN:N	2.73	0.47
1:A:2:ARG:NH1	1:A:251:ASP:CG	2.73	0.47
1:A:103:TRP:CE3	1:A:189:LEU:HD13	2.50	0.47
1:A:427:ASP:OD1	1:A:427:ASP:C	2.57	0.47
2:B:110:ILE:O	2:B:111:GLY:C	2.57	0.47
2:B:241:SER:HB3	2:B:320:ARG:NH2	2.29	0.47
2:B:381:THR:O	2:B:383:ALA:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:436:GLY:O	2:B:438:ASP:N	2.48	0.47
1:C:409:THR:C	1:C:411:GLU:N	2.73	0.47
2:D:67:PHE:CE1	2:D:87:PHE:CD1	2.89	0.47
2:D:103:TYR:O	2:D:104:ALA:C	2.57	0.47
2:D:191:THR:O	2:D:195:LEU:HB2	2.15	0.47
2:D:335:ILE:C	2:D:337:THR:N	2.73	0.47
2:D:381:THR:O	2:D:383:ALA:N	2.48	0.47
2:D:404:PHE:CD1	2:D:404:PHE:N	2.83	0.47
2:F:191:THR:O	2:F:195:LEU:HB2	2.15	0.47
2:F:204:VAL:HG21	2:F:231:ILE:HG23	1.97	0.47
2:F:265:GLY:O	2:F:266:HIS:O	2.33	0.47
2:F:335:ILE:C	2:F:337:THR:N	2.73	0.47
1:G:24:ILE:CD1	1:G:52:TYR:CE1	2.97	0.47
1:G:384:ILE:O	1:G:384:ILE:HG23	2.14	0.47
1:G:409:THR:C	1:G:411:GLU:N	2.73	0.47
2:H:149:PHE:O	2:H:150:THR:C	2.56	0.47
2:H:204:VAL:HG21	2:H:231:ILE:HG23	1.97	0.47
2:H:335:ILE:C	2:H:337:THR:N	2.73	0.47
2:H:436:GLY:O	2:H:438:ASP:N	2.48	0.47
3:I:59:ARG:HG2	3:I:59:ARG:O	2.14	0.47
1:A:287:THR:N	1:A:290:GLU:OE1	2.48	0.46
1:A:297:ASP:OD2	1:A:299:LYS:HE2	2.14	0.46
1:A:409:THR:C	1:A:411:GLU:N	2.73	0.46
2:B:9:VAL:HG21	2:B:149:PHE:HD1	1.80	0.46
2:B:132:LEU:HD21	2:B:164:LYS:HE3	1.96	0.46
2:B:256:GLN:HA	2:B:260:VAL:HG13	1.97	0.46
2:B:335:ILE:C	2:B:337:THR:N	2.73	0.46
2:B:353:VAL:HB	1:C:179:ASP:OD1	2.15	0.46
2:D:19:ALA:HB2	2:D:228:ASN:HB3	1.96	0.46
2:D:145:THR:O	2:D:149:PHE:HB3	2.15	0.46
1:E:35:SER:CB	1:E:59:ASN:HA	2.42	0.46
1:E:82:PRO:HB2	1:E:83:PHE:H	1.56	0.46
1:E:242:LEU:CD1	1:E:250:ALA:HB3	2.45	0.46
1:E:409:THR:C	1:E:411:GLU:N	2.73	0.46
2:F:114:ILE:O	2:F:118:VAL:HG23	2.16	0.46
2:F:243:ARG:NH2	2:F:252:LEU:CB	2.78	0.46
2:F:244:PHE:CD2	2:F:245:ASP:N	2.76	0.46
2:F:324:VAL:HG12	2:F:326:LYS:H	1.81	0.46
2:F:436:GLY:O	2:F:438:ASP:N	2.48	0.46
1:G:237:GLY:HA3	1:G:376:THR:OG1	2.15	0.46
1:G:254:LYS:CE	1:G:352:LYS:NZ	2.71	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:297:ASP:OD2	1:G:299:LYS:HE2	2.14	0.46
1:G:360:PRO:HG2	1:G:371:LEU:CB	2.38	0.46
2:H:114:ILE:O	2:H:118:VAL:HG23	2.16	0.46
2:H:191:THR:O	2:H:195:LEU:HB2	2.15	0.46
2:H:243:ARG:NH2	2:H:252:LEU:CB	2.78	0.46
2:H:328:VAL:O	2:H:330:ALA:N	2.38	0.46
1:A:199:ASP:C	1:A:265:LEU:HD13	2.40	0.46
1:A:259:MET:HE1	1:A:378:ILE:HG21	1.98	0.46
1:A:260:VAL:HG21	2:B:407:TRP:HZ2	1.80	0.46
1:C:103:TRP:CE3	1:C:189:LEU:HD13	2.50	0.46
1:C:168:THR:N	1:C:200:GLU:O	2.43	0.46
1:C:431:GLU:HA	1:C:434:GLN:HG3	1.97	0.46
2:D:243:ARG:NH2	2:D:252:LEU:CB	2.78	0.46
1:E:242:LEU:HD22	1:E:250:ALA:N	2.19	0.46
1:E:259:MET:HE1	1:E:378:ILE:HG21	1.97	0.46
2:F:256:GLN:HA	2:F:260:VAL:HG13	1.97	0.46
1:G:2:ARG:NH1	1:G:251:ASP:CG	2.73	0.46
1:G:179:ASP:OD2	4:G:600:GDP:O2'	2.15	0.46
1:G:198:THR:HG23	1:G:200:GLU:H	1.79	0.46
2:H:265:GLY:O	2:H:266:HIS:O	2.33	0.46
2:H:324:VAL:HG12	2:H:326:LYS:H	1.81	0.46
1:A:198:THR:HG23	1:A:200:GLU:H	1.79	0.46
1:A:307:PRO:HB3	1:A:312:TYR:CZ	2.49	0.46
2:B:148:GLY:O	2:B:151:SER:CB	2.61	0.46
2:B:210:TYR:CZ	2:B:227:LEU:HD11	2.51	0.46
2:B:265:GLY:O	2:B:266:HIS:O	2.33	0.46
2:B:324:VAL:HG12	2:B:326:LYS:H	1.81	0.46
2:B:384:ILE:C	2:B:386:GLU:N	2.72	0.46
1:C:242:LEU:HD11	1:C:250:ALA:HB3	1.97	0.46
1:C:360:PRO:HG2	1:C:371:LEU:CB	2.38	0.46
2:D:210:TYR:CZ	2:D:227:LEU:HD11	2.51	0.46
2:D:324:VAL:HG12	2:D:326:LYS:H	1.81	0.46
1:E:115:VAL:CG2	1:E:152:LEU:HD23	2.44	0.46
1:E:156:LYS:HA	1:E:156:LYS:CE	2.38	0.46
1:E:274:PRO:HG2	1:E:371:LEU:CD2	2.43	0.46
1:E:324:SER:OG	1:E:326:LYS:HB3	2.16	0.46
2:F:63:PRO:HG2	2:F:87:PHE:CG	2.51	0.46
2:F:243:ARG:NH2	2:F:252:LEU:HB2	2.30	0.46
1:G:194:LEU:C	1:G:196:GLU:N	2.70	0.46
1:G:332:MET:CE	1:G:351:VAL:HG11	2.32	0.46
2:H:110:ILE:O	2:H:111:GLY:C	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:117:LEU:HD11	2:H:121:ARG:NH2	2.30	0.46
2:H:243:ARG:NH2	2:H:252:LEU:HB2	2.30	0.46
2:H:244:PHE:CD2	2:H:245:ASP:N	2.76	0.46
3:I:83:LEU:HB2	3:I:116:MET:HE1	1.96	0.46
3:I:100:GLY:C	3:I:101:VAL:HG23	2.39	0.46
1:A:383:ALA:C	1:A:385:GLN:N	2.72	0.46
1:A:421:ALA:O	1:A:422:GLU:C	2.58	0.46
2:B:19:ALA:HB2	2:B:228:ASN:HB3	1.96	0.46
2:B:204:VAL:HG21	2:B:231:ILE:HG23	1.97	0.46
1:C:199:ASP:C	1:C:265:LEU:HD13	2.41	0.46
1:C:427:ASP:OD1	1:C:427:ASP:C	2.57	0.46
2:D:166:LYS:CE	2:D:199:ASP:OD1	2.62	0.46
1:E:288:VAL:C	1:E:290:GLU:N	2.70	0.46
1:E:427:ASP:OD1	1:E:427:ASP:C	2.57	0.46
2:F:110:ILE:O	2:F:111:GLY:C	2.57	0.46
2:F:117:LEU:HD11	2:F:121:ARG:NH2	2.30	0.46
2:F:145:THR:O	2:F:149:PHE:HB3	2.15	0.46
1:G:259:MET:HE1	1:G:378:ILE:HG21	1.97	0.46
2:H:103:TYR:O	2:H:104:ALA:C	2.57	0.46
2:H:256:GLN:HA	2:H:260:VAL:HG13	1.97	0.46
3:I:54:LYS:O	3:I:122:GLY:N	2.49	0.46
3:I:72:VAL:HG11	3:I:83:LEU:HD22	1.98	0.46
1:A:70:LEU:O	1:A:99:ALA:HB2	2.15	0.46
1:A:154:ILE:HD12	1:A:155:SER:N	2.31	0.46
2:B:63:PRO:HG3	2:B:87:PHE:CG	2.50	0.46
2:B:317:LEU:CD1	2:B:351:PHE:CD2	2.97	0.46
1:C:72:PRO:O	1:C:73:GLY:C	2.58	0.46
1:C:134:GLY:HA3	1:C:165:ILE:HG12	1.97	0.46
1:C:154:ILE:HD12	1:C:155:SER:N	2.31	0.46
2:D:401:LYS:C	2:D:403:ALA:H	2.24	0.46
1:E:12:CYS:C	1:E:14:ASN:N	2.71	0.46
1:E:168:THR:N	1:E:200:GLU:O	2.43	0.46
1:E:250:ALA:HB1	1:E:254:LYS:CB	2.44	0.46
1:E:383:ALA:C	1:E:385:GLN:N	2.72	0.46
2:F:95:GLY:C	2:F:97:GLU:H	2.23	0.46
2:F:103:TYR:O	2:F:104:ALA:C	2.57	0.46
2:F:185:TYR:OH	2:F:399:TYR:HA	2.15	0.46
2:F:349:THR:HG22	1:G:178:SER:O	2.13	0.46
1:G:324:SER:OG	1:G:326:LYS:HB3	2.15	0.46
1:G:431:GLU:HA	1:G:434:GLN:HG3	1.98	0.46
2:H:95:GLY:C	2:H:97:GLU:H	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:392:ASP:OD2	2:H:422:ARG:NE	2.48	0.46
2:B:23:LEU:CD2	2:B:232:GLY:O	2.64	0.46
2:B:62:VAL:HA	2:B:86:LEU:O	2.15	0.46
2:B:348:PRO:HD3	1:C:398:MET:HB3	1.97	0.46
1:C:70:LEU:O	1:C:99:ALA:HB2	2.15	0.46
1:C:259:MET:HE1	1:C:378:ILE:HG21	1.98	0.46
2:D:110:ILE:O	2:D:111:GLY:C	2.58	0.46
2:D:204:VAL:HG21	2:D:231:ILE:HG23	1.97	0.46
1:E:435:TYR:C	1:E:437:ASP:N	2.72	0.46
2:F:67:PHE:CE1	2:F:87:PHE:CD1	2.89	0.46
2:F:81:GLY:O	2:F:82:THR:C	2.59	0.46
2:F:230:LEU:O	2:F:231:ILE:C	2.57	0.46
2:F:316:CYS:HB3	2:F:378:LEU:HD12	1.94	0.46
2:F:328:VAL:O	2:F:330:ALA:N	2.38	0.46
1:G:156:LYS:HA	1:G:156:LYS:CE	2.38	0.46
1:G:196:GLU:O	1:G:197:ASN:OD1	2.34	0.46
1:G:208:ALA:O	1:G:212:ILE:HG13	2.16	0.46
1:G:245:PRO:CB	2:H:73:THR:HG21	2.45	0.46
1:G:245:PRO:CA	2:H:73:THR:HG21	2.44	0.46
1:G:287:THR:N	1:G:290:GLU:OE1	2.48	0.46
1:G:342:TYR:HD2	3:I:64:TYR:OH	1.99	0.46
2:H:11:GLN:O	2:H:15:GLN:HG3	2.15	0.46
2:H:63:PRO:HG2	2:H:87:PHE:CG	2.51	0.46
2:H:185:TYR:OH	2:H:399:TYR:HA	2.15	0.46
2:H:210:TYR:CZ	2:H:227:LEU:HD11	2.51	0.46
2:H:316:CYS:HB3	2:H:378:LEU:HD12	1.95	0.46
1:A:196:GLU:O	1:A:197:ASN:OD1	2.34	0.46
1:A:237:GLY:HA3	1:A:376:THR:OG1	2.15	0.46
1:A:245:PRO:HA	2:B:73:THR:CG2	2.46	0.46
1:A:431:GLU:HA	1:A:434:GLN:HG3	1.97	0.46
2:B:114:ILE:O	2:B:118:VAL:HG23	2.15	0.46
2:B:166:LYS:CE	2:B:199:ASP:OD1	2.62	0.46
1:C:196:GLU:O	1:C:197:ASN:OD1	2.34	0.46
1:C:237:GLY:HA3	1:C:376:THR:OG1	2.15	0.46
2:D:63:PRO:HG2	2:D:87:PHE:CG	2.51	0.46
2:D:328:VAL:O	2:D:330:ALA:N	2.38	0.46
1:E:199:ASP:C	1:E:265:LEU:HD13	2.41	0.46
1:E:208:ALA:O	1:E:212:ILE:HG13	2.16	0.46
1:E:230:LEU:CG	1:E:302:MET:HE2	2.46	0.46
1:E:360:PRO:HG2	1:E:371:LEU:CB	2.38	0.46
2:F:11:GLN:O	2:F:15:GLN:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:210:TYR:CZ	2:F:227:LEU:HD11	2.51	0.46
2:F:210:TYR:CD2	2:F:227:LEU:HD21	2.51	0.46
2:F:226:ASN:O	2:F:227:LEU:C	2.59	0.46
2:F:392:ASP:OD2	2:F:422:ARG:NE	2.48	0.46
1:G:102:ASN:ND2	1:G:104:ALA:HB3	2.31	0.46
1:G:383:ALA:C	1:G:385:GLN:N	2.72	0.46
2:H:61:HIS:O	2:H:62:VAL:C	2.59	0.46
2:H:81:GLY:O	2:H:82:THR:C	2.59	0.46
2:H:145:THR:O	2:H:149:PHE:HB3	2.15	0.46
2:H:210:TYR:CD2	2:H:227:LEU:HD21	2.51	0.46
1:A:230:LEU:CG	1:A:302:MET:HE2	2.46	0.46
2:B:5:ILE:HD11	2:B:64:ARG:NH2	2.31	0.46
2:B:104:ALA:HB1	2:B:413:MET:HG3	1.96	0.46
2:B:145:THR:O	2:B:149:PHE:HB3	2.15	0.46
1:C:230:LEU:CG	1:C:302:MET:HE2	2.46	0.46
1:C:297:ASP:OD2	1:C:299:LYS:HE2	2.14	0.46
1:C:383:ALA:C	1:C:385:GLN:N	2.72	0.46
1:C:421:ALA:O	1:C:422:GLU:C	2.58	0.46
2:D:114:ILE:O	2:D:118:VAL:HG23	2.16	0.46
2:D:130:THR:O	2:D:131:GLY:C	2.59	0.46
2:D:226:ASN:O	2:D:229:ARG:N	2.48	0.46
1:E:113:GLU:CG	1:E:114:LEU:N	2.79	0.46
2:F:63:PRO:HD2	2:F:87:PHE:HA	1.97	0.46
2:F:226:ASN:O	2:F:229:ARG:N	2.48	0.46
2:F:381:THR:O	2:F:383:ALA:N	2.49	0.46
2:F:388:TRP:HA	2:F:388:TRP:HE3	1.79	0.46
1:G:35:SER:CB	1:G:59:ASN:HA	2.42	0.46
1:G:199:ASP:C	1:G:265:LEU:HD13	2.41	0.46
2:H:19:ALA:HB2	2:H:228:ASN:HB3	1.96	0.46
2:H:119:LEU:HD11	2:H:156:ARG:HD2	1.97	0.46
2:H:226:ASN:O	2:H:227:LEU:C	2.59	0.46
1:A:11:GLN:O	1:A:14:ASN:HB3	2.16	0.46
1:A:134:GLY:HA3	1:A:165:ILE:HG12	1.97	0.46
1:A:435:TYR:C	1:A:437:ASP:N	2.72	0.46
2:B:130:THR:O	2:B:131:GLY:C	2.59	0.46
1:C:11:GLN:O	1:C:14:ASN:HB3	2.16	0.46
2:D:23:LEU:CD2	2:D:232:GLY:O	2.64	0.46
2:D:104:ALA:HB1	2:D:413:MET:HG3	1.95	0.46
2:D:226:ASN:O	2:D:227:LEU:C	2.59	0.46
1:E:72:PRO:O	1:E:73:GLY:C	2.58	0.46
1:E:196:GLU:O	1:E:197:ASN:OD1	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:287:THR:N	1:E:290:GLU:OE1	2.48	0.46
1:E:431:GLU:HA	1:E:434:GLN:HG3	1.98	0.46
1:G:133:GLN:O	1:G:165:ILE:CD1	2.64	0.46
1:G:154:ILE:HD12	1:G:155:SER:N	2.31	0.46
1:G:230:LEU:CG	1:G:302:MET:HE2	2.46	0.46
1:G:250:ALA:HB1	1:G:254:LYS:CB	2.44	0.46
2:H:63:PRO:HD2	2:H:87:PHE:HA	1.98	0.46
2:H:230:LEU:O	2:H:231:ILE:C	2.57	0.46
1:A:133:GLN:O	1:A:165:ILE:CD1	2.64	0.46
1:A:310:GLY:HA3	1:A:436:GLN:NE2	2.29	0.46
2:B:95:GLY:C	2:B:97:GLU:H	2.23	0.46
2:B:119:LEU:HD11	2:B:156:ARG:HD2	1.97	0.46
2:B:210:TYR:CD2	2:B:227:LEU:HD21	2.51	0.46
2:B:256:GLN:O	2:B:260:VAL:HG13	2.15	0.46
1:C:72:PRO:O	1:C:74:THR:N	2.50	0.46
1:C:137:LEU:HD22	1:C:154:ILE:HG23	1.97	0.46
1:C:310:GLY:HA3	1:C:436:GLN:NE2	2.29	0.46
1:C:408:TYR:O	1:C:411:GLU:HB2	2.15	0.46
2:D:95:GLY:C	2:D:97:GLU:H	2.23	0.46
1:E:11:GLN:O	1:E:14:ASN:HB3	2.16	0.46
1:E:98:GLY:C	1:E:100:GLY:H	2.24	0.46
1:E:133:GLN:O	1:E:165:ILE:CD1	2.64	0.46
1:E:154:ILE:HD12	1:E:155:SER:N	2.31	0.46
1:E:175:PRO:HG2	1:E:207:GLU:OE1	2.16	0.46
2:F:119:LEU:HD11	2:F:156:ARG:HD2	1.97	0.46
2:F:328:VAL:C	2:F:330:ALA:N	2.73	0.46
1:G:113:GLU:CG	1:G:114:LEU:N	2.79	0.46
1:G:245:PRO:HB3	2:H:73:THR:HG22	1.98	0.46
1:G:245:PRO:HB3	2:H:73:THR:HG21	1.97	0.46
1:G:248:LEU:HD21	2:H:179:THR:HG22	1.92	0.46
1:G:257:VAL:CG2	2:H:407:TRP:HB3	2.28	0.46
2:H:23:LEU:CD2	2:H:232:GLY:O	2.64	0.46
2:H:52:PHE:O	2:H:64:ARG:HB3	2.16	0.46
2:H:328:VAL:C	2:H:330:ALA:N	2.73	0.46
2:H:381:THR:O	2:H:383:ALA:N	2.49	0.46
2:H:384:ILE:C	2:H:386:GLU:N	2.72	0.46
2:H:388:TRP:HA	2:H:388:TRP:HE3	1.79	0.46
3:I:77:PHE:HB2	3:I:116:MET:HE3	1.98	0.46
1:A:72:PRO:O	1:A:73:GLY:C	2.58	0.45
1:A:72:PRO:O	1:A:74:THR:N	2.50	0.45
1:A:94:PHE:CD2	1:A:94:PHE:N	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:GLY:C	1:A:100:GLY:H	2.24	0.45
1:A:175:PRO:HG2	1:A:207:GLU:OE1	2.17	0.45
1:A:208:ALA:O	1:A:212:ILE:HG13	2.16	0.45
1:A:210:TYR:O	1:A:211:ASP:C	2.57	0.45
2:B:5:ILE:CG2	2:B:6:SER:H	2.29	0.45
2:B:384:ILE:HG22	2:B:384:ILE:O	2.15	0.45
1:C:6:HIS:HB3	1:C:21:TRP:HZ2	1.81	0.45
1:C:98:GLY:C	1:C:100:GLY:H	2.24	0.45
1:C:175:PRO:HG2	1:C:207:GLU:OE1	2.17	0.45
2:D:210:TYR:CD2	2:D:227:LEU:HD21	2.51	0.45
1:E:72:PRO:O	1:E:74:THR:N	2.49	0.45
1:E:102:ASN:ND2	1:E:104:ALA:HB3	2.31	0.45
1:E:134:GLY:HA3	1:E:165:ILE:HG12	1.97	0.45
1:E:421:ALA:O	1:E:422:GLU:C	2.58	0.45
2:F:203:MET:SD	2:F:267:PHE:CB	3.04	0.45
1:G:175:PRO:HG2	1:G:207:GLU:OE1	2.17	0.45
1:G:257:VAL:O	2:H:404:PHE:HB3	2.15	0.45
1:G:408:TYR:O	1:G:411:GLU:HB2	2.15	0.45
2:H:104:ALA:HB1	2:H:413:MET:HG3	1.95	0.45
2:H:203:MET:SD	2:H:267:PHE:CB	3.04	0.45
2:H:226:ASN:O	2:H:229:ARG:N	2.48	0.45
2:B:117:LEU:HD11	2:B:121:ARG:NH2	2.31	0.45
2:B:155:GLU:HA	2:B:197:HIS:CE1	2.49	0.45
2:B:226:ASN:O	2:B:227:LEU:C	2.59	0.45
2:B:226:ASN:O	2:B:229:ARG:N	2.48	0.45
2:B:328:VAL:C	2:B:330:ALA:N	2.73	0.45
2:B:401:LYS:C	2:B:403:ALA:H	2.24	0.45
1:C:12:CYS:C	1:C:14:ASN:N	2.71	0.45
1:C:209:LEU:HD23	1:C:227:LEU:HD13	1.98	0.45
1:C:423:SER:O	1:C:424:ASN:C	2.60	0.45
2:D:117:LEU:HD11	2:D:121:ARG:NH2	2.30	0.45
1:E:94:PHE:CD2	1:E:94:PHE:N	2.84	0.45
1:E:332:MET:CE	1:E:351:VAL:HG11	2.32	0.45
1:E:380:ASN:HD22	1:E:380:ASN:C	2.24	0.45
1:E:409:THR:HA	1:E:413:MET:HB3	1.99	0.45
2:F:23:LEU:CD2	2:F:232:GLY:O	2.64	0.45
2:F:152:LEU:C	2:F:152:LEU:CD1	2.89	0.45
1:G:11:GLN:O	1:G:14:ASN:HB3	2.16	0.45
1:G:98:GLY:C	1:G:100:GLY:H	2.24	0.45
1:G:409:THR:HA	1:G:413:MET:HB3	1.99	0.45
2:H:152:LEU:C	2:H:152:LEU:CD1	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:425:MET:O	2:H:426:ALA:C	2.60	0.45
1:A:12:CYS:C	1:A:14:ASN:N	2.71	0.45
1:A:113:GLU:CG	1:A:114:LEU:N	2.79	0.45
1:A:137:LEU:HD22	1:A:154:ILE:HG23	1.97	0.45
1:A:408:TYR:O	1:A:411:GLU:HB2	2.15	0.45
2:B:152:LEU:C	2:B:152:LEU:CD1	2.89	0.45
2:B:203:MET:SD	2:B:267:PHE:CB	3.04	0.45
2:B:231:ILE:C	2:B:233:GLN:N	2.73	0.45
2:B:346:TRP:HZ2	2:B:435:VAL:HG12	1.81	0.45
1:C:133:GLN:O	1:C:165:ILE:CD1	2.64	0.45
1:C:313:LEU:O	1:C:347:ILE:HD12	2.16	0.45
2:D:11:GLN:O	2:D:15:GLN:HG3	2.15	0.45
2:D:328:VAL:C	2:D:330:ALA:N	2.73	0.45
2:D:384:ILE:HG22	2:D:384:ILE:O	2.15	0.45
1:E:67:LEU:HD12	1:E:92:PHE:CD2	2.51	0.45
1:E:187:ALA:O	1:E:188:THR:C	2.57	0.45
1:E:210:TYR:CE2	1:E:227:LEU:HD11	2.52	0.45
2:F:19:ALA:HB2	2:F:228:ASN:HB3	1.96	0.45
2:F:104:ALA:HB1	2:F:413:MET:HG3	1.95	0.45
2:F:384:ILE:C	2:F:386:GLU:N	2.72	0.45
2:F:425:MET:O	2:F:426:ALA:C	2.60	0.45
1:G:82:PRO:HB2	1:G:83:PHE:H	1.55	0.45
1:G:313:LEU:O	1:G:347:ILE:HD12	2.16	0.45
1:G:325:MET:HE1	1:G:355:VAL:HG21	1.99	0.45
1:G:380:ASN:C	1:G:380:ASN:HD22	2.24	0.45
1:G:435:TYR:C	1:G:437:ASP:N	2.72	0.45
2:H:401:LYS:C	2:H:403:ALA:H	2.24	0.45
1:A:67:LEU:HD12	1:A:92:PHE:CD2	2.51	0.45
1:A:135:PHE:N	1:A:135:PHE:CD1	2.85	0.45
1:A:250:ALA:HB1	1:A:254:LYS:CB	2.43	0.45
1:A:423:SER:O	1:A:424:ASN:C	2.60	0.45
2:B:11:GLN:O	2:B:15:GLN:HG3	2.15	0.45
2:B:100:ALA:C	2:B:102:ASN:H	2.24	0.45
2:B:392:ASP:OD2	2:B:422:ARG:CZ	2.65	0.45
2:B:413:MET:C	2:B:414:GLU:CG	2.90	0.45
1:C:67:LEU:HD12	1:C:92:PHE:CD2	2.51	0.45
1:C:70:LEU:HD21	1:C:149:MET:HE3	1.99	0.45
1:C:113:GLU:CG	1:C:114:LEU:N	2.79	0.45
1:C:135:PHE:CD1	1:C:135:PHE:N	2.84	0.45
1:C:319:PHE:CD2	1:C:323:MET:HE1	2.52	0.45
1:C:435:TYR:C	1:C:437:ASP:N	2.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:7:ILE:HG13	2:D:137:VAL:HG22	1.97	0.45
2:D:152:LEU:C	2:D:152:LEU:CD1	2.89	0.45
2:D:256:GLN:O	2:D:260:VAL:HG13	2.15	0.45
2:D:423:GLU:O	2:D:426:ALA:HB3	2.16	0.45
1:E:288:VAL:N	1:E:289:PRO:CD	2.79	0.45
1:E:408:TYR:O	1:E:411:GLU:HB2	2.15	0.45
2:F:268:PRO:CA	2:F:379:SER:O	2.65	0.45
2:F:346:TRP:HZ2	2:F:435:VAL:HG12	1.81	0.45
1:G:72:PRO:O	1:G:73:GLY:C	2.58	0.45
1:G:72:PRO:O	1:G:74:THR:N	2.50	0.45
1:G:94:PHE:N	1:G:94:PHE:CD2	2.84	0.45
1:G:257:VAL:HG11	2:H:407:TRP:CE2	2.52	0.45
1:A:24:ILE:CD1	1:A:52:TYR:CE1	2.97	0.45
1:A:319:PHE:CD2	1:A:323:MET:HE1	2.52	0.45
2:B:81:GLY:O	2:B:82:THR:C	2.59	0.45
2:B:317:LEU:CD1	2:B:351:PHE:CE2	2.99	0.45
2:B:408:TYR:CG	2:B:418:PHE:HZ	2.34	0.45
1:C:24:ILE:CD1	1:C:52:TYR:CE1	2.97	0.45
1:C:35:SER:CB	1:C:59:ASN:HA	2.42	0.45
1:C:94:PHE:CD2	1:C:94:PHE:N	2.84	0.45
1:C:208:ALA:O	1:C:212:ILE:HG13	2.16	0.45
2:D:61:HIS:O	2:D:62:VAL:C	2.59	0.45
2:D:243:ARG:NH2	2:D:252:LEU:HB2	2.30	0.45
1:E:210:TYR:O	1:E:211:ASP:C	2.57	0.45
1:E:319:PHE:CD2	1:E:323:MET:HE1	2.52	0.45
1:E:324:SER:O	1:E:326:LYS:N	2.50	0.45
1:E:325:MET:HE1	1:E:355:VAL:HG21	1.99	0.45
2:F:100:ALA:C	2:F:102:ASN:H	2.24	0.45
2:F:155:GLU:HA	2:F:197:HIS:CE1	2.49	0.45
2:F:212:ILE:HD11	2:F:302:MET:H	1.82	0.45
2:F:317:LEU:CD1	2:F:351:PHE:CE2	2.99	0.45
1:G:209:LEU:HD23	1:G:227:LEU:HD13	1.98	0.45
1:G:273:ALA:CB	1:G:274:PRO:CD	2.93	0.45
1:G:319:PHE:CD2	1:G:323:MET:HE1	2.52	0.45
1:G:324:SER:O	1:G:326:LYS:N	2.50	0.45
1:G:409:THR:O	1:G:412:GLY:N	2.48	0.45
2:H:100:ALA:C	2:H:102:ASN:H	2.24	0.45
2:H:144:GLY:H	5:H:500:GTP:PG	2.40	0.45
2:H:212:ILE:HD11	2:H:302:MET:H	1.82	0.45
2:H:346:TRP:HZ2	2:H:435:VAL:HG12	1.81	0.45
1:A:288:VAL:N	1:A:289:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:LEU:O	1:A:347:ILE:HD12	2.16	0.45
2:B:308:ARG:O	2:B:309:HIS:HB3	2.16	0.45
2:B:316:CYS:HB3	2:B:378:LEU:HD12	1.95	0.45
2:B:334:THR:CG2	2:B:335:ILE:N	2.79	0.45
2:B:423:GLU:O	2:B:426:ALA:HB3	2.16	0.45
1:C:332:MET:HE3	1:C:351:VAL:CG1	2.32	0.45
1:C:413:MET:HG3	1:C:414:ASP:N	2.22	0.45
2:D:100:ALA:C	2:D:102:ASN:H	2.24	0.45
2:D:144:GLY:H	5:D:500:GTP:PG	2.39	0.45
2:D:303:VAL:O	2:D:303:VAL:CG1	2.64	0.45
2:D:316:CYS:HB3	2:D:378:LEU:HD12	1.95	0.45
2:D:317:LEU:CD1	2:D:351:PHE:CE2	2.99	0.45
2:D:334:THR:CG2	2:D:335:ILE:N	2.79	0.45
2:D:413:MET:C	2:D:414:GLU:CG	2.90	0.45
1:E:209:LEU:HD23	1:E:227:LEU:HD13	1.98	0.45
2:F:115:ILE:CG1	2:F:152:LEU:HD13	2.46	0.45
2:F:144:GLY:H	5:F:500:GTP:PG	2.40	0.45
2:F:401:LYS:C	2:F:403:ALA:H	2.24	0.45
2:F:413:MET:C	2:F:414:GLU:CG	2.90	0.45
1:G:188:THR:HG23	1:G:425:MET:HE3	1.98	0.45
1:G:210:TYR:CE2	1:G:227:LEU:HD11	2.52	0.45
1:G:242:LEU:HD22	1:G:250:ALA:N	2.19	0.45
1:G:288:VAL:N	1:G:289:PRO:CD	2.79	0.45
1:G:333:LEU:O	1:G:334:ASN:C	2.58	0.45
2:H:62:VAL:CG1	2:H:91:GLN:NE2	2.80	0.45
2:H:155:GLU:HA	2:H:197:HIS:CE1	2.49	0.45
2:H:268:PRO:CA	2:H:379:SER:O	2.65	0.45
2:H:317:LEU:CD1	2:H:351:PHE:CE2	2.99	0.45
3:I:80:PHE:CE1	3:I:119:LEU:HD21	2.52	0.45
1:A:4:ILE:HD12	1:A:239:THR:HG21	1.98	0.45
1:A:209:LEU:HD23	1:A:227:LEU:HD13	1.98	0.45
1:A:210:TYR:CE2	1:A:227:LEU:HD11	2.52	0.45
1:A:312:TYR:HA	1:A:381:SER:HA	1.99	0.45
1:A:324:SER:OG	1:A:326:LYS:HB3	2.15	0.45
2:B:204:VAL:O	2:B:204:VAL:HG12	2.17	0.45
2:B:253:THR:HG21	1:C:105:LYS:NZ	2.32	0.45
1:C:210:TYR:CE2	1:C:227:LEU:HD11	2.51	0.45
1:C:324:SER:OG	1:C:326:LYS:HB3	2.15	0.45
2:D:62:VAL:CG1	2:D:91:GLN:NE2	2.80	0.45
2:D:63:PRO:HD2	2:D:87:PHE:HA	1.98	0.45
2:D:103:TYR:CD1	2:D:148:GLY:HA2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:203:MET:SD	2:D:267:PHE:CB	3.04	0.45
1:E:95:GLY:C	1:E:97:SER:H	2.25	0.45
1:E:106:GLY:O	1:E:149:MET:HB2	2.17	0.45
1:E:135:PHE:N	1:E:135:PHE:CD1	2.85	0.45
1:E:313:LEU:O	1:E:347:ILE:HD12	2.16	0.45
1:E:333:LEU:O	1:E:334:ASN:C	2.58	0.45
2:F:52:PHE:O	2:F:64:ARG:HB3	2.16	0.45
2:F:62:VAL:CG1	2:F:91:GLN:NE2	2.80	0.45
2:F:295:CYS:SG	2:F:375:VAL:HG11	2.57	0.45
2:F:393:HIS:O	2:F:394:LYS:C	2.59	0.45
1:G:106:GLY:O	1:G:149:MET:HB2	2.16	0.45
1:G:135:PHE:N	1:G:135:PHE:CD1	2.85	0.45
2:H:67:PHE:CE1	2:H:87:PHE:CD1	2.89	0.45
2:H:413:MET:C	2:H:414:GLU:CG	2.90	0.45
1:A:6:HIS:HB3	1:A:21:TRP:HZ2	1.81	0.45
1:A:8:GLN:CG	1:A:67:LEU:HD22	2.47	0.45
1:A:35:SER:CB	1:A:59:ASN:HA	2.42	0.45
1:A:70:LEU:HD21	1:A:149:MET:HE3	1.98	0.45
1:A:188:THR:HG23	1:A:425:MET:HE3	1.98	0.45
2:B:132:LEU:H	2:B:132:LEU:CD2	2.23	0.45
2:B:434:GLU:C	2:B:436:GLY:N	2.74	0.45
1:C:8:GLN:CG	1:C:67:LEU:HD22	2.47	0.45
1:C:102:ASN:ND2	1:C:104:ALA:HB3	2.31	0.45
1:C:192:HIS:HD1	1:C:424:ASN:CG	2.20	0.45
1:C:194:LEU:O	1:C:265:LEU:HD23	2.17	0.45
1:C:273:ALA:CB	1:C:274:PRO:CD	2.93	0.45
1:C:288:VAL:N	1:C:289:PRO:CD	2.80	0.45
1:C:324:SER:O	1:C:326:LYS:N	2.50	0.45
2:D:81:GLY:O	2:D:82:THR:C	2.59	0.45
2:D:119:LEU:HD11	2:D:156:ARG:HD2	1.97	0.45
2:D:212:ILE:HD11	2:D:302:MET:H	1.82	0.45
2:D:388:TRP:CD2	2:D:425:MET:HE1	2.52	0.45
1:E:194:LEU:O	1:E:265:LEU:HD23	2.16	0.45
1:E:312:TYR:HA	1:E:381:SER:HA	1.99	0.45
2:F:182:VAL:O	2:F:184:PRO:CD	2.65	0.45
2:F:408:TYR:CG	2:F:418:PHE:HZ	2.34	0.45
1:G:67:LEU:HD12	1:G:92:PHE:CD2	2.51	0.45
1:G:254:LYS:HA	1:G:257:VAL:HG12	1.99	0.45
1:G:421:ALA:O	1:G:422:GLU:C	2.58	0.45
2:H:103:TYR:CD1	2:H:148:GLY:HA2	2.52	0.45
2:H:295:CYS:SG	2:H:375:VAL:HG11	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:393:HIS:O	2:H:394:LYS:C	2.59	0.45
1:A:102:ASN:ND2	1:A:104:ALA:HB3	2.31	0.45
1:A:102:ASN:OD1	1:A:408:TYR:CZ	2.70	0.45
1:A:273:ALA:CB	1:A:274:PRO:CD	2.93	0.45
1:A:325:MET:HE1	1:A:355:VAL:HG21	1.99	0.45
2:B:103:TYR:CD1	2:B:148:GLY:HA2	2.52	0.45
1:C:102:ASN:OD1	1:C:408:TYR:CZ	2.70	0.45
1:C:409:THR:O	1:C:412:GLY:N	2.48	0.45
2:D:204:VAL:O	2:D:204:VAL:HG12	2.17	0.45
2:D:274:PRO:HB2	2:D:371:VAL:HG21	1.98	0.45
2:D:346:TRP:HZ2	2:D:435:VAL:HG12	1.81	0.45
2:D:408:TYR:CG	2:D:418:PHE:HZ	2.34	0.45
1:E:115:VAL:HG21	1:E:152:LEU:HD21	1.98	0.45
2:F:61:HIS:O	2:F:62:VAL:C	2.59	0.45
2:F:182:VAL:O	2:F:183:GLU:C	2.60	0.45
2:F:274:PRO:HB2	2:F:371:VAL:HG21	1.98	0.45
2:F:334:THR:CG2	2:F:335:ILE:N	2.79	0.45
1:G:6:HIS:HB3	1:G:21:TRP:HZ2	1.81	0.45
1:G:95:GLY:C	1:G:97:SER:H	2.25	0.45
2:H:115:ILE:CG1	2:H:152:LEU:HD13	2.46	0.45
2:H:182:VAL:O	2:H:184:PRO:CD	2.65	0.45
2:H:308:ARG:O	2:H:309:HIS:HB3	2.16	0.45
1:A:106:GLY:O	1:A:149:MET:HB2	2.16	0.45
1:A:189:LEU:HD23	1:A:421:ALA:CB	2.47	0.45
1:A:324:SER:O	1:A:326:LYS:N	2.50	0.45
1:A:409:THR:O	1:A:412:GLY:N	2.48	0.45
2:B:212:ILE:HD11	2:B:302:MET:H	1.82	0.45
2:B:234:ILE:C	2:B:234:ILE:CD1	2.86	0.45
2:B:243:ARG:NH2	2:B:252:LEU:HB2	2.30	0.45
2:B:276:ILE:CG2	2:B:369:ALA:CB	2.91	0.45
2:B:295:CYS:SG	2:B:375:VAL:HG11	2.57	0.45
2:B:303:VAL:O	2:B:303:VAL:CG1	2.64	0.45
1:C:23:VAL:O	1:C:25:SER:N	2.50	0.45
1:C:312:TYR:HA	1:C:381:SER:HA	1.99	0.45
1:C:380:ASN:HD22	1:C:380:ASN:C	2.24	0.45
2:D:345:ASP:C	2:D:347:CYS:N	2.68	0.45
2:D:392:ASP:OD2	2:D:422:ARG:CZ	2.65	0.45
1:E:12:CYS:O	1:E:13:GLY:C	2.59	0.45
1:E:23:VAL:O	1:E:25:SER:N	2.50	0.45
1:E:188:THR:HG23	1:E:425:MET:HE3	1.98	0.45
2:F:384:ILE:HG22	2:F:384:ILE:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:384:ILE:O	2:F:385:ALA:C	2.59	0.45
2:F:388:TRP:CD2	2:F:425:MET:HE1	2.52	0.45
