



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 10:49 PM UTC

PDB ID : 6ZG6 / pdb_00006zg6
EMDB ID : EMD-11194
Title : COPII on membranes, outer coat vertex
Authors : Zanetti, G.; Hutchings, J.
Deposited on : 2020-06-18
Resolution : 12.00 Å (reported)
Based on initial model : 2PM6

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:

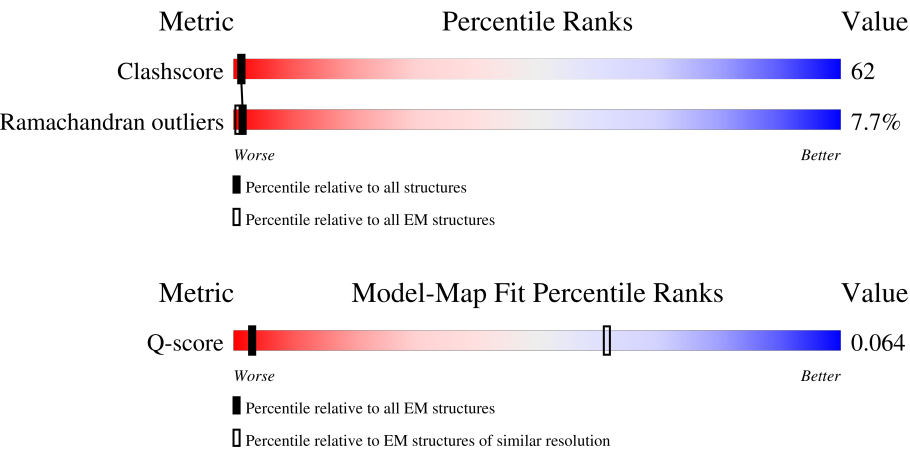
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 12.00 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	-
Q-score	-	25397	93 (11.50 - 12.50)

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	1273	
1	C	1273	
1	E	1273	
1	G	1273	
2	B	297	

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Mol	Chain	Length	Quality of chain
2	D	297	5% 41% 52% 6%
2	F	297	6% 41% 52% 6%
2	H	297	5% 42% 51% 6%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 21036 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Protein transport protein SEC31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	383	Total	C	N	O	S	0	0
			2957	1859	505	586	7		
1	C	383	Total	C	N	O	S	0	0
			2957	1859	505	586	7		
1	E	383	Total	C	N	O	S	0	0
			2957	1859	505	586	7		
1	G	383	Total	C	N	O	S	0	0
			2957	1859	505	586	7		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	367	SER	THR	conflict	UNP P38968
C	367	SER	THR	conflict	UNP P38968
E	367	SER	THR	conflict	UNP P38968
G	367	SER	THR	conflict	UNP P38968

- Molecule 2 is a protein called Protein transport protein SEC13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	279	Total	C	N	O	S	0	0
			2196	1403	375	415	3		
2	D	279	Total	C	N	O	S	0	0
			2196	1403	375	415	3		
2	F	279	Total	C	N	O	S	0	0
			2196	1403	375	415	3		
2	H	279	Total	C	N	O	S	0	0
			2196	1403	375	415	3		

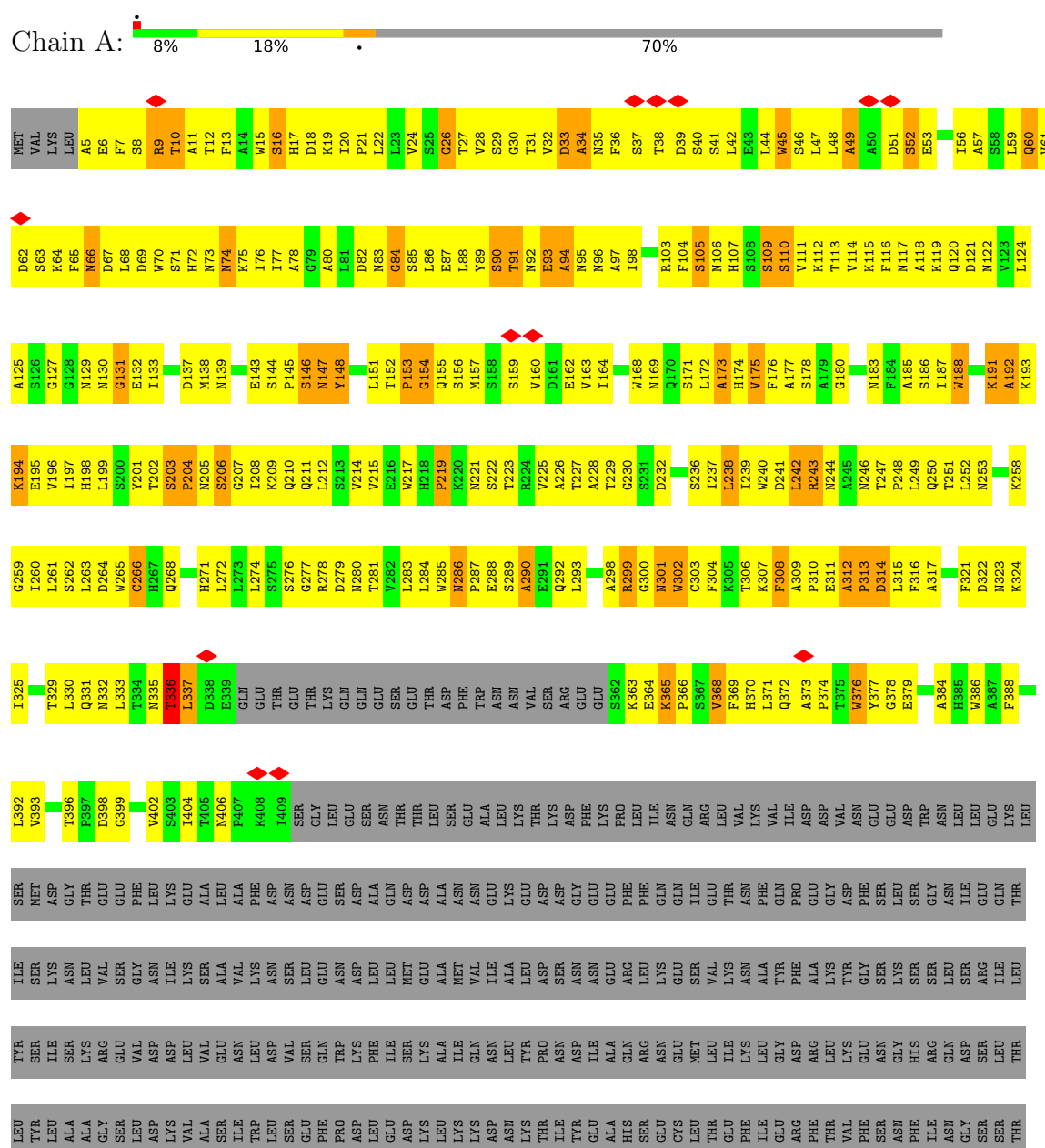
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	29	Total 29	O 29	0
3	B	78	Total 78	O 78	0
3	C	27	Total 27	O 27	0
3	D	78	Total 78	O 78	0
3	E	29	Total 29	O 29	0
3	F	78	Total 78	O 78	0
3	G	27	Total 27	O 27	0
3	H	78	Total 78	O 78	0

3 Residue-property plots

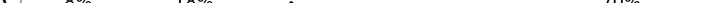
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

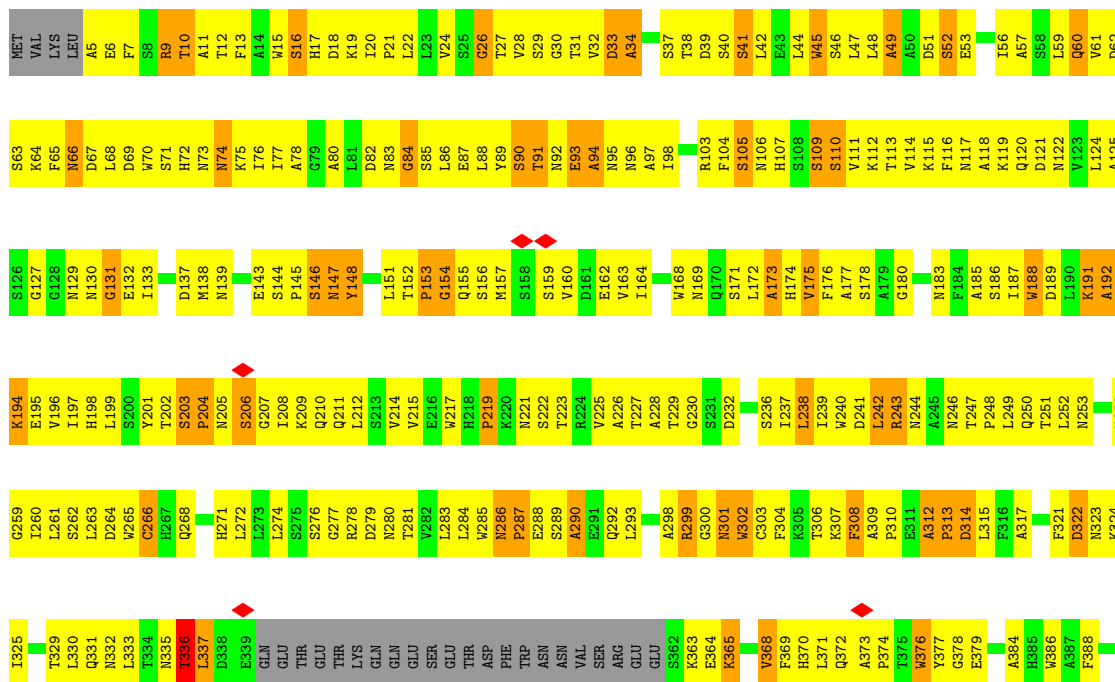
• Molecule 1: Protein transport protein SEC31



LYS	ASP	GLY	ARG	VAL	ASN	GLY	VAL	VAL	ARG	SER	PRO	THR	THR	ALA	ILE
THR	PHE	VAL	ASN	LEU	ASN	GLY	VAL	THR	ARG	ARG	GLN	THR	THR	THR	ASN
GLY	LEU	PRO	LYS	LEU	LYS	PRO	PRO	SER	LYS	ALA	PHE	ALA	SER	THR	ASN
ALA	GLU	ALA	LEU	GLU	ALA	PRO	ALA	SER	VAL	VAL	ALA	PRO	VAL	SER	LEU
MET	GLU	ALA	ALA	GLU	ALA	PRO	ARG	ARG	SER	VAL	PRO	VAL	HIS	ALA	ILE
VAL	LEU	ILE	ARG	ALA	ILE	PRO	LEU	LEU	VAL	VAL	ILE	THR	THR	LYS	PHX
HIS	VAL	GLN	GLU	VAL	GLN	ALA	ALA	SER	PRO	PRO	PRO	GLY	GLY	THR	LEU
ASN	THR	ASN	ASN	THR	ASN	PRO	ASN	SER	ASN	ILE	MET	LYS	LYS	GLU	GLU
ILE	PRO	PRO	SER	PRO	PRO	ASN	ASN	ASN	ILE	ILE	PRO	TYR	TYR	ALA	PHE
ALA	LEU	SER	SER	LEU	PRO	THR	PRO	THR	LEU	LEU	ILE	ALA	ALA	LYS	ILE
THR	THR	GLN	GLN	THR	GLY	ALA	ALA	THR	SER	THR	GLY	PRO	PRO	ASN	ASN
ASN	PRO	GLY	ALA	ALA	ALA	PRO	PRO	THR	PRO	THR	ASP	ASN	LYS	LEU	THR
LYS	LYS	ALA	ALA	THR	ALA	THR	THR	ALA	THR	THR	TYR	GLN	GLN	ASN	SER
ALA	TYR	THR	THR	THR	THR	ALA	ALA	GLN	THR	THR	THR	PRO	PRO	VAL	SER
GLU	SER	PRO	PRO	SER	PRO	THR	THR	SER	LEU	LEU	ASN	PRO	PRO	VAL	SER
GLY	GLN	GLY	THR	GLN	THR	GLN	GLN	GLY	GLY	ILE	ASP	GLN	MET	VAL	GLY
ASN	LEU	ASN	LEU	LEU	LEU	PRO	PRO	ASN	ILE	PRO	THR	SER	SER	PRO	THR
TRP	LYS	SER	SER	LYS	SER	GLY	GLY	PHE	PRO	ALA	THR	PRO	PHE	THR	GLU
LEU	ASP	THR	SER	ASP	ASN	ASN	ASN	PRO	PRO	ALA	ILE	THR	THR	LEU	LEU
THR	CYS	THR	SER	CYS	SER	SER	SER	ILE	ALA	ASN	ILE	VAL	VAL	GLY	THR
GLY	ASP	GLY	ALA	ASP	ALA	SER	SER	GLY	ALA	ASN	PRO	ASN	THR	MET	THR
VAL	LYS	VAL	LYS	LYS	PRO	TYR	TYR	THR	ALA	ALA	GLN	LYS	ASN	PRO	GLU
ARG	LEU	ARG	PRO	ARG	PRO	PRO	PRO	ILE	SER	SER	PRO	THR	ASN	SER	PHE
LEU	LEU	ILE	SER	ILE	LEU	GLY	GLY	THR	PRO	PRO	VAL	ARG	THR	ASN	LEU
ILE	ILE	GLY	SER	PHE	LEU	PRO	PRO	TYR	PRO	PRO	ILE	THR	THR	SER	PRO
GLY	LEU	THR	GLN	GLN	GLN	ASN	ASN	THR	ASN	ASN	GLN	THR	THR	GLN	GLY
ALA	ALA	GLU	PRO	GLN	THR	THR	THR	THR	LEU	GLY	ASN	ASN	GLY	ALA	VAL
GLU	GLU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
ASN	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
LEU	GLY	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
LEU	GLY	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
LEU	GLY	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
LEU	GLY	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
LEU	GLY	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
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LEU	GLY	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
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THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
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THR	LEU	THR	THR	GLN	THR	THR	THR	THR	SER	VAL	ASN	THR	THR	ALA	VAL
LEU	GLY	THR	THR	GLN											

- Molecule 1: Protein transport protein SEC31

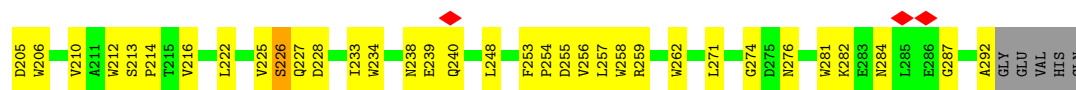
Chain C:  8% 18% 2% 70%



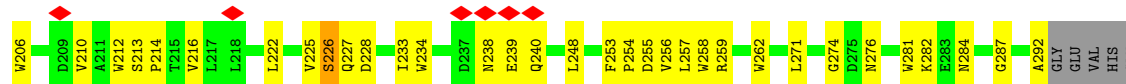
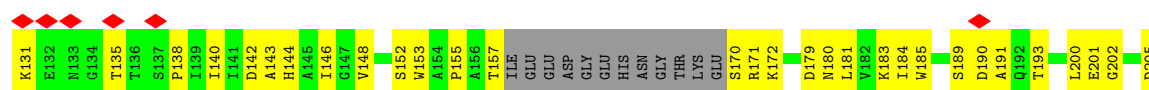
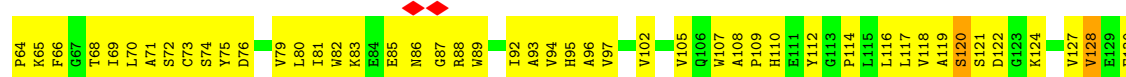
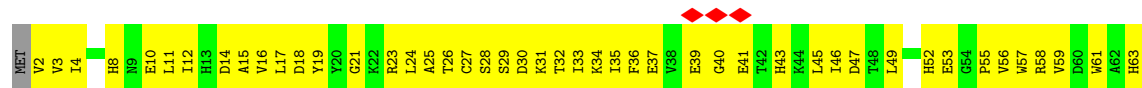
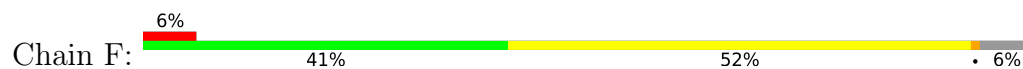


Chain G: 8% 18% . 70%

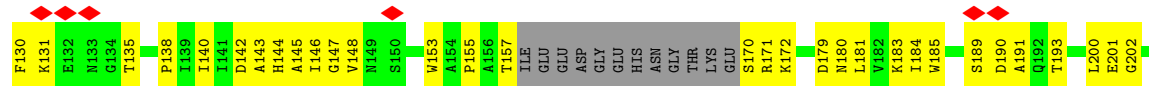
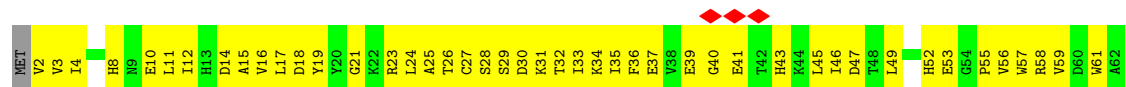
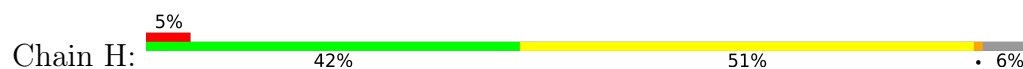




• Molecule 2: Protein transport protein SEC13



• Molecule 2: Protein transport protein SEC13



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	14099	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; 3d ctf correction	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.5, 3.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	10.996	Depositor
Minimum map value	-4.095	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.135	Depositor
Recommended contour level	2.3	Depositor
Map size ($\text{\AA}$)	340.48, 340.48, 340.48	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.66, 2.66, 2.66	Depositor

5 Model quality

5.1 Standard geometry

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	0.58	0/3030	1.21	35/4129 (0.8%)
1	C	0.58	0/3030	1.21	36/4129 (0.9%)
1	E	0.58	0/3030	1.21	38/4129 (0.9%)
1	G	0.58	0/3030	1.21	35/4129 (0.8%)
2	B	0.47	0/2256	0.99	6/3079 (0.2%)
2	D	0.47	0/2256	0.99	6/3079 (0.2%)
2	F	0.47	0/2256	0.99	6/3079 (0.2%)
2	H	0.48	0/2256	0.99	6/3079 (0.2%)
All	All	0.54	0/21144	1.12	168/28832 (0.6%)

There are no bond length outliers.

All (168) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	243	ARG	N-CA-C	-11.35	98.82	112.89
1	G	243	ARG	N-CA-C	-11.33	98.84	112.89
1	A	243	ARG	N-CA-C	-11.31	98.87	112.89
1	E	243	ARG	N-CA-C	-11.29	98.89	112.89
1	E	157	MET	N-CA-C	9.66	124.26	108.52
1	A	157	MET	N-CA-C	9.66	124.26	108.52
1	G	157	MET	N-CA-C	9.66	124.26	108.52
1	C	157	MET	N-CA-C	9.64	124.23	108.52
1	G	34	ALA	N-CA-C	-9.03	102.28	113.38
1	A	34	ALA	N-CA-C	-9.01	102.29	113.38
1	C	34	ALA	N-CA-C	-8.99	102.32	113.38
1	E	34	ALA	N-CA-C	-8.97	102.35	113.38
1	E	175	VAL	N-CA-C	8.05	121.55	108.99
1	A	175	VAL	N-CA-C	8.02	121.50	108.99
1	C	175	VAL	N-CA-C	8.02	121.50	108.99
1	G	175	VAL	N-CA-C	8.02	121.50	108.99
2	D	226	SER	N-CA-C	7.98	121.29	109.24
2	F	226	SER	N-CA-C	7.96	121.26	109.24
2	B	226	SER	N-CA-C	7.94	121.24	109.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	226	SER	N-CA-C	7.91	121.18	109.24
1	G	312	ALA	CA-C-N	7.31	128.97	119.84
1	G	312	ALA	C-N-CA	7.31	128.97	119.84
1	C	312	ALA	CA-C-N	7.28	128.94	119.84
1	C	312	ALA	C-N-CA	7.28	128.94	119.84
1	E	312	ALA	CA-C-N	7.28	128.94	119.84
1	E	312	ALA	C-N-CA	7.28	128.94	119.84
1	A	312	ALA	CA-C-N	7.26	128.91	119.84
1	A	312	ALA	C-N-CA	7.26	128.91	119.84
1	G	26	GLY	N-CA-C	-7.21	102.87	112.82
1	C	26	GLY	N-CA-C	-7.19	102.89	112.82
1	E	26	GLY	N-CA-C	-7.17	102.92	112.82
1	A	26	GLY	N-CA-C	-7.17	102.92	112.82
2	D	128	VAL	N-CA-C	7.10	118.34	108.12
2	F	128	VAL	N-CA-C	7.07	118.31	108.12
2	H	128	VAL	N-CA-C	7.07	118.30	108.12
2	B	128	VAL	N-CA-C	7.06	118.29	108.12
1	A	206	SER	N-CA-C	-6.82	103.03	112.30
1	C	206	SER	N-CA-C	-6.82	103.03	112.30
1	G	206	SER	N-CA-C	-6.81	103.03	112.30
1	E	206	SER	N-CA-C	-6.80	103.05	112.30
1	G	286	ASN	CA-C-N	6.67	128.18	119.84
1	G	286	ASN	C-N-CA	6.67	128.18	119.84
1	E	286	ASN	CA-C-N	6.67	128.18	119.84
1	E	286	ASN	C-N-CA	6.67	128.18	119.84
1	A	286	ASN	CA-C-N	6.65	128.16	119.84
1	A	286	ASN	C-N-CA	6.65	128.16	119.84
1	C	286	ASN	CA-C-N	6.62	128.12	119.84
1	C	286	ASN	C-N-CA	6.62	128.12	119.84
1	E	308	PHE	N-CA-C	-6.60	99.77	110.20
2	B	120	SER	N-CA-C	6.59	119.91	109.50
1	G	308	PHE	N-CA-C	-6.59	99.79	110.20
1	C	308	PHE	N-CA-C	-6.58	99.80	110.20
2	F	120	SER	N-CA-C	6.58	119.89	109.50
2	H	120	SER	N-CA-C	6.57	119.88	109.50
2	D	120	SER	N-CA-C	6.56	119.87	109.50
1	A	308	PHE	N-CA-C	-6.56	99.84	110.20
1	A	156	SER	N-CA-C	6.53	124.72	110.80
1	C	156	SER	N-CA-C	6.53	124.71	110.80
1	G	156	SER	N-CA-C	6.53	124.71	110.80
1	E	156	SER	N-CA-C	6.52	124.69	110.80
1	E	309	ALA	N-CA-C	-6.46	98.27	109.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	309	ALA	N-CA-C	-6.46	98.28	109.58
1	G	309	ALA	N-CA-C	-6.44	98.30	109.58
1	A	309	ALA	N-CA-C	-6.42	98.34	109.58
1	A	314	ASP	N-CA-C	-6.42	105.20	113.16
1	E	314	ASP	N-CA-C	-6.38	105.24	113.16
1	C	314	ASP	N-CA-C	-6.37	105.27	113.16
1	G	314	ASP	N-CA-C	-6.36	105.28	113.16
1	A	377	TYR	N-CA-C	6.28	118.50	109.14
1	E	377	TYR	N-CA-C	6.28	118.50	109.14
1	G	377	TYR	N-CA-C	6.28	118.50	109.14
1	C	377	TYR	N-CA-C	6.26	118.47	109.14
1	G	90	SER	N-CA-C	6.20	120.43	112.12
1	A	90	SER	N-CA-C	6.19	120.41	112.12
1	E	90	SER	N-CA-C	6.15	120.36	112.12
1	C	90	SER	N-CA-C	6.14	120.35	112.12
2	B	143	ALA	N-CA-C	6.12	121.68	113.72
2	F	143	ALA	N-CA-C	6.11	121.66	113.72
2	H	143	ALA	N-CA-C	6.10	121.66	113.72
2	D	143	ALA	N-CA-C	6.09	121.63	113.72
1	C	173	ALA	CA-C-N	6.05	128.39	120.28
1	C	173	ALA	C-N-CA	6.05	128.39	120.28
1	G	173	ALA	CA-C-N	6.03	128.36	120.28
1	G	173	ALA	C-N-CA	6.03	128.36	120.28
1	E	173	ALA	CA-C-N	6.03	128.36	120.28
1	E	173	ALA	C-N-CA	6.03	128.36	120.28
1	E	378	GLY	N-CA-C	6.02	123.36	115.36
1	C	378	GLY	N-CA-C	6.02	123.36	115.36
1	C	188	TRP	N-CA-C	6.00	118.69	108.90
1	A	173	ALA	CA-C-N	6.00	128.32	120.28
1	A	173	ALA	C-N-CA	6.00	128.32	120.28
1	A	378	GLY	N-CA-C	6.00	123.34	115.36
1	G	378	GLY	N-CA-C	6.00	123.34	115.36
1	E	188	TRP	N-CA-C	5.99	118.66	108.90
1	G	188	TRP	N-CA-C	5.99	118.66	108.90
1	A	188	TRP	N-CA-C	5.97	118.64	108.90
1	A	131	GLY	N-CA-C	-5.91	105.97	115.08
1	G	131	GLY	N-CA-C	-5.91	105.98	115.08
1	C	253	ASN	N-CA-C	5.90	119.07	110.17
1	E	131	GLY	N-CA-C	-5.89	106.01	115.08
1	C	131	GLY	N-CA-C	-5.89	106.01	115.08
1	A	253	ASN	N-CA-C	5.88	119.06	110.17
2	D	179	ASP	N-CA-C	-5.87	105.70	112.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	253	ASN	N-CA-C	5.84	119.00	110.17
2	H	179	ASP	N-CA-C	-5.84	105.73	112.92
1	E	253	ASN	N-CA-C	5.84	118.99	110.17
2	B	179	ASP	N-CA-C	-5.82	105.77	112.92
2	F	179	ASP	N-CA-C	-5.81	105.78	112.92
1	A	192	ALA	N-CA-C	-5.71	105.98	113.17
1	E	192	ALA	N-CA-C	-5.70	105.99	113.17
1	E	66	ASN	N-CA-C	-5.69	106.97	114.31
1	G	66	ASN	N-CA-C	-5.69	106.97	114.31
1	G	336	THR	N-CA-C	-5.69	98.68	110.80
1	A	66	ASN	N-CA-C	-5.68	106.98	114.31
1	C	66	ASN	N-CA-C	-5.67	106.99	114.31
1	C	192	ALA	N-CA-C	-5.67	106.02	113.17
1	G	192	ALA	N-CA-C	-5.67	106.03	113.17
1	A	336	THR	N-CA-C	-5.66	98.75	110.80
1	C	336	THR	N-CA-C	-5.66	98.75	110.80
1	E	336	THR	N-CA-C	-5.65	98.76	110.80
1	C	39	ASP	N-CA-C	5.59	117.81	109.59
1	A	39	ASP	N-CA-C	5.58	117.79	109.59
1	E	39	ASP	N-CA-C	5.57	117.77	109.59
1	G	39	ASP	N-CA-C	5.56	117.77	109.59
1	E	376	TRP	N-CA-C	5.50	116.96	111.07
1	C	376	TRP	N-CA-C	5.47	116.92	111.07
1	A	376	TRP	N-CA-C	5.45	116.90	111.07
1	G	376	TRP	N-CA-C	5.44	116.89	111.07
2	H	287	GLY	N-CA-C	-5.38	107.59	115.72
1	G	154	GLY	N-CA-C	5.38	125.92	113.18
1	A	154	GLY	N-CA-C	5.36	125.89	113.18
1	C	154	GLY	N-CA-C	5.36	125.87	113.18
2	B	287	GLY	N-CA-C	-5.35	107.64	115.72
1	E	154	GLY	N-CA-C	5.35	125.85	113.18
1	A	384	ALA	N-CA-C	5.34	117.18	110.24
1	G	384	ALA	N-CA-C	5.34	117.18	110.24
2	D	287	GLY	N-CA-C	-5.34	107.66	115.72
2	F	287	GLY	N-CA-C	-5.34	107.66	115.72
1	C	384	ALA	N-CA-C	5.33	117.17	110.24
1	G	177	ALA	N-CA-C	5.33	118.11	109.06
1	E	177	ALA	N-CA-C	5.32	118.11	109.06
1	C	177	ALA	N-CA-C	5.32	118.10	109.06
1	E	384	ALA	N-CA-C	5.32	117.16	110.24
1	A	177	ALA	N-CA-C	5.31	118.09	109.06
1	G	219	PRO	N-CA-C	5.21	120.45	114.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	219	PRO	N-CA-C	5.19	120.43	114.20
1	A	219	PRO	N-CA-C	5.18	120.41	114.20
1	C	219	PRO	N-CA-C	5.17	120.40	114.20
1	E	406	ASN	CA-C-N	5.08	125.07	119.89
1	E	406	ASN	C-N-CA	5.08	125.07	119.89
1	E	396	THR	CA-C-N	5.05	124.83	119.28
1	E	396	THR	C-N-CA	5.05	124.83	119.28
1	C	41	SER	N-CA-C	5.03	119.89	113.55
1	C	191	LYS	N-CA-C	-5.03	107.00	113.23
1	E	45	TRP	N-CA-C	5.03	117.02	109.23
1	G	406	ASN	CA-C-N	5.03	125.02	119.89
1	G	406	ASN	C-N-CA	5.03	125.02	119.89
1	G	396	THR	CA-C-N	5.03	124.81	119.28
1	G	396	THR	C-N-CA	5.03	124.81	119.28
1	E	191	LYS	N-CA-C	-5.02	107.00	113.23
1	C	45	TRP	N-CA-C	5.02	117.01	109.23
1	A	45	TRP	N-CA-C	5.02	117.00	109.23
1	E	41	SER	N-CA-C	5.01	119.87	113.55
1	A	191	LYS	N-CA-C	-5.00	107.03	113.23
1	A	406	ASN	CA-C-N	5.00	124.99	119.89
1	A	406	ASN	C-N-CA	5.00	124.99	119.89
1	C	406	ASN	CA-C-N	5.00	124.99	119.89
1	C	406	ASN	C-N-CA	5.00	124.99	119.89

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	2957	0	2835	499	0
1	C	2957	0	2832	495	0
1	E	2957	0	2834	507	0
1	G	2957	0	2832	502	0
2	B	2196	0	2138	189	0
2	D	2196	0	2138	189	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	2196	0	2138	186	0
2	H	2196	0	2138	185	0
3	A	29	0	0	17	0
3	B	78	0	0	23	0
3	C	27	0	0	15	0
3	D	78	0	0	24	0
3	E	29	0	0	15	0
3	F	78	0	0	23	0
3	G	27	0	0	16	0
3	H	78	0	0	23	0
All	All	21036	0	19885	2512	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 62.

