



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 02:38 PM UTC

PDB ID : 3E8K / pdb_00003e8k
Title : Crystal structure of HK97 Prohead II
Authors : Gertsman, I.; Speir, J.; Johnson, J.E.
Deposited on : 2008-08-20
Resolution : 3.65 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

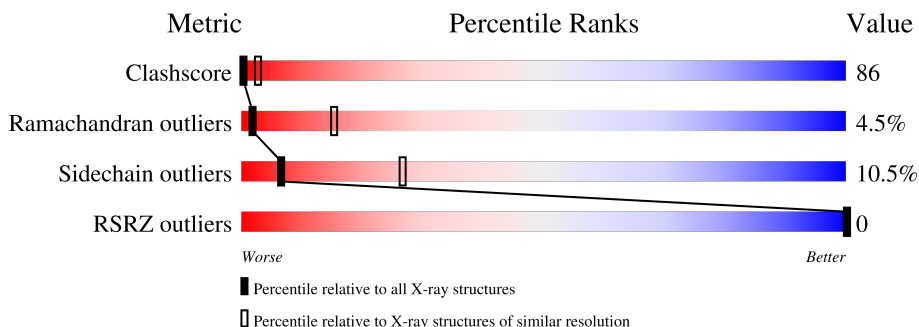
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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))
Clashscore	190562	1009 (3.76-3.56)
Ramachandran outliers	187476	1054 (3.78-3.54)
Sidechain outliers	187428	1052 (3.78-3.54)
RSRZ outliers	180081	1061 (3.78-3.54)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	273	
1	B	273	
1	C	273	
1	D	273	
1	E	273	
1	F	273	
1	G	273	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13590 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 Major capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	0	0
			1978	1238	346	384	10			
1	B	250	Total	C	N	O	S	0	0	0
			1934	1209	339	377	9			
1	C	248	Total	C	N	O	S	0	0	0
			1918	1198	337	375	8			
1	D	254	Total	C	N	O	S	0	0	0
			1961	1228	343	381	9			
1	E	255	Total	C	N	O	S	0	0	0
			1970	1233	345	383	9			
1	F	248	Total	C	N	O	S	0	0	0
			1918	1198	337	375	8			
1	G	247	Total	C	N	O	S	0	0	0
			1911	1193	336	374	8			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	159	ALA	-	linker	UNP P49861
A	160	PRO	-	linker	UNP P49861
A	161	GLY	-	linker	UNP P49861
A	162	ASP	-	linker	UNP P49861
A	336	PHE	TRP	engineered mutation	UNP P49861
B	159	ALA	-	linker	UNP P49861
B	160	PRO	-	linker	UNP P49861
B	161	GLY	-	linker	UNP P49861
B	162	ASP	-	linker	UNP P49861
B	336	PHE	TRP	engineered mutation	UNP P49861
C	159	ALA	-	linker	UNP P49861
C	160	PRO	-	linker	UNP P49861
C	161	GLY	-	linker	UNP P49861
C	162	ASP	-	linker	UNP P49861
C	336	PHE	TRP	engineered mutation	UNP P49861

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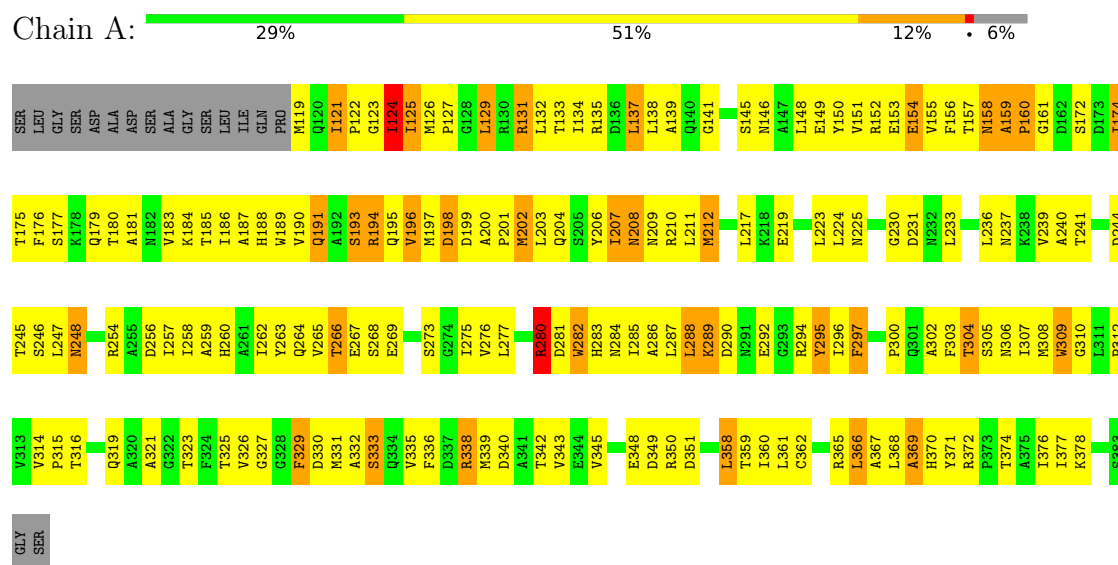
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Chain	Residue	Modelled	Actual	Comment	Reference
D	159	ALA	-	linker	UNP P49861
D	160	PRO	-	linker	UNP P49861
D	161	GLY	-	linker	UNP P49861
D	162	ASP	-	linker	UNP P49861
D	336	PHE	TRP	engineered mutation	UNP P49861
E	159	ALA	-	linker	UNP P49861
E	160	PRO	-	linker	UNP P49861
E	161	GLY	-	linker	UNP P49861
E	162	ASP	-	linker	UNP P49861
E	336	PHE	TRP	engineered mutation	UNP P49861
F	159	ALA	-	linker	UNP P49861
F	160	PRO	-	linker	UNP P49861
F	161	GLY	-	linker	UNP P49861
F	162	ASP	-	linker	UNP P49861
F	336	PHE	TRP	engineered mutation	UNP P49861
G	159	ALA	-	linker	UNP P49861
G	160	PRO	-	linker	UNP P49861
G	161	GLY	-	linker	UNP P49861
G	162	ASP	-	linker	UNP P49861
G	336	PHE	TRP	engineered mutation	UNP P49861