1:G:8:GLN:CG	1:G:67:LEU:HD22	2.47	0.45
1:G:115:VAL:HG21	1:G:152:LEU:HD21	1.98	0.45
1:G:134:GLY:HA3	1:G:165:ILE:HG12	1.97	0.45
1:G:312:TYR:HA	1:G:381:SER:HA	1.99	0.45
2:H:182:VAL:O	2:H:183:GLU:C	2.60	0.45
2:H:384:ILE:HG22	2:H:384:ILE:O	2.15	0.45
2:H:408:TYR:CG	2:H:418:PHE:HZ	2.34	0.45
3:I:97:LEU:HB3	3:I:100:GLY:O	2.16	0.45
1:A:194:LEU:O	1:A:265:LEU:HD23	2.16	0.44
2:B:4:CYS:SG	2:B:252:LEU:CD1	3.02	0.44
2:B:108:TYR:O	2:B:109:THR:C	2.61	0.44
2:B:402:ARG:O	2:B:405:VAL:N	2.49	0.44
2:B:404:PHE:CD1	2:B:404:PHE:N	2.83	0.44
1:C:167:ASN:HA	1:C:200:GLU:O	2.17	0.44
1:C:189:LEU:HD23	1:C:421:ALA:CB	2.47	0.44
2:D:108:TYR:O	2:D:109:THR:C	2.61	0.44
2:D:231:ILE:C	2:D:233:GLN:N	2.73	0.44
2:D:295:CYS:SG	2:D:375:VAL:HG11	2.57	0.44
2:D:425:MET:O	2:D:426:ALA:C	2.60	0.44
1:E:6:HIS:HB3	1:E:21:TRP:HZ2	1.81	0.44
1:E:52:TYR:HE1	1:E:240:THR:HB	1.82	0.44
1:E:137:LEU:HD22	1:E:154:ILE:HG23	1.97	0.44
1:E:409:THR:O	1:E:412:GLY:N	2.48	0.44
2:F:103:TYR:CD1	2:F:148:GLY:HA2	2.52	0.44
2:F:153:LEU:O	2:F:157:LEU:HG	2.18	0.44
2:F:231:ILE:HD13	2:F:231:ILE:H	1.82	0.44
2:F:303:VAL:O	2:F:303:VAL:CG1	2.65	0.44
2:F:344:VAL:CG1	2:F:345:ASP:N	2.78	0.44
2:F:423:GLU:O	2:F:426:ALA:HB3	2.16	0.44
1:G:52:TYR:HE1	1:G:240:THR:HB	1.83	0.44
1:G:189:LEU:HD23	1:G:421:ALA:CB	2.47	0.44
1:G:194:LEU:O	1:G:265:LEU:HD23	2.16	0.44
2:H:130:THR:O	2:H:131:GLY:C	2.59	0.44
2:H:153:LEU:O	2:H:157:LEU:HG	2.18	0.44
2:H:274:PRO:HB2	2:H:371:VAL:HG21	1.98	0.44
2:H:334:THR:CG2	2:H:335:ILE:N	2.79	0.44
2:H:384:ILE:O	2:H:385:ALA:C	2.59	0.44
1:A:14:ASN:O	1:A:17:GLY:N	2.50	0.44
1:A:99:ALA:O	1:A:100:GLY:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:GLN:O	1:A:282:GLN:CG	2.65	0.44
1:A:333:LEU:O	1:A:334:ASN:C	2.58	0.44
2:B:344:VAL:CG1	2:B:345:ASP:N	2.78	0.44
2:B:384:ILE:O	2:B:385:ALA:C	2.59	0.44
2:B:388:TRP:CD2	2:B:425:MET:HE1	2.52	0.44
1:C:4:ILE:HD12	1:C:239:THR:HG21	1.99	0.44
1:C:95:GLY:C	1:C:97:SER:H	2.25	0.44
1:C:161:TYR:C	1:C:163:ASP:N	2.71	0.44
1:C:257:VAL:CG1	2:D:407:TRP:CD1	2.98	0.44
1:C:325:MET:HE1	1:C:355:VAL:HG21	1.99	0.44
2:D:234:ILE:C	2:D:234:ILE:CD1	2.85	0.44
2:D:271:THR:O	2:D:376:CYS:HA	2.17	0.44
2:D:384:ILE:O	2:D:385:ALA:C	2.59	0.44
1:E:8:GLN:CG	1:E:67:LEU:HD22	2.47	0.44
1:E:167:ASN:HD21	1:E:252:LEU:HD22	1.82	0.44
1:E:242:LEU:HD22	1:E:250:ALA:O	2.17	0.44
1:E:273:ALA:CB	1:E:274:PRO:CD	2.93	0.44
2:F:30:ILE:O	2:F:31:GLN:O	2.35	0.44
2:F:30:ILE:HD11	2:F:61:HIS:CD2	2.51	0.44
2:F:108:TYR:O	2:F:109:THR:C	2.61	0.44
2:F:229:ARG:NH1	2:F:229:ARG:HG2	2.31	0.44
2:F:308:ARG:O	2:F:309:HIS:HB3	2.17	0.44
1:G:4:ILE:HD12	1:G:239:THR:HG21	1.98	0.44
1:G:12:CYS:O	1:G:13:GLY:C	2.59	0.44
1:G:237:GLY:O	1:G:241:CYS:CB	2.61	0.44
1:G:423:SER:O	1:G:424:ASN:C	2.60	0.44
2:H:108:TYR:O	2:H:109:THR:C	2.61	0.44
2:H:204:VAL:O	2:H:204:VAL:HG12	2.17	0.44
2:H:229:ARG:NH1	2:H:229:ARG:HG2	2.31	0.44
2:H:231:ILE:HD13	2:H:231:ILE:H	1.82	0.44
2:H:303:VAL:O	2:H:303:VAL:CG1	2.65	0.44
2:H:345:ASP:C	2:H:347:CYS:N	2.68	0.44
2:H:388:TRP:CD2	2:H:425:MET:HE1	2.52	0.44
2:H:392:ASP:OD2	2:H:422:ARG:CZ	2.64	0.44
1:A:11:GLN:O	1:A:15:GLN:N	2.41	0.44
1:A:95:GLY:C	1:A:97:SER:H	2.25	0.44
1:A:288:VAL:N	1:A:289:PRO:HD2	2.32	0.44
2:B:7:ILE:HG13	2:B:137:VAL:HG22	1.97	0.44
2:B:182:VAL:O	2:B:184:PRO:CD	2.65	0.44
2:B:425:MET:O	2:B:426:ALA:C	2.60	0.44
1:C:282:GLN:O	1:C:282:GLN:CG	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:288:VAL:N	1:C:289:PRO:HD2	2.32	0.44
1:C:409:THR:HA	1:C:413:MET:HB3	1.99	0.44
2:D:393:HIS:O	2:D:394:LYS:C	2.59	0.44
1:E:102:ASN:OD1	1:E:408:TYR:CZ	2.70	0.44
1:E:237:GLY:O	1:E:241:CYS:CB	2.61	0.44
1:E:257:VAL:O	1:E:257:VAL:CG1	2.64	0.44
2:F:130:THR:O	2:F:131:GLY:C	2.59	0.44
1:G:23:VAL:O	1:G:25:SER:N	2.50	0.44
1:G:102:ASN:OD1	1:G:408:TYR:CZ	2.70	0.44
2:H:271:THR:O	2:H:376:CYS:HA	2.17	0.44
2:H:344:VAL:CG1	2:H:345:ASP:N	2.78	0.44
1:A:167:ASN:HA	1:A:200:GLU:O	2.17	0.44
2:B:271:THR:O	2:B:376:CYS:HA	2.17	0.44
1:C:14:ASN:O	1:C:17:GLY:N	2.50	0.44
1:C:250:ALA:HB1	1:C:254:LYS:CB	2.44	0.44
2:D:8:HIS:HA	2:D:138:PHE:HB2	1.99	0.44
2:D:119:LEU:O	2:D:120:ASP:C	2.60	0.44
1:E:423:SER:O	1:E:424:ASN:C	2.60	0.44
2:F:204:VAL:O	2:F:204:VAL:HG12	2.17	0.44
2:F:262:TYR:CZ	1:G:403:ALA:O	2.70	0.44
2:F:272:TYR:CE2	2:F:274:PRO:HD2	2.53	0.44
2:F:392:ASP:OD2	2:F:422:ARG:CZ	2.65	0.44
1:G:2:ARG:HD3	2:H:98:ASP:OD2	2.18	0.44
1:G:310:GLY:HA3	1:G:436:GLN:NE2	2.29	0.44
2:H:8:HIS:HA	2:H:138:PHE:HB2	1.99	0.44
1:A:23:VAL:O	1:A:25:SER:N	2.50	0.44
1:A:52:TYR:HE1	1:A:240:THR:HB	1.82	0.44
1:A:380:ASN:C	1:A:380:ASN:HD22	2.24	0.44
2:B:8:HIS:HA	2:B:138:PHE:HB2	2.00	0.44
2:B:88:HIS:C	2:B:90:GLU:N	2.74	0.44
2:B:268:PRO:CA	2:B:379:SER:O	2.65	0.44
2:B:274:PRO:C	2:B:275:VAL:CA	2.89	0.44
2:B:274:PRO:HB2	2:B:371:VAL:HG21	1.98	0.44
2:B:362:VAL:HG13	2:B:368:LEU:CG	2.48	0.44
2:B:363:VAL:CG1	2:B:364:PRO:HD2	2.48	0.44
1:C:42:LEU:C	1:C:44:LEU:H	2.26	0.44
1:C:106:GLY:O	1:C:149:MET:HB2	2.17	0.44
1:C:167:ASN:HD21	1:C:252:LEU:HD22	1.82	0.44
1:C:188:THR:HG23	1:C:425:MET:HE3	1.98	0.44
1:C:257:VAL:O	1:C:257:VAL:CG1	2.64	0.44
2:D:11:GLN:NE2	2:D:74:VAL:CG2	2.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:182:VAL:O	2:D:184:PRO:CD	2.65	0.44
2:D:276:ILE:CG2	2:D:369:ALA:CB	2.91	0.44
2:D:308:ARG:O	2:D:309:HIS:HB3	2.16	0.44
2:D:402:ARG:O	2:D:405:VAL:N	2.49	0.44
1:E:167:ASN:HA	1:E:200:GLU:O	2.17	0.44
1:E:189:LEU:HD23	1:E:421:ALA:CB	2.47	0.44
1:E:310:GLY:HA3	1:E:436:GLN:NE2	2.29	0.44
2:F:8:HIS:HA	2:F:138:PHE:HB2	2.00	0.44
2:F:23:LEU:O	2:F:26:LEU:HB3	2.17	0.44
2:F:217:LEU:HD13	2:F:277:SER:N	2.33	0.44
1:G:137:LEU:HD22	1:G:154:ILE:HG23	1.98	0.44
1:G:167:ASN:HD21	1:G:252:LEU:HD22	1.82	0.44
1:G:242:LEU:HD22	1:G:250:ALA:O	2.17	0.44
2:H:23:LEU:O	2:H:26:LEU:HB3	2.17	0.44
2:H:30:ILE:O	2:H:31:GLN:O	2.35	0.44
2:H:272:TYR:CE2	2:H:274:PRO:HD2	2.53	0.44
2:H:343:PHE:CE1	2:H:351:PHE:HE1	2.36	0.44
2:H:423:GLU:O	2:H:426:ALA:HB3	2.16	0.44
1:A:12:CYS:O	1:A:13:GLY:C	2.59	0.44
1:A:105:LYS:HG2	1:A:110:GLU:CG	2.48	0.44
2:B:272:TYR:CE2	2:B:274:PRO:HD2	2.53	0.44
2:B:393:HIS:O	2:B:394:LYS:C	2.60	0.44
1:C:99:ALA:O	1:C:100:GLY:C	2.60	0.44
2:D:272:TYR:CE2	2:D:274:PRO:HD2	2.53	0.44
2:D:362:VAL:HG13	2:D:368:LEU:CG	2.48	0.44
2:D:384:ILE:C	2:D:386:GLU:N	2.72	0.44
1:E:4:ILE:HD12	1:E:239:THR:HG21	1.98	0.44
1:E:147:SER:HB2	1:E:190:SER:CB	2.41	0.44
2:F:343:PHE:CE1	2:F:351:PHE:HE1	2.36	0.44
2:F:402:ARG:O	2:F:405:VAL:N	2.49	0.44
1:G:204:ILE:HD13	1:G:231:VAL:CG2	2.45	0.44
2:H:121:ARG:HG2	2:H:121:ARG:HH11	1.83	0.44
2:H:217:LEU:HD13	2:H:277:SER:N	2.33	0.44
2:H:363:VAL:CG1	2:H:364:PRO:HD2	2.48	0.44
2:H:402:ARG:O	2:H:405:VAL:N	2.49	0.44
1:A:42:LEU:C	1:A:44:LEU:H	2.25	0.44
2:B:182:VAL:O	2:B:183:GLU:C	2.60	0.44
2:B:349:THR:O	1:C:181:VAL:CG1	2.65	0.44
1:C:24:ILE:CG2	1:C:25:SER:N	2.80	0.44
1:C:105:LYS:HG2	1:C:110:GLU:CG	2.48	0.44
2:D:64:ARG:HD2	2:D:125:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:182:VAL:O	2:D:183:GLU:C	2.60	0.44
1:E:105:LYS:HG2	1:E:110:GLU:CG	2.48	0.44
1:E:161:TYR:C	1:E:163:ASP:N	2.71	0.44
1:E:161:TYR:O	1:E:163:ASP:N	2.51	0.44
2:F:50:ASN:HD22	2:F:50:ASN:HA	1.60	0.44
2:F:271:THR:O	2:F:376:CYS:HA	2.17	0.44
2:F:325:PRO:CD	1:G:223:THR:HA	2.30	0.44
2:F:434:GLU:C	2:F:436:GLY:N	2.74	0.44
1:G:23:VAL:O	1:G:24:ILE:C	2.60	0.44
1:G:105:LYS:HG2	1:G:110:GLU:CG	2.48	0.44
1:G:161:TYR:O	1:G:163:ASP:N	2.51	0.44
3:I:60:ASN:HB2	3:I:126:VAL:CG1	2.48	0.44
3:I:77:PHE:CD2	3:I:83:LEU:HD13	2.52	0.44
1:A:23:VAL:O	1:A:24:ILE:C	2.60	0.44
1:A:115:VAL:HG21	1:A:152:LEU:HD21	1.98	0.44
1:A:242:LEU:HD23	1:A:242:LEU:HA	1.76	0.44
1:A:287:THR:O	1:A:288:VAL:CG2	2.58	0.44
2:B:12:ALA:HB2	5:B:500:GTP:C8	2.52	0.44
2:B:23:LEU:O	2:B:26:LEU:HB3	2.17	0.44
2:B:64:ARG:HD2	2:B:125:LEU:HD22	1.99	0.44
1:C:23:VAL:O	1:C:24:ILE:C	2.60	0.44
1:C:52:TYR:HE1	1:C:240:THR:HB	1.83	0.44
1:C:72:PRO:HG2	1:C:73:GLY:H	1.83	0.44
1:C:115:VAL:HG21	1:C:152:LEU:HD21	1.99	0.44
1:C:346:TRP:CG	2:D:401:LYS:HD2	2.52	0.44
2:D:363:VAL:CG1	2:D:364:PRO:HD2	2.48	0.44
2:D:390:ARG:HG3	2:D:390:ARG:HH11	1.83	0.44
1:E:67:LEU:HD12	1:E:92:PHE:CE2	2.52	0.44
1:E:288:VAL:N	1:E:289:PRO:HD2	2.32	0.44
1:E:301:MET:O	1:E:303:ALA:N	2.51	0.44
1:E:332:MET:HE3	1:E:351:VAL:CG1	2.32	0.44
1:E:352:LYS:HD3	1:E:352:LYS:C	2.43	0.44
1:E:390:ARG:O	1:E:391:ILE:C	2.61	0.44
2:F:121:ARG:NH1	2:F:121:ARG:HG2	2.33	0.44
2:F:345:ASP:C	2:F:347:CYS:N	2.68	0.44
2:F:363:VAL:CG1	2:F:364:PRO:HD2	2.48	0.44
1:G:67:LEU:HD12	1:G:92:PHE:CE2	2.52	0.44
1:G:301:MET:O	1:G:303:ALA:N	2.51	0.44
2:H:121:ARG:HG2	2:H:121:ARG:NH1	2.33	0.44
2:H:362:VAL:HG13	2:H:368:LEU:CG	2.48	0.44
3:I:46:LEU:N	3:I:46:LEU:HD12	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:80:PHE:CZ	3:I:104:ILE:HB	2.53	0.44
3:I:102:ARG:HB3	3:I:103:TYR:CE1	2.52	0.44
1:A:257:VAL:O	1:A:257:VAL:CG1	2.64	0.44
1:A:409:THR:HA	1:A:413:MET:HB3	1.99	0.44
2:B:115:ILE:CG1	2:B:152:LEU:HD13	2.46	0.44
2:B:121:ARG:HG2	2:B:121:ARG:NH1	2.33	0.44
2:B:153:LEU:O	2:B:157:LEU:HG	2.18	0.44
2:B:175:PRO:CG	2:B:304:LYS:HG2	2.47	0.44
2:B:390:ARG:HH11	2:B:390:ARG:HG3	1.83	0.44
1:C:12:CYS:O	1:C:13:GLY:C	2.59	0.44
2:D:23:LEU:O	2:D:26:LEU:HB3	2.17	0.44
2:D:50:ASN:HD22	2:D:50:ASN:HA	1.61	0.44
2:D:153:LEU:O	2:D:157:LEU:HG	2.18	0.44
2:D:175:PRO:CG	2:D:304:LYS:HG2	2.47	0.44
2:D:274:PRO:C	2:D:275:VAL:CA	2.88	0.44
1:E:7:ILE:N	1:E:136:GLN:O	2.51	0.44
1:E:161:TYR:CD1	1:E:161:TYR:N	2.86	0.44
2:F:5:ILE:CG2	2:F:135:PHE:CB	2.96	0.44
2:F:414:GLU:C	2:F:416:GLY:N	2.74	0.44
1:G:7:ILE:N	1:G:136:GLN:O	2.51	0.44
1:G:167:ASN:HA	1:G:200:GLU:O	2.17	0.44
1:G:288:VAL:N	1:G:289:PRO:HD2	2.32	0.44
2:H:5:ILE:CG2	2:H:135:PHE:CB	2.95	0.44
2:H:12:ALA:HB2	5:H:500:GTP:C8	2.52	0.44
2:H:404:PHE:CD1	2:H:404:PHE:N	2.83	0.44
2:H:414:GLU:C	2:H:416:GLY:N	2.74	0.44
1:A:72:PRO:HG2	1:A:73:GLY:H	1.83	0.43
1:A:167:ASN:HD21	1:A:252:LEU:HD22	1.82	0.43
2:B:54:SER:O	2:B:61:HIS:O	2.35	0.43
1:C:37:HIS:O	1:C:38:GLY:C	2.61	0.43
1:C:141:LEU:N	1:C:141:LEU:HD12	2.33	0.43
1:C:242:LEU:HD23	1:C:242:LEU:HA	1.76	0.43
2:D:229:ARG:NH1	2:D:229:ARG:HG2	2.31	0.43
1:E:6:HIS:HB3	1:E:65:ALA:CB	2.48	0.43
1:E:23:VAL:O	1:E:24:ILE:C	2.60	0.43
1:E:72:PRO:HG2	1:E:73:GLY:H	1.83	0.43
1:E:168:THR:CG2	1:E:201:THR:HG23	2.48	0.43
1:E:243:ARG:HH21	1:E:252:LEU:N	2.12	0.43
1:E:282:GLN:O	1:E:282:GLN:CG	2.65	0.43
1:E:330:GLU:O	1:E:331:GLN:C	2.61	0.43
2:F:7:ILE:HG13	2:F:137:VAL:HG22	1.97	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:119:LEU:O	2:F:120:ASP:C	2.61	0.43
2:F:362:VAL:HG13	2:F:368:LEU:CG	2.48	0.43
1:G:6:His:HB3	1:G:65:ALA:CB	2.48	0.43
2:H:7:ILE:HG13	2:H:137:VAL:HG22	1.98	0.43
2:H:50:ASN:HD22	2:H:50:ASN:HA	1.61	0.43
2:H:119:LEU:O	2:H:120:ASP:C	2.61	0.43
2:H:304:LYS:HG3	2:H:304:LYS:O	2.18	0.43
1:A:24:ILE:CG2	1:A:25:SER:N	2.80	0.43
1:A:70:LEU:HB2	1:A:99:ALA:CB	2.49	0.43
1:A:204:ILE:HD13	1:A:231:VAL:CG2	2.45	0.43
1:A:239:THR:CG2	1:A:240:THR:N	2.81	0.43
1:A:240:THR:HG23	1:A:241:CYS:N	2.33	0.43
1:A:262:PHE:HA	1:A:263:PRO:HD2	1.65	0.43
1:A:295:MET:SD	1:A:375:ALA:HB3	2.58	0.43
2:B:296:PHE:HZ	2:B:351:PHE:HZ	1.66	0.43
1:C:70:LEU:HB2	1:C:99:ALA:CB	2.49	0.43
1:C:295:MET:SD	1:C:375:ALA:HB3	2.57	0.43
2:D:5:ILE:CG2	2:D:135:PHE:CB	2.96	0.43
2:D:132:LEU:H	2:D:132:LEU:CD2	2.23	0.43
2:D:268:PRO:CA	2:D:379:SER:O	2.65	0.43
2:D:434:GLU:C	2:D:436:GLY:N	2.74	0.43
2:F:121:ARG:HG2	2:F:121:ARG:HH11	1.83	0.43
2:F:276:ILE:O	2:F:369:ALA:CA	2.66	0.43
2:F:292:THR:O	2:F:295:CYS:HB2	2.18	0.43
2:F:304:LYS:HG3	2:F:304:LYS:O	2.19	0.43
2:F:349:THR:CG2	1:G:178:SER:C	2.72	0.43
1:G:72:PRO:HG2	1:G:73:GLY:H	1.83	0.43
1:G:269:MET:HB2	1:G:301:MET:HE3	2.00	0.43
1:G:390:ARG:O	1:G:391:ILE:C	2.61	0.43
1:G:402:LYS:O	1:G:403:ALA:C	2.61	0.43
2:H:175:PRO:CG	2:H:304:LYS:HG2	2.47	0.43
2:H:276:ILE:O	2:H:369:ALA:CA	2.66	0.43
2:B:229:ARG:NH1	2:B:229:ARG:HG2	2.31	0.43
2:B:292:THR:O	2:B:295:CYS:HB2	2.18	0.43
1:C:7:ILE:N	1:C:136:GLN:O	2.51	0.43
1:C:67:LEU:HD12	1:C:92:PHE:CE2	2.52	0.43
1:C:248:LEU:HD21	2:D:179:THR:HG21	1.97	0.43
1:C:333:LEU:O	1:C:334:ASN:C	2.58	0.43
2:D:12:ALA:HB2	5:D:500:GTP:C8	2.53	0.43
2:D:199:ASP:OD2	2:D:256:GLN:NE2	2.46	0.43
2:D:209:ILE:CD1	2:D:231:ILE:HD11	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:70:LEU:HB2	1:E:99:ALA:CB	2.49	0.43
1:E:70:LEU:HD21	1:E:149:MET:HE3	1.99	0.43
1:E:99:ALA:O	1:E:100:GLY:C	2.60	0.43
1:E:204:ILE:HD13	1:E:231:VAL:CG2	2.45	0.43
2:F:5:ILE:CG1	2:F:6:SER:N	2.82	0.43
2:F:12:ALA:HB2	5:F:500:GTP:C8	2.52	0.43
1:G:282:GLN:O	1:G:282:GLN:CG	2.65	0.43
2:H:5:ILE:CG1	2:H:6:SER:N	2.82	0.43
2:H:143:GLY:O	2:H:147:SER:OG	2.33	0.43
2:H:255:PHE:O	2:H:259:LEU:N	2.50	0.43
2:H:377:MET:HG3	2:H:377:MET:O	2.18	0.43
1:A:67:LEU:HD12	1:A:92:PHE:CE2	2.52	0.43
1:A:161:TYR:CD1	1:A:161:TYR:N	2.86	0.43
1:A:269:MET:HB2	1:A:301:MET:HE3	2.00	0.43
2:B:121:ARG:HG2	2:B:121:ARG:HH11	1.83	0.43
1:C:242:LEU:HD22	1:C:250:ALA:O	2.17	0.43
1:C:287:THR:O	1:C:288:VAL:CG2	2.58	0.43
1:C:402:LYS:O	1:C:403:ALA:C	2.61	0.43
2:D:121:ARG:NH1	2:D:121:ARG:HG2	2.33	0.43
2:D:217:LEU:HD13	2:D:277:SER:N	2.32	0.43
2:D:425:MET:O	2:D:428:LEU:N	2.45	0.43
1:E:37:HIS:O	1:E:38:GLY:C	2.61	0.43
2:F:390:ARG:HH11	2:F:390:ARG:HG3	1.83	0.43
2:F:404:PHE:CD1	2:F:404:PHE:N	2.83	0.43
1:G:37:HIS:O	1:G:38:GLY:C	2.61	0.43
1:G:70:LEU:HB2	1:G:99:ALA:CB	2.49	0.43
1:G:70:LEU:HD21	1:G:149:MET:HE3	1.98	0.43
1:G:161:TYR:C	1:G:163:ASP:N	2.71	0.43
1:G:161:TYR:CD1	1:G:161:TYR:N	2.86	0.43
1:G:332:MET:HE3	1:G:351:VAL:CG1	2.32	0.43
2:H:4:CYS:SG	2:H:252:LEU:CD1	3.02	0.43
2:H:292:THR:O	2:H:295:CYS:HB2	2.18	0.43
1:A:7:ILE:N	1:A:136:GLN:O	2.51	0.43
1:A:243:ARG:HH21	1:A:252:LEU:N	2.12	0.43
1:A:301:MET:O	1:A:303:ALA:N	2.51	0.43
1:A:399:PHE:O	1:A:402:LYS:N	2.29	0.43
1:A:402:LYS:O	1:A:403:ALA:C	2.61	0.43
1:C:161:TYR:O	1:C:163:ASP:N	2.51	0.43
1:C:204:ILE:HD13	1:C:231:VAL:CG2	2.45	0.43
1:C:240:THR:HG23	1:C:241:CYS:N	2.33	0.43
2:D:115:ILE:CG1	2:D:152:LEU:HD13	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:231:ILE:HD13	2:D:231:ILE:H	1.82	0.43
2:D:304:LYS:HG3	2:D:304:LYS:O	2.18	0.43
1:E:269:MET:HB2	1:E:301:MET:HE3	2.00	0.43
1:E:295:MET:SD	1:E:375:ALA:HB3	2.57	0.43
1:E:402:LYS:O	1:E:403:ALA:C	2.61	0.43
2:F:175:PRO:CG	2:F:304:LYS:HG2	2.47	0.43
2:F:209:ILE:CD1	2:F:231:ILE:HD11	2.47	0.43
2:F:296:PHE:HZ	2:F:351:PHE:HZ	1.66	0.43
2:F:310:GLY:HA3	2:F:383:ALA:CA	2.48	0.43
1:G:99:ALA:O	1:G:100:GLY:C	2.60	0.43
1:G:168:THR:CG2	1:G:201:THR:HG23	2.48	0.43
1:G:295:MET:SD	1:G:375:ALA:HB3	2.57	0.43
1:G:330:GLU:O	1:G:331:GLN:C	2.61	0.43
2:H:64:ARG:HD2	2:H:125:LEU:HD22	1.99	0.43
2:H:296:PHE:HZ	2:H:351:PHE:HZ	1.66	0.43
2:H:390:ARG:HH11	2:H:390:ARG:HG3	1.83	0.43
2:H:434:GLU:C	2:H:436:GLY:N	2.74	0.43
1:A:37:HIS:O	1:A:38:GLY:C	2.61	0.43
1:A:141:LEU:N	1:A:141:LEU:HD12	2.32	0.43
1:A:161:TYR:O	1:A:163:ASP:N	2.51	0.43
2:B:8:HIS:CD2	2:B:138:PHE:CD1	3.07	0.43
2:B:209:ILE:CD1	2:B:231:ILE:HD11	2.47	0.43
2:B:217:LEU:HD13	2:B:277:SER:N	2.33	0.43
2:B:231:ILE:HD13	2:B:231:ILE:H	1.82	0.43
2:B:234:ILE:CG1	2:B:270:ALA:HB1	2.37	0.43
2:B:304:LYS:HG3	2:B:304:LYS:O	2.18	0.43
1:C:156:LYS:NZ	1:C:159:GLU:OE1	2.47	0.43
1:C:301:MET:C	1:C:303:ALA:N	2.77	0.43
1:C:301:MET:O	1:C:303:ALA:N	2.51	0.43
1:C:359:PRO:CB	1:C:360:PRO:HD2	2.45	0.43
2:D:122:ILE:CD1	2:D:157:LEU:HD21	2.35	0.43
2:D:343:PHE:HZ	2:D:351:PHE:CZ	2.36	0.43
1:E:212:ILE:O	1:E:212:ILE:HG22	2.18	0.43
1:E:435:TYR:C	1:E:437:ASP:H	2.27	0.43
2:F:11:GLN:NE2	2:F:74:VAL:CG2	2.76	0.43
2:F:64:ARG:HD2	2:F:125:LEU:HD22	1.99	0.43
2:F:231:ILE:C	2:F:233:GLN:N	2.73	0.43
2:F:255:PHE:O	2:F:259:LEU:N	2.50	0.43
2:F:377:MET:HG3	2:F:377:MET:O	2.18	0.43
1:G:243:ARG:HH21	1:G:252:LEU:N	2.13	0.43
2:H:310:GLY:HA3	2:H:383:ALA:CA	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:LEU:HD22	1:A:250:ALA:O	2.17	0.43
1:A:352:LYS:C	1:A:352:LYS:HD3	2.43	0.43
1:A:435:TYR:C	1:A:437:ASP:H	2.27	0.43
2:B:105:ARG:O	2:B:110:ILE:CG2	2.64	0.43
2:B:140:SER:O	2:B:141:PHE:C	2.62	0.43
2:B:397:LEU:HD23	2:B:397:LEU:HA	1.81	0.43
1:C:161:TYR:CD1	1:C:161:TYR:N	2.86	0.43
1:C:168:THR:CG2	1:C:201:THR:HG23	2.48	0.43
2:D:88:HIS:C	2:D:90:GLU:N	2.74	0.43
2:D:296:PHE:HZ	2:D:351:PHE:HZ	1.66	0.43
1:E:11:GLN:O	1:E:15:GLN:N	2.41	0.43
1:E:42:LEU:C	1:E:44:LEU:H	2.25	0.43
1:G:11:GLN:O	1:G:15:GLN:N	2.41	0.43
1:G:253:ARG:HD3	2:H:407:TRP:CH2	2.53	0.43
1:G:280:SER:OG	1:G:281:GLN:N	2.49	0.43
2:H:166:LYS:CE	2:H:199:ASP:OD1	2.62	0.43
1:A:6:HIS:HB3	1:A:65:ALA:CB	2.49	0.43
1:A:168:THR:CG2	1:A:201:THR:HG23	2.48	0.43
1:A:192:HIS:NE2	1:A:420:GLU:HG2	2.34	0.43
1:A:249:ASN:OD1	2:B:71:GLU:OE1	2.36	0.43
2:B:5:ILE:HD11	2:B:64:ARG:NH1	2.27	0.43
2:B:104:ALA:HB3	2:B:408:TYR:HD2	1.84	0.43
2:B:439:SER:HA	1:C:401:ARG:NH2	2.32	0.43
1:C:153:LEU:HD13	1:C:153:LEU:N	2.34	0.43
1:C:178:SER:C	1:C:180:THR:H	2.27	0.43
1:C:210:TYR:O	1:C:214:PHE:N	2.52	0.43
1:C:345:GLU:C	1:C:347:ILE:N	2.77	0.43
2:D:8:HIS:CD2	2:D:138:PHE:CD1	3.07	0.43
2:D:140:SER:O	2:D:141:PHE:C	2.62	0.43
2:D:268:PRO:C	2:D:269:LEU:HD23	2.44	0.43
2:D:280:LYS:O	2:D:282:TYR:N	2.52	0.43
2:D:301:GLN:O	2:D:302:MET:C	2.61	0.43
1:E:141:LEU:N	1:E:141:LEU:HD12	2.33	0.43
1:E:431:GLU:O	1:E:434:GLN:N	2.48	0.43
2:F:8:HIS:CD2	2:F:138:PHE:CD1	3.07	0.43
2:F:104:ALA:HB3	2:F:408:TYR:HD2	1.84	0.43
2:F:166:LYS:CE	2:F:199:ASP:OD1	2.62	0.43
2:F:238:ILE:O	2:F:242:LEU:CB	2.67	0.43
2:F:343:PHE:HZ	2:F:351:PHE:CZ	2.36	0.43
1:G:14:ASN:O	1:G:17:GLY:N	2.50	0.43
1:G:435:TYR:C	1:G:437:ASP:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:8:HIS:CD2	2:H:138:PHE:CD1	3.07	0.43
2:H:209:ILE:CD1	2:H:231:ILE:HD11	2.47	0.43
1:A:346:TRP:CD1	2:B:401:LYS:HZ2	2.37	0.43
2:B:268:PRO:C	2:B:269:LEU:HD23	2.44	0.43
2:B:296:PHE:CG	2:B:341:ILE:HD12	2.53	0.43
2:B:343:PHE:CE1	2:B:351:PHE:HE1	2.36	0.43
2:B:399:TYR:C	2:B:401:LYS:N	2.77	0.43
1:C:6:HIS:HB3	1:C:65:ALA:CB	2.48	0.43
1:C:118:VAL:O	1:C:122:VAL:HG13	2.19	0.43
1:C:269:MET:HB2	1:C:301:MET:HE3	2.00	0.43
1:C:352:LYS:C	1:C:352:LYS:HD3	2.43	0.43
1:C:390:ARG:O	1:C:391:ILE:C	2.61	0.43
2:D:4:CYS:SG	2:D:252:LEU:CD1	3.02	0.43
2:D:5:ILE:CG1	2:D:6:SER:N	2.82	0.43
2:D:104:ALA:HB3	2:D:408:TYR:HD2	1.84	0.43
2:D:292:THR:O	2:D:295:CYS:HB2	2.18	0.43
2:D:343:PHE:CE1	2:D:351:PHE:HE1	2.36	0.43
2:D:428:LEU:HD12	2:D:428:LEU:HA	1.78	0.43
1:E:68:VAL:HG11	1:E:153:LEU:HD21	2.00	0.43
1:E:178:SER:C	1:E:180:THR:H	2.27	0.43
1:E:210:TYR:O	1:E:214:PHE:N	2.52	0.43
2:F:4:CYS:SG	2:F:252:LEU:CD1	3.02	0.43
2:F:209:ILE:CD1	2:F:231:ILE:CD1	2.97	0.43
1:G:210:TYR:O	1:G:214:PHE:N	2.52	0.43
1:G:212:ILE:O	1:G:212:ILE:HG22	2.18	0.43
1:G:253:ARG:HD3	2:H:407:TRP:HH2	1.82	0.43
2:H:100:ALA:O	2:H:102:ASN:N	2.49	0.43
2:H:262:TYR:HB3	2:H:263:PRO:HD2	2.00	0.43
1:A:118:VAL:O	1:A:122:VAL:HG13	2.19	0.43
1:A:178:SER:C	1:A:180:THR:H	2.27	0.43
1:A:210:TYR:O	1:A:214:PHE:N	2.52	0.43
1:A:345:GLU:C	1:A:347:ILE:N	2.77	0.43
1:A:389:LYS:O	1:A:390:ARG:C	2.62	0.43
2:B:49:PHE:HE1	2:B:61:HIS:CE1	2.34	0.43
2:B:209:ILE:CD1	2:B:231:ILE:CD1	2.97	0.43
2:B:301:GLN:O	2:B:302:MET:C	2.61	0.43
2:B:377:MET:HG3	2:B:377:MET:O	2.18	0.43
2:B:414:GLU:C	2:B:416:GLY:N	2.74	0.43
1:C:239:THR:CG2	1:C:240:THR:N	2.80	0.43
1:C:243:ARG:HH21	1:C:252:LEU:N	2.12	0.43
1:C:389:LYS:O	1:C:390:ARG:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:209:ILE:CD1	2:D:231:ILE:CD1	2.97	0.43
1:E:24:ILE:CG2	1:E:25:SER:N	2.80	0.43
1:E:238:VAL:HB	1:E:239:THR:H	1.65	0.43
1:G:243:ARG:HD3	1:G:243:ARG:N	2.26	0.43
2:H:104:ALA:HB3	2:H:408:TYR:HD2	1.84	0.43
2:H:204:VAL:CG1	2:H:209:ILE:HD11	2.42	0.43
2:H:238:ILE:O	2:H:242:LEU:CB	2.67	0.43
2:H:343:PHE:HZ	2:H:351:PHE:CZ	2.36	0.43
1:A:280:SER:OG	1:A:281:GLN:N	2.49	0.42
1:A:390:ARG:O	1:A:391:ILE:C	2.61	0.42
2:B:16:ILE:CG2	2:B:17:GLY:N	2.82	0.42
2:B:63:PRO:HG3	2:B:87:PHE:CD1	2.54	0.42
2:B:425:MET:O	2:B:428:LEU:N	2.45	0.42
1:C:435:TYR:C	1:C:437:ASP:H	2.27	0.42
2:D:234:ILE:CG1	2:D:270:ALA:HB1	2.38	0.42
1:E:121:VAL:C	1:E:123:ARG:N	2.77	0.42
1:E:280:SER:OG	1:E:281:GLN:N	2.49	0.42
2:F:30:ILE:O	2:F:31:GLN:C	2.62	0.42
2:F:100:ALA:O	2:F:102:ASN:N	2.49	0.42
2:F:204:VAL:CG1	2:F:209:ILE:HD11	2.42	0.42
2:F:268:PRO:C	2:F:269:LEU:HD23	2.44	0.42
2:F:378:LEU:HD12	2:F:378:LEU:O	2.19	0.42
1:G:24:ILE:CG2	1:G:25:SER:N	2.80	0.42
1:G:359:PRO:CB	1:G:360:PRO:HD2	2.45	0.42
2:H:11:GLN:NE2	2:H:74:VAL:CG2	2.76	0.42
2:H:70:LEU:HD13	2:H:145:THR:CB	2.46	0.42
2:H:378:LEU:HD12	2:H:378:LEU:O	2.19	0.42
1:A:153:LEU:HD13	1:A:153:LEU:N	2.34	0.42
1:A:330:GLU:O	1:A:331:GLN:C	2.61	0.42
2:B:262:TYR:HB3	2:B:263:PRO:HD2	2.00	0.42
2:B:280:LYS:O	2:B:282:TYR:N	2.52	0.42
2:B:343:PHE:HZ	2:B:351:PHE:CZ	2.36	0.42
2:B:378:LEU:HD12	2:B:378:LEU:O	2.19	0.42
1:C:118:VAL:O	1:C:119:LEU:C	2.62	0.42
1:C:179:ASP:O	1:C:179:ASP:CG	2.61	0.42
2:D:16:ILE:CG2	2:D:17:GLY:N	2.82	0.42
2:D:121:ARG:HG2	2:D:121:ARG:HH11	1.83	0.42
2:D:399:TYR:C	2:D:401:LYS:N	2.77	0.42
1:E:103:TRP:HB2	1:E:186:ASN:HA	2.01	0.42
2:F:105:ARG:O	2:F:110:ILE:CG2	2.64	0.42
2:F:140:SER:O	2:F:141:PHE:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:262:TYR:HB3	2:F:263:PRO:HD2	2.01	0.42
2:F:265:GLY:O	2:F:266:HIS:C	2.63	0.42
1:G:345:GLU:C	1:G:347:ILE:N	2.77	0.42
2:H:147:SER:HB2	2:H:186:ASN:O	2.19	0.42
2:H:209:ILE:CD1	2:H:231:ILE:CD1	2.97	0.42
2:H:238:ILE:HD11	2:H:378:LEU:HD23	2.01	0.42
3:I:80:PHE:CE2	3:I:104:ILE:HB	2.54	0.42
1:A:212:ILE:O	1:A:212:ILE:HG22	2.18	0.42
1:A:250:ALA:CB	1:A:254:LYS:HE2	2.49	0.42
2:B:50:ASN:HD22	2:B:50:ASN:HA	1.60	0.42
2:B:147:SER:HB2	2:B:186:ASN:O	2.19	0.42
2:B:276:ILE:O	2:B:369:ALA:CA	2.66	0.42
2:B:363:VAL:HG13	2:B:364:PRO:HD2	2.02	0.42
1:C:192:HIS:NE2	1:C:420:GLU:HG2	2.34	0.42