All (2512) 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:E:35:ASN:HB3	1:G:174:HIS:CE1	1.35	1.57
1:A:35:ASN:HB3	1:C:174:HIS:CE1	1.37	1.54
1:C:314:ASP:OD2	1:C:376:TRP:CD2	1.64	1.48
1:E:314:ASP:OD2	1:E:376:TRP:CD2	1.64	1.47
1:G:314:ASP:OD2	1:G:376:TRP:CD2	1.64	1.47
1:A:314:ASP:OD2	1:A:376:TRP:CD2	1.64	1.47
1:E:33:ASP:O	1:G:196:VAL:CB	1.64	1.44
1:A:314:ASP:OD2	1:A:376:TRP:CE2	1.76	1.38
1:C:314:ASP:OD2	1:C:376:TRP:CE2	1.76	1.38
1:E:33:ASP:C	1:G:196:VAL:HG11	1.49	1.38
1:G:314:ASP:OD2	1:G:376:TRP:CE2	1.76	1.38
1:A:33:ASP:O	1:C:196:VAL:CB	1.70	1.36
1:E:314:ASP:OD2	1:E:376:TRP:CE2	1.76	1.36
1:E:33:ASP:C	1:G:196:VAL:CG1	1.98	1.35
1:A:33:ASP:C	1:C:196:VAL:CG1	2.00	1.35
1:A:33:ASP:C	1:C:196:VAL:HG11	1.51	1.31
1:E:32:VAL:HB	1:G:195:GLU:O	1.26	1.30
1:A:313:PRO:HG3	3:A:1309:HOH:O	1.14	1.30
1:G:268:GLN:HG3	3:G:1307:HOH:O	1.32	1.29
1:G:313:PRO:HG3	3:G:1307:HOH:O	1.14	1.29
1:C:313:PRO:HG3	3:C:1307:HOH:O	1.14	1.28
1:C:268:GLN:HB3	1:C:374:PRO:O	1.15	1.27
1:E:268:GLN:HB3	1:E:374:PRO:O	1.15	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:313:PRO:HG3	3:E:1309:HOH:O	1.14	1.26
1:G:268:GLN:HB3	1:G:374:PRO:O	1.15	1.25
1:A:268:GLN:HB3	1:A:374:PRO:O	1.15	1.24
1:A:268:GLN:HG3	3:A:1309:HOH:O	1.32	1.24
1:A:32:VAL:HB	1:C:195:GLU:O	1.31	1.24
1:E:268:GLN:CB	1:E:374:PRO:O	1.87	1.23
1:C:268:GLN:CB	1:C:374:PRO:O	1.87	1.23
1:C:268:GLN:HG3	3:C:1307:HOH:O	1.32	1.23
1:E:268:GLN:HG3	3:E:1309:HOH:O	1.32	1.23
1:A:268:GLN:CB	1:A:374:PRO:O	1.87	1.21
1:G:268:GLN:CB	1:G:374:PRO:O	1.87	1.21
1:C:321:PHE:CB	1:E:246:ASN:HD21	1.55	1.19
1:A:246:ASN:HD21	1:G:321:PHE:CB	1.56	1.17
1:C:314:ASP:CG	1:C:376:TRP:CE2	2.22	1.17
1:G:314:ASP:CG	1:G:376:TRP:CE2	2.22	1.16
1:E:35:ASN:CB	1:G:174:HIS:CE1	2.26	1.16
1:E:314:ASP:CG	1:E:376:TRP:CE2	2.22	1.15
1:A:314:ASP:CG	1:A:376:TRP:CE2	2.22	1.15
1:A:35:ASN:CB	1:C:174:HIS:CE1	2.30	1.14
1:E:22:LEU:HD11	1:E:94:ALA:HB1	1.30	1.13
1:G:22:LEU:HD11	1:G:94:ALA:HB1	1.30	1.12
1:A:33:ASP:O	1:C:196:VAL:CG1	0.83	1.12
1:G:93:GLU:HB2	1:G:96:ASN:HD22	1.16	1.10
1:E:33:ASP:O	1:G:196:VAL:CG1	0.81	1.10
1:A:93:GLU:HB2	1:A:96:ASN:HD22	1.16	1.10
1:G:268:GLN:CG	3:G:1307:HOH:O	1.91	1.09
1:A:22:LEU:HD11	1:A:94:ALA:HB1	1.30	1.09
1:C:321:PHE:HB2	1:E:246:ASN:ND2	1.68	1.09
1:E:314:ASP:OD2	1:E:376:TRP:CE3	2.06	1.09
1:C:22:LEU:HD11	1:C:94:ALA:HB1	1.30	1.08
1:C:314:ASP:OD2	1:C:376:TRP:CE3	2.06	1.08
1:E:268:GLN:CG	3:E:1309:HOH:O	1.91	1.08
1:A:268:GLN:CG	3:A:1309:HOH:O	1.91	1.08
1:G:314:ASP:OD2	1:G:376:TRP:CE3	2.06	1.08
1:C:93:GLU:HB2	1:C:96:ASN:HD22	1.16	1.07
1:A:246:ASN:ND2	1:G:321:PHE:HB2	1.69	1.07
1:A:314:ASP:OD2	1:A:376:TRP:CE3	2.06	1.07
1:E:93:GLU:HB2	1:E:96:ASN:HD22	1.16	1.06
1:C:268:GLN:CG	3:C:1307:HOH:O	1.91	1.06
1:C:268:GLN:HE21	1:C:313:PRO:HD3	1.19	1.05
1:E:268:GLN:HE21	1:E:313:PRO:HD3	1.19	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ASN:HB3	1:C:174:HIS:NE2	1.72	1.04
1:A:268:GLN:HE21	1:A:313:PRO:HD3	1.19	1.02
1:A:246:ASN:HD21	1:G:321:PHE:HB2	1.23	1.02
2:B:11:LEU:O	2:B:28:SER:HB2	1.61	1.01
2:B:128:VAL:HG22	2:B:138:PRO:HB3	1.43	1.01
1:C:34:ALA:HB1	1:E:243:ARG:HE	1.22	1.01
2:D:128:VAL:HG22	2:D:138:PRO:HB3	1.43	1.01
1:E:35:ASN:HB3	1:G:174:HIS:NE2	1.74	1.00
1:G:154:GLY:O	1:G:155:GLN:HG2	1.61	1.00
1:C:34:ALA:CB	1:E:243:ARG:HE	1.74	1.00
1:A:154:GLY:O	1:A:155:GLN:HG2	1.61	1.00
1:C:154:GLY:O	1:C:155:GLN:HG2	1.61	1.00
1:E:36:PHE:CD2	1:G:194:LYS:CB	2.22	1.00
1:G:268:GLN:HE21	1:G:313:PRO:HD3	1.19	1.00
2:F:11:LEU:O	2:F:28:SER:HB2	1.61	1.00
2:F:128:VAL:HG22	2:F:138:PRO:HB3	1.43	1.00
1:C:321:PHE:HB3	1:E:246:ASN:HD21	1.25	1.00
2:D:11:LEU:O	2:D:28:SER:HB2	1.61	1.00
2:H:128:VAL:HG22	2:H:138:PRO:HB3	1.43	1.00
1:E:154:GLY:O	1:E:155:GLN:HG2	1.61	0.99
1:G:304:PHE:HD1	1:G:304:PHE:H	1.04	0.99
1:E:35:ASN:CB	1:G:174:HIS:NE2	2.26	0.99
1:A:268:GLN:HA	1:A:373:ALA:HB1	1.45	0.99
1:A:35:ASN:CB	1:C:174:HIS:NE2	2.26	0.98
1:E:304:PHE:HD1	1:E:304:PHE:H	1.04	0.98
1:G:268:GLN:HA	1:G:373:ALA:HB1	1.45	0.98
1:C:268:GLN:HA	1:C:373:ALA:HB1	1.45	0.98
2:H:11:LEU:O	2:H:28:SER:HB2	1.61	0.98
1:A:243:ARG:HE	1:G:34:ALA:CB	1.76	0.98
1:A:304:PHE:HD1	1:A:304:PHE:H	1.04	0.98
1:E:268:GLN:HA	1:E:373:ALA:HB1	1.45	0.97
1:C:304:PHE:H	1:C:304:PHE:HD1	1.03	0.97
1:A:246:ASN:HD21	1:G:321:PHE:HB3	1.28	0.97
1:G:202:THR:C	1:G:204:PRO:HD2	1.89	0.97
1:A:202:THR:C	1:A:204:PRO:HD2	1.89	0.97
1:E:202:THR:C	1:E:204:PRO:HD2	1.89	0.96
1:A:243:ARG:HE	1:G:34:ALA:HB1	1.25	0.96
1:C:75:LYS:HZ1	1:C:94:ALA:H	1.14	0.96
1:A:75:LYS:HZ1	1:A:94:ALA:H	1.12	0.96
1:E:32:VAL:HG23	1:G:155:GLN:NE2	1.81	0.95
1:A:364:GLU:O	1:A:365:LYS:HB2	1.66	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:32:VAL:CG2	1:E:197:ILE:HD11	1.96	0.95
1:A:93:GLU:HB2	1:A:96:ASN:ND2	1.81	0.95
1:A:33:ASP:HB2	1:C:192:ALA:CB	1.97	0.95
1:C:32:VAL:HB	1:E:197:ILE:HD11	1.45	0.95
1:C:202:THR:C	1:C:204:PRO:HD2	1.89	0.94
1:G:364:GLU:O	1:G:365:LYS:HB2	1.66	0.94
1:A:32:VAL:HG23	1:C:155:GLN:NE2	1.82	0.94
1:C:93:GLU:HB2	1:C:96:ASN:ND2	1.81	0.94
1:G:93:GLU:HB2	1:G:96:ASN:ND2	1.81	0.94
1:A:370:HIS:CE1	2:B:75:TYR:CE2	2.56	0.94
1:A:197:ILE:HD11	1:G:32:VAL:HB	1.48	0.94
1:A:370:HIS:CE1	2:B:75:TYR:HE2	1.86	0.93
1:E:75:LYS:HZ1	1:E:94:ALA:H	1.15	0.93
1:E:93:GLU:HB2	1:E:96:ASN:ND2	1.81	0.93
1:C:22:LEU:CD1	1:C:94:ALA:HB1	1.99	0.93
1:E:22:LEU:CD1	1:E:94:ALA:HB1	1.98	0.93
1:G:299:ARG:HE	1:G:323:ASN:HB2	1.32	0.93
1:E:268:GLN:HG3	3:E:1321:HOH:O	1.67	0.93
1:G:22:LEU:CD1	1:G:94:ALA:HB1	1.99	0.93
1:G:268:GLN:HG3	3:G:1319:HOH:O	1.67	0.93
1:A:22:LEU:CD1	1:A:94:ALA:HB1	1.99	0.93
1:C:370:HIS:CE1	2:D:75:TYR:CE2	2.56	0.93
1:E:32:VAL:CB	1:G:195:GLU:O	2.16	0.93
1:E:72:HIS:CE1	1:E:118:ALA:HA	2.04	0.93
1:A:10:THR:HG23	1:A:28:VAL:HG12	1.50	0.93
1:E:364:GLU:O	1:E:365:LYS:HB2	1.66	0.93
1:E:370:HIS:CE1	2:F:75:TYR:HE2	1.86	0.93
1:G:368:VAL:O	1:G:370:HIS:N	2.02	0.93
1:G:370:HIS:CE1	2:H:75:TYR:HE2	1.86	0.93
1:A:268:GLN:HG3	3:A:1321:HOH:O	1.67	0.92
1:E:299:ARG:HE	1:E:323:ASN:HB2	1.33	0.92
1:C:370:HIS:CE1	2:D:75:TYR:HE2	1.86	0.92
1:G:125:ALA:HB2	1:G:168:TRP:CH2	2.05	0.92
1:C:368:VAL:O	1:C:370:HIS:N	2.02	0.92
1:G:72:HIS:CE1	1:G:118:ALA:HA	2.04	0.92
1:A:368:VAL:O	1:A:370:HIS:N	2.02	0.92
1:C:31:THR:HG22	1:C:32:VAL:H	1.33	0.92
1:G:370:HIS:CE1	2:H:75:TYR:CE2	2.56	0.92
1:C:268:GLN:HG3	3:C:1319:HOH:O	1.67	0.92
1:E:368:VAL:O	1:E:370:HIS:N	2.02	0.92
1:E:370:HIS:CE1	2:F:75:TYR:CE2	2.56	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:32:VAL:CB	1:E:197:ILE:HD11	1.98	0.92
1:C:72:HIS:CE1	1:C:118:ALA:HA	2.04	0.92
1:A:197:ILE:HD11	1:G:32:VAL:CG2	1.99	0.92
1:A:299:ARG:HE	1:A:323:ASN:HB2	1.32	0.92
1:A:72:HIS:CE1	1:A:118:ALA:HA	2.04	0.92
1:E:32:VAL:HG11	1:G:194:LYS:C	1.78	0.92
1:G:31:THR:HG22	1:G:32:VAL:H	1.33	0.92
1:E:31:THR:HG22	1:E:32:VAL:H	1.33	0.92
1:C:364:GLU:O	1:C:365:LYS:HB2	1.66	0.91
1:E:313:PRO:C	1:E:376:TRP:HE1	1.79	0.91
1:C:16:SER:O	1:C:310:PRO:HG3	1.69	0.91
1:G:10:THR:HG23	1:G:28:VAL:HG12	1.50	0.91
1:A:31:THR:HG22	1:A:32:VAL:H	1.33	0.91
1:C:313:PRO:C	1:C:376:TRP:HE1	1.79	0.91
1:E:125:ALA:HB2	1:E:168:TRP:CH2	2.04	0.91
1:A:16:SER:O	1:A:310:PRO:HG3	1.69	0.91
1:A:125:ALA:HB2	1:A:168:TRP:CH2	2.05	0.91
1:A:313:PRO:C	1:A:376:TRP:HE1	1.79	0.91
1:C:299:ARG:HE	1:C:323:ASN:HB2	1.32	0.91
1:E:16:SER:O	1:E:310:PRO:HG3	1.69	0.91
1:G:16:SER:O	1:G:310:PRO:HG3	1.69	0.91
1:E:10:THR:HG23	1:E:28:VAL:HG12	1.50	0.91
1:E:314:ASP:CG	1:E:376:TRP:CD2	2.48	0.91
1:A:314:ASP:N	1:A:376:TRP:HE1	1.69	0.91
1:C:10:THR:HG23	1:C:28:VAL:HG12	1.50	0.91
1:C:125:ALA:HB2	1:C:168:TRP:CH2	2.05	0.91
1:E:33:ASP:HB2	1:G:192:ALA:CB	2.01	0.91
1:E:36:PHE:CD2	1:G:194:LYS:CG	2.53	0.91
1:E:32:VAL:HG23	1:G:155:GLN:HE21	1.32	0.90
1:C:34:ALA:HB1	1:E:243:ARG:NE	1.86	0.90
1:G:314:ASP:N	1:G:376:TRP:HE1	1.69	0.90
1:A:314:ASP:CG	1:A:376:TRP:CD2	2.48	0.90
1:C:314:ASP:N	1:C:376:TRP:HE1	1.69	0.90
1:E:314:ASP:N	1:E:376:TRP:HE1	1.69	0.90
1:A:197:ILE:HD11	1:G:32:VAL:CB	2.02	0.90
1:A:246:ASN:ND2	1:G:321:PHE:CB	2.29	0.90
1:C:314:ASP:CG	1:C:376:TRP:CD2	2.48	0.90
1:E:370:HIS:HE1	2:F:75:TYR:CE2	1.90	0.90
1:C:244:ASN:HD21	1:C:246:ASN:ND2	1.70	0.90
1:A:32:VAL:HG23	1:C:155:GLN:HE21	1.35	0.90
1:G:313:PRO:C	1:G:376:TRP:HE1	1.79	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ASN:HD21	1:A:246:ASN:ND2	1.70	0.89
2:D:81:ILE:HB	3:D:303:HOH:O	1.73	0.89
1:G:370:HIS:HE1	2:H:75:TYR:CE2	1.90	0.89
2:H:81:ILE:HD13	2:H:93:ALA:HB3	1.54	0.89
1:E:35:ASN:HB3	1:G:174:HIS:HE1	1.06	0.89
2:B:81:ILE:HD13	2:B:93:ALA:HB3	1.54	0.89
1:E:244:ASN:HD21	1:E:246:ASN:ND2	1.70	0.89
1:G:244:ASN:HD21	1:G:246:ASN:ND2	1.70	0.89
2:F:81:ILE:HB	3:F:303:HOH:O	1.73	0.89
1:E:106:ASN:HD22	1:E:106:ASN:N	1.70	0.88
1:C:106:ASN:HD22	1:C:106:ASN:N	1.70	0.88
1:E:202:THR:O	1:E:204:PRO:HD2	1.74	0.88
1:C:202:THR:O	1:C:204:PRO:HD2	1.74	0.88
1:C:370:HIS:HE1	2:D:75:TYR:CE2	1.90	0.88
2:B:81:ILE:HB	3:B:303:HOH:O	1.73	0.88
1:C:268:GLN:HE21	1:C:313:PRO:CD	1.87	0.88
1:A:35:ASN:HB3	1:C:174:HIS:HE1	1.09	0.87
1:C:321:PHE:CB	1:E:246:ASN:ND2	2.27	0.87
1:A:32:VAL:HG11	1:C:194:LYS:C	1.80	0.87
1:G:268:GLN:HE21	1:G:313:PRO:CD	1.87	0.87
1:G:314:ASP:CG	1:G:376:TRP:CD2	2.48	0.87
2:H:81:ILE:HB	3:H:303:HOH:O	1.73	0.87
1:E:268:GLN:HE21	1:E:313:PRO:CD	1.87	0.87
1:A:106:ASN:N	1:A:106:ASN:HD22	1.70	0.86
1:E:314:ASP:OD2	1:E:376:TRP:CZ2	2.28	0.86
1:G:314:ASP:OD2	1:G:376:TRP:CZ2	2.28	0.86
1:A:370:HIS:HE1	2:B:75:TYR:CE2	1.90	0.86
1:C:314:ASP:OD2	1:C:376:TRP:CZ2	2.28	0.86
2:D:81:ILE:HD13	2:D:93:ALA:HB3	1.54	0.86
1:A:243:ARG:NE	1:G:34:ALA:HB1	1.90	0.86
1:A:268:GLN:HE21	1:A:313:PRO:CD	1.87	0.86
2:F:81:ILE:HD13	2:F:93:ALA:HB3	1.54	0.86
1:G:202:THR:O	1:G:204:PRO:HD2	1.74	0.86
1:G:106:ASN:HD22	1:G:106:ASN:N	1.70	0.86
1:A:10:THR:CG2	1:A:28:VAL:HG12	2.06	0.86
1:A:314:ASP:OD2	1:A:376:TRP:CZ2	2.28	0.85
1:G:75:LYS:HZ1	1:G:94:ALA:H	1.23	0.85
1:A:32:VAL:CB	1:C:195:GLU:O	2.21	0.85
2:D:83:LYS:O	2:D:89:TRP:HA	1.76	0.85
1:A:119:LYS:HB2	1:A:173:ALA:HB2	1.59	0.85
2:H:83:LYS:O	2:H:89:TRP:HA	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:THR:O	1:A:204:PRO:HD2	1.74	0.85
1:E:75:LYS:NZ	1:E:94:ALA:H	1.74	0.85
1:E:10:THR:CG2	1:E:28:VAL:HG12	2.06	0.85
1:G:75:LYS:NZ	1:G:94:ALA:H	1.74	0.85
1:G:10:THR:CG2	1:G:28:VAL:HG12	2.06	0.85
1:A:34:ALA:CA	1:C:196:VAL:HG11	2.06	0.85
1:C:119:LYS:HB2	1:C:173:ALA:HB2	1.59	0.85
1:C:10:THR:CG2	1:C:28:VAL:HG12	2.06	0.85
2:B:83:LYS:O	2:B:89:TRP:HA	1.76	0.84
2:D:12:ILE:HA	2:D:28:SER:HB3	1.59	0.84
2:F:12:ILE:HA	2:F:28:SER:HB3	1.59	0.84
2:F:83:LYS:O	2:F:89:TRP:HA	1.76	0.84
1:C:75:LYS:NZ	1:C:94:ALA:H	1.74	0.84
2:D:257:LEU:HD13	2:D:271:LEU:HD21	1.59	0.84
2:B:12:ILE:HA	2:B:28:SER:HB3	1.59	0.84
1:C:321:PHE:HB2	1:E:246:ASN:HD21	1.24	0.84
2:F:257:LEU:HD13	2:F:271:LEU:HD21	1.60	0.84
1:C:117:ASN:HD22	1:C:118:ALA:N	1.75	0.84
1:E:33:ASP:O	1:G:196:VAL:HB	1.74	0.84
1:E:119:LYS:HB2	1:E:173:ALA:HB2	1.59	0.84
1:E:34:ALA:CA	1:G:196:VAL:HG11	2.08	0.84
1:A:75:LYS:NZ	1:A:94:ALA:H	1.74	0.84
1:G:119:LYS:HB2	1:G:173:ALA:HB2	1.59	0.84
2:H:257:LEU:HD13	2:H:271:LEU:HD21	1.59	0.84
1:G:117:ASN:HD22	1:G:118:ALA:N	1.75	0.84
2:B:257:LEU:HD13	2:B:271:LEU:HD21	1.59	0.83
1:A:117:ASN:HD22	1:A:118:ALA:N	1.75	0.83
1:A:30:GLY:HA3	1:A:321:PHE:HE2	1.43	0.83
1:A:268:GLN:NE2	1:A:313:PRO:HD3	1.94	0.83
1:C:30:GLY:HA3	1:C:321:PHE:HE2	1.43	0.83
1:G:73:ASN:O	1:G:75:LYS:N	2.11	0.83
1:A:33:ASP:HB2	1:C:192:ALA:HB2	1.59	0.83
1:G:74:ASN:HD22	1:G:74:ASN:N	1.77	0.83
1:E:30:GLY:HA3	1:E:321:PHE:HE2	1.44	0.82
1:E:268:GLN:NE2	1:E:313:PRO:HD3	1.94	0.82
1:E:74:ASN:HD22	1:E:74:ASN:N	1.77	0.82
1:E:117:ASN:HD22	1:E:118:ALA:N	1.75	0.82
1:A:73:ASN:O	1:A:75:LYS:N	2.11	0.82
1:G:30:GLY:HA3	1:G:321:PHE:HE2	1.44	0.82
2:H:12:ILE:HA	2:H:28:SER:HB3	1.59	0.82
1:G:268:GLN:NE2	1:G:313:PRO:HD3	1.94	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:ALA:N	1:G:196:VAL:HG11	1.94	0.82
1:A:36:PHE:CD2	1:C:194:LYS:CG	2.56	0.82
1:A:74:ASN:HD22	1:A:74:ASN:N	1.77	0.82
1:G:31:THR:HG22	1:G:32:VAL:N	1.95	0.82
1:C:74:ASN:HD22	1:C:74:ASN:N	1.77	0.81
1:E:73:ASN:O	1:E:75:LYS:N	2.11	0.81
1:A:34:ALA:N	1:C:196:VAL:HG11	1.95	0.81
1:A:133:ILE:HD11	1:A:163:VAL:HG21	1.62	0.81
1:G:314:ASP:N	1:G:376:TRP:NE1	2.29	0.81
1:A:31:THR:HG22	1:A:32:VAL:N	1.95	0.81
1:C:133:ILE:HD11	1:C:163:VAL:HG21	1.62	0.81
1:E:133:ILE:HD11	1:E:163:VAL:HG21	1.62	0.81
1:G:133:ILE:HD11	1:G:163:VAL:HG21	1.62	0.81
1:C:336:THR:HB	2:D:96:ALA:O	1.80	0.81
1:C:268:GLN:NE2	1:C:313:PRO:HD3	1.94	0.81
1:E:32:VAL:CG2	1:G:155:GLN:HE21	1.93	0.81
1:G:370:HIS:CG	1:G:371:LEU:H	1.99	0.81
1:A:336:THR:HB	2:B:96:ALA:O	1.80	0.81
1:E:336:THR:HB	2:F:96:ALA:O	1.80	0.81
1:C:221:ASN:HD22	1:C:222:SER:N	1.79	0.81
1:G:292:GLN:O	1:G:368:VAL:HG23	1.81	0.81
1:G:336:THR:HB	2:H:96:ALA:O	1.80	0.81
1:C:300:GLY:O	1:C:301:ASN:HB2	1.81	0.80
1:E:31:THR:HG22	1:E:32:VAL:N	1.95	0.80
1:E:202:THR:C	1:E:204:PRO:CD	2.55	0.80
1:C:292:GLN:O	1:C:368:VAL:HG23	1.81	0.80
1:C:314:ASP:N	1:C:376:TRP:NE1	2.29	0.80
1:E:300:GLY:O	1:E:301:ASN:HB2	1.81	0.80
1:G:221:ASN:HD22	1:G:222:SER:N	1.79	0.80
1:E:221:ASN:HD22	1:E:222:SER:N	1.79	0.80
1:E:292:GLN:O	1:E:368:VAL:HG23	1.81	0.80
1:G:202:THR:C	1:G:204:PRO:CD	2.55	0.80
1:G:300:GLY:O	1:G:301:ASN:HB2	1.81	0.80
1:A:314:ASP:N	1:A:376:TRP:NE1	2.29	0.80
1:C:31:THR:HG22	1:C:32:VAL:N	1.95	0.80
1:C:73:ASN:O	1:C:75:LYS:N	2.11	0.80
1:G:74:ASN:HD22	1:G:74:ASN:H	1.30	0.80
1:A:370:HIS:CG	1:A:371:LEU:H	1.99	0.80
1:G:19:LYS:O	1:G:21:PRO:HD3	1.82	0.80
1:C:202:THR:C	1:C:204:PRO:CD	2.55	0.80
1:A:202:THR:C	1:A:204:PRO:CD	2.55	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:370:HIS:CG	1:C:371:LEU:H	1.99	0.79
1:E:314:ASP:N	1:E:376:TRP:NE1	2.29	0.79
1:A:19:LYS:O	1:A:21:PRO:HD3	1.82	0.79
1:A:292:GLN:O	1:A:368:VAL:HG23	1.81	0.79
1:A:300:GLY:O	1:A:301:ASN:HB2	1.81	0.79
1:E:33:ASP:HB2	1:G:192:ALA:HB2	1.64	0.79
1:A:33:ASP:O	1:C:196:VAL:HB	1.80	0.79
1:C:19:LYS:O	1:C:21:PRO:HD3	1.82	0.79
1:E:32:VAL:O	1:G:196:VAL:HA	1.82	0.79
1:A:315:LEU:HD11	2:B:146:ILE:HD12	1.64	0.79
1:E:34:ALA:HA	1:G:196:VAL:HG21	1.65	0.79
1:E:370:HIS:CG	1:E:371:LEU:H	1.99	0.79
1:C:250:GLN:NE2	1:C:251:THR:H	1.81	0.79
1:E:72:HIS:O	1:E:74:ASN:ND2	2.16	0.79
1:E:34:ALA:O	1:G:189:ASP:HA	1.81	0.79
1:G:72:HIS:O	1:G:74:ASN:ND2	2.16	0.79
1:A:250:GLN:NE2	1:A:251:THR:H	1.81	0.79
1:G:315:LEU:HD11	2:H:146:ILE:HD12	1.64	0.78
1:A:221:ASN:HD22	1:A:222:SER:N	1.79	0.78
1:A:268:GLN:HG3	1:A:313:PRO:HG3	1.65	0.78
1:E:33:ASP:O	1:G:196:VAL:HG12	0.97	0.78
1:E:19:LYS:O	1:E:21:PRO:HD3	1.82	0.78
1:G:333:LEU:HD23	3:G:1301:HOH:O	1.59	0.78
1:C:315:LEU:HD11	2:D:146:ILE:HD12	1.65	0.78
1:A:56:ILE:HD13	1:A:95:ASN:HA	1.65	0.78
1:A:80:ALA:HB1	1:A:111:VAL:HG12	1.65	0.78
1:E:74:ASN:HD22	1:E:74:ASN:H	1.30	0.78
1:E:196:VAL:HG23	1:E:197:ILE:HG13	1.66	0.78
1:E:250:GLN:NE2	1:E:251:THR:H	1.81	0.78
1:G:250:GLN:NE2	1:G:251:THR:H	1.81	0.78
1:A:174:HIS:NE2	1:A:191:LYS:HB2	1.99	0.78
1:C:74:ASN:HD22	1:C:74:ASN:H	1.30	0.78
1:G:80:ALA:HB1	1:G:111:VAL:HG12	1.65	0.78
1:C:72:HIS:O	1:C:74:ASN:ND2	2.16	0.77
1:C:56:ILE:HD13	1:C:95:ASN:HA	1.65	0.77
1:C:196:VAL:HG23	1:C:197:ILE:HG13	1.66	0.77
1:E:268:GLN:HG3	1:E:313:PRO:HG3	1.65	0.77
1:A:304:PHE:CD1	1:A:304:PHE:N	2.52	0.77
1:A:93:GLU:CB	1:A:96:ASN:HD22	1.97	0.77
1:C:174:HIS:NE2	1:C:191:LYS:HB2	1.99	0.77
1:E:56:ILE:HD13	1:E:95:ASN:HA	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:196:VAL:HG23	1:G:197:ILE:HG13	1.66	0.77
1:A:72:HIS:O	1:A:74:ASN:ND2	2.16	0.77
1:C:93:GLU:CB	1:C:96:ASN:HD22	1.97	0.77
1:E:315:LEU:HD11	2:F:146:ILE:HD12	1.64	0.77
1:G:56:ILE:HD13	1:G:95:ASN:HA	1.65	0.77
1:A:32:VAL:CG2	1:C:155:GLN:HE21	1.97	0.77
1:C:73:ASN:C	1:C:75:LYS:H	1.92	0.77
1:A:196:VAL:HG23	1:A:197:ILE:HG13	1.66	0.77
1:A:333:LEU:HD23	3:A:1301:HOH:O	1.59	0.77
1:E:93:GLU:CB	1:E:96:ASN:HD22	1.97	0.77
1:G:73:ASN:C	1:G:75:LYS:H	1.92	0.77
1:G:93:GLU:CB	1:G:96:ASN:HD22	1.97	0.77
1:A:33:ASP:O	1:C:196:VAL:HG11	0.95	0.77
1:E:80:ALA:HB1	1:E:111:VAL:HG12	1.65	0.77
1:G:174:HIS:NE2	1:G:191:LYS:HB2	1.99	0.77
1:G:268:GLN:HG3	1:G:313:PRO:HG3	1.65	0.76
1:C:268:GLN:HG3	1:C:313:PRO:HG3	1.65	0.76
1:C:151:LEU:HD12	1:C:152:THR:H	1.50	0.76
1:E:174:HIS:NE2	1:E:191:LYS:HB2	1.99	0.76
1:A:74:ASN:HD22	1:A:74:ASN:H	1.30	0.76
1:E:33:ASP:O	1:G:196:VAL:HG11	0.95	0.76
1:A:73:ASN:C	1:A:75:LYS:H	1.92	0.76
1:C:80:ALA:HB1	1:C:111:VAL:HG12	1.65	0.76
1:E:73:ASN:C	1:E:75:LYS:H	1.92	0.76
2:F:10:GLU:HB2	3:F:311:HOH:O	1.86	0.76
2:H:10:GLU:HB2	3:H:311:HOH:O	1.86	0.76
1:G:393:VAL:HG22	1:G:404:ILE:HG13	1.67	0.76
1:A:372:GLN:O	1:A:372:GLN:HG3	1.86	0.76
1:A:393:VAL:HG22	1:A:404:ILE:HG13	1.67	0.76
1:G:80:ALA:HB2	1:G:114:VAL:HG23	1.67	0.76
1:A:32:VAL:O	1:C:196:VAL:HA	1.86	0.75
2:D:10:GLU:HB2	3:D:311:HOH:O	1.86	0.75
1:C:80:ALA:HB2	1:C:114:VAL:HG23	1.68	0.75
1:A:151:LEU:HD12	1:A:152:THR:H	1.51	0.75
1:E:372:GLN:HG3	1:E:372:GLN:O	1.86	0.75
1:G:372:GLN:HG3	1:G:372:GLN:O	1.86	0.75
1:C:393:VAL:HG22	1:C:404:ILE:HG13	1.67	0.75
1:E:393:VAL:HG22	1:E:404:ILE:HG13	1.67	0.75
1:G:276:SER:OG	1:G:303:CYS:HB2	1.88	0.74
1:E:151:LEU:HD12	1:E:152:THR:H	1.51	0.74
2:F:117:LEU:HA	3:F:306:HOH:O	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:SER:HB2	1:C:104:PHE:O	1.88	0.74
1:G:133:ILE:CD1	1:G:163:VAL:HG21	2.17	0.74
1:E:85:SER:HB2	1:E:104:PHE:O	1.88	0.74
1:A:276:SER:OG	1:A:303:CYS:HB2	1.88	0.74
2:H:117:LEU:HA	3:H:306:HOH:O	1.86	0.74
1:A:85:SER:HB2	1:A:104:PHE:O	1.88	0.74
1:A:314:ASP:CG	1:A:376:TRP:NE1	2.46	0.74
1:C:314:ASP:CG	1:C:376:TRP:NE1	2.46	0.74
1:A:393:VAL:HG21	2:B:17:LEU:HG	1.69	0.74
2:B:10:GLU:HB2	3:B:311:HOH:O	1.86	0.74
1:C:276:SER:OG	1:C:303:CYS:HB2	1.88	0.74
1:C:372:GLN:HG3	1:C:372:GLN:O	1.86	0.74
1:E:80:ALA:HB2	1:E:114:VAL:HG23	1.68	0.74
1:E:314:ASP:CG	1:E:376:TRP:NE1	2.46	0.74
1:G:85:SER:HB2	1:G:104:PHE:O	1.88	0.74
1:G:151:LEU:HD12	1:G:152:THR:H	1.51	0.74
1:A:33:ASP:O	1:C:196:VAL:HG12	0.93	0.74
2:B:117:LEU:HA	3:B:306:HOH:O	1.86	0.74
1:C:133:ILE:CD1	1:C:163:VAL:HG21	2.17	0.74
1:E:34:ALA:O	1:G:189:ASP:CA	2.19	0.74
1:A:80:ALA:HB2	1:A:114:VAL:HG23	1.68	0.73
1:G:314:ASP:CG	1:G:376:TRP:NE1	2.46	0.73
1:E:276:SER:OG	1:E:303:CYS:HB2	1.88	0.73
1:A:133:ILE:CD1	1:A:163:VAL:HG21	2.17	0.73
2:D:117:LEU:HA	3:D:306:HOH:O	1.86	0.73
1:G:304:PHE:CD1	1:G:304:PHE:N	2.52	0.73
1:A:10:THR:HG23	1:A:28:VAL:CG1	2.18	0.73
1:A:31:THR:CG2	1:A:32:VAL:H	2.02	0.73
1:C:10:THR:HG23	1:C:28:VAL:CG1	2.18	0.73
1:C:393:VAL:HG21	2:D:17:LEU:HG	1.69	0.73
2:D:255:ASP:OD2	2:D:274:GLY:HA3	1.89	0.73
1:E:31:THR:CG2	1:E:32:VAL:H	2.02	0.73
1:C:31:THR:CG2	1:C:32:VAL:H	2.02	0.73
1:E:133:ILE:CD1	1:E:163:VAL:HG21	2.17	0.73
1:G:10:THR:HG23	1:G:28:VAL:CG1	2.18	0.73
1:E:93:GLU:CB	1:E:96:ASN:ND2	2.52	0.73
1:A:34:ALA:HA	1:C:196:VAL:HG11	1.71	0.73
1:A:35:ASN:HB2	1:C:191:LYS:HB2	1.70	0.73
1:A:78:ALA:CB	1:A:114:VAL:HG11	2.19	0.73
1:E:78:ALA:CB	1:E:114:VAL:HG11	2.19	0.73
1:C:93:GLU:CB	1:C:96:ASN:ND2	2.52	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:255:ASP:OD2	2:F:274:GLY:HA3	1.89	0.72
1:G:93:GLU:CB	1:G:96:ASN:ND2	2.52	0.72
1:G:393:VAL:HG21	2:H:17:LEU:HG	1.69	0.72
2:B:255:ASP:OD2	2:B:274:GLY:HA3	1.89	0.72
1:E:393:VAL:HG21	2:F:17:LEU:HG	1.69	0.72
2:H:255:ASP:OD2	2:H:274:GLY:HA3	1.89	0.72
1:C:78:ALA:CB	1:C:114:VAL:HG11	2.19	0.72
1:E:36:PHE:CD2	1:G:194:LYS:HB3	2.23	0.72
1:G:78:ALA:CB	1:G:114:VAL:HG11	2.19	0.72
1:E:36:PHE:HD2	1:G:193:LYS:O	1.17	0.72
1:A:93:GLU:CB	1:A:96:ASN:ND2	2.52	0.72
1:C:202:THR:OG1	1:C:209:LYS:HD3	1.90	0.72
1:A:34:ALA:HA	1:C:196:VAL:HG21	1.71	0.71
1:A:171:SER:O	1:A:172:LEU:HD23	1.91	0.71
1:A:202:THR:OG1	1:A:209:LYS:HD3	1.90	0.71
1:C:69:ASP:OD2	1:C:116:PHE:HB2	1.91	0.71
1:C:331:GLN:OE1	1:C:333:LEU:HD21	1.91	0.71
1:E:69:ASP:OD2	1:E:116:PHE:HB2	1.90	0.71
1:E:314:ASP:H	1:E:376:TRP:HZ2	1.38	0.71
1:A:69:ASP:OD2	1:A:116:PHE:HB2	1.91	0.71
1:E:10:THR:HG23	1:E:28:VAL:CG1	2.18	0.71
2:B:105:VAL:HG23	2:B:118:VAL:HG22	1.73	0.71
1:E:331:GLN:OE1	1:E:333:LEU:HD21	1.91	0.71
1:G:171:SER:O	1:G:172:LEU:HD23	1.90	0.71
1:G:314:ASP:H	1:G:376:TRP:HZ2	1.38	0.71
2:H:74:SER:HB3	2:H:76:ASP:OD1	1.91	0.71
1:A:32:VAL:CG2	1:C:155:GLN:NE2	2.54	0.70
1:G:109:SER:O	1:G:110:SER:HB2	1.91	0.70
2:H:105:VAL:HG23	2:H:118:VAL:HG22	1.73	0.70
1:E:171:SER:O	1:E:172:LEU:HD23	1.91	0.70
1:G:31:THR:CG2	1:G:32:VAL:H	2.02	0.70
1:G:202:THR:OG1	1:G:209:LYS:HD3	1.90	0.70
1:G:69:ASP:OD2	1:G:116:PHE:HB2	1.90	0.70
2:D:105:VAL:HG23	2:D:118:VAL:HG22	1.73	0.70
1:G:336:THR:CB	2:H:96:ALA:O	2.40	0.70
1:C:171:SER:O	1:C:172:LEU:HD23	1.90	0.70
1:C:289:SER:OG	1:C:290:ALA:N	2.24	0.70
1:A:164:ILE:HG12	1:A:180:GLY:HA2	1.74	0.70
2:H:274:GLY:C	2:H:276:ASN:H	2.00	0.70
1:A:289:SER:OG	1:A:290:ALA:N	2.24	0.70
2:F:105:VAL:HG23	2:F:118:VAL:HG22	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:PHE:CE1	1:C:194:LYS:O	2.40	0.70
1:E:202:THR:OG1	1:E:209:LYS:HD3	1.90	0.70
1:C:75:LYS:HZ1	1:C:94:ALA:N	1.90	0.69
1:C:333:LEU:HD23	3:C:1301:HOH:O	1.59	0.69
1:E:35:ASN:HB2	1:G:191:LYS:HB2	1.74	0.69
1:A:331:GLN:OE1	1:A:333:LEU:HD21	1.91	0.69
1:C:314:ASP:H	1:C:376:TRP:HZ2	1.38	0.69
2:D:74:SER:HB3	2:D:76:ASP:OD1	1.91	0.69
2:D:274:GLY:C	2:D:276:ASN:H	2.00	0.69
1:A:117:ASN:HD22	1:A:118:ALA:H	1.39	0.69
1:A:203:SER:O	1:A:205:ASN:N	2.26	0.69
2:D:144:HIS:CE1	2:D:183:LYS:HD2	2.28	0.69
1:E:35:ASN:HB2	1:G:174:HIS:NE2	2.06	0.69
1:C:203:SER:O	1:C:205:ASN:N	2.26	0.69
1:E:212:LEU:HD13	1:E:227:THR:HG21	1.74	0.69
1:E:336:THR:CB	2:F:96:ALA:O	2.40	0.69
1:G:212:LEU:HD13	1:G:227:THR:HG21	1.74	0.69
1:G:331:GLN:OE1	1:G:333:LEU:HD21	1.91	0.69
2:B:74:SER:HB3	2:B:76:ASP:OD1	1.91	0.69
1:E:333:LEU:HD23	3:E:1301:HOH:O	1.59	0.69
1:G:221:ASN:HD22	1:G:221:ASN:C	2.01	0.69
1:E:32:VAL:HG11	1:G:194:LYS:O	1.91	0.69
1:E:109:SER:O	1:E:110:SER:HB2	1.91	0.69
1:E:203:SER:O	1:E:205:ASN:N	2.26	0.69
1:G:164:ILE:HG12	1:G:180:GLY:HA2	1.74	0.69
1:G:203:SER:O	1:G:205:ASN:N	2.26	0.69
1:A:28:VAL:HG22	1:A:29:SER:H	1.58	0.69
1:A:94:ALA:O	1:A:95:ASN:HB2	1.92	0.69
1:A:314:ASP:H	1:A:376:TRP:HZ2	1.38	0.69
1:C:94:ALA:O	1:C:95:ASN:HB2	1.92	0.69
1:E:185:ALA:HB3	1:E:199:LEU:HB2	1.75	0.69
2:F:144:HIS:CE1	2:F:183:LYS:HD2	2.28	0.69
1:A:212:LEU:HD13	1:A:227:THR:HG21	1.74	0.69
1:C:28:VAL:HG22	1:C:29:SER:H	1.58	0.69
1:C:32:VAL:HG21	1:E:197:ILE:HD11	1.75	0.69
1:C:336:THR:CB	2:D:96:ALA:O	2.40	0.69
1:E:314:ASP:OD2	1:E:376:TRP:CZ3	2.46	0.69
2:F:74:SER:HB3	2:F:76:ASP:OD1	1.91	0.69
1:G:117:ASN:HD22	1:G:118:ALA:H	1.39	0.69
2:H:144:HIS:CE1	2:H:183:LYS:HD2	2.28	0.69
1:C:212:LEU:HD13	1:C:227:THR:HG21	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:THR:CB	2:B:96:ALA:O	2.40	0.68
2:B:24:LEU:HB3	2:B:36:PHE:HB2	1.75	0.68
2:B:53:GLU:HG3	3:B:328:HOH:O	1.93	0.68
1:C:164:ILE:HG12	1:C:180:GLY:HA2	1.74	0.68
2:B:274:GLY:C	2:B:276:ASN:H	2.00	0.68
1:C:185:ALA:HB3	1:C:199:LEU:HB2	1.75	0.68
1:G:28:VAL:HG22	1:G:29:SER:H	1.58	0.68
1:G:314:ASP:OD2	1:G:376:TRP:CZ3	2.46	0.68
1:G:94:ALA:O	1:G:95:ASN:HB2	1.92	0.68
1:A:185:ALA:HB3	1:A:199:LEU:HB2	1.75	0.68
1:E:107:HIS:ND1	1:E:111:VAL:HG22	2.09	0.68
2:F:274:GLY:C	2:F:276:ASN:H	2.00	0.68
2:H:53:GLU:HG3	3:H:328:HOH:O	1.93	0.68
1:C:75:LYS:NZ	1:C:94:ALA:HB2	2.08	0.68
1:C:280:ASN:C	1:C:298:ALA:HB3	2.19	0.68
1:G:185:ALA:HB3	1:G:199:LEU:HB2	1.75	0.68
1:A:75:LYS:HZ1	1:A:94:ALA:N	1.88	0.68
1:A:107:HIS:ND1	1:A:111:VAL:HG22	2.09	0.68
2:B:144:HIS:CE1	2:B:183:LYS:HD2	2.28	0.68
1:C:109:SER:O	1:C:110:SER:HB2	1.91	0.68
2:D:24:LEU:HB3	2:D:36:PHE:HB2	1.76	0.68
1:A:75:LYS:NZ	1:A:94:ALA:HB2	2.08	0.68
1:A:249:LEU:O	1:A:249:LEU:HD23	1.94	0.68
1:A:280:ASN:C	1:A:298:ALA:HB3	2.19	0.68
2:D:53:GLU:HG3	3:D:328:HOH:O	1.93	0.68
1:E:75:LYS:NZ	1:E:94:ALA:HB2	2.08	0.68
1:A:109:SER:O	1:A:110:SER:HB2	1.91	0.68
1:C:402:VAL:HG11	2:D:24:LEU:HD21	1.76	0.68
1:E:86:LEU:CD2	1:E:104:PHE:HB2	2.24	0.68
1:E:280:ASN:C	1:E:298:ALA:HB3	2.19	0.68
1:C:314:ASP:OD2	1:C:376:TRP:CZ3	2.46	0.68
1:E:94:ALA:O	1:E:95:ASN:HB2	1.92	0.68
1:E:164:ILE:HG12	1:E:180:GLY:HA2	1.74	0.68
1:E:241:ASP:C	1:E:243:ARG:H	2.02	0.68
1:G:75:LYS:NZ	1:G:94:ALA:HB2	2.08	0.68
1:G:86:LEU:CD2	1:G:104:PHE:HB2	2.24	0.68
1:E:28:VAL:HG22	1:E:29:SER:H	1.58	0.67
1:E:117:ASN:HD22	1:E:118:ALA:H	1.39	0.67
2:F:53:GLU:HG3	3:F:328:HOH:O	1.93	0.67
1:E:34:ALA:HA	1:G:196:VAL:HG11	1.75	0.67
1:E:249:LEU:HD23	1:E:249:LEU:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:402:VAL:HG11	2:F:24:LEU:HD21	1.76	0.67
2:F:24:LEU:HB3	2:F:36:PHE:HB2	1.76	0.67
1:G:107:HIS:ND1	1:G:111:VAL:HG22	2.09	0.67
1:A:86:LEU:CD2	1:A:104:PHE:HB2	2.24	0.67
1:A:314:ASP:OD2	1:A:376:TRP:CZ3	2.46	0.67
1:A:402:VAL:HG11	2:B:24:LEU:HD21	1.76	0.67
1:E:32:VAL:CG2	1:G:155:GLN:NE2	2.52	0.67
1:E:32:VAL:HG12	1:G:196:VAL:HG12	1.75	0.67
1:G:280:ASN:C	1:G:298:ALA:HB3	2.19	0.67
1:G:402:VAL:HG11	2:H:24:LEU:HD21	1.76	0.67
2:H:233:ILE:HD11	2:H:248:LEU:HD13	1.76	0.67
1:A:32:VAL:HG11	1:C:194:LYS:O	1.95	0.67
1:A:35:ASN:HB2	1:C:174:HIS:NE2	2.10	0.67
1:G:241:ASP:C	1:G:243:ARG:H	2.02	0.67
1:G:289:SER:OG	1:G:290:ALA:N	2.24	0.67
1:C:241:ASP:C	1:C:243:ARG:H	2.02	0.67
1:E:36:PHE:CE1	1:G:194:LYS:O	2.36	0.67
1:E:124:LEU:HG	1:E:125:ALA:N	2.10	0.67
1:A:36:PHE:CD2	1:C:192:ALA:O	2.47	0.67
2:B:233:ILE:HD11	2:B:248:LEU:HD13	1.76	0.67
1:C:107:HIS:ND1	1:C:111:VAL:HG22	2.09	0.67
1:C:124:LEU:HG	1:C:125:ALA:N	2.10	0.67
2:B:157:THR:OG1	2:B:170:SER:HB2	1.95	0.67
1:C:86:LEU:CD2	1:C:104:PHE:HB2	2.24	0.67
2:F:157:THR:OG1	2:F:170:SER:HB2	1.95	0.67
2:B:3:VAL:C	2:B:4:ILE:HD12	2.21	0.66
1:E:106:ASN:N	1:E:106:ASN:ND2	2.42	0.66
2:H:157:THR:OG1	2:H:170:SER:HB2	1.95	0.66
1:G:249:LEU:HD23	1:G:249:LEU:O	1.94	0.66
1:C:75:LYS:NZ	1:C:94:ALA:N	2.44	0.66
1:C:96:ASN:HB2	3:C:1309:HOH:O	1.96	0.66
1:C:249:LEU:O	1:C:249:LEU:HD23	1.94	0.66
1:G:124:LEU:HG	1:G:125:ALA:N	2.10	0.66
1:E:96:ASN:HB2	3:E:1311:HOH:O	1.96	0.66
1:E:75:LYS:NZ	1:E:94:ALA:N	2.44	0.66
1:E:221:ASN:HD22	1:E:221:ASN:C	2.01	0.66
1:G:75:LYS:NZ	1:G:94:ALA:N	2.44	0.66
2:H:3:VAL:C	2:H:4:ILE:HD12	2.21	0.66
2:H:24:LEU:HB3	2:H:36:PHE:HB2	1.76	0.66
1:A:241:ASP:C	1:A:243:ARG:H	2.02	0.66
1:C:117:ASN:HD22	1:C:118:ALA:H	1.39	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:233:ILE:HD11	2:D:248:LEU:HD13	1.76	0.66
1:E:30:GLY:HA3	1:E:321:PHE:CE2	2.29	0.66
1:C:304:PHE:HD1	1:C:304:PHE:N	1.87	0.66
1:E:32:VAL:CG1	1:G:194:LYS:C	2.64	0.66
1:A:337:LEU:HD21	2:B:97:VAL:CG1	2.26	0.65
2:F:233:ILE:HD11	2:F:248:LEU:HD13	1.76	0.65
1:G:30:GLY:HA3	1:G:321:PHE:CE2	2.30	0.65
1:G:96:ASN:HB2	3:G:1309:HOH:O	1.96	0.65
2:F:3:VAL:C	2:F:4:ILE:HD12	2.21	0.65
1:A:96:ASN:HB2	3:A:1311:HOH:O	1.96	0.65
1:A:221:ASN:HD22	1:A:221:ASN:C	2.01	0.65
2:B:40:GLY:N	3:B:305:HOH:O	2.30	0.65
1:E:36:PHE:CD2	1:G:192:ALA:O	2.49	0.65
1:E:75:LYS:HZ1	1:E:94:ALA:N	1.91	0.65
1:E:250:GLN:HE21	1:E:251:THR:H	1.45	0.65
1:E:337:LEU:HD21	2:F:97:VAL:CG1	2.26	0.65
1:G:337:LEU:HD21	2:H:97:VAL:CG1	2.26	0.65
2:D:157:THR:OG1	2:D:170:SER:HB2	1.95	0.65
1:A:124:LEU:HG	1:A:125:ALA:N	2.10	0.65
2:B:102:VAL:CG2	3:B:304:HOH:O	2.45	0.65
2:F:102:VAL:CG2	3:F:304:HOH:O	2.45	0.65
1:G:124:LEU:HG	1:G:125:ALA:H	1.62	0.65
1:G:325:ILE:N	1:G:325:ILE:HD12	2.12	0.65
1:C:32:VAL:CG2	1:E:197:ILE:CD1	2.74	0.65
1:G:250:GLN:HE21	1:G:251:THR:H	1.45	0.65
1:C:124:LEU:HG	1:C:125:ALA:H	1.62	0.65
1:C:337:LEU:HD21	2:D:97:VAL:CG1	2.26	0.65
2:D:40:GLY:N	3:D:305:HOH:O	2.30	0.65
1:E:125:ALA:HB2	1:E:168:TRP:HH2	1.62	0.65
1:A:30:GLY:HA3	1:A:321:PHE:CE2	2.30	0.65
1:A:124:LEU:HG	1:A:125:ALA:H	1.62	0.65
2:F:40:GLY:N	3:F:305:HOH:O	2.30	0.65
1:G:106:ASN:HD22	1:G:106:ASN:H	1.46	0.65
1:G:106:ASN:N	1:G:106:ASN:ND2	2.42	0.65
1:A:20:ILE:HG13	1:A:20:ILE:O	1.97	0.64
1:A:325:ILE:N	1:A:325:ILE:HD12	2.12	0.64
1:C:221:ASN:HD22	1:C:221:ASN:C	2.01	0.64
2:D:3:VAL:C	2:D:4:ILE:HD12	2.21	0.64
1:E:325:ILE:HD12	1:E:325:ILE:N	2.12	0.64
2:H:238:ASN:HD22	2:H:240:GLN:H	1.45	0.64
1:E:124:LEU:HG	1:E:125:ALA:H	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:116:PHE:HE1	1:G:138:MET:HE3	1.63	0.64
2:H:18:ASP:HB2	3:H:337:HOH:O	1.98	0.64
2:D:102:VAL:CG2	3:D:304:HOH:O	2.45	0.64
1:A:75:LYS:NZ	1:A:94:ALA:N	2.44	0.64
1:E:20:ILE:O	1:E:20:ILE:HG13	1.97	0.64
2:D:33:ILE:HD11	2:D:56:VAL:HG11	1.80	0.64
1:A:125:ALA:HB2	1:A:168:TRP:HH2	1.62	0.64
1:A:212:LEU:HD22	1:A:227:THR:CG2	2.28	0.64
2:B:33:ILE:HD11	2:B:56:VAL:HG11	1.80	0.64
2:B:238:ASN:HD22	2:B:240:GLN:H	1.44	0.64
1:C:325:ILE:HD12	1:C:325:ILE:N	2.12	0.64
1:E:289:SER:OG	1:E:290:ALA:N	2.24	0.64
1:C:116:PHE:HE1	1:C:138:MET:HE3	1.63	0.64
2:D:18:ASP:HB2	3:D:337:HOH:O	1.97	0.64
2:F:33:ILE:HD11	2:F:56:VAL:HG11	1.80	0.64
1:A:206:SER:O	1:A:208:ILE:HG13	1.98	0.63
1:A:239:ILE:HB	1:A:250:GLN:HB3	1.81	0.63
1:C:106:ASN:HD22	1:C:106:ASN:H	1.46	0.63
1:C:125:ALA:HB2	1:C:168:TRP:HH2	1.62	0.63
2:F:18:ASP:HB2	3:F:337:HOH:O	1.97	0.63
1:G:20:ILE:HG13	1:G:20:ILE:O	1.97	0.63
1:G:206:SER:O	1:G:208:ILE:HG13	1.98	0.63
1:A:304:PHE:HD1	1:A:304:PHE:N	1.87	0.63
1:C:30:GLY:HA3	1:C:321:PHE:CE2	2.30	0.63
2:H:102:VAL:CG2	3:H:304:HOH:O	2.45	0.63
2:B:18:ASP:HB2	3:B:337:HOH:O	1.98	0.63
1:C:51:ASP:O	1:C:53:GLU:HG3	1.99	0.63
1:E:51:ASP:O	1:E:53:GLU:HG3	1.99	0.63
2:H:68:THR:C	2:H:69:ILE:HD12	2.23	0.63
1:E:212:LEU:HD22	1:E:227:THR:CG2	2.28	0.63
2:F:238:ASN:HD22	2:F:240:GLN:H	1.44	0.63
2:H:40:GLY:N	3:H:305:HOH:O	2.30	0.63
1:A:116:PHE:HE1	1:A:138:MET:HE3	1.63	0.63
1:C:20:ILE:O	1:C:20:ILE:HG13	1.97	0.63
2:F:68:THR:C	2:F:69:ILE:HD12	2.23	0.63
2:D:68:THR:C	2:D:69:ILE:HD12	2.23	0.63
1:A:32:VAL:HG12	1:C:196:VAL:HG12	1.81	0.63
1:C:250:GLN:HE21	1:C:251:THR:H	1.45	0.63
2:D:238:ASN:HD22	2:D:240:GLN:H	1.44	0.63
1:G:193:LYS:O	1:G:194:LYS:HB3	1.99	0.63
1:G:212:LEU:HD22	1:G:227:THR:CG2	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:23:ARG:NH1	2:H:68:THR:HG21	2.14	0.63
2:H:33:ILE:HD11	2:H:56:VAL:HG11	1.80	0.63
2:B:68:THR:C	2:B:69:ILE:HD12	2.24	0.63
1:C:78:ALA:HB3	1:C:114:VAL:HG11	1.80	0.63
1:C:147:ASN:O	1:C:148:TYR:C	2.42	0.63
1:C:239:ILE:HB	1:C:250:GLN:HB3	1.81	0.63
1:C:314:ASP:OD1	1:C:376:TRP:CD1	2.52	0.63
1:E:314:ASP:OD1	1:E:376:TRP:CD1	2.52	0.63
1:A:250:GLN:HE21	1:A:251:THR:H	1.44	0.62
1:C:212:LEU:HD22	1:C:227:THR:CG2	2.28	0.62
1:C:280:ASN:HB3	1:C:300:GLY:C	2.24	0.62
1:A:78:ALA:HB3	1:A:114:VAL:HG11	1.80	0.62
1:A:197:ILE:HD11	1:G:32:VAL:HG21	1.77	0.62
1:A:268:GLN:OE1	1:A:374:PRO:HD2	1.99	0.62
1:C:206:SER:O	1:C:208:ILE:HG13	1.98	0.62
1:E:78:ALA:HB3	1:E:114:VAL:HG11	1.80	0.62
1:E:280:ASN:HB3	1:E:300:GLY:C	2.24	0.62
1:A:147:ASN:O	1:A:148:TYR:C	2.42	0.62
1:A:280:ASN:HB3	1:A:300:GLY:C	2.24	0.62
2:D:157:THR:O	2:D:157:THR:HG22	2.00	0.62
1:A:193:LYS:O	1:A:194:LYS:HB3	1.99	0.62
2:B:23:ARG:NH1	2:B:68:THR:HG21	2.14	0.62
1:E:206:SER:O	1:E:208:ILE:HG13	1.98	0.62
1:G:51:ASP:O	1:G:53:GLU:HG3	1.99	0.62
1:A:243:ARG:HE	1:G:34:ALA:HB2	1.63	0.62
1:A:314:ASP:OD1	1:A:376:TRP:CD1	2.52	0.62
1:E:116:PHE:HE1	1:E:138:MET:HE3	1.63	0.62
1:E:239:ILE:HB	1:E:250:GLN:HB3	1.81	0.62
2:B:257:LEU:CD1	2:B:271:LEU:HD21	2.30	0.62
1:C:192:ALA:O	1:C:194:LYS:HG2	2.00	0.62
1:C:268:GLN:CA	1:C:373:ALA:HB1	2.27	0.62
1:E:370:HIS:HE1	2:F:75:TYR:CD2	2.18	0.62
2:D:128:VAL:CG2	2:D:138:PRO:HB3	2.27	0.62
1:E:392:LEU:HD13	3:E:1302:HOH:O	2.00	0.62
1:G:192:ALA:O	1:G:194:LYS:HG2	2.00	0.62
1:G:314:ASP:OD1	1:G:376:TRP:CD1	2.52	0.62
1:A:51:ASP:O	1:A:53:GLU:HG3	1.99	0.62
1:C:193:LYS:O	1:C:194:LYS:HB3	1.99	0.62
1:E:62:ASP:CG	1:E:103:ARG:HH12	2.08	0.62
1:E:193:LYS:O	1:E:194:LYS:HB3	1.99	0.62
1:G:370:HIS:HE1	2:H:75:TYR:CD2	2.18	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:66:PHE:HE1	2:B:114:PRO:HD3	1.65	0.61
2:D:257:LEU:CD1	2:D:271:LEU:HD21	2.30	0.61
1:E:147:ASN:O	1:E:148:TYR:C	2.42	0.61
2:F:157:THR:O	2:F:157:THR:HG22	2.00	0.61
1:A:192:ALA:O	1:A:194:LYS:HG2	2.00	0.61
1:C:34:ALA:CB	1:E:243:ARG:NE	2.52	0.61
1:E:32:VAL:CG1	1:G:194:LYS:O	2.48	0.61
1:E:241:ASP:OD1	1:E:243:ARG:HB2	2.00	0.61
2:F:128:VAL:CG2	2:F:138:PRO:HB3	2.27	0.61
1:G:268:GLN:OE1	1:G:374:PRO:HD2	1.99	0.61
2:F:23:ARG:NH1	2:F:68:THR:HG21	2.14	0.61
1:G:78:ALA:HB3	1:G:114:VAL:HG11	1.80	0.61
1:G:239:ILE:HB	1:G:250:GLN:HB3	1.81	0.61
1:C:304:PHE:N	1:C:304:PHE:CD1	2.52	0.61
1:E:106:ASN:HD22	1:E:106:ASN:H	1.46	0.61
1:G:241:ASP:OD1	1:G:243:ARG:HB2	2.00	0.61
2:H:37:GLU:HG2	2:H:46:ILE:HG13	1.82	0.61
2:H:66:PHE:HE1	2:H:114:PRO:HD3	1.65	0.61
1:A:33:ASP:C	1:C:196:VAL:HG12	1.95	0.61
1:A:33:ASP:HB2	1:C:192:ALA:HB1	1.81	0.61
1:A:106:ASN:HD22	1:A:106:ASN:H	1.46	0.61
1:C:62:ASP:CG	1:C:103:ARG:HH12	2.08	0.61
1:C:241:ASP:OD1	1:C:243:ARG:HB2	2.00	0.61
1:E:304:PHE:CD1	1:E:304:PHE:N	2.52	0.61
2:B:102:VAL:HG23	3:B:304:HOH:O	2.00	0.61
1:C:244:ASN:ND2	1:C:246:ASN:ND2	2.47	0.61
1:C:370:HIS:HE1	2:D:75:TYR:CD2	2.18	0.61
2:D:37:GLU:HG2	2:D:46:ILE:HG13	1.82	0.61
2:D:102:VAL:HG23	3:D:304:HOH:O	2.00	0.61
2:F:66:PHE:HE1	2:F:114:PRO:HD3	1.65	0.61
2:F:102:VAL:HG23	3:F:304:HOH:O	2.01	0.61
1:G:280:ASN:HB3	1:G:300:GLY:C	2.24	0.61
2:H:155:PRO:HG3	2:H:214:PRO:HA	1.83	0.61
1:A:153:PRO:HB2	1:A:188:TRP:CZ3	2.35	0.61
1:C:153:PRO:HB2	1:C:188:TRP:CZ3	2.35	0.61
2:D:66:PHE:HE1	2:D:114:PRO:HD3	1.65	0.61
1:E:268:GLN:OE1	1:E:374:PRO:HD2	1.99	0.61
2:H:30:ASP:OD1	2:H:32:THR:N	2.34	0.61
1:A:62:ASP:CG	1:A:103:ARG:HH12	2.08	0.61
2:B:189:SER:C	2:B:191:ALA:H	2.09	0.61
1:C:268:GLN:OE1	1:C:374:PRO:HD2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:52:HIS:HA	3:D:328:HOH:O	2.01	0.61
1:E:36:PHE:CD2	1:G:194:LYS:HG2	2.35	0.61
1:G:62:ASP:CG	1:G:103:ARG:HH12	2.08	0.61
1:G:153:PRO:HB2	1:G:188:TRP:CZ3	2.35	0.61
1:G:392:LEU:HD13	3:G:1302:HOH:O	2.00	0.61
1:A:370:HIS:HE1	2:B:75:TYR:CD2	2.18	0.61
1:E:244:ASN:ND2	1:E:246:ASN:ND2	2.47	0.61
2:F:257:LEU:CD1	2:F:271:LEU:HD21	2.30	0.61
1:A:244:ASN:HD21	1:A:246:ASN:HD22	1.49	0.61
2:B:200:LEU:HB3	2:B:234:TRP:CZ3	2.36	0.61
1:C:34:ALA:HB2	1:E:243:ARG:HE	1.62	0.61
1:E:192:ALA:O	1:E:194:LYS:HG2	2.00	0.61
1:G:202:THR:O	1:G:202:THR:HG22	2.01	0.61
2:D:23:ARG:NH1	2:D:68:THR:HG21	2.14	0.60
1:E:105:SER:C	1:E:107:HIS:H	2.09	0.60
2:B:30:ASP:OD1	2:B:32:THR:N	2.34	0.60
2:D:12:ILE:HA	2:D:28:SER:CB	2.30	0.60
1:E:202:THR:O	1:E:202:THR:HG22	2.01	0.60
2:F:4:ILE:HG13	2:F:43:HIS:ND1	2.16	0.60
2:H:200:LEU:HB3	2:H:234:TRP:CZ3	2.36	0.60
1:A:31:THR:CG2	1:A:32:VAL:N	2.64	0.60
1:A:241:ASP:OD1	1:A:243:ARG:HB2	2.00	0.60
1:A:330:LEU:O	1:A:371:LEU:HD21	2.02	0.60
1:A:392:LEU:HD13	3:A:1302:HOH:O	2.00	0.60
1:C:392:LEU:HD13	3:C:1302:HOH:O	2.00	0.60
2:D:189:SER:C	2:D:191:ALA:H	2.09	0.60
2:D:155:PRO:HG3	2:D:214:PRO:HA	1.82	0.60
1:E:153:PRO:HB2	1:E:188:TRP:CZ3	2.35	0.60
1:E:187:ILE:HG22	1:E:196:VAL:HG22	1.83	0.60
2:F:189:SER:C	2:F:191:ALA:H	2.09	0.60
1:G:105:SER:C	1:G:107:HIS:H	2.09	0.60
1:G:147:ASN:O	1:G:148:TYR:C	2.42	0.60
1:A:105:SER:C	1:A:107:HIS:H	2.09	0.60
1:C:187:ILE:HG22	1:C:196:VAL:HG22	1.83	0.60
2:D:30:ASP:OD1	2:D:32:THR:N	2.34	0.60
1:G:78:ALA:HB1	1:G:114:VAL:HG11	1.84	0.60
1:A:36:PHE:CD2	1:C:194:LYS:HG2	2.36	0.60
2:B:157:THR:O	2:B:157:THR:HG22	2.00	0.60
1:C:92:ASN:O	1:C:93:GLU:HB2	2.02	0.60
2:D:4:ILE:HG13	2:D:43:HIS:ND1	2.16	0.60
2:D:200:LEU:HB3	2:D:234:TRP:CZ3	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:155:PRO:HG3	2:F:214:PRO:HA	1.83	0.60
1:G:187:ILE:HG22	1:G:196:VAL:HG22	1.83	0.60
1:G:370:HIS:CG	1:G:371:LEU:N	2.68	0.60
1:A:217:TRP:CD2	1:A:225:VAL:HG22	2.37	0.60
1:A:244:ASN:ND2	1:A:246:ASN:ND2	2.47	0.60
1:A:272:LEU:HD22	1:A:284:LEU:HD11	1.83	0.60
2:B:12:ILE:HA	2:B:28:SER:CB	2.30	0.60
2:B:155:PRO:HG3	2:B:214:PRO:HA	1.82	0.60
1:C:105:SER:C	1:C:107:HIS:H	2.09	0.60
2:F:12:ILE:HA	2:F:28:SER:CB	2.30	0.60
2:F:37:GLU:HG2	2:F:46:ILE:HG13	1.82	0.60
1:C:71:SER:O	1:C:73:ASN:N	2.34	0.60
1:C:396:THR:HG23	3:C:1310:HOH:O	2.01	0.60
2:D:29:SER:HA	2:D:55:PRO:HB3	1.84	0.60
2:D:225:VAL:HG13	2:D:257:LEU:HB2	1.84	0.60
1:E:78:ALA:HB1	1:E:114:VAL:HG11	1.83	0.60
2:F:225:VAL:HG13	2:F:257:LEU:HB2	1.84	0.60
1:G:217:TRP:CD2	1:G:225:VAL:HG22	2.37	0.60
1:A:227:THR:HG22	1:A:227:THR:O	2.02	0.60
1:A:386:TRP:HA	3:A:1302:HOH:O	2.01	0.60
2:B:37:GLU:HG2	2:B:46:ILE:HG13	1.82	0.60
1:C:217:TRP:CD2	1:C:225:VAL:HG22	2.37	0.60
1:G:314:ASP:OD2	1:G:376:TRP:CH2	2.55	0.60
1:G:330:LEU:O	1:G:371:LEU:HD21	2.02	0.60
2:H:52:HIS:HA	3:H:328:HOH:O	2.01	0.60
2:H:189:SER:C	2:H:191:ALA:H	2.09	0.60
1:A:32:VAL:CG1	1:C:194:LYS:O	2.50	0.60
1:C:330:LEU:O	1:C:371:LEU:HD21	2.02	0.60
1:E:71:SER:O	1:E:73:ASN:N	2.34	0.60
1:E:217:TRP:CD2	1:E:225:VAL:HG22	2.37	0.60
1:E:396:THR:HG23	3:E:1312:HOH:O	2.01	0.60
2:F:200:LEU:HB3	2:F:234:TRP:CZ3	2.36	0.60
