



Full wwPDB/EMDataBank EM Map/Model Validation Report ⓘ

Dec 3, 2019 – 07:16 PM EST

PDB ID : 5M0Q
EMDB ID: : EMD-4138
Title : Cryo-EM reconstruction of the maedi-visna virus (MVV) intasome
Authors : Ballandras-Colas, A.; Maskell, D.; Pye, V.E.; Locke, J.; Swuec, S.; Kotecha, A.; Costa, A.; Cherepanov, P.
Deposited on : 2016-10-05
Resolution : 4.91 Å(reported)

This is a Full wwPDB/EMDataBank EM Map/Model Validation Report
for a publicly released PDB/EMDB 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.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

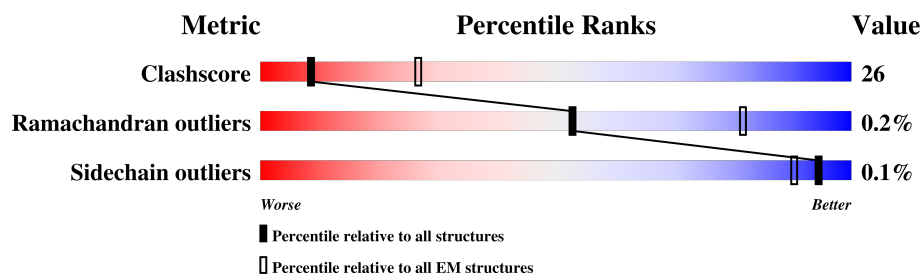
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.91 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	281	
1	B	281	
1	C	281	
1	D	281	
1	E	281	
1	F	281	
1	G	281	
1	H	281	
1	I	281	

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Mol	Chain	Length	Quality of chain
1	J	281	
1	K	281	
1	L	281	
1	M	281	
1	N	281	
1	O	281	
1	P	281	
2	Q	21	
2	S	21	
3	R	19	
3	T	19	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 33171 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 integrase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	275	Total	C	N	O	S	0	0
			2201	1400	385	407	9		
1	B	256	Total	C	N	O	S	0	0
			2075	1321	363	383	8		
1	C	261	Total	C	N	O	S	0	0
			2123	1353	371	391	8		
1	D	216	Total	C	N	O	S	0	0
			1729	1110	297	316	6		
1	E	257	Total	C	N	O	S	0	0
			2090	1333	365	384	8		
1	F	266	Total	C	N	O	S	0	0
			2148	1367	378	395	8		
1	G	205	Total	C	N	O	S	0	0
			1657	1051	284	314	8		
1	H	217	Total	C	N	O	S	0	0
			1761	1129	308	318	6		
1	I	275	Total	C	N	O	S	0	0
			2201	1400	385	407	9		
1	J	256	Total	C	N	O	S	0	0
			2075	1321	363	383	8		
1	K	261	Total	C	N	O	S	0	0
			2123	1353	371	391	8		
1	L	216	Total	C	N	O	S	0	0
			1729	1110	297	316	6		
1	M	256	Total	C	N	O	S	0	0
			2076	1322	363	383	8		
1	N	264	Total	C	N	O	S	0	0
			2131	1355	376	392	8		
1	O	205	Total	C	N	O	S	0	0
			1657	1051	284	314	8		
1	P	217	Total	C	N	O	S	0	0
			1761	1129	308	318	6		

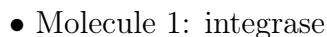
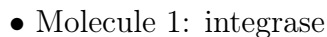
- Molecule 2 is a DNA chain called vDNA, non-transferred strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Q	21	Total 428	C 203	N 79	O 126	P 20	0	0
2	S	21	Total 428	C 203	N 79	O 126	P 20	0	0

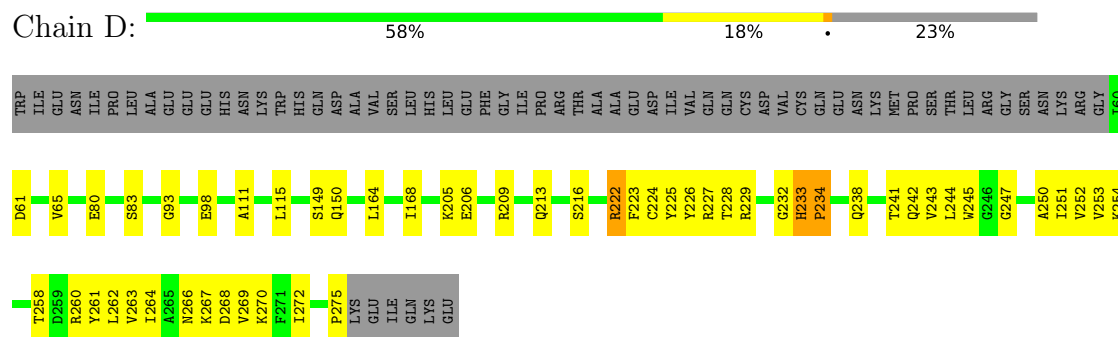
- Molecule 3 is a DNA chain called vDNA, transferred strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	R	19	Total 389	C 183	N 75	O 112	P 19	0	0
3	T	19	Total 389	C 183	N 75	O 112	P 19	0	0

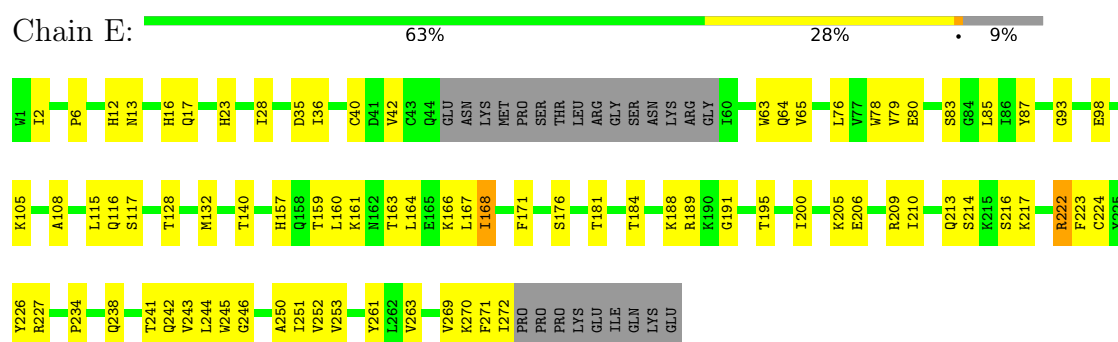
- Molecule 1: integrase



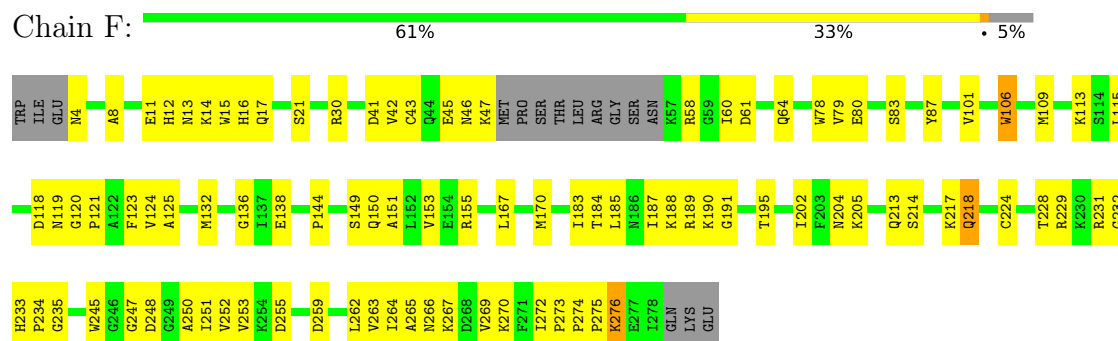
- Molecule 1: integrase



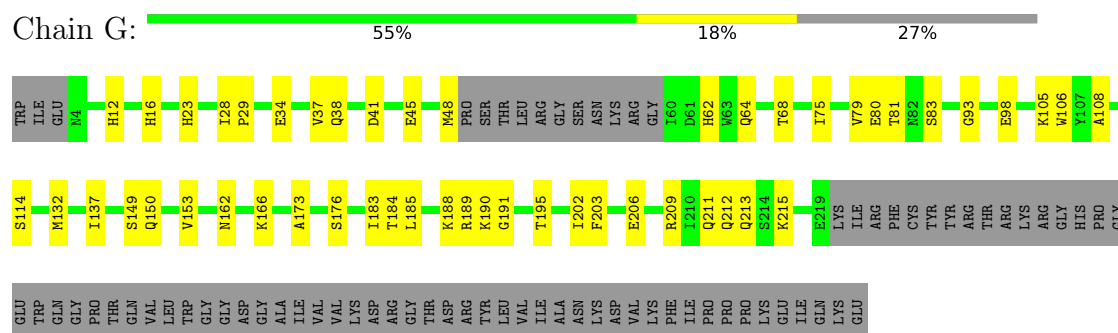
- Molecule 1: integrase

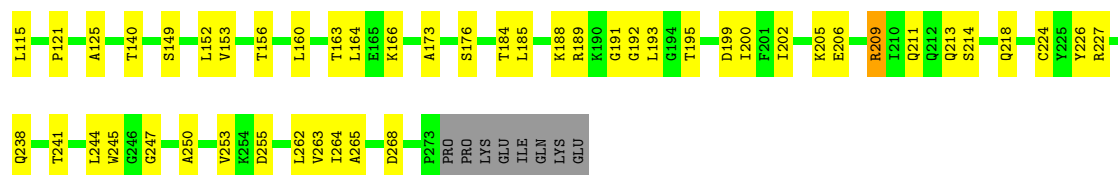


- Molecule 1: integrase



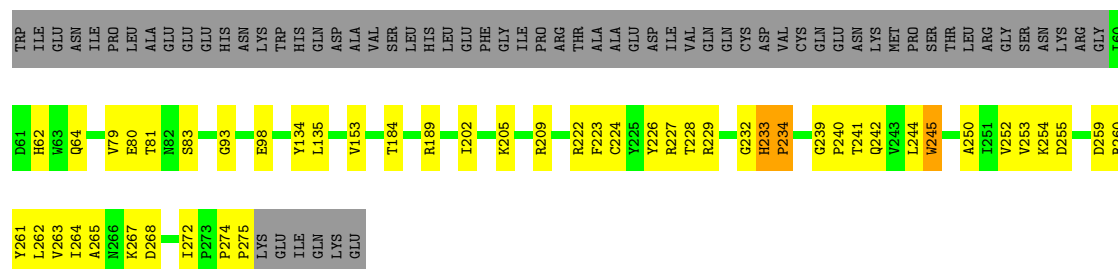
- Molecule 1: integrase





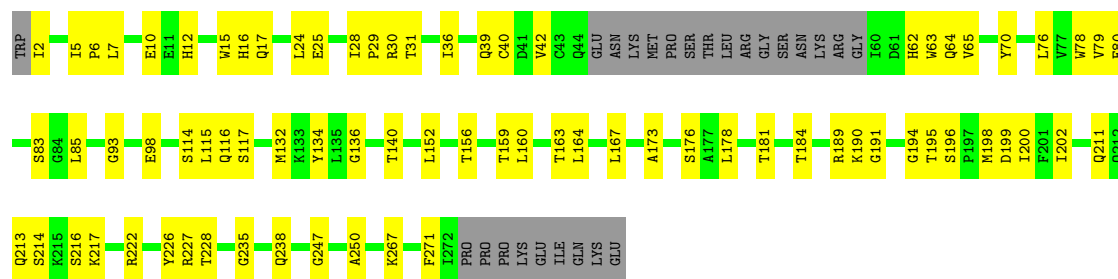
- Molecule 1: integrase

Chain L: 59% 16% 23%



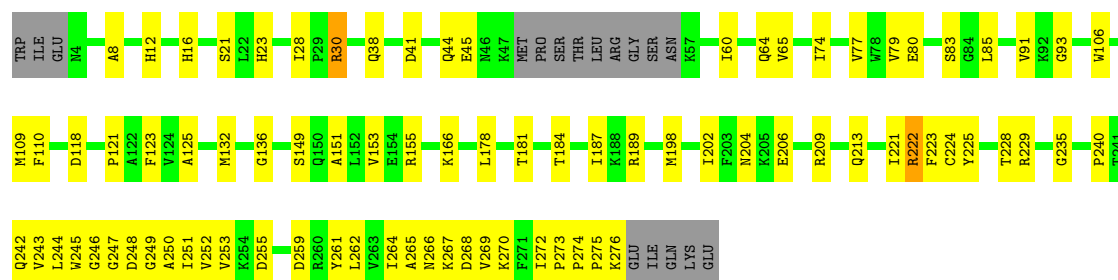
- Molecule 1: integrase

Chain M: 64% 27% 9%



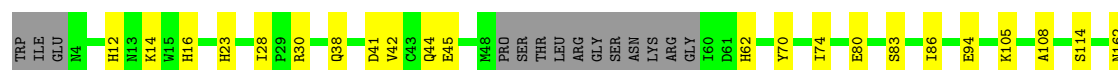
- Molecule 1: integrase

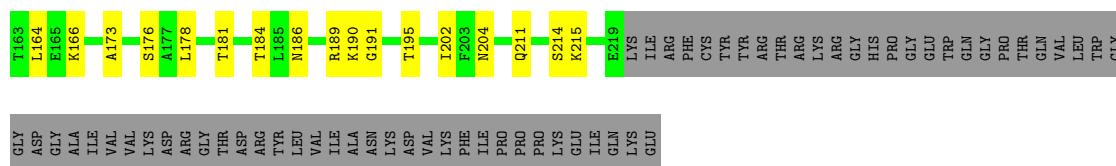
Chain N: 64% 29% 6%



- Molecule 1: integrase

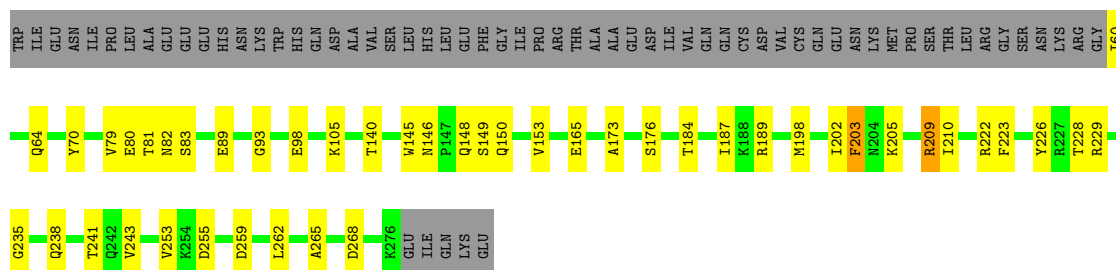
Chain O: 59% 14% 27%





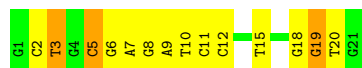
- Molecule 1: integrase

Chain P: 61% 16% 23%



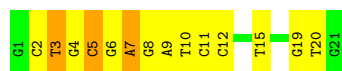
- Molecule 2: vDNA, non-transferred strand

Chain Q: 33% 52% 14%



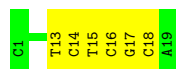
- Molecule 2: vDNA, non-transferred strand

Chain S: 33% 52% 14%



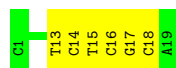
- Molecule 3: vDNA, transferred strand

Chain R: 68% 32%



- Molecule 3: vDNA, transferred strand

Chain T: 68% 32%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	94283	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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 > 2$	RMSZ	# $ Z > 2$
1	A	0.91	6/2254 (0.3%)	0.94	3/3053 (0.1%)
1	B	0.75	4/2124 (0.2%)	0.82	3/2874 (0.1%)
1	C	0.54	0/2174	0.70	0/2942
1	D	0.65	3/1772 (0.2%)	0.73	0/2401
1	E	0.69	2/2140 (0.1%)	0.76	0/2896
1	F	0.78	3/2199 (0.1%)	0.81	2/2975 (0.1%)
1	G	0.55	1/1693 (0.1%)	0.67	0/2290
1	H	0.59	0/1805	0.72	0/2441
1	I	0.89	5/2254 (0.2%)	0.93	2/3053 (0.1%)
1	J	0.73	3/2124 (0.1%)	0.84	2/2874 (0.1%)
1	K	0.58	2/2174 (0.1%)	0.69	1/2942 (0.0%)
1	L	0.62	1/1772 (0.1%)	0.68	0/2401
1	M	0.62	0/2124	0.73	0/2873
1	N	0.71	2/2182 (0.1%)	0.75	1/2953 (0.0%)
1	O	0.48	0/1693	0.62	0/2290
1	P	0.63	2/1805 (0.1%)	0.75	1/2441 (0.0%)
2	Q	2.08	14/479 (2.9%)	1.43	7/738 (0.9%)
2	S	2.08	13/479 (2.7%)	1.43	7/738 (0.9%)
3	R	2.08	11/436 (2.5%)	1.29	4/670 (0.6%)
3	T	2.08	10/436 (2.3%)	1.29	4/670 (0.6%)
All	All	0.83	82/34119 (0.2%)	0.82	37/46515 (0.1%)

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

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

All (82) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	T	15	DT	C5-C7	-9.45	1.44	1.50
3	R	15	DT	C5-C7	-9.30	1.44	1.50
3	T	13	DT	C5-C7	-7.36	1.45	1.50
1	B	78	TRP	CB-CG	-7.30	1.37	1.50
1	J	78	TRP	CB-CG	-7.28	1.37	1.50
1	N	222	ARG	CZ-NH2	7.28	1.42	1.33
1	K	209	ARG	CZ-NH2	7.24	1.42	1.33
1	E	222	ARG	CZ-NH2	7.23	1.42	1.33
1	P	209	ARG	CZ-NH2	7.22	1.42	1.33
1	B	222	ARG	CZ-NH2	7.20	1.42	1.33
1	F	231	ARG	CZ-NH2	7.19	1.42	1.33
1	D	222	ARG	CZ-NH2	7.18	1.42	1.33
3	R	13	DT	C5-C7	-7.18	1.45	1.50
1	A	209	ARG	CZ-NH2	7.18	1.42	1.33
1	J	222	ARG	CZ-NH2	7.17	1.42	1.33
1	I	209	ARG	CZ-NH2	7.16	1.42	1.33
1	I	209	ARG	CZ-NH1	7.00	1.42	1.33
1	E	222	ARG	CZ-NH1	7.00	1.42	1.33
1	N	222	ARG	CZ-NH1	6.99	1.42	1.33
1	K	209	ARG	CZ-NH1	6.98	1.42	1.33
1	B	222	ARG	CZ-NH1	6.96	1.42	1.33
1	P	209	ARG	CZ-NH1	6.96	1.42	1.33
1	J	222	ARG	CZ-NH1	6.93	1.42	1.33
1	A	209	ARG	CZ-NH1	6.93	1.42	1.33
1	D	222	ARG	CZ-NH1	6.92	1.42	1.33
1	F	231	ARG	CZ-NH1	6.90	1.42	1.33
3	R	15	DT	C4-C5	-6.39	1.39	1.45
2	S	10	DT	C5-C7	-6.36	1.46	1.50
2	S	3	DT	C5-C7	-6.34	1.46	1.50
3	T	15	DT	C4-C5	-6.32	1.39	1.45
2	Q	3	DT	C5-C7	-6.25	1.46	1.50
2	Q	10	DT	C5-C7	-6.24	1.46	1.50
3	T	13	DT	C3'-O3'	-6.19	1.35	1.44
1	A	78	TRP	CB-CG	-6.17	1.39	1.50
3	R	13	DT	C3'-O3'	-6.16	1.35	1.44
1	A	203	PHE	CB-CG	-6.14	1.41	1.51
1	I	78	TRP	CB-CG	-6.13	1.39	1.50
1	I	106	TRP	CB-CG	-6.04	1.39	1.50
1	A	106	TRP	CB-CG	-6.02	1.39	1.50
3	R	14	DC	N3-C4	-5.99	1.29	1.33
3	T	16	DC	C4-C5	-5.96	1.38	1.43
3	R	16	DC	C4-C5	-5.96	1.38	1.43
3	T	14	DC	N3-C4	-5.94	1.29	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Q	9	DA	C2'-C1'	-5.92	1.46	1.52
2	S	9	DA	C2'-C1'	-5.91	1.46	1.52
2	Q	8	DG	C3'-O3'	-5.89	1.36	1.44
2	S	8	DG	C3'-O3'	-5.87	1.36	1.44
1	B	63	TRP	CB-CG	-5.77	1.39	1.50
3	R	16	DC	C5-C6	-5.71	1.29	1.34
2	Q	9	DA	N9-C4	-5.71	1.34	1.37
1	D	245	TRP	CB-CG	-5.70	1.40	1.50
2	S	9	DA	N9-C4	-5.70	1.34	1.37
3	T	16	DC	N1-C6	-5.63	1.33	1.37
3	R	16	DC	N1-C6	-5.61	1.33	1.37
3	T	16	DC	C5-C6	-5.60	1.29	1.34
2	S	9	DA	N9-C8	-5.53	1.33	1.37
2	S	11	DC	C4-C5	-5.53	1.38	1.43
1	L	245	TRP	CB-CG	-5.52	1.40	1.50
2	Q	12	DC	C3'-O3'	-5.52	1.36	1.44
2	Q	11	DC	C4-C5	-5.49	1.38	1.43
2	Q	9	DA	N9-C8	-5.47	1.33	1.37
2	S	12	DC	C3'-O3'	-5.43	1.36	1.44
2	S	12	DC	N1-C6	-5.41	1.33	1.37
3	R	18	DC	N3-C4	-5.34	1.30	1.33
2	S	11	DC	N1-C6	-5.34	1.33	1.37
2	Q	12	DC	N1-C6	-5.31	1.33	1.37
2	S	5	DC	N1-C6	-5.30	1.33	1.37
3	T	15	DT	N3-C4	-5.29	1.34	1.38
2	S	10	DT	N1-C6	-5.26	1.34	1.38
3	T	18	DC	N3-C4	-5.26	1.30	1.33
3	R	15	DT	N3-C4	-5.26	1.34	1.38
2	Q	11	DC	N1-C6	-5.25	1.34	1.37
1	G	106	TRP	CB-CG	-5.24	1.40	1.50
2	Q	5	DC	N1-C6	-5.21	1.34	1.37
1	I	15	TRP	CB-CG	-5.18	1.41	1.50
1	A	15	TRP	CB-CG	-5.17	1.41	1.50
2	Q	10	DT	N1-C6	-5.17	1.34	1.38
2	Q	9	DA	C6-N6	-5.15	1.29	1.33
1	F	106	TRP	CB-CG	-5.12	1.41	1.50
2	S	9	DA	C6-N6	-5.09	1.29	1.33
3	R	15	DT	C5-C6	-5.04	1.30	1.34
2	Q	10	DT	C4-C5	-5.02	1.40	1.45