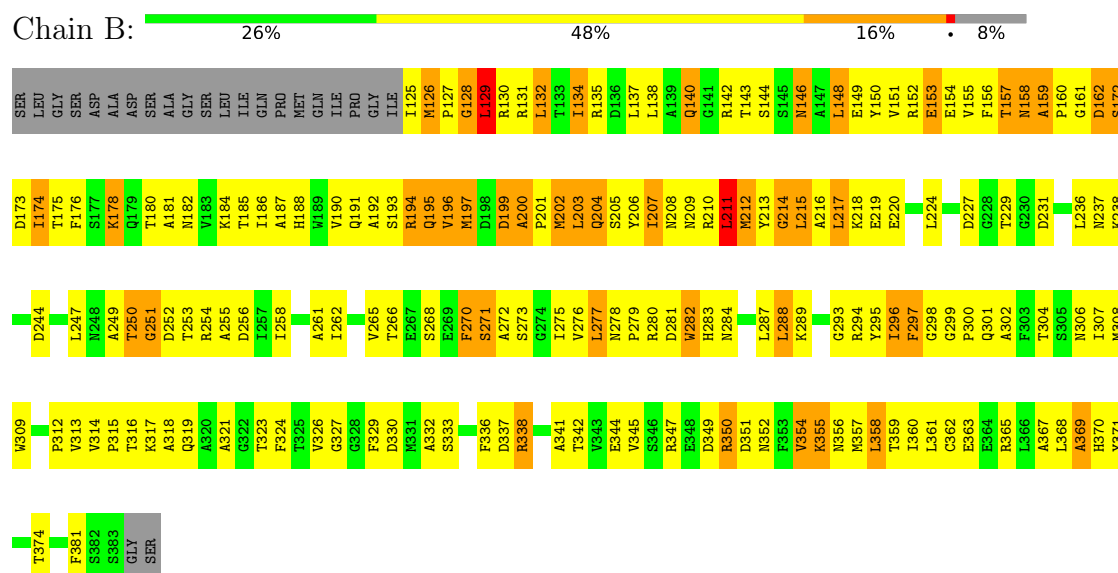
3 Residue-property plots

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

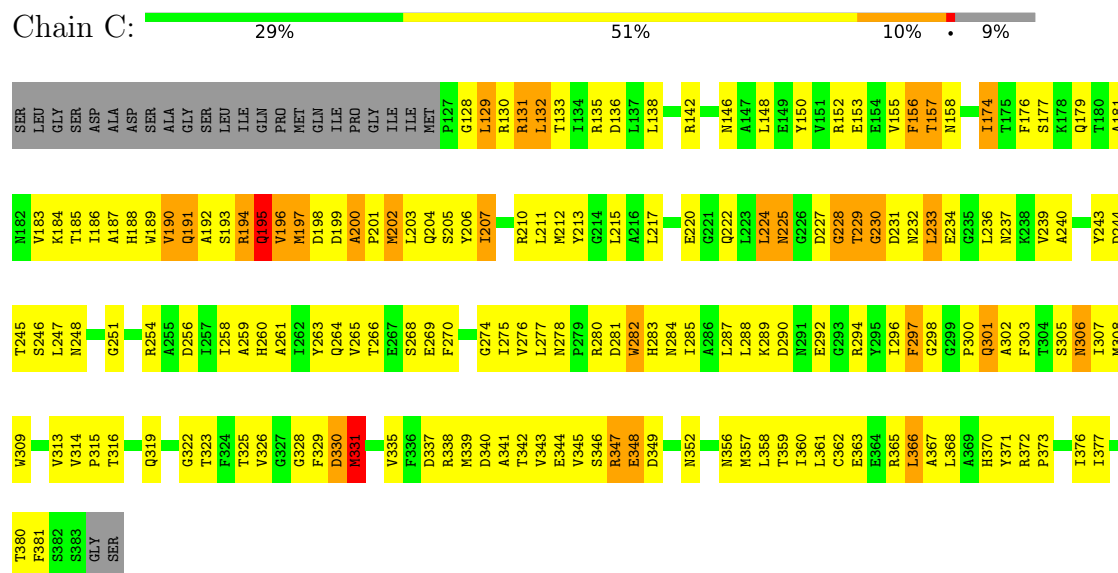
• Molecule 1: Major capsid protein



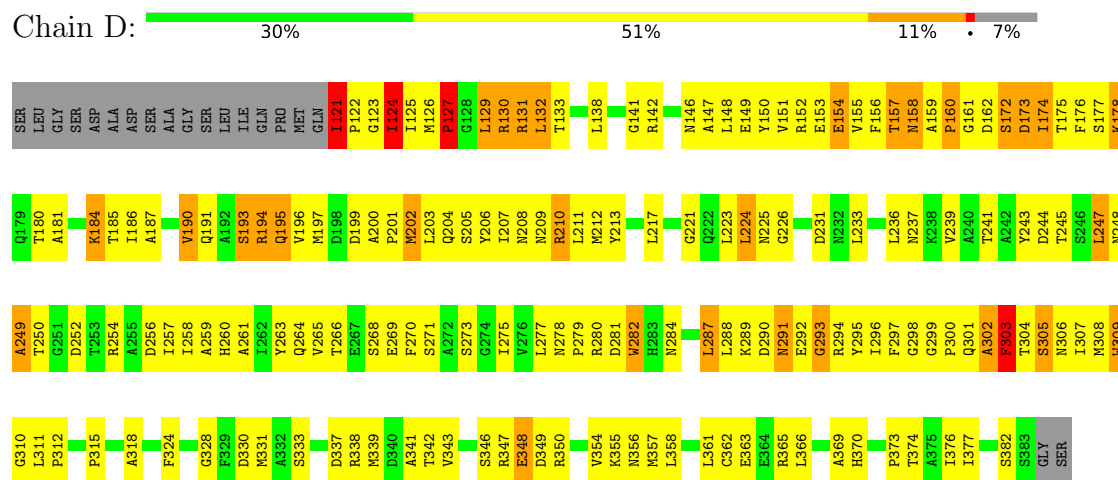
• Molecule 1: Major capsid protein



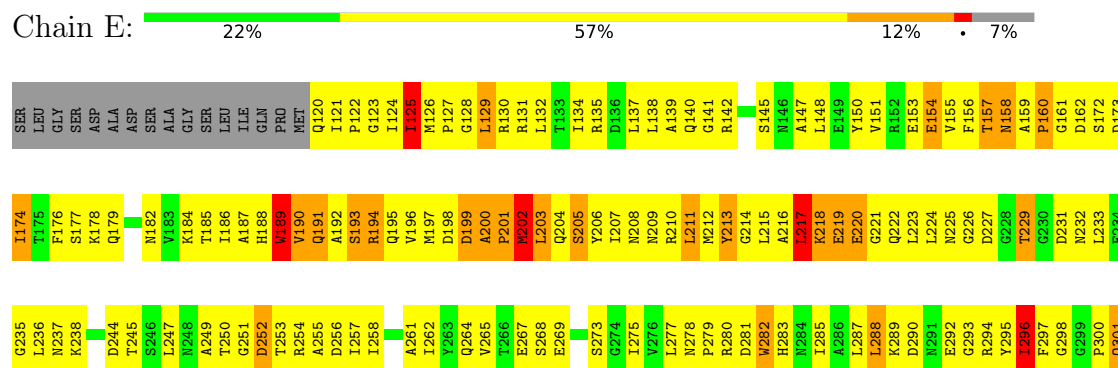
- Molecule 1: Major capsid protein

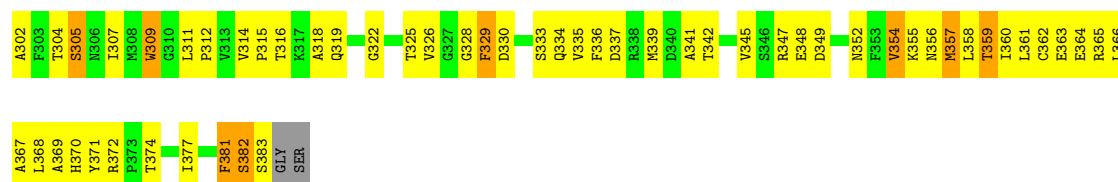


- Molecule 1: Major capsid protein



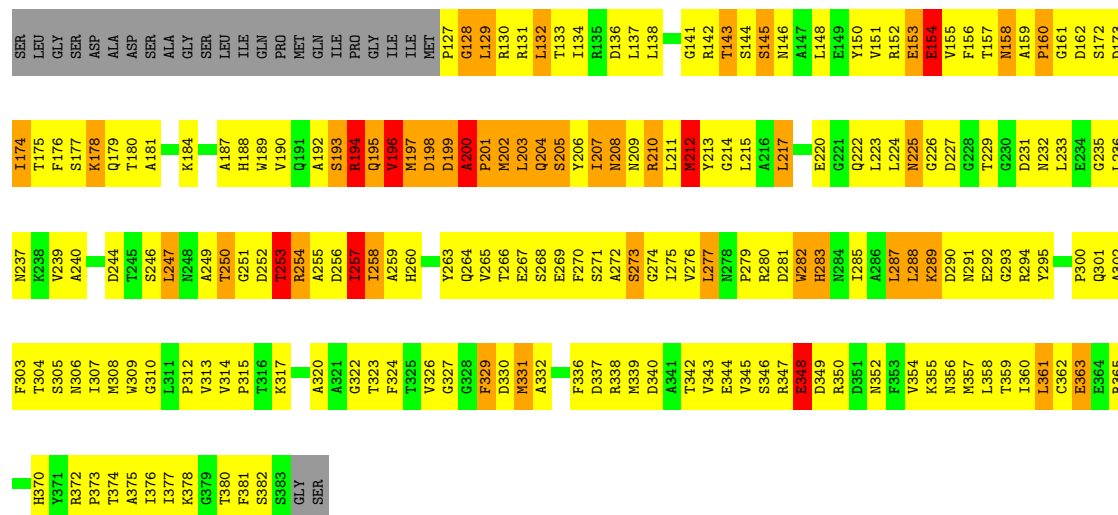
- Molecule 1: Major capsid protein





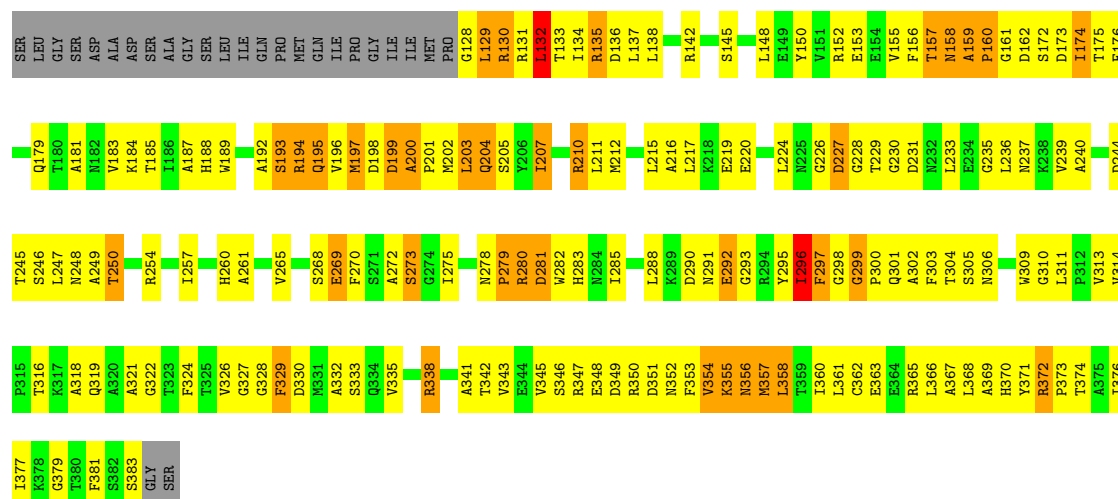
- Molecule 1: Major capsid protein

Chain F: 19% 54% 15% 9%



- Molecule 1: Major capsid protein

Chain G: 27% 49% 13% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	553.03Å 574.39Å 587.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 3.65 35.00 – 3.65	Depositor EDS
% Data completeness (in resolution range)	64.8 (35.00-3.65) 54.3 (35.00-3.65)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 3.66Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.366 , (Not available) 0.311 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	72.5	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.23$, $\langle L^2 \rangle = 0.09$	Xtriage
Estimated twinning fraction	0.276 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.51	EDS
Total number of atoms	13590	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.58% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.59	3/2013 (0.1%)	0.99	13/2730 (0.5%)
1	B	0.56	3/1968 (0.2%)	1.17	22/2669 (0.8%)
1	C	0.49	1/1952 (0.1%)	0.95	6/2647 (0.2%)
1	D	0.49	2/1996 (0.1%)	1.03	19/2708 (0.7%)
1	E	0.56	2/2005 (0.1%)	1.07	16/2720 (0.6%)
1	F	0.57	0/1952	1.15	20/2647 (0.8%)
1	G	0.52	0/1944	1.19	24/2636 (0.9%)
All	All	0.54	11/13830 (0.1%)	1.08	120/18757 (0.6%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	329	PHE	C-N	-9.49	1.21	1.33
1	A	212	MET	C-N	-9.44	1.21	1.33
1	A	338	ARG	C-N	8.97	1.44	1.33
1	E	288	LEU	C-N	7.97	1.44	1.33
1	D	288	LEU	C-N	-7.91	1.22	1.33
1	B	288	LEU	C-N	-6.75	1.24	1.33
1	A	329	PHE	C-N	-6.14	1.26	1.33
1	C	338	ARG	C-N	6.11	1.42	1.33
1	B	338	ARG	C-N	-5.99	1.25	1.33
1	B	178	LYS	CA-CB	-5.34	1.45	1.52
1	D	338	ARG	C-N	-5.32	1.26	1.33

All (120) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	195	GLN	N-CA-C	-17.61	91.46	111.71
1	G	207	ILE	N-CA-C	15.32	125.16	110.30
1	D	250	THR	N-CA-C	14.47	127.09	111.03
1	G	228	GLY	N-CA-C	13.27	133.63	115.32
1	E	202	MET	N-CA-C	13.11	125.27	110.97
1	B	203	LEU	N-CA-C	-12.42	96.30	111.33
1	B	202	MET	N-CA-C	-11.82	98.11	111.82
1	F	250	THR	N-CA-C	-11.63	95.12	110.24
1	B	250	THR	N-CA-C	11.54	125.09	111.02
1	G	227	ASP	N-CA-C	10.47	126.19	113.41
1	E	193	SER	N-CA-C	10.36	125.39	109.96
1	E	217	LEU	N-CA-C	-9.75	99.67	112.34
1	G	207	ILE	CB-CA-C	-9.59	99.82	111.81
1	B	250	THR	CB-CA-C	-9.44	95.92	110.92
1	A	202	MET	N-CA-C	-9.29	99.97	111.11
1	G	281	ASP	N-CA-C	-9.25	101.77	112.87
1	B	204	GLN	N-CA-C	8.96	120.74	110.97
1	F	212	MET	O-C-N	8.76	131.20	122.09
1	F	257	ILE	CB-CA-C	-8.45	101.25	111.81
1	E	211	LEU	N-CA-C	8.34	121.50	111.82
1	B	196	VAL	N-CA-C	-8.24	92.19	109.34
1	D	123	GLY	N-CA-C	-8.20	99.97	112.51
1	F	288	LEU	CA-C-N	-8.06	109.18	122.39
1	F	288	LEU	C-N-CA	-8.06	109.18	122.39
1	G	297	PHE	N-CA-C	-8.03	102.00	112.68
1	B	197	MET	N-CA-C	7.94	124.39	111.37
1	E	189	TRP	N-CA-C	7.78	120.20	109.54
1	F	157	THR	N-CA-C	-7.78	99.86	110.68
1	B	369	ALA	O-C-N	-7.68	112.82	123.11
1	D	193	SER	N-CA-CB	-7.68	99.01	110.61
1	B	211	LEU	N-CA-C	7.67	120.76	111.40
1	D	302	ALA	N-CA-C	-7.65	101.14	111.54
1	F	332	ALA	N-CA-CB	-7.48	100.56	110.88
