



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:38 AM GMT

PDB ID : 2NN6
Title : Structure of the human RNA exosome composed of Rrp41, Rrp45, Rrp46, Rrp43, Mtr3, Rrp42, Csl4, Rrp4, and Rrp40
Authors : Lima, C.D.
Deposited on : 2006-10-23
Resolution : 3.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

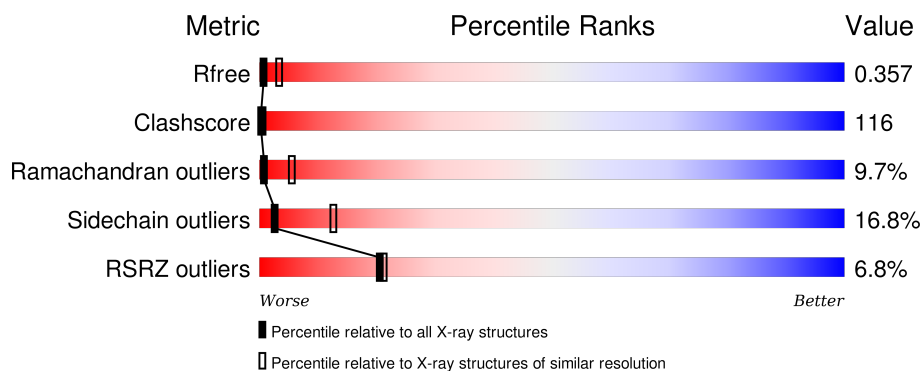
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1005 (3.42-3.30)
Clashscore	102246	1076 (3.42-3.30)
Ramachandran outliers	100387	1059 (3.42-3.30)
Sidechain outliers	100360	1058 (3.42-3.30)
RSRZ outliers	91569	1010 (3.42-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	358	 3% 15% 55% 23% • 5%
2	B	249	 3% 12% 63% 18% • 6%
3	C	278	 5% 10% 68% 17% • •
4	D	237	 3% 11% 59% 16% 14%
5	E	305	 12% 11% 63% 15% • 10%

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Mol	Chain	Length	Quality of chain
6	F	272	<div><div><div></div><div></div><div></div><div></div></div><div>7%12%56%14%18%</div></div>
7	G	289	<div><div><div></div><div></div><div></div><div></div></div><div>2%15%46%19%18%</div></div>
8	H	308	<div><div><div></div><div></div><div></div><div></div></div><div>4%15%54%12%19%</div></div>
9	I	209	<div><div><div></div><div></div><div></div><div></div></div><div>16%15%56%15%14%</div></div>

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 16858 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Polymyositis/scleroderma autoantigen 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2611	1651	464	477	19			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	CLONING ARTIFACT	UNP Q86Y41
A	-15	GLY	-	CLONING ARTIFACT	UNP Q86Y41
A	-14	SER	-	CLONING ARTIFACT	UNP Q86Y41
A	-13	SER	-	CLONING ARTIFACT	UNP Q86Y41
A	-12	HIS	-	CLONING ARTIFACT	UNP Q86Y41
A	-11	HIS	-	CLONING ARTIFACT	UNP Q86Y41
A	-10	HIS	-	CLONING ARTIFACT	UNP Q86Y41
A	-9	HIS	-	CLONING ARTIFACT	UNP Q86Y41
A	-8	HIS	-	CLONING ARTIFACT	UNP Q86Y41
A	-7	HIS	-	CLONING ARTIFACT	UNP Q86Y41
A	-6	SER	-	CLONING ARTIFACT	UNP Q86Y41
A	-5	GLN	-	CLONING ARTIFACT	UNP Q86Y41
A	-4	ASP	-	CLONING ARTIFACT	UNP Q86Y41
A	-3	PRO	-	CLONING ARTIFACT	UNP Q86Y41
A	-2	ASN	-	CLONING ARTIFACT	UNP Q86Y41
A	-1	SER	-	CLONING ARTIFACT	UNP Q86Y41
A	0	HIS	-	CLONING ARTIFACT	UNP Q86Y41

- Molecule 2 is a protein called Exosome complex exonuclease RRP41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	235	Total	C	N	O	S	0	0	0
			1779	1095	339	336	9			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	CLONING ARTIFACT	UNP Q9NPD3
B	-3	ALA	-	CLONING ARTIFACT	UNP Q9NPD3
B	-2	ASP	-	CLONING ARTIFACT	UNP Q9NPD3
B	-1	PRO	-	CLONING ARTIFACT	UNP Q9NPD3
B	0	MET	-	CLONING ARTIFACT	UNP Q9NPD3

- Molecule 3 is a protein called Exosome complex exonuclease RRP43.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	270	Total	C	N	O	S	0	0	0
			2058	1298	344	402	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	ASP	-	CLONING ARTIFACT	UNP Q96B26
C	0	PRO	-	CLONING ARTIFACT	UNP Q96B26

- Molecule 4 is a protein called Exosome complex exonuclease RRP46.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	205	Total	C	N	O	S	0	0	0
			1534	956	275	291	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	SER	-	CLONING ARTIFACT	UNP Q9NQ4
D	0	LEU	-	CLONING ARTIFACT	UNP Q9NQ4

- Molecule 5 is a protein called Exosome complex exonuclease RRP42.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	275	Total	C	N	O	S	0	0	0
			2109	1320	361	413	15			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-13	MET	-	CLONING ARTIFACT	UNP Q15024
E	-12	GLY	-	CLONING ARTIFACT	UNP Q15024
E	-11	SER	-	CLONING ARTIFACT	UNP Q15024

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-10	SER	-	CLONING ARTIFACT	UNP Q15024
E	-9	HIS	-	CLONING ARTIFACT	UNP Q15024
E	-8	HIS	-	CLONING ARTIFACT	UNP Q15024
E	-7	HIS	-	CLONING ARTIFACT	UNP Q15024
E	-6	HIS	-	CLONING ARTIFACT	UNP Q15024
E	-5	HIS	-	CLONING ARTIFACT	UNP Q15024
E	-4	HIS	-	CLONING ARTIFACT	UNP Q15024
E	-3	SER	-	CLONING ARTIFACT	UNP Q15024
E	-2	GLN	-	CLONING ARTIFACT	UNP Q15024
E	-1	ASP	-	CLONING ARTIFACT	UNP Q15024
E	0	PRO	-	CLONING ARTIFACT	UNP Q15024
E	274	VAL	LEU	VARIANT	UNP Q15024

- Molecule 6 is a protein called Exosome component 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	223	Total	C	N	O	S	0	0	0
			1635	1019	311	298	7			

- Molecule 7 is a protein called Exosome complex exonuclease RRP40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	236	Total	C	N	O	S	0	0	0
			1793	1128	318	337	10			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-14	MET	-	CLONING ARTIFACT	UNP Q9NQ5
G	-13	GLY	-	CLONING ARTIFACT	UNP Q9NQ5
G	-12	SER	-	CLONING ARTIFACT	UNP Q9NQ5
G	-11	SER	-	CLONING ARTIFACT	UNP Q9NQ5
G	-10	HIS	-	CLONING ARTIFACT	UNP Q9NQ5
G	-9	HIS	-	CLONING ARTIFACT	UNP Q9NQ5
G	-8	HIS	-	CLONING ARTIFACT	UNP Q9NQ5
G	-7	HIS	-	CLONING ARTIFACT	UNP Q9NQ5
G	-6	HIS	-	CLONING ARTIFACT	UNP Q9NQ5
G	-5	HIS	-	CLONING ARTIFACT	UNP Q9NQ5
G	-4	SER	-	CLONING ARTIFACT	UNP Q9NQ5
G	-3	GLN	-	CLONING ARTIFACT	UNP Q9NQ5
G	-2	ASP	-	CLONING ARTIFACT	UNP Q9NQ5
G	-1	PRO	-	CLONING ARTIFACT	UNP Q9NQ5

- Molecule 8 is a protein called Exosome complex exonuclease RRP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	250	Total	C	N	O	S	0	0	0
			1956	1238	341	365	12			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-14	MET	-	CLONING ARTIFACT	UNP Q13868
H	-13	GLY	-	CLONING ARTIFACT	UNP Q13868
H	-12	SER	-	CLONING ARTIFACT	UNP Q13868
H	-11	SER	-	CLONING ARTIFACT	UNP Q13868
H	-10	HIS	-	CLONING ARTIFACT	UNP Q13868
H	-9	HIS	-	CLONING ARTIFACT	UNP Q13868
H	-8	HIS	-	CLONING ARTIFACT	UNP Q13868
H	-7	HIS	-	CLONING ARTIFACT	UNP Q13868
H	-6	HIS	-	CLONING ARTIFACT	UNP Q13868
H	-5	HIS	-	CLONING ARTIFACT	UNP Q13868
H	-4	SER	-	CLONING ARTIFACT	UNP Q13868
H	-3	GLN	-	CLONING ARTIFACT	UNP Q13868
H	-2	ASP	-	CLONING ARTIFACT	UNP Q13868
H	-1	PRO	-	CLONING ARTIFACT	UNP Q13868
H	0	HIS	-	CLONING ARTIFACT	UNP Q13868

- Molecule 9 is a protein called 3'-5' exoribonuclease CSL4 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	180	Total	C	N	O	S	0	0	0
			1383	870	241	262	10			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	-13	MET	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-12	GLY	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-11	SER	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-10	SER	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-9	HIS	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-8	HIS	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-7	HIS	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-6	HIS	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-5	HIS	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-4	HIS	-	CLONING ARTIFACT	UNP Q9Y3B2

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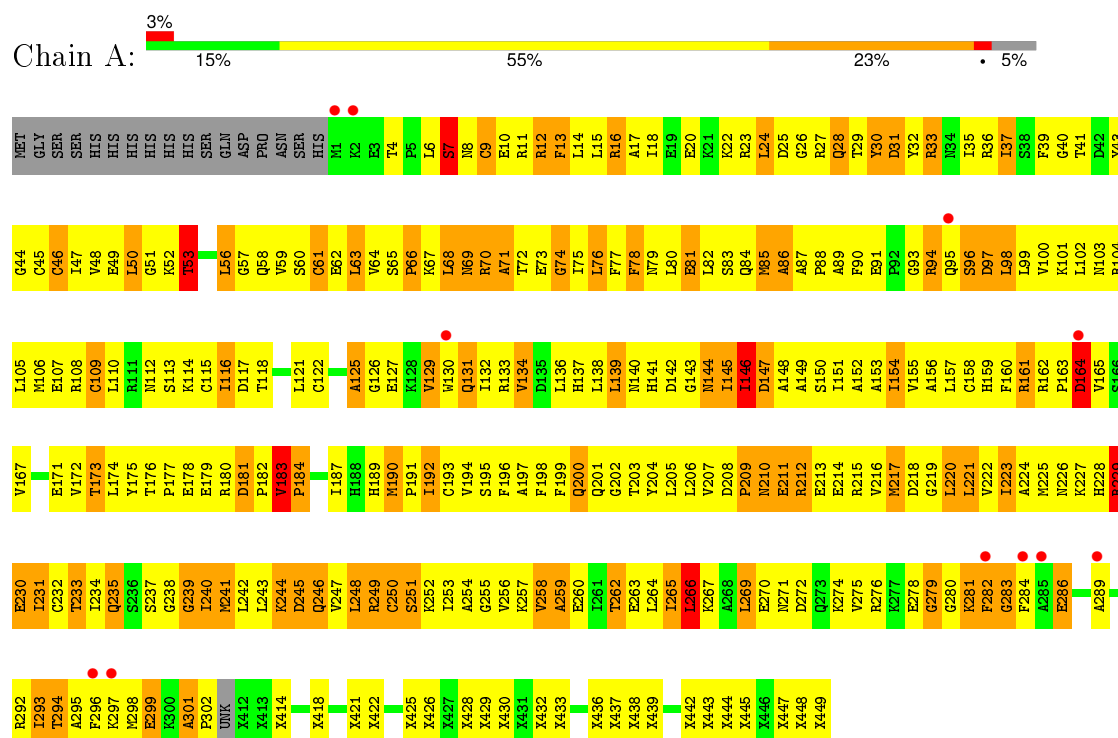
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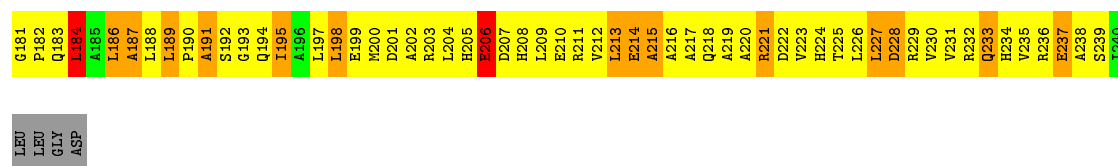
Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	SER	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-2	GLN	-	CLONING ARTIFACT	UNP Q9Y3B2
I	-1	ASP	-	CLONING ARTIFACT	UNP Q9Y3B2
I	0	PRO	-	CLONING ARTIFACT	UNP Q9Y3B2

3 Residue-property plots

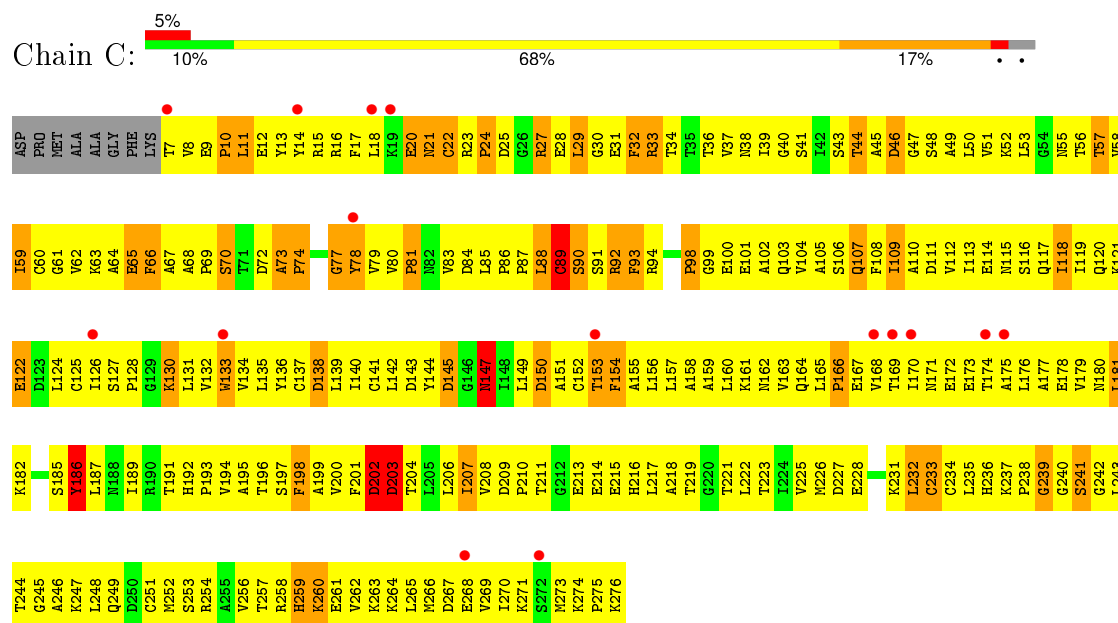
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Polymyositis/scleroderma autoantigen 1

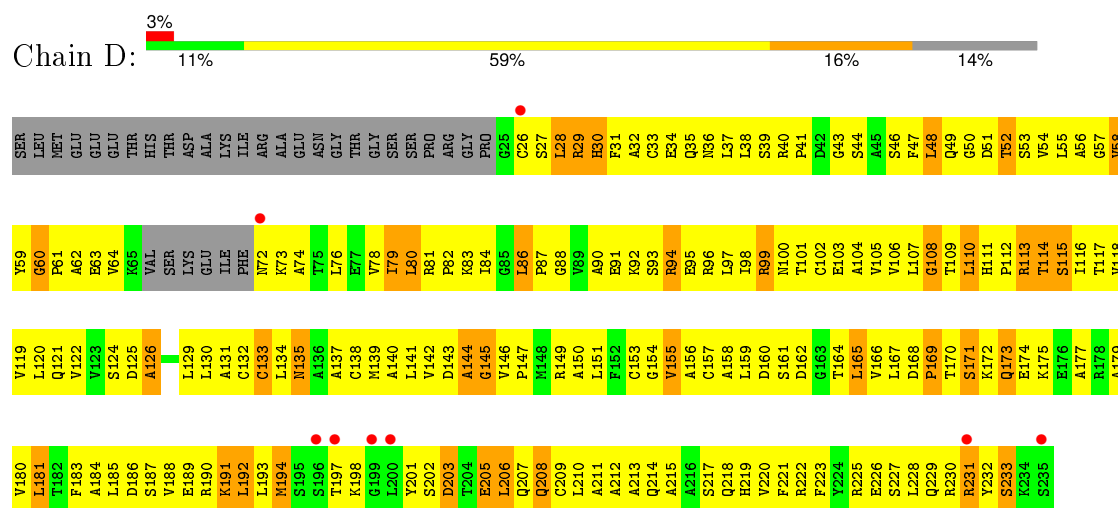




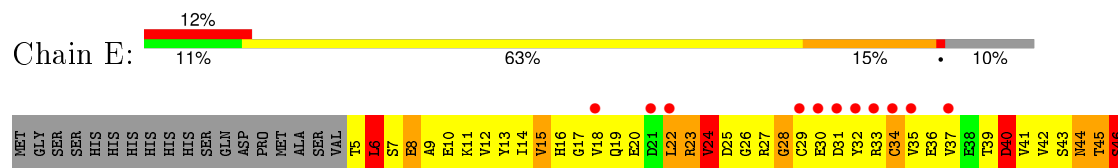
• Molecule 3: Exosome complex exonuclease RRP43

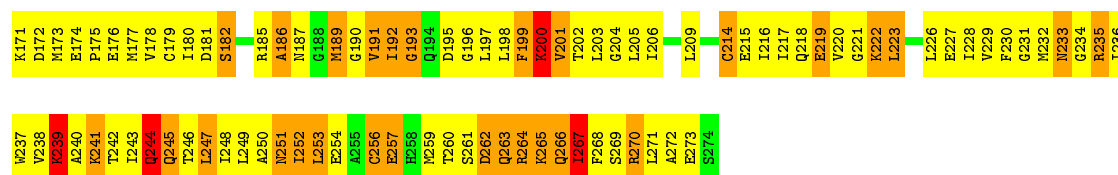


• Molecule 4: Exosome complex exonuclease RRP46

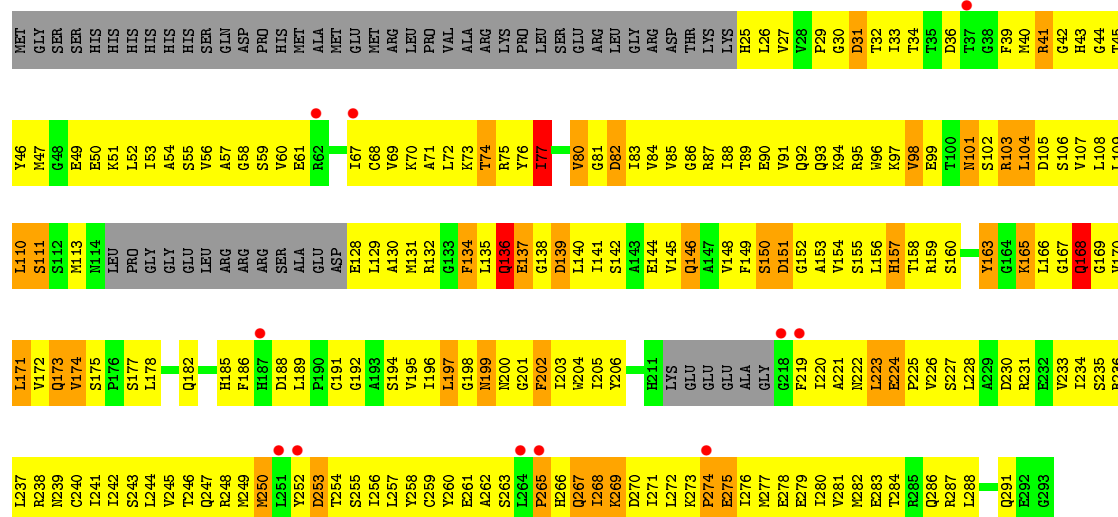
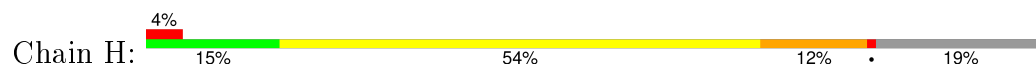


• Molecule 5: Exosome complex exonuclease RRP42

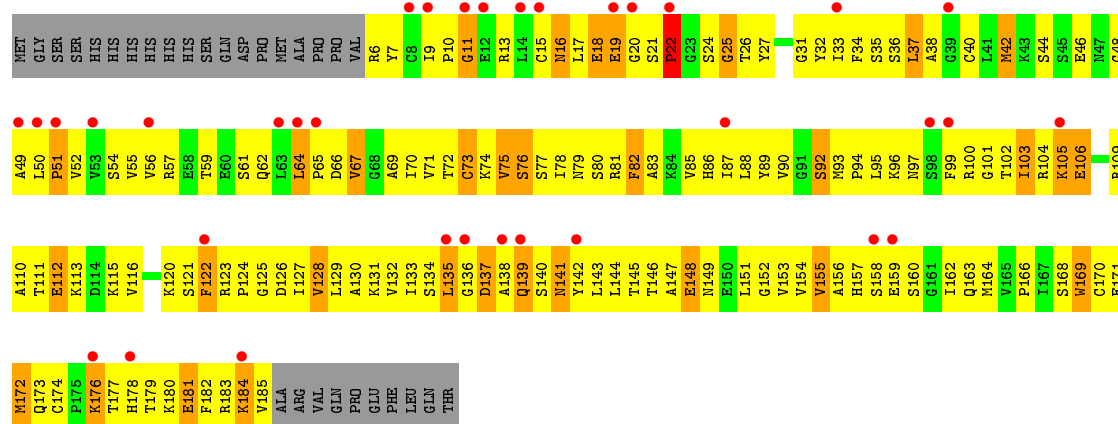
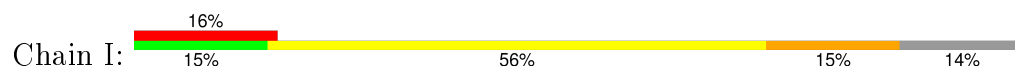




• Molecule 8: Exosome complex exonuclease RRP4



• Molecule 9: 3'-5' exoribonuclease CSL4 homolog



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 3 2	Depositor
Cell constants a, b, c, α , β , γ	307.80Å 307.80Å 307.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.98 – 3.35 34.85 – 3.35	Depositor EDS
% Data completeness (in resolution range)	97.7 (14.98-3.35) 97.8 (34.85-3.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.32Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.291 , 0.344 0.308 , 0.357	Depositor DCC
R_{free} test set	3465 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	87.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.20 , 62.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.33$, $\langle L^2 \rangle = 0.17$	Xtriage
Outliers	1 of 69964 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	16858	wwPDB-VP
Average B, all atoms (Å ²)	119.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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	0.62	0/2418	0.87	4/3256 (0.1%)
2	B	0.51	0/1804	0.81	2/2439 (0.1%)
3	C	0.46	0/2092	0.73	0/2839
4	D	0.54	0/1552	0.79	1/2097 (0.0%)
5	E	0.41	0/2138	0.72	0/2890
6	F	0.41	0/1658	0.69	0/2247
7	G	0.62	0/1819	0.91	2/2451 (0.1%)
8	H	0.39	0/1985	0.72	0/2679
9	I	0.41	0/1407	0.74	1/1899 (0.1%)
All	All	0.50	0/16873	0.78	10/22797 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	266	LEU	CA-CB-CG	-7.27	98.57	115.30
7	G	253	LEU	CA-CB-CG	-6.87	99.50	115.30
1	A	53	THR	N-CA-C	-6.70	92.92	111.00
1	A	33	ARG	N-CA-C	-5.80	95.33	111.00
7	G	193	GLY	N-CA-C	5.79	127.58	113.10
9	I	180	LYS	N-CA-C	-5.61	95.86	111.00
4	D	60	GLY	N-CA-C	5.60	127.10	113.10
1	A	56	LEU	CA-CB-CG	-5.46	102.74	115.30
2	B	184	LEU	CA-CB-CG	5.43	127.80	115.30
2	B	187	ALA	N-CA-C	-5.22	96.91	111.00

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	2611	0	2673	640	0
2	B	1779	0	1770	414	0
3	C	2058	0	2084	608	0
4	D	1534	0	1572	415	0
5	E	2109	0	2122	495	0
6	F	1635	0	1686	409	0
7	G	1793	0	1827	495	0
8	H	1956	0	2002	414	0
9	I	1383	0	1405	329	0
All	All	16858	0	17141	3953	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 116.