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	203	PHE	N-CA-CB	-7.01	97.98	110.60
3	T	15	DT	N3-C4-O4	6.96	124.08	119.90
2	Q	7	DA	O4'-C4'-C3'	-6.93	101.73	104.50
3	R	15	DT	N3-C4-O4	6.92	124.06	119.90
2	S	7	DA	O4'-C4'-C3'	-6.81	101.78	104.50
1	B	209	ARG	NE-CZ-NH1	6.65	123.63	120.30
2	S	19	DG	O4'-C1'-N9	-6.18	103.67	108.00
2	Q	19	DG	O4'-C1'-N9	-6.14	103.70	108.00
1	A	118	ASP	CB-CG-OD1	6.13	123.81	118.30
1	A	60	ILE	N-CA-C	-6.10	94.52	111.00
1	A	231	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	K	7	LEU	CA-CB-CG	6.05	129.21	115.30
1	I	231	ARG	NE-CZ-NH2	-6.03	117.28	120.30
3	T	15	DT	C5-C4-O4	-6.03	120.68	124.90
3	R	15	DT	C5-C4-O4	-5.98	120.72	124.90
2	Q	5	DC	O4'-C1'-N1	-5.96	103.83	108.00
2	S	10	DT	N3-C4-O4	5.93	123.46	119.90
2	S	5	DC	O4'-C1'-N1	-5.89	103.88	108.00
2	Q	10	DT	N3-C4-O4	5.81	123.39	119.90
3	R	17	DG	O4'-C1'-N9	5.63	111.94	108.00
3	T	17	DG	O4'-C1'-N9	5.63	111.94	108.00
1	B	178	LEU	CA-CB-CG	5.61	128.19	115.30
1	F	276	LYS	CB-CA-C	5.58	121.56	110.40
1	N	30	ARG	NE-CZ-NH2	-5.58	117.51	120.30
2	Q	3	DT	OP1-P-O3'	5.49	117.28	105.20
2	S	3	DT	OP1-P-O3'	5.48	117.26	105.20
1	J	104	MET	CA-CB-CG	5.42	122.51	113.30
1	F	218	GLN	N-CA-C	5.37	125.51	111.00
3	R	13	DT	N3-C4-O4	5.32	123.09	119.90
3	T	13	DT	N3-C4-O4	5.26	123.06	119.90
1	B	189	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	I	243	VAL	N-CA-C	-5.17	97.04	111.00
1	J	178	LEU	CA-CB-CG	5.14	127.13	115.30
2	Q	15	DT	N3-C4-O4	5.12	122.97	119.90
2	S	15	DT	N3-C4-O4	5.10	122.96	119.90
2	S	20	DT	C4'-C3'-C2'	-5.09	98.52	103.10
2	Q	20	DT	C4'-C3'-C2'	-5.05	98.55	103.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	62	HIS	Peptide

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Mol	Chain	Res	Type	Group
1	L	239	GLY	Peptide

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	2201	0	2164	346	0
1	B	2075	0	2046	73	0
1	C	2123	0	2095	40	0
1	D	1729	0	1708	114	0
1	E	2090	0	2063	124	0
1	F	2148	0	2119	137	0
1	G	1657	0	1626	53	0
1	H	1761	0	1764	106	0
1	I	2201	0	2165	334	0
1	J	2075	0	2046	153	0
1	K	2123	0	2095	57	0
1	L	1729	0	1708	87	0
1	M	2076	0	2050	86	0
1	N	2131	0	2099	105	0
1	O	1657	0	1626	28	0
1	P	1761	0	1764	63	0
2	Q	428	0	237	14	0
2	S	428	0	237	44	0
3	R	389	0	212	0	0
3	T	389	0	212	0	0
All	All	33171	0	32036	1669	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 26.