1	B	272	ALA	N-CA-C	7.47	120.91	108.73
1	D	157	THR	N-CA-C	-7.46	100.31	110.68
1	G	292	GLU	N-CA-C	-7.29	104.83	113.21
1	B	157	THR	N-CA-C	-7.22	99.51	110.70
1	F	194	ARG	CB-CA-C	-7.21	96.46	110.46
1	A	122	PRO	N-CA-C	-7.15	101.32	113.12
1	G	157	THR	N-CA-C	-7.10	103.47	111.07
1	D	226	GLY	N-CA-C	7.09	129.98	113.18
1	G	200	ALA	N-CA-C	-7.00	104.53	113.77
1	C	330	ASP	N-CA-C	-6.99	103.67	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	272	ALA	CB-CA-C	-6.97	97.73	109.65
1	D	305	SER	N-CA-C	-6.94	103.72	111.28
1	C	224	LEU	O-C-N	6.92	129.29	122.09
1	D	193	SER	N-CA-C	6.86	122.49	113.30
1	B	194	ARG	CB-CA-C	-6.83	96.83	110.42
1	F	258	ILE	N-CA-C	-6.82	102.06	111.89
1	F	204	GLN	CB-CA-C	-6.81	98.03	110.63
1	B	195	GLN	CB-CA-C	-6.76	96.97	110.42
1	E	157	THR	N-CA-C	-6.76	100.23	110.70
1	E	203	LEU	N-CA-CB	-6.66	100.19	109.91
1	A	280	ARG	N-CA-C	6.63	122.24	111.37
1	B	214	GLY	N-CA-C	-6.59	104.61	113.24
1	C	251	GLY	N-CA-C	6.51	123.38	114.92
1	E	202	MET	CB-CA-C	-6.46	101.02	110.96
1	C	331	MET	N-CA-CB	-6.43	100.60	111.27
1	F	205	SER	N-CA-C	-6.38	97.22	110.80
1	D	121	ILE	CA-C-N	6.34	126.25	119.85
1	D	121	ILE	C-N-CA	6.34	126.25	119.85
1	F	200	ALA	C-N-CD	-6.26	99.35	125.00
1	G	210	ARG	N-CA-CB	-6.25	99.93	110.49
1	G	129	LEU	N-CA-C	-6.22	104.26	112.34
1	F	251	GLY	N-CA-C	6.17	123.57	115.36
1	G	273	SER	N-CA-CB	-6.13	101.51	110.40
1	B	212	MET	N-CA-C	-6.08	104.34	110.97
1	F	273	SER	CB-CA-C	6.08	119.24	109.02
1	B	271	SER	CB-CA-C	-6.08	99.87	111.48
1	G	358	LEU	N-CA-C	6.01	118.83	109.52
1	A	338	ARG	CA-C-N	-5.99	111.87	121.58
1	A	338	ARG	C-N-CA	-5.99	111.87	121.58
1	F	250	THR	CB-CA-C	5.98	120.22	109.64
1	G	135	ARG	N-CA-C	5.95	117.44	111.07
1	A	338	ARG	O-C-N	5.95	130.46	122.49
1	E	252	ASP	N-CA-C	-5.95	101.68	110.48
1	F	331	MET	N-CA-C	5.95	120.25	111.87
1	B	288	LEU	O-C-N	-5.91	116.15	123.36
1	E	218	LYS	N-CA-C	5.85	120.44	113.12
1	A	333	SER	N-CA-CB	5.78	119.72	111.05
1	C	297	PHE	N-CA-C	-5.72	100.72	109.65
1	D	249	ALA	CB-CA-C	-5.72	101.51	112.43
1	G	250	THR	N-CA-C	-5.68	104.29	111.11
1	D	202	MET	N-CA-C	-5.65	102.05	111.37
1	G	299	GLY	N-CA-C	-5.63	100.86	112.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	128	GLY	N-CA-C	-5.62	99.85	113.18
1	E	218	LYS	CB-CA-C	-5.62	100.29	109.56
1	A	248	ASN	N-CA-C	-5.62	102.71	110.35
1	B	314	VAL	N-CA-C	5.57	113.67	108.15
1	D	172	SER	N-CA-C	-5.57	106.81	113.21
1	E	381	PHE	N-CA-C	-5.54	101.45	109.59
1	C	331	MET	N-CA-C	5.54	121.27	113.02
1	A	196	VAL	N-CA-C	-5.52	105.12	110.42
1	E	192	ALA	CB-CA-C	-5.47	100.85	112.78
1	F	253	THR	CB-CA-C	-5.42	100.85	109.80
1	B	194	ARG	N-CA-C	5.39	122.28	110.80
1	D	210	ARG	N-CA-C	5.39	119.80	111.56
1	G	280	ARG	CB-CA-C	-5.34	100.92	110.70
1	F	272	ALA	CB-CA-C	-5.33	100.53	109.65
1	E	198	ASP	O-C-N	5.31	128.45	122.19
1	A	333	SER	N-CA-C	-5.30	101.70	109.81
1	F	350	ARG	CB-CA-C	-5.29	110.45	116.54
1	E	221	GLY	N-CA-C	-5.28	106.25	113.27
1	F	208	ASN	N-CA-C	5.26	122.00	110.80
1	D	124	ILE	N-CA-C	5.25	117.41	108.86
1	G	273	SER	N-CA-C	5.22	120.13	113.55
1	G	194	ARG	CB-CA-C	-5.20	99.57	110.17
1	G	203	LEU	N-CA-C	-5.20	104.68	111.02
1	G	159	ALA	CA-C-N	5.20	126.33	119.84
1	G	159	ALA	C-N-CA	5.20	126.33	119.84
1	A	159	ALA	CA-C-N	5.16	126.29	119.84
1	A	159	ALA	C-N-CA	5.16	126.29	119.84
1	D	178	LYS	N-CA-C	-5.13	102.10	110.20
1	E	203	LEU	CB-CA-C	-5.08	103.13	110.96
1	A	247	LEU	N-CA-C	5.06	117.58	111.40
1	D	224	LEU	N-CA-C	5.06	117.77	111.24
1	D	250	THR	CB-CA-C	-5.05	103.13	110.95
1	B	272	ALA	N-CA-CB	-5.04	102.21	110.42
1	D	291	ASN	N-CA-C	-5.04	106.06	113.72
1	B	251	GLY	N-CA-C	5.01	127.83	113.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	369	ALA	Mainchain