All (3953) 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)
4:D:202:SER:N	4:D:205:GLU:HG3	1.49	1.25
8:H:220:ILE:HA	8:H:223:LEU:HD13	1.26	1.18
1:A:230:GLU:HB3	2:B:205:HIS:HA	1.22	1.18
9:I:24:SER:HB3	9:I:54:SER:HB2	1.24	1.18
3:C:126:ILE:HB	3:C:131:LEU:HB3	1.25	1.17
9:I:123:ARG:HB3	9:I:124:PRO:HD2	1.23	1.15
1:A:145:ILE:H	1:A:145:ILE:HD12	1.12	1.15
7:G:253:LEU:HA	7:G:256:CYS:SG	1.88	1.14
7:G:253:LEU:HD23	7:G:256:CYS:SG	1.88	1.14
7:G:216:ILE:H	7:G:216:ILE:HD12	1.14	1.13
1:A:143:GLY:HA2	1:A:214:GLU:HG3	1.28	1.12
1:A:422:UNK:HA	1:A:425:UNK:CG	1.79	1.12
1:A:302:PRO:HB2	1:A:414:UNK:HG1	1.32	1.11
7:G:123:LYS:HA	7:G:128:PHE:HB3	1.33	1.11
7:G:34:LEU:HB3	7:G:76:ARG:HA	1.32	1.10
3:C:32:PHE:HE2	3:C:262:VAL:HG13	1.11	1.10
9:I:156:ALA:HB1	9:I:164:MET:HB2	1.25	1.09
5:E:17:GLY:HA2	8:H:231:ARG:HE	1.06	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:62:VAL:HG21	6:F:161:ALA:HA	1.33	1.09
7:G:86:ARG:HB3	7:G:100:TRP:HB3	1.29	1.09
2:B:173:SER:O	2:B:177:GLU:HG3	1.52	1.08
7:G:24:GLY:HA2	7:G:85:LEU:HD23	1.10	1.08
5:E:37:VAL:HG22	5:E:51:VAL:HG22	1.32	1.07
4:D:202:SER:H	4:D:205:GLU:CG	1.66	1.07
2:B:176:GLU:H	2:B:176:GLU:CD	1.58	1.07
5:E:116:LYS:HG2	5:E:198:PRO:HD3	1.35	1.07
5:E:37:VAL:HG11	5:E:158:ALA:HB1	1.34	1.07
8:H:76:TYR:HB3	8:H:102:SER:HB3	1.37	1.06
6:F:50:LYS:H	6:F:50:LYS:HD2	1.17	1.06
6:F:216:MET:HG3	6:F:221:GLN:HB2	1.30	1.06
3:C:269:VAL:HG13	3:C:273:MET:HB2	1.32	1.06
9:I:145:THR:HG22	9:I:147:ALA:H	1.17	1.06
1:A:429:UNK:CG	3:C:249:GLN:HE21	1.69	1.06
3:C:50:LEU:HD11	3:C:57:THR:HG22	1.34	1.06
7:G:202:THR:HB	7:G:205:LEU:HD13	1.33	1.05
1:A:244:LYS:O	1:A:247:VAL:HG22	1.56	1.05
7:G:161:LEU:HB3	7:G:192:ILE:HD12	1.07	1.05
6:F:200:THR:H	6:F:203:GLU:HB2	1.22	1.05
1:A:165:VAL:HG21	1:A:175:TYR:H	1.17	1.05
4:D:173:GLN:N	4:D:173:GLN:HE21	1.56	1.03
5:E:40:ASP:HA	5:E:48:SER:HB2	1.33	1.03
4:D:96:ARG:HG3	4:D:99:ARG:HH21	1.24	1.03
6:F:134:VAL:HA	6:F:176:MET:HA	1.37	1.03
6:F:197:LEU:HD13	6:F:243:LEU:HG	1.40	1.03
1:A:41:THR:HG22	1:A:283:GLY:HA2	1.38	1.03
5:E:53:LEU:HD22	5:E:151:ALA:HB2	1.41	1.03
1:A:140:ASN:OD1	4:D:40:ARG:HB2	1.58	1.03
7:G:47:ALA:HB3	7:G:78:LEU:HB3	1.39	1.02
2:B:69:ALA:HB2	2:B:115:HIS:HB2	1.37	1.02
9:I:112:GLU:HG3	9:I:147:ALA:HB1	1.41	1.02
9:I:127:ILE:HD13	9:I:155:VAL:HG21	1.41	1.01
7:G:226:LEU:HD22	7:G:227:GLU:H	1.25	1.01
6:F:255:LEU:HD12	6:F:256:GLN:N	1.74	1.01
2:B:7:SER:HB2	2:B:12:ARG:HA	1.40	1.01
3:C:47:GLY:HA3	3:C:163:VAL:HG22	1.38	1.01
7:G:170:ASN:HD21	7:G:173:MET:HB3	1.21	1.00
6:F:127:GLN:O	6:F:131:GLU:HB2	1.60	1.00
1:A:192:ILE:HD13	1:A:193:CYS:H	1.23	1.00
2:B:69:ALA:HB3	2:B:112:THR:HG22	1.43	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:69:PRO:HD3	3:C:132:VAL:HB	1.40	1.00
4:D:184:ALA:HB3	4:D:194:MET:HB3	1.39	1.00
1:A:249:ARG:HH11	1:A:249:ARG:HB3	1.22	1.00
1:A:167:VAL:HG22	1:A:172:VAL:HA	1.42	1.00
3:C:27:ARG:HD2	3:C:31:GLU:HG2	1.42	0.99
9:I:40:CYS:HB3	9:I:56:VAL:HB	1.43	0.99
1:A:40:GLY:HA3	1:A:45:CYS:SG	2.02	0.99
9:I:129:LEU:H	9:I:129:LEU:HD23	1.28	0.99
4:D:29:ARG:HD2	4:D:50:GLY:HA3	1.45	0.99
1:A:162:ARG:O	1:A:183:VAL:HA	1.60	0.99
1:A:429:UNK:HG2	3:C:249:GLN:HB3	1.45	0.98
3:C:259:HIS:HB3	3:C:260:LYS:HZ1	1.22	0.98
1:A:246:GLN:HA	1:A:249:ARG:HE	1.27	0.98
7:G:197:LEU:O	7:G:237:TRP:HA	1.62	0.98
6:F:134:VAL:HG22	6:F:176:MET:HG2	1.44	0.98
1:A:302:PRO:HB2	1:A:414:UNK:CG	1.94	0.98
4:D:28:LEU:HD23	4:D:28:LEU:H	1.29	0.98
3:C:178:GLU:H	3:C:181:LEU:HG	1.29	0.98
8:H:29:PRO:HD3	8:H:57:ALA:HA	1.46	0.98
4:D:141:LEU:HD12	4:D:146:VAL:HB	1.42	0.98
4:D:81:ARG:HG2	4:D:87:PRO:HB3	1.46	0.98
1:A:78:PHE:HB2	1:A:134:VAL:HG23	1.45	0.98
1:A:429:UNK:HG1	3:C:249:GLN:NE2	1.79	0.97
1:A:301:ALA:HB1	1:A:302:PRO:HD2	1.44	0.97
7:G:260:THR:HG22	7:G:262:ASP:H	1.25	0.97
2:B:48:LEU:HG	2:B:127:LEU:HD11	1.43	0.97
3:C:45:ALA:HA	3:C:63:LYS:HE3	1.46	0.97
1:A:422:UNK:HA	1:A:425:UNK:HG3	1.43	0.97
5:E:5:THR:N	8:H:87:ARG:HE	1.60	0.97
5:E:9:ALA:HB1	8:H:167:GLY:HA3	1.43	0.97
5:E:17:GLY:N	8:H:231:ARG:HH21	1.61	0.97
9:I:19:GLU:HG2	9:I:51:PRO:HD2	1.47	0.97
2:B:57:ILE:HD12	2:B:57:ILE:H	1.27	0.96
2:B:221:ARG:HH11	2:B:221:ARG:HB3	1.28	0.96
8:H:80:VAL:HG12	8:H:81:GLY:H	1.29	0.96
8:H:148:VAL:HG22	8:H:154:VAL:HA	1.47	0.96
9:I:129:LEU:HD22	9:I:154:VAL:HG22	1.48	0.96
3:C:48:SER:H	3:C:162:ASN:HD22	1.06	0.96
2:B:45:THR:HG23	2:B:130:ASP:H	1.30	0.95
9:I:130:ALA:HA	9:I:151:LEU:HD11	1.44	0.95
3:C:199:ALA:HB2	3:C:210:PRO:HB3	1.45	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ILE:HG13	1:A:234:ILE:HG22	1.48	0.95
3:C:32:PHE:CE2	3:C:262:VAL:HG13	2.01	0.95
3:C:48:SER:N	3:C:162:ASN:HD22	1.64	0.95
2:B:172:LEU:HD12	2:B:172:LEU:H	1.32	0.95
1:A:192:ILE:HD13	1:A:193:CYS:N	1.82	0.95
6:F:116:GLY:O	6:F:120:ARG:HB2	1.65	0.95
1:A:422:UNK:CA	1:A:425:UNK:HG3	1.97	0.95
6:F:185:LEU:HD21	6:F:243:LEU:HD23	1.46	0.95
2:B:137:CYS:HA	2:B:140:ALA:HB3	1.49	0.94
1:A:429:UNK:HG1	3:C:249:GLN:HE21	1.28	0.94
7:G:270:ARG:HH11	7:G:270:ARG:HA	1.31	0.94
3:C:273:MET:HG2	3:C:276:LYS:HE2	1.47	0.94
5:E:11:LYS:HA	5:E:14:ILE:HD12	1.47	0.94
7:G:146:GLU:CD	7:G:187:ASN:HD21	1.70	0.94
4:D:202:SER:H	4:D:205:GLU:HG3	0.78	0.94
1:A:22:LYS:HD2	7:G:243:ILE:HD13	1.50	0.93
7:G:152:ASN:HA	7:G:155:ASN:HB2	1.48	0.93
7:G:170:ASN:ND2	7:G:173:MET:HB3	1.82	0.93
8:H:174:VAL:O	8:H:201:GLY:HA3	1.68	0.93
4:D:165:LEU:HD23	4:D:165:LEU:H	1.32	0.93
1:A:66:PRO:HD3	1:A:129:VAL:HB	1.50	0.93
1:A:264:LEU:H	1:A:264:LEU:HD22	1.32	0.93
7:G:219:GLU:O	7:G:222:LYS:HD3	1.68	0.93
8:H:110:LEU:HD12	8:H:110:LEU:H	1.34	0.93
5:E:238:CYS:HA	6:F:228:SER:HA	1.51	0.93
3:C:48:SER:H	3:C:162:ASN:ND2	1.65	0.93
3:C:150:ASP:OD2	3:C:196:THR:HA	1.69	0.92
4:D:72:ASN:HA	4:D:113:ARG:H	1.35	0.92
7:G:197:LEU:HB3	7:G:238:VAL:HG22	1.48	0.92
9:I:74:LYS:HZ3	9:I:126:ASP:H	1.10	0.92
5:E:9:ALA:HB1	8:H:167:GLY:CA	1.99	0.92
3:C:56:THR:HA	3:C:143:ASP:O	1.68	0.92
3:C:50:LEU:HD13	3:C:59:ILE:HG13	1.51	0.92
2:B:111:LEU:HD13	2:B:152:MET:HA	1.49	0.92
1:A:107:GLU:HA	1:A:110:LEU:CD1	1.99	0.92
5:E:230:VAL:HG13	5:E:234:GLY:HA2	1.50	0.92
5:E:17:GLY:HA2	8:H:231:ARG:NE	1.84	0.92
8:H:170:VAL:HG11	8:H:205:ILE:HB	1.52	0.92
1:A:265:ILE:O	1:A:269:LEU:HB2	1.68	0.92
3:C:260:LYS:HE3	3:C:263:LYS:HD2	1.52	0.92
1:A:231:ILE:H	1:A:231:ILE:HD12	1.35	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:78:ALA:HB3	2:B:81:SER:HB2	1.50	0.92
9:I:133:ILE:HG22	9:I:134:SER:H	1.33	0.92
1:A:138:LEU:HD11	1:A:141:HIS:HB2	1.50	0.92
2:B:214:GLU:HA	2:B:214:GLU:OE1	1.70	0.92
7:G:161:LEU:HB3	7:G:192:ILE:CD1	1.98	0.91
7:G:49:GLU:HB3	9:I:160:SER:HA	1.52	0.91
5:E:263:GLY:O	5:E:267:HIS:HB3	1.69	0.91
1:A:436:UNK:HA	3:C:257:THR:HG23	1.51	0.91
1:A:86:ALA:O	4:D:40:ARG:HG2	1.70	0.91
1:A:107:GLU:HA	1:A:110:LEU:HD12	1.51	0.91
4:D:73:LYS:N	4:D:112:PRO:HA	1.86	0.91
9:I:126:ASP:HA	9:I:155:VAL:HG11	1.53	0.91
3:C:242:GLY:HA3	4:D:191:LYS:HD3	1.51	0.90
6:F:53:ALA:CB	6:F:167:LEU:HB2	2.02	0.90
8:H:77:ILE:HG23	8:H:104:LEU:HD21	1.51	0.90
1:A:147:ASP:O	1:A:151:ILE:HG13	1.69	0.90
9:I:87:ILE:HD11	9:I:99:PHE:HD2	1.35	0.90
5:E:7:SER:HB3	5:E:10:GLU:CD	1.92	0.90
9:I:9:ILE:HD12	9:I:10:PRO:HD2	1.53	0.90
3:C:193:PRO:HB3	3:C:227:ASP:HA	1.51	0.90
4:D:40:ARG:HB3	4:D:41:PRO:HD3	1.52	0.90
3:C:213:GLU:O	3:C:216:HIS:HB3	1.72	0.90
3:C:177:ALA:HA	3:C:181:LEU:HD11	1.54	0.90
3:C:237:LYS:O	4:D:194:MET:HG2	1.72	0.90
7:G:119:ILE:N	7:G:119:ILE:HD12	1.87	0.90
5:E:209:ARG:HA	5:E:209:ARG:HH11	1.37	0.90
6:F:104:PRO:O	6:F:110:ARG:HG2	1.72	0.89
4:D:159:LEU:HA	4:D:164:THR:O	1.72	0.89
4:D:100:ASN:HA	4:D:103:GLU:OE1	1.72	0.89
7:G:161:LEU:CB	7:G:192:ILE:HD12	2.00	0.89
1:A:86:ALA:HB1	1:A:138:LEU:HD12	1.52	0.89
1:A:8:ASN:O	1:A:11:ARG:HG2	1.73	0.89
3:C:115:ASN:HD21	4:D:198:LYS:HG3	1.34	0.89
7:G:248:ILE:HG21	7:G:271:LEU:HD21	1.53	0.89
3:C:260:LYS:O	3:C:264:LYS:HG2	1.72	0.89
7:G:41:ALA:HB3	7:G:98:VAL:HG22	1.54	0.89
1:A:271:ASN:HA	1:A:274:LYS:HE2	1.55	0.89
3:C:262:VAL:HA	3:C:265:LEU:HD12	1.55	0.88
3:C:77:GLY:HA3	3:C:124:LEU:HB2	1.55	0.88
4:D:186:ASP:HA	4:D:193:LEU:HD11	1.54	0.88
1:A:230:GLU:CB	2:B:205:HIS:HA	2.04	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:ARG:O	1:A:252:LYS:HB3	1.72	0.88
2:B:156:VAL:HG13	2:B:188:LEU:O	1.72	0.88
5:E:8:GLU:HB2	5:E:11:LYS:NZ	1.87	0.88
3:C:60:CYS:HA	3:C:139:LEU:HG	1.55	0.88
1:A:165:VAL:CG2	1:A:175:TYR:H	1.85	0.88
1:A:246:GLN:HA	1:A:249:ARG:NE	1.88	0.88
7:G:116:VAL:HG13	7:G:233:ASN:ND2	1.87	0.88
6:F:215:LEU:HD21	6:F:220:ASN:HA	1.56	0.88
2:B:101:GLN:O	2:B:105:THR:HG23	1.74	0.88
7:G:242:THR:HG23	7:G:244:GLN:H	1.39	0.88
8:H:75:ARG:HB3	8:H:102:SER:HA	1.55	0.88
1:A:164:ASP:HA	1:A:174:LEU:HD22	1.55	0.88
1:A:182:PRO:O	1:A:183:VAL:HG13	1.73	0.88
7:G:198:LEU:HD12	7:G:236:ILE:C	1.93	0.88
3:C:23:ARG:HD3	3:C:207:ILE:HG21	1.55	0.88
1:A:190:MET:N	1:A:226:ASN:HD21	1.72	0.88
4:D:181:LEU:HA	4:D:197:THR:OG1	1.73	0.87
4:D:219:HIS:N	4:D:222:ARG:HH21	1.72	0.87
7:G:242:THR:H	7:G:245:GLN:NE2	1.72	0.87
2:B:57:ILE:HD11	2:B:117:ARG:HB3	1.56	0.87
3:C:243:LEU:HG	3:C:244:THR:H	1.38	0.87
4:D:170:THR:HG21	4:D:172:LYS:HD3	1.56	0.87
2:B:143:LEU:HA	2:B:146:LEU:CD1	2.04	0.87
1:A:53:THR:HG23	1:A:142:ASP:H	1.39	0.87
2:B:198:LEU:HD13	2:B:198:LEU:O	1.74	0.87
3:C:86:PRO:HB2	3:C:87:PRO:HD2	1.54	0.87
2:B:79:THR:HA	2:B:88:ARG:CZ	2.05	0.87
1:A:414:UNK:HB1	4:D:26:CYS:HB2	1.57	0.86
3:C:211:THR:H	3:C:214:GLU:HB3	1.37	0.86
7:G:20:ARG:H	7:G:35:LEU:HD21	1.40	0.86
5:E:257:GLU:HA	6:F:234:THR:HG21	1.56	0.86
7:G:270:ARG:HH11	7:G:270:ARG:CA	1.88	0.86
5:E:57:ASP:HB2	5:E:142:LEU:HB2	1.57	0.86
1:A:71:ALA:HB1	1:A:126:GLY:HA2	1.57	0.86
4:D:173:GLN:H	4:D:173:GLN:HE21	1.22	0.86
8:H:94:LYS:O	8:H:109:LEU:HG	1.75	0.86
1:A:13:PHE:HA	1:A:16:ARG:HB2	1.56	0.86
3:C:60:CYS:HB3	3:C:159:ALA:HB2	1.57	0.86
3:C:235:LEU:HD12	4:D:206:LEU:HD21	1.54	0.86
8:H:220:ILE:HG23	8:H:223:LEU:HD22	1.57	0.86
1:A:234:ILE:CD1	2:B:200:MET:H	1.88	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:155:ASN:O	7:G:156:VAL:HG23	1.76	0.86
8:H:139:ASP:HB2	8:H:141:ILE:HD11	1.57	0.86
9:I:104:ARG:HD3	9:I:141:ASN:HB2	1.58	0.86
7:G:222:LYS:HZ1	7:G:268:PHE:CB	1.89	0.86
6:F:153:ASP:OD1	6:F:157:ALA:HB3	1.77	0.85
3:C:94:ARG:HH12	3:C:100:GLU:H	1.23	0.85
4:D:158:ALA:O	4:D:165:LEU:HA	1.76	0.85
1:A:217:MET:SD	1:A:220:LEU:HB2	2.16	0.85
8:H:195:VAL:HG22	8:H:205:ILE:HG23	1.57	0.85
7:G:243:ILE:HG23	7:G:244:GLN:H	1.40	0.85
1:A:59:VAL:HG13	1:A:134:VAL:HG13	1.58	0.85
3:C:12:GLU:HG3	3:C:15:ARG:HD2	1.59	0.85
3:C:270:ILE:O	3:C:274:LYS:HB3	1.76	0.85
9:I:128:VAL:HB	9:I:153:VAL:HG23	1.59	0.85
6:F:51:GLY:HA3	6:F:172:ALA:HB2	1.57	0.85
5:E:74:PRO:HB2	5:E:129:ARG:HA	1.57	0.85
1:A:231:ILE:HD12	1:A:231:ILE:N	1.92	0.85
3:C:104:VAL:HG13	4:D:93:SER:HB2	1.56	0.85
1:A:145:ILE:H	1:A:145:ILE:CD1	1.87	0.84
1:A:234:ILE:HD11	2:B:200:MET:H	1.40	0.84
5:E:56:THR:OG1	5:E:148:LEU:HD13	1.76	0.84
5:E:123:THR:HG21	5:E:192:LEU:HB2	1.58	0.84
1:A:249:ARG:HH11	1:A:249:ARG:CB	1.90	0.84
2:B:99:GLY:HA2	2:B:102:LEU:HD23	1.60	0.84
5:E:240:ARG:HG2	5:E:241:LYS:N	1.91	0.84
5:E:264:LYS:HA	5:E:267:HIS:CD2	2.12	0.84
9:I:123:ARG:HB3	9:I:124:PRO:CD	2.06	0.84
3:C:94:ARG:HH11	3:C:99:GLY:HA2	1.41	0.84
7:G:128:PHE:HE1	7:G:140:LEU:HB3	1.41	0.84
1:A:77:PHE:O	1:A:133:ARG:HA	1.78	0.84
1:A:144:ASN:HB2	1:A:209:PRO:HD2	1.58	0.84
6:F:158:LEU:HD22	6:F:212:THR:HG21	1.59	0.84
2:B:142:THR:O	2:B:146:LEU:HG	1.78	0.84
1:A:167:VAL:HG13	1:A:171:GLU:O	1.78	0.84
1:A:56:LEU:HB3	1:A:137:HIS:HB2	1.60	0.84
1:A:234:ILE:HD13	2:B:198:LEU:CD1	2.08	0.84
9:I:148:GLU:HB2	9:I:151:LEU:HB2	1.60	0.84
2:B:139:ASN:O	2:B:143:LEU:HG	1.77	0.84
1:A:264:LEU:N	1:A:264:LEU:HD22	1.92	0.84
7:G:119:ILE:HD11	7:G:235:ARG:HH21	1.42	0.84
9:I:156:ALA:CB	9:I:164:MET:HB2	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:227:LEU:O	5:E:239:MET:HG2	1.78	0.84
1:A:439:UNK:HG3	3:C:261:GLU:HB2	1.58	0.83
7:G:244:GLN:NE2	7:G:244:GLN:HA	1.90	0.83
7:G:264:ARG:H	7:G:264:ARG:NH1	1.75	0.83
9:I:112:GLU:H	9:I:112:GLU:CD	1.80	0.83
4:D:159:LEU:HB2	4:D:179:ALA:HB3	1.60	0.83
3:C:94:ARG:NH1	3:C:99:GLY:HA2	1.93	0.83
1:A:33:ARG:HH21	1:A:50:LEU:HD22	1.43	0.83
9:I:168:SER:O	9:I:185:VAL:HG21	1.78	0.83
6:F:103:ALA:HB3	6:F:106:ALA:HB2	1.60	0.83
5:E:227:LEU:HB3	5:E:240:ARG:H	1.43	0.83
1:A:211:GLU:O	1:A:215:ARG:HD2	1.79	0.83
7:G:242:THR:N	7:G:245:GLN:HE22	1.74	0.83
4:D:211:ALA:O	4:D:214:GLN:HB2	1.78	0.83
1:A:234:ILE:HD11	2:B:200:MET:N	1.92	0.83
7:G:215:GLU:O	7:G:219:GLU:N	2.11	0.83
6:F:96:LEU:HG	6:F:127:GLN:HE21	1.41	0.83
5:E:118:SER:HA	5:E:196:ASN:ND2	1.91	0.83
1:A:145:ILE:N	1:A:145:ILE:HD12	1.92	0.83
6:F:53:ALA:HB1	6:F:164:ALA:O	1.79	0.83
2:B:41:GLU:HA	2:B:45:THR:O	1.79	0.82
8:H:76:TYR:CB	8:H:102:SER:HB3	2.07	0.82
6:F:129:ALA:O	6:F:132:PRO:HD2	1.78	0.82
7:G:243:ILE:HG23	7:G:244:GLN:N	1.94	0.82
5:E:264:LYS:HD3	5:E:268:ALA:HB2	1.60	0.82
5:E:120:ASP:OD2	5:E:192:LEU:HD11	1.80	0.82
4:D:112:PRO:HG2	4:D:113:ARG:NH2	1.94	0.82
7:G:50:ARG:NE	7:G:75:ASP:HA	1.94	0.82
1:A:429:UNK:HG3	3:C:249:GLN:O	1.78	0.82
1:A:115:CYS:HB2	1:A:189:HIS:O	1.79	0.82
7:G:120:VAL:HG22	7:G:162:ILE:HD11	1.59	0.82
4:D:120:LEU:HD23	4:D:133:CYS:HB3	1.62	0.82
5:E:18:VAL:O	5:E:209:ARG:HG2	1.78	0.82
1:A:436:UNK:HG3	3:C:257:THR:OG1	1.79	0.82
4:D:74:ALA:HB1	4:D:116:ILE:HD11	1.60	0.82
1:A:85:MET:HA	4:D:59:TYR:HE1	1.45	0.82
9:I:123:ARG:HB2	9:I:183:ARG:HH21	1.42	0.82
9:I:75:VAL:HA	9:I:85:VAL:HG12	1.60	0.82
6:F:50:LYS:N	6:F:50:LYS:HD2	1.91	0.82
1:A:177:PRO:O	1:A:180:ARG:HG2	1.80	0.82
2:B:182:PRO:HA	2:B:202:ALA:HB1	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:13:TYR:HB2	8:H:168:GLN:OE1	1.80	0.82
3:C:46:ASP:O	3:C:163:VAL:HA	1.79	0.81
3:C:199:ALA:HB3	3:C:207:ILE:HG13	1.62	0.81
4:D:184:ALA:CB	4:D:194:MET:HB3	2.10	0.81
7:G:228:ILE:HG22	7:G:238:VAL:HA	1.62	0.81
7:G:41:ALA:O	7:G:98:VAL:HG13	1.79	0.81
6:F:62:VAL:HG11	6:F:160:ALA:O	1.80	0.81
2:B:143:LEU:HA	2:B:146:LEU:HD12	1.61	0.81
8:H:282:MET:O	8:H:286:GLN:HG3	1.80	0.81
8:H:91:VAL:HG13	8:H:96:TRP:HA	1.60	0.81
2:B:73:CYS:SG	2:B:122:ILE:HB	2.21	0.81
8:H:140:LEU:C	8:H:141:ILE:HD12	2.00	0.81
5:E:101:LEU:HD12	5:E:102:GLY:H	1.45	0.81
2:B:100:LEU:HD23	2:B:103:ARG:HD3	1.63	0.81
5:E:23:ARG:NH2	5:E:211:VAL:HG11	1.94	0.81
5:E:264:LYS:HA	5:E:267:HIS:HD2	1.44	0.81
4:D:54:VAL:HG13	4:D:121:GLN:O	1.81	0.81
4:D:28:LEU:N	4:D:28:LEU:HD23	1.96	0.81
5:E:105:ILE:HG21	5:E:152:ILE:HD13	1.63	0.81
8:H:33:ILE:HG21	8:H:67:ILE:HD13	1.61	0.81
2:B:41:GLU:HB3	2:B:46:LYS:HG3	1.62	0.81
4:D:73:LYS:CA	4:D:112:PRO:HA	2.10	0.81
7:G:242:THR:H	7:G:245:GLN:HE22	1.24	0.81
7:G:128:PHE:CE1	7:G:140:LEU:HB3	2.16	0.81
5:E:83:VAL:HG13	5:E:139:VAL:HB	1.60	0.81
7:G:262:ASP:OD1	7:G:263:GLN:N	2.13	0.81
8:H:188:ASP:HB3	8:H:194:SER:OG	1.81	0.81
3:C:27:ARG:HD2	3:C:31:GLU:CG	2.11	0.80
3:C:83:VAL:HG23	3:C:106:SER:HA	1.63	0.80
6:F:53:ALA:HB2	6:F:168:ALA:H	1.46	0.80
6:F:39:VAL:HG21	6:F:251:LEU:HD21	1.63	0.80
1:A:104:ARG:NH1	1:A:104:ARG:O	2.14	0.80
1:A:37:ILE:N	1:A:37:ILE:HD12	1.97	0.80
2:B:186:LEU:HD12	2:B:195:ILE:HG23	1.63	0.80
5:E:15:VAL:HA	5:E:206:ILE:HG22	1.62	0.80
5:E:22:LEU:HD13	8:H:231:ARG:HB3	1.63	0.80
3:C:147:ASN:ND2	3:C:150:ASP:H	1.79	0.80
6:F:53:ALA:HB2	6:F:167:LEU:HB2	1.64	0.80
2:B:197:LEU:HD13	2:B:198:LEU:N	1.96	0.80
7:G:34:LEU:CB	7:G:76:ARG:HA	2.09	0.80
9:I:168:SER:HG	9:I:169:TRP:HE3	1.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:156:LEU:O	3:C:160:LEU:HD13	1.81	0.80
6:F:259:LEU:HD13	9:I:9:ILE:CD1	2.12	0.80
1:A:221:LEU:HG	1:A:222:VAL:N	1.94	0.80
9:I:102:THR:HG22	9:I:104:ARG:HH12	1.44	0.80
5:E:169:ARG:HH21	5:E:182:LEU:HB3	1.44	0.80
3:C:84:ASP:O	3:C:85:LEU:HD23	1.82	0.80
4:D:79:ILE:CD1	4:D:119:VAL:HG22	2.11	0.80
5:E:56:THR:HB	5:E:145:GLY:H	1.46	0.80
1:A:161:ARG:HB3	1:A:183:VAL:HB	1.64	0.80
9:I:15:CYS:HB3	9:I:33:ILE:HD12	1.63	0.80
2:B:16:ARG:HH21	2:B:21:LEU:C	1.85	0.80
5:E:186:PRO:HG2	5:E:187:TYR:HD1	1.47	0.80
3:C:237:LYS:NZ	3:C:240:GLY:H	1.80	0.80
9:I:156:ALA:HB1	9:I:164:MET:CB	2.07	0.80
5:E:205:LYS:HE2	5:E:208:TYR:HA	1.64	0.80
6:F:237:TRP:CE3	6:F:237:TRP:HA	2.16	0.80
2:B:17:ARG:HB2	2:B:20:GLU:HG2	1.63	0.80
7:G:111:VAL:HG12	7:G:112:LYS:H	1.47	0.79
7:G:20:ARG:H	7:G:35:LEU:CD2	1.94	0.79
7:G:34:LEU:HD22	7:G:76:ARG:HG3	1.64	0.79
6:F:96:LEU:H	6:F:96:LEU:HD23	1.46	0.79
6:F:264:ARG:HA	9:I:7:TYR:OH	1.81	0.79
9:I:89:TYR:HD2	9:I:92:SER:HA	1.46	0.79
7:G:216:ILE:CD1	7:G:216:ILE:H	1.90	0.79
3:C:195:ALA:HB2	3:C:225:VAL:HG22	1.63	0.79
6:F:43:ALA:HB2	6:F:167:LEU:HD13	1.65	0.79
2:B:77:SER:HA	2:B:125:GLN:OE1	1.83	0.79
7:G:242:THR:HG23	7:G:244:GLN:N	1.96	0.79
5:E:232:SER:O	5:E:264:LYS:HE2	1.83	0.79
7:G:19:ALA:HB1	7:G:35:LEU:HD13	1.64	0.79
3:C:192:HIS:H	3:C:228:GLU:CD	1.86	0.79
1:A:230:GLU:HB3	2:B:205:HIS:CA	2.09	0.79
8:H:165:LYS:HD2	8:H:166:LEU:N	1.98	0.79
5:E:25:ASP:C	8:H:239:ASN:HD21	1.85	0.79
8:H:129:LEU:HA	8:H:132:ARG:HG2	1.64	0.79
7:G:198:LEU:HD21	7:G:235:ARG:HB3	1.64	0.79
7:G:197:LEU:HB3	7:G:238:VAL:CG2	2.13	0.79
5:E:240:ARG:HG2	5:E:241:LYS:H	1.47	0.79
1:A:106:MET:CE	1:A:150:SER:HA	2.13	0.79
3:C:88:LEU:HD12	6:F:65:ALA:HB2	1.63	0.79
6:F:170:ALA:HB1	9:I:38:ALA:CB	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:178:VAL:HG12	7:G:179:CYS:H	1.47	0.79
7:G:50:ARG:HE	7:G:75:ASP:HA	1.47	0.79
1:A:88:PRO:HG2	1:A:89:ALA:H	1.45	0.79
7:G:26:VAL:HA	7:G:84:ARG:HA	1.63	0.79
6:F:185:LEU:HD11	6:F:243:LEU:HB3	1.65	0.78
8:H:254:THR:HA	8:H:257:LEU:HD12	1.64	0.78
9:I:133:ILE:HB	9:I:143:LEU:HB2	1.63	0.78
9:I:74:LYS:NZ	9:I:126:ASP:H	1.79	0.78
5:E:241:LYS:HD2	6:F:224:GLY:HA2	1.65	0.78
3:C:118:ILE:HG13	3:C:119:ILE:H	1.47	0.78
5:E:12:VAL:HG13	5:E:13:TYR:H	1.47	0.78
7:G:205:LEU:HB3	7:G:209:LEU:HD11	1.64	0.78
4:D:134:LEU:HD13	4:D:154:GLY:HA3	1.64	0.78
3:C:69:PRO:HB2	3:C:74:PRO:O	1.82	0.78
6:F:255:LEU:HD12	6:F:256:GLN:H	1.45	0.78
6:F:40:TYR:CD1	6:F:56:GLU:HG3	2.18	0.78
2:B:36:GLY:HA3	2:B:51:VAL:CG1	2.13	0.78
8:H:136:GLN:H	8:H:136:GLN:NE2	1.82	0.78
3:C:160:LEU:O	3:C:187:LEU:HD13	1.83	0.78
9:I:129:LEU:HD23	9:I:129:LEU:N	1.99	0.78
4:D:105:VAL:O	4:D:149:ARG:HG2	1.83	0.78
8:H:76:TYR:O	8:H:104:LEU:HD21	1.83	0.78
8:H:96:TRP:NE1	8:H:131:MET:HB3	1.98	0.78
2:B:99:GLY:CA	2:B:102:LEU:HD23	2.14	0.78
7:G:19:ALA:H	7:G:22:VAL:CG2	1.97	0.78
3:C:66:PHE:HE1	6:F:109:ARG:HH12	1.30	0.78
4:D:137:ALA:O	4:D:140:ALA:HB3	1.83	0.78
8:H:266:HIS:O	8:H:268:ILE:N	2.16	0.78
1:A:240:ILE:HD12	1:A:240:ILE:N	1.99	0.78
7:G:127:ILE:HG21	7:G:139:SER:HB3	1.66	0.78
9:I:104:ARG:NH1	9:I:141:ASN:HA	1.99	0.78
5:E:152:ILE:O	5:E:156:VAL:HB	1.84	0.78
3:C:78:TYR:O	3:C:135:LEU:HG	1.84	0.77
2:B:218:GLN:NE2	2:B:221:ARG:HD3	1.99	0.77
6:F:134:VAL:HG22	6:F:176:MET:CG	2.14	0.77
1:A:109:CYS:HA	1:A:112:ASN:HB2	1.65	0.77
5:E:116:LYS:HG2	5:E:198:PRO:CD	2.13	0.77
4:D:82:PRO:HA	4:D:122:VAL:CG2	2.14	0.77
6:F:34:THR:HG22	6:F:197:LEU:HD22	1.66	0.77
4:D:181:LEU:HG	4:D:197:THR:HG21	1.66	0.77
1:A:271:ASN:HA	1:A:274:LYS:CE	2.13	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:153:SER:O	5:E:156:VAL:HG12	1.85	0.77
1:A:106:MET:HE2	1:A:150:SER:HA	1.65	0.77
3:C:37:VAL:HG12	3:C:51:VAL:HG22	1.65	0.77
5:E:51:VAL:HG11	5:E:154:ILE:HG21	1.65	0.77
7:G:264:ARG:O	7:G:268:PHE:N	2.18	0.77
2:B:135:ALA:HB1	2:B:158:ALA:O	1.85	0.77
5:E:140:LEU:C	5:E:141:LEU:HD23	2.04	0.77
3:C:23:ARG:NH1	3:C:207:ILE:HB	1.99	0.77
4:D:107:LEU:HD21	4:D:110:LEU:HD22	1.65	0.77
7:G:166:PHE:HA	7:G:177:MET:HA	1.67	0.77
7:G:264:ARG:HH11	7:G:264:ARG:HB2	1.49	0.77
4:D:183:PHE:CE1	4:D:210:LEU:HA	2.20	0.77
6:F:55:LEU:HD12	6:F:160:ALA:O	1.85	0.77
2:B:186:LEU:HD11	2:B:188:LEU:HB2	1.67	0.77
8:H:262:ALA:O	8:H:265:PRO:HD2	1.85	0.77
1:A:286:GLU:HA	1:A:289:ALA:HB3	1.66	0.77
3:C:157:LEU:HD11	3:C:193:PRO:O	1.85	0.77
4:D:97:LEU:HB3	4:D:194:MET:CE	2.15	0.77
8:H:170:VAL:HG12	8:H:205:ILE:HD13	1.65	0.77
8:H:96:TRP:HE1	8:H:131:MET:HB3	1.49	0.77
5:E:260:LYS:HB3	6:F:234:THR:OG1	1.85	0.77
6:F:97:LEU:HB3	6:F:145:GLU:HA	1.65	0.77
2:B:79:THR:O	2:B:85:ARG:HA	1.85	0.77
9:I:87:ILE:HD11	9:I:99:PHE:CD2	2.19	0.77
2:B:73:CYS:HA	2:B:122:ILE:O	1.85	0.77
3:C:178:GLU:H	3:C:181:LEU:CG	1.96	0.77
6:F:66:VAL:HG22	6:F:146:VAL:HG13	1.67	0.76
1:A:86:ALA:HA	1:A:139:LEU:O	1.86	0.76
1:A:211:GLU:O	1:A:214:GLU:HB2	1.84	0.76
7:G:123:LYS:CA	7:G:128:PHE:HB3	2.14	0.76
5:E:8:GLU:HB2	5:E:11:LYS:HZ3	1.49	0.76
2:B:121:ASP:HB2	2:B:123:TYR:CZ	2.20	0.76
1:A:143:GLY:HA2	1:A:214:GLU:CG	2.11	0.76
8:H:76:TYR:HB3	8:H:102:SER:CB	2.15	0.76
5:E:105:ILE:HA	5:E:108:THR:OG1	1.84	0.76
9:I:154:VAL:O	9:I:155:VAL:HG23	1.85	0.76
6:F:94:GLY:HA3	6:F:142:ALA:O	1.85	0.76
7:G:116:VAL:HG11	7:G:132:VAL:HG13	1.66	0.76
7:G:226:LEU:HD22	7:G:227:GLU:N	2.00	0.76
7:G:198:LEU:HA	7:G:236:ILE:O	1.85	0.76
5:E:37:VAL:HG11	5:E:158:ALA:CB	2.15	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:12:GLU:O	3:C:15:ARG:HG2	1.85	0.76
9:I:103:ILE:HG23	9:I:142:TYR:HB2	1.68	0.76
7:G:222:LYS:HZ1	7:G:269:SER:N	1.84	0.76
8:H:256:ILE:HA	8:H:259:CYS:SG	2.26	0.76
6:F:239:GLU:HG3	6:F:240:ALA:H	1.50	0.76
5:E:120:ASP:OD1	5:E:192:LEU:HD21	1.86	0.76
2:B:42:GLN:OE1	2:B:136:ALA:HB2	1.86	0.76
4:D:189:GLU:C	4:D:191:LYS:H	1.87	0.76
1:A:142:ASP:OD1	1:A:211:GLU:HB2	1.86	0.76
9:I:103:ILE:HG21	9:I:144:LEU:HD11	1.68	0.76
5:E:202:THR:O	5:E:212:VAL:HG22	1.86	0.76
7:G:114:ASP:O	7:G:165:GLN:HA	1.86	0.76
3:C:17:PHE:HB3	3:C:22:CYS:SG	2.25	0.76
3:C:94:ARG:NH1	3:C:100:GLU:H	1.84	0.76
9:I:123:ARG:HG3	9:I:183:ARG:HE	1.48	0.76
1:A:59:VAL:HG13	1:A:134:VAL:CG1	2.15	0.76
1:A:428:UNK:O	1:A:432:UNK:HG2	1.86	0.76
9:I:22:PRO:HG2	9:I:26:THR:HB	1.66	0.76
7:G:117:ILE:HG23	7:G:192:ILE:HD11	1.68	0.76
7:G:25:GLN:C	7:G:84:ARG:HG3	2.06	0.76
1:A:78:PHE:HB2	1:A:134:VAL:CG2	2.16	0.76
6:F:237:TRP:HE3	6:F:237:TRP:HA	1.50	0.76
6:F:252:TYR:HA	6:F:255:LEU:HD21	1.67	0.75
6:F:55:LEU:HB2	6:F:62:VAL:HG13	1.66	0.75
7:G:172:ASP:HB3	9:I:124:PRO:HG3	1.67	0.75
1:A:121:LEU:HD12	1:A:122:CYS:N	2.01	0.75
1:A:421:UNK:O	1:A:425:UNK:HG3	1.85	0.75
2:B:184:LEU:HB2	2:B:200:MET:HB2	1.67	0.75
3:C:83:VAL:CG2	3:C:106:SER:HA	2.16	0.75
2:B:46:LYS:HD3	2:B:128:GLN:CB	2.15	0.75
8:H:108:LEU:HD23	8:H:108:LEU:H	1.50	0.75
8:H:174:VAL:HG22	8:H:201:GLY:CA	2.16	0.75
3:C:57:THR:O	3:C:141:CYS:HA	1.86	0.75
3:C:193:PRO:HB3	3:C:227:ASP:CA	2.16	0.75
1:A:11:ARG:HG2	1:A:12:ARG:H	1.51	0.75
7:G:20:ARG:N	7:G:35:LEU:HD21	2.01	0.75
9:I:69:ALA:O	9:I:132:VAL:HG23	1.85	0.75
6:F:33:PRO:O	6:F:34:THR:HG23	1.86	0.75
3:C:164:GLN:HG2	3:C:186:TYR:CB	2.16	0.75
4:D:53:SER:N	4:D:124:SER:HB3	2.01	0.75
7:G:202:THR:CB	7:G:205:LEU:HD13	2.15	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:73:LYS:HB3	5:E:76:GLU:OE2	1.87	0.75
2:B:182:PRO:HA	2:B:202:ALA:CB	2.16	0.75
4:D:112:PRO:HG2	4:D:113:ARG:CZ	2.17	0.75
8:H:91:VAL:HG11	8:H:96:TRP:CD1	2.22	0.75
1:A:183:VAL:H	1:A:184:PRO:HD3	1.51	0.75
4:D:53:SER:H	4:D:124:SER:HB3	1.51	0.75
5:E:249:PRO:O	5:E:252:ILE:HG22	1.85	0.75
2:B:147:ASP:C	2:B:149:GLY:H	1.90	0.75
9:I:16:ASN:ND2	9:I:18:GLU:HG2	2.01	0.75
1:A:234:ILE:HG13	2:B:200:MET:HE3	1.67	0.75
9:I:73:CYS:HB3	9:I:87:ILE:HA	1.69	0.75
9:I:86:HIS:HA	9:I:101:GLY:CA	2.17	0.75
3:C:237:LYS:HZ2	4:D:194:MET:N	1.84	0.75
6:F:150:LEU:HD11	6:F:157:ALA:HB1	1.69	0.75
9:I:127:ILE:CD1	9:I:155:VAL:HG21	2.15	0.75
4:D:131:ALA:HA	4:D:134:LEU:HD12	1.68	0.75
3:C:127:SER:HB2	3:C:131:LEU:HD12	1.69	0.74
3:C:7:THR:HB	3:C:10:PRO:CD	2.17	0.74
9:I:10:PRO:HA	9:I:35:SER:O	1.87	0.74
1:A:100:VAL:HG12	1:A:101:LYS:N	2.01	0.74
1:A:263:GLU:O	1:A:267:LYS:HB2	1.87	0.74
7:G:152:ASN:CA	7:G:155:ASN:HB2	2.16	0.74
9:I:73:CYS:HB3	9:I:87:ILE:HG22	1.69	0.74
7:G:260:THR:HB	7:G:263:GLN:H	1.52	0.74
5:E:238:CYS:CA	6:F:228:SER:HA	2.17	0.74
1:A:78:PHE:CB	1:A:134:VAL:HG23	2.17	0.74
1:A:24:LEU:C	1:A:26:GLY:H	1.89	0.74
6:F:181:VAL:HG11	6:F:248:CYS:HA	1.68	0.74
9:I:10:PRO:HD3	9:I:38:ALA:HB2	1.69	0.74
3:C:127:SER:HB3	3:C:131:LEU:HB2	1.67	0.74
3:C:236:HIS:CE1	3:C:238:PRO:HD3	2.23	0.74
4:D:193:LEU:O	4:D:194:MET:HB2	1.87	0.74
2:B:79:THR:HA	2:B:88:ARG:NH2	2.01	0.74
8:H:96:TRP:CH2	8:H:110:LEU:HG	2.23	0.74
5:E:216:LEU:HA	5:E:219:GLU:OE1	1.86	0.74
3:C:109:ILE:H	3:C:109:ILE:HD13	1.53	0.74
1:A:425:UNK:HA	3:C:249:GLN:HG3	1.68	0.74
7:G:136:GLU:HB2	7:G:137:PRO:HD2	1.69	0.74
5:E:127:SER:H	5:E:131:HIS:HB2	1.52	0.74
8:H:136:GLN:H	8:H:136:GLN:HE21	1.32	0.74
3:C:17:PHE:HB3	3:C:22:CYS:O	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:273:MET:HA	3:C:276:LYS:HG2	1.70	0.74
5:E:249:PRO:HG3	6:F:245:LEU:HD11	1.69	0.74
2:B:195:ILE:HD12	2:B:195:ILE:N	2.02	0.74
7:G:226:LEU:HD13	7:G:227:GLU:N	2.03	0.74
5:E:264:LYS:CD	5:E:268:ALA:HB2	2.17	0.74
1:A:429:UNK:CG	3:C:249:GLN:NE2	2.44	0.74
1:A:255:GLY:O	1:A:258:VAL:HG13	1.88	0.74
9:I:133:ILE:HD12	9:I:143:LEU:HB3	1.69	0.74
7:G:215:GLU:O	7:G:219:GLU:HB2	1.86	0.74
8:H:237:LEU:O	8:H:241:ILE:HG13	1.88	0.74
2:B:24:ILE:HG22	2:B:42:GLN:HA	1.70	0.74
7:G:148:ALA:O	7:G:151:ARG:HG2	1.87	0.74
8:H:25:HIS:HB3	8:H:60:VAL:HB	1.68	0.74
3:C:259:HIS:HB3	3:C:260:LYS:NZ	2.01	0.74
3:C:25:ASP:HB3	3:C:27:ARG:HG3	1.69	0.74
6:F:36:LEU:HD21	6:F:39:VAL:CG2	2.17	0.74
1:A:99:LEU:O	1:A:103:ASN:HB2	1.88	0.74
5:E:227:LEU:HD12	5:E:239:MET:HA	1.69	0.74
8:H:150:SER:C	8:H:152:GLY:H	1.92	0.74
1:A:242:LEU:C	1:A:246:GLN:HE22	1.91	0.73
2:B:205:HIS:CD2	2:B:206:GLU:N	2.55	0.73
7:G:242:THR:O	7:G:245:GLN:NE2	2.21	0.73
7:G:118:GLY:O	7:G:161:LEU:HA	1.88	0.73
7:G:32:GLU:C	7:G:33:LEU:HD13	2.08	0.73
3:C:259:HIS:O	3:C:263:LYS:HG3	1.87	0.73
1:A:32:TYR:HE1	1:A:207:VAL:HG12	1.54	0.73
4:D:58:VAL:HG13	4:D:118:VAL:HG22	1.69	0.73
5:E:251:SER:HA	5:E:254:GLU:CD	2.08	0.73
5:E:154:ILE:HD12	5:E:270:LEU:HD13	1.69	0.73
3:C:164:GLN:HA	3:C:186:TYR:HB3	1.70	0.73
3:C:12:GLU:HA	3:C:15:ARG:HG2	1.70	0.73
6:F:214:ALA:C	6:F:223:ALA:HB3	2.09	0.73
1:A:112:ASN:HD21	2:B:201:ASP:HB3	1.53	0.73
7:G:244:GLN:HE21	7:G:244:GLN:HA	1.50	0.73
7:G:157:GLN:O	7:G:160:ASP:HB2	1.89	0.73
7:G:42:GLU:OE2	7:G:47:ALA:HA	1.88	0.73
9:I:67:VAL:HG13	9:I:135:LEU:HD21	1.69	0.73
2:B:69:ALA:HB3	2:B:112:THR:CG2	2.17	0.73
5:E:63:LYS:O	5:E:135:LEU:HA	1.88	0.73
7:G:78:LEU:HD12	7:G:79:VAL:H	1.54	0.73
5:E:184:ASP:CB	5:E:187:TYR:HB2	2.19	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:120:VAL:HA	7:G:130:VAL:HA	1.70	0.73
1:A:442:UNK:HG2	1:A:443:UNK:N	2.03	0.73
6:F:166:ALA:HA	6:F:169:LEU:HD12	1.70	0.73
7:G:116:VAL:HG11	7:G:132:VAL:CG1	2.19	0.73
7:G:166:PHE:HB3	7:G:177:MET:HB3	1.70	0.73
7:G:178:VAL:HG12	7:G:179:CYS:N	2.02	0.73
9:I:102:THR:HG22	9:I:104:ARG:NH1	2.04	0.73
6:F:222:VAL:HG13	6:F:225:LEU:HD21	1.71	0.73
2:B:12:ARG:HH21	2:B:18:ALA:HA	1.51	0.73
5:E:93:PHE:HB3	5:E:97:GLY:HA3	1.70	0.73
1:A:14:LEU:HD22	1:A:216:VAL:HG21	1.70	0.73
1:A:235:GLN:HG2	2:B:199:GLU:OE2	1.89	0.73
9:I:105:LYS:HZ1	9:I:146:THR:HG23	1.53	0.73
9:I:128:VAL:HG23	9:I:152:GLY:O	1.89	0.73
2:B:46:LYS:HD3	2:B:128:GLN:HB3	1.71	0.73
3:C:110:ALA:HA	3:C:113:ILE:HD12	1.70	0.73
7:G:191:VAL:HG12	7:G:191:VAL:O	1.89	0.73
5:E:116:LYS:HE3	5:E:196:ASN:O	1.88	0.73
8:H:59:SER:OG	8:H:70:LYS:HB2	1.89	0.73
6:F:93:ARG:HA	6:F:140:PRO:HA	1.71	0.73
4:D:197:THR:C	4:D:198:LYS:HD2	2.08	0.72
2:B:204:LEU:HD11	2:B:208:HIS:HB2	1.69	0.72
2:B:95:SER:O	2:B:98:MET:HB3	1.89	0.72
4:D:58:VAL:CG2	4:D:140:ALA:HB1	2.17	0.72
5:E:44:ASN:O	5:E:45:THR:HG23	1.88	0.72
7:G:216:ILE:N	7:G:216:ILE:HD12	1.99	0.72
8:H:98:VAL:HG23	8:H:106:SER:O	1.89	0.72
1:A:201:GLN:HB2	1:A:203:THR:HG23	1.71	0.72
1:A:264:LEU:H	1:A:264:LEU:CD2	2.02	0.72
9:I:162:ILE:CD1	9:I:176:LYS:HB3	2.18	0.72
7:G:249:LEU:O	7:G:252:ILE:HG22	1.88	0.72
5:E:16:HIS:CD2	8:H:225:PRO:HB3	2.24	0.72
1:A:439:UNK:CG	3:C:261:GLU:HB2	2.19	0.72
6:F:174:VAL:HG23	6:F:176:MET:CE	2.19	0.72
1:A:243:LEU:O	1:A:247:VAL:HG13	1.89	0.72
9:I:173:GLN:HG3	9:I:179:THR:O	1.89	0.72
5:E:23:ARG:CZ	5:E:211:VAL:HG11	2.20	0.72
5:E:12:VAL:HG13	5:E:13:TYR:N	2.05	0.72
5:E:202:THR:HA	5:E:226:LEU:O	1.89	0.72
1:A:176:THR:HB	1:A:180:ARG:NH1	2.03	0.72
1:A:293:ILE:HG22	1:A:294:THR:H	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:143:LEU:O	9:I:144:LEU:HD23	1.89	0.72
7:G:222:LYS:NZ	7:G:269:SER:N	2.36	0.72
8:H:102:SER:C	8:H:104:LEU:H	1.93	0.72
4:D:95:GLU:O	4:D:98:ILE:HG22	1.90	0.72
2:B:130:ASP:OD2	2:B:174:HIS:HB2	1.89	0.72
4:D:81:ARG:O	4:D:122:VAL:HG23	1.88	0.72
6:F:128:GLU:HA	6:F:131:GLU:OE2	1.88	0.72
8:H:200:ASN:ND2	8:H:202:PHE:HB2	2.04	0.72
6:F:44:GLY:CA	6:F:52:SER:HB2	2.19	0.72
6:F:46:LEU:HB2	6:F:52:SER:OG	1.90	0.72
3:C:27:ARG:O	3:C:28:GLU:HG2	1.89	0.72
7:G:117:ILE:HD12	7:G:198:LEU:HD11	1.72	0.72
5:E:23:ARG:HG2	5:E:28:GLY:O	1.89	0.72
3:C:243:LEU:N	4:D:191:LYS:HG2	2.04	0.72
4:D:183:PHE:HE1	4:D:210:LEU:HA	1.55	0.72
6:F:53:ALA:CB	6:F:164:ALA:O	2.37	0.72
2:B:22:ARG:NH1	2:B:173:SER:HB2	2.04	0.72
8:H:197:LEU:N	8:H:197:LEU:HD23	2.05	0.72
8:H:170:VAL:O	8:H:204:TRP:HA	1.89	0.72
6:F:185:LEU:CD2	6:F:243:LEU:HD23	2.19	0.72
1:A:73:GLU:HB2	1:A:118:THR:OG1	1.89	0.72
6:F:209:ALA:HA	6:F:230:GLU:HB3	1.71	0.72
8:H:197:LEU:H	8:H:197:LEU:HD23	1.54	0.72
9:I:19:GLU:O	9:I:50:LEU:HB3	1.90	0.72
4:D:151:LEU:HD21	7:G:29:PRO:CG	2.20	0.72
1:A:22:LYS:HD2	7:G:243:ILE:CD1	2.20	0.72
2:B:45:THR:HG23	2:B:130:ASP:N	2.04	0.71
8:H:197:LEU:HB3	8:H:203:ILE:HG23	1.72	0.71
1:A:74:GLY:HA3	1:A:121:LEU:HD11	1.71	0.71
2:B:218:GLN:HA	2:B:221:ARG:HD2	1.70	0.71
7:G:199:PHE:N	7:G:199:PHE:CD2	2.57	0.71
7:G:228:ILE:HG22	7:G:238:VAL:HG12	1.70	0.71
8:H:172:VAL:HG23	8:H:203:ILE:O	1.88	0.71
6:F:187:LEU:HD11	6:F:239:GLU:OE2	1.90	0.71
6:F:197:LEU:HD13	6:F:243:LEU:CG	2.19	0.71
3:C:77:GLY:N	3:C:121:LYS:HB3	2.05	0.71
4:D:92:LYS:O	4:D:95:GLU:HG2	1.90	0.71
1:A:212:ARG:HA	1:A:215:ARG:HH11	1.55	0.71
1:A:82:LEU:HG	1:A:99:LEU:HD13	1.69	0.71
2:B:205:HIS:O	2:B:207:ASP:N	2.22	0.71
2:B:34:ALA:O	2:B:35:ASP:HB2	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:244:THR:HB	3:C:247:LYS:CB	2.20	0.71
9:I:162:ILE:HG22	9:I:163:GLN:H	1.55	0.71
3:C:77:GLY:H	3:C:121:LYS:HB3	1.53	0.71
2:B:176:GLU:CD	2:B:176:GLU:N	2.37	0.71
7:G:153:ARG:HB3	7:G:154:PRO:CD	2.21	0.71
6:F:264:ARG:HA	9:I:7:TYR:CZ	2.26	0.71
4:D:97:LEU:HB3	4:D:194:MET:HE2	1.70	0.71
9:I:86:HIS:HA	9:I:101:GLY:HA3	1.71	0.71
3:C:244:THR:HB	3:C:247:LYS:HB3	1.73	0.71
4:D:211:ALA:HA	4:D:214:GLN:OE1	1.89	0.71
2:B:209:LEU:O	2:B:210:GLU:C	2.28	0.71
8:H:247:GLN:HG2	8:H:281:VAL:HG21	1.72	0.71
1:A:422:UNK:C	1:A:425:UNK:HG3	2.21	0.71
5:E:184:ASP:HB3	5:E:187:TYR:HB2	1.73	0.71
2:B:175:VAL:O	2:B:178:ALA:HB3	1.91	0.71
6:F:37:ARG:HB3	6:F:38:PRO:HD2	1.73	0.71
5:E:226:LEU:HD12	5:E:227:LEU:H	1.56	0.71
8:H:141:ILE:HG22	8:H:142:SER:O	1.91	0.71
3:C:178:GLU:N	3:C:181:LEU:HG	2.04	0.71
9:I:19:GLU:HA	9:I:50:LEU:HD22	1.72	0.71
4:D:165:LEU:CD2	4:D:165:LEU:H	2.03	0.71
6:F:170:ALA:HB1	9:I:38:ALA:HB3	1.73	0.71
1:A:231:ILE:CD1	1:A:231:ILE:H	2.02	0.71
1:A:96:SER:O	1:A:98:LEU:N	2.24	0.71
6:F:158:LEU:HD23	6:F:158:LEU:C	2.11	0.71
2:B:6:LEU:C	2:B:13:VAL:HG22	2.11	0.71
5:E:170:VAL:O	5:E:171:LEU:HD23	1.91	0.71
1:A:35:ILE:HG22	1:A:50:LEU:HD23	1.73	0.70
2:B:189:LEU:HD11	2:B:194:GLN:HB2	1.73	0.70
4:D:29:ARG:CD	4:D:50:GLY:HA3	2.20	0.70
6:F:185:LEU:HG	6:F:197:LEU:HD12	1.73	0.70
4:D:188:VAL:HG12	4:D:189:GLU:HG2	1.71	0.70
2:B:189:LEU:HD23	2:B:189:LEU:N	2.06	0.70
7:G:179:CYS:HA	7:G:189:MET:HG3	1.73	0.70
6:F:226:LEU:HD12	6:F:226:LEU:N	2.05	0.70
1:A:41:THR:HG22	1:A:283:GLY:CA	2.19	0.70
7:G:98:VAL:HG12	7:G:99:TYR:N	2.06	0.70
7:G:149:THR:HG22	7:G:150:LYS:N	2.06	0.70
4:D:232:TYR:OH	7:G:103:SER:HB3	1.91	0.70
4:D:29:ARG:H	4:D:168:ASP:CB	2.04	0.70
8:H:165:LYS:O	8:H:166:LEU:HD23	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:61:GLU:HG3	8:H:70:LYS:HG2	1.73	0.70
2:B:111:LEU:HD11	2:B:153:ARG:N	2.06	0.70
7:G:195:ASP:O	7:G:237:TRP:HZ2	1.75	0.70
5:E:123:THR:HB	5:E:192:LEU:HG	1.72	0.70
8:H:31:ASP:O	8:H:53:ILE:HA	1.91	0.70
8:H:200:ASN:HD21	8:H:202:PHE:HB2	1.57	0.70
3:C:199:ALA:HB2	3:C:210:PRO:CB	2.18	0.70
7:G:228:ILE:O	7:G:228:ILE:HD12	1.91	0.70
8:H:84:VAL:HG13	8:H:200:ASN:OD1	1.91	0.70
6:F:177:TYR:HB3	9:I:27:TYR:OH	1.92	0.70
1:A:165:VAL:HG21	1:A:175:TYR:N	2.01	0.70
9:I:181:GLU:HG2	9:I:182:PHE:N	2.05	0.70
2:B:57:ILE:HD12	2:B:57:ILE:N	2.04	0.70
4:D:151:LEU:HD21	7:G:29:PRO:HG2	1.74	0.70
3:C:249:GLN:O	3:C:252:MET:HB2	1.91	0.70
3:C:23:ARG:C	3:C:25:ASP:H	1.94	0.70
7:G:111:VAL:HG12	7:G:112:LYS:N	2.06	0.70
5:E:172:GLU:HA	5:E:179:ASP:HB3	1.74	0.70
2:B:235:VAL:HG13	8:H:26:LEU:HD23	1.72	0.70
3:C:77:GLY:CA	3:C:124:LEU:HB2	2.21	0.70
1:A:254:ALA:O	1:A:258:VAL:HG12	1.92	0.70
1:A:83:SER:O	1:A:90:PHE:HB3	1.92	0.70
2:B:102:LEU:O	2:B:105:THR:OG1	2.08	0.70
4:D:115:SER:C	4:D:116:ILE:HD12	2.12	0.70
1:A:130:TRP:CZ3	1:A:162:ARG:HG3	2.27	0.70
5:E:69:PRO:HD3	5:E:132:CYS:SG	2.31	0.70
6:F:149:LEU:C	6:F:149:LEU:HD23	2.11	0.70
2:B:78:ALA:HB1	2:B:80:PHE:CE1	2.27	0.70
9:I:85:VAL:HG23	9:I:103:ILE:HB	1.73	0.70
1:A:75:ILE:HG22	1:A:76:LEU:N	2.07	0.70
3:C:108:PHE:HA	3:C:111:ASP:OD1	1.92	0.69
3:C:32:PHE:HE2	3:C:262:VAL:CG1	1.97	0.69
4:D:181:LEU:HD12	4:D:181:LEU:N	2.07	0.69
2:B:181:GLY:N	2:B:182:PRO:CD	2.55	0.69
8:H:191:CYS:HB2	8:H:260:TYR:CZ	2.27	0.69
5:E:116:LYS:HZ1	5:E:118:SER:HB3	1.57	0.69
5:E:257:GLU:HG3	5:E:260:LYS:HE3	1.74	0.69
6:F:158:LEU:HD22	6:F:212:THR:CG2	2.22	0.69
3:C:236:HIS:NE2	3:C:238:PRO:HD3	2.06	0.69
3:C:50:LEU:HB2	3:C:59:ILE:HG23	1.75	0.69
8:H:113:MET:SD	8:H:134:PHE:HB3	2.33	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:221:ARG:NH1	2:B:221:ARG:HB3	2.07	0.69
4:D:225:ARG:HH21	7:G:28:LEU:CD2	2.05	0.69
4:D:225:ARG:O	4:D:229:GLN:HG3	1.92	0.69
3:C:136:TYR:HB3	6:F:110:ARG:NE	2.08	0.69
4:D:107:LEU:HD22	4:D:147:PRO:HB2	1.74	0.69
7:G:266:GLN:O	7:G:268:PHE:N	2.26	0.69
8:H:178:LEU:HD13	8:H:245:VAL:HG13	1.73	0.69
8:H:273:LYS:HA	8:H:277:MET:SD	2.32	0.69
3:C:60:CYS:SG	3:C:156:LEU:HD12	2.33	0.69
9:I:24:SER:HB3	9:I:54:SER:CB	2.14	0.69
1:A:228:HIS:O	1:A:230:GLU:HG3	1.92	0.69
1:A:23:ARG:HG3	1:A:27:ARG:HG2	1.74	0.69
4:D:170:THR:O	4:D:174:GLU:HG3	1.92	0.69
7:G:46:GLY:HA2	7:G:78:LEU:O	1.93	0.69
2:B:188:LEU:HD12	2:B:194:GLN:O	1.92	0.69
4:D:78:VAL:HG22	4:D:118:VAL:HB	1.73	0.69
8:H:53:ILE:HG22	8:H:54:ALA:N	2.06	0.69
5:E:251:SER:O	5:E:255:MET:HG2	1.91	0.69
6:F:95:ARG:HG3	6:F:96:LEU:N	2.07	0.69
1:A:66:PRO:HD3	1:A:129:VAL:CB	2.22	0.69
5:E:69:PRO:HG3	5:E:74:PRO:O	1.92	0.69
3:C:154:PHE:CE1	3:C:262:VAL:HB	2.28	0.69
4:D:189:GLU:HB2	4:D:191:LYS:HB2	1.75	0.69
4:D:201:TYR:HB2	4:D:205:GLU:CB	2.22	0.69
1:A:121:LEU:HB2	1:A:130:TRP:HB2	1.73	0.69
3:C:124:LEU:O	3:C:133:TRP:HB2	1.92	0.69
3:C:59:ILE:O	3:C:139:LEU:HA	1.93	0.69
7:G:31:GLU:O	7:G:78:LEU:HA	1.93	0.69
3:C:45:ALA:HA	3:C:63:LYS:CE	2.22	0.69
3:C:109:ILE:CD1	3:C:109:ILE:H	2.04	0.69
3:C:109:ILE:O	3:C:112:VAL:HB	1.92	0.69
3:C:47:GLY:HA3	3:C:163:VAL:CG2	2.17	0.69
2:B:189:LEU:HD23	2:B:189:LEU:H	1.56	0.69
7:G:228:ILE:HA	7:G:237:TRP:O	1.93	0.69
5:E:226:LEU:HD12	5:E:240:ARG:O	1.93	0.69
5:E:128:PRO:O	5:E:129:ARG:HB2	1.91	0.69
6:F:174:VAL:HG23	6:F:176:MET:SD	2.32	0.68
1:A:245:ASP:O	1:A:248:LEU:HB2	1.93	0.68
7:G:179:CYS:O	7:G:189:MET:HG2	1.92	0.68
7:G:24:GLY:HA2	7:G:85:LEU:CD2	2.05	0.68
7:G:269:SER:HA	7:G:272:ALA:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:203:LEU:HA	7:G:206:ILE:HD12	1.75	0.68
1:A:66:PRO:CD	1:A:129:VAL:HB	2.22	0.68
6:F:37:ARG:CZ	6:F:57:ALA:HB1	2.23	0.68
3:C:29:LEU:HD21	3:C:254:ARG:NH1	2.07	0.68
6:F:192:ALA:HB1	6:F:193:PRO:HD2	1.75	0.68
6:F:36:LEU:HD21	6:F:39:VAL:HG21	1.74	0.68
6:F:55:LEU:HB2	6:F:62:VAL:CG1	2.22	0.68
1:A:20:GLU:OE1	1:A:20:GLU:HA	1.93	0.68
2:B:22:ARG:NH2	2:B:173:SER:HA	2.08	0.68
6:F:156:SER:HB2	6:F:198:ASP:OD2	1.93	0.68
7:G:99:TYR:CD1	7:G:99:TYR:N	2.61	0.68
5:E:126:ILE:HB	5:E:131:HIS:CB	2.22	0.68
3:C:164:GLN:HG2	3:C:186:TYR:HB3	1.76	0.68
3:C:240:GLY:O	3:C:242:GLY:N	2.26	0.68
1:A:244:LYS:HD2	1:A:245:ASP:N	2.07	0.68
2:B:209:LEU:CD1	2:B:213:LEU:HB2	2.23	0.68
9:I:148:GLU:CB	9:I:151:LEU:HB2	2.22	0.68
8:H:174:VAL:HG22	8:H:201:GLY:HA2	1.75	0.68
1:A:41:THR:O	1:A:282:PHE:HB3	1.93	0.68
9:I:46:GLU:OE2	9:I:52:VAL:HG23	1.93	0.68
2:B:209:LEU:HD11	2:B:213:LEU:HB2	1.75	0.68
8:H:165:LYS:HD2	8:H:166:LEU:H	1.58	0.68
2:B:134:TYR:O	2:B:138:VAL:HG23	1.93	0.68
4:D:192:LEU:HD23	4:D:192:LEU:O	1.93	0.68
1:A:104:ARG:HH12	1:A:108:ARG:N	1.92	0.68
1:A:12:ARG:HD3	1:A:13:PHE:N	2.09	0.68
5:E:108:THR:O	5:E:112:ILE:HG13	1.93	0.68
1:A:176:THR:N	1:A:177:PRO:HD2	2.09	0.68
2:B:159:CYS:SG	2:B:220:ALA:HA	2.33	0.68
5:E:33:ARG:O	5:E:35:VAL:HG23	1.93	0.68
3:C:131:LEU:HD12	3:C:170:ILE:HD11	1.75	0.68
3:C:239:GLY:HA2	4:D:193:LEU:O	1.93	0.68
9:I:164:MET:HB3	9:I:173:GLN:N	2.08	0.68
7:G:215:GLU:C	7:G:219:GLU:HB2	2.13	0.68
7:G:222:LYS:NZ	7:G:268:PHE:CB	2.56	0.68
5:E:206:ILE:N	5:E:206:ILE:HD12	2.08	0.68
5:E:58:ILE:HD13	5:E:151:ALA:HB1	1.75	0.68
1:A:177:PRO:HG2	1:A:178:GLU:OE2	1.93	0.68
5:E:106:ALA:O	5:E:110:TYR:HB2	1.94	0.68
6:F:118:GLU:HB3	6:F:119:GLU:OE1	1.94	0.68
1:A:422:UNK:HA	1:A:425:UNK:HG1	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:35:GLN:HB2	4:D:231:ARG:HH21	1.58	0.68
2:B:135:ALA:O	2:B:139:ASN:ND2	2.27	0.68
3:C:111:ASP:OD2	3:C:112:VAL:N	2.26	0.68
4:D:170:THR:HB	4:D:173:GLN:H	1.59	0.68
5:E:60:VAL:CG1	5:E:137:VAL:HG12	2.24	0.68
7:G:140:LEU:HD23	7:G:177:MET:O	1.94	0.68
8:H:110:LEU:H	8:H:110:LEU:CD1	2.07	0.68
8:H:236:ARG:HH12	8:H:269:LYS:HB3	1.59	0.68
2:B:36:GLY:HA3	2:B:51:VAL:HG13	1.74	0.68
2:B:6:LEU:O	2:B:13:VAL:HG22	1.93	0.68
6:F:238:ALA:O	6:F:242:ARG:HG3	1.94	0.68
5:E:232:SER:HA	5:E:271:GLN:OE1	1.94	0.68
3:C:59:ILE:HD11	3:C:142:LEU:HD11	1.75	0.67
6:F:53:ALA:HB1	6:F:167:LEU:HB2	1.75	0.67
9:I:9:ILE:CD1	9:I:10:PRO:HD2	2.23	0.67
4:D:64:VAL:CG2	4:D:115:SER:HB3	2.23	0.67
8:H:203:ILE:N	8:H:203:ILE:HD12	2.09	0.67
8:H:88:ILE:HG12	8:H:98:VAL:HG12	1.74	0.67
8:H:235:SER:O	8:H:238:ARG:HB3	1.94	0.67
3:C:237:LYS:HE2	3:C:240:GLY:HA3	1.75	0.67
3:C:242:GLY:CA	4:D:191:LYS:HD3	2.24	0.67
6:F:53:ALA:HB2	6:F:168:ALA:N	2.09	0.67
1:A:190:MET:SD	1:A:190:MET:N	2.68	0.67
1:A:231:ILE:HG22	1:A:232:CYS:H	1.59	0.67
1:A:23:ARG:HB2	1:A:27:ARG:H	1.59	0.67
2:B:77:SER:O	2:B:88:ARG:HD2	1.93	0.67
9:I:133:ILE:HG22	9:I:134:SER:N	2.09	0.67
9:I:145:THR:HG22	9:I:147:ALA:N	1.99	0.67
4:D:151:LEU:O	4:D:187:SER:HB3	1.94	0.67
1:A:266:LEU:O	1:A:270:GLU:HG2	1.93	0.67
8:H:96:TRP:HB2	8:H:108:LEU:HD21	1.74	0.67
2:B:135:ALA:HA	2:B:158:ALA:HB3	1.76	0.67
8:H:53:ILE:HD12	8:H:53:ILE:N	2.10	0.67
9:I:90:VAL:H	9:I:94:PRO:CG	2.07	0.67
5:E:25:ASP:CA	8:H:239:ASN:HD21	2.08	0.67
4:D:153:CYS:SG	4:D:217:SER:HB2	2.34	0.67
1:A:234:ILE:HD13	2:B:198:LEU:HD11	1.76	0.67
7:G:238:VAL:O	7:G:239:LYS:HB2	1.94	0.67
9:I:130:ALA:CA	9:I:151:LEU:HD11	2.19	0.67
8:H:167:GLY:O	8:H:168:GLN:HB2	1.93	0.67
7:G:205:LEU:HB3	7:G:209:LEU:CD1	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:118:ILE:HG13	3:C:119:ILE:N	2.09	0.67
3:C:237:LYS:HZ1	3:C:240:GLY:H	1.42	0.67
7:G:223:LEU:H	7:G:223:LEU:HD12	1.58	0.67
5:E:203:LEU:O	5:E:226:LEU:N	2.26	0.67
5:E:28:GLY:N	5:E:31:ASP:OD2	2.28	0.67
5:E:167:ARG:HG2	5:E:169:ARG:HH11	1.59	0.67
3:C:72:ASP:O	3:C:74:PRO:HD3	1.94	0.67
7:G:243:ILE:O	7:G:246:THR:HB	1.94	0.67
9:I:87:ILE:HG12	9:I:103:ILE:HD11	1.76	0.67
8:H:205:ILE:N	8:H:205:ILE:HD12	2.09	0.67
8:H:267:GLN:O	8:H:269:LYS:N	2.24	0.67
8:H:252:TYR:O	8:H:255:SER:HB3	1.94	0.67
3:C:200:VAL:HG12	3:C:201:PHE:N	2.09	0.67
3:C:216:HIS:C	3:C:218:ALA:H	1.97	0.67
3:C:37:VAL:HA	3:C:50:LEU:O	1.94	0.67
3:C:62:VAL:HA	3:C:136:TYR:O	1.95	0.67
1:A:234:ILE:O	1:A:234:ILE:HD12	1.95	0.67
5:E:258:THR:HG23	5:E:261:ARG:CZ	2.25	0.67
8:H:204:TRP:CZ3	8:H:206:TYR:HB3	2.30	0.67
5:E:126:ILE:HB	5:E:131:HIS:HB2	1.75	0.67
3:C:94:ARG:HH12	3:C:100:GLU:N	1.91	0.67
3:C:108:PHE:O	3:C:112:VAL:HG23	1.95	0.67
6:F:110:ARG:NH1	6:F:112:ALA:HB2	2.09	0.67
1:A:84:GLN:NE2	1:A:91:GLU:HA	2.09	0.67
4:D:74:ALA:HB1	4:D:116:ILE:CD1	2.25	0.67
5:E:203:LEU:O	5:E:225:SER:HA	1.95	0.67
6:F:118:GLU:HA	6:F:118:GLU:OE1	1.94	0.67
3:C:249:GLN:HA	3:C:249:GLN:NE2	2.10	0.67
7:G:215:GLU:HA	7:G:218:GLN:CD	2.15	0.67
5:E:203:LEU:HD22	5:E:255:MET:HB3	1.77	0.67
6:F:95:ARG:HA	6:F:136:LEU:HD22	1.77	0.67
5:E:101:LEU:HD12	5:E:102:GLY:N	2.09	0.67
2:B:149:GLY:O	8:H:56:VAL:HG13	1.93	0.67
8:H:44:GLY:HA2	8:H:56:VAL:HG23	1.76	0.67
4:D:143:ASP:C	4:D:145:GLY:H	1.98	0.67
3:C:239:GLY:HA2	4:D:194:MET:HB2	1.77	0.67
1:A:235:GLN:HA	2:B:199:GLU:OE2	1.95	0.67
2:B:184:LEU:HB2	2:B:200:MET:CB	2.25	0.67
7:G:127:ILE:HG23	7:G:140:LEU:O	1.95	0.67
7:G:149:THR:O	7:G:150:LYS:HD2	1.95	0.67
8:H:185:HIS:ND1	8:H:186:PHE:N	2.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ARG:HD2	1:A:229:ARG:O	1.95	0.66
5:E:206:ILE:HD13	5:E:211:VAL:HG23	1.77	0.66
8:H:200:ASN:HD21	8:H:202:PHE:HD1	1.43	0.66
6:F:108:ARG:NE	6:F:108:ARG:N	2.43	0.66
5:E:161:PHE:HB3	5:E:274:VAL:HG11	1.77	0.66
3:C:7:THR:HB	3:C:10:PRO:HD3	1.77	0.66
1:A:139:LEU:N	1:A:139:LEU:HD13	2.10	0.66
1:A:32:TYR:HE1	1:A:207:VAL:CG1	2.08	0.66
5:E:153:SER:OG	5:E:200:ILE:HB	1.95	0.66
6:F:156:SER:O	6:F:158:LEU:N	2.27	0.66
7:G:38:GLN:NE2	7:G:39:GLU:HB3	2.10	0.66
3:C:14:TYR:OH	3:C:214:GLU:HG3	1.96	0.66
4:D:29:ARG:H	4:D:168:ASP:CG	1.99	0.66
7:G:24:GLY:CA	7:G:85:LEU:HD23	2.06	0.66
5:E:8:GLU:HB2	5:E:11:LYS:HZ2	1.59	0.66
8:H:76:TYR:O	8:H:77:ILE:HG23	1.96	0.66
1:A:176:THR:HB	1:A:180:ARG:HH12	1.59	0.66
6:F:32:ASP:HB2	6:F:35:ARG:HB3	1.76	0.66
3:C:139:LEU:HD23	3:C:155:ALA:HB3	1.77	0.66
1:A:271:ASN:HA	1:A:274:LYS:NZ	2.11	0.66
8:H:88:ILE:HB	8:H:138:GLY:HA2	1.76	0.66
8:H:91:VAL:HG13	8:H:95:ARG:O	1.95	0.66
3:C:109:ILE:N	3:C:109:ILE:HD13	2.10	0.66
9:I:40:CYS:O	9:I:55:VAL:HG13	1.96	0.66
1:A:20:GLU:HG3	7:G:243:ILE:HD12	1.75	0.66
7:G:199:PHE:CZ	7:G:236:ILE:HB	2.31	0.66
5:E:20:GLU:HG3	8:H:231:ARG:NE	2.10	0.66
8:H:106:SER:HA	8:H:154:VAL:HG13	1.76	0.66
2:B:24:ILE:CG2	2:B:42:GLN:HA	2.25	0.66
3:C:60:CYS:CA	3:C:139:LEU:HG	2.26	0.66
1:A:190:MET:N	1:A:226:ASN:ND2	2.42	0.66
5:E:9:ALA:O	5:E:12:VAL:HG12	1.95	0.66
8:H:108:LEU:HD11	8:H:135:LEU:HD21	1.78	0.66
8:H:233:VAL:O	8:H:237:LEU:HG	1.94	0.66
7:G:181:ASP:O	7:G:185:ARG:N	2.29	0.66
3:C:17:PHE:CB	3:C:22:CYS:O	2.44	0.66
3:C:70:SER:OG	3:C:73:ALA:HB3	1.96	0.66
1:A:87:ALA:HB1	1:A:88:PRO:HD2	1.77	0.66
5:E:241:LYS:HD3	5:E:241:LYS:O	1.95	0.66
5:E:51:VAL:HG11	5:E:154:ILE:CG2	2.25	0.66
5:E:230:VAL:CG1	5:E:234:GLY:HA2	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:GLN:N	1:A:218:ASP:OD2	2.29	0.66
6:F:51:GLY:HA3	6:F:168:ALA:O	1.96	0.66
7:G:199:PHE:CE2	7:G:236:ILE:HB	2.31	0.66
5:E:258:THR:HG23	5:E:261:ARG:NH2	2.11	0.66
8:H:205:ILE:HG22	8:H:234:ILE:HG22	1.77	0.66
5:E:273:VAL:HG13	5:E:276:LYS:HD2	1.77	0.66
8:H:266:HIS:NE2	8:H:280:ILE:HG12	2.11	0.66
2:B:133:THR:O	2:B:136:ALA:HB3	1.96	0.66
4:D:218:GLN:C	4:D:222:ARG:HE	1.99	0.66
6:F:150:LEU:HD21	6:F:157:ALA:HB1	1.77	0.66
6:F:253:PRO:HG2	6:F:254:VAL:H	1.61	0.66
1:A:115:CYS:HB3	1:A:189:HIS:HB2	1.77	0.66
4:D:135:ASN:O	4:D:139:MET:HG2	1.95	0.66
7:G:243:ILE:O	7:G:247:LEU:HD23	1.96	0.66
7:G:157:GLN:HB2	7:G:160:ASP:OD2	1.96	0.66