2:H:157:THR:HG22	2:H:157:THR:O	2.00	0.60
1:A:78:ALA:HB1	1:A:114:VAL:HG11	1.84	0.59
2:B:4:ILE:HG13	2:B:43:HIS:ND1	2.16	0.59
1:E:314:ASP:OD2	1:E:376:TRP:CH2	2.55	0.59
2:F:29:SER:HA	2:F:55:PRO:HB3	1.84	0.59
1:E:330:LEU:O	1:E:371:LEU:HD21	2.02	0.59
2:F:30:ASP:OD1	2:F:32:THR:N	2.34	0.59
1:C:272:LEU:HD22	1:C:284:LEU:HD11	1.83	0.59
2:D:120:SER:HB3	2:D:122:ASP:OD1	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:180:ASN:HD22	2:F:180:ASN:N	2.00	0.59
1:G:71:SER:O	1:G:73:ASN:N	2.34	0.59
2:B:180:ASN:HD22	2:B:180:ASN:N	2.00	0.59
1:C:202:THR:O	1:C:202:THR:HG22	2.01	0.59
1:E:268:GLN:CA	1:E:373:ALA:HB1	2.27	0.59
1:E:272:LEU:HD22	1:E:284:LEU:HD11	1.83	0.59
2:F:52:HIS:HA	3:F:328:HOH:O	2.01	0.59
2:F:120:SER:HB3	2:F:122:ASP:OD1	2.03	0.59
1:G:15:TRP:HB3	1:G:310:PRO:HD3	1.85	0.59
1:G:272:LEU:HD22	1:G:284:LEU:HD11	1.83	0.59
2:H:216:VAL:O	2:H:216:VAL:HG12	2.03	0.59
1:E:40:SER:OG	1:E:61:VAL:HG23	2.02	0.59
1:E:92:ASN:O	1:E:93:GLU:HB2	2.02	0.59
1:E:386:TRP:HA	3:E:1302:HOH:O	2.01	0.59
1:G:386:TRP:HA	3:G:1302:HOH:O	2.01	0.59
2:H:102:VAL:HG23	3:H:304:HOH:O	2.00	0.59
1:A:15:TRP:HB3	1:A:310:PRO:HD3	1.85	0.59
1:A:71:SER:O	1:A:73:ASN:N	2.34	0.59
1:A:202:THR:O	1:A:202:THR:HG22	2.01	0.59
2:B:52:HIS:HA	3:B:328:HOH:O	2.01	0.59
1:C:227:THR:HG22	1:C:227:THR:O	2.02	0.59
1:C:306:THR:HA	1:C:317:ALA:O	2.03	0.59
1:E:306:THR:HA	1:E:317:ALA:O	2.03	0.59
1:G:315:LEU:HD11	2:H:146:ILE:CD1	2.33	0.59
2:H:4:ILE:HG13	2:H:43:HIS:ND1	2.16	0.59
2:H:12:ILE:HA	2:H:28:SER:CB	2.30	0.59
2:B:29:SER:HA	2:B:55:PRO:HB3	1.84	0.59
1:G:84:GLY:HA3	1:G:110:SER:H	1.68	0.59
1:G:129:ASN:HA	1:G:162:GLU:HB3	1.84	0.59
1:A:88:LEU:HD13	1:A:138:MET:SD	2.43	0.59
1:A:146:SER:O	1:A:147:ASN:HB2	2.02	0.59
1:A:228:ALA:HB2	1:A:263:LEU:HD11	1.85	0.59
1:A:314:ASP:CG	1:A:376:TRP:CD1	2.81	0.59
1:A:370:HIS:CG	1:A:371:LEU:N	2.68	0.59
2:B:120:SER:HB3	2:B:122:ASP:OD1	2.03	0.59
1:C:321:PHE:HB3	1:E:246:ASN:ND2	2.07	0.59
1:G:88:LEU:HD13	1:G:138:MET:SD	2.43	0.59
1:G:314:ASP:CG	1:G:376:TRP:CD1	2.81	0.59
2:H:19:TYR:CD2	2:H:64:PRO:HG2	2.38	0.59
1:C:146:SER:O	1:C:147:ASN:HB2	2.02	0.59
1:C:314:ASP:OD2	1:C:376:TRP:CH2	2.55	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:370:HIS:CE1	2:F:75:TYR:CD2	2.90	0.59
1:G:75:LYS:HZ1	1:G:94:ALA:HB2	1.68	0.59
1:G:146:SER:O	1:G:147:ASN:HB2	2.02	0.59
1:A:129:ASN:C	1:A:131:GLY:H	2.11	0.59
1:A:187:ILE:HG22	1:A:196:VAL:HG22	1.84	0.59
2:B:216:VAL:O	2:B:216:VAL:HG12	2.03	0.59
2:B:225:VAL:HG13	2:B:257:LEU:HB2	1.84	0.59
1:C:40:SER:OG	1:C:61:VAL:HG23	2.02	0.59
1:C:106:ASN:N	1:C:106:ASN:ND2	2.42	0.59
2:F:19:TYR:CD2	2:F:64:PRO:HG2	2.38	0.59
1:G:40:SER:OG	1:G:61:VAL:HG23	2.02	0.59
1:G:112:LYS:HG3	1:G:164:ILE:HG22	1.85	0.59
1:A:32:VAL:CG1	1:C:194:LYS:C	2.65	0.58
1:A:112:LYS:HG3	1:A:164:ILE:HG22	1.85	0.58
1:A:243:ARG:NE	1:G:34:ALA:CB	2.54	0.58
1:C:112:LYS:HG3	1:C:164:ILE:HG22	1.85	0.58
2:D:180:ASN:HD22	2:D:180:ASN:N	2.00	0.58
1:E:84:GLY:HA3	1:E:110:SER:H	1.68	0.58
1:E:175:VAL:HG12	1:E:176:PHE:N	2.18	0.58
2:F:83:LYS:HB2	2:F:92:ILE:HD13	1.85	0.58
1:A:92:ASN:O	1:A:93:GLU:HB2	2.02	0.58
1:A:314:ASP:OD2	1:A:376:TRP:CH2	2.55	0.58
1:A:370:HIS:CE1	2:B:75:TYR:CD2	2.90	0.58
1:E:15:TRP:HB3	1:E:310:PRO:HD3	1.85	0.58
1:E:228:ALA:HB2	1:E:263:LEU:HD11	1.85	0.58
1:G:396:THR:HG23	3:G:1310:HOH:O	2.02	0.58
2:H:225:VAL:HG13	2:H:257:LEU:HB2	1.84	0.58
1:A:268:GLN:HG3	1:A:313:PRO:CG	2.34	0.58
1:A:268:GLN:CD	3:A:1309:HOH:O	2.36	0.58
2:B:83:LYS:HB2	2:B:92:ILE:HD13	1.85	0.58
1:C:78:ALA:HB1	1:C:114:VAL:HG11	1.84	0.58
1:C:228:ALA:HB2	1:C:263:LEU:HD11	1.85	0.58
1:C:314:ASP:CG	1:C:376:TRP:CD1	2.81	0.58
1:C:386:TRP:HA	3:C:1302:HOH:O	2.01	0.58
1:E:112:LYS:HG3	1:E:164:ILE:HG22	1.85	0.58
1:G:289:SER:O	1:G:290:ALA:HB2	2.03	0.58
2:H:29:SER:HA	2:H:55:PRO:HB3	1.84	0.58
1:A:40:SER:OG	1:A:61:VAL:HG23	2.02	0.58
1:A:129:ASN:HA	1:A:162:GLU:HB3	1.84	0.58
1:C:15:TRP:HB3	1:C:310:PRO:HD3	1.85	0.58
2:D:83:LYS:HB2	2:D:92:ILE:HD13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:146:SER:O	1:E:147:ASN:HB2	2.02	0.58
1:G:227:THR:O	1:G:227:THR:HG22	2.02	0.58
1:G:228:ALA:HB2	1:G:263:LEU:HD11	1.85	0.58
1:G:306:THR:HA	1:G:317:ALA:O	2.03	0.58
1:A:289:SER:O	1:A:290:ALA:HB2	2.03	0.58
1:C:289:SER:O	1:C:290:ALA:HB2	2.03	0.58
2:D:19:TYR:CD2	2:D:64:PRO:HG2	2.38	0.58
1:E:227:THR:O	1:E:227:THR:HG22	2.02	0.58
1:E:289:SER:O	1:E:290:ALA:HB2	2.03	0.58
1:C:129:ASN:C	1:C:131:GLY:H	2.11	0.58
1:C:175:VAL:HG12	1:C:176:PHE:N	2.18	0.58
2:D:216:VAL:O	2:D:216:VAL:HG12	2.03	0.58
1:E:33:ASP:C	1:G:196:VAL:CB	2.58	0.58
1:E:228:ALA:HB1	1:E:260:ILE:HG21	1.85	0.58
1:A:283:LEU:HD22	1:A:292:GLN:HE21	1.69	0.58
1:A:396:THR:HG23	3:A:1312:HOH:O	2.02	0.58
2:B:19:TYR:CD2	2:B:64:PRO:HG2	2.38	0.58
1:E:129:ASN:HA	1:E:162:GLU:HB3	1.84	0.58
1:E:314:ASP:CG	1:E:376:TRP:CD1	2.81	0.58
1:E:329:THR:HB	1:E:331:GLN:O	2.04	0.58
2:F:222:LEU:HB2	2:F:234:TRP:HB2	1.85	0.58
1:G:370:HIS:CE1	2:H:75:TYR:CD2	2.91	0.58
2:H:222:LEU:HB2	2:H:234:TRP:HB2	1.85	0.58
1:C:370:HIS:CE1	2:D:75:TYR:CD2	2.90	0.58
1:E:306:THR:O	1:E:307:LYS:HD3	2.04	0.58
1:E:314:ASP:N	1:E:376:TRP:CE2	2.72	0.58
1:G:314:ASP:N	1:G:376:TRP:CE2	2.72	0.58
2:H:83:LYS:HB2	2:H:92:ILE:HD13	1.85	0.58
2:H:120:SER:HB3	2:H:122:ASP:OD1	2.03	0.58
1:C:88:LEU:HD13	1:C:138:MET:SD	2.43	0.58
1:C:315:LEU:HD11	2:D:146:ILE:CD1	2.33	0.58
1:E:32:VAL:O	1:G:196:VAL:CA	2.50	0.58
1:G:92:ASN:O	1:G:93:GLU:HB2	2.02	0.58
1:G:268:GLN:HB2	1:G:374:PRO:O	1.98	0.58
1:G:329:THR:HB	1:G:331:GLN:O	2.04	0.58
2:H:257:LEU:CD1	2:H:271:LEU:HD21	2.30	0.58
1:A:306:THR:HA	1:A:317:ALA:O	2.03	0.58
1:C:11:ALA:HB1	1:C:26:GLY:O	2.04	0.58
2:D:108:ALA:HB1	2:D:109:PRO:CD	2.34	0.58
1:E:88:LEU:HD13	1:E:138:MET:SD	2.43	0.58
2:H:108:ALA:HB1	2:H:109:PRO:CD	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:ALA:HB1	1:A:260:ILE:HG21	1.85	0.57
1:A:314:ASP:N	1:A:376:TRP:CE2	2.72	0.57
1:A:314:ASP:N	1:A:376:TRP:CZ2	2.72	0.57
2:B:24:LEU:HG	2:B:25:ALA:N	2.19	0.57
1:C:129:ASN:HA	1:C:162:GLU:HB3	1.84	0.57
2:D:222:LEU:HB2	2:D:234:TRP:HB2	1.85	0.57
1:G:72:HIS:ND1	1:G:118:ALA:HA	2.19	0.57
1:C:283:LEU:HD22	1:C:292:GLN:HE21	1.69	0.57
1:C:365:LYS:HD2	1:C:365:LYS:O	2.04	0.57
2:F:216:VAL:O	2:F:216:VAL:HG12	2.03	0.57
1:G:11:ALA:HB1	1:G:26:GLY:O	2.04	0.57
1:C:84:GLY:HA3	1:C:110:SER:H	1.68	0.57
1:E:11:ALA:HB1	1:E:26:GLY:O	2.04	0.57
1:E:72:HIS:ND1	1:E:118:ALA:HA	2.19	0.57
1:E:221:ASN:ND2	1:E:223:THR:H	2.03	0.57
1:G:306:THR:O	1:G:307:LYS:HD3	2.04	0.57
1:G:365:LYS:O	1:G:365:LYS:HD2	2.04	0.57
1:A:44:LEU:HD23	1:A:56:ILE:HB	1.87	0.57
1:C:116:PHE:CE1	1:C:138:MET:HE3	2.39	0.57
1:C:228:ALA:HB1	1:C:260:ILE:HG21	1.85	0.57
1:C:306:THR:O	1:C:307:LYS:HD3	2.04	0.57
1:E:129:ASN:C	1:E:131:GLY:H	2.11	0.57
2:H:24:LEU:HG	2:H:25:ALA:N	2.20	0.57
2:H:180:ASN:N	2:H:180:ASN:HD22	2.00	0.57
1:A:145:PRO:O	1:A:146:SER:C	2.48	0.57
1:C:129:ASN:ND2	1:C:162:GLU:OE1	2.38	0.57
1:E:129:ASN:ND2	1:E:162:GLU:OE1	2.38	0.57
1:G:44:LEU:HD23	1:G:56:ILE:HB	1.87	0.57
1:G:129:ASN:C	1:G:131:GLY:H	2.11	0.57
1:A:11:ALA:HB1	1:A:26:GLY:O	2.04	0.57
1:A:74:ASN:N	1:A:74:ASN:ND2	2.50	0.57
1:A:84:GLY:HA3	1:A:110:SER:H	1.68	0.57
1:A:306:THR:O	1:A:307:LYS:HD3	2.04	0.57
2:B:108:ALA:HB1	2:B:109:PRO:CD	2.34	0.57
2:B:222:LEU:HB2	2:B:234:TRP:HB2	1.85	0.57
1:C:113:THR:HG22	1:C:114:VAL:N	2.20	0.57
1:C:262:SER:HB2	1:C:304:PHE:O	2.05	0.57
1:C:314:ASP:N	1:C:376:TRP:CE2	2.72	0.57
1:E:71:SER:HA	1:E:116:PHE:CG	2.40	0.57
1:E:113:THR:HG22	1:E:114:VAL:N	2.20	0.57
2:F:108:ALA:HB1	2:F:109:PRO:CD	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:221:ASN:ND2	1:G:223:THR:H	2.03	0.57
1:C:44:LEU:HD23	1:C:56:ILE:HB	1.87	0.57
1:C:72:HIS:ND1	1:C:118:ALA:HA	2.19	0.57
1:C:292:GLN:O	1:C:368:VAL:CG2	2.53	0.57
1:E:32:VAL:O	1:G:196:VAL:CB	2.53	0.57
1:E:35:ASN:CB	1:G:174:HIS:HE1	1.93	0.57
1:E:262:SER:HB2	1:E:304:PHE:O	2.05	0.57
2:F:24:LEU:HG	2:F:25:ALA:N	2.20	0.57
1:G:228:ALA:HB1	1:G:260:ILE:HG21	1.85	0.57
1:A:113:THR:HG22	1:A:114:VAL:N	2.20	0.57
1:A:175:VAL:HG12	1:A:176:PHE:N	2.18	0.57
1:C:241:ASP:O	1:C:243:ARG:N	2.38	0.57
2:D:4:ILE:HG13	2:D:43:HIS:CG	2.39	0.57
2:D:24:LEU:HG	2:D:25:ALA:N	2.20	0.57
1:A:172:LEU:C	1:A:174:HIS:H	2.13	0.57
1:A:241:ASP:O	1:A:243:ARG:N	2.38	0.57
1:A:329:THR:HB	1:A:331:GLN:O	2.04	0.57
2:B:4:ILE:HG13	2:B:43:HIS:CG	2.40	0.57
1:C:221:ASN:ND2	1:C:223:THR:H	2.03	0.57
1:E:74:ASN:N	1:E:74:ASN:ND2	2.50	0.57
1:E:116:PHE:CE1	1:E:138:MET:HE3	2.39	0.57
1:E:241:ASP:O	1:E:243:ARG:N	2.38	0.57
1:E:315:LEU:HD11	2:F:146:ILE:CD1	2.33	0.57
1:G:241:ASP:O	1:G:243:ARG:N	2.38	0.57
1:G:283:LEU:HD22	1:G:292:GLN:HE21	1.69	0.57
1:A:221:ASN:ND2	1:A:223:THR:H	2.03	0.57
1:E:153:PRO:HB2	1:E:188:TRP:CE3	2.40	0.57
2:F:4:ILE:HG13	2:F:43:HIS:CG	2.40	0.57
1:G:71:SER:HA	1:G:116:PHE:CG	2.40	0.57
1:G:116:PHE:CE1	1:G:138:MET:HE3	2.39	0.57
1:C:71:SER:HA	1:C:116:PHE:CG	2.40	0.56
1:C:74:ASN:N	1:C:74:ASN:ND2	2.50	0.56
2:D:4:ILE:HD12	2:D:4:ILE:N	2.20	0.56
1:G:17:HIS:HB2	1:G:73:ASN:HB2	1.87	0.56
1:G:129:ASN:ND2	1:G:162:GLU:OE1	2.38	0.56
2:H:255:ASP:CG	2:H:256:VAL:H	2.14	0.56
1:A:71:SER:HA	1:A:116:PHE:CG	2.40	0.56
1:A:365:LYS:HD2	1:A:365:LYS:O	2.04	0.56
1:E:44:LEU:HD23	1:E:56:ILE:HB	1.87	0.56
1:E:145:PRO:O	1:E:147:ASN:N	2.38	0.56
1:G:21:PRO:HB2	1:G:47:LEU:HD11	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:262:SER:HB2	1:G:304:PHE:O	2.05	0.56
2:H:4:ILE:HD12	2:H:4:ILE:N	2.20	0.56
2:H:4:ILE:HG13	2:H:43:HIS:CG	2.40	0.56
1:A:17:HIS:HB2	1:A:73:ASN:HB2	1.87	0.56
1:A:21:PRO:HB2	1:A:47:LEU:HD11	1.86	0.56
1:A:106:ASN:N	1:A:106:ASN:ND2	2.42	0.56
1:A:116:PHE:CE1	1:A:138:MET:HE3	2.39	0.56
1:A:129:ASN:ND2	1:A:162:GLU:OE1	2.38	0.56
1:A:145:PRO:O	1:A:147:ASN:N	2.39	0.56
2:B:4:ILE:HD12	2:B:4:ILE:N	2.20	0.56
2:B:66:PHE:CE1	2:B:114:PRO:HD3	2.41	0.56
1:C:145:PRO:O	1:C:147:ASN:N	2.38	0.56
2:D:255:ASP:CG	2:D:256:VAL:H	2.13	0.56
1:E:17:HIS:HB2	1:E:73:ASN:HB2	1.87	0.56
1:E:21:PRO:HB2	1:E:47:LEU:HD11	1.86	0.56
1:E:33:ASP:C	1:G:196:VAL:HG12	1.96	0.56
1:E:365:LYS:HD2	1:E:365:LYS:O	2.04	0.56
1:G:155:GLN:CB	1:G:195:GLU:HB3	2.35	0.56
1:G:175:VAL:HG12	1:G:176:PHE:N	2.18	0.56
1:G:292:GLN:O	1:G:368:VAL:CG2	2.53	0.56
1:G:365:LYS:NZ	1:G:371:LEU:HD22	2.21	0.56
2:H:56:VAL:HA	2:H:74:SER:HB2	1.87	0.56
1:A:72:HIS:ND1	1:A:118:ALA:HA	2.19	0.56
1:C:329:THR:HB	1:C:331:GLN:O	2.04	0.56
1:E:155:GLN:CB	1:E:195:GLU:HB3	2.35	0.56
1:G:244:ASN:ND2	1:G:246:ASN:ND2	2.47	0.56
1:G:314:ASP:N	1:G:376:TRP:CZ2	2.72	0.56
1:A:197:ILE:CD1	1:G:32:VAL:CG2	2.78	0.56
1:A:262:SER:HB2	1:A:304:PHE:O	2.05	0.56
1:C:280:ASN:HB3	1:C:300:GLY:O	2.06	0.56
2:D:8:HIS:ND1	2:D:30:ASP:OD2	2.39	0.56
1:E:283:LEU:HD22	1:E:292:GLN:HE21	1.69	0.56
2:F:8:HIS:ND1	2:F:30:ASP:OD2	2.39	0.56
2:F:66:PHE:CE1	2:F:114:PRO:HD3	2.41	0.56
1:G:87:GLU:HG2	1:G:89:TYR:CE1	2.41	0.56
1:G:113:THR:HG22	1:G:114:VAL:N	2.20	0.56
2:B:255:ASP:CG	2:B:256:VAL:H	2.14	0.56
1:C:21:PRO:HB2	1:C:47:LEU:HD11	1.86	0.56
1:C:145:PRO:O	1:C:146:SER:C	2.48	0.56
1:C:172:LEU:C	1:C:174:HIS:H	2.13	0.56
1:E:145:PRO:O	1:E:146:SER:C	2.48	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:PRO:HB2	1:A:188:TRP:CE3	2.41	0.56
1:C:17:HIS:HB2	1:C:73:ASN:HB2	1.87	0.56
1:C:74:ASN:H	1:C:74:ASN:ND2	2.02	0.56
1:C:74:ASN:O	1:C:76:ILE:HG12	2.06	0.56
1:C:120:GLN:HG3	1:C:122:ASN:OD1	2.06	0.56
1:C:153:PRO:HB2	1:C:188:TRP:CE3	2.41	0.56
1:G:12:THR:HG23	1:G:12:THR:O	2.06	0.56
1:G:73:ASN:C	1:G:75:LYS:N	2.59	0.56
1:G:120:GLN:HG3	1:G:122:ASN:OD1	2.06	0.56
1:G:125:ALA:HB2	1:G:168:TRP:HH2	1.62	0.56
1:A:365:LYS:NZ	1:A:371:LEU:HD22	2.21	0.56
1:C:155:GLN:CB	1:C:195:GLU:HB3	2.35	0.56
1:E:42:LEU:HD21	1:E:89:TYR:CD2	2.41	0.56
2:F:4:ILE:HD12	2:F:4:ILE:N	2.20	0.56
1:G:145:PRO:O	1:G:147:ASN:N	2.39	0.56
1:G:333:LEU:CD2	3:G:1301:HOH:O	2.13	0.56
1:A:74:ASN:O	1:A:76:ILE:HG12	2.06	0.56
1:A:312:ALA:CB	1:A:315:LEU:HD12	2.36	0.56
1:E:244:ASN:HD21	1:E:246:ASN:HD22	1.49	0.56
1:G:153:PRO:HB2	1:G:188:TRP:CE3	2.40	0.56
1:G:178:SER:HB2	1:G:186:SER:HB2	1.88	0.56
1:G:244:ASN:HD21	1:G:246:ASN:HD22	1.49	0.56
1:G:260:ILE:CG2	1:G:261:LEU:N	2.69	0.56
2:H:180:ASN:N	2:H:180:ASN:ND2	2.53	0.56
1:A:80:ALA:HB2	1:A:114:VAL:CG2	2.36	0.56
1:C:365:LYS:NZ	1:C:371:LEU:HD22	2.21	0.56
1:E:33:ASP:C	1:G:196:VAL:HB	2.27	0.56
1:E:87:GLU:HG2	1:E:89:TYR:CE1	2.41	0.56
1:E:337:LEU:CD2	2:F:97:VAL:HG12	2.36	0.56
1:E:365:LYS:NZ	1:E:371:LEU:HD22	2.21	0.56
1:G:280:ASN:HB3	1:G:300:GLY:O	2.06	0.56
1:A:12:THR:O	1:A:12:THR:HG23	2.06	0.55
1:A:42:LEU:HD21	1:A:89:TYR:CD2	2.41	0.55
1:A:120:GLN:HG3	1:A:122:ASN:OD1	2.06	0.55
1:A:203:SER:N	1:A:204:PRO:CD	2.69	0.55
1:A:268:GLN:CA	1:A:373:ALA:HB1	2.27	0.55
2:B:8:HIS:ND1	2:B:30:ASP:OD2	2.39	0.55
2:B:180:ASN:N	2:B:180:ASN:ND2	2.53	0.55
1:C:162:GLU:O	1:C:164:ILE:HG23	2.06	0.55
1:C:203:SER:N	1:C:204:PRO:CD	2.69	0.55
1:E:12:THR:HG23	1:E:12:THR:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:280:ASN:HB3	1:E:300:GLY:O	2.06	0.55
1:A:155:GLN:CB	1:A:195:GLU:HB3	2.35	0.55
1:A:260:ILE:CG2	1:A:261:LEU:N	2.69	0.55
1:C:32:VAL:HG21	1:E:197:ILE:CD1	2.35	0.55
1:C:42:LEU:HD21	1:C:89:TYR:CD2	2.41	0.55
1:C:312:ALA:CB	1:C:315:LEU:HD12	2.36	0.55
1:E:203:SER:N	1:E:204:PRO:CD	2.69	0.55
1:E:312:ALA:CB	1:E:315:LEU:HD12	2.36	0.55
2:F:56:VAL:HA	2:F:74:SER:HB2	1.87	0.55
2:F:69:ILE:HD12	2:F:69:ILE:N	2.22	0.55
1:G:145:PRO:O	1:G:146:SER:C	2.48	0.55
1:G:162:GLU:O	1:G:164:ILE:HG23	2.06	0.55
1:G:203:SER:N	1:G:204:PRO:CD	2.69	0.55
1:G:314:ASP:CG	1:G:376:TRP:CG	2.84	0.55
1:G:337:LEU:CD2	2:H:97:VAL:HG12	2.36	0.55
2:H:66:PHE:CE1	2:H:114:PRO:HD3	2.41	0.55
1:A:314:ASP:CG	1:A:376:TRP:CG	2.84	0.55
1:C:178:SER:HB2	1:C:186:SER:HB2	1.88	0.55
1:C:268:GLN:HG3	1:C:313:PRO:CG	2.34	0.55
1:C:337:LEU:CD2	2:D:97:VAL:HG12	2.36	0.55
2:D:56:VAL:HA	2:D:74:SER:HB2	1.87	0.55
1:E:36:PHE:N	1:G:189:ASP:HB3	2.21	0.55
1:E:260:ILE:CG2	1:E:261:LEU:N	2.69	0.55
1:E:268:GLN:HG3	1:E:313:PRO:CG	2.34	0.55
1:G:74:ASN:O	1:G:76:ILE:HG12	2.06	0.55
2:F:255:ASP:CG	2:F:256:VAL:H	2.14	0.55
1:G:312:ALA:CB	1:G:315:LEU:HD12	2.36	0.55
1:A:162:GLU:O	1:A:164:ILE:HG23	2.06	0.55
1:A:280:ASN:HB3	1:A:300:GLY:O	2.06	0.55
1:C:12:THR:HG23	1:C:12:THR:O	2.06	0.55
1:C:75:LYS:HZ1	1:C:94:ALA:HB2	1.72	0.55
1:C:87:GLU:HG2	1:C:89:TYR:CE1	2.41	0.55
1:E:314:ASP:CG	1:E:376:TRP:CG	2.84	0.55
1:E:33:ASP:HB2	1:G:192:ALA:HB1	1.87	0.55
1:E:38:THR:O	1:E:64:LYS:HE2	2.07	0.55
1:E:80:ALA:CB	1:E:111:VAL:HG12	2.37	0.55
2:H:8:HIS:ND1	2:H:30:ASP:OD2	2.39	0.55
1:A:104:PHE:CD1	1:A:104:PHE:N	2.75	0.55
1:A:315:LEU:HD11	2:B:146:ILE:CD1	2.33	0.55
1:C:38:THR:O	1:C:64:LYS:HE2	2.07	0.55
1:C:241:ASP:C	1:C:243:ARG:N	2.64	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:314:ASP:CG	1:C:376:TRP:CG	2.84	0.55
1:E:74:ASN:O	1:E:76:ILE:HG12	2.06	0.55
1:E:75:LYS:HZ1	1:E:94:ALA:HB2	1.71	0.55
1:E:104:PHE:N	1:E:104:PHE:CD1	2.75	0.55
1:E:120:GLN:HG3	1:E:122:ASN:OD1	2.06	0.55
1:E:199:LEU:HD13	1:E:240:TRP:CG	2.42	0.55
1:G:42:LEU:HD21	1:G:89:TYR:CD2	2.41	0.55
1:A:41:SER:O	1:A:42:LEU:HB3	2.07	0.55
1:A:106:ASN:H	1:A:106:ASN:ND2	2.05	0.55
2:B:73:CYS:HB2	2:B:102:VAL:CG1	2.37	0.55
1:C:247:THR:CG2	1:C:248:PRO:HD2	2.37	0.55
2:D:69:ILE:HD12	2:D:69:ILE:N	2.21	0.55
1:E:162:GLU:O	1:E:164:ILE:HG23	2.06	0.55
1:E:241:ASP:C	1:E:243:ARG:N	2.65	0.55
1:G:199:LEU:HD13	1:G:240:TRP:CG	2.42	0.55
1:A:32:VAL:O	1:C:196:VAL:CA	2.54	0.55
1:C:196:VAL:C	1:C:197:ILE:HG13	2.32	0.55
2:D:66:PHE:CE1	2:D:114:PRO:HD3	2.41	0.55
1:E:247:THR:CG2	1:E:248:PRO:HD2	2.37	0.55
1:G:59:LEU:HD22	1:G:98:ILE:HG12	1.89	0.55
1:G:247:THR:CG2	1:G:248:PRO:HD2	2.37	0.55
1:A:196:VAL:C	1:A:197:ILE:HG13	2.32	0.55
1:C:26:GLY:HA2	1:C:42:LEU:HA	1.89	0.55
2:B:56:VAL:HA	2:B:74:SER:HB2	1.87	0.54
1:C:80:ALA:CB	1:C:111:VAL:HG12	2.37	0.54
1:C:260:ILE:CG2	1:C:261:LEU:N	2.69	0.54
1:E:172:LEU:C	1:E:174:HIS:H	2.13	0.54
1:G:48:LEU:O	1:G:49:ALA:O	2.25	0.54
1:A:87:GLU:HG2	1:A:89:TYR:CE1	2.41	0.54
1:C:106:ASN:H	1:C:106:ASN:ND2	2.04	0.54
2:D:180:ASN:N	2:D:180:ASN:ND2	2.53	0.54
1:E:26:GLY:HA2	1:E:42:LEU:HA	1.89	0.54
1:G:26:GLY:HA2	1:G:42:LEU:HA	1.89	0.54
1:G:66:ASN:N	1:G:80:ALA:O	2.39	0.54
2:B:45:LEU:O	2:B:46:ILE:HD13	2.08	0.54
2:D:73:CYS:HB2	2:D:102:VAL:CG1	2.37	0.54
1:E:59:LEU:HD22	1:E:98:ILE:HG12	1.89	0.54
1:E:196:VAL:C	1:E:197:ILE:HG13	2.32	0.54
1:G:268:GLN:CA	1:G:373:ALA:HB1	2.27	0.54
2:H:69:ILE:HD12	2:H:69:ILE:N	2.22	0.54
1:A:337:LEU:CD2	2:B:97:VAL:HG12	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:LEU:HD23	2:B:94:VAL:HG23	1.90	0.54
1:C:80:ALA:HB2	1:C:114:VAL:CG2	2.36	0.54
1:E:106:ASN:ND2	1:E:106:ASN:H	2.04	0.54
1:E:304:PHE:HD1	1:E:304:PHE:N	1.87	0.54
2:H:80:LEU:CD2	2:H:94:VAL:HG23	2.38	0.54
1:A:35:ASN:CB	1:C:174:HIS:HE1	1.97	0.54
1:A:178:SER:HB2	1:A:186:SER:HB2	1.89	0.54
1:C:244:ASN:HD21	1:C:246:ASN:HD22	1.49	0.54
1:E:41:SER:O	1:E:42:LEU:HB3	2.07	0.54
2:F:73:CYS:HB2	2:F:102:VAL:CG1	2.37	0.54
2:F:80:LEU:HD23	2:F:94:VAL:HG23	1.90	0.54
1:G:38:THR:O	1:G:64:LYS:HE2	2.07	0.54
1:A:73:ASN:C	1:A:75:LYS:N	2.58	0.54
1:A:74:ASN:ND2	1:A:74:ASN:H	2.02	0.54
1:C:59:LEU:HD22	1:C:98:ILE:HG12	1.89	0.54
1:E:178:SER:HB2	1:E:186:SER:HB2	1.89	0.54
1:G:41:SER:O	1:G:42:LEU:HB3	2.07	0.54
1:G:80:ALA:CB	1:G:111:VAL:HG12	2.37	0.54
1:C:46:SER:HB2	1:C:56:ILE:HD11	1.89	0.54
1:C:199:LEU:HD13	1:C:240:TRP:CG	2.42	0.54
1:A:32:VAL:O	1:C:196:VAL:CB	2.56	0.54
1:C:19:LYS:C	1:C:21:PRO:HD3	2.33	0.54
1:G:241:ASP:C	1:G:243:ARG:N	2.65	0.54
1:A:75:LYS:HZ1	1:A:94:ALA:HB2	1.72	0.54
1:A:199:LEU:HD13	1:A:240:TRP:CG	2.42	0.54
1:A:241:ASP:C	1:A:243:ARG:N	2.64	0.54
2:B:39:GLU:HB2	3:B:305:HOH:O	2.08	0.54
2:B:69:ILE:HD12	2:B:69:ILE:N	2.22	0.54
1:G:304:PHE:HD1	1:G:304:PHE:N	1.87	0.54
1:A:38:THR:O	1:A:64:LYS:HE2	2.07	0.54
1:A:48:LEU:O	1:A:49:ALA:O	2.25	0.54
2:F:45:LEU:O	2:F:46:ILE:HD13	2.08	0.54
1:A:59:LEU:HD22	1:A:98:ILE:HG12	1.89	0.53
1:A:247:THR:CG2	1:A:248:PRO:HD2	2.37	0.53
2:H:73:CYS:HB2	2:H:102:VAL:CG1	2.37	0.53
1:A:19:LYS:C	1:A:21:PRO:HD3	2.33	0.53
1:A:26:GLY:HA2	1:A:42:LEU:HA	1.89	0.53
1:A:175:VAL:HG13	1:A:188:TRP:O	2.08	0.53
1:E:48:LEU:O	1:E:49:ALA:O	2.25	0.53
1:E:80:ALA:HB2	1:E:114:VAL:CG2	2.36	0.53
1:E:314:ASP:N	1:E:376:TRP:CZ2	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:19:LYS:C	1:G:21:PRO:HD3	2.33	0.53
1:G:46:SER:HB2	1:G:56:ILE:HD11	1.89	0.53
1:G:172:LEU:C	1:G:174:HIS:H	2.13	0.53
1:G:259:GLY:HA3	1:G:278:ARG:HH11	1.74	0.53
1:C:62:ASP:OD1	1:C:62:ASP:N	2.36	0.53
2:H:117:LEU:HD12	3:H:306:HOH:O	2.08	0.53
1:A:7:PHE:O	1:A:324:LYS:HD3	2.08	0.53
1:A:110:SER:OG	1:A:129:ASN:ND2	2.41	0.53
1:A:203:SER:C	1:A:205:ASN:H	2.17	0.53
2:B:25:ALA:HB2	2:B:61:TRP:CZ2	2.44	0.53
2:B:29:SER:C	2:B:31:LYS:H	2.16	0.53
1:C:41:SER:O	1:C:42:LEU:HB3	2.07	0.53
2:D:49:LEU:HB3	2:D:82:TRP:CZ3	2.44	0.53
1:E:19:LYS:C	1:E:21:PRO:HD3	2.33	0.53
2:F:49:LEU:HB3	2:F:82:TRP:CZ3	2.44	0.53
1:G:104:PHE:N	1:G:104:PHE:CD1	2.75	0.53
1:G:110:SER:OG	1:G:129:ASN:ND2	2.41	0.53
1:G:196:VAL:C	1:G:197:ILE:HG13	2.32	0.53
1:A:13:PHE:HA	1:A:24:VAL:O	2.09	0.53
1:C:7:PHE:O	1:C:324:LYS:HD3	2.08	0.53
2:D:25:ALA:HB2	2:D:61:TRP:CZ2	2.44	0.53
2:D:29:SER:C	2:D:31:LYS:H	2.16	0.53
2:D:39:GLU:HB2	3:D:305:HOH:O	2.08	0.53
1:E:7:PHE:O	1:E:324:LYS:HD3	2.08	0.53
1:G:175:VAL:HG13	1:G:188:TRP:O	2.08	0.53
2:H:29:SER:C	2:H:31:LYS:H	2.16	0.53
2:H:39:GLU:HB2	3:H:305:HOH:O	2.08	0.53
2:H:128:VAL:CG2	2:H:138:PRO:HB3	2.27	0.53
1:A:46:SER:HB2	1:A:56:ILE:HD11	1.90	0.53
1:C:48:LEU:O	1:C:49:ALA:O	2.25	0.53
1:C:104:PHE:N	1:C:104:PHE:CD1	2.75	0.53
1:C:110:SER:OG	1:C:129:ASN:ND2	2.41	0.53
1:E:110:SER:OG	1:E:129:ASN:ND2	2.41	0.53
1:E:285:TRP:CZ3	1:E:292:GLN:HG3	2.44	0.53
2:F:29:SER:C	2:F:31:LYS:H	2.16	0.53
1:G:7:PHE:O	1:G:324:LYS:HD3	2.08	0.53
1:G:13:PHE:HA	1:G:24:VAL:O	2.09	0.53
1:A:337:LEU:HD11	2:B:97:VAL:HB	1.91	0.53
1:C:13:PHE:HA	1:C:24:VAL:O	2.09	0.53
1:C:203:SER:C	1:C:205:ASN:H	2.17	0.53
2:D:45:LEU:O	2:D:46:ILE:HD13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:80:LEU:CD2	2:D:94:VAL:HG23	2.38	0.53
1:E:203:SER:C	1:E:205:ASN:H	2.17	0.53
1:E:292:GLN:O	1:E:368:VAL:CG2	2.53	0.53
2:F:25:ALA:HB2	2:F:61:TRP:CZ2	2.44	0.53
1:G:90:SER:O	1:G:91:THR:HB	2.08	0.53
1:G:203:SER:C	1:G:205:ASN:H	2.16	0.53
2:B:80:LEU:CD2	2:B:94:VAL:HG23	2.38	0.53
2:B:117:LEU:HD12	3:B:306:HOH:O	2.08	0.53
1:C:57:ALA:O	1:C:98:ILE:HG22	2.09	0.53
1:C:337:LEU:HD11	2:D:97:VAL:HB	1.91	0.53
1:E:259:GLY:HA3	1:E:278:ARG:HH11	1.74	0.53
1:E:337:LEU:HD11	2:F:97:VAL:HB	1.91	0.53
1:E:364:GLU:O	1:E:365:LYS:CB	2.47	0.53
2:F:180:ASN:N	2:F:180:ASN:ND2	2.53	0.53
1:G:75:LYS:HZ1	1:G:94:ALA:N	1.99	0.53
1:G:285:TRP:CZ3	1:G:292:GLN:HG3	2.44	0.53
2:H:45:LEU:O	2:H:46:ILE:HD13	2.08	0.53
1:A:259:GLY:HA3	1:A:278:ARG:HH11	1.74	0.53
1:E:90:SER:O	1:E:91:THR:HB	2.09	0.53
1:G:57:ALA:O	1:G:98:ILE:HG22	2.09	0.53
1:G:268:GLN:CD	3:G:1307:HOH:O	2.36	0.53
1:A:57:ALA:O	1:A:98:ILE:HG22	2.09	0.53
1:A:199:LEU:HD13	1:A:240:TRP:CD2	2.44	0.53
1:C:285:TRP:CZ3	1:C:292:GLN:HG3	2.44	0.53
1:E:268:GLN:CD	3:E:1309:HOH:O	2.36	0.53
2:F:39:GLU:HB2	3:F:305:HOH:O	2.08	0.53
2:H:25:ALA:HB2	2:H:61:TRP:CZ2	2.44	0.53
2:B:238:ASN:HD22	2:B:240:GLN:N	2.07	0.52
1:C:199:LEU:HD13	1:C:240:TRP:CD2	2.44	0.52
1:C:314:ASP:N	1:C:376:TRP:CZ2	2.72	0.52
2:D:80:LEU:HD23	2:D:94:VAL:HG23	1.90	0.52
1:E:13:PHE:HA	1:E:24:VAL:O	2.09	0.52
2:F:33:ILE:CD1	2:F:56:VAL:HG11	2.39	0.52
2:F:80:LEU:CD2	2:F:94:VAL:HG23	2.38	0.52
1:G:80:ALA:HB2	1:G:114:VAL:CG2	2.36	0.52
1:G:106:ASN:ND2	1:G:106:ASN:H	2.04	0.52
1:G:337:LEU:HD11	2:H:97:VAL:HB	1.91	0.52
1:A:33:ASP:C	1:C:196:VAL:HB	2.33	0.52
1:A:197:ILE:CD1	1:G:32:VAL:HG21	2.38	0.52
1:A:286:ASN:HB2	1:A:293:LEU:HD11	1.92	0.52
1:A:365:LYS:HZ3	1:A:371:LEU:HD22	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:49:LEU:HB3	2:B:82:TRP:CZ3	2.44	0.52
1:E:175:VAL:HG13	1:E:188:TRP:O	2.08	0.52
1:G:199:LEU:HD13	1:G:240:TRP:CD2	2.44	0.52
2:H:33:ILE:CD1	2:H:56:VAL:HG11	2.39	0.52
1:E:46:SER:HB2	1:E:56:ILE:HD11	1.89	0.52
1:G:286:ASN:HB2	1:G:293:LEU:HD11	1.92	0.52
2:H:33:ILE:HB	2:H:49:LEU:HB2	1.92	0.52
1:A:27:THR:HB	1:A:40:SER:CB	2.40	0.52
1:C:175:VAL:HG13	1:C:188:TRP:O	2.08	0.52
1:C:286:ASN:HB2	1:C:293:LEU:HD11	1.92	0.52
1:A:90:SER:O	1:A:91:THR:HB	2.08	0.52
1:A:252:LEU:HD13	1:A:285:TRP:CG	2.45	0.52
2:D:33:ILE:CD1	2:D:56:VAL:HG11	2.39	0.52
1:E:137:ASP:OD1	1:E:139:ASN:HB2	2.10	0.52
1:E:268:GLN:HB2	1:E:374:PRO:O	1.98	0.52
2:F:117:LEU:HD12	3:F:306:HOH:O	2.08	0.52
1:G:312:ALA:HB1	1:G:315:LEU:HD12	1.92	0.52
1:A:80:ALA:CB	1:A:111:VAL:HG12	2.37	0.52
1:A:261:LEU:HB2	1:A:277:GLY:HA2	1.92	0.52
2:B:33:ILE:CD1	2:B:56:VAL:HG11	2.39	0.52
2:B:69:ILE:HG22	2:B:70:LEU:N	2.25	0.52
1:C:90:SER:O	1:C:91:THR:HB	2.09	0.52
1:C:137:ASP:OD1	1:C:139:ASN:HB2	2.10	0.52
2:D:69:ILE:HG22	2:D:70:LEU:N	2.25	0.52
2:F:69:ILE:HG22	2:F:70:LEU:N	2.25	0.52
1:G:137:ASP:OD1	1:G:139:ASN:HB2	2.10	0.52
1:G:252:LEU:HD13	1:G:285:TRP:CG	2.45	0.52
2:H:80:LEU:HD23	2:H:94:VAL:HG23	1.90	0.52
1:C:154:GLY:O	1:C:155:GLN:CG	2.48	0.52
1:C:259:GLY:HA3	1:C:278:ARG:HH11	1.73	0.52
1:C:312:ALA:HB1	1:C:315:LEU:HD12	1.92	0.52
2:D:117:LEU:HD12	3:D:306:HOH:O	2.08	0.52
1:A:285:TRP:CZ3	1:A:292:GLN:HG3	2.44	0.52
1:A:292:GLN:O	1:A:368:VAL:CG2	2.53	0.52
1:C:27:THR:HB	1:C:40:SER:CB	2.40	0.52
1:E:312:ALA:HB1	1:E:315:LEU:HD12	1.92	0.52
1:G:27:THR:HB	1:G:40:SER:CB	2.40	0.52
1:G:261:LEU:HB2	1:G:277:GLY:HA2	1.92	0.52
2:H:49:LEU:HB3	2:H:82:TRP:CZ3	2.44	0.52
1:A:312:ALA:HB1	1:A:315:LEU:HD12	1.92	0.52
2:D:238:ASN:HD22	2:D:240:GLN:N	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:66:ASN:N	1:E:80:ALA:O	2.39	0.52
1:E:252:LEU:HD13	1:E:285:TRP:CG	2.45	0.52
1:E:286:ASN:HB2	1:E:293:LEU:HD11	1.92	0.52
2:H:238:ASN:HD22	2:H:240:GLN:N	2.08	0.52
1:A:172:LEU:C	1:A:174:HIS:N	2.69	0.51
2:B:128:VAL:CG2	2:B:138:PRO:HB3	2.27	0.51
1:E:57:ALA:O	1:E:98:ILE:HG22	2.09	0.51
1:E:199:LEU:HD13	1:E:240:TRP:CD2	2.44	0.51
2:H:69:ILE:HG22	2:H:70:LEU:N	2.25	0.51
1:A:155:GLN:HG3	1:A:194:LYS:HB2	1.92	0.51
1:C:155:GLN:HG3	1:C:194:LYS:HB2	1.92	0.51
1:C:252:LEU:HD13	1:C:285:TRP:CG	2.45	0.51
1:C:365:LYS:HZ3	1:C:371:LEU:HD22	1.75	0.51
1:E:117:ASN:HD22	1:E:117:ASN:C	2.17	0.51
1:C:274:LEU:HG	1:C:308:PHE:CZ	2.46	0.51
2:H:95:HIS:CE1	2:H:128:VAL:HG21	2.46	0.51
2:B:95:HIS:CE1	2:B:128:VAL:HG21	2.46	0.51
1:C:66:ASN:N	1:C:80:ALA:O	2.39	0.51
1:C:203:SER:C	1:C:205:ASN:N	2.69	0.51
1:G:365:LYS:HZ3	1:G:371:LEU:HD22	1.76	0.51
1:A:137:ASP:OD1	1:A:139:ASN:HB2	2.10	0.51
1:A:203:SER:C	1:A:205:ASN:N	2.69	0.51
2:B:33:ILE:HB	2:B:49:LEU:HB2	1.92	0.51
1:C:261:LEU:HB2	1:C:277:GLY:HA2	1.92	0.51
1:E:155:GLN:HG3	1:E:194:LYS:HB2	1.92	0.51
1:C:15:TRP:HB3	1:C:310:PRO:CD	2.41	0.51
1:C:28:VAL:HG22	1:C:29:SER:N	2.26	0.51
1:C:283:LEU:HD13	1:C:292:GLN:NE2	2.26	0.51
1:E:274:LEU:HG	1:E:308:PHE:CZ	2.46	0.51
1:G:268:GLN:HG3	1:G:313:PRO:CG	2.34	0.51
1:A:15:TRP:HB3	1:A:310:PRO:CD	2.41	0.51
1:A:237:ILE:HB	1:A:252:LEU:HB2	1.93	0.51
1:C:72:HIS:HE1	1:C:118:ALA:HA	1.72	0.51
1:E:15:TRP:HB3	1:E:310:PRO:CD	2.41	0.51
1:E:261:LEU:HB2	1:E:277:GLY:HA2	1.92	0.51
1:G:74:ASN:H	1:G:74:ASN:ND2	2.02	0.51
1:A:117:ASN:HD22	1:A:117:ASN:C	2.17	0.51
2:D:33:ILE:HB	2:D:49:LEU:HB2	1.92	0.51
2:D:95:HIS:CE1	2:D:128:VAL:HG21	2.46	0.51
1:E:27:THR:HB	1:E:40:SER:CB	2.40	0.51
1:E:203:SER:C	1:E:205:ASN:N	2.69	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:4:ILE:HG22	2:F:4:ILE:O	2.11	0.51
1:G:204:PRO:C	1:G:206:SER:H	2.19	0.51
1:G:237:ILE:HB	1:G:252:LEU:HB2	1.93	0.51
2:H:105:VAL:CG2	2:H:116:LEU:HD21	2.41	0.51
1:C:212:LEU:HD13	1:C:227:THR:CG2	2.41	0.50
1:C:237:ILE:HB	1:C:252:LEU:HB2	1.93	0.50
2:F:33:ILE:HB	2:F:49:LEU:HB2	1.92	0.50
2:H:112:TYR:CZ	2:H:171:ARG:HG2	2.46	0.50
1:A:124:LEU:CG	1:A:125:ALA:H	2.25	0.50
2:B:105:VAL:CG2	2:B:116:LEU:HD21	2.41	0.50
2:B:259:ARG:HG3	2:B:259:ARG:HH11	1.77	0.50
1:C:51:ASP:O	1:C:52:SER:C	2.54	0.50
1:E:51:ASP:O	1:E:52:SER:C	2.54	0.50
2:F:95:HIS:CE1	2:F:128:VAL:HG21	2.46	0.50
2:F:238:ASN:HD22	2:F:240:GLN:N	2.07	0.50
2:H:26:THR:O	2:H:33:ILE:HG23	2.12	0.50
1:A:62:ASP:OD1	1:A:62:ASP:N	2.36	0.50
1:A:70:TRP:HD1	1:A:71:SER:O	1.94	0.50
1:A:204:PRO:C	1:A:206:SER:H	2.19	0.50
1:A:274:LEU:HG	1:A:308:PHE:CZ	2.46	0.50
2:B:26:THR:O	2:B:33:ILE:HG23	2.12	0.50
2:B:200:LEU:HD13	2:B:234:TRP:CE3	2.47	0.50
1:C:70:TRP:HD1	1:C:71:SER:O	1.94	0.50
1:C:221:ASN:C	1:C:221:ASN:ND2	2.69	0.50
1:E:212:LEU:HD13	1:E:227:THR:CG2	2.41	0.50
1:E:221:ASN:C	1:E:221:ASN:ND2	2.69	0.50
1:G:70:TRP:HD1	1:G:71:SER:O	1.94	0.50
1:A:268:GLN:CB	3:A:1309:HOH:O	2.46	0.50
1:C:22:LEU:CD1	1:C:94:ALA:CB	2.82	0.50
1:E:70:TRP:HD1	1:E:71:SER:O	1.94	0.50
2:F:200:LEU:HD13	2:F:234:TRP:CE3	2.47	0.50
1:G:155:GLN:HG3	1:G:194:LYS:HB2	1.92	0.50
1:G:271:HIS:O	1:G:272:LEU:HD23	2.12	0.50
2:H:4:ILE:O	2:H:4:ILE:HG22	2.11	0.50
1:A:51:ASP:O	1:A:52:SER:C	2.54	0.50
2:B:29:SER:C	2:B:31:LYS:N	2.70	0.50
1:C:73:ASN:C	1:C:75:LYS:N	2.58	0.50
1:C:268:GLN:CD	3:C:1307:HOH:O	2.36	0.50
1:C:268:GLN:HB2	1:C:374:PRO:O	1.98	0.50
1:E:75:LYS:HZ1	1:E:94:ALA:CB	2.25	0.50
2:F:259:ARG:HH11	2:F:259:ARG:HG3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:75:LYS:HZ1	1:G:94:ALA:CB	2.25	0.50
2:H:30:ASP:OD1	2:H:30:ASP:C	2.55	0.50
1:A:268:GLN:HE21	1:A:313:PRO:CG	2.25	0.50
1:C:11:ALA:HB3	1:C:325:ILE:HD11	1.93	0.50
2:D:105:VAL:CG2	2:D:116:LEU:HD21	2.41	0.50
2:D:200:LEU:HD13	2:D:234:TRP:CE3	2.47	0.50
1:E:237:ILE:HB	1:E:252:LEU:HB2	1.93	0.50
1:G:51:ASP:O	1:G:52:SER:C	2.54	0.50
2:H:259:ARG:HH11	2:H:259:ARG:HG3	1.76	0.50
1:G:11:ALA:HB3	1:G:325:ILE:HD11	1.93	0.50
1:A:271:HIS:O	1:A:272:LEU:HD23	2.12	0.50
2:D:26:THR:O	2:D:33:ILE:HG23	2.12	0.50
2:D:112:TYR:CZ	2:D:171:ARG:HG2	2.46	0.50
1:E:268:GLN:HE21	1:E:313:PRO:CG	2.25	0.50
1:G:203:SER:C	1:G:205:ASN:N	2.69	0.50
1:G:268:GLN:HE21	1:G:313:PRO:CG	2.25	0.50
1:G:274:LEU:HG	1:G:308:PHE:CZ	2.46	0.50
2:H:200:LEU:HD13	2:H:234:TRP:CE3	2.47	0.50
1:A:36:PHE:N	1:C:189:ASP:HB3	2.27	0.50
2:B:4:ILE:O	2:B:4:ILE:HG22	2.11	0.50
1:G:283:LEU:HD13	1:G:292:GLN:NE2	2.26	0.50
1:A:66:ASN:N	1:A:80:ALA:O	2.39	0.49
1:C:124:LEU:CG	1:C:125:ALA:H	2.24	0.49
2:D:4:ILE:HG22	2:D:4:ILE:O	2.11	0.49
2:F:105:VAL:CG2	2:F:116:LEU:HD21	2.41	0.49
2:F:112:TYR:CZ	2:F:171:ARG:HG2	2.46	0.49
1:G:314:ASP:CB	1:G:376:TRP:CE2	2.95	0.49
1:A:11:ALA:HB3	1:A:325:ILE:HD11	1.93	0.49
1:A:283:LEU:HD13	1:A:292:GLN:NE2	2.26	0.49
2:D:95:HIS:HE1	2:D:138:PRO:HG3	1.77	0.49
1:G:249:LEU:HD23	1:G:249:LEU:C	2.38	0.49
1:A:212:LEU:HD13	1:A:227:THR:CG2	2.41	0.49
1:C:264:ASP:HB2	1:C:307:LYS:HD3	1.94	0.49
1:C:325:ILE:N	1:C:325:ILE:CD1	2.76	0.49
1:C:371:LEU:O	1:C:372:GLN:C	2.55	0.49
1:E:22:LEU:CD1	1:E:94:ALA:CB	2.82	0.49
1:E:264:ASP:HB2	1:E:307:LYS:HD3	1.95	0.49
1:E:283:LEU:HD13	1:E:292:GLN:NE2	2.26	0.49
1:G:314:ASP:OD1	1:G:376:TRP:CG	2.65	0.49
1:A:75:LYS:HZ1	1:A:94:ALA:CB	2.25	0.49
1:A:246:ASN:ND2	1:G:321:PHE:HB3	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:30:ASP:OD1	2:B:30:ASP:C	2.55	0.49
2:B:95:HIS:HE1	2:B:138:PRO:HG3	1.77	0.49
2:B:112:TYR:CZ	2:B:171:ARG:HG2	2.46	0.49
1:C:268:GLN:HE21	1:C:313:PRO:CG	2.25	0.49
2:D:30:ASP:OD1	2:D:30:ASP:C	2.55	0.49
1:E:371:LEU:O	1:E:372:GLN:C	2.55	0.49
1:G:57:ALA:O	1:G:98:ILE:CG2	2.60	0.49
2:H:95:HIS:HE1	2:H:138:PRO:HG3	1.77	0.49
1:A:57:ALA:O	1:A:98:ILE:CG2	2.60	0.49
1:C:271:HIS:O	1:C:272:LEU:HD23	2.12	0.49
1:E:36:PHE:CD2	1:G:193:LYS:O	1.71	0.49
1:G:15:TRP:HB3	1:G:310:PRO:CD	2.41	0.49
1:G:62:ASP:OD1	1:G:62:ASP:N	2.36	0.49
1:G:371:LEU:O	1:G:372:GLN:C	2.55	0.49
2:H:63:HIS:CD2	3:H:312:HOH:O	2.65	0.49
1:A:15:TRP:HZ3	1:A:307:LYS:O	1.96	0.49
1:A:33:ASP:OD1	1:A:37:SER:HB3	2.13	0.49
1:A:337:LEU:CD2	2:B:97:VAL:CG1	2.90	0.49
1:A:371:LEU:O	1:A:372:GLN:C	2.55	0.49
2:B:74:SER:C	2:B:76:ASP:N	2.71	0.49
2:B:274:GLY:C	2:B:276:ASN:N	2.69	0.49
1:E:15:TRP:HZ3	1:E:307:LYS:O	1.96	0.49
1:G:75:LYS:HD2	1:G:91:THR:HG22	1.95	0.49
2:H:148:VAL:O	3:H:301:HOH:O	2.20	0.49
1:A:130:ASN:HB3	1:A:132:GLU:HG3	1.95	0.49
1:A:314:ASP:OD1	1:A:376:TRP:CG	2.65	0.49
2:B:184:ILE:N	2:B:184:ILE:HD12	2.28	0.49
1:C:34:ALA:HB1	1:E:243:ARG:CZ	2.43	0.49
1:C:57:ALA:O	1:C:98:ILE:CG2	2.60	0.49
1:C:314:ASP:OD1	1:C:376:TRP:CG	2.65	0.49
2:D:148:VAL:O	3:D:301:HOH:O	2.20	0.49
1:E:11:ALA:HB3	1:E:325:ILE:HD11	1.93	0.49
1:E:268:GLN:CB	3:E:1309:HOH:O	2.46	0.49
1:G:402:VAL:HG11	2:H:24:LEU:CD2	2.42	0.49
1:A:115:LYS:O	1:A:124:LEU:HD12	2.13	0.49
1:A:284:LEU:HD23	1:A:371:LEU:HD11	1.94	0.49
2:B:8:HIS:CE1	2:B:34:LYS:HE2	2.48	0.49
1:C:32:VAL:CG2	1:E:197:ILE:CG1	2.91	0.49
1:C:33:ASP:OD1	1:C:37:SER:HB3	2.13	0.49
1:C:75:LYS:HZ1	1:C:94:ALA:CB	2.25	0.49
1:C:402:VAL:HG11	2:D:24:LEU:CD2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:184:ILE:HD12	2:D:184:ILE:N	2.28	0.49
2:D:259:ARG:HH11	2:D:259:ARG:HG3	1.77	0.49
1:E:29:SER:HB2	1:E:82:ASP:OD1	2.13	0.49
1:E:33:ASP:OD1	1:E:37:SER:HB3	2.13	0.49
1:E:325:ILE:N	1:E:325:ILE:CD1	2.76	0.49
2:F:26:THR:O	2:F:33:ILE:HG23	2.12	0.49
1:G:29:SER:HB2	1:G:82:ASP:OD1	2.13	0.49
1:G:284:LEU:HD23	1:G:371:LEU:HD11	1.95	0.49
1:C:172:LEU:C	1:C:174:HIS:N	2.69	0.49
1:E:57:ALA:O	1:E:98:ILE:CG2	2.60	0.49
1:E:172:LEU:C	1:E:174:HIS:N	2.69	0.49
1:E:249:LEU:HD23	1:E:249:LEU:C	2.38	0.49
1:E:271:HIS:O	1:E:272:LEU:HD23	2.12	0.49
1:E:314:ASP:OD1	1:E:376:TRP:CG	2.65	0.49
1:G:115:LYS:O	1:G:124:LEU:HD12	2.13	0.49
2:B:148:VAL:O	3:B:301:HOH:O	2.20	0.49
1:C:204:PRO:C	1:C:206:SER:H	2.19	0.49
1:C:370:HIS:CG	1:C:371:LEU:N	2.68	0.49
2:F:63:HIS:CD2	3:F:312:HOH:O	2.65	0.49
1:E:284:LEU:HD23	1:E:371:LEU:HD11	1.94	0.48
2:F:30:ASP:OD1	2:F:30:ASP:C	2.55	0.48
2:F:95:HIS:HE1	2:F:138:PRO:HG3	1.77	0.48
2:F:184:ILE:HD12	2:F:184:ILE:N	2.28	0.48
1:G:15:TRP:HZ3	1:G:307:LYS:O	1.96	0.48
1:G:130:ASN:HB3	1:G:132:GLU:HG3	1.95	0.48
1:G:187:ILE:HB	1:G:197:ILE:HB	1.95	0.48
1:G:337:LEU:CD2	2:H:97:VAL:CG1	2.90	0.48
2:H:8:HIS:CE1	2:H:34:LYS:HE2	2.48	0.48
1:A:22:LEU:CD1	1:A:94:ALA:CB	2.82	0.48
1:A:75:LYS:HD2	1:A:91:THR:HG22	1.95	0.48
1:C:115:LYS:O	1:C:124:LEU:HD12	2.13	0.48
1:C:115:LYS:O	1:C:168:TRP:HZ3	1.97	0.48
1:C:364:GLU:O	1:C:365:LYS:CB	2.47	0.48
2:D:172:LYS:HA	2:D:185:TRP:O	2.13	0.48
1:E:34:ALA:HA	1:G:196:VAL:CG2	2.40	0.48
1:G:105:SER:C	1:G:107:HIS:N	2.71	0.48
1:G:115:LYS:O	1:G:168:TRP:HZ3	1.96	0.48
1:G:124:LEU:CG	1:G:125:ALA:H	2.24	0.48
1:G:172:LEU:C	1:G:174:HIS:N	2.69	0.48
2:H:225:VAL:HG13	2:H:257:LEU:CB	2.43	0.48
1:A:105:SER:C	1:A:107:HIS:N	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:63:HIS:CD2	3:B:312:HOH:O	2.65	0.48
2:B:172:LYS:HA	2:B:185:TRP:O	2.13	0.48
2:F:274:GLY:C	2:F:276:ASN:N	2.69	0.48
1:G:325:ILE:N	1:G:325:ILE:CD1	2.76	0.48
2:H:57:TRP:O	2:H:58:ARG:HG2	2.14	0.48
1:A:86:LEU:HD23	1:A:104:PHE:HB2	1.96	0.48
1:A:219:PRO:HG3	1:A:266:CYS:O	2.13	0.48
2:B:119:ALA:HB1	2:B:148:VAL:HG12	1.96	0.48
2:B:233:ILE:CD1	2:B:248:LEU:HD13	2.43	0.48
1:C:284:LEU:HD23	1:C:371:LEU:HD11	1.95	0.48
2:D:63:HIS:CD2	3:D:312:HOH:O	2.65	0.48
1:E:337:LEU:CD2	2:F:97:VAL:CG1	2.90	0.48
2:F:148:VAL:O	3:F:301:HOH:O	2.20	0.48
1:G:33:ASP:OD1	1:G:37:SER:HB3	2.13	0.48
1:G:70:TRP:C	1:G:71:SER:O	2.55	0.48
2:H:274:GLY:C	2:H:276:ASN:N	2.69	0.48
1:A:221:ASN:C	1:A:221:ASN:ND2	2.69	0.48
1:C:249:LEU:HD23	1:C:249:LEU:C	2.37	0.48
2:D:59:VAL:HA	2:D:71:ALA:O	2.14	0.48
2:D:108:ALA:HA	2:D:153:TRP:CD1	2.49	0.48
2:D:119:ALA:HB1	2:D:148:VAL:HG12	1.96	0.48
1:E:115:LYS:O	1:E:124:LEU:HD12	2.13	0.48
1:E:124:LEU:CG	1:E:125:ALA:N	2.76	0.48
2:F:29:SER:C	2:F:31:LYS:N	2.70	0.48
1:G:264:ASP:HB2	1:G:307:LYS:HD3	1.94	0.48
2:H:172:LYS:HA	2:H:185:TRP:O	2.13	0.48
1:A:109:SER:O	1:A:110:SER:CB	2.61	0.48
1:A:249:LEU:HD23	1:A:249:LEU:C	2.38	0.48
1:A:264:ASP:HB2	1:A:307:LYS:HD3	1.94	0.48
1:A:268:GLN:HB2	1:A:374:PRO:O	1.98	0.48
2:B:72:SER:O	2:B:79:VAL:HG13	2.14	0.48
2:B:212:TRP:CD2	2:B:222:LEU:HD21	2.49	0.48
1:C:42:LEU:HD23	1:C:98:ILE:HD11	1.96	0.48
1:C:105:SER:C	1:C:107:HIS:N	2.71	0.48
1:E:124:LEU:CG	1:E:125:ALA:H	2.24	0.48
1:E:187:ILE:HB	1:E:197:ILE:HB	1.95	0.48
1:E:331:GLN:HG2	1:E:371:LEU:HD23	1.96	0.48
1:E:402:VAL:HG11	2:F:24:LEU:CD2	2.42	0.48
2:F:57:TRP:O	2:F:58:ARG:HG2	2.13	0.48
1:G:268:GLN:CB	3:G:1307:HOH:O	2.46	0.48
2:H:69:ILE:CG2	2:H:70:LEU:N	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:SER:HB2	1:A:82:ASP:OD1	2.13	0.48
1:A:117:ASN:ND2	1:A:118:ALA:N	2.54	0.48
2:B:69:ILE:CG2	2:B:70:LEU:N	2.77	0.48
1:C:29:SER:HB2	1:C:82:ASP:OD1	2.13	0.48
1:C:124:LEU:CG	1:C:125:ALA:N	2.76	0.48
2:D:212:TRP:CD2	2:D:222:LEU:HD21	2.49	0.48
1:G:28:VAL:HG22	1:G:29:SER:N	2.26	0.48
1:G:186:SER:HB3	1:G:188:TRP:NE1	2.29	0.48
2:H:108:ALA:HA	2:H:153:TRP:CD1	2.49	0.48
1:A:114:VAL:HA	1:A:125:ALA:O	2.14	0.48
2:B:59:VAL:HA	2:B:71:ALA:O	2.14	0.48
1:C:114:VAL:HA	1:C:125:ALA:O	2.14	0.48
1:C:337:LEU:CD2	2:D:97:VAL:CG1	2.90	0.48
1:E:31:THR:O	1:E:32:VAL:HG23	2.13	0.48
1:E:73:ASN:C	1:E:75:LYS:N	2.59	0.48
1:E:105:SER:C	1:E:107:HIS:N	2.71	0.48
1:E:186:SER:HB3	1:E:188:TRP:NE1	2.29	0.48
1:E:365:LYS:HZ3	1:E:371:LEU:HD22	1.79	0.48
2:F:59:VAL:HA	2:F:71:ALA:O	2.14	0.48
2:F:74:SER:CB	2:F:76:ASP:OD1	2.61	0.48
2:F:108:ALA:HA	2:F:153:TRP:CD1	2.49	0.48
1:G:42:LEU:CD2	1:G:98:ILE:HD11	2.44	0.48
1:G:114:VAL:HA	1:G:125:ALA:O	2.14	0.48
2:H:15:ALA:HA	2:H:25:ALA:O	2.14	0.48
2:H:59:VAL:HA	2:H:71:ALA:O	2.14	0.48
1:A:42:LEU:HD23	1:A:98:ILE:HD11	1.96	0.48
2:B:57:TRP:O	2:B:58:ARG:HG2	2.13	0.48
1:C:10:THR:O	1:C:11:ALA:HB2	2.14	0.48
1:C:15:TRP:HZ3	1:C:307:LYS:O	1.96	0.48
1:C:187:ILE:HB	1:C:197:ILE:HB	1.95	0.48
2:D:57:TRP:O	2:D:58:ARG:HG2	2.14	0.48
2:D:274:GLY:C	2:D:276:ASN:N	2.69	0.48
1:E:10:THR:O	1:E:11:ALA:HB2	2.14	0.48
2:H:184:ILE:HD12	2:H:184:ILE:N	2.28	0.48
1:A:31:THR:O	1:A:32:VAL:HG23	2.13	0.48
1:A:42:LEU:CD2	1:A:98:ILE:HD11	2.44	0.48
3:A:1306:HOH:O	1:C:193:LYS:NZ	2.46	0.48
2:B:37:GLU:HG2	2:B:46:ILE:CG1	2.44	0.48
2:B:225:VAL:HG13	2:B:257:LEU:CB	2.44	0.48
1:C:331:GLN:HG2	1:C:371:LEU:HD23	1.96	0.48
2:D:72:SER:O	2:D:79:VAL:HG13	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:74:SER:C	2:D:76:ASP:N	2.71	0.48
2:F:87:GLY:C	2:F:88:ARG:HG3	2.39	0.48
1:G:331:GLN:HG2	1:G:371:LEU:HD23	1.96	0.48
2:B:18:ASP:CG	2:B:23:ARG:HB3	2.39	0.47
1:C:92:ASN:O	1:C:93:GLU:CB	2.62	0.47
1:C:202:THR:HG1	1:C:209:LYS:HD3	1.79	0.47
2:D:8:HIS:CE1	2:D:34:LYS:HE2	2.48	0.47
2:D:18:ASP:CG	2:D:23:ARG:HB3	2.39	0.47
2:D:87:GLY:C	2:D:88:ARG:HG3	2.39	0.47
1:E:72:HIS:HE1	1:E:118:ALA:HA	1.72	0.47
2:F:18:ASP:OD2	2:F:23:ARG:HB3	2.14	0.47
2:F:29:SER:O	2:F:31:LYS:HG3	2.14	0.47
1:G:219:PRO:HG3	1:G:266:CYS:O	2.13	0.47
2:H:212:TRP:CD2	2:H:222:LEU:HD21	2.49	0.47
2:B:31:LYS:O	3:B:302:HOH:O	2.20	0.47
