



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 06:42 PM UTC

PDB ID : 2C9F / pdb_00002c9f
EMDB ID : EMD-1178
Title : THE QUASI-ATOMIC MODEL OF THE ADENOVIRUS TYPE 3 PENTON DODECAHEDRON
Authors : Fuschiotti, P.; Schoehn, G.; Fender, P.; Fabry, C.M.S.; Hewat, E.A.; Chroboczek, J.; Ruigrok, R.W.H.; Conway, J.F.
Deposited on : 2005-12-12
Resolution : 16.50 Å (reported)

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:

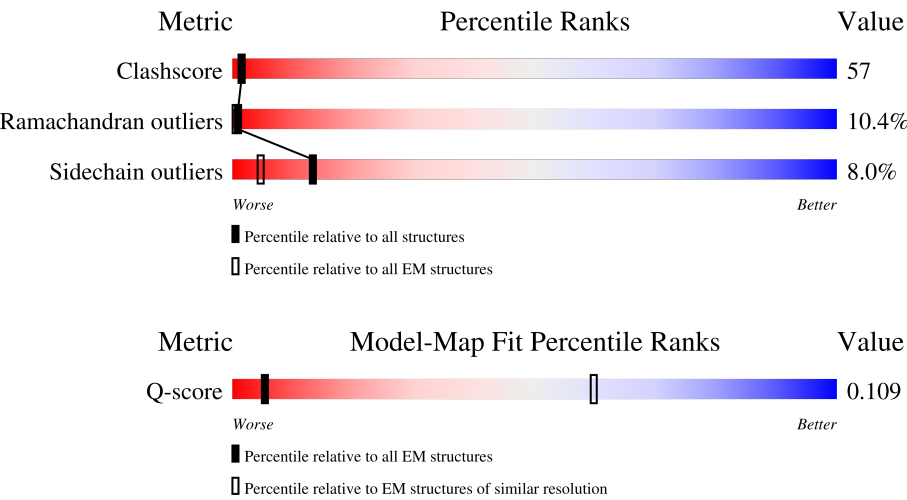
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 16.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	228 (8.80 - 9.80)

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	523	
1	B	523	
1	C	523	
1	D	523	

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Mol	Chain	Length	Quality of chain
1	E	523	16%27%42%14%16%
2	S	19	53%21%32%47%
2	T	19	53%26%26%47%
2	U	19	53%21%32%47%
2	V	19	53%21%32%47%
2	W	19	53%26%26%47%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18025 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 PENTON PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	440	Total	C	N	O	S	0	0
			3519	2227	608	672	12		
1	B	440	Total	C	N	O	S	0	0
			3519	2227	608	672	12		
1	C	440	Total	C	N	O	S	0	0
			3519	2227	608	672	12		
1	D	440	Total	C	N	O	S	0	0
			3519	2227	608	672	12		
1	E	440	Total	C	N	O	S	0	0
			3519	2227	608	672	12		

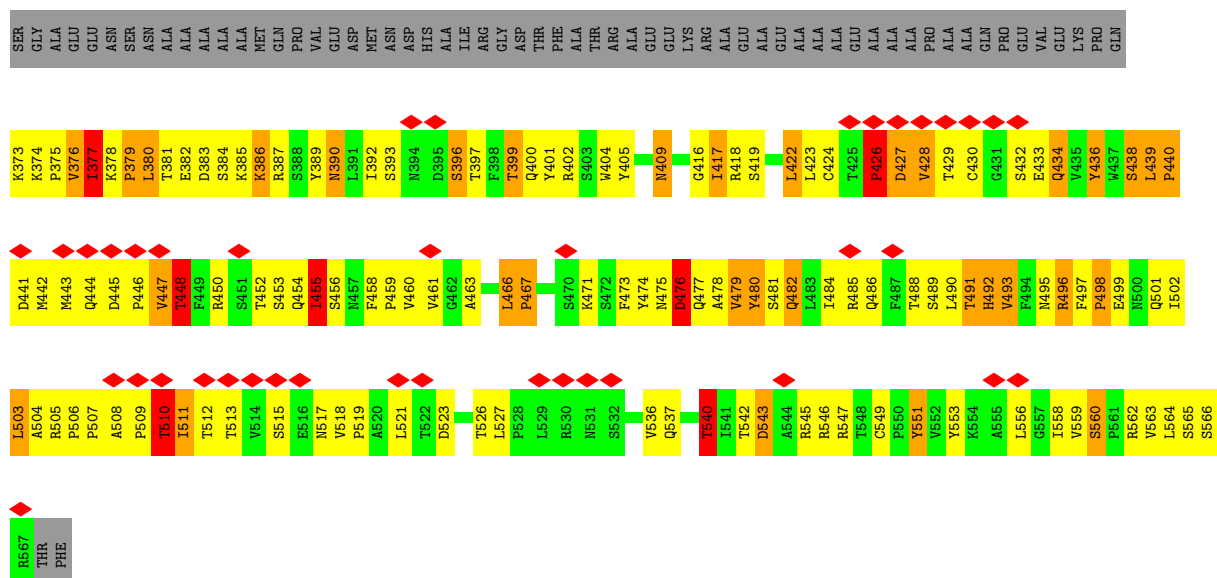
- Molecule 2 is a protein called FIBER.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	S	10	Total	C	N	O	0	0
			86	58	11	17		
2	T	10	Total	C	N	O	0	0
			86	58	11	17		
2	U	10	Total	C	N	O	0	0
			86	58	11	17		
2	V	10	Total	C	N	O	0	0
			86	58	11	17		
2	W	10	Total	C	N	O	0	0
			86	58	11	17		

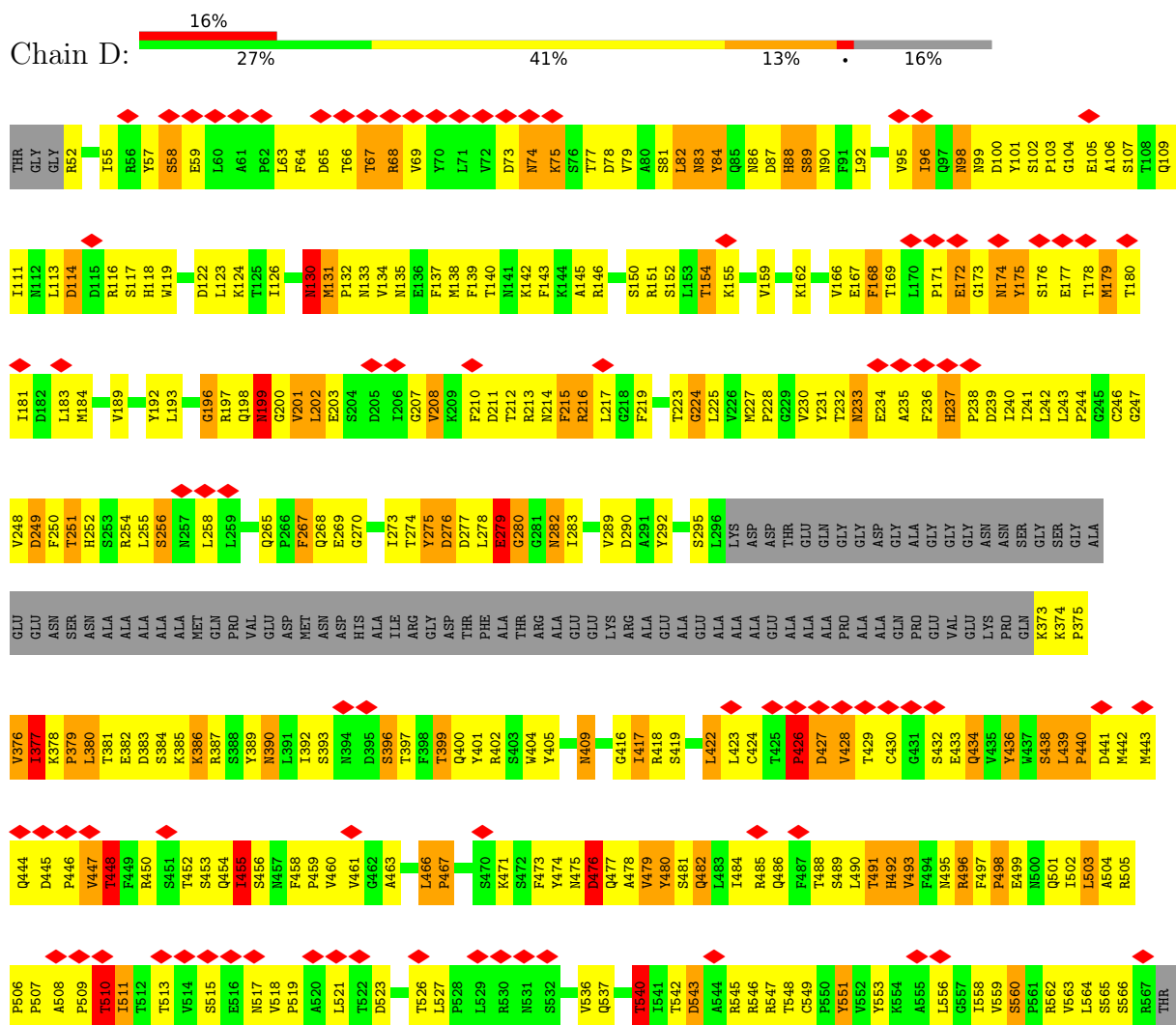


Frequency	Percentage
Daily	16%
Often	27%
Sometimes	42%
Rarely	13%
Never	16%

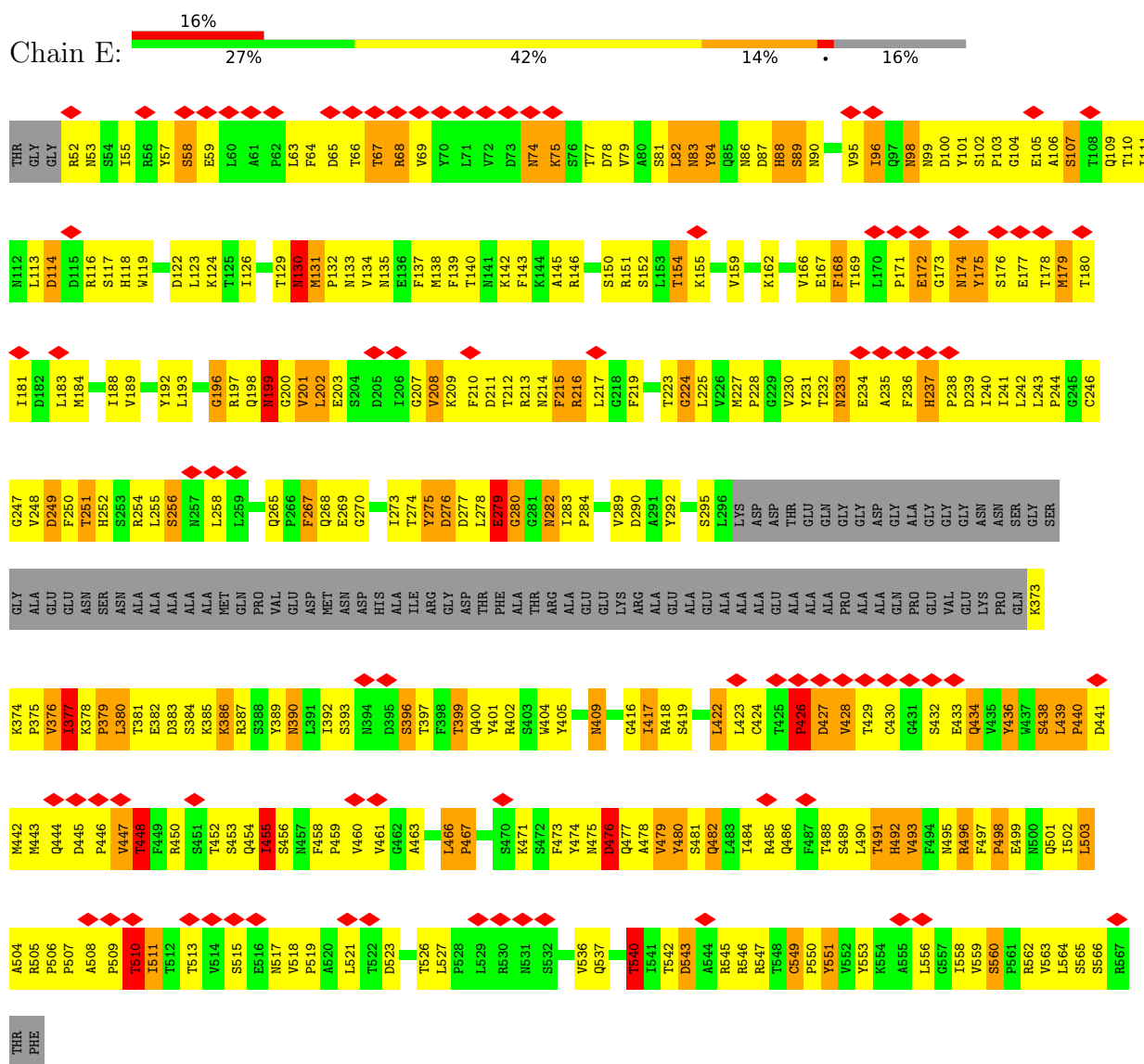




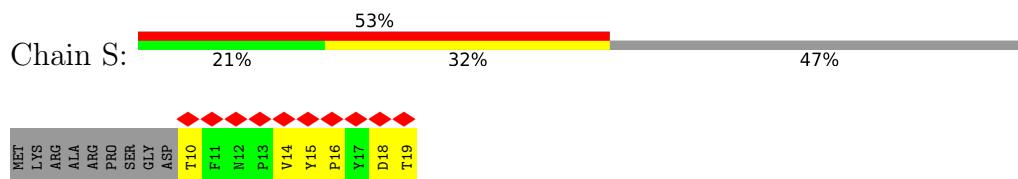
• Molecule 1: PENTON PROTEIN



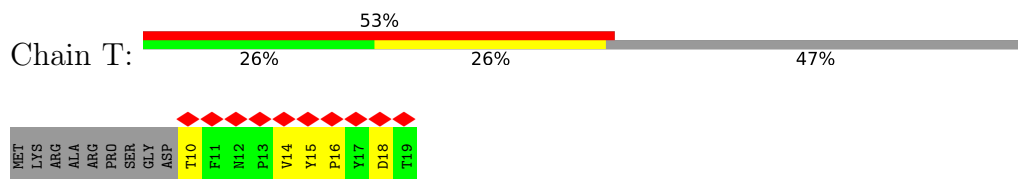
• Molecule 1: PENTON PROTEIN



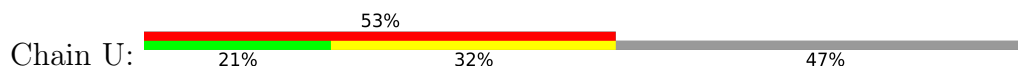
- Molecule 2: FIBER

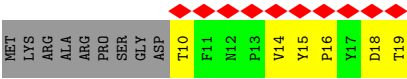


- Molecule 2: FIBER

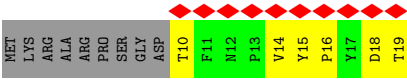


- Molecule 2: FIBER

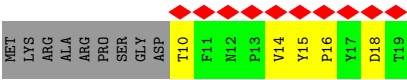
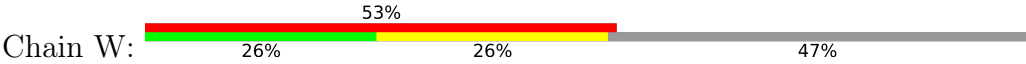




● Molecule 2: FIBER



● Molecule 2: FIBER



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	1849	Depositor
Resolution determination method	Not provided	
CTF correction method	AMPLITUDE, PHASE	Depositor
Microscope	FEI/PHILIPS CM200T	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	40930	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	509.000	Depositor
Minimum map value	-335.000	Depositor
Average map value	3.055	Depositor
Map value standard deviation	52.415	Depositor
Recommended contour level	91.9	Depositor
Map size ($\text{\AA}$)	382.23, 382.23, 382.23	wwPDB
Map dimensions	279, 279, 279	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.37, 1.37, 1.37	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	0.78	4/3602 (0.1%)	1.25	38/4904 (0.8%)
1	B	0.78	4/3602 (0.1%)	1.25	39/4904 (0.8%)
1	C	0.78	4/3602 (0.1%)	1.25	38/4904 (0.8%)
1	D	0.78	4/3602 (0.1%)	1.25	38/4904 (0.8%)
1	E	0.78	4/3602 (0.1%)	1.25	39/4904 (0.8%)
2	S	0.66	0/90	1.05	0/125
2	T	0.67	0/90	1.06	0/125
2	U	0.66	0/90	1.05	0/125
2	V	0.67	0/90	1.06	0/125
2	W	0.66	0/90	1.06	0/125
All	All	0.78	20/18460 (0.1%)	1.24	192/25145 (0.8%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	179	MET	SD-CE	5.58	1.93	1.79
1	B	179	MET	SD-CE	5.55	1.93	1.79
1	A	179	MET	SD-CE	5.54	1.93	1.79
1	B	377	ILE	CA-CB	5.53	1.61	1.54
1	E	179	MET	SD-CE	5.52	1.93	1.79
1	D	377	ILE	CA-CB	5.52	1.61	1.54
1	D	179	MET	SD-CE	5.51	1.93	1.79
1	C	377	ILE	CA-CB	5.49	1.61	1.54
1	E	377	ILE	CA-CB	5.48	1.61	1.54
1	A	377	ILE	CA-CB	5.44	1.61	1.54
1	D	448	THR	CA-CB	-5.33	1.44	1.53
1	A	480	TYR	C-O	5.32	1.30	1.23
1	C	480	TYR	C-O	5.32	1.30	1.23
1	B	448	THR	CA-CB	-5.30	1.44	1.53
1	D	480	TYR	C-O	5.30	1.30	1.23
1	E	448	THR	CA-CB	-5.29	1.44	1.53
1	E	480	TYR	C-O	5.29	1.30	1.23
1	C	448	THR	CA-CB	-5.27	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	480	TYR	C-O	5.25	1.30	1.23
1	A	448	THR	CA-CB	-5.22	1.44	1.53

All (192) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	480	TYR	N-CA-C	-17.66	91.37	113.97
1	A	480	TYR	N-CA-C	-17.64	91.40	113.97
1	D	480	TYR	N-CA-C	-17.64	91.40	113.97
1	B	480	TYR	N-CA-C	-17.60	91.44	113.97
1	E	480	TYR	N-CA-C	-17.58	91.46	113.97
1	C	265	GLN	CA-C-N	8.91	130.98	119.84
1	C	265	GLN	C-N-CA	8.91	130.98	119.84
1	E	265	GLN	CA-C-N	8.88	130.93	119.84
1	E	265	GLN	C-N-CA	8.88	130.93	119.84
1	B	265	GLN	CA-C-N	8.85	130.90	119.84
1	B	265	GLN	C-N-CA	8.85	130.90	119.84
1	D	265	GLN	CA-C-N	8.82	130.87	119.84
1	D	265	GLN	C-N-CA	8.82	130.87	119.84
1	A	265	GLN	CA-C-N	8.82	130.86	119.84
1	A	265	GLN	C-N-CA	8.82	130.86	119.84
1	C	466	LEU	CA-C-N	8.74	130.77	119.84
1	C	466	LEU	C-N-CA	8.74	130.77	119.84
1	D	466	LEU	CA-C-N	8.74	130.76	119.84
1	D	466	LEU	C-N-CA	8.74	130.76	119.84
1	A	466	LEU	CA-C-N	8.72	130.75	119.84
1	A	466	LEU	C-N-CA	8.72	130.75	119.84
1	B	439	LEU	CA-C-N	8.72	130.75	119.84
1	B	439	LEU	C-N-CA	8.72	130.75	119.84
1	C	439	LEU	CA-C-N	8.72	130.74	119.84
1	C	439	LEU	C-N-CA	8.72	130.74	119.84
1	B	466	LEU	CA-C-N	8.70	130.72	119.84
1	B	466	LEU	C-N-CA	8.70	130.72	119.84
1	E	466	LEU	CA-C-N	8.70	130.72	119.84
1	E	466	LEU	C-N-CA	8.70	130.72	119.84
1	D	439	LEU	CA-C-N	8.66	130.66	119.84
1	D	439	LEU	C-N-CA	8.66	130.66	119.84
1	E	439	LEU	CA-C-N	8.63	130.62	119.84
1	E	439	LEU	C-N-CA	8.63	130.62	119.84
1	A	439	LEU	CA-C-N	8.61	130.60	119.84
1	A	439	LEU	C-N-CA	8.61	130.60	119.84
1	E	106	ALA	N-CA-C	-7.74	102.78	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	ALA	N-CA-C	-7.74	102.78	111.14
1	C	106	ALA	N-CA-C	-7.71	102.81	111.14
1	D	106	ALA	N-CA-C	-7.70	102.83	111.14
1	B	106	ALA	N-CA-C	-7.67	102.86	111.14
1	A	96	ILE	N-CA-C	7.34	117.87	110.23
1	B	96	ILE	N-CA-C	7.31	117.83	110.23
1	D	96	ILE	N-CA-C	7.29	117.81	110.23
1	E	96	ILE	N-CA-C	7.29	117.81	110.23
1	E	445	ASP	CA-C-N	7.28	128.94	119.84
1	E	445	ASP	C-N-CA	7.28	128.94	119.84
1	C	445	ASP	CA-C-N	7.26	128.92	119.84
1	C	445	ASP	C-N-CA	7.26	128.92	119.84
1	B	445	ASP	CA-C-N	7.25	128.90	119.84
1	B	445	ASP	C-N-CA	7.25	128.90	119.84
1	D	445	ASP	CA-C-N	7.23	128.87	119.84
1	D	445	ASP	C-N-CA	7.23	128.87	119.84
1	A	445	ASP	CA-C-N	7.22	128.87	119.84
1	A	445	ASP	C-N-CA	7.22	128.87	119.84
1	C	96	ILE	N-CA-C	7.19	117.91	110.36
1	E	448	THR	N-CA-C	7.16	122.19	113.17
1	A	476	ASP	N-CA-C	-7.12	104.33	112.87
1	E	476	ASP	N-CA-C	-7.12	104.33	112.87
1	B	448	THR	N-CA-C	7.11	122.13	113.17
1	A	448	THR	N-CA-C	7.11	122.12	113.17
1	D	448	THR	N-CA-C	7.10	122.11	113.17
1	B	476	ASP	N-CA-C	-7.09	104.36	112.87
1	D	476	ASP	N-CA-C	-7.09	104.36	112.87
1	C	448	THR	N-CA-C	7.07	122.08	113.17
1	C	476	ASP	N-CA-C	-7.06	104.40	112.87
1	C	510	THR	N-CA-C	-6.65	100.44	110.28
1	A	510	THR	N-CA-C	-6.63	100.47	110.28
1	B	510	THR	N-CA-C	-6.61	100.49	110.28
1	E	203	GLU	N-CA-C	-6.57	104.20	111.36
1	C	203	GLU	N-CA-C	-6.57	104.20	111.36
1	D	510	THR	N-CA-C	-6.54	100.60	110.28
1	E	510	THR	N-CA-C	-6.54	100.60	110.28
1	A	203	GLU	N-CA-C	-6.52	104.25	111.36
1	D	203	GLU	N-CA-C	-6.49	104.29	111.36
1	B	203	GLU	N-CA-C	-6.46	104.32	111.36
1	C	282	ASN	N-CA-C	-6.31	99.41	109.76
1	D	282	ASN	N-CA-C	-6.30	99.42	109.76
1	E	282	ASN	N-CA-C	-6.26	99.49	109.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	282	ASN	N-CA-C	-6.25	99.51	109.76
1	C	237	HIS	CA-C-N	-6.25	113.54	119.85
1	C	237	HIS	C-N-CA	-6.25	113.54	119.85
1	E	237	HIS	CA-C-N	-6.24	113.55	119.85
1	E	237	HIS	C-N-CA	-6.24	113.55	119.85
1	B	282	ASN	N-CA-C	-6.23	99.54	109.76
1	B	237	HIS	CA-C-N	-6.22	113.57	119.85
1	B	237	HIS	C-N-CA	-6.22	113.57	119.85
1	A	154	THR	N-CA-C	6.21	119.15	109.52
1	B	154	THR	N-CA-C	6.20	119.13	109.52
1	E	154	THR	N-CA-C	6.20	119.13	109.52
1	A	237	HIS	CA-C-N	-6.19	113.60	119.85
1	A	237	HIS	C-N-CA	-6.19	113.60	119.85
1	C	154	THR	N-CA-C	6.17	119.08	109.52
1	D	74	ASN	N-CA-C	6.16	121.53	111.37
1	D	237	HIS	CA-C-N	-6.15	113.64	119.85
1	D	237	HIS	C-N-CA	-6.15	113.64	119.85
1	D	154	THR	N-CA-C	6.14	119.04	109.52
1	A	74	ASN	N-CA-C	6.14	121.50	111.37
1	C	74	ASN	N-CA-C	6.14	121.50	111.37
1	C	105	GLU	N-CA-C	-6.13	104.91	112.38
1	E	74	ASN	N-CA-C	6.11	121.45	111.37
1	E	105	GLU	N-CA-C	-6.09	104.94	112.38
1	B	74	ASN	N-CA-C	6.09	121.41	111.37
1	B	105	GLU	N-CA-C	-6.07	104.97	112.38
1	D	105	GLU	N-CA-C	-6.05	105.00	112.38
1	E	131	MET	CA-C-N	6.04	125.80	119.76
1	E	131	MET	C-N-CA	6.04	125.80	119.76
1	A	275	TYR	N-CA-C	-6.03	104.61	111.07
1	C	131	MET	CA-C-N	6.03	125.79	119.76
1	C	131	MET	C-N-CA	6.03	125.79	119.76
1	D	275	TYR	N-CA-C	-6.03	104.61	111.07
1	E	275	TYR	N-CA-C	-6.02	104.62	111.07
1	C	275	TYR	N-CA-C	-6.02	104.63	111.07
1	A	105	GLU	N-CA-C	-6.02	105.04	112.38
1	A	131	MET	CA-C-N	6.02	125.78	119.76
1	A	131	MET	C-N-CA	6.02	125.78	119.76
1	B	131	MET	CA-C-N	6.01	125.77	119.76
1	B	131	MET	C-N-CA	6.01	125.77	119.76
1	B	275	TYR	N-CA-C	-6.00	104.64	111.07
1	D	131	MET	CA-C-N	6.00	125.76	119.76
1	D	131	MET	C-N-CA	6.00	125.76	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	224	GLY	N-CA-C	-5.91	105.98	115.08
1	D	224	GLY	N-CA-C	-5.91	105.98	115.08
1	B	224	GLY	N-CA-C	-5.90	105.99	115.08
1	A	224	GLY	N-CA-C	-5.89	106.01	115.08
1	C	224	GLY	N-CA-C	-5.84	106.08	115.08
1	B	491	THR	N-CA-C	5.56	117.85	109.23
1	A	489	SER	N-CA-C	-5.55	100.76	109.25
1	B	489	SER	N-CA-C	-5.55	100.76	109.25
1	C	489	SER	N-CA-C	-5.51	100.81	109.25
1	D	491	THR	N-CA-C	5.51	117.78	109.23
1	E	489	SER	N-CA-C	-5.51	100.81	109.25
1	A	491	THR	N-CA-C	5.50	117.76	109.23
1	E	491	THR	N-CA-C	5.50	117.75	109.23
1	B	152	SER	N-CA-C	5.49	118.03	109.52
1	C	491	THR	N-CA-C	5.49	117.75	109.23
1	D	489	SER	N-CA-C	-5.49	100.85	109.25
1	D	152	SER	N-CA-C	5.47	118.00	109.52
1	C	267	PHE	N-CA-C	5.47	119.43	112.87
1	D	267	PHE	N-CA-C	5.47	119.44	112.87
1	E	152	SER	N-CA-C	5.47	118.00	109.52
1	C	152	SER	N-CA-C	5.46	117.99	109.52
1	A	152	SER	N-CA-C	5.46	117.98	109.52
1	E	267	PHE	N-CA-C	5.43	119.39	112.87
1	C	77	THR	N-CA-C	5.43	116.89	110.97
1	A	267	PHE	N-CA-C	5.42	119.37	112.87
1	B	77	THR	N-CA-C	5.42	116.87	110.97
1	A	77	THR	N-CA-C	5.41	116.87	110.97
1	B	267	PHE	N-CA-C	5.41	119.36	112.87
1	C	84	TYR	N-CA-C	-5.40	99.30	110.80
1	D	77	THR	N-CA-C	5.40	116.85	110.97
1	D	84	TYR	N-CA-C	-5.40	99.31	110.80
1	D	551	TYR	N-CA-C	5.40	119.42	113.21
1	E	77	THR	N-CA-C	5.39	116.84	110.97
1	A	551	TYR	N-CA-C	5.38	119.40	113.21
1	E	551	TYR	N-CA-C	5.37	119.39	113.21
1	B	84	TYR	N-CA-C	-5.37	99.36	110.80
1	A	84	TYR	N-CA-C	-5.37	99.37	110.80
1	E	84	TYR	N-CA-C	-5.34	99.43	110.80
1	B	551	TYR	N-CA-C	5.32	119.33	113.21
1	C	551	TYR	N-CA-C	5.31	119.32	113.21
1	C	549	CYS	CA-C-N	5.30	125.62	119.47
1	C	549	CYS	C-N-CA	5.30	125.62	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	549	CYS	CA-C-N	5.29	125.60	119.47
1	E	549	CYS	C-N-CA	5.29	125.60	119.47
1	B	549	CYS	CA-C-N	5.28	125.59	119.47
1	B	549	CYS	C-N-CA	5.28	125.59	119.47
1	D	549	CYS	CA-C-N	5.27	125.59	119.47
1	D	549	CYS	C-N-CA	5.27	125.59	119.47
1	E	540	THR	N-CA-C	5.26	117.18	108.13
1	A	549	CYS	CA-C-N	5.26	125.57	119.47
1	A	549	CYS	C-N-CA	5.26	125.57	119.47
1	B	540	THR	N-CA-C	5.24	117.14	108.13
1	C	540	THR	N-CA-C	5.22	117.11	108.13
1	D	492	HIS	N-CA-C	-5.21	105.64	112.72
1	D	540	THR	N-CA-C	5.21	117.09	108.13
1	B	493	VAL	CB-CA-C	-5.20	105.22	112.04
1	C	492	HIS	N-CA-C	-5.20	105.65	112.72
1	A	492	HIS	N-CA-C	-5.20	105.65	112.72
1	E	493	VAL	CB-CA-C	-5.20	105.23	112.04
1	E	396	SER	N-CA-C	5.19	117.61	110.35
1	B	492	HIS	N-CA-C	-5.19	105.66	112.72
1	E	492	HIS	N-CA-C	-5.19	105.66	112.72
1	A	540	THR	N-CA-C	5.18	117.05	108.13
1	A	493	VAL	CB-CA-C	-5.18	105.25	112.04
1	C	493	VAL	CB-CA-C	-5.16	105.28	112.04
1	C	396	SER	N-CA-C	5.16	117.57	110.35
1	D	493	VAL	CB-CA-C	-5.15	105.29	112.04
1	A	396	SER	N-CA-C	5.12	117.52	110.35
1	B	396	SER	N-CA-C	5.12	117.51	110.35
1	D	396	SER	N-CA-C	5.10	117.49	110.35
1	B	188	ILE	N-CA-C	-5.02	105.60	110.42
1	E	188	ILE	N-CA-C	-5.01	105.61	110.42

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	3519	0	3452	447	0
1	B	3519	0	3452	434	0
1	C	3519	0	3452	432	0
1	D	3519	0	3452	447	0
1	E	3519	0	3452	446	0
2	S	86	0	73	18	0
2	T	86	0	73	16	0
2	U	86	0	73	19	0
2	V	86	0	73	17	0
2	W	86	0	73	17	0
All	All	18025	0	17625	2047	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 57.