All (1669) 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:L:227:ARG:CD	1:L:234:PRO:HB2	1.25	1.58
1:L:227:ARG:CD	1:L:234:PRO:CB	1.91	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:227:ARG:CD	1:D:234:PRO:HB2	1.45	1.45
1:E:223:PHE:CZ	1:E:272:ILE:CG2	1.99	1.45
1:L:227:ARG:HD3	1:L:234:PRO:CB	1.46	1.45
1:L:223:PHE:CB	1:L:241:THR:O	1.70	1.37
1:A:12:HIS:CE1	1:A:43:CYS:SG	2.19	1.35
1:E:223:PHE:CZ	1:E:272:ILE:HG21	1.55	1.34
1:F:248:ASP:HB2	2:S:3:DT:N3	1.41	1.33
1:A:52:LEU:HD13	1:D:232:GLY:O	1.28	1.33
1:A:240:PRO:HG3	1:H:223:PHE:CZ	1.64	1.31
1:A:51:THR:OG1	1:F:266:ASN:ND2	1.58	1.30
1:I:77:VAL:HG12	1:I:79:VAL:CG2	1.61	1.30
1:A:148:GLN:HB3	2:S:4:DG:O5'	1.30	1.30
1:E:223:PHE:CE2	1:E:272:ILE:HG21	1.65	1.29
1:L:223:PHE:HB2	1:L:241:THR:O	1.14	1.28
1:A:77:VAL:HG12	1:A:79:VAL:CG2	1.63	1.28
1:B:9:GLU:OE1	1:B:261:TYR:CG	1.88	1.26
1:A:2:ILE:O	1:A:5:ILE:HG13	1.13	1.25
1:E:223:PHE:CE2	1:E:272:ILE:CB	2.20	1.24
1:E:223:PHE:CE2	1:E:272:ILE:CG2	2.18	1.24
1:E:160:LEU:CD1	1:E:181:THR:HG21	1.68	1.23
1:E:191:GLY:O	1:E:195:THR:HG22	1.34	1.23
1:B:9:GLU:OE1	1:B:261:TYR:CD2	1.90	1.23
1:J:9:GLU:OE1	1:J:36:ILE:HD13	1.10	1.22
1:A:3:GLU:O	1:A:6:PRO:HD2	1.41	1.21
1:A:64:GLN:O	1:A:79:VAL:HB	1.39	1.20
1:F:187:ILE:O	1:F:190:LYS:NZ	1.74	1.20
1:N:221:ILE:O	1:N:274:PRO:CG	1.88	1.19
1:N:221:ILE:O	1:N:274:PRO:HG3	1.37	1.18
1:I:240:PRO:HG3	1:P:223:PHE:CZ	1.77	1.18
1:I:2:ILE:CG2	1:I:5:ILE:HD12	1.75	1.17
1:A:223:PHE:HA	1:A:242:GLN:HA	1.19	1.17
1:M:217:LYS:NZ	1:P:209:ARG:HD2	1.60	1.17
1:I:62:HIS:ND1	1:I:81:THR:HG21	1.60	1.17
1:A:77:VAL:HG21	1:A:157:HIS:CE1	1.79	1.17
1:L:244:LEU:HD12	1:L:252:VAL:O	1.46	1.16
1:A:148:GLN:OE1	2:S:4:DG:O4'	1.65	1.15
1:A:223:PHE:CE1	1:A:242:GLN:HB3	1.81	1.15
1:E:223:PHE:CE2	1:E:272:ILE:CD1	2.29	1.15
1:A:37:VAL:HG13	1:A:43:CYS:HB2	1.18	1.15
1:J:9:GLU:OE1	1:J:36:ILE:CD1	1.95	1.15
1:A:116:GLN:HG2	1:A:140:THR:OG1	1.42	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:223:PHE:CE2	1:E:272:ILE:HB	1.83	1.14
1:L:227:ARG:HD2	1:L:234:PRO:CB	1.62	1.14
1:I:108:ALA:CA	1:J:183:ILE:HD11	1.77	1.13
1:I:108:ALA:HA	1:J:183:ILE:CD1	1.78	1.13
1:A:12:HIS:NE2	1:A:43:CYS:SG	2.19	1.13
1:A:207:GLN:HB3	1:D:222:ARG:NH2	1.61	1.13
1:J:16:HIS:CE1	1:J:42:VAL:HG21	1.83	1.13
1:A:223:PHE:CD1	1:A:242:GLN:HB3	1.84	1.12
1:E:223:PHE:HE2	1:E:272:ILE:HD13	1.11	1.12
1:A:2:ILE:O	1:A:5:ILE:CG1	1.96	1.12
1:E:160:LEU:HD11	1:E:181:THR:HG21	1.31	1.12
1:A:46:ASN:HB2	1:I:166:LYS:HE2	1.31	1.12
1:F:248:ASP:CB	2:S:3:DT:H3	1.62	1.12
1:K:227:ARG:HH12	1:P:140:THR:HG23	1.07	1.12
1:A:77:VAL:HG12	1:A:79:VAL:HG23	1.25	1.12
1:M:17:GLN:NE2	1:M:184:THR:HG22	1.65	1.12
1:I:2:ILE:HG23	1:I:5:ILE:HD12	1.20	1.11
1:A:207:GLN:OE1	1:D:222:ARG:NH1	1.84	1.11
1:F:15:TRP:HB3	1:F:17:GLN:HE22	1.09	1.11
1:A:148:GLN:HB3	2:S:4:DG:C5'	1.78	1.11
1:M:15:TRP:HB3	1:M:17:GLN:HE22	0.98	1.11
1:I:63:TRP:O	1:I:115:LEU:HD12	1.50	1.10
1:B:222:ARG:NH1	1:B:273:PRO:HA	1.65	1.10
1:N:224:CYS:HA	1:N:272:ILE:HG13	1.27	1.10
1:I:2:ILE:HG23	1:I:5:ILE:CD1	1.82	1.10
1:E:223:PHE:HE2	1:E:272:ILE:CD1	1.63	1.09
1:I:57:LYS:O	1:I:81:THR:OG1	1.71	1.09
1:J:33:ALA:O	1:J:36:ILE:HG22	1.51	1.08
1:M:271:PHE:CD2	1:P:82:ASN:ND2	2.19	1.08
1:A:184:THR:CG2	1:A:188:LYS:HG3	1.84	1.08
1:I:77:VAL:HG11	1:I:153:VAL:HG23	1.27	1.07
1:I:184:THR:HB	1:I:188:LYS:HE2	1.10	1.07
1:I:63:TRP:CD2	1:I:106:TRP:HH2	1.72	1.07
1:J:183:ILE:HG23	1:J:187:ILE:CD1	1.84	1.07
1:L:227:ARG:HD2	1:L:234:PRO:HB3	1.27	1.07
1:L:252:VAL:HB	1:L:262:LEU:O	1.55	1.06
1:A:77:VAL:HG11	1:A:153:VAL:HG23	1.27	1.06
1:E:251:ILE:HG12	1:E:269:VAL:HG21	1.35	1.06
1:A:211:GLN:O	1:A:215:LYS:HG2	1.54	1.06
1:F:60:ILE:HG21	1:F:204:ASN:HB3	1.35	1.06
1:F:15:TRP:CB	1:F:17:GLN:HE22	1.68	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:38:GLN:O	1:N:273:PRO:HG3	1.54	1.06
1:D:227:ARG:HD2	1:D:234:PRO:HB2	1.33	1.06
1:A:184:THR:HG22	1:A:188:LYS:CG	1.86	1.06
1:I:77:VAL:HG12	1:I:79:VAL:HG23	1.33	1.06
1:I:143:ILE:CG2	1:I:144:PRO:HD2	1.86	1.05
1:D:233:HIS:CB	1:D:234:PRO:HD2	1.86	1.05
1:L:233:HIS:CB	1:L:234:PRO:HD2	1.86	1.05
1:E:223:PHE:CZ	1:E:272:ILE:HG22	1.88	1.05
1:A:148:GLN:CB	2:S:4:DG:O5'	2.04	1.05
1:E:223:PHE:CD2	1:E:272:ILE:HD12	1.90	1.05
1:L:252:VAL:CB	1:L:262:LEU:O	2.05	1.05
1:D:227:ARG:CD	1:D:234:PRO:CB	2.35	1.04
1:F:15:TRP:HB3	1:F:17:GLN:NE2	1.72	1.04
1:J:15:TRP:CZ2	1:L:134:TYR:CE2	2.44	1.04
1:I:78:TRP:HB3	1:I:106:TRP:CZ2	1.90	1.04
1:A:77:VAL:CG1	1:A:79:VAL:CG2	2.35	1.04
1:D:233:HIS:CB	1:D:234:PRO:CD	2.34	1.04
1:L:233:HIS:CB	1:L:234:PRO:CD	2.34	1.04
1:A:178:LEU:O	1:A:182:LEU:HG	1.57	1.03
1:I:39:GLN:NE2	1:N:276:LYS:O	1.91	1.03
1:A:3:GLU:O	1:A:6:PRO:CD	2.06	1.03
1:I:77:VAL:CG1	1:I:79:VAL:CG2	2.36	1.03
1:L:252:VAL:CG1	1:L:262:LEU:O	2.07	1.03
1:C:20:VAL:O	1:C:24:LEU:HG	1.59	1.02
1:D:227:ARG:HD3	1:D:234:PRO:HB2	1.03	1.02
1:O:202:ILE:HG23	1:P:202:ILE:HG23	1.38	1.02
1:E:223:PHE:CE2	1:E:272:ILE:HD13	1.93	1.02
1:I:211:GLN:O	1:I:215:LYS:HG2	1.59	1.02
1:E:167:LEU:HB3	1:E:171:PHE:HE2	1.22	1.02
1:I:77:VAL:CG1	1:I:153:VAL:HG23	1.89	1.02
1:J:183:ILE:HG23	1:J:187:ILE:HD12	1.05	1.02
1:D:227:ARG:HD3	1:D:234:PRO:CB	1.90	1.01
1:B:222:ARG:HH12	1:B:273:PRO:HA	1.12	1.01
1:A:77:VAL:CG1	1:A:153:VAL:HG23	1.89	1.01
1:I:64:GLN:HG3	1:I:81:THR:HG22	1.43	1.01
1:I:184:THR:O	1:I:188:LYS:HB3	1.61	1.00
1:A:244:LEU:HD13	1:A:253:VAL:HA	1.44	1.00
1:A:148:GLN:HB2	2:S:4:DG:P	2.01	1.00
1:I:143:ILE:HG22	1:I:144:PRO:HD2	1.39	1.00
1:A:126:GLU:O	1:A:130:LEU:HG	1.62	0.99
1:A:52:LEU:HD22	1:D:233:HIS:CB	1.92	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:251:ILE:CG2	1:F:264:ILE:HB	1.92	0.99
1:A:207:GLN:HG3	1:D:222:ARG:CZ	1.93	0.98
1:F:248:ASP:O	2:S:2:DC:O2	1.81	0.98
1:E:222:ARG:HD2	1:H:203:PHE:HE1	1.24	0.98
1:A:184:THR:HG22	1:A:188:LYS:HG3	1.01	0.98
1:A:203:PHE:HZ	1:D:222:ARG:HD3	1.22	0.98
1:A:207:GLN:CD	1:D:222:ARG:NH1	2.16	0.98
1:A:221:ILE:HG21	1:A:242:GLN:OE1	1.62	0.98
1:L:223:PHE:HB3	1:L:241:THR:O	1.62	0.98
1:A:144:PRO:HB2	1:A:145:TRP:CE3	2.00	0.97
1:I:63:TRP:CD2	1:I:106:TRP:CH2	2.51	0.97
1:A:65:VAL:HB	1:A:77:VAL:O	1.63	0.97
1:I:118:ASP:OD1	1:I:123:PHE:CE2	2.18	0.97
1:J:14:LYS:HE2	1:J:15:TRP:HE1	1.30	0.96
1:A:184:THR:O	1:A:188:LYS:HB2	1.61	0.96
1:A:52:LEU:CD1	1:D:232:GLY:O	2.13	0.96
1:B:9:GLU:OE1	1:B:261:TYR:CB	2.14	0.96
1:I:184:THR:CB	1:I:188:LYS:HE2	1.96	0.96
1:A:203:PHE:CZ	1:D:222:ARG:HD3	2.00	0.96
1:J:183:ILE:CG2	1:J:187:ILE:HD12	1.95	0.96
1:A:203:PHE:HZ	1:D:222:ARG:CD	1.79	0.95
1:N:60:ILE:HG21	1:N:204:ASN:HB3	1.43	0.95
1:A:203:PHE:CZ	1:D:222:ARG:CD	2.49	0.95
1:L:227:ARG:CD	1:L:234:PRO:HB3	1.85	0.95
1:A:184:THR:HA	1:A:188:LYS:HG2	1.48	0.95
1:D:226:TYR:O	1:D:238:GLN:HB2	1.66	0.95
1:A:223:PHE:CA	1:A:242:GLN:HA	1.97	0.95
1:L:252:VAL:HG12	1:L:262:LEU:O	1.67	0.95
1:D:251:ILE:HG23	1:D:266:ASN:OD1	1.65	0.95
1:A:223:PHE:CD1	1:A:242:GLN:CB	2.50	0.94
1:M:217:LYS:HZ1	1:P:209:ARG:HD2	1.18	0.94
1:E:222:ARG:O	1:E:243:VAL:HG23	1.68	0.94
1:E:222:ARG:CD	1:H:203:PHE:HE1	1.81	0.94
1:I:107:TYR:HD1	1:I:112:PRO:CD	1.80	0.94
1:A:223:PHE:CD1	1:A:242:GLN:CA	2.50	0.93
1:I:108:ALA:HA	1:J:183:ILE:HD11	0.94	0.93
1:N:247:GLY:H	1:N:251:ILE:HG22	1.33	0.93
1:A:166:LYS:HB3	1:I:42:VAL:HG12	1.49	0.93
1:M:15:TRP:HB3	1:M:17:GLN:NE2	1.83	0.93
1:E:245:TRP:HE3	1:E:252:VAL:HG23	1.34	0.93
1:A:37:VAL:CG1	1:A:43:CYS:HB2	1.96	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:227:ARG:HH12	1:P:140:THR:CG2	1.80	0.93
1:A:55:SER:CB	2:S:5:DC:OP1	2.16	0.93
1:M:271:PHE:CE2	1:P:82:ASN:ND2	2.34	0.93
1:A:223:PHE:HA	1:A:242:GLN:CA	1.99	0.93
1:E:167:LEU:O	1:E:171:PHE:HD2	1.52	0.92
1:H:60:ILE:HB	1:H:208:GLN:OE1	1.70	0.92
1:A:184:THR:HA	1:A:188:LYS:CG	1.99	0.92
1:B:19:ALA:HB1	1:B:33:ALA:HB1	1.49	0.92
1:N:221:ILE:O	1:N:274:PRO:HG2	1.68	0.92
1:I:220:LYS:NZ	1:I:274:PRO:HG3	1.85	0.91
1:M:222:ARG:NH1	1:P:203:PHE:CE1	2.38	0.91
1:A:120:GLY:O	1:A:124:VAL:HG23	1.70	0.91
1:A:2:ILE:HG23	1:A:5:ILE:HD11	1.50	0.91
1:D:225:TYR:O	1:D:269:VAL:HA	1.71	0.91
1:E:223:PHE:HZ	1:E:272:ILE:CG2	1.68	0.91
1:I:17:GLN:HE21	1:I:22:LEU:HB2	1.33	0.91
1:I:62:HIS:ND1	1:I:81:THR:CG2	2.34	0.91
1:F:251:ILE:HG22	1:F:264:ILE:O	1.70	0.91
1:A:65:VAL:CG1	1:A:78:TRP:HA	2.01	0.91
1:E:160:LEU:CD1	1:E:181:THR:CG2	2.48	0.90
1:I:64:GLN:CG	1:I:81:THR:HG22	2.01	0.90
1:F:250:ALA:HB3	2:S:2:DC:H1'	1.52	0.90
1:A:37:VAL:HG13	1:A:43:CYS:CB	2.00	0.90
1:M:271:PHE:HD2	1:P:82:ASN:ND2	1.62	0.90
1:I:118:ASP:OD1	1:I:123:PHE:HE2	1.50	0.90
1:J:17:GLN:OE1	1:K:188:LYS:HB3	1.71	0.89
1:I:78:TRP:CE3	1:I:106:TRP:CZ3	2.59	0.89
1:K:227:ARG:NH1	1:P:140:THR:HG23	1.87	0.89
1:A:116:GLN:CG	1:A:140:THR:OG1	2.20	0.89
1:G:206:GLU:OE2	1:H:203:PHE:HD2	1.54	0.89
1:F:248:ASP:HB2	2:S:3:DT:H3	0.76	0.89
1:A:244:LEU:HB2	1:A:252:VAL:HG12	1.55	0.89
1:A:80:GLU:OE1	1:A:83:SER:N	2.05	0.89
1:E:223:PHE:HZ	1:E:272:ILE:HG21	1.24	0.88
1:I:201:PHE:O	1:I:205:LYS:HG2	1.72	0.88
1:B:244:LEU:HD13	1:B:261:TYR:CE1	2.08	0.88
1:A:221:ILE:CG2	1:A:242:GLN:HB2	2.04	0.88
1:A:46:ASN:CB	1:I:166:LYS:HE2	2.03	0.88
1:E:223:PHE:HD2	1:E:272:ILE:HD12	1.33	0.88
1:I:68:THR:CG2	1:I:75:ILE:HB	2.04	0.88
1:M:271:PHE:HD2	1:P:82:ASN:HD21	0.90	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:118:ASP:O	1:I:123:PHE:HD2	1.56	0.87
1:I:244:LEU:HB2	1:I:252:VAL:HG12	1.55	0.87
1:D:251:ILE:HD11	1:D:269:VAL:HG11	1.55	0.87
1:H:244:LEU:HB2	1:H:252:VAL:HG12	1.54	0.87
1:A:223:PHE:CD1	1:A:242:GLN:HA	2.10	0.87
1:I:107:TYR:HD1	1:I:112:PRO:HD2	1.40	0.87
1:M:15:TRP:CB	1:M:17:GLN:HE22	1.86	0.87
1:A:12:HIS:HE1	1:A:43:CYS:SG	1.85	0.87
1:A:63:TRP:HA	1:A:81:THR:HG23	1.54	0.87
1:E:167:LEU:HB3	1:E:171:PHE:CE2	2.10	0.87
1:H:143:ILE:CG2	1:H:144:PRO:HD2	2.05	0.87
1:A:207:GLN:CG	1:D:222:ARG:CZ	2.53	0.86
1:A:207:GLN:HB3	1:D:222:ARG:HH22	1.37	0.86
1:I:52:LEU:HD23	1:I:52:LEU:O	1.76	0.86
1:F:149:SER:O	1:F:153:VAL:HG23	1.77	0.85
1:A:148:GLN:CB	2:S:4:DG:P	2.65	0.85
1:A:221:ILE:HD13	1:A:242:GLN:OE1	1.75	0.85
1:D:251:ILE:HD13	1:D:269:VAL:HG21	1.58	0.85
1:A:77:VAL:CG2	1:A:157:HIS:CE1	2.58	0.85
1:O:202:ILE:HG23	1:P:202:ILE:CG2	2.05	0.85
1:D:223:PHE:O	1:D:272:ILE:HB	1.76	0.85
1:E:164:LEU:O	1:E:168:ILE:HG22	1.77	0.85
1:A:224:CYS:SG	1:A:243:VAL:HG22	2.17	0.85
1:N:224:CYS:HA	1:N:272:ILE:CG1	2.06	0.85
1:P:79:VAL:HG11	1:P:153:VAL:HG22	1.59	0.85
1:A:207:GLN:CB	1:D:222:ARG:NH2	2.40	0.84
1:F:248:ASP:CB	2:S:3:DT:N3	2.29	0.84
1:J:78:TRP:HB2	1:J:87:TYR:HB3	1.60	0.84
1:F:250:ALA:CB	2:S:2:DC:H1'	2.06	0.84
1:I:153:VAL:HG22	1:I:157:HIS:CE1	2.13	0.84
1:C:61:ASP:OD2	1:C:205:LYS:NZ	2.11	0.84
1:N:222:ARG:O	1:N:243:VAL:HG23	1.78	0.84
1:I:107:TYR:CD1	1:I:112:PRO:HD2	2.13	0.83
1:H:185:LEU:HB3	1:H:189:ARG:CZ	2.09	0.83
1:I:52:LEU:HD22	1:L:234:PRO:HD2	1.57	0.83
1:B:9:GLU:OE1	1:B:261:TYR:HB2	1.78	0.83
1:I:78:TRP:CE3	1:I:106:TRP:CE3	2.66	0.83
1:F:58:ARG:HH12	1:F:149:SER:HB3	1.43	0.83
1:I:244:LEU:CD1	1:I:261:TYR:CD1	2.61	0.83
1:F:30:ARG:HD2	1:F:60:ILE:HD11	1.61	0.83
1:E:223:PHE:CD2	1:E:272:ILE:CD1	2.57	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:ASN:OD1	1:I:166:LYS:HG2	1.77	0.82
1:E:222:ARG:HD2	1:H:203:PHE:CE1	2.13	0.82
1:F:250:ALA:HB3	2:S:2:DC:C1'	2.09	0.82
1:E:223:PHE:CD2	1:E:272:ILE:HB	2.14	0.82
1:A:62:HIS:O	1:A:81:THR:OG1	1.97	0.82
1:E:222:ARG:HG3	1:E:243:VAL:HG21	1.60	0.82
1:E:245:TRP:HE3	1:E:252:VAL:CG2	1.93	0.82
1:I:226:TYR:CE1	1:I:241:THR:HG22	2.15	0.82
1:A:37:VAL:CG1	1:A:43:CYS:CB	2.57	0.81
1:I:154:GLU:HA	1:I:157:HIS:ND1	1.94	0.81
1:I:263:VAL:CG2	1:L:252:VAL:HG11	2.09	0.81
1:B:20:VAL:O	1:B:24:LEU:HG	1.79	0.81
1:F:17:GLN:NE2	1:G:184:THR:HG22	1.95	0.81
1:B:244:LEU:CD1	1:B:261:TYR:CE1	2.62	0.81
1:B:219:GLU:O	1:B:220:LYS:HD2	1.81	0.81
1:I:51:THR:CG2	1:N:266:ASN:HD22	1.93	0.81
1:F:251:ILE:HG21	1:F:264:ILE:HB	1.63	0.81
1:A:2:ILE:HG23	1:A:5:ILE:CD1	2.10	0.81
1:A:2:ILE:C	1:A:5:ILE:HG13	2.00	0.81
1:A:210:ILE:O	1:A:214:SER:N	2.15	0.80
1:A:65:VAL:CB	1:A:77:VAL:O	2.28	0.80
1:A:65:VAL:HG11	1:A:78:TRP:HA	1.62	0.80
1:I:51:THR:CG2	1:N:266:ASN:ND2	2.44	0.80
1:I:63:TRP:O	1:I:115:LEU:CD1	2.29	0.80
1:I:63:TRP:CD1	1:I:112:PRO:HB3	2.16	0.80
1:N:225:TYR:N	1:N:272:ILE:HD11	1.97	0.80
1:N:250:ALA:HB3	2:Q:2:DC:H1'	1.61	0.80
1:A:148:GLN:CB	2:S:4:DG:C5'	2.59	0.80
1:J:16:HIS:CE1	1:J:42:VAL:CG2	2.65	0.80
1:E:167:LEU:O	1:E:171:PHE:CD2	2.34	0.80
1:A:252:VAL:HG22	1:D:252:VAL:HG21	1.64	0.80
1:I:52:LEU:HD22	1:L:233:HIS:CB	2.12	0.79
1:M:217:LYS:HZ1	1:P:209:ARG:CD	1.94	0.79
1:A:65:VAL:CG1	1:A:77:VAL:O	2.30	0.79
1:N:60:ILE:HG21	1:N:204:ASN:CB	2.12	0.79
1:D:251:ILE:CD1	1:D:269:VAL:HG21	2.12	0.79
1:E:128:THR:O	1:E:132:MET:HG2	1.82	0.79
1:I:61:ASP:HB3	1:I:113:LYS:H	1.47	0.79
1:I:226:TYR:CE1	1:I:241:THR:CG2	2.66	0.79
1:M:17:GLN:HE21	1:M:184:THR:HG22	1.44	0.79
1:H:245:TRP:HB3	1:H:252:VAL:CG2	2.13	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:SER:CB	2:S:5:DC:C5'	2.61	0.78
1:A:46:ASN:HB2	1:I:166:LYS:CE	2.12	0.78
1:I:63:TRP:CZ3	1:I:80:GLU:HB2	2.19	0.78
1:D:227:ARG:HD2	1:D:234:PRO:CB	2.08	0.78
1:I:68:THR:HG22	1:I:75:ILE:HB	1.65	0.78
1:N:243:VAL:HG22	1:N:251:ILE:HD12	1.64	0.78
1:H:143:ILE:HG22	1:H:144:PRO:HD2	1.65	0.78
1:A:61:ASP:HA	1:A:63:TRP:HE1	1.49	0.78
1:I:107:TYR:CD1	1:I:112:PRO:CD	2.65	0.78
1:I:63:TRP:CE2	1:I:106:TRP:CH2	2.72	0.78
1:E:223:PHE:CE2	1:E:272:ILE:CG1	2.66	0.77
1:J:20:VAL:O	1:J:24:LEU:HG	1.85	0.77
1:A:166:LYS:HB3	1:I:42:VAL:CG1	2.15	0.77
1:I:76:LEU:O	1:I:88:ALA:HB1	1.85	0.77
1:E:195:THR:O	1:E:195:THR:HG23	1.82	0.77
1:F:15:TRP:CZ3	1:G:183:ILE:HG21	2.20	0.77
1:H:251:ILE:HD13	1:H:269:VAL:HG21	1.66	0.77
1:I:204:ASN:O	1:I:208:GLN:N	2.18	0.77
1:N:209:ARG:NH1	1:N:213:GLN:NE2	2.33	0.77
1:A:193:LEU:HD13	1:D:275:PRO:O	1.83	0.77
1:J:161:LYS:HD3	1:J:164:LEU:HD11	1.66	0.77
1:E:251:ILE:HD12	1:E:253:VAL:HG13	1.66	0.76
1:B:244:LEU:CD1	1:B:261:TYR:CD1	2.68	0.76
1:A:223:PHE:HD1	1:A:242:GLN:CB	1.95	0.76
1:A:76:LEU:O	1:A:88:ALA:HB1	1.85	0.76
1:I:143:ILE:HG23	1:I:144:PRO:HD2	1.66	0.76
1:B:8:ALA:HB2	1:B:26:PHE:CG	2.20	0.76
1:G:211:GLN:O	1:G:215:LYS:HG3	1.84	0.76
1:I:220:LYS:HZ1	1:I:274:PRO:HG3	1.47	0.76
1:J:36:ILE:CD1	1:J:261:TYR:HE2	1.97	0.76
1:E:251:ILE:CG1	1:E:269:VAL:HG21	2.15	0.76
1:I:184:THR:HB	1:I:188:LYS:CE	2.05	0.76
1:P:187:ILE:HG12	1:P:198:MET:SD	2.25	0.76
1:A:188:LYS:HE2	1:I:15:TRP:HB3	1.67	0.76
1:E:17:GLN:HG3	1:E:184:THR:HG23	1.67	0.76
1:F:250:ALA:HB1	1:F:263:VAL:HG13	1.68	0.76
1:H:251:ILE:HD13	1:H:269:VAL:CG2	2.14	0.76
1:I:2:ILE:HG22	1:I:5:ILE:HD12	1.66	0.76
1:B:244:LEU:HD13	1:B:261:TYR:HE1	1.49	0.76
1:A:203:PHE:CZ	1:D:222:ARG:HD2	2.20	0.76
1:P:145:TRP:O	1:P:145:TRP:CG	2.39	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:63:TRP:NE1	1:I:112:PRO:HB3	2.01	0.75