2:B:108:ALA:HA	2:B:153:TRP:CD1	2.49	0.47
1:C:16:SER:HB2	1:C:18:ASP:OD1	2.14	0.47
1:C:75:LYS:HD2	1:C:91:THR:HG22	1.95	0.47
1:C:186:SER:HB3	1:C:188:TRP:NE1	2.29	0.47
2:D:29:SER:C	2:D:31:LYS:N	2.70	0.47
2:D:74:SER:CB	2:D:76:ASP:OD1	2.61	0.47
1:E:32:VAL:C	1:G:196:VAL:HG12	2.40	0.47
1:E:42:LEU:HD23	1:E:98:ILE:HD11	1.96	0.47
1:E:154:GLY:O	1:E:155:GLN:CG	2.48	0.47
2:F:8:HIS:CE1	2:F:34:LYS:HE2	2.48	0.47
2:F:172:LYS:HA	2:F:185:TRP:O	2.13	0.47
1:G:271:HIS:CE1	1:G:288:GLU:OE2	2.67	0.47
2:H:29:SER:O	2:H:31:LYS:HG3	2.14	0.47
2:H:119:ALA:HB1	2:H:148:VAL:HG12	1.96	0.47
1:A:92:ASN:O	1:A:93:GLU:CB	2.62	0.47
2:B:87:GLY:C	2:B:88:ARG:HG3	2.39	0.47
1:C:268:GLN:CB	3:C:1307:HOH:O	2.46	0.47
1:E:28:VAL:HG22	1:E:29:SER:N	2.26	0.47
2:F:18:ASP:CG	2:F:23:ARG:HB3	2.39	0.47
1:G:31:THR:O	1:G:32:VAL:HG23	2.13	0.47
1:G:212:LEU:HD13	1:G:227:THR:CG2	2.41	0.47
2:H:18:ASP:CG	2:H:23:ARG:HB3	2.39	0.47
1:A:331:GLN:HG2	1:A:371:LEU:HD23	1.95	0.47
2:D:18:ASP:OD2	2:D:23:ARG:HB3	2.14	0.47
1:E:91:THR:O	1:E:91:THR:HG22	2.14	0.47
1:E:130:ASN:HB3	1:E:132:GLU:HG3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:93:GLU:O	1:G:94:ALA:C	2.57	0.47
1:G:337:LEU:HD21	2:H:140:ILE:HD11	1.97	0.47
2:H:74:SER:C	2:H:76:ASP:N	2.71	0.47
2:H:233:ILE:CD1	2:H:248:LEU:HD13	2.43	0.47
1:A:115:LYS:O	1:A:168:TRP:HZ3	1.97	0.47
2:B:15:ALA:HA	2:B:25:ALA:O	2.14	0.47
2:B:109:PRO:HD2	2:B:112:TYR:CD2	2.50	0.47
1:C:42:LEU:CD2	1:C:98:ILE:HD11	2.44	0.47
1:C:120:GLN:C	1:C:122:ASN:H	2.22	0.47
2:D:29:SER:O	2:D:31:LYS:HG3	2.14	0.47
1:E:42:LEU:CD2	1:E:98:ILE:HD11	2.44	0.47
2:F:74:SER:C	2:F:76:ASP:N	2.71	0.47
1:A:16:SER:HB2	1:A:18:ASP:OD1	2.14	0.47
1:C:117:ASN:HD22	1:C:117:ASN:C	2.17	0.47
1:C:271:HIS:CE1	1:C:288:GLU:OE2	2.67	0.47
2:D:259:ARG:HG3	2:D:259:ARG:NH1	2.30	0.47
1:E:75:LYS:HD2	1:E:91:THR:HG22	1.95	0.47
1:E:93:GLU:O	1:E:94:ALA:C	2.57	0.47
1:E:114:VAL:HA	1:E:125:ALA:O	2.14	0.47
1:E:204:PRO:C	1:E:206:SER:H	2.19	0.47
1:E:219:PRO:HG3	1:E:266:CYS:O	2.13	0.47
1:E:271:HIS:CE1	1:E:288:GLU:OE2	2.67	0.47
2:F:72:SER:O	2:F:79:VAL:HG13	2.14	0.47
2:H:37:GLU:HG2	2:H:46:ILE:CG1	2.44	0.47
2:H:72:SER:O	2:H:79:VAL:HG13	2.14	0.47
1:A:10:THR:O	1:A:11:ALA:HB2	2.14	0.47
1:A:93:GLU:O	1:A:94:ALA:C	2.57	0.47
1:A:187:ILE:HB	1:A:197:ILE:HB	1.95	0.47
1:A:325:ILE:N	1:A:325:ILE:CD1	2.76	0.47
2:B:255:ASP:CG	2:B:256:VAL:N	2.72	0.47
1:C:31:THR:O	1:C:32:VAL:HG23	2.13	0.47
1:C:133:ILE:HD11	1:C:163:VAL:CG2	2.41	0.47
1:C:219:PRO:HG3	1:C:266:CYS:O	2.13	0.47
2:D:109:PRO:HD2	2:D:112:TYR:CD2	2.50	0.47
2:D:225:VAL:HG13	2:D:257:LEU:CB	2.43	0.47
1:E:16:SER:HB2	1:E:18:ASP:OD1	2.14	0.47
1:E:115:LYS:O	1:E:168:TRP:HZ3	1.97	0.47
2:F:27:CYS:HB2	2:F:56:VAL:CG1	2.44	0.47
2:F:37:GLU:HG2	2:F:46:ILE:CG1	2.44	0.47
2:F:69:ILE:CG2	2:F:70:LEU:N	2.77	0.47
2:F:212:TRP:CD2	2:F:222:LEU:HD21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:255:ASP:CG	2:F:256:VAL:N	2.72	0.47
2:F:259:ARG:HG3	2:F:259:ARG:NH1	2.30	0.47
1:G:10:THR:O	1:G:11:ALA:HB2	2.14	0.47
1:G:120:GLN:C	1:G:122:ASN:H	2.22	0.47
2:H:18:ASP:OD2	2:H:23:ARG:HB3	2.14	0.47
2:H:27:CYS:HB2	2:H:56:VAL:CG1	2.45	0.47
2:H:87:GLY:C	2:H:88:ARG:HG3	2.39	0.47
2:H:109:PRO:HD2	2:H:112:TYR:CD2	2.50	0.47
2:H:119:ALA:HB1	2:H:148:VAL:CG1	2.45	0.47
2:H:259:ARG:HG3	2:H:259:ARG:NH1	2.30	0.47
1:A:91:THR:HG22	1:A:91:THR:O	2.14	0.47
1:A:133:ILE:HD11	1:A:163:VAL:CG2	2.41	0.47
2:B:27:CYS:HB2	2:B:56:VAL:CG1	2.45	0.47
2:B:119:ALA:HB1	2:B:148:VAL:CG1	2.45	0.47
2:D:15:ALA:HA	2:D:25:ALA:O	2.14	0.47
2:D:27:CYS:HB2	2:D:56:VAL:CG1	2.44	0.47
2:D:69:ILE:CG2	2:D:70:LEU:N	2.77	0.47
2:D:121:SER:HA	3:D:301:HOH:O	2.15	0.47
2:D:255:ASP:CG	2:D:256:VAL:N	2.72	0.47
1:E:336:THR:OG1	2:F:96:ALA:O	2.33	0.47
2:F:109:PRO:HD2	2:F:112:TYR:CD2	2.50	0.47
1:G:124:LEU:CG	1:G:125:ALA:N	2.76	0.47
2:H:124:LYS:HE2	2:H:142:ASP:OD1	2.15	0.47
1:C:78:ALA:HB3	1:C:114:VAL:CG1	2.45	0.47
2:D:119:ALA:HB1	2:D:148:VAL:CG1	2.45	0.47
1:E:70:TRP:C	1:E:71:SER:O	2.55	0.47
1:E:314:ASP:CB	1:E:376:TRP:CE2	2.95	0.47
1:E:337:LEU:HD21	2:F:140:ILE:HD11	1.97	0.47
2:F:119:ALA:HB1	2:F:148:VAL:HG12	1.96	0.47
2:F:200:LEU:HB3	2:F:234:TRP:CH2	2.50	0.47
2:B:34:LYS:HB3	2:B:36:PHE:HE1	1.79	0.47
1:C:130:ASN:HB3	1:C:132:GLU:HG3	1.95	0.47
1:C:314:ASP:CB	1:C:376:TRP:CE2	2.95	0.47
1:E:370:HIS:CG	1:E:371:LEU:N	2.68	0.47
1:G:78:ALA:HB3	1:G:114:VAL:CG1	2.45	0.47
1:G:92:ASN:O	1:G:93:GLU:CB	2.62	0.47
2:H:34:LYS:HB3	2:H:36:PHE:HE1	1.80	0.47
1:A:72:HIS:HE1	1:A:118:ALA:HA	1.72	0.46
1:A:271:HIS:CE1	1:A:288:GLU:OE2	2.68	0.46
2:B:93:ALA:HB1	3:B:336:HOH:O	2.14	0.46
1:C:93:GLU:O	1:C:94:ALA:C	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:312:ALA:O	1:E:314:ASP:N	2.49	0.46
2:F:225:VAL:HG13	2:F:257:LEU:CB	2.43	0.46
1:G:15:TRP:CZ3	1:G:317:ALA:N	2.83	0.46
1:G:16:SER:HB2	1:G:18:ASP:OD1	2.14	0.46
1:G:42:LEU:HD23	1:G:98:ILE:HD11	1.96	0.46
1:G:68:LEU:HA	1:G:78:ALA:O	2.16	0.46
1:G:91:THR:HG22	1:G:91:THR:O	2.14	0.46
2:H:93:ALA:HB1	3:H:336:HOH:O	2.14	0.46
2:H:102:VAL:HG22	3:H:304:HOH:O	2.14	0.46
2:H:255:ASP:CG	2:H:256:VAL:N	2.72	0.46
1:A:120:GLN:C	1:A:122:ASN:H	2.22	0.46
1:A:186:SER:HB3	1:A:188:TRP:NE1	2.29	0.46
2:B:18:ASP:OD2	2:B:23:ARG:HB3	2.14	0.46
2:B:29:SER:O	2:B:31:LYS:HG3	2.14	0.46
2:B:259:ARG:HG3	2:B:259:ARG:NH1	2.30	0.46
1:C:86:LEU:HD23	1:C:104:PHE:HB2	1.96	0.46
1:C:91:THR:HG22	1:C:91:THR:O	2.14	0.46
1:E:117:ASN:ND2	1:E:118:ALA:N	2.54	0.46
1:E:133:ILE:HD11	1:E:163:VAL:CG2	2.41	0.46
2:F:34:LYS:HB3	2:F:36:PHE:HE1	1.80	0.46
2:F:124:LYS:HE2	2:F:142:ASP:OD1	2.15	0.46
1:A:45:TRP:CD1	1:A:45:TRP:N	2.84	0.46
1:A:183:ASN:HA	1:A:211:GLN:HA	1.97	0.46
2:B:124:LYS:HE2	2:B:142:ASP:OD1	2.15	0.46
1:C:151:LEU:CD1	1:C:152:THR:H	2.25	0.46
1:C:337:LEU:HD21	2:D:140:ILE:HD11	1.97	0.46
1:C:392:LEU:CD1	3:C:1302:HOH:O	2.61	0.46
1:E:15:TRP:CZ3	1:E:317:ALA:N	2.83	0.46
1:E:92:ASN:O	1:E:93:GLU:CB	2.62	0.46
1:E:120:GLN:C	1:E:122:ASN:H	2.22	0.46
1:E:202:THR:CG2	1:E:209:LYS:HD3	2.46	0.46
2:F:93:ALA:HB1	3:F:336:HOH:O	2.14	0.46
1:G:312:ALA:O	1:G:314:ASP:N	2.49	0.46
1:A:127:GLY:HA2	1:A:132:GLU:O	2.16	0.46
1:A:402:VAL:HG11	2:B:24:LEU:CD2	2.42	0.46
1:C:219:PRO:HD3	1:C:265:TRP:CD1	2.51	0.46
1:C:244:ASN:C	1:C:244:ASN:HD22	2.24	0.46
2:D:34:LYS:HB3	2:D:36:PHE:HE1	1.80	0.46
1:E:68:LEU:HA	1:E:78:ALA:O	2.15	0.46
2:F:15:ALA:HA	2:F:25:ALA:O	2.14	0.46
1:A:68:LEU:HD22	1:A:77:ILE:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:THR:CG2	1:A:209:LYS:HD3	2.45	0.46
1:A:243:ARG:CZ	1:G:34:ALA:HB1	2.44	0.46
1:A:252:LEU:HD13	1:A:285:TRP:CB	2.45	0.46
1:A:279:ASP:OD2	1:A:281:THR:HG22	2.16	0.46
1:C:252:LEU:HD13	1:C:285:TRP:CB	2.46	0.46
1:C:279:ASP:OD2	1:C:281:THR:HG22	2.16	0.46
1:E:151:LEU:CD1	1:E:152:THR:H	2.25	0.46
1:E:252:LEU:HD13	1:E:285:TRP:CB	2.46	0.46
2:F:117:LEU:HB2	2:F:153:TRP:NE1	2.31	0.46
1:G:212:LEU:HD22	1:G:227:THR:HG22	1.98	0.46
2:H:66:PHE:CD1	2:H:114:PRO:HB3	2.51	0.46
1:A:169:ASN:OD1	1:A:172:LEU:HB2	2.16	0.46
1:C:32:VAL:HG23	1:E:197:ILE:CG1	2.46	0.46
1:C:68:LEU:HD22	1:C:77:ILE:HG22	1.98	0.46
2:D:37:GLU:HG2	2:D:46:ILE:CG1	2.44	0.46
2:D:93:ALA:HB1	3:D:336:HOH:O	2.14	0.46
1:E:86:LEU:HD23	1:E:104:PHE:HB2	1.96	0.46
1:E:279:ASP:OD2	1:E:281:THR:HG22	2.16	0.46
2:F:119:ALA:HB1	2:F:148:VAL:CG1	2.45	0.46
1:G:45:TRP:N	1:G:45:TRP:CD1	2.84	0.46
1:G:127:GLY:HA2	1:G:132:GLU:O	2.16	0.46
1:G:183:ASN:HA	1:G:211:GLN:HA	1.97	0.46
1:G:244:ASN:C	1:G:244:ASN:HD22	2.24	0.46
1:G:337:LEU:HD21	2:H:97:VAL:HG11	1.97	0.46
1:A:15:TRP:CZ3	1:A:317:ALA:N	2.83	0.46
1:A:32:VAL:C	1:C:196:VAL:HG12	2.41	0.46
1:A:154:GLY:O	1:A:155:GLN:CG	2.48	0.46
1:A:260:ILE:HG23	1:A:261:LEU:N	2.31	0.46
1:A:336:THR:OG1	2:B:96:ALA:O	2.33	0.46
1:A:337:LEU:HD21	2:B:140:ILE:HD11	1.97	0.46
1:C:45:TRP:N	1:C:45:TRP:CD1	2.84	0.46
1:C:127:GLY:HA2	1:C:132:GLU:O	2.16	0.46
2:D:117:LEU:HB2	2:D:153:TRP:NE1	2.31	0.46
2:D:200:LEU:HB3	2:D:234:TRP:CH2	2.50	0.46
1:E:32:VAL:O	1:G:196:VAL:HB	2.15	0.46
1:E:68:LEU:HD22	1:E:77:ILE:HG22	1.98	0.46
1:E:127:GLY:HA2	1:E:132:GLU:O	2.16	0.46
1:G:252:LEU:HD13	1:G:285:TRP:CB	2.45	0.46
1:G:392:LEU:CD1	3:G:1302:HOH:O	2.61	0.46
2:H:31:LYS:O	3:H:302:HOH:O	2.20	0.46
1:A:244:ASN:C	1:A:244:ASN:HD22	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:ASN:HB3	1:G:302:TRP:CD2	2.50	0.46
1:A:329:THR:C	1:A:331:GLN:N	2.73	0.46
1:C:15:TRP:CZ3	1:C:317:ALA:N	2.83	0.46
1:C:70:TRP:C	1:C:71:SER:O	2.55	0.46
1:C:169:ASN:OD1	1:C:172:LEU:HB2	2.16	0.46
1:C:300:GLY:O	1:C:301:ASN:CB	2.59	0.46
1:C:314:ASP:CG	1:C:376:TRP:CZ2	2.87	0.46
1:E:392:LEU:HA	3:E:1302:HOH:O	2.16	0.46
2:F:121:SER:HA	3:F:301:HOH:O	2.15	0.46
1:G:22:LEU:CD1	1:G:94:ALA:CB	2.82	0.46
1:G:117:ASN:HD22	1:G:117:ASN:C	2.17	0.46
1:G:202:THR:CG2	1:G:209:LYS:HD3	2.46	0.46
1:A:7:PHE:HB2	1:A:8:SER:H	1.51	0.46
1:A:212:LEU:HD22	1:A:227:THR:HG22	1.98	0.46
1:C:68:LEU:HA	1:C:78:ALA:O	2.16	0.46
1:C:337:LEU:HD21	2:D:97:VAL:HG11	1.97	0.46
2:D:124:LYS:HE2	2:D:142:ASP:OD1	2.15	0.46
1:E:244:ASN:HD22	1:E:244:ASN:C	2.24	0.46
2:F:66:PHE:CD1	2:F:114:PRO:HB3	2.51	0.46
1:G:83:ASN:O	1:G:84:GLY:C	2.59	0.46
1:A:314:ASP:CB	1:A:376:TRP:CE2	2.95	0.46
2:B:127:VAL:HA	3:B:306:HOH:O	2.15	0.46
1:C:259:GLY:HA3	1:C:278:ARG:NH1	2.31	0.46
1:E:260:ILE:HG23	1:E:261:LEU:N	2.31	0.46
1:G:74:ASN:N	1:G:74:ASN:ND2	2.50	0.46
1:G:169:ASN:HB3	1:G:172:LEU:O	2.16	0.46
1:A:28:VAL:HG22	1:A:29:SER:N	2.26	0.45
1:A:259:GLY:HA3	1:A:278:ARG:NH1	2.31	0.45
2:B:117:LEU:HB2	2:B:153:TRP:NE1	2.31	0.45
2:B:284:ASN:HB2	3:B:346:HOH:O	2.16	0.45
1:C:202:THR:CG2	1:C:209:LYS:HD3	2.45	0.45
2:D:66:PHE:CD1	2:D:114:PRO:HB3	2.51	0.45
2:F:127:VAL:HA	3:F:306:HOH:O	2.15	0.45
1:G:117:ASN:ND2	1:G:118:ALA:N	2.54	0.45
1:G:336:THR:OG1	2:H:96:ALA:O	2.33	0.45
1:G:392:LEU:HA	3:G:1302:HOH:O	2.16	0.45
2:H:121:SER:HA	3:H:301:HOH:O	2.15	0.45
1:A:312:ALA:O	1:A:314:ASP:N	2.48	0.45
1:C:392:LEU:HA	3:C:1302:HOH:O	2.16	0.45
1:E:45:TRP:CD1	1:E:45:TRP:N	2.84	0.45
1:E:169:ASN:OD1	1:E:172:LEU:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:259:GLY:HA3	1:E:278:ARG:NH1	2.31	0.45
1:E:337:LEU:HD21	2:F:97:VAL:HG11	1.97	0.45
1:G:154:GLY:O	1:G:155:GLN:CG	2.48	0.45
1:G:279:ASP:OD2	1:G:281:THR:HG22	2.16	0.45
1:A:169:ASN:HB3	1:A:172:LEU:O	2.16	0.45
2:B:121:SER:HA	3:B:301:HOH:O	2.15	0.45
2:B:191:ALA:HB1	2:B:193:THR:HG22	1.99	0.45
1:C:15:TRP:CH2	1:C:317:ALA:HB2	2.52	0.45
1:C:169:ASN:HB3	1:C:172:LEU:O	2.16	0.45
1:C:312:ALA:O	1:C:314:ASP:N	2.48	0.45
2:D:127:VAL:HA	3:D:306:HOH:O	2.15	0.45
1:E:219:PRO:HD3	1:E:265:TRP:CD1	2.51	0.45
2:H:191:ALA:HB1	2:H:193:THR:HG22	1.99	0.45
1:A:68:LEU:HA	1:A:78:ALA:O	2.15	0.45
2:B:35:ILE:HG13	2:B:89:TRP:CE2	2.52	0.45
2:B:102:VAL:HG22	3:B:304:HOH:O	2.14	0.45
2:D:284:ASN:HB2	3:D:346:HOH:O	2.16	0.45
1:G:86:LEU:HD23	1:G:104:PHE:HB2	1.96	0.45
1:G:109:SER:O	1:G:110:SER:CB	2.61	0.45
1:G:202:THR:HG1	1:G:209:LYS:HD3	1.79	0.45
1:G:329:THR:C	1:G:331:GLN:N	2.73	0.45
1:A:15:TRP:CH2	1:A:317:ALA:HB2	2.52	0.45
1:A:151:LEU:CD1	1:A:152:THR:H	2.25	0.45
1:A:193:LYS:O	1:A:194:LYS:CB	2.65	0.45
2:B:25:ALA:HB2	2:B:61:TRP:HZ2	1.81	0.45
1:C:129:ASN:C	1:C:131:GLY:N	2.74	0.45
1:C:183:ASN:HA	1:C:211:GLN:HA	1.97	0.45
1:E:83:ASN:O	1:E:84:GLY:C	2.59	0.45
1:E:155:GLN:HB2	1:E:195:GLU:HB3	1.99	0.45
1:G:68:LEU:HD22	1:G:77:ILE:HG22	1.98	0.45
1:G:219:PRO:HD3	1:G:265:TRP:CD1	2.51	0.45
2:H:117:LEU:HB2	2:H:153:TRP:NE1	2.31	0.45
1:A:83:ASN:O	1:A:84:GLY:C	2.58	0.45
1:A:129:ASN:C	1:A:131:GLY:N	2.74	0.45
2:B:239:GLU:HG3	3:B:345:HOH:O	2.16	0.45
1:C:83:ASN:O	1:C:84:GLY:C	2.59	0.45
1:E:183:ASN:HA	1:E:211:GLN:HA	1.97	0.45
1:G:5:ALA:N	3:G:1306:HOH:O	2.49	0.45
1:G:162:GLU:HG3	1:G:164:ILE:HG23	1.99	0.45
1:A:337:LEU:HD21	2:B:97:VAL:HG11	1.97	0.45
1:E:162:GLU:HG3	1:E:164:ILE:HG23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:29:SER:C	2:H:31:LYS:N	2.70	0.45
2:H:105:VAL:HG22	2:H:116:LEU:HD11	1.99	0.45
2:H:200:LEU:HB3	2:H:234:TRP:CH2	2.50	0.45
2:H:238:ASN:ND2	2:H:240:GLN:H	2.14	0.45
1:A:219:PRO:HD3	1:A:265:TRP:CD1	2.51	0.45
2:D:191:ALA:HB1	2:D:193:THR:HG22	1.99	0.45
1:E:20:ILE:O	1:E:20:ILE:CG1	2.65	0.45
1:E:63:SER:HB3	1:E:82:ASP:HB2	1.98	0.45
2:F:233:ILE:CD1	2:F:248:LEU:HD13	2.43	0.45
1:G:260:ILE:HG23	1:G:261:LEU:N	2.31	0.45
2:H:30:ASP:OD1	2:H:32:THR:HG23	2.17	0.45
2:H:284:ASN:HB2	3:H:346:HOH:O	2.16	0.45
1:A:63:SER:HB3	1:A:82:ASP:HB2	1.98	0.45
1:A:78:ALA:HB3	1:A:114:VAL:CG1	2.45	0.45
1:A:392:LEU:HA	3:A:1302:HOH:O	2.16	0.45
2:B:66:PHE:CD1	2:B:114:PRO:HB3	2.51	0.45
2:B:200:LEU:HB3	2:B:234:TRP:CH2	2.50	0.45
1:C:5:ALA:N	3:C:1306:HOH:O	2.49	0.45
2:D:35:ILE:HG13	2:D:89:TRP:CE2	2.51	0.45
1:E:129:ASN:HA	1:E:162:GLU:CB	2.47	0.45
1:E:152:THR:HA	1:E:153:PRO:HD3	1.81	0.45
1:E:197:ILE:HG22	1:E:198:HIS:N	2.32	0.45
1:E:232:ASP:HA	1:E:259:GLY:H	1.82	0.45
1:G:169:ASN:OD1	1:G:172:LEU:HB2	2.16	0.45
2:H:74:SER:CB	2:H:76:ASP:OD1	2.61	0.45
2:H:239:GLU:HG3	3:H:345:HOH:O	2.16	0.45
1:A:155:GLN:HB3	1:A:195:GLU:HB3	1.99	0.45
1:A:312:ALA:N	1:A:313:PRO:CD	2.80	0.45
1:C:129:ASN:HA	1:C:162:GLU:CB	2.47	0.45
1:C:162:GLU:HG3	1:C:164:ILE:HG23	1.99	0.45
1:C:197:ILE:HG22	1:C:198:HIS:N	2.32	0.45
1:E:5:ALA:N	3:E:1308:HOH:O	2.49	0.45
1:E:78:ALA:HB3	1:E:114:VAL:CG1	2.45	0.45
1:E:169:ASN:HB3	1:E:172:LEU:O	2.16	0.45
2:F:191:ALA:HB1	2:F:193:THR:HG22	1.99	0.45
1:G:15:TRP:CH2	1:G:317:ALA:HB2	2.52	0.45
1:G:232:ASP:O	1:G:258:LYS:HA	2.17	0.45
1:A:119:LYS:CB	1:A:173:ALA:HB2	2.40	0.44
1:A:232:ASP:O	1:A:258:LYS:HA	2.17	0.44
2:B:181:LEU:CD2	2:B:201:GLU:HG2	2.47	0.44
1:C:27:THR:O	1:C:65:PHE:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:336:THR:OG1	2:D:96:ALA:O	2.33	0.44
1:C:399:GLY:O	2:D:11:LEU:HD12	2.17	0.44
2:D:233:ILE:CD1	2:D:248:LEU:HD13	2.43	0.44
1:E:155:GLN:HB3	1:E:195:GLU:HB3	1.99	0.44
1:E:212:LEU:HB3	1:E:227:THR:HG23	1.99	0.44
1:G:155:GLN:HB3	1:G:195:GLU:HB3	1.99	0.44
1:G:221:ASN:C	1:G:221:ASN:ND2	2.69	0.44
1:G:289:SER:O	1:G:290:ALA:CB	2.65	0.44
1:G:300:GLY:O	1:G:301:ASN:CB	2.59	0.44
1:G:399:GLY:O	2:H:11:LEU:HD12	2.17	0.44
2:H:25:ALA:HB2	2:H:61:TRP:HZ2	1.81	0.44
1:A:75:LYS:NZ	1:A:94:ALA:CB	2.80	0.44
1:A:197:ILE:CG1	1:G:32:VAL:CG2	2.95	0.44
1:A:212:LEU:HB3	1:A:227:THR:HG23	1.98	0.44
1:C:212:LEU:HB3	1:C:227:THR:HG23	1.98	0.44
1:C:260:ILE:HG23	1:C:261:LEU:N	2.31	0.44
2:D:4:ILE:HG21	2:D:36:PHE:CE2	2.52	0.44
1:E:27:THR:O	1:E:65:PHE:HB2	2.17	0.44
1:E:86:LEU:HD21	1:E:104:PHE:HB2	1.99	0.44
2:F:4:ILE:HG21	2:F:36:PHE:CE2	2.52	0.44
2:F:35:ILE:HG13	2:F:89:TRP:CE2	2.52	0.44
2:F:181:LEU:CD2	2:F:201:GLU:HG2	2.47	0.44
2:F:284:ASN:HB2	3:F:346:HOH:O	2.16	0.44
1:G:75:LYS:HZ2	1:G:94:ALA:N	2.15	0.44
2:H:4:ILE:HG21	2:H:36:PHE:CE2	2.52	0.44
2:H:181:LEU:CD2	2:H:201:GLU:HG2	2.47	0.44
1:A:86:LEU:HD21	1:A:104:PHE:HB2	1.99	0.44
1:A:162:GLU:HG3	1:A:164:ILE:HG23	1.99	0.44
1:C:32:VAL:HG21	1:E:196:VAL:HG23	2.00	0.44
1:C:63:SER:HB3	1:C:82:ASP:HB2	1.98	0.44
1:C:88:LEU:CD1	1:C:138:MET:SD	3.06	0.44
1:C:232:ASP:O	1:C:258:LYS:HA	2.17	0.44
2:D:181:LEU:CD2	2:D:201:GLU:HG2	2.47	0.44
2:D:239:GLU:HG3	3:D:345:HOH:O	2.16	0.44
1:E:300:GLY:O	1:E:301:ASN:CB	2.59	0.44
1:E:379:GLU:HG2	2:F:258:TRP:CZ2	2.53	0.44
2:F:213:SER:HB2	2:F:262:TRP:CE2	2.53	0.44
1:G:312:ALA:N	1:G:313:PRO:CD	2.80	0.44
2:H:127:VAL:HA	3:H:306:HOH:O	2.15	0.44
1:A:129:ASN:HA	1:A:162:GLU:CB	2.47	0.44
2:B:4:ILE:HG21	2:B:36:PHE:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:74:SER:CB	2:B:76:ASP:OD1	2.61	0.44
2:D:31:LYS:O	3:D:302:HOH:O	2.20	0.44
1:E:15:TRP:CH2	1:E:317:ALA:HB2	2.52	0.44
1:E:116:PHE:CE1	1:E:124:LEU:HD13	2.53	0.44
1:E:392:LEU:CD1	3:E:1302:HOH:O	2.61	0.44
2:F:152:SER:OG	2:F:210:VAL:O	2.33	0.44
2:F:239:GLU:HG3	3:F:345:HOH:O	2.16	0.44
1:G:259:GLY:HA3	1:G:278:ARG:NH1	2.31	0.44
1:A:70:TRP:C	1:A:71:SER:O	2.55	0.44
1:A:197:ILE:HG22	1:A:198:HIS:N	2.32	0.44
1:A:399:GLY:O	2:B:11:LEU:HD12	2.17	0.44
2:B:238:ASN:HD22	2:B:238:ASN:C	2.26	0.44
1:C:86:LEU:HD21	1:C:104:PHE:HB2	1.99	0.44
1:C:119:LYS:CB	1:C:173:ALA:HB2	2.41	0.44
1:C:232:ASP:HA	1:C:259:GLY:H	1.82	0.44
2:D:213:SER:HB2	2:D:262:TRP:CE2	2.53	0.44
1:E:88:LEU:CD1	1:E:138:MET:SD	3.06	0.44
1:E:129:ASN:C	1:E:131:GLY:N	2.74	0.44
1:E:312:ALA:N	1:E:313:PRO:CD	2.80	0.44
2:F:105:VAL:HG22	2:F:116:LEU:HD11	1.99	0.44
1:A:162:GLU:HG3	1:A:164:ILE:CG2	2.48	0.44
1:A:379:GLU:HG2	2:B:258:TRP:CZ2	2.53	0.44
1:C:117:ASN:ND2	1:C:118:ALA:N	2.54	0.44
2:D:25:ALA:HB2	2:D:61:TRP:HZ2	1.81	0.44
1:E:232:ASP:O	1:E:258:LYS:HA	2.17	0.44
2:F:189:SER:C	2:F:191:ALA:N	2.76	0.44
1:G:24:VAL:CG2	1:G:70:TRP:CZ3	3.01	0.44
1:G:88:LEU:CD1	1:G:138:MET:SD	3.06	0.44
1:G:162:GLU:HG3	1:G:164:ILE:CG2	2.48	0.44
1:A:27:THR:O	1:A:65:PHE:HB2	2.17	0.44
1:A:116:PHE:CE1	1:A:124:LEU:HD13	2.53	0.44
1:A:204:PRO:HG2	1:A:208:ILE:O	2.18	0.44
2:B:14:ASP:HB3	2:B:27:CYS:SG	2.58	0.44
1:C:232:ASP:HA	1:C:259:GLY:N	2.33	0.44
2:D:14:ASP:HB3	2:D:27:CYS:SG	2.58	0.44
1:G:379:GLU:HG2	2:H:258:TRP:CZ2	2.53	0.44
2:H:64:PRO:HD2	3:H:312:HOH:O	2.17	0.44
2:H:213:SER:HB2	2:H:262:TRP:CE2	2.53	0.44
1:A:16:SER:HB2	1:A:17:HIS:H	1.70	0.44
1:A:34:ALA:HA	1:C:196:VAL:CG1	2.45	0.44
1:C:312:ALA:N	1:C:313:PRO:CD	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:379:GLU:HG2	2:D:258:TRP:CZ2	2.53	0.44
2:F:31:LYS:O	3:F:302:HOH:O	2.20	0.44
1:G:42:LEU:O	1:G:42:LEU:HG	2.18	0.44
1:G:63:SER:HB3	1:G:82:ASP:HB2	1.98	0.44
1:G:74:ASN:O	1:G:75:LYS:C	2.61	0.44
1:G:197:ILE:HG22	1:G:198:HIS:N	2.32	0.44
2:H:35:ILE:HG13	2:H:89:TRP:CE2	2.52	0.44
1:A:5:ALA:N	3:A:1308:HOH:O	2.49	0.44
1:A:67:ASP:OD2	1:A:113:THR:HG23	2.18	0.44
1:A:289:SER:O	1:A:290:ALA:CB	2.65	0.44
2:B:213:SER:HB2	2:B:262:TRP:CE2	2.53	0.44
1:C:24:VAL:CG2	1:C:70:TRP:CZ3	3.01	0.44
1:C:162:GLU:HG3	1:C:164:ILE:CG2	2.48	0.44
2:D:63:HIS:CE1	2:D:65:LYS:HB3	2.53	0.44
2:D:85:GLU:O	2:D:86:ASN:HB2	2.18	0.44
2:D:105:VAL:HG22	2:D:116:LEU:HD11	1.99	0.44
2:D:112:TYR:N	2:D:112:TYR:CD1	2.86	0.44
2:D:238:ASN:HD22	2:D:238:ASN:C	2.26	0.44
1:E:212:LEU:HD22	1:E:227:THR:HG22	1.98	0.44
1:E:232:ASP:HA	1:E:259:GLY:N	2.33	0.44
2:F:30:ASP:OD1	2:F:32:THR:HG23	2.17	0.44
1:G:116:PHE:CE1	1:G:124:LEU:HD13	2.53	0.44
1:G:212:LEU:HB3	1:G:227:THR:HG23	1.98	0.44
2:H:14:ASP:HB3	2:H:27:CYS:SG	2.58	0.44
2:H:74:SER:C	2:H:76:ASP:H	2.26	0.44
2:H:85:GLU:O	2:H:86:ASN:HB2	2.18	0.44
1:A:24:VAL:CG2	1:A:70:TRP:CZ3	3.01	0.43
1:A:33:ASP:C	1:C:196:VAL:CB	2.63	0.43
1:A:232:ASP:HA	1:A:259:GLY:H	1.83	0.43
1:C:204:PRO:HG2	1:C:208:ILE:O	2.18	0.43
1:C:212:LEU:HD22	1:C:227:THR:HG22	1.98	0.43
1:E:36:PHE:CD1	1:G:194:LYS:O	2.71	0.43
1:E:204:PRO:HG2	1:E:208:ILE:O	2.18	0.43
1:E:242:LEU:N	1:E:242:LEU:HD23	2.33	0.43
2:F:74:SER:C	2:F:76:ASP:H	2.26	0.43
2:F:85:GLU:O	2:F:86:ASN:HB2	2.18	0.43
2:F:112:TYR:CD1	2:F:112:TYR:N	2.86	0.43
2:F:238:ASN:HD22	2:F:238:ASN:C	2.26	0.43
1:G:232:ASP:HA	1:G:259:GLY:H	1.82	0.43
1:A:232:ASP:HA	1:A:259:GLY:N	2.33	0.43
2:B:30:ASP:OD1	2:B:32:THR:HG23	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:22:LEU:HD21	1:C:95:ASN:ND2	2.33	0.43
2:D:30:ASP:OD1	2:D:32:THR:HG23	2.17	0.43
1:E:252:LEU:HD13	1:E:285:TRP:CD2	2.53	0.43
1:E:399:GLY:O	2:F:11:LEU:HD12	2.17	0.43
1:G:204:PRO:HG3	1:G:210:GLN:HG3	2.00	0.43
1:G:236:SER:C	1:G:237:ILE:HD12	2.44	0.43
2:H:63:HIS:CE1	2:H:65:LYS:HB3	2.53	0.43
1:A:155:GLN:HB2	1:A:195:GLU:HB3	1.99	0.43
1:A:364:GLU:O	1:A:365:LYS:CB	2.47	0.43
2:B:63:HIS:CE1	2:B:65:LYS:HB3	2.53	0.43
1:C:155:GLN:HB2	1:C:195:GLU:HB3	1.99	0.43
1:C:204:PRO:HG3	1:C:210:GLN:HG3	2.00	0.43
2:D:152:SER:OG	2:D:210:VAL:O	2.33	0.43
2:D:281:TRP:CD1	2:D:281:TRP:N	2.87	0.43
2:F:63:HIS:CE1	2:F:65:LYS:HB3	2.53	0.43
2:F:281:TRP:CD1	2:F:281:TRP:N	2.87	0.43
1:G:155:GLN:HB2	1:G:195:GLU:HB3	1.99	0.43
1:G:242:LEU:N	1:G:242:LEU:HD23	2.33	0.43
1:A:42:LEU:HG	1:A:42:LEU:O	2.18	0.43
1:C:42:LEU:HG	1:C:42:LEU:O	2.18	0.43
1:C:223:THR:O	1:C:241:ASP:HA	2.19	0.43
1:E:24:VAL:CG2	1:E:70:TRP:CZ3	3.01	0.43
1:E:42:LEU:HG	1:E:42:LEU:O	2.18	0.43
1:G:22:LEU:HD21	1:G:95:ASN:ND2	2.33	0.43
1:G:129:ASN:HA	1:G:162:GLU:CB	2.47	0.43
2:H:238:ASN:HD22	2:H:238:ASN:C	2.26	0.43
1:C:116:PHE:CE1	1:C:124:LEU:HD13	2.53	0.43
1:C:155:GLN:HB3	1:C:195:GLU:HB3	1.99	0.43
1:C:242:LEU:HD23	1:C:242:LEU:N	2.33	0.43
2:D:102:VAL:HG22	3:D:304:HOH:O	2.14	0.43
1:E:289:SER:O	1:E:290:ALA:CB	2.65	0.43
2:F:14:ASP:HB3	2:F:27:CYS:SG	2.58	0.43
2:H:46:ILE:O	2:H:46:ILE:HG22	2.19	0.43
1:A:20:ILE:O	1:A:20:ILE:CG1	2.65	0.43
1:A:22:LEU:HD21	1:A:95:ASN:ND2	2.33	0.43
1:A:193:LYS:NZ	3:A:1307:HOH:O	2.46	0.43
1:C:211:GLN:O	1:C:229:THR:HA	2.19	0.43
2:D:189:SER:C	2:D:191:ALA:N	2.76	0.43
1:G:152:THR:HA	1:G:153:PRO:HD3	1.81	0.43
1:A:223:THR:O	1:A:241:ASP:HA	2.19	0.43
2:B:107:TRP:CH2	2:B:130:PHE:HE2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:LEU:HD13	1:C:285:TRP:CD2	2.53	0.43
2:D:74:SER:C	2:D:76:ASP:H	2.26	0.43
2:D:226:SER:HB3	2:D:228:ASP:OD1	2.19	0.43
1:E:196:VAL:O	1:E:197:ILE:HG13	2.19	0.43
1:E:223:THR:O	1:E:241:ASP:HA	2.19	0.43
2:F:102:VAL:HG22	3:F:304:HOH:O	2.14	0.43
1:G:252:LEU:HD13	1:G:285:TRP:CD2	2.53	0.43
2:H:145:ALA:O	2:H:147:GLY:N	2.50	0.43
2:H:227:GLN:HA	2:H:256:VAL:HG13	2.01	0.43
1:A:88:LEU:CD1	1:A:138:MET:SD	3.06	0.43
1:A:268:GLN:NE2	3:A:1309:HOH:O	2.51	0.43
1:A:392:LEU:CD1	3:A:1302:HOH:O	2.61	0.43
2:B:85:GLU:O	2:B:86:ASN:HB2	2.18	0.43
2:B:105:VAL:HG22	2:B:116:LEU:HD11	1.99	0.43
2:B:226:SER:HB3	2:B:228:ASP:OD1	2.19	0.43
2:B:227:GLN:HA	2:B:256:VAL:HG13	2.01	0.43
1:C:268:GLN:NE2	3:C:1307:HOH:O	2.51	0.43
1:C:289:SER:O	1:C:290:ALA:CB	2.65	0.43
1:G:201:TYR:CD2	1:G:238:LEU:HD11	2.54	0.43
1:G:223:THR:O	1:G:241:ASP:HA	2.19	0.43
2:H:112:TYR:N	2:H:112:TYR:CD1	2.86	0.43
2:H:226:SER:HB3	2:H:228:ASP:OD1	2.19	0.43
1:A:201:TYR:CD2	1:A:238:LEU:HD11	2.54	0.43
1:A:242:LEU:N	1:A:242:LEU:HD23	2.33	0.43
2:B:112:TYR:N	2:B:112:TYR:CD1	2.86	0.43
1:E:34:ALA:HA	1:G:196:VAL:CG1	2.47	0.43
1:E:67:ASP:OD2	1:E:113:THR:HG23	2.18	0.43
1:E:201:TYR:CD2	1:E:238:LEU:HD11	2.54	0.43
1:G:59:LEU:O	1:G:60:GLN:C	2.62	0.43
1:G:232:ASP:HA	1:G:259:GLY:N	2.33	0.43
1:G:399:GLY:HA3	2:H:11:LEU:CD1	2.49	0.43
1:A:314:ASP:CG	1:A:376:TRP:CZ2	2.87	0.43
1:A:404:ILE:N	1:A:404:ILE:HD12	2.34	0.43
1:C:7:PHE:CD1	1:C:7:PHE:N	2.87	0.43
1:C:201:TYR:CD2	1:C:238:LEU:HD11	2.54	0.43
1:C:236:SER:C	1:C:237:ILE:HD12	2.44	0.43
1:C:302:TRP:CD2	1:E:246:ASN:HB3	2.54	0.43
2:D:238:ASN:ND2	2:D:240:GLN:H	2.14	0.43
1:E:109:SER:O	1:E:110:SER:CB	2.61	0.43
1:E:162:GLU:HG3	1:E:164:ILE:CG2	2.48	0.43
2:F:25:ALA:HB2	2:F:61:TRP:HZ2	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:226:SER:HB3	2:F:228:ASP:OD1	2.19	0.43
1:G:67:ASP:OD2	1:G:113:THR:HG23	2.18	0.43
1:G:204:PRO:HG2	1:G:208:ILE:O	2.18	0.43
1:G:302:TRP:CD1	1:G:321:PHE:CD1	3.07	0.43
1:G:314:ASP:CB	1:G:376:TRP:CZ2	3.02	0.43
1:A:32:VAL:O	1:C:196:VAL:HB	2.19	0.42
1:A:124:LEU:CG	1:A:125:ALA:N	2.76	0.42
1:A:196:VAL:O	1:A:197:ILE:HG13	2.19	0.42
1:A:252:LEU:HD13	1:A:285:TRP:CD2	2.53	0.42
1:A:399:GLY:HA3	2:B:11:LEU:CD1	2.49	0.42
2:B:205:ASP:O	2:B:206:TRP:C	2.62	0.42
1:C:196:VAL:O	1:C:197:ILE:HG13	2.19	0.42
1:C:404:ILE:HD12	1:C:404:ILE:N	2.34	0.42
2:D:64:PRO:HD2	3:D:312:HOH:O	2.18	0.42
2:D:205:ASP:O	2:D:206:TRP:C	2.62	0.42
1:E:74:ASN:O	1:E:75:LYS:C	2.61	0.42
2:F:64:PRO:HD2	3:F:312:HOH:O	2.18	0.42
1:A:59:LEU:O	1:A:60:GLN:C	2.62	0.42
1:A:197:ILE:CG1	1:G:32:VAL:HG23	2.49	0.42
1:A:211:GLN:O	1:A:229:THR:HA	2.19	0.42
2:B:64:PRO:HD2	3:B:312:HOH:O	2.18	0.42
2:B:74:SER:C	2:B:76:ASP:H	2.26	0.42
1:C:74:ASN:O	1:C:75:LYS:C	2.61	0.42
1:C:314:ASP:CB	1:C:376:TRP:CZ2	3.02	0.42
2:D:30:ASP:OD1	2:D:32:THR:OG1	2.36	0.42
2:D:145:ALA:O	2:D:147:GLY:N	2.50	0.42
1:E:22:LEU:HD21	1:E:95:ASN:ND2	2.33	0.42
1:E:66:ASN:HD22	1:E:66:ASN:HA	1.64	0.42
1:E:187:ILE:HD13	1:E:187:ILE:HA	1.88	0.42
1:E:193:LYS:O	1:E:194:LYS:CB	2.65	0.42
1:E:236:SER:C	1:E:237:ILE:HD12	2.44	0.42
1:E:314:ASP:CG	1:E:376:TRP:CZ2	2.87	0.42
1:E:314:ASP:CB	1:E:376:TRP:CZ2	3.02	0.42
1:G:27:THR:HB	1:G:40:SER:HB2	2.01	0.42
1:G:86:LEU:HD21	1:G:104:PHE:HB2	1.99	0.42
1:G:330:LEU:HD12	1:G:330:LEU:HA	1.87	0.42
1:A:29:SER:OG	1:A:66:ASN:ND2	2.53	0.42
1:A:302:TRP:CD1	1:A:321:PHE:CD1	3.07	0.42
2:B:30:ASP:OD1	2:B:32:THR:OG1	2.36	0.42
2:D:227:GLN:HA	2:D:256:VAL:HG13	2.01	0.42
1:E:74:ASN:ND2	1:E:74:ASN:H	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:204:PRO:HG3	1:E:210:GLN:HG3	2.00	0.42
1:E:302:TRP:CD1	1:E:321:PHE:CD1	3.07	0.42
1:E:404:ILE:HD12	1:E:404:ILE:N	2.34	0.42
2:F:63:HIS:CD2	2:F:110:HIS:HB3	2.54	0.42
2:H:225:VAL:CG2	2:H:271:LEU:HD11	2.50	0.42
1:A:72:HIS:C	1:A:74:ASN:H	2.28	0.42
1:A:236:SER:C	1:A:237:ILE:HD12	2.44	0.42
1:C:202:THR:O	1:C:202:THR:CG2	2.67	0.42
1:C:302:TRP:CD1	1:C:321:PHE:CD1	3.07	0.42
2:D:63:HIS:CD2	2:D:110:HIS:HB3	2.54	0.42
1:E:34:ALA:CA	1:G:196:VAL:HG21	2.43	0.42
2:F:227:GLN:HA	2:F:256:VAL:HG13	2.01	0.42
1:G:27:THR:O	1:G:65:PHE:HB2	2.18	0.42
2:B:63:HIS:CD2	2:B:110:HIS:HB3	2.54	0.42
2:B:189:SER:C	2:B:191:ALA:N	2.76	0.42
2:B:282:LYS:HB3	2:B:292:ALA:HB2	2.02	0.42
2:D:107:TRP:CH2	2:D:130:PHE:HE2	2.37	0.42
1:E:7:PHE:CD1	1:E:7:PHE:N	2.87	0.42
1:E:29:SER:OG	1:E:66:ASN:ND2	2.53	0.42
1:G:202:THR:O	1:G:202:THR:CG2	2.67	0.42
1:G:211:GLN:O	1:G:229:THR:HA	2.19	0.42
1:G:247:THR:HG23	1:G:248:PRO:HD2	2.02	0.42
2:H:233:ILE:N	2:H:233:ILE:HD12	2.35	0.42
1:A:215:VAL:HA	1:A:226:ALA:O	2.20	0.42
1:C:29:SER:OG	1:C:66:ASN:ND2	2.53	0.42
1:C:67:ASP:OD2	1:C:113:THR:HG23	2.18	0.42
1:C:152:THR:HA	1:C:153:PRO:HD3	1.81	0.42
1:E:211:GLN:O	1:E:229:THR:HA	2.19	0.42
2:F:16:VAL:HG12	2:F:61:TRP:HD1	1.84	0.42
2:F:46:ILE:HG22	2:F:46:ILE:O	2.19	0.42
2:F:107:TRP:CH2	2:F:130:PHE:HE2	2.37	0.42
1:G:15:TRP:HZ3	1:G:317:ALA:H	1.67	0.42
1:G:31:THR:OG1	1:G:321:PHE:HD2	2.03	0.42
2:H:63:HIS:CD2	2:H:110:HIS:HB3	2.54	0.42
2:H:107:TRP:CH2	2:H:130:PHE:HE2	2.37	0.42
2:H:155:PRO:CG	2:H:214:PRO:HA	2.49	0.42
2:H:248:LEU:HD12	2:H:248:LEU:HA	1.86	0.42
1:C:6:GLU:OE2	1:C:324:LYS:HB2	2.20	0.42
1:C:274:LEU:HA	1:C:274:LEU:HD23	1.69	0.42
1:C:329:THR:C	1:C:331:GLN:N	2.73	0.42
1:E:247:THR:HG23	1:E:248:PRO:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:205:ASP:O	2:F:206:TRP:C	2.62	0.42
1:G:29:SER:OG	1:G:66:ASN:ND2	2.53	0.42
1:G:151:LEU:CD1	1:G:152:THR:H	2.25	0.42
1:G:196:VAL:O	1:G:197:ILE:HG13	2.19	0.42
2:H:282:LYS:HB3	2:H:292:ALA:HB2	2.02	0.42
1:A:31:THR:OG1	1:A:321:PHE:HD2	2.03	0.42
2:B:281:TRP:CD1	2:B:281:TRP:N	2.87	0.42
1:C:59:LEU:O	1:C:60:GLN:C	2.62	0.42
1:E:6:GLU:OE2	1:E:324:LYS:HB2	2.20	0.42
1:E:59:LEU:O	1:E:60:GLN:C	2.62	0.42
1:E:237:ILE:HD12	1:E:237:ILE:N	2.35	0.42
1:G:215:VAL:HA	1:G:226:ALA:O	2.20	0.42
2:H:281:TRP:CD1	2:H:281:TRP:N	2.87	0.42
1:A:314:ASP:CB	1:A:376:TRP:CZ2	3.02	0.42
1:C:15:TRP:HZ3	1:C:317:ALA:H	1.67	0.42
1:C:330:LEU:HD12	1:C:330:LEU:HA	1.87	0.42
1:E:15:TRP:HZ3	1:E:317:ALA:H	1.67	0.42
1:G:9:ARG:O	1:G:10:THR:C	2.63	0.42
1:G:72:HIS:C	1:G:74:ASN:H	2.28	0.42
1:G:144:SER:C	1:G:146:SER:N	2.77	0.42
1:G:261:LEU:N	1:G:277:GLY:HA2	2.35	0.42
2:H:16:VAL:HG12	2:H:61:TRP:HD1	1.85	0.42
1:A:6:GLU:OE2	1:A:324:LYS:HB2	2.20	0.42
1:A:74:ASN:O	1:A:75:LYS:C	2.61	0.42
1:A:196:VAL:HG23	1:G:32:VAL:HG21	2.02	0.42
1:A:204:PRO:C	1:A:205:ASN:CG	2.88	0.42
2:B:16:VAL:HG12	2:B:61:TRP:HD1	1.85	0.42
2:B:238:ASN:ND2	2:B:240:GLN:H	2.14	0.42
1:C:72:HIS:C	1:C:74:ASN:H	2.27	0.42
1:C:125:ALA:HB2	1:C:168:TRP:CZ3	2.53	0.42
1:C:215:VAL:HA	1:C:226:ALA:O	2.20	0.42
1:E:9:ARG:HB3	1:E:10:THR:H	1.65	0.42
1:E:84:GLY:HA2	1:E:111:VAL:HG23	2.02	0.42
1:E:202:THR:O	1:E:202:THR:CG2	2.67	0.42
1:E:329:THR:C	1:E:331:GLN:N	2.73	0.42
1:G:7:PHE:HB2	1:G:8:SER:H	1.51	0.42
1:G:268:GLN:NE2	3:G:1307:HOH:O	2.51	0.42
1:G:404:ILE:N	1:G:404:ILE:HD12	2.34	0.42
1:A:15:TRP:HZ3	1:A:317:ALA:H	1.68	0.41
2:B:238:ASN:HB2	3:B:345:HOH:O	2.20	0.41
1:C:229:THR:HG22	1:C:230:GLY:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:286:ASN:HA	1:C:287:PRO:HD2	1.83	0.41
2:D:121:SER:CA	3:D:301:HOH:O	2.68	0.41
2:F:49:LEU:HA	3:F:334:HOH:O	2.20	0.41
2:F:121:SER:CA	3:F:301:HOH:O	2.68	0.41
2:F:233:ILE:N	2:F:233:ILE:HD12	2.35	0.41
1:G:70:TRP:O	1:G:71:SER:C	2.63	0.41
1:A:84:GLY:HA2	1:A:111:VAL:HG23	2.03	0.41
1:A:229:THR:HG22	1:A:230:GLY:N	2.35	0.41
2:B:52:HIS:CD2	2:B:56:VAL:HG22	2.55	0.41
1:C:84:GLY:HA2	1:C:111:VAL:HG23	2.03	0.41
1:C:237:ILE:HD12	1:C:237:ILE:N	2.35	0.41
2:D:16:VAL:HG12	2:D:61:TRP:HD1	1.85	0.41
2:D:46:ILE:O	2:D:46:ILE:HG22	2.19	0.41
2:D:155:PRO:CG	2:D:214:PRO:HA	2.49	0.41
1:E:9:ARG:O	1:E:10:THR:C	2.63	0.41
1:E:399:GLY:HA3	2:F:11:LEU:CD1	2.49	0.41
2:F:213:SER:HB2	2:F:262:TRP:CD2	2.55	0.41
1:G:6:GLU:OE2	1:G:324:LYS:HB2	2.20	0.41
1:G:125:ALA:CB	1:G:168:TRP:CH2	2.92	0.41
1:G:271:HIS:HB3	1:G:286:ASN:OD1	2.20	0.41
1:G:272:LEU:HD23	1:G:272:LEU:HA	1.81	0.41
2:H:238:ASN:HB2	3:H:345:HOH:O	2.20	0.41
2:B:225:VAL:CG1	2:B:257:LEU:O	2.69	0.41
2:B:225:VAL:CG2	2:B:271:LEU:HD11	2.49	0.41
1:C:70:TRP:O	1:C:71:SER:C	2.63	0.41
1:C:214:VAL:HB	1:C:228:ALA:HB3	2.03	0.41
2:D:238:ASN:HB2	3:D:345:HOH:O	2.20	0.41
2:D:282:LYS:HB3	2:D:292:ALA:HB2	2.02	0.41
1:E:261:LEU:N	1:E:277:GLY:HA2	2.35	0.41
1:E:279:ASP:C	1:E:281:THR:H	2.29	0.41
2:F:30:ASP:OD1	2:F:32:THR:OG1	2.36	0.41
2:H:4:ILE:N	2:H:4:ILE:CD1	2.83	0.41
1:A:66:ASN:HD22	1:A:66:ASN:HA	1.64	0.41
1:A:144:SER:C	1:A:146:SER:H	2.28	0.41
1:A:279:ASP:C	1:A:281:THR:H	2.29	0.41
2:B:23:ARG:NH1	2:B:68:THR:CG2	2.83	0.41
2:B:46:ILE:O	2:B:46:ILE:HG22	2.19	0.41
2:B:121:SER:CA	3:B:301:HOH:O	2.68	0.41
2:B:233:ILE:HD12	2:B:233:ILE:N	2.35	0.41
1:C:20:ILE:O	1:C:20:ILE:CG1	2.65	0.41
1:C:127:GLY:HA3	1:C:163:VAL:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:247:THR:HG23	1:C:248:PRO:HD2	2.02	0.41
2:D:225:VAL:CG2	2:D:271:LEU:HD11	2.50	0.41
1:E:9:ARG:HA	1:E:324:LYS:HA	2.02	0.41
1:E:27:THR:HB	1:E:40:SER:HB2	2.01	0.41
1:E:72:HIS:C	1:E:74:ASN:H	2.28	0.41
1:E:215:VAL:HA	1:E:226:ALA:O	2.20	0.41
1:E:268:GLN:CA	1:E:374:PRO:O	2.63	0.41
2:F:155:PRO:CG	2:F:214:PRO:HA	2.49	0.41
1:G:9:ARG:HA	1:G:324:LYS:HA	2.02	0.41
2:H:2:VAL:HG13	2:H:41:GLU:HA	2.03	0.41
1:A:204:PRO:HG3	1:A:210:GLN:HG3	2.00	0.41
1:A:261:LEU:N	1:A:277:GLY:HA2	2.35	0.41
1:A:272:LEU:HD23	1:A:272:LEU:HA	1.81	0.41
1:C:9:ARG:HA	1:C:324:LYS:HA	2.02	0.41
1:C:261:LEU:N	1:C:277:GLY:HA2	2.35	0.41
1:C:399:GLY:HA3	2:D:11:LEU:CD1	2.49	0.41
2:D:52:HIS:CD2	2:D:56:VAL:HG22	2.55	0.41
1:E:96:ASN:O	1:E:97:ALA:HB2	2.21	0.41
1:E:214:VAL:HB	1:E:228:ALA:HB3	2.03	0.41
1:E:229:THR:HG22	1:E:230:GLY:N	2.35	0.41
2:F:4:ILE:N	2:F:4:ILE:CD1	2.83	0.41
2:F:23:ARG:NH1	2:F:68:THR:CG2	2.83	0.41
2:F:282:LYS:HB3	2:F:292:ALA:HB2	2.02	0.41
1:G:78:ALA:CB	1:G:114:VAL:CG1	2.95	0.41
1:G:96:ASN:O	1:G:97:ALA:HB2	2.21	0.41
1:A:70:TRP:O	1:A:71:SER:C	2.63	0.41
1:A:144:SER:C	1:A:146:SER:N	2.78	0.41
1:A:271:HIS:HB3	1:A:286:ASN:OD1	2.21	0.41
2:B:4:ILE:N	2:B:4:ILE:CD1	2.83	0.41
1:C:9:ARG:O	1:C:10:THR:C	2.63	0.41
1:C:27:THR:HB	1:C:40:SER:HB2	2.01	0.41
1:C:113:THR:CG2	1:C:114:VAL:N	2.84	0.41
2:D:213:SER:HB2	2:D:262:TRP:CD2	2.55	0.41
1:E:268:GLN:NE2	3:E:1309:HOH:O	2.51	0.41
2:H:52:HIS:CD2	2:H:56:VAL:HG22	2.55	0.41
1:C:144:SER:C	1:C:146:SER:H	2.28	0.41
2:D:4:ILE:N	2:D:4:ILE:CD1	2.83	0.41
1:E:36:PHE:HD2	1:G:192:ALA:O	2.02	0.41
1:E:36:PHE:N	1:G:189:ASP:CB	2.78	0.41
1:E:125:ALA:HB2	1:E:168:TRP:CZ3	2.53	0.41
1:E:365:LYS:O	1:E:366:PRO:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:46:ILE:O	2:F:47:ASP:HB2	2.21	0.41
2:F:225:VAL:CG2	2:F:271:LEU:HD11	2.50	0.41
2:H:49:LEU:HA	3:H:334:HOH:O	2.20	0.41
2:H:120:SER:C	2:H:122:ASP:H	2.29	0.41
2:H:205:ASP:O	2:H:206:TRP:C	2.62	0.41
1:A:9:ARG:O	1:A:10:THR:C	2.63	0.41
1:A:36:PHE:N	1:C:189:ASP:CB	2.84	0.41
1:A:125:ALA:HB2	1:A:168:TRP:CZ3	2.53	0.41
2:B:24:LEU:HG	2:B:25:ALA:H	1.86	0.41
1:C:144:SER:C	1:C:146:SER:N	2.78	0.41
1:C:204:PRO:C	1:C:205:ASN:CG	2.88	0.41
1:E:32:VAL:CG1	1:G:195:GLU:O	2.69	0.41
1:E:113:THR:CG2	1:E:114:VAL:N	2.84	0.41
1:E:127:GLY:HA3	1:E:163:VAL:HB	2.03	0.41
1:E:252:LEU:HB3	1:E:285:TRP:CE3	2.55	0.41
1:G:279:ASP:C	1:G:281:THR:H	2.29	0.41
1:G:381:SER:HA	1:G:382:PRO:HD3	1.99	0.41
1:A:7:PHE:CD1	1:A:7:PHE:N	2.87	0.41
1:A:27:THR:HB	1:A:40:SER:HB2	2.01	0.41
1:A:113:THR:CG2	1:A:114:VAL:N	2.84	0.41
1:A:203:SER:O	1:A:204:PRO:C	2.64	0.41
1:A:237:ILE:HD12	1:A:237:ILE:N	2.35	0.41
1:A:252:LEU:HB3	1:A:285:TRP:CE3	2.55	0.41
1:A:365:LYS:O	1:A:366:PRO:C	2.64	0.41
2:B:120:SER:C	2:B:122:ASP:H	2.29	0.41
1:C:96:ASN:O	1:C:97:ALA:HB2	2.21	0.41
1:C:252:LEU:HB3	1:C:285:TRP:CE3	2.55	0.41
1:C:396:THR:HB	1:C:398:ASP:OD2	2.21	0.41
2:D:23:ARG:HH12	2:D:68:THR:HG21	1.86	0.41
2:D:225:VAL:CG1	2:D:257:LEU:O	2.69	0.41
2:D:233:ILE:HD12	2:D:233:ILE:N	2.35	0.41
1:E:31:THR:OG1	1:E:321:PHE:HD2	2.03	0.41
1:E:144:SER:C	1:E:146:SER:H	2.28	0.41
2:F:238:ASN:ND2	2:F:240:GLN:H	2.14	0.41
1:G:41:SER:O	1:G:42:LEU:CB	2.67	0.41
1:G:84:GLY:HA2	1:G:111:VAL:HG23	2.03	0.41
1:G:127:GLY:HA3	1:G:163:VAL:HB	2.03	0.41
1:G:252:LEU:HB3	1:G:285:TRP:CE3	2.55	0.41
2:H:17:LEU:HB3	2:H:21:GLY:HA2	2.03	0.41
2:H:213:SER:HB2	2:H:262:TRP:CD2	2.55	0.41
1:A:9:ARG:HA	1:A:324:LYS:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:ALA:HA	1:C:196:VAL:CG2	2.44	0.41
1:A:127:GLY:HA3	1:A:163:VAL:HB	2.03	0.41
1:A:396:THR:HB	1:A:398:ASP:OD2	2.21	0.41
2:B:46:ILE:O	2:B:47:ASP:HB2	2.21	0.41
2:D:87:GLY:O	2:D:88:ARG:HG3	2.21	0.41
2:D:253:PHE:HB3	2:D:254:PRO:HD2	2.03	0.41
1:E:70:TRP:O	1:E:71:SER:C	2.63	0.41
2:F:253:PHE:HB3	2:F:254:PRO:HD2	2.03	0.41
1:G:144:SER:C	1:G:146:SER:H	2.28	0.41
1:G:187:ILE:HD13	1:G:187:ILE:HA	1.88	0.41
1:G:214:VAL:HB	1:G:228:ALA:HB3	2.03	0.41
2:H:17:LEU:HD23	2:H:24:LEU:HA	2.03	0.41
1:A:96:ASN:O	1:A:97:ALA:HB2	2.21	0.40
1:A:214:VAL:HB	1:A:228:ALA:HB3	2.03	0.40
2:B:81:ILE:HD13	2:B:93:ALA:CB	2.40	0.40
2:B:213:SER:HB2	2:B:262:TRP:CD2	2.55	0.40
1:C:271:HIS:HB3	1:C:286:ASN:OD1	2.21	0.40
1:E:78:ALA:CB	1:E:114:VAL:CG1	2.95	0.40
2:F:225:VAL:CG1	2:F:257:LEU:O	2.69	0.40
1:G:217:TRP:CE3	1:G:225:VAL:HG22	2.56	0.40
2:H:87:GLY:O	2:H:88:ARG:HG3	2.21	0.40
1:A:15:TRP:HH2	1:A:316:PHE:C	2.29	0.40
2:B:78:LYS:HG2	2:B:96:ALA:CB	2.52	0.40
2:B:87:GLY:O	2:B:88:ARG:HG3	2.21	0.40
2:D:23:ARG:NH1	2:D:68:THR:CG2	2.83	0.40
2:D:212:TRP:HA	2:D:222:LEU:HD23	2.02	0.40
1:E:244:ASN:ND2	1:E:244:ASN:C	2.80	0.40
2:F:52:HIS:CD2	2:F:56:VAL:HG22	2.55	0.40
2:F:212:TRP:HA	2:F:222:LEU:HD23	2.02	0.40
1:G:268:GLN:CA	1:G:374:PRO:O	2.63	0.40
1:G:373:ALA:HA	1:G:374:PRO:HD3	1.95	0.40
2:H:78:LYS:HG2	2:H:96:ALA:CB	2.52	0.40
1:A:19:LYS:HD3	1:A:311:GLU:HG3	2.03	0.40
2:B:2:VAL:HG13	2:B:41:GLU:HA	2.03	0.40
2:B:17:LEU:HB3	2:B:21:GLY:HA2	2.03	0.40
1:C:301:ASN:N	1:C:322:ASP:OD2	2.51	0.40
2:D:46:ILE:O	2:D:47:ASP:HB2	2.21	0.40
1:E:75:LYS:NZ	1:E:94:ALA:CB	2.80	0.40
1:E:271:HIS:HB3	1:E:286:ASN:OD1	2.21	0.40
1:G:229:THR:HG22	1:G:230:GLY:N	2.35	0.40
2:H:46:ILE:O	2:H:47:ASP:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:212:TRP:HA	2:H:222:LEU:HD23	2.02	0.40
1:A:116:PHE:CD1	1:A:124:LEU:HD13	2.57	0.40
1:A:252:LEU:CD2	1:A:290:ALA:HA	2.52	0.40
2:B:69:ILE:HA	2:B:82:TRP:O	2.22	0.40
1:C:48:LEU:O	1:C:49:ALA:C	2.64	0.40
1:C:217:TRP:CE3	1:C:225:VAL:HG22	2.56	0.40
1:C:244:ASN:ND2	1:C:244:ASN:C	2.80	0.40
1:C:279:ASP:C	1:C:281:THR:H	2.29	0.40
2:D:17:LEU:HB3	2:D:21:GLY:HA2	2.02	0.40
1:E:15:TRP:HH2	1:E:316:PHE:C	2.29	0.40
1:E:19:LYS:HD3	1:E:311:GLU:HG3	2.03	0.40
1:E:289:SER:HG	1:E:291:GLU:HG3	1.87	0.40
1:E:330:LEU:HD12	1:E:330:LEU:HA	1.87	0.40
1:E:396:THR:HB	1:E:398:ASP:OD2	2.21	0.40
2:F:2:VAL:HG13	2:F:41:GLU:HA	2.03	0.40
2:F:17:LEU:HB3	2:F:21:GLY:HA2	2.03	0.40
1:G:314:ASP:CG	1:G:376:TRP:CZ2	2.87	0.40
1:A:41:SER:O	1:A:42:LEU:CB	2.67	0.40
1:A:202:THR:O	1:A:202:THR:CG2	2.67	0.40
2:B:152:SER:OG	2:B:210:VAL:O	2.33	0.40
2:B:155:PRO:CG	2:B:214:PRO:HA	2.49	0.40
1:C:203:SER:O	1:C:204:PRO:C	2.64	0.40
2:D:2:VAL:HG13	2:D:41:GLU:HA	2.03	0.40
2:D:49:LEU:HA	3:D:334:HOH:O	2.20	0.40
1:E:217:TRP:CE3	1:E:225:VAL:HG22	2.56	0.40
2:F:120:SER:C	2:F:122:ASP:H	2.29	0.40
1:G:15:TRP:HH2	1:G:316:PHE:C	2.29	0.40
1:G:40:SER:HB3	1:G:64:LYS:HG2	2.04	0.40
1:G:169:ASN:HD22	1:G:170:GLN:N	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	377/1273 (30%)	267 (71%)	64 (17%)	46 (12%)	0	4
1	C	377/1273 (30%)	267 (71%)	64 (17%)	46 (12%)	0	4
1	E	377/1273 (30%)	267 (71%)	64 (17%)	46 (12%)	0	4
1	G	377/1273 (30%)	267 (71%)	64 (17%)	46 (12%)	0	4
2	B	275/297 (93%)	241 (88%)	30 (11%)	4 (2%)	8	40
2	D	275/297 (93%)	241 (88%)	30 (11%)	4 (2%)	8	40
2	F	275/297 (93%)	241 (88%)	30 (11%)	4 (2%)	8	40
2	H	275/297 (93%)	241 (88%)	30 (11%)	4 (2%)	8	40
All	All	2608/6280 (42%)	2032 (78%)	376 (14%)	200 (8%)	1	10