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	1978	0	1946	320	0
1	B	1934	0	1897	362	0
1	C	1918	0	1878	354	0
1	D	1961	0	1929	347	0
1	E	1970	0	1937	389	0
1	F	1918	0	1878	372	0
1	G	1911	0	1870	300	0
All	All	13590	0	13335	2329	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 86.

All (2329) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:127:PRO:HB2	1:E:213:TYR:CD1	1.32	1.62
1:D:125:ILE:HD11	1:D:208:ASN:CG	1.32	1.54
1:D:125:ILE:HD11	1:D:208:ASN:ND2	1.26	1.45
1:C:196:VAL:HG12	1:C:203:LEU:CD1	1.44	1.45
1:B:201:PRO:O	1:B:204:GLN:CB	1.67	1.41
1:D:127:PRO:CG	1:D:212:MET:HE3	1.52	1.37
1:G:197:MET:CE	1:G:358:LEU:HD21	1.56	1.36
1:C:213:TYR:CZ	1:C:217:LEU:HD11	1.64	1.33
1:E:233:LEU:CD1	1:E:366:LEU:HD11	1.56	1.33
1:D:203:LEU:O	1:D:207:ILE:HD13	1.24	1.32
1:E:127:PRO:CB	1:E:213:TYR:HD1	1.44	1.30
1:F:199:ASP:O	1:F:201:PRO:HD2	1.31	1.29
1:E:206:TYR:O	1:E:210:ARG:HB2	1.28	1.29
1:G:197:MET:HE2	1:G:358:LEU:CD2	1.61	1.29
1:C:196:VAL:CG1	1:C:203:LEU:HD11	1.59	1.29
1:C:194:ARG:O	1:C:196:VAL:N	1.66	1.28
1:F:203:LEU:O	1:F:206:TYR:CB	1.80	1.27
1:F:203:LEU:O	1:F:206:TYR:HB3	1.29	1.26
1:A:287:LEU:C	1:A:288:LEU:HD23	1.58	1.26
1:E:227:ASP:HB3	1:E:229:THR:CG2	1.65	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:LEU:HD12	1:B:211:LEU:O	1.28	1.26
1:E:202:MET:O	1:E:205:SER:HB3	1.07	1.25
1:G:197:MET:CE	1:G:358:LEU:CD2	2.13	1.24
1:C:210:ARG:NH2	1:D:153:GLU:CD	1.97	1.23
1:B:193:SER:O	1:B:196:VAL:CG2	1.87	1.23
1:C:346:SER:O	1:C:359:THR:HG22	1.36	1.23
1:G:278:ASN:OD1	1:G:279:PRO:HD2	1.38	1.22
1:A:287:LEU:HD12	1:A:287:LEU:O	1.39	1.21
1:D:125:ILE:CD1	1:D:208:ASN:OD1	1.89	1.20
1:B:215:LEU:C	1:B:215:LEU:CD2	2.12	1.20
1:A:285:ILE:O	1:A:288:LEU:CD2	1.91	1.19
1:E:202:MET:HE3	1:E:203:LEU:H	1.07	1.18
1:D:125:ILE:CD1	1:D:208:ASN:CG	2.17	1.18
1:A:285:ILE:O	1:A:288:LEU:HD21	1.02	1.17
1:D:247:LEU:HD23	1:D:247:LEU:O	1.45	1.17
1:A:368:LEU:HD21	1:A:370:HIS:NE2	1.60	1.16
1:B:201:PRO:C	1:B:204:GLN:H	1.52	1.16
1:D:190:VAL:HG12	1:D:211:LEU:HD21	1.28	1.16
1:A:269:GLU:HB3	1:F:217:LEU:HD21	1.22	1.15
1:F:203:LEU:C	1:F:203:LEU:CD2	2.18	1.15
1:C:129:LEU:HD11	1:D:331:MET:CE	1.75	1.15
1:C:129:LEU:HD11	1:D:331:MET:HE1	1.19	1.14
1:C:233:LEU:N	1:C:233:LEU:HD23	1.49	1.14
1:D:190:VAL:CG1	1:D:211:LEU:HD21	1.78	1.14
1:E:127:PRO:CB	1:E:213:TYR:CD1	2.23	1.14
1:D:127:PRO:HD3	1:D:212:MET:HE2	1.23	1.13
1:B:250:THR:HB	1:B:251:GLY:CA	1.76	1.13
1:C:213:TYR:CE2	1:C:217:LEU:HD11	1.84	1.13
1:C:195:GLN:HE22	1:C:198:ASP:CB	1.60	1.13
1:C:196:VAL:CG1	1:C:203:LEU:HD21	1.78	1.13
1:D:127:PRO:HD3	1:D:212:MET:CE	1.76	1.13
1:F:194:ARG:O	1:F:197:MET:HB3	1.48	1.13
1:F:200:ALA:HB3	1:F:201:PRO:HD3	1.20	1.13
1:C:196:VAL:CG1	1:C:203:LEU:CD1	2.22	1.13
1:A:285:ILE:C	1:A:288:LEU:HD21	1.74	1.12
1:B:131:ARG:NH2	1:B:220:GLU:OE1	1.81	1.12
1:F:142:ARG:HG3	1:F:337:ASP:HB2	1.16	1.12
1:B:215:LEU:C	1:B:215:LEU:HD23	1.65	1.12
1:D:125:ILE:CD1	1:D:208:ASN:ND2	2.12	1.12
1:G:338:ARG:HH11	1:G:338:ARG:CG	1.58	1.12
1:C:225:ASN:HB3	1:C:237:ASN:HD22	1.08	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:LEU:N	1:B:277:LEU:HD23	1.52	1.11
1:F:203:LEU:C	1:F:203:LEU:HD23	1.68	1.11
1:F:343:VAL:HG12	1:F:362:CYS:HB3	1.24	1.11
1:G:198:ASP:O	1:G:199:ASP:OD1	1.69	1.10
1:C:232:ASN:C	1:C:233:LEU:HD23	1.76	1.10
1:F:142:ARG:CG	1:F:337:ASP:HB2	1.79	1.10
1:B:193:SER:O	1:B:196:VAL:HG23	1.49	1.10
1:B:212:MET:O	1:B:215:LEU:N	1.83	1.10
1:B:127:PRO:HA	1:B:129:LEU:HD13	1.18	1.09
1:E:215:LEU:O	1:E:218:LYS:HB3	1.52	1.09
1:E:227:ASP:HB3	1:E:229:THR:HG23	1.31	1.09
1:A:125:ILE:CG2	1:A:204:GLN:NE2	2.15	1.09
1:B:201:PRO:O	1:B:204:GLN:HB3	1.44	1.09
1:E:194:ARG:HA	1:E:358:LEU:CD1	1.82	1.09
1:E:202:MET:HE3	1:E:203:LEU:N	1.67	1.09
1:C:287:LEU:HD22	1:C:300:PRO:HB3	1.35	1.09
1:A:288:LEU:HD23	1:A:288:LEU:N	1.56	1.09
1:F:246:SER:C	1:F:247:LEU:HD23	1.77	1.08
1:B:296:ILE:HD13	1:B:296:ILE:H	1.16	1.08
1:C:196:VAL:HG13	1:C:203:LEU:HD21	1.08	1.08
1:E:202:MET:O	1:E:205:SER:CB	2.01	1.08
1:F:247:LEU:HD23	1:F:247:LEU:N	1.48	1.08
1:G:129:LEU:CD2	1:G:131:ARG:HB2	1.84	1.08
1:A:287:LEU:C	1:A:288:LEU:CD2	2.27	1.07
1:C:130:ARG:HG3	1:D:271:SER:HB2	1.36	1.07
1:G:158:ASN:OD1	1:G:172:SER:HA	1.53	1.07
1:A:197:MET:SD	1:A:203:LEU:HD13	1.95	1.07
1:A:153:GLU:OE1	1:F:210:ARG:NH2	1.88	1.07
1:C:194:ARG:NH1	1:C:347:ARG:HH22	1.51	1.07
1:D:122:PRO:HG3	1:D:343:VAL:O	1.54	1.06
1:E:203:LEU:O	1:E:206:TYR:N	1.85	1.06
1:D:127:PRO:HG3	1:D:212:MET:CE	1.83	1.06
1:G:129:LEU:HD22	1:G:131:ARG:HB2	1.12	1.06
1:B:250:THR:CB	1:B:251:GLY:HA3	1.78	1.06
1:G:197:MET:HE2	1:G:358:LEU:HD22	1.37	1.06
1:B:217:LEU:CD1	1:B:217:LEU:C	2.30	1.05
1:C:196:VAL:CG1	1:C:203:LEU:CD2	2.35	1.05
1:D:129:LEU:HD22	1:D:130:ARG:H	1.16	1.05
1:A:202:MET:O	1:A:206:TYR:N	1.88	1.05
1:C:195:GLN:NE2	1:C:198:ASP:HB3	1.70	1.04
1:G:329:PHE:HA	1:G:332:ALA:HB3	1.39	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:187:ALA:HB2	1:C:363:GLU:HA	1.39	1.04
1:D:247:LEU:HD23	1:D:247:LEU:C	1.81	1.04
1:F:324:PHE:HD2	1:F:381:PHE:CE1	1.73	1.04
1:C:203:LEU:O	1:C:206:TYR:N	1.88	1.04
1:D:203:LEU:O	1:D:207:ILE:CD1	2.04	1.04
1:G:199:ASP:C	1:G:201:PRO:HD2	1.82	1.04
1:B:217:LEU:C	1:B:217:LEU:HD13	1.77	1.04
1:B:201:PRO:O	1:B:204:GLN:CA	2.07	1.03
1:D:249:ALA:O	1:D:252:ASP:OD2	1.75	1.03
1:F:194:ARG:NH1	1:F:347:ARG:NH1	2.06	1.03
1:B:158:ASN:HB2	1:B:172:SER:HA	1.35	1.03
1:B:195:GLN:C	1:B:197:MET:N	2.06	1.03
1:C:196:VAL:HG13	1:C:203:LEU:CD2	1.87	1.03
1:D:127:PRO:CD	1:D:212:MET:CE	2.36	1.03
1:G:158:ASN:HD22	1:G:159:ALA:N	1.54	1.03
1:B:201:PRO:O	1:B:204:GLN:N	1.91	1.03
1:C:195:GLN:HE22	1:C:198:ASP:HB3	0.89	1.03
1:A:127:PRO:HB3	1:A:212:MET:HB3	1.39	1.02
1:B:215:LEU:HD23	1:B:215:LEU:O	1.56	1.02
1:E:233:LEU:HD11	1:E:366:LEU:HD11	1.03	1.02
1:C:201:PRO:O	1:C:204:GLN:HB2	1.59	1.02
1:F:210:ARG:HH11	1:F:210:ARG:HG2	1.20	1.01
1:F:282:TRP:CZ3	1:F:308:MET:HE3	1.95	1.01
1:D:125:ILE:HD11	1:D:208:ASN:HD21	1.26	1.01
1:G:197:MET:HE1	1:G:358:LEU:HD21	1.43	1.01
1:F:131:ARG:NH2	1:F:220:GLU:OE1	1.93	1.01
1:B:250:THR:HB	1:B:251:GLY:HA3	1.01	1.00
1:F:203:LEU:HD22	1:F:204:GLN:N	1.74	1.00
1:B:201:PRO:O	1:B:204:GLN:HB2	1.61	1.00
1:G:296:ILE:HG22	1:G:297:PHE:N	1.76	1.00
1:A:125:ILE:CG2	1:A:204:GLN:HE22	1.71	1.00
1:A:368:LEU:CD2	1:A:370:HIS:NE2	2.24	1.00
1:E:194:ARG:HA	1:E:358:LEU:HD13	1.39	1.00
1:E:227:ASP:HB3	1:E:229:THR:HG21	1.41	1.00
1:C:357:MET:HE1	1:D:178:LYS:HG2	1.42	1.00
1:F:324:PHE:CD2	1:F:381:PHE:HE1	1.78	1.00
1:G:338:ARG:HH11	1:G:338:ARG:HG3	0.86	0.99
1:C:194:ARG:O	1:C:196:VAL:HG23	1.62	0.99
1:G:303:PHE:HD2	1:G:304:THR:H	1.07	0.99
1:A:125:ILE:HG21	1:A:204:GLN:NE2	1.74	0.99
1:G:184:LYS:NZ	1:G:230:GLY:O	1.93	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:LEU:HD11	1:A:366:LEU:HD11	1.43	0.98
1:F:204:GLN:C	1:F:206:TYR:H	1.63	0.98
1:E:125:ILE:CD1	1:E:127:PRO:HD3	1.92	0.98
1:F:329:PHE:HD1	1:F:329:PHE:N	1.62	0.98
1:C:202:MET:O	1:C:205:SER:N	1.96	0.98
1:C:213:TYR:CE2	1:C:217:LEU:HD21	1.97	0.98
1:G:202:MET:O	1:G:205:SER:OG	1.81	0.97
1:B:249:ALA:HB3	1:B:252:ASP:OD2	1.64	0.97
1:G:227:ASP:OD1	1:G:227:ASP:O	1.82	0.97
1:F:244:ASP:OD2	1:F:247:LEU:HD21	1.63	0.97
1:F:202:MET:O	1:F:205:SER:N	1.97	0.97
1:G:301:GLN:HG3	1:G:302:ALA:H	1.26	0.97
1:E:157:THR:HG22	1:E:267:GLU:HG3	1.45	0.97
1:E:210:ARG:HH22	1:F:153:GLU:CD	1.73	0.96
1:B:211:LEU:HD12	1:B:211:LEU:C	1.72	0.96
1:C:270:PHE:HE2	1:C:331:MET:HG2	1.30	0.96
1:C:201:PRO:O	1:C:204:GLN:N	1.99	0.95
1:C:130:ARG:CG	1:D:271:SER:HB2	1.95	0.95
1:E:233:LEU:HD11	1:E:366:LEU:CD1	1.96	0.95