All (2047) 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:B:68:ARG:NH1	1:B:560:SER:HB3	1.68	1.09
1:D:68:ARG:NH1	1:D:560:SER:HB3	1.68	1.09
1:C:68:ARG:NH1	1:C:560:SER:HB3	1.68	1.09
1:A:68:ARG:NH1	1:A:560:SER:HB3	1.68	1.08
1:E:68:ARG:NH1	1:E:560:SER:HB3	1.68	1.08
1:A:442:MET:HE1	1:A:559:VAL:HG21	1.39	1.05
1:E:442:MET:HE1	1:E:559:VAL:HG21	1.39	1.04
1:B:197:ARG:HE	1:B:198:GLN:HE21	1.05	1.03
1:A:477:GLN:O	1:A:481:SER:HB2	1.59	1.03
1:E:477:GLN:O	1:E:481:SER:HB2	1.59	1.02
1:B:442:MET:HE1	1:B:559:VAL:HG21	1.39	1.02
1:D:466:LEU:HD12	1:D:467:PRO:HD2	1.41	1.02
1:D:442:MET:HE1	1:D:559:VAL:HG21	1.39	1.01
1:D:477:GLN:O	1:D:481:SER:HB2	1.59	1.01
1:D:197:ARG:HE	1:D:198:GLN:NE2	1.59	1.01
1:E:197:ARG:HE	1:E:198:GLN:NE2	1.59	1.01
1:A:197:ARG:HE	1:A:198:GLN:HE21	1.05	1.01
1:B:197:ARG:HE	1:B:198:GLN:NE2	1.59	1.01
1:B:477:GLN:O	1:B:481:SER:HB2	1.59	1.01
1:C:466:LEU:HD12	1:C:467:PRO:HD2	1.41	1.01
1:A:68:ARG:HG2	1:A:68:ARG:HH11	1.26	1.00
1:A:488:THR:CG2	1:B:479:VAL:HG12	1.91	1.00
1:C:197:ARG:HE	1:C:198:GLN:NE2	1.59	1.00
1:C:477:GLN:O	1:C:481:SER:HB2	1.59	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:466:LEU:HD12	1:B:467:PRO:HD2	1.41	1.00
1:E:481:SER:O	1:E:485:ARG:N	1.95	1.00
1:A:481:SER:O	1:A:485:ARG:N	1.95	1.00
1:C:68:ARG:HG2	1:C:68:ARG:HH11	1.26	1.00
1:B:481:SER:O	1:B:485:ARG:N	1.95	1.00
1:C:442:MET:HE1	1:C:559:VAL:HG21	1.39	1.00
1:D:68:ARG:HG2	1:D:68:ARG:HH11	1.26	1.00
1:E:466:LEU:HD12	1:E:467:PRO:HD2	1.41	0.99
1:B:68:ARG:HG2	1:B:68:ARG:HH11	1.26	0.99
1:A:197:ARG:HE	1:A:198:GLN:NE2	1.59	0.99
1:C:481:SER:O	1:C:485:ARG:N	1.95	0.99
1:E:68:ARG:HH11	1:E:68:ARG:HG2	1.25	0.99
1:D:481:SER:O	1:D:485:ARG:N	1.95	0.99
1:A:466:LEU:HD12	1:A:467:PRO:HD2	1.41	0.98
1:C:197:ARG:HE	1:C:198:GLN:HE21	1.05	0.98
1:D:490:LEU:HB2	1:E:230:VAL:HG11	1.45	0.98
1:A:479:VAL:HG12	1:E:488:THR:CG2	1.94	0.98
1:A:484:ILE:HG21	1:B:480:TYR:CE1	1.97	0.98
1:A:479:VAL:HG12	1:E:488:THR:HG23	1.46	0.97
1:C:488:THR:HG23	1:D:479:VAL:HG12	1.45	0.97
1:C:490:LEU:HB2	1:D:230:VAL:HG11	1.47	0.97
1:D:484:ILE:HG21	1:E:480:TYR:CE1	1.99	0.97
1:E:477:GLN:O	1:E:481:SER:CB	2.13	0.97
1:C:477:GLN:O	1:C:481:SER:CB	2.13	0.97
1:D:477:GLN:O	1:D:481:SER:CB	2.13	0.97
1:A:488:THR:HG23	1:B:479:VAL:HG12	1.46	0.96
1:A:477:GLN:O	1:A:481:SER:CB	2.13	0.96
1:B:477:GLN:O	1:B:481:SER:CB	2.13	0.95
1:A:480:TYR:CE1	1:E:484:ILE:HG21	2.00	0.95
1:C:488:THR:CG2	1:D:479:VAL:HG12	1.97	0.95
1:D:488:THR:CG2	1:E:479:VAL:HG12	1.96	0.95
1:A:230:VAL:HG11	1:E:490:LEU:HB2	1.48	0.95
1:E:197:ARG:HE	1:E:198:GLN:HE21	1.05	0.95
1:D:132:PRO:HA	1:D:175:TYR:OH	1.67	0.94
1:D:488:THR:HG23	1:E:479:VAL:HG12	1.49	0.94
1:D:197:ARG:HE	1:D:198:GLN:HE21	1.05	0.94
1:E:132:PRO:HA	1:E:175:TYR:OH	1.67	0.94
1:D:230:VAL:HG13	1:D:501:GLN:NE2	1.83	0.94
1:B:230:VAL:HG13	1:B:501:GLN:NE2	1.83	0.93
1:C:230:VAL:HG13	1:C:501:GLN:NE2	1.83	0.93
1:E:230:VAL:HG13	1:E:501:GLN:NE2	1.83	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:PRO:HA	1:B:175:TYR:OH	1.67	0.92
1:C:132:PRO:HA	1:C:175:TYR:OH	1.67	0.92
1:A:230:VAL:HG13	1:A:501:GLN:NE2	1.83	0.92
1:A:132:PRO:HA	1:A:175:TYR:OH	1.67	0.91
1:E:68:ARG:HH12	1:E:560:SER:HB3	1.36	0.91
1:A:484:ILE:CG2	1:B:480:TYR:CE1	2.54	0.91
1:D:274:THR:HG22	1:D:276:ASP:H	1.37	0.90
1:E:274:THR:HG22	1:E:276:ASP:H	1.37	0.90
1:C:68:ARG:HH12	1:C:560:SER:HB3	1.36	0.89
1:B:274:THR:HG22	1:B:276:ASP:H	1.37	0.89
1:B:83:ASN:HA	1:B:86:ASN:HD22	1.38	0.89
1:D:83:ASN:HA	1:D:86:ASN:HD22	1.38	0.88
1:A:68:ARG:HH12	1:A:560:SER:HB3	1.36	0.88
1:C:275:TYR:CE1	1:C:402:ARG:HD3	2.09	0.88
1:B:275:TYR:CE1	1:B:402:ARG:HD3	2.09	0.87
1:C:83:ASN:HA	1:C:86:ASN:HD22	1.38	0.87
1:A:275:TYR:CE1	1:A:402:ARG:HD3	2.09	0.87
1:A:377:ILE:O	1:A:379:PRO:HD3	1.75	0.87
1:C:274:THR:HG22	1:C:276:ASP:H	1.37	0.87
1:C:377:ILE:O	1:C:379:PRO:HD3	1.75	0.87
1:A:217:LEU:HB2	1:A:232:THR:HG21	1.57	0.87
1:E:83:ASN:HA	1:E:86:ASN:HD22	1.38	0.87
1:B:377:ILE:O	1:B:379:PRO:HD3	1.75	0.87
1:D:217:LEU:HB2	1:D:232:THR:HG21	1.56	0.87
1:A:274:THR:HG22	1:A:276:ASP:H	1.37	0.87
1:B:217:LEU:HB2	1:B:232:THR:HG21	1.57	0.87
1:D:275:TYR:CE1	1:D:402:ARG:HD3	2.09	0.87
1:D:68:ARG:HH12	1:D:560:SER:HB3	1.36	0.87
1:E:275:TYR:CE1	1:E:402:ARG:HD3	2.09	0.86
1:C:484:ILE:HG21	1:D:480:TYR:CE1	2.10	0.86
1:A:83:ASN:HA	1:A:86:ASN:HD22	1.38	0.86
1:C:100:ASP:OD2	1:D:450:ARG:NH1	2.09	0.86
1:D:377:ILE:O	1:D:379:PRO:HD3	1.75	0.86
1:E:377:ILE:O	1:E:379:PRO:HD3	1.75	0.86
1:B:68:ARG:HH12	1:B:560:SER:HB3	1.36	0.86
1:B:100:ASP:OD2	1:C:450:ARG:NH1	2.09	0.85
1:E:217:LEU:HB2	1:E:232:THR:HG21	1.57	0.85
1:A:473:PHE:O	1:A:511:ILE:HA	1.77	0.85
1:C:217:LEU:HB2	1:C:232:THR:HG21	1.57	0.85
1:D:473:PHE:O	1:D:511:ILE:HA	1.77	0.85
1:E:526:THR:HG21	1:E:562:ARG:HH21	1.42	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:526:THR:HG21	1:C:562:ARG:HH21	1.42	0.84
1:E:473:PHE:O	1:E:511:ILE:HA	1.77	0.84
1:A:484:ILE:HG21	1:B:480:TYR:CD1	2.12	0.84
1:B:526:THR:HG21	1:B:562:ARG:HH21	1.42	0.84
1:C:473:PHE:O	1:C:511:ILE:HA	1.77	0.83
1:D:526:THR:HG21	1:D:562:ARG:HH21	1.42	0.83
1:B:473:PHE:O	1:B:511:ILE:HA	1.77	0.83
1:A:526:THR:HG21	1:A:562:ARG:HH21	1.42	0.82
1:A:488:THR:HG23	1:B:479:VAL:O	1.78	0.82
1:D:179:MET:HE2	1:D:485:ARG:NH2	1.95	0.82
1:C:485:ARG:NE	1:D:234:GLU:OE2	2.12	0.82
1:B:179:MET:HE2	1:B:485:ARG:NH2	1.95	0.82
1:B:542:THR:CG2	1:B:546:ARG:HA	2.10	0.81
1:C:67:THR:HG21	1:D:447:VAL:HG22	1.61	0.81
1:D:542:THR:CG2	1:D:546:ARG:HA	2.10	0.81
1:A:484:ILE:CG2	1:B:480:TYR:CD1	2.63	0.81
1:A:490:LEU:HB2	1:B:230:VAL:HG11	1.62	0.81
1:E:179:MET:HE2	1:E:485:ARG:NH2	1.95	0.81
1:C:542:THR:CG2	1:C:546:ARG:HA	2.10	0.81
1:A:179:MET:HE2	1:A:485:ARG:NH2	1.95	0.81
1:B:488:THR:HG23	1:C:479:VAL:HG12	1.62	0.81
1:C:179:MET:HE2	1:C:485:ARG:NH2	1.95	0.81
1:D:485:ARG:NE	1:E:234:GLU:OE2	2.12	0.81
1:E:197:ARG:NE	1:E:198:GLN:HE21	1.80	0.80
1:C:197:ARG:NE	1:C:198:GLN:HE21	1.80	0.80
1:E:542:THR:CG2	1:E:546:ARG:HA	2.10	0.80
1:A:542:THR:CG2	1:A:546:ARG:HA	2.10	0.80
1:C:490:LEU:CB	1:D:230:VAL:HG11	2.11	0.80
1:D:490:LEU:CB	1:E:230:VAL:HG11	2.12	0.80
1:A:197:ARG:NE	1:A:198:GLN:HE21	1.80	0.80
1:A:234:GLU:OE2	1:E:485:ARG:NE	2.14	0.80
1:B:197:ARG:NE	1:B:198:GLN:HE21	1.80	0.79
1:A:480:TYR:CE1	1:E:484:ILE:CG2	2.65	0.79
1:B:466:LEU:HD12	1:B:467:PRO:CD	2.12	0.79
1:D:197:ARG:NE	1:D:198:GLN:HE21	1.80	0.79
1:E:466:LEU:HD12	1:E:467:PRO:CD	2.12	0.79
1:C:466:LEU:HD12	1:C:467:PRO:CD	2.12	0.79
1:D:104:GLY:O	1:D:107:SER:HB3	1.83	0.79
1:D:68:ARG:NH1	1:D:68:ARG:HG2	1.97	0.79
1:A:466:LEU:HD12	1:A:467:PRO:CD	2.12	0.78
1:D:466:LEU:HD12	1:D:467:PRO:CD	2.12	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:104:GLY:O	1:E:107:SER:HB3	1.83	0.78
1:A:401:TYR:CD1	1:A:502:ILE:HG12	2.19	0.78
1:D:100:ASP:OD2	1:E:450:ARG:NH1	2.15	0.78
1:D:230:VAL:HG13	1:D:501:GLN:HE22	1.47	0.78
1:A:230:VAL:HG11	1:E:490:LEU:CB	2.13	0.78
1:D:401:TYR:CD1	1:D:502:ILE:HG12	2.19	0.78
1:E:401:TYR:CD1	1:E:502:ILE:HG12	2.19	0.78
1:A:104:GLY:O	1:A:107:SER:HB3	1.83	0.78
1:A:217:LEU:HB2	1:A:232:THR:CG2	2.14	0.77
1:B:104:GLY:O	1:B:107:SER:HB3	1.83	0.77
1:C:217:LEU:HB2	1:C:232:THR:CG2	2.14	0.77
1:E:68:ARG:NH1	1:E:68:ARG:HG2	1.97	0.77
1:A:230:VAL:HG13	1:A:501:GLN:HE22	1.47	0.77
1:B:488:THR:CG2	1:C:479:VAL:HG12	2.14	0.77
1:B:401:TYR:CD1	1:B:502:ILE:HG12	2.19	0.77
1:C:104:GLY:O	1:C:107:SER:HB3	1.83	0.77
1:C:401:TYR:CD1	1:C:502:ILE:HG12	2.19	0.77
1:D:217:LEU:HB2	1:D:232:THR:CG2	2.14	0.77
1:A:480:TYR:CD1	1:E:484:ILE:HG21	2.19	0.77
1:C:230:VAL:HG13	1:C:501:GLN:HE22	1.47	0.77
1:B:145:ALA:HB3	1:B:168:PHE:HE1	1.50	0.77
1:D:484:ILE:CG2	1:E:480:TYR:CE1	2.66	0.77
1:B:217:LEU:HB2	1:B:232:THR:CG2	2.14	0.76
1:D:145:ALA:HB3	1:D:168:PHE:HE1	1.50	0.76
1:E:376:VAL:HG23	1:E:377:ILE:N	2.01	0.76
1:A:214:ASN:C	1:A:214:ASN:HD22	1.93	0.76
1:E:217:LEU:HB2	1:E:232:THR:CG2	2.14	0.76
1:C:376:VAL:HG23	1:C:377:ILE:N	2.01	0.76
1:E:145:ALA:HB3	1:E:168:PHE:HE1	1.50	0.76
1:E:214:ASN:C	1:E:214:ASN:HD22	1.93	0.76
1:E:230:VAL:HG13	1:E:501:GLN:HE22	1.47	0.76
1:A:67:THR:HG21	1:B:447:VAL:HG22	1.65	0.76
1:B:376:VAL:HG23	1:B:377:ILE:N	2.01	0.76
1:C:145:ALA:HB3	1:C:168:PHE:HE1	1.50	0.76
1:B:111:ILE:HD13	1:C:447:VAL:HG11	1.67	0.76
1:C:135:ASN:HA	1:C:172:GLU:HG2	1.68	0.76
1:A:145:ALA:HB3	1:A:168:PHE:HE1	1.50	0.76
1:A:376:VAL:HG23	1:A:377:ILE:N	2.01	0.76
1:D:135:ASN:HA	1:D:172:GLU:HG2	1.68	0.76
1:D:376:VAL:HG23	1:D:377:ILE:N	2.01	0.76
1:B:96:ILE:HG22	1:B:98:ASN:H	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:230:VAL:HG13	1:B:501:GLN:HE22	1.47	0.75
1:B:134:VAL:HG13	1:B:140:THR:O	1.87	0.75
1:B:542:THR:HG22	1:B:546:ARG:HA	1.69	0.75
1:D:214:ASN:C	1:D:214:ASN:HD22	1.93	0.75
1:D:134:VAL:HG13	1:D:140:THR:O	1.87	0.75
1:A:96:ILE:HG22	1:A:98:ASN:H	1.51	0.75
1:B:214:ASN:C	1:B:214:ASN:HD22	1.93	0.75
1:B:526:THR:HG21	1:B:562:ARG:NH2	2.02	0.75
1:A:135:ASN:HA	1:A:172:GLU:HG2	1.68	0.75
1:A:526:THR:HG21	1:A:562:ARG:NH2	2.02	0.75
1:B:146:ARG:O	1:B:246:CYS:HB2	1.87	0.75
1:B:135:ASN:HA	1:B:172:GLU:HG2	1.68	0.74
1:C:68:ARG:NH1	1:C:68:ARG:HG2	1.97	0.74
1:C:96:ILE:HG22	1:C:98:ASN:H	1.51	0.74
1:E:135:ASN:HA	1:E:172:GLU:HG2	1.68	0.74
1:C:214:ASN:HD22	1:C:214:ASN:C	1.93	0.74
1:C:551:TYR:CE2	1:D:422:LEU:HD21	2.22	0.74
1:A:277:ASP:HB3	1:A:417:ILE:HD11	1.70	0.74
1:B:277:ASP:HB3	1:B:417:ILE:HD11	1.70	0.74
1:D:146:ARG:O	1:D:246:CYS:HB2	1.87	0.74
1:D:484:ILE:HG21	1:E:480:TYR:CD1	2.22	0.74
1:E:146:ARG:O	1:E:246:CYS:HB2	1.87	0.74
1:E:526:THR:HG21	1:E:562:ARG:NH2	2.02	0.74
1:E:542:THR:HG22	1:E:546:ARG:HA	1.68	0.74
1:A:134:VAL:HG13	1:A:140:THR:O	1.87	0.74
1:C:134:VAL:HG13	1:C:140:THR:O	1.87	0.74
1:C:146:ARG:O	1:C:246:CYS:HB2	1.87	0.74
1:D:542:THR:HG22	1:D:546:ARG:HA	1.69	0.74
1:E:134:VAL:HG13	1:E:140:THR:O	1.87	0.74
1:D:96:ILE:HG22	1:D:98:ASN:H	1.51	0.74
1:D:510:THR:O	1:D:511:ILE:HB	1.88	0.73
1:A:542:THR:HG22	1:A:546:ARG:HA	1.69	0.73
1:C:277:ASP:HB3	1:C:417:ILE:HD11	1.70	0.73
1:D:277:ASP:HB3	1:D:417:ILE:HD11	1.70	0.73
1:E:277:ASP:HB3	1:E:417:ILE:HD11	1.70	0.73
1:D:526:THR:HG21	1:D:562:ARG:NH2	2.02	0.73
1:A:510:THR:O	1:A:511:ILE:HB	1.88	0.73
1:B:510:THR:O	1:B:511:ILE:HB	1.88	0.73
1:C:526:THR:HG21	1:C:562:ARG:NH2	2.02	0.73
1:A:146:ARG:O	1:A:246:CYS:HB2	1.87	0.73
1:A:450:ARG:NH1	1:E:100:ASP:OD2	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:542:THR:HG22	1:C:546:ARG:HA	1.69	0.73
1:A:447:VAL:HG22	1:E:67:THR:HG21	1.70	0.72
1:A:488:THR:HG22	1:B:479:VAL:HG12	1.70	0.72
1:B:484:ILE:HG21	1:C:480:TYR:CE1	2.24	0.72
2:V:10:THR:O	2:V:10:THR:HG22	1.89	0.72
1:E:96:ILE:HG22	1:E:98:ASN:H	1.51	0.72
1:B:154:THR:HG22	1:B:155:LYS:HG3	1.71	0.72
1:C:193:LEU:HD11	1:C:496:ARG:HH12	1.54	0.72
2:U:10:THR:O	2:U:10:THR:HG22	1.89	0.72
1:A:193:LEU:HD11	1:A:496:ARG:HH12	1.54	0.72
1:C:510:THR:O	1:C:511:ILE:HB	1.88	0.72
1:D:193:LEU:HD11	1:D:496:ARG:HH12	1.54	0.72
2:T:10:THR:HG22	2:T:10:THR:O	1.89	0.72
1:C:215:PHE:O	1:C:216:ARG:HB2	1.89	0.72
1:A:488:THR:CG2	1:B:479:VAL:CG1	2.66	0.72
1:B:68:ARG:NH1	1:B:68:ARG:HG2	1.97	0.72
1:C:111:ILE:HD13	1:D:447:VAL:HG11	1.71	0.71
1:D:154:THR:HG22	1:D:155:LYS:HG3	1.72	0.71
1:B:215:PHE:O	1:B:216:ARG:HB2	1.89	0.71
1:C:154:THR:HG22	1:C:155:LYS:HG3	1.72	0.71
1:D:130:ASN:HA	1:D:517:ASN:CG	2.16	0.71
1:E:154:THR:HG22	1:E:155:LYS:HG3	1.72	0.71
1:B:193:LEU:HD11	1:B:496:ARG:HH12	1.54	0.71
1:B:275:TYR:CZ	1:B:402:ARG:HD3	2.26	0.71
1:C:484:ILE:HG21	1:D:480:TYR:CD1	2.25	0.71
1:C:275:TYR:CZ	1:C:402:ARG:HD3	2.26	0.71
1:E:130:ASN:HA	1:E:517:ASN:CG	2.16	0.71
1:E:510:THR:O	1:E:511:ILE:HB	1.88	0.71
1:A:422:LEU:HD23	1:A:423:LEU:N	2.06	0.71
1:B:274:THR:HG22	1:B:276:ASP:N	2.06	0.71
1:E:193:LEU:HD11	1:E:496:ARG:HH12	1.54	0.71
1:D:215:PHE:O	1:D:216:ARG:HB2	1.90	0.70
2:W:10:THR:HG22	2:W:10:THR:O	1.89	0.70
1:C:502:ILE:HG22	1:C:503:LEU:N	2.06	0.70
1:D:275:TYR:CZ	1:D:402:ARG:HD3	2.26	0.70
1:D:422:LEU:HD23	1:D:423:LEU:N	2.06	0.70
1:E:376:VAL:O	1:E:378:LYS:N	2.25	0.70
1:A:275:TYR:CZ	1:A:402:ARG:HD3	2.26	0.70
1:A:488:THR:HG22	1:B:479:VAL:CG1	2.21	0.70
2:S:10:THR:O	2:S:10:THR:HG22	1.89	0.70
1:A:479:VAL:O	1:E:488:THR:HG23	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:376:VAL:O	1:C:378:LYS:N	2.25	0.70
1:E:376:VAL:HG23	1:E:377:ILE:H	1.57	0.70
1:A:215:PHE:O	1:A:216:ARG:HB2	1.89	0.70
1:B:376:VAL:O	1:B:378:LYS:N	2.25	0.70
1:A:130:ASN:HA	1:A:517:ASN:CG	2.16	0.70
1:D:376:VAL:O	1:D:378:LYS:N	2.24	0.70
1:C:130:ASN:HA	1:C:517:ASN:CG	2.16	0.70
1:A:154:THR:HG22	1:A:155:LYS:HG3	1.72	0.70
1:B:422:LEU:HD23	1:B:423:LEU:N	2.06	0.70
1:C:484:ILE:CG2	1:D:480:TYR:CE1	2.75	0.70
1:A:98:ASN:HD22	1:A:99:ASN:N	1.90	0.70
1:E:422:LEU:HD23	1:E:423:LEU:N	2.06	0.70
1:A:376:VAL:O	1:A:378:LYS:N	2.25	0.69
1:B:98:ASN:HD22	1:B:99:ASN:N	1.90	0.69
1:B:130:ASN:HA	1:B:517:ASN:CG	2.16	0.69
1:C:422:LEU:HD23	1:C:423:LEU:N	2.06	0.69
1:A:479:VAL:CG1	1:E:488:THR:CG2	2.70	0.69
1:A:502:ILE:HG22	1:A:503:LEU:N	2.06	0.69
1:D:98:ASN:HD22	1:D:99:ASN:N	1.90	0.69
1:A:438:SER:C	1:A:440:PRO:HD3	2.17	0.69
1:A:485:ARG:NE	1:B:234:GLU:OE2	2.25	0.69
1:C:438:SER:C	1:C:440:PRO:HD3	2.17	0.69
1:B:376:VAL:HG23	1:B:377:ILE:H	1.57	0.69
1:D:274:THR:HG22	1:D:276:ASP:N	2.06	0.69
1:A:68:ARG:NH1	1:A:68:ARG:HG2	1.97	0.69
1:A:376:VAL:HG23	1:A:377:ILE:H	1.57	0.69
1:B:438:SER:C	1:B:440:PRO:HD3	2.17	0.69
1:C:98:ASN:HD22	1:C:99:ASN:N	1.90	0.69
1:E:438:SER:C	1:E:440:PRO:HD3	2.17	0.69
1:A:274:THR:HG22	1:A:276:ASP:N	2.06	0.69
1:E:98:ASN:HD22	1:E:99:ASN:N	1.90	0.69
1:E:274:THR:HG22	1:E:276:ASP:N	2.06	0.69
1:E:275:TYR:CZ	1:E:402:ARG:HD3	2.26	0.69
1:E:283:ILE:O	1:E:399:THR:HG23	1.93	0.69
1:B:490:LEU:HB2	1:C:230:VAL:HG11	1.74	0.69
1:B:502:ILE:HG22	1:B:503:LEU:N	2.06	0.69
1:C:488:THR:CG2	1:D:479:VAL:CG1	2.71	0.69
1:E:215:PHE:O	1:E:216:ARG:HB2	1.89	0.69
1:B:283:ILE:O	1:B:399:THR:HG23	1.93	0.69
1:C:455:ILE:HD12	1:C:456:SER:H	1.58	0.69
1:D:67:THR:HG21	1:E:447:VAL:HG22	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:376:VAL:HG23	1:C:377:ILE:H	1.57	0.69
1:D:438:SER:C	1:D:440:PRO:HD3	2.17	0.69
1:A:83:ASN:HA	1:A:86:ASN:ND2	2.09	0.68
1:A:283:ILE:O	1:A:399:THR:HG23	1.93	0.68
1:A:211:ASP:OD1	1:A:213:ARG:HG2	1.94	0.68
1:C:211:ASP:OD1	1:C:213:ARG:HG2	1.93	0.68
1:C:274:THR:HG22	1:C:276:ASP:N	2.05	0.68
1:C:283:ILE:O	1:C:399:THR:HG23	1.93	0.68
1:D:488:THR:HG23	1:E:479:VAL:O	1.93	0.68
1:E:502:ILE:HG22	1:E:503:LEU:N	2.06	0.68
1:D:211:ASP:OD1	1:D:213:ARG:HG2	1.93	0.68
1:E:83:ASN:HA	1:E:86:ASN:ND2	2.09	0.68
1:E:426:PRO:O	1:E:427:ASP:HB3	1.93	0.68
1:A:497:PHE:HD1	1:A:503:LEU:HB3	1.59	0.68
1:D:455:ILE:HD12	1:D:456:SER:H	1.58	0.68
1:D:502:ILE:HG22	1:D:503:LEU:N	2.06	0.68
1:B:455:ILE:HD12	1:B:456:SER:H	1.58	0.68
1:A:480:TYR:CD1	1:E:484:ILE:CG2	2.77	0.67
1:B:83:ASN:HA	1:B:86:ASN:ND2	2.09	0.67
1:C:556:LEU:HD21	1:D:434:GLN:HG2	1.75	0.67
1:D:485:ARG:HH21	1:E:234:GLU:CD	2.02	0.67
1:D:426:PRO:O	1:D:427:ASP:HB3	1.94	0.67
1:E:455:ILE:HD12	1:E:456:SER:H	1.58	0.67
1:A:455:ILE:HD12	1:A:456:SER:H	1.59	0.67
1:B:274:THR:HG22	1:B:275:TYR:N	2.10	0.67
1:C:179:MET:HE2	1:C:485:ARG:HH22	1.60	0.67
1:D:283:ILE:O	1:D:399:THR:HG23	1.93	0.67
1:E:497:PHE:HD1	1:E:503:LEU:HB3	1.59	0.67
1:A:422:LEU:HD21	1:E:551:TYR:CE2	2.30	0.67
1:B:179:MET:HE2	1:B:485:ARG:HH22	1.60	0.67
1:B:214:ASN:HD21	1:B:216:ARG:HB3	1.60	0.67
1:A:183:LEU:HD21	1:B:236:PHE:HE2	1.59	0.67
1:B:211:ASP:OD1	1:B:213:ARG:HG2	1.93	0.67
1:C:214:ASN:HD21	1:C:216:ARG:HB3	1.60	0.67
1:C:497:PHE:HD1	1:C:503:LEU:HB3	1.59	0.67
1:D:215:PHE:HB3	1:D:283:ILE:HG23	1.77	0.67
1:D:217:LEU:CB	1:D:232:THR:HG21	2.24	0.67
1:C:274:THR:HG22	1:C:275:TYR:N	2.10	0.67
1:E:211:ASP:OD1	1:E:213:ARG:HG2	1.94	0.67
1:E:214:ASN:HD21	1:E:216:ARG:HB3	1.60	0.66
1:A:217:LEU:CB	1:A:232:THR:HG21	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:ALA:HB3	1:B:168:PHE:CE1	2.31	0.66
1:C:215:PHE:HB3	1:C:283:ILE:HG23	1.77	0.66
1:C:217:LEU:CB	1:C:232:THR:HG21	2.24	0.66
1:D:497:PHE:HD1	1:D:503:LEU:HB3	1.59	0.66
1:B:475:ASN:C	1:B:477:GLN:H	2.03	0.66
1:D:475:ASN:C	1:D:477:GLN:H	2.03	0.66
1:A:426:PRO:O	1:A:427:ASP:HB3	1.94	0.66
1:C:83:ASN:HA	1:C:86:ASN:ND2	2.09	0.66
1:E:215:PHE:HB3	1:E:283:ILE:HG23	1.77	0.66
1:E:217:LEU:CB	1:E:232:THR:HG21	2.25	0.66
1:E:475:ASN:C	1:E:477:GLN:H	2.03	0.66
1:B:426:PRO:O	1:B:427:ASP:HB3	1.93	0.66
1:B:497:PHE:HD1	1:B:503:LEU:HB3	1.59	0.66
1:A:475:ASN:C	1:A:477:GLN:N	2.53	0.66
1:C:426:PRO:O	1:C:427:ASP:HB3	1.94	0.66
1:A:145:ALA:HB3	1:A:168:PHE:CE1	2.31	0.66
1:D:551:TYR:CE2	1:E:422:LEU:HD21	2.31	0.66
1:D:376:VAL:HG23	1:D:377:ILE:H	1.57	0.66
1:D:133:ASN:HB2	1:D:175:TYR:CD2	2.32	0.65
1:D:488:THR:CG2	1:E:479:VAL:CG1	2.73	0.65
1:A:179:MET:HE2	1:A:485:ARG:HH22	1.60	0.65
1:A:438:SER:HB3	1:A:459:PRO:O	1.97	0.65
1:E:475:ASN:C	1:E:477:GLN:N	2.53	0.65
1:A:214:ASN:HD21	1:A:216:ARG:HB3	1.60	0.65
1:C:133:ASN:HB2	1:C:175:TYR:CD2	2.32	0.65
1:D:179:MET:HE2	1:D:485:ARG:HH22	1.60	0.65
1:D:274:THR:HG22	1:D:275:TYR:N	2.10	0.65
1:D:485:ARG:NH1	1:D:505:ARG:NH2	2.44	0.65
1:A:490:LEU:CB	1:B:230:VAL:HG11	2.27	0.65
1:A:57:TYR:O	1:A:58:SER:C	2.40	0.65
1:B:133:ASN:HB2	1:B:175:TYR:CD2	2.32	0.65
1:B:217:LEU:CB	1:B:232:THR:HG21	2.24	0.65
1:E:133:ASN:HB2	1:E:175:TYR:CD2	2.31	0.65
1:B:224:GLY:O	1:B:225:LEU:HD23	1.97	0.65
1:B:485:ARG:NH1	1:B:505:ARG:NH2	2.44	0.65
1:E:179:MET:HE2	1:E:485:ARG:HH22	1.60	0.65
1:A:215:PHE:HB3	1:A:283:ILE:HG23	1.77	0.65
1:B:207:GLY:O	1:B:208:VAL:HB	1.97	0.65
1:C:57:TYR:O	1:C:58:SER:C	2.40	0.65
1:A:485:ARG:NH1	1:A:505:ARG:NH2	2.44	0.65
1:E:207:GLY:O	1:E:208:VAL:HB	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:485:ARG:NH1	1:E:505:ARG:NH2	2.44	0.65
1:A:224:GLY:O	1:A:225:LEU:HD23	1.97	0.64
1:D:214:ASN:HD21	1:D:216:ARG:HB3	1.60	0.64
1:D:484:ILE:CG2	1:E:480:TYR:CD1	2.80	0.64
1:E:274:THR:HG22	1:E:275:TYR:N	2.10	0.64
1:A:274:THR:HG22	1:A:275:TYR:N	2.10	0.64
1:C:145:ALA:HB3	1:C:168:PHE:CE1	2.31	0.64
1:D:224:GLY:O	1:D:225:LEU:HD23	1.97	0.64
2:W:18:ASP:OD1	2:W:18:ASP:O	2.15	0.64
1:B:215:PHE:HB3	1:B:283:ILE:HG23	1.77	0.64
1:B:475:ASN:C	1:B:477:GLN:N	2.53	0.64
1:C:485:ARG:NH1	1:C:505:ARG:NH2	2.44	0.64
2:V:18:ASP:OD1	2:V:18:ASP:O	2.15	0.64
1:A:133:ASN:HB2	1:A:175:TYR:CD2	2.32	0.64
1:B:511:ILE:HG22	1:B:511:ILE:O	1.97	0.64
1:C:475:ASN:C	1:C:477:GLN:H	2.03	0.64
1:D:57:TYR:O	1:D:58:SER:C	2.40	0.64
1:E:145:ALA:HB3	1:E:168:PHE:CE1	2.31	0.64
2:S:18:ASP:OD1	2:S:18:ASP:O	2.15	0.64
1:B:64:PHE:HD1	1:C:118:HIS:NE2	1.95	0.64
1:C:496:ARG:HD3	2:U:14:VAL:HG12	1.80	0.64
1:D:83:ASN:HA	1:D:86:ASN:ND2	2.09	0.64
1:C:434:GLN:NE2	1:C:436:TYR:HE2	1.96	0.64
1:D:145:ALA:HB3	1:D:168:PHE:CE1	2.31	0.64
1:D:496:ARG:HD3	2:V:14:VAL:HG12	1.80	0.64
2:T:18:ASP:OD1	2:T:18:ASP:O	2.15	0.64
2:U:18:ASP:O	2:U:18:ASP:OD1	2.15	0.64
1:A:475:ASN:C	1:A:477:GLN:H	2.03	0.64
1:B:57:TYR:O	1:B:58:SER:C	2.40	0.64
1:B:67:THR:HG21	1:C:447:VAL:HG22	1.80	0.64
1:C:488:THR:HG23	1:D:479:VAL:O	1.97	0.64
1:A:443:MET:HE3	1:A:527:LEU:HB2	1.80	0.64
1:B:438:SER:HB3	1:B:459:PRO:O	1.97	0.64
1:C:466:LEU:CD1	1:C:467:PRO:HD2	2.24	0.64
1:E:210:PHE:HD2	1:E:240:ILE:HG22	1.63	0.64
1:E:434:GLN:NE2	1:E:436:TYR:HE2	1.96	0.64
1:E:224:GLY:O	1:E:225:LEU:HD23	1.97	0.64
1:E:511:ILE:O	1:E:511:ILE:HG22	1.97	0.64
1:C:511:ILE:O	1:C:511:ILE:HG22	1.97	0.64
1:D:438:SER:HB3	1:D:459:PRO:O	1.97	0.64
1:E:57:TYR:O	1:E:58:SER:C	2.40	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:466:LEU:CD1	1:E:467:PRO:HD2	2.24	0.64
1:A:210:PHE:HD2	1:A:240:ILE:HG22	1.63	0.63
1:A:434:GLN:NE2	1:A:436:TYR:HE2	1.96	0.63
1:A:542:THR:HG21	1:A:546:ARG:HA	1.80	0.63
1:B:68:ARG:NE	1:C:527:LEU:HD21	2.12	0.63
1:D:443:MET:HE3	1:D:527:LEU:HB2	1.80	0.63
1:D:511:ILE:HG22	1:D:511:ILE:O	1.97	0.63
1:B:496:ARG:HD3	2:T:14:VAL:HG12	1.80	0.63
1:C:210:PHE:HD2	1:C:240:ILE:HG22	1.63	0.63
1:C:224:GLY:O	1:C:225:LEU:HD23	1.97	0.63
1:D:434:GLN:NE2	1:D:436:TYR:HE2	1.96	0.63
1:E:134:VAL:HA	1:E:140:THR:OG1	1.98	0.63
1:E:438:SER:HB3	1:E:459:PRO:O	1.97	0.63
1:A:207:GLY:O	1:A:208:VAL:HB	1.97	0.63
1:C:558:ILE:HD11	1:D:463:ALA:HB3	1.79	0.63
1:A:98:ASN:HD22	1:A:98:ASN:C	2.06	0.63
1:A:134:VAL:HA	1:A:140:THR:OG1	1.99	0.63
1:D:207:GLY:O	1:D:208:VAL:HB	1.97	0.63
1:D:228:PRO:HG3	2:U:15:TYR:CE1	2.34	0.63
1:A:111:ILE:HD13	1:B:447:VAL:HG11	1.81	0.63
1:A:234:GLU:CD	1:E:485:ARG:HH21	2.06	0.63
1:A:511:ILE:HG22	1:A:511:ILE:O	1.97	0.63
1:E:171:PRO:O	1:E:174:ASN:ND2	2.32	0.63
1:A:496:ARG:HD3	2:S:14:VAL:HG12	1.80	0.63
1:B:484:ILE:CG2	1:C:480:TYR:CE1	2.82	0.63
1:C:443:MET:HE3	1:C:527:LEU:HB2	1.80	0.63
1:D:98:ASN:HD22	1:D:98:ASN:C	2.06	0.63
1:C:542:THR:HG21	1:C:546:ARG:HA	1.80	0.63
1:A:100:ASP:OD2	1:B:450:ARG:NH1	2.32	0.63
1:B:434:GLN:NE2	1:B:436:TYR:HE2	1.96	0.63
1:B:443:MET:HE3	1:B:527:LEU:HB2	1.80	0.63
1:C:134:VAL:HA	1:C:140:THR:OG1	1.99	0.63
1:C:207:GLY:O	1:C:208:VAL:HB	1.97	0.63
1:D:134:VAL:HA	1:D:140:THR:OG1	1.98	0.62
1:D:475:ASN:C	1:D:477:GLN:N	2.53	0.62
1:E:138:MET:O	1:E:139:PHE:HB2	1.98	0.62
1:B:138:MET:O	1:B:139:PHE:HB2	1.99	0.62
1:B:542:THR:HG21	1:B:546:ARG:HA	1.80	0.62
1:C:138:MET:O	1:C:139:PHE:HB2	1.99	0.62
1:D:171:PRO:O	1:D:174:ASN:ND2	2.32	0.62
1:D:210:PHE:HD2	1:D:240:ILE:HG22	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:443:MET:HE3	1:E:527:LEU:HB2	1.80	0.62
1:A:171:PRO:O	1:A:174:ASN:ND2	2.32	0.62
1:D:556:LEU:HD21	1:E:434:GLN:HG2	1.80	0.62
1:B:74:ASN:OD1	1:C:434:GLN:OE1	2.17	0.62
1:B:134:VAL:HA	1:B:140:THR:OG1	1.98	0.62
1:C:98:ASN:HD22	1:C:98:ASN:C	2.06	0.62
1:E:98:ASN:HD22	1:E:98:ASN:C	2.06	0.62
1:D:496:ARG:C	1:D:497:PHE:HD2	2.07	0.62
1:A:479:VAL:HG12	1:A:479:VAL:O	2.00	0.62
1:C:438:SER:HB3	1:C:459:PRO:O	1.97	0.62
1:E:159:VAL:HG23	1:E:159:VAL:O	2.00	0.62
1:E:211:ASP:OD1	1:E:212:THR:N	2.31	0.62
1:A:496:ARG:C	1:A:497:PHE:HD2	2.08	0.62
1:A:551:TYR:CE2	1:B:422:LEU:HD21	2.35	0.62
1:C:171:PRO:O	1:C:174:ASN:ND2	2.32	0.62
1:B:177:GLU:HG3	1:B:178:THR:N	2.15	0.62
1:D:154:THR:HG22	1:D:155:LYS:N	2.14	0.62
1:E:154:THR:HG22	1:E:155:LYS:N	2.14	0.62
1:E:496:ARG:HD3	2:W:14:VAL:HG12	1.80	0.62
1:B:210:PHE:HD2	1:B:240:ILE:HG22	1.63	0.62
1:C:496:ARG:C	1:C:497:PHE:HD2	2.07	0.62
1:D:542:THR:HG21	1:D:546:ARG:HA	1.80	0.62
1:E:177:GLU:HG3	1:E:178:THR:N	2.15	0.62
1:A:177:GLU:HG3	1:A:178:THR:N	2.15	0.62
1:A:383:ASP:OD1	1:A:387:ARG:HD2	2.00	0.62
1:B:100:ASP:CG	1:C:450:ARG:HH12	2.07	0.62
1:C:485:ARG:HH21	1:D:234:GLU:CD	2.08	0.62
1:E:496:ARG:C	1:E:497:PHE:HD2	2.08	0.62
1:E:542:THR:HG21	1:E:546:ARG:HA	1.80	0.62
1:A:154:THR:HG22	1:A:155:LYS:N	2.14	0.61
1:B:171:PRO:O	1:B:174:ASN:ND2	2.32	0.61
1:B:479:VAL:HG12	1:B:479:VAL:O	2.00	0.61
1:A:159:VAL:HG23	1:A:159:VAL:O	2.00	0.61
1:C:479:VAL:HG12	1:C:479:VAL:O	2.00	0.61
1:D:292:TYR:CD1	1:D:376:VAL:HG12	2.35	0.61
1:A:466:LEU:CD1	1:A:467:PRO:HD2	2.24	0.61
1:C:177:GLU:HG3	1:C:178:THR:N	2.15	0.61
1:C:292:TYR:CD1	1:C:376:VAL:HG12	2.35	0.61
1:C:383:ASP:OD1	1:C:387:ARG:HD2	2.00	0.61
1:A:214:ASN:C	1:A:214:ASN:ND2	2.58	0.61
1:C:154:THR:HG22	1:C:155:LYS:N	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:475:ASN:C	1:C:477:GLN:N	2.54	0.61
1:D:138:MET:O	1:D:139:PHE:HB2	1.98	0.61
1:D:466:LEU:CD1	1:D:467:PRO:HD2	2.24	0.61
1:B:98:ASN:HD22	1:B:98:ASN:C	2.06	0.61
1:B:154:THR:HG22	1:B:155:LYS:N	2.14	0.61
1:B:496:ARG:C	1:B:497:PHE:CD2	2.78	0.61
1:D:177:GLU:HG3	1:D:178:THR:N	2.15	0.61
1:A:138:MET:O	1:A:139:PHE:HB2	1.98	0.61
1:D:376:VAL:CG2	1:D:377:ILE:H	2.14	0.61
1:D:383:ASP:OD1	1:D:387:ARG:HD2	2.00	0.61
1:A:428:VAL:HG21	1:A:515:SER:N	2.16	0.61
1:C:99:ASN:HB3	1:D:450:ARG:NH2	2.16	0.61
1:A:292:TYR:CD1	1:A:376:VAL:HG12	2.35	0.61
1:A:479:VAL:CG1	1:E:488:THR:HG22	2.31	0.61
1:C:496:ARG:C	1:C:497:PHE:CD2	2.78	0.61
1:D:428:VAL:HG21	1:D:515:SER:N	2.16	0.61
1:A:496:ARG:C	1:A:497:PHE:CD2	2.78	0.61
1:B:214:ASN:C	1:B:214:ASN:ND2	2.58	0.61
1:B:292:TYR:CD1	1:B:376:VAL:HG12	2.35	0.61
1:B:428:VAL:HG21	1:B:515:SER:N	2.16	0.61
1:C:183:LEU:HD21	1:D:236:PHE:HE2	1.65	0.61
1:D:496:ARG:C	1:D:497:PHE:CD2	2.78	0.61
1:B:159:VAL:O	1:B:159:VAL:HG23	2.00	0.61
1:B:496:ARG:C	1:B:497:PHE:HD2	2.07	0.61
1:C:428:VAL:HG21	1:C:515:SER:N	2.16	0.61
1:D:495:ASN:O	1:D:497:PHE:N	2.34	0.61
1:E:383:ASP:OD1	1:E:387:ARG:HD2	2.00	0.61
1:E:496:ARG:C	1:E:497:PHE:CD2	2.78	0.61
1:A:447:VAL:HG11	1:E:111:ILE:HD13	1.83	0.60
1:A:495:ASN:O	1:A:497:PHE:N	2.34	0.60
1:D:479:VAL:HG12	1:D:479:VAL:O	2.00	0.60
2:W:18:ASP:O	2:W:18:ASP:CG	2.44	0.60
1:A:236:PHE:HE2	1:E:183:LEU:HD21	1.66	0.60
1:B:383:ASP:OD1	1:B:387:ARG:HD2	2.00	0.60
1:C:376:VAL:CG2	1:C:377:ILE:H	2.14	0.60
1:C:484:ILE:CG2	1:D:480:TYR:CD1	2.83	0.60
1:B:376:VAL:CG2	1:B:377:ILE:H	2.14	0.60
1:C:159:VAL:HG23	1:C:159:VAL:O	2.00	0.60
1:D:273:ILE:HG23	1:D:273:ILE:O	2.02	0.60
1:E:292:TYR:CD1	1:E:376:VAL:HG12	2.35	0.60
1:E:478:ALA:HB1	1:E:508:ALA:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:479:VAL:HA	1:E:482:GLN:HB3	1.83	0.60
1:C:68:ARG:NE	1:D:527:LEU:HD21	2.16	0.60
1:E:214:ASN:C	1:E:214:ASN:ND2	2.58	0.60
1:A:173:GLY:O	1:A:175:TYR:CD1	2.55	0.60
1:B:479:VAL:HA	1:B:482:GLN:HB3	1.83	0.60
1:C:67:THR:HG21	1:D:447:VAL:CG2	2.29	0.60
1:C:495:ASN:O	1:C:497:PHE:N	2.35	0.60
1:A:478:ALA:HB1	1:A:508:ALA:HB3	1.83	0.60
1:A:479:VAL:HA	1:A:482:GLN:HB3	1.83	0.60
1:A:491:THR:HB	1:A:493:VAL:HG23	1.84	0.60
1:B:488:THR:HG23	1:C:479:VAL:O	2.02	0.60
1:D:159:VAL:HG23	1:D:159:VAL:O	2.00	0.60
1:B:273:ILE:O	1:B:273:ILE:HG23	2.02	0.60
1:C:479:VAL:HA	1:C:482:GLN:HB3	1.83	0.60
1:C:491:THR:HB	1:C:493:VAL:HG23	1.84	0.60
1:D:479:VAL:HA	1:D:482:GLN:HB3	1.83	0.60
1:D:488:THR:HG22	1:E:479:VAL:HG12	1.82	0.60
1:E:173:GLY:O	1:E:175:TYR:CD1	2.55	0.60
1:E:495:ASN:O	1:E:497:PHE:N	2.35	0.60
2:T:18:ASP:O	2:T:18:ASP:CG	2.44	0.60
1:A:376:VAL:CG2	1:A:377:ILE:N	2.65	0.60
1:A:497:PHE:CD2	1:A:497:PHE:N	2.69	0.60
1:B:478:ALA:HB1	1:B:508:ALA:HB3	1.83	0.60
1:E:52:ARG:N	1:E:116:ARG:HH12	2.00	0.60
2:S:18:ASP:O	2:S:18:ASP:CG	2.44	0.60
1:B:173:GLY:O	1:B:175:TYR:CD1	2.55	0.60
1:C:488:THR:HG22	1:D:479:VAL:HG12	1.84	0.60
1:D:211:ASP:OD1	1:D:212:THR:N	2.31	0.60
2:U:18:ASP:O	2:U:18:ASP:CG	2.44	0.60
2:V:18:ASP:O	2:V:18:ASP:CG	2.44	0.60
1:C:52:ARG:N	1:C:116:ARG:HH12	2.00	0.59
1:C:173:GLY:O	1:C:175:TYR:CD1	2.55	0.59
1:E:273:ILE:O	1:E:273:ILE:HG23	2.02	0.59
1:E:428:VAL:HG21	1:E:515:SER:N	2.16	0.59
1:B:52:ARG:N	1:B:116:ARG:HH12	2.00	0.59
1:B:497:PHE:CD2	1:B:497:PHE:N	2.69	0.59
1:D:173:GLY:O	1:D:175:TYR:CD1	2.55	0.59
1:D:210:PHE:CD2	1:D:240:ILE:HG22	2.37	0.59
1:D:233:ASN:OD1	1:D:507:PRO:HG3	2.02	0.59
1:D:278:LEU:HD22	1:D:404:TRP:HA	1.84	0.59
1:E:376:VAL:CG2	1:E:377:ILE:N	2.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:479:VAL:HG12	1:E:479:VAL:O	2.00	0.59
1:B:387:ARG:HG2	1:B:387:ARG:HH11	1.68	0.59
1:D:491:THR:HB	1:D:493:VAL:HG23	1.84	0.59
1:E:279:GLU:O	1:E:280:GLY:C	2.45	0.59
1:C:273:ILE:HG23	1:C:273:ILE:O	2.02	0.59
1:C:536:VAL:HG23	1:C:536:VAL:O	2.02	0.59
1:E:233:ASN:OD1	1:E:507:PRO:HG3	2.02	0.59
1:C:237:HIS:CD2	1:C:238:PRO:O	2.56	0.59
1:C:278:LEU:HD22	1:C:404:TRP:HA	1.84	0.59
1:E:237:HIS:CD2	1:E:238:PRO:O	2.56	0.59
1:A:237:HIS:CD2	1:A:238:PRO:O	2.56	0.59
1:A:479:VAL:HG12	1:E:488:THR:HG22	1.80	0.59
1:B:495:ASN:O	1:B:497:PHE:N	2.34	0.59
1:C:211:ASP:OD1	1:C:212:THR:N	2.31	0.59
1:D:208:VAL:HG22	1:D:242:LEU:CD2	2.33	0.59
1:E:491:THR:HB	1:E:493:VAL:HG23	1.83	0.59
1:E:536:VAL:HG23	1:E:536:VAL:O	2.02	0.59
1:A:376:VAL:CG2	1:A:377:ILE:H	2.14	0.59
1:B:536:VAL:HG23	1:B:536:VAL:O	2.02	0.59
1:C:208:VAL:HG22	1:C:242:LEU:CD2	2.33	0.59
1:C:488:THR:HG22	1:D:479:VAL:CG1	2.33	0.59
1:C:490:LEU:HB2	1:D:230:VAL:CG1	2.28	0.59
1:C:497:PHE:CD2	1:C:497:PHE:N	2.69	0.59
1:D:111:ILE:HD13	1:E:447:VAL:HG11	1.82	0.59
1:D:279:GLU:O	1:D:280:GLY:C	2.45	0.59
1:D:478:ALA:HB1	1:D:508:ALA:HB3	1.83	0.59
1:A:211:ASP:OD1	1:A:212:THR:N	2.31	0.59
1:A:536:VAL:HG23	1:A:536:VAL:O	2.02	0.59
1:B:210:PHE:CD2	1:B:240:ILE:HG22	2.37	0.59
1:B:409:ASN:OD1	1:B:409:ASN:N	2.36	0.59
1:A:210:PHE:CD2	1:A:240:ILE:HG22	2.37	0.59
1:D:376:VAL:CG2	1:D:377:ILE:N	2.65	0.59
1:E:208:VAL:HG22	1:E:242:LEU:CD2	2.33	0.59
1:E:376:VAL:CG2	1:E:377:ILE:H	2.14	0.59
1:B:278:LEU:HD22	1:B:404:TRP:HA	1.84	0.59
1:D:475:ASN:HB3	1:E:474:TYR:CE2	2.38	0.59
1:E:122:ASP:OD1	1:E:526:THR:HG22	2.03	0.59
1:E:433:GLU:OE1	1:E:433:GLU:HA	2.03	0.59
1:A:233:ASN:OD1	1:A:507:PRO:HG3	2.03	0.58
1:C:210:PHE:CD2	1:C:240:ILE:HG22	2.37	0.58
1:C:376:VAL:CG2	1:C:377:ILE:N	2.65	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:536:VAL:O	1:D:536:VAL:HG23	2.02	0.58
1:A:52:ARG:N	1:A:116:ARG:HH12	2.00	0.58
1:A:208:VAL:HG22	1:A:242:LEU:CD2	2.33	0.58
1:A:278:LEU:HD22	1:A:404:TRP:HA	1.84	0.58
1:B:433:GLU:OE1	1:B:433:GLU:HA	2.03	0.58
1:B:477:GLN:O	1:B:481:SER:N	2.36	0.58
1:C:478:ALA:HB1	1:C:508:ALA:HB3	1.83	0.58
1:A:295:SER:OG	1:A:375:PRO:HD3	2.03	0.58
1:B:233:ASN:OD1	1:B:507:PRO:HG3	2.02	0.58
1:B:491:THR:HB	1:B:493:VAL:HG23	1.84	0.58
1:C:409:ASN:OD1	1:C:409:ASN:N	2.36	0.58
1:D:57:TYR:CD2	1:E:448:THR:HG22	2.39	0.58
1:D:183:LEU:HD21	1:E:236:PHE:HE2	1.67	0.58
1:D:496:ARG:O	2:V:16:PRO:HD3	2.03	0.58
1:A:68:ARG:NE	1:B:527:LEU:HD21	2.18	0.58
1:A:434:GLN:HG2	1:E:556:LEU:HD21	1.83	0.58
1:A:477:GLN:O	1:A:481:SER:N	2.36	0.58
1:A:556:LEU:HD21	1:B:434:GLN:HG2	1.86	0.58
1:B:274:THR:CG2	1:B:275:TYR:N	2.67	0.58
1:B:376:VAL:CG2	1:B:377:ILE:N	2.65	0.58
1:E:387:ARG:HH11	1:E:387:ARG:HG2	1.67	0.58
1:A:387:ARG:HG2	1:A:387:ARG:HH11	1.67	0.58
1:A:401:TYR:HD1	1:A:502:ILE:HG12	1.69	0.58
1:A:409:ASN:OD1	1:A:409:ASN:N	2.36	0.58
1:A:433:GLU:OE1	1:A:433:GLU:HA	2.03	0.58
1:A:474:TYR:CE2	1:E:475:ASN:HB3	2.38	0.58
1:B:122:ASP:OD1	1:B:526:THR:HG22	2.03	0.58
1:B:279:GLU:O	1:B:280:GLY:C	2.45	0.58
1:D:237:HIS:CD2	1:D:238:PRO:O	2.56	0.58
1:D:295:SER:OG	1:D:375:PRO:HD3	2.03	0.58
1:D:558:ILE:HD11	1:E:463:ALA:HB3	1.86	0.58
1:E:210:PHE:CD2	1:E:240:ILE:HG22	2.37	0.58
1:E:497:PHE:CD2	1:E:497:PHE:N	2.69	0.58
1:A:496:ARG:O	2:S:16:PRO:HD3	2.03	0.58
1:B:401:TYR:HD1	1:B:502:ILE:HG12	1.69	0.58
1:C:295:SER:OG	1:C:375:PRO:HD3	2.03	0.58
1:C:433:GLU:HA	1:C:433:GLU:OE1	2.03	0.58
1:C:477:GLN:O	1:C:481:SER:N	2.36	0.58
1:D:52:ARG:N	1:D:116:ARG:HH12	2.00	0.58