1:L:227:ARG:HD3	1:L:234:PRO:HB2	0.76	0.75
1:A:254:LYS:HE2	1:A:261:TYR:CE1	2.20	0.75
1:F:250:ALA:HB1	1:F:263:VAL:CG1	2.15	0.75
1:E:222:ARG:CD	1:H:203:PHE:CE1	2.67	0.75
1:I:60:ILE:O	1:I:61:ASP:HB2	1.87	0.75
1:F:15:TRP:CB	1:F:17:GLN:NE2	2.41	0.75
1:J:79:VAL:HG13	1:J:86:ILE:HG22	1.67	0.75
1:A:40:CYS:SG	1:A:41:ASP:N	2.59	0.75
1:I:40:CYS:SG	1:I:41:ASP:N	2.59	0.75
1:A:82:ASN:ND2	1:D:269:VAL:O	2.19	0.75
1:A:223:PHE:HD1	1:A:242:GLN:HA	1.47	0.75
1:B:9:GLU:HG2	1:B:36:ILE:CD1	2.17	0.75
1:E:223:PHE:HE2	1:E:272:ILE:HG21	1.45	0.75
1:H:183:ILE:CG2	1:H:188:LYS:HZ3	1.99	0.75
1:E:271:PHE:CD2	1:H:82:ASN:ND2	2.53	0.74
1:I:63:TRP:CD1	1:I:112:PRO:CB	2.69	0.74
1:F:17:GLN:HG2	1:G:188:LYS:CB	2.17	0.74
1:A:166:LYS:CB	1:I:42:VAL:HG12	2.17	0.74
1:B:19:ALA:HB1	1:B:33:ALA:CB	2.17	0.74
1:A:240:PRO:CG	1:H:223:PHE:CZ	2.59	0.74
1:I:77:VAL:CG1	1:I:79:VAL:HG22	2.17	0.74
1:A:144:PRO:HB2	1:A:145:TRP:HE3	1.53	0.74
1:E:269:VAL:O	1:H:82:ASN:OD1	2.05	0.74
1:J:78:TRP:N	1:J:87:TYR:O	2.19	0.74
1:A:223:PHE:HE1	1:A:242:GLN:HB3	1.53	0.74
1:G:206:GLU:OE2	1:H:203:PHE:CD2	2.40	0.74
1:F:118:ASP:O	1:F:123:PHE:HD2	1.71	0.74
1:I:51:THR:HG21	1:N:266:ASN:HD22	1.51	0.74
1:D:206:GLU:OE2	1:D:209:ARG:NH2	2.20	0.74
1:I:143:ILE:HG22	1:I:144:PRO:CD	2.16	0.74
1:J:15:TRP:CZ2	1:L:134:TYR:CZ	2.76	0.74
1:I:52:LEU:HD13	1:L:232:GLY:O	1.88	0.74
1:A:148:GLN:NE2	2:S:4:DG:C8	2.56	0.73
1:A:252:VAL:CG2	1:D:252:VAL:HG21	2.18	0.73
1:E:222:ARG:O	1:E:243:VAL:CG2	2.36	0.73
1:F:30:ARG:CD	1:F:60:ILE:HD11	2.18	0.73
1:J:17:GLN:NE2	1:J:25:GLU:OE1	2.20	0.73
1:F:248:ASP:HB2	2:S:3:DT:C2	2.21	0.73
1:I:23:HIS:ND1	1:I:28:ILE:O	2.20	0.73
1:I:52:LEU:CD2	1:L:234:PRO:HD2	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:ILE:HG23	1:A:242:GLN:HB2	1.68	0.73
1:C:79:VAL:HG11	1:C:153:VAL:HG22	1.70	0.73
1:F:60:ILE:CG2	1:F:204:ASN:HB3	2.17	0.73
1:M:17:GLN:OE1	1:M:17:GLN:N	2.20	0.73
1:H:152:LEU:O	1:H:156:THR:OG1	2.03	0.73
1:I:87:TYR:HB3	1:I:106:TRP:HE1	1.52	0.73
1:G:80:GLU:OE1	1:G:83:SER:N	2.20	0.73
1:J:15:TRP:CH2	1:L:134:TYR:CE2	2.77	0.73
1:N:209:ARG:HH12	1:N:213:GLN:NE2	1.85	0.73
1:D:258:THR:O	1:D:258:THR:HG22	1.89	0.72
1:E:205:LYS:HG2	1:F:202:ILE:HD13	1.71	0.72
1:J:198:MET:HG2	1:J:202:ILE:HD11	1.70	0.72
1:N:209:ARG:HH12	1:N:213:GLN:HE22	1.35	0.72
1:L:223:PHE:CE1	1:L:240:PRO:HB2	2.24	0.72
1:M:222:ARG:CZ	1:P:203:PHE:CZ	2.72	0.72
1:A:65:VAL:HG12	1:A:78:TRP:HA	1.70	0.72
1:M:217:LYS:NZ	1:P:209:ARG:CD	2.47	0.72
1:C:115:LEU:O	1:C:140:THR:OG1	2.07	0.72
1:H:183:ILE:CG2	1:H:188:LYS:NZ	2.53	0.72
1:I:107:TYR:HA	1:I:112:PRO:HG3	1.68	0.72
1:I:244:LEU:CD1	1:I:261:TYR:HD1	2.00	0.72
1:J:14:LYS:HE2	1:J:15:TRP:NE1	2.04	0.72
1:M:16:HIS:CE1	1:M:42:VAL:HG11	2.24	0.72
1:I:64:GLN:OE1	1:I:152:LEU:HB2	1.88	0.72
1:L:227:ARG:HH11	1:L:234:PRO:CB	2.02	0.72
1:A:244:LEU:HD13	1:A:253:VAL:CA	2.18	0.72
1:I:78:TRP:HE3	1:I:106:TRP:CZ3	2.07	0.72
1:D:226:TYR:HE1	1:D:241:THR:HG22	1.55	0.72
1:I:143:ILE:CG2	1:I:144:PRO:CD	2.68	0.72
1:M:222:ARG:NH1	1:P:203:PHE:CD1	2.58	0.72
1:B:94:GLU:O	1:B:122:ALA:HB2	1.90	0.72
1:A:77:VAL:HG21	1:A:157:HIS:HE1	1.54	0.72
1:E:245:TRP:CE3	1:E:252:VAL:HG23	2.22	0.72
1:A:166:LYS:O	1:I:42:VAL:CG1	2.38	0.72
1:A:148:GLN:CG	2:S:4:DG:H5"	2.20	0.71
1:D:251:ILE:HD11	1:D:269:VAL:CG1	2.20	0.71
1:A:204:ASN:O	1:A:208:GLN:N	2.23	0.71
1:I:107:TYR:HD1	1:I:112:PRO:CG	2.03	0.71
1:C:41:ASP:O	1:C:45:GLU:N	2.22	0.71
1:J:161:LYS:HD3	1:J:164:LEU:CD1	2.19	0.71
1:A:82:ASN:OD1	1:D:270:LYS:HA	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:244:LEU:HD11	1:I:261:TYR:CD1	2.24	0.71
1:A:67:TYR:CZ	1:A:94:GLU:HB2	2.26	0.71
1:H:159:THR:HG22	1:H:185:LEU:HD11	1.72	0.71
1:B:132:MET:O	1:B:136:GLY:N	2.24	0.71
1:F:17:GLN:HG2	1:G:188:LYS:HB2	1.73	0.71
1:A:115:LEU:N	1:A:138:GLU:O	2.24	0.71
1:J:17:GLN:HE21	1:J:22:LEU:HD23	1.56	0.70
1:M:115:LEU:O	1:M:140:THR:OG1	2.08	0.70
1:A:51:THR:OG1	1:F:266:ASN:CG	2.29	0.70
1:A:55:SER:CB	2:S:5:DC:H5"	2.21	0.70
1:I:22:LEU:HD12	1:I:26:PHE:CD2	2.26	0.70
1:N:253:VAL:O	1:N:262:LEU:N	2.23	0.70
1:L:227:ARG:HH11	1:L:234:PRO:HB2	1.51	0.70
1:F:118:ASP:C	1:F:120:GLY:H	1.94	0.70
1:F:17:GLN:HE21	1:G:184:THR:HG22	1.56	0.70
1:I:64:GLN:HG3	1:I:81:THR:CG2	2.20	0.70
1:I:253:VAL:O	1:I:262:LEU:N	2.24	0.70
1:L:227:ARG:HH11	1:L:234:PRO:HG2	1.55	0.70
1:A:254:LYS:NZ	1:A:261:TYR:CD1	2.59	0.70
1:A:253:VAL:O	1:A:262:LEU:N	2.24	0.70
1:K:20:VAL:O	1:K:24:LEU:HG	1.90	0.70
1:A:244:LEU:HB2	1:A:252:VAL:CG1	2.21	0.70
1:F:30:ARG:CZ	1:F:60:ILE:HD11	2.22	0.70
1:L:227:ARG:HD3	1:L:234:PRO:CA	2.21	0.70
1:P:226:TYR:O	1:P:238:GLN:N	2.25	0.70
1:I:68:THR:HG22	1:I:75:ILE:O	1.91	0.70
1:J:36:ILE:O	1:J:40:CYS:N	2.24	0.70
1:J:64:GLN:O	1:J:79:VAL:N	2.24	0.69
1:F:248:ASP:CB	2:S:3:DT:C2	2.74	0.69
1:D:226:TYR:HA	1:D:268:ASP:O	1.92	0.69
1:I:64:GLN:O	1:I:79:VAL:HB	1.92	0.69
1:N:228:THR:O	1:N:235:GLY:N	2.25	0.69
1:A:63:TRP:O	1:A:115:LEU:HD12	1.92	0.69
1:G:202:ILE:HD13	1:H:205:LYS:HG2	1.73	0.69
1:L:227:ARG:HH11	1:L:234:PRO:CG	2.05	0.69
1:A:132:MET:O	1:A:136:GLY:N	2.25	0.69
1:A:245:TRP:CH2	1:D:244:LEU:HB3	2.27	0.69
1:I:77:VAL:HG21	1:I:157:HIS:NE2	2.08	0.69
1:J:206:GLU:O	1:J:210:ILE:HD12	1.92	0.69
1:M:228:THR:O	1:M:235:GLY:N	2.26	0.69
1:C:253:VAL:O	1:C:262:LEU:N	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:222:ARG:HB2	1:D:272:ILE:O	1.91	0.69
1:J:8:ALA:CB	1:J:28:ILE:HD13	2.21	0.69
1:J:80:GLU:OE1	1:J:83:SER:N	2.25	0.69
1:N:272:ILE:CG2	1:N:273:PRO:HD2	2.23	0.69
1:A:166:LYS:O	1:I:42:VAL:HG13	1.92	0.69
1:I:63:TRP:CG	1:I:106:TRP:CH2	2.80	0.69
1:J:132:MET:O	1:J:136:GLY:N	2.25	0.69
1:A:184:THR:CA	1:A:188:LYS:HB2	2.23	0.69
1:G:62:HIS:CD2	1:G:81:THR:HG21	2.27	0.69
1:I:132:MET:O	1:I:136:GLY:N	2.25	0.69
1:K:253:VAL:O	1:K:262:LEU:N	2.25	0.69
1:A:148:GLN:OE1	2:S:4:DG:C1'	2.40	0.69
1:A:184:THR:O	1:A:188:LYS:CB	2.39	0.69
1:J:16:HIS:CG	1:J:42:VAL:HG11	2.28	0.69
1:B:244:LEU:CD1	1:B:261:TYR:HE1	2.04	0.69
1:I:115:LEU:N	1:I:138:GLU:O	2.24	0.69
1:I:2:ILE:N	1:I:2:ILE:HD12	2.07	0.69
1:A:55:SER:CB	2:S:5:DC:P	2.80	0.69
1:I:186:ASN:O	1:I:197:PRO:HD2	1.93	0.69
1:J:161:LYS:CD	1:J:164:LEU:CD1	2.71	0.69
1:J:200:ILE:O	1:J:204:ASN:OD1	2.11	0.69
1:M:25:GLU:HB2	1:M:190:LYS:NZ	2.08	0.68
1:I:244:LEU:HB2	1:I:252:VAL:CG1	2.22	0.68
1:K:80:GLU:OE1	1:K:83:SER:N	2.26	0.68
1:I:108:ALA:CB	1:J:179:ALA:HB1	2.23	0.68
1:A:244:LEU:HD21	1:A:261:TYR:CD1	2.29	0.68
1:K:206:GLU:OE2	1:K:209:ARG:NE	2.20	0.68
1:E:242:GLN:OE1	1:E:244:LEU:HD21	1.94	0.68
1:I:244:LEU:CD1	1:I:261:TYR:CE1	2.77	0.68
1:A:223:PHE:HD1	1:A:242:GLN:CA	1.98	0.68
1:J:161:LYS:CD	1:J:164:LEU:HD11	2.22	0.68
1:D:244:LEU:HD11	1:D:261:TYR:CE1	2.29	0.68
1:I:78:TRP:HB3	1:I:106:TRP:CE2	2.29	0.68
1:N:224:CYS:C	1:N:272:ILE:CD1	2.62	0.68
1:I:240:PRO:HG3	1:P:223:PHE:CE2	2.25	0.68
1:A:231:ARG:NH2	2:Q:19:DG:O4'	2.26	0.68
1:E:164:LEU:O	1:E:168:ILE:CG2	2.42	0.68
1:I:63:TRP:CD1	1:I:106:TRP:CZ3	2.82	0.68
1:M:25:GLU:HB2	1:M:190:LYS:HZ1	1.59	0.68
1:H:60:ILE:HD12	1:H:60:ILE:N	2.10	0.67
1:N:132:MET:O	1:N:136:GLY:N	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:41:ASP:O	1:K:45:GLU:N	2.26	0.67
1:M:173:ALA:O	1:M:176:SER:OG	2.11	0.67
1:M:36:ILE:O	1:M:40:CYS:N	2.27	0.67
1:I:107:TYR:O	1:I:110:PHE:O	2.11	0.67
1:I:118:ASP:O	1:I:123:PHE:CD2	2.44	0.67
1:I:116:GLN:NE2	1:I:149:SER:O	2.26	0.67
1:A:203:PHE:CE2	1:D:222:ARG:HD2	2.29	0.67
1:I:63:TRP:HE1	1:I:112:PRO:HB3	1.60	0.67
1:A:184:THR:C	1:A:188:LYS:HB2	2.15	0.67
1:A:240:PRO:HG3	1:H:223:PHE:CE2	2.25	0.67
1:I:184:THR:O	1:I:188:LYS:CB	2.39	0.67
1:J:176:SER:O	1:J:179:ALA:HB3	1.94	0.67
1:F:248:ASP:HB3	2:S:3:DT:O2	1.94	0.67
1:F:251:ILE:O	1:F:263:VAL:HA	1.95	0.67
1:I:220:LYS:HZ2	1:I:274:PRO:HG3	1.57	0.67
1:N:247:GLY:N	1:N:251:ILE:HG22	2.07	0.67
1:I:65:VAL:CG1	1:I:76:LEU:HD11	2.25	0.67
1:A:244:LEU:CD1	1:A:253:VAL:HA	2.23	0.67
1:B:9:GLU:HG2	1:B:36:ILE:HD11	1.77	0.67
1:E:270:LYS:HA	1:H:82:ASN:OD1	1.94	0.67
1:I:152:LEU:O	1:I:156:THR:HG23	1.95	0.67
1:E:234:PRO:HA	1:H:148:GLN:NE2	2.10	0.66
1:I:207:GLN:OE1	1:L:222:ARG:NH2	2.28	0.66
1:E:36:ILE:O	1:E:40:CYS:N	2.27	0.66
1:I:77:VAL:CG1	1:I:79:VAL:HG21	2.23	0.66
1:L:223:PHE:HB3	1:L:242:GLN:HA	1.77	0.66
1:N:60:ILE:CG2	1:N:204:ASN:HB3	2.24	0.66
1:A:244:LEU:HD22	1:A:252:VAL:HG12	1.76	0.66
1:C:13:ASN:O	1:C:16:HIS:NE2	2.27	0.66
1:C:80:GLU:OE1	1:C:83:SER:N	2.28	0.66
1:A:145:TRP:HE1	1:F:232:GLY:H	1.42	0.66
1:H:60:ILE:HG12	1:H:204:ASN:HB3	1.76	0.66
1:M:222:ARG:HD2	1:P:203:PHE:CE1	2.31	0.66
1:N:246:GLY:HA2	1:N:251:ILE:CG2	2.25	0.66
1:A:244:LEU:HD21	1:A:261:TYR:CE1	2.30	0.66
1:F:132:MET:O	1:F:136:GLY:N	2.29	0.66
1:N:240:PRO:CB	1:N:272:ILE:CD1	2.74	0.66
1:E:2:ILE:O	1:E:6:PRO:CD	2.43	0.66
1:N:224:CYS:C	1:N:272:ILE:HD12	2.16	0.66
1:F:187:ILE:HG23	1:F:188:LYS:N	2.11	0.66
1:J:183:ILE:O	1:J:187:ILE:HB	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:178:LEU:O	1:M:181:THR:OG1	2.13	0.66
1:M:217:LYS:HZ3	1:P:209:ARG:HD2	1.58	0.66
1:A:148:GLN:HB2	2:S:4:DG:OP2	1.96	0.66
1:H:182:LEU:HB3	1:H:186:ASN:ND2	2.10	0.66
1:O:16:HIS:CE1	1:O:42:VAL:HG11	2.31	0.66
1:P:223:PHE:HD1	1:P:241:THR:O	1.78	0.66
1:K:115:LEU:O	1:K:140:THR:OG1	2.13	0.65
1:L:265:ALA:HB1	1:L:267:LYS:HG2	1.77	0.65
1:E:2:ILE:O	1:E:6:PRO:HD3	1.96	0.65
1:A:254:LYS:CE	1:A:261:TYR:CE1	2.79	0.65
1:D:258:THR:HG22	1:D:260:ARG:HB2	1.79	0.65
1:D:80:GLU:OE1	1:D:83:SER:N	2.29	0.65
1:F:228:THR:O	1:F:235:GLY:N	2.28	0.65
1:E:191:GLY:O	1:E:195:THR:CG2	2.28	0.65
1:H:244:LEU:HB2	1:H:252:VAL:CG1	2.25	0.65
1:I:118:ASP:OD1	1:I:123:PHE:CD2	2.50	0.65
1:O:184:THR:O	1:O:189:ARG:N	2.29	0.65
1:H:143:ILE:HG23	1:H:144:PRO:HD2	1.77	0.65
1:I:73:LYS:HD3	1:I:90:ARG:NH1	2.12	0.65
1:A:207:GLN:CG	1:D:222:ARG:NH1	2.59	0.65
1:A:59:GLY:HA3	1:A:62:HIS:HB2	1.77	0.65
1:D:213:GLN:O	1:D:216:SER:OG	2.09	0.65
1:H:60:ILE:CB	1:H:208:GLN:OE1	2.44	0.65
1:M:181:THR:O	1:M:184:THR:OG1	2.13	0.65
1:A:3:GLU:O	1:A:6:PRO:HD3	1.97	0.65
1:F:272:ILE:HG21	1:F:276:LYS:HD2	1.77	0.65
1:E:271:PHE:CE2	1:H:82:ASN:ND2	2.64	0.65
1:O:162:ASN:O	1:O:166:LYS:HG3	1.96	0.65
1:A:15:TRP:O	1:I:188:LYS:HD2	1.98	0.64
1:C:121:PRO:O	1:C:125:ALA:N	2.30	0.64
1:F:61:ASP:OD2	1:F:205:LYS:HD3	1.96	0.64
1:M:117:SER:OG	1:M:140:THR:O	2.11	0.64
1:N:240:PRO:HB2	1:N:272:ILE:HD12	1.78	0.64
1:A:77:VAL:CG1	1:A:79:VAL:HG21	2.23	0.64
1:I:5:ILE:HG12	1:I:28:ILE:CD1	2.27	0.64
1:I:60:ILE:O	1:I:61:ASP:CB	2.44	0.64
1:A:64:GLN:HG3	1:A:81:THR:HG22	1.79	0.64
1:H:251:ILE:CD1	1:H:269:VAL:HG22	2.27	0.64
1:A:231:ARG:NH2	2:Q:18:DG:N3	2.44	0.64
1:I:251:ILE:HD11	1:I:264:ILE:HB	1.79	0.64
1:I:2:ILE:HD13	1:M:39:GLN:OE1	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:19:ALA:HB1	1:J:33:ALA:HB1	1.79	0.64
1:J:67:TYR:O	1:J:67:TYR:CD1	2.50	0.64
1:D:254:LYS:O	1:D:254:LYS:HG3	1.96	0.64
1:N:222:ARG:O	1:N:243:VAL:CG2	2.46	0.64
1:P:80:GLU:OE1	1:P:83:SER:N	2.29	0.64
1:A:184:THR:CA	1:A:188:LYS:CG	2.76	0.64
1:I:245:TRP:O	1:I:252:VAL:N	2.31	0.64
1:I:63:TRP:HZ3	1:I:80:GLU:HB2	1.60	0.64
1:J:15:TRP:CE2	1:L:134:TYR:CZ	2.86	0.64
1:B:213:GLN:O	1:B:218:GLN:NE2	2.32	0.63
1:A:145:TRP:HE1	1:F:232:GLY:N	1.94	0.63
1:I:77:VAL:HG12	1:I:79:VAL:HG21	1.72	0.63
1:J:193:LEU:HD11	1:L:209:ARG:NH2	2.12	0.63
1:N:265:ALA:HB1	1:N:267:LYS:HG2	1.80	0.63
1:A:95:THR:OG1	1:A:98:GLU:HB2	1.96	0.63
1:B:218:GLN:OE1	1:B:218:GLN:N	2.30	0.63
1:C:206:GLU:OE2	1:C:209:ARG:NE	2.31	0.63
1:E:78:TRP:N	1:E:87:TYR:O	2.32	0.63
1:I:51:THR:HG21	1:N:266:ASN:ND2	2.13	0.63
1:J:198:MET:HG2	1:J:202:ILE:CD1	2.28	0.63
1:J:36:ILE:HG23	1:J:37:VAL:N	2.13	0.63
1:A:263:VAL:HG23	1:D:263:VAL:HG23	1.79	0.63
1:A:2:ILE:CG2	1:A:5:ILE:HD11	2.28	0.63
1:A:55:SER:CB	2:S:5:DC:H5'	2.28	0.63
1:A:193:LEU:CD1	1:D:275:PRO:O	2.46	0.63
1:J:16:HIS:CD2	1:J:42:VAL:HG11	2.33	0.63
1:M:5:ILE:HG12	1:M:28:ILE:HB	1.80	0.63
1:N:121:PRO:O	1:N:125:ALA:N	2.30	0.63
1:A:77:VAL:CG1	1:A:79:VAL:HG22	2.25	0.63
1:B:80:GLU:OE1	1:B:83:SER:N	2.31	0.63
1:G:212:GLN:HA	1:G:215:LYS:HD2	1.79	0.63
1:I:130:LEU:HG	1:I:130:LEU:O	1.99	0.63
1:A:53:ARG:O	1:D:233:HIS:CB	2.47	0.63
1:G:62:HIS:ND1	1:G:114:SER:OG	2.22	0.63
1:I:150:GLN:HE21	1:I:150:GLN:HA	1.63	0.63
1:M:213:GLN:O	1:M:216:SER:OG	2.10	0.63
1:C:78:TRP:N	1:C:87:TYR:O	2.31	0.63
1:E:251:ILE:CD1	1:E:253:VAL:HG13	2.29	0.63
1:F:78:TRP:N	1:F:87:TYR:O	2.32	0.63
1:G:212:GLN:HA	1:G:215:LYS:CD	2.27	0.63
1:K:202:ILE:HD13	1:L:205:LYS:HG2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:217:LYS:HZ3	1:P:209:ARG:HB3	1.64	0.63
1:A:73:LYS:HD3	1:A:90:ARG:NH1	2.14	0.63
1:A:77:VAL:HG12	1:A:79:VAL:HG21	1.74	0.62
1:B:161:LYS:HA	1:B:164:LEU:HD12	1.81	0.62
1:E:271:PHE:HD2	1:H:82:ASN:ND2	1.97	0.62
1:I:198:MET:O	1:I:202:ILE:HG12	2.00	0.62
1:A:156:THR:O	1:A:159:THR:N	2.32	0.62
1:A:251:ILE:HD11	1:A:264:ILE:HB	1.79	0.62
1:I:156:THR:O	1:I:159:THR:N	2.32	0.62
1:I:184:THR:C	1:I:188:LYS:HB3	2.18	0.62
1:L:252:VAL:HG12	1:L:263:VAL:CA	2.28	0.62
1:M:217:LYS:CE	1:P:209:ARG:HD2	2.29	0.62
1:F:250:ALA:CB	2:S:2:DC:C1'	2.73	0.62
1:I:184:THR:CA	1:I:188:LYS:HB3	2.29	0.62
1:O:211:GLN:O	1:O:215:LYS:N	2.32	0.62
1:A:76:LEU:CD2	1:A:78:TRP:CZ2	2.82	0.62
1:E:195:THR:O	1:E:195:THR:CG2	2.47	0.62
1:I:17:GLN:NE2	1:I:22:LEU:HD22	2.14	0.62
1:I:62:HIS:CE1	1:I:81:THR:HG21	2.31	0.62
1:I:209:ARG:NH1	1:J:199:ASP:OD2	2.33	0.62
1:J:198:MET:O	1:J:202:ILE:HD12	1.99	0.62
1:K:191:GLY:O	1:K:195:THR:OG1	2.15	0.62
1:A:3:GLU:C	1:A:5:ILE:H	2.02	0.62
1:E:244:LEU:HB3	1:H:245:TRP:CZ2	2.35	0.62
1:I:184:THR:HA	1:I:188:LYS:CB	2.30	0.62
1:I:244:LEU:HD12	1:I:252:VAL:HG12	1.81	0.62
1:L:80:GLU:OE1	1:L:83:SER:N	2.31	0.62
1:F:248:ASP:O	2:S:3:DT:C2	2.52	0.62
1:A:2:ILE:CG2	1:A:5:ILE:CD1	2.78	0.62
1:A:37:VAL:HG11	1:A:43:CYS:HB3	1.81	0.62
1:I:63:TRP:CG	1:I:106:TRP:HH2	2.18	0.62
1:I:62:HIS:HB3	1:I:81:THR:OG1	1.99	0.62
1:L:227:ARG:NH1	1:L:234:PRO:HB2	2.14	0.62
1:M:226:TYR:O	1:M:238:GLN:N	2.32	0.62
1:E:227:ARG:NH2	1:H:148:GLN:O	2.32	0.62
1:I:61:ASP:HB2	1:I:113:LYS:HB3	1.82	0.62
1:I:17:GLN:HE21	1:I:22:LEU:CB	2.10	0.62
1:I:76:LEU:CD2	1:I:78:TRP:CZ2	2.82	0.62
1:M:2:ILE:O	1:M:6:PRO:HD3	1.99	0.62
1:A:245:TRP:O	1:A:252:VAL:N	2.31	0.62
1:H:204:ASN:O	1:H:208:GLN:HG3	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:201:PHE:CZ	1:I:205:LYS:HD3	2.33	0.61
1:I:226:TYR:CD1	1:I:241:THR:HG22	2.35	0.61
1:J:180:GLY:O	1:J:184:THR:HG23	2.01	0.61
1:N:246:GLY:HA2	1:N:251:ILE:HG22	1.82	0.61
1:I:117:SER:OG	1:I:139:HIS:NE2	2.31	0.61
1:J:20:VAL:HG12	1:J:24:LEU:HD11	1.81	0.61
1:K:36:ILE:O	1:K:40:CYS:N	2.32	0.61
1:A:222:ARG:O	1:A:243:VAL:N	2.32	0.61
1:A:224:CYS:N	1:A:241:THR:O	2.33	0.61
1:D:241:THR:OG1	1:D:254:LYS:HG2	2.00	0.61