2:D:276:ILE:O	2:D:369:ALA:CA	2.66	0.42
2:D:310:GLY:HA3	2:D:383:ALA:CA	2.49	0.42
1:E:14:ASN:O	1:E:17:GLY:N	2.51	0.42
1:E:240:THR:HG23	1:E:241:CYS:N	2.33	0.42
1:E:345:GLU:C	1:E:347:ILE:N	2.77	0.42
1:E:399:PHE:O	1:E:402:LYS:N	2.29	0.42
2:F:7:ILE:HD11	2:F:137:VAL:CG2	2.44	0.42
2:F:238:ILE:HD11	2:F:378:LEU:HD23	2.01	0.42
2:F:280:LYS:O	2:F:282:TYR:N	2.52	0.42
1:G:42:LEU:C	1:G:44:LEU:H	2.26	0.42
1:G:68:VAL:HG11	1:G:153:LEU:HD21	2.00	0.42
1:G:141:LEU:N	1:G:141:LEU:HD12	2.33	0.42
1:G:254:LYS:HA	1:G:257:VAL:CG1	2.49	0.42
1:G:348:PRO:HG3	2:H:397:LEU:HB2	2.01	0.42
1:G:399:PHE:O	1:G:402:LYS:N	2.29	0.42
1:G:431:GLU:O	1:G:434:GLN:N	2.48	0.42
2:H:30:ILE:O	2:H:31:GLN:C	2.62	0.42
2:H:105:ARG:O	2:H:110:ILE:CG2	2.64	0.42
2:H:140:SER:O	2:H:141:PHE:C	2.62	0.42
2:H:265:GLY:O	2:H:266:HIS:C	2.62	0.42
2:H:268:PRO:C	2:H:269:LEU:HD23	2.44	0.42
2:B:115:ILE:CG2	2:B:116:ASP:H	2.32	0.42
2:B:260:VAL:HG22	1:C:407:TRP:CE2	2.54	0.42
1:C:250:ALA:CB	1:C:254:LYS:HE2	2.49	0.42
2:D:147:SER:HB2	2:D:186:ASN:O	2.19	0.42
2:D:262:TYR:HB3	2:D:263:PRO:HD2	2.00	0.42
2:D:378:LEU:HD12	2:D:378:LEU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:192:HIS:NE2	1:E:420:GLU:HG2	2.34	0.42
1:E:297:ASP:CG	1:E:299:LYS:HE2	2.45	0.42
1:E:359:PRO:CB	1:E:360:PRO:HD2	2.45	0.42
2:F:70:LEU:HD13	2:F:145:THR:CB	2.46	0.42
2:F:147:SER:HB2	2:F:186:ASN:O	2.19	0.42
2:F:262:TYR:OH	1:G:403:ALA:CA	2.39	0.42
1:G:103:TRP:HB2	1:G:186:ASN:HA	2.01	0.42
1:G:121:VAL:C	1:G:123:ARG:N	2.77	0.42
1:G:153:LEU:HD13	1:G:153:LEU:N	2.34	0.42
2:H:280:LYS:O	2:H:282:TYR:N	2.52	0.42
3:I:65:PHE:CE2	3:I:67:GLY:CA	3.02	0.42
3:I:105:TYR:HA	3:I:112:LYS:HA	2.00	0.42
1:A:68:VAL:HG11	1:A:153:LEU:HD21	2.00	0.42
1:A:359:PRO:CB	1:A:360:PRO:HD2	2.45	0.42
2:B:119:LEU:O	2:B:120:ASP:C	2.61	0.42
2:B:329:ASN:HB3	1:C:210:TYR:CE1	2.52	0.42
1:C:106:GLY:O	1:C:149:MET:CA	2.68	0.42
1:C:121:VAL:C	1:C:123:ARG:N	2.76	0.42
1:C:243:ARG:N	1:C:243:ARG:HD3	2.26	0.42
1:E:175:PRO:O	1:E:177:VAL:N	2.53	0.42
1:E:250:ALA:CB	1:E:254:LYS:HE2	2.50	0.42
1:E:273:ALA:HB1	1:E:291:LEU:HG	2.01	0.42
1:G:192:HIS:NE2	1:G:420:GLU:HG2	2.34	0.42
1:G:253:ARG:O	1:G:257:VAL:HG12	2.19	0.42
2:H:184:PRO:HG2	2:H:398:MET:CE	2.40	0.42
3:I:107:ILE:HD11	3:I:139:THR:HG23	2.01	0.42
1:A:301:MET:C	1:A:303:ALA:N	2.77	0.42
2:B:25:CYS:SG	2:B:26:LEU:N	2.92	0.42
2:B:207:GLU:O	2:B:210:TYR:N	2.51	0.42
2:B:231:ILE:C	2:B:233:GLN:H	2.28	0.42
2:B:238:ILE:O	2:B:242:LEU:CB	2.67	0.42
1:C:102:ASN:ND2	1:C:408:TYR:HA	2.20	0.42
2:D:12:ALA:C	2:D:14:VAL:N	2.75	0.42
2:D:105:ARG:O	2:D:110:ILE:CG2	2.64	0.42
2:D:238:ILE:O	2:D:242:LEU:CB	2.67	0.42
2:D:265:GLY:O	2:D:266:HIS:C	2.62	0.42
1:E:98:GLY:O	1:E:100:GLY:N	2.49	0.42
1:E:242:LEU:HB3	1:E:250:ALA:O	2.20	0.42
1:E:243:ARG:HD3	1:E:243:ARG:N	2.26	0.42
2:F:16:ILE:CG2	2:F:17:GLY:N	2.82	0.42
2:F:119:LEU:HD11	2:F:156:ARG:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:296:PHE:CG	2:F:341:ILE:HD12	2.53	0.42
2:H:7:ILE:HD11	2:H:137:VAL:CG2	2.44	0.42
2:H:296:PHE:CG	2:H:341:ILE:HD12	2.53	0.42
1:A:102:ASN:ND2	1:A:408:TYR:HA	2.20	0.42
1:A:103:TRP:HB2	1:A:186:ASN:HA	2.01	0.42
1:A:121:VAL:C	1:A:123:ARG:N	2.76	0.42
1:C:147:SER:CB	1:C:190:SER:HB3	2.42	0.42
1:C:212:ILE:O	1:C:212:ILE:HG22	2.18	0.42
1:C:307:PRO:O	1:C:309:HIS:N	2.53	0.42
2:D:363:VAL:HG13	2:D:364:PRO:HD2	2.02	0.42
2:D:377:MET:HG3	2:D:377:MET:O	2.18	0.42
2:D:414:GLU:C	2:D:416:GLY:N	2.74	0.42
1:E:261:PRO:HB2	1:E:262:PHE:CD1	2.54	0.42
2:F:115:ILE:CG2	2:F:116:ASP:H	2.32	0.42
2:F:363:VAL:HG13	2:F:364:PRO:HD2	2.02	0.42
1:G:242:LEU:HB3	1:G:250:ALA:O	2.20	0.42
1:G:273:ALA:HB1	1:G:291:LEU:HG	2.02	0.42
2:H:16:ILE:CG2	2:H:17:GLY:N	2.82	0.42
2:H:119:LEU:HD11	2:H:156:ARG:HD3	2.01	0.42
2:H:175:PRO:HG3	2:H:304:LYS:CB	2.50	0.42
2:H:301:GLN:O	2:H:302:MET:C	2.61	0.42
2:H:363:VAL:HG13	2:H:364:PRO:HD2	2.02	0.42
3:I:62:ASP:O	3:I:63:ARG:C	2.63	0.42
3:I:102:ARG:HB3	3:I:103:TYR:CD1	2.54	0.42
1:A:106:GLY:O	1:A:149:MET:CA	2.68	0.42
1:A:118:VAL:O	1:A:119:LEU:C	2.62	0.42
1:A:185:TYR:HD2	1:A:185:TYR:HA	1.76	0.42
1:A:238:VAL:HB	1:A:239:THR:H	1.65	0.42
1:A:261:PRO:HB2	1:A:262:PHE:CD1	2.54	0.42
1:A:307:PRO:O	1:A:309:HIS:N	2.53	0.42
2:B:119:LEU:HD11	2:B:156:ARG:HD3	2.02	0.42
2:B:175:PRO:HG3	2:B:304:LYS:CB	2.50	0.42
2:B:310:GLY:HA3	2:B:383:ALA:CA	2.49	0.42
2:B:346:TRP:O	1:C:398:MET:HB2	2.20	0.42
2:B:362:VAL:HG13	2:B:368:LEU:CB	2.50	0.42
1:C:68:VAL:HG11	1:C:153:LEU:HD21	2.00	0.42
2:D:115:ILE:CG2	2:D:116:ASP:H	2.32	0.42
2:D:119:LEU:HD11	2:D:156:ARG:HD3	2.01	0.42
2:D:296:PHE:CG	2:D:341:ILE:HD12	2.53	0.42
1:E:138:THR:O	1:E:139:HIS:HB3	2.19	0.42
1:E:301:MET:C	1:E:303:ALA:N	2.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:307:PRO:O	1:E:309:HIS:N	2.53	0.42
2:F:175:PRO:HG3	2:F:304:LYS:CB	2.50	0.42
2:F:274:PRO:C	2:F:275:VAL:CA	2.89	0.42
1:G:175:PRO:O	1:G:177:VAL:N	2.53	0.42
1:G:297:ASP:CG	1:G:299:LYS:HE2	2.45	0.42
2:H:115:ILE:CG2	2:H:116:ASP:H	2.32	0.42
2:H:274:PRO:C	2:H:275:VAL:CA	2.89	0.42
3:I:62:ASP:C	3:I:63:ARG:HG2	2.45	0.42
3:I:84:LEU:HD21	3:I:104:ILE:HG13	2.01	0.42
1:A:275:LEU:HD12	1:A:275:LEU:HA	1.78	0.42
1:A:297:ASP:CG	1:A:299:LYS:HE2	2.45	0.42
1:A:343:PHE:CD2	1:A:350:ASN:ND2	2.88	0.42
1:A:399:PHE:O	1:A:401:ARG:N	2.53	0.42
2:B:11:GLN:NE2	2:B:74:VAL:CG2	2.76	0.42
2:B:13:GLY:HA2	2:B:16:ILE:CG2	2.50	0.42
2:B:24:TYR:O	2:B:25:CYS:C	2.63	0.42
2:B:213:CYS:O	2:B:219:ILE:HG13	2.20	0.42
1:C:103:TRP:HB2	1:C:186:ASN:HA	2.01	0.42
1:C:171:VAL:O	1:C:171:VAL:HG12	2.20	0.42
1:C:273:ALA:HB1	1:C:291:LEU:HG	2.01	0.42
2:D:207:GLU:O	2:D:210:TYR:N	2.51	0.42
2:D:213:CYS:O	2:D:219:ILE:HG13	2.20	0.42
1:E:153:LEU:HD13	1:E:153:LEU:N	2.34	0.42
1:E:399:PHE:O	1:E:401:ARG:N	2.53	0.42
2:F:15:GLN:NE2	5:F:500:GTP:N7	2.67	0.42
2:F:301:GLN:O	2:F:302:MET:C	2.61	0.42
1:G:240:THR:HG23	1:G:241:CYS:N	2.34	0.42
1:G:261:PRO:HB2	1:G:262:PHE:CD1	2.54	0.42
1:G:307:PRO:O	1:G:309:HIS:N	2.53	0.42
1:G:389:LYS:O	1:G:390:ARG:C	2.62	0.42
2:H:213:CYS:O	2:H:219:ILE:HG13	2.20	0.42
2:B:12:ALA:C	2:B:14:VAL:N	2.75	0.42
2:B:238:ILE:HD11	2:B:378:LEU:HD23	2.01	0.42
2:B:255:PHE:O	2:B:257:THR:N	2.53	0.42
1:C:280:SER:OG	1:C:281:GLN:N	2.49	0.42
1:C:343:PHE:CD2	1:C:350:ASN:ND2	2.88	0.42
2:D:24:TYR:O	2:D:25:CYS:C	2.63	0.42
2:D:175:PRO:HG3	2:D:304:LYS:CB	2.50	0.42
2:D:231:ILE:C	2:D:233:GLN:H	2.28	0.42
2:D:362:VAL:HG13	2:D:368:LEU:CB	2.50	0.42
1:E:48:ARG:HG2	1:E:243:ARG:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:343:PHE:CD2	1:E:350:ASN:ND2	2.88	0.42
2:F:11:GLN:CG	2:F:74:VAL:HG21	2.50	0.42
2:F:213:CYS:O	2:F:219:ILE:HG13	2.20	0.42
2:F:231:ILE:C	2:F:233:GLN:H	2.28	0.42
2:F:335:ILE:C	2:F:337:THR:H	2.28	0.42
1:G:143:GLY:O	1:G:147:SER:OG	2.38	0.42
1:G:301:MET:C	1:G:303:ALA:N	2.77	0.42
1:G:306:ASP:HA	1:G:307:PRO:HD3	1.92	0.42
2:H:255:PHE:O	2:H:257:THR:N	2.53	0.42
2:H:362:VAL:HG13	2:H:368:LEU:CB	2.50	0.42
2:H:428:LEU:HD12	2:H:428:LEU:HA	1.78	0.42
2:B:11:GLN:CG	2:B:74:VAL:HG21	2.50	0.41
2:B:151:SER:HB3	2:B:193:THR:CG2	2.34	0.41
1:C:133:GLN:CG	1:C:165:ILE:HD11	2.49	0.41
1:C:150:GLY:HA2	1:C:153:LEU:CD2	2.42	0.41
1:C:242:LEU:HB3	1:C:250:ALA:O	2.20	0.41
1:C:249:ASN:OD1	2:D:71:GLU:CD	2.62	0.41
1:C:306:ASP:HA	1:C:307:PRO:HD3	1.91	0.41
1:C:330:GLU:O	1:C:331:GLN:C	2.61	0.41
1:C:399:PHE:O	1:C:401:ARG:N	2.53	0.41
1:C:417:GLU:O	1:C:420:GLU:HB3	2.20	0.41
2:D:11:GLN:CG	2:D:74:VAL:HG21	2.50	0.41
2:D:15:GLN:NE2	5:D:500:GTP:N7	2.67	0.41
2:D:238:ILE:HD11	2:D:378:LEU:HD23	2.01	0.41
2:D:243:ARG:NH2	2:D:252:LEU:HG	2.35	0.41
1:E:118:VAL:O	1:E:122:VAL:HG13	2.19	0.41
1:E:143:GLY:O	1:E:147:SER:OG	2.38	0.41
1:E:262:PHE:HA	1:E:263:PRO:HD2	1.65	0.41
2:F:71:GLU:HA	2:F:72:PRO:HD3	1.88	0.41
2:F:132:LEU:H	2:F:132:LEU:CD2	2.23	0.41
2:F:255:PHE:O	2:F:257:THR:N	2.53	0.41
2:F:347:CYS:SG	1:G:181:VAL:HG13	2.60	0.41
2:F:362:VAL:HG13	2:F:368:LEU:CB	2.50	0.41
1:G:118:VAL:O	1:G:119:LEU:C	2.62	0.41
1:G:399:PHE:O	1:G:401:ARG:N	2.53	0.41
2:H:11:GLN:CG	2:H:74:VAL:HG21	2.50	0.41
2:H:15:GLN:NE2	5:H:500:GTP:N7	2.67	0.41
2:H:231:ILE:C	2:H:233:GLN:H	2.28	0.41
2:H:335:ILE:C	2:H:337:THR:H	2.28	0.41
1:A:11:GLN:O	1:A:12:CYS:C	2.63	0.41
1:A:25:SER:O	1:A:28:HIS:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:LEU:HD12	1:A:49:ILE:CD1	2.49	0.41
1:A:48:ARG:HG2	1:A:243:ARG:HB3	2.01	0.41
1:A:138:THR:O	1:A:139:HIS:HB3	2.19	0.41
1:A:171:VAL:HG12	1:A:171:VAL:O	2.20	0.41
1:A:273:ALA:HB1	1:A:291:LEU:HG	2.01	0.41
1:A:417:GLU:O	1:A:420:GLU:HB3	2.20	0.41
2:B:243:ARG:NH2	2:B:252:LEU:HG	2.35	0.41
2:B:265:GLY:O	2:B:266:HIS:C	2.63	0.41
2:B:305:CYS:SG	2:B:383:ALA:HB1	2.60	0.41
1:C:19:LYS:HG3	1:C:228:ASN:HB2	2.01	0.41
1:C:175:PRO:O	1:C:177:VAL:N	2.53	0.41
2:D:30:ILE:HD11	2:D:61:HIS:CD2	2.54	0.41
2:D:305:CYS:SG	2:D:383:ALA:HB1	2.60	0.41
1:E:118:VAL:O	1:E:119:LEU:C	2.62	0.41
1:E:171:VAL:O	1:E:171:VAL:HG12	2.20	0.41
2:F:13:GLY:HA2	2:F:16:ILE:CG2	2.50	0.41
2:F:243:ARG:NH2	2:F:252:LEU:HG	2.35	0.41
1:G:2:ARG:HH21	2:H:99:ALA:N	2.16	0.41
1:G:118:VAL:O	1:G:122:VAL:HG13	2.19	0.41
1:G:138:THR:O	1:G:139:HIS:HB3	2.20	0.41
2:H:132:LEU:H	2:H:132:LEU:CD2	2.23	0.41
2:H:243:ARG:NH2	2:H:252:LEU:HG	2.35	0.41
3:I:91:LEU:O	3:I:92:SER:C	2.62	0.41
3:I:105:TYR:CD1	3:I:111:ARG:C	2.98	0.41
2:B:15:GLN:NE2	5:B:500:GTP:N7	2.67	0.41
1:C:118:VAL:O	1:C:121:VAL:N	2.54	0.41
1:C:297:ASP:CG	1:C:299:LYS:HE2	2.45	0.41
1:C:352:LYS:HG2	2:D:181:VAL:HG23	2.02	0.41
2:D:13:GLY:HA2	2:D:16:ILE:CG2	2.50	0.41
2:D:25:CYS:SG	2:D:26:LEU:N	2.92	0.41
2:D:255:PHE:O	2:D:257:THR:N	2.53	0.41
1:E:25:SER:O	1:E:28:HIS:N	2.53	0.41
1:E:389:LYS:O	1:E:390:ARG:C	2.62	0.41
2:F:184:PRO:HG2	2:F:398:MET:CE	2.40	0.41
1:G:11:GLN:O	1:G:12:CYS:C	2.63	0.41
1:G:48:ARG:HG2	1:G:243:ARG:HB3	2.01	0.41
1:G:171:VAL:O	1:G:171:VAL:HG12	2.20	0.41
2:H:12:ALA:C	2:H:14:VAL:N	2.75	0.41
2:H:13:GLY:HA2	2:H:16:ILE:CG2	2.50	0.41
3:I:80:PHE:CZ	3:I:104:ILE:HD12	2.56	0.41
1:A:118:VAL:O	1:A:121:VAL:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:GLY:HA2	1:A:153:LEU:CD2	2.42	0.41
1:A:175:PRO:O	1:A:177:VAL:N	2.53	0.41
2:B:224:TYR:HD2	2:B:224:TYR:HA	1.73	0.41
2:B:242:LEU:HD11	2:B:250:VAL:HG23	2.02	0.41
2:B:332:ILE:CD1	2:B:353:VAL:HG22	2.51	0.41
1:C:261:PRO:HB2	1:C:262:PHE:CD1	2.54	0.41
2:D:332:ILE:CD1	2:D:353:VAL:HG22	2.51	0.41
2:D:344:VAL:CG1	2:D:345:ASP:N	2.78	0.41
2:D:383:ALA:C	2:D:385:ALA:N	2.78	0.41
2:F:12:ALA:C	2:F:14:VAL:N	2.75	0.41
1:G:98:GLY:O	1:G:100:GLY:N	2.49	0.41
1:G:254:LYS:CA	1:G:257:VAL:HG12	2.50	0.41
1:G:352:LYS:CG	2:H:181:VAL:CG2	2.93	0.41
2:H:25:CYS:SG	2:H:26:LEU:N	2.92	0.41
2:H:242:LEU:HD11	2:H:250:VAL:HG23	2.02	0.41
2:H:251:ASP:CA	2:H:254:GLU:HG3	2.48	0.41
2:H:318:LEU:HB2	2:H:376:CYS:SG	2.61	0.41
1:A:119:LEU:O	1:A:122:VAL:HG22	2.21	0.41
1:A:242:LEU:HB3	1:A:250:ALA:O	2.20	0.41
2:B:210:TYR:O	2:B:211:ASP:C	2.64	0.41
1:C:11:GLN:O	1:C:12:CYS:C	2.63	0.41
1:C:399:PHE:O	1:C:402:LYS:N	2.29	0.41
2:D:173:PRO:HG3	2:D:183:GLU:CD	2.45	0.41
2:D:242:LEU:HD11	2:D:250:VAL:HG23	2.02	0.41
1:E:182:VAL:O	1:E:184:PRO:N	2.54	0.41
2:F:25:CYS:SG	2:F:26:LEU:N	2.92	0.41
2:F:297:GLU:HA	2:F:298:PRO:HD2	1.87	0.41
2:F:305:CYS:SG	2:F:383:ALA:HB1	2.60	0.41
2:F:318:LEU:HB2	2:F:376:CYS:SG	2.61	0.41
1:G:118:VAL:O	1:G:121:VAL:N	2.54	0.41
2:H:71:GLU:HA	2:H:72:PRO:HD3	1.88	0.41
2:H:161:TYR:C	2:H:163:LYS:N	2.77	0.41
2:H:386:GLU:O	2:H:387:ALA:C	2.63	0.41
1:A:105:LYS:HG2	1:A:110:GLU:HG3	2.03	0.41
2:B:383:ALA:C	2:B:385:ALA:N	2.78	0.41
1:C:119:LEU:O	1:C:122:VAL:HG22	2.21	0.41
1:C:138:THR:O	1:C:139:HIS:HB3	2.20	0.41
1:C:168:THR:HB	1:C:198:THR:HG21	2.03	0.41
1:C:259:MET:HE3	1:C:268:PHE:CZ	2.56	0.41
2:D:184:PRO:O	2:D:185:TYR:C	2.62	0.41
2:D:251:ASP:CA	2:D:254:GLU:HG3	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:273:ALA:HB2	2:D:375:VAL:HB	2.03	0.41
2:D:335:ILE:C	2:D:337:THR:H	2.28	0.41
1:E:106:GLY:O	1:E:149:MET:CA	2.68	0.41
1:E:135:PHE:CD1	1:E:166:MET:SD	3.14	0.41
1:E:168:THR:HB	1:E:198:THR:HG21	2.03	0.41
1:E:202:TYR:CE2	1:E:268:PHE:HD1	2.38	0.41
2:F:251:ASP:CA	2:F:254:GLU:HG3	2.49	0.41
2:F:273:ALA:HB2	2:F:375:VAL:HB	2.03	0.41
2:F:332:ILE:CD1	2:F:353:VAL:HG22	2.51	0.41
2:F:428:LEU:HD12	2:F:428:LEU:HA	1.79	0.41
1:G:106:GLY:O	1:G:149:MET:CA	2.68	0.41
1:G:343:PHE:CD2	1:G:350:ASN:ND2	2.88	0.41
2:H:305:CYS:SG	2:H:383:ALA:HB1	2.60	0.41
3:I:108:ASP:O	3:I:133:PHE:CE2	2.74	0.41
1:A:19:LYS:HG3	1:A:228:ASN:HB2	2.01	0.41
1:A:26:ASP:C	1:A:26:ASP:OD1	2.64	0.41
1:A:168:THR:HB	1:A:198:THR:HG21	2.03	0.41
2:B:34:GLY:O	2:B:61:HIS:HB2	2.20	0.41
2:B:166:LYS:HB2	2:B:199:ASP:OD1	2.20	0.41
2:B:173:PRO:HG3	2:B:183:GLU:CD	2.45	0.41
2:B:292:THR:HG21	2:B:331:ALA:HB1	2.02	0.41
1:C:105:LYS:HG2	1:C:110:GLU:HG3	2.03	0.41
2:D:161:TYR:C	2:D:163:LYS:N	2.77	0.41
2:D:166:LYS:HB2	2:D:199:ASP:OD1	2.20	0.41
2:D:255:PHE:O	2:D:259:LEU:N	2.50	0.41
2:D:318:LEU:HB2	2:D:376:CYS:SG	2.61	0.41
1:E:70:LEU:HB2	1:E:99:ALA:HB2	2.03	0.41
1:E:118:VAL:O	1:E:121:VAL:N	2.54	0.41
2:F:161:TYR:C	2:F:163:LYS:N	2.77	0.41
2:F:166:LYS:HB2	2:F:199:ASP:OD1	2.20	0.41
2:F:173:PRO:HG3	2:F:183:GLU:CD	2.45	0.41
2:F:386:GLU:O	2:F:387:ALA:C	2.63	0.41
1:G:26:ASP:C	1:G:26:ASP:OD1	2.64	0.41
1:G:156:LYS:NZ	1:G:159:GLU:OE1	2.47	0.41
1:G:168:THR:HB	1:G:198:THR:HG21	2.03	0.41
1:G:333:LEU:HD11	1:G:337:ASN:HD21	1.85	0.41
1:G:417:GLU:O	1:G:420:GLU:HB3	2.21	0.41
2:H:166:LYS:HB2	2:H:199:ASP:OD1	2.20	0.41
2:H:207:GLU:C	2:H:209:ILE:H	2.29	0.41
2:H:287:SER:O	2:H:291:ILE:HG12	2.21	0.41
2:H:332:ILE:CD1	2:H:353:VAL:HG22	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:GLN:CG	1:A:165:ILE:HD11	2.49	0.41
2:B:7:ILE:HD11	2:B:137:VAL:CG2	2.44	0.41
2:B:273:ALA:HB2	2:B:375:VAL:HB	2.03	0.41
1:C:26:ASP:C	1:C:26:ASP:OD1	2.64	0.41
1:C:44:LEU:HD12	1:C:49:ILE:CD1	2.49	0.41
1:C:48:ARG:HG2	1:C:243:ARG:HB3	2.01	0.41
2:D:172:TYR:OH	2:D:387:ALA:C	2.64	0.41
2:D:217:LEU:HD13	2:D:277:SER:CA	2.48	0.41
1:E:20:PHE:CD2	1:E:235:MET:CG	3.04	0.41
1:E:26:ASP:C	1:E:26:ASP:OD1	2.64	0.41
1:E:105:LYS:HG2	1:E:110:GLU:HG3	2.03	0.41
2:F:172:TYR:OH	2:F:387:ALA:C	2.64	0.41
2:F:207:GLU:C	2:F:209:ILE:H	2.29	0.41
2:F:242:LEU:HD11	2:F:250:VAL:HG23	2.02	0.41
2:F:287:SER:O	2:F:291:ILE:HG12	2.21	0.41
2:F:313:MET:O	2:F:314:ALA:CB	2.68	0.41
1:G:70:LEU:HB2	1:G:99:ALA:HB2	2.03	0.41
1:G:105:LYS:HG2	1:G:110:GLU:HG3	2.03	0.41
1:G:182:VAL:O	1:G:184:PRO:N	2.54	0.41
1:G:262:PHE:HA	1:G:263:PRO:HD2	1.65	0.41
2:H:147:SER:OG	2:H:148:GLY:N	2.54	0.41
2:H:173:PRO:HG3	2:H:183:GLU:CD	2.45	0.41
2:H:273:ALA:HB2	2:H:375:VAL:HB	2.03	0.41
3:I:105:TYR:CE1	3:I:111:ARG:C	2.99	0.41
1:A:135:PHE:CD1	1:A:166:MET:SD	3.14	0.41
1:A:182:VAL:O	1:A:184:PRO:N	2.54	0.41
1:A:243:ARG:N	1:A:243:ARG:HD3	2.26	0.41
1:A:259:MET:HE3	1:A:268:PHE:CZ	2.56	0.41
1:A:288:VAL:O	1:A:289:PRO:C	2.64	0.41
1:A:333:LEU:HD11	1:A:337:ASN:HD21	1.85	0.41
2:B:95:GLY:O	2:B:96:LYS:C	2.64	0.41
2:B:149:PHE:CD1	2:B:150:THR:N	2.89	0.41
2:B:172:TYR:OH	2:B:387:ALA:C	2.64	0.41
2:B:207:GLU:C	2:B:209:ILE:H	2.29	0.41
2:B:318:LEU:HB2	2:B:376:CYS:SG	2.61	0.41
2:B:335:ILE:C	2:B:337:THR:H	2.28	0.41
2:B:401:LYS:O	2:B:402:ARG:HB2	2.21	0.41
1:C:82:PRO:C	1:C:84:GLY:N	2.78	0.41
1:C:262:PHE:HA	1:C:263:PRO:HD2	1.65	0.41
1:C:288:VAL:O	1:C:289:PRO:C	2.64	0.41
1:C:333:LEU:HD11	1:C:337:ASN:HD21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:207:GLU:C	2:D:209:ILE:H	2.29	0.41
2:D:401:LYS:O	2:D:402:ARG:HB2	2.21	0.41
1:E:311:ARG:HG2	1:E:311:ARG:NH1	2.34	0.41
1:E:333:LEU:HD11	1:E:337:ASN:HD21	1.85	0.41
2:F:95:GLY:O	2:F:96:LYS:C	2.64	0.41
2:F:147:SER:OG	2:F:148:GLY:N	2.54	0.41
2:F:184:PRO:O	2:F:185:TYR:C	2.62	0.41
2:F:326:LYS:HE2	1:G:214:PHE:HB2	2.01	0.41
2:F:383:ALA:C	2:F:385:ALA:N	2.78	0.41
1:G:135:PHE:CD1	1:G:166:MET:SD	3.14	0.41
1:G:165:ILE:H	1:G:165:ILE:CD1	2.31	0.41
1:G:202:TYR:CE2	1:G:268:PHE:HD1	2.38	0.41
1:G:308:ARG:HG2	3:I:64:TYR:CE2	2.56	0.41
1:G:311:ARG:HG2	1:G:311:ARG:NH1	2.34	0.41
2:H:172:TYR:OH	2:H:387:ALA:C	2.64	0.41
2:H:313:MET:O	2:H:314:ALA:CB	2.68	0.41
3:I:65:PHE:CE2	3:I:67:GLY:HA2	2.56	0.41
1:A:70:LEU:HB2	1:A:99:ALA:HB2	2.03	0.41
2:B:386:GLU:O	2:B:387:ALA:C	2.63	0.41
1:C:70:LEU:HB2	1:C:99:ALA:HB2	2.03	0.41
1:C:78:VAL:O	1:C:84:GLY:HA3	2.21	0.41
1:C:114:LEU:HD12	1:C:117:SER:OG	2.21	0.41
1:C:135:PHE:CD1	1:C:166:MET:SD	3.14	0.41
1:C:182:VAL:O	1:C:184:PRO:N	2.54	0.41
1:C:238:VAL:HB	1:C:239:THR:H	1.66	0.41
1:C:291:LEU:HD21	1:C:373:MET:HG2	2.03	0.41
1:C:346:TRP:CB	2:D:401:LYS:CD	2.93	0.41
2:D:292:THR:HG21	2:D:331:ALA:HB1	2.02	0.41
1:E:82:PRO:C	1:E:84:GLY:N	2.78	0.41
1:E:417:GLU:O	1:E:420:GLU:HB3	2.21	0.41
2:F:149:PHE:CD1	2:F:150:THR:N	2.89	0.41
2:F:292:THR:HG21	2:F:331:ALA:HB1	2.02	0.41
2:F:425:MET:O	2:F:428:LEU:N	2.45	0.41
1:G:14:ASN:O	1:G:15:GLN:C	2.64	0.41
1:G:20:PHE:CD2	1:G:235:MET:CG	3.04	0.41
1:G:258:ASN:CA	2:H:404:PHE:HD2	2.26	0.41
2:H:95:GLY:O	2:H:96:LYS:C	2.64	0.41
2:H:401:LYS:O	2:H:402:ARG:HB2	2.21	0.41
1:A:20:PHE:CD2	1:A:235:MET:CG	3.04	0.40
1:A:78:VAL:O	1:A:84:GLY:HA3	2.22	0.40
1:A:147:SER:CB	1:A:190:SER:HB3	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:ARG:HG2	1:A:311:ARG:NH1	2.34	0.40
2:B:11:GLN:HG3	2:B:74:VAL:HG21	2.04	0.40
2:B:184:PRO:O	2:B:185:TYR:C	2.62	0.40
2:B:217:LEU:HD13	2:B:277:SER:CA	2.48	0.40
2:B:287:SER:O	2:B:291:ILE:HG12	2.21	0.40
1:C:52:TYR:C	1:C:53:TYR:CD1	2.99	0.40
1:C:275:LEU:HD12	1:C:275:LEU:HA	1.78	0.40
2:D:23:LEU:HD11	2:D:361:THR:O	2.21	0.40
2:D:149:PHE:CD1	2:D:150:THR:N	2.89	0.40
2:D:161:TYR:O	2:D:162:GLY:C	2.64	0.40
1:E:11:GLN:HA	1:E:74:THR:HG21	2.03	0.40
1:E:119:LEU:O	1:E:122:VAL:HG22	2.21	0.40
1:E:259:MET:HE3	1:E:268:PHE:CZ	2.56	0.40
2:F:401:LYS:O	2:F:402:ARG:HB2	2.21	0.40
2:H:98:ASP:OD1	2:H:98:ASP:N	2.55	0.40
2:H:149:PHE:CD1	2:H:150:THR:N	2.89	0.40
2:H:292:THR:HG21	2:H:331:ALA:HB1	2.02	0.40
2:H:425:MET:O	2:H:428:LEU:N	2.45	0.40
1:A:11:GLN:HA	1:A:74:THR:HG21	2.04	0.40
1:A:114:LEU:HD12	1:A:117:SER:OG	2.21	0.40
1:A:306:ASP:HA	1:A:307:PRO:HD3	1.91	0.40
2:B:161:TYR:C	2:B:163:LYS:N	2.77	0.40
2:B:251:ASP:CA	2:B:254:GLU:HG3	2.48	0.40
2:B:428:LEU:HD12	2:B:428:LEU:HA	1.79	0.40
1:C:20:PHE:CD2	1:C:235:MET:CG	3.04	0.40
1:C:311:ARG:HG2	1:C:311:ARG:NH1	2.34	0.40
2:D:11:GLN:HG3	2:D:74:VAL:HG21	2.04	0.40
2:D:95:GLY:O	2:D:96:LYS:C	2.64	0.40
2:F:98:ASP:OD1	2:F:98:ASP:N	2.55	0.40
2:F:408:TYR:O	2:F:409:VAL:C	2.63	0.40
1:G:114:LEU:HD12	1:G:117:SER:OG	2.21	0.40
1:G:119:LEU:O	1:G:122:VAL:HG22	2.21	0.40
2:H:297:GLU:HA	2:H:298:PRO:HD2	1.87	0.40
2:H:383:ALA:C	2:H:385:ALA:N	2.78	0.40
3:I:80:PHE:CZ	3:I:113:ILE:HB	2.56	0.40
1:A:52:TYR:C	1:A:53:TYR:CD1	2.99	0.40
1:A:82:PRO:C	1:A:84:GLY:N	2.78	0.40
1:A:202:TYR:CE2	1:A:268:PHE:HD1	2.38	0.40
1:A:260:VAL:CG2	2:B:407:TRP:HE1	2.30	0.40
1:A:422:GLU:O	1:A:426:ASN:CB	2.67	0.40
2:B:272:TYR:O	2:B:300:ASN:ND2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:CYS:O	1:C:14:ASN:N	2.55	0.40
1:C:349:ASN:C	1:C:349:ASN:ND2	2.77	0.40
2:D:100:ALA:HB2	2:D:105:ARG:HD3	2.02	0.40
2:D:272:TYR:O	2:D:300:ASN:ND2	2.54	0.40
2:D:386:GLU:O	2:D:387:ALA:C	2.63	0.40
1:E:2:ARG:NH2	2:F:98:ASP:HA	2.37	0.40
1:E:14:ASN:O	1:E:15:GLN:C	2.64	0.40
1:E:150:GLY:HA2	1:E:153:LEU:CD2	2.42	0.40
1:E:306:ASP:HA	1:E:307:PRO:HD3	1.91	0.40
2:F:325:PRO:HG2	1:G:224:TYR:H	1.85	0.40
1:G:11:GLN:HA	1:G:74:THR:HG21	2.04	0.40
1:G:82:PRO:C	1:G:84:GLY:N	2.78	0.40
1:G:259:MET:HE3	1:G:268:PHE:CZ	2.56	0.40
1:G:291:LEU:HD21	1:G:373:MET:HG2	2.03	0.40
2:H:184:PRO:O	2:H:185:TYR:C	2.62	0.40
1:A:11:GLN:HG3	1:A:74:THR:HG23	2.04	0.40
1:C:11:GLN:HG3	1:C:74:THR:HG23	2.04	0.40
1:C:98:GLY:O	1:C:100:GLY:N	2.49	0.40
1:C:139:HIS:HE1	1:C:168:THR:CG2	2.34	0.40
1:C:422:GLU:O	1:C:426:ASN:CB	2.67	0.40
2:D:398:MET:HE3	2:D:398:MET:HB2	1.78	0.40
1:E:52:TYR:C	1:E:53:TYR:CD1	2.99	0.40
1:E:132:LEU:O	1:E:164:ARG:HD2	2.21	0.40
1:E:175:PRO:HG2	1:E:207:GLU:CD	2.47	0.40
2:F:320:ARG:O	2:F:373:ARG:HA	2.22	0.40
2:F:392:ASP:OD2	2:F:392:ASP:C	2.64	0.40
1:G:133:GLN:CG	1:G:165:ILE:HD11	2.49	0.40
1:G:147:SER:CB	1:G:190:SER:HB3	2.42	0.40
2:H:320:ARG:O	2:H:373:ARG:HA	2.22	0.40
1:A:12:CYS:O	1:A:14:ASN:N	2.55	0.40
1:A:291:LEU:HD21	1:A:373:MET:HG2	2.03	0.40
2:B:23:LEU:HD11	2:B:361:THR:O	2.21	0.40
2:B:98:ASP:OD1	2:B:98:ASP:N	2.55	0.40
2:B:255:PHE:O	2:B:259:LEU:N	2.50	0.40
2:B:392:ASP:OD2	2:B:392:ASP:C	2.64	0.40
1:C:11:GLN:HA	1:C:74:THR:HG21	2.04	0.40
1:C:315:VAL:CG1	1:C:377:PHE:CE1	3.05	0.40
2:D:100:ALA:O	2:D:102:ASN:N	2.49	0.40
1:E:12:CYS:O	1:E:14:ASN:N	2.55	0.40
1:E:114:LEU:HD12	1:E:117:SER:OG	2.21	0.40
1:E:204:ILE:HG23	1:E:209:LEU:HD11	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:11:GLN:HG3	2:F:74:VAL:HG21	2.03	0.40
2:F:11:GLN:N	5:F:500:GTP:O2B	2.55	0.40
2:F:161:TYR:O	2:F:162:GLY:C	2.64	0.40
1:G:52:TYR:C	1:G:53:TYR:CD1	2.99	0.40
1:G:132:LEU:O	1:G:164:ARG:HD2	2.21	0.40
1:G:150:GLY:HA2	1:G:153:LEU:CD2	2.42	0.40
1:G:188:THR:O	1:G:191:VAL:HG12	2.21	0.40
1:G:204:ILE:HG23	1:G:209:LEU:HD11	2.04	0.40
2:H:11:GLN:N	5:H:500:GTP:O2B	2.55	0.40
2:H:392:ASP:OD2	2:H:392:ASP:C	2.64	0.40
2:H:399:TYR:C	2:H:401:LYS:N	2.77	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	424/445 (95%)	274 (65%)	94 (22%)	56 (13%)	0	4
1	C	424/445 (95%)	274 (65%)	94 (22%)	56 (13%)	0	4
1	E	424/445 (95%)	274 (65%)	94 (22%)	56 (13%)	0	4
1	G	424/445 (95%)	274 (65%)	94 (22%)	56 (13%)	0	4
2	B	423/452 (94%)	279 (66%)	87 (21%)	57 (14%)	0	4
2	D	423/452 (94%)	281 (66%)	85 (20%)	57 (14%)	0	4
2	F	423/452 (94%)	279 (66%)	87 (21%)	57 (14%)	0	4
2	H	423/452 (94%)	278 (66%)	88 (21%)	57 (14%)	0	4
3	I	93/95 (98%)	72 (77%)	15 (16%)	6 (6%)	1	12
All	All	3481/3683 (94%)	2285 (66%)	738 (21%)	458 (13%)	0	4