1:E:477:GLN:O	1:E:481:SER:N	2.36	0.58
1:A:274:THR:CG2	1:A:275:TYR:N	2.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:GLU:O	1:A:280:GLY:C	2.45	0.58
1:C:387:ARG:HG2	1:C:387:ARG:HH11	1.68	0.58
1:D:387:ARG:HG2	1:D:387:ARG:HH11	1.67	0.58
1:C:233:ASN:OD1	1:C:507:PRO:HG3	2.02	0.58
1:C:496:ARG:O	2:U:16:PRO:HD3	2.03	0.58
2:S:15:TYR:HD2	2:S:16:PRO:N	2.02	0.58
1:B:211:ASP:OD1	1:B:212:THR:N	2.31	0.58
1:B:237:HIS:CD2	1:B:238:PRO:O	2.56	0.58
1:C:122:ASP:OD1	1:C:526:THR:HG22	2.04	0.58
1:C:279:GLU:O	1:C:280:GLY:C	2.45	0.58
1:D:274:THR:CG2	1:D:275:TYR:N	2.67	0.58
1:D:433:GLU:OE1	1:D:433:GLU:HA	2.03	0.58
1:A:502:ILE:O	1:A:504:ALA:N	2.36	0.58
1:B:295:SER:OG	1:B:375:PRO:HD3	2.03	0.58
1:C:214:ASN:C	1:C:214:ASN:ND2	2.58	0.58
1:E:278:LEU:HD22	1:E:404:TRP:HA	1.84	0.58
1:C:100:ASP:CG	1:D:450:ARG:HH12	2.10	0.57
1:C:274:THR:CG2	1:C:275:TYR:N	2.67	0.57
1:D:439:LEU:N	1:D:440:PRO:HD3	2.19	0.57
1:D:477:GLN:O	1:D:481:SER:N	2.36	0.57
1:E:295:SER:OG	1:E:375:PRO:HD3	2.03	0.57
2:T:15:TYR:HD2	2:T:16:PRO:N	2.02	0.57
2:W:15:TYR:HD2	2:W:16:PRO:N	2.02	0.57
1:B:99:ASN:HB3	1:C:450:ARG:NH2	2.19	0.57
1:B:376:VAL:C	1:B:378:LYS:N	2.62	0.57
1:B:496:ARG:O	2:T:16:PRO:HD3	2.03	0.57
1:C:502:ILE:O	1:C:504:ALA:N	2.37	0.57
1:D:376:VAL:C	1:D:378:LYS:N	2.62	0.57
1:D:122:ASP:OD1	1:D:526:THR:HG22	2.03	0.57
1:D:498:PRO:HG2	1:D:499:GLU:OE2	2.04	0.57
1:E:496:ARG:O	2:W:16:PRO:HD3	2.03	0.57
1:A:475:ASN:HB3	1:B:474:TYR:CE2	2.39	0.57
1:A:498:PRO:HG2	1:A:499:GLU:OE2	2.04	0.57
1:A:518:VAL:HG23	1:A:519:PRO:HD2	1.87	0.57
1:B:208:VAL:HG22	1:B:242:LEU:CD2	2.33	0.57
1:B:484:ILE:HG21	1:C:480:TYR:CD1	2.39	0.57
1:D:497:PHE:CD2	1:D:497:PHE:N	2.69	0.57
1:E:113:LEU:O	1:E:114:ASP:C	2.47	0.57
1:E:409:ASN:OD1	1:E:409:ASN:N	2.36	0.57
1:E:502:ILE:O	1:E:504:ALA:N	2.37	0.57
1:E:518:VAL:HG23	1:E:519:PRO:HD2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:LEU:O	1:A:114:ASP:C	2.47	0.57
1:A:122:ASP:OD1	1:A:526:THR:HG22	2.03	0.57
1:C:475:ASN:HB3	1:D:474:TYR:CE2	2.39	0.57
1:A:484:ILE:HG23	1:B:480:TYR:CE1	2.40	0.57
1:B:466:LEU:CD1	1:B:467:PRO:HD2	2.24	0.57
1:C:113:LEU:O	1:C:114:ASP:C	2.47	0.57
1:C:175:TYR:CD1	1:C:175:TYR:N	2.72	0.57
1:D:502:ILE:O	1:D:504:ALA:N	2.37	0.57
1:E:376:VAL:C	1:E:378:LYS:N	2.62	0.57
1:B:175:TYR:H	1:B:175:TYR:HD1	1.52	0.57
1:B:498:PRO:HG2	1:B:499:GLU:OE2	2.05	0.57
1:C:498:PRO:HG2	1:C:499:GLU:OE2	2.04	0.57
2:U:15:TYR:HD2	2:U:16:PRO:N	2.02	0.57
1:A:273:ILE:HG23	1:A:273:ILE:O	2.02	0.57
1:B:113:LEU:O	1:B:114:ASP:C	2.47	0.57
1:B:175:TYR:CD1	1:B:175:TYR:N	2.72	0.57
1:B:502:ILE:O	1:B:504:ALA:N	2.37	0.57
1:E:258:LEU:CD1	1:E:428:VAL:HA	2.35	0.57
1:E:498:PRO:HG2	1:E:499:GLU:OE2	2.05	0.57
1:A:88:HIS:ND1	1:A:553:TYR:O	2.38	0.57
1:B:490:LEU:CB	1:C:230:VAL:HG11	2.34	0.57
1:E:274:THR:CG2	1:E:275:TYR:N	2.67	0.57
2:S:15:TYR:HD2	2:S:16:PRO:CD	2.18	0.57
2:U:15:TYR:HD2	2:U:16:PRO:CD	2.18	0.57
2:V:15:TYR:HD2	2:V:16:PRO:N	2.02	0.57
1:A:175:TYR:CD1	1:A:175:TYR:N	2.72	0.57
1:A:376:VAL:C	1:A:378:LYS:N	2.62	0.57
1:B:88:HIS:ND1	1:B:553:TYR:O	2.38	0.57
1:B:258:LEU:CD1	1:B:428:VAL:HA	2.35	0.57
1:A:99:ASN:HB3	1:B:450:ARG:NH2	2.20	0.56
1:A:258:LEU:CD1	1:A:428:VAL:HA	2.35	0.56
1:C:68:ARG:NH1	1:C:68:ARG:CG	2.67	0.56
1:E:401:TYR:HD1	1:E:502:ILE:HG12	1.69	0.56
1:A:175:TYR:HD1	1:A:175:TYR:H	1.52	0.56
1:A:463:ALA:HB3	1:E:558:ILE:HD11	1.88	0.56
1:C:556:LEU:C	1:C:556:LEU:HD12	2.30	0.56
1:D:88:HIS:ND1	1:D:553:TYR:O	2.38	0.56
1:D:409:ASN:OD1	1:D:409:ASN:N	2.36	0.56
1:A:130:ASN:HA	1:A:517:ASN:ND2	2.21	0.56
1:A:151:ARG:HB3	1:A:201:VAL:H	1.70	0.56
1:B:461:VAL:HB	1:B:527:LEU:HD13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:556:LEU:C	1:B:556:LEU:HD12	2.30	0.56
1:C:258:LEU:CD1	1:C:428:VAL:HA	2.35	0.56
1:D:461:VAL:HB	1:D:527:LEU:HD13	1.88	0.56
1:D:488:THR:HG22	1:E:479:VAL:CG1	2.34	0.56
1:E:69:VAL:CG2	1:E:559:VAL:HB	2.36	0.56
1:E:151:ARG:HB3	1:E:201:VAL:H	1.70	0.56
1:E:175:TYR:CD1	1:E:175:TYR:N	2.72	0.56
1:E:439:LEU:N	1:E:440:PRO:HD3	2.19	0.56
2:V:15:TYR:HD2	2:V:16:PRO:CD	2.18	0.56
1:A:556:LEU:HD12	1:A:556:LEU:C	2.31	0.56
1:C:439:LEU:N	1:C:440:PRO:HD3	2.19	0.56
1:D:113:LEU:O	1:D:114:ASP:C	2.47	0.56
1:A:429:THR:O	1:A:430:CYS:HB2	2.05	0.56
1:B:429:THR:O	1:B:430:CYS:HB2	2.05	0.56
1:D:427:ASP:C	1:D:427:ASP:OD1	2.49	0.56
1:D:429:THR:O	1:D:430:CYS:HB2	2.05	0.56
1:E:130:ASN:HA	1:E:517:ASN:ND2	2.21	0.56
1:A:243:LEU:HG	1:A:401:TYR:HE2	1.71	0.56
1:B:154:THR:CG2	1:B:155:LYS:N	2.69	0.56
1:C:86:ASN:HB3	1:C:90:ASN:O	2.06	0.56
1:C:132:PRO:HD2	1:C:551:TYR:CE2	2.41	0.56
1:C:151:ARG:HB3	1:C:201:VAL:H	1.70	0.56
1:C:461:VAL:HB	1:C:527:LEU:HD13	1.88	0.56
1:D:132:PRO:HD2	1:D:551:TYR:CE2	2.41	0.56
1:D:154:THR:CG2	1:D:155:LYS:N	2.69	0.56
1:D:258:LEU:CD1	1:D:428:VAL:HA	2.35	0.56
1:E:429:THR:O	1:E:430:CYS:HB2	2.05	0.56
1:E:556:LEU:C	1:E:556:LEU:HD12	2.30	0.56
1:A:427:ASP:C	1:A:427:ASP:OD1	2.49	0.56
1:B:86:ASN:HB3	1:B:90:ASN:O	2.06	0.56
1:B:439:LEU:N	1:B:440:PRO:HD3	2.19	0.56
1:C:69:VAL:CG2	1:C:559:VAL:HB	2.36	0.56
1:D:67:THR:OG1	1:D:68:ARG:N	2.39	0.56
1:D:130:ASN:HA	1:D:517:ASN:ND2	2.21	0.56
1:E:86:ASN:HB3	1:E:90:ASN:O	2.06	0.56
1:E:132:PRO:HD2	1:E:551:TYR:CE2	2.41	0.56
1:E:427:ASP:C	1:E:427:ASP:OD1	2.49	0.56
1:A:67:THR:OG1	1:B:447:VAL:HG23	2.06	0.56
1:A:86:ASN:HB3	1:A:90:ASN:O	2.06	0.56
1:A:154:THR:CG2	1:A:155:LYS:N	2.69	0.56
1:A:447:VAL:CG2	1:E:67:THR:HG21	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:PRO:HD2	1:B:551:TYR:CE2	2.41	0.56
1:C:427:ASP:C	1:C:427:ASP:OD1	2.49	0.56
1:D:150:SER:HB3	1:D:199:ASN:HD22	1.71	0.56
1:D:518:VAL:HG23	1:D:519:PRO:HD2	1.87	0.56
1:E:279:GLU:O	1:E:280:GLY:O	2.24	0.56
1:A:69:VAL:CG2	1:A:559:VAL:HB	2.36	0.56
1:C:243:LEU:HG	1:C:401:TYR:HE2	1.71	0.56
1:C:279:GLU:O	1:C:280:GLY:O	2.24	0.56
1:D:151:ARG:HB3	1:D:201:VAL:H	1.70	0.56
1:A:130:ASN:C	1:A:130:ASN:HD22	2.14	0.56
1:C:88:HIS:HD2	1:D:267:PHE:CZ	2.24	0.56
1:C:130:ASN:HA	1:C:517:ASN:ND2	2.21	0.56
1:C:130:ASN:C	1:C:130:ASN:HD22	2.14	0.56
1:D:86:ASN:HB3	1:D:90:ASN:O	2.06	0.56
1:D:556:LEU:C	1:D:556:LEU:HD12	2.31	0.56
1:E:175:TYR:H	1:E:175:TYR:HD1	1.52	0.56
2:W:15:TYR:HD2	2:W:16:PRO:CD	2.18	0.56
1:B:69:VAL:CG2	1:B:559:VAL:HB	2.36	0.55
1:C:197:ARG:HG3	1:C:198:GLN:HG3	1.88	0.55
1:A:132:PRO:HD2	1:A:551:TYR:CE2	2.41	0.55
1:A:279:GLU:O	1:A:280:GLY:O	2.24	0.55
1:B:427:ASP:C	1:B:427:ASP:OD1	2.49	0.55
1:C:150:SER:HB3	1:C:199:ASN:HD22	1.71	0.55
1:E:154:THR:CG2	1:E:155:LYS:N	2.69	0.55
1:E:243:LEU:HG	1:E:401:TYR:HE2	1.71	0.55
2:T:15:TYR:HD2	2:T:16:PRO:CD	2.18	0.55
1:A:235:ALA:C	1:A:236:PHE:HD1	2.15	0.55
1:B:65:ASP:O	1:B:66:THR:HB	2.06	0.55
1:B:150:SER:HB3	1:B:199:ASN:HD22	1.71	0.55
1:B:151:ARG:HB3	1:B:201:VAL:H	1.71	0.55
1:B:518:VAL:HG23	1:B:519:PRO:HD2	1.87	0.55
1:D:130:ASN:HD22	1:D:130:ASN:C	2.14	0.55
1:A:150:SER:HB3	1:A:199:ASN:HD22	1.71	0.55
1:A:461:VAL:HB	1:A:527:LEU:HD13	1.88	0.55
1:B:130:ASN:HA	1:B:517:ASN:ND2	2.21	0.55
1:D:69:VAL:CG2	1:D:559:VAL:HB	2.36	0.55
1:D:197:ARG:HG3	1:D:198:GLN:HG3	1.89	0.55
1:C:154:THR:CG2	1:C:155:LYS:N	2.69	0.55
1:C:518:VAL:HG23	1:C:519:PRO:HD2	1.87	0.55
1:D:65:ASP:O	1:D:66:THR:HB	2.06	0.55
1:D:243:LEU:HG	1:D:401:TYR:HE2	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:65:ASP:O	1:C:66:THR:HB	2.06	0.55
1:D:175:TYR:HD1	1:D:175:TYR:H	1.52	0.55
1:E:88:HIS:ND1	1:E:553:TYR:O	2.38	0.55
1:A:67:THR:OG1	1:A:68:ARG:N	2.39	0.55
1:A:404:TRP:NE1	1:A:417:ILE:HG21	2.22	0.55
1:C:175:TYR:HD1	1:C:175:TYR:H	1.52	0.55
1:E:150:SER:HB3	1:E:199:ASN:HD22	1.71	0.55
1:B:444:GLN:O	1:B:446:PRO:HD3	2.07	0.55
1:C:444:GLN:O	1:C:446:PRO:HD3	2.07	0.55
1:E:65:ASP:O	1:E:66:THR:HB	2.06	0.55
1:E:444:GLN:O	1:E:446:PRO:HD3	2.07	0.55
1:E:461:VAL:HB	1:E:527:LEU:HD13	1.88	0.55
1:C:235:ALA:C	1:C:236:PHE:HD1	2.15	0.55
1:D:175:TYR:CD1	1:D:175:TYR:N	2.72	0.55
1:D:401:TYR:HD1	1:D:502:ILE:HG12	1.69	0.55
1:E:442:MET:CE	1:E:559:VAL:HG21	2.27	0.55
1:A:439:LEU:N	1:A:440:PRO:HD3	2.19	0.55
1:C:376:VAL:C	1:C:378:LYS:N	2.62	0.55
1:C:429:THR:O	1:C:430:CYS:HB2	2.05	0.55
1:E:67:THR:OG1	1:E:68:ARG:N	2.39	0.55
1:E:130:ASN:C	1:E:130:ASN:HD22	2.14	0.55
1:E:235:ALA:C	1:E:236:PHE:HD1	2.15	0.55
1:A:444:GLN:O	1:A:446:PRO:HD3	2.07	0.54
1:B:197:ARG:HG3	1:B:198:GLN:HG3	1.89	0.54
1:B:279:GLU:O	1:B:280:GLY:O	2.24	0.54
1:C:375:PRO:O	1:C:377:ILE:N	2.40	0.54
1:A:122:ASP:OD1	1:A:526:THR:CG2	2.56	0.54
1:A:228:PRO:HG3	2:W:15:TYR:CE1	2.42	0.54
1:A:375:PRO:O	1:A:377:ILE:N	2.40	0.54
1:B:67:THR:OG1	1:B:68:ARG:N	2.39	0.54
1:B:122:ASP:OD1	1:B:526:THR:CG2	2.56	0.54
1:B:428:VAL:CG1	1:B:513:THR:HB	2.38	0.54
1:E:197:ARG:HG3	1:E:198:GLN:HG3	1.88	0.54
1:E:375:PRO:O	1:E:377:ILE:N	2.41	0.54
1:B:52:ARG:N	1:B:116:ARG:NH1	2.56	0.54
1:C:171:PRO:HG2	1:C:174:ASN:ND2	2.23	0.54
1:E:52:ARG:N	1:E:116:ARG:NH1	2.56	0.54
1:E:495:ASN:O	1:E:498:PRO:HD3	2.08	0.54
1:B:130:ASN:HD22	1:B:130:ASN:C	2.14	0.54
1:B:235:ALA:C	1:B:236:PHE:HD1	2.15	0.54
1:B:375:PRO:O	1:B:377:ILE:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:428:VAL:CG1	1:C:513:THR:HB	2.38	0.54
1:C:542:THR:CG2	1:C:547:ARG:N	2.70	0.54
1:E:404:TRP:NE1	1:E:417:ILE:HG21	2.22	0.54
1:A:495:ASN:O	1:A:498:PRO:HD3	2.08	0.54
1:A:563:VAL:HG12	1:A:564:LEU:N	2.23	0.54
1:B:484:ILE:CG2	1:C:480:TYR:CD1	2.90	0.54
1:B:556:LEU:HD21	1:C:434:GLN:HG2	1.89	0.54
1:C:404:TRP:NE1	1:C:417:ILE:HG21	2.22	0.54
1:D:171:PRO:HG2	1:D:174:ASN:ND2	2.23	0.54
1:D:428:VAL:CG1	1:D:513:THR:HB	2.38	0.54
1:B:98:ASN:C	1:B:98:ASN:ND2	2.66	0.54
1:B:495:ASN:O	1:B:498:PRO:HD3	2.08	0.54
1:C:88:HIS:ND1	1:C:553:TYR:O	2.38	0.54
1:E:214:ASN:O	1:E:216:ARG:N	2.41	0.54
1:B:243:LEU:HG	1:B:401:TYR:HE2	1.71	0.54
1:B:389:TYR:O	1:B:390:ASN:C	2.51	0.54
1:B:404:TRP:NE1	1:B:417:ILE:HG21	2.22	0.54
1:C:98:ASN:C	1:C:98:ASN:ND2	2.66	0.54
1:D:67:THR:HG21	1:E:447:VAL:CG2	2.37	0.54
1:D:235:ALA:C	1:D:236:PHE:HD1	2.15	0.54
1:A:65:ASP:O	1:A:66:THR:HB	2.06	0.54
1:B:542:THR:CG2	1:B:547:ARG:N	2.70	0.54
1:C:122:ASP:OD1	1:C:526:THR:CG2	2.56	0.54
1:D:563:VAL:HG12	1:D:564:LEU:N	2.23	0.54
1:E:428:VAL:CG1	1:E:513:THR:HB	2.38	0.54
1:A:52:ARG:N	1:A:116:ARG:NH1	2.56	0.54
1:A:542:THR:CG2	1:A:547:ARG:N	2.71	0.54
1:B:96:ILE:O	1:C:448:THR:HB	2.07	0.54
1:B:485:ARG:NE	1:C:234:GLU:OE2	2.38	0.54
1:C:214:ASN:O	1:C:216:ARG:N	2.41	0.54
1:C:389:TYR:O	1:C:390:ASN:C	2.51	0.54
1:D:404:TRP:HE1	1:D:417:ILE:HG21	1.73	0.54
1:E:171:PRO:HG2	1:E:174:ASN:ND2	2.23	0.54
1:E:542:THR:CG2	1:E:547:ARG:N	2.70	0.54
1:B:64:PHE:CD1	1:C:118:HIS:NE2	2.76	0.54
1:B:177:GLU:CG	1:B:178:THR:N	2.71	0.54
1:B:214:ASN:O	1:B:216:ARG:N	2.41	0.54
1:B:243:LEU:HG	1:B:401:TYR:CE2	2.43	0.54
1:B:249:ASP:C	1:B:249:ASP:OD1	2.51	0.54
1:C:223:THR:HG21	1:C:227:MET:SD	2.48	0.54
1:A:404:TRP:HE1	1:A:417:ILE:HG21	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:243:LEU:HG	1:D:401:TYR:CE2	2.43	0.53
1:D:279:GLU:O	1:D:280:GLY:O	2.24	0.53
1:D:375:PRO:O	1:D:377:ILE:N	2.40	0.53
1:E:122:ASP:OD1	1:E:526:THR:CG2	2.55	0.53
1:A:558:ILE:HD11	1:B:463:ALA:HB3	1.90	0.53
1:B:223:THR:HG21	1:B:227:MET:SD	2.49	0.53
1:C:563:VAL:HG12	1:C:564:LEU:N	2.23	0.53
1:D:52:ARG:N	1:D:116:ARG:NH1	2.56	0.53
1:D:122:ASP:OD1	1:D:526:THR:CG2	2.56	0.53
1:D:249:ASP:C	1:D:249:ASP:OD1	2.51	0.53
1:D:542:THR:CG2	1:D:547:ARG:N	2.71	0.53
1:E:243:LEU:HG	1:E:401:TYR:CE2	2.44	0.53
1:A:171:PRO:HG2	1:A:174:ASN:ND2	2.23	0.53
1:C:228:PRO:HG3	2:T:15:TYR:CE1	2.43	0.53
1:D:404:TRP:NE1	1:D:417:ILE:HG21	2.22	0.53
1:A:197:ARG:HG3	1:A:198:GLN:HG3	1.89	0.53
1:A:214:ASN:O	1:A:216:ARG:N	2.41	0.53
1:A:230:VAL:CG1	1:E:490:LEU:HB2	2.31	0.53
1:A:428:VAL:CG1	1:A:513:THR:HB	2.38	0.53
1:B:214:ASN:ND2	1:B:216:ARG:HB3	2.24	0.53
1:B:404:TRP:HE1	1:B:417:ILE:HG21	1.73	0.53
1:B:563:VAL:HG12	1:B:564:LEU:N	2.23	0.53
1:C:495:ASN:O	1:C:498:PRO:HD3	2.08	0.53
1:A:67:THR:HG21	1:B:447:VAL:CG2	2.37	0.53
1:A:98:ASN:C	1:A:98:ASN:ND2	2.66	0.53
1:A:486:GLN:HE22	1:A:495:ASN:ND2	2.07	0.53
1:A:542:THR:HG22	1:A:543:ASP:H	1.74	0.53
1:C:243:LEU:HG	1:C:401:TYR:CE2	2.44	0.53
1:D:214:ASN:O	1:D:216:ARG:N	2.41	0.53
1:D:495:ASN:O	1:D:498:PRO:HD3	2.08	0.53
1:D:542:THR:HG22	1:D:543:ASP:H	1.74	0.53
1:A:389:TYR:O	1:A:390:ASN:C	2.51	0.53
1:B:488:THR:CG2	1:C:479:VAL:CG1	2.86	0.53
1:B:542:THR:HG22	1:B:543:ASP:H	1.74	0.53
1:C:88:HIS:CD2	1:D:267:PHE:CZ	2.96	0.53
1:D:444:GLN:O	1:D:446:PRO:HD3	2.07	0.53
1:E:404:TRP:HE1	1:E:417:ILE:HG21	1.73	0.53
1:A:442:MET:HB2	1:A:537:GLN:OE1	2.08	0.53
1:B:442:MET:HB2	1:B:537:GLN:OE1	2.09	0.53
1:C:177:GLU:CG	1:C:178:THR:N	2.71	0.53
1:C:542:THR:HG22	1:C:543:ASP:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:214:ASN:ND2	1:D:216:ARG:HB3	2.24	0.53
1:D:442:MET:HB2	1:D:537:GLN:OE1	2.09	0.53
1:D:486:GLN:HE22	1:D:495:ASN:ND2	2.07	0.53
1:A:223:THR:HG21	1:A:227:MET:SD	2.49	0.53
1:B:57:TYR:OH	1:B:109:GLN:NE2	2.42	0.53
1:C:52:ARG:N	1:C:116:ARG:NH1	2.56	0.53
1:C:486:GLN:HE22	1:C:495:ASN:ND2	2.07	0.53
1:D:74:ASN:O	1:D:75:LYS:C	2.52	0.53
1:E:442:MET:HB2	1:E:537:GLN:OE1	2.08	0.53
1:A:57:TYR:OH	1:A:109:GLN:NE2	2.42	0.53
1:A:249:ASP:C	1:A:249:ASP:OD1	2.52	0.53
1:B:486:GLN:HE22	1:B:495:ASN:ND2	2.07	0.53
1:C:74:ASN:O	1:C:75:LYS:C	2.52	0.53
1:C:249:ASP:C	1:C:249:ASP:OD1	2.52	0.53
1:D:392:ILE:HA	1:D:400:GLN:HE21	1.74	0.53
1:C:404:TRP:HE1	1:C:417:ILE:HG21	1.73	0.53
1:B:392:ILE:HA	1:B:400:GLN:HE21	1.74	0.52
1:C:57:TYR:OH	1:C:109:GLN:NE2	2.42	0.52
1:D:223:THR:HG21	1:D:227:MET:SD	2.49	0.52
1:E:151:ARG:HB3	1:E:201:VAL:N	2.24	0.52
1:E:486:GLN:HE22	1:E:495:ASN:ND2	2.07	0.52
1:A:527:LEU:HD21	1:E:68:ARG:NE	2.25	0.52
1:C:214:ASN:ND2	1:C:216:ARG:HB3	2.24	0.52
1:D:68:ARG:NH1	1:D:68:ARG:CG	2.67	0.52
1:D:151:ARG:HB3	1:D:201:VAL:N	2.24	0.52
1:D:491:THR:HG23	2:V:15:TYR:CE1	2.45	0.52
1:E:126:ILE:HG12	1:E:521:LEU:HD23	1.91	0.52
1:E:223:THR:HG21	1:E:227:MET:SD	2.49	0.52
1:E:389:TYR:O	1:E:390:ASN:C	2.51	0.52
1:E:392:ILE:HA	1:E:400:GLN:HE21	1.74	0.52
1:E:455:ILE:HA	1:E:458:PHE:CE2	2.44	0.52
1:E:563:VAL:HG12	1:E:564:LEU:N	2.23	0.52
1:A:88:HIS:CD2	1:B:267:PHE:CZ	2.97	0.52
1:B:74:ASN:O	1:B:75:LYS:C	2.52	0.52
1:B:474:TYR:CD1	1:B:511:ILE:HD11	2.45	0.52
1:D:57:TYR:OH	1:D:109:GLN:NE2	2.42	0.52
1:D:455:ILE:HA	1:D:458:PHE:CE2	2.45	0.52
1:E:249:ASP:C	1:E:249:ASP:OD1	2.51	0.52
1:A:474:TYR:CD1	1:A:511:ILE:HD11	2.45	0.52
1:A:491:THR:HG23	2:S:15:TYR:CE1	2.45	0.52
1:B:171:PRO:HG2	1:B:174:ASN:ND2	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:401:TYR:HD1	1:C:502:ILE:HG12	1.68	0.52
1:D:383:ASP:C	1:D:384:SER:O	2.52	0.52
1:A:243:LEU:HG	1:A:401:TYR:CE2	2.44	0.52
1:A:455:ILE:HA	1:A:458:PHE:CE2	2.44	0.52
1:E:57:TYR:OH	1:E:109:GLN:NE2	2.42	0.52
1:A:74:ASN:O	1:A:75:LYS:C	2.52	0.52
1:C:392:ILE:HA	1:C:400:GLN:HE21	1.74	0.52
1:C:442:MET:HB2	1:C:537:GLN:OE1	2.08	0.52
1:D:474:TYR:CD1	1:D:511:ILE:HD11	2.45	0.52
1:D:511:ILE:HD12	1:D:511:ILE:N	2.25	0.52
1:E:231:TYR:HD1	1:E:501:GLN:HB3	1.75	0.52
1:E:511:ILE:HD12	1:E:511:ILE:N	2.25	0.52
1:A:214:ASN:ND2	1:A:216:ARG:HB3	2.24	0.52
1:A:418:ARG:O	1:A:418:ARG:HG2	2.10	0.52
1:A:455:ILE:HD12	1:A:456:SER:N	2.25	0.52
1:B:455:ILE:HA	1:B:458:PHE:CE2	2.44	0.52
1:B:491:THR:HG23	2:T:15:TYR:CE1	2.45	0.52
1:C:102:SER:O	1:C:103:PRO:C	2.52	0.52
1:C:178:THR:OG1	1:C:509:PRO:HD2	2.10	0.52
1:C:455:ILE:HA	1:C:458:PHE:CE2	2.44	0.52
1:C:485:ARG:NH1	1:C:505:ARG:HH22	2.07	0.52
1:D:68:ARG:NE	1:E:527:LEU:HD21	2.25	0.52
1:D:98:ASN:C	1:D:98:ASN:ND2	2.66	0.52
1:D:389:TYR:O	1:D:390:ASN:C	2.51	0.52
1:E:74:ASN:O	1:E:75:LYS:C	2.52	0.52
1:E:177:GLU:CG	1:E:178:THR:N	2.71	0.52
1:E:455:ILE:HD12	1:E:456:SER:N	2.25	0.52
1:A:126:ILE:HG12	1:A:521:LEU:HD23	1.91	0.52
1:A:151:ARG:HB3	1:A:201:VAL:N	2.24	0.52
1:A:177:GLU:CG	1:A:178:THR:N	2.71	0.52
1:C:151:ARG:HB3	1:C:201:VAL:N	2.24	0.52
1:D:177:GLU:CG	1:D:178:THR:N	2.72	0.52
1:E:214:ASN:ND2	1:E:216:ARG:HB3	2.24	0.52
1:A:231:TYR:HD1	1:A:501:GLN:HB3	1.75	0.52
1:A:448:THR:HG22	1:E:57:TYR:CD2	2.45	0.52
1:B:383:ASP:C	1:B:384:SER:O	2.52	0.52
1:C:74:ASN:OD1	1:D:434:GLN:OE1	2.28	0.52
1:C:491:THR:HG23	2:U:15:TYR:CE1	2.45	0.52
1:D:490:LEU:HB2	1:E:230:VAL:CG1	2.29	0.52
1:E:98:ASN:C	1:E:98:ASN:ND2	2.66	0.52
1:E:474:TYR:CD1	1:E:511:ILE:HD11	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ARG:HB3	1:B:201:VAL:N	2.24	0.52
1:B:277:ASP:O	1:B:417:ILE:HD13	2.10	0.52
1:B:485:ARG:NH1	1:B:505:ARG:HH22	2.07	0.52
1:C:231:TYR:HD1	1:C:501:GLN:HB3	1.75	0.52
1:C:277:ASP:O	1:C:417:ILE:HD13	2.10	0.52
1:C:474:TYR:CD1	1:C:511:ILE:HD11	2.45	0.52
1:E:228:PRO:HG3	2:V:15:TYR:CE1	2.45	0.52
1:E:491:THR:HG23	2:W:15:TYR:CE1	2.45	0.52
1:B:228:PRO:HB3	2:S:15:TYR:HE1	1.75	0.51
1:B:231:TYR:HD1	1:B:501:GLN:HB3	1.75	0.51
1:E:154:THR:CG2	1:E:155:LYS:HG3	2.41	0.51
1:E:277:ASP:O	1:E:417:ILE:HD13	2.10	0.51
1:A:88:HIS:HD2	1:B:267:PHE:CZ	2.28	0.51
1:C:511:ILE:N	1:C:511:ILE:HD12	2.25	0.51
1:D:178:THR:OG1	1:D:509:PRO:HD2	2.10	0.51
1:D:277:ASP:O	1:D:417:ILE:HD13	2.10	0.51
1:A:392:ILE:HA	1:A:400:GLN:HE21	1.74	0.51
1:B:126:ILE:HG12	1:B:521:LEU:HD23	1.91	0.51
1:C:551:TYR:CZ	1:D:422:LEU:HD21	2.45	0.51
1:D:418:ARG:O	1:D:418:ARG:HG2	2.10	0.51
1:E:132:PRO:HA	1:E:175:TYR:CZ	2.45	0.51
1:A:497:PHE:CD1	1:A:503:LEU:HB3	2.44	0.51
1:E:387:ARG:HG2	1:E:387:ARG:NH1	2.26	0.51
1:E:418:ARG:HG2	1:E:418:ARG:O	2.10	0.51
1:A:387:ARG:HG2	1:A:387:ARG:NH1	2.26	0.51
1:B:178:THR:OG1	1:B:509:PRO:HD2	2.10	0.51
1:C:67:THR:OG1	1:C:68:ARG:N	2.39	0.51
1:D:485:ARG:NH1	1:D:505:ARG:HH22	2.07	0.51
1:A:484:ILE:HG23	1:B:480:TYR:HE1	1.75	0.51
1:A:485:ARG:HH21	1:B:234:GLU:CD	2.18	0.51
1:C:477:GLN:O	1:C:481:SER:HB3	2.07	0.51
1:D:74:ASN:OD1	1:E:434:GLN:OE1	2.27	0.51
1:E:542:THR:HG22	1:E:543:ASP:H	1.74	0.51
1:D:135:ASN:H	1:D:140:THR:HG1	1.59	0.51
1:D:227:MET:HB2	1:D:228:PRO:HD3	1.92	0.51
1:D:477:GLN:O	1:D:481:SER:HB3	2.07	0.51
1:A:178:THR:OG1	1:A:509:PRO:HD2	2.10	0.51
1:B:511:ILE:HD12	1:B:511:ILE:N	2.25	0.51
1:C:132:PRO:HA	1:C:175:TYR:CZ	2.45	0.51
1:D:126:ILE:HG12	1:D:521:LEU:HD23	1.91	0.51
1:B:102:SER:O	1:B:103:PRO:C	2.52	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:292:TYR:HD1	1:D:376:VAL:HG12	1.75	0.51
1:D:376:VAL:C	1:D:378:LYS:H	2.19	0.51
1:E:237:HIS:CD2	1:E:423:LEU:HD11	2.46	0.51
1:A:292:TYR:HD1	1:A:376:VAL:HG12	1.75	0.51
1:C:64:PHE:HD1	1:D:118:HIS:NE2	2.09	0.51
1:C:126:ILE:HG12	1:C:521:LEU:HD23	1.91	0.51
1:E:485:ARG:NH1	1:E:505:ARG:HH22	2.07	0.51
1:A:277:ASP:O	1:A:417:ILE:HD13	2.10	0.50
1:A:376:VAL:C	1:A:378:LYS:H	2.19	0.50
1:C:67:THR:CG2	1:D:447:VAL:CG2	2.89	0.50
1:C:292:TYR:HD1	1:C:376:VAL:HG12	1.75	0.50
1:D:214:ASN:C	1:D:214:ASN:ND2	2.58	0.50
1:D:237:HIS:CD2	1:D:423:LEU:HD11	2.46	0.50
1:E:227:MET:HB2	1:E:228:PRO:HD3	1.92	0.50
1:E:477:GLN:O	1:E:481:SER:HB3	2.07	0.50
1:B:442:MET:CE	1:B:559:VAL:HG21	2.28	0.50
1:C:171:PRO:CA	1:D:409:ASN:HD22	2.24	0.50
1:A:135:ASN:H	1:A:140:THR:HG1	1.59	0.50
1:B:228:PRO:HG3	2:S:15:TYR:CE1	2.46	0.50
1:B:497:PHE:HD1	1:B:503:LEU:CB	2.25	0.50
1:B:551:TYR:CE2	1:C:422:LEU:HD21	2.47	0.50
1:D:102:SER:O	1:D:103:PRO:C	2.52	0.50
1:E:102:SER:O	1:E:103:PRO:C	2.52	0.50
1:E:422:LEU:HD23	1:E:423:LEU:H	1.76	0.50
1:A:102:SER:O	1:A:103:PRO:C	2.53	0.50
1:B:295:SER:CB	1:B:375:PRO:CG	2.90	0.50
1:C:497:PHE:HD1	1:C:503:LEU:CB	2.25	0.50
1:D:154:THR:CG2	1:D:155:LYS:HG3	2.41	0.50
1:E:135:ASN:OD1	1:E:135:ASN:C	2.55	0.50
1:A:511:ILE:HD12	1:A:511:ILE:N	2.25	0.50
1:B:418:ARG:O	1:B:418:ARG:HG2	2.10	0.50
1:C:237:HIS:CD2	1:C:423:LEU:HD11	2.46	0.50
1:D:64:PHE:HD1	1:E:118:HIS:NE2	2.09	0.50
1:A:373:LYS:O	1:A:374:LYS:HG3	2.12	0.50
1:B:154:THR:CG2	1:B:155:LYS:HG3	2.40	0.50
1:B:237:HIS:CD2	1:B:423:LEU:HD11	2.46	0.50
1:C:227:MET:HB2	1:C:228:PRO:HD3	1.92	0.50
1:C:543:ASP:OD1	1:C:547:ARG:HG2	2.12	0.50
1:D:231:TYR:HD1	1:D:501:GLN:HB3	1.75	0.50
1:E:178:THR:OG1	1:E:509:PRO:HD2	2.10	0.50
2:S:15:TYR:HD2	2:S:16:PRO:HD2	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:15:TYR:HD2	2:T:16:PRO:HD2	1.77	0.50
1:A:383:ASP:C	1:A:384:SER:O	2.52	0.50
1:A:447:VAL:HA	1:E:63:LEU:HD12	1.93	0.50
1:B:135:ASN:C	1:B:135:ASN:OD1	2.55	0.50
1:B:387:ARG:HG2	1:B:387:ARG:NH1	2.26	0.50
1:B:553:TYR:HE2	1:C:432:SER:N	2.09	0.50
1:C:387:ARG:HG2	1:C:387:ARG:NH1	2.26	0.50
1:C:418:ARG:HG2	1:C:418:ARG:O	2.10	0.50
1:D:132:PRO:HA	1:D:175:TYR:CZ	2.45	0.50
1:D:422:LEU:HD23	1:D:423:LEU:H	1.76	0.50
1:D:543:ASP:OD1	1:D:547:ARG:HG2	2.12	0.50
2:U:15:TYR:HD2	2:U:16:PRO:HD2	1.76	0.50
1:A:237:HIS:CD2	1:A:423:LEU:HD11	2.46	0.50
1:A:485:ARG:NH1	1:A:505:ARG:HH22	2.07	0.50
1:B:132:PRO:HA	1:B:175:TYR:CZ	2.45	0.50
1:B:542:THR:HG22	1:B:543:ASP:N	2.27	0.50
1:C:130:ASN:HD22	1:C:130:ASN:N	2.10	0.50
1:D:228:PRO:CB	2:U:15:TYR:HE1	2.25	0.50
1:E:384:SER:O	1:E:386:LYS:N	2.45	0.50
1:A:497:PHE:HD1	1:A:503:LEU:CB	2.25	0.50
1:C:376:VAL:C	1:C:378:LYS:H	2.19	0.50
1:D:243:LEU:CD2	1:D:244:PRO:HD3	2.42	0.50
1:D:373:LYS:O	1:D:374:LYS:HG3	2.12	0.50
1:D:484:ILE:CG2	1:E:480:TYR:HE1	2.22	0.50
1:E:295:SER:CB	1:E:375:PRO:CG	2.90	0.50
2:V:15:TYR:HD2	2:V:16:PRO:HD2	1.77	0.50
1:B:68:ARG:NH1	1:B:68:ARG:CG	2.67	0.49
1:B:227:MET:HB2	1:B:228:PRO:HD3	1.92	0.49
1:B:292:TYR:HD1	1:B:376:VAL:HG12	1.76	0.49
1:C:151:ARG:CB	1:C:201:VAL:H	2.25	0.49
1:C:173:GLY:O	1:C:175:TYR:CE1	2.65	0.49
1:D:63:LEU:HD12	1:E:447:VAL:HA	1.93	0.49
1:D:243:LEU:CG	1:D:401:TYR:HE2	2.25	0.49
1:D:384:SER:O	1:D:386:LYS:N	2.45	0.49
1:E:131:MET:HA	1:E:551:TYR:CD2	2.47	0.49
1:E:173:GLY:O	1:E:175:TYR:CE1	2.65	0.49
1:E:376:VAL:O	1:E:377:ILE:C	2.55	0.49
1:A:227:MET:HB2	1:A:228:PRO:HD3	1.92	0.49
1:A:502:ILE:C	1:A:504:ALA:H	2.20	0.49
1:B:543:ASP:OD1	1:B:547:ARG:HG2	2.12	0.49
1:D:100:ASP:CG	1:E:450:ARG:HH12	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:455:ILE:HD12	1:D:456:SER:N	2.25	0.49
1:E:542:THR:HG22	1:E:543:ASP:N	2.27	0.49
1:C:295:SER:CB	1:C:375:PRO:CG	2.90	0.49
1:D:131:MET:HA	1:D:551:TYR:CD2	2.47	0.49
1:D:197:ARG:HG3	1:D:198:GLN:N	2.27	0.49
1:D:240:ILE:HD11	1:D:273:ILE:HG21	1.95	0.49
1:D:392:ILE:HD11	1:D:396:SER:OG	2.13	0.49
1:D:542:THR:HG22	1:D:543:ASP:N	2.27	0.49
1:E:201:VAL:O	1:E:201:VAL:HG13	2.12	0.49
2:W:10:THR:O	2:W:10:THR:CG2	2.60	0.49
1:A:74:ASN:OD1	1:B:434:GLN:OE1	2.30	0.49
1:A:173:GLY:O	1:A:175:TYR:CE1	2.65	0.49
1:A:243:LEU:CD2	1:A:244:PRO:HD3	2.42	0.49
1:A:243:LEU:CG	1:A:401:TYR:HE2	2.25	0.49
1:B:132:PRO:CA	1:B:175:TYR:OH	2.53	0.49
1:B:243:LEU:CG	1:B:401:TYR:HE2	2.25	0.49
1:C:63:LEU:HD12	1:D:447:VAL:HA	1.95	0.49
1:C:197:ARG:HG3	1:C:198:GLN:N	2.27	0.49
1:C:392:ILE:HD11	1:C:396:SER:OG	2.13	0.49
1:D:295:SER:CB	1:D:375:PRO:CG	2.90	0.49
1:D:491:THR:HG22	1:D:492:HIS:N	2.27	0.49
1:E:197:ARG:HG3	1:E:198:GLN:N	2.27	0.49
1:A:130:ASN:HD22	1:A:130:ASN:N	2.10	0.49
1:A:295:SER:CB	1:A:375:PRO:CG	2.90	0.49
1:A:542:THR:HG22	1:A:543:ASP:N	2.27	0.49
1:B:131:MET:HA	1:B:551:TYR:CD2	2.47	0.49
1:B:201:VAL:O	1:B:201:VAL:HG13	2.12	0.49
1:B:243:LEU:CD2	1:B:244:PRO:HD3	2.42	0.49
1:B:384:SER:O	1:B:386:LYS:N	2.45	0.49
1:B:392:ILE:HD11	1:B:396:SER:OG	2.13	0.49
1:C:135:ASN:C	1:C:135:ASN:OD1	2.55	0.49
1:C:154:THR:CG2	1:C:155:LYS:HG3	2.41	0.49
1:C:240:ILE:HD11	1:C:273:ILE:HG21	1.95	0.49
1:C:373:LYS:O	1:C:374:LYS:HG3	2.12	0.49
1:C:501:GLN:OE1	1:C:501:GLN:HA	2.12	0.49
1:C:518:VAL:CG2	1:C:519:PRO:HD2	2.43	0.49
1:D:151:ARG:CB	1:D:201:VAL:H	2.25	0.49
1:D:173:GLY:O	1:D:175:TYR:CE1	2.65	0.49
1:D:387:ARG:HG2	1:D:387:ARG:NH1	2.26	0.49
1:D:501:GLN:OE1	1:D:501:GLN:HA	2.12	0.49
1:D:518:VAL:CG2	1:D:519:PRO:HD2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:151:ARG:CB	1:E:201:VAL:H	2.26	0.49
1:E:376:VAL:C	1:E:378:LYS:H	2.19	0.49
1:E:502:ILE:C	1:E:504:ALA:H	2.20	0.49
1:A:68:ARG:NH1	1:A:68:ARG:CG	2.67	0.49
1:A:131:MET:HA	1:A:551:TYR:CD2	2.47	0.49
1:A:384:SER:O	1:A:386:LYS:N	2.45	0.49
1:A:495:ASN:ND2	1:A:498:PRO:HB3	2.28	0.49
1:B:373:LYS:O	1:B:374:LYS:HG3	2.12	0.49
1:B:502:ILE:C	1:B:504:ALA:H	2.20	0.49
1:C:243:LEU:CD2	1:C:244:PRO:HD3	2.43	0.49
1:D:502:ILE:C	1:D:504:ALA:H	2.20	0.49
1:E:68:ARG:NH1	1:E:68:ARG:CG	2.67	0.49
1:E:243:LEU:CG	1:E:401:TYR:HE2	2.25	0.49
1:E:373:LYS:O	1:E:374:LYS:HG3	2.12	0.49
1:E:518:VAL:CG2	1:E:519:PRO:HD2	2.42	0.49
1:B:130:ASN:HD22	1:B:130:ASN:N	2.10	0.49
1:B:376:VAL:O	1:B:377:ILE:C	2.55	0.49
1:C:131:MET:HA	1:C:551:TYR:CD2	2.47	0.49
1:D:130:ASN:HD22	1:D:130:ASN:N	2.10	0.49
1:A:151:ARG:CB	1:A:201:VAL:H	2.25	0.49
1:A:240:ILE:HD11	1:A:273:ILE:HG21	1.95	0.49
1:B:491:THR:HG22	1:B:492:HIS:N	2.27	0.49
1:C:243:LEU:CG	1:C:401:TYR:HE2	2.25	0.49
1:C:491:THR:HG22	1:C:492:HIS:N	2.27	0.49
1:C:542:THR:HG22	1:C:543:ASP:N	2.27	0.49
1:D:135:ASN:C	1:D:135:ASN:OD1	2.55	0.49
1:D:495:ASN:ND2	1:D:498:PRO:HB3	2.28	0.49
1:A:501:GLN:OE1	1:A:501:GLN:HA	2.12	0.49
1:A:518:VAL:CG2	1:A:519:PRO:HD2	2.43	0.49
1:A:540:THR:HG22	1:A:540:THR:O	2.13	0.49
1:C:422:LEU:HD23	1:C:423:LEU:H	1.76	0.49
1:C:455:ILE:HD12	1:C:456:SER:N	2.25	0.49
1:D:201:VAL:HG13	1:D:201:VAL:O	2.12	0.49
1:D:497:PHE:HD1	1:D:503:LEU:CB	2.25	0.49
1:E:130:ASN:HD22	1:E:130:ASN:N	2.10	0.49
1:E:474:TYR:HH	1:E:476:ASP:CG	2.20	0.49
2:U:10:THR:O	2:U:10:THR:CG2	2.60	0.49
1:B:237:HIS:HD2	1:B:238:PRO:O	1.96	0.49
1:C:201:VAL:HG13	1:C:201:VAL:O	2.12	0.49
1:C:383:ASP:C	1:C:384:SER:O	2.52	0.49
1:C:495:ASN:ND2	1:C:498:PRO:HB3	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:502:ILE:C	1:C:504:ALA:H	2.20	0.49
1:D:57:TYR:CE2	1:E:448:THR:HG22	2.48	0.49
1:D:237:HIS:HD2	1:D:238:PRO:O	1.96	0.49
1:E:501:GLN:HA	1:E:501:GLN:OE1	2.12	0.49
1:E:540:THR:O	1:E:540:THR:HG22	2.13	0.49
1:B:173:GLY:O	1:B:175:TYR:CE1	2.65	0.48
1:B:197:ARG:HG3	1:B:198:GLN:N	2.27	0.48
1:E:543:ASP:OD1	1:E:547:ARG:HG2	2.12	0.48
2:W:15:TYR:HD2	2:W:16:PRO:HD2	1.76	0.48
1:A:132:PRO:HA	1:A:175:TYR:CZ	2.45	0.48
1:A:434:GLN:OE1	1:E:74:ASN:OD1	2.30	0.48
1:A:447:VAL:HG23	1:E:67:THR:OG1	2.12	0.48
1:B:376:VAL:C	1:B:378:LYS:H	2.19	0.48
1:B:518:VAL:CG2	1:B:519:PRO:HD2	2.43	0.48
1:E:243:LEU:CD2	1:E:244:PRO:HD3	2.42	0.48
1:E:491:THR:HG22	1:E:492:HIS:N	2.27	0.48
1:A:154:THR:CG2	1:A:155:LYS:HG3	2.40	0.48
1:A:201:VAL:HG13	1:A:201:VAL:O	2.12	0.48
1:A:392:ILE:HD11	1:A:396:SER:OG	2.13	0.48
1:B:135:ASN:H	1:B:140:THR:HG1	1.59	0.48
1:B:151:ARG:CB	1:B:201:VAL:H	2.26	0.48
1:B:495:ASN:ND2	1:B:498:PRO:HB3	2.28	0.48
1:D:244:PRO:HA	1:D:275:TYR:CD2	2.49	0.48
1:D:540:THR:O	1:D:540:THR:HG22	2.13	0.48
1:D:553:TYR:HE2	1:E:432:SER:N	2.11	0.48
1:E:392:ILE:HD11	1:E:396:SER:OG	2.13	0.48
1:A:135:ASN:C	1:A:135:ASN:OD1	2.55	0.48
1:A:197:ARG:HG3	1:A:198:GLN:N	2.27	0.48
1:A:237:HIS:HD2	1:A:238:PRO:O	1.96	0.48
1:B:228:PRO:HG3	2:S:15:TYR:CD1	2.48	0.48
1:E:237:HIS:HD2	1:E:238:PRO:O	1.96	0.48
1:E:292:TYR:HD1	1:E:376:VAL:HG12	1.75	0.48
1:E:495:ASN:ND2	1:E:498:PRO:HB3	2.28	0.48
1:E:497:PHE:O	1:E:499:GLU:N	2.45	0.48
1:A:142:LYS:O	1:A:143:PHE:HB3	2.14	0.48
1:A:477:GLN:O	1:A:481:SER:HB3	2.07	0.48
1:A:543:ASP:OD1	1:A:547:ARG:HG2	2.12	0.48
1:D:497:PHE:O	1:D:499:GLU:N	2.45	0.48
1:B:142:LYS:HD3	1:B:167:GLU:OE2	2.14	0.48
1:B:142:LYS:O	1:B:143:PHE:HB3	2.14	0.48
1:B:497:PHE:CD1	1:B:503:LEU:HB3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:501:GLN:OE1	1:B:501:GLN:HA	2.12	0.48
1:C:142:LYS:O	1:C:143:PHE:HB3	2.14	0.48
1:E:383:ASP:C	1:E:384:SER:O	2.52	0.48
2:V:10:THR:O	2:V:10:THR:CG2	2.60	0.48
1:A:142:LYS:HD3	1:A:167:GLU:OE2	2.14	0.48
1:A:422:LEU:HD23	1:A:423:LEU:H	1.76	0.48
1:A:491:THR:HG22	1:A:492:HIS:N	2.27	0.48
1:B:455:ILE:HD12	1:B:456:SER:N	2.25	0.48
1:B:491:THR:HG22	1:B:493:VAL:N	2.29	0.48
1:C:244:PRO:HA	1:C:275:TYR:CD2	2.49	0.48
1:C:497:PHE:CD1	1:C:503:LEU:HB3	2.44	0.48
1:A:130:ASN:N	1:A:130:ASN:ND2	2.61	0.48
1:A:244:PRO:HA	1:A:275:TYR:CD2	2.49	0.48
1:B:75:LYS:O	1:B:78:ASP:OD1	2.32	0.48
1:B:211:ASP:HA	1:B:506:PRO:CG	2.44	0.48
1:C:193:LEU:HD22	1:C:197:ARG:NH1	2.29	0.48
1:C:384:SER:O	1:C:386:LYS:N	2.45	0.48
1:C:540:THR:O	1:C:540:THR:HG22	2.13	0.48
1:D:376:VAL:O	1:D:377:ILE:C	2.55	0.48
1:E:491:THR:HG22	1:E:493:VAL:N	2.29	0.48
1:A:118:HIS:NE2	1:E:64:PHE:HD1	2.12	0.48
1:A:376:VAL:O	1:A:377:ILE:C	2.55	0.48
1:B:87:ASP:O	1:B:89:SER:N	2.46	0.48
1:C:135:ASN:H	1:C:140:THR:HG1	1.60	0.48
1:D:454:GLN:O	1:D:456:SER:N	2.47	0.48
1:E:145:ALA:HA	1:E:248:VAL:HA	1.96	0.48
1:E:240:ILE:HD11	1:E:273:ILE:HG21	1.95	0.48
1:E:244:PRO:HA	1:E:275:TYR:CD2	2.49	0.48
1:E:269:GLU:HG3	1:E:269:GLU:O	2.14	0.48
1:A:239:ASP:HB3	1:A:405:TYR:HB2	1.96	0.48
1:A:454:GLN:O	1:A:456:SER:N	2.47	0.48
1:B:193:LEU:HD22	1:B:197:ARG:NH1	2.29	0.48
1:B:215:PHE:CE1	1:B:241:ILE:HD11	2.49	0.48
1:B:240:ILE:HD11	1:B:273:ILE:HG21	1.95	0.48
1:B:542:THR:HG22	1:B:547:ARG:H	1.79	0.48
1:C:171:PRO:HA	1:D:409:ASN:HD22	1.79	0.48
1:D:228:PRO:HG3	2:U:15:TYR:CD1	2.49	0.48
1:E:130:ASN:N	1:E:130:ASN:ND2	2.61	0.48
1:A:128:HIS:CE1	1:B:432:SER:HG	2.32	0.47
1:B:145:ALA:HA	1:B:248:VAL:HA	1.96	0.47
1:B:183:LEU:HD21	1:C:236:PHE:HE2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:PRO:HA	1:B:275:TYR:CD2	2.49	0.47
1:C:442:MET:CE	1:C:559:VAL:HG21	2.28	0.47
1:C:491:THR:HG22	1:C:493:VAL:N	2.29	0.47
1:C:497:PHE:O	1:C:499:GLU:N	2.46	0.47
1:D:215:PHE:CE1	1:D:241:ILE:HD11	2.49	0.47
1:E:75:LYS:O	1:E:78:ASP:OD1	2.32	0.47
1:E:454:GLN:O	1:E:456:SER:N	2.47	0.47
1:B:540:THR:O	1:B:540:THR:HG22	2.13	0.47
1:C:75:LYS:O	1:C:78:ASP:OD1	2.32	0.47
1:D:193:LEU:HD22	1:D:197:ARG:NH1	2.29	0.47
1:D:211:ASP:HA	1:D:506:PRO:CG	2.44	0.47
1:D:461:VAL:HB	1:D:527:LEU:CD1	2.44	0.47
1:E:142:LYS:HD3	1:E:167:GLU:OE2	2.14	0.47
1:A:269:GLU:O	1:A:269:GLU:HG3	2.14	0.47
1:A:450:ARG:NH2	1:E:99:ASN:HB3	2.29	0.47
1:A:491:THR:HG22	1:A:493:VAL:N	2.29	0.47
1:B:142:LYS:HG2	1:B:169:THR:HG22	1.97	0.47
1:B:180:THR:HG21	1:B:258:LEU:CD2	2.44	0.47
1:C:180:THR:HG21	1:C:258:LEU:CD2	2.44	0.47
1:E:497:PHE:CD1	1:E:503:LEU:HB3	2.44	0.47
1:B:422:LEU:HD23	1:B:423:LEU:H	1.76	0.47
1:C:376:VAL:O	1:C:377:ILE:C	2.55	0.47
1:A:171:PRO:HA	1:B:409:ASN:HD22	1.80	0.47
1:A:211:ASP:HA	1:A:506:PRO:CG	2.44	0.47
1:A:277:ASP:O	1:A:279:GLU:N	2.46	0.47
1:C:131:MET:SD	1:C:138:MET:HG3	2.55	0.47
1:D:142:LYS:HD3	1:D:167:GLU:OE2	2.14	0.47
1:D:145:ALA:HA	1:D:248:VAL:HA	1.96	0.47
1:D:180:THR:HG21	1:D:258:LEU:CD2	2.44	0.47
1:E:180:THR:HG21	1:E:258:LEU:CD2	2.44	0.47
1:E:211:ASP:HA	1:E:506:PRO:CG	2.44	0.47