1:C:287:LEU:HD22	1:C:300:PRO:CB	1.96	0.95
1:D:127:PRO:CD	1:D:212:MET:HE3	1.97	0.94
1:A:125:ILE:HG23	1:A:204:GLN:HE22	1.32	0.94
1:D:282:TRP:HE1	1:D:304:THR:HA	1.32	0.94
1:G:129:LEU:HD22	1:G:131:ARG:CB	1.97	0.94
1:F:200:ALA:O	1:F:202:MET:N	2.01	0.94
1:G:301:GLN:HG3	1:G:302:ALA:N	1.82	0.94
1:B:288:LEU:O	1:B:296:ILE:HD11	1.68	0.94
1:E:227:ASP:CB	1:E:229:THR:HG23	1.98	0.94
1:D:125:ILE:CD1	1:D:208:ASN:HD21	1.77	0.93
1:E:157:THR:HG22	1:E:267:GLU:CG	1.98	0.93
1:C:183:VAL:HA	1:C:367:ALA:HB2	1.49	0.93
1:D:125:ILE:HD11	1:D:208:ASN:OD1	1.57	0.93
1:F:203:LEU:O	1:F:203:LEU:HD23	1.66	0.93
1:F:345:VAL:HG13	1:F:358:LEU:HD21	1.50	0.93
1:E:207:ILE:HG13	1:E:208:ASN:H	1.32	0.93
1:A:195:GLN:HG3	1:A:196:VAL:HG23	1.51	0.93
1:B:207:ILE:O	1:B:211:LEU:HB3	1.67	0.93
1:F:197:MET:O	1:F:197:MET:SD	2.27	0.93
1:C:366:LEU:HD22	1:C:367:ALA:H	1.32	0.93
1:G:174:ILE:HD13	1:G:174:ILE:H	1.33	0.93
1:G:329:PHE:H	1:G:329:PHE:HD2	0.98	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:VAL:HG22	1:A:377:ILE:HD13	1.51	0.92
1:B:288:LEU:O	1:B:296:ILE:CD1	2.16	0.92
1:C:213:TYR:HE2	1:C:217:LEU:HD21	1.34	0.92
1:F:253:THR:HG23	1:F:256:ASP:OD1	1.68	0.92
1:D:127:PRO:CG	1:D:212:MET:CE	2.42	0.92
1:B:277:LEU:N	1:B:277:LEU:CD2	2.29	0.92
1:F:225:ASN:HB3	1:F:237:ASN:HD22	1.33	0.92
1:G:351:ASP:O	1:G:355:LYS:HG2	1.70	0.91
1:F:200:ALA:CB	1:F:201:PRO:HD3	2.00	0.91
1:G:304:THR:HG22	1:G:305:SER:H	1.36	0.91
1:A:158:ASN:CG	1:A:172:SER:HA	1.94	0.91
1:F:194:ARG:NH1	1:F:347:ARG:HH12	1.64	0.91
1:G:132:LEU:HB2	1:G:136:ASP:HB2	1.52	0.91
1:F:200:ALA:HB3	1:F:201:PRO:CD	1.99	0.91
1:G:196:VAL:HG22	1:G:202:MET:HE2	1.49	0.91
1:A:174:ILE:H	1:A:174:ILE:HD13	1.33	0.91
1:G:303:PHE:HD2	1:G:304:THR:N	1.69	0.91
1:E:158:ASN:CG	1:E:172:SER:HA	1.95	0.91
1:G:329:PHE:HA	1:G:332:ALA:CB	1.99	0.91
1:F:282:TRP:HZ3	1:F:308:MET:HE3	1.35	0.91
1:A:263:TYR:OH	1:A:267:GLU:OE2	1.87	0.91
1:B:195:GLN:C	1:B:197:MET:H	1.66	0.91
1:C:213:TYR:CE1	1:C:217:LEU:HD11	2.05	0.91
1:C:233:LEU:HD11	1:C:366:LEU:CD1	2.01	0.90
1:F:199:ASP:O	1:F:201:PRO:CD	2.18	0.90
1:E:174:ILE:HD13	1:E:174:ILE:H	1.36	0.90
1:D:126:MET:SD	1:D:127:PRO:HD2	2.11	0.90
1:F:202:MET:SD	1:F:203:LEU:N	2.45	0.90
1:C:347:ARG:O	1:C:349:ASP:N	2.05	0.90
1:E:233:LEU:HD13	1:E:366:LEU:HD11	1.53	0.90
1:E:345:VAL:HG22	1:E:360:ILE:HA	1.54	0.90
1:G:338:ARG:HG3	1:G:338:ARG:NH1	1.67	0.89
1:F:174:ILE:H	1:F:174:ILE:HD13	1.36	0.89
1:F:211:LEU:HD21	1:F:362:CYS:SG	2.13	0.89
1:B:195:GLN:O	1:B:197:MET:N	2.04	0.89
1:D:194:ARG:HG2	1:D:195:GLN:H	1.37	0.89
1:F:194:ARG:O	1:F:197:MET:CB	2.20	0.89
1:A:127:PRO:HD3	1:A:212:MET:HE3	1.52	0.89
1:C:206:TYR:OH	1:C:210:ARG:NH1	2.05	0.89
1:E:220:GLU:OE2	1:E:316:THR:CG2	2.21	0.89
1:C:344:GLU:HB2	1:C:361:LEU:HD11	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:VAL:CG1	1:B:374:THR:HB	2.03	0.89
1:B:215:LEU:C	1:B:215:LEU:HD22	1.96	0.89
1:E:206:TYR:O	1:E:210:ARG:CB	2.19	0.89
1:F:354:VAL:HG13	1:F:355:LYS:HG3	1.52	0.89
1:G:327:GLY:O	1:G:329:PHE:CD2	2.25	0.89
1:E:155:VAL:HG23	1:E:174:ILE:HG22	1.53	0.89
1:F:247:LEU:N	1:F:247:LEU:CD2	2.30	0.88
1:C:233:LEU:N	1:C:233:LEU:CD2	2.30	0.88
1:G:200:ALA:O	1:G:204:GLN:N	2.06	0.88
1:D:158:ASN:CG	1:D:172:SER:HA	1.97	0.88
1:D:190:VAL:HG12	1:D:211:LEU:CD2	2.03	0.88
1:D:247:LEU:HD21	1:D:260:HIS:HB3	1.56	0.88
1:F:343:VAL:CG1	1:F:362:CYS:HB3	2.01	0.88
1:B:127:PRO:CA	1:B:129:LEU:HD13	2.02	0.88
1:A:195:GLN:HG3	1:A:196:VAL:H	1.37	0.88
1:F:158:ASN:CG	1:F:172:SER:HA	1.98	0.88
1:A:376:ILE:C	1:A:377:ILE:HD12	1.99	0.88
1:C:366:LEU:HD22	1:C:367:ALA:N	1.89	0.87
1:E:137:LEU:HD22	1:E:329:PHE:HB2	1.56	0.87
1:F:155:VAL:HG23	1:F:174:ILE:HG22	1.56	0.87
1:F:131:ARG:HD2	1:F:315:PRO:O	1.74	0.87
1:B:185:THR:HG22	1:B:365:ARG:HG2	1.54	0.87
1:B:155:VAL:CG1	1:B:374:THR:CB	2.52	0.87
1:B:345:VAL:HG12	1:B:360:ILE:HA	1.56	0.87
1:E:295:TYR:OH	1:F:256:ASP:OD2	1.91	0.87
1:A:155:VAL:HG23	1:A:174:ILE:HG22	1.54	0.87
1:B:127:PRO:C	1:B:129:LEU:H	1.81	0.87
1:B:342:THR:O	1:B:362:CYS:HA	1.72	0.87
1:C:194:ARG:CZ	1:C:347:ARG:HH22	1.88	0.87
1:F:361:LEU:HD13	1:F:361:LEU:O	1.75	0.87
1:C:130:ARG:HG3	1:D:271:SER:CB	2.04	0.86
1:B:131:ARG:NH2	1:B:220:GLU:CD	2.32	0.86
1:C:287:LEU:CD2	1:C:300:PRO:CB	2.52	0.86
1:A:141:GLY:O	1:A:336:PHE:HA	1.74	0.86
1:A:343:VAL:HG12	1:A:362:CYS:HB2	1.54	0.86
1:B:201:PRO:C	1:B:204:GLN:N	2.33	0.86
1:G:198:ASP:O	1:G:199:ASP:CG	2.16	0.86
1:G:200:ALA:N	1:G:201:PRO:CD	2.38	0.86
1:B:159:ALA:O	1:B:172:SER:HB3	1.73	0.86
1:C:213:TYR:CE2	1:C:217:LEU:CD1	2.58	0.86
1:G:316:THR:HG22	1:G:318:ALA:H	1.37	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:233:LEU:CD1	1:E:366:LEU:CD1	2.51	0.86
1:G:155:VAL:HG11	1:G:374:THR:OG1	1.75	0.86
1:D:122:PRO:HG3	1:D:343:VAL:HG23	1.58	0.86
1:G:199:ASP:HB3	1:G:202:MET:HB3	1.56	0.85
1:A:153:GLU:CD	1:F:210:ARG:HH21	1.84	0.85
1:D:127:PRO:HG3	1:D:212:MET:HE3	0.87	0.85
1:D:155:VAL:HG12	1:D:374:THR:OG1	1.76	0.85
1:A:300:PRO:HA	1:A:303:PHE:HB3	1.59	0.85
1:E:207:ILE:HG13	1:E:208:ASN:N	1.91	0.85
1:C:197:MET:SD	1:C:358:LEU:CD1	2.65	0.85
1:D:207:ILE:HG13	1:D:211:LEU:HD12	1.57	0.85
1:C:203:LEU:O	1:C:206:TYR:CB	2.25	0.85
1:C:258:ILE:HD11	1:C:275:ILE:HG12	1.59	0.85
1:C:366:LEU:C	1:C:366:LEU:HD13	2.01	0.85
1:E:202:MET:CE	1:E:203:LEU:N	2.39	0.85
1:G:329:PHE:HD2	1:G:329:PHE:N	1.75	0.84
1:B:194:ARG:NH2	1:B:347:ARG:NH2	2.25	0.84
1:B:132:LEU:HD23	1:B:132:LEU:H	1.42	0.84
1:B:156:PHE:HB3	1:B:158:ASN:OD1	1.78	0.84
1:E:213:TYR:O	1:E:217:LEU:HB2	1.77	0.84
1:F:203:LEU:CD2	1:F:204:GLN:N	2.38	0.84
1:A:195:GLN:O	1:A:199:ASP:CG	2.20	0.83
1:E:220:GLU:OE2	1:E:316:THR:HG21	1.77	0.83
1:A:296:ILE:HG23	1:A:297:PHE:CD2	2.12	0.83
1:E:355:LYS:O	1:E:357:MET:HG2	1.78	0.83
1:B:296:ILE:H	1:B:296:ILE:CD1	1.91	0.83
1:D:194:ARG:HG2	1:D:195:GLN:N	1.91	0.83
1:B:194:ARG:HH22	1:B:347:ARG:HH22	1.23	0.83
1:F:142:ARG:HG2	1:F:337:ASP:O	1.78	0.83
1:F:253:THR:O	1:F:254:ARG:C	2.21	0.83
1:G:132:LEU:HB2	1:G:136:ASP:CB	2.08	0.83
1:C:210:ARG:HH22	1:D:153:GLU:CD	1.83	0.83
1:E:210:ARG:NH2	1:F:153:GLU:OE1	2.10	0.83
1:G:366:LEU:C	1:G:366:LEU:HD12	2.03	0.83
1:C:196:VAL:HG12	1:C:203:LEU:CG	2.08	0.83
1:F:202:MET:HG3	1:F:203:LEU:H	1.43	0.83
1:C:233:LEU:CD1	1:C:366:LEU:HD11	2.09	0.82
1:D:132:LEU:HD23	1:D:132:LEU:H	1.41	0.82
1:A:159:ALA:HB1	1:A:160:PRO:HD2	1.62	0.82
1:A:194:ARG:O	1:A:198:ASP:HB2	1.79	0.82
1:B:217:LEU:HD13	1:B:217:LEU:O	1.78	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:316:THR:HG22	1:B:318:ALA:H	1.44	0.82
1:C:210:ARG:NH2	1:D:153:GLU:OE1	2.03	0.82
1:E:210:ARG:NH2	1:F:153:GLU:CD	2.37	0.82
1:A:275:ILE:HD12	1:A:308:MET:SD	2.20	0.82
1:D:129:LEU:HD22	1:D:130:ARG:N	1.94	0.82
1:F:194:ARG:HH12	1:F:347:ARG:HH12	1.26	0.82
1:G:332:ALA:HB1	1:G:376:ILE:HD11	1.62	0.82
1:E:138:LEU:HD23	1:E:329:PHE:HB3	1.59	0.82
1:A:129:LEU:HD23	1:A:129:LEU:H	1.45	0.81
1:B:277:LEU:HD23	1:B:277:LEU:H	1.43	0.81
1:C:270:PHE:CE2	1:C:331:MET:HG2	2.14	0.81
1:D:202:MET:HA	1:D:205:SER:OG	1.80	0.81
1:E:132:LEU:HD23	1:E:132:LEU:H	1.43	0.81
1:C:202:MET:O	1:C:203:LEU:C	2.23	0.81
1:F:129:LEU:H	1:F:129:LEU:HD12	1.45	0.81
1:F:203:LEU:O	1:F:206:TYR:HB2	1.76	0.81
1:G:138:LEU:HD23	1:G:329:PHE:HB3	1.61	0.81
1:G:158:ASN:ND2	1:G:159:ALA:N	2.29	0.81
1:B:207:ILE:O	1:B:211:LEU:CB	2.28	0.81
1:F:194:ARG:CZ	1:F:347:ARG:NH1	2.44	0.81
1:D:190:VAL:CG1	1:D:211:LEU:CD2	2.59	0.81
1:G:290:ASP:HB3	1:G:292:GLU:HB3	1.63	0.81
1:F:287:LEU:HD23	1:F:287:LEU:H	1.46	0.81
1:E:203:LEU:O	1:E:204:GLN:C	2.23	0.80
1:B:336:PHE:HB2	1:B:367:ALA:HB3	1.63	0.80