All (458) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	VAL
1	A	24	ILE
1	A	32	PRO
1	A	50	ASN
1	A	82	PRO
1	A	97	SER
1	A	128	SER
1	A	176	LYS
1	A	183	GLU
1	A	218	LYS
1	A	238	VAL
1	A	239	THR
1	A	240	THR
1	A	252	LEU
1	A	263	PRO
1	A	266	HIS
1	A	273	ALA
1	A	278	ARG
1	A	280	SER
1	A	281	GLN
1	A	282	GLN
1	A	288	VAL
1	A	294	GLN
1	A	295	MET
1	A	343	PHE
1	A	344	VAL
1	A	346	TRP
1	A	369	ARG
1	A	403	ALA
2	B	56	THR
2	B	58	ALA
2	B	96	LYS
2	B	97	GLU
2	B	108	TYR
2	B	109	THR
2	B	141	PHE
2	B	183	GLU
2	B	217	LEU
2	B	240	ALA
2	B	249	ASN
2	B	255	PHE
2	B	266	HIS
2	B	309	HIS

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Mol	Chain	Res	Type
2	B	346	TRP
2	B	370	LYS
2	B	387	ALA
2	B	403	ALA
2	B	437	VAL
1	C	23	VAL
1	C	24	ILE
1	C	32	PRO
1	C	50	ASN
1	C	82	PRO
1	C	97	SER
1	C	128	SER
1	C	176	LYS
1	C	183	GLU
1	C	218	LYS
1	C	238	VAL
1	C	239	THR
1	C	240	THR
1	C	252	LEU
1	C	263	PRO
1	C	266	HIS
1	C	273	ALA
1	C	278	ARG
1	C	280	SER
1	C	281	GLN
1	C	282	GLN
1	C	288	VAL
1	C	294	GLN
1	C	295	MET
1	C	343	PHE
1	C	344	VAL
1	C	346	TRP
1	C	369	ARG
1	C	403	ALA
2	D	56	THR
2	D	58	ALA
2	D	63	PRO
2	D	96	LYS
2	D	97	GLU
2	D	108	TYR
2	D	109	THR
2	D	141	PHE