1:A:474:TYR:HD1	1:A:511:ILE:HD11	1.80	0.47
1:B:130:ASN:N	1:B:130:ASN:ND2	2.61	0.47
1:B:488:THR:HG22	1:C:479:VAL:CG1	2.45	0.47
1:C:215:PHE:CE1	1:C:241:ILE:HD11	2.49	0.47
1:C:237:HIS:HD2	1:C:238:PRO:O	1.96	0.47
1:D:142:LYS:HG2	1:D:169:THR:HG22	1.97	0.47
1:D:491:THR:HG22	1:D:493:VAL:N	2.29	0.47
1:E:142:LYS:O	1:E:143:PHE:HB3	2.14	0.47
2:V:15:TYR:C	2:V:15:TYR:CD2	2.92	0.47
1:B:96:ILE:O	1:C:448:THR:CB	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:434:GLN:NE2	1:B:436:TYR:CE2	2.81	0.47
1:C:130:ASN:N	1:C:130:ASN:ND2	2.61	0.47
1:C:142:LYS:HD3	1:C:167:GLU:OE2	2.14	0.47
1:C:142:LYS:HG2	1:C:169:THR:HG22	1.97	0.47
1:C:211:ASP:HA	1:C:506:PRO:CG	2.44	0.47
1:C:454:GLN:O	1:C:456:SER:N	2.47	0.47
1:C:553:TYR:HE2	1:D:432:SER:N	2.12	0.47
1:E:142:LYS:HG2	1:E:169:THR:HG22	1.97	0.47
2:U:15:TYR:C	2:U:15:TYR:CD2	2.92	0.47
1:A:75:LYS:O	1:A:78:ASP:OD1	2.32	0.47
1:A:215:PHE:CE1	1:A:241:ILE:HD11	2.50	0.47
1:B:497:PHE:O	1:B:499:GLU:N	2.46	0.47
1:C:83:ASN:CA	1:C:86:ASN:HD22	2.21	0.47
1:D:289:VAL:HG13	1:D:290:ASP:N	2.30	0.47
1:D:542:THR:CG2	1:D:547:ARG:H	2.28	0.47
1:A:497:PHE:O	1:A:499:GLU:N	2.46	0.47
1:B:131:MET:SD	1:B:138:MET:HG3	2.55	0.47
1:B:454:GLN:O	1:B:456:SER:N	2.47	0.47
1:C:269:GLU:HG3	1:C:269:GLU:O	2.14	0.47
1:D:130:ASN:N	1:D:130:ASN:ND2	2.61	0.47
1:A:78:ASP:HB2	1:A:82:LEU:HD12	1.97	0.47
1:A:180:THR:HG21	1:A:258:LEU:CD2	2.44	0.47
1:A:193:LEU:HD22	1:A:197:ARG:NH1	2.29	0.47
1:A:450:ARG:HH12	1:E:100:ASP:CG	2.23	0.47
1:A:461:VAL:HB	1:A:527:LEU:CD1	2.45	0.47
1:A:485:ARG:CZ	1:A:505:ARG:HH22	2.28	0.47
1:B:542:THR:CG2	1:B:547:ARG:H	2.28	0.47
1:C:88:HIS:HD2	1:D:267:PHE:HZ	1.63	0.47
1:D:78:ASP:HB2	1:D:82:LEU:HD12	1.97	0.47
1:D:132:PRO:CA	1:D:175:TYR:OH	2.53	0.47
1:D:142:LYS:O	1:D:143:PHE:HB3	2.14	0.47
1:D:542:THR:HG22	1:D:547:ARG:H	1.79	0.47
1:E:78:ASP:HB2	1:E:82:LEU:HD12	1.97	0.47
1:E:542:THR:HG22	1:E:547:ARG:H	1.79	0.47
1:A:145:ALA:HA	1:A:248:VAL:HA	1.96	0.46
1:B:447:VAL:HG12	1:B:448:THR:HG23	1.97	0.46
1:D:131:MET:SD	1:D:138:MET:HG3	2.55	0.46
1:E:87:ASP:O	1:E:89:SER:N	2.46	0.46
1:E:239:ASP:HB3	1:E:405:TYR:HB2	1.96	0.46
1:E:289:VAL:HG13	1:E:290:ASP:N	2.30	0.46
1:E:461:VAL:HB	1:E:527:LEU:CD1	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:15:TYR:C	2:T:15:TYR:CD2	2.92	0.46
1:A:96:ILE:O	1:B:448:THR:HB	2.16	0.46
1:B:231:TYR:CD1	1:B:501:GLN:HB3	2.51	0.46
1:C:67:THR:OG1	1:D:447:VAL:HG23	2.14	0.46
1:C:542:THR:HG22	1:C:547:ARG:H	1.79	0.46
1:D:75:LYS:O	1:D:78:ASP:OD1	2.32	0.46
1:D:239:ASP:HB3	1:D:405:TYR:HB2	1.96	0.46
1:D:269:GLU:HG3	1:D:269:GLU:O	2.14	0.46
1:E:193:LEU:HD22	1:E:197:ARG:NH1	2.29	0.46
1:A:542:THR:CG2	1:A:547:ARG:H	2.28	0.46
1:A:542:THR:HG22	1:A:547:ARG:H	1.79	0.46
1:B:228:PRO:CB	2:S:15:TYR:HE1	2.28	0.46
1:C:145:ALA:HA	1:C:248:VAL:HA	1.96	0.46
1:C:231:TYR:CD1	1:C:501:GLN:HB3	2.51	0.46
1:E:474:TYR:HD1	1:E:511:ILE:HD11	1.80	0.46
1:A:67:THR:CG2	1:B:447:VAL:CG2	2.94	0.46
1:A:434:GLN:NE2	1:A:436:TYR:CE2	2.81	0.46
1:B:474:TYR:HD1	1:B:511:ILE:HD11	1.80	0.46
1:C:78:ASP:HB2	1:C:82:LEU:HD12	1.97	0.46
1:C:289:VAL:HG13	1:C:290:ASP:N	2.30	0.46
1:D:434:GLN:NE2	1:D:436:TYR:CE2	2.81	0.46
1:E:215:PHE:CE1	1:E:241:ILE:HD11	2.50	0.46
1:E:542:THR:CG2	1:E:547:ARG:H	2.28	0.46
1:A:267:PHE:CZ	1:E:88:HIS:HD2	2.34	0.46
1:A:295:SER:CB	1:A:375:PRO:HG2	2.46	0.46
1:A:474:TYR:HH	1:A:476:ASP:CG	2.24	0.46
1:B:452:THR:OG1	1:B:453:SER:N	2.49	0.46
1:B:461:VAL:HB	1:B:527:LEU:CD1	2.45	0.46
1:B:558:ILE:HD11	1:C:463:ALA:HB3	1.97	0.46
1:C:295:SER:CB	1:C:375:PRO:HG2	2.46	0.46
1:C:461:VAL:HB	1:C:527:LEU:CD1	2.45	0.46
1:C:542:THR:CG2	1:C:547:ARG:H	2.27	0.46
1:D:87:ASP:O	1:D:89:SER:N	2.46	0.46
1:D:123:LEU:HD13	1:D:559:VAL:HG22	1.98	0.46
1:E:295:SER:CB	1:E:375:PRO:HG2	2.46	0.46
1:E:497:PHE:HD1	1:E:503:LEU:CB	2.25	0.46
2:W:15:TYR:C	2:W:15:TYR:CD2	2.92	0.46
1:A:267:PHE:CZ	1:E:88:HIS:CD2	3.04	0.46
1:B:289:VAL:HG13	1:B:290:ASP:N	2.30	0.46
1:B:477:GLN:OE1	1:B:477:GLN:HA	2.16	0.46
1:C:87:ASP:O	1:C:89:SER:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:452:THR:OG1	1:C:453:SER:N	2.49	0.46
1:C:477:GLN:OE1	1:C:477:GLN:HA	2.16	0.46
1:E:123:LEU:HD13	1:E:559:VAL:HG22	1.98	0.46
2:U:15:TYR:CD2	2:U:16:PRO:HD2	2.51	0.46
1:A:142:LYS:HG2	1:A:169:THR:HG22	1.97	0.46
1:A:447:VAL:HG12	1:A:448:THR:HG23	1.97	0.46
1:B:239:ASP:HB3	1:B:405:TYR:HB2	1.96	0.46
1:B:295:SER:CB	1:B:375:PRO:HG2	2.46	0.46
1:B:477:GLN:O	1:B:481:SER:HB3	2.07	0.46
1:C:474:TYR:HD1	1:C:511:ILE:HD11	1.80	0.46
1:E:447:VAL:HG12	1:E:448:THR:HG23	1.97	0.46
1:E:485:ARG:CZ	1:E:505:ARG:HH22	2.28	0.46
1:A:553:TYR:HE2	1:B:432:SER:N	2.14	0.46
1:C:239:ASP:HB3	1:C:405:TYR:HB2	1.96	0.46
1:C:242:LEU:HD22	1:C:247:GLY:HA2	1.98	0.46
1:C:485:ARG:CZ	1:C:505:ARG:HH22	2.28	0.46
1:D:485:ARG:CZ	1:D:505:ARG:HH22	2.29	0.46
2:S:15:TYR:C	2:S:15:TYR:CD2	2.92	0.46
1:B:243:LEU:HD23	1:B:243:LEU:HA	1.82	0.46
1:B:485:ARG:CZ	1:B:505:ARG:HH22	2.28	0.46
1:C:481:SER:O	1:C:482:GLN:C	2.59	0.46
1:D:217:LEU:HD23	1:D:217:LEU:HA	1.74	0.46
1:D:477:GLN:OE1	1:D:477:GLN:HA	2.15	0.46
1:E:131:MET:SD	1:E:138:MET:HG3	2.55	0.46
1:E:452:THR:OG1	1:E:453:SER:N	2.49	0.46
1:E:477:GLN:OE1	1:E:477:GLN:HA	2.16	0.46
2:W:15:TYR:CD2	2:W:16:PRO:HD2	2.50	0.46
1:A:132:PRO:CA	1:A:175:TYR:OH	2.53	0.46
1:B:243:LEU:HD21	1:B:401:TYR:CE2	2.51	0.46
1:D:295:SER:CB	1:D:375:PRO:HG2	2.46	0.46
1:E:242:LEU:HD22	1:E:247:GLY:HA2	1.98	0.46
1:E:250:PHE:O	1:E:252:HIS:N	2.49	0.46
1:A:131:MET:SD	1:A:138:MET:HG3	2.55	0.45
1:B:242:LEU:HD22	1:B:247:GLY:HA2	1.98	0.45
1:B:277:ASP:O	1:B:279:GLU:N	2.46	0.45
1:C:123:LEU:HD13	1:C:559:VAL:HG22	1.98	0.45
1:D:231:TYR:CD1	1:D:501:GLN:HB3	2.51	0.45
1:D:545:ARG:O	1:D:546:ARG:HB2	2.16	0.45
1:E:231:TYR:CD1	1:E:501:GLN:HB3	2.51	0.45
1:A:63:LEU:HD12	1:B:447:VAL:HA	1.98	0.45
1:A:225:LEU:CD2	1:A:397:THR:HB	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:GLU:HG3	1:B:269:GLU:O	2.14	0.45
1:C:171:PRO:O	1:C:172:GLU:C	2.59	0.45
1:C:237:HIS:HE1	1:C:424:CYS:O	2.00	0.45
1:C:243:LEU:HD21	1:C:401:TYR:CE2	2.51	0.45
1:C:556:LEU:CD2	1:D:434:GLN:HG2	2.44	0.45
1:D:497:PHE:CD1	1:D:503:LEU:HB3	2.44	0.45
1:E:243:LEU:HD21	1:E:401:TYR:CE2	2.51	0.45
2:S:15:TYR:CD2	2:S:16:PRO:HD2	2.51	0.45
2:T:15:TYR:CD2	2:T:16:PRO:HD2	2.51	0.45
1:A:432:SER:N	1:E:553:TYR:HE2	2.14	0.45
1:A:477:GLN:OE1	1:A:477:GLN:HA	2.16	0.45
1:B:207:GLY:O	1:B:208:VAL:CB	2.64	0.45
1:B:491:THR:HG23	2:T:15:TYR:CZ	2.52	0.45
1:C:223:THR:HG22	1:C:225:LEU:HB2	1.99	0.45
1:D:474:TYR:HD1	1:D:511:ILE:HD11	1.80	0.45
1:A:123:LEU:HD13	1:A:559:VAL:HG22	1.98	0.45
1:A:289:VAL:HG13	1:A:290:ASP:N	2.30	0.45
1:C:243:LEU:HA	1:C:243:LEU:HD23	1.82	0.45
1:C:250:PHE:O	1:C:252:HIS:N	2.49	0.45
1:C:295:SER:HB3	1:C:375:PRO:HG2	1.98	0.45
1:C:545:ARG:O	1:C:546:ARG:HB2	2.16	0.45
1:D:79:VAL:HG13	1:E:267:PHE:HD2	1.82	0.45
1:D:223:THR:HG22	1:D:225:LEU:HB2	1.99	0.45
1:D:243:LEU:HD21	1:D:401:TYR:CE2	2.51	0.45
1:D:250:PHE:O	1:D:252:HIS:N	2.49	0.45
1:D:452:THR:OG1	1:D:453:SER:N	2.49	0.45
1:E:177:GLU:HG3	1:E:178:THR:H	1.82	0.45
1:A:243:LEU:HD21	1:A:401:TYR:CE2	2.51	0.45
1:A:481:SER:O	1:A:482:GLN:C	2.59	0.45
1:B:64:PHE:O	1:B:65:ASP:HB2	2.17	0.45
1:B:78:ASP:HB2	1:B:82:LEU:HD12	1.97	0.45
1:D:242:LEU:HD22	1:D:247:GLY:HA2	1.98	0.45
1:D:485:ARG:NH2	1:E:234:GLU:OE1	2.50	0.45
1:E:171:PRO:O	1:E:172:GLU:C	2.59	0.45
1:A:223:THR:HG22	1:A:225:LEU:HB2	1.99	0.45
1:A:250:PHE:O	1:A:252:HIS:N	2.49	0.45
1:A:439:LEU:N	1:A:440:PRO:CD	2.79	0.45
1:B:439:LEU:N	1:B:440:PRO:CD	2.79	0.45
1:C:129:THR:HB	1:C:130:ASN:H	1.63	0.45
1:C:225:LEU:CD2	1:C:397:THR:HB	2.47	0.45
1:C:447:VAL:HG12	1:C:448:THR:HG23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:64:PHE:O	1:D:65:ASP:HB2	2.17	0.45
1:D:474:TYR:HH	1:D:476:ASP:CG	2.24	0.45
1:E:225:LEU:CD2	1:E:397:THR:HB	2.47	0.45
1:E:382:GLU:HA	1:E:387:ARG:O	2.17	0.45
1:A:228:PRO:CB	2:W:15:TYR:HE1	2.29	0.45
1:A:243:LEU:O	1:A:244:PRO:C	2.59	0.45
1:A:491:THR:HG23	2:S:15:TYR:CZ	2.52	0.45
1:D:243:LEU:O	1:D:244:PRO:C	2.59	0.45
1:D:295:SER:HB3	1:D:375:PRO:HG2	1.99	0.45
1:D:447:VAL:HG12	1:D:448:THR:HG23	1.97	0.45
1:D:491:THR:HG23	2:V:15:TYR:CZ	2.52	0.45
2:V:15:TYR:CD2	2:V:16:PRO:HD2	2.51	0.45
1:A:177:GLU:CG	1:A:178:THR:H	2.30	0.45
1:B:123:LEU:HD13	1:B:559:VAL:HG22	1.98	0.45
1:B:223:THR:HG22	1:B:225:LEU:HB2	1.99	0.45
1:B:231:TYR:H	1:B:501:GLN:HE21	1.65	0.45
1:D:382:GLU:HA	1:D:387:ARG:O	2.17	0.45
1:D:481:SER:O	1:D:482:GLN:C	2.59	0.45
1:E:129:THR:HB	1:E:130:ASN:H	1.63	0.45
1:E:439:LEU:N	1:E:440:PRO:CD	2.79	0.45
1:A:64:PHE:HD1	1:B:118:HIS:NE2	2.15	0.45
1:A:171:PRO:CA	1:B:409:ASN:HD22	2.30	0.45
1:A:250:PHE:O	1:A:251:THR:C	2.60	0.45
1:A:417:ILE:HD12	1:A:417:ILE:HA	1.80	0.45
1:A:442:MET:CE	1:A:559:VAL:HG21	2.27	0.45
1:B:295:SER:HB3	1:B:375:PRO:HG2	1.98	0.45
1:B:382:GLU:HA	1:B:387:ARG:O	2.17	0.45
1:C:381:THR:O	1:C:381:THR:CG2	2.65	0.45
1:D:225:LEU:CD2	1:D:397:THR:HB	2.47	0.45
1:D:237:HIS:HE1	1:D:424:CYS:O	2.00	0.45
1:E:545:ARG:O	1:E:546:ARG:HB2	2.17	0.45
1:A:242:LEU:HD22	1:A:247:GLY:HA2	1.98	0.45
1:A:295:SER:HB3	1:A:375:PRO:HG2	1.98	0.45
1:A:474:TYR:CD1	1:A:511:ILE:CD1	3.00	0.45
1:A:480:TYR:HE1	1:E:484:ILE:CG2	2.24	0.45
1:B:177:GLU:CG	1:B:178:THR:H	2.30	0.45
1:B:225:LEU:CD2	1:B:397:THR:HB	2.47	0.45
1:B:446:PRO:HG2	1:B:460:VAL:O	2.17	0.45
1:B:545:ARG:O	1:B:546:ARG:HB2	2.17	0.45
1:C:474:TYR:CD1	1:C:511:ILE:CD1	3.00	0.45
1:A:231:TYR:CD1	1:A:501:GLN:HB3	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:237:HIS:HE1	1:E:424:CYS:O	2.00	0.44
1:E:250:PHE:O	1:E:251:THR:C	2.60	0.44
1:E:381:THR:HG22	1:E:382:GLU:HG3	1.99	0.44
1:A:237:HIS:HE1	1:A:424:CYS:O	2.00	0.44
1:A:381:THR:HG22	1:A:382:GLU:HG3	1.99	0.44
1:A:446:PRO:HG2	1:A:460:VAL:O	2.17	0.44
1:A:452:THR:OG1	1:A:453:SER:N	2.49	0.44
1:B:171:PRO:O	1:B:172:GLU:O	2.36	0.44
1:B:237:HIS:HE1	1:B:424:CYS:O	1.99	0.44
1:C:202:LEU:N	1:C:202:LEU:HD23	2.33	0.44
1:D:171:PRO:O	1:D:172:GLU:O	2.36	0.44
1:D:250:PHE:O	1:D:251:THR:C	2.60	0.44
1:D:379:PRO:O	1:D:380:LEU:C	2.61	0.44
1:E:392:ILE:HG13	1:E:393:SER:N	2.32	0.44
1:A:88:HIS:HD2	1:B:267:PHE:HZ	1.63	0.44
1:A:382:GLU:HA	1:A:387:ARG:O	2.17	0.44
1:B:250:PHE:O	1:B:251:THR:C	2.60	0.44
1:C:379:PRO:O	1:C:380:LEU:C	2.61	0.44
1:C:485:ARG:NH2	1:D:234:GLU:OE1	2.49	0.44
1:D:392:ILE:HG13	1:D:393:SER:N	2.32	0.44
1:E:458:PHE:O	1:E:546:ARG:NH2	2.50	0.44
1:E:506:PRO:HA	1:E:507:PRO:HD3	1.81	0.44
1:A:171:PRO:O	1:A:172:GLU:C	2.59	0.44
1:A:267:PHE:HB3	1:E:79:VAL:HG13	2.00	0.44
1:A:466:LEU:HA	1:A:467:PRO:HD3	1.78	0.44
1:B:250:PHE:O	1:B:252:HIS:N	2.49	0.44
1:B:458:PHE:O	1:B:546:ARG:NH2	2.50	0.44
1:C:171:PRO:O	1:C:172:GLU:O	2.36	0.44
1:C:177:GLU:CG	1:C:178:THR:H	2.30	0.44
1:D:79:VAL:HG13	1:E:267:PHE:CD2	2.52	0.44
1:E:64:PHE:O	1:E:65:ASP:HB2	2.17	0.44
1:E:231:TYR:H	1:E:501:GLN:HE21	1.65	0.44
1:E:446:PRO:HG2	1:E:460:VAL:O	2.17	0.44
1:A:69:VAL:HG22	1:A:559:VAL:HB	2.00	0.44
1:A:202:LEU:N	1:A:202:LEU:HD23	2.33	0.44
1:A:244:PRO:HA	1:A:275:TYR:CE2	2.53	0.44
1:A:379:PRO:O	1:A:380:LEU:C	2.61	0.44
1:A:381:THR:O	1:A:381:THR:CG2	2.65	0.44
1:A:545:ARG:O	1:A:546:ARG:HB2	2.16	0.44
1:D:177:GLU:CG	1:D:178:THR:H	2.30	0.44
1:E:207:GLY:HA3	1:E:246:CYS:SG	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:244:PRO:HA	1:E:275:TYR:CE2	2.53	0.44
1:A:64:PHE:O	1:A:65:ASP:HB2	2.17	0.44
1:A:171:PRO:O	1:A:172:GLU:O	2.36	0.44
1:A:417:ILE:C	1:A:419:SER:N	2.76	0.44
1:B:474:TYR:CD1	1:B:511:ILE:CD1	3.00	0.44
1:C:64:PHE:O	1:C:65:ASP:HB2	2.17	0.44
1:C:446:PRO:HG2	1:C:460:VAL:O	2.17	0.44
1:D:79:VAL:HG13	1:E:267:PHE:HB3	1.99	0.44
1:D:99:ASN:HB3	1:E:450:ARG:NH2	2.32	0.44
1:D:202:LEU:N	1:D:202:LEU:HD23	2.33	0.44
1:E:177:GLU:CG	1:E:178:THR:H	2.30	0.44
1:E:295:SER:HB3	1:E:375:PRO:HG2	1.98	0.44
1:E:379:PRO:O	1:E:380:LEU:C	2.61	0.44
1:E:474:TYR:CD1	1:E:511:ILE:CD1	3.01	0.44
1:E:491:THR:HG23	2:W:15:TYR:CZ	2.52	0.44
1:A:207:GLY:HA3	1:A:246:CYS:SG	2.58	0.44
1:B:113:LEU:HB3	1:B:119:TRP:CE2	2.53	0.44
1:B:244:PRO:HA	1:B:275:TYR:CE2	2.53	0.44
1:B:384:SER:C	1:B:386:LYS:N	2.76	0.44
1:C:243:LEU:O	1:C:244:PRO:C	2.59	0.44
1:A:113:LEU:HB3	1:A:119:TRP:CE2	2.53	0.44
1:A:189:VAL:O	1:A:192:TYR:N	2.51	0.44
1:B:243:LEU:O	1:B:244:PRO:C	2.59	0.44
1:C:57:TYR:CD2	1:D:448:THR:HG22	2.53	0.44
1:C:130:ASN:C	1:C:130:ASN:ND2	2.76	0.44
1:C:382:GLU:HA	1:C:387:ARG:O	2.17	0.44
1:C:491:THR:HG23	2:U:15:TYR:CZ	2.52	0.44
1:D:171:PRO:O	1:D:172:GLU:C	2.59	0.44
1:D:207:GLY:HA3	1:D:246:CYS:SG	2.58	0.44
1:D:244:PRO:HA	1:D:275:TYR:CE2	2.53	0.44
1:D:381:THR:HG22	1:D:382:GLU:HG3	1.99	0.44
1:E:171:PRO:O	1:E:172:GLU:O	2.35	0.44
1:E:202:LEU:N	1:E:202:LEU:HD23	2.33	0.44
1:E:243:LEU:O	1:E:244:PRO:C	2.59	0.44
1:C:69:VAL:O	1:C:69:VAL:HG23	2.18	0.44
1:C:69:VAL:HG22	1:C:559:VAL:HB	2.00	0.44
1:D:556:LEU:CD2	1:E:434:GLN:HG2	2.46	0.44
1:E:69:VAL:HG22	1:E:559:VAL:HB	2.00	0.44
1:E:481:SER:O	1:E:482:GLN:C	2.59	0.44
1:A:255:LEU:O	1:A:256:SER:C	2.61	0.43
1:A:384:SER:C	1:A:386:LYS:N	2.76	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:MET:HE3	1:B:254:ARG:NH1	2.33	0.43
1:B:189:VAL:O	1:B:192:TYR:N	2.51	0.43
1:C:381:THR:HG22	1:C:382:GLU:HG3	1.99	0.43
1:C:466:LEU:HA	1:C:467:PRO:HD3	1.78	0.43
1:D:67:THR:OG1	1:E:447:VAL:HG23	2.18	0.43
1:D:381:THR:O	1:D:381:THR:CG2	2.65	0.43
1:B:392:ILE:HG13	1:B:393:SER:N	2.32	0.43
1:C:255:LEU:O	1:C:256:SER:C	2.62	0.43
1:C:392:ILE:HG13	1:C:393:SER:N	2.32	0.43
1:C:506:PRO:HA	1:C:507:PRO:HD3	1.81	0.43
1:D:130:ASN:C	1:D:130:ASN:ND2	2.76	0.43
1:E:189:VAL:O	1:E:192:TYR:N	2.51	0.43
1:E:223:THR:HG22	1:E:225:LEU:HB2	1.99	0.43
1:A:130:ASN:C	1:A:130:ASN:ND2	2.76	0.43
1:B:171:PRO:O	1:B:172:GLU:C	2.59	0.43
1:B:202:LEU:N	1:B:202:LEU:HD23	2.33	0.43
1:C:250:PHE:O	1:C:251:THR:C	2.60	0.43
1:D:113:LEU:HB3	1:D:119:TRP:CE2	2.53	0.43
1:D:192:TYR:CD1	1:D:196:GLY:HA3	2.54	0.43
1:D:446:PRO:HG2	1:D:460:VAL:O	2.17	0.43
1:D:458:PHE:O	1:D:546:ARG:NH2	2.50	0.43
1:D:474:TYR:CD1	1:D:511:ILE:CD1	3.00	0.43
1:E:278:LEU:C	1:E:279:GLU:O	2.60	0.43
1:A:564:LEU:O	1:A:565:SER:HB3	2.19	0.43
1:B:428:VAL:C	1:B:430:CYS:N	2.76	0.43
1:C:542:THR:HG23	1:C:547:ARG:N	2.34	0.43
1:D:131:MET:HA	1:D:132:PRO:HD3	1.80	0.43
1:E:479:VAL:O	1:E:479:VAL:CG1	2.66	0.43
1:B:79:VAL:HG13	1:C:267:PHE:HD2	1.83	0.43
1:C:113:LEU:HB3	1:C:119:TRP:CE2	2.53	0.43
1:C:207:GLY:HA3	1:C:246:CYS:SG	2.58	0.43
1:C:278:LEU:C	1:C:279:GLU:O	2.60	0.43
1:C:428:VAL:HG13	1:C:513:THR:HB	2.01	0.43
1:D:189:VAL:O	1:D:192:TYR:N	2.51	0.43
1:D:255:LEU:O	1:D:256:SER:C	2.61	0.43
1:E:75:LYS:HE2	1:E:75:LYS:HB3	1.88	0.43
1:E:96:ILE:HD13	1:E:96:ILE:HA	1.82	0.43
1:E:113:LEU:HB3	1:E:119:TRP:CE2	2.53	0.43
1:E:138:MET:HE3	1:E:254:ARG:NH1	2.33	0.43
1:A:99:ASN:OD1	1:A:99:ASN:C	2.62	0.43
1:B:88:HIS:CD2	1:C:267:PHE:CZ	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:TYR:CD1	1:B:196:GLY:HA3	2.54	0.43
1:C:181:ILE:O	1:C:184:MET:HB2	2.19	0.43
1:C:384:SER:C	1:C:386:LYS:N	2.76	0.43
1:D:99:ASN:OD1	1:D:99:ASN:C	2.62	0.43
1:D:428:VAL:HG13	1:D:513:THR:HB	2.01	0.43
1:D:564:LEU:O	1:D:565:SER:HB3	2.19	0.43
1:E:102:SER:C	1:E:103:PRO:O	2.61	0.43
1:E:130:ASN:C	1:E:130:ASN:ND2	2.76	0.43
1:E:223:THR:CG2	1:E:225:LEU:HB2	2.49	0.43
1:A:83:ASN:CA	1:A:86:ASN:HD22	2.21	0.43
1:A:231:TYR:H	1:A:501:GLN:HE21	1.65	0.43
1:A:392:ILE:HG13	1:A:393:SER:N	2.32	0.43
1:B:69:VAL:O	1:B:69:VAL:HG23	2.18	0.43
1:B:130:ASN:C	1:B:130:ASN:ND2	2.76	0.43
1:B:181:ILE:O	1:B:184:MET:HB2	2.19	0.43
1:C:171:PRO:C	1:D:409:ASN:HD22	2.26	0.43
1:D:64:PHE:CD1	1:E:118:HIS:NE2	2.86	0.43
1:D:231:TYR:H	1:D:501:GLN:HE21	1.65	0.43
1:D:278:LEU:C	1:D:279:GLU:O	2.60	0.43
1:E:384:SER:C	1:E:386:LYS:N	2.76	0.43
1:E:422:LEU:CD2	1:E:423:LEU:N	2.80	0.43
1:E:428:VAL:HG13	1:E:513:THR:HB	2.00	0.43
1:A:177:GLU:HG3	1:A:178:THR:H	1.82	0.43
1:B:69:VAL:HG22	1:B:559:VAL:HB	2.00	0.43
1:B:126:ILE:HG12	1:B:521:LEU:CD2	2.49	0.43
1:B:381:THR:HG22	1:B:382:GLU:HG3	2.00	0.43
1:B:481:SER:O	1:B:482:GLN:C	2.59	0.43
1:B:502:ILE:C	1:B:504:ALA:N	2.77	0.43
1:C:189:VAL:O	1:C:192:TYR:N	2.51	0.43
1:C:192:TYR:CD1	1:C:196:GLY:HA3	2.54	0.43
1:C:417:ILE:C	1:C:419:SER:N	2.76	0.43
1:C:458:PHE:O	1:C:546:ARG:NH2	2.50	0.43
1:E:132:PRO:CA	1:E:175:TYR:OH	2.53	0.43
1:A:422:LEU:HD21	1:E:551:TYR:CZ	2.53	0.43
1:A:448:THR:HG22	1:E:57:TYR:CE2	2.54	0.43
1:B:207:GLY:HA3	1:B:246:CYS:SG	2.58	0.43
1:B:223:THR:CG2	1:B:225:LEU:HB2	2.49	0.43
1:B:379:PRO:O	1:B:380:LEU:C	2.61	0.43
1:B:474:TYR:HH	1:B:476:ASP:CG	2.25	0.43
1:C:99:ASN:OD1	1:C:99:ASN:C	2.62	0.43
1:C:231:TYR:H	1:C:501:GLN:HE21	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:502:ILE:C	1:C:504:ALA:N	2.77	0.43
1:D:138:MET:HE3	1:D:254:ARG:NH1	2.33	0.43
1:E:126:ILE:HG12	1:E:521:LEU:CD2	2.49	0.43
1:E:200:GLY:O	1:E:201:VAL:C	2.62	0.43
1:E:381:THR:O	1:E:381:THR:CG2	2.65	0.43
1:A:87:ASP:OD1	1:A:89:SER:HB3	2.19	0.43
1:A:192:TYR:CD1	1:A:196:GLY:HA3	2.54	0.43
1:A:223:THR:CG2	1:A:225:LEU:HB2	2.49	0.43
1:A:234:GLU:OE1	1:E:485:ARG:NH2	2.52	0.43
1:A:447:VAL:CG2	1:E:67:THR:CG2	2.97	0.43
1:B:95:VAL:O	1:B:95:VAL:HG12	2.19	0.43
1:B:381:THR:O	1:B:381:THR:CG2	2.65	0.43
1:C:243:LEU:HD23	1:C:244:PRO:HD3	2.01	0.43
1:D:551:TYR:CZ	1:E:422:LEU:HD21	2.54	0.43
1:E:243:LEU:HD23	1:E:244:PRO:HD3	2.01	0.43
1:A:96:ILE:HD13	1:A:96:ILE:HA	1.82	0.42
1:A:138:MET:HE3	1:A:254:ARG:NH1	2.33	0.42
1:A:493:VAL:HG21	1:B:232:THR:HB	2.00	0.42
1:B:58:SER:OG	1:B:59:GLU:N	2.52	0.42
1:B:243:LEU:HD23	1:B:244:PRO:HD3	2.01	0.42
1:B:542:THR:HG23	1:B:547:ARG:N	2.34	0.42
1:C:58:SER:OG	1:C:59:GLU:N	2.52	0.42
1:C:96:ILE:O	1:D:448:THR:HB	2.19	0.42
1:C:200:GLY:O	1:C:201:VAL:C	2.62	0.42
1:D:57:TYR:CG	1:E:448:THR:HG22	2.55	0.42
1:A:96:ILE:HG22	1:A:98:ASN:N	2.28	0.42
1:A:177:GLU:O	1:A:178:THR:C	2.63	0.42
1:A:228:PRO:HB3	2:W:15:TYR:HE1	1.84	0.42
1:C:138:MET:HE3	1:C:254:ARG:NH1	2.33	0.42
1:C:244:PRO:HA	1:C:275:TYR:CE2	2.53	0.42
1:C:422:LEU:CD2	1:C:423:LEU:N	2.80	0.42
1:D:69:VAL:HG22	1:D:559:VAL:HB	2.00	0.42
1:D:177:GLU:O	1:D:178:THR:C	2.62	0.42
1:D:223:THR:CG2	1:D:225:LEU:HB2	2.49	0.42
1:E:87:ASP:OD1	1:E:89:SER:HB3	2.19	0.42
1:E:192:TYR:CD1	1:E:196:GLY:HA3	2.54	0.42
1:E:277:ASP:O	1:E:279:GLU:N	2.46	0.42
1:E:502:ILE:C	1:E:504:ALA:N	2.77	0.42
1:A:132:PRO:CD	1:A:551:TYR:CE2	3.02	0.42
1:B:200:GLY:O	1:B:201:VAL:C	2.62	0.42
1:C:223:THR:CG2	1:C:225:LEU:HB2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:384:SER:C	1:D:386:LYS:N	2.76	0.42
1:E:228:PRO:CB	2:V:15:TYR:HE1	2.33	0.42
2:T:10:THR:O	2:T:10:THR:CG2	2.60	0.42
1:A:126:ILE:HG12	1:A:521:LEU:CD2	2.49	0.42
1:A:479:VAL:O	1:A:479:VAL:CG1	2.66	0.42
1:B:177:GLU:HG3	1:B:178:THR:H	1.82	0.42
1:C:87:ASP:OD1	1:C:89:SER:HB3	2.19	0.42
1:C:177:GLU:HG3	1:C:178:THR:H	1.82	0.42
1:D:69:VAL:O	1:D:69:VAL:HG23	2.18	0.42
1:D:506:PRO:HA	1:D:507:PRO:HD3	1.81	0.42
1:E:177:GLU:O	1:E:178:THR:C	2.63	0.42
1:E:542:THR:HG23	1:E:547:ARG:N	2.34	0.42
1:E:549:CYS:HA	1:E:550:PRO:HD3	1.89	0.42
2:V:15:TYR:HD2	2:V:15:TYR:C	2.28	0.42
1:A:200:GLY:O	1:A:201:VAL:C	2.62	0.42
1:A:243:LEU:HD23	1:A:244:PRO:HD3	2.01	0.42
1:A:428:VAL:HG13	1:A:513:THR:HB	2.00	0.42
1:B:87:ASP:OD1	1:B:89:SER:HB3	2.19	0.42
1:B:129:THR:HB	1:B:130:ASN:H	1.63	0.42
1:B:428:VAL:HG13	1:B:513:THR:HB	2.00	0.42
1:C:282:ASN:HA	1:C:402:ARG:HA	2.02	0.42
1:D:181:ILE:O	1:D:184:MET:HB2	2.19	0.42
1:D:228:PRO:HB3	2:U:15:TYR:HE1	1.83	0.42
1:E:69:VAL:O	1:E:69:VAL:HG23	2.18	0.42
1:E:83:ASN:CA	1:E:86:ASN:HD22	2.21	0.42
1:E:99:ASN:C	1:E:99:ASN:OD1	2.62	0.42
1:E:255:LEU:O	1:E:256:SER:C	2.61	0.42
1:E:282:ASN:HA	1:E:402:ARG:HA	2.02	0.42
1:A:58:SER:OG	1:A:59:GLU:N	2.52	0.42
1:A:268:GLN:O	1:A:269:GLU:C	2.62	0.42
1:A:488:THR:HG23	1:B:479:VAL:C	2.42	0.42
1:B:75:LYS:HE2	1:B:75:LYS:HB3	1.88	0.42
1:B:109:GLN:C	1:B:110:THR:HG23	2.45	0.42
1:B:132:PRO:CD	1:B:551:TYR:CE2	3.02	0.42
1:B:542:THR:HG21	1:B:546:ARG:HD2	2.01	0.42
1:D:95:VAL:O	1:D:95:VAL:HG12	2.19	0.42
1:D:268:GLN:O	1:D:269:GLU:C	2.62	0.42
1:A:422:LEU:CD2	1:A:423:LEU:N	2.80	0.42
1:A:458:PHE:O	1:A:546:ARG:NH2	2.50	0.42
1:B:137:PHE:HE1	1:B:547:ARG:NE	2.18	0.42
1:B:177:GLU:O	1:B:178:THR:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:207:GLY:O	1:C:208:VAL:CB	2.64	0.42
1:D:200:GLY:O	1:D:201:VAL:C	2.62	0.42
1:E:132:PRO:CD	1:E:551:TYR:CE2	3.02	0.42
1:E:181:ILE:O	1:E:184:MET:HB2	2.19	0.42
1:E:428:VAL:C	1:E:430:CYS:N	2.76	0.42
1:E:564:LEU:O	1:E:565:SER:HB3	2.19	0.42
2:T:15:TYR:HD2	2:T:15:TYR:C	2.28	0.42
1:A:137:PHE:HE1	1:A:547:ARG:NE	2.18	0.42
1:A:502:ILE:C	1:A:504:ALA:N	2.77	0.42
1:B:117:SER:HA	1:B:566:SER:HA	2.02	0.42
1:B:523:ASP:OD1	1:B:523:ASP:C	2.63	0.42
1:D:502:ILE:C	1:D:504:ALA:N	2.77	0.42
1:E:95:VAL:O	1:E:95:VAL:HG12	2.19	0.42
1:E:109:GLN:C	1:E:110:THR:HG23	2.45	0.42
1:E:268:GLN:O	1:E:269:GLU:C	2.62	0.42
1:A:95:VAL:O	1:A:95:VAL:HG12	2.19	0.42
1:A:228:PRO:HG3	2:W:15:TYR:CD1	2.54	0.42
1:B:88:HIS:HD2	1:C:267:PHE:CZ	2.38	0.42
1:C:126:ILE:HG12	1:C:521:LEU:CD2	2.49	0.42
1:C:268:GLN:O	1:C:269:GLU:C	2.62	0.42
1:C:277:ASP:O	1:C:279:GLU:N	2.46	0.42
1:C:523:ASP:OD1	1:C:523:ASP:C	2.63	0.42
1:D:282:ASN:HA	1:D:402:ARG:HA	2.02	0.42
1:D:542:THR:HG21	1:D:546:ARG:HD2	2.02	0.42
2:S:10:THR:O	2:S:10:THR:CG2	2.60	0.42
2:U:15:TYR:HD2	2:U:15:TYR:C	2.27	0.42
1:A:87:ASP:O	1:A:89:SER:N	2.46	0.42
1:A:278:LEU:C	1:A:279:GLU:O	2.60	0.42
1:A:547:ARG:O	1:A:548:THR:C	2.63	0.42
1:B:99:ASN:OD1	1:B:99:ASN:C	2.62	0.42
1:B:102:SER:C	1:B:103:PRO:O	2.61	0.42
1:B:426:PRO:O	1:B:427:ASP:CB	2.67	0.42
1:B:479:VAL:O	1:B:479:VAL:CG1	2.66	0.42
1:C:109:GLN:C	1:C:110:THR:HG23	2.45	0.42
1:C:132:PRO:CD	1:C:551:TYR:CE2	3.02	0.42
1:D:117:SER:HA	1:D:566:SER:HA	2.02	0.42
1:E:179:MET:CE	1:E:485:ARG:NH2	2.77	0.42
1:E:243:LEU:HD23	1:E:243:LEU:HA	1.82	0.42
1:A:69:VAL:O	1:A:69:VAL:HG23	2.18	0.41
1:A:109:GLN:C	1:A:110:THR:HG23	2.45	0.41
1:A:150:SER:OG	1:A:162:LYS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:GLY:O	1:A:208:VAL:CB	2.64	0.41
1:A:243:LEU:HD23	1:A:243:LEU:HA	1.82	0.41
1:B:73:ASP:OD1	1:B:73:ASP:N	2.53	0.41
1:B:79:VAL:HG13	1:C:267:PHE:CD2	2.54	0.41
1:B:83:ASN:CA	1:B:86:ASN:HD22	2.21	0.41
1:D:417:ILE:C	1:D:419:SER:N	2.76	0.41
1:D:542:THR:HG23	1:D:547:ARG:N	2.34	0.41
1:E:58:SER:OG	1:E:59:GLU:N	2.52	0.41
1:E:117:SER:HA	1:E:566:SER:HA	2.02	0.41
1:E:137:PHE:HE1	1:E:547:ARG:NE	2.18	0.41
1:E:197:ARG:C	1:E:199:ASN:H	2.28	0.41
1:A:181:ILE:O	1:A:184:MET:HB2	2.19	0.41
1:B:224:GLY:O	1:B:397:THR:HB	2.21	0.41
1:B:243:LEU:CG	1:B:401:TYR:CE2	3.03	0.41
1:B:422:LEU:CD2	1:B:423:LEU:N	2.80	0.41
1:C:137:PHE:HE1	1:C:547:ARG:NE	2.18	0.41
1:C:542:THR:HG21	1:C:546:ARG:HD2	2.02	0.41
1:D:87:ASP:OD1	1:D:89:SER:HB3	2.19	0.41
1:D:109:GLN:C	1:D:110:THR:HG23	2.45	0.41
1:D:126:ILE:HG12	1:D:521:LEU:CD2	2.49	0.41
1:D:132:PRO:CD	1:D:551:TYR:CE2	3.02	0.41
1:D:207:GLY:O	1:D:208:VAL:CB	2.64	0.41
1:A:542:THR:HG23	1:A:547:ARG:N	2.34	0.41
1:B:63:LEU:C	1:B:64:PHE:CD2	2.99	0.41
1:C:95:VAL:O	1:C:95:VAL:HG12	2.19	0.41
1:C:117:SER:HA	1:C:566:SER:HA	2.02	0.41
1:C:177:GLU:O	1:C:178:THR:C	2.63	0.41
1:C:224:GLY:O	1:C:397:THR:HB	2.20	0.41
1:D:224:GLY:O	1:D:397:THR:HB	2.21	0.41
1:A:117:SER:HA	1:A:566:SER:HA	2.01	0.41
1:A:179:MET:CE	1:A:485:ARG:NH2	2.77	0.41
1:A:428:VAL:C	1:A:430:CYS:N	2.76	0.41
1:A:474:TYR:CE2	1:A:476:ASP:CG	2.99	0.41
1:B:255:LEU:O	1:B:256:SER:C	2.62	0.41
1:B:547:ARG:O	1:B:548:THR:C	2.63	0.41
1:D:73:ASP:OD1	1:D:73:ASP:N	2.53	0.41
1:E:63:LEU:C	1:E:64:PHE:CD2	2.99	0.41
1:A:63:LEU:C	1:A:64:PHE:CD2	2.99	0.41
1:A:183:LEU:HD21	1:B:236:PHE:CE2	2.47	0.41
1:A:217:LEU:HD23	1:A:217:LEU:HA	1.74	0.41
1:A:224:GLY:O	1:A:397:THR:HB	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:THR:HG21	1:A:493:VAL:HG22	2.03	0.41
1:A:549:CYS:HA	1:A:550:PRO:HD3	1.89	0.41
1:B:217:LEU:HD23	1:B:217:LEU:HA	1.74	0.41
1:B:268:GLN:O	1:B:269:GLU:C	2.62	0.41
1:B:417:ILE:HD12	1:B:417:ILE:HA	1.80	0.41
1:B:417:ILE:C	1:B:419:SER:N	2.76	0.41
1:B:564:LEU:O	1:B:565:SER:HB3	2.19	0.41
1:C:63:LEU:C	1:C:64:PHE:CD2	2.99	0.41
1:C:211:ASP:C	1:C:212:THR:CG2	2.94	0.41
1:C:228:PRO:HG3	2:T:15:TYR:CD1	2.55	0.41
1:C:439:LEU:O	1:C:441:ASP:N	2.54	0.41
1:C:474:TYR:CE2	1:C:476:ASP:CG	2.99	0.41
1:C:479:VAL:O	1:C:479:VAL:CG1	2.66	0.41
1:C:564:LEU:O	1:C:565:SER:HB3	2.19	0.41
1:D:63:LEU:C	1:D:64:PHE:CD2	2.99	0.41
1:D:474:TYR:CE2	1:D:476:ASP:CG	2.99	0.41
1:A:401:TYR:CE1	1:A:502:ILE:HG12	2.56	0.41
1:A:523:ASP:OD1	1:A:523:ASP:C	2.63	0.41
1:B:491:THR:HG21	1:B:493:VAL:HG22	2.02	0.41
1:C:64:PHE:CD1	1:D:118:HIS:NE2	2.88	0.41
1:C:150:SER:OG	1:C:162:LYS:HB2	2.21	0.41
1:C:243:LEU:CG	1:C:401:TYR:CE2	3.03	0.41
1:D:137:PHE:HE1	1:D:547:ARG:NE	2.18	0.41
1:D:154:THR:CG2	1:D:155:LYS:H	2.34	0.41
1:D:243:LEU:HD23	1:D:244:PRO:HD3	2.01	0.41
1:D:392:ILE:HD11	1:D:396:SER:CB	2.51	0.41
1:D:422:LEU:CD2	1:D:423:LEU:N	2.80	0.41
1:E:217:LEU:HD23	1:E:217:LEU:HA	1.74	0.41
1:E:563:VAL:CG1	1:E:564:LEU:N	2.84	0.41
1:A:196:GLY:O	1:A:201:VAL:HG12	2.21	0.41
1:B:114:ASP:OD2	1:B:116:ARG:NH1	2.54	0.41
1:B:282:ASN:HA	1:B:402:ARG:HA	2.02	0.41
1:B:474:TYR:CE2	1:B:476:ASP:CG	2.99	0.41
1:C:405:TYR:O	1:C:409:ASN:OD1	2.39	0.41
1:C:428:VAL:C	1:C:430:CYS:N	2.76	0.41
1:C:441:ASP:HB2	1:C:537:GLN:OE1	2.21	0.41
1:C:563:VAL:CG1	1:C:564:LEU:N	2.84	0.41
1:D:547:ARG:O	1:D:548:THR:C	2.63	0.41
1:A:282:ASN:HA	1:A:402:ARG:HA	2.02	0.41
1:A:542:THR:HG21	1:A:546:ARG:HD2	2.02	0.41
1:A:563:VAL:CG1	1:A:564:LEU:N	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:ASP:OD2	1:C:116:ARG:NH1	2.54	0.41
1:C:434:GLN:NE2	1:C:436:TYR:CE2	2.81	0.41
1:D:150:SER:OG	1:D:162:LYS:HB2	2.21	0.41
1:D:523:ASP:OD1	1:D:523:ASP:C	2.63	0.41
1:E:231:TYR:OH	1:E:284:PRO:O	2.34	0.41
1:E:405:TYR:O	1:E:409:ASN:OD1	2.39	0.41
1:E:417:ILE:C	1:E:419:SER:N	2.76	0.41
1:A:73:ASP:OD1	1:A:73:ASP:N	2.53	0.41
1:A:114:ASP:OD2	1:A:116:ARG:NH1	2.54	0.41
1:A:154:THR:CG2	1:A:155:LYS:H	2.34	0.41
1:A:197:ARG:C	1:A:199:ASN:H	2.28	0.41
1:A:267:PHE:HD2	1:E:79:VAL:HG13	1.86	0.41
1:A:551:TYR:CZ	1:B:422:LEU:HD21	2.55	0.41
1:B:196:GLY:O	1:B:201:VAL:HG12	2.21	0.41
1:B:417:ILE:C	1:B:419:SER:H	2.29	0.41
1:B:563:VAL:CG1	1:B:564:LEU:N	2.84	0.41
1:C:75:LYS:HB3	1:C:75:LYS:HE2	1.88	0.41
1:C:197:ARG:C	1:C:199:ASN:H	2.28	0.41
1:C:491:THR:HG21	1:C:493:VAL:HG22	2.03	0.41
1:D:58:SER:OG	1:D:59:GLU:N	2.52	0.41
1:D:83:ASN:OD1	1:D:92:LEU:N	2.38	0.41
1:D:102:SER:C	1:D:103:PRO:O	2.61	0.41
1:D:114:ASP:OD2	1:D:116:ARG:NH1	2.54	0.41
1:D:439:LEU:O	1:D:441:ASP:N	2.54	0.41
1:D:479:VAL:CG1	1:D:479:VAL:O	2.66	0.41
1:E:224:GLY:O	1:E:397:THR:HB	2.20	0.41
1:E:434:GLN:NE2	1:E:436:TYR:CE2	2.81	0.41
1:E:523:ASP:OD1	1:E:523:ASP:C	2.63	0.41
2:V:18:ASP:O	2:V:19:THR:HB	2.21	0.41
1:A:441:ASP:HB2	1:A:537:GLN:OE1	2.21	0.41
1:B:441:ASP:HB2	1:B:537:GLN:OE1	2.21	0.41
1:C:96:ILE:HD13	1:C:96:ILE:HA	1.82	0.41
1:C:154:THR:CG2	1:C:155:LYS:H	2.34	0.41
1:C:439:LEU:N	1:C:440:PRO:CD	2.79	0.41
1:D:88:HIS:CD2	1:E:267:PHE:CZ	3.09	0.41
1:D:417:ILE:HA	1:D:417:ILE:HD12	1.79	0.41
1:D:491:THR:HG21	1:D:493:VAL:HG22	2.03	0.41
1:E:114:ASP:OD2	1:E:116:ARG:NH1	2.54	0.41
1:E:150:SER:OG	1:E:162:LYS:HB2	2.21	0.41
1:E:211:ASP:C	1:E:212:THR:CG2	2.94	0.41
1:E:491:THR:HG21	1:E:493:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:542:THR:HG21	1:E:546:ARG:HD2	2.02	0.41
1:A:135:ASN:N	1:A:140:THR:OG1	2.54	0.40
1:A:267:PHE:CD2	1:E:79:VAL:HG13	2.56	0.40
1:A:439:LEU:O	1:A:441:ASP:N	2.54	0.40
1:B:149:VAL:HG13	1:B:195:VAL:HG11	2.04	0.40
1:C:53:ASN:ND2	1:C:53:ASN:O	2.54	0.40
1:D:197:ARG:C	1:D:199:ASN:H	2.28	0.40
1:D:441:ASP:HB2	1:D:537:GLN:OE1	2.21	0.40
1:E:225:LEU:HD23	1:E:397:THR:HB	2.03	0.40
1:E:243:LEU:CG	1:E:401:TYR:CE2	3.03	0.40
1:E:474:TYR:CE2	1:E:476:ASP:CG	2.99	0.40
2:S:18:ASP:O	2:S:19:THR:HB	2.21	0.40
1:A:211:ASP:C	1:A:212:THR:CG2	2.94	0.40
1:B:53:ASN:ND2	1:B:53:ASN:O	2.54	0.40
1:B:278:LEU:C	1:B:279:GLU:O	2.60	0.40
1:B:373:LYS:O	1:B:374:LYS:CG	2.69	0.40
1:C:225:LEU:HD23	1:C:397:THR:HB	2.04	0.40
1:C:373:LYS:O	1:C:374:LYS:CG	2.70	0.40
1:D:88:HIS:HD2	1:E:267:PHE:CZ	2.39	0.40
1:D:401:TYR:CE1	1:D:502:ILE:HG12	2.56	0.40
1:D:417:ILE:C	1:D:419:SER:H	2.29	0.40
1:D:495:ASN:O	1:D:496:ARG:C	2.64	0.40
1:E:441:ASP:HB2	1:E:537:GLN:OE1	2.21	0.40
1:B:150:SER:OG	1:B:162:LYS:HB2	2.21	0.40
1:C:149:VAL:HG13	1:C:195:VAL:HG11	2.03	0.40
1:C:208:VAL:HG22	1:C:242:LEU:HD22	2.03	0.40
1:D:75:LYS:HB3	1:D:75:LYS:HE2	1.88	0.40
1:D:211:ASP:C	1:D:212:THR:CG2	2.94	0.40
1:A:454:GLN:O	1:A:455:ILE:C	2.65	0.40
1:B:405:TYR:O	1:B:409:ASN:OD1	2.39	0.40
1:C:220:ASP:HB3	1:C:223:THR:HB	2.04	0.40
1:D:177:GLU:HG3	1:D:178:THR:H	1.82	0.40
1:D:428:VAL:C	1:D:430:CYS:N	2.76	0.40
1:D:436:TYR:HD1	1:D:460:VAL:HG21	1.86	0.40
1:D:442:MET:CE	1:D:559:VAL:HG21	2.28	0.40
1:E:196:GLY:O	1:E:201:VAL:HG12	2.21	0.40
1:E:209:LYS:NZ	1:E:502:ILE:O	2.54	0.40
1:E:373:LYS:O	1:E:374:LYS:CG	2.70	0.40
1:A:220:ASP:HB3	1:A:223:THR:HB	2.04	0.40
1:A:373:LYS:O	1:A:374:LYS:CG	2.70	0.40
1:A:409:ASN:HD22	1:E:171:PRO:CA	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:ASP:C	1:B:212:THR:CG2	2.94	0.40
1:B:392:ILE:HD11	1:B:396:SER:CB	2.51	0.40
1:B:401:TYR:CE1	1:B:502:ILE:HG12	2.56	0.40
1:C:392:ILE:HD11	1:C:396:SER:CB	2.51	0.40
1:C:436:TYR:HD1	1:C:460:VAL:HG21	1.86	0.40
1:D:179:MET:CE	1:D:485:ARG:NH2	2.77	0.40
1:D:225:LEU:HD23	1:D:397:THR:HB	2.03	0.40
1:D:384:SER:C	1:D:386:LYS:H	2.30	0.40
1:D:405:TYR:O	1:D:409:ASN:OD1	2.39	0.40
1:E:53:ASN:O	1:E:53:ASN:ND2	2.54	0.40
1:E:434:GLN:HE21	1:E:436:TYR:HE2	1.69	0.40
1:E:439:LEU:O	1:E:441:ASP:N	2.54	0.40
1:E:536:VAL:O	1:E:536:VAL:CG2	2.69	0.40
2:U:18:ASP:O	2:U:19:THR:HB	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	436/523 (83%)	321 (74%)	69 (16%)	46 (11%)	0	6
1	B	436/523 (83%)	320 (73%)	70 (16%)	46 (11%)	0	6
1	C	436/523 (83%)	321 (74%)	69 (16%)	46 (11%)	0	6
1	D	436/523 (83%)	321 (74%)	69 (16%)	46 (11%)	0	6
1	E	436/523 (83%)	321 (74%)	69 (16%)	46 (11%)	0	6
2	S	8/19 (42%)	5 (62%)	3 (38%)	0	100	100
2	T	8/19 (42%)	5 (62%)	3 (38%)	0	100	100
2	U	8/19 (42%)	5 (62%)	3 (38%)	0	100	100
2	V	8/19 (42%)	5 (62%)	3 (38%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	W	8/19 (42%)	5 (62%)	3 (38%)	0	100	100
All	All	2220/2710 (82%)	1629 (73%)	361 (16%)	230 (10%)	1	6