1:D:155:VAL:CG1	1:D:374:THR:CB	2.60	0.80
1:D:155:VAL:CG1	1:D:374:THR:OG1	2.29	0.80
1:D:303:PHE:HA	1:D:306:ASN:HB3	1.63	0.80
1:E:211:LEU:HD21	1:E:360:ILE:HD13	1.63	0.80
1:C:207:ILE:HA	1:C:211:LEU:HB3	1.63	0.80
1:E:215:LEU:O	1:E:218:LYS:CB	2.27	0.80
1:E:322:GLY:HA2	1:E:381:PHE:HB2	1.63	0.80
1:F:327:GLY:N	1:F:329:PHE:HE1	1.79	0.80
1:D:295:TYR:HD1	1:D:299:GLY:HA2	1.46	0.80
1:B:125:ILE:HG12	1:B:127:PRO:HD3	1.64	0.80
1:B:158:ASN:H	1:B:158:ASN:ND2	1.76	0.80
1:C:184:LYS:HD2	1:C:231:ASP:HA	1.64	0.80
1:F:202:MET:CG	1:F:203:LEU:N	2.44	0.80
1:A:266:THR:HG21	1:F:279:PRO:HB3	1.64	0.80
1:C:233:LEU:CD1	1:C:366:LEU:CD1	2.60	0.80
1:G:281:ASP:OD2	1:G:322:GLY:N	2.12	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:338:ARG:CG	1:G:338:ARG:NH1	2.30	0.79
1:B:127:PRO:O	1:B:129:LEU:HD22	1.83	0.79
1:B:129:LEU:HD23	1:B:129:LEU:C	2.07	0.79
1:C:131:ARG:NH2	1:C:220:GLU:OE1	2.14	0.79
1:D:349:ASP:OD1	1:D:350:ARG:N	2.16	0.79
1:F:195:GLN:O	1:F:198:ASP:N	2.12	0.79
1:B:159:ALA:HB1	1:B:160:PRO:HD2	1.62	0.79
1:F:244:ASP:OD2	1:F:247:LEU:CD2	2.30	0.79
1:A:123:GLY:O	1:A:124:ILE:HG23	1.81	0.79
1:G:199:ASP:C	1:G:201:PRO:CD	2.56	0.79
1:C:194:ARG:HG2	1:C:195:GLN:N	1.97	0.79
1:E:215:LEU:O	1:E:218:LYS:N	2.16	0.79
1:E:342:THR:O	1:E:362:CYS:HA	1.81	0.79
1:D:159:ALA:HB1	1:D:160:PRO:HD2	1.65	0.79
1:B:194:ARG:HH22	1:B:347:ARG:NH2	1.81	0.79
1:D:247:LEU:O	1:D:247:LEU:CD2	2.30	0.79
1:D:356:ASN:CG	1:E:178:LYS:HZ1	1.89	0.79
1:E:123:GLY:C	1:E:124:ILE:HG13	2.07	0.79
1:F:288:LEU:HD23	1:F:289:LYS:N	1.98	0.79
1:A:287:LEU:CA	1:A:288:LEU:HD23	2.13	0.78
1:C:225:ASN:HB3	1:C:237:ASN:ND2	1.94	0.78
1:F:282:TRP:HZ3	1:F:308:MET:CE	1.96	0.78
1:B:358:LEU:N	1:B:358:LEU:HD12	1.98	0.78
1:C:347:ARG:C	1:C:349:ASP:H	1.88	0.78
1:F:203:LEU:O	1:F:206:TYR:N	2.17	0.78
1:G:156:PHE:CE2	1:G:158:ASN:HB3	2.19	0.78
1:C:201:PRO:O	1:C:204:GLN:CB	2.30	0.78
1:G:155:VAL:CG1	1:G:374:THR:HG21	2.14	0.78
1:B:276:VAL:C	1:B:277:LEU:HD23	2.07	0.78
1:C:343:VAL:HG12	1:C:362:CYS:HB2	1.66	0.78
1:E:216:ALA:C	1:E:218:LYS:N	2.36	0.78
1:A:190:VAL:HG12	1:A:211:LEU:HD21	1.64	0.78
1:B:193:SER:O	1:B:196:VAL:HG22	1.81	0.78
1:G:224:LEU:HD21	1:G:319:GLN:HB2	1.66	0.78
1:C:197:MET:SD	1:C:358:LEU:HD11	2.23	0.78
1:D:194:ARG:CG	1:D:195:GLN:H	1.94	0.78
1:F:200:ALA:O	1:F:201:PRO:C	2.26	0.78
1:G:156:PHE:CD2	1:G:158:ASN:HB3	2.18	0.77
1:A:197:MET:SD	1:A:197:MET:C	2.67	0.77
1:A:269:GLU:HB3	1:F:217:LEU:CD2	2.11	0.77
1:F:324:PHE:CD2	1:F:381:PHE:CE1	2.61	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:138:LEU:CD2	1:G:329:PHE:HB3	2.14	0.77
1:E:190:VAL:N	1:E:360:ILE:HD11	1.98	0.77
1:B:155:VAL:HG11	1:B:374:THR:HB	1.64	0.77
1:F:198:ASP:C	1:F:200:ALA:N	2.38	0.77
1:E:194:ARG:HG3	1:E:358:LEU:HD11	1.66	0.77
1:E:203:LEU:C	1:E:205:SER:N	2.40	0.77
1:F:210:ARG:HG2	1:F:210:ARG:NH1	1.97	0.77
1:A:129:LEU:HD23	1:A:129:LEU:N	2.00	0.77
1:C:346:SER:O	1:C:359:THR:CG2	2.26	0.77
1:D:129:LEU:HD13	1:D:131:ARG:N	2.00	0.77
1:D:131:ARG:HG2	1:D:132:LEU:N	2.00	0.77
1:A:155:VAL:HG11	1:A:374:THR:OG1	1.85	0.76
1:B:296:ILE:C	1:B:298:GLY:H	1.91	0.76
1:C:195:GLN:O	1:C:196:VAL:C	2.28	0.76
1:E:207:ILE:HA	1:E:211:LEU:HB2	1.67	0.76
1:G:366:LEU:HD12	1:G:367:ALA:N	2.00	0.76
1:E:125:ILE:HD13	1:E:127:PRO:HD3	1.66	0.76
1:F:207:ILE:HD12	1:F:208:ASN:N	2.00	0.76
1:C:213:TYR:CE2	1:C:217:LEU:CD2	2.68	0.76
1:G:132:LEU:HB2	1:G:136:ASP:CG	2.11	0.76
1:A:137:LEU:HD22	1:A:329:PHE:HB2	1.68	0.76
1:D:141:GLY:O	1:D:142:ARG:HG2	1.85	0.76
1:G:203:LEU:C	1:G:205:SER:H	1.93	0.76
1:B:195:GLN:O	1:B:196:VAL:C	2.29	0.76
1:D:356:ASN:OD1	1:E:178:LYS:NZ	2.19	0.76
1:G:290:ASP:C	1:G:292:GLU:H	1.92	0.76
1:A:153:GLU:CD	1:A:372:ARG:HH21	1.93	0.76
1:C:186:ILE:HD13	1:C:222:GLN:HG3	1.66	0.76
1:C:227:ASP:O	1:C:232:ASN:HB2	1.86	0.76
1:A:146:ASN:HD22	1:G:145:SER:HB2	1.50	0.75
1:A:366:LEU:HD12	1:A:366:LEU:C	2.11	0.75
1:F:253:THR:CG2	1:F:256:ASP:OD1	2.34	0.75
1:G:183:VAL:HA	1:G:367:ALA:HB2	1.67	0.75
1:B:131:ARG:HH21	1:B:220:GLU:CD	1.94	0.75
1:E:296:ILE:HG23	1:E:297:PHE:N	2.02	0.75
1:G:327:GLY:N	1:G:329:PHE:HE2	1.83	0.75
1:B:126:MET:N	1:B:126:MET:SD	2.60	0.75
1:E:125:ILE:HD11	1:E:127:PRO:HD3	1.66	0.75
1:G:145:SER:O	1:G:338:ARG:HD3	1.85	0.75
1:E:189:TRP:HE3	1:E:189:TRP:O	1.70	0.75
1:B:296:ILE:HD13	1:B:296:ILE:N	1.98	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:MET:HB2	1:B:336:PHE:HE2	1.52	0.74
1:D:191:GLN:NE2	1:E:176:PHE:CE2	2.53	0.74
1:F:226:GLY:H	1:F:235:GLY:HA3	1.51	0.74
1:A:176:PHE:HE1	1:F:190:VAL:HG13	1.51	0.74
1:B:158:ASN:HB2	1:B:172:SER:CA	2.16	0.74
1:A:121:ILE:N	1:A:121:ILE:HD12	2.02	0.74
1:B:192:ALA:O	1:B:357:MET:HB2	1.87	0.74
1:C:194:ARG:NH1	1:C:347:ARG:NH2	2.34	0.74
1:F:239:VAL:HG12	1:F:373:PRO:HB3	1.70	0.74
1:G:196:VAL:HG22	1:G:202:MET:CE	2.17	0.74
1:A:287:LEU:O	1:A:287:LEU:CD1	2.30	0.74
1:B:130:ARG:NH2	1:C:330:ASP:OD2	2.20	0.74
1:C:192:ALA:O	1:C:357:MET:HB3	1.87	0.74
1:G:285:ILE:HA	1:G:288:LEU:HG	1.70	0.74
1:C:187:ALA:CB	1:C:363:GLU:HA	2.15	0.74
1:C:194:ARG:O	1:C:195:GLN:C	2.30	0.74
1:C:130:ARG:CB	1:D:271:SER:CB	2.66	0.74
1:D:158:ASN:ND2	1:D:158:ASN:H	1.82	0.74
1:D:197:MET:SD	1:D:202:MET:HE2	2.27	0.74
1:C:197:MET:HA	1:C:197:MET:HE3	1.69	0.74
1:E:316:THR:HG22	1:E:318:ALA:H	1.53	0.74
1:G:327:GLY:O	1:G:329:PHE:HD2	1.71	0.74
1:B:210:ARG:HH22	1:C:153:GLU:HG3	1.52	0.74
1:E:156:PHE:HD2	1:E:158:ASN:N	1.86	0.74
1:C:146:ASN:ND2	1:C:365:ARG:NH2	2.36	0.73
1:G:193:SER:O	1:G:196:VAL:HB	1.87	0.73
1:B:201:PRO:CB	1:B:204:GLN:HB2	2.18	0.73
1:F:203:LEU:HD22	1:F:204:GLN:CA	2.19	0.73
1:B:258:ILE:H	1:B:258:ILE:HD12	1.54	0.73
1:E:153:GLU:N	1:E:371:TYR:O	2.21	0.73
1:F:158:ASN:ND2	1:F:158:ASN:H	1.83	0.73
1:F:342:THR:O	1:F:362:CYS:HA	1.88	0.73
1:G:203:LEU:O	1:G:205:SER:N	2.21	0.73
1:A:195:GLN:NE2	1:B:149:GLU:OE2	2.21	0.73
1:G:327:GLY:O	1:G:329:PHE:CE2	2.42	0.73
1:A:284:ASN:O	1:A:288:LEU:HD22	1.88	0.73
1:B:162:ASP:O	1:B:172:SER:C	2.30	0.73
1:C:129:LEU:CD1	1:D:331:MET:HE1	2.10	0.73
1:C:194:ARG:O	1:C:196:VAL:CG2	2.36	0.73
1:B:203:LEU:O	1:B:207:ILE:HG13	1.88	0.73
1:B:212:MET:O	1:B:213:TYR:C	2.28	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:200:ALA:O	1:G:204:GLN:CB	2.37	0.73
1:E:304:THR:HG21	1:F:309:TRP:O	1.88	0.73
1:F:343:VAL:HG12	1:F:362:CYS:CB	2.11	0.73
1:B:295:TYR:HB3	1:B:298:GLY:O	1.89	0.73
1:B:296:ILE:O	1:B:298:GLY:N	2.22	0.73
1:C:265:VAL:HG22	1:C:377:ILE:HD13	1.71	0.73
1:A:155:VAL:HG13	1:A:374:THR:HG21	1.71	0.72
1:A:307:ILE:C	1:A:307:ILE:HD12	2.14	0.72
1:A:349:ASP:OD1	1:A:350:ARG:HG3	1.89	0.72
1:C:357:MET:CE	1:D:178:LYS:HG2	2.19	0.72
1:E:207:ILE:HG22	1:E:211:LEU:HD22	1.68	0.72
1:A:207:ILE:HG13	1:A:211:LEU:HD12	1.71	0.72
1:F:358:LEU:HD23	1:F:359:THR:N	2.04	0.72
1:D:247:LEU:CD2	1:D:260:HIS:HB3	2.20	0.72
1:D:349:ASP:OD1	1:D:350:ARG:HG3	1.89	0.72
1:E:125:ILE:HG13	1:E:212:MET:HB3	1.70	0.72
1:F:204:GLN:C	1:F:206:TYR:N	2.32	0.72
1:G:278:ASN:OD1	1:G:279:PRO:CD	2.30	0.72
1:D:193:SER:O	1:D:194:ARG:HB3	1.89	0.72
1:E:130:ARG:HB3	1:F:271:SER:OG	1.89	0.72
1:C:131:ARG:HH22	1:C:220:GLU:CD	1.97	0.72
1:C:194:ARG:C	1:C:196:VAL:N	2.41	0.72
1:C:210:ARG:NH2	1:D:153:GLU:OE2	2.22	0.72
1:A:207:ILE:H	1:A:207:ILE:HD12	1.55	0.72
1:C:202:MET:HE2	1:C:203:LEU:HD23	1.71	0.72
1:D:156:PHE:HD2	1:D:158:ASN:N	1.88	0.72
1:F:198:ASP:C	1:F:198:ASP:OD2	2.30	0.72
1:D:132:LEU:H	1:D:132:LEU:CD2	2.02	0.72
1:G:197:MET:HE3	1:G:358:LEU:HD21	1.68	0.72
1:E:159:ALA:HB1	1:E:160:PRO:HD2	1.70	0.71
1:F:198:ASP:C	1:F:200:ALA:H	1.95	0.71
1:G:199:ASP:O	1:G:202:MET:N	2.23	0.71