7:G:163:TYR:O	7:G:189:MET:HB2	1.96	0.66
8:H:192:GLY:HA3	8:H:233:VAL:HG21	1.76	0.66
8:H:45:THR:HG23	8:H:69:VAL:HG23	1.78	0.66
3:C:252:MET:CE	4:D:203:ASP:HB2	2.26	0.66
7:G:140:LEU:HD22	7:G:141:SER:N	2.11	0.66
7:G:23:LEU:HD23	7:G:25:GLN:HE22	1.61	0.66
9:I:173:GLN:HG2	9:I:174:CYS:N	2.11	0.66
7:G:252:ILE:HG22	7:G:253:LEU:HG	1.78	0.66
6:F:200:THR:N	6:F:203:GLU:HB2	2.03	0.66
8:H:141:ILE:N	8:H:141:ILE:HD12	2.11	0.65
1:A:61:CYS:SG	1:A:160:PHE:HE2	2.18	0.65
3:C:235:LEU:CD1	4:D:206:LEU:HD21	2.26	0.65
6:F:97:LEU:N	6:F:144:LEU:O	2.28	0.65
6:F:217:PRO:O	6:F:220:ASN:N	2.28	0.65
1:A:176:THR:HA	1:A:179:GLU:HB2	1.78	0.65
6:F:62:VAL:HG13	6:F:164:ALA:HB2	1.78	0.65
1:A:211:GLU:HA	1:A:211:GLU:OE1	1.95	0.65
1:A:88:PRO:HG2	1:A:89:ALA:N	2.11	0.65
4:D:63:GLU:HB2	7:G:136:GLU:HB3	1.79	0.65
7:G:248:ILE:CG2	7:G:271:LEU:HD21	2.24	0.65
2:B:232:ARG:O	2:B:235:VAL:HG12	1.96	0.65
3:C:88:LEU:HD23	3:C:142:LEU:HA	1.77	0.65
3:C:191:THR:HA	3:C:228:GLU:OE1	1.96	0.65
1:A:11:ARG:O	1:A:15:LEU:HG	1.96	0.65
4:D:73:LYS:O	4:D:114:THR:HG23	1.95	0.65
6:F:135:ARG:HB3	6:F:175:GLU:HB3	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:85:VAL:HA	8:H:141:ILE:O	1.96	0.65
8:H:91:VAL:HG22	8:H:96:TRP:HA	1.76	0.65
3:C:167:GLU:HG2	3:C:182:LYS:O	1.97	0.65
3:C:271:LYS:O	3:C:275:PRO:CG	2.45	0.65
8:H:148:VAL:HG13	8:H:153:ALA:O	1.96	0.65
9:I:19:GLU:CG	9:I:51:PRO:HD2	2.23	0.65
9:I:70:ILE:N	9:I:70:ILE:HD12	2.12	0.65
3:C:210:PRO:HB2	3:C:215:GLU:HB2	1.79	0.65
6:F:217:PRO:O	6:F:219:LEU:N	2.30	0.65
6:F:216:MET:CG	6:F:221:GLN:HB2	2.17	0.65
4:D:48:LEU:N	4:D:48:LEU:HD12	2.11	0.65
7:G:34:LEU:HD23	7:G:34:LEU:N	2.12	0.65
5:E:16:HIS:O	5:E:20:GLU:HG2	1.97	0.65
6:F:96:LEU:H	6:F:96:LEU:CD2	2.09	0.65
3:C:27:ARG:C	3:C:28:GLU:HG2	2.17	0.65
4:D:197:THR:O	4:D:198:LYS:HD2	1.96	0.65
1:A:49:GLU:C	1:A:51:GLY:H	2.00	0.65
7:G:20:ARG:HB3	7:G:35:LEU:HD11	1.79	0.65
8:H:243:SER:HB3	8:H:277:MET:HG2	1.79	0.65
2:B:226:LEU:HD22	2:B:227:LEU:HD23	1.78	0.65
3:C:149:LEU:H	3:C:149:LEU:HD12	1.60	0.65
1:A:199:PHE:CE1	1:A:206:LEU:HB2	2.31	0.65
1:A:155:VAL:HG22	1:A:265:ILE:HG23	1.78	0.65
5:E:23:ARG:HG3	5:E:23:ARG:HH11	1.62	0.65
8:H:195:VAL:HG13	8:H:204:TRP:O	1.97	0.65
3:C:164:GLN:CB	3:C:186:TYR:HB3	2.27	0.65
1:A:301:ALA:HB1	1:A:302:PRO:CD	2.23	0.65
7:G:266:GLN:O	7:G:267:ILE:C	2.35	0.65
1:A:61:CYS:SG	1:A:162:ARG:HA	2.37	0.65
3:C:14:TYR:O	3:C:17:PHE:HD2	1.79	0.65
3:C:59:ILE:HD12	3:C:59:ILE:H	1.62	0.65
1:A:151:ILE:HG22	1:A:155:VAL:HG21	1.79	0.65
9:I:109:ARG:O	9:I:145:THR:HG23	1.96	0.65
8:H:52:LEU:C	8:H:53:ILE:HD12	2.17	0.65
3:C:39:ILE:HG12	3:C:269:VAL:HG11	1.79	0.64
4:D:210:LEU:HD11	4:D:214:GLN:HE22	1.62	0.64
1:A:224:ALA:O	1:A:231:ILE:HA	1.97	0.64
4:D:116:ILE:N	4:D:116:ILE:HD12	2.13	0.64
7:G:19:ALA:H	7:G:22:VAL:HG21	1.63	0.64
5:E:118:SER:HA	5:E:196:ASN:HD22	1.59	0.64
5:E:53:LEU:HD22	5:E:151:ALA:CB	2.24	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:16:ASN:HA	9:I:33:ILE:HG13	1.79	0.64
5:E:126:ILE:HD12	5:E:131:HIS:HB3	1.79	0.64
8:H:33:ILE:HG22	8:H:34:THR:N	2.11	0.64
1:A:231:ILE:HD11	2:B:206:GLU:HA	1.78	0.64
1:A:88:PRO:CG	1:A:89:ALA:H	2.10	0.64
2:B:184:LEU:HA	2:B:200:MET:HA	1.78	0.64
5:E:168:VAL:N	5:E:190:ILE:HD12	2.12	0.64
9:I:93:MET:N	9:I:94:PRO:HD2	2.11	0.64
8:H:129:LEU:HA	8:H:132:ARG:CG	2.27	0.64
3:C:27:ARG:HB3	3:C:31:GLU:HG2	1.79	0.64
1:A:302:PRO:CB	1:A:414:UNK:HG1	2.20	0.64
1:A:85:MET:HA	4:D:59:TYR:CE1	2.31	0.64
2:B:111:LEU:C	2:B:113:GLN:H	1.99	0.64
4:D:79:ILE:HD13	4:D:119:VAL:HG13	1.80	0.64
8:H:98:VAL:HG23	8:H:106:SER:OG	1.97	0.64
7:G:182:SER:HA	7:G:185:ARG:HD2	1.78	0.64
3:C:237:LYS:NZ	4:D:194:MET:N	2.45	0.64
1:A:104:ARG:HH22	1:A:108:ARG:HA	1.63	0.64
9:I:168:SER:OG	9:I:169:TRP:HE3	1.81	0.64
5:E:37:VAL:HG22	5:E:51:VAL:CG2	2.21	0.64
2:B:36:GLY:O	2:B:50:VAL:HG13	1.98	0.64
3:C:177:ALA:HA	3:C:181:LEU:CD1	2.25	0.64
8:H:144:GLU:HB3	8:H:157:HIS:O	1.98	0.64
3:C:115:ASN:ND2	4:D:198:LYS:HG3	2.08	0.64
6:F:178:ASP:HB3	6:F:216:MET:HE3	1.79	0.64
1:A:234:ILE:HD13	2:B:198:LEU:HD13	1.79	0.64
1:A:162:ARG:HG2	1:A:162:ARG:HH11	1.62	0.64
3:C:185:SER:O	3:C:186:TYR:C	2.35	0.64
3:C:169:THR:HB	3:C:176:LEU:O	1.98	0.64
8:H:228:LEU:O	8:H:228:LEU:HD23	1.97	0.64
3:C:161:LYS:HE3	3:C:189:ILE:HG12	1.79	0.64
3:C:232:LEU:HD22	4:D:202:SER:C	2.17	0.64
4:D:90:ALA:O	4:D:94:ARG:HG3	1.97	0.64
9:I:129:LEU:HD22	9:I:154:VAL:CG2	2.23	0.64
7:G:218:GLN:O	7:G:221:GLY:N	2.30	0.64
7:G:264:ARG:HH11	7:G:264:ARG:CB	2.11	0.64
2:B:12:ARG:NH1	2:B:16:ARG:NH1	2.46	0.64
3:C:63:LYS:NZ	6:F:108:ARG:HA	2.12	0.64
5:E:140:LEU:HD12	5:E:141:LEU:H	1.62	0.64
4:D:181:LEU:CA	4:D:197:THR:OG1	2.43	0.64
9:I:66:ASP:HB3	9:I:69:ALA:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:96:LEU:O	6:F:127:GLN:NE2	2.31	0.64
5:E:7:SER:N	8:H:87:ARG:HH22	1.95	0.64
9:I:16:ASN:HB2	9:I:31:GLY:O	1.98	0.64
3:C:23:ARG:HH11	3:C:207:ILE:HB	1.62	0.64
3:C:191:THR:HB	3:C:227:ASP:OD1	1.97	0.64
3:C:232:LEU:HD23	4:D:206:LEU:HD22	1.78	0.64
1:A:196:PHE:CZ	1:A:254:ALA:HB2	2.32	0.64
6:F:34:THR:HG22	6:F:197:LEU:CD2	2.28	0.64
2:B:218:GLN:HA	2:B:221:ARG:CD	2.27	0.64
8:H:58:GLY:HA3	8:H:70:LYS:O	1.98	0.64
3:C:34:THR:O	3:C:53:LEU:HA	1.97	0.64
6:F:149:LEU:HD23	6:F:150:LEU:N	2.13	0.64
1:A:146:ILE:HA	1:A:149:ALA:HB3	1.78	0.64
2:B:198:LEU:C	2:B:198:LEU:HD22	2.18	0.64
4:D:125:ASP:O	4:D:126:ALA:HB2	1.98	0.64
4:D:132:CYS:HA	4:D:135:ASN:HD21	1.62	0.64
7:G:168:VAL:O	7:G:175:PRO:HA	1.98	0.64
7:G:196:GLY:HA3	7:G:237:TRP:NE1	2.12	0.64
5:E:56:THR:HA	5:E:143:GLU:HB3	1.80	0.64
1:A:75:ILE:HD12	1:A:75:ILE:N	2.13	0.64
6:F:31:ARG:HH21	6:F:35:ARG:NE	1.95	0.64
6:F:214:ALA:O	6:F:223:ALA:HB3	1.98	0.64
1:A:189:HIS:HB3	1:A:226:ASN:ND2	2.12	0.64
1:A:95:GLN:O	1:A:96:SER:C	2.36	0.64
9:I:127:ILE:H	9:I:155:VAL:HB	1.63	0.64
7:G:104:GLN:HE22	7:G:202:THR:CG2	2.11	0.64
2:B:69:ALA:HA	2:B:115:HIS:O	1.97	0.64
3:C:32:PHE:CE1	3:C:258:ARG:HB3	2.32	0.63
4:D:52:THR:HG23	4:D:124:SER:O	1.98	0.63
9:I:20:GLY:HA3	9:I:51:PRO:O	1.98	0.63
3:C:109:ILE:O	3:C:113:ILE:HG13	1.97	0.63
6:F:167:LEU:O	6:F:171:ASP:HB2	1.98	0.63
9:I:10:PRO:HD3	9:I:38:ALA:CB	2.27	0.63
1:A:240:ILE:HD13	1:A:242:LEU:HD11	1.79	0.63
9:I:162:ILE:HD13	9:I:176:LYS:HB3	1.79	0.63
5:E:89:ALA:HB2	5:E:141:LEU:O	1.97	0.63
3:C:12:GLU:CA	3:C:15:ARG:HG2	2.27	0.63
6:F:122:LEU:O	6:F:126:LEU:HB2	1.98	0.63
8:H:102:SER:C	8:H:104:LEU:N	2.52	0.63
8:H:80:VAL:HG12	8:H:81:GLY:N	2.08	0.63
2:B:8:ASP:O	2:B:9:GLN:HG3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:23:ARG:HD3	3:C:207:ILE:CG2	2.28	0.63
6:F:215:LEU:HA	6:F:223:ALA:H	1.62	0.63
2:B:204:LEU:HD21	2:B:208:HIS:HB2	1.79	0.63
9:I:109:ARG:CZ	9:I:109:ARG:HA	2.28	0.63
9:I:78:ILE:HD13	9:I:124:PRO:HD3	1.80	0.63
6:F:124:LEU:HD13	6:F:125:ALA:N	2.12	0.63
5:E:56:THR:CB	5:E:145:GLY:H	2.10	0.63
2:B:143:LEU:HD23	2:B:143:LEU:N	2.13	0.63
7:G:90:PRO:O	7:G:94:SER:HB3	1.98	0.63
1:A:418:UNK:HG2	4:D:208:GLN:HB3	1.79	0.63
2:B:131:GLY:HA2	2:B:177:GLU:CD	2.19	0.63
5:E:53:LEU:HD13	5:E:151:ALA:CB	2.29	0.63
2:B:218:GLN:HE21	2:B:218:GLN:HA	1.63	0.63
3:C:59:ILE:HD12	3:C:140:ILE:O	1.99	0.63
1:A:199:PHE:HB2	1:A:204:TYR:HB2	1.80	0.63
1:A:253:ILE:HA	1:A:256:VAL:CG2	2.28	0.63
7:G:113:GLY:HA2	7:G:166:PHE:O	1.98	0.63
7:G:20:ARG:HB2	7:G:35:LEU:HD21	1.80	0.63
5:E:55:HIS:H	5:E:145:GLY:HA3	1.63	0.63
2:B:7:SER:HB3	2:B:13:VAL:H	1.63	0.63
5:E:185:ASP:N	5:E:186:PRO:HD2	2.13	0.63
6:F:100:PHE:CB	6:F:123:ALA:HB2	2.28	0.63
3:C:36:THR:O	3:C:51:VAL:HA	1.97	0.63
1:A:83:SER:O	1:A:86:ALA:HB3	1.99	0.63
7:G:152:ASN:HA	7:G:155:ASN:HD22	1.64	0.63
1:A:59:VAL:HG22	1:A:134:VAL:HG12	1.81	0.63
1:A:75:ILE:HG22	1:A:76:LEU:H	1.62	0.63
9:I:18:GLU:O	9:I:19:GLU:HB2	1.98	0.63
2:B:218:GLN:NE2	2:B:218:GLN:HA	2.13	0.63
7:G:145:PHE:O	7:G:146:GLU:HG2	1.98	0.63
5:E:231:THR:HG22	5:E:232:SER:N	2.12	0.63
5:E:26:GLY:C	8:H:270:ASP:HB3	2.19	0.63
3:C:204:THR:HB	3:C:247:LYS:HE2	1.81	0.63
2:B:47:ALA:HB1	2:B:125:GLN:O	1.99	0.63
4:D:29:ARG:HD2	4:D:50:GLY:CA	2.27	0.63
7:G:25:GLN:O	7:G:84:ARG:HG3	1.97	0.63
8:H:42:GLY:N	8:H:67:ILE:O	2.32	0.63
4:D:225:ARG:HH21	7:G:28:LEU:HD23	1.64	0.63
1:A:444:UNK:HG2	1:A:445:UNK:N	2.13	0.63
3:C:39:ILE:CG1	3:C:269:VAL:HG11	2.29	0.63
6:F:62:VAL:HG11	6:F:160:ALA:C	2.18	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:178:ASP:HB3	6:F:216:MET:CE	2.29	0.63
9:I:148:GLU:HB2	9:I:151:LEU:CB	2.29	0.63
2:B:31:PHE:CD2	2:B:31:PHE:N	2.64	0.63
2:B:17:ARG:HB2	2:B:20:GLU:CG	2.29	0.63
9:I:21:SER:O	9:I:52:VAL:HG13	1.98	0.63
7:G:100:TRP:CZ3	7:G:102:ASP:HB3	2.33	0.62
7:G:114:ASP:HB2	7:G:166:PHE:CE2	2.34	0.62
8:H:33:ILE:HB	8:H:52:LEU:HD23	1.81	0.62
3:C:127:SER:CB	3:C:131:LEU:HB2	2.28	0.62
1:A:196:PHE:HZ	1:A:254:ALA:HB2	1.62	0.62
1:A:35:ILE:HA	1:A:49:GLU:O	1.98	0.62
4:D:173:GLN:H	4:D:173:GLN:NE2	1.96	0.62
9:I:132:VAL:HG13	9:I:144:LEU:HD23	1.82	0.62
5:E:202:THR:C	5:E:203:LEU:HD12	2.19	0.62
8:H:195:VAL:CG2	8:H:205:ILE:HG23	2.30	0.62
5:E:273:VAL:HA	5:E:276:LYS:HG3	1.81	0.62
2:B:147:ASP:HA	8:H:72:LEU:HD11	1.80	0.62
8:H:33:ILE:HD12	8:H:33:ILE:N	2.13	0.62
3:C:53:LEU:HD12	3:C:53:LEU:N	2.13	0.62
3:C:55:ASN:O	3:C:143:ASP:HB3	1.99	0.62
4:D:97:LEU:HD12	4:D:97:LEU:H	1.64	0.62
1:A:146:ILE:HD12	1:A:146:ILE:N	2.15	0.62
4:D:108:GLY:HA2	4:D:147:PRO:HG2	1.81	0.62
4:D:74:ALA:HB3	4:D:109:THR:HA	1.80	0.62
9:I:127:ILE:HD12	9:I:127:ILE:N	2.13	0.62
9:I:13:ARG:HB2	9:I:33:ILE:O	1.98	0.62
2:B:209:LEU:HA	2:B:212:VAL:HG22	1.80	0.62
7:G:243:ILE:CG2	7:G:244:GLN:H	2.12	0.62
9:I:133:ILE:HB	9:I:143:LEU:CB	2.29	0.62
7:G:266:GLN:O	7:G:270:ARG:N	2.30	0.62
5:E:23:ARG:HD3	5:E:29:CYS:HA	1.81	0.62
2:B:139:ASN:O	2:B:142:THR:N	2.33	0.62
1:A:93:GLY:O	1:A:94:ARG:HB2	1.99	0.62
3:C:109:ILE:HG22	3:C:156:LEU:HD22	1.80	0.62
3:C:246:ALA:O	3:C:249:GLN:HB2	1.99	0.62
4:D:192:LEU:HD12	4:D:210:LEU:HD13	1.80	0.62
5:E:11:LYS:O	5:E:15:VAL:HG22	2.00	0.62
8:H:90:GLU:O	8:H:97:LYS:HB2	2.00	0.62
5:E:53:LEU:CD2	5:E:151:ALA:HB2	2.25	0.62
7:G:148:ALA:O	7:G:151:ARG:CG	2.47	0.62
5:E:161:PHE:CD2	5:E:274:VAL:HG11	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:89:CYS:HB2	3:C:144:TYR:HB2	1.80	0.62
3:C:27:ARG:CD	3:C:31:GLU:HG2	2.22	0.62
2:B:46:LYS:N	2:B:128:GLN:O	2.30	0.62
7:G:192:ILE:HG22	7:G:193:GLY:N	2.14	0.62
1:A:131:GLN:OE1	1:A:132:ILE:N	2.31	0.62
5:E:100:ASP:HA	6:F:120:ARG:HH22	1.64	0.62
5:E:52:LYS:HG2	5:E:57:ASP:OD1	1.99	0.62
5:E:265:VAL:HG12	5:E:266:LEU:N	2.13	0.62
6:F:36:LEU:HB2	6:F:250:ARG:NH1	2.14	0.62
7:G:116:VAL:CG1	7:G:132:VAL:HG13	2.29	0.62
9:I:59:THR:HG22	9:I:61:SER:O	1.99	0.62
3:C:274:LYS:HB3	3:C:275:PRO:HD3	1.80	0.62
1:A:146:ILE:C	1:A:149:ALA:HB3	2.20	0.62
7:G:242:THR:HG22	7:G:245:GLN:CD	2.19	0.62
5:E:8:GLU:HA	5:E:11:LYS:HG2	1.81	0.62
3:C:201:PHE:CE2	3:C:218:ALA:HA	2.35	0.62
7:G:119:ILE:N	7:G:119:ILE:CD1	2.55	0.62
1:A:175:TYR:HB3	1:A:177:PRO:HG2	1.82	0.62
5:E:281:GLY:HA2	5:E:284:ARG:HB3	1.80	0.62
3:C:79:VAL:HG12	3:C:121:LYS:NZ	2.15	0.62
6:F:40:TYR:HB3	6:F:56:GLU:HB2	1.82	0.62
9:I:42:MET:HB2	9:I:56:VAL:HG22	1.80	0.62
4:D:49:GLN:N	4:D:52:THR:O	2.32	0.62
5:E:8:GLU:O	5:E:11:LYS:HG2	2.00	0.62
5:E:238:CYS:HA	6:F:229:GLY:H	1.63	0.62
6:F:233:LEU:N	6:F:236:SER:HB3	2.15	0.62
8:H:149:PHE:O	8:H:151:ASP:N	2.33	0.62
4:D:201:TYR:CE1	4:D:206:LEU:HD13	2.35	0.61
1:A:302:PRO:HA	4:D:27:SER:HB2	1.82	0.61
7:G:242:THR:CA	7:G:245:GLN:HE22	2.13	0.61
7:G:132:VAL:HG12	7:G:132:VAL:O	1.99	0.61
9:I:126:ASP:HA	9:I:155:VAL:CG1	2.30	0.61
9:I:105:LYS:NZ	9:I:146:THR:HG23	2.14	0.61
8:H:84:VAL:HG12	8:H:85:VAL:N	2.15	0.61
5:E:56:THR:HB	5:E:145:GLY:N	2.14	0.61
2:B:69:ALA:N	2:B:112:THR:O	2.30	0.61
2:B:115:HIS:HB3	2:B:118:SER:HB2	1.82	0.61
2:B:143:LEU:HA	2:B:146:LEU:CG	2.29	0.61
5:E:69:PRO:HG3	5:E:132:CYS:SG	2.40	0.61
3:C:8:VAL:O	3:C:11:LEU:HD21	2.00	0.61
3:C:125:CYS:HA	3:C:132:VAL:HA	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:SER:OG	1:A:115:CYS:HB3	2.00	0.61
4:D:125:ASP:OD1	4:D:126:ALA:N	2.33	0.61
2:B:36:GLY:CA	2:B:148:ALA:HB2	2.29	0.61
5:E:120:ASP:C	5:E:122:LYS:N	2.53	0.61
3:C:199:ALA:CB	3:C:210:PRO:HB3	2.24	0.61
6:F:150:LEU:HD21	6:F:157:ALA:CB	2.30	0.61
6:F:150:LEU:HG	6:F:152:GLU:O	2.01	0.61
7:G:34:LEU:HD13	7:G:75:ASP:O	2.00	0.61
8:H:234:ILE:HA	8:H:237:LEU:HD12	1.81	0.61
8:H:87:ARG:HG3	8:H:87:ARG:HH11	1.66	0.61
4:D:232:TYR:HE2	7:G:103:SER:HA	1.64	0.61
8:H:258:TYR:CE2	8:H:287:ARG:HG2	2.35	0.61
3:C:235:LEU:HD23	3:C:236:HIS:N	2.15	0.61
1:A:148:ALA:HA	1:A:151:ILE:HD12	1.81	0.61
4:D:170:THR:N	4:D:173:GLN:HB2	2.15	0.61
8:H:198:GLY:O	8:H:200:ASN:N	2.34	0.61
8:H:249:MET:CE	8:H:250:MET:H	2.14	0.61
9:I:44:SER:HB3	9:I:52:VAL:O	2.00	0.61
3:C:80:VAL:HB	3:C:135:LEU:O	1.99	0.61
3:C:86:PRO:HG2	3:C:88:LEU:HB2	1.83	0.61
4:D:186:ASP:HB3	4:D:190:ARG:N	2.14	0.61
5:E:246:SER:OG	6:F:221:GLN:HB3	1.99	0.61
6:F:215:LEU:HG	6:F:221:GLN:O	2.00	0.61
4:D:58:VAL:HG22	4:D:140:ALA:HB1	1.82	0.61
9:I:67:VAL:HG13	9:I:135:LEU:CD2	2.29	0.61
9:I:156:ALA:O	9:I:163:GLN:HA	1.99	0.61
8:H:198:GLY:C	8:H:200:ASN:H	2.03	0.61
2:B:7:SER:HB3	2:B:13:VAL:CG2	2.30	0.61
9:I:90:VAL:H	9:I:94:PRO:HG3	1.66	0.61
8:H:284:THR:HG22	8:H:288:LEU:HD12	1.81	0.61
3:C:195:ALA:CB	3:C:225:VAL:HG22	2.30	0.61
3:C:206:LEU:HD23	3:C:206:LEU:H	1.65	0.61
3:C:259:HIS:CD2	3:C:263:LYS:HE3	2.35	0.61
9:I:10:PRO:HB3	9:I:36:SER:O	2.01	0.61
1:A:302:PRO:HA	4:D:27:SER:CB	2.30	0.61
2:B:161:ALA:HB3	2:B:184:LEU:CD2	2.31	0.61
7:G:173:MET:HB2	9:I:78:ILE:HD11	1.81	0.61
1:A:183:VAL:N	1:A:184:PRO:HD3	2.15	0.61
3:C:178:GLU:O	3:C:181:LEU:HB2	2.00	0.61
2:B:57:ILE:H	2:B:57:ILE:CD1	2.02	0.61
5:E:123:THR:CG2	5:E:192:LEU:HB2	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:158:THR:HB	8:H:163:TYR:O	2.01	0.61
1:A:140:ASN:HD21	4:D:39:SER:N	1.99	0.61
1:A:10:GLU:O	1:A:14:LEU:HB2	2.00	0.61
2:B:205:HIS:HD2	2:B:206:GLU:N	1.95	0.61
4:D:64:VAL:HG23	4:D:115:SER:HB3	1.82	0.61
9:I:74:LYS:HG2	9:I:126:ASP:O	2.00	0.61
6:F:31:ARG:HH21	6:F:35:ARG:HE	1.47	0.61
8:H:182:GLN:HB2	8:H:186:PHE:HE1	1.64	0.61
1:A:429:UNK:HG2	3:C:249:GLN:HE21	1.63	0.61
6:F:181:VAL:HG23	6:F:217:PRO:HD3	1.83	0.61
7:G:123:LYS:HD3	7:G:128:PHE:CD2	2.35	0.61
9:I:104:ARG:HH11	9:I:141:ASN:HA	1.65	0.61
5:E:227:LEU:CD1	5:E:239:MET:HA	2.30	0.61
1:A:177:PRO:HA	1:A:180:ARG:NE	2.16	0.61
7:G:146:GLU:CD	7:G:187:ASN:ND2	2.50	0.61
8:H:283:GLU:O	8:H:286:GLN:HB2	2.01	0.61
8:H:277:MET:HA	8:H:280:ILE:HD12	1.82	0.61
6:F:202:LEU:HA	6:F:205:GLU:OE2	1.99	0.61
4:D:214:GLN:HB3	4:D:218:GLN:HE21	1.66	0.61
7:G:127:ILE:CG2	7:G:139:SER:HB3	2.28	0.61
5:E:10:GLU:O	5:E:14:ILE:HG13	2.01	0.61
7:G:205:LEU:HD11	7:G:257:GLU:OE1	1.99	0.61
1:A:422:UNK:O	1:A:426:UNK:N	2.34	0.61
3:C:118:ILE:HB	3:C:189:ILE:HG21	1.81	0.61
3:C:126:ILE:HG22	3:C:131:LEU:HD13	1.83	0.61
6:F:153:ASP:HA	6:F:157:ALA:HB2	1.83	0.61
1:A:46:CYS:O	1:A:56:LEU:HD12	2.00	0.61
5:E:60:VAL:HG11	5:E:137:VAL:HG12	1.82	0.61
1:A:61:CYS:SG	1:A:160:PHE:CE2	2.94	0.61
6:F:236:SER:O	6:F:239:GLU:HG2	2.01	0.61
2:B:115:HIS:HB3	2:B:118:SER:CB	2.31	0.61
8:H:49:GLU:O	8:H:50:GLU:HB2	2.01	0.61
3:C:192:HIS:N	3:C:228:GLU:OE2	2.31	0.60
3:C:260:LYS:HA	3:C:260:LYS:HE3	1.83	0.60
1:A:220:LEU:HG	1:A:221:LEU:N	2.16	0.60
7:G:19:ALA:N	7:G:22:VAL:HG21	2.16	0.60
9:I:145:THR:O	9:I:151:LEU:HD21	2.00	0.60
6:F:135:ARG:N	6:F:175:GLU:O	2.29	0.60
2:B:125:GLN:OE1	2:B:126:VAL:N	2.34	0.60
7:G:169:ALA:HA	7:G:175:PRO:HB3	1.83	0.60
7:G:178:VAL:HG12	7:G:180:ILE:H	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:16:HIS:NE2	8:H:225:PRO:HG3	2.16	0.60
7:G:205:LEU:C	7:G:209:LEU:HD12	2.22	0.60
5:E:252:ILE:HG22	5:E:253:PHE:CD1	2.36	0.60
2:B:56:GLU:HG2	2:B:57:ILE:HD12	1.83	0.60
5:E:140:LEU:HD12	5:E:141:LEU:N	2.16	0.60
5:E:140:LEU:HG	5:E:142:LEU:HD21	1.82	0.60
8:H:46:TYR:HD2	8:H:55:SER:HB3	1.66	0.60
4:D:180:VAL:O	4:D:197:THR:HG23	2.01	0.60
6:F:60:THR:HG21	6:F:157:ALA:HA	1.83	0.60
4:D:41:PRO:HB3	4:D:59:TYR:CD1	2.36	0.60
7:G:114:ASP:C	7:G:165:GLN:NE2	2.54	0.60
7:G:223:LEU:HD21	7:G:271:LEU:HB3	1.82	0.60
8:H:96:TRP:CZ2	8:H:131:MET:HG2	2.36	0.60
5:E:238:CYS:CB	6:F:228:SER:HA	2.31	0.60
6:F:32:ASP:HB2	6:F:35:ARG:CB	2.31	0.60
2:B:218:GLN:NE2	2:B:221:ARG:CD	2.63	0.60
9:I:25:GLY:HA3	9:I:55:VAL:HB	1.82	0.60
1:A:255:GLY:HA2	1:A:258:VAL:CG1	2.31	0.60
2:B:209:LEU:O	2:B:213:LEU:N	2.32	0.60
7:G:119:ILE:O	7:G:131:ASP:N	2.29	0.60
7:G:25:GLN:O	7:G:85:LEU:N	2.31	0.60
5:E:211:VAL:HG12	5:E:212:VAL:N	2.17	0.60
8:H:173:GLN:HA	8:H:173:GLN:HE21	1.66	0.60
3:C:127:SER:N	3:C:131:LEU:HB2	2.16	0.60
3:C:170:ILE:HA	3:C:174:THR:O	2.01	0.60
4:D:210:LEU:O	4:D:213:ALA:HB3	2.02	0.60
2:B:195:ILE:N	2:B:195:ILE:CD1	2.64	0.60
5:E:226:LEU:HD12	5:E:227:LEU:N	2.16	0.60
5:E:257:GLU:HA	6:F:234:THR:CG2	2.31	0.60
8:H:252:TYR:H	8:H:255:SER:HB3	1.64	0.60
5:E:147:ASN:CG	5:E:213:ASP:HA	2.22	0.60
4:D:219:HIS:HA	4:D:222:ARG:NE	2.16	0.60
6:F:51:GLY:CA	6:F:172:ALA:HB2	2.28	0.60
1:A:20:GLU:O	1:A:22:LYS:HG3	2.00	0.60
8:H:96:TRP:HB2	8:H:108:LEU:CD2	2.32	0.60
8:H:31:ASP:O	8:H:53:ILE:HG23	2.01	0.60
6:F:191:PRO:HG2	6:F:192:ALA:H	1.64	0.60
3:C:9:GLU:N	3:C:10:PRO:HD2	2.15	0.60
1:A:198:PHE:HD1	1:A:219:GLY:O	1.85	0.60
1:A:32:TYR:CE1	1:A:207:VAL:HG12	2.37	0.60
5:E:62:VAL:HG13	5:E:135:LEU:HB3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:140:LEU:HD22	7:G:141:SER:H	1.66	0.60
7:G:222:LYS:NZ	7:G:268:PHE:HB2	2.16	0.60
7:G:260:THR:HG22	7:G:262:ASP:N	2.08	0.60
6:F:239:GLU:HG3	6:F:240:ALA:N	2.16	0.60
6:F:35:ARG:O	6:F:35:ARG:HD2	2.01	0.60
9:I:57:ARG:HE	9:I:59:THR:HB	1.66	0.60
9:I:64:LEU:H	9:I:96:LYS:HE2	1.67	0.60
3:C:37:VAL:HG13	3:C:51:VAL:HG13	1.84	0.60
4:D:184:ALA:HB3	4:D:194:MET:CB	2.24	0.60
4:D:205:GLU:O	4:D:208:GLN:OE1	2.19	0.60
9:I:26:THR:O	9:I:36:SER:HB3	2.02	0.60
9:I:25:GLY:HA3	9:I:55:VAL:CG2	2.32	0.60
4:D:38:LEU:HD12	4:D:38:LEU:N	2.15	0.60
9:I:106:GLU:OE2	9:I:109:ARG:HB2	2.00	0.60
5:E:203:LEU:HD12	5:E:203:LEU:N	2.16	0.60
2:B:141:ALA:O	2:B:144:ALA:HB3	2.00	0.60
6:F:44:GLY:HA2	6:F:52:SER:HB2	1.82	0.60
3:C:232:LEU:HD13	4:D:202:SER:CA	2.32	0.60
4:D:58:VAL:HG21	4:D:140:ALA:C	2.22	0.60
7:G:243:ILE:CG2	7:G:244:GLN:N	2.65	0.60
7:G:78:LEU:HD12	7:G:79:VAL:N	2.16	0.60
8:H:40:MET:HE3	8:H:41:ARG:O	2.02	0.60
5:E:19:GLN:HA	5:E:209:ARG:CB	2.31	0.60
8:H:110:LEU:HD11	8:H:131:MET:SD	2.41	0.60
8:H:170:VAL:CG1	8:H:205:ILE:HB	2.29	0.60
5:E:273:VAL:HA	5:E:276:LYS:HZ3	1.66	0.60
2:B:221:ARG:HH11	2:B:221:ARG:CB	2.10	0.60
4:D:159:LEU:HD13	4:D:164:THR:C	2.22	0.60
8:H:253:ASP:CG	8:H:254:THR:H	2.05	0.60
1:A:11:ARG:CG	1:A:12:ARG:N	2.65	0.59
4:D:28:LEU:CD2	4:D:28:LEU:H	2.00	0.59
4:D:41:PRO:HB3	4:D:59:TYR:CE1	2.37	0.59
7:G:226:LEU:HD11	7:G:228:ILE:HG23	1.84	0.59
9:I:112:GLU:CD	9:I:112:GLU:N	2.54	0.59
6:F:100:PHE:HD2	6:F:119:GLU:HG3	1.66	0.59
4:D:153:CYS:HB2	4:D:220:VAL:HG11	1.83	0.59
9:I:6:ARG:HD2	9:I:6:ARG:N	2.17	0.59
3:C:101:GLU:HA	3:C:104:VAL:HG23	1.84	0.59
3:C:256:VAL:O	3:C:259:HIS:HB2	2.01	0.59
3:C:78:TYR:HB3	3:C:134:VAL:HA	1.84	0.59
1:A:189:HIS:C	1:A:226:ASN:HD21	2.04	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:161:LEU:HD12	7:G:161:LEU:N	2.17	0.59
5:E:17:GLY:H	8:H:231:ARG:HH21	1.48	0.59
2:B:143:LEU:H	2:B:143:LEU:CD2	2.14	0.59
3:C:164:GLN:CA	3:C:186:TYR:HB3	2.31	0.59
4:D:197:THR:CG2	4:D:198:LYS:N	2.64	0.59
6:F:253:PRO:O	6:F:257:GLN:HG3	2.03	0.59
2:B:84:GLU:O	2:B:85:ARG:HB2	2.02	0.59
1:A:84:GLN:HB3	4:D:119:VAL:HG21	1.84	0.59
7:G:228:ILE:HG22	7:G:238:VAL:CA	2.31	0.59
7:G:23:LEU:HA	7:G:25:GLN:OE1	2.01	0.59
7:G:34:LEU:C	7:G:35:LEU:HD22	2.22	0.59
5:E:146:GLY:HA2	5:E:216:LEU:HD21	1.83	0.59
1:A:130:TRP:CH2	1:A:162:ARG:HG3	2.36	0.59
1:A:98:LEU:O	1:A:102:LEU:N	2.35	0.59
2:B:154:ASP:HB2	2:B:191:ALA:HB2	1.85	0.59
7:G:42:GLU:HG3	7:G:48:VAL:HG23	1.83	0.59
9:I:174:CYS:SG	9:I:177:THR:HG23	2.42	0.59
5:E:168:VAL:H	5:E:190:ILE:HD12	1.66	0.59
2:B:235:VAL:HG13	2:B:236:ARG:N	2.18	0.59
8:H:111:SER:HB2	8:H:157:HIS:NE2	2.18	0.59
3:C:237:LYS:NZ	4:D:193:LEU:C	2.56	0.59
6:F:170:ALA:HA	6:F:176:MET:HE1	1.83	0.59
1:A:86:ALA:HB1	1:A:138:LEU:CD1	2.28	0.59
2:B:47:ALA:HA	2:B:127:LEU:HG	1.84	0.59
4:D:78:VAL:CG2	4:D:118:VAL:HB	2.33	0.59
4:D:29:ARG:H	4:D:168:ASP:HB3	1.66	0.59
7:G:31:GLU:O	7:G:78:LEU:HD12	2.03	0.59
7:G:260:THR:C	7:G:262:ASP:N	2.54	0.59
2:B:148:ALA:O	2:B:150:ILE:N	2.36	0.59
2:B:12:ARG:NH1	2:B:16:ARG:HH12	1.99	0.59
7:G:232:MET:C	7:G:234:GLY:H	2.05	0.59
3:C:144:TYR:O	3:C:145:ASP:HB2	2.03	0.59
2:B:204:LEU:HD23	2:B:205:HIS:O	2.02	0.59
2:B:46:LYS:HD2	2:B:46:LYS:N	2.18	0.59
4:D:173:GLN:HE21	4:D:173:GLN:CA	2.10	0.59
5:E:238:CYS:HB2	6:F:228:SER:HA	1.84	0.59
1:A:41:THR:HA	1:A:283:GLY:N	2.17	0.59
5:E:86:SER:O	5:E:89:ALA:N	2.34	0.59
8:H:246:THR:HB	8:H:247:GLN:OE1	2.03	0.59
9:I:70:ILE:HA	9:I:131:LYS:HA	1.84	0.59
3:C:107:GLN:OE1	3:C:108:PHE:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:207:GLN:HG3	4:D:208:GLN:H	1.67	0.59
1:A:146:ILE:CA	1:A:149:ALA:HB3	2.32	0.59
2:B:198:LEU:HD22	2:B:199:GLU:N	2.16	0.59
4:D:29:ARG:HG3	4:D:30:HIS:N	2.17	0.59
7:G:119:ILE:HA	7:G:160:ASP:O	2.02	0.59
5:E:227:LEU:HB3	5:E:240:ARG:N	2.14	0.59
5:E:153:SER:HB3	5:E:200:ILE:H	1.68	0.59
6:F:185:LEU:HA	6:F:198:ASP:H	1.68	0.59
5:E:120:ASP:C	5:E:122:LYS:H	2.05	0.59
2:B:233:GLN:OE1	2:B:234:HIS:N	2.35	0.59
3:C:232:LEU:HD13	4:D:202:SER:HA	1.84	0.59
1:A:20:GLU:HG3	7:G:243:ILE:CD1	2.33	0.59
8:H:142:SER:OG	8:H:166:LEU:HD11	2.02	0.59
7:G:98:VAL:CG1	7:G:99:TYR:N	2.66	0.59
5:E:140:LEU:CG	5:E:142:LEU:HD21	2.33	0.59
9:I:72:THR:OG1	9:I:89:TYR:HB2	2.02	0.59
8:H:288:LEU:O	8:H:291:GLN:HB3	2.02	0.59
3:C:57:THR:HB	3:C:142:LEU:HD12	1.85	0.59
1:A:246:GLN:C	1:A:248:LEU:N	2.53	0.59
2:B:154:ASP:CG	2:B:155:PHE:N	2.56	0.59
2:B:79:THR:HG22	2:B:88:ARG:HE	1.67	0.59
4:D:170:THR:HB	4:D:173:GLN:NE2	2.18	0.59
5:E:205:LYS:O	5:E:222:SER:HB2	2.03	0.59
9:I:18:GLU:CD	9:I:18:GLU:N	2.56	0.59
3:C:78:TYR:H	3:C:124:LEU:CD1	2.15	0.59
4:D:219:HIS:N	4:D:222:ARG:NH2	2.48	0.59
6:F:252:TYR:CD1	6:F:252:TYR:O	2.56	0.59
7:G:227:GLU:HG3	7:G:239:LYS:HB3	1.84	0.59
9:I:103:ILE:C	9:I:104:ARG:HD2	2.23	0.59
7:G:222:LYS:HZ1	7:G:268:PHE:C	2.05	0.59
5:E:9:ALA:HB1	8:H:167:GLY:HA2	1.81	0.59
8:H:141:ILE:HG13	8:H:165:LYS:HG2	1.85	0.59
8:H:88:ILE:HG22	8:H:89:THR:O	2.02	0.59
2:B:124:VAL:HG11	2:B:137:CYS:HB3	1.85	0.59
5:E:123:THR:CB	5:E:192:LEU:HG	2.33	0.59
3:C:136:TYR:HB3	6:F:110:ARG:HE	1.66	0.58
3:C:59:ILE:HD11	3:C:142:LEU:HD21	1.85	0.58
6:F:252:TYR:HA	6:F:255:LEU:CD2	2.31	0.58
2:B:173:SER:C	2:B:176:GLU:OE2	2.41	0.58
2:B:184:LEU:HB2	2:B:200:MET:CG	2.32	0.58
4:D:40:ARG:HB3	4:D:41:PRO:CD	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:127:ILE:HG23	7:G:140:LEU:C	2.23	0.58
9:I:132:VAL:HG13	9:I:144:LEU:CD2	2.33	0.58
5:E:241:LYS:HD3	5:E:241:LYS:C	2.23	0.58
5:E:229:SER:HB2	5:E:237:THR:OG1	2.03	0.58
4:D:214:GLN:HB3	4:D:218:GLN:NE2	2.17	0.58
6:F:64:CYS:SG	6:F:165:ALA:N	2.76	0.58
2:B:79:THR:HA	2:B:88:ARG:NE	2.19	0.58
7:G:226:LEU:HD22	7:G:239:LYS:O	2.04	0.58
7:G:33:LEU:O	7:G:77:LEU:N	2.36	0.58
7:G:216:ILE:CA	7:G:219:GLU:HB2	2.33	0.58
8:H:276:ILE:HG22	8:H:280:ILE:CG1	2.33	0.58
4:D:61:PRO:HG3	7:G:107:ARG:CZ	2.32	0.58
4:D:111:HIS:NE2	4:D:113:ARG:NH2	2.52	0.58
5:E:64:ALA:HA	5:E:135:LEU:HD23	1.85	0.58
7:G:47:ALA:O	7:G:77:LEU:HA	2.02	0.58
9:I:162:ILE:CD1	9:I:177:THR:HG22	2.33	0.58
7:G:270:ARG:HA	7:G:270:ARG:NH1	2.12	0.58
1:A:177:PRO:HA	1:A:180:ARG:HE	1.67	0.58
5:E:73:LYS:HB3	5:E:76:GLU:CD	2.24	0.58
1:A:28:GLN:HG2	1:A:29:THR:N	2.19	0.58
3:C:60:CYS:SG	3:C:159:ALA:CB	2.91	0.58
1:A:249:ARG:CB	1:A:249:ARG:NH1	2.64	0.58
7:G:76:ARG:HG2	7:G:77:LEU:N	2.18	0.58
3:C:167:GLU:OE1	3:C:167:GLU:HA	2.04	0.58
3:C:166:PRO:CB	3:C:181:LEU:HB2	2.34	0.58
3:C:63:LYS:HE2	3:C:63:LYS:HA	1.84	0.58
5:E:69:PRO:HB3	5:E:132:CYS:CB	2.33	0.58
3:C:274:LYS:HB3	3:C:275:PRO:CD	2.34	0.58
9:I:112:GLU:OE2	9:I:113:LYS:HG2	2.03	0.58
9:I:74:LYS:HZ1	9:I:125:GLY:HA2	1.68	0.58
7:G:222:LYS:HZ1	7:G:268:PHE:HB3	1.69	0.58
5:E:23:ARG:O	5:E:24:VAL:HG13	2.03	0.58
7:G:104:GLN:OE1	7:G:202:THR:HG23	2.02	0.58
1:A:44:GLY:HA3	1:A:160:PHE:HD1	1.68	0.58
6:F:32:ASP:HB2	6:F:35:ARG:H	1.67	0.58
9:I:70:ILE:HG13	9:I:131:LYS:HG3	1.85	0.58
9:I:136:GLY:C	9:I:138:ALA:H	2.07	0.58
6:F:247:GLY:O	6:F:250:ARG:HB3	2.03	0.58
1:A:223:ILE:CD1	1:A:251:SER:HA	2.34	0.58
1:A:243:LEU:C	1:A:247:VAL:HG13	2.24	0.58
4:D:73:LYS:O	4:D:114:THR:CG2	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:141:LEU:HD12	4:D:146:VAL:CB	2.26	0.58
6:F:213:VAL:HB	6:F:225:LEU:HA	1.84	0.58
8:H:83:ILE:H	8:H:199:ASN:HD22	1.51	0.58
5:E:154:ILE:HG23	5:E:155:ALA:N	2.19	0.58
1:A:178:GLU:O	1:A:182:PRO:HD2	2.04	0.58
5:E:231:THR:O	5:E:232:SER:C	2.41	0.58
5:E:267:HIS:O	5:E:271:GLN:HB2	2.04	0.58
5:E:139:VAL:HG12	5:E:140:LEU:N	2.18	0.58
3:C:29:LEU:HD21	3:C:254:ARG:HH12	1.69	0.58
6:F:97:LEU:O	6:F:146:VAL:N	2.37	0.58
1:A:234:ILE:C	1:A:234:ILE:HD12	2.24	0.58
4:D:28:LEU:HD12	4:D:31:PHE:CE1	2.39	0.58
9:I:164:MET:HA	9:I:173:GLN:O	2.03	0.58
9:I:75:VAL:HG12	9:I:76:SER:N	2.18	0.58
5:E:6:LEU:N	8:H:87:ARG:HH21	2.02	0.58
9:I:73:CYS:O	9:I:128:VAL:N	2.31	0.58
7:G:248:ILE:HG22	7:G:271:LEU:HD11	1.85	0.58
8:H:205:ILE:CG2	8:H:234:ILE:HG22	2.34	0.58
2:B:143:LEU:HA	2:B:146:LEU:HG	1.85	0.58
1:A:286:GLU:CA	1:A:289:ALA:HB3	2.34	0.58
6:F:36:LEU:HB3	6:F:250:ARG:NH2	2.19	0.58
2:B:99:GLY:O	2:B:102:LEU:HB2	2.03	0.58
6:F:138:ARG:HB3	6:F:139:TYR:CE1	2.39	0.58
5:E:116:LYS:HG3	5:E:118:SER:CB	2.34	0.58
5:E:237:THR:C	6:F:229:GLY:H	2.07	0.58
3:C:60:CYS:SG	3:C:159:ALA:HB3	2.44	0.58
3:C:222:LEU:HD23	3:C:223:THR:N	2.19	0.58
3:C:50:LEU:HD13	3:C:59:ILE:CG1	2.31	0.58
3:C:232:LEU:HD22	4:D:202:SER:O	2.04	0.58
4:D:205:GLU:O	4:D:207:GLN:N	2.37	0.58
7:G:173:MET:HG3	9:I:78:ILE:O	2.03	0.58
7:G:228:ILE:CG2	7:G:238:VAL:HG12	2.33	0.58
9:I:162:ILE:HG22	9:I:163:GLN:N	2.18	0.58
5:E:23:ARG:HG3	5:E:23:ARG:NH1	2.19	0.58
1:A:76:LEU:HG	1:A:132:ILE:O	2.04	0.58
1:A:176:THR:HA	1:A:179:GLU:CD	2.24	0.58
6:F:32:ASP:CG	6:F:35:ARG:HB3	2.24	0.58
6:F:108:ARG:H	6:F:108:ARG:NE	2.01	0.58
3:C:200:VAL:HG13	3:C:206:LEU:HB3	1.86	0.57
4:D:197:THR:HG21	4:D:201:TYR:HE2	1.69	0.57
4:D:215:ALA:HA	4:D:218:GLN:CD	2.25	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:62:VAL:HG22	6:F:164:ALA:HB3	1.86	0.57
1:A:7:SER:OG	1:A:8:ASN:N	2.35	0.57
7:G:222:LYS:HZ1	7:G:268:PHE:HB2	1.69	0.57
5:E:19:GLN:HA	5:E:209:ARG:HB2	1.84	0.57
6:F:30:THR:HG22	6:F:31:ARG:N	2.18	0.57
3:C:90:SER:HB2	3:C:92:ARG:HG2	1.85	0.57
3:C:243:LEU:H	4:D:191:LYS:HG2	1.69	0.57
4:D:96:ARG:O	4:D:99:ARG:HB3	2.04	0.57
2:B:172:LEU:CD1	2:B:172:LEU:H	2.10	0.57
9:I:103:ILE:HD12	9:I:103:ILE:N	2.18	0.57
8:H:198:GLY:O	8:H:200:ASN:O	2.22	0.57
5:E:229:SER:OG	5:E:237:THR:C	2.42	0.57
2:B:17:ARG:N	2:B:20:GLU:HG2	2.18	0.57
8:H:32:THR:HA	8:H:52:LEU:O	2.04	0.57
8:H:150:SER:C	8:H:152:GLY:N	2.58	0.57
4:D:97:LEU:HB3	4:D:194:MET:HE1	1.85	0.57
1:A:199:PHE:CZ	1:A:206:LEU:HD22	2.40	0.57
7:G:19:ALA:HA	7:G:34:LEU:O	2.04	0.57
6:F:213:VAL:CB	6:F:225:LEU:HA	2.34	0.57
4:D:210:LEU:CD1	4:D:214:GLN:HE22	2.17	0.57
4:D:84:ILE:O	4:D:84:ILE:HD12	2.04	0.57
5:E:240:ARG:HG3	6:F:226:LEU:HG	1.85	0.57
8:H:76:TYR:C	8:H:77:ILE:HG13	2.25	0.57
8:H:43:HIS:N	8:H:68:CYS:SG	2.77	0.57
1:A:289:ALA:HB1	1:A:297:LYS:HD3	1.86	0.57
5:E:32:TYR:CZ	5:E:213:ASP:HB2	2.40	0.57
3:C:107:GLN:NE2	3:C:111:ASP:OD1	2.37	0.57
3:C:126:ILE:CB	3:C:131:LEU:HB3	2.17	0.57
1:A:418:UNK:CG	4:D:208:GLN:HB3	2.34	0.57
1:A:113:SER:C	1:A:115:CYS:N	2.56	0.57
1:A:146:ILE:O	1:A:149:ALA:HB3	2.04	0.57
1:A:223:ILE:HD13	1:A:251:SER:HA	1.86	0.57
1:A:231:ILE:HG22	1:A:232:CYS:N	2.19	0.57
7:G:110:PRO:CB	7:G:166:PHE:CZ	2.87	0.57
7:G:27:VAL:HG23	7:G:79:VAL:HG11	1.87	0.57
9:I:102:THR:O	9:I:103:ILE:HG13	2.05	0.57
2:B:17:ARG:CB	2:B:20:GLU:HG2	2.33	0.57
9:I:15:CYS:SG	9:I:16:ASN:N	2.77	0.57
6:F:113:PRO:O	6:F:115:GLY:N	2.37	0.57
1:A:256:VAL:O	1:A:259:ALA:HB3	2.05	0.57
1:A:257:LYS:O	1:A:258:VAL:C	2.43	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:SER:O	1:A:100:VAL:N	2.25	0.57
4:D:170:THR:H	4:D:173:GLN:HB2	1.70	0.57
7:G:33:LEU:HD22	7:G:77:LEU:O	2.04	0.57
9:I:74:LYS:HA	9:I:127:ILE:HA	1.87	0.57
2:B:51:VAL:HG23	2:B:122:ILE:HG13	1.85	0.57
2:B:236:ARG:O	2:B:239:SER:HB3	2.04	0.57
9:I:116:VAL:HG12	9:I:120:LYS:HB2	1.87	0.57
1:A:429:UNK:O	1:A:432:UNK:N	2.37	0.57
3:C:245:GLY:O	3:C:249:GLN:N	2.38	0.57
4:D:47:PHE:C	4:D:48:LEU:HD12	2.24	0.57
4:D:52:THR:OG1	4:D:126:ALA:HB3	2.05	0.57
7:G:148:ALA:O	7:G:149:THR:O	2.22	0.57
2:B:225:THR:O	2:B:228:ASP:HB3	2.05	0.57
6:F:55:LEU:HD11	6:F:163:THR:CG2	2.35	0.57
1:A:47:ILE:HD12	1:A:47:ILE:N	2.19	0.57
4:D:82:PRO:HA	4:D:122:VAL:HG21	1.86	0.57
7:G:114:ASP:O	7:G:165:GLN:NE2	2.38	0.57
9:I:141:ASN:O	9:I:142:TYR:HD2	1.86	0.57
6:F:124:LEU:HD22	6:F:124:LEU:O	2.04	0.57
6:F:135:ARG:HG2	6:F:136:LEU:N	2.20	0.57
8:H:129:LEU:CA	8:H:132:ARG:HG2	2.34	0.57
4:D:134:LEU:CD1	4:D:154:GLY:HA3	2.34	0.57
9:I:79:ASN:C	9:I:81:ARG:H	2.07	0.57
5:E:203:LEU:HD21	5:E:258:THR:HB	1.87	0.57
3:C:260:LYS:HE3	3:C:263:LYS:CD	2.30	0.57
2:B:81:SER:HB2	2:B:127:LEU:O	2.05	0.57
7:G:242:THR:HG22	7:G:245:GLN:OE1	2.05	0.57
7:G:111:VAL:CG1	7:G:112:LYS:H	2.12	0.57
7:G:42:GLU:CD	7:G:47:ALA:HA	2.25	0.57
8:H:97:LYS:HA	8:H:107:VAL:HG22	1.85	0.57
8:H:85:VAL:HG13	8:H:141:ILE:O	2.04	0.57
5:E:112:ILE:HG12	5:E:238:CYS:HB3	1.87	0.57
6:F:237:TRP:C	6:F:239:GLU:H	2.06	0.57
6:F:237:TRP:C	6:F:239:GLU:N	2.57	0.57
8:H:72:LEU:HG	8:H:73:LYS:H	1.69	0.57
1:A:436:UNK:HA	3:C:257:THR:CG2	2.29	0.56
4:D:94:ARG:HA	4:D:97:LEU:HD13	1.86	0.56
6:F:180:VAL:HG22	6:F:216:MET:SD	2.44	0.56
1:A:114:LYS:C	1:A:116:ILE:H	2.08	0.56
1:A:219:GLY:HA2	1:A:238:GLY:HA3	1.86	0.56
1:A:246:GLN:O	1:A:248:LEU:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:107:LEU:C	4:D:107:LEU:HD23	2.25	0.56
8:H:105:ASP:O	8:H:154:VAL:HG12	2.04	0.56
1:A:61:CYS:O	1:A:62:GLU:HG3	2.05	0.56
3:C:166:PRO:HB2	3:C:181:LEU:HB2	1.86	0.56
5:E:140:LEU:HD21	5:E:142:LEU:HD21	1.87	0.56
2:B:227:LEU:HD23	2:B:227:LEU:N	2.20	0.56
8:H:47:MET:HA	8:H:51:LYS:O	2.05	0.56
2:B:28:MET:HA	2:B:38:ALA:HA	1.87	0.56
3:C:124:LEU:HD22	3:C:133:TRP:HB3	1.86	0.56
4:D:112:PRO:HG2	4:D:113:ARG:NE	2.20	0.56
4:D:57:GLY:O	4:D:118:VAL:HA	2.06	0.56
7:G:259:MET:HB3	7:G:263:GLN:HB3	1.87	0.56
2:B:217:ALA:O	2:B:221:ARG:HG3	2.05	0.56
8:H:268:ILE:O	8:H:270:ASP:N	2.38	0.56
2:B:121:ASP:HB2	2:B:123:TYR:OH	2.05	0.56
3:C:38:ASN:CB	3:C:41:SER:OG	2.53	0.56
3:C:81:PRO:HG3	3:C:113:ILE:HD12	1.87	0.56
4:D:192:LEU:HD23	4:D:194:MET:H	1.70	0.56
4:D:197:THR:HG23	4:D:198:LYS:N	2.20	0.56
3:C:126:ILE:CG2	3:C:131:LEU:HD13	2.35	0.56
1:A:25:ASP:OD2	1:A:27:ARG:HD2	2.04	0.56
2:B:212:VAL:HG23	2:B:213:LEU:N	2.19	0.56
4:D:141:LEU:O	4:D:142:VAL:C	2.44	0.56
9:I:145:THR:HG22	9:I:146:THR:N	2.20	0.56
5:E:15:VAL:HA	5:E:206:ILE:CG2	2.34	0.56
8:H:172:VAL:CG2	8:H:203:ILE:HB	2.35	0.56
5:E:10:GLU:CB	8:H:169:GLY:HA2	2.35	0.56
5:E:8:GLU:HG2	5:E:9:ALA:N	2.20	0.56
6:F:187:LEU:HD21	6:F:239:GLU:OE2	2.05	0.56
5:E:231:THR:O	5:E:233:LYS:N	2.38	0.56
5:E:232:SER:O	5:E:267:HIS:NE2	2.38	0.56
6:F:260:VAL:HG13	9:I:7:TYR:CD2	2.41	0.56
6:F:45:LEU:HD13	6:F:46:LEU:HD23	1.86	0.56
6:F:44:GLY:H	6:F:52:SER:HB2	1.70	0.56
2:B:70:LEU:HD23	2:B:71:VAL:H	1.70	0.56
2:B:27:ARG:O	2:B:39:TYR:N	2.36	0.56
5:E:164:ARG:HG2	5:E:191:ARG:HD2	1.87	0.56
3:C:196:THR:O	3:C:223:THR:HG23	2.05	0.56
4:D:214:GLN:C	4:D:218:GLN:HE21	2.08	0.56
1:A:197:ALA:HA	1:A:220:LEU:HD12	1.87	0.56
5:E:205:LYS:C	5:E:206:ILE:HD12	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:227:LEU:HD12	5:E:239:MET:CA	2.35	0.56
3:C:63:LYS:HZ3	6:F:108:ARG:HA	1.71	0.56
3:C:164:GLN:CG	3:C:186:TYR:HB3	2.35	0.56
6:F:44:GLY:N	6:F:52:SER:HB2	2.20	0.56
7:G:107:ARG:NH1	7:G:107:ARG:HB3	2.20	0.56
2:B:93:ARG:O	2:B:96:CYS:SG	2.64	0.56
5:E:62:VAL:HG11	5:E:135:LEU:HD13	1.87	0.56
9:I:164:MET:HE3	9:I:172:MET:HB3	1.88	0.56
7:G:220:VAL:C	7:G:222:LYS:N	2.59	0.56
6:F:124:LEU:C	6:F:124:LEU:HD22	2.26	0.56
6:F:213:VAL:HG12	6:F:225:LEU:HA	1.87	0.56
8:H:249:MET:HE3	8:H:250:MET:H	1.70	0.56
5:E:229:SER:O	5:E:236:VAL:HA	2.05	0.56
1:A:78:PHE:HA	1:A:134:VAL:O	2.06	0.56
3:C:178:GLU:H	3:C:181:LEU:CD1	2.19	0.56
8:H:149:PHE:HB3	8:H:151:ASP:OD1	2.06	0.56
2:B:26:ALA:HB2	2:B:40:ILE:HD12	1.86	0.56
6:F:153:ASP:HA	6:F:157:ALA:CB	2.36	0.56
6:F:181:VAL:CG2	6:F:217:PRO:HD3	2.35	0.56
1:A:246:GLN:HE21	1:A:247:VAL:N	2.04	0.56
7:G:141:SER:C	7:G:143:LEU:H	2.07	0.56
8:H:76:TYR:CE1	8:H:200:ASN:HB3	2.40	0.56
6:F:158:LEU:HD23	6:F:158:LEU:O	2.06	0.56
2:B:36:GLY:HA3	2:B:51:VAL:HG12	1.86	0.56
2:B:121:ASP:N	2:B:121:ASP:OD2	2.32	0.56
7:G:149:THR:HG22	7:G:150:LYS:H	1.70	0.56
3:C:108:PHE:HE1	3:C:234:CYS:SG	2.29	0.56
1:A:144:ASN:ND2	1:A:147:ASP:OD2	2.32	0.56
1:A:35:ILE:HD12	1:A:35:ILE:C	2.26	0.56
1:A:86:ALA:HB3	1:A:90:PHE:CD1	2.41	0.56
4:D:73:LYS:H	4:D:112:PRO:HA	1.66	0.56
7:G:263:GLN:O	7:G:267:ILE:HB	2.06	0.56
5:E:7:SER:HB3	8:H:87:ARG:HH12	1.71	0.56
6:F:185:LEU:HD11	6:F:243:LEU:CB	2.34	0.56
8:H:40:MET:HE3	8:H:41:ARG:H	1.69	0.56
1:A:223:ILE:HG21	1:A:254:ALA:HB1	1.87	0.56
7:G:165:GLN:HG2	7:G:189:MET:CE	2.36	0.56
7:G:168:VAL:HG23	7:G:176:GLU:H	1.70	0.56
5:E:23:ARG:HB2	5:E:27:ARG:HB2	1.88	0.56
6:F:177:TYR:O	9:I:27:TYR:CE1	2.59	0.56
5:E:37:VAL:HG23	5:E:154:ILE:HD11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:184:GLY:C	6:F:198:ASP:HA	2.26	0.56
6:F:158:LEU:HD13	6:F:212:THR:CB	2.35	0.56
9:I:18:GLU:OE2	9:I:18:GLU:N	2.39	0.56
7:G:146:GLU:OE1	7:G:187:ASN:ND2	2.33	0.56
2:B:159:CYS:SG	2:B:220:ALA:N	2.78	0.56
8:H:144:GLU:HB2	8:H:163:TYR:CD2	2.39	0.56
3:C:237:LYS:O	3:C:239:GLY:N	2.39	0.56
1:A:245:ASP:O	1:A:248:LEU:N	2.32	0.56
2:B:98:MET:O	2:B:102:LEU:CD2	2.54	0.56
8:H:91:VAL:HG22	8:H:96:TRP:CA	2.35	0.56
5:E:53:LEU:O	5:E:56:THR:HG22	2.05	0.56
2:B:12:ARG:NH2	2:B:18:ALA:HA	2.21	0.56
5:E:26:GLY:O	8:H:270:ASP:HB3	2.05	0.56
9:I:46:GLU:CD	9:I:52:VAL:HG23	2.25	0.56
9:I:170:CYS:O	9:I:171:GLU:HG3	2.06	0.56
3:C:69:PRO:CD	3:C:132:VAL:HB	2.26	0.56
2:B:75:TYR:OH	2:B:126:VAL:HG21	2.06	0.56
4:D:138:CYS:SG	4:D:139:MET:HE2	2.46	0.56
7:G:47:ALA:N	7:G:78:LEU:O	2.39	0.56
8:H:148:VAL:HG22	8:H:154:VAL:CA	2.31	0.56
8:H:91:VAL:CG1	8:H:96:TRP:HA	2.34	0.56
3:C:7:THR:HB	3:C:10:PRO:HD2	1.86	0.55
3:C:260:LYS:NZ	3:C:263:LYS:HZ2	2.03	0.55
3:C:47:GLY:HA2	3:C:162:ASN:HD22	1.71	0.55
6:F:36:LEU:HG	6:F:37:ARG:O	2.04	0.55
1:A:209:PRO:HA	1:A:213:GLU:OE1	2.06	0.55
2:B:172:LEU:O	2:B:173:SER:O	2.24	0.55
7:G:170:ASN:CG	7:G:173:MET:HB3	2.26	0.55
9:I:86:HIS:HA	9:I:101:GLY:HA2	1.86	0.55
3:C:47:GLY:HA2	3:C:162:ASN:ND2	2.21	0.55
1:A:151:ILE:O	1:A:155:VAL:HB	2.05	0.55
1:A:213:GLU:O	1:A:214:GLU:C	2.44	0.55
2:B:111:LEU:HD11	2:B:153:ARG:HG3	1.88	0.55
1:A:229:ARG:O	2:B:206:GLU:HB2	2.05	0.55
2:B:46:LYS:O	2:B:127:LEU:N	2.37	0.55
4:D:28:LEU:HA	4:D:168:ASP:HB3	1.89	0.55
7:G:123:LYS:HD3	7:G:128:PHE:HD2	1.71	0.55
7:G:20:ARG:CA	7:G:35:LEU:HD21	2.36	0.55
9:I:111:THR:HG22	9:I:112:GLU:H	1.72	0.55
9:I:162:ILE:HB	9:I:174:CYS:HB2	1.88	0.55
5:E:56:THR:HB	5:E:144:CYS:HA	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:32:ASP:CB	6:F:35:ARG:HB3	2.35	0.55
7:G:149:THR:C	7:G:150:LYS:HD2	2.27	0.55
8:H:25:HIS:HB3	8:H:60:VAL:CB	2.35	0.55
5:E:266:LEU:HA	5:E:269:SER:OG	2.05	0.55
3:C:106:SER:O	3:C:109:ILE:HG12	2.06	0.55
3:C:127:SER:CB	3:C:131:LEU:HD12	2.36	0.55
2:B:106:PHE:N	2:B:106:PHE:CD1	2.74	0.55
7:G:242:THR:C	7:G:245:GLN:HE22	2.09	0.55
7:G:244:GLN:O	7:G:247:LEU:N	2.39	0.55
5:E:58:ILE:HD11	5:E:148:LEU:CD1	2.36	0.55
6:F:50:LYS:N	6:F:50:LYS:CD	2.65	0.55
1:A:78:PHE:HA	1:A:134:VAL:HG23	1.88	0.55
1:A:178:GLU:N	1:A:178:GLU:OE2	2.39	0.55
8:H:242:ILE:HD12	8:H:273:LYS:HE2	1.88	0.55
8:H:182:GLN:HB2	8:H:186:PHE:CE1	2.41	0.55
3:C:208:VAL:CG1	3:C:209:ASP:N	2.68	0.55
3:C:194:VAL:O	3:C:259:HIS:CE1	2.60	0.55
6:F:253:PRO:HA	6:F:256:GLN:HG2	1.89	0.55
6:F:259:LEU:HD23	6:F:259:LEU:C	2.26	0.55
1:A:246:GLN:O	1:A:247:VAL:C	2.41	0.55
2:B:183:GLN:H	2:B:202:ALA:HB2	1.70	0.55
4:D:48:LEU:HG	4:D:53:SER:HB2	1.87	0.55
7:G:48:VAL:HG22	7:G:77:LEU:HD21	1.89	0.55
5:E:126:ILE:HB	5:E:131:HIS:C	2.25	0.55
4:D:181:LEU:HG	4:D:197:THR:CG2	2.35	0.55
6:F:60:THR:HG21	6:F:160:ALA:CB	2.36	0.55
5:E:65:GLU:O	5:E:133:TRP:HA	2.06	0.55
7:G:108:TYR:CE2	7:G:116:VAL:HG21	2.42	0.55
8:H:80:VAL:CG1	8:H:81:GLY:H	2.13	0.55
3:C:88:LEU:O	3:C:90:SER:N	2.40	0.55
6:F:178:ASP:CG	6:F:216:MET:HB3	2.26	0.55
7:G:142:TYR:C	7:G:143:LEU:HD23	2.27	0.55
7:G:226:LEU:HD13	7:G:226:LEU:C	2.26	0.55
7:G:19:ALA:N	7:G:22:VAL:CG2	2.69	0.55
7:G:259:MET:HG2	7:G:263:GLN:HG2	1.86	0.55
8:H:84:VAL:CG1	8:H:85:VAL:N	2.69	0.55
2:B:218:GLN:HE22	2:B:221:ARG:HD3	1.71	0.55
5:E:140:LEU:CD2	5:E:142:LEU:HD21	2.36	0.55
5:E:86:SER:O	5:E:89:ALA:HB3	2.06	0.55
2:B:222:ASP:O	2:B:223:VAL:C	2.44	0.55
8:H:275:GLU:O	8:H:278:GLU:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:126:ILE:HB	3:C:131:LEU:CB	2.18	0.55
1:A:299:GLU:HG2	4:D:30:HIS:HA	1.87	0.55
7:G:242:THR:HG22	7:G:245:GLN:NE2	2.21	0.55
7:G:23:LEU:CD2	7:G:25:GLN:HE22	2.20	0.55
5:E:12:VAL:CG1	5:E:13:TYR:H	2.19	0.55
5:E:141:LEU:N	5:E:141:LEU:HD23	2.20	0.55
3:C:101:GLU:O	3:C:102:ALA:C	2.45	0.55
3:C:111:ASP:O	3:C:115:ASN:N	2.40	0.55
4:D:192:LEU:C	4:D:192:LEU:HD23	2.27	0.55
1:A:421:UNK:HB2	4:D:207:GLN:HB2	1.89	0.55
2:B:111:LEU:C	2:B:113:GLN:N	2.60	0.55
7:G:136:GLU:HB2	7:G:137:PRO:CD	2.35	0.55
8:H:95:ARG:HD2	8:H:107:VAL:HG11	1.89	0.55
5:E:151:ALA:O	5:E:154:ILE:HG22	2.07	0.55
1:A:181:ASP:HB2	1:A:182:PRO:CD	2.37	0.55
6:F:233:LEU:HG	6:F:236:SER:H	1.72	0.55
2:B:143:LEU:HD23	2:B:143:LEU:H	1.71	0.55
3:C:58:VAL:HG12	3:C:155:ALA:CB	2.36	0.55
3:C:249:GLN:HA	3:C:252:MET:HB2	1.89	0.55
3:C:57:THR:HB	3:C:142:LEU:CG	2.37	0.55
3:C:89:CYS:HB2	3:C:144:TYR:CB	2.36	0.55
6:F:39:VAL:HG21	6:F:251:LEU:CD2	2.36	0.55
1:A:189:HIS:HB3	1:A:226:ASN:CG	2.27	0.55
4:D:50:GLY:C	4:D:52:THR:H	2.10	0.55
7:G:230:PHE:CD2	7:G:236:ILE:HD12	2.41	0.55
7:G:49:GLU:HB3	9:I:160:SER:CA	2.32	0.55
9:I:86:HIS:CG	9:I:101:GLY:HA3	2.41	0.55
5:E:204:CYS:HA	5:E:225:SER:HA	1.87	0.55
1:A:78:PHE:CA	1:A:134:VAL:HG23	2.37	0.55
2:B:51:VAL:CG2	2:B:122:ILE:HG13	2.37	0.55
2:B:159:CYS:SG	2:B:220:ALA:CA	2.95	0.55
3:C:213:GLU:HA	3:C:213:GLU:OE1	2.07	0.55
4:D:188:VAL:HG12	4:D:189:GLU:CG	2.37	0.55
6:F:67:SER:O	6:F:68:GLY:O	2.25	0.55
1:A:205:LEU:C	1:A:205:LEU:HD23	2.27	0.55
1:A:80:LEU:O	1:A:103:ASN:ND2	2.40	0.55
2:B:176:GLU:OE2	2:B:176:GLU:N	2.38	0.55
2:B:161:ALA:HB3	2:B:184:LEU:HD22	1.88	0.55
7:G:119:ILE:H	7:G:119:ILE:HD12	1.70	0.55
9:I:78:ILE:HG13	9:I:78:ILE:O	2.07	0.55
7:G:260:THR:HB	7:G:263:GLN:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:264:ARG:HA	7:G:267:ILE:CG2	2.37	0.55
7:G:203:LEU:HA	7:G:206:ILE:CD1	2.36	0.55
6:F:117:CYS:SG	6:F:118:GLU:N	2.80	0.55
3:C:107:GLN:NE2	3:C:111:ASP:HB3	2.22	0.54
4:D:96:ARG:HG3	4:D:99:ARG:NH2	2.08	0.54
6:F:216:MET:O	6:F:217:PRO:O	2.25	0.54
1:A:51:GLY:O	1:A:52:LYS:HB2	2.07	0.54
2:B:111:LEU:CD1	2:B:153:ARG:N	2.70	0.54
4:D:32:ALA:O	4:D:48:LEU:N	2.33	0.54
9:I:156:ALA:HB3	9:I:164:MET:H	1.71	0.54
5:E:239:MET:C	5:E:239:MET:SD	2.86	0.54
3:C:60:CYS:CB	3:C:139:LEU:HG	2.37	0.54
3:C:52:LYS:HA	3:C:56:THR:O	2.06	0.54
3:C:91:SER:C	3:C:93:PHE:H	2.11	0.54
4:D:193:LEU:O	4:D:194:MET:CB	2.55	0.54
6:F:149:LEU:HD21	6:F:151:LEU:HD23	1.89	0.54
6:F:55:LEU:HD11	6:F:163:THR:HB	1.88	0.54
1:A:198:PHE:C	1:A:199:PHE:CD1	2.81	0.54
2:B:81:SER:OG	2:B:129:ALA:N	2.41	0.54
4:D:146:VAL:HG13	4:D:147:PRO:HD2	1.88	0.54
4:D:49:GLN:HE21	4:D:132:CYS:HA	1.72	0.54
7:G:118:GLY:C	7:G:119:ILE:HD12	2.27	0.54
7:G:128:PHE:CE2	7:G:156:VAL:HG11	2.42	0.54
6:F:35:ARG:C	6:F:35:ARG:HD2	2.26	0.54
2:B:137:CYS:CA	2:B:140:ALA:HB3	2.30	0.54
4:D:160:ASP:C	4:D:162:ASP:H	2.10	0.54
5:E:231:THR:CG2	5:E:232:SER:N	2.70	0.54
3:C:216:HIS:CD2	3:C:217:LEU:N	2.76	0.54
6:F:130:LEU:HD21	6:F:162:LEU:HD23	1.89	0.54
6:F:97:LEU:HG	6:F:145:GLU:HG3	1.89	0.54
7:G:144:SER:C	7:G:180:ILE:HG23	2.27	0.54
7:G:21:THR:O	7:G:22:VAL:C	2.45	0.54
9:I:158:SER:HB2	9:I:174:CYS:HB3	1.87	0.54
6:F:139:TYR:HB3	6:F:142:ALA:HB3	1.89	0.54
5:E:116:LYS:NZ	5:E:118:SER:HB3	2.22	0.54
2:B:151:PRO:HB3	8:H:56:VAL:HG23	1.88	0.54
8:H:258:TYR:CB	8:H:288:LEU:HG	2.37	0.54
3:C:57:THR:O	3:C:142:LEU:N	2.36	0.54
1:A:264:LEU:O	1:A:265:ILE:C	2.43	0.54
4:D:102:CYS:C	4:D:104:ALA:N	2.58	0.54
7:G:18:ALA:HB3	7:G:33:LEU:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:229:VAL:HG23	7:G:237:TRP:HE3	1.72	0.54
5:E:10:GLU:HB2	8:H:169:GLY:HA2	1.89	0.54
6:F:233:LEU:H	6:F:236:SER:HB3	1.71	0.54
8:H:44:GLY:HA2	8:H:56:VAL:CG2	2.37	0.54
9:I:16:ASN:HB2	9:I:18:GLU:OE1	2.07	0.54
4:D:165:LEU:CD2	4:D:165:LEU:N	2.69	0.54
5:E:90:THR:C	5:E:92:GLU:H	2.11	0.54
3:C:98:PRO:HB2	3:C:103:GLN:CG	2.37	0.54
3:C:23:ARG:C	3:C:25:ASP:N	2.61	0.54
4:D:180:VAL:C	4:D:181:LEU:HD12	2.28	0.54
1:A:82:LEU:HB3	1:A:90:PHE:CE1	2.41	0.54
4:D:83:LYS:NZ	4:D:125:ASP:H	2.05	0.54
2:B:142:THR:HG22	2:B:146:LEU:HD21	1.88	0.54
8:H:128:GLU:HB3	8:H:132:ARG:NH2	2.22	0.54
3:C:105:ALA:O	3:C:108:PHE:N	2.41	0.54
3:C:147:ASN:HD21	3:C:150:ASP:H	1.55	0.54
3:C:60:CYS:HB3	3:C:155:ALA:O	2.08	0.54
1:A:53:THR:HG23	1:A:142:ASP:N	2.15	0.54
2:B:79:THR:HG22	2:B:88:ARG:HG2	1.89	0.54
8:H:109:LEU:HD23	8:H:109:LEU:C	2.28	0.54
2:B:6:LEU:O	2:B:13:VAL:HG13	2.08	0.54
3:C:64:ALA:CB	3:C:165:LEU:HD11	2.38	0.54
1:A:428:UNK:HG1	3:C:246:ALA:O	2.07	0.54
6:F:130:LEU:HD23	6:F:130:LEU:N	2.22	0.54
1:A:242:LEU:O	2:B:195:ILE:HD13	2.07	0.54
9:I:111:THR:HG1	9:I:184:LYS:HE3	1.73	0.54
9:I:155:VAL:HG13	9:I:157:HIS:NE2	2.22	0.54
7:G:266:GLN:C	7:G:268:PHE:N	2.59	0.54
5:E:241:LYS:HB3	6:F:225:LEU:H	1.72	0.54
1:A:165:VAL:HG22	1:A:178:GLU:HB2	1.87	0.54
2:B:48:LEU:CG	2:B:127:LEU:HD11	2.29	0.54
2:B:209:LEU:O	2:B:213:LEU:HB3	2.07	0.54
8:H:271:ILE:CG2	8:H:277:MET:HG3	2.38	0.54
5:E:147:ASN:CB	5:E:213:ASP:HA	2.37	0.54
3:C:120:GLN:HB3	3:C:122:GLU:HG2	1.90	0.54
3:C:200:VAL:HG22	3:C:206:LEU:CB	2.38	0.54
9:I:40:CYS:SG	9:I:56:VAL:HG21	2.48	0.54
1:A:32:TYR:CE1	1:A:208:ASP:HB2	2.43	0.54
4:D:51:ASP:O	4:D:124:SER:OG	2.25	0.54
7:G:123:LYS:HB2	7:G:128:PHE:HD2	1.73	0.54
7:G:170:ASN:HD21	7:G:173:MET:CB	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:7:SER:H	8:H:87:ARG:HH22	1.54	0.54
5:E:154:ILE:CD1	5:E:270:LEU:HD13	2.36	0.54
5:E:238:CYS:HA	6:F:228:SER:CA	2.31	0.54
5:E:154:ILE:HD12	5:E:270:LEU:CD1	2.36	0.54
8:H:188:ASP:OD1	8:H:194:SER:HB3	2.08	0.54
4:D:225:ARG:NH2	7:G:28:LEU:HD23	2.22	0.54
2:B:159:CYS:SG	2:B:219:ALA:C	2.86	0.54
6:F:261:ARG:O	6:F:265:ARG:HG2	2.08	0.54
3:C:72:ASP:O	3:C:74:PRO:CD	2.56	0.54
4:D:190:ARG:HG3	4:D:214:GLN:HG3	1.89	0.54
6:F:130:LEU:O	6:F:133:ALA:HB3	2.08	0.54
4:D:40:ARG:CB	4:D:41:PRO:HD3	2.27	0.54
6:F:213:VAL:CG1	6:F:225:LEU:HA	2.38	0.54
1:A:76:LEU:HG	1:A:77:PHE:N	2.21	0.54
3:C:61:GLY:HA3	6:F:105:PHE:CD2	2.43	0.54
5:E:110:TYR:O	5:E:114:ASN:HB2	2.08	0.54
5:E:86:SER:HB3	5:E:89:ALA:HB2	1.90	0.54
5:E:71:LEU:O	5:E:74:PRO:HD3	2.07	0.54
8:H:53:ILE:CG2	8:H:54:ALA:N	2.71	0.54
8:H:276:ILE:O	8:H:279:GLU:N	2.41	0.54
1:A:28:GLN:HB3	1:A:31:ASP:OD2	2.08	0.54