All (230) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	LEU
1	A	130	ASN
1	A	172	GLU
1	A	174	ASN
1	A	201	VAL
1	A	216	ARG
1	A	280	GLY
1	A	376	VAL
1	A	447	VAL
1	A	455	ILE
1	A	467	PRO
1	A	479	VAL
1	A	496	ARG
1	B	82	LEU
1	B	130	ASN
1	B	172	GLU
1	B	174	ASN
1	B	201	VAL
1	B	216	ARG
1	B	280	GLY
1	B	376	VAL
1	B	447	VAL
1	B	467	PRO
1	B	479	VAL
1	B	496	ARG
1	C	82	LEU
1	C	130	ASN
1	C	172	GLU
1	C	174	ASN
1	C	201	VAL
1	C	216	ARG
1	C	280	GLY
1	C	376	VAL
1	C	447	VAL
1	C	455	ILE
1	C	467	PRO

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Mol	Chain	Res	Type
1	C	479	VAL
1	C	496	ARG
1	D	82	LEU
1	D	130	ASN
1	D	172	GLU
1	D	174	ASN
1	D	201	VAL
1	D	216	ARG
1	D	280	GLY
1	D	376	VAL
1	D	447	VAL
1	D	455	ILE
1	D	467	PRO
1	D	479	VAL
1	D	496	ARG
1	E	82	LEU
1	E	130	ASN
1	E	172	GLU
1	E	174	ASN
1	E	201	VAL
1	E	216	ARG
1	E	280	GLY
1	E	376	VAL
1	E	447	VAL
1	E	455	ILE
1	E	467	PRO
1	E	479	VAL
1	E	496	ARG
1	A	58	SER
1	A	84	TYR
1	A	175	TYR
1	A	196	GLY
1	A	215	PHE
1	A	219	PHE
1	A	251	THR
1	A	279	GLU
1	A	377	ILE
1	A	385	LYS
1	A	386	LYS
1	A	426	PRO
1	A	440	PRO
1	A	503	LEU