1:F:17:GLN:HG2	1:G:188:LYS:HB3	1.82	0.61
1:F:60:ILE:HG21	1:F:204:ASN:CB	2.20	0.61
1:H:251:ILE:CD1	1:H:269:VAL:CG2	2.77	0.61
1:I:150:GLN:O	1:I:153:VAL:HG12	2.00	0.61
1:J:14:LYS:HB2	1:J:15:TRP:HD1	1.65	0.61
1:L:233:HIS:CB	1:N:248:ASP:OD2	2.48	0.61
1:B:160:LEU:O	1:B:163:THR:OG1	2.14	0.61
1:B:78:TRP:N	1:B:87:TYR:O	2.33	0.61
1:D:251:ILE:HD11	1:D:269:VAL:CB	2.31	0.61
1:I:153:VAL:HG22	1:I:157:HIS:HE1	1.65	0.61
1:J:78:TRP:HD1	1:J:87:TYR:HD1	1.47	0.61
1:M:271:PHE:HE2	1:P:82:ASN:ND2	1.95	0.61
1:E:222:ARG:HD3	1:H:203:PHE:CE1	2.35	0.61
1:I:244:LEU:HD11	1:I:261:TYR:CE1	2.36	0.61
1:J:198:MET:O	1:J:202:ILE:HG13	2.00	0.61
1:J:36:ILE:HD12	1:J:261:TYR:HE2	1.66	0.61
1:J:78:TRP:CD1	1:J:87:TYR:HD1	2.19	0.61
1:F:14:LYS:HD3	1:H:134:TYR:CE1	2.36	0.61
1:A:148:GLN:OE1	2:S:4:DG:N9	2.33	0.61
1:B:185:LEU:HD22	1:B:189:ARG:NH1	2.15	0.61
1:G:162:ASN:O	1:G:166:LYS:HG3	2.00	0.61
1:I:223:PHE:HA	1:I:241:THR:O	2.01	0.61
1:I:55:SER:CB	2:Q:5:DC:H5"	2.30	0.61
1:B:191:GLY:O	1:B:195:THR:OG1	2.09	0.61
1:F:144:PRO:HG2	1:F:150:GLN:HE22	1.66	0.61
1:I:247:GLY:N	1:I:250:ALA:O	2.33	0.61
1:I:57:LYS:O	1:I:81:THR:CB	2.48	0.61
1:K:20:VAL:HG12	1:K:24:LEU:HD11	1.83	0.61
1:M:134:TYR:CE1	1:O:14:LYS:HD3	2.35	0.61
1:A:145:TRP:NE1	1:F:232:GLY:N	2.47	0.61
1:A:184:THR:HA	1:A:188:LYS:CB	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:86:ILE:HG13	1:I:186:ASN:OD1	2.00	0.61
1:J:206:GLU:O	1:J:210:ILE:CD1	2.49	0.61
1:N:245:TRP:O	1:N:252:VAL:N	2.34	0.61
1:A:184:THR:CB	1:A:188:LYS:HG3	2.31	0.60
1:A:63:TRP:CA	1:A:81:THR:HG23	2.30	0.60
1:I:223:PHE:HB3	1:I:241:THR:O	2.01	0.60
1:M:222:ARG:CZ	1:P:203:PHE:CE1	2.84	0.60
1:A:95:THR:OG1	1:A:98:GLU:CB	2.49	0.60
1:J:198:MET:O	1:J:202:ILE:CG1	2.50	0.60
1:N:266:ASN:OD1	1:N:267:LYS:N	2.34	0.60
1:E:223:PHE:HE2	1:E:272:ILE:CG1	2.08	0.60
1:E:234:PRO:HA	1:H:148:GLN:HE22	1.66	0.60
1:E:80:GLU:OE1	1:E:83:SER:N	2.35	0.60
1:F:41:ASP:O	1:F:45:GLU:N	2.35	0.60
1:H:186:ASN:O	1:H:198:MET:HB2	2.01	0.60
1:N:178:LEU:O	1:N:181:THR:OG1	2.14	0.60
1:I:117:SER:HA	1:I:150:GLN:OE1	2.01	0.60
1:N:246:GLY:HA2	1:N:251:ILE:HB	1.83	0.60
1:B:8:ALA:CB	1:B:26:PHE:CG	2.85	0.60
1:I:17:GLN:HG2	1:I:18:ASP:O	2.02	0.60
1:I:226:TYR:CD1	1:I:241:THR:CG2	2.84	0.60
1:A:190:LYS:N	1:I:21:SER:OG	2.35	0.60
1:A:212:GLN:HG3	1:D:213:GLN:HB3	1.84	0.60
1:E:159:THR:O	1:E:163:THR:HG23	2.00	0.60
1:H:115:LEU:O	1:H:140:THR:OG1	2.14	0.60
1:J:16:HIS:HB2	1:K:166:LYS:HD3	1.84	0.60
1:I:51:THR:HG22	1:N:266:ASN:ND2	2.16	0.60
1:I:184:THR:O	1:I:189:ARG:N	2.35	0.60
1:N:184:THR:O	1:N:189:ARG:N	2.34	0.60
1:F:13:ASN:O	1:F:16:HIS:CE1	2.55	0.59
1:A:254:LYS:HE2	1:A:261:TYR:HE1	1.67	0.59
1:G:212:GLN:HA	1:G:215:LYS:CG	2.32	0.59
1:H:80:GLU:OE1	1:H:83:SER:N	2.27	0.59
1:L:252:VAL:HG12	1:L:263:VAL:HB	1.84	0.59
1:M:156:THR:O	1:M:160:LEU:CB	2.50	0.59
1:O:202:ILE:HD13	1:P:205:LYS:HG2	1.85	0.59
1:A:166:LYS:HD3	1:I:43:CYS:HA	1.85	0.59
1:A:97:GLN:O	1:A:101:VAL:HG23	2.03	0.59
1:E:222:ARG:HG3	1:E:243:VAL:CG2	2.30	0.59
1:F:30:ARG:NH1	1:F:60:ILE:HD11	2.18	0.59
1:H:173:ALA:O	1:H:176:SER:OG	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:200:ILE:HD12	1:K:192:GLY:CA	2.32	0.59
1:L:227:ARG:NH1	1:L:234:PRO:HG2	2.16	0.59
1:I:146:ASN:HD21	2:Q:3:DT:H5"	1.67	0.59
1:I:226:TYR:CE1	1:I:241:THR:HG21	2.35	0.59
1:J:19:ALA:HB1	1:J:33:ALA:CB	2.33	0.59
1:I:63:TRP:HD1	1:I:112:PRO:CB	2.15	0.59
1:I:77:VAL:HG12	1:I:79:VAL:HG22	1.69	0.59
1:J:203:PHE:O	1:J:206:GLU:HG2	2.03	0.59
1:F:30:ARG:NE	1:F:60:ILE:HD11	2.17	0.59
1:I:147:PRO:O	1:I:150:GLN:N	2.35	0.59
1:A:184:THR:O	1:A:189:ARG:N	2.35	0.59
1:I:63:TRP:CE3	1:I:106:TRP:HH2	2.20	0.59
1:I:76:LEU:HD21	1:I:78:TRP:CZ2	2.38	0.59
1:K:226:TYR:O	1:K:238:GLN:N	2.35	0.59
1:A:76:LEU:HD21	1:A:78:TRP:CZ2	2.37	0.59
1:I:87:TYR:CB	1:I:106:TRP:HE1	2.15	0.59
1:I:184:THR:HA	1:I:188:LYS:HB2	1.84	0.59
1:J:253:VAL:O	1:J:262:LEU:N	2.35	0.59
1:A:148:GLN:CB	2:S:4:DG:H5"	2.33	0.59
1:A:70:TYR:CE1	1:A:71:GLU:HB2	2.38	0.58
1:B:181:THR:O	1:B:184:THR:OG1	2.18	0.58
1:B:36:ILE:O	1:B:40:CYS:N	2.36	0.58
1:C:173:ALA:O	1:C:176:SER:OG	2.18	0.58
1:F:253:VAL:O	1:F:262:LEU:N	2.35	0.58
1:I:201:PHE:HZ	1:I:205:LYS:HZ3	1.50	0.58
1:A:244:LEU:CB	1:A:252:VAL:HG12	2.32	0.58
1:A:52:LEU:HD22	1:D:234:PRO:HD2	1.86	0.58
1:I:80:GLU:OE1	1:I:83:SER:N	2.35	0.58
1:N:151:ALA:HB1	1:N:155:ARG:HH12	1.68	0.58
1:A:48:MET:SD	1:F:270:LYS:NZ	2.77	0.58
1:H:185:LEU:HB3	1:H:189:ARG:NH2	2.17	0.58
1:I:108:ALA:O	1:J:183:ILE:HG12	2.03	0.58
1:P:145:TRP:O	1:P:145:TRP:CD1	2.55	0.58
1:I:73:LYS:HD3	1:I:90:ARG:CZ	2.34	0.58
1:K:185:LEU:HD22	1:K:189:ARG:NH1	2.18	0.58
1:J:200:ILE:HD12	1:K:192:GLY:HA2	1.86	0.58
1:I:52:LEU:HD22	1:L:234:PRO:CD	2.32	0.58
1:M:222:ARG:CD	1:P:203:PHE:CE1	2.86	0.58
1:E:160:LEU:HD13	1:E:181:THR:CG2	2.34	0.58
1:H:210:ILE:O	1:H:213:GLN:N	2.37	0.58
1:I:97:GLN:O	1:I:101:VAL:HG23	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:87:TYR:HB3	1:I:106:TRP:NE1	2.18	0.58
1:M:202:ILE:HG23	1:N:202:ILE:HG23	1.86	0.58
1:B:244:LEU:HD12	1:B:261:TYR:HD1	1.68	0.58
1:E:23:HIS:ND1	1:E:28:ILE:O	2.37	0.58
1:N:225:TYR:N	1:N:272:ILE:CD1	2.65	0.58
1:D:111:ALA:HB3	1:D:205:LYS:NZ	2.18	0.58
1:I:26:PHE:O	1:I:28:ILE:HG23	2.03	0.58
1:I:39:GLN:OE1	1:N:275:PRO:HB2	2.03	0.58
1:I:63:TRP:HD1	1:I:112:PRO:HB2	1.69	0.58
1:N:272:ILE:HG23	1:N:273:PRO:HD2	1.85	0.58
1:D:222:ARG:O	1:D:243:VAL:HG23	2.03	0.58
1:E:160:LEU:HD13	1:E:181:THR:HG21	1.80	0.58
1:N:240:PRO:HB3	1:N:272:ILE:CD1	2.34	0.58
1:A:65:VAL:HG12	1:A:77:VAL:O	2.03	0.57
1:I:226:TYR:HE1	1:I:241:THR:HG22	1.67	0.57
1:I:108:ALA:CB	1:J:183:ILE:HD11	2.32	0.57
1:L:227:ARG:NE	1:L:234:PRO:HB2	2.09	0.57
1:M:12:HIS:CD2	1:M:17:GLN:O	2.57	0.57
1:N:240:PRO:HB2	1:N:272:ILE:CD1	2.33	0.57
1:G:212:GLN:HA	1:G:215:LYS:HG3	1.85	0.57
1:J:78:TRP:O	1:J:87:TYR:N	2.35	0.57
1:L:226:TYR:CE1	1:L:241:THR:HG21	2.39	0.57
1:N:12:HIS:O	1:N:16:HIS:N	2.35	0.57
1:M:222:ARG:HD2	1:P:203:PHE:CZ	2.39	0.57
1:A:17:GLN:OE1	1:I:188:LYS:HG2	2.04	0.57
1:C:36:ILE:O	1:C:40:CYS:N	2.38	0.57
1:J:82:ASN:HD22	1:J:82:ASN:C	2.06	0.57
1:D:227:ARG:HH12	2:S:5:DC:P	2.28	0.57
1:I:79:VAL:HG21	1:I:153:VAL:HG23	1.86	0.57
1:I:108:ALA:HB2	1:J:179:ALA:HB1	1.87	0.57
1:J:36:ILE:CG2	1:J:37:VAL:N	2.67	0.57
1:A:52:LEU:CD2	1:D:233:HIS:CB	2.78	0.57
1:E:251:ILE:HG21	1:E:271:PHE:HZ	1.68	0.57
1:H:245:TRP:HE3	1:H:252:VAL:HG23	1.69	0.57
1:J:79:VAL:HG22	1:J:86:ILE:HG22	1.87	0.57
1:D:251:ILE:O	1:D:264:ILE:HB	2.04	0.57
1:H:60:ILE:HG22	1:H:61:ASP:OD1	2.03	0.57
1:M:80:GLU:OE1	1:M:83:SER:N	2.37	0.57
1:E:64:GLN:N	1:E:79:VAL:O	2.36	0.57
1:I:60:ILE:HG22	1:I:61:ASP:OD1	2.04	0.57
1:K:191:GLY:N	1:K:195:THR:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:226:TYR:O	1:H:238:GLN:N	2.38	0.57
1:I:22:LEU:HD12	1:I:26:PHE:CE2	2.38	0.57
1:E:250:ALA:HB1	1:E:263:VAL:CG1	2.35	0.57
1:L:252:VAL:HG12	1:L:263:VAL:HA	1.85	0.57
1:M:152:LEU:O	1:M:156:THR:OG1	2.12	0.57
1:O:202:ILE:CG2	1:P:202:ILE:HG23	2.26	0.57
1:I:150:GLN:NE2	1:I:150:GLN:HA	2.20	0.56
1:J:36:ILE:CD1	1:J:261:TYR:CE2	2.84	0.56
1:K:121:PRO:O	1:K:125:ALA:N	2.36	0.56
1:G:34:GLU:HA	1:G:37:VAL:HG22	1.86	0.56
1:I:63:TRP:CG	1:I:106:TRP:CZ3	2.93	0.56
1:I:223:PHE:CB	1:I:241:THR:O	2.53	0.56
1:I:223:PHE:CA	1:I:241:THR:O	2.52	0.56
1:J:161:LYS:HD2	1:J:164:LEU:CD1	2.35	0.56
1:K:149:SER:O	1:K:153:VAL:HG23	2.06	0.56
1:M:211:GLN:O	1:M:214:SER:OG	2.23	0.56
1:N:41:ASP:O	1:N:45:GLU:N	2.36	0.56
1:E:176:SER:OG	1:F:101:VAL:HG22	2.05	0.56
1:I:64:GLN:N	1:I:79:VAL:O	2.23	0.56
1:A:65:VAL:HG12	1:A:78:TRP:CA	2.36	0.56
1:D:226:TYR:HE1	1:D:241:THR:CG2	2.17	0.56
1:E:223:PHE:CZ	1:E:272:ILE:CB	2.68	0.56
1:A:152:LEU:O	1:A:156:THR:HG23	2.04	0.56
1:A:223:PHE:HA	1:A:241:THR:O	2.05	0.56
1:A:52:LEU:CD2	1:D:234:PRO:HD2	2.35	0.56
1:F:184:THR:O	1:F:189:ARG:N	2.37	0.56
1:A:148:GLN:HG3	2:S:4:DG:H5"	1.87	0.56
1:B:185:LEU:O	1:B:189:ARG:NH2	2.38	0.56
1:D:224:CYS:HB2	1:D:270:LYS:O	2.05	0.56
1:E:184:THR:O	1:E:189:ARG:N	2.35	0.56
1:L:252:VAL:HG12	1:L:263:VAL:CB	2.36	0.56
1:A:144:PRO:HB2	1:A:145:TRP:CZ3	2.39	0.56
1:B:19:ALA:CB	1:B:33:ALA:HB1	2.30	0.56
1:F:61:ASP:O	1:F:113:LYS:HB3	2.06	0.56
1:N:106:TRP:O	1:N:110:PHE:N	2.38	0.56
1:A:155:ARG:NH2	2:S:6:DG:N3	2.53	0.56
1:B:173:ALA:O	1:B:176:SER:OG	2.23	0.56
1:F:43:CYS:SG	1:G:166:LYS:NZ	2.68	0.56
1:H:244:LEU:CB	1:H:252:VAL:HG12	2.30	0.56
1:A:51:THR:HG21	1:F:266:ASN:HB2	1.88	0.56
1:F:245:TRP:CZ3	1:F:247:GLY:HA3	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:5:ILE:HG12	1:J:28:ILE:HB	1.87	0.56
1:K:13:ASN:O	1:K:16:HIS:NE2	2.38	0.56
1:N:74:ILE:O	1:N:91:VAL:N	2.39	0.56
1:A:178:LEU:O	1:A:182:LEU:CG	2.45	0.56
1:F:15:TRP:HB2	1:F:17:GLN:OE1	2.06	0.56
1:G:191:GLY:O	1:G:195:THR:OG1	2.14	0.56
1:I:5:ILE:HG12	1:I:28:ILE:HD13	1.87	0.56
1:M:227:ARG:NE	1:P:148:GLN:OE1	2.38	0.56
1:B:8:ALA:HB2	1:B:26:PHE:CB	2.36	0.56
1:I:263:VAL:HG21	1:L:252:VAL:HG11	1.86	0.56
1:H:70:TYR:OH	1:H:165:GLU:OE1	2.23	0.55
1:I:244:LEU:HD13	1:I:261:TYR:CE1	2.39	0.55
1:J:161:LYS:CD	1:J:164:LEU:HD12	2.36	0.55
1:M:227:ARG:NH2	1:P:148:GLN:O	2.38	0.55
1:N:243:VAL:HG22	1:N:251:ILE:CD1	2.33	0.55
1:A:68:THR:HG1	1:A:157:HIS:CD2	2.24	0.55
1:D:254:LYS:HA	1:D:261:TYR:HD1	1.70	0.55
1:J:15:TRP:CZ2	1:L:134:TYR:CD2	2.92	0.55
1:P:253:VAL:O	1:P:262:LEU:N	2.37	0.55
1:A:150:GLN:O	1:A:150:GLN:HG3	2.05	0.55
1:E:244:LEU:CD1	1:E:261:TYR:CE1	2.88	0.55
1:A:66:ASP:N	1:A:153:VAL:HG21	2.22	0.55
1:A:68:THR:OG1	1:A:157:HIS:NE2	2.31	0.55
1:F:11:GLU:OE2	1:F:15:TRP:CD1	2.59	0.55
1:G:48:MET:HG3	1:G:48:MET:O	2.06	0.55
1:J:20:VAL:HG12	1:J:24:LEU:CD1	2.35	0.55
1:P:209:ARG:HG2	1:P:210:ILE:N	2.21	0.55
1:B:76:LEU:N	1:B:89:GLU:O	2.37	0.55
1:D:262:LEU:HB2	1:D:264:ILE:HD11	1.87	0.55
1:I:76:LEU:HD23	1:I:78:TRP:CZ2	2.42	0.55
1:J:85:LEU:HD11	1:J:186:ASN:CG	2.27	0.55
1:N:246:GLY:HA2	1:N:251:ILE:CB	2.37	0.55
1:A:23:HIS:O	1:A:27:GLY:N	2.40	0.55
1:A:53:ARG:O	1:D:234:PRO:HD2	2.06	0.55
1:I:23:HIS:O	1:I:27:GLY:N	2.40	0.55
1:J:67:TYR:CG	1:J:67:TYR:O	2.59	0.55
1:F:191:GLY:O	1:F:195:THR:OG1	2.12	0.55
1:I:202:ILE:HG23	1:J:202:ILE:HG12	1.88	0.55
1:L:254:LYS:HA	1:L:261:TYR:HA	1.88	0.55
1:A:224:CYS:SG	1:A:243:VAL:CG2	2.92	0.55
1:A:73:LYS:HD3	1:A:90:ARG:CZ	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:245:TRP:CE3	1:E:252:VAL:CG2	2.84	0.55
1:I:201:PHE:CE1	1:I:205:LYS:HD3	2.42	0.55
1:A:166:LYS:CD	1:I:43:CYS:HA	2.36	0.55
1:A:36:ILE:HG12	1:E:2:ILE:HD11	1.88	0.55
1:D:226:TYR:O	1:D:238:GLN:CB	2.49	0.55
1:F:46:ASN:HB2	1:G:162:ASN:OD1	2.07	0.55
1:L:255:ASP:N	1:L:260:ARG:O	2.36	0.55
1:N:60:ILE:HD13	1:N:204:ASN:HB3	1.88	0.55
1:C:193:LEU:HD12	1:C:193:LEU:C	2.27	0.54
1:A:79:VAL:HG21	1:A:153:VAL:HG23	1.88	0.54
1:F:11:GLU:OE2	1:F:15:TRP:NE1	2.40	0.54
1:A:166:LYS:HG2	1:I:42:VAL:O	2.07	0.54
1:L:265:ALA:O	1:L:268:ASP:N	2.40	0.54
1:P:229:ARG:NH2	1:P:268:ASP:OD1	2.40	0.54
1:A:2:ILE:HD11	1:E:35:ASP:OD2	2.06	0.54
1:F:12:HIS:O	1:F:16:HIS:N	2.37	0.54
1:G:37:VAL:HG23	1:G:38:GLN:N	2.22	0.54
1:H:182:LEU:O	1:H:186:ASN:CB	2.54	0.54
1:H:184:THR:O	1:H:189:ARG:N	2.39	0.54
1:I:12:HIS:CE1	1:I:37:VAL:HG12	2.42	0.54
1:I:34:GLU:O	1:I:37:VAL:HG22	2.07	0.54
1:J:30:ARG:NH2	1:J:60:ILE:HD12	2.21	0.54
1:K:173:ALA:O	1:K:176:SER:OG	2.25	0.54
1:D:251:ILE:CD1	1:D:269:VAL:HG11	2.30	0.54
1:H:186:ASN:O	1:H:198:MET:CB	2.55	0.54
1:J:198:MET:O	1:J:202:ILE:CD1	2.55	0.54
1:A:223:PHE:CA	1:A:241:THR:O	2.55	0.54
1:F:11:GLU:CD	1:F:15:TRP:CD1	2.81	0.54
1:G:202:ILE:HD13	1:H:205:LYS:CG	2.37	0.54
1:H:206:GLU:OE1	1:H:209:ARG:NH2	2.41	0.54
1:I:51:THR:HG22	1:N:266:ASN:HD22	1.69	0.54
1:D:258:THR:CG2	1:D:258:THR:O	2.56	0.54
1:K:211:GLN:O	1:K:214:SER:OG	2.14	0.54
1:N:166:LYS:NZ	1:O:16:HIS:O	2.41	0.54
1:F:248:ASP:CB	2:S:3:DT:O2	2.56	0.54
1:A:166:LYS:O	1:I:42:VAL:HG11	2.07	0.54
1:A:37:VAL:CG1	1:A:43:CYS:HB3	2.34	0.54
1:F:17:GLN:NE2	1:G:188:LYS:HG3	2.22	0.54
1:H:60:ILE:HG22	1:H:61:ASP:N	2.22	0.54
1:I:184:THR:CA	1:I:188:LYS:CB	2.86	0.54
1:I:68:THR:HG23	1:I:68:THR:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:151:ALA:HB1	1:N:155:ARG:NH1	2.22	0.54
1:C:184:THR:O	1:C:189:ARG:N	2.37	0.54
1:G:29:PRO:HG3	1:G:211:GLN:HG3	1.90	0.54
1:L:254:LYS:HB3	1:L:261:TYR:CE1	2.41	0.54
1:H:183:ILE:HG21	1:H:188:LYS:HZ3	1.73	0.54
1:K:20:VAL:HG12	1:K:24:LEU:CD1	2.38	0.54
1:B:244:LEU:HD13	1:B:261:TYR:CD1	2.40	0.54
1:F:118:ASP:C	1:F:120:GLY:N	2.58	0.54
1:F:213:GLN:O	1:F:217:LYS:HB2	2.08	0.54
1:I:66:ASP:N	1:I:153:VAL:HG21	2.22	0.54
1:J:191:GLY:O	1:J:195:THR:OG1	2.15	0.54
1:K:247:GLY:CA	1:K:250:ALA:O	2.55	0.54
1:L:223:PHE:CE1	1:L:240:PRO:CB	2.90	0.54
1:A:231:ARG:NE	2:Q:18:DG:H21	2.06	0.53
1:E:64:GLN:O	1:E:79:VAL:N	2.39	0.53
1:I:127:SER:HA	1:I:130:LEU:HB3	1.90	0.53
1:I:190:LYS:HG2	1:I:196:SER:N	2.22	0.53
1:H:213:GLN:O	1:H:216:SER:OG	2.26	0.53
1:I:240:PRO:HG3	1:P:223:PHE:CE1	2.38	0.53
1:N:221:ILE:HG21	1:N:242:GLN:OE1	2.09	0.53
1:A:240:PRO:HG3	1:H:223:PHE:HZ	1.57	0.53
1:D:224:CYS:SG	1:D:269:VAL:HB	2.48	0.53
1:E:222:ARG:O	1:E:243:VAL:CB	2.56	0.53
1:P:255:ASP:O	1:P:259:ASP:N	2.41	0.53
1:I:52:LEU:O	1:I:52:LEU:CD2	2.54	0.53
1:A:126:GLU:HG2	1:A:130:LEU:HD11	1.89	0.53
1:A:207:GLN:CB	1:D:222:ARG:CZ	2.82	0.53
1:I:255:ASP:O	1:I:259:ASP:N	2.42	0.53
1:F:15:TRP:CE2	1:G:188:LYS:NZ	2.76	0.53
1:M:28:ILE:O	1:M:29:PRO:C	2.47	0.53
1:N:118:ASP:OD1	1:N:123:PHE:CE2	2.62	0.53
1:A:221:ILE:CG2	1:A:242:GLN:CB	2.84	0.53
1:A:255:ASP:O	1:A:259:ASP:N	2.42	0.53
1:A:76:LEU:HD23	1:A:78:TRP:CZ2	2.42	0.53
1:C:193:LEU:HD12	1:C:193:LEU:O	2.08	0.53
1:H:245:TRP:HB3	1:H:252:VAL:HG21	1.90	0.53
1:G:93:GLY:N	1:G:98:GLU:OE1	2.42	0.53
1:A:3:GLU:C	1:A:5:ILE:N	2.63	0.53
1:B:229:ARG:NH2	1:B:268:ASP:OD1	2.42	0.53
1:F:251:ILE:HG12	1:F:253:VAL:HG13	1.90	0.53
1:G:23:HIS:ND1	1:G:28:ILE:O	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:57:LYS:HA	1:I:81:THR:O	2.08	0.53
1:J:15:TRP:CD1	1:J:15:TRP:N	2.76	0.53
1:J:206:GLU:O	1:J:210:ILE:HG13	2.09	0.53
1:K:199:ASP:O	1:L:209:ARG:NH1	2.42	0.53
1:B:34:GLU:OE2	1:B:60:ILE:N	2.42	0.53
1:F:251:ILE:HG22	1:F:264:ILE:C	2.29	0.53
1:P:223:PHE:CD1	1:P:241:THR:O	2.61	0.53
1:A:252:VAL:HG22	1:D:252:VAL:CG2	2.38	0.52
1:F:121:PRO:O	1:F:125:ALA:N	2.42	0.52
1:G:79:VAL:HG11	1:G:153:VAL:HG22	1.91	0.52
1:O:41:ASP:O	1:O:45:GLU:N	2.37	0.52
1:C:17:GLN:CD	1:C:22:LEU:HD21	2.30	0.52
1:H:185:LEU:HD22	1:H:189:ARG:NH1	2.24	0.52
1:K:199:ASP:HB3	1:L:209:ARG:NH1	2.24	0.52
1:I:244:LEU:CB	1:I:252:VAL:HG12	2.32	0.52
1:J:23:HIS:ND1	1:J:28:ILE:O	2.34	0.52
1:M:2:ILE:O	1:M:6:PRO:CD	2.56	0.52
1:I:255:ASP:O	1:I:258:THR:OG1	2.19	0.52
1:J:68:THR:O	1:J:75:ILE:N	2.42	0.52
1:M:156:THR:O	1:M:160:LEU:HB2	2.09	0.52
1:H:245:TRP:N	1:H:252:VAL:HB	2.25	0.52