3:C:232:LEU:HD13	4:D:203:ASP:N	2.23	0.53
3:C:237:LYS:HZ3	3:C:240:GLY:H	1.55	0.53
1:A:36:ARG:C	1:A:37:ILE:HD12	2.28	0.53
2:B:100:LEU:HA	2:B:103:ARG:HD3	1.90	0.53
2:B:190:PRO:O	2:B:191:ALA:C	2.46	0.53
2:B:204:LEU:HD11	2:B:208:HIS:CB	2.37	0.53
2:B:41:GLU:CA	2:B:45:THR:O	2.53	0.53
4:D:121:GLN:NE2	4:D:122:VAL:N	2.56	0.53
9:I:100:ARG:CG	9:I:101:GLY:H	2.20	0.53
8:H:202:PHE:C	8:H:203:ILE:HD12	2.27	0.53
8:H:236:ARG:NH1	8:H:269:LYS:HB3	2.22	0.53
1:A:67:LYS:HG2	1:A:68:LEU:H	1.74	0.53
3:C:109:ILE:O	3:C:113:ILE:N	2.29	0.53
3:C:57:THR:OG1	3:C:142:LEU:HB2	2.07	0.53
4:D:98:ILE:CG2	4:D:99:ARG:N	2.71	0.53
6:F:97:LEU:O	6:F:146:VAL:HG23	2.07	0.53
1:A:12:ARG:HD3	1:A:12:ARG:C	2.29	0.53
1:A:245:ASP:O	1:A:249:ARG:NH2	2.41	0.53
2:B:104:GLN:O	2:B:107:GLU:HB3	2.08	0.53
7:G:178:VAL:CG1	7:G:179:CYS:H	2.21	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:76:TYR:CA	8:H:102:SER:HB3	2.38	0.53
8:H:113:MET:HG3	8:H:113:MET:O	2.07	0.53
8:H:165:LYS:HE2	8:H:219:PHE:HE1	1.72	0.53
5:E:13:TYR:CE1	8:H:231:ARG:HG3	2.43	0.53
8:H:76:TYR:CD2	8:H:77:ILE:N	2.75	0.53
5:E:217:GLN:O	5:E:220:ALA:HB3	2.08	0.53
5:E:184:ASP:HB2	5:E:187:TYR:HB2	1.90	0.53
3:C:38:ASN:HB3	3:C:41:SER:OG	2.08	0.53
4:D:214:GLN:C	4:D:218:GLN:NE2	2.61	0.53
2:B:105:THR:OG1	2:B:106:PHE:CD1	2.61	0.53
2:B:110:ILE:O	2:B:111:LEU:HB2	2.09	0.53
5:E:42:VAL:C	5:E:44:ASN:H	2.12	0.53
9:I:73:CYS:HB3	9:I:87:ILE:CG2	2.38	0.53
5:E:120:ASP:CG	5:E:192:LEU:HD11	2.29	0.53
5:E:185:ASP:N	5:E:186:PRO:CD	2.71	0.53
2:B:223:VAL:O	2:B:227:LEU:HG	2.07	0.53
2:B:228:ASP:O	2:B:232:ARG:HG3	2.08	0.53
1:A:13:PHE:CD2	1:A:13:PHE:C	2.81	0.53
1:A:15:LEU:HD21	1:A:216:VAL:HB	1.89	0.53
1:A:197:ALA:CA	1:A:220:LEU:HD12	2.38	0.53
1:A:48:VAL:HG21	1:A:152:ALA:HA	1.90	0.53
7:G:250:ALA:O	7:G:253:LEU:HB2	2.09	0.53
8:H:109:LEU:HD23	8:H:110:LEU:N	2.24	0.53
7:G:203:LEU:O	7:G:204:GLY:C	2.47	0.53
2:B:145:VAL:O	2:B:146:LEU:C	2.47	0.53
9:I:71:VAL:CG2	9:I:72:THR:N	2.71	0.53
9:I:93:MET:N	9:I:94:PRO:CD	2.71	0.53
8:H:189:LEU:HD13	8:H:257:LEU:CD2	2.38	0.53
1:A:28:GLN:O	1:A:31:ASP:OD1	2.27	0.53
9:I:79:ASN:C	9:I:81:ARG:N	2.60	0.53
3:C:65:GLU:O	3:C:134:VAL:N	2.37	0.53
6:F:169:LEU:O	6:F:174:VAL:HG22	2.08	0.53
6:F:181:VAL:HG23	6:F:217:PRO:CD	2.39	0.53
6:F:252:TYR:HD1	6:F:255:LEU:HD11	1.72	0.53
1:A:243:LEU:N	1:A:246:GLN:HE22	2.07	0.53
1:A:241:MET:HB3	2:B:194:GLN:NE2	2.23	0.53
4:D:38:LEU:CD1	4:D:38:LEU:H	2.22	0.53
5:E:42:VAL:HG12	5:E:44:ASN:H	1.73	0.53
9:I:129:LEU:CD2	9:I:154:VAL:HG22	2.31	0.53
9:I:126:ASP:HB3	9:I:183:ARG:HH22	1.73	0.53
8:H:244:LEU:O	8:H:249:MET:N	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:247:GLN:O	8:H:248:ARG:C	2.46	0.53
7:G:149:THR:CG2	7:G:150:LYS:N	2.69	0.53
7:G:115:HIS:N	7:G:115:HIS:ND1	2.56	0.53
8:H:71:ALA:HB3	8:H:74:THR:OG1	2.09	0.53
1:A:421:UNK:O	1:A:425:UNK:CG	2.54	0.53
3:C:210:PRO:HA	3:C:214:GLU:OE2	2.08	0.53
3:C:244:THR:HG22	3:C:246:ALA:H	1.73	0.53
6:F:40:TYR:C	6:F:40:TYR:CD1	2.81	0.53
1:A:101:LYS:HD2	1:A:105:LEU:HD22	1.91	0.53
1:A:15:LEU:HA	1:A:18:ILE:HG12	1.90	0.53
1:A:226:ASN:O	1:A:228:HIS:N	2.41	0.53
1:A:23:ARG:HH21	1:A:27:ARG:NH1	2.05	0.53
1:A:158:CYS:CB	1:A:269:LEU:HD11	2.39	0.53
1:A:83:SER:OG	1:A:85:MET:HG2	2.08	0.53
2:B:156:VAL:HG13	2:B:188:LEU:C	2.29	0.53
4:D:74:ALA:HA	4:D:114:THR:HG23	1.90	0.53
9:I:106:GLU:CD	9:I:106:GLU:H	2.12	0.53
5:E:7:SER:CB	8:H:87:ARG:HH12	2.22	0.53
6:F:158:LEU:CD2	6:F:158:LEU:C	2.77	0.53
5:E:120:ASP:HB3	5:E:123:THR:OG1	2.09	0.53
8:H:40:MET:CE	8:H:41:ARG:H	2.21	0.53
3:C:126:ILE:HG23	3:C:168:VAL:CG1	2.38	0.53
3:C:15:ARG:HA	3:C:18:LEU:HD12	1.90	0.53
3:C:201:PHE:CD2	3:C:219:THR:HG23	2.44	0.53
1:A:260:GLU:O	1:A:263:GLU:HB3	2.09	0.53
1:A:262:THR:O	1:A:265:ILE:HG13	2.06	0.53
2:B:210:GLU:O	2:B:214:GLU:HB2	2.08	0.53
9:I:123:ARG:HB2	9:I:183:ARG:NH2	2.20	0.53
8:H:191:CYS:O	8:H:233:VAL:HG13	2.09	0.53
1:A:433:UNK:O	1:A:436:UNK:HG2	2.08	0.53
3:C:7:THR:C	3:C:10:PRO:HD2	2.29	0.53
1:A:240:ILE:HD13	1:A:242:LEU:HD21	1.91	0.53
5:E:47:GLY:O	5:E:61:GLY:HA2	2.09	0.53
7:G:42:GLU:OE1	7:G:48:VAL:N	2.42	0.53
7:G:49:GLU:HA	7:G:50:ARG:CZ	2.39	0.53
1:A:181:ASP:HB2	1:A:182:PRO:HD3	1.91	0.53
2:B:7:SER:HB3	2:B:13:VAL:HG23	1.90	0.53
7:G:87:HIS:ND1	7:G:98:VAL:O	2.39	0.53
8:H:149:PHE:C	8:H:151:ASP:N	2.61	0.53
3:C:40:GLY:HA2	3:C:162:ASN:ND2	2.24	0.53
1:A:189:HIS:CB	1:A:226:ASN:ND2	2.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:GLU:OE1	1:A:81:GLU:O	2.27	0.53
2:B:186:LEU:HG	2:B:187:ALA:N	2.14	0.53
2:B:78:ALA:HB3	2:B:81:SER:CB	2.32	0.53
2:B:92:ASP:O	2:B:96:CYS:SG	2.60	0.53
4:D:26:CYS:O	4:D:167:LEU:HD12	2.09	0.53
7:G:48:VAL:HG22	7:G:77:LEU:CD2	2.39	0.53
9:I:151:LEU:HG	9:I:152:GLY:H	1.74	0.53
7:G:270:ARG:N	7:G:270:ARG:HH11	2.07	0.53
8:H:110:LEU:HD12	8:H:110:LEU:N	2.13	0.53
5:E:116:LYS:HG3	5:E:118:SER:HB3	1.90	0.53
6:F:178:ASP:OD1	6:F:179:LEU:N	2.42	0.53
1:A:146:ILE:HA	1:A:149:ALA:CB	2.39	0.53
1:A:198:PHE:CD1	1:A:219:GLY:O	2.62	0.53
1:A:83:SER:OG	1:A:84:GLN:N	2.38	0.53
2:B:192:SER:OG	2:B:194:GLN:HG3	2.08	0.53
9:I:87:ILE:HG23	9:I:103:ILE:CD1	2.38	0.53
8:H:102:SER:OG	8:H:104:LEU:HG	2.09	0.53
8:H:108:LEU:HB2	8:H:156:LEU:O	2.08	0.53
1:A:165:VAL:HB	1:A:174:LEU:HA	1.90	0.53
3:C:258:ARG:O	3:C:262:VAL:HG22	2.08	0.52
4:D:205:GLU:O	4:D:209:CYS:SG	2.68	0.52
6:F:178:ASP:OD1	6:F:216:MET:HB3	2.10	0.52
5:E:48:SER:HA	5:E:60:VAL:O	2.08	0.52
7:G:222:LYS:NZ	7:G:268:PHE:HB3	2.23	0.52
7:G:223:LEU:HG	7:G:272:ALA:HA	1.91	0.52
5:E:105:ILE:HG12	5:E:149:PHE:HE1	1.74	0.52
5:E:108:THR:HG1	5:E:149:PHE:HZ	1.55	0.52
1:A:40:GLY:CA	1:A:45:CYS:SG	2.89	0.52
5:E:126:ILE:CD1	5:E:131:HIS:HB3	2.39	0.52
5:E:69:PRO:CG	5:E:132:CYS:SG	2.97	0.52
4:D:149:ARG:HG3	4:D:150:ALA:N	2.24	0.52
1:A:286:GLU:HA	1:A:289:ALA:CB	2.37	0.52
3:C:139:LEU:N	3:C:139:LEU:HD12	2.24	0.52
6:F:218:VAL:HG21	9:I:11:GLY:O	2.09	0.52
9:I:69:ALA:O	9:I:132:VAL:N	2.40	0.52
8:H:102:SER:CB	8:H:104:LEU:HG	2.39	0.52
8:H:106:SER:CA	8:H:154:VAL:HG13	2.39	0.52
5:E:156:VAL:O	5:E:160:LEU:HD13	2.09	0.52
5:E:249:PRO:CG	6:F:245:LEU:HD11	2.38	0.52
3:C:206:LEU:HD22	3:C:247:LYS:NZ	2.24	0.52
3:C:65:GLU:OE2	6:F:109:ARG:NH1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:46:LYS:HD3	2:B:128:GLN:HB2	1.91	0.52
2:B:130:ASP:OD2	2:B:174:HIS:CB	2.57	0.52
4:D:28:LEU:CD2	4:D:28:LEU:N	2.67	0.52
4:D:46:SER:HA	4:D:55:LEU:HA	1.91	0.52
9:I:135:LEU:HB2	9:I:142:TYR:CE2	2.43	0.52
8:H:137:GLU:HA	8:H:137:GLU:OE2	2.09	0.52
8:H:87:ARG:HG3	8:H:87:ARG:NH1	2.24	0.52
1:A:165:VAL:H	1:A:174:LEU:HD22	1.74	0.52
4:D:61:PRO:HB2	7:G:135:SER:OG	2.09	0.52
1:A:276:ARG:HG3	1:A:276:ARG:HH11	1.74	0.52
3:C:240:GLY:C	3:C:242:GLY:H	2.12	0.52
6:F:250:ARG:O	6:F:253:PRO:HD2	2.09	0.52
2:B:161:ALA:HB1	2:B:215:ALA:HB3	1.90	0.52
4:D:107:LEU:HD23	4:D:107:LEU:O	2.09	0.52
4:D:172:LYS:HB2	4:D:173:GLN:NE2	2.24	0.52
9:I:127:ILE:H	9:I:155:VAL:CB	2.21	0.52
7:G:260:THR:O	7:G:262:ASP:N	2.43	0.52
5:E:146:GLY:HA2	5:E:216:LEU:CD2	2.38	0.52
7:G:202:THR:HG22	7:G:204:GLY:N	2.25	0.52
2:B:139:ASN:O	2:B:143:LEU:CG	2.54	0.52
1:A:71:ALA:O	1:A:126:GLY:N	2.42	0.52
7:G:201:VAL:HG23	7:G:234:GLY:HA2	1.90	0.52
6:F:174:VAL:HG23	6:F:176:MET:HE1	1.90	0.52
1:A:12:ARG:HD3	1:A:13:PHE:CA	2.40	0.52
1:A:15:LEU:O	1:A:16:ARG:C	2.47	0.52
1:A:253:ILE:HA	1:A:256:VAL:HG23	1.90	0.52
2:B:102:LEU:HD22	2:B:102:LEU:H	1.75	0.52
7:G:116:VAL:CG1	7:G:117:ILE:N	2.72	0.52
7:G:157:GLN:NE2	7:G:157:GLN:HA	2.25	0.52
7:G:48:VAL:O	9:I:159:GLU:HG3	2.09	0.52
9:I:129:LEU:CD2	9:I:129:LEU:N	2.69	0.52
8:H:172:VAL:O	8:H:202:PHE:HA	2.08	0.52
5:E:252:ILE:CG2	5:E:253:PHE:N	2.71	0.52
2:B:66:PRO:O	2:B:116:PRO:HA	2.09	0.52
5:E:192:LEU:HD13	5:E:192:LEU:C	2.29	0.52
1:A:24:LEU:C	1:A:26:GLY:N	2.58	0.52
3:C:171:ASN:ND2	3:C:176:LEU:HD13	2.25	0.52
3:C:111:ASP:HB2	4:D:198:LYS:HE3	1.92	0.52
3:C:59:ILE:HD11	3:C:142:LEU:CG	2.39	0.52
3:C:56:THR:HG22	3:C:143:ASP:O	2.09	0.52
3:C:86:PRO:HG2	3:C:88:LEU:CB	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:251:LEU:C	6:F:253:PRO:HD2	2.29	0.52
6:F:259:LEU:HD13	9:I:9:ILE:HD12	1.92	0.52
1:A:262:THR:HA	1:A:265:ILE:CD1	2.40	0.52
1:A:294:THR:HA	4:D:231:ARG:HD2	1.91	0.52
2:B:173:SER:OG	2:B:174:HIS:N	2.40	0.52
1:A:233:THR:HG22	2:B:201:ASP:OD1	2.09	0.52
4:D:102:CYS:O	4:D:103:GLU:C	2.47	0.52
4:D:112:PRO:HG2	4:D:113:ARG:HH21	1.69	0.52
7:G:33:LEU:HD13	7:G:33:LEU:N	2.24	0.52
7:G:173:MET:HB2	9:I:78:ILE:CD1	2.39	0.52
5:E:58:ILE:HD12	5:E:58:ILE:N	2.24	0.52
1:A:61:CYS:C	1:A:62:GLU:HG3	2.30	0.52
2:B:49:ALA:CB	2:B:124:VAL:HG22	2.40	0.52
2:B:137:CYS:O	2:B:141:ALA:N	2.33	0.52
5:E:66:MET:HA	5:E:126:ILE:HD11	1.90	0.52
4:D:226:GLU:O	4:D:229:GLN:HB2	2.09	0.52
1:A:242:LEU:CA	1:A:246:GLN:HE22	2.22	0.52
4:D:33:CYS:HB2	4:D:47:PHE:CD1	2.45	0.52
9:I:123:ARG:CB	9:I:124:PRO:HD2	2.14	0.52
5:E:226:LEU:HD11	5:E:239:MET:HE2	1.92	0.52
8:H:82:ASP:OD1	8:H:199:ASN:ND2	2.43	0.52
2:B:151:PRO:HB3	8:H:56:VAL:CG2	2.39	0.52
6:F:108:ARG:CD	6:F:108:ARG:N	2.73	0.52
3:C:48:SER:C	3:C:159:ALA:HA	2.30	0.52
3:C:23:ARG:NH1	3:C:214:GLU:OE2	2.43	0.52
3:C:59:ILE:HD11	3:C:142:LEU:CD1	2.40	0.52
6:F:255:LEU:CD1	6:F:256:GLN:N	2.62	0.52
1:A:50:LEU:HD12	1:A:148:ALA:HB2	1.92	0.52
1:A:247:VAL:O	1:A:251:SER:OG	2.26	0.52
4:D:43:GLY:N	4:D:58:VAL:O	2.42	0.52
7:G:20:ARG:CB	7:G:35:LEU:HD11	2.37	0.52
9:I:102:THR:N	9:I:103:ILE:HD12	2.25	0.52
5:E:257:GLU:C	5:E:259:GLY:N	2.59	0.52
1:A:182:PRO:C	1:A:183:VAL:HG22	2.30	0.52
2:B:143:LEU:CA	2:B:146:LEU:HG	2.40	0.52
8:H:33:ILE:CG2	8:H:34:THR:N	2.72	0.52
1:A:444:UNK:CG	1:A:445:UNK:N	2.73	0.52
6:F:170:ALA:HB2	6:F:176:MET:HE3	1.91	0.52
6:F:252:TYR:CD1	6:F:255:LEU:HD11	2.45	0.52
6:F:64:CYS:SG	6:F:165:ALA:HA	2.49	0.52
2:B:93:ARG:O	2:B:97:GLU:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:33:CYS:SG	4:D:34:GLU:N	2.83	0.52
4:D:86:LEU:HB2	4:D:87:PRO:HD2	1.91	0.52
7:G:192:ILE:CG2	7:G:193:GLY:N	2.72	0.52
5:E:10:GLU:HA	8:H:168:GLN:C	2.29	0.52
5:E:8:GLU:HA	5:E:11:LYS:CG	2.40	0.52
5:E:51:VAL:HG21	5:E:154:ILE:HG23	1.91	0.52
1:A:159:HIS:O	1:A:161:ARG:HD3	2.10	0.52
8:H:258:TYR:CD2	8:H:287:ARG:HG2	2.45	0.52
6:F:61:LYS:HB3	6:F:151:LEU:HD12	1.92	0.52
1:A:11:ARG:HG2	1:A:12:ARG:N	2.20	0.52
1:A:115:CYS:HA	1:A:189:HIS:CD2	2.45	0.52
1:A:225:MET:SD	1:A:255:GLY:CA	2.98	0.52
7:G:116:VAL:HG22	7:G:233:ASN:CG	2.31	0.52
7:G:144:SER:O	7:G:180:ILE:HG23	2.10	0.52
7:G:239:LYS:C	7:G:239:LYS:HD2	2.31	0.52
7:G:253:LEU:HA	7:G:256:CYS:HG	1.73	0.52
7:G:215:GLU:O	7:G:216:ILE:C	2.47	0.52
8:H:204:TRP:C	8:H:205:ILE:HD12	2.31	0.52
5:E:51:VAL:CG2	5:E:155:ALA:HB2	2.40	0.52
2:B:66:PRO:HG2	2:B:67:ASP:H	1.73	0.52
7:G:149:THR:CG2	7:G:150:LYS:H	2.23	0.52
7:G:201:VAL:HG23	7:G:234:GLY:CA	2.40	0.52
8:H:36:ASP:HB2	8:H:39:PHE:CE1	2.45	0.52
6:F:188:ALA:HB1	6:F:189:PRO:HD2	1.91	0.52
3:C:232:LEU:H	4:D:202:SER:HA	1.75	0.51
1:A:436:UNK:CG	3:C:257:THR:OG1	2.55	0.51
1:A:237:SER:O	1:A:240:ILE:HD11	2.09	0.51
1:A:265:ILE:O	1:A:269:LEU:N	2.35	0.51
4:D:29:ARG:NH1	4:D:52:THR:HB	2.25	0.51
7:G:117:ILE:H	7:G:233:ASN:HD21	1.58	0.51
9:I:87:ILE:HG23	9:I:103:ILE:HD13	1.91	0.51
7:G:264:ARG:HH11	7:G:264:ARG:H	1.56	0.51
6:F:213:VAL:HG12	6:F:226:LEU:H	1.75	0.51
1:A:439:UNK:CB	3:C:257:THR:HG22	2.40	0.51
3:C:199:ALA:O	3:C:206:LEU:HB2	2.10	0.51
3:C:9:GLU:O	3:C:11:LEU:HG	2.10	0.51
6:F:36:LEU:HD21	6:F:251:LEU:HD21	1.92	0.51
1:A:146:ILE:HD12	1:A:146:ILE:H	1.75	0.51
1:A:246:GLN:O	1:A:250:CYS:SG	2.68	0.51
1:A:262:THR:HA	1:A:265:ILE:HD11	1.92	0.51
7:G:240:ALA:HB3	7:G:246:THR:OG1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:233:ASN:OD1	7:G:233:ASN:N	2.44	0.51
7:G:230:PHE:CE2	7:G:236:ILE:HG23	2.44	0.51
7:G:199:PHE:HE2	7:G:238:VAL:HG13	1.75	0.51
7:G:33:LEU:HD11	7:G:79:VAL:HG23	1.92	0.51
7:G:220:VAL:O	7:G:222:LYS:N	2.44	0.51
8:H:104:LEU:N	8:H:104:LEU:HD23	2.24	0.51
8:H:102:SER:HB2	8:H:104:LEU:HG	1.92	0.51
6:F:185:LEU:HG	6:F:197:LEU:CD1	2.41	0.51
6:F:211:LEU:HG	6:F:212:THR:N	2.25	0.51
1:A:167:VAL:HG22	1:A:172:VAL:CA	2.27	0.51
5:E:86:SER:HB3	5:E:141:LEU:O	2.09	0.51
5:E:117:SER:C	5:E:119:VAL:H	2.12	0.51
3:C:83:VAL:HG21	3:C:109:ILE:HD11	1.93	0.51
3:C:79:VAL:HG12	3:C:121:LYS:HZ3	1.76	0.51
3:C:225:VAL:HB	3:C:233:CYS:HB3	1.93	0.51
3:C:260:LYS:C	3:C:264:LYS:HZ3	2.13	0.51
2:B:22:ARG:CZ	2:B:173:SER:HA	2.40	0.51
5:E:62:VAL:HA	5:E:136:TYR:O	2.10	0.51
5:E:81:PHE:HA	5:E:137:VAL:O	2.11	0.51
7:G:195:ASP:O	7:G:237:TRP:CZ2	2.61	0.51
9:I:130:ALA:HB1	9:I:145:THR:O	2.11	0.51
9:I:172:MET:SD	9:I:185:VAL:HG22	2.51	0.51
8:H:204:TRP:CE3	8:H:206:TYR:HD2	2.27	0.51
1:A:134:VAL:HG11	1:A:157:LEU:HD21	1.92	0.51
1:A:77:PHE:HB3	1:A:133:ARG:HG3	1.92	0.51
2:B:139:ASN:O	2:B:140:ALA:C	2.47	0.51
9:I:71:VAL:HG22	9:I:72:THR:N	2.25	0.51
3:C:66:PHE:HB3	3:C:126:ILE:CD1	2.40	0.51
3:C:200:VAL:HG22	3:C:206:LEU:HB2	1.92	0.51
9:I:35:SER:OG	9:I:55:VAL:HG21	2.10	0.51
1:A:271:ASN:O	1:A:275:VAL:HG23	2.10	0.51
2:B:163:PHE:HB2	2:B:212:VAL:CG1	2.40	0.51
2:B:172:LEU:HB3	2:B:176:GLU:HG2	1.92	0.51
2:B:161:ALA:HB2	2:B:216:ALA:HB2	1.91	0.51
4:D:58:VAL:HG21	4:D:140:ALA:O	2.11	0.51
4:D:139:MET:HA	4:D:142:VAL:CG2	2.40	0.51
4:D:28:LEU:HD12	4:D:31:PHE:CZ	2.46	0.51
5:E:45:THR:HB	5:E:62:VAL:O	2.11	0.51
9:I:112:GLU:HG3	9:I:147:ALA:CB	2.27	0.51
9:I:85:VAL:O	9:I:103:ILE:HD12	2.10	0.51
6:F:213:VAL:HG12	6:F:226:LEU:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:GLY:CA	1:A:129:VAL:HG21	2.40	0.51
6:F:233:LEU:HD23	6:F:233:LEU:H	1.75	0.51
4:D:160:ASP:OD1	4:D:164:THR:HB	2.10	0.51
8:H:243:SER:O	8:H:247:GLN:N	2.29	0.51
9:I:44:SER:HB3	9:I:52:VAL:HB	1.92	0.51
3:C:116:SER:O	3:C:117:GLN:HB2	2.10	0.51
3:C:23:ARG:NH2	3:C:31:GLU:HB3	2.26	0.51
4:D:197:THR:CG2	4:D:201:TYR:HE2	2.23	0.51
4:D:181:LEU:CB	4:D:197:THR:OG1	2.58	0.51
9:I:25:GLY:HA3	9:I:55:VAL:CB	2.39	0.51
1:A:225:MET:HE1	2:B:206:GLU:HG3	1.93	0.51
1:A:228:HIS:HB2	1:A:230:GLU:OE2	2.10	0.51
7:G:218:GLN:C	7:G:221:GLY:H	2.14	0.51
5:E:27:ARG:HD2	5:E:31:ASP:HB2	1.93	0.51
5:E:273:VAL:HG22	5:E:276:LYS:NZ	2.25	0.51
2:B:36:GLY:HA3	2:B:148:ALA:HB2	1.92	0.51
2:B:18:ALA:HB1	2:B:169:LEU:HA	1.91	0.51
3:C:43:SER:C	3:C:45:ALA:H	2.14	0.51
8:H:242:ILE:HG13	8:H:243:SER:N	2.25	0.51
3:C:47:GLY:CA	3:C:162:ASN:HD22	2.24	0.51
3:C:50:LEU:HD12	3:C:51:VAL:N	2.25	0.51
1:A:248:LEU:HA	1:A:251:SER:OG	2.11	0.51
4:D:38:LEU:CD1	4:D:38:LEU:N	2.73	0.51
7:G:42:GLU:CG	7:G:48:VAL:HG23	2.40	0.51
9:I:126:ASP:C	9:I:127:ILE:HD12	2.31	0.51
5:E:240:ARG:HA	6:F:225:LEU:O	2.10	0.51
8:H:178:LEU:CD1	8:H:245:VAL:HG13	2.38	0.51
2:B:169:LEU:N	2:B:169:LEU:HD12	2.26	0.51
8:H:243:SER:HA	8:H:277:MET:HE3	1.92	0.51
1:A:263:GLU:HB3	1:A:264:LEU:HD22	1.92	0.51
1:A:237:SER:HA	2:B:104:GLN:OE1	2.11	0.51
1:A:234:ILE:CD1	2:B:199:GLU:HA	2.41	0.51
4:D:112:PRO:CG	4:D:113:ARG:NH2	2.69	0.51
4:D:29:ARG:HG2	4:D:168:ASP:OD2	2.10	0.51
7:G:160:ASP:C	7:G:161:LEU:HD12	2.31	0.51
9:I:109:ARG:HH12	9:I:145:THR:HG21	1.76	0.51
6:F:177:TYR:HB3	9:I:27:TYR:CZ	2.45	0.51
5:E:152:ILE:O	5:E:156:VAL:CB	2.58	0.51
1:A:130:TRP:HH2	1:A:163:PRO:HG2	1.75	0.51
6:F:237:TRP:O	6:F:239:GLU:N	2.44	0.51
3:C:43:SER:O	3:C:45:ALA:N	2.32	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:167:ARG:HD3	5:E:187:TYR:HB3	1.93	0.51
9:I:92:SER:C	9:I:94:PRO:HD2	2.31	0.51
9:I:48:GLY:O	9:I:49:ALA:HB3	2.11	0.51
3:C:201:PHE:O	3:C:203:ASP:N	2.44	0.51
1:A:47:ILE:HG12	1:A:284:PHE:HE1	1.76	0.51
8:H:96:TRP:HE3	8:H:108:LEU:HG	1.76	0.51
8:H:84:VAL:CG1	8:H:200:ASN:OD1	2.59	0.51
8:H:76:TYR:HD2	8:H:77:ILE:H	1.59	0.51
1:A:165:VAL:CG2	1:A:178:GLU:HB2	2.41	0.51
2:B:139:ASN:HA	2:B:142:THR:HB	1.93	0.51
5:E:90:THR:C	5:E:92:GLU:N	2.62	0.51
6:F:265:ARG:HG3	6:F:265:ARG:HH11	1.75	0.51
3:C:107:GLN:HE21	3:C:111:ASP:HB3	1.76	0.51
3:C:12:GLU:O	3:C:16:ARG:N	2.44	0.51
3:C:260:LYS:CE	3:C:263:LYS:HD2	2.34	0.51
1:A:144:ASN:HB3	1:A:208:ASP:OD1	2.10	0.51
1:A:302:PRO:HA	4:D:27:SER:CA	2.41	0.51
5:E:39:THR:HB	5:E:162:ASN:ND2	2.26	0.51
5:E:40:ASP:CA	5:E:48:SER:HB2	2.24	0.51
7:G:123:LYS:HA	7:G:128:PHE:CB	2.23	0.51
7:G:20:ARG:CB	7:G:35:LEU:HD21	2.41	0.51
9:I:157:HIS:HA	9:I:162:ILE:O	2.10	0.51
9:I:166:PRO:HA	9:I:172:MET:HA	1.93	0.51
5:E:14:ILE:HB	5:E:221:CYS:SG	2.51	0.51
8:H:170:VAL:O	8:H:204:TRP:CD1	2.64	0.51
9:I:27:TYR:HB3	9:I:34:PHE:O	2.10	0.51
5:E:58:ILE:C	5:E:59:LEU:HD12	2.30	0.51
6:F:184:GLY:O	6:F:198:ASP:N	2.44	0.51
2:B:115:HIS:ND1	8:H:103:ARG:HG3	2.26	0.51
6:F:111:ARG:O	6:F:111:ARG:HG3	2.11	0.51
3:C:25:ASP:OD1	3:C:27:ARG:HD3	2.11	0.51
3:C:44:THR:O	6:F:107:GLY:O	2.27	0.51
1:A:51:GLY:O	1:A:52:LYS:CB	2.59	0.51
4:D:72:ASN:CA	4:D:113:ARG:H	2.15	0.51
4:D:139:MET:N	4:D:139:MET:HE2	2.26	0.51
7:G:199:PHE:CE2	7:G:236:ILE:O	2.64	0.51
8:H:106:SER:HA	8:H:154:VAL:O	2.11	0.51
5:E:118:SER:HB2	5:E:196:ASN:HB3	1.92	0.51
8:H:29:PRO:CD	8:H:57:ALA:HA	2.29	0.51
2:B:226:LEU:HD22	2:B:227:LEU:CD2	2.41	0.51
3:C:201:PHE:HD2	3:C:219:THR:HG23	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:28:GLU:O	3:C:30:GLY:N	2.44	0.50
3:C:44:THR:OG1	6:F:152:GLU:HG3	2.11	0.50
6:F:40:TYR:HB3	6:F:56:GLU:CB	2.41	0.50
6:F:98:CYS:HA	6:F:146:VAL:O	2.10	0.50
1:A:109:CYS:SG	1:A:110:LEU:HD23	2.51	0.50
1:A:224:ALA:HB3	1:A:233:THR:H	1.76	0.50
2:B:45:THR:C	2:B:46:LYS:HD2	2.32	0.50
4:D:73:LYS:N	4:D:112:PRO:CA	2.69	0.50
5:E:82:PHE:O	5:E:138:ASP:HA	2.10	0.50
7:G:242:THR:N	7:G:245:GLN:NE2	2.42	0.50
8:H:76:TYR:CD1	8:H:200:ASN:HB3	2.46	0.50
8:H:30:GLY:N	8:H:54:ALA:O	2.43	0.50
5:E:93:PHE:HB3	5:E:97:GLY:CA	2.41	0.50
9:I:44:SER:CB	9:I:52:VAL:HB	2.40	0.50
9:I:79:ASN:HB2	9:I:82:PHE:O	2.10	0.50
4:D:129:LEU:HD23	4:D:129:LEU:C	2.32	0.50
4:D:208:GLN:O	4:D:212:ALA:N	2.32	0.50
6:F:37:ARG:HB3	6:F:38:PRO:CD	2.41	0.50
9:I:25:GLY:HA2	9:I:37:LEU:HB2	1.92	0.50
2:B:75:TYR:CE1	2:B:126:VAL:HG23	2.45	0.50
7:G:249:LEU:O	7:G:253:LEU:HG	2.11	0.50
5:E:238:CYS:CA	6:F:229:GLY:H	2.23	0.50
7:G:104:GLN:HE22	7:G:202:THR:HG21	1.75	0.50
1:A:75:ILE:CG2	1:A:76:LEU:N	2.75	0.50
2:B:144:ALA:O	2:B:147:ASP:HB3	2.11	0.50
8:H:266:HIS:C	8:H:268:ILE:H	2.13	0.50
8:H:136:GLN:N	8:H:136:GLN:NE2	2.57	0.50
6:F:100:PHE:CD2	6:F:119:GLU:HG3	2.46	0.50
4:D:227:SER:HA	4:D:230:ARG:HG2	1.92	0.50
3:C:249:GLN:CA	3:C:249:GLN:NE2	2.73	0.50
4:D:215:ALA:N	4:D:218:GLN:NE2	2.59	0.50
4:D:96:ARG:HG2	4:D:99:ARG:HE	1.76	0.50
6:F:179:LEU:O	6:F:216:MET:HA	2.11	0.50
9:I:10:PRO:CD	9:I:38:ALA:HB2	2.41	0.50
1:A:141:HIS:NE2	1:A:211:GLU:OE2	2.45	0.50
1:A:302:PRO:HA	4:D:27:SER:HA	1.93	0.50
9:I:88:LEU:HD12	9:I:88:LEU:N	2.26	0.50
7:G:268:PHE:C	7:G:270:ARG:N	2.65	0.50
5:E:23:ARG:HG2	5:E:27:ARG:O	2.10	0.50
5:E:17:GLY:CA	8:H:231:ARG:HE	1.99	0.50
1:A:162:ARG:CZ	1:A:162:ARG:HB3	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:185:LEU:CG	6:F:243:LEU:HD23	2.42	0.50
6:F:31:ARG:HE	6:F:35:ARG:HE	1.59	0.50
8:H:59:SER:HG	8:H:70:LYS:HB2	1.75	0.50
1:A:31:ASP:OD1	1:A:31:ASP:N	2.44	0.50
3:C:49:ALA:CB	3:C:159:ALA:N	2.75	0.50
3:C:174:THR:HG22	3:C:175:ALA:N	2.27	0.50
3:C:31:GLU:O	3:C:31:GLU:HG3	2.12	0.50
1:A:151:ILE:HG22	1:A:155:VAL:CG2	2.41	0.50
1:A:217:MET:O	1:A:217:MET:HG3	2.11	0.50
1:A:225:MET:CE	2:B:206:GLU:HG3	2.41	0.50
1:A:294:THR:HB	4:D:35:GLN:O	2.12	0.50
7:G:111:VAL:CG1	7:G:112:LYS:N	2.72	0.50
9:I:130:ALA:HA	9:I:151:LEU:CD1	2.31	0.50
8:H:174:VAL:HG22	8:H:201:GLY:HA3	1.94	0.50
1:A:177:PRO:C	1:A:180:ARG:HG2	2.30	0.50
5:E:86:SER:HB2	5:E:140:LEU:HD11	1.93	0.50
6:F:100:PHE:HB3	6:F:123:ALA:HB2	1.94	0.50
3:C:200:VAL:CG1	3:C:201:PHE:N	2.74	0.50
3:C:193:PRO:CB	3:C:227:ASP:HA	2.33	0.50
3:C:237:LYS:HZ3	4:D:194:MET:HA	1.75	0.50
6:F:179:LEU:O	6:F:217:PRO:HD2	2.12	0.50
1:A:84:GLN:O	1:A:87:ALA:O	2.29	0.50
2:B:111:LEU:CD1	2:B:153:ARG:H	2.24	0.50
7:G:144:SER:OG	7:G:178:VAL:HG13	2.11	0.50
9:I:155:VAL:CG1	9:I:157:HIS:NE2	2.75	0.50
5:E:56:THR:CG2	5:E:145:GLY:H	2.24	0.50
5:E:146:GLY:C	5:E:148:LEU:N	2.64	0.50
1:A:175:TYR:HB3	1:A:178:GLU:OE2	2.12	0.50
5:E:265:VAL:HG12	5:E:266:LEU:HG	1.94	0.50
2:B:29:GLY:HA2	2:B:37:SER:OG	2.11	0.50
3:C:153:THR:OG1	3:C:194:VAL:CG1	2.60	0.50
3:C:60:CYS:HB3	3:C:159:ALA:CB	2.33	0.50
3:C:68:ALA:N	3:C:132:VAL:HG12	2.26	0.50
1:A:49:GLU:C	1:A:51:GLY:N	2.65	0.50
1:A:84:GLN:C	1:A:86:ALA:H	2.14	0.50
1:A:84:GLN:C	1:A:86:ALA:N	2.65	0.50
4:D:35:GLN:HG2	4:D:36:ASN:N	2.26	0.50
9:I:87:ILE:C	9:I:88:LEU:HD12	2.32	0.50
9:I:73:CYS:CB	9:I:87:ILE:HG22	2.40	0.50
7:G:216:ILE:HA	7:G:219:GLU:HB2	1.93	0.50
7:G:220:VAL:C	7:G:222:LYS:H	2.14	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:139:TYR:CD1	6:F:139:TYR:N	2.79	0.50
8:H:98:VAL:CG2	8:H:106:SER:O	2.60	0.50
5:E:157:LYS:O	5:E:160:LEU:N	2.42	0.50
5:E:172:GLU:HG3	5:E:179:ASP:CG	2.32	0.50
9:I:121:SER:HB3	9:I:122:PHE:CE2	2.46	0.50
3:C:55:ASN:O	3:C:143:ASP:CB	2.59	0.50
2:B:204:LEU:CD1	2:B:208:HIS:HB2	2.38	0.50
9:I:133:ILE:HG13	9:I:144:LEU:CA	2.41	0.50
7:G:260:THR:HG22	7:G:262:ASP:HB3	1.93	0.50
5:E:23:ARG:NH2	5:E:214:ALA:HB2	2.27	0.50
8:H:244:LEU:HD22	8:H:249:MET:HG2	1.94	0.50
5:E:154:ILE:HG23	5:E:155:ALA:H	1.75	0.50
5:E:116:LYS:HB2	5:E:237:THR:CG2	2.42	0.50
7:G:205:LEU:O	7:G:209:LEU:N	2.35	0.50
2:B:17:ARG:CA	2:B:20:GLU:HG2	2.42	0.50
5:E:111:ARG:O	5:E:114:ASN:HB3	2.12	0.50
9:I:90:VAL:N	9:I:94:PRO:HG3	2.26	0.50
9:I:44:SER:OG	9:I:52:VAL:HB	2.12	0.50
5:E:274:VAL:O	5:E:278:GLU:HG3	2.10	0.50
8:H:146:GLN:OE1	8:H:157:HIS:HB2	2.12	0.50
3:C:187:LEU:HD23	3:C:187:LEU:C	2.33	0.50
3:C:260:LYS:HA	3:C:263:LYS:HD2	1.94	0.50
3:C:271:LYS:O	3:C:275:PRO:HG3	2.12	0.50
6:F:254:VAL:HA	6:F:257:GLN:OE1	2.11	0.50
7:G:242:THR:H	7:G:245:GLN:CD	2.16	0.50
7:G:198:LEU:HD12	7:G:237:TRP:N	2.27	0.50
7:G:32:GLU:HA	7:G:77:LEU:O	2.12	0.50
1:A:76:LEU:HD23	1:A:76:LEU:C	2.32	0.50
5:E:123:THR:HG21	5:E:192:LEU:CB	2.38	0.50
5:E:25:ASP:HB2	8:H:239:ASN:OD1	2.11	0.50
8:H:271:ILE:HG21	8:H:280:ILE:HD11	1.94	0.50
8:H:150:SER:O	8:H:152:GLY:N	2.45	0.50
5:E:189:CYS:O	5:E:191:ARG:N	2.35	0.50
3:C:198:PHE:HE2	3:C:251:CYS:HA	1.75	0.50
3:C:147:ASN:OD1	3:C:150:ASP:HB2	2.12	0.50
1:A:302:PRO:CA	4:D:27:SER:HB2	2.42	0.50
2:B:172:LEU:C	2:B:173:SER:O	2.49	0.50
4:D:62:ALA:O	4:D:115:SER:N	2.38	0.50
7:G:50:ARG:HB3	7:G:76:ARG:CB	2.42	0.50
5:E:150:ASP:HA	5:E:153:SER:HG	1.77	0.50
1:A:167:VAL:HG21	1:A:172:VAL:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:103:GLN:O	3:C:104:VAL:C	2.51	0.49
3:C:202:ASP:C	3:C:204:THR:H	2.15	0.49
1:A:212:ARG:O	1:A:216:VAL:HG22	2.12	0.49
1:A:7:SER:O	1:A:11:ARG:HD2	2.12	0.49
4:D:58:VAL:HB	4:D:144:ALA:HB2	1.94	0.49
7:G:192:ILE:CG2	7:G:193:GLY:H	2.25	0.49
5:E:243:GLY:O	6:F:128:GLU:HB3	2.11	0.49
2:B:7:SER:HB3	2:B:13:VAL:HG22	1.93	0.49
5:E:165:ILE:HG23	5:E:166:PRO:HD2	1.92	0.49
1:A:187:ILE:HD12	1:A:187:ILE:N	2.27	0.49
1:A:63:LEU:H	1:A:63:LEU:HD23	1.77	0.49
3:C:194:VAL:O	3:C:225:VAL:HA	2.13	0.49
3:C:196:THR:O	3:C:223:THR:HA	2.12	0.49
3:C:237:LYS:NZ	3:C:240:GLY:N	2.56	0.49
3:C:242:GLY:HA3	4:D:191:LYS:HB3	1.93	0.49
9:I:25:GLY:HA3	9:I:55:VAL:HG23	1.95	0.49
2:B:105:THR:OG1	2:B:106:PHE:CE1	2.65	0.49
2:B:47:ALA:HB2	2:B:126:VAL:HA	1.94	0.49
1:A:241:MET:HG2	2:B:194:GLN:NE2	2.27	0.49
7:G:233:ASN:ND2	7:G:235:ARG:HG3	2.28	0.49
8:H:172:VAL:HG21	8:H:203:ILE:HB	1.95	0.49
5:E:215:THR:O	5:E:218:GLU:HB2	2.12	0.49
1:A:176:THR:C	1:A:180:ARG:CZ	2.80	0.49
6:F:32:ASP:OD1	6:F:35:ARG:HB3	2.12	0.49
1:A:192:ILE:CD1	1:A:193:CYS:H	2.11	0.49
8:H:42:GLY:HA3	8:H:68:CYS:SG	2.52	0.49
6:F:265:ARG:O	6:F:269:ALA:HB2	2.11	0.49
3:C:208:VAL:HG12	3:C:209:ASP:N	2.27	0.49
6:F:67:SER:O	6:F:144:LEU:HG	2.12	0.49
6:F:66:VAL:HG23	6:F:168:ALA:CB	2.43	0.49
6:F:252:TYR:C	6:F:255:LEU:HG	2.33	0.49
6:F:97:LEU:HD23	6:F:145:GLU:HB2	1.92	0.49
1:A:147:ASP:N	1:A:147:ASP:OD2	2.45	0.49
4:D:112:PRO:C	4:D:114:THR:H	2.15	0.49
4:D:82:PRO:HA	4:D:122:VAL:HB	1.93	0.49
7:G:168:VAL:O	7:G:175:PRO:CA	2.60	0.49
8:H:88:ILE:HB	8:H:137:GLU:O	2.12	0.49
3:C:179:VAL:C	3:C:181:LEU:H	2.16	0.49
1:A:187:ILE:HD12	1:A:187:ILE:H	1.77	0.49
3:C:127:SER:H	3:C:131:LEU:CB	2.26	0.49
3:C:210:PRO:HB2	3:C:215:GLU:CB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:126:LEU:CD2	6:F:130:LEU:HG	2.43	0.49
6:F:96:LEU:N	6:F:96:LEU:CD2	2.74	0.49
8:H:172:VAL:HG12	8:H:174:VAL:HG12	1.94	0.49
8:H:170:VAL:CG1	8:H:205:ILE:HD13	2.38	0.49
8:H:83:ILE:O	8:H:84:VAL:HG23	2.12	0.49
1:A:173:THR:O	1:A:174:LEU:HD23	2.12	0.49
1:A:64:VAL:HG12	1:A:65:SER:N	2.27	0.49
6:F:156:SER:C	6:F:158:LEU:N	2.65	0.49
2:B:16:ARG:HH21	2:B:21:LEU:CA	2.25	0.49
9:I:64:LEU:N	9:I:65:PRO:CD	2.76	0.49
8:H:36:ASP:HB2	8:H:39:PHE:CZ	2.47	0.49
3:C:101:GLU:O	3:C:103:GLN:N	2.45	0.49
3:C:62:VAL:HG22	3:C:137:CYS:HA	1.94	0.49
3:C:246:ALA:HA	3:C:249:GLN:HB2	1.93	0.49
6:F:36:LEU:HD12	6:F:37:ARG:N	2.28	0.49
9:I:9:ILE:O	9:I:11:GLY:N	2.42	0.49
1:A:107:GLU:HA	1:A:110:LEU:HD11	1.89	0.49
1:A:253:ILE:HA	1:A:256:VAL:HG21	1.93	0.49
1:A:46:CYS:C	1:A:47:ILE:HD12	2.32	0.49
2:B:194:GLN:C	2:B:195:ILE:HD12	2.32	0.49
1:A:233:THR:HG23	2:B:201:ASP:HA	1.94	0.49
2:B:212:VAL:CG2	2:B:213:LEU:N	2.75	0.49
2:B:48:LEU:HD12	2:B:127:LEU:HD21	1.93	0.49
4:D:28:LEU:HD22	4:D:167:LEU:HD13	1.94	0.49
9:I:100:ARG:HG2	9:I:101:GLY:N	2.27	0.49
1:A:162:ARG:HH11	1:A:162:ARG:CG	2.25	0.49
1:A:161:ARG:HB3	1:A:183:VAL:O	2.11	0.49
6:F:199:PRO:HB2	6:F:204:GLU:HB2	1.95	0.49
2:B:69:ALA:HB3	2:B:112:THR:CB	2.42	0.49
2:B:12:ARG:HD2	2:B:14:ASP:OD2	2.13	0.49
5:E:69:PRO:HB3	5:E:132:CYS:HB2	1.95	0.49
8:H:252:TYR:CE1	8:H:255:SER:HB2	2.48	0.49
5:E:161:PHE:CB	5:E:274:VAL:HG11	2.41	0.49
3:C:105:ALA:O	3:C:106:SER:C	2.51	0.49
4:D:214:GLN:O	4:D:218:GLN:HG3	2.12	0.49
1:A:98:LEU:N	1:A:98:LEU:CD2	2.75	0.49
2:B:45:THR:HA	2:B:128:GLN:O	2.13	0.49
4:D:47:PHE:O	4:D:53:SER:HB2	2.13	0.49
4:D:83:LYS:H	4:D:122:VAL:HB	1.78	0.49
9:I:123:ARG:H	9:I:183:ARG:NE	2.10	0.49
9:I:74:LYS:N	9:I:86:HIS:O	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:264:ARG:O	7:G:265:LYS:C	2.51	0.49
1:A:43:TYR:HB3	1:A:161:ARG:HG2	1.94	0.49
1:A:45:CYS:HB2	1:A:58:GLN:HE22	1.76	0.49
5:E:122:LYS:C	5:E:124:LEU:H	2.14	0.49
5:E:167:ARG:HA	5:E:190:ILE:HB	1.94	0.49
4:D:227:SER:O	4:D:230:ARG:HB2	2.13	0.49
3:C:56:THR:CA	3:C:143:ASP:O	2.52	0.49
3:C:253:SER:O	3:C:256:VAL:HB	2.12	0.49
3:C:56:THR:HG22	3:C:145:ASP:N	2.27	0.49
4:D:215:ALA:HA	4:D:218:GLN:NE2	2.28	0.49
1:A:223:ILE:HG21	1:A:254:ALA:CB	2.42	0.49
2:B:45:THR:OG1	2:B:130:ASP:HB3	2.13	0.49
1:A:295:ALA:HA	4:D:231:ARG:HH12	1.78	0.49
7:G:42:GLU:OE2	7:G:46:GLY:O	2.30	0.49
9:I:111:THR:HG22	9:I:112:GLU:OE2	2.13	0.49
2:B:116:PRO:C	2:B:118:SER:H	2.16	0.49
8:H:72:LEU:H	8:H:72:LEU:HD23	1.77	0.49
9:I:16:ASN:N	9:I:16:ASN:ND2	2.59	0.49
3:C:126:ILE:HG23	3:C:168:VAL:HG12	1.95	0.49
3:C:12:GLU:C	3:C:15:ARG:HG2	2.33	0.49
3:C:49:ALA:HB2	3:C:159:ALA:N	2.27	0.49
6:F:253:PRO:O	6:F:255:LEU:N	2.45	0.49
1:A:146:ILE:CD1	1:A:146:ILE:H	2.25	0.49
7:G:116:VAL:HG22	7:G:233:ASN:CB	2.43	0.49
7:G:140:LEU:CD2	7:G:141:SER:H	2.25	0.49
7:G:179:CYS:HA	7:G:189:MET:CG	2.43	0.49
7:G:50:ARG:HE	7:G:75:ASP:CA	2.22	0.49
7:G:83:GLY:HA3	7:G:102:ASP:O	2.12	0.49
7:G:216:ILE:O	7:G:220:VAL:N	2.42	0.49
5:E:203:LEU:O	5:E:225:SER:CA	2.61	0.49
5:E:157:LYS:HG3	5:E:158:ALA:H	1.77	0.49
5:E:53:LEU:CB	5:E:56:THR:HG23	2.43	0.49
1:A:179:GLU:C	1:A:181:ASP:H	2.15	0.49
4:D:160:ASP:CG	4:D:164:THR:HB	2.33	0.49
8:H:276:ILE:HG22	8:H:280:ILE:HG13	1.93	0.49
1:A:29:THR:OG1	1:A:30:TYR:CE1	2.65	0.49
3:C:263:LYS:O	3:C:267:ASP:OD2	2.31	0.49
9:I:22:PRO:HG2	9:I:26:THR:CB	2.38	0.49
1:A:9:CYS:O	1:A:10:GLU:C	2.52	0.49
1:A:86:ALA:CB	1:A:138:LEU:HD12	2.34	0.49
2:B:173:SER:O	2:B:177:GLU:CG	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:105:THR:HG22	2:B:197:LEU:HB2	1.95	0.49
4:D:63:GLU:OE2	4:D:113:ARG:HB3	2.13	0.49
7:G:228:ILE:HG22	7:G:238:VAL:CG1	2.42	0.49
5:E:224:ALA:HB2	5:E:243:GLY:HA3	1.95	0.49
2:B:66:PRO:O	2:B:67:ASP:C	2.50	0.49
1:A:192:ILE:CD1	1:A:193:CYS:N	2.68	0.49
8:H:252:TYR:O	8:H:253:ASP:C	2.51	0.49
4:D:232:TYR:CE2	7:G:103:SER:HA	2.46	0.49
8:H:26:LEU:HD12	8:H:26:LEU:N	2.27	0.49
4:D:61:PRO:HG3	7:G:107:ARG:NH1	2.28	0.49
3:C:127:SER:H	3:C:131:LEU:HB2	1.76	0.49
3:C:147:ASN:OD1	3:C:150:ASP:CG	2.50	0.49
4:D:189:GLU:C	4:D:191:LYS:N	2.56	0.49
1:A:113:SER:C	1:A:115:CYS:H	2.16	0.49
1:A:139:LEU:N	1:A:139:LEU:CD1	2.76	0.49
1:A:231:ILE:O	2:B:203:ARG:HA	2.12	0.49
7:G:222:LYS:O	7:G:223:LEU:O	2.31	0.49
8:H:131:MET:HA	8:H:134:PHE:CD1	2.48	0.49
1:A:66:PRO:CG	1:A:129:VAL:HB	2.43	0.49
3:C:216:HIS:C	3:C:218:ALA:N	2.61	0.48
3:C:7:THR:O	3:C:10:PRO:HD2	2.13	0.48
1:A:35:ILE:O	1:A:35:ILE:HD12	2.13	0.48
1:A:84:GLN:O	1:A:86:ALA:N	2.45	0.48
4:D:74:ALA:CA	4:D:114:THR:HG23	2.43	0.48
9:I:104:ARG:NH1	9:I:141:ASN:CA	2.73	0.48
5:E:206:ILE:HG22	5:E:206:ILE:O	2.12	0.48
8:H:108:LEU:HD23	8:H:108:LEU:N	2.25	0.48
4:D:143:ASP:C	4:D:145:GLY:N	2.65	0.48
3:C:46:ASP:N	3:C:46:ASP:OD1	2.45	0.48
4:D:203:ASP:C	4:D:205:GLU:N	2.64	0.48
1:A:145:ILE:O	1:A:147:ASP:N	2.46	0.48
1:A:115:CYS:CB	1:A:189:HIS:HB2	2.43	0.48
1:A:80:LEU:O	1:A:99:LEU:HD11	2.13	0.48
7:G:20:ARG:HB2	7:G:35:LEU:CD2	2.41	0.48
5:E:15:VAL:HG13	5:E:221:CYS:HB3	1.95	0.48
6:F:135:ARG:HB2	6:F:177:TYR:CE2	2.48	0.48
5:E:7:SER:HB2	8:H:138:GLY:O	2.13	0.48
1:A:444:UNK:HA	3:C:265:LEU:HD23	1.95	0.48
3:C:67:ALA:C	3:C:132:VAL:HG12	2.33	0.48
3:C:149:LEU:HD22	3:C:223:THR:OG1	2.12	0.48
3:C:199:ALA:HB2	3:C:210:PRO:CG	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:154:PHE:CZ	3:C:266:MET:HB2	2.49	0.48
3:C:78:TYR:H	3:C:124:LEU:HD13	1.78	0.48
6:F:62:VAL:HG22	6:F:164:ALA:CB	2.42	0.48
1:A:15:LEU:O	1:A:18:ILE:N	2.41	0.48
1:A:15:LEU:CD2	1:A:216:VAL:HB	2.43	0.48
1:A:265:ILE:HG13	1:A:265:ILE:H	1.42	0.48
1:A:293:ILE:HG22	1:A:294:THR:N	2.26	0.48
9:I:126:ASP:OD1	9:I:183:ARG:CZ	2.62	0.48
6:F:139:TYR:OH	6:F:175:GLU:HB2	2.13	0.48
1:A:176:THR:N	1:A:177:PRO:CD	2.75	0.48
2:B:218:GLN:O	2:B:221:ARG:HG3	2.13	0.48
9:I:62:GLN:O	9:I:64:LEU:HG	2.12	0.48
9:I:79:ASN:O	9:I:81:ARG:N	2.47	0.48
3:C:116:SER:HB2	3:C:118:ILE:HG23	1.95	0.48
3:C:189:ILE:HD12	3:C:191:THR:O	2.13	0.48
3:C:20:GLU:O	3:C:21:ASN:C	2.51	0.48
4:D:190:ARG:CG	4:D:214:GLN:HG3	2.43	0.48
1:A:101:LYS:HD3	1:A:235:GLN:NE2	2.29	0.48
1:A:244:LYS:HB2	2:B:213:LEU:HD21	1.95	0.48
2:B:102:LEU:H	2:B:102:LEU:CD2	2.27	0.48
4:D:79:ILE:HD11	4:D:119:VAL:HG22	1.93	0.48
4:D:30:HIS:C	4:D:30:HIS:ND1	2.66	0.48
7:G:19:ALA:HB3	7:G:22:VAL:HG23	1.95	0.48
2:B:229:ARG:C	2:B:231:VAL:N	2.64	0.48
1:A:280:GLY:O	1:A:281:LYS:HB2	2.13	0.48
3:C:72:ASP:CG	3:C:73:ALA:N	2.67	0.48
3:C:242:GLY:CA	4:D:193:LEU:HD23	2.43	0.48
4:D:218:GLN:C	4:D:222:ARG:HH21	2.15	0.48
6:F:252:TYR:N	6:F:253:PRO:HD2	2.28	0.48
1:A:240:ILE:HB	1:A:242:LEU:HD21	1.96	0.48
5:E:40:ASP:HA	5:E:48:SER:CB	2.24	0.48
9:I:100:ARG:CG	9:I:101:GLY:N	2.76	0.48
5:E:29:CYS:SG	5:E:209:ARG:HG3	2.53	0.48
5:E:116:LYS:CE	5:E:118:SER:HB3	2.43	0.48
5:E:236:VAL:HG12	5:E:237:THR:O	2.14	0.48
5:E:112:ILE:CG2	5:E:237:THR:HG21	2.44	0.48
8:H:252:TYR:O	8:H:255:SER:N	2.42	0.48
4:D:151:LEU:HD11	7:G:29:PRO:HG2	1.96	0.48
8:H:40:MET:SD	8:H:41:ARG:N	2.85	0.48
3:C:11:LEU:HB2	3:C:12:GLU:OE2	2.13	0.48
3:C:149:LEU:HD12	3:C:149:LEU:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:209:ASP:OD1	3:C:209:ASP:O	2.31	0.48
4:D:201:TYR:HB2	4:D:205:GLU:CG	2.43	0.48
4:D:209:CYS:O	4:D:213:ALA:N	2.34	0.48
6:F:157:ALA:HA	6:F:160:ALA:CB	2.42	0.48
6:F:259:LEU:HD13	9:I:9:ILE:HD13	1.95	0.48
1:A:213:GLU:HA	1:A:216:VAL:CG2	2.43	0.48
1:A:240:ILE:H	1:A:240:ILE:HD12	1.72	0.48
1:A:252:LYS:HA	2:B:206:GLU:OE2	2.14	0.48
2:B:154:ASP:CG	2:B:155:PHE:H	2.16	0.48
6:F:187:LEU:HD21	6:F:237:TRP:HZ3	1.79	0.48
8:H:272:LEU:HG	8:H:274:PRO:HD2	1.95	0.48
3:C:126:ILE:HD12	3:C:131:LEU:HD22	1.95	0.48
3:C:237:LYS:HZ2	4:D:193:LEU:C	2.17	0.48
3:C:86:PRO:HB2	3:C:87:PRO:CD	2.30	0.48
1:A:144:ASN:HD22	1:A:145:ILE:N	2.10	0.48
1:A:246:GLN:C	1:A:248:LEU:H	2.17	0.48
1:A:52:LYS:HB2	1:A:142:ASP:OD2	2.12	0.48
4:D:28:LEU:HA	4:D:168:ASP:CB	2.43	0.48
4:D:54:VAL:HG12	4:D:55:LEU:N	2.28	0.48
7:G:244:GLN:O	7:G:245:GLN:C	2.51	0.48
7:G:114:ASP:HB2	7:G:166:PHE:CZ	2.49	0.48
7:G:166:PHE:HB3	7:G:177:MET:CB	2.42	0.48
6:F:135:ARG:HB2	6:F:177:TYR:HE2	1.78	0.48
8:H:76:TYR:H	8:H:102:SER:HB3	1.79	0.48
8:H:110:LEU:HD21	8:H:131:MET:CG	2.44	0.48
8:H:77:ILE:HG23	8:H:104:LEU:CD2	2.34	0.48
2:B:151:PRO:HA	8:H:56:VAL:HA	1.96	0.48
5:E:164:ARG:HE	5:E:191:ARG:NH1	2.12	0.48
8:H:224:GLU:OE1	8:H:224:GLU:O	2.32	0.48
3:C:104:VAL:HG13	4:D:93:SER:CB	2.38	0.48
3:C:147:ASN:C	3:C:149:LEU:N	2.67	0.48
1:A:429:UNK:CG	3:C:249:GLN:O	2.56	0.48
3:C:32:PHE:O	3:C:33:ARG:O	2.31	0.48
4:D:201:TYR:HB2	4:D:205:GLU:HB3	1.93	0.48
6:F:215:LEU:HG	6:F:221:GLN:C	2.34	0.48
1:A:114:LYS:C	1:A:116:ILE:N	2.67	0.48
1:A:212:ARG:HD2	1:A:215:ARG:NH1	2.29	0.48
1:A:96:SER:O	1:A:99:LEU:N	2.47	0.48
7:G:244:GLN:O	7:G:246:THR:N	2.47	0.48
7:G:174:GLU:HG3	7:G:175:PRO:HD2	1.94	0.48
7:G:76:ARG:HG2	7:G:77:LEU:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:31:ARG:NH2	6:F:35:ARG:NE	2.61	0.48
8:H:69:VAL:HG12	8:H:70:LYS:N	2.29	0.48
9:I:136:GLY:O	9:I:138:ALA:N	2.44	0.48
5:E:34:CYS:HB2	8:H:272:LEU:HD11	1.96	0.48
3:C:118:ILE:HG22	3:C:189:ILE:HD12	1.96	0.48
3:C:65:GLU:OE2	6:F:109:ARG:CZ	2.62	0.48
6:F:103:ALA:HB2	6:F:151:LEU:HA	1.95	0.48
9:I:24:SER:O	9:I:25:GLY:C	2.51	0.48
1:A:293:ILE:O	1:A:295:ALA:N	2.47	0.48
4:D:112:PRO:O	4:D:114:THR:N	2.43	0.48
7:G:18:ALA:O	7:G:33:LEU:HA	2.14	0.48
9:I:102:THR:CG2	9:I:104:ARG:HH12	2.22	0.48
9:I:126:ASP:OD2	9:I:126:ASP:C	2.52	0.48
5:E:16:HIS:CE1	8:H:225:PRO:HG3	2.48	0.48
8:H:86:GLY:O	8:H:140:LEU:HA	2.14	0.48
6:F:35:ARG:HH22	6:F:196:LEU:CD2	2.27	0.48
5:E:78:TYR:HD2	5:E:78:TYR:H	1.61	0.48
6:F:255:LEU:CD1	6:F:256:GLN:H	2.23	0.48
7:G:19:ALA:CB	7:G:34:LEU:O	2.62	0.48
8:H:192:GLY:C	8:H:233:VAL:HG11	2.34	0.48
8:H:197:LEU:CB	8:H:203:ILE:HG13	2.44	0.48
5:E:112:ILE:HG23	5:E:237:THR:HG21	1.96	0.48
5:E:51:VAL:HG23	5:E:155:ALA:HB2	1.95	0.48
2:B:52:TYR:O	2:B:53:GLY:O	2.32	0.48
2:B:7:SER:HB3	2:B:13:VAL:N	2.28	0.48
5:E:125:CYS:O	5:E:126:ILE:O	2.32	0.48
5:E:69:PRO:CD	5:E:132:CYS:SG	3.00	0.48
5:E:190:ILE:O	5:E:190:ILE:HG22	2.13	0.48
1:A:278:GLU:O	1:A:279:GLY:C	2.51	0.48
3:C:103:GLN:O	3:C:106:SER:HB2	2.14	0.47
3:C:153:THR:HG21	3:C:195:ALA:H	1.79	0.47
6:F:169:LEU:HB3	6:F:176:MET:SD	2.54	0.47
9:I:22:PRO:O	9:I:26:THR:HG21	2.13	0.47
1:A:144:ASN:HD22	1:A:144:ASN:C	2.17	0.47
1:A:201:GLN:O	1:A:202:GLY:C	2.52	0.47
1:A:81:GLU:OE1	1:A:137:HIS:HA	2.14	0.47
2:B:207:ASP:N	2:B:207:ASP:OD2	2.41	0.47
2:B:208:HIS:O	2:B:212:VAL:HG22	2.14	0.47
4:D:36:ASN:HA	4:D:44:SER:HB2	1.95	0.47
8:H:174:VAL:HG23	8:H:175:SER:O	2.14	0.47
3:C:176:LEU:C	3:C:176:LEU:HD23	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:138:ALA:HB3	9:I:139:GLN:NE2	2.29	0.47
3:C:271:LYS:O	3:C:275:PRO:HG2	2.14	0.47
3:C:79:VAL:HB	3:C:135:LEU:HD12	1.96	0.47
2:B:204:LEU:CG	2:B:208:HIS:HB2	2.44	0.47
5:E:46:SER:HB2	5:E:47:GLY:H	1.52	0.47
7:G:244:GLN:CA	7:G:244:GLN:NE2	2.72	0.47
7:G:170:ASN:ND2	7:G:173:MET:HE2	2.29	0.47
9:I:133:ILE:HG13	9:I:144:LEU:HA	1.95	0.47
6:F:135:ARG:CG	6:F:136:LEU:N	2.76	0.47
8:H:195:VAL:HG12	8:H:196:ILE:N	2.29	0.47
8:H:243:SER:HA	8:H:277:MET:CE	2.43	0.47
1:A:70:ARG:C	1:A:72:THR:H	2.16	0.47
7:G:29:PRO:CB	7:G:80:THR:O	2.62	0.47
3:C:27:ARG:NH2	3:C:209:ASP:O	2.44	0.47
3:C:193:PRO:HB3	3:C:227:ASP:N	2.29	0.47
3:C:237:LYS:HZ1	3:C:240:GLY:N	2.10	0.47
3:C:259:HIS:O	3:C:263:LYS:CG	2.60	0.47
3:C:57:THR:CB	3:C:142:LEU:HD12	2.44	0.47
3:C:237:LYS:HD3	4:D:192:LEU:CD2	2.44	0.47
4:D:98:ILE:HG23	4:D:99:ARG:N	2.29	0.47
1:A:249:ARG:O	1:A:252:LYS:N	2.46	0.47
2:B:111:LEU:N	2:B:111:LEU:HD12	2.29	0.47
5:E:40:ASP:OD1	5:E:162:ASN:HB3	2.14	0.47
7:G:226:LEU:CD2	7:G:239:LYS:O	2.61	0.47
9:I:145:THR:CG2	9:I:146:THR:N	2.78	0.47
7:G:214:CYS:SG	7:G:214:CYS:O	2.71	0.47
5:E:16:HIS:HB3	8:H:231:ARG:NH2	2.29	0.47
6:F:200:THR:HG22	6:F:201:ARG:N	2.29	0.47
1:A:162:ARG:C	1:A:183:VAL:HG12	2.34	0.47
2:B:135:ALA:O	2:B:138:VAL:HB	2.15	0.47
5:E:119:VAL:O	5:E:121:LEU:HG	2.15	0.47
5:E:120:ASP:O	5:E:122:LYS:N	2.47	0.47
5:E:25:ASP:HA	8:H:239:ASN:HD21	1.78	0.47
6:F:45:LEU:CD1	6:F:46:LEU:HD23	2.44	0.47
6:F:193:PRO:HB2	6:F:195:TRP:CZ3	2.49	0.47
4:D:191:LYS:O	4:D:193:LEU:N	2.46	0.47
6:F:215:LEU:HD23	6:F:216:MET:C	2.35	0.47
1:A:189:HIS:CB	1:A:226:ASN:HD21	2.28	0.47
1:A:198:PHE:N	1:A:198:PHE:CD1	2.81	0.47
1:A:219:GLY:HA3	1:A:240:ILE:HG13	1.97	0.47
1:A:257:LYS:O	1:A:259:ALA:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:188:LEU:HG	2:B:189:LEU:N	2.30	0.47
7:G:191:VAL:O	7:G:192:ILE:HB	2.14	0.47
7:G:269:SER:HA	7:G:272:ALA:CB	2.43	0.47
5:E:22:LEU:HD13	8:H:231:ARG:CB	2.38	0.47
6:F:30:THR:CG2	6:F:31:ARG:N	2.77	0.47
5:E:83:VAL:HG21	5:E:106:ALA:HA	1.96	0.47
5:E:119:VAL:O	5:E:119:VAL:HG23	2.13	0.47
3:C:107:GLN:O	3:C:110:ALA:HB3	2.14	0.47
3:C:111:ASP:OD2	3:C:111:ASP:C	2.53	0.47
3:C:57:THR:HB	3:C:142:LEU:CD1	2.43	0.47
9:I:22:PRO:HB2	9:I:26:THR:HG22	1.96	0.47
1:A:240:ILE:CD1	1:A:240:ILE:N	2.68	0.47
2:B:102:LEU:HD22	2:B:102:LEU:N	2.29	0.47
1:A:234:ILE:HD12	2:B:199:GLU:HA	1.95	0.47
2:B:84:GLU:HA	5:E:63:LYS:NZ	2.29	0.47
7:G:192:ILE:HG22	7:G:193:GLY:H	1.78	0.47
5:E:58:ILE:HD13	5:E:151:ALA:CB	2.44	0.47
7:G:98:VAL:CG1	7:G:99:TYR:H	2.27	0.47
3:C:164:GLN:HA	3:C:186:TYR:CB	2.42	0.47
3:C:164:GLN:HG2	3:C:186:TYR:HB2	1.96	0.47
3:C:101:GLU:CG	4:D:96:ARG:HH12	2.27	0.47
3:C:17:PHE:CB	3:C:22:CYS:SG	3.01	0.47
1:A:96:SER:C	1:A:98:LEU:N	2.65	0.47
2:B:204:LEU:CD2	2:B:208:HIS:HB2	2.44	0.47
4:D:82:PRO:HA	4:D:122:VAL:CB	2.44	0.47
7:G:130:VAL:HG22	7:G:131:ASP:N	2.30	0.47
7:G:196:GLY:HA3	7:G:237:TRP:HE1	1.78	0.47
7:G:20:ARG:HB2	7:G:35:LEU:CG	2.44	0.47
7:G:35:LEU:HD22	7:G:35:LEU:N	2.29	0.47
7:G:266:GLN:O	7:G:269:SER:N	2.48	0.47
8:H:76:TYR:N	8:H:102:SER:HB3	2.29	0.47
1:A:75:ILE:H	1:A:75:ILE:HD12	1.79	0.47
4:D:158:ALA:HB1	4:D:177:ALA:HB2	1.97	0.47
8:H:129:LEU:HD23	8:H:132:ARG:HG3	1.96	0.47
1:A:286:GLU:O	1:A:289:ALA:HB3	2.15	0.47
5:E:147:ASN:HB2	5:E:213:ASP:HA	1.95	0.47
3:C:198:PHE:CE2	3:C:251:CYS:HA	2.50	0.47
3:C:260:LYS:HB3	3:C:264:LYS:HZ1	1.79	0.47
9:I:24:SER:O	9:I:54:SER:HA	2.15	0.47
9:I:10:PRO:CA	9:I:35:SER:O	2.62	0.47
3:C:9:GLU:H	3:C:10:PRO:HD2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:86:PRO:C	3:C:88:LEU:H	2.17	0.47
6:F:64:CYS:SG	6:F:165:ALA:CA	3.03	0.47
6:F:60:THR:C	6:F:61:LYS:HD2	2.35	0.47
1:A:104:ARG:HG2	2:B:97:GLU:OE1	2.14	0.47
1:A:238:GLY:O	1:A:239:GLY:O	2.32	0.47
4:D:112:PRO:O	4:D:114:THR:HG22	2.14	0.47
4:D:37:LEU:H	4:D:44:SER:CB	2.27	0.47
7:G:228:ILE:C	7:G:228:ILE:HD12	2.35	0.47
7:G:230:PHE:HD2	7:G:236:ILE:HD12	1.80	0.47
9:I:102:THR:C	9:I:103:ILE:HG13	2.35	0.47
9:I:128:VAL:CG2	9:I:129:LEU:N	2.78	0.47
9:I:146:THR:HA	9:I:151:LEU:HG	1.97	0.47
7:G:262:ASP:CG	7:G:263:GLN:N	2.68	0.47
8:H:197:LEU:N	8:H:197:LEU:CD2	2.75	0.47
5:E:237:THR:C	6:F:229:GLY:N	2.67	0.47
5:E:148:LEU:HD12	5:E:148:LEU:O	2.14	0.47
5:E:53:LEU:O	5:E:56:THR:CG2	2.62	0.47
6:F:239:GLU:CG	6:F:240:ALA:N	2.78	0.47
2:B:122:ILE:HD12	2:B:122:ILE:N	2.30	0.47
8:H:30:GLY:C	8:H:53:ILE:HG23	2.34	0.47
9:I:90:VAL:H	9:I:94:PRO:HG2	1.79	0.47
8:H:271:ILE:HG22	8:H:277:MET:HG3	1.96	0.47
4:D:134:LEU:HD13	4:D:154:GLY:CA	2.40	0.47
7:G:28:LEU:HD22	7:G:28:LEU:N	2.30	0.47
9:I:96:LYS:HB2	9:I:96:LYS:NZ	2.29	0.47
8:H:40:MET:HE3	8:H:41:ARG:N	2.29	0.47
5:E:163:THR:O	5:E:165:ILE:N	2.43	0.47
3:C:127:SER:N	3:C:131:LEU:CB	2.77	0.47
3:C:57:THR:HB	3:C:142:LEU:HG	1.96	0.47
3:C:201:PHE:CE1	3:C:207:ILE:HD11	2.50	0.47
4:D:88:GLY:N	4:D:91:GLU:HG3	2.30	0.47
1:A:225:MET:HB2	1:A:258:VAL:HG11	1.96	0.47
1:A:295:ALA:N	4:D:231:ARG:NH1	2.63	0.47
1:A:83:SER:O	1:A:90:PHE:CB	2.62	0.47
4:D:170:THR:HG22	4:D:172:LYS:H	1.80	0.47
5:E:12:VAL:CG1	5:E:13:TYR:N	2.74	0.47
5:E:118:SER:OG	5:E:198:PRO:HD3	2.14	0.47
2:B:54:PRO:HB3	2:B:120:ILE:HD11	1.96	0.47
2:B:226:LEU:HD23	2:B:226:LEU:C	2.36	0.47
3:C:89:CYS:O	6:F:48:GLN:HG3	2.15	0.47
4:D:208:GLN:OE1	4:D:208:GLN:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:ARG:NH1	1:A:107:GLU:HB3	2.30	0.47
1:A:198:PHE:HB3	1:A:202:GLY:HA2	1.96	0.47
4:D:112:PRO:HD2	4:D:113:ARG:HH21	1.79	0.47
4:D:64:VAL:HG21	4:D:115:SER:HB3	1.95	0.47
4:D:167:LEU:O	4:D:168:ASP:HB3	2.15	0.47
1:A:165:VAL:H	1:A:174:LEU:CD2	2.27	0.47
2:B:139:ASN:HA	2:B:142:THR:CB	2.45	0.47
8:H:188:ASP:HA	8:H:194:SER:HB3	1.97	0.47
8:H:277:MET:HA	8:H:280:ILE:CD1	2.44	0.47
2:B:74:GLN:H	2:B:123:TYR:HD2	1.63	0.47
7:G:107:ARG:HB3	7:G:107:ARG:HH11	1.78	0.47
3:C:243:LEU:HG	3:C:244:THR:N	2.19	0.47
3:C:262:VAL:HA	3:C:265:LEU:CD1	2.38	0.47
3:C:37:VAL:CG1	3:C:51:VAL:HG13	2.44	0.47
4:D:156:ALA:HA	4:D:181:LEU:O	2.15	0.47
6:F:170:ALA:O	6:F:173:GLY:N	2.48	0.47
6:F:180:VAL:HG13	6:F:223:ALA:CB	2.45	0.47
1:A:95:GLN:O	1:A:97:ASP:N	2.48	0.47
4:D:101:THR:O	4:D:104:ALA:HB3	2.15	0.47
4:D:35:GLN:HB2	4:D:231:ARG:NH2	2.29	0.47
7:G:117:ILE:HD12	7:G:235:ARG:HB2	1.97	0.47
9:I:106:GLU:N	9:I:106:GLU:CD	2.68	0.47
6:F:139:TYR:CE1	6:F:175:GLU:HB2	2.50	0.47
6:F:226:LEU:H	6:F:226:LEU:HD12	1.80	0.47
5:E:10:GLU:HA	8:H:168:GLN:O	2.15	0.47
8:H:197:LEU:HB2	8:H:203:ILE:HG13	1.96	0.47
6:F:186:SER:C	6:F:187:LEU:HD12	2.35	0.47
8:H:258:TYR:HE2	8:H:287:ARG:HG2	1.78	0.47
7:G:232:MET:C	7:G:234:GLY:N	2.68	0.47
3:C:12:GLU:OE2	3:C:12:GLU:N	2.48	0.46
3:C:225:VAL:C	3:C:226:MET:HG3	2.36	0.46
3:C:227:ASP:HB3	3:C:231:LYS:H	1.79	0.46
9:I:24:SER:OG	9:I:55:VAL:O	2.19	0.46
1:A:271:ASN:CA	1:A:274:LYS:NZ	2.77	0.46
2:B:92:ASP:O	2:B:93:ARG:C	2.54	0.46
1:A:65:SER:HA	1:A:127:GLU:O	2.15	0.46
1:A:162:ARG:HH22	1:A:184:PRO:HD2	1.79	0.46
5:E:231:THR:HG22	5:E:232:SER:OG	2.14	0.46
5:E:186:PRO:HG2	5:E:187:TYR:CD1	2.38	0.46
8:H:243:SER:HB3	8:H:277:MET:CG	2.44	0.46
9:I:44:SER:N	9:I:52:VAL:O	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:130:LYS:CE	3:C:130:LYS:O	2.63	0.46
3:C:242:GLY:HA3	4:D:191:LYS:CD	2.33	0.46
3:C:259:HIS:O	3:C:262:VAL:HG23	2.15	0.46
3:C:32:PHE:CE2	3:C:262:VAL:CG1	2.83	0.46
1:A:140:ASN:ND2	4:D:38:LEU:HA	2.30	0.46
4:D:76:LEU:CD2	4:D:102:CYS:HB2	2.45	0.46
7:G:119:ILE:O	7:G:130:VAL:HG23	2.15	0.46
7:G:31:GLU:H	7:G:78:LEU:HD12	1.81	0.46
9:I:74:LYS:HB2	9:I:127:ILE:HG13	1.97	0.46
5:E:261:ARG:HD2	5:E:262:VAL:CG2	2.45	0.46
5:E:7:SER:N	8:H:87:ARG:NH2	2.62	0.46
1:A:153:ALA:O	1:A:156:ALA:HB3	2.15	0.46
5:E:126:ILE:H	5:E:132:CYS:HA	1.80	0.46
8:H:53:ILE:HG22	8:H:54:ALA:H	1.74	0.46
8:H:276:ILE:HG22	8:H:280:ILE:HD11	1.95	0.46
2:B:235:VAL:CG1	8:H:26:LEU:HD23	2.41	0.46
9:I:44:SER:HB3	9:I:52:VAL:CB	2.45	0.46
7:G:107:ARG:HH11	7:G:107:ARG:CB	2.29	0.46
3:C:172:GLU:O	3:C:173:GLU:HB2	2.15	0.46
1:A:436:UNK:O	1:A:437:UNK:C	2.63	0.46
3:C:147:ASN:CG	3:C:197:SER:HB2	2.35	0.46
3:C:264:LYS:HA	3:C:267:ASP:HB2	1.97	0.46
3:C:52:LYS:HD3	3:C:57:THR:HG23	1.96	0.46
4:D:139:MET:HA	4:D:142:VAL:HG23	1.96	0.46
9:I:102:THR:H	9:I:103:ILE:CD1	2.28	0.46
9:I:146:THR:HB	9:I:152:GLY:HA2	1.97	0.46
1:A:59:VAL:HB	1:A:160:PHE:CD1	2.51	0.46
8:H:271:ILE:HD13	8:H:280:ILE:CD1	2.45	0.46
1:A:442:UNK:CG	1:A:443:UNK:N	2.75	0.46
1:A:117:ASP:OD1	1:A:118:THR:N	2.49	0.46
4:D:220:VAL:O	4:D:223:PHE:HB3	2.15	0.46