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Mol	Chain	Res	Type
1	B	58	SER
1	B	84	TYR
1	B	175	TYR
1	B	196	GLY
1	B	215	PHE
1	B	219	PHE
1	B	251	THR
1	B	279	GLU
1	B	377	ILE
1	B	385	LYS
1	B	386	LYS
1	B	426	PRO
1	B	440	PRO
1	B	455	ILE
1	B	503	LEU
1	C	58	SER
1	C	84	TYR
1	C	175	TYR
1	C	196	GLY
1	C	215	PHE
1	C	219	PHE
1	C	251	THR
1	C	279	GLU
1	C	377	ILE
1	C	385	LYS
1	C	386	LYS
1	C	426	PRO
1	C	440	PRO
1	C	503	LEU
1	D	58	SER
1	D	84	TYR
1	D	175	TYR
1	D	196	GLY
1	D	215	PHE
1	D	219	PHE
1	D	251	THR
1	D	279	GLU
1	D	377	ILE
1	D	385	LYS
1	D	386	LYS
1	D	426	PRO
1	D	440	PRO

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Mol	Chain	Res	Type
1	D	503	LEU
1	E	58	SER
1	E	84	TYR
1	E	175	TYR
1	E	196	GLY
1	E	215	PHE
1	E	219	PHE
1	E	251	THR
1	E	279	GLU
1	E	377	ILE
1	E	385	LYS
1	E	386	LYS
1	E	426	PRO
1	E	440	PRO
1	E	503	LEU
1	A	75	LYS
1	A	81	SER
1	A	88	HIS
1	A	89	SER
1	A	101	TYR
1	A	114	ASP
1	A	176	SER
1	A	199	ASN
1	A	233	ASN
1	A	270	GLY
1	A	498	PRO
1	A	511	ILE
1	B	75	LYS
1	B	81	SER
1	B	88	HIS
1	B	89	SER
1	B	101	TYR
1	B	114	ASP
1	B	176	SER
1	B	199	ASN
1	B	233	ASN
1	B	270	GLY
1	B	498	PRO
1	B	511	ILE
1	C	75	LYS
1	C	81	SER
1	C	88	HIS