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Mol	Chain	Res	Type
2	D	183	GLU
2	D	217	LEU
2	D	240	ALA
2	D	249	ASN
2	D	255	PHE
2	D	266	HIS
2	D	309	HIS
2	D	346	TRP
2	D	370	LYS
2	D	387	ALA
2	D	403	ALA
2	D	437	VAL
1	E	23	VAL
1	E	24	ILE
1	E	32	PRO
1	E	50	ASN
1	E	82	PRO
1	E	97	SER
1	E	128	SER
1	E	176	LYS
1	E	183	GLU
1	E	218	LYS
1	E	238	VAL
1	E	239	THR
1	E	240	THR
1	E	252	LEU
1	E	263	PRO
1	E	266	HIS
1	E	273	ALA
1	E	278	ARG
1	E	280	SER
1	E	281	GLN
1	E	282	GLN
1	E	288	VAL
1	E	294	GLN
1	E	295	MET
1	E	343	PHE
1	E	344	VAL
1	E	346	TRP
1	E	369	ARG
1	E	403	ALA
2	F	63	PRO

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Mol	Chain	Res	Type
2	F	96	LYS
2	F	97	GLU
2	F	108	TYR
2	F	109	THR
2	F	141	PHE
2	F	183	GLU
2	F	217	LEU
2	F	240	ALA
2	F	249	ASN
2	F	255	PHE
2	F	266	HIS
2	F	309	HIS
2	F	346	TRP
2	F	370	LYS
2	F	387	ALA
2	F	403	ALA
2	F	437	VAL
1	G	23	VAL
1	G	24	ILE
1	G	32	PRO
1	G	50	ASN
1	G	82	PRO
1	G	97	SER
1	G	128	SER
1	G	176	LYS
1	G	183	GLU
1	G	218	LYS
1	G	238	VAL
1	G	239	THR
1	G	240	THR
1	G	252	LEU
1	G	263	PRO
1	G	266	HIS
1	G	273	ALA
1	G	278	ARG
1	G	280	SER
1	G	281	GLN
1	G	282	GLN
1	G	288	VAL
1	G	294	GLN
1	G	295	MET
1	G	343	PHE

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Mol	Chain	Res	Type
1	G	344	VAL
1	G	346	TRP
1	G	369	ARG
1	G	403	ALA
2	H	63	PRO
2	H	96	LYS
2	H	97	GLU
2	H	108	TYR
2	H	109	THR
2	H	141	PHE
2	H	183	GLU
2	H	217	LEU
2	H	240	ALA
2	H	249	ASN
2	H	255	PHE
2	H	266	HIS
2	H	309	HIS
2	H	346	TRP
2	H	370	LYS
2	H	387	ALA
2	H	403	ALA
2	H	437	VAL
1	A	38	GLY
1	A	73	GLY
1	A	175	PRO
1	A	265	LEU
1	A	279	GLY
1	A	298	ALA
1	A	300	ASN
1	A	311	ARG
2	B	24	TYR
2	B	73	THR
2	B	83	TYR
2	B	103	TYR
2	B	111	GLY
2	B	131	GLY
2	B	218	ASP
2	B	219	ILE
2	B	238	ILE
2	B	265	GLY
2	B	281	ALA
2	B	314	ALA

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Mol	Chain	Res	Type
2	B	339	ARG
2	B	342	GLN
2	B	373	ARG
2	B	386	GLU
1	C	38	GLY
1	C	73	GLY
1	C	175	PRO
1	C	265	LEU
1	C	279	GLY
1	C	298	ALA
1	C	300	ASN
1	C	311	ARG
2	D	24	TYR
2	D	73	THR
2	D	83	TYR
2	D	103	TYR
2	D	111	GLY
2	D	131	GLY
2	D	218	ASP
2	D	219	ILE
2	D	238	ILE
2	D	265	GLY
2	D	281	ALA
2	D	314	ALA
2	D	339	ARG
2	D	342	GLN
2	D	373	ARG
2	D	386	GLU
1	E	38	GLY
1	E	73	GLY
1	E	175	PRO
1	E	265	LEU
1	E	279	GLY
1	E	298	ALA
1	E	300	ASN
1	E	311	ARG
2	F	24	TYR
2	F	73	THR
2	F	83	TYR
2	F	103	TYR
2	F	111	GLY
2	F	131	GLY