2:B:62:ALA:O	2:B:63:ARG:C	2.54	0.46
3:C:249:GLN:C	3:C:252:MET:HB2	2.36	0.46
4:D:40:ARG:HG3	4:D:40:ARG:NH1	2.29	0.46
9:I:127:ILE:CD1	9:I:127:ILE:N	2.77	0.46
5:E:19:GLN:HA	5:E:209:ARG:CG	2.46	0.46
8:H:205:ILE:HG22	8:H:234:ILE:CG2	2.45	0.46
8:H:205:ILE:CD1	8:H:205:ILE:N	2.79	0.46
5:E:151:ALA:O	5:E:154:ILE:CG2	2.63	0.46
1:A:62:GLU:O	1:A:130:TRP:HA	2.15	0.46
6:F:156:SER:C	6:F:158:LEU:H	2.19	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:237:TRP:O	6:F:241:VAL:HG23	2.15	0.46
9:I:19:GLU:HG2	9:I:51:PRO:CD	2.32	0.46
7:G:181:ASP:HB3	7:G:186:ALA:N	2.31	0.46
3:C:176:LEU:HD23	3:C:176:LEU:O	2.16	0.46
7:G:94:SER:C	7:G:96:GLY:H	2.19	0.46
3:C:105:ALA:O	3:C:109:ILE:CD1	2.63	0.46
3:C:58:VAL:HG13	3:C:139:LEU:HB3	1.97	0.46
3:C:51:VAL:HG23	3:C:155:ALA:HA	1.97	0.46
3:C:216:HIS:CG	3:C:217:LEU:N	2.82	0.46
3:C:216:HIS:O	3:C:218:ALA:N	2.48	0.46
3:C:23:ARG:NH2	3:C:27:ARG:NE	2.64	0.46
3:C:72:ASP:CG	3:C:73:ALA:H	2.18	0.46
1:A:151:ILE:O	1:A:152:ALA:C	2.54	0.46
1:A:201:GLN:O	1:A:203:THR:N	2.49	0.46
2:B:197:LEU:HD22	2:B:198:LEU:H	1.79	0.46
1:A:231:ILE:CG2	2:B:200:MET:HE1	2.46	0.46
4:D:79:ILE:O	4:D:119:VAL:HA	2.15	0.46
5:E:61:GLY:O	5:E:137:VAL:HA	2.15	0.46
7:G:136:GLU:CD	7:G:136:GLU:N	2.69	0.46
7:G:198:LEU:HD11	7:G:235:ARG:C	2.35	0.46
8:H:95:ARG:HB3	8:H:109:LEU:HD12	1.98	0.46
9:I:15:CYS:CB	9:I:33:ILE:HD12	2.42	0.46
5:E:92:GLU:HB2	5:E:93:PHE:H	1.52	0.46
9:I:70:ILE:N	9:I:70:ILE:CD1	2.76	0.46
6:F:144:LEU:HD21	6:F:146:VAL:HG22	1.96	0.46
1:A:224:ALA:HB3	1:A:233:THR:N	2.30	0.46
4:D:74:ALA:HA	4:D:114:THR:O	2.16	0.46
7:G:116:VAL:HG22	7:G:233:ASN:HB3	1.97	0.46
2:B:147:ASP:C	2:B:149:GLY:N	2.61	0.46
2:B:54:PRO:O	8:H:103:ARG:HA	2.15	0.46
3:C:84:ASP:OD1	3:C:85:LEU:N	2.49	0.46
9:I:90:VAL:N	9:I:94:PRO:CG	2.76	0.46
1:A:70:ARG:HB3	1:A:73:GLU:OE2	2.16	0.46
8:H:50:GLU:C	8:H:51:LYS:HD2	2.36	0.46
8:H:171:LEU:H	8:H:171:LEU:HD23	1.81	0.46
4:D:197:THR:HG21	4:D:201:TYR:CE2	2.51	0.46
6:F:133:ALA:HB2	6:F:180:VAL:CG2	2.46	0.46
6:F:248:CYS:O	6:F:252:TYR:HB2	2.15	0.46
4:D:112:PRO:CD	4:D:113:ARG:HH21	2.28	0.46
4:D:125:ASP:O	4:D:126:ALA:CB	2.63	0.46
4:D:138:CYS:SG	4:D:139:MET:CE	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:170:THR:HG22	4:D:171:SER:N	2.31	0.46
7:G:153:ARG:C	7:G:155:ASN:H	2.18	0.46
7:G:260:THR:O	7:G:261:SER:C	2.53	0.46
8:H:174:VAL:HG23	8:H:178:LEU:HD12	1.97	0.46
6:F:240:ALA:O	6:F:244:GLY:N	2.49	0.46
2:B:17:ARG:O	2:B:20:GLU:HG2	2.15	0.46
9:I:16:ASN:HB3	9:I:32:TYR:HA	1.98	0.46
2:B:70:LEU:CD2	2:B:71:VAL:H	2.29	0.46
8:H:272:LEU:CD1	8:H:274:PRO:HD2	2.46	0.46
3:C:107:GLN:O	3:C:111:ASP:N	2.41	0.46
3:C:88:LEU:HD12	6:F:65:ALA:CB	2.42	0.46
4:D:91:GLU:O	4:D:92:LYS:C	2.54	0.46
6:F:220:ASN:O	6:F:220:ASN:OD1	2.33	0.46
1:A:199:PHE:CD1	1:A:199:PHE:N	2.83	0.46
1:A:249:ARG:CA	1:A:249:ARG:NH1	2.78	0.46
2:B:188:LEU:HD11	2:B:193:GLY:HA2	1.98	0.46
2:B:200:MET:SD	2:B:200:MET:C	2.94	0.46
7:G:110:PRO:HB2	7:G:166:PHE:CZ	2.51	0.46
8:H:140:LEU:HD13	8:H:204:TRP:NE1	2.30	0.46
5:E:55:HIS:O	5:E:143:GLU:HG2	2.16	0.46
1:A:176:THR:O	1:A:180:ARG:CZ	2.64	0.46
5:E:119:VAL:O	5:E:121:LEU:N	2.48	0.46
2:B:27:ARG:N	2:B:39:TYR:O	2.48	0.46
3:C:228:GLU:CD	3:C:228:GLU:H	2.19	0.46
6:F:61:LYS:CB	6:F:151:LEU:HD12	2.46	0.46
6:F:253:PRO:O	6:F:256:GLN:HG2	2.16	0.46
1:A:212:ARG:CA	1:A:215:ARG:HH11	2.25	0.46
1:A:270:GLU:C	1:A:274:LYS:HZ3	2.20	0.46
2:B:106:PHE:O	2:B:109:ALA:O	2.34	0.46
2:B:111:LEU:O	2:B:113:GLN:N	2.49	0.46
2:B:189:LEU:CD2	2:B:189:LEU:N	2.76	0.46
7:G:240:ALA:O	7:G:241:LYS:C	2.54	0.46
7:G:222:LYS:HZ1	7:G:268:PHE:CA	2.29	0.46
8:H:88:ILE:HD11	8:H:141:ILE:HD11	1.97	0.46
5:E:114:ASN:ND2	5:E:114:ASN:C	2.69	0.46
5:E:86:SER:HB2	5:E:140:LEU:CD1	2.46	0.46
8:H:273:LYS:O	8:H:277:MET:HB2	2.16	0.46
7:G:28:LEU:HB3	7:G:29:PRO:HD2	1.97	0.46
8:H:182:GLN:HA	8:H:185:HIS:HB3	1.97	0.46
1:A:296:PHE:HE2	1:A:298:MET:SD	2.38	0.46
4:D:157:CYS:HA	4:D:166:VAL:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:247:LEU:HG	5:E:248:ASP:H	1.81	0.46
3:C:109:ILE:CG2	3:C:156:LEU:HD22	2.45	0.46
3:C:201:PHE:HE1	3:C:207:ILE:HD11	1.81	0.46
6:F:149:LEU:CD2	6:F:151:LEU:HD23	2.45	0.46
3:C:55:ASN:ND2	6:F:47:SER:OG	2.49	0.46
1:A:23:ARG:NH2	1:A:27:ARG:NH1	2.63	0.46
1:A:249:ARG:O	1:A:252:LYS:CB	2.55	0.46
2:B:96:CYS:O	2:B:97:GLU:C	2.54	0.46
7:G:219:GLU:OE2	7:G:265:LYS:HA	2.16	0.46
5:E:228:VAL:HA	5:E:239:MET:HB2	1.97	0.46
5:E:253:PHE:HA	5:E:256:MET:HB3	1.98	0.46
5:E:232:SER:HA	5:E:267:HIS:CE1	2.51	0.46
6:F:100:PHE:HB2	6:F:123:ALA:CA	2.46	0.46
8:H:149:PHE:C	8:H:151:ASP:H	2.19	0.46
5:E:164:ARG:O	5:E:165:ILE:C	2.53	0.46
3:C:101:GLU:HB2	4:D:96:ARG:NH2	2.31	0.45
3:C:79:VAL:HA	3:C:135:LEU:HB2	1.98	0.45
3:C:47:GLY:O	3:C:62:VAL:HB	2.15	0.45
6:F:252:TYR:O	6:F:255:LEU:HG	2.16	0.45
1:A:104:ARG:HH12	1:A:107:GLU:C	2.19	0.45
7:G:139:SER:H	7:G:176:GLU:HA	1.80	0.45
9:I:74:LYS:O	9:I:86:HIS:HB2	2.16	0.45
5:E:240:ARG:CG	6:F:225:LEU:O	2.64	0.45
6:F:125:ALA:HB1	6:F:226:LEU:HD21	1.98	0.45
5:E:216:LEU:O	5:E:217:GLN:C	2.54	0.45
1:A:183:VAL:N	1:A:184:PRO:CD	2.80	0.45
5:E:141:LEU:C	5:E:142:LEU:HD23	2.36	0.45
5:E:119:VAL:HG23	5:E:121:LEU:HG	1.99	0.45
6:F:56:GLU:HA	6:F:60:THR:O	2.16	0.45
1:A:113:SER:O	1:A:115:CYS:N	2.49	0.45
1:A:140:ASN:HD21	4:D:39:SER:H	1.63	0.45
1:A:243:LEU:O	1:A:246:GLN:N	2.50	0.45
4:D:141:LEU:CD1	4:D:146:VAL:HB	2.31	0.45
5:E:273:VAL:CA	5:E:276:LYS:HZ3	2.28	0.45
1:A:74:GLY:CA	1:A:121:LEU:HD11	2.43	0.45
1:A:78:PHE:CD1	1:A:79:ASN:N	2.84	0.45
6:F:199:PRO:CG	6:F:204:GLU:HB2	2.46	0.45
2:B:49:ALA:HB1	2:B:124:VAL:HG22	1.98	0.45
5:E:77:GLY:O	5:E:121:LEU:HD23	2.15	0.45
8:H:247:GLN:HG2	8:H:281:VAL:CG2	2.43	0.45
3:C:267:ASP:HA	3:C:270:ILE:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:89:CYS:HA	3:C:142:LEU:O	2.16	0.45
3:C:89:CYS:HA	3:C:143:ASP:HA	1.98	0.45
1:A:264:LEU:HD13	1:A:264:LEU:HA	1.60	0.45
1:A:263:GLU:HA	1:A:266:LEU:HD12	1.97	0.45
9:I:74:LYS:NZ	9:I:125:GLY:HA2	2.31	0.45
7:G:260:THR:N	7:G:263:GLN:HB2	2.31	0.45
5:E:23:ARG:HH21	5:E:214:ALA:HB2	1.81	0.45
5:E:9:ALA:O	8:H:168:GLN:N	2.50	0.45
6:F:31:ARG:NH2	6:F:35:ARG:HE	2.12	0.45
5:E:74:PRO:O	5:E:132:CYS:SG	2.74	0.45
3:C:94:ARG:NH1	3:C:100:GLU:N	2.55	0.45
4:D:99:ARG:HH11	4:D:99:ARG:HG3	1.81	0.45
6:F:248:CYS:SG	6:F:249:GLN:N	2.89	0.45
6:F:179:LEU:HD12	6:F:252:TYR:HE1	1.81	0.45
1:A:12:ARG:CD	1:A:13:PHE:N	2.78	0.45
2:B:189:LEU:CD2	2:B:194:GLN:O	2.65	0.45
4:D:112:PRO:CG	4:D:113:ARG:HH21	2.28	0.45
1:A:141:HIS:O	4:D:40:ARG:HD3	2.16	0.45
5:E:60:VAL:HA	5:E:138:ASP:O	2.15	0.45
8:H:244:LEU:HD11	8:H:259:CYS:SG	2.56	0.45
8:H:94:LYS:O	8:H:109:LEU:CG	2.58	0.45
5:E:260:LYS:HD3	6:F:234:THR:HB	1.99	0.45
1:A:66:PRO:HB3	1:A:129:VAL:HG11	1.98	0.45
9:I:13:ARG:CB	9:I:33:ILE:O	2.64	0.45
5:E:66:MET:HB3	5:E:126:ILE:CD1	2.46	0.45
8:H:261:GLU:HB3	8:H:287:ARG:NH1	2.32	0.45
3:C:264:LYS:O	3:C:268:GLU:HG2	2.17	0.45
3:C:66:PHE:CD1	3:C:66:PHE:N	2.79	0.45
4:D:186:ASP:HA	4:D:193:LEU:CD1	2.38	0.45
4:D:186:ASP:HB3	4:D:191:LYS:N	2.32	0.45
9:I:26:THR:N	9:I:36:SER:OG	2.49	0.45
1:A:145:ILE:CD1	1:A:145:ILE:N	2.59	0.45
1:A:234:ILE:HG13	2:B:200:MET:HB3	1.99	0.45
4:D:111:HIS:ND1	4:D:112:PRO:O	2.50	0.45
5:E:226:LEU:HD11	5:E:239:MET:CE	2.46	0.45
5:E:235:VAL:HG12	5:E:236:VAL:H	1.82	0.45
5:E:235:VAL:HG12	5:E:236:VAL:N	2.31	0.45
8:H:61:GLU:CG	8:H:70:LYS:HG2	2.45	0.45
6:F:100:PHE:HB2	6:F:123:ALA:HA	1.98	0.45
9:I:6:ARG:CD	9:I:6:ARG:N	2.79	0.45
1:A:429:UNK:O	1:A:430:UNK:C	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:107:GLN:O	3:C:108:PHE:C	2.52	0.45
3:C:39:ILE:HG13	3:C:269:VAL:HG11	1.96	0.45
3:C:269:VAL:HG12	3:C:269:VAL:O	2.15	0.45
3:C:49:ALA:CB	3:C:158:ALA:HB3	2.47	0.45
3:C:90:SER:HB2	3:C:92:ARG:CG	2.45	0.45
6:F:169:LEU:C	6:F:174:VAL:HG22	2.37	0.45
5:E:109:LEU:HD21	5:E:156:VAL:CG2	2.47	0.45
4:D:158:ALA:HB1	4:D:177:ALA:CB	2.46	0.45
1:A:70:ARG:H	1:A:70:ARG:HG3	1.51	0.45
4:D:225:ARG:HH21	7:G:28:LEU:HD21	1.80	0.45
9:I:21:SER:O	9:I:52:VAL:HG22	2.17	0.45
6:F:157:ALA:HA	6:F:160:ALA:HB3	1.99	0.45
6:F:248:CYS:O	6:F:252:TYR:N	2.42	0.45
1:A:35:ILE:HD12	1:A:37:ILE:HD11	1.98	0.45
1:A:241:MET:HG2	2:B:194:GLN:HE22	1.81	0.45
7:G:230:PHE:HE2	7:G:236:ILE:HG23	1.81	0.45
5:E:203:LEU:HD22	5:E:255:MET:CB	2.46	0.45
5:E:101:LEU:CD1	5:E:102:GLY:N	2.78	0.45
5:E:153:SER:C	5:E:156:VAL:HG12	2.35	0.45
5:E:270:LEU:C	5:E:272:SER:N	2.69	0.45
1:A:68:LEU:O	1:A:69:ASN:O	2.35	0.45
8:H:53:ILE:CG2	8:H:54:ALA:H	2.30	0.45
5:E:167:ARG:O	5:E:169:ARG:NH1	2.49	0.45
8:H:247:GLN:CG	8:H:281:VAL:HG21	2.44	0.45
7:G:181:ASP:HB3	7:G:186:ALA:H	1.82	0.45
8:H:41:ARG:H	8:H:41:ARG:HG3	1.62	0.45
2:B:229:ARG:O	2:B:230:VAL:C	2.54	0.45
1:A:421:UNK:HG2	1:A:422:UNK:N	2.31	0.45
3:C:23:ARG:O	3:C:25:ASP:N	2.49	0.45
3:C:237:LYS:HG2	4:D:194:MET:HA	1.98	0.45
6:F:251:LEU:HD22	6:F:254:VAL:HB	1.98	0.45
6:F:66:VAL:HG23	6:F:168:ALA:HB1	1.99	0.45
1:A:101:LYS:O	1:A:105:LEU:CB	2.65	0.45
2:B:103:ARG:O	2:B:104:GLN:C	2.54	0.45
4:D:73:LYS:H	4:D:112:PRO:CA	2.28	0.45
4:D:37:LEU:H	4:D:44:SER:HB2	1.82	0.45
4:D:58:VAL:HA	4:D:117:THR:O	2.16	0.45
7:G:144:SER:CB	7:G:178:VAL:HG13	2.47	0.45
7:G:260:THR:CG2	7:G:262:ASP:HB3	2.45	0.45
5:E:112:ILE:HG23	5:E:237:THR:CG2	2.46	0.45
1:A:60:SER:OG	1:A:133:ARG:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:252:ILE:HG21	6:F:241:VAL:HG11	1.99	0.45
8:H:283:GLU:HA	8:H:286:GLN:HB2	1.99	0.45
1:A:72:THR:HA	1:A:125:ALA:HB1	1.99	0.45
9:I:70:ILE:CG1	9:I:131:LYS:HG3	2.45	0.45
8:H:111:SER:CB	8:H:157:HIS:NE2	2.79	0.45
1:A:429:UNK:HG2	3:C:249:GLN:CB	2.31	0.45
3:C:18:LEU:O	3:C:21:ASN:N	2.50	0.45
3:C:237:LYS:HZ2	4:D:192:LEU:HD23	1.81	0.45
3:C:271:LYS:O	3:C:271:LYS:HG2	2.17	0.45
3:C:99:GLY:O	3:C:102:ALA:HB3	2.17	0.45
4:D:156:ALA:O	4:D:169:PRO:HD3	2.17	0.45
1:A:140:ASN:HD22	4:D:38:LEU:HA	1.82	0.45
5:E:65:GLU:HB2	5:E:134:VAL:HB	1.99	0.45
7:G:123:LYS:HB2	7:G:128:PHE:CD2	2.52	0.45
7:G:85:LEU:HD12	7:G:86:ARG:N	2.32	0.45
9:I:73:CYS:HB3	9:I:87:ILE:CA	2.43	0.45
8:H:87:ARG:HA	8:H:139:ASP:O	2.17	0.45
5:E:270:LEU:O	5:E:272:SER:N	2.49	0.45
1:A:74:GLY:HA3	1:A:121:LEU:CD1	2.45	0.45
2:B:120:ILE:N	2:B:120:ILE:HD12	2.32	0.45
3:C:166:PRO:HB2	3:C:181:LEU:HD12	1.99	0.45
9:I:16:ASN:C	9:I:18:GLU:H	2.20	0.45
9:I:70:ILE:CD1	9:I:131:LYS:HG3	2.46	0.45
9:I:170:CYS:C	9:I:171:GLU:HG3	2.37	0.45
3:C:147:ASN:O	3:C:147:ASN:ND2	2.50	0.45
3:C:209:ASP:N	3:C:210:PRO:CD	2.79	0.45
3:C:232:LEU:HD13	4:D:202:SER:C	2.37	0.45
3:C:49:ALA:HB1	3:C:158:ALA:HB3	1.99	0.45
3:C:56:THR:CG2	3:C:145:ASP:N	2.80	0.45
4:D:192:LEU:O	4:D:192:LEU:CD2	2.62	0.45
6:F:255:LEU:HD12	6:F:256:GLN:CA	2.44	0.45
1:A:101:LYS:CD	1:A:105:LEU:HD22	2.47	0.45
7:G:112:LYS:HB3	7:G:113:GLY:H	1.59	0.45
7:G:270:ARG:HD3	7:G:270:ARG:HA	1.78	0.45
8:H:172:VAL:N	8:H:203:ILE:O	2.50	0.45
8:H:233:VAL:O	8:H:236:ARG:HG2	2.17	0.45
8:H:260:TYR:O	8:H:263:SER:HB2	2.17	0.45
6:F:158:LEU:HD13	6:F:212:THR:HB	1.98	0.45
9:I:16:ASN:N	9:I:16:ASN:HD22	2.15	0.45
2:B:121:ASP:HB2	2:B:123:TYR:CE2	2.50	0.45
3:C:199:ALA:O	3:C:207:ILE:N	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:17:PHE:CZ	3:C:24:PRO:HB3	2.53	0.44
1:A:223:ILE:HG23	1:A:224:ALA:N	2.31	0.44
1:A:224:ALA:N	1:A:233:THR:O	2.50	0.44
1:A:234:ILE:CG1	2:B:200:MET:HB3	2.47	0.44
4:D:139:MET:SD	4:D:142:VAL:HG21	2.57	0.44
7:G:153:ARG:HB3	7:G:154:PRO:HD3	1.96	0.44
6:F:96:LEU:N	6:F:96:LEU:HD23	2.18	0.44
8:H:172:VAL:HG12	8:H:174:VAL:CG1	2.47	0.44
8:H:198:GLY:C	8:H:200:ASN:N	2.70	0.44
8:H:76:TYR:HB2	8:H:101:ASN:O	2.17	0.44
8:H:83:ILE:HG12	8:H:199:ASN:ND2	2.32	0.44
5:E:215:THR:OG1	5:E:218:GLU:HG3	2.16	0.44
5:E:249:PRO:HA	5:E:252:ILE:HB	1.98	0.44
5:E:99:ASP:O	5:E:100:ASP:O	2.34	0.44
3:C:133:TRP:CH2	3:C:165:LEU:HD13	2.52	0.44
3:C:60:CYS:CB	3:C:155:ALA:O	2.65	0.44
3:C:7:THR:N	3:C:10:PRO:HG3	2.32	0.44
6:F:126:LEU:HD23	6:F:162:LEU:HD23	1.98	0.44
1:A:270:GLU:HA	1:A:270:GLU:OE2	2.16	0.44
2:B:98:MET:O	2:B:102:LEU:HD23	2.16	0.44
2:B:46:LYS:CD	2:B:128:GLN:HB3	2.43	0.44
2:B:111:LEU:CD1	2:B:153:ARG:HG3	2.46	0.44
4:D:141:LEU:HA	4:D:144:ALA:HB3	1.98	0.44
4:D:48:LEU:N	4:D:48:LEU:CD1	2.79	0.44
7:G:242:THR:O	7:G:243:ILE:C	2.54	0.44
7:G:126:ASP:O	7:G:142:TYR:N	2.50	0.44
9:I:126:ASP:OD1	9:I:183:ARG:NH1	2.50	0.44
5:E:230:VAL:HA	5:E:235:VAL:O	2.17	0.44
6:F:185:LEU:HD13	6:F:240:ALA:HB1	1.98	0.44
3:C:60:CYS:SG	3:C:156:LEU:HA	2.57	0.44
3:C:157:LEU:HD12	3:C:194:VAL:HG13	1.99	0.44
3:C:261:GLU:O	3:C:265:LEU:HG	2.16	0.44
6:F:110:ARG:HH11	6:F:112:ALA:HB2	1.79	0.44
1:A:100:VAL:CG1	1:A:101:LYS:N	2.67	0.44
1:A:249:ARG:N	1:A:249:ARG:NH1	2.65	0.44
1:A:252:LYS:O	1:A:255:GLY:N	2.50	0.44
4:D:126:ALA:O	4:D:171:SER:N	2.46	0.44
7:G:244:GLN:C	7:G:246:THR:N	2.70	0.44
7:G:161:LEU:O	7:G:162:ILE:HG13	2.18	0.44
9:I:86:HIS:CD2	9:I:101:GLY:HA3	2.52	0.44
6:F:114:PRO:O	6:F:116:GLY:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:32:PHE:CZ	3:C:258:ARG:HB3	2.53	0.44
6:F:150:LEU:CD1	6:F:157:ALA:HB1	2.41	0.44
2:B:156:VAL:HG22	2:B:189:LEU:HA	1.99	0.44
2:B:209:LEU:O	2:B:211:ARG:N	2.51	0.44
7:G:118:GLY:HA2	7:G:119:ILE:HD12	1.98	0.44
7:G:157:GLN:NE2	7:G:157:GLN:CA	2.77	0.44
9:I:135:LEU:HD23	9:I:135:LEU:N	2.33	0.44
7:G:263:GLN:O	7:G:264:ARG:C	2.55	0.44
5:E:10:GLU:OE2	8:H:87:ARG:NH2	2.50	0.44
5:E:58:ILE:O	5:E:59:LEU:HD12	2.18	0.44
1:A:61:CYS:SG	1:A:163:PRO:HD2	2.56	0.44
5:E:126:ILE:HG22	5:E:127:SER:N	2.33	0.44
5:E:67:GLY:HA2	5:E:131:HIS:HA	2.00	0.44
3:C:206:LEU:CD2	3:C:247:LYS:NZ	2.81	0.44
1:A:195:SER:HB3	1:A:220:LEU:HD21	1.99	0.44
1:A:257:LYS:C	1:A:259:ALA:N	2.68	0.44
1:A:33:ARG:NH1	1:A:210:ASN:HA	2.32	0.44
1:A:235:GLN:CA	2:B:199:GLU:OE2	2.66	0.44
2:B:22:ARG:O	2:B:23:LYS:C	2.56	0.44
4:D:107:LEU:HD22	4:D:147:PRO:CB	2.47	0.44
7:G:152:ASN:HB2	7:G:155:ASN:O	2.17	0.44
7:G:190:GLY:O	7:G:192:ILE:N	2.45	0.44
7:G:199:PHE:N	7:G:199:PHE:HD2	2.14	0.44
7:G:216:ILE:O	7:G:220:VAL:HG23	2.18	0.44
7:G:260:THR:C	7:G:262:ASP:H	2.20	0.44
8:H:108:LEU:O	8:H:108:LEU:HG	2.17	0.44
8:H:172:VAL:HB	8:H:203:ILE:HD13	2.00	0.44
2:B:31:PHE:HB3	5:E:143:GLU:OE1	2.17	0.44
5:E:237:THR:C	6:F:229:GLY:HA3	2.38	0.44
5:E:253:PHE:CE2	6:F:241:VAL:HB	2.53	0.44
2:B:57:ILE:HG13	2:B:117:ARG:O	2.18	0.44
5:E:69:PRO:O	5:E:70:LYS:HB2	2.17	0.44
3:C:198:PHE:CD1	3:C:198:PHE:N	2.84	0.44
3:C:80:VAL:O	3:C:136:TYR:HA	2.18	0.44
3:C:147:ASN:C	3:C:149:LEU:H	2.21	0.44
3:C:270:ILE:O	3:C:275:PRO:HD3	2.17	0.44
3:C:30:GLY:HA2	3:C:208:VAL:HB	1.98	0.44
6:F:55:LEU:HD11	6:F:163:THR:CB	2.48	0.44
2:B:75:TYR:HE1	2:B:126:VAL:HG23	1.82	0.44
7:G:119:ILE:N	7:G:130:VAL:HG23	2.32	0.44
7:G:33:LEU:O	7:G:77:LEU:HB2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:135:LEU:HD23	9:I:135:LEU:H	1.81	0.44
5:E:8:GLU:HG2	5:E:9:ALA:H	1.82	0.44
2:B:120:ILE:HG22	2:B:122:ILE:HD11	2.00	0.44
5:E:195:GLU:HB3	5:E:232:SER:HB3	2.00	0.44
5:E:167:ARG:HB3	5:E:187:TYR:O	2.17	0.44
8:H:185:HIS:CG	8:H:186:PHE:H	2.34	0.44
8:H:274:PRO:HB2	8:H:275:GLU:OE1	2.18	0.44
1:A:448:UNK:O	1:A:449:UNK:C	2.64	0.44
3:C:94:ARG:NH1	3:C:99:GLY:CA	2.73	0.44
3:C:99:GLY:H	3:C:102:ALA:HB3	1.83	0.44
4:D:94:ARG:NH1	4:D:130:LEU:HD21	2.32	0.44
6:F:251:LEU:O	6:F:253:PRO:N	2.51	0.44
9:I:55:VAL:HG12	9:I:56:VAL:N	2.33	0.44
1:A:96:SER:O	1:A:97:ASP:C	2.56	0.44
4:D:80:LEU:HB2	4:D:120:LEU:HB2	1.98	0.44
7:G:170:ASN:ND2	7:G:173:MET:CE	2.81	0.44
2:B:138:VAL:O	2:B:142:THR:OG1	2.32	0.44
3:C:206:LEU:HD22	3:C:247:LYS:CE	2.47	0.44
3:C:260:LYS:HB3	3:C:264:LYS:NZ	2.33	0.44
3:C:37:VAL:HG23	3:C:269:VAL:HG21	2.00	0.44
6:F:53:ALA:HB3	6:F:64:CYS:HB2	1.99	0.44
2:B:161:ALA:HB2	2:B:216:ALA:N	2.33	0.44
2:B:76:SER:O	2:B:125:GLN:OE1	2.35	0.44
5:E:65:GLU:HA	5:E:65:GLU:OE2	2.18	0.44
9:I:75:VAL:CG1	9:I:76:SER:N	2.81	0.44
6:F:138:ARG:HD2	6:F:175:GLU:CG	2.47	0.44
5:E:101:LEU:O	5:E:105:ILE:HG13	2.18	0.44
5:E:238:CYS:HA	6:F:229:GLY:N	2.32	0.44
5:E:53:LEU:HB2	5:E:56:THR:HG23	1.99	0.44
1:A:75:ILE:CG2	1:A:76:LEU:H	2.27	0.44
5:E:90:THR:OG1	5:E:93:PHE:HB2	2.17	0.44
6:F:100:PHE:N	6:F:123:ALA:HB2	2.33	0.44
4:D:227:SER:O	4:D:230:ARG:N	2.51	0.44
4:D:230:ARG:O	4:D:233:SER:OG	2.35	0.44
3:C:198:PHE:N	3:C:198:PHE:HD1	2.15	0.44
3:C:244:THR:HG22	3:C:246:ALA:N	2.32	0.44
3:C:260:LYS:CA	3:C:260:LYS:HE3	2.47	0.44
9:I:40:CYS:O	9:I:55:VAL:CG1	2.65	0.44
1:A:85:MET:HE2	4:D:57:GLY:HA3	2.00	0.44
2:B:162:GLY:HA3	2:B:172:LEU:HD21	1.99	0.44
4:D:119:VAL:C	4:D:120:LEU:HD12	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:132:VAL:O	7:G:132:VAL:CG1	2.65	0.44
9:I:127:ILE:H	9:I:155:VAL:CG2	2.31	0.44
5:E:202:THR:O	5:E:212:VAL:HG13	2.18	0.44
8:H:96:TRP:HZ2	8:H:134:PHE:HD1	1.66	0.44
8:H:132:ARG:HG3	8:H:132:ARG:HH11	1.82	0.44
8:H:27:VAL:HG22	8:H:60:VAL:CG2	2.48	0.44
7:G:200:LYS:O	7:G:201:VAL:HG13	2.18	0.44
3:C:147:ASN:ND2	3:C:197:SER:OG	2.50	0.43
3:C:21:ASN:O	3:C:22:CYS:HB3	2.17	0.43
3:C:262:VAL:HA	3:C:265:LEU:HB2	2.00	0.43
4:D:201:TYR:CD1	4:D:201:TYR:C	2.90	0.43
6:F:251:LEU:O	6:F:252:TYR:C	2.56	0.43
9:I:10:PRO:HB3	9:I:37:LEU:O	2.18	0.43
2:B:104:GLN:NE2	2:B:197:LEU:HD23	2.33	0.43
7:G:117:ILE:HB	7:G:235:ARG:HG3	1.99	0.43
7:G:141:SER:C	7:G:143:LEU:N	2.71	0.43
7:G:153:ARG:C	7:G:155:ASN:N	2.70	0.43
7:G:226:LEU:HD11	7:G:228:ILE:HG13	1.99	0.43
9:I:158:SER:OG	9:I:159:GLU:N	2.51	0.43
9:I:67:VAL:O	9:I:132:VAL:HB	2.18	0.43
5:E:258:THR:OG1	5:E:261:ARG:NH2	2.51	0.43
8:H:197:LEU:HA	8:H:203:ILE:HA	1.99	0.43
5:E:154:ILE:O	5:E:157:LYS:HG3	2.18	0.43
8:H:73:LYS:HE3	8:H:73:LYS:HB2	1.69	0.43
9:I:13:ARG:HA	9:I:33:ILE:O	2.17	0.43
1:A:30:TYR:N	1:A:30:TYR:CD1	2.86	0.43
8:H:275:GLU:N	8:H:275:GLU:OE1	2.51	0.43
8:H:226:VAL:HG12	8:H:230:ASP:HB2	2.00	0.43
2:B:164:VAL:HG12	2:B:165:ASP:N	2.33	0.43
1:A:421:UNK:C	1:A:425:UNK:HG3	2.46	0.43
3:C:200:VAL:HG12	3:C:201:PHE:H	1.78	0.43
4:D:189:GLU:O	4:D:191:LYS:N	2.50	0.43
6:F:64:CYS:HA	6:F:147:SER:O	2.19	0.43
6:F:149:LEU:C	6:F:149:LEU:CD2	2.83	0.43
4:D:141:LEU:HD13	4:D:141:LEU:HA	1.83	0.43
4:D:76:LEU:HD11	4:D:118:VAL:HG23	2.00	0.43
7:G:242:THR:CG2	7:G:244:GLN:HB2	2.49	0.43
9:I:132:VAL:HG22	9:I:144:LEU:HD22	1.99	0.43
8:H:141:ILE:CD1	8:H:141:ILE:N	2.79	0.43
8:H:96:TRP:CG	8:H:135:LEU:HD22	2.53	0.43
7:G:205:LEU:O	7:G:206:ILE:C	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:181:LEU:HB3	3:C:182:LYS:H	1.45	0.43
3:C:227:ASP:HB3	3:C:231:LYS:HB2	1.99	0.43
3:C:244:THR:HB	3:C:247:LYS:H	1.84	0.43
3:C:23:ARG:NH2	3:C:27:ARG:CZ	2.81	0.43
3:C:86:PRO:CB	3:C:87:PRO:HD2	2.37	0.43
6:F:144:LEU:HG	6:F:145:GLU:N	2.32	0.43
1:A:271:ASN:N	1:A:274:LYS:NZ	2.67	0.43
7:G:245:GLN:NE2	7:G:245:GLN:N	2.67	0.43
7:G:165:GLN:HG2	7:G:189:MET:SD	2.59	0.43
7:G:31:GLU:HB2	7:G:79:VAL:CG2	2.48	0.43
9:I:133:ILE:HD11	9:I:144:LEU:O	2.18	0.43
8:H:244:LEU:HA	8:H:244:LEU:HD23	1.85	0.43
2:B:222:ASP:C	2:B:224:HIS:N	2.68	0.43
7:G:115:HIS:HD1	7:G:115:HIS:N	2.16	0.43
3:C:103:GLN:O	3:C:106:SER:N	2.52	0.43
3:C:78:TYR:CD2	3:C:134:VAL:HG22	2.54	0.43
3:C:118:ILE:O	3:C:189:ILE:HB	2.17	0.43
1:A:109:CYS:CA	1:A:112:ASN:HB2	2.44	0.43
1:A:20:GLU:HB3	1:A:22:LYS:HG3	2.00	0.43
2:B:111:LEU:HD11	2:B:153:ARG:H	1.76	0.43
4:D:82:PRO:HG2	4:D:84:ILE:O	2.19	0.43
7:G:162:ILE:HD12	7:G:162:ILE:N	2.34	0.43
9:I:85:VAL:CG2	9:I:103:ILE:HB	2.44	0.43
9:I:104:ARG:N	9:I:104:ARG:HD2	2.32	0.43
9:I:129:LEU:HG	9:I:129:LEU:O	2.18	0.43
5:E:105:ILE:HG12	5:E:149:PHE:CE1	2.54	0.43
5:E:118:SER:HB2	5:E:196:ASN:C	2.39	0.43
1:A:176:THR:HB	1:A:180:ARG:CZ	2.48	0.43
6:F:187:LEU:HD12	6:F:187:LEU:N	2.33	0.43
8:H:277:MET:HA	8:H:280:ILE:CG1	2.49	0.43
2:B:72:ASN:O	2:B:121:ASP:HA	2.19	0.43
1:A:444:UNK:O	1:A:447:UNK:HG3	2.18	0.43
3:C:222:LEU:HD23	3:C:222:LEU:C	2.39	0.43
3:C:227:ASP:CB	3:C:231:LYS:HB2	2.48	0.43
3:C:221:THR:O	3:C:238:PRO:HD2	2.19	0.43
4:D:191:LYS:O	4:D:192:LEU:C	2.57	0.43
4:D:205:GLU:C	4:D:207:GLN:H	2.21	0.43
1:A:80:LEU:HD12	1:A:81:GLU:N	2.34	0.43
2:B:209:LEU:C	2:B:211:ARG:N	2.70	0.43
4:D:83:LYS:HZ3	4:D:125:ASP:H	1.65	0.43
4:D:138:CYS:O	4:D:142:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:43:GLY:HA3	4:D:144:ALA:HB2	2.01	0.43
7:G:86:ARG:CB	7:G:100:TRP:HE3	2.32	0.43
7:G:130:VAL:CG2	7:G:131:ASP:N	2.81	0.43
5:E:205:LYS:HG3	5:E:210:HIS:HB3	2.00	0.43
5:E:261:ARG:HD2	5:E:262:VAL:HG22	2.00	0.43
5:E:27:ARG:HB3	5:E:31:ASP:HB2	2.01	0.43
8:H:165:LYS:HE2	8:H:219:PHE:CE1	2.53	0.43
5:E:13:TYR:HE1	8:H:231:ARG:HG3	1.83	0.43
7:G:205:LEU:HD12	7:G:205:LEU:N	2.33	0.43
1:A:66:PRO:HD2	1:A:127:GLU:O	2.18	0.43
6:F:185:LEU:HD11	6:F:243:LEU:CG	2.48	0.43
4:D:160:ASP:OD2	4:D:164:THR:N	2.51	0.43
6:F:119:GLU:OE1	6:F:119:GLU:N	2.51	0.43
3:C:10:PRO:O	3:C:11:LEU:C	2.57	0.43
3:C:39:ILE:HD12	3:C:158:ALA:HB1	2.00	0.43
1:A:81:GLU:OE1	1:A:81:GLU:C	2.57	0.43
4:D:73:LYS:C	4:D:111:HIS:O	2.56	0.43
4:D:79:ILE:HD12	4:D:79:ILE:H	1.83	0.43
7:G:19:ALA:H	7:G:22:VAL:CB	2.29	0.43
9:I:128:VAL:CB	9:I:153:VAL:HG23	2.41	0.43
5:E:116:LYS:NZ	5:E:116:LYS:O	2.39	0.43
1:A:153:ALA:O	1:A:157:LEU:HD23	2.19	0.43
6:F:264:ARG:HA	9:I:7:TYR:CE2	2.52	0.43
6:F:207:ALA:HB1	6:F:209:ALA:O	2.18	0.43
3:C:151:ALA:O	3:C:155:ALA:HB2	2.19	0.43
1:A:429:UNK:CG	3:C:249:GLN:HB3	2.33	0.43
3:C:48:SER:N	3:C:162:ASN:ND2	2.39	0.43
3:C:59:ILE:HD11	3:C:142:LEU:CD2	2.47	0.43
1:A:33:ARG:NH2	1:A:50:LEU:HD13	2.33	0.43
2:B:100:LEU:O	2:B:103:ARG:N	2.52	0.43
2:B:174:HIS:O	2:B:177:GLU:HB2	2.19	0.43
2:B:181:GLY:N	2:B:182:PRO:HD2	2.33	0.43
5:E:201:VAL:N	5:E:228:VAL:O	2.45	0.43
8:H:145:VAL:HG22	8:H:156:LEU:CD2	2.49	0.43
8:H:76:TYR:CE1	8:H:84:VAL:HG21	2.54	0.43
1:A:24:LEU:O	1:A:26:GLY:N	2.52	0.43
8:H:226:VAL:HG12	8:H:227:SER:N	2.34	0.43
3:C:152:CYS:O	3:C:153:THR:C	2.57	0.43
1:A:225:MET:SD	1:A:255:GLY:N	2.91	0.43
2:B:189:LEU:O	2:B:191:ALA:N	2.51	0.43
1:A:248:LEU:CD1	2:B:209:LEU:HD23	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:138:ALA:HA	7:G:175:PRO:O	2.19	0.43
7:G:21:THR:C	7:G:23:LEU:N	2.70	0.43
7:G:26:VAL:HG22	7:G:84:ARG:HB2	2.01	0.43
8:H:102:SER:HB2	8:H:104:LEU:CD2	2.49	0.43
1:A:162:ARG:NH1	1:A:162:ARG:CG	2.81	0.43
1:A:182:PRO:O	1:A:183:VAL:CG1	2.56	0.43
6:F:197:LEU:HD13	6:F:243:LEU:CD2	2.48	0.43
2:B:54:PRO:HA	2:B:120:ILE:CD1	2.48	0.43
8:H:185:HIS:C	8:H:186:PHE:CD1	2.92	0.43
7:G:17:ARG:HG2	7:G:17:ARG:HH11	1.84	0.43
6:F:216:MET:O	6:F:220:ASN:HA	2.18	0.43
6:F:252:TYR:N	6:F:253:PRO:CD	2.82	0.43
1:A:145:ILE:O	1:A:148:ALA:N	2.52	0.43
4:D:173:GLN:NE2	4:D:173:GLN:CA	2.81	0.43
5:E:9:ALA:O	5:E:12:VAL:CG1	2.64	0.43
5:E:270:LEU:HA	5:E:273:VAL:HG23	2.00	0.43
1:A:64:VAL:CG2	1:A:131:GLN:HB2	2.49	0.43
2:B:7:SER:CB	2:B:12:ARG:HA	2.29	0.43
5:E:139:VAL:CG1	5:E:140:LEU:N	2.81	0.43
2:B:222:ASP:O	2:B:224:HIS:N	2.52	0.43
9:I:95:LEU:O	9:I:97:ASN:ND2	2.51	0.43
3:C:117:GLN:O	3:C:118:ILE:C	2.57	0.43
3:C:138:ASP:C	3:C:139:LEU:HD12	2.39	0.43
3:C:244:THR:HB	3:C:247:LYS:HB2	1.99	0.43
1:A:158:CYS:HB3	1:A:269:LEU:HD11	2.01	0.43
1:A:144:ASN:CB	1:A:209:PRO:HD2	2.40	0.43
1:A:17:ALA:O	1:A:20:GLU:HB2	2.18	0.43
1:A:33:ARG:NH2	1:A:50:LEU:HD22	2.24	0.43
2:B:106:PHE:C	2:B:108:ALA:N	2.69	0.43
7:G:170:ASN:N	7:G:170:ASN:HD22	2.17	0.43
7:G:178:VAL:HG11	7:G:180:ILE:HG12	2.01	0.43
9:I:83:ALA:HB3	9:I:105:LYS:HG3	1.99	0.43
5:E:11:LYS:HA	5:E:14:ILE:CD1	2.33	0.43
5:E:224:ALA:CB	5:E:243:GLY:HA3	2.48	0.43
8:H:135:LEU:HD12	8:H:135:LEU:N	2.33	0.43
8:H:88:ILE:HG13	8:H:139:ASP:H	1.83	0.43
2:B:138:VAL:HG11	2:B:158:ALA:HB2	2.01	0.43
8:H:33:ILE:CD1	8:H:33:ILE:N	2.81	0.43
2:B:227:LEU:H	2:B:227:LEU:HD23	1.81	0.43
3:C:252:MET:SD	4:D:203:ASP:HB2	2.59	0.42
1:A:20:GLU:HB3	1:A:22:LYS:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:ILE:HG22	1:A:241:MET:H	1.84	0.42
1:A:253:ILE:CA	1:A:256:VAL:HG23	2.48	0.42
1:A:262:THR:O	1:A:265:ILE:N	2.52	0.42
4:D:30:HIS:HB3	4:D:50:GLY:HA2	2.01	0.42
5:E:60:VAL:HG13	5:E:138:ASP:O	2.18	0.42
7:G:235:ARG:C	7:G:236:ILE:HD13	2.40	0.42
9:I:87:ILE:O	9:I:87:ILE:HG13	2.18	0.42
5:E:14:ILE:HG21	5:E:221:CYS:SG	2.59	0.42
5:E:150:ASP:O	5:E:153:SER:OG	2.37	0.42
5:E:273:VAL:O	5:E:277:GLU:OE1	2.36	0.42
2:B:139:ASN:HA	2:B:142:THR:OG1	2.19	0.42
2:B:145:VAL:O	2:B:148:ALA:N	2.51	0.42
5:E:52:LYS:HE3	5:E:54:GLY:O	2.20	0.42
5:E:161:PHE:HD2	5:E:274:VAL:HG11	1.83	0.42
1:A:276:ARG:NH1	1:A:276:ARG:HG3	2.34	0.42
8:H:222:ASN:O	8:H:224:GLU:N	2.52	0.42
3:C:130:LYS:HA	3:C:130:LYS:HE2	1.99	0.42
1:A:422:UNK:O	1:A:425:UNK:HG3	2.19	0.42
6:F:181:VAL:O	6:F:214:ALA:HB1	2.20	0.42
1:A:205:LEU:HD23	1:A:206:LEU:N	2.34	0.42
2:B:22:ARG:HG2	2:B:171:ASP:OD1	2.18	0.42
4:D:56:ALA:HB3	4:D:140:ALA:HB2	2.00	0.42
7:G:141:SER:OG	7:G:144:SER:OG	2.33	0.42
7:G:50:ARG:HB3	7:G:75:ASP:C	2.39	0.42
9:I:162:ILE:CB	9:I:174:CYS:HB2	2.49	0.42
7:G:268:PHE:O	7:G:271:LEU:N	2.52	0.42
8:H:108:LEU:HB3	8:H:156:LEU:HB2	2.00	0.42
8:H:82:ASP:H	8:H:145:VAL:HB	1.83	0.42
5:E:252:ILE:HG23	5:E:253:PHE:N	2.33	0.42
6:F:140:PRO:O	6:F:141:ARG:C	2.58	0.42
2:B:229:ARG:O	2:B:231:VAL:N	2.52	0.42
3:C:112:VAL:O	3:C:113:ILE:C	2.58	0.42
3:C:38:ASN:C	3:C:41:SER:HG	2.21	0.42
4:D:218:GLN:HB2	4:D:222:ARG:NH2	2.34	0.42
1:A:101:LYS:HD3	1:A:235:GLN:HE21	1.84	0.42
1:A:113:SER:O	1:A:114:LYS:C	2.57	0.42
1:A:225:MET:SD	1:A:255:GLY:HA2	2.60	0.42
1:A:240:ILE:CD1	1:A:242:LEU:HD11	2.46	0.42
2:B:207:ASP:C	2:B:209:LEU:H	2.22	0.42
4:D:108:GLY:C	4:D:110:LEU:N	2.70	0.42
4:D:228:LEU:HA	4:D:231:ARG:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:35:LEU:O	7:G:37:GLU:N	2.51	0.42
9:I:85:VAL:O	9:I:103:ILE:CD1	2.68	0.42
9:I:74:LYS:NZ	9:I:126:ASP:O	2.52	0.42
5:E:227:LEU:C	5:E:227:LEU:HD13	2.39	0.42
5:E:30:GLU:OE2	5:E:261:ARG:NH1	2.50	0.42
6:F:213:VAL:HG12	6:F:225:LEU:CA	2.50	0.42
8:H:84:VAL:HA	8:H:198:GLY:HA3	2.01	0.42
5:E:146:GLY:C	5:E:148:LEU:H	2.22	0.42
1:A:122:CYS:SG	1:A:129:VAL:HG23	2.59	0.42
6:F:35:ARG:NH2	6:F:196:LEU:HD21	2.34	0.42
6:F:198:ASP:HA	6:F:199:PRO:HD2	1.89	0.42
9:I:18:GLU:CD	9:I:18:GLU:H	2.22	0.42
1:A:69:ASN:O	1:A:71:ALA:N	2.51	0.42
3:C:124:LEU:O	3:C:133:TRP:CB	2.66	0.42
3:C:66:PHE:HB3	3:C:126:ILE:HD11	2.01	0.42
3:C:150:ASP:HA	3:C:153:THR:HG22	2.00	0.42
3:C:249:GLN:CA	3:C:252:MET:HB2	2.49	0.42
4:D:91:GLU:O	4:D:94:ARG:N	2.52	0.42
1:A:10:GLU:HA	1:A:10:GLU:OE1	2.20	0.42
1:A:56:LEU:O	1:A:136:LEU:HA	2.19	0.42
1:A:141:HIS:CE1	1:A:211:GLU:OE2	2.72	0.42
1:A:250:CYS:O	1:A:251:SER:C	2.57	0.42
2:B:102:LEU:O	2:B:103:ARG:C	2.56	0.42
2:B:205:HIS:C	2:B:205:HIS:CD2	2.91	0.42
4:D:73:LYS:O	4:D:112:PRO:HA	2.19	0.42
7:G:50:ARG:HB3	7:G:76:ARG:HB3	2.01	0.42
5:E:204:CYS:SG	5:E:222:SER:CB	3.07	0.42
8:H:175:SER:C	8:H:177:SER:H	2.21	0.42
4:D:159:LEU:O	4:D:177:ALA:HB1	2.19	0.42
2:B:235:VAL:CG1	2:B:236:ARG:N	2.82	0.42
7:G:251:ASN:HA	7:G:254:GLU:OE2	2.20	0.42
3:C:110:ALA:O	3:C:113:ILE:N	2.52	0.42
3:C:132:VAL:HG22	3:C:133:TRP:N	2.35	0.42
3:C:12:GLU:O	3:C:15:ARG:N	2.52	0.42
3:C:252:MET:HE1	4:D:203:ASP:HB2	2.02	0.42
6:F:165:ALA:O	6:F:166:ALA:C	2.57	0.42
1:A:112:ASN:ND2	1:A:233:THR:HG23	2.34	0.42
1:A:191:PRO:HD3	1:A:226:ASN:ND2	2.33	0.42
1:A:219:GLY:HA3	1:A:240:ILE:CG1	2.49	0.42
1:A:225:MET:HA	1:A:230:GLU:O	2.19	0.42
1:A:245:ASP:C	1:A:249:ARG:HH21	2.22	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:110:LEU:O	4:D:111:HIS:C	2.57	0.42
4:D:29:ARG:HB3	4:D:168:ASP:OD1	2.19	0.42
5:E:64:ALA:HB1	5:E:133:TRP:NE1	2.35	0.42
7:G:162:ILE:HG22	7:G:163:TYR:N	2.35	0.42
7:G:215:GLU:HA	7:G:218:GLN:NE2	2.34	0.42
5:E:53:LEU:O	5:E:55:HIS:N	2.52	0.42
6:F:197:LEU:HB2	6:F:243:LEU:HD21	2.01	0.42
2:B:234:HIS:ND1	2:B:234:HIS:O	2.53	0.42
3:C:99:GLY:O	3:C:100:GLU:C	2.58	0.42
3:C:12:GLU:O	3:C:13:TYR:C	2.58	0.42
3:C:153:THR:OG1	3:C:194:VAL:HA	2.19	0.42
3:C:17:PHE:CA	3:C:22:CYS:SG	3.08	0.42
3:C:150:ASP:CG	3:C:196:THR:HA	2.36	0.42
3:C:88:LEU:C	3:C:90:SER:H	2.22	0.42
1:A:6:LEU:O	1:A:7:SER:O	2.37	0.42
9:I:162:ILE:HD11	9:I:176:LYS:HB3	1.99	0.42
6:F:124:LEU:O	6:F:128:GLU:HG3	2.19	0.42
5:E:105:ILE:HA	5:E:108:THR:HG1	1.83	0.42
2:B:20:GLU:HG3	2:B:20:GLU:O	2.20	0.42
2:B:218:GLN:HE21	2:B:218:GLN:CA	2.23	0.42
5:E:69:PRO:HG2	5:E:74:PRO:HA	2.02	0.42
9:I:181:GLU:HG2	9:I:182:PHE:H	1.79	0.42
7:G:232:MET:O	7:G:234:GLY:N	2.52	0.42
3:C:107:GLN:CD	3:C:107:GLN:C	2.78	0.42
3:C:124:LEU:HD11	3:C:135:LEU:HD11	2.02	0.42
3:C:124:LEU:HA	3:C:124:LEU:HD23	1.91	0.42
3:C:160:LEU:HA	3:C:163:VAL:HG23	2.01	0.42
3:C:64:ALA:HB3	3:C:165:LEU:HD11	2.01	0.42
3:C:154:PHE:HE1	3:C:262:VAL:HB	1.80	0.42
6:F:215:LEU:HD23	6:F:216:MET:N	2.35	0.42
6:F:36:LEU:HD12	6:F:37:ARG:H	1.85	0.42
1:A:116:ILE:HD12	1:A:116:ILE:H	1.83	0.42
1:A:144:ASN:HB2	1:A:209:PRO:CD	2.40	0.42
1:A:202:GLY:C	1:A:204:TYR:H	2.22	0.42
1:A:262:THR:HG22	1:A:266:LEU:HD11	2.01	0.42
2:B:102:LEU:O	2:B:106:PHE:CD1	2.73	0.42
7:G:128:PHE:CD1	7:G:128:PHE:N	2.88	0.42
7:G:170:ASN:HD21	7:G:173:MET:CE	2.32	0.42
5:E:260:LYS:HB3	6:F:234:THR:CB	2.49	0.42
5:E:270:LEU:C	5:E:272:SER:H	2.22	0.42
5:E:167:ARG:HA	5:E:190:ILE:CG1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:271:ILE:HG21	8:H:280:ILE:CD1	2.50	0.42
7:G:90:PRO:HA	7:G:94:SER:HB3	2.02	0.42
2:B:237:GLU:OE1	2:B:238:ALA:N	2.53	0.42
3:C:89:CYS:HB3	3:C:141:CYS:O	2.20	0.42
3:C:88:LEU:CD2	3:C:142:LEU:HA	2.48	0.42
3:C:78:TYR:O	3:C:124:LEU:HD13	2.19	0.42
3:C:242:GLY:HA2	4:D:191:LYS:O	2.20	0.42
4:D:192:LEU:HD23	4:D:194:MET:N	2.34	0.42
1:A:196:PHE:N	1:A:221:LEU:O	2.43	0.42
1:A:33:ARG:HH21	1:A:50:LEU:CD2	2.23	0.42
2:B:161:ALA:C	2:B:172:LEU:HD11	2.40	0.42
1:A:231:ILE:N	2:B:204:LEU:O	2.51	0.42
4:D:40:ARG:HH11	4:D:40:ARG:HG3	1.84	0.42
7:G:116:VAL:HG13	7:G:117:ILE:N	2.34	0.42
7:G:141:SER:HG	7:G:144:SER:HG	1.64	0.42
7:G:228:ILE:CD1	7:G:228:ILE:C	2.87	0.42
7:G:214:CYS:SG	7:G:216:ILE:HD13	2.60	0.42
8:H:200:ASN:HD21	8:H:202:PHE:CB	2.31	0.42
5:E:16:HIS:CG	8:H:225:PRO:HB3	2.54	0.42
5:E:272:SER:OG	5:E:273:VAL:N	2.53	0.42
6:F:200:THR:HB	6:F:203:GLU:H	1.85	0.42
1:A:59:VAL:HB	1:A:160:PHE:CG	2.54	0.42
8:H:45:THR:HG21	8:H:67:ILE:HG22	2.02	0.42
1:A:70:ARG:O	1:A:72:THR:N	2.44	0.42
8:H:111:SER:HB2	8:H:157:HIS:CE1	2.55	0.42
5:E:164:ARG:CG	5:E:191:ARG:HD2	2.50	0.42
3:C:198:PHE:CE2	3:C:251:CYS:HB3	2.55	0.42
3:C:31:GLU:O	3:C:33:ARG:N	2.53	0.42
6:F:253:PRO:HG2	6:F:254:VAL:N	2.31	0.42
1:A:199:PHE:HE1	1:A:206:LEU:HB2	1.78	0.42
1:A:246:GLN:O	1:A:249:ARG:HG2	2.20	0.42
1:A:260:GLU:O	1:A:264:LEU:CD2	2.68	0.42
1:A:87:ALA:HB3	1:A:90:PHE:CD2	2.55	0.42
2:B:111:LEU:N	2:B:111:LEU:CD1	2.83	0.42
7:G:161:LEU:HD22	7:G:192:ILE:HG21	2.02	0.42
7:G:27:VAL:CG2	7:G:79:VAL:HG11	2.49	0.42
8:H:83:ILE:CG1	8:H:199:ASN:ND2	2.83	0.42
8:H:91:VAL:HG22	8:H:97:LYS:H	1.84	0.42
5:E:116:LYS:HG2	5:E:198:PRO:CG	2.49	0.42
5:E:116:LYS:HD3	5:E:198:PRO:HB3	2.02	0.42
6:F:35:ARG:HH22	6:F:196:LEU:HD21	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:63:LYS:HG3	6:F:105:PHE:HA	2.02	0.42
6:F:265:ARG:NH1	6:F:265:ARG:HG3	2.33	0.42
8:H:171:LEU:O	8:H:171:LEU:HD23	2.19	0.42
3:C:150:ASP:O	3:C:153:THR:HG22	2.20	0.42
3:C:89:CYS:O	3:C:90:SER:HB3	2.20	0.42
1:A:36:ARG:HA	1:A:37:ILE:HD12	2.01	0.42
2:B:109:ALA:O	2:B:110:ILE:HB	2.20	0.42
2:B:47:ALA:CB	2:B:125:GLN:O	2.66	0.42
2:B:190:PRO:O	2:B:192:SER:N	2.53	0.42
2:B:96:CYS:SG	2:B:97:GLU:N	2.92	0.42
5:E:45:THR:CG2	5:E:63:LYS:HB2	2.50	0.42
7:G:144:SER:O	7:G:179:CYS:HB2	2.20	0.42
9:I:111:THR:HG22	9:I:112:GLU:N	2.34	0.42
9:I:153:VAL:HG22	9:I:154:VAL:N	2.35	0.42
8:H:83:ILE:HG12	8:H:199:ASN:HD21	1.85	0.42
1:A:76:LEU:HA	1:A:131:GLN:OE1	2.19	0.42
2:B:54:PRO:CB	2:B:120:ILE:HD11	2.50	0.42
2:B:145:VAL:C	2:B:147:ASP:N	2.73	0.42
1:A:167:VAL:CG2	1:A:172:VAL:HG13	2.50	0.42
9:I:18:GLU:O	9:I:19:GLU:CB	2.67	0.42
3:C:153:THR:OG1	3:C:194:VAL:HG13	2.19	0.41
1:A:295:ALA:HA	4:D:33:CYS:O	2.19	0.41
2:B:41:GLU:CB	2:B:46:LYS:HG3	2.43	0.41
7:G:156:VAL:O	7:G:157:GLN:HG2	2.19	0.41
7:G:19:ALA:HB1	7:G:35:LEU:CD1	2.42	0.41
9:I:133:ILE:CG2	9:I:134:SER:H	2.17	0.41
9:I:135:LEU:HD13	9:I:142:TYR:CZ	2.54	0.41
9:I:129:LEU:CD2	9:I:152:GLY:O	2.68	0.41
9:I:174:CYS:SG	9:I:177:THR:CG2	3.08	0.41
5:E:254:GLU:HG3	5:E:254:GLU:H	1.51	0.41
1:A:162:ARG:NH1	1:A:162:ARG:O	2.54	0.41
9:I:16:ASN:CA	9:I:33:ILE:HG13	2.48	0.41
7:G:98:VAL:HG12	7:G:99:TYR:H	1.83	0.41
5:E:167:ARG:NH1	5:E:187:TYR:HD2	2.18	0.41
3:C:57:THR:O	3:C:142:LEU:HG	2.20	0.41
3:C:199:ALA:HB3	3:C:207:ILE:CG1	2.42	0.41
3:C:37:VAL:CG2	3:C:269:VAL:HG21	2.50	0.41
3:C:90:SER:O	3:C:93:PHE:HB2	2.21	0.41
1:A:101:LYS:HB3	1:A:101:LYS:HE3	1.78	0.41
7:G:170:ASN:OD1	7:G:173:MET:HB3	2.19	0.41
7:G:189:MET:HB3	7:G:189:MET:HE3	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:197:LEU:O	7:G:237:TRP:CA	2.51	0.41
9:I:129:LEU:HD23	9:I:152:GLY:O	2.20	0.41
7:G:220:VAL:O	7:G:220:VAL:HG12	2.20	0.41
8:H:109:LEU:HD23	8:H:110:LEU:O	2.20	0.41
2:B:224:HIS:ND1	2:B:225:THR:N	2.68	0.41
9:I:82:PHE:CD1	9:I:82:PHE:N	2.88	0.41
1:A:262:THR:O	1:A:263:GLU:C	2.59	0.41
1:A:56:LEU:HD12	1:A:57:GLY:H	1.85	0.41
4:D:74:ALA:HB2	4:D:114:THR:HG23	2.03	0.41
4:D:38:LEU:H	4:D:38:LEU:HD12	1.83	0.41
7:G:222:LYS:NZ	7:G:269:SER:H	2.15	0.41
8:H:130:ALA:HB1	8:H:134:PHE:CZ	2.54	0.41
8:H:191:CYS:SG	8:H:237:LEU:HD11	2.60	0.41
2:B:30:VAL:HB	2:B:31:PHE:H	1.63	0.41
5:E:199:CYS:O	5:E:229:SER:HA	2.20	0.41
5:E:116:LYS:HB2	5:E:237:THR:HG23	2.02	0.41
8:H:72:LEU:H	8:H:72:LEU:CD2	2.33	0.41
9:I:16:ASN:O	9:I:18:GLU:N	2.53	0.41
7:G:145:PHE:O	7:G:146:GLU:CG	2.66	0.41
7:G:29:PRO:HB3	7:G:80:THR:O	2.20	0.41
6:F:188:ALA:HB3	6:F:194:THR:HB	2.02	0.41
1:A:425:UNK:HG2	1:A:426:UNK:N	2.35	0.41
3:C:99:GLY:N	3:C:102:ALA:HB3	2.35	0.41
3:C:246:ALA:O	3:C:249:GLN:N	2.53	0.41
6:F:55:LEU:O	6:F:56:GLU:HG2	2.19	0.41
2:B:163:PHE:HB2	2:B:212:VAL:HG12	2.01	0.41
7:G:20:ARG:HB2	7:G:35:LEU:HG	2.02	0.41
5:E:8:GLU:CA	5:E:11:LYS:HG2	2.49	0.41
8:H:250:MET:HA	8:H:250:MET:CE	2.50	0.41
5:E:257:GLU:CG	5:E:260:LYS:HE3	2.47	0.41
3:C:101:GLU:C	3:C:103:GLN:N	2.74	0.41
1:A:8:ASN:HA	1:A:11:ARG:HD2	2.02	0.41
1:A:195:SER:HA	1:A:221:LEU:O	2.21	0.41
1:A:37:ILE:N	1:A:37:ILE:CD1	2.64	0.41
7:G:215:GLU:O	7:G:219:GLU:CB	2.64	0.41
8:H:91:VAL:CG2	8:H:96:TRP:HA	2.45	0.41
5:E:113:PHE:HZ	5:E:156:VAL:HG13	1.85	0.41
5:E:194:VAL:HG23	5:E:196:ASN:H	1.84	0.41
6:F:211:LEU:HA	6:F:227:GLY:HA2	2.03	0.41
5:E:245:GLY:HA2	6:F:132:PRO:HB3	2.02	0.41
8:H:30:GLY:HA2	8:H:53:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:239:ASN:O	8:H:242:ILE:HG12	2.21	0.41
2:B:58:ARG:HD3	2:B:58:ARG:HA	1.90	0.41
3:C:147:ASN:C	3:C:147:ASN:HD22	2.23	0.41
3:C:38:ASN:HD22	3:C:50:LEU:HB3	1.86	0.41
4:D:110:LEU:HB3	4:D:111:HIS:H	1.71	0.41
5:E:227:LEU:N	5:E:240:ARG:O	2.36	0.41
8:H:178:LEU:HA	8:H:250:MET:CE	2.51	0.41
8:H:191:CYS:HB2	8:H:260:TYR:CE2	2.56	0.41
8:H:88:ILE:HD11	8:H:141:ILE:CD1	2.51	0.41
2:B:142:THR:O	2:B:146:LEU:CG	2.60	0.41
2:B:145:VAL:O	2:B:147:ASP:N	2.53	0.41
9:I:15:CYS:HB3	9:I:33:ILE:CD1	2.42	0.41
8:H:276:ILE:HG22	8:H:280:ILE:CD1	2.50	0.41
8:H:129:LEU:O	8:H:132:ARG:HG2	2.21	0.41
8:H:258:TYR:HB2	8:H:288:LEU:HG	2.01	0.41
8:H:291:GLN:O	8:H:291:GLN:HG2	2.19	0.41
9:I:79:ASN:HB3	9:I:82:PHE:H	1.85	0.41
2:B:60:SER:O	2:B:62:ALA:N	2.54	0.41
1:A:436:UNK:C	1:A:438:UNK:N	2.83	0.41
3:C:79:VAL:CG1	3:C:121:LYS:HZ1	2.33	0.41
3:C:144:TYR:CD1	3:C:145:ASP:N	2.88	0.41
3:C:207:ILE:H	3:C:207:ILE:HG12	1.47	0.41
1:A:449:UNK:O	3:C:276:LYS:NZ	2.54	0.41
6:F:169:LEU:O	6:F:172:ALA:HB3	2.20	0.41
9:I:42:MET:O	9:I:54:SER:O	2.39	0.41
1:A:194:VAL:HG11	1:A:254:ALA:HA	2.03	0.41
1:A:247:VAL:C	1:A:250:CYS:HG	2.20	0.41
1:A:99:LEU:HD12	1:A:99:LEU:HA	1.75	0.41
7:G:265:LYS:HB3	7:G:266:GLN:OE1	2.21	0.41
5:E:17:GLY:CA	8:H:231:ARG:HH21	2.30	0.41
6:F:186:SER:O	6:F:196:LEU:N	2.46	0.41
6:F:233:LEU:H	6:F:236:SER:CB	2.34	0.41
3:C:63:LYS:HZ2	6:F:108:ARG:HA	1.83	0.41
5:E:86:SER:C	5:E:88:SER:N	2.72	0.41
5:E:120:ASP:O	5:E:123:THR:N	2.53	0.41
2:B:159:CYS:SG	2:B:223:VAL:HG21	2.60	0.41
9:I:139:GLN:O	9:I:140:SER:HB2	2.20	0.41
5:E:49:ALA:HB3	5:E:159:ALA:HB2	2.01	0.41
3:C:147:ASN:O	3:C:149:LEU:N	2.54	0.41
3:C:150:ASP:OD2	3:C:195:ALA:O	2.39	0.41
3:C:274:LYS:CB	3:C:275:PRO:CD	2.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:59:ILE:HD12	3:C:59:ILE:N	2.32	0.41
6:F:126:LEU:HD22	6:F:130:LEU:HG	2.03	0.41
1:A:18:ILE:C	1:A:20:GLU:N	2.72	0.41
1:A:23:ARG:NH2	1:A:27:ARG:CZ	2.83	0.41
1:A:140:ASN:ND2	4:D:39:SER:N	2.67	0.41
9:I:145:THR:HG21	9:I:147:ALA:HB3	2.03	0.41
9:I:156:ALA:HB3	9:I:164:MET:O	2.21	0.41
8:H:96:TRP:O	8:H:108:LEU:HD23	2.20	0.41
8:H:165:LYS:NZ	8:H:166:LEU:O	2.45	0.41
5:E:37:VAL:CG2	5:E:154:ILE:HD11	2.49	0.41
5:E:257:GLU:C	5:E:259:GLY:H	2.23	0.41
5:E:256:MET:CE	6:F:241:VAL:HG21	2.51	0.41
2:B:69:ALA:HB2	2:B:115:HIS:CB	2.27	0.41
4:D:105:VAL:C	4:D:149:ARG:HG2	2.40	0.41
9:I:79:ASN:CB	9:I:82:PHE:H	2.34	0.41
1:A:63:LEU:N	1:A:63:LEU:HD23	2.35	0.41
3:C:101:GLU:O	3:C:104:VAL:N	2.54	0.41
3:C:111:ASP:O	3:C:115:ASN:ND2	2.54	0.41
3:C:139:LEU:HD21	3:C:156:LEU:HB2	2.02	0.41
3:C:50:LEU:HD12	3:C:51:VAL:H	1.86	0.41
3:C:101:GLU:HB2	4:D:96:ARG:HH22	1.86	0.41
3:C:110:ALA:O	3:C:113:ILE:HB	2.21	0.41
3:C:170:ILE:HG23	3:C:174:THR:O	2.21	0.41
3:C:201:PHE:C	3:C:202:ASP:OD2	2.59	0.41
3:C:215:GLU:O	3:C:218:ALA:HB3	2.21	0.41
3:C:267:ASP:O	3:C:270:ILE:HD12	2.21	0.41
1:A:144:ASN:ND2	1:A:146:ILE:CD1	2.84	0.41
1:A:35:ILE:CD1	1:A:37:ILE:HD11	2.51	0.41
2:B:100:LEU:HA	2:B:103:ARG:HG3	2.03	0.41
2:B:77:SER:CA	2:B:125:GLN:OE1	2.61	0.41
2:B:172:LEU:HD22	2:B:183:GLN:HB3	2.02	0.41
2:B:79:THR:HG22	2:B:88:ARG:NE	2.33	0.41
1:A:244:LYS:HD2	1:A:245:ASP:CA	2.51	0.41
2:B:100:LEU:O	2:B:101:GLN:C	2.58	0.41
4:D:139:MET:O	4:D:140:ALA:C	2.59	0.41
4:D:29:ARG:N	4:D:168:ASP:HB3	2.35	0.41
1:A:295:ALA:CA	4:D:231:ARG:HH12	2.34	0.41
4:D:41:PRO:HG3	4:D:59:TYR:CE1	2.56	0.41
7:G:48:VAL:HG12	7:G:50:ARG:NH2	2.36	0.41
7:G:161:LEU:CD1	7:G:161:LEU:N	2.84	0.41
7:G:173:MET:CG	7:G:174:GLU:N	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:162:ILE:HB	9:I:174:CYS:CB	2.51	0.41
8:H:204:TRP:HE3	8:H:206:TYR:HD2	1.66	0.41
5:E:12:VAL:O	5:E:15:VAL:HG23	2.20	0.41
5:E:206:ILE:CD1	5:E:206:ILE:N	2.77	0.41
8:H:106:SER:HB2	8:H:156:LEU:HD11	2.03	0.41
5:E:157:LYS:O	5:E:160:LEU:HB2	2.21	0.41
5:E:252:ILE:O	5:E:256:MET:HB2	2.21	0.41
2:B:139:ASN:O	2:B:143:LEU:CD2	2.68	0.41
2:B:12:ARG:HH12	2:B:16:ARG:HH12	1.66	0.41
5:E:140:LEU:HG	5:E:142:LEU:CD2	2.50	0.41
5:E:76:GLU:HA	5:E:125:CYS:SG	2.61	0.41
5:E:126:ILE:O	5:E:128:PRO:HD3	2.21	0.41
5:E:77:GLY:HA3	5:E:124:LEU:O	2.20	0.41
8:H:189:LEU:HD13	8:H:257:LEU:HG	2.02	0.41
7:G:148:ALA:O	7:G:149:THR:C	2.59	0.41
3:C:29:LEU:CD2	3:C:254:ARG:NH1	2.81	0.41
7:G:115:HIS:CD2	7:G:232:MET:HG2	2.56	0.41
9:I:136:GLY:C	9:I:138:ALA:N	2.73	0.41
4:D:155:VAL:HG22	4:D:185:LEU:HD11	2.01	0.41
3:C:232:LEU:CD2	4:D:206:LEU:HD22	2.50	0.41
6:F:149:LEU:HD23	6:F:150:LEU:C	2.42	0.41
6:F:150:LEU:CD2	6:F:157:ALA:HB1	2.48	0.41
6:F:166:ALA:HA	6:F:169:LEU:CD1	2.46	0.41
1:A:154:ILE:HG22	1:A:155:VAL:N	2.36	0.41
1:A:56:LEU:HD12	1:A:56:LEU:HA	1.71	0.41
1:A:84:GLN:O	1:A:84:GLN:OE1	2.38	0.41
4:D:100:ASN:C	4:D:102:CYS:N	2.72	0.41
9:I:102:THR:C	9:I:103:ILE:CG1	2.89	0.41
9:I:74:LYS:HD3	9:I:75:VAL:O	2.21	0.41
5:E:211:VAL:CG1	5:E:212:VAL:N	2.82	0.41
5:E:216:LEU:C	5:E:218:GLU:N	2.70	0.41
2:B:16:ARG:HA	2:B:20:GLU:OE1	2.21	0.41
3:C:235:LEU:HD23	3:C:235:LEU:C	2.41	0.40
6:F:103:ALA:HA	6:F:104:PRO:HD3	1.82	0.40
6:F:253:PRO:C	6:F:255:LEU:N	2.74	0.40
6:F:37:ARG:NH2	6:F:57:ALA:HB1	2.37	0.40
8:H:220:ILE:O	8:H:221:ALA:C	2.59	0.40
1:A:109:CYS:HA	1:A:112:ASN:CB	2.45	0.40
1:A:258:VAL:O	1:A:259:ALA:C	2.57	0.40
2:B:89:PRO:HA	2:B:92:ASP:OD2	2.20	0.40
4:D:100:ASN:O	4:D:102:CYS:N	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:39:THR:O	5:E:40:ASP:HB2	2.21	0.40
6:F:135:ARG:CG	6:F:136:LEU:H	2.34	0.40
5:E:215:THR:HB	5:E:217:GLN:NE2	2.36	0.40
7:G:203:LEU:O	7:G:206:ILE:N	2.54	0.40
7:G:202:THR:CG2	7:G:205:LEU:HD13	2.51	0.40
2:B:6:LEU:HB3	2:B:7:SER:H	1.48	0.40
3:C:178:GLU:O	3:C:181:LEU:CB	2.68	0.40
7:G:115:HIS:H	7:G:115:HIS:HD1	1.68	0.40
3:C:79:VAL:CB	3:C:135:LEU:HD12	2.52	0.40
6:F:130:LEU:CD2	6:F:162:LEU:HD23	2.50	0.40
6:F:180:VAL:HG13	6:F:223:ALA:HB2	2.03	0.40
6:F:54:TYR:HD1	6:F:63:LEU:CD2	2.34	0.40
7:G:198:LEU:HD13	7:G:237:TRP:HB2	2.03	0.40
7:G:33:LEU:HD22	7:G:33:LEU:N	2.35	0.40
7:G:48:VAL:CG2	7:G:77:LEU:HD21	2.49	0.40
7:G:252:ILE:HG22	7:G:253:LEU:N	2.36	0.40
1:A:175:TYR:HB3	1:A:177:PRO:CG	2.50	0.40
1:A:175:TYR:C	1:A:177:PRO:HD2	2.40	0.40
2:B:49:ALA:HB2	2:B:124:VAL:HG13	2.02	0.40
6:F:120:ARG:HG3	6:F:120:ARG:HH11	1.86	0.40
9:I:92:SER:H	9:I:94:PRO:HD2	1.85	0.40
1:A:150:SER:H	1:A:150:SER:HG	1.67	0.40
4:D:230:ARG:HA	4:D:233:SER:OG	2.20	0.40
6:F:179:LEU:HD21	9:I:10:PRO:HG2	2.04	0.40
4:D:111:HIS:CD2	4:D:113:ARG:NH2	2.90	0.40
4:D:73:LYS:O	4:D:111:HIS:O	2.39	0.40
5:E:42:VAL:C	5:E:44:ASN:N	2.75	0.40
7:G:48:VAL:HG22	7:G:77:LEU:HG	2.03	0.40
8:H:195:VAL:CG1	8:H:196:ILE:N	2.84	0.40
5:E:236:VAL:HG21	6:F:234:THR:HA	2.04	0.40
1:A:64:VAL:HG12	1:A:65:SER:H	1.85	0.40
5:E:264:LYS:O	5:E:264:LYS:HD3	2.21	0.40
4:D:153:CYS:HB3	4:D:221:PHE:CE2	2.56	0.40
2:B:26:ALA:HB2	2:B:40:ILE:CD1	2.51	0.40
4:D:175:LYS:HA	4:D:175:LYS:HD2	1.81	0.40
3:C:201:PHE:HE1	3:C:207:ILE:CD1	2.34	0.40
3:C:78:TYR:H	3:C:124:LEU:HD12	1.84	0.40
3:C:89:CYS:HB2	3:C:144:TYR:N	2.36	0.40
4:D:181:LEU:CD1	4:D:181:LEU:N	2.78	0.40
3:C:241:SER:O	4:D:191:LYS:HD3	2.22	0.40
4:D:202:SER:O	4:D:205:GLU:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:GLY:H	1:A:211:GLU:CD	2.24	0.40
1:A:211:GLU:OE1	1:A:211:GLU:CA	2.65	0.40
1:A:243:LEU:N	1:A:246:GLN:NE2	2.69	0.40
2:B:100:LEU:O	2:B:103:ARG:HB2	2.21	0.40
4:D:111:HIS:CE1	4:D:112:PRO:O	2.75	0.40
7:G:127:ILE:HA	7:G:140:LEU:O	2.21	0.40
9:I:76:SER:HB2	9:I:77:SER:H	1.62	0.40
5:E:258:THR:CG2	5:E:261:ARG:NH2	2.83	0.40
6:F:127:GLN:O	6:F:131:GLU:CB	2.50	0.40
8:H:236:ARG:NH2	8:H:267:GLN:OE1	2.54	0.40
5:E:105:ILE:HG21	5:E:152:ILE:CD1	2.42	0.40
5:E:238:CYS:N	6:F:229:GLY:H	2.19	0.40
1:A:66:PRO:HD3	1:A:129:VAL:N	2.36	0.40
2:B:140:ALA:HA	2:B:143:LEU:HD11	2.03	0.40
2:B:51:VAL:HG22	2:B:52:TYR:N	2.37	0.40
8:H:52:LEU:HD21	8:H:67:ILE:HD12	2.04	0.40
8:H:160:SER:O	8:H:163:TYR:C	2.59	0.40
7:G:231:GLY:O	7:G:234:GLY:N	2.51	0.40
5:E:189:CYS:C	5:E:191:ARG:N	2.75	0.40
6:F:266:ARG:O	6:F:269:ALA:HB3	2.21	0.40
1:A:418:UNK:O	1:A:421:UNK:HG3	2.21	0.40
3:C:194:VAL:HG12	3:C:195:ALA:H	1.85	0.40
3:C:20:GLU:O	3:C:20:GLU:OE1	2.39	0.40
3:C:37:VAL:HG11	3:C:154:PHE:CE2	2.56	0.40
3:C:65:GLU:O	3:C:134:VAL:HB	2.22	0.40
6:F:102:ARG:O	6:F:103:ALA:C	2.60	0.40
6:F:54:TYR:OH	6:F:61:LYS:CG	2.69	0.40
1:A:201:GLN:O	1:A:203:THR:HG23	2.21	0.40
1:A:23:ARG:NH1	1:A:206:LEU:HG	2.37	0.40
1:A:96:SER:HB3	1:A:100:VAL:HG23	2.03	0.40
2:B:111:LEU:HD13	2:B:152:MET:CA	2.35	0.40
2:B:154:ASP:OD2	2:B:189:LEU:HA	2.21	0.40
5:E:45:THR:O	5:E:46:SER:O	2.39	0.40
7:G:166:PHE:HB2	7:G:176:GLU:O	2.21	0.40
9:I:111:THR:HG23	9:I:184:LYS:CE	2.51	0.40
7:G:260:THR:H	7:G:263:GLN:HB2	1.87	0.40
8:H:155:SER:O	8:H:156:LEU:HD23	2.21	0.40
8:H:92:GLN:O	8:H:94:LYS:N	2.55	0.40
4:D:160:ASP:C	4:D:162:ASP:N	2.73	0.40
9:I:110:ALA:HB1	9:I:122:PHE:HZ	1.87	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 X-ray entries followed by that with respect to entries of similar resolution.