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Mol	Chain	Res	Type
1	C	89	SER
1	C	101	TYR
1	C	114	ASP
1	C	176	SER
1	C	199	ASN
1	C	233	ASN
1	C	270	GLY
1	C	498	PRO
1	C	511	ILE
1	D	75	LYS
1	D	81	SER
1	D	88	HIS
1	D	89	SER
1	D	101	TYR
1	D	114	ASP
1	D	176	SER
1	D	199	ASN
1	D	233	ASN
1	D	270	GLY
1	D	498	PRO
1	D	511	ILE
1	E	75	LYS
1	E	81	SER
1	E	88	HIS
1	E	89	SER
1	E	101	TYR
1	E	114	ASP
1	E	176	SER
1	E	199	ASN
1	E	233	ASN
1	E	270	GLY
1	E	498	PRO
1	E	511	ILE
1	A	55	ILE
1	A	67	THR
1	A	208	VAL
1	A	380	LEU
1	B	55	ILE
1	B	67	THR
1	B	208	VAL
1	B	380	LEU
1	C	55	ILE

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Mol	Chain	Res	Type
1	C	67	THR
1	C	208	VAL
1	C	380	LEU
1	D	55	ILE
1	D	67	THR
1	D	208	VAL
1	D	380	LEU
1	E	55	ILE
1	E	67	THR
1	E	208	VAL
1	E	380	LEU
1	A	390	ASN
1	B	390	ASN
1	C	390	ASN
1	D	390	ASN
1	E	390	ASN
1	D	416	GLY
1	A	379	PRO
1	A	416	GLY
1	B	379	PRO
1	B	416	GLY
1	C	379	PRO
1	C	416	GLY
1	D	379	PRO
1	E	379	PRO
1	E	416	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	399/451 (88%)	367 (92%)	32 (8%)	11	31
1	B	399/451 (88%)	366 (92%)	33 (8%)	10	30
1	C	399/451 (88%)	366 (92%)	33 (8%)	10	30
1	D	399/451 (88%)	367 (92%)	32 (8%)	11	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	399/451 (88%)	366 (92%)	33 (8%)	10	30
2	S	10/17 (59%)	10 (100%)	0	100	100
2	T	10/17 (59%)	10 (100%)	0	100	100
2	U	10/17 (59%)	10 (100%)	0	100	100
2	V	10/17 (59%)	10 (100%)	0	100	100
2	W	10/17 (59%)	10 (100%)	0	100	100
All	All	2045/2340 (87%)	1882 (92%)	163 (8%)	13	31

All (163) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	ARG
1	A	83	ASN
1	A	98	ASN
1	A	124	LYS
1	A	130	ASN
1	A	166	VAL
1	A	168	PHE
1	A	199	ASN
1	A	202	LEU
1	A	249	ASP
1	A	256	SER
1	A	276	ASP
1	A	279	GLU
1	A	399	THR
1	A	409	ASN
1	A	417	ILE
1	A	422	LEU
1	A	426	PRO
1	A	427	ASP
1	A	428	VAL
1	A	434	GLN
1	A	436	TYR
1	A	438	SER
1	A	448	THR
1	A	455	ILE
1	A	471	LYS
1	A	476	ASP
1	A	482	GLN
1	A	510	THR

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Mol	Chain	Res	Type
1	A	540	THR
1	A	543	ASP
1	A	560	SER
1	B	68	ARG
1	B	83	ASN
1	B	98	ASN
1	B	107	SER
1	B	124	LYS
1	B	130	ASN
1	B	166	VAL
1	B	168	PHE
1	B	199	ASN
1	B	202	LEU
1	B	249	ASP
1	B	256	SER
1	B	276	ASP
1	B	279	GLU
1	B	399	THR
1	B	409	ASN
1	B	417	ILE
1	B	422	LEU
1	B	426	PRO
1	B	427	ASP
1	B	428	VAL
1	B	434	GLN
1	B	436	TYR
1	B	438	SER
1	B	448	THR
1	B	455	ILE
1	B	471	LYS
1	B	476	ASP
1	B	482	GLN
1	B	510	THR
1	B	540	THR
1	B	543	ASP
1	B	560	SER
1	C	68	ARG
1	C	83	ASN
1	C	98	ASN
1	C	124	LYS
1	C	130	ASN
1	C	166	VAL

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Mol	Chain	Res	Type
1	C	168	PHE
1	C	199	ASN
1	C	202	LEU
1	C	249	ASP
1	C	256	SER
1	C	276	ASP
1	C	279	GLU
1	C	399	THR
1	C	409	ASN
1	C	417	ILE
1	C	422	LEU
1	C	426	PRO
1	C	427	ASP
1	C	428	VAL
1	C	434	GLN
1	C	436	TYR
1	C	438	SER
1	C	448	THR
1	C	455	ILE
1	C	471	LYS
1	C	476	ASP
1	C	482	GLN
1	C	510	THR
1	C	512	THR
1	C	540	THR
1	C	543	ASP
1	C	560	SER
1	D	68	ARG
1	D	83	ASN
1	D	98	ASN
1	D	124	LYS
1	D	130	ASN
1	D	166	VAL
1	D	168	PHE
1	D	199	ASN
1	D	202	LEU
1	D	249	ASP
1	D	256	SER
1	D	276	ASP
1	D	279	GLU
1	D	399	THR
1	D	409	ASN

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Mol	Chain	Res	Type
1	D	417	ILE
1	D	422	LEU
1	D	426	PRO
1	D	427	ASP
1	D	428	VAL
1	D	434	GLN
1	D	436	TYR
1	D	438	SER
1	D	448	THR
1	D	455	ILE
1	D	471	LYS
1	D	476	ASP
1	D	482	GLN
1	D	510	THR
1	D	540	THR
1	D	543	ASP
1	D	560	SER
1	E	68	ARG
1	E	83	ASN
1	E	98	ASN
1	E	107	SER
1	E	124	LYS
1	E	130	ASN
1	E	166	VAL
1	E	168	PHE
1	E	199	ASN
1	E	202	LEU
1	E	249	ASP
1	E	256	SER
1	E	276	ASP
1	E	279	GLU
1	E	399	THR
1	E	409	ASN
1	E	417	ILE
1	E	422	LEU
1	E	426	PRO
1	E	427	ASP
1	E	428	VAL
1	E	434	GLN
1	E	436	TYR
1	E	438	SER
1	E	448	THR

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Mol	Chain	Res	Type
1	E	455	ILE
1	E	471	LYS
1	E	476	ASP
1	E	482	GLN
1	E	510	THR
1	E	540	THR
1	E	543	ASP
1	E	560	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (89) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	86	ASN
1	A	98	ASN
1	A	109	GLN
1	A	130	ASN
1	A	174	ASN
1	A	198	GLN
1	A	199	ASN
1	A	214	ASN
1	A	237	HIS
1	A	268	GLN
1	A	400	GLN
1	A	434	GLN
1	A	457	ASN
1	A	469	HIS
1	A	495	ASN
1	A	501	GLN
1	A	524	HIS
1	B	53	ASN
1	B	86	ASN
1	B	98	ASN
1	B	109	GLN
1	B	130	ASN
1	B	174	ASN
1	B	198	GLN
1	B	199	ASN
1	B	214	ASN
1	B	237	HIS
1	B	268	GLN
1	B	400	GLN

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Mol	Chain	Res	Type
1	B	434	GLN
1	B	457	ASN
1	B	469	HIS
1	B	486	GLN
1	B	501	GLN
1	B	524	HIS
1	C	53	ASN
1	C	86	ASN
1	C	98	ASN
1	C	109	GLN
1	C	130	ASN
1	C	174	ASN
1	C	198	GLN
1	C	199	ASN
1	C	214	ASN
1	C	237	HIS
1	C	268	GLN
1	C	400	GLN
1	C	434	GLN
1	C	457	ASN
1	C	469	HIS
1	C	486	GLN
1	C	501	GLN
1	C	524	HIS
1	D	86	ASN
1	D	98	ASN
1	D	109	GLN
1	D	130	ASN
1	D	174	ASN
1	D	198	GLN
1	D	199	ASN
1	D	214	ASN
1	D	237	HIS
1	D	268	GLN
1	D	400	GLN
1	D	434	GLN
1	D	457	ASN
1	D	469	HIS
1	D	486	GLN
1	D	501	GLN
1	D	524	HIS
1	E	53	ASN

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Mol	Chain	Res	Type
1	E	86	ASN
1	E	98	ASN
1	E	109	GLN
1	E	130	ASN
1	E	174	ASN
1	E	198	GLN
1	E	199	ASN
1	E	214	ASN
1	E	237	HIS
1	E	268	GLN
1	E	400	GLN
1	E	434	GLN
1	E	457	ASN
1	E	469	HIS
1	E	486	GLN
1	E	501	GLN
1	E	524	HIS

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 ⓘ

There are no chain breaks in this entry.