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Mol	Chain	Res	Type
2	F	218	ASP
2	F	219	ILE
2	F	238	ILE
2	F	265	GLY
2	F	281	ALA
2	F	314	ALA
2	F	339	ARG
2	F	342	GLN
2	F	373	ARG
2	F	386	GLU
1	G	38	GLY
1	G	73	GLY
1	G	175	PRO
1	G	265	LEU
1	G	279	GLY
1	G	298	ALA
1	G	300	ASN
1	G	311	ARG
2	H	24	TYR
2	H	73	THR
2	H	83	TYR
2	H	103	TYR
2	H	111	GLY
2	H	131	GLY
2	H	218	ASP
2	H	219	ILE
2	H	238	ILE
2	H	265	GLY
2	H	281	ALA
2	H	314	ALA
2	H	339	ARG
2	H	342	GLN
2	H	373	ARG
2	H	386	GLU
3	I	51	LYS
3	I	135	LYS
1	A	34	GLY
1	A	83	PHE
1	A	99	ALA
1	A	100	GLY
1	A	302	MET
1	A	386	GLU

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Mol	Chain	Res	Type
2	B	48	SER
2	B	104	ALA
2	B	148	GLY
2	B	149	PHE
2	B	173	PRO
2	B	239	THR
2	B	245	ASP
2	B	279	GLU
2	B	330	ALA
2	B	336	LYS
2	B	369	ALA
1	C	34	GLY
1	C	83	PHE
1	C	99	ALA
1	C	100	GLY
1	C	302	MET
1	C	386	GLU
2	D	48	SER
2	D	104	ALA
2	D	148	GLY
2	D	149	PHE
2	D	173	PRO
2	D	239	THR
2	D	245	ASP
2	D	263	PRO
2	D	279	GLU
2	D	330	ALA
2	D	336	LYS
2	D	369	ALA
1	E	34	GLY
1	E	83	PHE
1	E	99	ALA
1	E	100	GLY
1	E	302	MET
1	E	386	GLU
2	F	48	SER
2	F	59	GLY
2	F	104	ALA
2	F	148	GLY
2	F	149	PHE
2	F	173	PRO
2	F	239	THR

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Mol	Chain	Res	Type
2	F	245	ASP
2	F	263	PRO
2	F	279	GLU
2	F	330	ALA
2	F	336	LYS
2	F	369	ALA
1	G	34	GLY
1	G	83	PHE
1	G	99	ALA
1	G	100	GLY
1	G	302	MET
1	G	386	GLU
2	H	48	SER
2	H	59	GLY
2	H	104	ALA
2	H	148	GLY
2	H	149	PHE
2	H	173	PRO
2	H	239	THR
2	H	245	ASP
2	H	263	PRO
2	H	279	GLU
2	H	330	ALA
2	H	336	LYS
2	H	369	ALA
3	I	63	ARG
3	I	67	GLY
1	A	96	GLN
1	A	395	PHE
2	B	129	CYS
2	B	263	PRO
2	B	300	ASN
2	B	348	PRO
1	C	96	GLN
1	C	395	PHE
2	D	129	CYS
2	D	300	ASN
2	D	348	PRO
1	E	96	GLN
1	E	395	PHE
2	F	300	ASN
2	F	348	PRO

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Mol	Chain	Res	Type
1	G	96	GLN
1	G	395	PHE
2	H	300	ASN
2	H	348	PRO
3	I	101	VAL
1	A	57	ALA
1	A	74	THR
1	A	285	ALA
1	A	424	ASN
2	B	256	GLN
2	B	303	VAL
2	B	382	THR
1	C	57	ALA
1	C	74	THR
1	C	285	ALA
1	C	424	ASN
2	D	256	GLN
2	D	303	VAL
2	D	382	THR
1	E	57	ALA
1	E	74	THR
1	E	285	ALA
1	E	424	ASN
2	F	129	CYS
2	F	256	GLN
2	F	303	VAL
2	F	307	PRO
2	F	382	THR
1	G	57	ALA
1	G	74	THR
1	G	285	ALA
1	G	424	ASN
2	H	129	CYS
2	H	256	GLN
2	H	303	VAL
2	H	382	THR
1	A	51	VAL
1	A	58	GLY
1	A	145	THR
1	A	162	PRO
1	A	400	ARG
2	B	62	VAL

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Mol	Chain	Res	Type
2	B	273	ALA
2	B	307	PRO
1	C	51	VAL
1	C	58	GLY
1	C	145	THR
1	C	162	PRO
1	C	400	ARG
2	D	273	ALA
2	D	307	PRO
1	E	51	VAL
1	E	58	GLY
1	E	145	THR
1	E	162	PRO
1	E	400	ARG
2	F	273	ALA
1	G	51	VAL
1	G	58	GLY
1	G	145	THR
1	G	162	PRO
1	G	400	ARG
2	H	273	ALA
2	H	307	PRO
1	A	195	VAL
1	C	195	VAL
1	E	195	VAL
2	F	31	GLN
1	G	195	VAL
2	H	31	GLN
2	B	115	ILE
1	C	72	PRO
2	D	115	ILE
1	E	72	PRO
2	F	115	ILE
2	H	115	ILE
3	I	98	PRO
1	A	72	PRO
1	G	72	PRO

5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	367/381 (96%)	307 (84%)	60 (16%)	2	10
1	C	367/381 (96%)	307 (84%)	60 (16%)	2	10
1	E	367/381 (96%)	307 (84%)	60 (16%)	2	10
1	G	367/381 (96%)	307 (84%)	60 (16%)	2	10
2	B	354/378 (94%)	288 (81%)	66 (19%)	1	8
2	D	354/378 (94%)	289 (82%)	65 (18%)	1	8
2	F	354/378 (94%)	289 (82%)	65 (18%)	1	8
2	H	354/378 (94%)	290 (82%)	64 (18%)	2	9
3	I	85/85 (100%)	56 (66%)	29 (34%)	0	1
All	All	2969/3121 (95%)	2440 (82%)	529 (18%)	4	9

All (529) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ILE
1	A	26	ASP
1	A	32	PRO
1	A	41	ASP
1	A	67	LEU
1	A	68	VAL
1	A	90	ASP
1	A	94	PHE
1	A	121	VAL
1	A	122	VAL
1	A	129	CYS
1	A	135	PHE
1	A	141	LEU
1	A	145	THR
1	A	149	MET
1	A	151	THR
1	A	153	LEU
1	A	161	TYR
1	A	163	ASP
1	A	165	ILE
1	A	174	SER
1	A	193	GLN

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Mol	Chain	Res	Type
1	A	198	THR
1	A	201	THR
1	A	203	CYS
1	A	207	GLU
1	A	211	ASP
1	A	214	PHE
1	A	227	LEU
1	A	229	HIS
1	A	230	LEU
1	A	232	SER
1	A	236	SER
1	A	240	THR
1	A	265	LEU
1	A	267	PHE
1	A	275	LEU
1	A	282	GLN
1	A	284	ARG
1	A	299	LYS
1	A	306	ASP
1	A	309	HIS
1	A	314	THR
1	A	322	ARG
1	A	324	SER
1	A	325	MET
1	A	331	GLN
1	A	343	PHE
1	A	344	VAL
1	A	352	LYS
1	A	353	THR
1	A	369	ARG
1	A	387	LEU
1	A	413	MET
1	A	414	ASP
1	A	424	ASN
1	A	427	ASP
1	A	431	GLU
1	A	432	TYR
1	A	437	ASP
2	B	6	SER
2	B	7	ILE
2	B	16	ILE
2	B	20	CYS

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Mol	Chain	Res	Type
2	B	31	GLN
2	B	36	MET
2	B	48	SER
2	B	50	ASN
2	B	60	LYS
2	B	61	HIS
2	B	62	VAL
2	B	73	THR
2	B	74	VAL
2	B	79	ARG
2	B	82	THR
2	B	84	ARG
2	B	87	PHE
2	B	88	HIS
2	B	90	GLU
2	B	98	ASP
2	B	109	THR
2	B	115	ILE
2	B	120	ASP
2	B	125	LEU
2	B	130	THR
2	B	135	PHE
2	B	141	PHE
2	B	150	THR
2	B	152	LEU
2	B	154	MET
2	B	155	GLU
2	B	172	TYR
2	B	173	PRO
2	B	183	GLU
2	B	192	HIS
2	B	204	VAL
2	B	219	ILE
2	B	224	TYR
2	B	231	ILE
2	B	234	ILE
2	B	243	ARG
2	B	244	PHE
2	B	253	THR
2	B	260	VAL
2	B	267	PHE
2	B	269	LEU

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Mol	Chain	Res	Type
2	B	279	GLU
2	B	280	LYS
2	B	288	VAL
2	B	290	GLU
2	B	303	VAL
2	B	325	PRO
2	B	328	VAL
2	B	334	THR
2	B	345	ASP
2	B	352	LYS
2	B	368	LEU
2	B	376	CYS
2	B	377	MET
2	B	378	LEU
2	B	415	GLU
2	B	417	GLU
2	B	420	GLU
2	B	431	ASP
2	B	432	TYR
2	B	433	GLU
1	C	24	ILE
1	C	26	ASP
1	C	32	PRO
1	C	41	ASP
1	C	67	LEU
1	C	68	VAL
1	C	90	ASP
1	C	94	PHE
1	C	121	VAL
1	C	122	VAL
1	C	129	CYS
1	C	135	PHE
1	C	141	LEU
1	C	145	THR
1	C	149	MET
1	C	151	THR
1	C	153	LEU
1	C	161	TYR
1	C	163	ASP
1	C	165	ILE
1	C	174	SER
1	C	193	GLN

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Mol	Chain	Res	Type
1	C	198	THR
1	C	201	THR
1	C	203	CYS
1	C	207	GLU
1	C	211	ASP
1	C	214	PHE
1	C	227	LEU
1	C	229	HIS
1	C	230	LEU
1	C	232	SER
1	C	236	SER
1	C	240	THR
1	C	265	LEU
1	C	267	PHE
1	C	275	LEU
1	C	282	GLN
1	C	284	ARG
1	C	299	LYS
1	C	306	ASP
1	C	309	HIS
1	C	314	THR
1	C	322	ARG
1	C	324	SER
1	C	325	MET
1	C	331	GLN
1	C	343	PHE
1	C	344	VAL
1	C	352	LYS
1	C	353	THR
1	C	369	ARG
1	C	387	LEU
1	C	413	MET
1	C	414	ASP
1	C	424	ASN
1	C	427	ASP
1	C	431	GLU
1	C	432	TYR
1	C	437	ASP
2	D	6	SER
2	D	7	ILE
2	D	16	ILE
2	D	20	CYS

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Mol	Chain	Res	Type
2	D	31	GLN
2	D	36	MET
2	D	48	SER
2	D	50	ASN
2	D	60	LYS
2	D	73	THR
2	D	74	VAL
2	D	79	ARG
2	D	82	THR
2	D	84	ARG
2	D	87	PHE
2	D	88	HIS
2	D	90	GLU
2	D	98	ASP
2	D	109	THR
2	D	115	ILE
2	D	120	ASP
2	D	125	LEU
2	D	130	THR
2	D	135	PHE
2	D	141	PHE
2	D	150	THR
2	D	152	LEU
2	D	154	MET
2	D	155	GLU
2	D	172	TYR
2	D	173	PRO
2	D	183	GLU
2	D	192	HIS
2	D	204	VAL
2	D	219	ILE
2	D	224	TYR
2	D	231	ILE
2	D	234	ILE
2	D	243	ARG
2	D	244	PHE
2	D	253	THR
2	D	260	VAL
2	D	267	PHE
2	D	269	LEU
2	D	279	GLU
2	D	280	LYS

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Mol	Chain	Res	Type
2	D	288	VAL
2	D	290	GLU
2	D	291	ILE
2	D	303	VAL
2	D	325	PRO
2	D	328	VAL
2	D	334	THR
2	D	345	ASP
2	D	352	LYS
2	D	368	LEU
2	D	376	CYS
2	D	377	MET
2	D	378	LEU
2	D	415	GLU
2	D	417	GLU
2	D	420	GLU
2	D	431	ASP
2	D	432	TYR
2	D	433	GLU
1	E	24	ILE
1	E	26	ASP
1	E	32	PRO
1	E	41	ASP
1	E	67	LEU
1	E	68	VAL
1	E	90	ASP
1	E	94	PHE
1	E	121	VAL
1	E	122	VAL
1	E	129	CYS
1	E	135	PHE
1	E	141	LEU
1	E	145	THR
1	E	149	MET
1	E	151	THR
1	E	153	LEU
1	E	161	TYR
1	E	163	ASP
1	E	165	ILE
1	E	174	SER
1	E	193	GLN
1	E	198	THR

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Mol	Chain	Res	Type
1	E	201	THR
1	E	203	CYS
1	E	207	GLU
1	E	211	ASP
1	E	214	PHE
1	E	227	LEU
1	E	229	HIS
1	E	230	LEU
1	E	232	SER
1	E	236	SER
1	E	240	THR
1	E	265	LEU
1	E	267	PHE
1	E	275	LEU
1	E	282	GLN
1	E	284	ARG
1	E	299	LYS
1	E	306	ASP
1	E	309	HIS
1	E	314	THR
1	E	322	ARG
1	E	324	SER
1	E	325	MET
1	E	331	GLN
1	E	343	PHE
1	E	344	VAL
1	E	352	LYS
1	E	353	THR
1	E	369	ARG
1	E	387	LEU
1	E	413	MET
1	E	414	ASP
1	E	424	ASN
1	E	427	ASP
1	E	431	GLU
1	E	432	TYR
1	E	437	ASP
2	F	6	SER
2	F	7	ILE
2	F	16	ILE
2	F	20	CYS
2	F	31	GLN

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Mol	Chain	Res	Type
2	F	36	MET
2	F	48	SER
2	F	50	ASN
2	F	60	LYS
2	F	73	THR
2	F	74	VAL
2	F	79	ARG
2	F	82	THR
2	F	84	ARG
2	F	87	PHE
2	F	88	HIS
2	F	90	GLU
2	F	98	ASP
2	F	109	THR
2	F	115	ILE
2	F	120	ASP
2	F	125	LEU
2	F	130	THR
2	F	135	PHE
2	F	141	PHE
2	F	150	THR
2	F	152	LEU
2	F	154	MET
2	F	155	GLU
2	F	172	TYR
2	F	173	PRO
2	F	183	GLU
2	F	192	HIS
2	F	204	VAL
2	F	219	ILE
2	F	224	TYR
2	F	231	ILE
2	F	234	ILE
2	F	243	ARG
2	F	244	PHE
2	F	253	THR
2	F	260	VAL
2	F	267	PHE
2	F	269	LEU
2	F	279	GLU
2	F	280	LYS
2	F	288	VAL

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Mol	Chain	Res	Type
2	F	290	GLU
2	F	291	ILE
2	F	303	VAL
2	F	325	PRO
2	F	328	VAL
2	F	334	THR
2	F	345	ASP
2	F	352	LYS
2	F	368	LEU
2	F	376	CYS
2	F	377	MET
2	F	378	LEU
2	F	415	GLU
2	F	417	GLU
2	F	420	GLU
2	F	431	ASP
2	F	432	TYR
2	F	433	GLU
1	G	24	ILE
1	G	26	ASP
1	G	32	PRO
1	G	41	ASP
1	G	67	LEU
1	G	68	VAL
1	G	90	ASP
1	G	94	PHE
1	G	121	VAL
1	G	122	VAL
1	G	129	CYS
1	G	135	PHE
1	G	141	LEU
1	G	145	THR
1	G	149	MET
1	G	151	THR
1	G	153	LEU
1	G	158	ARG
1	G	161	TYR
1	G	163	ASP
1	G	165	ILE
1	G	174	SER
1	G	193	GLN
1	G	198	THR

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Mol	Chain	Res	Type
1	G	201	THR
1	G	203	CYS
1	G	207	GLU
1	G	211	ASP
1	G	214	PHE
1	G	227	LEU
1	G	229	HIS
1	G	230	LEU
1	G	232	SER
1	G	236	SER
1	G	240	THR
1	G	265	LEU
1	G	267	PHE
1	G	275	LEU
1	G	282	GLN
1	G	284	ARG
1	G	299	LYS
1	G	306	ASP
1	G	309	HIS
1	G	314	THR
1	G	322	ARG
1	G	324	SER
1	G	325	MET
1	G	331	GLN
1	G	343	PHE
1	G	344	VAL
1	G	353	THR
1	G	369	ARG
1	G	387	LEU
1	G	413	MET
1	G	414	ASP
1	G	424	ASN
1	G	427	ASP
1	G	431	GLU
1	G	432	TYR
1	G	437	ASP
2	H	6	SER
2	H	7	ILE
2	H	16	ILE
2	H	20	CYS
2	H	31	GLN
2	H	36	MET

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Mol	Chain	Res	Type
2	H	48	SER
2	H	50	ASN
2	H	73	THR
2	H	74	VAL
2	H	79	ARG
2	H	82	THR
2	H	84	ARG
2	H	87	PHE
2	H	88	HIS
2	H	90	GLU
2	H	98	ASP
2	H	109	THR
2	H	115	ILE
2	H	120	ASP
2	H	125	LEU
2	H	130	THR
2	H	135	PHE
2	H	141	PHE
2	H	150	THR
2	H	152	LEU
2	H	154	MET
2	H	155	GLU
2	H	172	TYR
2	H	173	PRO
2	H	183	GLU
2	H	192	HIS
2	H	204	VAL
2	H	219	ILE
2	H	224	TYR
2	H	231	ILE
2	H	234	ILE
2	H	243	ARG
2	H	244	PHE
2	H	253	THR
2	H	260	VAL
2	H	267	PHE
2	H	269	LEU
2	H	279	GLU
2	H	280	LYS
2	H	288	VAL
2	H	290	GLU
2	H	291	ILE

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Mol	Chain	Res	Type
2	H	303	VAL
2	H	325	PRO
2	H	328	VAL
2	H	334	THR
2	H	345	ASP
2	H	352	LYS
2	H	368	LEU
2	H	376	CYS
2	H	377	MET
2	H	378	LEU
2	H	415	GLU
2	H	417	GLU
2	H	420	GLU
2	H	431	ASP
2	H	432	TYR
2	H	433	GLU
3	I	47	SER
3	I	49	GLU
3	I	50	LYS
3	I	51	LYS
3	I	54	LYS
3	I	56	ARG
3	I	59	ARG
3	I	72	VAL
3	I	75	ASP
3	I	76	ARG
3	I	78	ARG
3	I	79	SER
3	I	86	ASP
3	I	88	THR
3	I	89	ARG
3	I	90	SER
3	I	93	ASP
3	I	95	ILE
3	I	102	ARG
3	I	106	THR
3	I	108	ASP
3	I	112	LYS
3	I	117	ASP
3	I	120	GLU
3	I	131	ASN
3	I	132	PHE

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Mol	Chain	Res	Type
3	I	135	LYS
3	I	136	VAL
3	I	140	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (134) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	91	ASN
1	A	101	ASN
1	A	102	ASN
1	A	133	GLN
1	A	136	GLN
1	A	139	HIS
1	A	186	ASN
1	A	266	HIS
1	A	282	GLN
1	A	331	GLN
1	A	334	ASN
1	A	336	GLN
1	A	337	ASN
1	A	349	ASN
1	A	380	ASN
1	A	385	GLN
1	A	406	HIS
1	A	434	GLN
1	A	436	GLN
2	B	11	GLN
2	B	15	GLN
2	B	50	ASN
2	B	61	HIS
2	B	91	GLN
2	B	101	ASN
2	B	107	HIS
2	B	133	GLN
2	B	139	HIS
2	B	197	HIS
2	B	216	ASN
2	B	226	ASN
2	B	256	GLN
2	B	309	HIS
1	C	14	ASN

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Mol	Chain	Res	Type
1	C	43	GLN
1	C	91	ASN
1	C	102	ASN
1	C	107	HIS
1	C	133	GLN
1	C	136	GLN
1	C	139	HIS
1	C	186	ASN
1	C	266	HIS
1	C	282	GLN
1	C	331	GLN
1	C	334	ASN
1	C	336	GLN
1	C	337	ASN
1	C	349	ASN
1	C	380	ASN
1	C	385	GLN
1	C	406	HIS
1	C	434	GLN
1	C	436	GLN
2	D	11	GLN
2	D	15	GLN
2	D	50	ASN
2	D	91	GLN
2	D	133	GLN
2	D	139	HIS
2	D	197	HIS
2	D	216	ASN
2	D	226	ASN
2	D	256	GLN
2	D	309	HIS
1	E	14	ASN
1	E	43	GLN
1	E	91	ASN
1	E	101	ASN
1	E	102	ASN
1	E	133	GLN
1	E	136	GLN
1	E	139	HIS
1	E	186	ASN
1	E	282	GLN
1	E	331	GLN

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Mol	Chain	Res	Type
1	E	334	ASN
1	E	336	GLN
1	E	337	ASN
1	E	349	ASN
1	E	380	ASN
1	E	385	GLN
1	E	406	HIS
1	E	434	GLN
1	E	436	GLN
2	F	8	HIS
2	F	11	GLN
2	F	15	GLN
2	F	50	ASN
2	F	61	HIS
2	F	91	GLN
2	F	133	GLN
2	F	139	HIS
2	F	197	HIS
2	F	216	ASN
2	F	226	ASN
2	F	256	GLN
2	F	309	HIS
1	G	43	GLN
1	G	91	ASN
1	G	102	ASN
1	G	133	GLN
1	G	136	GLN
1	G	139	HIS
1	G	186	ASN
1	G	282	GLN
1	G	309	HIS
1	G	331	GLN
1	G	334	ASN
1	G	336	GLN
1	G	337	ASN
1	G	349	ASN
1	G	380	ASN
1	G	385	GLN
1	G	406	HIS
1	G	434	GLN
1	G	436	GLN
2	H	8	HIS

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Mol	Chain	Res	Type
2	H	11	GLN
2	H	15	GLN
2	H	50	ASN
2	H	91	GLN
2	H	101	ASN
2	H	133	GLN
2	H	139	HIS
2	H	197	HIS
2	H	216	ASN
2	H	226	ASN
2	H	256	GLN
2	H	309	HIS
2	H	406	HIS
3	I	96	ASN
3	I	131	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

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
5	GTP	H	500	-	33,34,34	1.90	4 (12%)	50,54,54	1.03	5 (10%)
4	GDP	C	600	-	29,30,30	2.85	11 (37%)	45,47,47	3.47	16 (35%)
4	GDP	A	600	-	29,30,30	2.84	11 (37%)	45,47,47	3.47	16 (35%)
5	GTP	B	500	-	33,34,34	2.04	5 (15%)	50,54,54	1.37	6 (12%)
4	GDP	G	600	-	29,30,30	2.85	11 (37%)	45,47,47	3.47	16 (35%)
5	GTP	F	500	-	33,34,34	1.90	4 (12%)	50,54,54	1.03	5 (10%)
4	GDP	E	600	-	29,30,30	2.84	11 (37%)	45,47,47	3.47	16 (35%)
5	GTP	D	500	-	33,34,34	1.90	4 (12%)	50,54,54	1.04	5 (10%)

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
5	GTP	H	500	-	-	3/22/38/38	0/3/3/3
4	GDP	C	600	-	-	4/16/32/32	0/3/3/3
4	GDP	A	600	-	-	4/16/32/32	0/3/3/3
5	GTP	B	500	-	-	3/22/38/38	0/3/3/3
4	GDP	G	600	-	-	4/16/32/32	0/3/3/3
5	GTP	F	500	-	-	3/22/38/38	0/3/3/3
4	GDP	E	600	-	-	4/16/32/32	0/3/3/3
5	GTP	D	500	-	-	3/22/38/38	0/3/3/3

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	600	GDP	PA-O3A	7.53	1.67	1.59
4	G	600	GDP	PA-O3A	7.50	1.67	1.59
4	A	600	GDP	PA-O3A	7.47	1.67	1.59
4	E	600	GDP	PA-O3A	7.42	1.67	1.59
5	H	500	GTP	PA-O3A	-5.94	1.53	1.59
5	F	500	GTP	PA-O3A	-5.94	1.53	1.59
5	B	500	GTP	PA-O3A	-5.91	1.53	1.59
4	C	600	GDP	O6-C6	5.90	1.34	1.23
4	E	600	GDP	C8-N9	5.90	1.50	1.37
4	G	600	GDP	C8-N9	5.90	1.50	1.37
4	C	600	GDP	C8-N9	5.90	1.50	1.37
4	G	600	GDP	O6-C6	5.90	1.34	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	600	GDP	O6-C6	5.90	1.34	1.23
4	A	600	GDP	C8-N9	5.89	1.50	1.37
5	D	500	GTP	PA-O3A	-5.88	1.53	1.59
4	A	600	GDP	O6-C6	5.88	1.34	1.23
5	B	500	GTP	PB-O3A	-5.79	1.53	1.59
5	D	500	GTP	PB-O3A	-5.73	1.53	1.59
5	F	500	GTP	PB-O3A	-5.72	1.53	1.59
5	H	500	GTP	PB-O3A	-5.70	1.53	1.59
5	B	500	GTP	PB-O3B	5.45	1.65	1.59
5	H	500	GTP	PB-O3B	5.44	1.65	1.59
5	D	500	GTP	PB-O3B	5.44	1.65	1.59
5	F	500	GTP	PB-O3B	5.38	1.65	1.59
4	E	600	GDP	C2-N1	4.77	1.49	1.37
4	A	600	GDP	C2-N1	4.75	1.49	1.37
4	G	600	GDP	C2-N1	4.75	1.49	1.37
4	C	600	GDP	C2-N1	4.74	1.49	1.37
4	G	600	GDP	PB-O2B	-3.93	1.40	1.54
4	A	600	GDP	PB-O2B	-3.93	1.40	1.54
4	C	600	GDP	PB-O2B	-3.92	1.40	1.54
4	E	600	GDP	PB-O2B	-3.91	1.40	1.54
5	B	500	GTP	PG-O1G	3.78	1.62	1.50
4	A	600	GDP	O4'-C1'	3.40	1.49	1.42
4	C	600	GDP	O4'-C1'	3.38	1.49	1.42
4	G	600	GDP	O4'-C1'	3.37	1.49	1.42
4	E	600	GDP	O4'-C1'	3.35	1.49	1.42
4	G	600	GDP	C8-N7	3.04	1.41	1.32
4	A	600	GDP	C8-N7	3.03	1.41	1.32
4	E	600	GDP	C8-N7	2.99	1.40	1.32
4	C	600	GDP	C8-N7	2.99	1.40	1.32
4	G	600	GDP	C5-N7	-2.86	1.33	1.39
4	A	600	GDP	C5-N7	-2.86	1.33	1.39
4	C	600	GDP	C5-N7	-2.81	1.33	1.39
4	E	600	GDP	C5-N7	-2.78	1.33	1.39
4	C	600	GDP	C5-C4	2.64	1.46	1.38
4	E	600	GDP	C5-C4	2.63	1.45	1.38
4	G	600	GDP	C5-C4	2.63	1.45	1.38
4	A	600	GDP	C5-C4	2.63	1.45	1.38
4	G	600	GDP	PB-O3B	2.47	1.64	1.54
4	E	600	GDP	PB-O3B	2.47	1.64	1.54
4	E	600	GDP	C2-N3	-2.46	1.27	1.33
4	C	600	GDP	PB-O3B	2.45	1.63	1.54
4	A	600	GDP	PB-O3B	2.45	1.63	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	600	GDP	C2-N3	-2.43	1.27	1.33
4	G	600	GDP	C2-N3	-2.43	1.27	1.33
4	C	600	GDP	C2-N3	-2.42	1.27	1.33
5	H	500	GTP	PB-O2B	-2.04	1.45	1.55
5	D	500	GTP	PB-O2B	-2.03	1.45	1.55
5	F	500	GTP	PB-O2B	-2.03	1.45	1.55
5	B	500	GTP	PB-O2B	-2.02	1.46	1.55