1:G:200:ALA:N	1:G:201:PRO:HD2	2.04	0.71
1:B:250:THR:CB	1:B:251:GLY:CA	2.49	0.71
1:E:127:PRO:O	1:E:129:LEU:HD22	1.90	0.71
1:C:357:MET:HE1	1:D:178:LYS:CG	2.20	0.71
1:G:303:PHE:CD2	1:G:304:THR:N	2.57	0.71
1:B:156:PHE:HD2	1:B:158:ASN:N	1.88	0.71
1:B:296:ILE:C	1:B:298:GLY:N	2.45	0.71
1:E:125:ILE:HG12	1:E:126:MET:N	2.05	0.71
1:E:333:SER:HB2	1:E:369:ALA:O	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:ILE:C	1:B:127:PRO:HD3	2.14	0.71
1:E:137:LEU:CD2	1:E:329:PHE:HB2	2.20	0.71
1:A:195:GLN:HG3	1:A:196:VAL:N	2.06	0.71
1:B:134:ILE:HD13	1:B:220:GLU:HG3	1.72	0.71
1:E:123:GLY:O	1:E:124:ILE:HG13	1.91	0.71
1:F:206:TYR:O	1:F:208:ASN:N	2.24	0.71
1:F:249:ALA:O	1:F:250:THR:C	2.32	0.71
1:B:158:ASN:ND2	1:B:172:SER:HB2	2.04	0.71
1:B:199:ASP:OD2	1:B:199:ASP:C	2.34	0.71
1:E:158:ASN:H	1:E:158:ASN:ND2	1.86	0.71
1:G:297:PHE:H	1:G:297:PHE:HD2	1.38	0.71
1:C:146:ASN:HD21	1:C:365:ARG:NH2	1.89	0.71
1:C:195:GLN:O	1:C:198:ASP:N	2.22	0.71
1:F:192:ALA:O	1:F:357:MET:SD	2.49	0.71
1:C:198:ASP:O	1:C:199:ASP:CG	2.34	0.71
1:C:203:LEU:O	1:C:206:TYR:HB3	1.89	0.71
1:C:347:ARG:C	1:C:349:ASP:N	2.43	0.71
1:A:203:LEU:O	1:A:204:GLN:C	2.32	0.70
1:G:227:ASP:OD1	1:G:227:ASP:C	2.34	0.70
1:D:347:ARG:HB2	1:D:358:LEU:HG	1.71	0.70
1:E:142:ARG:HA	1:E:337:ASP:H	1.54	0.70
1:G:290:ASP:C	1:G:292:GLU:N	2.47	0.70
1:F:206:TYR:HD2	1:F:207:ILE:N	1.89	0.70
1:A:273:SER:OG	1:A:330:ASP:HB2	1.91	0.70
1:G:278:ASN:O	1:G:280:ARG:N	2.24	0.70
1:A:350:ARG:O	1:A:351:ASP:CG	2.35	0.70
1:D:307:ILE:HD12	1:D:307:ILE:O	1.92	0.70
1:B:211:LEU:O	1:B:211:LEU:CD1	2.24	0.70
1:C:203:LEU:O	1:C:204:GLN:C	2.33	0.70
1:E:126:MET:CE	1:E:129:LEU:HD21	2.21	0.70
1:E:194:ARG:CA	1:E:358:LEU:CD1	2.67	0.70
1:F:329:PHE:HD1	1:F:329:PHE:H	0.82	0.70
1:B:249:ALA:CB	1:B:252:ASP:OD2	2.40	0.70
1:C:194:ARG:C	1:C:196:VAL:H	1.99	0.70
1:C:196:VAL:HG12	1:C:203:LEU:HD11	0.72	0.70
1:F:327:GLY:N	1:F:329:PHE:CE1	2.59	0.70
1:G:194:ARG:C	1:G:197:MET:H	2.00	0.70
1:G:200:ALA:O	1:G:204:GLN:HB3	1.92	0.70
1:A:207:ILE:HD12	1:A:207:ILE:N	2.05	0.70
1:B:288:LEU:O	1:B:296:ILE:HD13	1.91	0.70
1:A:194:ARG:HB2	1:A:358:LEU:HD23	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:122:PRO:CG	1:D:343:VAL:HG23	2.21	0.70
1:G:185:THR:OG1	1:G:365:ARG:HG2	1.90	0.70
1:G:296:ILE:HG22	1:G:297:PHE:H	1.54	0.70
1:D:129:LEU:HD13	1:D:130:ARG:N	2.07	0.70
1:E:216:ALA:C	1:E:218:LYS:H	1.99	0.70
1:A:125:ILE:HG21	1:A:204:GLN:HE21	1.55	0.69
1:A:194:ARG:O	1:A:198:ASP:CB	2.39	0.69
1:F:275:ILE:HD12	1:F:275:ILE:N	2.06	0.69
1:G:197:MET:CE	1:G:358:LEU:HD22	2.04	0.69
1:F:159:ALA:HB1	1:F:160:PRO:HD2	1.73	0.69
1:C:292:GLU:HG2	1:C:294:ARG:NE	2.06	0.69
1:F:156:PHE:HD2	1:F:158:ASN:N	1.89	0.69
1:F:329:PHE:N	1:F:329:PHE:CD1	2.35	0.69
1:A:127:PRO:HB3	1:A:212:MET:CB	2.20	0.69
1:B:134:ILE:H	1:B:134:ILE:HD12	1.58	0.69
1:D:209:ASN:O	1:D:213:TYR:CB	2.40	0.69
1:G:296:ILE:CG2	1:G:297:PHE:N	2.48	0.69
1:C:224:LEU:CD1	1:C:225:ASN:CG	2.66	0.69
1:F:361:LEU:HD13	1:F:361:LEU:C	2.17	0.69
1:G:155:VAL:CG1	1:G:374:THR:CG2	2.70	0.69
1:A:123:GLY:C	1:A:124:ILE:HG12	2.15	0.69
1:B:155:VAL:CG1	1:B:374:THR:OG1	2.41	0.69
1:B:200:ALA:HB1	1:B:201:PRO:CD	2.23	0.69
1:E:382:SER:O	1:E:383:SER:HB2	1.92	0.69
1:F:197:MET:SD	1:F:197:MET:C	2.74	0.69
1:B:156:PHE:O	1:B:158:ASN:ND2	2.25	0.69
1:B:216:ALA:O	1:B:217:LEU:C	2.34	0.69
1:E:258:ILE:HD11	1:E:381:PHE:HZ	1.58	0.69
1:E:200:ALA:O	1:E:201:PRO:C	2.33	0.69
1:C:323:THR:HA	1:C:380:THR:HG22	1.75	0.68
1:G:297:PHE:CG	1:G:298:GLY:N	2.61	0.68
1:A:125:ILE:N	1:A:125:ILE:HD12	2.08	0.68
1:D:148:LEU:HD12	1:D:181:ALA:HB3	1.74	0.68
1:B:125:ILE:HG12	1:B:127:PRO:CD	2.22	0.68
1:D:333:SER:HB3	1:D:369:ALA:O	1.92	0.68
1:E:184:LYS:HD2	1:E:231:ASP:HA	1.76	0.68
1:E:203:LEU:O	1:E:205:SER:N	2.27	0.68
1:G:198:ASP:O	1:G:199:ASP:CB	2.40	0.68
1:B:127:PRO:C	1:B:129:LEU:N	2.51	0.68
1:C:155:VAL:HG23	1:C:174:ILE:HG22	1.75	0.68
1:C:213:TYR:CZ	1:C:217:LEU:CD1	2.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:132:LEU:CD2	1:F:136:ASP:HB2	2.24	0.68
1:F:131:ARG:NH2	1:F:220:GLU:CD	2.51	0.68
1:B:275:ILE:HD11	1:B:313:VAL:HG22	1.75	0.68
1:F:202:MET:HG3	1:F:203:LEU:N	2.08	0.68
1:F:327:GLY:C	1:F:329:PHE:CE1	2.72	0.68
1:B:341:ALA:HA	1:B:363:GLU:O	1.94	0.68
1:C:130:ARG:CB	1:D:271:SER:HB2	2.24	0.68
1:F:142:ARG:NH2	1:F:340:ASP:OD1	2.27	0.68
1:C:153:GLU:OE2	1:C:372:ARG:NH2	2.27	0.68
1:D:162:ASP:C	1:D:173:ASP:H	2.01	0.68
1:C:194:ARG:C	1:C:196:VAL:HG23	2.18	0.67
1:E:220:GLU:HG2	1:E:316:THR:HG21	1.77	0.67
1:A:300:PRO:HA	1:A:303:PHE:CB	2.24	0.67
1:B:275:ILE:HG22	1:B:326:VAL:HG22	1.76	0.67
1:G:158:ASN:ND2	1:G:159:ALA:H	1.92	0.67
1:C:197:MET:SD	1:C:197:MET:N	2.65	0.67
1:G:187:ALA:HB2	1:G:363:GLU:HA	1.76	0.67
1:A:194:ARG:O	1:A:198:ASP:OD2	2.12	0.67
1:C:188:HIS:O	1:C:361:LEU:HA	1.95	0.67
1:C:200:ALA:C	1:C:202:MET:H	2.00	0.67
1:C:192:ALA:HB1	1:D:151:VAL:HG11	1.76	0.67
1:E:219:GLU:OE2	1:E:364:GLU:OE1	2.11	0.67
1:G:158:ASN:HD22	1:G:159:ALA:H	1.41	0.67
1:E:194:ARG:NH1	1:E:347:ARG:NH2	2.43	0.67
1:E:224:LEU:HD11	1:E:319:GLN:OE1	1.94	0.67
1:F:194:ARG:HB2	1:F:356:ASN:OD1	1.95	0.67
1:C:207:ILE:O	1:C:212:MET:HB2	1.95	0.67
1:C:227:ASP:O	1:C:229:THR:N	2.28	0.67
1:C:361:LEU:HD12	1:C:361:LEU:O	1.95	0.67
1:D:184:LYS:HZ3	1:D:184:LYS:HA	1.60	0.67
1:F:211:LEU:HD23	1:F:211:LEU:C	2.20	0.67
1:A:156:PHE:C	1:A:158:ASN:H	2.03	0.67
1:B:208:ASN:O	1:B:212:MET:HG2	1.95	0.67
1:C:192:ALA:CB	1:D:151:VAL:HG11	2.25	0.67
1:C:244:ASP:H	1:C:264:GLN:HE22	1.42	0.67
1:G:199:ASP:O	1:G:202:MET:HB3	1.94	0.67
1:B:188:HIS:CD2	1:B:214:GLY:HA3	2.30	0.67
1:B:201:PRO:C	1:B:204:GLN:HB2	2.20	0.67
1:C:174:ILE:H	1:C:174:ILE:HD13	1.60	0.67
1:D:295:TYR:CD1	1:D:299:GLY:HA2	2.28	0.67
1:G:329:PHE:CD2	1:G:329:PHE:N	2.48	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:VAL:HG22	1:A:360:ILE:HA	1.76	0.67
1:D:174:ILE:HG12	1:D:176:PHE:HE2	1.59	0.67
1:D:209:ASN:O	1:D:213:TYR:HB2	1.95	0.67
1:G:200:ALA:HB3	1:G:201:PRO:HD3	1.76	0.66
1:A:195:GLN:CG	1:A:196:VAL:H	2.06	0.66
1:C:129:LEU:H	1:C:129:LEU:HD22	1.60	0.66
1:D:301:GLN:O	1:D:306:ASN:HB2	1.95	0.66
1:D:339:MET:HB3	1:D:365:ARG:HB2	1.77	0.66
1:E:188:HIS:NE2	1:E:190:VAL:HG13	2.11	0.66
1:G:129:LEU:C	1:G:131:ARG:H	2.02	0.66
1:B:209:ASN:HB3	1:C:331:MET:HE3	1.77	0.66
1:D:121:ILE:HD13	1:D:121:ILE:C	2.20	0.66
1:F:206:TYR:CD2	1:F:207:ILE:N	2.64	0.66
1:B:158:ASN:CB	1:B:172:SER:HA	2.18	0.66
1:C:233:LEU:HD12	1:C:366:LEU:HD11	1.76	0.66
1:D:174:ILE:HG12	1:D:176:PHE:CE2	2.30	0.66
1:E:227:ASP:CB	1:E:229:THR:CG2	2.56	0.66
1:B:125:ILE:N	1:B:208:ASN:HB3	2.11	0.66
1:C:307:ILE:O	1:C:307:ILE:HG13	1.95	0.66
1:D:184:LYS:HG3	1:D:233:LEU:HD23	1.77	0.66
1:D:187:ALA:HB2	1:D:363:GLU:HB3	1.76	0.66
1:D:249:ALA:C	1:D:252:ASP:OD2	2.38	0.66
1:D:270:PHE:HE2	1:D:331:MET:HB3	1.61	0.66
1:G:270:PHE:CE1	1:G:372:ARG:CZ	2.78	0.66
1:B:125:ILE:HG12	1:B:127:PRO:CG	2.25	0.66
1:A:191:GLN:H	1:A:191:GLN:HE21	1.41	0.66
1:F:210:ARG:C	1:F:210:ARG:HD3	2.21	0.66
1:F:370:HIS:HB3	1:F:373:PRO:HG3	1.78	0.66
1:D:155:VAL:HG11	1:D:374:THR:CB	2.26	0.66
1:E:236:LEU:HD23	1:E:370:HIS:HE1	1.61	0.66
1:F:132:LEU:HD22	1:F:136:ASP:HB2	1.76	0.66
1:B:199:ASP:O	1:B:200:ALA:HB2	1.95	0.65
1:E:296:ILE:HG23	1:E:297:PHE:H	1.61	0.65
1:F:141:GLY:O	1:F:336:PHE:HA	1.95	0.65
1:C:233:LEU:HD11	1:C:366:LEU:HD12	1.78	0.65
1:F:275:ILE:HG23	1:F:326:VAL:HG12	1.78	0.65
1:B:126:MET:N	1:B:127:PRO:HD3	2.11	0.65
1:B:194:ARG:HD2	1:B:357:MET:HA	1.78	0.65
1:G:345:VAL:HG11	1:G:358:LEU:HD21	1.78	0.65
1:C:368:LEU:HD21	1:C:370:HIS:NE2	2.12	0.65