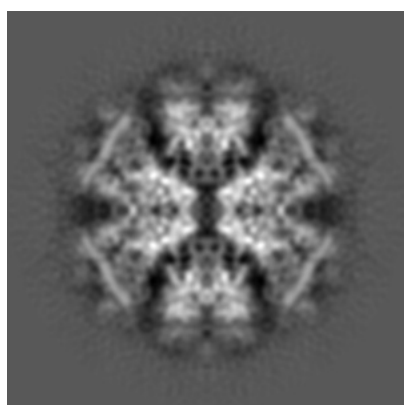
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1178. These allow visual inspection of the internal detail of the map and identification of artifacts.

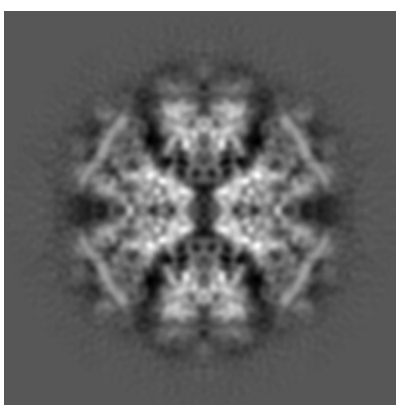
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

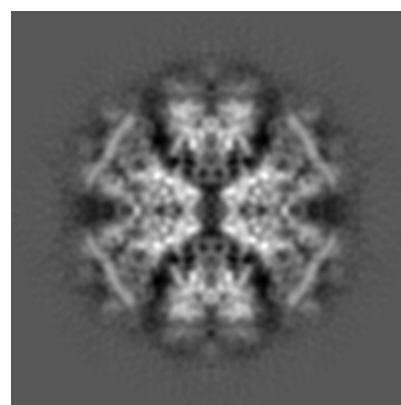
6.1.1 Primary map



X



Y

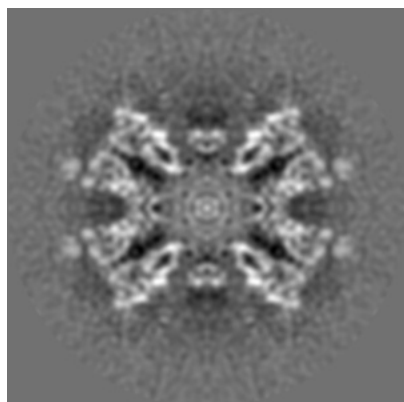


Z

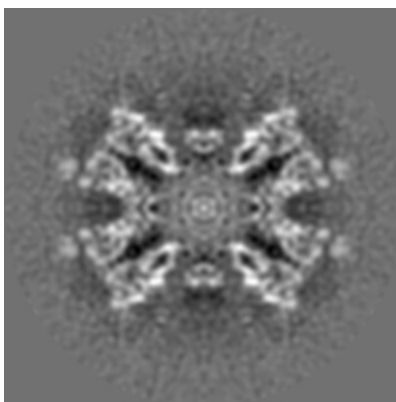
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

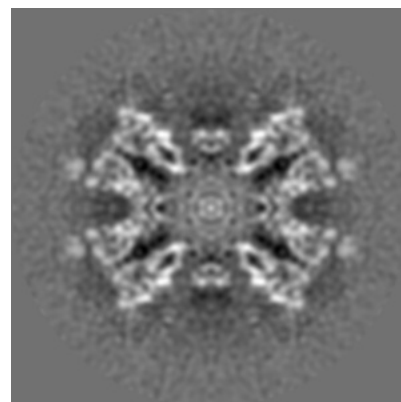
6.2.1 Primary map



X Index: 139



Y Index: 139

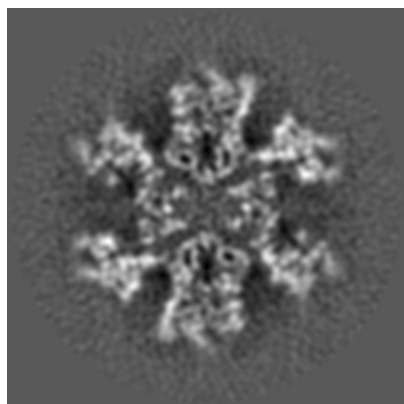


Z Index: 139

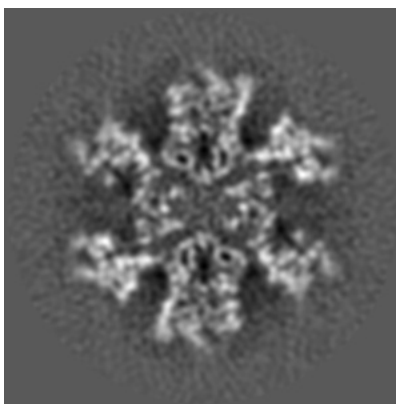
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

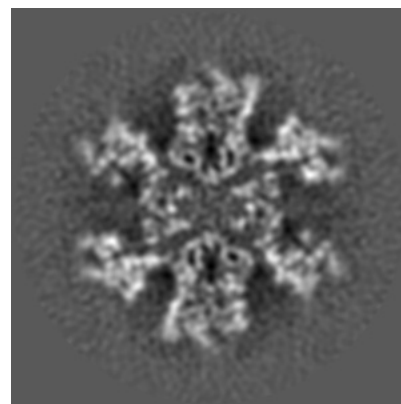
6.3.1 Primary map



X Index: 164



Y Index: 164

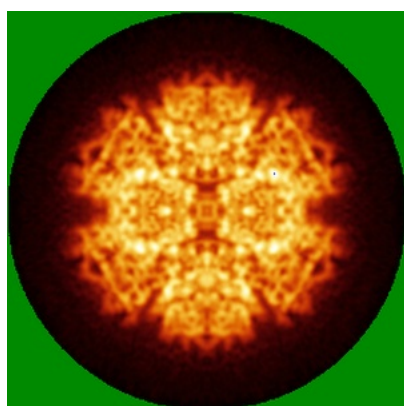


Z Index: 164

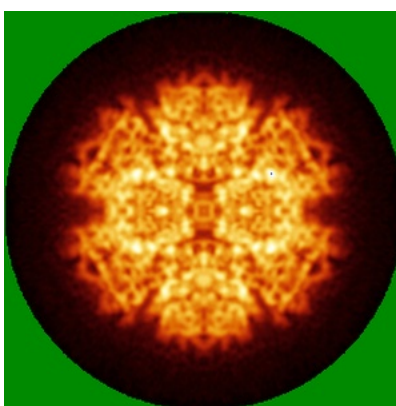
The images above show the largest variance slices of the map in three orthogonal directions.

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

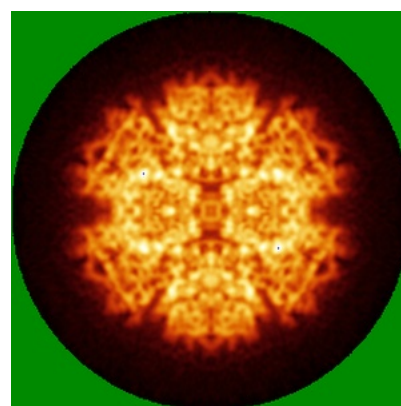
6.4.1 Primary map



X



Y

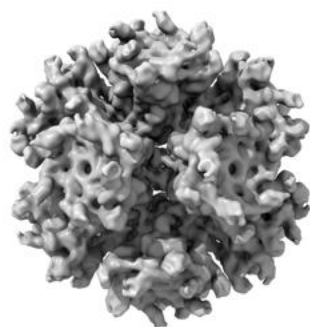


Z

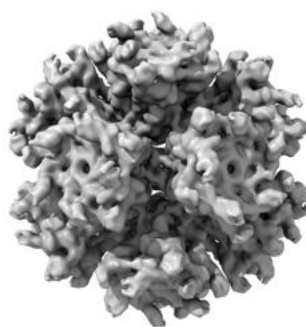
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

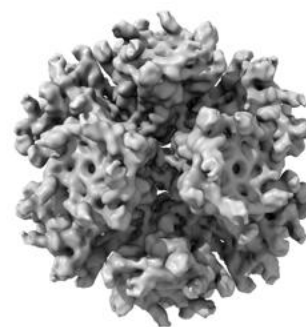
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 91.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

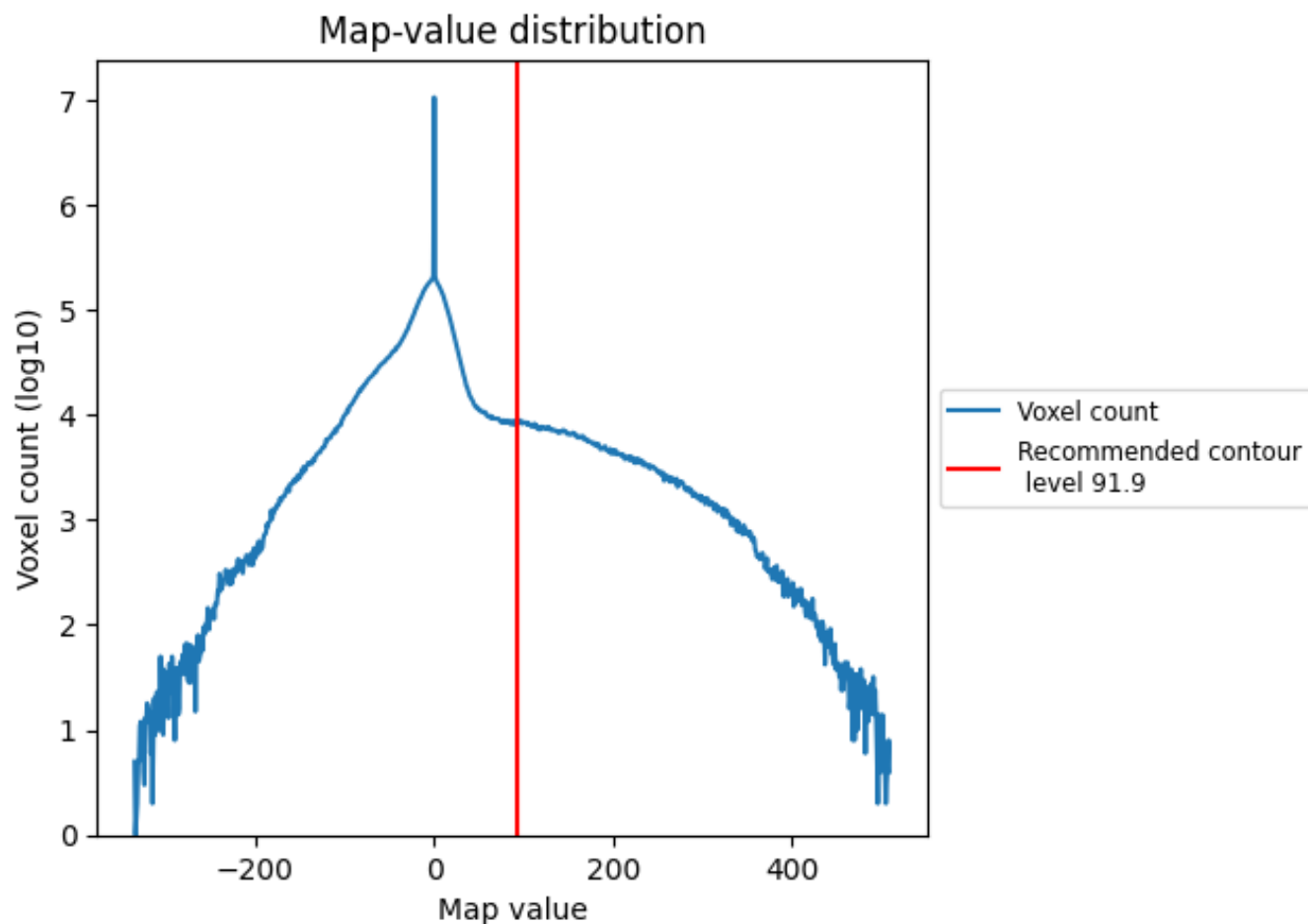
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

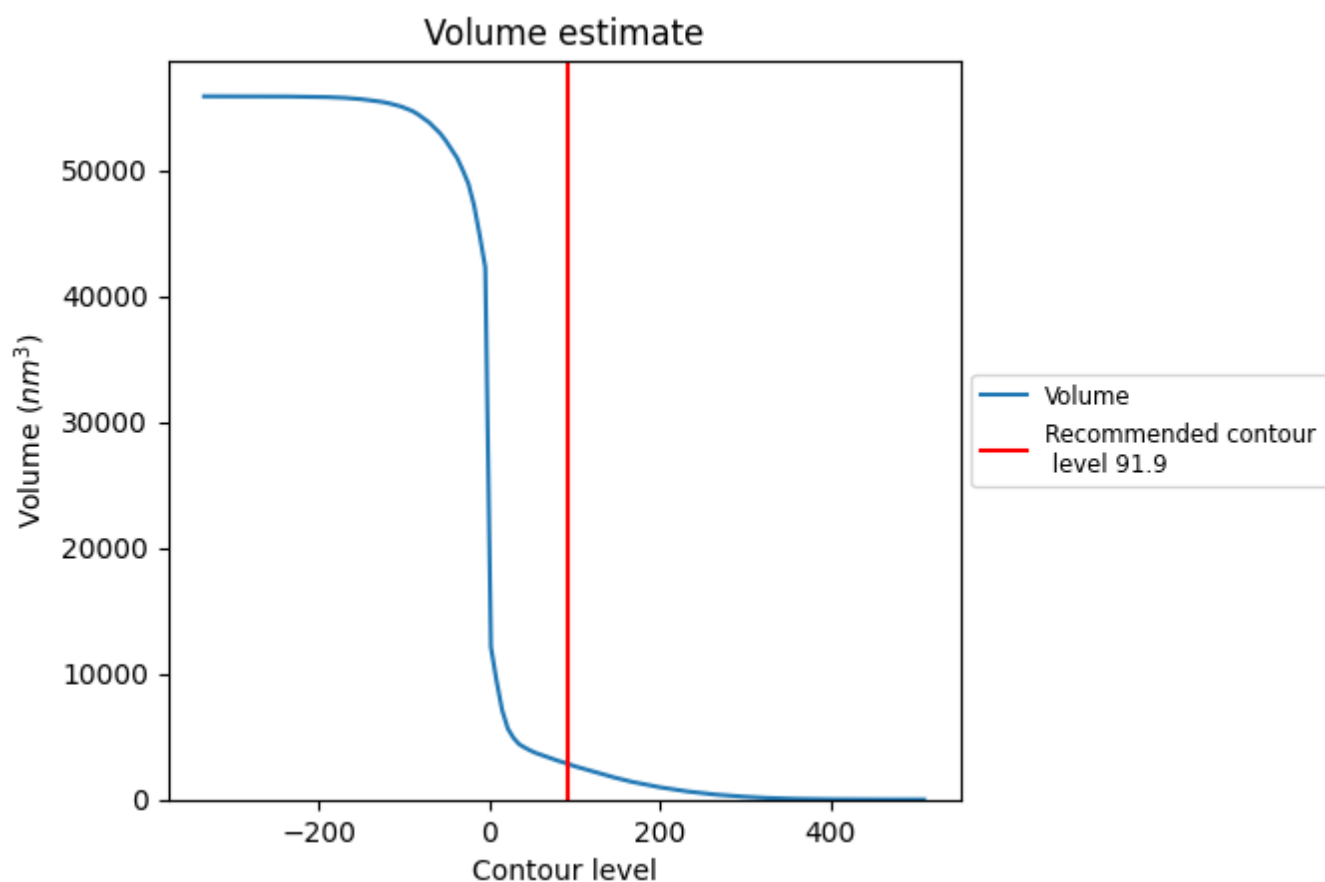
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

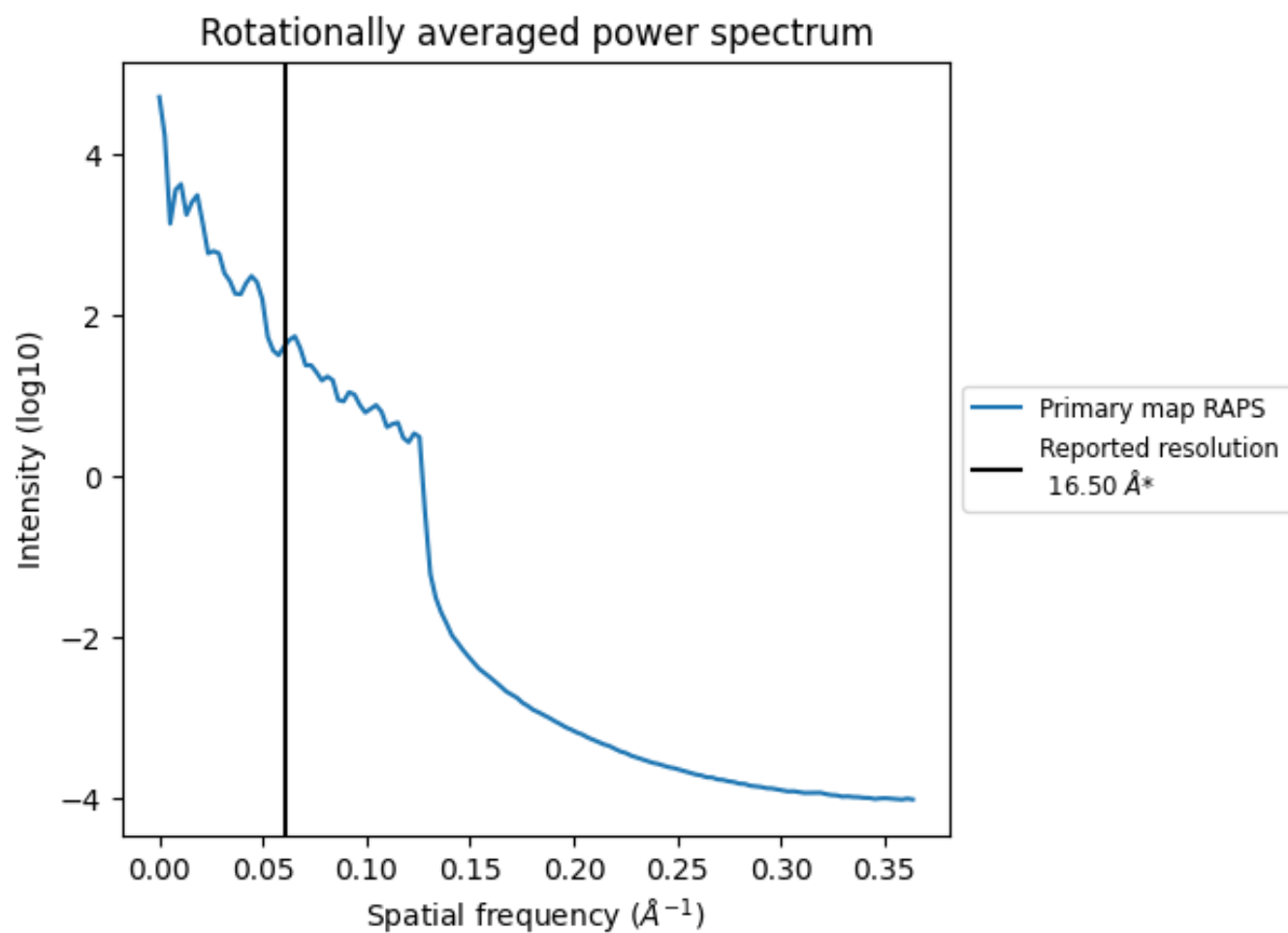
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2826 nm³; this corresponds to an approximate mass of 2552 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 0.061 Å⁻¹

8 Fourier-Shell correlation

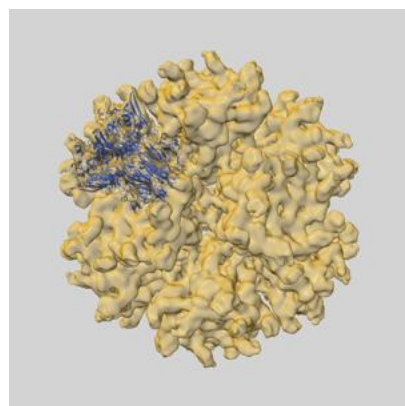
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

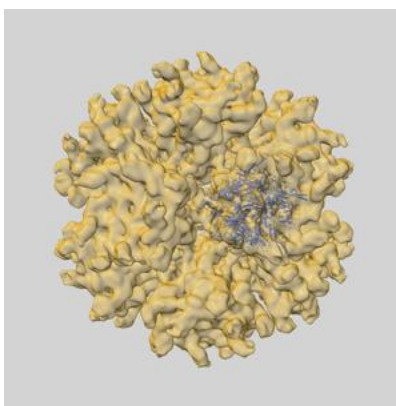
This section contains information regarding the fit between EMDB map EMD-1178 and PDB model 2C9F. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlays

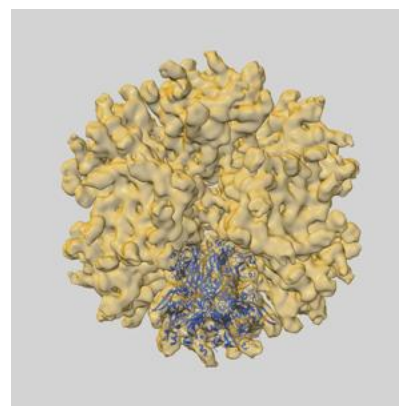
9.1.1 Map-model overlay [i](#)



X

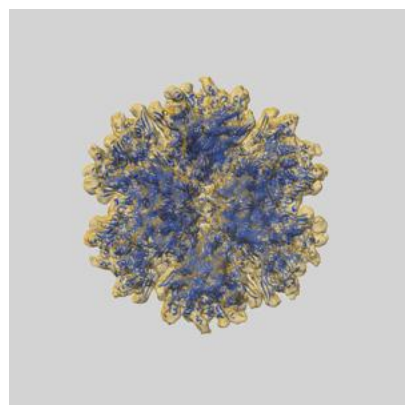


Y

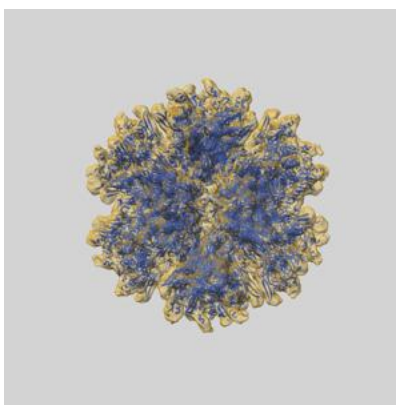


Z

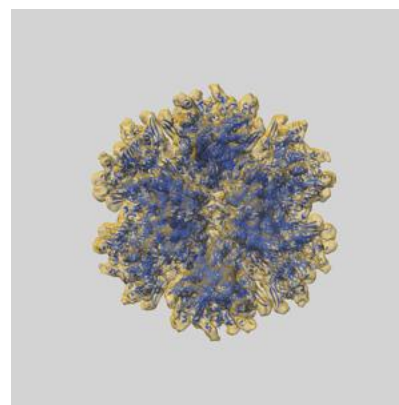
9.1.2 Map-model assembly overlay [i](#)



X



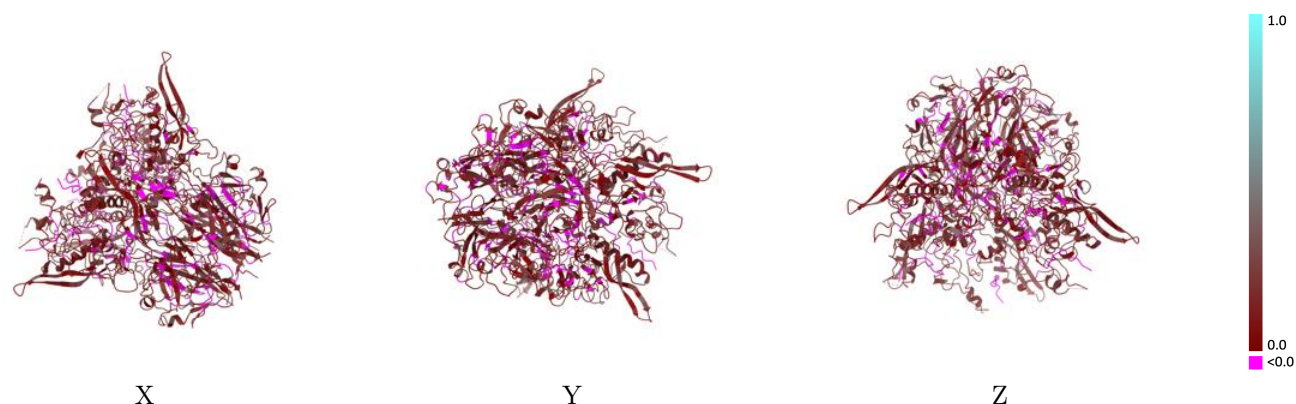
Y



Z

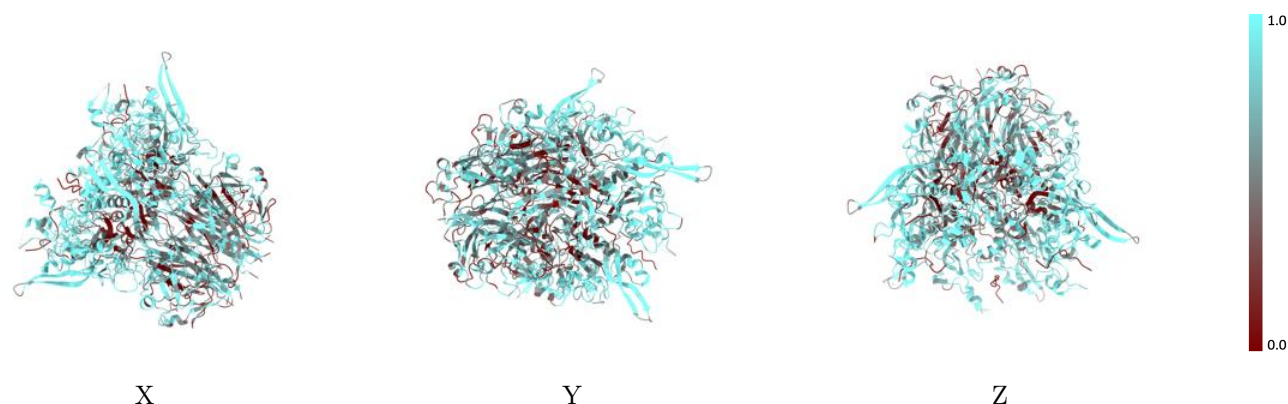
The images above show the 3D surface view of the map at the recommended contour level 91.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



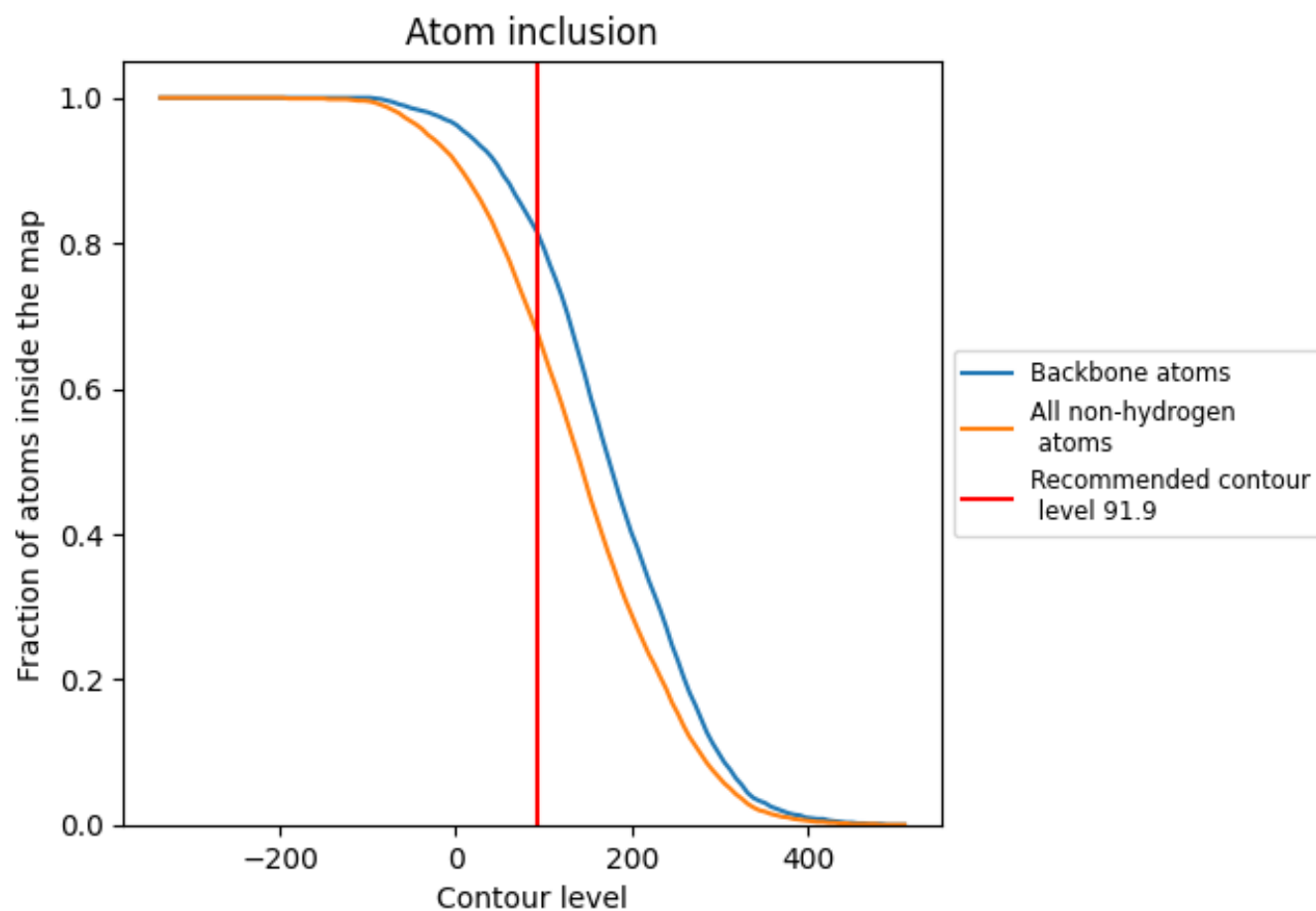
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (91.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 68% 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 (91.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6790	0.1090
A	0.6930	0.1140
B	0.6960	0.1170
C	0.6960	0.1160
D	0.6960	0.1170
E	0.6950	0.1140
S	0.0360	-0.1530
T	0.0240	-0.1540
U	0.0240	-0.1490
V	0.0240	-0.1550
W	0.0240	-0.1590

1.0

0.0

<0.0