1:H:80:GLU:HG3	1:H:201:PHE:HD2	1.74	0.52
1:N:272:ILE:HG22	1:N:273:PRO:HD2	1.90	0.52
1:N:65:VAL:HG13	1:N:77:VAL:O	2.09	0.52
1:A:188:LYS:HE2	1:I:15:TRP:CB	2.37	0.52
1:A:57:LYS:O	1:A:82:ASN:N	2.42	0.52
1:C:17:GLN:OE1	1:C:22:LEU:HD21	2.10	0.52
1:C:226:TYR:O	1:C:238:GLN:N	2.37	0.52
1:H:64:GLN:O	1:H:79:VAL:N	2.43	0.52
1:I:107:TYR:CD1	1:I:112:PRO:CG	2.91	0.52
1:I:187:ILE:CD1	1:J:110:PHE:O	2.57	0.52
1:A:221:ILE:CG2	1:A:242:GLN:OE1	2.48	0.52
1:A:2:ILE:O	1:A:5:ILE:CD1	2.55	0.52
1:C:211:GLN:O	1:C:214:SER:OG	2.14	0.52
1:C:265:ALA:O	1:C:268:ASP:N	2.43	0.52
1:E:245:TRP:O	1:E:252:VAL:N	2.27	0.52
1:H:121:PRO:O	1:H:125:ALA:N	2.43	0.52
1:K:20:VAL:O	1:K:24:LEU:CG	2.58	0.52
1:M:191:GLY:N	1:M:195:THR:O	2.43	0.52
1:E:226:TYR:O	1:E:238:GLN:N	2.40	0.52
1:A:145:TRP:CD1	1:F:232:GLY:HA2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:178:LEU:O	1:H:181:THR:OG1	2.21	0.52
1:I:201:PHE:HZ	1:I:205:LYS:NZ	2.07	0.52
1:I:56:ASN:O	1:I:81:THR:HB	2.09	0.52
1:I:76:LEU:O	1:I:88:ALA:CB	2.56	0.52
1:J:200:ILE:HD13	1:K:193:LEU:CD1	2.40	0.52
1:O:173:ALA:O	1:O:176:SER:OG	2.28	0.52
1:A:231:ARG:HB3	2:Q:19:DG:H21	1.73	0.52
1:B:193:LEU:HD12	1:C:193:LEU:HD11	1.92	0.52
1:B:23:HIS:ND1	1:B:28:ILE:O	2.39	0.52
1:E:63:TRP:O	1:E:116:GLN:N	2.42	0.52
1:E:227:ARG:NE	1:H:148:GLN:OE1	2.43	0.52
1:A:76:LEU:O	1:A:88:ALA:CB	2.55	0.52
1:E:245:TRP:CE2	1:E:246:GLY:O	2.63	0.52
1:F:245:TRP:CZ3	1:F:247:GLY:CA	2.93	0.52
1:J:206:GLU:HG3	1:J:207:GLN:HG3	1.92	0.52
1:A:18:ASP:OD1	1:A:18:ASP:O	2.28	0.51
1:A:208:GLN:HG2	1:A:208:GLN:O	2.10	0.51
1:A:244:LEU:CD2	1:A:261:TYR:CD1	2.92	0.51
1:E:117:SER:OG	1:E:140:THR:O	2.18	0.51
1:I:2:ILE:N	1:I:2:ILE:CD1	2.73	0.51
1:I:64:GLN:HE21	1:I:81:THR:HG22	1.75	0.51
1:J:105:LYS:O	1:J:108:ALA:HB3	2.10	0.51
1:J:159:THR:O	1:J:163:THR:HG23	2.10	0.51
1:J:218:GLN:OE1	1:J:218:GLN:N	2.43	0.51
1:A:207:GLN:HB3	1:D:222:ARG:CZ	2.34	0.51
1:A:58:ARG:HA	1:D:267:LYS:HG2	1.92	0.51
1:B:8:ALA:HB1	1:B:26:PHE:CD2	2.46	0.51
1:H:182:LEU:O	1:H:186:ASN:HB2	2.09	0.51
1:I:68:THR:HB	1:I:157:HIS:CD2	2.45	0.51
1:D:228:THR:O	1:D:234:PRO:HA	2.11	0.51
1:N:64:GLN:O	1:N:79:VAL:N	2.43	0.51
1:A:148:GLN:HB3	2:S:4:DG:C4'	2.39	0.51
1:A:63:TRP:CZ3	1:A:80:GLU:HB2	2.46	0.51
1:A:70:TYR:CD1	1:A:71:GLU:HB2	2.46	0.51
1:D:233:HIS:CB	1:D:234:PRO:HD3	2.35	0.51
1:H:251:ILE:HD11	1:H:269:VAL:HG22	1.92	0.51
1:H:60:ILE:N	1:H:60:ILE:CD1	2.73	0.51
1:A:263:VAL:HG23	1:D:263:VAL:CG2	2.41	0.51
1:F:274:PRO:N	1:F:275:PRO:CD	2.73	0.51
1:H:107:TYR:CE2	1:H:135:LEU:HD22	2.46	0.51
1:E:195:THR:OG1	1:E:200:ILE:HD11	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:228:THR:O	1:L:234:PRO:HA	2.11	0.51
1:A:231:ARG:HE	2:Q:18:DG:H21	1.58	0.51
1:A:55:SER:N	2:S:5:DC:OP1	2.43	0.51
1:D:226:TYR:CE1	1:D:241:THR:HG22	2.42	0.51
1:F:119:ASN:O	1:F:124:VAL:CG2	2.59	0.51
1:P:146:ASN:O	1:P:150:GLN:HB2	2.11	0.51
1:A:223:PHE:CD1	1:A:242:GLN:N	2.78	0.51
1:A:99:PHE:CG	1:A:122:ALA:HB1	2.46	0.51
1:C:111:ALA:HB3	1:C:205:LYS:NZ	2.26	0.51
1:A:203:PHE:CE2	1:D:222:ARG:CD	2.91	0.51
1:A:68:THR:OG1	1:A:157:HIS:CD2	2.64	0.51
1:G:29:PRO:HG3	1:G:211:GLN:NE2	2.26	0.51
1:I:107:TYR:CA	1:I:112:PRO:HG3	2.40	0.51
1:I:47:LYS:O	1:N:270:LYS:NZ	2.26	0.51
1:L:241:THR:HG21	1:L:253:VAL:HG21	1.93	0.51
1:A:211:GLN:O	1:A:215:LYS:CG	2.44	0.51
1:A:63:TRP:CE2	1:A:80:GLU:HG2	2.45	0.51
1:I:187:ILE:HA	1:I:196:SER:CB	2.41	0.51
1:I:201:PHE:CZ	1:I:205:LYS:NZ	2.78	0.51
1:I:22:LEU:CD1	1:I:26:PHE:CE2	2.94	0.51
1:G:68:THR:O	1:G:75:ILE:N	2.40	0.50
1:I:22:LEU:CD1	1:I:26:PHE:CD2	2.95	0.50
1:I:66:ASP:OD1	1:I:67:TYR:N	2.44	0.50
1:J:206:GLU:O	1:J:210:ILE:CG1	2.59	0.50
1:O:178:LEU:O	1:O:181:THR:OG1	2.21	0.50
1:P:60:ILE:HD11	1:P:82:ASN:HD22	1.75	0.50
1:C:30:ARG:NH1	1:C:211:GLN:OE1	2.44	0.50
1:D:223:PHE:CE2	1:D:272:ILE:HG21	2.45	0.50
1:H:228:THR:O	1:H:235:GLY:N	2.44	0.50
1:H:93:GLY:N	1:H:98:GLU:OE1	2.43	0.50
1:I:88:ALA:H	1:I:182:LEU:HD21	1.77	0.50
1:J:14:LYS:CB	1:J:15:TRP:CD1	2.94	0.50
1:A:39:GLN:NE2	1:F:276:LYS:O	2.39	0.50
1:A:66:ASP:OD1	1:A:67:TYR:N	2.44	0.50
1:F:11:GLU:O	1:F:15:TRP:HD1	1.93	0.50
1:E:227:ARG:CZ	1:H:148:GLN:OE1	2.59	0.50
1:J:8:ALA:HB3	1:J:28:ILE:HD13	1.91	0.50
1:M:191:GLY:O	1:M:195:THR:OG1	2.24	0.50
1:N:187:ILE:HG12	1:N:198:MET:SD	2.51	0.50
1:P:93:GLY:N	1:P:98:GLU:OE1	2.45	0.50
1:A:184:THR:CA	1:A:188:LYS:CB	2.85	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:GLN:O	1:C:79:VAL:N	2.43	0.50
1:I:99:PHE:CG	1:I:122:ALA:HB1	2.46	0.50
1:L:226:TYR:HB2	1:L:264:ILE:HG21	1.92	0.50
1:M:222:ARG:NE	1:P:203:PHE:CZ	2.79	0.50
1:P:70:TYR:OH	1:P:165:GLU:OE1	2.30	0.50
1:A:207:GLN:HG3	1:D:222:ARG:NE	2.24	0.50
1:J:9:GLU:OE1	1:J:36:ILE:CG1	2.56	0.50
1:L:64:GLN:N	1:L:79:VAL:O	2.44	0.50
1:M:156:THR:O	1:M:160:LEU:HB3	2.10	0.50
1:A:183:ILE:HD13	1:I:15:TRP:CH2	2.47	0.50
1:E:210:ILE:O	1:E:214:SER:OG	2.07	0.50
1:A:184:THR:CB	1:A:188:LYS:CG	2.89	0.50
1:A:52:LEU:CG	1:D:232:GLY:O	2.60	0.50
1:I:64:GLN:NE2	1:I:81:THR:HG22	2.26	0.50
1:L:226:TYR:CE1	1:L:241:THR:CG2	2.94	0.50
1:C:20:VAL:HG12	1:C:24:LEU:HD11	1.94	0.50
1:F:46:ASN:C	1:G:162:ASN:HD21	2.14	0.50
1:H:181:THR:O	1:H:184:THR:OG1	2.28	0.50
1:L:233:HIS:CB	1:L:234:PRO:HD3	2.35	0.50
1:O:12:HIS:O	1:O:16:HIS:N	2.42	0.50
1:B:30:ARG:NH2	1:B:60:ILE:HD12	2.27	0.50
1:F:184:THR:HA	1:F:188:LYS:HB2	1.94	0.50
1:P:184:THR:O	1:P:189:ARG:N	2.39	0.50
1:A:66:ASP:H	1:A:153:VAL:HG21	1.77	0.49
1:E:157:HIS:O	1:E:161:LYS:HG3	2.12	0.49
1:P:89:GLU:OE2	1:P:105:LYS:NZ	2.41	0.49
1:E:16:HIS:HD2	1:E:167:LEU:HD21	1.77	0.49
1:M:16:HIS:CD2	1:M:42:VAL:HB	2.46	0.49
1:A:240:PRO:HG3	1:H:223:PHE:CE1	2.36	0.49
1:I:88:ALA:N	1:I:182:LEU:HD21	2.27	0.49
1:B:8:ALA:CB	1:B:26:PHE:CD2	2.95	0.49
1:D:223:PHE:HB3	1:D:242:GLN:HG2	1.95	0.49
1:D:262:LEU:CB	1:D:264:ILE:HD11	2.43	0.49
1:F:4:ASN:O	1:F:8:ALA:N	2.43	0.49
1:I:17:GLN:N	1:I:17:GLN:OE1	2.45	0.49
1:I:78:TRP:CZ3	1:I:106:TRP:CE3	3.00	0.49
1:K:2:ILE:CD1	1:K:250:ALA:HB3	2.43	0.49
1:N:60:ILE:CG2	1:N:204:ASN:CB	2.87	0.49
1:B:244:LEU:CD1	1:B:261:TYR:HD1	2.16	0.49
1:J:190:LYS:N	1:K:21:SER:OG	2.44	0.49
1:K:64:GLN:O	1:K:79:VAL:N	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:173:ALA:O	1:P:176:SER:OG	2.23	0.49
1:A:244:LEU:CD2	1:A:261:TYR:CE1	2.95	0.49
1:J:64:GLN:N	1:J:79:VAL:O	2.44	0.49
1:A:62:HIS:C	1:A:63:TRP:CD1	2.86	0.49
1:B:5:ILE:HB	1:B:6:PRO:HD3	1.95	0.49
1:F:273:PRO:C	1:F:275:PRO:HD2	2.33	0.49
1:G:173:ALA:O	1:G:176:SER:OG	2.28	0.49
1:L:226:TYR:HE1	1:L:241:THR:CG2	2.26	0.49
1:M:83:SER:CB	1:M:200:ILE:HB	2.42	0.49
1:N:224:CYS:CA	1:N:272:ILE:HG13	2.20	0.49
1:A:244:LEU:CD2	1:A:252:VAL:HG12	2.43	0.49
1:G:203:PHE:HB2	1:H:209:ARG:HH22	1.78	0.49
1:J:68:THR:HG21	1:J:157:HIS:CD2	2.47	0.49
1:B:182:LEU:O	1:B:186:ASN:ND2	2.45	0.49
1:G:185:LEU:HD22	1:G:189:ARG:NH1	2.28	0.49
1:I:77:VAL:CB	1:I:153:VAL:HG23	2.43	0.49
1:J:115:LEU:HD23	1:J:139:HIS:CD2	2.48	0.49
1:J:115:LEU:N	1:J:138:GLU:O	2.45	0.49
1:J:8:ALA:CB	1:J:28:ILE:CD1	2.89	0.49
1:A:166:LYS:CB	1:I:42:VAL:CG1	2.86	0.48
1:F:106:TRP:O	1:F:109:MET:N	2.45	0.48
1:F:255:ASP:O	1:F:259:ASP:N	2.46	0.48
1:I:63:TRP:CD1	1:I:106:TRP:HZ3	2.31	0.48
1:M:12:HIS:O	1:M:16:HIS:N	2.43	0.48
1:N:245:TRP:O	1:N:251:ILE:HB	2.13	0.48
1:A:77:VAL:CB	1:A:153:VAL:HG23	2.43	0.48
1:F:119:ASN:O	1:F:124:VAL:HG21	2.13	0.48
1:H:185:LEU:HD22	1:H:189:ARG:HD3	1.96	0.48
1:H:244:LEU:HD12	1:H:252:VAL:HG12	1.94	0.48
1:J:161:LYS:HD2	1:J:164:LEU:HD12	1.93	0.48
1:A:150:GLN:HB2	1:A:153:VAL:CG1	2.44	0.48
1:B:24:LEU:HD22	1:C:194:GLY:N	2.28	0.48
1:F:58:ARG:NH1	1:F:149:SER:HB3	2.21	0.48
1:F:46:ASN:CB	1:G:162:ASN:OD1	2.60	0.48
1:F:80:GLU:OE1	1:F:83:SER:N	2.47	0.48
1:N:187:ILE:HG12	1:N:198:MET:CE	2.43	0.48
1:A:59:GLY:N	1:A:62:HIS:HB3	2.28	0.48
1:J:68:THR:CG2	1:J:157:HIS:NE2	2.77	0.48
1:J:9:GLU:HG3	1:J:261:TYR:HB2	1.95	0.48
1:O:38:GLN:OE1	1:O:44:GLN:NE2	2.46	0.48
1:F:251:ILE:CG2	1:F:264:ILE:CB	2.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:41:ASP:O	1:G:45:GLU:N	2.41	0.48
1:K:60:ILE:N	1:K:82:ASN:OD1	2.47	0.48
1:N:60:ILE:O	1:N:80:GLU:OE2	2.30	0.48
1:A:2:ILE:CG2	1:A:5:ILE:HD12	2.44	0.48
1:E:164:LEU:O	1:E:168:ILE:N	2.46	0.48
1:I:79:VAL:HG21	1:I:153:VAL:CG2	2.44	0.48
1:I:68:THR:HB	1:I:157:HIS:HD2	1.79	0.48
1:J:20:VAL:O	1:J:24:LEU:CG	2.57	0.48
1:H:68:THR:O	1:H:75:ILE:N	2.46	0.48
1:I:63:TRP:CZ3	1:I:80:GLU:CB	2.93	0.48
1:J:36:ILE:HD13	1:J:261:TYR:CE2	2.48	0.48
1:M:132:MET:O	1:M:136:GLY:N	2.46	0.48
1:B:34:GLU:OE1	1:B:113:LYS:NZ	2.46	0.48
1:F:187:ILE:HG23	1:F:188:LYS:H	1.76	0.48
1:J:62:HIS:O	1:J:81:THR:N	2.42	0.48
1:A:148:GLN:CD	2:S:4:DG:C8	2.87	0.48
1:A:59:GLY:H	1:A:62:HIS:CB	2.27	0.48
1:A:63:TRP:N	1:A:63:TRP:CD1	2.82	0.48
1:D:111:ALA:HB3	1:D:205:LYS:HZ3	1.78	0.48
1:F:115:LEU:N	1:F:138:GLU:O	2.46	0.48
1:F:64:GLN:O	1:F:79:VAL:N	2.46	0.48
1:G:12:HIS:O	1:G:16:HIS:N	2.43	0.48
1:G:149:SER:O	1:G:153:VAL:HG23	2.14	0.48
1:J:79:VAL:CG1	1:J:86:ILE:HG22	2.40	0.48
1:A:184:THR:O	1:A:188:LYS:CA	2.62	0.48
1:D:269:VAL:O	1:D:269:VAL:HG23	2.14	0.48
1:A:63:TRP:HB3	1:A:79:VAL:O	2.14	0.47
1:E:2:ILE:O	1:E:6:PRO:HD2	2.11	0.47
1:F:224:CYS:SG	1:F:251:ILE:HD11	2.54	0.47
1:F:251:ILE:HG22	1:F:264:ILE:HB	1.91	0.47
1:H:210:ILE:O	1:H:213:GLN:HB3	2.14	0.47
1:A:188:LYS:HE2	1:I:15:TRP:CG	2.49	0.47
1:I:30:ARG:O	1:I:33:ALA:HB3	2.14	0.47
1:E:80:GLU:N	1:E:85:LEU:O	2.39	0.47
1:H:143:ILE:O	1:H:144:PRO:C	2.52	0.47
1:H:182:LEU:O	1:H:186:ASN:CG	2.52	0.47
1:L:227:ARG:CZ	1:L:234:PRO:HB2	2.44	0.47
1:M:12:HIS:NE2	1:M:17:GLN:O	2.47	0.47
1:A:262:LEU:HA	1:D:263:VAL:HG21	1.97	0.47
1:I:87:TYR:CD2	1:I:106:TRP:CD1	3.02	0.47
1:I:184:THR:O	1:I:188:LYS:CA	2.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:70:TYR:O	1:J:73:LYS:N	2.48	0.47
1:A:30:ARG:O	1:A:33:ALA:HB3	2.14	0.47
1:J:15:TRP:CH2	1:L:135:LEU:HD23	2.50	0.47
1:K:23:HIS:ND1	1:K:28:ILE:O	2.46	0.47
1:I:149:SER:OG	2:Q:3:DT:O5'	2.31	0.47
1:A:226:TYR:CE1	1:A:241:THR:HG22	2.50	0.47
1:A:59:GLY:CA	1:A:62:HIS:CB	2.92	0.47
1:G:209:ARG:NH2	1:H:203:PHE:CD2	2.83	0.47
1:N:223:PHE:O	1:N:272:ILE:N	2.43	0.47
1:O:16:HIS:CE1	1:O:42:VAL:HG21	2.49	0.47
1:A:13:ASN:O	1:A:16:HIS:NE2	2.48	0.47
1:A:178:LEU:HG	1:A:182:LEU:HD11	1.97	0.47
1:A:184:THR:HB	1:A:188:LYS:HB2	1.96	0.47
1:B:175:GLU:HA	1:B:178:LEU:HB3	1.95	0.47
1:E:65:VAL:HG22	1:E:78:TRP:HA	1.96	0.47
1:I:13:ASN:O	1:I:16:HIS:NE2	2.47	0.47
1:J:79:VAL:HG22	1:J:86:ILE:CG2	2.44	0.47
1:M:64:GLN:O	1:M:79:VAL:N	2.46	0.47
1:A:148:GLN:HB3	2:S:4:DG:H5''	1.81	0.47
1:A:244:LEU:HD12	1:A:244:LEU:N	2.30	0.47
1:I:196:SER:O	1:I:197:PRO:C	2.52	0.47
1:A:209:ARG:O	1:A:213:GLN:HB2	2.14	0.47
1:A:19:ALA:HB1	1:A:33:ALA:HB1	1.96	0.47
1:J:14:LYS:HB3	1:J:15:TRP:CD1	2.50	0.47
1:M:24:LEU:HD13	1:M:194:GLY:HA2	1.96	0.47
1:A:126:GLU:O	1:A:130:LEU:CG	2.50	0.47
1:A:175:GLU:N	1:A:175:GLU:OE1	2.47	0.47
1:A:67:TYR:CZ	1:A:94:GLU:CB	2.96	0.47
1:J:87:TYR:CD1	1:J:106:TRP:HD1	2.32	0.47
1:O:211:GLN:O	1:O:214:SER:N	2.47	0.47
1:A:152:LEU:HD21	2:S:5:DC:H4'	1.96	0.47
1:B:121:PRO:O	1:B:125:ALA:HB2	2.15	0.47
1:C:12:HIS:ND1	1:C:22:LEU:HD11	2.30	0.47
1:D:254:LYS:CG	1:D:254:LYS:O	2.63	0.47
1:E:206:GLU:OE2	1:E:209:ARG:NH2	2.47	0.47
1:J:15:TRP:HH2	1:L:135:LEU:HD23	1.79	0.47
1:N:38:GLN:OE1	1:N:44:GLN:OE1	2.32	0.47
1:I:155:ARG:NH2	2:Q:6:DG:N3	2.57	0.47
1:A:247:GLY:N	1:A:250:ALA:O	2.45	0.47
1:A:254:LYS:NZ	1:A:261:TYR:CE1	2.83	0.47
1:B:253:VAL:O	1:B:262:LEU:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:252:VAL:HG12	1:D:253:VAL:N	2.29	0.47
1:E:250:ALA:CB	1:E:263:VAL:CG1	2.93	0.47
1:I:66:ASP:H	1:I:153:VAL:HG21	1.80	0.47
1:I:175:GLU:OE1	1:I:175:GLU:N	2.47	0.47
1:B:43:CYS:SG	1:C:166:LYS:NZ	2.78	0.46
1:F:265:ALA:HB1	1:F:267:LYS:HG2	1.96	0.46
1:I:49:PRO:HG3	1:N:269:VAL:O	2.15	0.46
1:N:80:GLU:OE1	1:N:83:SER:N	2.48	0.46
1:P:146:ASN:O	1:P:150:GLN:CB	2.63	0.46
1:A:66:ASP:O	1:A:77:VAL:N	2.47	0.46
1:C:62:HIS:CG	1:C:114:SER:HG	2.28	0.46
1:M:196:SER:N	1:M:199:ASP:OD2	2.40	0.46
1:M:83:SER:HB2	1:M:200:ILE:HB	1.98	0.46
1:N:149:SER:O	1:N:153:VAL:HG23	2.16	0.46
1:A:60:ILE:O	1:A:61:ASP:HB2	2.15	0.46
1:D:65:VAL:HG23	1:D:115:LEU:HD11	1.97	0.46
1:E:164:LEU:C	1:E:168:ILE:HG22	2.33	0.46
1:K:209:ARG:O	1:K:213:GLN:HG3	2.15	0.46
1:K:224:CYS:N	1:K:241:THR:O	2.44	0.46
1:M:226:TYR:N	1:M:238:GLN:O	2.46	0.46
1:O:62:HIS:CG	1:O:114:SER:HG	2.29	0.46
1:A:60:ILE:O	1:A:60:ILE:HG23	2.16	0.46
1:C:21:SER:HA	1:C:24:LEU:HD12	1.96	0.46
1:D:258:THR:HG21	1:D:260:ARG:HD2	1.98	0.46
1:A:223:PHE:HB3	1:A:241:THR:O	2.16	0.46
1:D:164:LEU:O	1:D:168:ILE:HG23	2.16	0.46
1:F:15:TRP:O	1:F:16:HIS:HB2	2.15	0.46
1:A:14:LYS:NZ	1:J:134:TYR:O	2.41	0.46
1:I:202:ILE:HG22	1:J:202:ILE:HG23	1.98	0.46
1:K:199:ASP:HB3	1:L:209:ARG:CZ	2.46	0.46
1:I:263:VAL:HG23	1:L:252:VAL:HG11	1.96	0.46
1:N:224:CYS:CA	1:N:272:ILE:CG1	2.88	0.46
1:P:149:SER:O	1:P:153:VAL:HG23	2.16	0.46
1:A:77:VAL:HG11	1:A:79:VAL:HG21	1.97	0.46
1:D:93:GLY:N	1:D:98:GLU:OE1	2.49	0.46
1:E:250:ALA:HB1	1:E:263:VAL:HG13	1.98	0.46
1:D:224:CYS:HA	1:D:270:LYS:O	2.16	0.46
1:I:184:THR:HB	1:I:188:LYS:HB3	1.98	0.46
1:I:79:VAL:HG21	1:I:153:VAL:CB	2.46	0.46
1:J:65:VAL:CG2	1:J:78:TRP:CE3	2.99	0.46
1:E:12:HIS:O	1:E:16:HIS:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:251:ILE:HG22	1:F:264:ILE:CA	2.45	0.46
1:I:201:PHE:CE1	1:I:205:LYS:CD	2.99	0.46
1:J:79:VAL:HG13	1:J:86:ILE:CG2	2.41	0.46
1:N:21:SER:OG	1:O:190:LYS:N	2.49	0.46
1:A:153:VAL:O	1:A:156:THR:OG1	2.27	0.45
1:F:183:ILE:O	1:F:187:ILE:HG22	2.16	0.45
1:I:241:THR:OG1	1:I:242:GLN:N	2.48	0.45
1:J:68:THR:HG21	1:J:157:HIS:NE2	2.31	0.45
1:L:184:THR:O	1:L:189:ARG:N	2.49	0.45
1:N:30:ARG:NE	1:N:60:ILE:HD11	2.31	0.45
1:E:250:ALA:HB1	1:E:263:VAL:HG12	1.97	0.45
1:F:118:ASP:O	1:F:120:GLY:N	2.50	0.45
1:H:106:TRP:O	1:H:110:PHE:N	2.49	0.45
1:J:9:GLU:HG3	1:J:261:TYR:CD2	2.51	0.45
1:M:159:THR:O	1:M:163:THR:HG23	2.15	0.45
1:O:23:HIS:ND1	1:O:28:ILE:O	2.42	0.45
1:A:132:MET:O	1:A:137:ILE:N	2.50	0.45
1:A:79:VAL:HG21	1:A:153:VAL:CG2	2.47	0.45
1:A:37:VAL:HG11	1:A:43:CYS:CB	2.37	0.45
1:E:105:LYS:O	1:E:108:ALA:HB3	2.16	0.45
1:I:153:VAL:O	1:I:156:THR:OG1	2.27	0.45
1:J:4:ASN:HB2	1:J:28:ILE:CG2	2.46	0.45
1:M:65:VAL:HG23	1:M:115:LEU:HD11	1.98	0.45
1:N:224:CYS:CA	1:N:272:ILE:CD1	2.94	0.45
1:M:267:LYS:HA	1:P:81:THR:OG1	2.15	0.45
1:A:148:GLN:O	1:A:149:SER:C	2.53	0.45
1:G:132:MET:O	1:G:137:ILE:N	2.50	0.45
1:H:62:HIS:O	1:H:81:THR:HG23	2.16	0.45
1:H:92:LYS:N	1:H:98:GLU:OE2	2.41	0.45
1:J:203:PHE:CD1	1:J:206:GLU:OE2	2.69	0.45
1:K:3:GLU:HA	1:K:263:VAL:HG11	1.99	0.45
1:B:159:THR:O	1:B:163:THR:HG23	2.17	0.45
1:B:188:LYS:HB3	1:C:17:GLN:HE21	1.82	0.45
1:H:245:TRP:HB3	1:H:252:VAL:HG23	1.94	0.45
1:I:244:LEU:CD1	1:I:252:VAL:HG12	2.45	0.45