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	300/358 (84%)	209 (70%)	60 (20%)	31 (10%)	1	5
2	B	233/249 (94%)	156 (67%)	56 (24%)	21 (9%)	1	7
3	C	268/278 (96%)	193 (72%)	44 (16%)	31 (12%)	0	3
4	D	201/237 (85%)	157 (78%)	29 (14%)	15 (8%)	1	11
5	E	271/305 (89%)	200 (74%)	47 (17%)	24 (9%)	1	7
6	F	219/272 (80%)	166 (76%)	32 (15%)	21 (10%)	1	6
7	G	232/289 (80%)	152 (66%)	51 (22%)	29 (12%)	0	2
8	H	244/308 (79%)	182 (75%)	41 (17%)	21 (9%)	1	8
9	I	178/209 (85%)	122 (68%)	40 (22%)	16 (9%)	1	7
All	All	2146/2505 (86%)	1537 (72%)	400 (19%)	209 (10%)	1	5

All (209) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	SER
1	A	68	LEU
1	A	69	ASN
1	A	94	ARG
1	A	227	LYS
1	A	239	GLY
1	A	292	ARG
1	A	293	ILE
1	A	294	THR
1	A	301	ALA
2	B	30	VAL
2	B	35	ASP
2	B	62	ALA
2	B	110	ILE
2	B	149	GLY
2	B	173	SER