All (200) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	ASP
1	A	49	ALA
1	A	74	ASN
1	A	110	SER
1	A	143	GLU
1	A	146	SER
1	A	147	ASN
1	A	159	SER
1	A	203	SER
1	A	242	LEU
1	A	290	ALA
1	A	301	ASN
1	A	313	PRO
1	A	335	ASN
1	A	336	THR
1	A	365	LYS
1	A	369	PHE
2	B	131	LYS
1	C	33	ASP
1	C	49	ALA
1	C	74	ASN
1	C	110	SER
1	C	143	GLU
1	C	146	SER
1	C	147	ASN
1	C	159	SER
1	C	203	SER

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Mol	Chain	Res	Type
1	C	242	LEU
1	C	290	ALA
1	C	301	ASN
1	C	313	PRO
1	C	335	ASN
1	C	336	THR
1	C	365	LYS
1	C	369	PHE
2	D	131	LYS
1	E	33	ASP
1	E	49	ALA
1	E	74	ASN
1	E	110	SER
1	E	143	GLU
1	E	146	SER
1	E	147	ASN
1	E	159	SER
1	E	203	SER
1	E	242	LEU
1	E	290	ALA
1	E	301	ASN
1	E	313	PRO
1	E	335	ASN
1	E	336	THR
1	E	365	LYS
1	E	369	PHE
2	F	131	LYS
1	G	33	ASP
1	G	49	ALA
1	G	74	ASN
1	G	110	SER
1	G	143	GLU
1	G	146	SER
1	G	147	ASN
1	G	159	SER
1	G	203	SER
1	G	242	LEU
1	G	290	ALA
1	G	301	ASN
1	G	313	PRO
1	G	335	ASN
1	G	336	THR