1:I:40:CYS:SG	1:I:42:VAL:N	2.89	0.45
1:O:86:ILE:O	1:O:186:ASN:ND2	2.48	0.45
1:P:146:ASN:O	1:P:150:GLN:HG2	2.17	0.45
1:M:222:ARG:CD	1:P:203:PHE:CZ	2.99	0.45
1:J:78:TRP:CD1	1:J:87:TYR:CD1	3.02	0.45
1:K:218:GLN:NE2	1:K:244:LEU:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:21:SER:OG	1:G:190:LYS:N	2.46	0.45
1:I:38:GLN:O	1:N:273:PRO:CG	2.43	0.45
1:J:66:ASP:HB3	1:J:77:VAL:HB	1.98	0.45
1:A:120:GLY:O	1:A:124:VAL:CG2	2.55	0.45
1:J:181:THR:O	1:J:184:THR:OG1	2.29	0.45
1:L:255:ASP:O	1:L:259:ASP:N	2.49	0.45
1:M:62:HIS:CG	1:M:114:SER:HG	2.30	0.45
1:N:265:ALA:O	1:N:269:VAL:N	2.50	0.45
1:B:70:TYR:CD1	1:B:164:LEU:HD13	2.52	0.45
1:E:93:GLY:N	1:E:98:GLU:OE1	2.50	0.45
1:F:167:LEU:O	1:F:170:MET:N	2.48	0.45
1:J:28:ILE:O	1:J:29:PRO:C	2.52	0.45
1:N:253:VAL:HG21	1:N:264:ILE:HG13	1.99	0.45
1:A:58:ARG:CB	1:A:62:HIS:ND1	2.80	0.45
1:B:174:PHE:O	1:B:177:ALA:N	2.50	0.45
1:G:29:PRO:HG3	1:G:211:GLN:CD	2.37	0.45
1:M:16:HIS:NE2	1:M:42:VAL:HG11	2.31	0.45
1:M:93:GLY:N	1:M:98:GLU:OE1	2.50	0.45
1:B:245:TRP:O	1:B:252:VAL:N	2.50	0.44
1:F:187:ILE:CG2	1:F:188:LYS:N	2.79	0.44
1:F:250:ALA:CB	2:S:2:DC:O4'	2.65	0.44
1:F:266:ASN:OD1	1:F:267:LYS:N	2.48	0.44
1:I:51:THR:HG22	1:I:52:LEU:N	2.32	0.44
1:J:9:GLU:CG	1:J:261:TYR:HD2	2.30	0.44
1:L:229:ARG:HA	1:L:233:HIS:O	2.17	0.44
1:L:62:HIS:CD2	1:L:81:THR:HG21	2.50	0.44
1:B:76:LEU:O	1:B:88:ALA:HB1	2.16	0.44
1:F:47:LYS:O	1:G:162:ASN:ND2	2.49	0.44
1:F:250:ALA:HB2	2:S:2:DC:H1'	1.94	0.44
1:B:76:LEU:HD21	1:B:78:TRP:HE1	1.81	0.44
1:E:115:LEU:O	1:E:140:THR:OG1	2.33	0.44
1:G:105:LYS:O	1:G:108:ALA:HB3	2.16	0.44
1:G:209:ARG:O	1:G:213:GLN:HG3	2.17	0.44
1:I:132:MET:O	1:I:137:ILE:N	2.50	0.44
1:A:42:VAL:CG1	1:I:166:LYS:HB3	2.47	0.44
1:J:14:LYS:CB	1:J:15:TRP:HD1	2.27	0.44
1:K:152:LEU:O	1:K:156:THR:OG1	2.22	0.44
1:N:106:TRP:O	1:N:109:MET:N	2.50	0.44
1:N:30:ARG:CD	1:N:60:ILE:HD11	2.47	0.44
1:O:105:LYS:O	1:O:108:ALA:HB3	2.16	0.44
1:A:184:THR:CB	1:A:188:LYS:HB2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:VAL:HG21	1:A:153:VAL:CB	2.48	0.44
1:H:245:TRP:HB3	1:H:252:VAL:HB	1.98	0.44
1:I:79:VAL:HG21	1:I:153:VAL:HB	1.99	0.44
1:I:54:GLY:O	2:Q:3:DT:H2''	2.18	0.44
1:J:121:PRO:O	1:J:125:ALA:N	2.50	0.44
1:K:205:LYS:HG2	1:L:202:ILE:HD13	1.98	0.44
1:N:249:GLY:O	1:N:266:ASN:HB3	2.17	0.44
1:M:222:ARG:HD2	1:P:203:PHE:HE1	1.78	0.44
1:A:28:ILE:HD11	1:A:33:ALA:HB2	2.00	0.44
1:F:245:TRP:CH2	1:F:247:GLY:HA2	2.53	0.44
1:I:2:ILE:HG23	1:I:5:ILE:HD11	1.84	0.44
1:I:5:ILE:HG12	1:I:28:ILE:HD12	1.99	0.44
1:M:76:LEU:HD21	1:M:78:TRP:HE1	1.82	0.44
1:A:63:TRP:CD2	1:A:80:GLU:HA	2.52	0.44
1:E:76:LEU:HD21	1:E:78:TRP:HE1	1.82	0.44
1:F:272:ILE:HG22	1:F:273:PRO:O	2.18	0.44
1:H:60:ILE:CG2	1:H:61:ASP:N	2.80	0.44
1:I:252:VAL:HG11	1:L:245:TRP:CZ3	2.52	0.44
1:N:253:VAL:O	1:N:261:TYR:HA	2.18	0.44
1:B:80:GLU:OE1	1:B:82:ASN:N	2.47	0.44
1:I:185:LEU:HD23	1:I:189:ARG:HB2	1.99	0.44
1:L:274:PRO:O	1:L:275:PRO:C	2.56	0.44
1:A:210:ILE:HD12	1:A:210:ILE:C	2.38	0.44
1:A:3:GLU:O	1:A:5:ILE:N	2.50	0.44
1:E:160:LEU:HD12	1:E:181:THR:HG21	1.82	0.44
1:E:222:ARG:O	1:E:243:VAL:N	2.50	0.44
1:J:16:HIS:ND1	1:J:42:VAL:HB	2.33	0.44
1:M:85:LEU:HD22	1:M:198:MET:HA	1.98	0.44
1:A:185:LEU:HD23	1:A:189:ARG:HB2	1.99	0.44
1:A:222:ARG:O	1:A:242:GLN:CA	2.66	0.44
1:I:153:VAL:O	1:I:157:HIS:ND1	2.51	0.44
1:I:244:LEU:HD11	1:I:261:TYR:HD1	1.67	0.44
1:J:78:TRP:O	1:J:86:ILE:HA	2.18	0.44
1:K:184:THR:O	1:K:189:ARG:N	2.46	0.44
1:L:93:GLY:N	1:L:98:GLU:OE1	2.49	0.44
1:N:118:ASP:OD1	1:N:123:PHE:HE2	1.99	0.44
1:O:191:GLY:O	1:O:195:THR:OG1	2.12	0.44
1:A:155:ARG:NH2	2:S:7:DA:O4'	2.38	0.44
1:A:89:GLU:HA	1:A:178:LEU:HD21	2.00	0.43
1:A:4:ASN:OD1	1:A:7:LEU:HB3	2.18	0.43
1:B:62:HIS:O	1:B:81:THR:N	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:70:TYR:CD2	1:K:164:LEU:HD13	2.53	0.43
1:M:63:TRP:O	1:M:116:GLN:N	2.47	0.43
1:A:206:GLU:O	1:A:209:ARG:HG3	2.18	0.43
1:C:64:GLN:N	1:C:79:VAL:O	2.46	0.43
1:D:229:ARG:HA	1:D:233:HIS:O	2.17	0.43
1:D:226:TYR:CE1	1:D:241:THR:CG2	3.00	0.43
1:E:12:HIS:NE2	1:E:17:GLN:O	2.50	0.43
1:E:251:ILE:CD1	1:E:253:VAL:CG1	2.95	0.43
1:A:188:LYS:CE	1:I:15:TRP:HB3	2.45	0.43
1:J:173:ALA:O	1:J:176:SER:OG	2.32	0.43
1:B:76:LEU:HD12	1:B:77:VAL:H	1.82	0.43
1:I:118:ASP:C	1:I:120:GLY:H	2.21	0.43
1:I:70:TYR:O	1:I:73:LYS:N	2.51	0.43
1:J:117:SER:N	1:J:140:THR:O	2.47	0.43
1:M:184:THR:O	1:M:189:ARG:N	2.41	0.43
1:B:12:HIS:O	1:B:16:HIS:ND1	2.51	0.43
1:B:68:THR:OG1	1:B:161:LYS:NZ	2.47	0.43
1:F:251:ILE:HG23	1:F:251:ILE:O	2.19	0.43
1:H:245:TRP:HB3	1:H:252:VAL:CB	2.48	0.43
1:I:78:TRP:CB	1:I:106:TRP:CE2	2.99	0.43
1:I:78:TRP:N	1:I:87:TYR:O	2.39	0.43
1:L:224:CYS:C	1:L:272:ILE:HD12	2.39	0.43
1:B:176:SER:O	1:B:179:ALA:HB3	2.19	0.43
1:C:245:TRP:O	1:C:252:VAL:N	2.49	0.43
1:N:265:ALA:O	1:N:268:ASP:N	2.52	0.43
1:N:80:GLU:OE1	1:N:83:SER:OG	2.14	0.43
1:A:95:THR:OG1	1:A:98:GLU:HB3	2.19	0.43
1:D:251:ILE:CD1	1:D:269:VAL:CG2	2.92	0.43
1:E:224:CYS:N	1:E:241:THR:O	2.46	0.43
1:I:28:ILE:O	1:I:29:PRO:C	2.57	0.43
1:A:59:GLY:CA	1:A:62:HIS:HB2	2.43	0.43
1:F:250:ALA:HB3	2:S:2:DC:O4'	2.18	0.43
1:I:103:THR:O	1:I:107:TYR:HB3	2.19	0.43
1:I:77:VAL:HG11	1:I:79:VAL:HG21	2.00	0.43
1:J:14:LYS:HB2	1:J:15:TRP:CD1	2.49	0.43
1:O:80:GLU:OE1	1:O:83:SER:OG	2.36	0.43
1:C:80:GLU:N	1:C:85:LEU:O	2.48	0.43
1:F:151:ALA:HB1	1:F:155:ARG:NH1	2.33	0.43
1:I:2:ILE:O	1:I:5:ILE:CG1	2.67	0.43
1:N:23:HIS:ND1	1:N:28:ILE:O	2.46	0.43
1:A:59:GLY:O	1:A:62:HIS:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:229:ARG:NH1	1:I:232:GLY:O	2.51	0.43
1:N:253:VAL:HG22	1:N:262:LEU:O	2.18	0.43
1:C:218:GLN:NE2	1:C:244:LEU:O	2.46	0.43
1:J:15:TRP:HH2	1:L:135:LEU:CD2	2.32	0.43
1:K:247:GLY:N	1:K:250:ALA:O	2.52	0.43
1:K:76:LEU:HB2	1:K:91:VAL:HG21	2.00	0.43
1:N:222:ARG:HA	1:N:274:PRO:HG3	2.00	0.43
1:A:126:GLU:HG2	1:A:130:LEU:CD1	2.48	0.42
1:F:15:TRP:HZ3	1:G:183:ILE:HG21	1.79	0.42
1:F:17:GLN:CG	1:G:188:LYS:HB2	2.47	0.42
1:H:159:THR:CG2	1:H:185:LEU:HD11	2.44	0.42
1:J:226:TYR:O	1:J:238:GLN:N	2.52	0.42
1:K:2:ILE:HD13	1:K:250:ALA:HB3	2.00	0.42
1:A:12:HIS:O	1:A:16:HIS:N	2.51	0.42
1:D:225:TYR:O	1:D:269:VAL:CA	2.55	0.42
1:J:75:ILE:HD11	1:J:174:PHE:HZ	1.83	0.42
1:N:225:TYR:H	1:N:272:ILE:HD11	1.80	0.42
1:A:70:TYR:HE1	1:A:71:GLU:OE1	2.02	0.42
1:C:32:ALA:HB2	1:C:245:TRP:CE2	2.55	0.42
1:E:17:GLN:HE21	1:E:188:LYS:CB	2.32	0.42
1:I:89:GLU:HA	1:I:178:LEU:HD21	2.00	0.42
1:N:255:ASP:O	1:N:259:ASP:N	2.52	0.42
1:O:30:ARG:NH2	1:O:204:ASN:O	2.51	0.42
1:A:100:ARG:HE	1:A:127:SER:C	2.23	0.42
1:A:224:CYS:HG	1:A:243:VAL:HG22	1.78	0.42
1:C:35:ASP:O	1:C:39:GLN:N	2.46	0.42
1:F:17:GLN:N	1:F:17:GLN:OE1	2.50	0.42
1:J:142:GLY:O	1:J:143:ILE:C	2.55	0.42
1:A:210:ILE:HA	1:A:213:GLN:HB3	2.01	0.42
1:F:233:HIS:ND1	1:F:234:PRO:HD2	2.34	0.42
1:I:77:VAL:CG2	1:I:157:HIS:NE2	2.79	0.42
1:I:157:HIS:HA	1:I:160:LEU:HD12	2.02	0.42
1:J:75:ILE:CD1	1:J:161:LYS:NZ	2.82	0.42
1:N:244:LEU:CD2	1:N:261:TYR:CE1	3.01	0.42
1:N:80:GLU:N	1:N:85:LEU:O	2.49	0.42
1:A:167:LEU:HD22	1:A:170:MET:SD	2.60	0.42
1:A:190:LYS:N	1:I:21:SER:HG	2.17	0.42
1:A:222:ARG:O	1:A:242:GLN:HA	2.20	0.42
1:B:154:GLU:OE2	1:B:158:GLN:NE2	2.52	0.42
1:E:42:VAL:HG12	1:E:166:LYS:HG2	2.02	0.42
1:I:55:SER:CB	2:Q:5:DC:C5'	2.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:59:GLY:O	1:I:62:HIS:HB2	2.20	0.42
1:J:16:HIS:NE2	1:J:42:VAL:HG21	2.27	0.42
1:P:64:GLN:NE2	1:P:150:GLN:OE1	2.48	0.42
1:P:228:THR:O	1:P:235:GLY:N	2.49	0.42
1:A:77:VAL:HB	1:A:153:VAL:CG2	2.49	0.42
1:A:79:VAL:HG21	1:A:153:VAL:HB	2.02	0.42
1:E:17:GLN:HG3	1:E:184:THR:CG2	2.45	0.42
1:E:160:LEU:HD12	1:E:181:THR:CG2	2.43	0.42
1:F:21:SER:HB3	1:G:188:LYS:O	2.19	0.42
1:F:229:ARG:HA	1:F:233:HIS:O	2.19	0.42
1:F:245:TRP:HB3	1:F:252:VAL:HB	2.02	0.42
1:E:244:LEU:HB3	1:H:245:TRP:CH2	2.54	0.42
1:A:166:LYS:C	1:I:42:VAL:CG1	2.88	0.42
1:M:30:ARG:HG3	1:M:31:THR:HG23	2.00	0.42
1:H:70:TYR:CD2	1:H:164:LEU:HD13	2.54	0.42
1:H:224:CYS:HB2	1:H:269:VAL:HG13	2.02	0.42
1:I:77:VAL:HB	1:I:153:VAL:CG2	2.49	0.42
1:K:255:ASP:HB2	1:K:262:LEU:HD11	2.01	0.42
1:A:46:ASN:CB	1:I:166:LYS:CE	2.86	0.42
1:D:224:CYS:CA	1:D:270:LYS:O	2.68	0.42
1:E:222:ARG:O	1:E:243:VAL:HB	2.19	0.42
1:F:46:ASN:HB3	1:G:162:ASN:CG	2.40	0.42
1:I:17:GLN:NE2	1:I:22:LEU:HB2	2.16	0.42
1:B:144:PRO:HB2	1:B:150:GLN:CD	2.40	0.42
1:B:171:PHE:CD2	1:B:177:ALA:HB2	2.55	0.42
1:F:274:PRO:HD2	1:F:275:PRO:HD3	2.02	0.42
1:H:245:TRP:CE3	1:H:252:VAL:HG23	2.51	0.42
1:H:80:GLU:HG3	1:H:201:PHE:CD2	2.54	0.42
1:I:59:GLY:O	1:I:62:HIS:CB	2.68	0.42
1:I:51:THR:HG21	1:N:266:ASN:CB	2.49	0.42
1:A:58:ARG:HA	1:D:267:LYS:HA	2.01	0.41
1:E:217:LYS:NZ	1:H:211:GLN:HB2	2.35	0.41
1:I:100:ARG:HE	1:I:127:SER:C	2.23	0.41
1:I:130:LEU:CG	1:I:130:LEU:O	2.66	0.41
1:L:244:LEU:CD1	1:L:253:VAL:HA	2.49	0.41
1:L:64:GLN:O	1:L:79:VAL:N	2.53	0.41
1:M:83:SER:HB3	1:M:200:ILE:CG2	2.50	0.41
1:N:64:GLN:N	1:N:79:VAL:O	2.47	0.41
1:P:146:ASN:O	1:P:150:GLN:CG	2.68	0.41
1:P:265:ALA:O	1:P:268:ASP:N	2.53	0.41
1:H:187:ILE:HG12	1:H:198:MET:SD	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:251:ILE:HG23	1:H:266:ASN:OD1	2.20	0.41
1:J:127:SER:HA	1:J:130:LEU:HB3	2.01	0.41
1:J:65:VAL:HG22	1:J:78:TRP:CE3	2.55	0.41
1:L:250:ALA:HB1	1:L:263:VAL:CG2	2.50	0.41
1:N:229:ARG:NE	1:N:268:ASP:OD2	2.50	0.41
1:A:59:GLY:N	1:A:62:HIS:CB	2.84	0.41
1:B:244:LEU:HD11	1:B:261:TYR:CE1	2.51	0.41
1:D:223:PHE:HB3	1:D:242:GLN:CG	2.50	0.41
1:D:247:GLY:HA3	1:D:250:ALA:O	2.20	0.41
1:D:241:THR:HG1	1:D:254:LYS:HG2	1.82	0.41
1:G:64:GLN:NE2	1:G:150:GLN:OE1	2.47	0.41
1:I:175:GLU:HA	1:I:178:LEU:HB3	2.02	0.41
1:I:163:THR:HB	1:I:181:THR:HG22	2.03	0.41
1:A:166:LYS:CA	1:I:42:VAL:CG1	2.98	0.41
1:A:59:GLY:CA	1:A:62:HIS:HB3	2.51	0.41
1:D:268:ASP:N	1:D:268:ASP:OD1	2.54	0.41
1:L:79:VAL:HG11	1:L:153:VAL:HG22	2.01	0.41
1:I:203:PHE:CE1	1:I:207:GLN:HG3	2.55	0.41
1:A:231:ARG:HE	2:Q:18:DG:N2	2.18	0.41
1:I:161:LYS:HA	1:I:164:LEU:HD12	2.01	0.41
1:I:36:ILE:HG12	1:M:2:ILE:HG13	2.02	0.41
1:J:215:LYS:NZ	1:J:246:GLY:O	2.40	0.41
1:K:263:VAL:O	1:K:264:ILE:HD13	2.20	0.41
1:L:244:LEU:HD11	1:L:253:VAL:HA	2.02	0.41
1:N:224:CYS:CA	1:N:272:ILE:HD12	2.50	0.41
1:O:74:ILE:HD13	1:O:94:GLU:HG3	2.01	0.41
1:A:229:ARG:NH1	1:A:232:GLY:O	2.52	0.41
1:D:252:VAL:CG1	1:D:253:VAL:N	2.82	0.41
1:E:13:ASN:O	1:E:16:HIS:NE2	2.53	0.41
1:I:66:ASP:O	1:I:77:VAL:N	2.47	0.41
1:J:132:MET:O	1:J:137:ILE:N	2.52	0.41
1:J:160:LEU:C	1:J:160:LEU:HD23	2.41	0.41
1:M:70:TYR:CD2	1:M:164:LEU:HD13	2.56	0.41
1:O:70:TYR:CD2	1:O:164:LEU:HD13	2.55	0.41
1:A:76:LEU:HD23	1:A:78:TRP:CE2	2.56	0.41
1:E:213:GLN:O	1:E:216:SER:HB3	2.21	0.41
1:I:107:TYR:CB	1:I:112:PRO:HG3	2.50	0.41
1:I:167:LEU:HD22	1:I:170:MET:SD	2.60	0.41
1:K:32:ALA:HB2	1:K:245:TRP:CE2	2.56	0.41
1:L:223:PHE:O	1:L:272:ILE:N	2.48	0.41
1:N:91:VAL:HG12	1:N:93:GLY:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:SER:O	1:A:179:ALA:HB3	2.21	0.41
1:A:52:LEU:HD22	1:D:232:GLY:O	2.21	0.41
1:B:92:LYS:N	1:B:98:GLU:OE2	2.42	0.41
1:D:149:SER:OG	1:D:150:GLN:N	2.53	0.41
1:D:227:ARG:HD3	1:D:234:PRO:C	2.40	0.41
1:I:12:HIS:O	1:I:16:HIS:N	2.51	0.41
1:I:52:LEU:C	1:I:52:LEU:HD23	2.40	0.41
1:K:195:THR:HB	1:K:200:ILE:HD11	2.02	0.41
1:M:7:LEU:O	1:M:10:GLU:HB3	2.21	0.41
1:P:222:ARG:O	1:P:243:VAL:HG23	2.20	0.41
1:A:161:LYS:HA	1:A:164:LEU:HD12	2.01	0.41
1:D:224:CYS:CB	1:D:270:LYS:O	2.68	0.41
1:F:274:PRO:N	1:F:275:PRO:HD2	2.36	0.41
1:I:149:SER:HG	2:Q:3:DT:P	2.43	0.41
1:I:86:ILE:CG1	1:I:186:ASN:OD1	2.67	0.41
1:J:76:LEU:N	1:J:89:GLU:O	2.48	0.41
1:K:202:ILE:HG23	1:L:202:ILE:HG23	2.02	0.41
1:L:227:ARG:NH1	1:L:234:PRO:CG	2.77	0.41
1:M:167:LEU:HD12	1:M:181:THR:HG23	2.02	0.41
1:N:206:GLU:OE2	1:N:209:ARG:NH2	2.50	0.41
1:P:187:ILE:HG12	1:P:198:MET:CE	2.50	0.41
1:A:15:TRP:O	1:I:188:LYS:CD	2.66	0.41
1:A:223:PHE:CE1	1:A:242:GLN:CB	2.75	0.41
1:C:225:TYR:N	1:C:270:LYS:O	2.53	0.41
1:E:244:LEU:HD12	1:E:261:TYR:CE1	2.55	0.41
1:F:185:LEU:HD22	1:F:189:ARG:NH1	2.36	0.41
1:H:184:THR:HA	1:H:188:LYS:HB2	2.01	0.41
1:H:60:ILE:CG1	1:H:208:GLN:OE1	2.68	0.41
1:I:76:LEU:HD23	1:I:78:TRP:CE2	2.56	0.41
1:J:188:LYS:NZ	1:K:15:TRP:CE2	2.89	0.41
1:J:90:ARG:NH1	1:J:175:GLU:OE2	2.52	0.41
1:K:160:LEU:O	1:K:163:THR:OG1	2.34	0.41
1:D:223:PHE:O	1:D:272:ILE:CB	2.59	0.40
1:I:65:VAL:HG13	1:I:77:VAL:O	2.21	0.40
1:I:68:THR:N	1:I:75:ILE:O	2.51	0.40
1:I:78:TRP:O	1:I:87:TYR:N	2.48	0.40
1:A:60:ILE:O	1:A:60:ILE:CG2	2.69	0.40
1:B:16:HIS:CE1	1:B:42:VAL:HG21	2.55	0.40
1:D:61:ASP:OD2	1:D:205:LYS:NZ	2.40	0.40
1:F:214:SER:O	1:F:218:GLN:HB2	2.21	0.40
1:I:2:ILE:O	1:I:5:ILE:HG13	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:THR:HG23	1:A:157:HIS:HD2	1.87	0.40
1:A:67:TYR:CE2	1:A:94:GLU:HB2	2.56	0.40
1:K:8:ALA:HB2	1:K:26:PHE:CD1	2.56	0.40
1:A:52:LEU:HD22	1:D:234:PRO:CD	2.51	0.40
1:D:226:TYR:HB3	1:D:269:VAL:HG12	2.04	0.40
1:I:61:ASP:CB	1:I:113:LYS:HB3	2.49	0.40
1:I:17:GLN:HE21	1:I:22:LEU:HD22	1.85	0.40
1:I:244:LEU:HD12	1:I:261:TYR:HD1	1.84	0.40
1:I:76:LEU:HD23	1:I:78:TRP:NE1	2.37	0.40
1:J:255:ASP:O	1:J:258:THR:OG1	2.23	0.40
1:M:83:SER:HB3	1:M:200:ILE:HB	2.04	0.40
1:O:80:GLU:CD	1:O:83:SER:OG	2.60	0.40
1:C:22:LEU:O	1:C:26:PHE:HD2	2.04	0.40
1:E:244:LEU:HD13	1:H:245:TRP:HH2	1.86	0.40
1:F:118:ASP:O	1:F:123:PHE:CD2	2.61	0.40
1:F:224:CYS:HB2	1:F:269:VAL:HG13	2.03	0.40
1:F:224:CYS:SG	1:F:251:ILE:CD1	3.09	0.40
1:F:272:ILE:HG21	1:F:276:LYS:CD	2.47	0.40
1:F:16:HIS:CD2	1:F:42:VAL:HB	2.57	0.40
1:I:108:ALA:HA	1:J:183:ILE:CG1	2.47	0.40
1:I:88:ALA:O	1:I:182:LEU:HD11	2.21	0.40
1:I:184:THR:CB	1:I:188:LYS:HB3	2.51	0.40
1:I:195:THR:HB	1:I:199:ASP:OD2	2.21	0.40
1:J:84:GLY:O	1:J:85:LEU:C	2.60	0.40
1:K:265:ALA:O	1:K:268:ASP:N	2.53	0.40
1:M:247:GLY:N	1:M:250:ALA:O	2.52	0.40
1:N:8:ALA:CB	1:N:28:ILE:HD13	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	273/281 (97%)	248 (91%)	23 (8%)	2 (1%)	24	66
1	B	252/281 (90%)	238 (94%)	14 (6%)	0	100	100
1	C	257/281 (92%)	251 (98%)	6 (2%)	0	100	100
1	D	214/281 (76%)	207 (97%)	5 (2%)	2 (1%)	19	60
1	E	253/281 (90%)	249 (98%)	4 (2%)	0	100	100
1	F	262/281 (93%)	257 (98%)	5 (2%)	0	100	100
1	G	201/281 (72%)	198 (98%)	3 (2%)	0	100	100
1	H	215/281 (76%)	213 (99%)	2 (1%)	0	100	100
1	I	273/281 (97%)	257 (94%)	14 (5%)	2 (1%)	24	66
1	J	252/281 (90%)	245 (97%)	7 (3%)	0	100	100
1	K	257/281 (92%)	254 (99%)	3 (1%)	0	100	100
1	L	214/281 (76%)	203 (95%)	9 (4%)	2 (1%)	19	60
1	M	252/281 (90%)	244 (97%)	8 (3%)	0	100	100
1	N	260/281 (92%)	257 (99%)	3 (1%)	0	100	100
1	O	201/281 (72%)	200 (100%)	1 (0%)	0	100	100
1	P	215/281 (76%)	211 (98%)	4 (2%)	0	100	100
All	All	3851/4496 (86%)	3732 (97%)	111 (3%)	8 (0%)	53	84