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Mol	Chain	Res	Type
2	B	179	ALA
2	B	206	GLU
3	C	21	ASN
3	C	29	LEU
3	C	33	ARG
3	C	74	PRO
3	C	89	CYS
3	C	145	ASP
3	C	181	LEU
3	C	202	ASP
3	C	232	LEU
3	C	241	SER
4	D	60	GLY
4	D	110	LEU
4	D	126	ALA
4	D	145	GLY
4	D	169	PRO
5	E	23	ARG
5	E	46	SER
5	E	70	LYS
5	E	100	ASP
5	E	126	ILE
5	E	232	SER
6	F	68	GLY
6	F	157	ALA
6	F	190	GLY
6	F	217	PRO
6	F	218	VAL
7	G	44	PRO
7	G	149	THR
7	G	156	VAL
7	G	191	VAL
7	G	192	ILE
7	G	222	LYS
7	G	223	LEU
7	G	239	LYS
7	G	256	CYS
7	G	257	GLU
7	G	265	LYS
8	H	77	ILE
8	H	80	VAL
8	H	93	GLN

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Mol	Chain	Res	Type
8	H	136	GLN
8	H	137	GLU
8	H	150	SER
8	H	168	GLN
8	H	199	ASN
8	H	253	ASP
8	H	267	GLN
8	H	268	ILE
8	H	269	LYS
9	I	19	GLU
9	I	67	VAL
9	I	176	LYS
1	A	97	ASP
1	A	146	ILE
1	A	164	ASP
1	A	184	PRO
1	A	229	ARG
1	A	281	LYS
1	A	282	PHE
2	B	21	LEU
2	B	23	LYS
2	B	53	GLY
2	B	57	ILE
2	B	59	GLY
2	B	61	ARG
2	B	66	PRO
2	B	69	ALA
3	C	10	PRO
3	C	44	THR
3	C	70	SER
3	C	186	TYR
4	D	191	LYS
4	D	192	LEU
4	D	194	MET
4	D	206	LEU
5	E	24	VAL
5	E	28	GLY
5	E	54	GLY
5	E	125	CYS
5	E	265	VAL
6	F	34	THR
6	F	115	GLY