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Mol	Chain	Res	Type
1	G	365	LYS
1	G	369	PHE
2	H	131	LYS
1	A	10	THR
1	A	84	GLY
1	A	105	SER
1	A	160	VAL
1	A	194	LYS
1	A	238	LEU
1	A	266	CYS
1	A	322	ASP
1	A	332	ASN
1	A	337	LEU
1	A	388	PHE
2	B	135	THR
1	C	10	THR
1	C	84	GLY
1	C	105	SER
1	C	160	VAL
1	C	194	LYS
1	C	238	LEU
1	C	266	CYS
1	C	322	ASP
1	C	332	ASN
1	C	337	LEU
1	C	388	PHE
2	D	135	THR
1	E	10	THR
1	E	84	GLY
1	E	105	SER
1	E	160	VAL
1	E	194	LYS
1	E	238	LEU
1	E	266	CYS
1	E	322	ASP
1	E	332	ASN
1	E	337	LEU
1	E	388	PHE
2	F	135	THR
1	G	10	THR
1	G	84	GLY
1	G	105	SER

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Mol	Chain	Res	Type
1	G	160	VAL
1	G	194	LYS
1	G	238	LEU
1	G	266	CYS
1	G	322	ASP
1	G	332	ASN
1	G	337	LEU
1	G	388	PHE
2	H	135	THR
1	A	16	SER
1	A	52	SER
1	A	60	GLN
1	A	93	GLU
1	A	121	ASP
1	A	148	TYR
1	A	153	PRO
1	A	204	PRO
1	A	299	ARG
1	A	363	LYS
2	B	190	ASP
1	C	16	SER
1	C	52	SER
1	C	60	GLN
1	C	93	GLU
1	C	121	ASP
1	C	148	TYR
1	C	153	PRO
1	C	204	PRO
1	C	299	ARG
1	C	363	LYS
2	D	190	ASP
1	E	16	SER
1	E	52	SER
1	E	60	GLN
1	E	93	GLU
1	E	121	ASP
1	E	148	TYR
1	E	153	PRO
1	E	204	PRO
1	E	299	ARG
1	E	363	LYS
2	F	190	ASP