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	600	GDP	N9-C8-N7	-10.77	93.42	113.40
4	G	600	GDP	N9-C8-N7	-10.77	93.43	113.40
4	E	600	GDP	N9-C8-N7	-10.75	93.46	113.40
4	C	600	GDP	N9-C8-N7	-10.75	93.46	113.40
4	A	600	GDP	C8-N7-C5	9.23	120.70	104.26
4	C	600	GDP	C8-N7-C5	9.22	120.68	104.26
4	E	600	GDP	C8-N7-C5	9.21	120.66	104.26
4	G	600	GDP	C8-N7-C5	9.21	120.66	104.26
4	A	600	GDP	C6-C5-N7	8.57	145.89	130.29
4	C	600	GDP	C6-C5-N7	8.57	145.89	130.29
4	E	600	GDP	C6-C5-N7	8.57	145.88	130.29
4	G	600	GDP	C6-C5-N7	8.56	145.87	130.29
4	E	600	GDP	N2-C2-N3	6.31	131.99	119.67
4	C	600	GDP	N2-C2-N3	6.30	131.97	119.67
4	A	600	GDP	N2-C2-N3	6.29	131.96	119.67
4	G	600	GDP	N2-C2-N3	6.27	131.91	119.67
4	G	600	GDP	C6-C5-C4	-6.18	109.53	118.83
4	C	600	GDP	C6-C5-C4	-6.16	109.56	118.83
4	E	600	GDP	C6-C5-C4	-6.16	109.56	118.83
4	A	600	GDP	C6-C5-C4	-6.16	109.57	118.83
4	E	600	GDP	C8-N9-C4	5.87	117.03	106.03
4	G	600	GDP	C8-N9-C4	5.87	117.02	106.03
4	A	600	GDP	C8-N9-C4	5.86	117.01	106.03
4	C	600	GDP	C8-N9-C4	5.86	117.01	106.03
5	B	500	GTP	O2G-PG-O3B	5.04	121.55	104.64
4	G	600	GDP	C5-C6-N1	4.48	124.66	113.25
4	A	600	GDP	C5-C6-N1	4.48	124.65	113.25
4	E	600	GDP	C5-C6-N1	4.48	124.65	113.25
4	C	600	GDP	C5-C6-N1	4.48	124.64	113.25
5	B	500	GTP	O3G-PG-O3B	4.41	119.42	104.64
4	E	600	GDP	N2-C2-N1	-4.26	107.78	116.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	600	GDP	N2-C2-N1	-4.26	107.78	116.76
4	C	600	GDP	N2-C2-N1	-4.25	107.80	116.76
4	G	600	GDP	N2-C2-N1	-4.23	107.83	116.76
4	E	600	GDP	C2-N3-C4	4.11	119.38	112.30
4	C	600	GDP	C2-N3-C4	4.10	119.36	112.30
4	A	600	GDP	C2-N3-C4	4.08	119.33	112.30
4	G	600	GDP	C2-N3-C4	4.06	119.29	112.30
4	C	600	GDP	O6-C6-C5	-3.96	116.09	126.53
4	G	600	GDP	O6-C6-C5	-3.95	116.10	126.53
4	E	600	GDP	O6-C6-C5	-3.94	116.12	126.53
4	A	600	GDP	O6-C6-C5	-3.94	116.13	126.53
4	A	600	GDP	C4-C5-N7	-3.87	104.55	110.67
4	C	600	GDP	C4-C5-N7	-3.86	104.55	110.67
4	E	600	GDP	C4-C5-N7	-3.86	104.56	110.67
4	G	600	GDP	C4-C5-N7	-3.83	104.60	110.67
4	A	600	GDP	C2-N1-C6	-3.78	118.25	125.11
4	E	600	GDP	C2-N1-C6	-3.78	118.25	125.11
4	C	600	GDP	C2-N1-C6	-3.77	118.28	125.11
4	G	600	GDP	C2-N1-C6	-3.76	118.29	125.11
4	C	600	GDP	C2'-C3'-C4'	3.43	109.24	102.61
4	E	600	GDP	C2'-C3'-C4'	3.42	109.21	102.61
4	G	600	GDP	C2'-C3'-C4'	3.41	109.19	102.61
4	A	600	GDP	C2'-C3'-C4'	3.39	109.17	102.61
5	D	500	GTP	O2G-PG-O3B	2.98	114.63	104.64
5	F	500	GTP	O2G-PG-O3B	2.93	114.45	104.64
5	H	500	GTP	O2G-PG-O3B	2.92	114.43	104.64
4	E	600	GDP	C1'-N9-C8	-2.69	119.08	126.73
4	G	600	GDP	C1'-N9-C8	-2.68	119.11	126.73
4	A	600	GDP	C1'-N9-C8	-2.68	119.12	126.73
4	C	600	GDP	C1'-N9-C8	-2.68	119.13	126.73
5	B	500	GTP	O3G-PG-O2G	-2.67	97.80	107.80
5	D	500	GTP	O3G-PG-O3B	2.53	113.14	104.64
5	H	500	GTP	O3G-PG-O3B	2.49	112.99	104.64
5	F	500	GTP	O3G-PG-O3B	2.48	112.96	104.64
5	F	500	GTP	O3A-PB-O1B	-2.45	103.32	110.70
5	H	500	GTP	O3A-PB-O1B	-2.44	103.35	110.70
5	B	500	GTP	O3A-PB-O1B	-2.43	103.39	110.70
5	D	500	GTP	O3A-PB-O1B	-2.43	103.39	110.70
4	C	600	GDP	O2'-C2'-C3'	2.28	119.12	111.82
4	G	600	GDP	O2'-C2'-C3'	2.28	119.12	111.82
4	A	600	GDP	O2'-C2'-C3'	2.27	119.09	111.82
4	E	600	GDP	O2'-C2'-C3'	2.26	119.06	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	500	GTP	O2B-PB-O3A	2.21	113.25	107.27
5	B	500	GTP	O2B-PB-O3A	2.21	113.25	107.27
5	F	500	GTP	O2B-PB-O3A	2.20	113.22	107.27
5	H	500	GTP	O2B-PB-O3A	2.19	113.20	107.27
4	C	600	GDP	C4'-O4'-C1'	2.09	114.08	109.47
4	G	600	GDP	C4'-O4'-C1'	2.08	114.07	109.47
4	E	600	GDP	C4'-O4'-C1'	2.08	114.07	109.47
5	H	500	GTP	O5'-C5'-C4'	2.08	116.08	108.99
4	A	600	GDP	C4'-O4'-C1'	2.08	114.06	109.47
5	D	500	GTP	O5'-C5'-C4'	2.08	116.06	108.99
5	F	500	GTP	O5'-C5'-C4'	2.07	116.03	108.99
5	B	500	GTP	O5'-C5'-C4'	2.06	116.02	108.99

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	600	GDP	PA-O3A-PB-O2B
4	A	600	GDP	C5'-O5'-PA-O3A
4	A	600	GDP	C5'-O5'-PA-O1A
4	C	600	GDP	PA-O3A-PB-O2B
4	C	600	GDP	C5'-O5'-PA-O3A
4	C	600	GDP	C5'-O5'-PA-O1A
4	E	600	GDP	PA-O3A-PB-O2B
4	E	600	GDP	C5'-O5'-PA-O3A
4	E	600	GDP	C5'-O5'-PA-O1A
4	G	600	GDP	PA-O3A-PB-O2B
4	G	600	GDP	C5'-O5'-PA-O3A
4	G	600	GDP	C5'-O5'-PA-O1A
5	D	500	GTP	C3'-C4'-C5'-O5'
5	F	500	GTP	C3'-C4'-C5'-O5'
5	B	500	GTP	C3'-C4'-C5'-O5'
5	H	500	GTP	C3'-C4'-C5'-O5'
5	B	500	GTP	O4'-C4'-C5'-O5'
5	D	500	GTP	O4'-C4'-C5'-O5'
5	F	500	GTP	O4'-C4'-C5'-O5'
5	H	500	GTP	O4'-C4'-C5'-O5'
4	A	600	GDP	PA-O3A-PB-O3B
4	C	600	GDP	PA-O3A-PB-O3B
4	E	600	GDP	PA-O3A-PB-O3B
4	G	600	GDP	PA-O3A-PB-O3B
5	B	500	GTP	PG-O3B-PB-O1B

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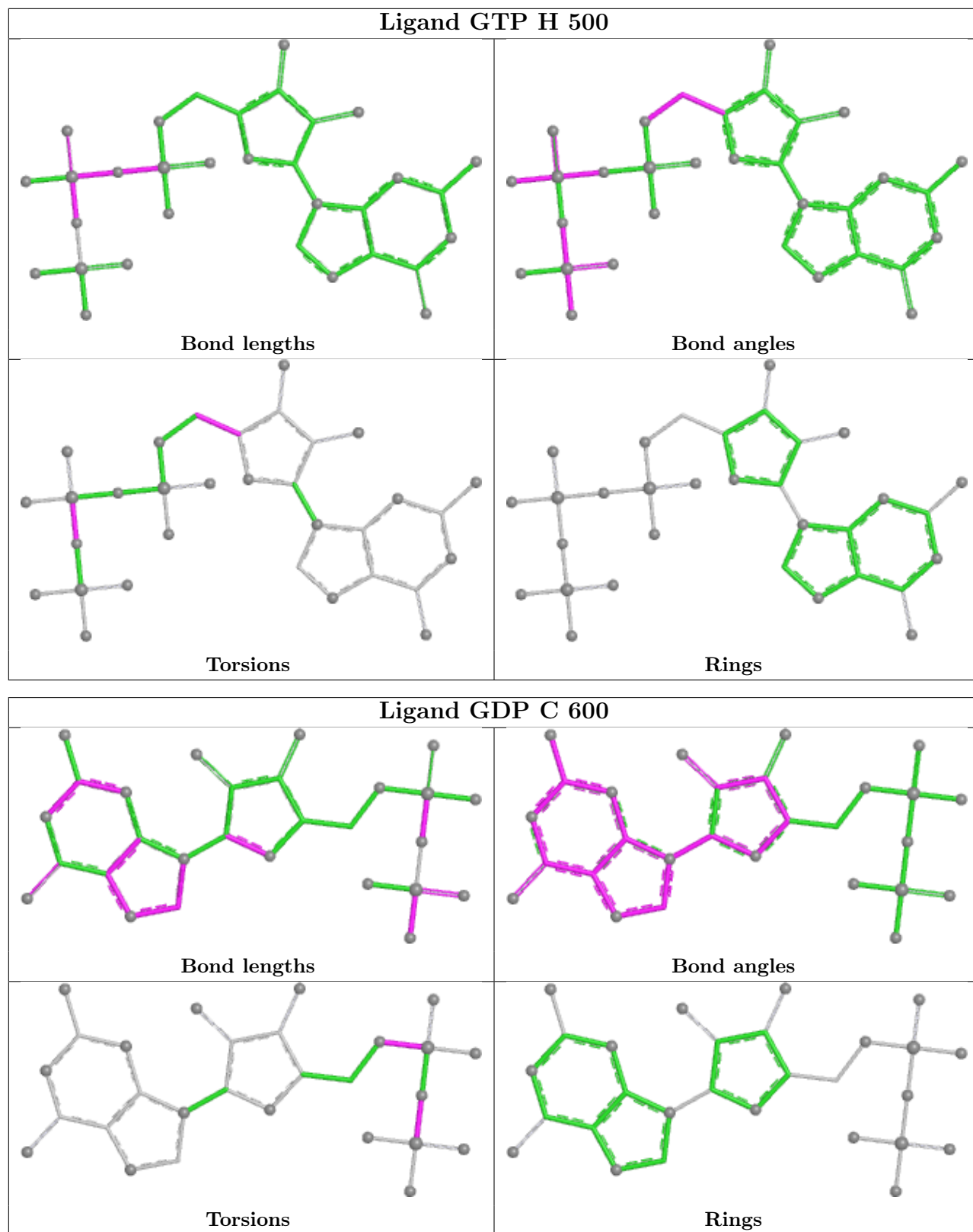
Mol	Chain	Res	Type	Atoms
5	D	500	GTP	PG-O3B-PB-O1B
5	F	500	GTP	PG-O3B-PB-O1B
5	H	500	GTP	PG-O3B-PB-O1B

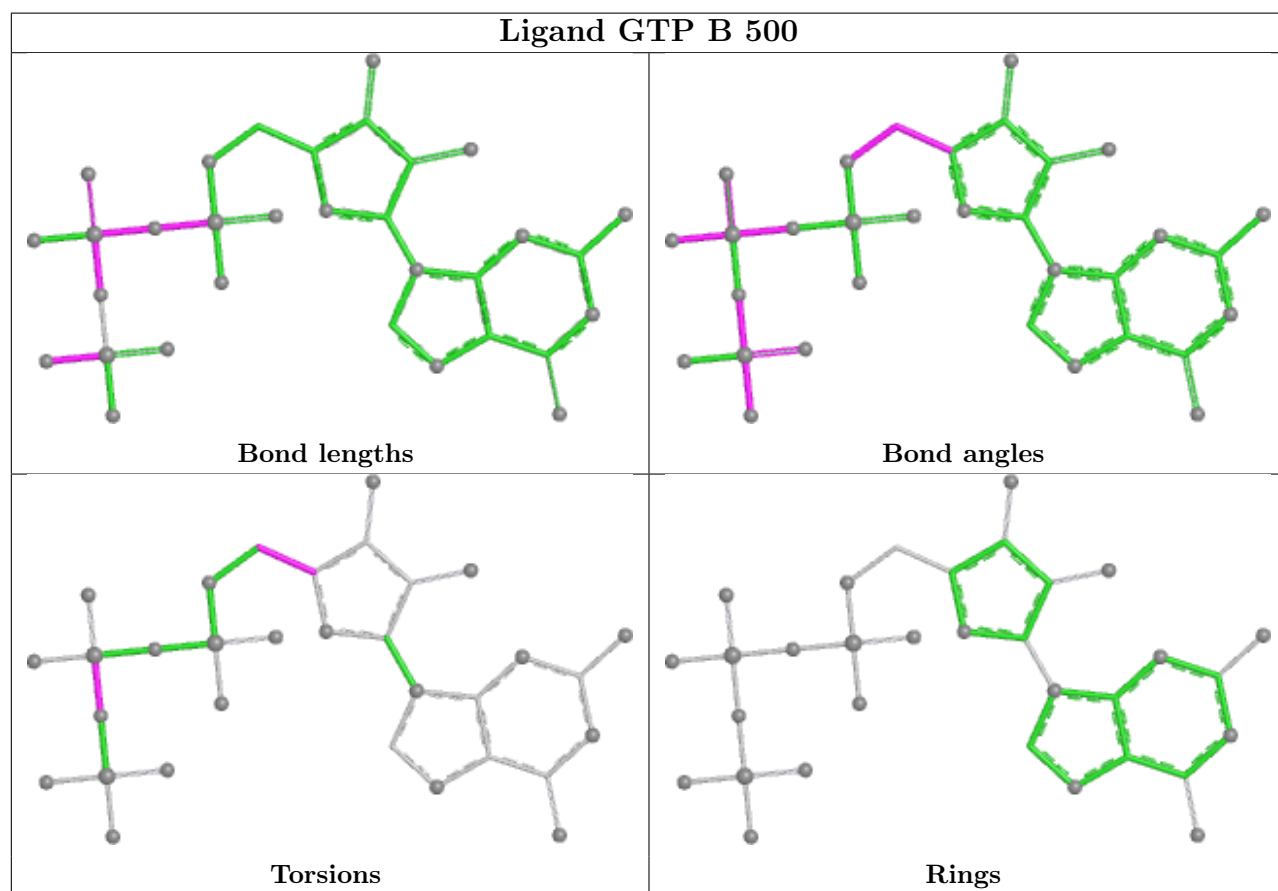
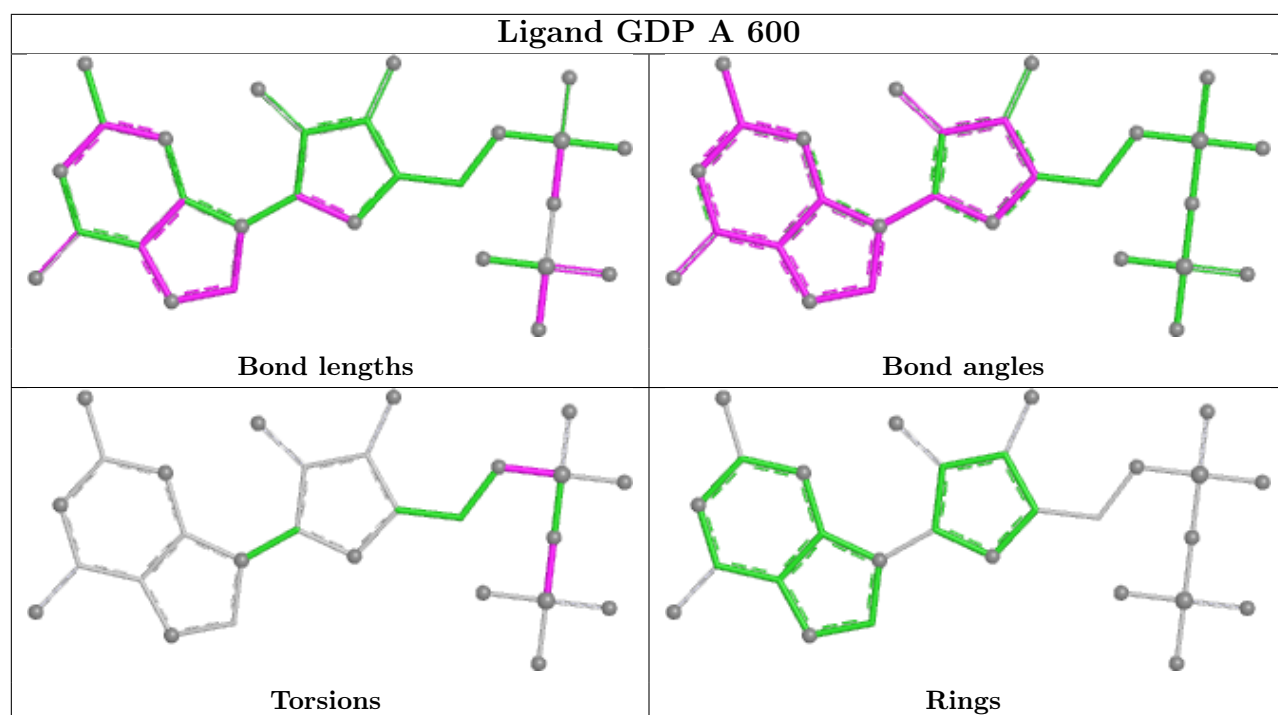
There are no ring outliers.

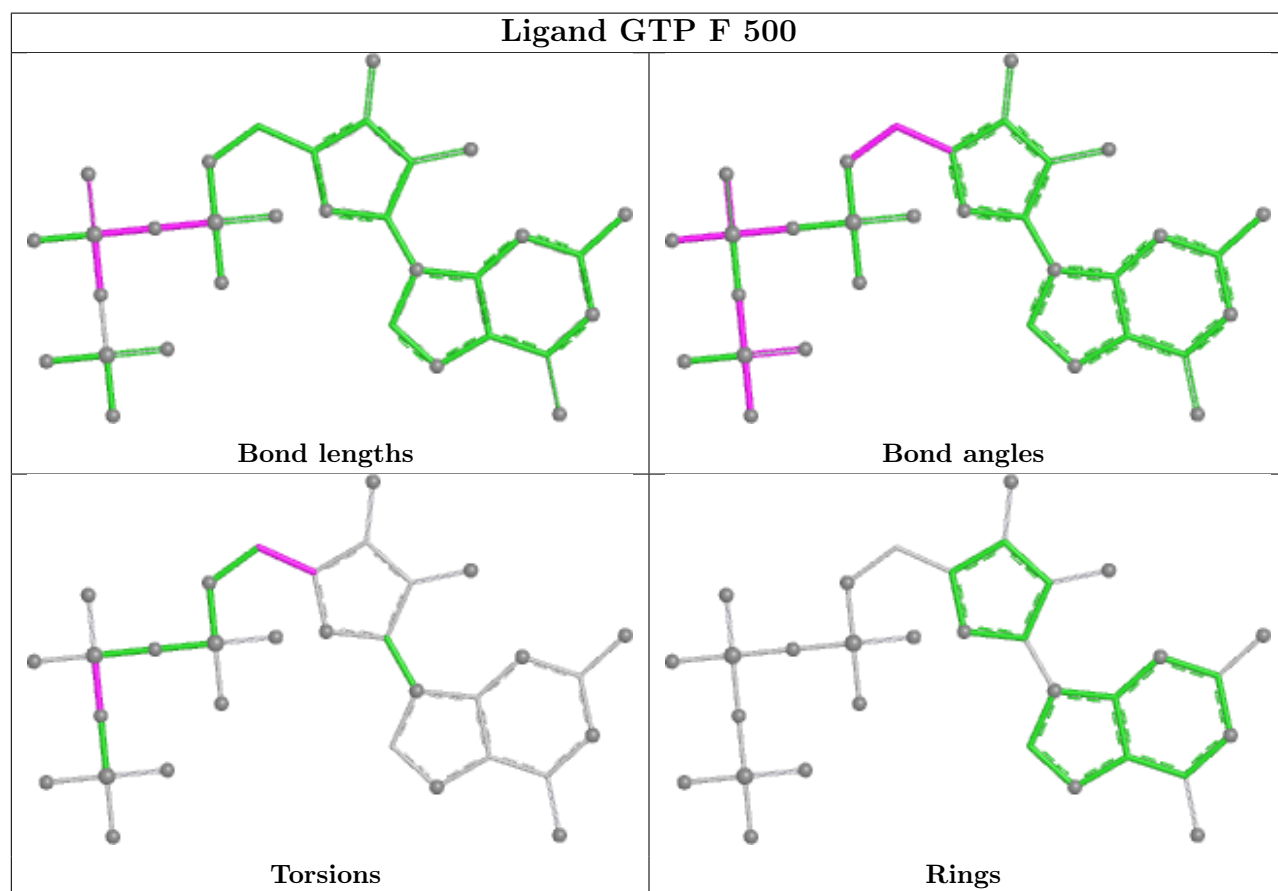
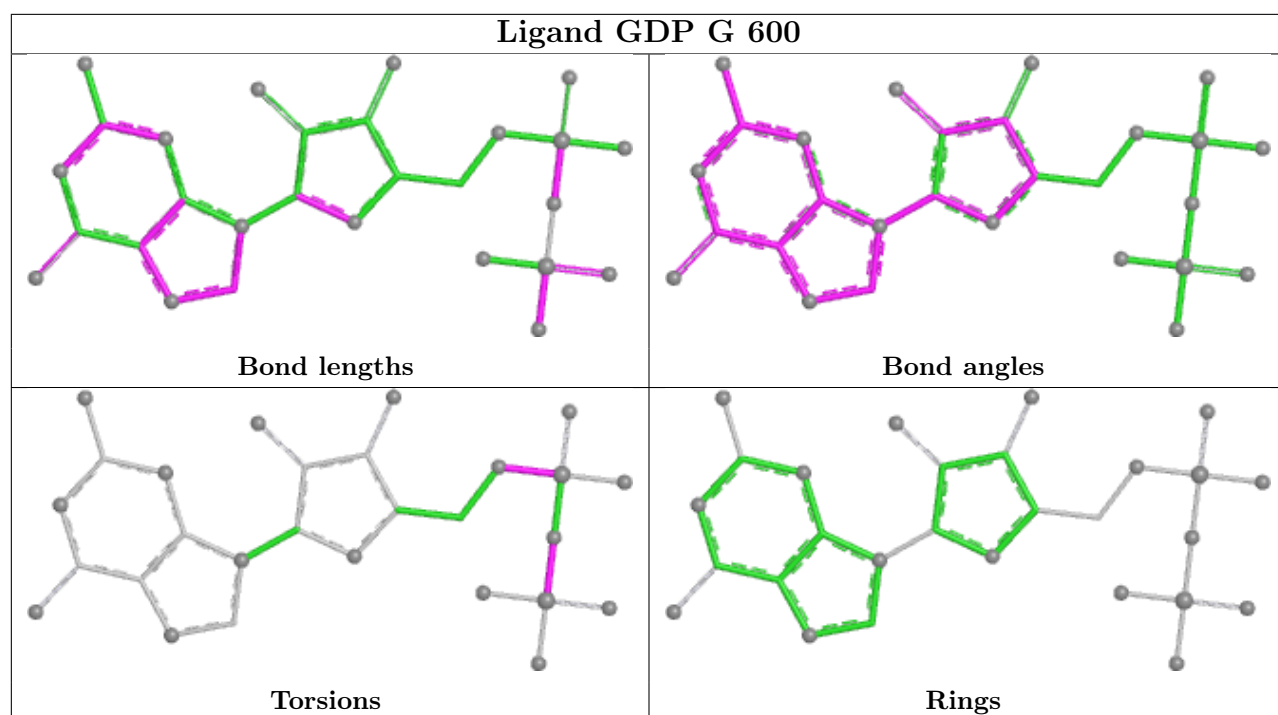
8 monomers are involved in 26 short contacts:

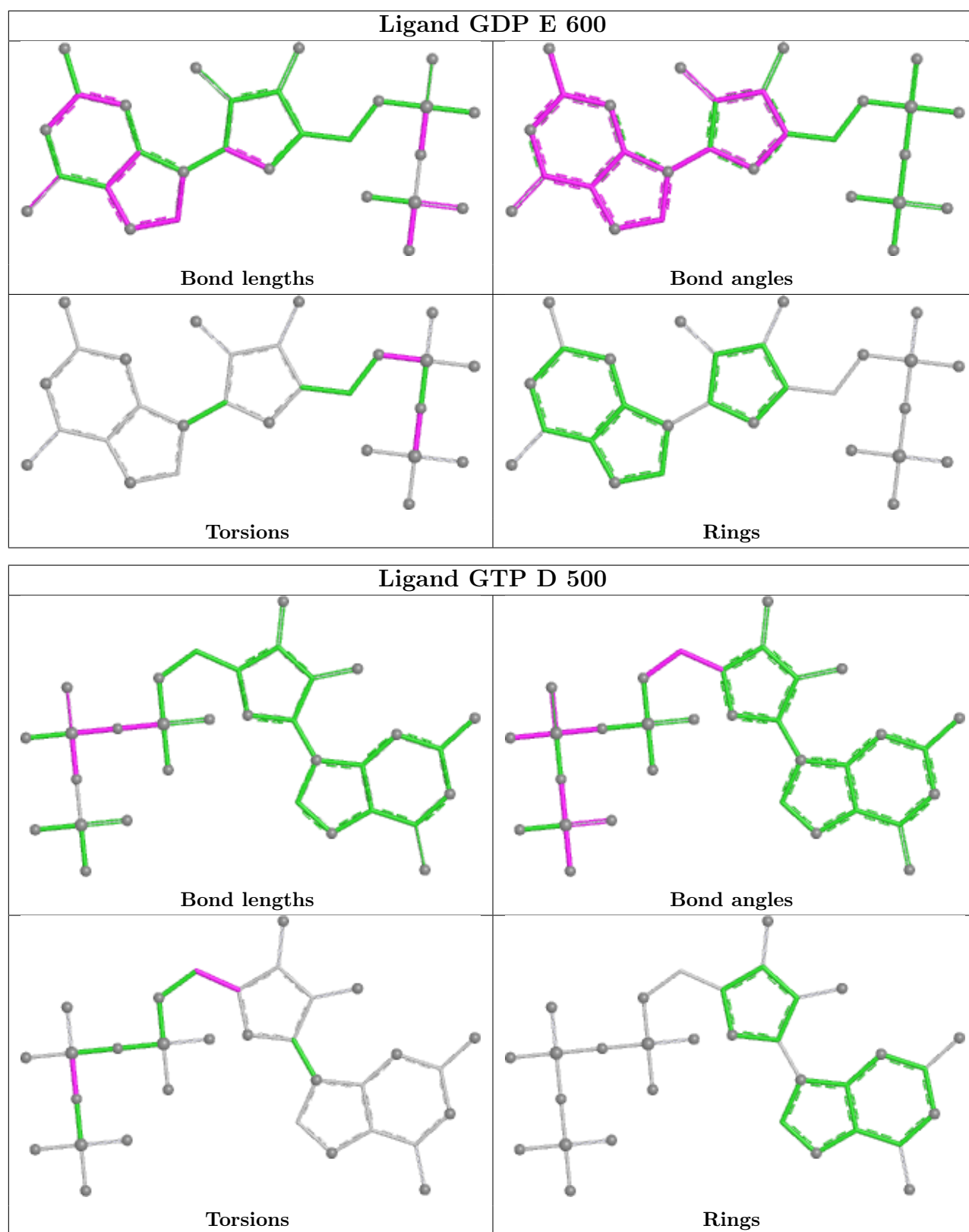
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	500	GTP	5	0
4	C	600	GDP	1	0
4	A	600	GDP	1	0
5	B	500	GTP	5	0
4	G	600	GDP	4	0
5	F	500	GTP	5	0
4	E	600	GDP	1	0
5	D	500	GTP	4	0

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	4
2	D	4
2	F	4
2	H	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	274:PRO	C	275:VAL	N	2.09
1	D	274:PRO	C	275:VAL	N	2.09
1	F	274:PRO	C	275:VAL	N	2.09
1	H	274:PRO	C	275:VAL	N	2.09
1	B	92:LEU	C	93:ILE	N	1.98
1	D	92:LEU	C	93:ILE	N	1.98
1	F	92:LEU	C	93:ILE	N	1.98
1	H	92:LEU	C	93:ILE	N	1.98
1	B	298:PRO	C	299:ALA	N	1.73
1	D	298:PRO	C	299:ALA	N	1.73
1	F	298:PRO	C	299:ALA	N	1.73
1	H	298:PRO	C	299:ALA	N	1.73
1	B	68:VAL	C	69:ASP	N	1.67
1	D	68:VAL	C	69:ASP	N	1.67
1	F	68:VAL	C	69:ASP	N	1.67
1	H	68:VAL	C	69:ASP	N	1.67

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1788. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 17



Y Index: 25



Z Index: 24

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

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 17



Y Index: 10

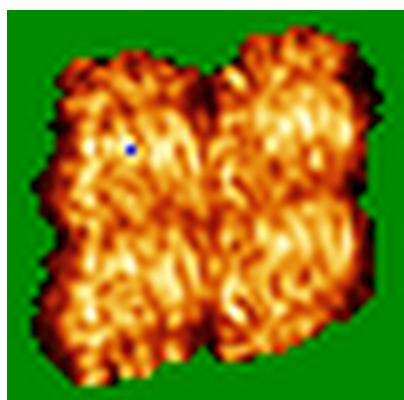


Z Index: 32

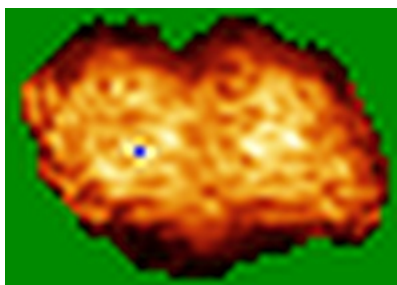
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

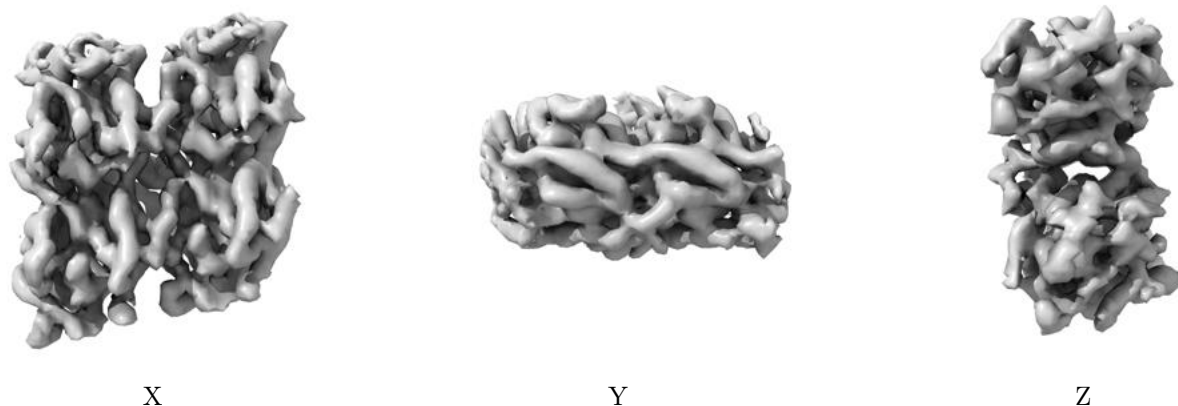


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.92. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

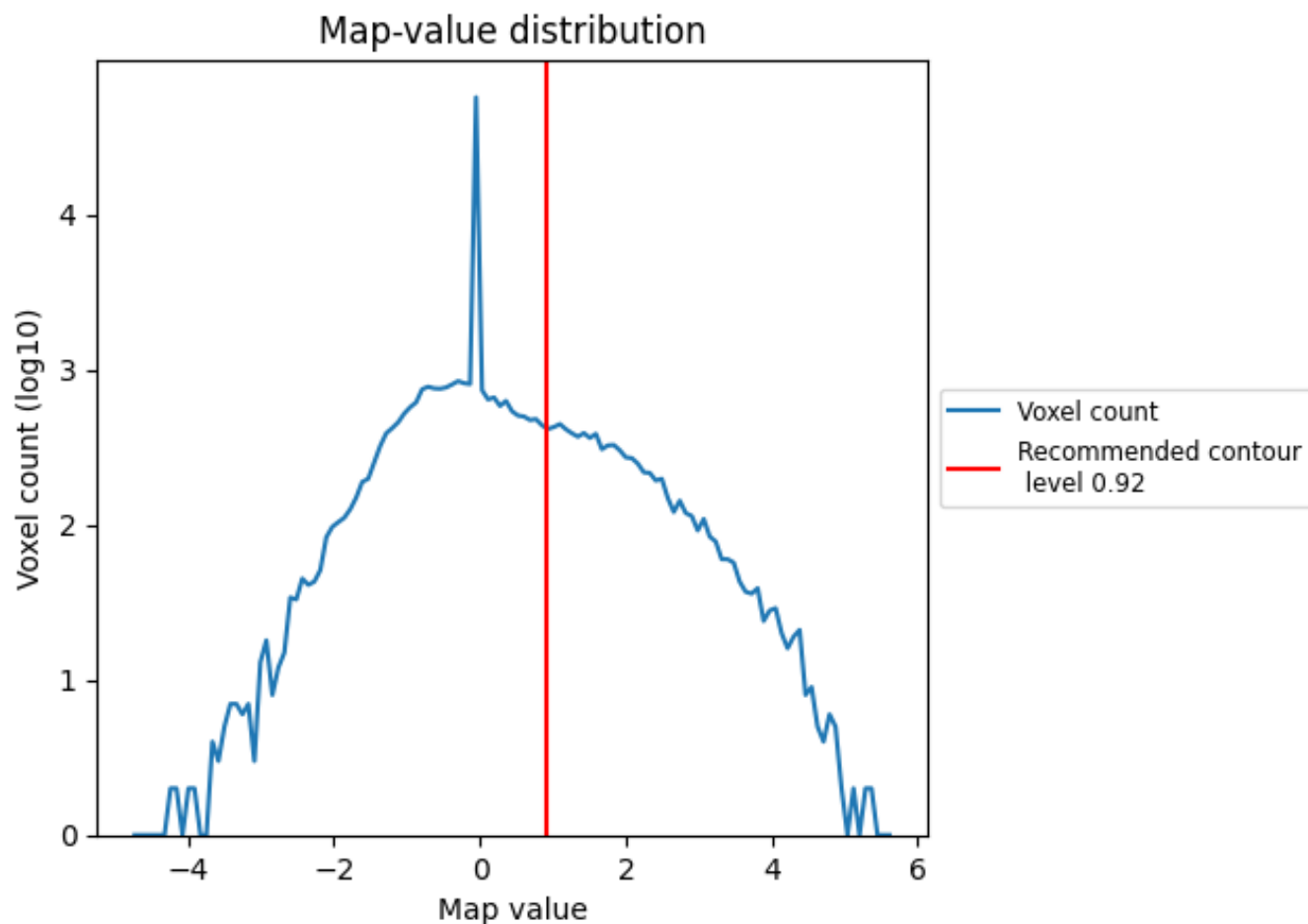
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

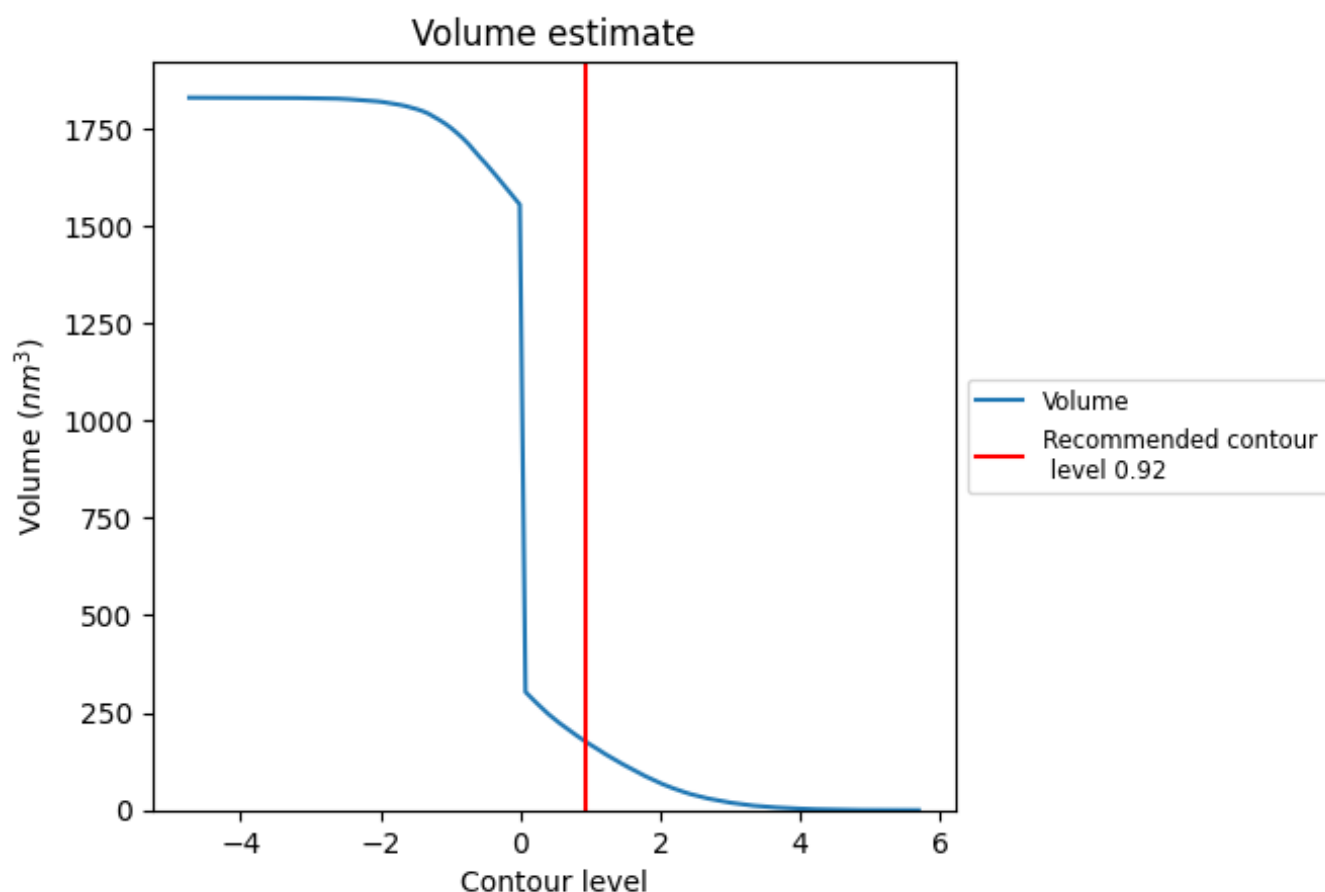
This section contains the results of statistical analysis of the map.

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 178 nm³; this corresponds to an approximate mass of 160 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.

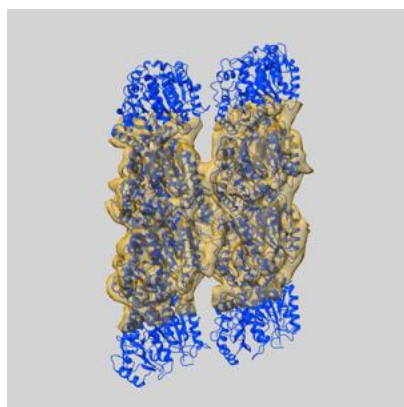
8 Fourier-Shell correlation

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

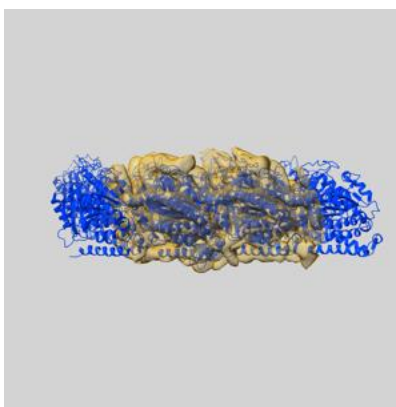
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1788 and PDB model 2XRP. Per-residue inclusion information can be found in section 3 on page 8.

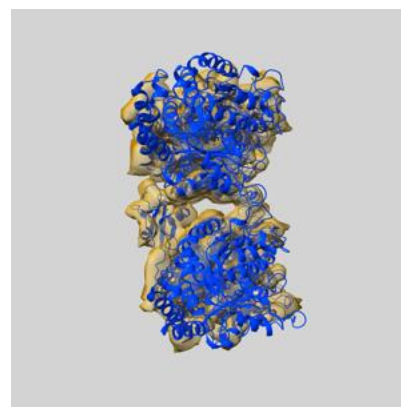
9.1 Map-model overlay [i](#)



X



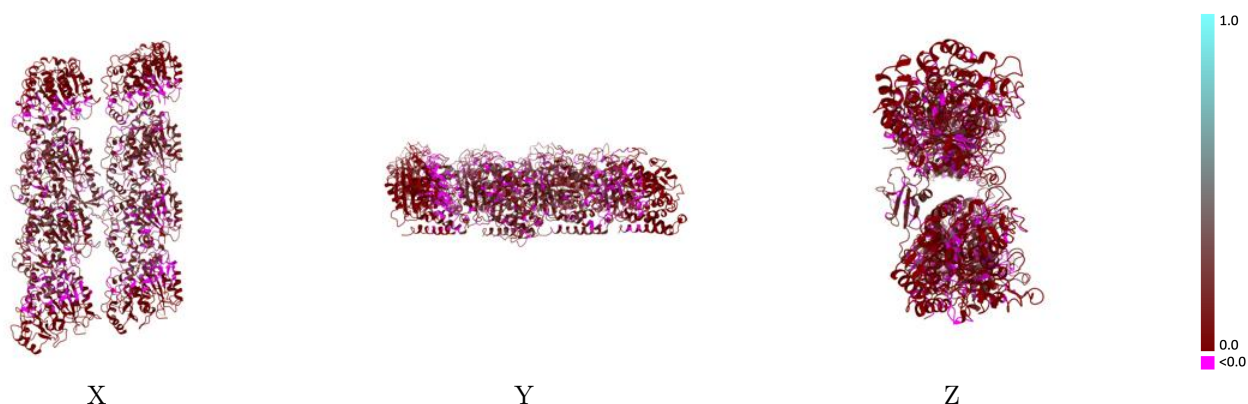
Y



Z

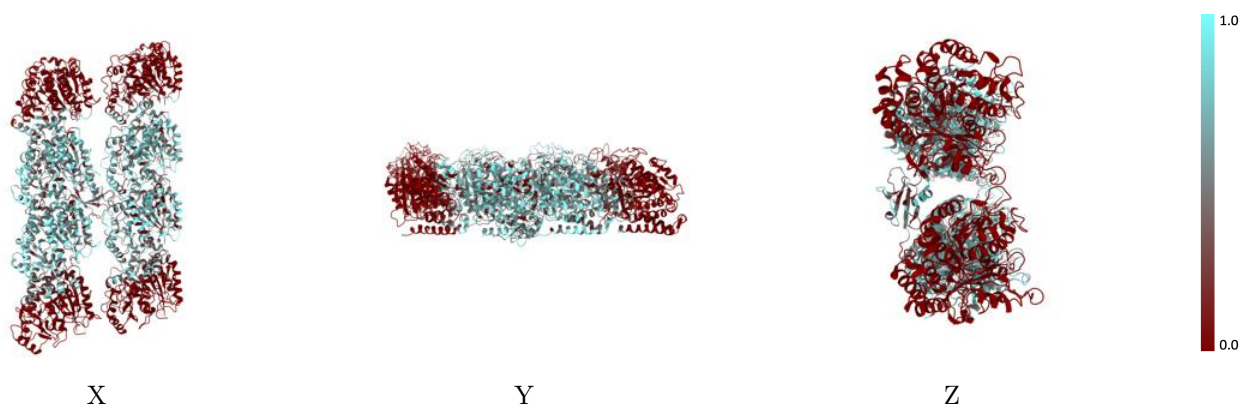
The images above show the 3D surface view of the map at the recommended contour level 0.92 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



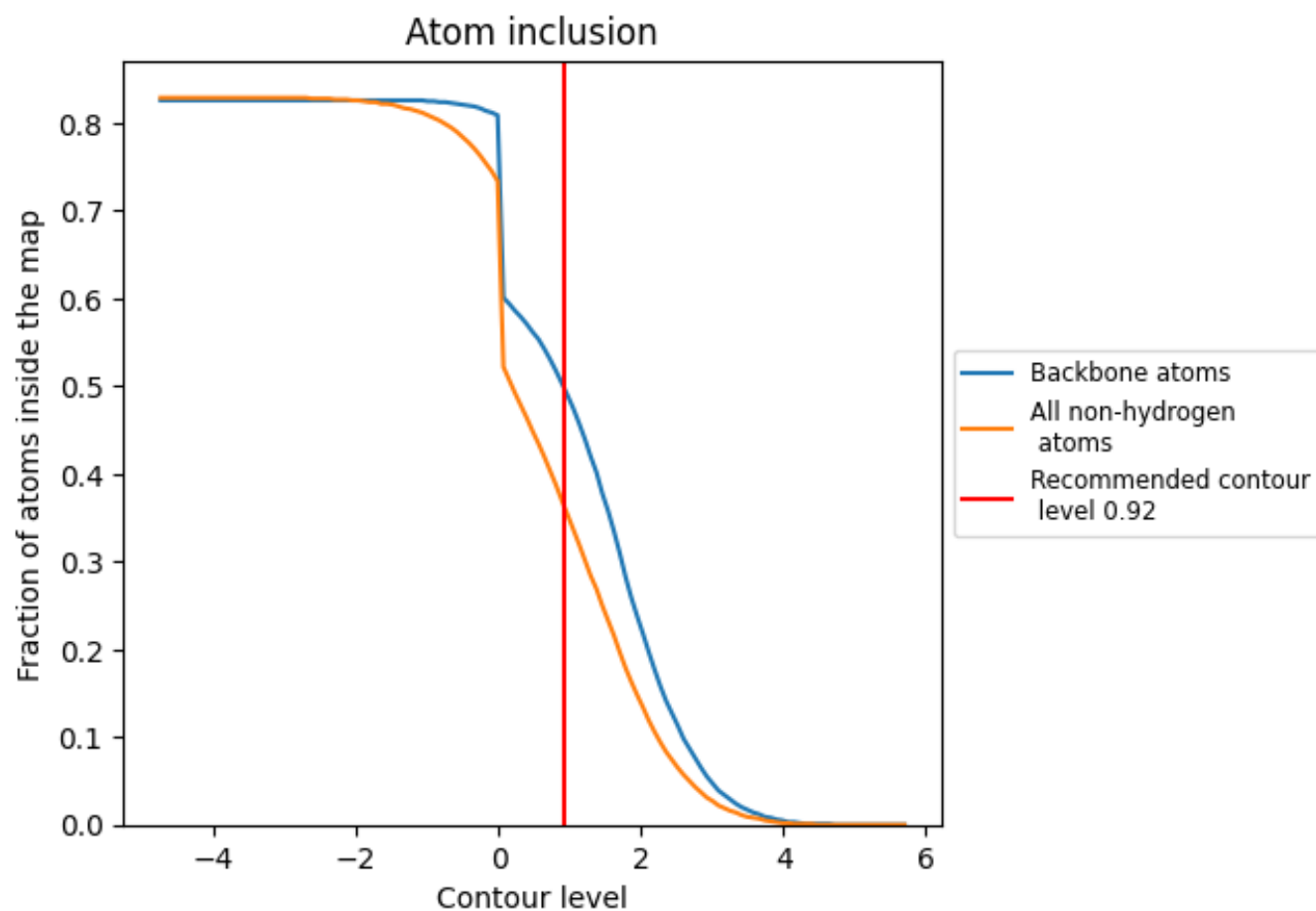
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.92).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 36% 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 (0.92) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3640	0.0680
A	0.1220	0.0190
B	0.6070	0.1210
C	0.6290	0.1220
D	0.1190	0.0120
E	0.1160	0.0180
F	0.6100	0.1240
G	0.5810	0.1040
H	0.1260	0.0140
I	0.4300	0.1140

1.0

0.0

<0.0