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Mol	Chain	Res	Type
7	G	92	SER
7	G	106	LYS
7	G	112	LYS
7	G	152	ASN
7	G	171	LYS
7	G	186	ALA
7	G	263	GLN
8	H	101	ASN
8	H	110	LEU
8	H	134	PHE
8	H	151	ASP
9	I	37	LEU
9	I	115	LYS
9	I	137	ASP
1	A	66	PRO
1	A	70	ARG
1	A	74	GLY
1	A	85	MET
1	A	96	SER
1	A	125	ALA
1	A	181	ASP
1	A	200	GLN
1	A	259	ALA
2	B	67	ASP
3	C	22	CYS
3	C	128	PRO
3	C	147	ASN
3	C	166	PRO
3	C	180	ASN
3	C	203	ASP
4	D	113	ARG
4	D	233	SER
5	E	34	CYS
5	E	164	ARG
6	F	191	PRO
6	F	220	ASN
6	F	223	ALA
7	G	20	ARG
7	G	182	SER
7	G	233	ASN
7	G	241	LYS
7	G	244	GLN

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Mol	Chain	Res	Type
8	H	223	LEU
8	H	265	PRO
9	I	17	LEU
1	A	86	ALA
2	B	85	ARG
2	B	191	ALA
2	B	215	ALA
3	C	88	LEU
3	C	90	SER
3	C	92	ARG
5	E	43	SER
5	E	120	ASP
5	E	163	THR
6	F	253	PRO
7	G	137	PRO
7	G	200	LYS
8	H	111	SER
8	H	159	ARG
9	I	11	GLY
9	I	22	PRO
9	I	64	LEU
9	I	92	SER
1	A	71	ALA
1	A	183	VAL
2	B	112	THR
3	C	73	ALA
3	C	98	PRO
3	C	239	GLY
5	E	6	LEU
5	E	40	ASP
5	E	75	ASN
5	E	190	ILE
5	E	271	GLN
6	F	57	ALA
6	F	222	VAL
6	F	236	SER
6	F	238	ALA
7	G	111	VAL
9	I	51	PRO
3	C	77	GLY
3	C	233	CYS
4	D	144	ALA

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Mol	Chain	Res	Type
4	D	161	SER
5	E	215	THR
6	F	37	ARG
6	F	69	PRO
6	F	193	PRO
6	F	198	ASP
9	I	184	LYS
1	A	279	GLY
6	F	114	PRO
7	G	267	ILE
1	A	283	GLY
3	C	24	PRO
3	C	118	ILE
5	E	281	GLY
7	G	153	ARG
3	C	81	PRO
4	D	106	VAL
4	D	108	GLY
5	E	41	VAL
6	F	32	ASP
7	G	43	GLY
8	H	274	PRO
9	I	155	VAL
9	I	25	GLY
9	I	75	VAL

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 X-ray entries followed by that with respect to entries of similar resolution.

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	264/280 (94%)	196 (74%)	68 (26%)	0	2
2	B	179/189 (95%)	146 (82%)	33 (18%)	2	9
3	C	232/237 (98%)	201 (87%)	31 (13%)	5	21
4	D	168/195 (86%)	144 (86%)	24 (14%)	4	19
5	E	240/265 (91%)	205 (85%)	35 (15%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	157/188 (84%)	135 (86%)	22 (14%)	4	20
7	G	192/234 (82%)	150 (78%)	42 (22%)	1	5
8	H	219/268 (82%)	194 (89%)	25 (11%)	7	29
9	I	157/183 (86%)	133 (85%)	24 (15%)	3	16
All	All	1808/2039 (89%)	1504 (83%)	304 (17%)	2	12

All (304) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	7	SER
1	A	9	CYS
1	A	12	ARG
1	A	13	PHE
1	A	16	ARG
1	A	24	LEU
1	A	28	GLN
1	A	30	TYR
1	A	31	ASP
1	A	37	ILE
1	A	39	PHE
1	A	46	CYS
1	A	50	LEU
1	A	53	THR
1	A	61	CYS
1	A	63	LEU
1	A	76	LEU
1	A	78	PHE
1	A	81	GLU
1	A	98	LEU
1	A	109	CYS
1	A	116	ILE
1	A	129	VAL
1	A	131	GLN
1	A	134	VAL
1	A	139	LEU
1	A	144	ASN
1	A	145	ILE
1	A	146	ILE
1	A	147	ASP
1	A	154	ILE

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Mol	Chain	Res	Type
1	A	161	ARG
1	A	164	ASP
1	A	173	THR
1	A	183	VAL
1	A	190	MET
1	A	192	ILE
1	A	209	PRO
1	A	210	ASN
1	A	211	GLU
1	A	212	ARG
1	A	217	MET
1	A	220	LEU
1	A	221	LEU
1	A	223	ILE
1	A	229	ARG
1	A	230	GLU
1	A	231	ILE
1	A	233	THR
1	A	235	GLN
1	A	240	ILE
1	A	241	MET
1	A	244	LYS
1	A	245	ASP
1	A	246	GLN
1	A	248	LEU
1	A	249	ARG
1	A	250	CYS
1	A	251	SER
1	A	258	VAL
1	A	262	THR
1	A	265	ILE
1	A	266	LEU
1	A	269	LEU
1	A	272	ASP
1	A	286	GLU
1	A	299	GLU
2	B	9	GLN
2	B	13	VAL
2	B	14	ASP
2	B	28	MET
2	B	31	PHE
2	B	44	ASN

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Mol	Chain	Res	Type
2	B	46	LYS
2	B	70	LEU
2	B	76	SER
2	B	80	PHE
2	B	97	GLU
2	B	106	PHE
2	B	121	ASP
2	B	133	THR
2	B	139	ASN
2	B	143	LEU
2	B	157	CYS
2	B	160	SER
2	B	172	LEU
2	B	176	GLU
2	B	184	LEU
2	B	186	LEU
2	B	189	LEU
2	B	195	ILE
2	B	198	LEU
2	B	206	GLU
2	B	213	LEU
2	B	214	GLU
2	B	221	ARG
2	B	227	LEU
2	B	228	ASP
2	B	233	GLN
2	B	237	GLU
3	C	11	LEU
3	C	20	GLU
3	C	27	ARG
3	C	32	PHE
3	C	46	ASP
3	C	57	THR
3	C	59	ILE
3	C	65	GLU
3	C	66	PHE
3	C	78	TYR
3	C	89	CYS
3	C	93	PHE
3	C	107	GLN
3	C	109	ILE
3	C	114	GLU

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Mol	Chain	Res	Type
3	C	122	GLU
3	C	130	LYS
3	C	133	TRP
3	C	138	ASP
3	C	147	ASN
3	C	150	ASP
3	C	153	THR
3	C	154	PHE
3	C	186	TYR
3	C	198	PHE
3	C	202	ASP
3	C	203	ASP
3	C	207	ILE
3	C	248	LEU
3	C	259	HIS
3	C	260	LYS
4	D	28	LEU
4	D	29	ARG
4	D	30	HIS
4	D	48	LEU
4	D	52	THR
4	D	58	VAL
4	D	79	ILE
4	D	80	LEU
4	D	86	LEU
4	D	94	ARG
4	D	99	ARG
4	D	114	THR
4	D	115	SER
4	D	133	CYS
4	D	135	ASN
4	D	155	VAL
4	D	165	LEU
4	D	171	SER
4	D	173	GLN
4	D	181	LEU
4	D	203	ASP
4	D	205	GLU
4	D	208	GLN
4	D	231	ARG
5	E	6	LEU
5	E	8	GLU

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Mol	Chain	Res	Type
5	E	15	VAL
5	E	22	LEU
5	E	24	VAL
5	E	36	GLU
5	E	40	ASP
5	E	44	ASN
5	E	45	THR
5	E	46	SER
5	E	53	LEU
5	E	55	HIS
5	E	56	THR
5	E	66	MET
5	E	78	TYR
5	E	84	ASP
5	E	99	ASP
5	E	101	LEU
5	E	115	ASN
5	E	141	LEU
5	E	150	ASP
5	E	153	SER
5	E	157	LYS
5	E	161	PHE
5	E	169	ARG
5	E	172	GLU
5	E	185	ASP
5	E	199	CYS
5	E	209	ARG
5	E	225	SER
5	E	237	THR
5	E	239	MET
5	E	248	ASP
5	E	254	GLU
5	E	267	HIS
6	F	34	THR
6	F	35	ARG
6	F	45	LEU
6	F	50	LYS
6	F	62	VAL
6	F	108	ARG
6	F	119	GLU
6	F	124	LEU
6	F	126	LEU

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Mol	Chain	Res	Type
6	F	130	LEU
6	F	144	LEU
6	F	174	VAL
6	F	175	GLU
6	F	183	CYS
6	F	195	TRP
6	F	196	LEU
6	F	226	LEU
6	F	233	LEU
6	F	237	TRP
6	F	239	GLU
6	F	245	LEU
6	F	249	GLN
7	G	25	GLN
7	G	33	LEU
7	G	37	GLU
7	G	49	GLU
7	G	50	ARG
7	G	75	ASP
7	G	77	LEU
7	G	86	ARG
7	G	99	TYR
7	G	100	TRP
7	G	109	VAL
7	G	115	HIS
7	G	119	ILE
7	G	120	VAL
7	G	128	PHE
7	G	130	VAL
7	G	136	GLU
7	G	140	LEU
7	G	143	LEU
7	G	150	LYS
7	G	158	VAL
7	G	170	ASN
7	G	189	MET
7	G	199	PHE
7	G	200	LYS
7	G	201	VAL
7	G	214	CYS
7	G	217	ILE
7	G	219	GLU

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Mol	Chain	Res	Type
7	G	235	ARG
7	G	239	LYS
7	G	244	GLN
7	G	245	GLN
7	G	247	LEU
7	G	251	ASN
7	G	252	ILE
7	G	262	ASP
7	G	264	ARG
7	G	266	GLN
7	G	267	ILE
7	G	270	ARG
7	G	273	GLU
8	H	31	ASP
8	H	41	ARG
8	H	74	THR
8	H	77	ILE
8	H	82	ASP
8	H	98	VAL
8	H	99	GLU
8	H	103	ARG
8	H	104	LEU
8	H	136	GLN
8	H	139	ASP
8	H	146	GLN
8	H	157	HIS
8	H	163	TYR
8	H	165	LYS
8	H	168	GLN
8	H	171	LEU
8	H	173	GLN
8	H	174	VAL
8	H	197	LEU
8	H	202	PHE
8	H	224	GLU
8	H	240	CYS
8	H	250	MET
8	H	275	GLU
9	I	16	ASN
9	I	18	GLU
9	I	22	PRO
9	I	42	MET

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Mol	Chain	Res	Type
9	I	73	CYS
9	I	76	SER
9	I	80	SER
9	I	82	PHE
9	I	103	ILE
9	I	105	LYS
9	I	106	GLU
9	I	112	GLU
9	I	122	PHE
9	I	128	VAL
9	I	135	LEU
9	I	137	ASP
9	I	139	GLN
9	I	141	ASN
9	I	148	GLU
9	I	149	ASN
9	I	169	TRP
9	I	172	MET
9	I	178	HIS
9	I	181	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (58) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	28	GLN
1	A	58	GLN
1	A	112	ASN
1	A	189	HIS
1	A	226	ASN
1	A	246	GLN
2	B	55	HIS
2	B	74	GLN
2	B	119	GLN
2	B	205	HIS
2	B	218	GLN
3	C	38	ASN
3	C	55	ASN
3	C	82	ASN
3	C	103	GLN
3	C	120	GLN
3	C	147	ASN

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Mol	Chain	Res	Type
3	C	162	ASN
3	C	171	ASN
3	C	180	ASN
3	C	216	HIS
3	C	249	GLN
4	D	49	GLN
4	D	121	GLN
4	D	135	ASN
4	D	173	GLN
4	D	207	GLN
4	D	218	GLN
5	E	114	ASN
5	E	115	ASN
5	E	131	HIS
5	E	162	ASN
6	F	127	GLN
6	F	220	ASN
6	F	221	GLN
6	F	249	GLN
6	F	256	GLN
7	G	25	GLN
7	G	38	GLN
7	G	155	ASN
7	G	157	GLN
7	G	170	ASN
7	G	187	ASN
7	G	244	GLN
7	G	245	GLN
8	H	64	ASN
8	H	136	GLN
8	H	173	GLN
8	H	199	ASN
8	H	211	HIS
8	H	239	ASN
8	H	286	GLN
9	I	16	ASN
9	I	97	ASN
9	I	139	GLN
9	I	149	ASN
9	I	178	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 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.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	302/358 (84%)	0.02	11 (3%)	46 46	15, 86, 175, 194	0
2	B	235/249 (94%)	0.10	7 (2%)	54 54	21, 99, 145, 181	0
3	C	270/278 (97%)	0.15	15 (5%)	28 27	66, 117, 171, 203	0
4	D	205/237 (86%)	0.08	8 (3%)	43 42	38, 94, 128, 157	0
5	E	275/305 (90%)	0.55	36 (13%)	5 4	87, 133, 181, 195	0
6	F	223/272 (81%)	0.11	18 (8%)	15 14	77, 131, 174, 189	0
7	G	236/289 (81%)	-0.07	7 (2%)	54 54	19, 98, 153, 189	0
8	H	250/308 (81%)	0.28	11 (4%)	38 37	94, 146, 185, 204	0
9	I	180/209 (86%)	0.60	34 (18%)	2 2	88, 142, 178, 193	0
All	All	2176/2505 (86%)	0.19	147 (6%)	20 21	15, 118, 176, 204	0

All (147) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	133	TRP	7.3
5	E	282	PRO	6.9
8	H	265	PRO	6.6
8	H	264	LEU	5.9
9	I	53	VAL	5.8
9	I	39	GLY	5.8
5	E	71	LEU	5.7
5	E	181	GLU	5.6
9	I	49	ALA	5.5
9	I	12	GLU	5.4
5	E	29	CYS	5.3
1	A	282	PHE	5.1
5	E	248	ASP	5.0
5	E	18	VAL	4.9
5	E	281	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
4	D	200	LEU	4.8
4	D	235	SER	4.6
9	I	19	GLU	4.6
4	D	26	CYS	4.6
7	G	75	ASP	4.6
8	H	219	PHE	4.3
3	C	14	TYR	4.3
5	E	168	VAL	4.2
1	A	1	MET	4.2
5	E	210	HIS	4.1
3	C	126	ILE	4.1
9	I	20	GLY	4.1
5	E	211	VAL	4.0
6	F	71	GLN	4.0
6	F	72	ALA	4.0
6	F	203	GLU	3.9
7	G	40	ASP	3.8
6	F	196	LEU	3.8
5	E	30	GLU	3.8
7	G	97	GLY	3.8
8	H	187	HIS	3.7
8	H	62	ARG	3.7
5	E	249	PRO	3.7
3	C	268	GLU	3.6
3	C	18	LEU	3.6
5	E	70	LYS	3.6
5	E	279	SER	3.6
4	D	231	ARG	3.6
1	A	289	ALA	3.5
5	E	78	TYR	3.5
7	G	74	GLY	3.5
1	A	164	ASP	3.5
8	H	251	LEU	3.5
4	D	196	SER	3.5
1	A	284	PHE	3.4
6	F	186	SER	3.4
6	F	188	ALA	3.4
6	F	195	TRP	3.4
6	F	92	LEU	3.4
3	C	168	VAL	3.3
5	E	206	ILE	3.3
9	I	11	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
3	C	174	THR	3.3
2	B	90	HIS	3.2
5	E	205	LYS	3.2
8	H	67	ILE	3.2
1	A	130	TRP	3.1
5	E	250	GLU	3.1
9	I	63	LEU	3.0
9	I	105	LYS	3.0
3	C	7	THR	3.0
6	F	231	GLY	3.0
9	I	50	LEU	3.0
9	I	136	GLY	3.0
9	I	135	LEU	3.0
5	E	31	ASP	2.9
5	E	283	LYS	2.9
9	I	8	CYS	2.9
3	C	175	ALA	2.9
9	I	65	PRO	2.9
6	F	194	THR	2.9
1	A	297	LYS	2.8
9	I	159	GLU	2.8
5	E	77	GLY	2.8
5	E	79	LEU	2.8
9	I	51	PRO	2.8
5	E	180	ILE	2.8
9	I	64	LEU	2.7
5	E	22	LEU	2.7
3	C	133	TRP	2.7
7	G	50	ARG	2.7
3	C	169	THR	2.7
9	I	14	LEU	2.7
6	F	193	PRO	2.7
9	I	99	PHE	2.6
9	I	142	TYR	2.6
5	E	33	ARG	2.6
7	G	38	GLN	2.6
5	E	21	ASP	2.6
3	C	78	TYR	2.6
9	I	15	CYS	2.6
8	H	37	THR	2.5
9	I	98	SER	2.5
6	F	182	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	272	SER	2.5
5	E	72	GLU	2.5
2	B	54	PRO	2.5
2	B	33	GLN	2.5
1	A	285	ALA	2.4
9	I	56	VAL	2.4
9	I	176	LYS	2.3
7	G	48	VAL	2.3
6	F	212	THR	2.3
9	I	87	ILE	2.3
8	H	252	TYR	2.3
2	B	61	ARG	2.3
9	I	184	LYS	2.3
9	I	139	GLN	2.3
4	D	72	ASN	2.3
6	F	202	LEU	2.3
5	E	158	ALA	2.3
2	B	120	ILE	2.3
5	E	247	LEU	2.3
8	H	274	PRO	2.2
5	E	32	TYR	2.2
9	I	9	ILE	2.2
3	C	19	LYS	2.2
6	F	192	ALA	2.2
1	A	2	LYS	2.2
3	C	170	ILE	2.2
9	I	138	ALA	2.2
9	I	178	HIS	2.2
9	I	122	PHE	2.1
9	I	33	ILE	2.1
6	F	141	ARG	2.1
5	E	34	CYS	2.1
4	D	197	THR	2.1
5	E	37	VAL	2.1
1	A	296	PHE	2.1
5	E	53	LEU	2.1
2	B	87	ARG	2.1
9	I	22	PRO	2.1
2	B	26	ALA	2.1
5	E	207	GLY	2.0
8	H	218	GLY	2.0
3	C	153	THR	2.0

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Mol	Chain	Res	Type	RSRZ
6	F	111	ARG	2.0
4	D	199	GLY	2.0
5	E	35	VAL	2.0
6	F	201	ARG	2.0
9	I	158	SER	2.0
1	A	95	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.