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Mol	Chain	Res	Type
1	G	16	SER
1	G	52	SER
1	G	60	GLN
1	G	93	GLU
1	G	121	ASP
1	G	148	TYR
1	G	153	PRO
1	G	204	PRO
1	G	299	ARG
1	G	363	LYS
2	H	190	ASP
1	A	91	THR
1	A	302	TRP
1	A	368	VAL
2	B	202	GLY
1	C	91	THR
1	C	302	TRP
1	C	368	VAL
2	D	202	GLY
1	E	91	THR
1	E	302	TRP
1	E	368	VAL
2	F	202	GLY
1	G	91	THR
1	G	302	TRP
1	G	368	VAL
2	H	202	GLY
1	A	9	ARG
1	A	94	ALA
1	A	109	SER
1	A	207	GLY
1	C	9	ARG
1	C	94	ALA
1	C	109	SER
1	C	207	GLY
1	E	9	ARG
1	E	94	ALA
1	E	109	SER
1	E	207	GLY
1	G	9	ARG
1	G	94	ALA
1	G	109	SER

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Mol	Chain	Res	Type
1	G	207	GLY
1	A	287	PRO
1	C	287	PRO
1	E	287	PRO
1	G	287	PRO

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	C	1

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Mol	Chain	Number of breaks
1	E	1
1	G	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	372:GLN	C	373:ALA	N	16.58
1	C	372:GLN	C	373:ALA	N	16.58
1	E	372:GLN	C	373:ALA	N	16.58
1	G	372:GLN	C	373:ALA	N	16.58

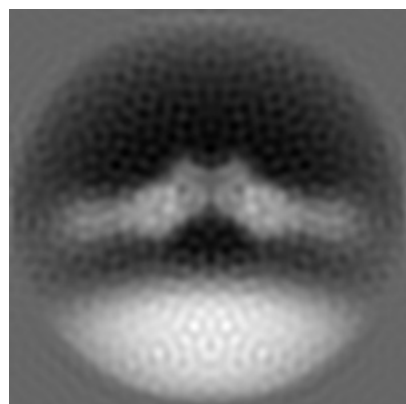
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11194. These allow visual inspection of the internal detail of the map and identification of artifacts.