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	233	HIS
1	L	233	HIS
1	I	119	ASN
1	I	240	PRO
1	A	4	ASN
1	A	240	PRO
1	D	234	PRO
1	L	234	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	235/246 (96%)	234 (100%)	1 (0%)	92	95
1	B	223/246 (91%)	223 (100%)	0	100	100
1	C	228/246 (93%)	228 (100%)	0	100	100
1	D	183/246 (74%)	183 (100%)	0	100	100
1	E	224/246 (91%)	223 (100%)	1 (0%)	92	95
1	F	230/246 (94%)	230 (100%)	0	100	100
1	G	181/246 (74%)	181 (100%)	0	100	100
1	H	189/246 (77%)	189 (100%)	0	100	100
1	I	235/246 (96%)	234 (100%)	1 (0%)	92	95
1	J	223/246 (91%)	222 (100%)	1 (0%)	92	95
1	K	228/246 (93%)	228 (100%)	0	100	100
1	L	183/246 (74%)	183 (100%)	0	100	100
1	M	223/246 (91%)	223 (100%)	0	100	100
1	N	228/246 (93%)	228 (100%)	0	100	100
1	O	181/246 (74%)	181 (100%)	0	100	100
1	P	189/246 (77%)	189 (100%)	0	100	100
All	All	3383/3936 (86%)	3379 (100%)	4 (0%)	94	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	210	ILE
1	E	168	ILE
1	I	223	PHE
1	J	82	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	I	150	GLN
1	M	16	HIS
1	N	213	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.