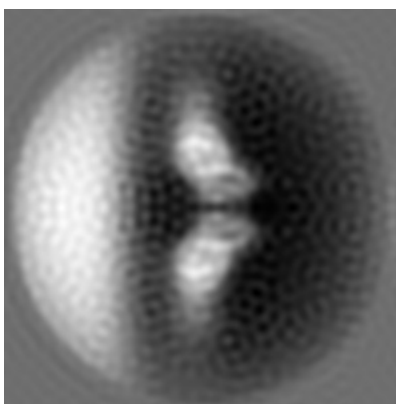
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

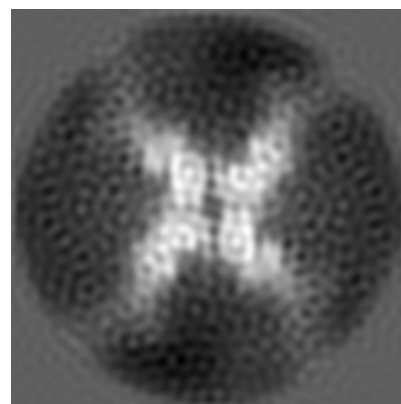
6.1.1 Primary map



X



Y

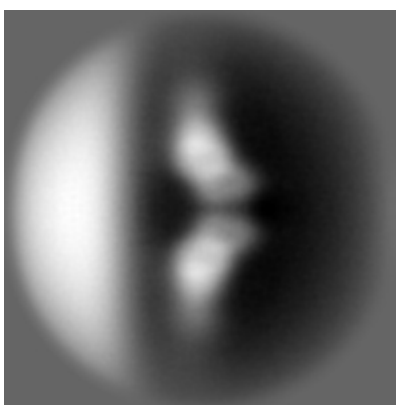


Z

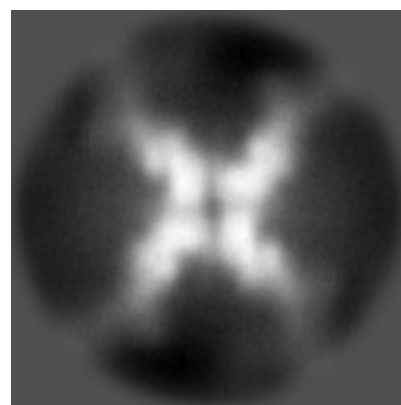
6.1.2 Raw map



X



Y

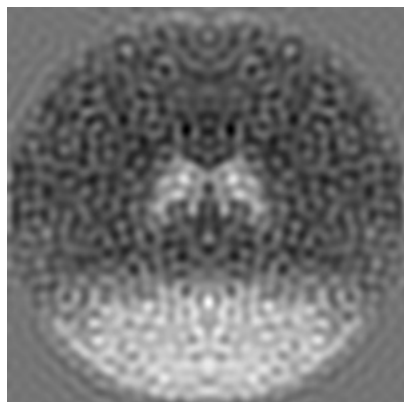


Z

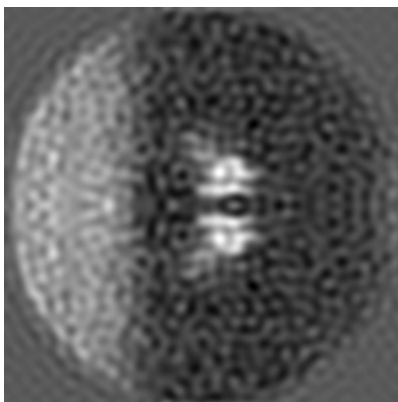
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

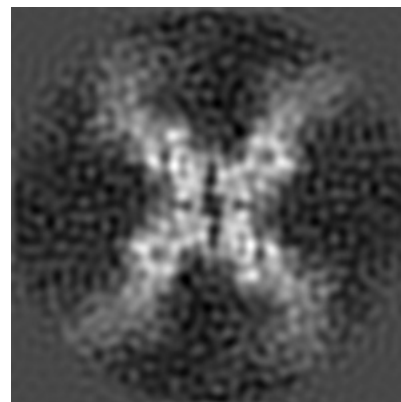
6.2.1 Primary map



X Index: 64

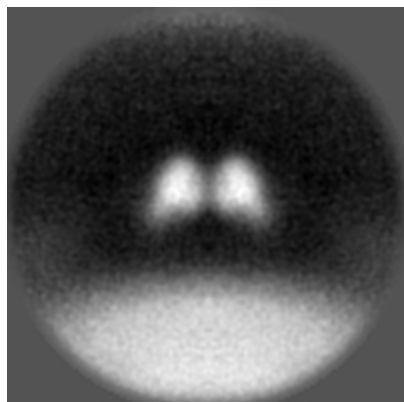


Y Index: 64

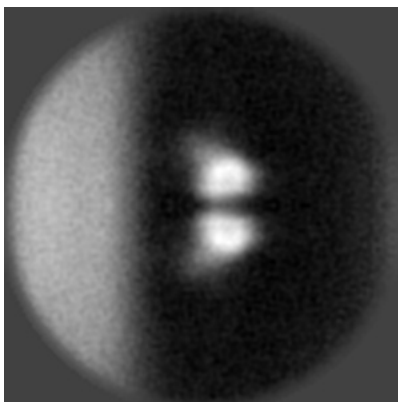


Z Index: 64

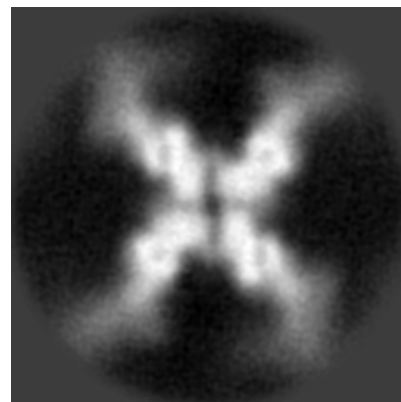
6.2.2 Raw map



X Index: 64



Y Index: 64

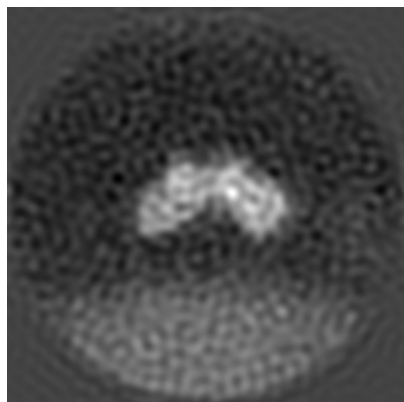


Z Index: 64

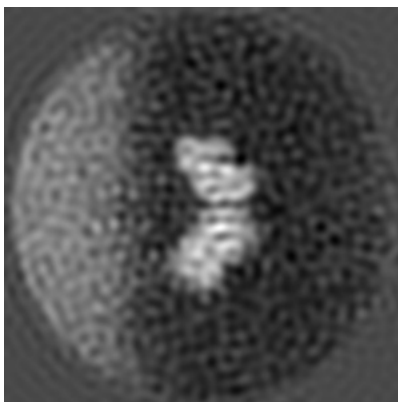
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

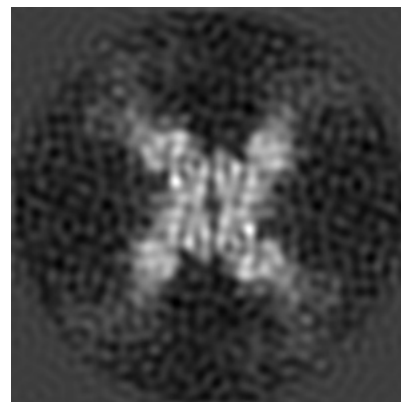
6.3.1 Primary map



X Index: 52

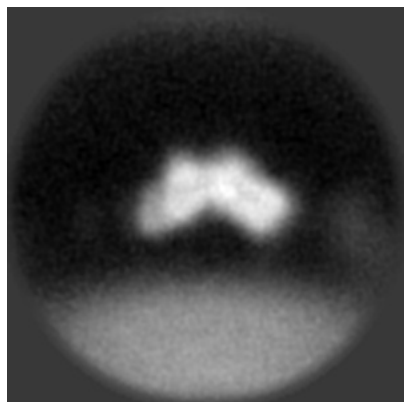


Y Index: 52

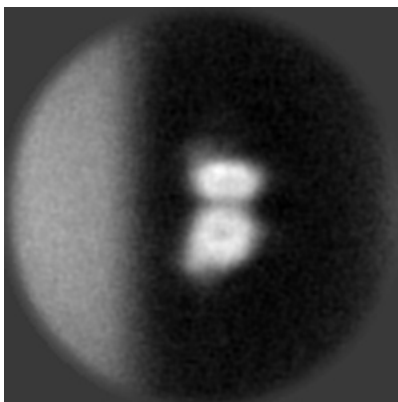


Z Index: 67

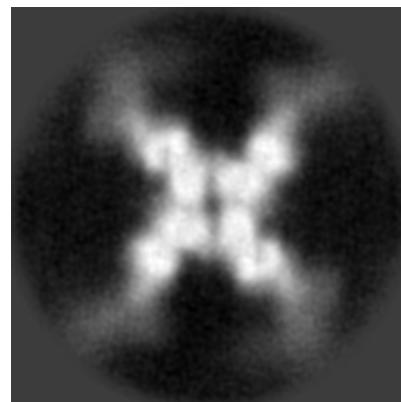
6.3.2 Raw map



X Index: 53



Y Index: 57

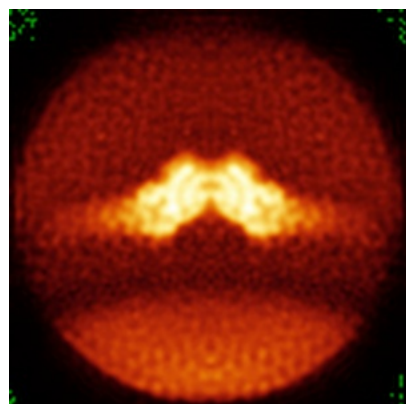


Z Index: 66

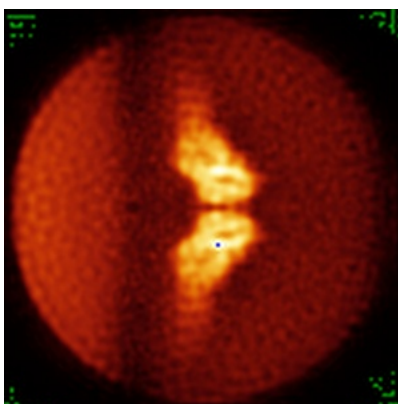
The images above show the largest variance slices of the map in three orthogonal directions.

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

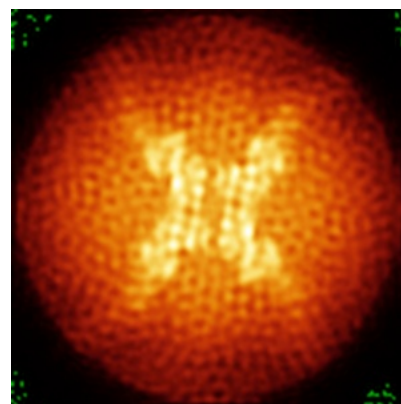
6.4.1 Primary map



X

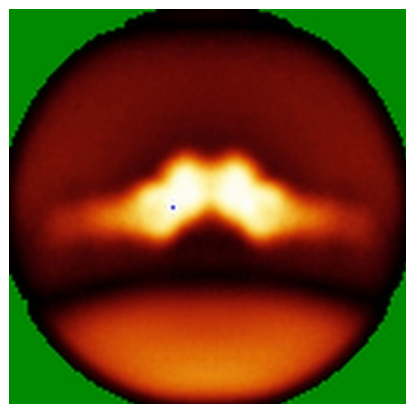


Y

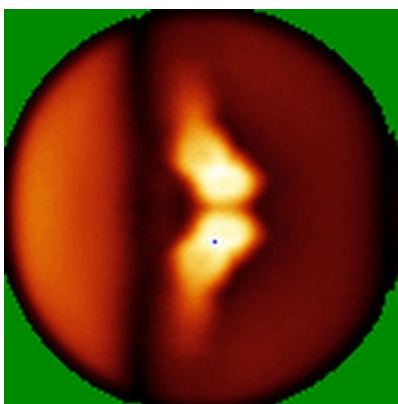


Z

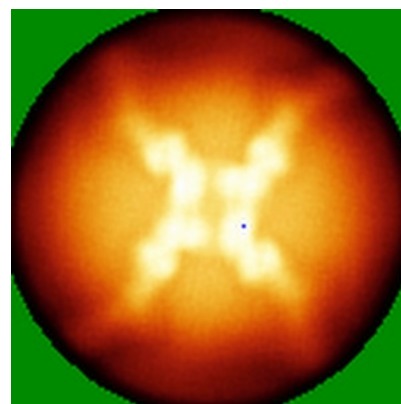
6.4.2 Raw map



X



Y

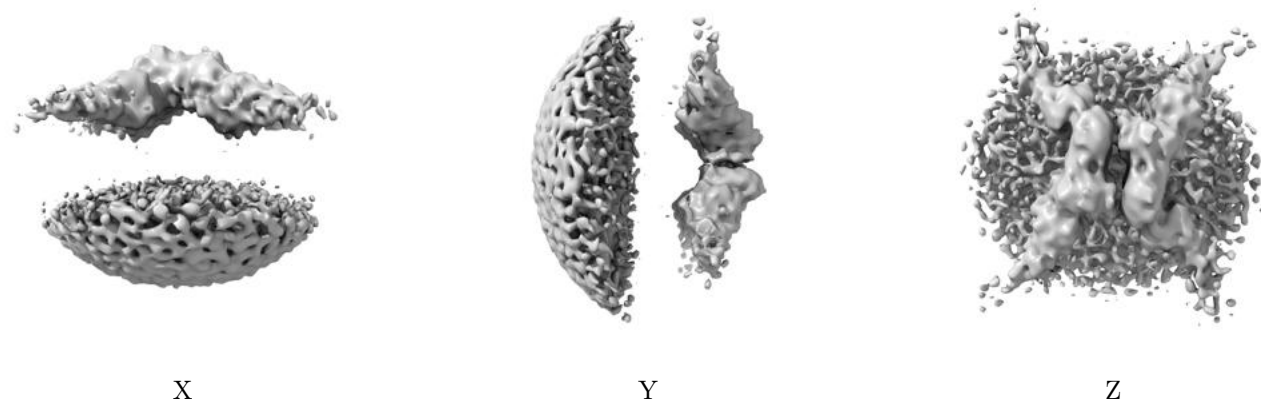


Z

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.

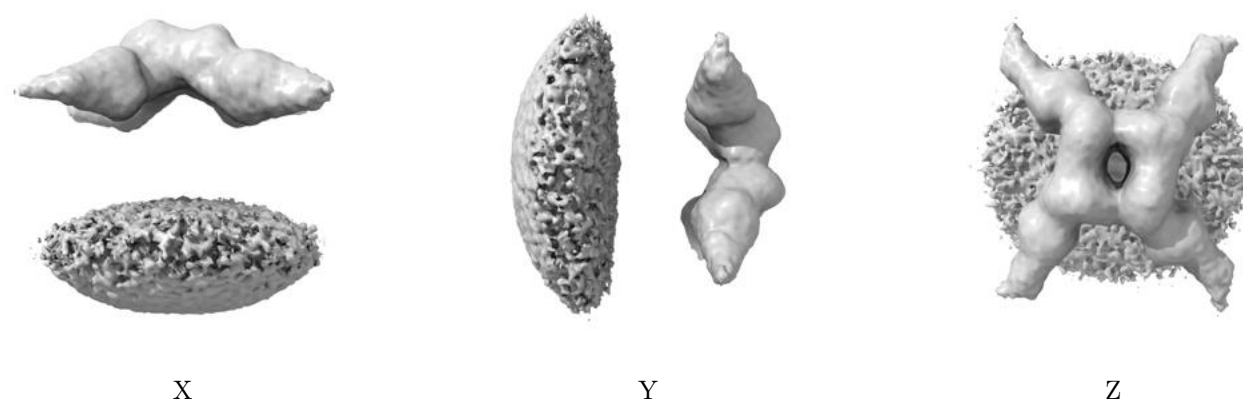
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

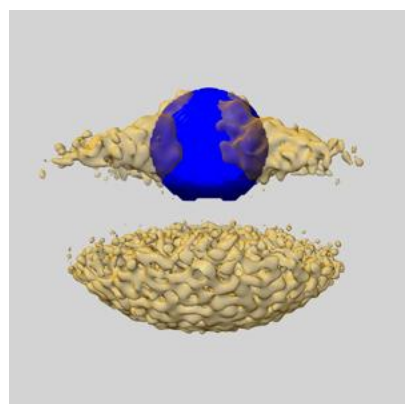
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

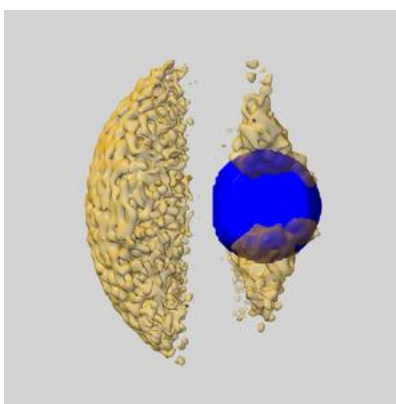
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

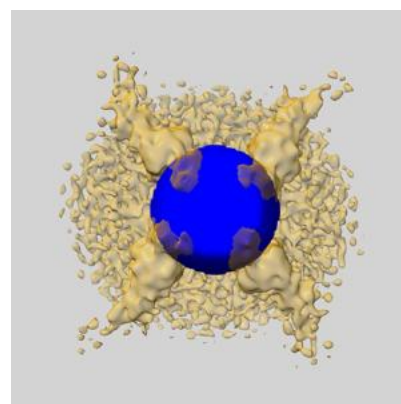
6.6.1 emd_11194_msk_1.map [i](#)



X



Y

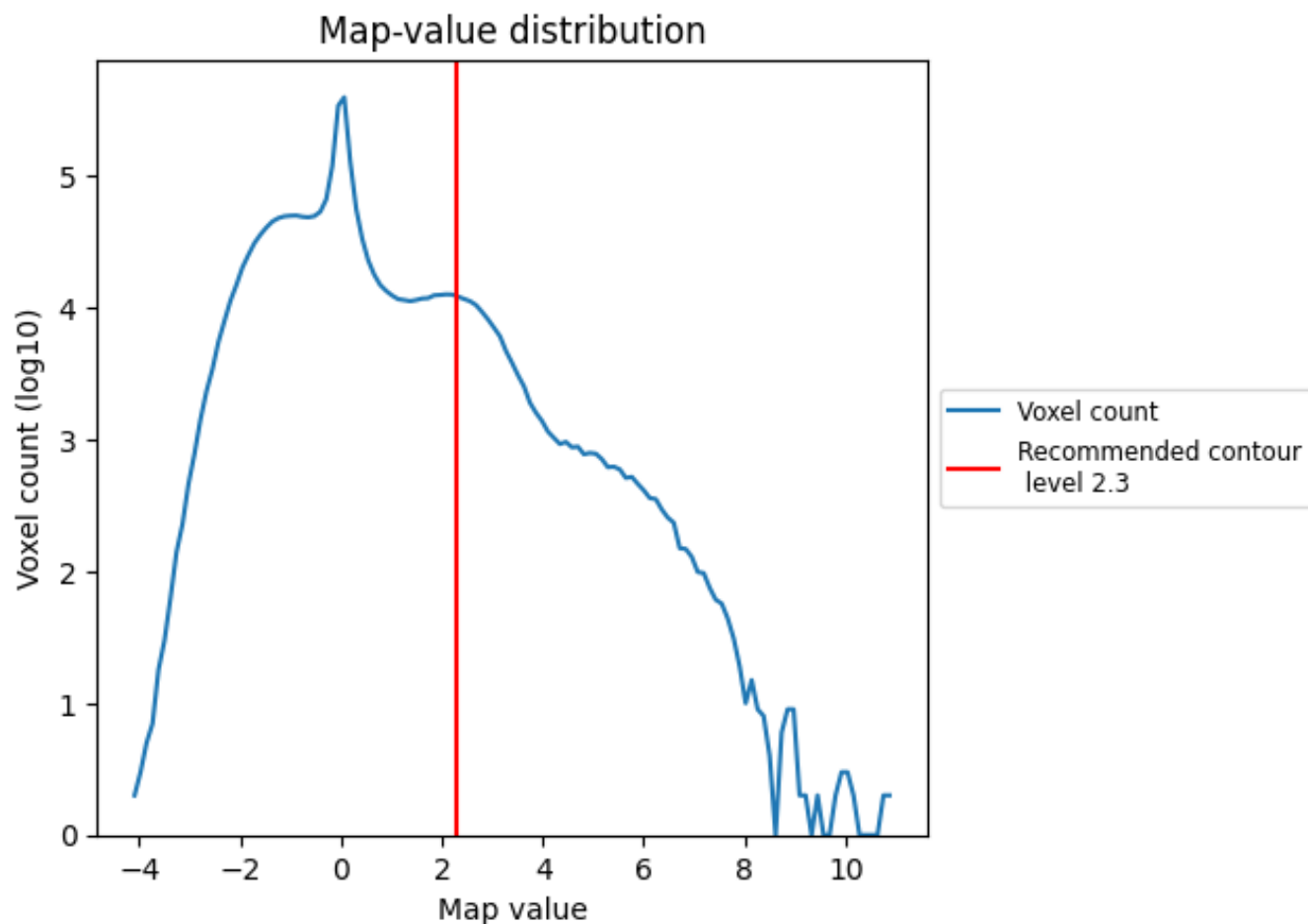


Z

7 Map analysis [i](#)

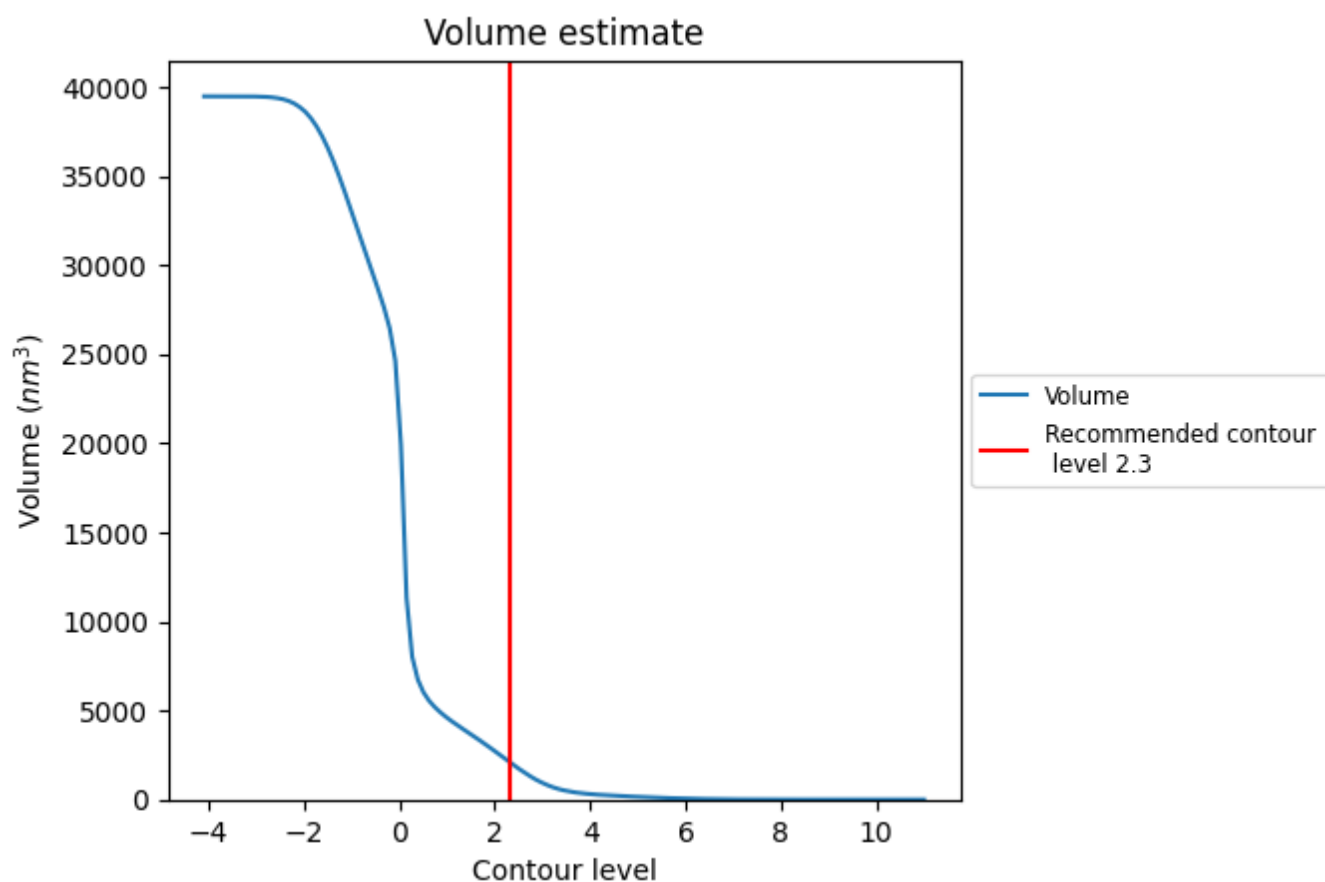
This section contains the results of statistical analysis of the map.

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.

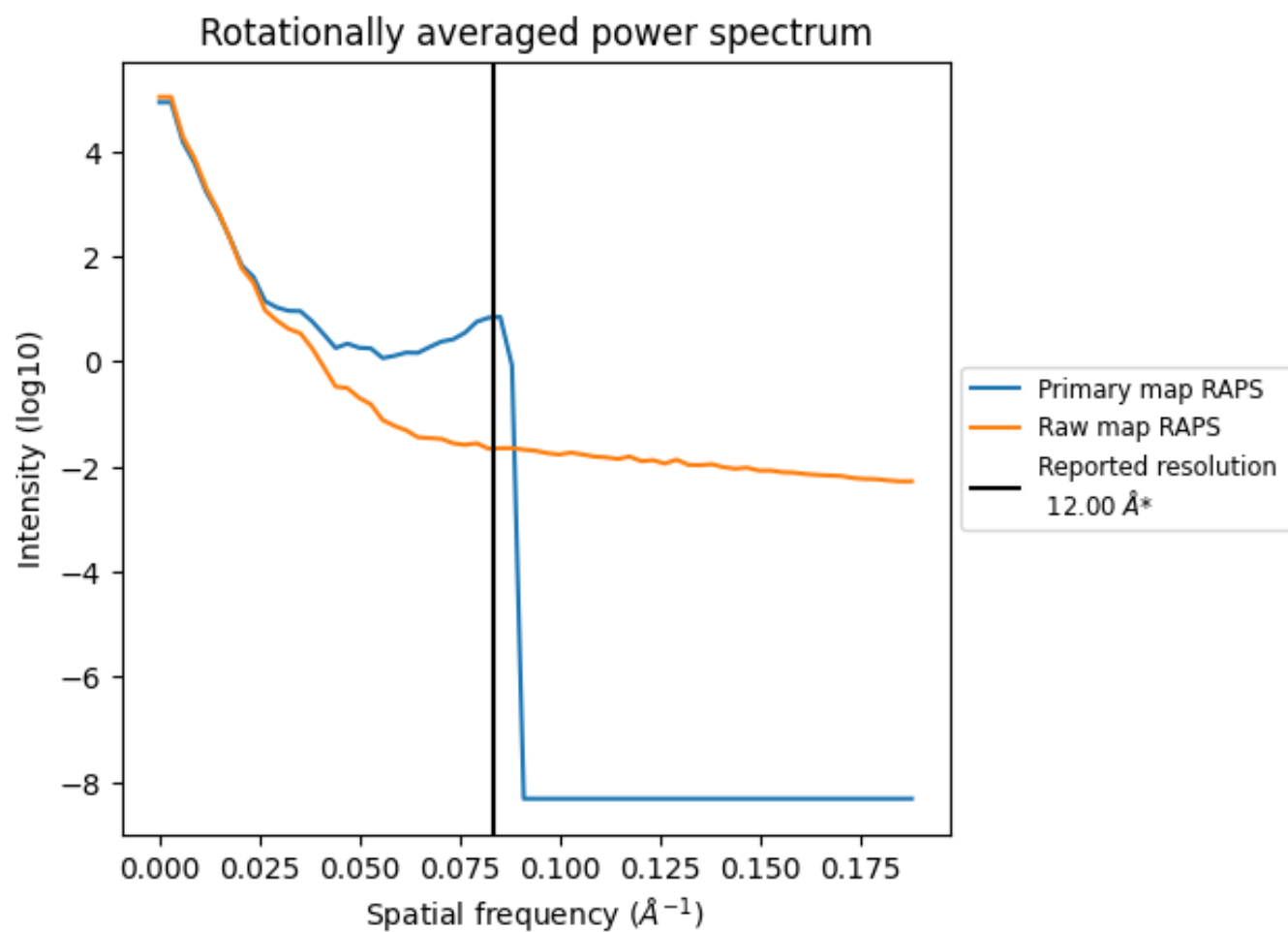
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2121 nm³; this corresponds to an approximate mass of 1916 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 ⓘ

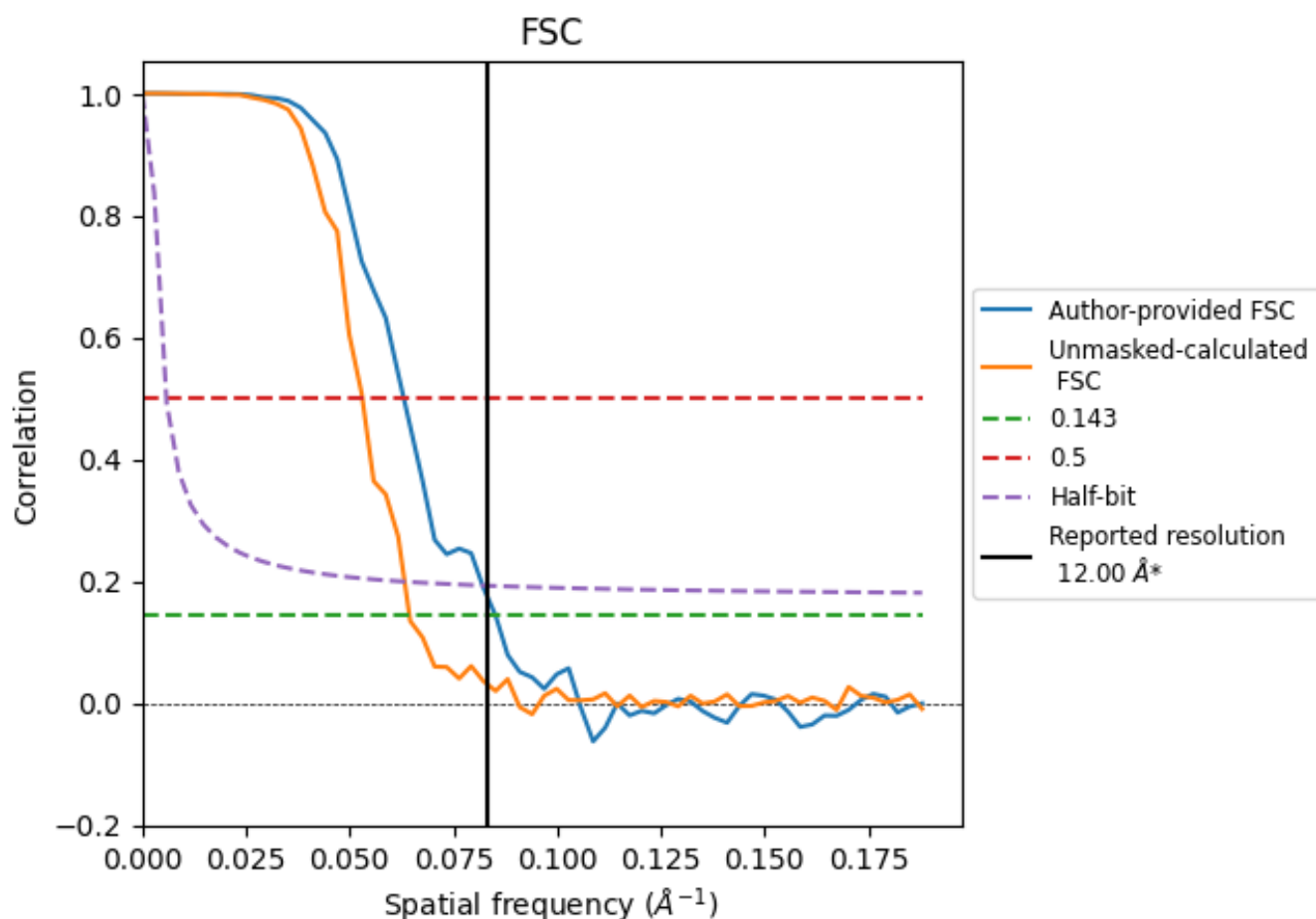


*Reported resolution corresponds to spatial frequency of 0.083 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.083 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	12.00	-	-
Author-provided FSC curve	11.74	15.87	12.18
Unmasked-calculated*	15.53	18.87	15.82

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 15.53 differs from the reported value 12.0 by more than 10 %

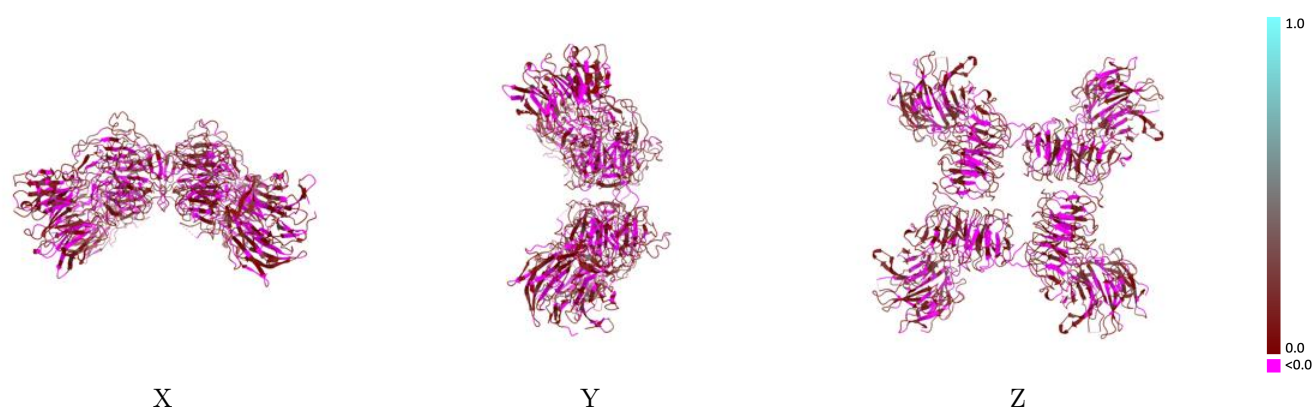
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11194 and PDB model 6ZG6. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

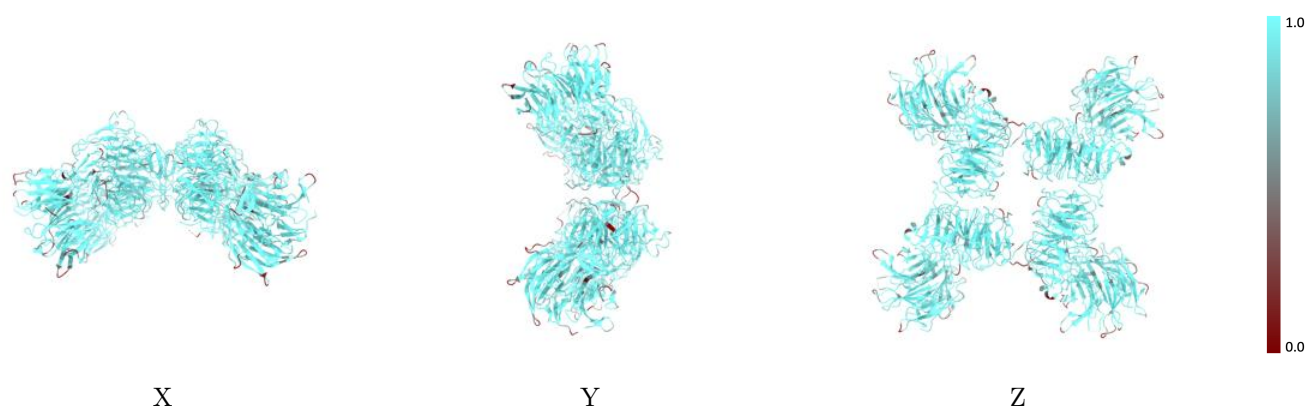
This section was not generated.

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



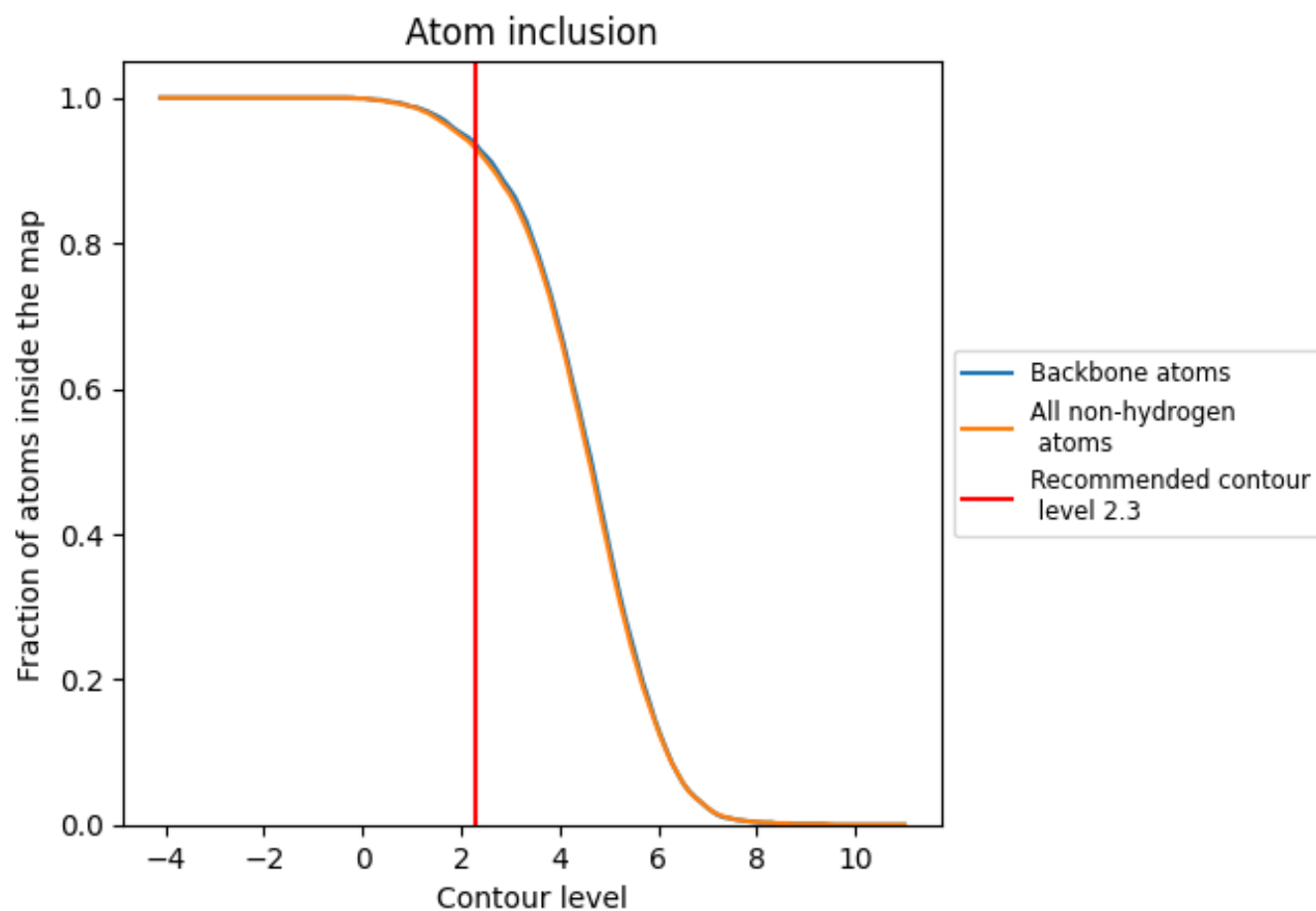
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 93% 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 (2.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9300	0.0640
A	0.9330	0.0610
B	0.9080	0.0640
C	0.9600	0.0670
D	0.9060	0.0630
E	0.9340	0.0600
F	0.9080	0.0630
G	0.9600	0.0680
H	0.9080	0.0640

1.0

0.0

<0.0