1:D:247:LEU:C	1:D:247:LEU:CD2	2.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:279:PRO:O	1:G:282:TRP:HB3	1.96	0.65
1:B:215:LEU:CD2	1:B:215:LEU:O	2.30	0.65
1:D:125:ILE:HD12	1:D:208:ASN:OD1	1.91	0.65
1:D:127:PRO:CB	1:D:212:MET:HB3	2.26	0.65
1:D:304:THR:OG1	1:D:315:PRO:HG3	1.97	0.65
1:E:212:MET:O	1:E:215:LEU:N	2.30	0.65
1:F:202:MET:SD	1:F:202:MET:C	2.80	0.65
1:F:258:ILE:HD11	1:F:275:ILE:HG21	1.77	0.65
1:B:194:ARG:HA	1:B:358:LEU:HD11	1.77	0.65
1:D:341:ALA:HA	1:D:363:GLU:O	1.96	0.65
1:E:200:ALA:O	1:E:202:MET:N	2.30	0.65
1:C:135:ARG:NH2	1:C:337:ASP:OD2	2.29	0.65
1:G:261:ALA:O	1:G:265:VAL:HG23	1.97	0.65
1:D:129:LEU:HD13	1:D:131:ARG:H	1.61	0.64
1:D:129:LEU:CD1	1:D:131:ARG:H	2.10	0.64
1:D:277:LEU:O	1:D:315:PRO:HA	1.98	0.64
1:D:224:LEU:HD12	1:D:225:ASN:ND2	2.12	0.64
1:G:265:VAL:HG22	1:G:377:ILE:HD13	1.78	0.64
1:B:155:VAL:HG12	1:B:374:THR:OG1	1.98	0.64
1:C:275:ILE:HD12	1:C:275:ILE:N	2.13	0.64
1:F:200:ALA:CB	1:F:201:PRO:CD	2.57	0.64
1:F:273:SER:O	1:F:312:PRO:HD2	1.98	0.64
1:B:146:ASN:HD22	1:B:146:ASN:N	1.95	0.64
1:F:198:ASP:O	1:F:200:ALA:N	2.29	0.64
1:G:159:ALA:HB1	1:G:160:PRO:HD2	1.80	0.64
1:G:345:VAL:HG12	1:G:358:LEU:HD11	1.80	0.64
1:B:217:LEU:C	1:B:217:LEU:HD12	2.21	0.64
1:E:258:ILE:HD11	1:E:381:PHE:CZ	2.33	0.64
1:F:148:LEU:O	1:F:180:THR:HG23	1.97	0.64
1:C:189:TRP:HA	1:C:360:ILE:O	1.97	0.64
1:C:268:SER:O	1:C:372:ARG:NH1	2.27	0.64
1:E:157:THR:HG22	1:E:267:GLU:HG2	1.80	0.64
1:E:289:LYS:HD3	1:E:293:GLY:HA2	1.77	0.64
1:F:211:LEU:O	1:F:214:GLY:N	2.28	0.64
1:A:275:ILE:HG23	1:A:326:VAL:HG22	1.80	0.64
1:D:193:SER:O	1:D:194:ARG:CB	2.46	0.64
1:E:366:LEU:C	1:E:366:LEU:HD12	2.23	0.64
1:G:196:VAL:C	1:G:198:ASP:H	2.06	0.64
1:B:131:ARG:NH2	1:B:220:GLU:OE2	2.27	0.64
1:D:265:VAL:HG22	1:D:377:ILE:HD13	1.80	0.64
1:D:270:PHE:CE2	1:D:331:MET:HB3	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:194:ARG:HD2	1:E:347:ARG:CZ	2.28	0.64
1:E:254:ARG:HG2	1:E:381:PHE:HE2	1.63	0.64
1:F:134:ILE:O	1:F:137:LEU:N	2.24	0.64
1:G:244:ASP:OD2	1:G:246:SER:HB3	1.98	0.64
1:F:224:LEU:HD13	1:F:237:ASN:ND2	2.13	0.63
1:C:195:GLN:NE2	1:C:198:ASP:CB	2.46	0.63
1:E:226:GLY:H	1:E:235:GLY:HA3	1.63	0.63
1:C:341:ALA:HB1	1:C:362:CYS:SG	2.39	0.63
1:F:375:ALA:C	1:F:376:ILE:HD12	2.24	0.63
1:G:155:VAL:HG22	1:G:156:PHE:N	2.12	0.63
1:B:215:LEU:HD22	1:B:216:ALA:N	2.12	0.63
1:D:129:LEU:HD11	1:D:131:ARG:HD3	1.79	0.63
1:E:229:THR:H	1:E:232:ASN:HB2	1.64	0.63
1:F:301:GLN:HG3	1:F:302:ALA:N	2.13	0.63
1:A:153:GLU:CD	1:F:210:ARG:NH2	2.51	0.63
1:C:196:VAL:CG1	1:C:203:LEU:CG	2.72	0.63
1:E:127:PRO:HG2	1:E:129:LEU:HD13	1.78	0.63
1:B:289:LYS:HD2	1:B:293:GLY:HA2	1.80	0.63
1:C:224:LEU:HD12	1:C:225:ASN:CG	2.24	0.63
1:C:278:ASN:ND2	1:C:280:ARG:HB3	2.14	0.63
1:C:287:LEU:CD2	1:C:300:PRO:HA	2.29	0.63
1:E:126:MET:HE3	1:E:129:LEU:HD21	1.80	0.63
1:E:254:ARG:CG	1:E:381:PHE:HE2	2.10	0.63
1:G:134:ILE:HG12	1:G:220:GLU:HG3	1.79	0.63
1:A:237:ASN:HB3	1:A:378:LYS:HD3	1.79	0.63
1:E:244:ASP:OD1	1:E:247:LEU:HG	1.98	0.63
1:F:202:MET:O	1:F:205:SER:HB3	1.97	0.63
1:G:310:GLY:C	1:G:311:LEU:HD22	2.24	0.63
1:E:296:ILE:CG2	1:E:297:PHE:N	2.61	0.63
1:G:194:ARG:C	1:G:196:VAL:N	2.51	0.63
1:G:199:ASP:CB	1:G:202:MET:HB3	2.29	0.63
1:B:201:PRO:HB3	1:B:204:GLN:HB2	1.79	0.63
1:G:275:ILE:HG23	1:G:326:VAL:HG22	1.79	0.63
1:G:135:ARG:HH21	1:G:219:GLU:CD	2.06	0.62
1:A:186:ILE:HD12	1:A:186:ILE:N	2.14	0.62
1:D:273:SER:HB3	1:D:328:GLY:HA2	1.81	0.62
1:D:300:PRO:HG2	1:E:301:GLN:HE21	1.64	0.62
1:B:276:VAL:C	1:B:277:LEU:CD2	2.70	0.62
1:D:307:ILE:CG2	1:D:312:PRO:HA	2.29	0.62
1:B:195:GLN:HA	1:B:197:MET:HG2	1.80	0.62
1:D:279:PRO:HG3	1:D:315:PRO:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:342:THR:O	1:D:362:CYS:HA	1.99	0.62
1:F:153:GLU:CD	1:F:372:ARG:HH21	2.08	0.62
1:G:135:ARG:NH2	1:G:219:GLU:OE2	2.33	0.62
1:G:145:SER:O	1:G:338:ARG:CD	2.47	0.62
1:G:157:THR:O	1:G:158:ASN:ND2	2.32	0.62
1:A:158:ASN:ND2	1:A:172:SER:HA	2.14	0.62
1:A:280:ARG:CG	1:A:281:ASP:N	2.62	0.62
1:B:148:LEU:HD23	1:B:148:LEU:O	1.99	0.62
1:C:287:LEU:CD2	1:C:300:PRO:CA	2.78	0.62
1:F:345:VAL:CG1	1:F:358:LEU:HD11	2.29	0.62
1:C:194:ARG:CZ	1:C:347:ARG:NH2	2.62	0.62
1:D:196:VAL:O	1:D:199:ASP:OD1	2.18	0.62
1:G:129:LEU:O	1:G:129:LEU:HD23	1.98	0.62
1:A:349:ASP:OD1	1:A:350:ARG:N	2.33	0.62
1:D:282:TRP:NE1	1:D:304:THR:HA	2.11	0.62
1:D:296:ILE:C	1:D:298:GLY:H	2.06	0.62
1:E:189:TRP:O	1:E:189:TRP:CE3	2.52	0.62
1:E:268:SER:HB2	1:E:372:ARG:HD3	1.82	0.62
1:F:308:MET:HG2	1:F:309:TRP:CE3	2.35	0.62
1:A:156:PHE:O	1:A:158:ASN:ND2	2.33	0.62
1:F:150:TYR:CE1	1:F:179:GLN:HB2	2.35	0.62
1:F:202:MET:SD	1:F:203:LEU:HA	2.40	0.62
1:A:197:MET:C	1:A:199:ASP:H	2.06	0.61
1:B:162:ASP:C	1:B:173:ASP:N	2.55	0.61
1:D:122:PRO:CG	1:D:343:VAL:O	2.39	0.61
1:E:174:ILE:H	1:E:174:ILE:CD1	2.12	0.61
1:G:257:ILE:HA	1:G:260:HIS:HD2	1.65	0.61
1:B:138:LEU:HD23	1:B:329:PHE:HB3	1.80	0.61
1:E:125:ILE:HG13	1:E:212:MET:CB	2.30	0.61
1:F:203:LEU:O	1:F:206:TYR:CA	2.47	0.61
1:F:206:TYR:C	1:F:208:ASN:N	2.52	0.61
1:A:134:ILE:HD13	1:A:314:VAL:HG11	1.83	0.61
1:A:240:ALA:HB1	1:A:376:ILE:HG22	1.82	0.61
1:D:303:PHE:N	1:D:303:PHE:CD1	2.67	0.61
1:E:233:LEU:HD13	1:E:366:LEU:CD1	2.25	0.61
1:F:194:ARG:NH2	1:G:363:GLU:OE1	2.33	0.61
1:A:207:ILE:H	1:A:207:ILE:CD1	2.12	0.61
1:B:284:ASN:O	1:B:288:LEU:HB2	2.00	0.61
1:C:357:MET:CE	1:D:178:LYS:CG	2.78	0.61
1:D:130:ARG:CZ	1:D:131:ARG:CB	2.79	0.61
1:D:191:GLN:OE1	1:D:191:GLN:N	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:194:ARG:O	1:D:197:MET:N	2.27	0.61
1:E:296:ILE:HG23	1:E:297:PHE:CD1	2.36	0.61
1:A:332:ALA:O	1:A:371:TYR:HB2	2.00	0.61
1:B:258:ILE:HD12	1:B:258:ILE:N	2.16	0.61
1:F:177:SER:HB3	1:F:179:GLN:HE21	1.66	0.61
1:G:199:ASP:CA	1:G:201:PRO:HD2	2.30	0.61
1:B:173:ASP:OD1	1:B:174:ILE:HD13	2.00	0.61
1:C:194:ARG:O	1:C:196:VAL:CA	2.48	0.61
1:C:213:TYR:CD2	1:C:217:LEU:HD11	2.36	0.61
1:C:277:LEU:O	1:C:315:PRO:HA	2.00	0.61
1:F:210:ARG:HD3	1:F:210:ARG:O	2.00	0.61
1:B:129:LEU:C	1:B:131:ARG:N	2.57	0.61
1:E:360:ILE:HD12	1:E:360:ILE:O	2.00	0.61
1:F:195:GLN:OE1	1:F:195:GLN:HA	2.01	0.61
1:F:224:LEU:HD13	1:F:237:ASN:HD21	1.65	0.61
1:G:155:VAL:HG13	1:G:374:THR:HG21	1.82	0.61
1:B:184:LYS:HD2	1:B:231:ASP:HA	1.82	0.61
1:E:134:ILE:H	1:E:134:ILE:HD12	1.64	0.61
1:E:258:ILE:H	1:E:258:ILE:HD12	1.66	0.61
1:G:194:ARG:O	1:G:197:MET:N	2.34	0.61
1:A:191:GLN:OE1	1:A:350:ARG:NH2	2.33	0.61
1:D:275:ILE:HG22	1:D:277:LEU:HD23	1.82	0.61
1:E:206:TYR:C	1:E:206:TYR:CD2	2.75	0.61
1:E:207:ILE:HG22	1:E:211:LEU:CD2	2.31	0.61
1:G:158:ASN:ND2	1:G:159:ALA:O	2.34	0.61
1:C:296:ILE:HG23	1:C:297:PHE:CD2	2.36	0.61
1:D:295:TYR:HE1	1:D:300:PRO:HD3	1.66	0.61
1:D:307:ILE:HG21	1:D:312:PRO:HA	1.81	0.61
1:E:212:MET:C	1:E:214:GLY:N	2.55	0.61
1:G:368:LEU:H	1:G:368:LEU:HD23	1.66	0.61
1:B:360:ILE:HG22	1:B:361:LEU:N	2.16	0.60
1:F:327:GLY:CA	1:F:329:PHE:HE1	2.14	0.60
1:F:344:GLU:HB2	1:F:361:LEU:HD11	1.82	0.60
1:C:343:VAL:HG12	1:C:362:CYS:CB	2.31	0.60
1:E:278:ASN:HB3	1:E:281:ASP:OD2	2.01	0.60
1:F:225:ASN:HD22	1:F:225:ASN:N	1.97	0.60
1:F:266:THR:HA	1:F:270:PHE:O	2.02	0.60
1:A:133:THR:HG22	1:A:135:ARG:H	1.66	0.60
1:A:296:ILE:HG23	1:A:297:PHE:CE2	2.35	0.60
1:E:258:ILE:HD12	1:E:258:ILE:N	2.15	0.60
1:E:273:SER:N	1:E:328:GLY:HA2	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:253:THR:HG23	1:F:256:ASP:CG	2.25	0.60
1:F:343:VAL:HA	1:F:361:LEU:O	2.01	0.60
1:A:194:ARG:HB2	1:A:358:LEU:CD2	2.30	0.60
1:A:233:LEU:HD11	1:A:366:LEU:CD1	2.26	0.60
1:A:368:LEU:HD23	1:A:370:HIS:NE2	2.12	0.60
1:C:224:LEU:HD12	1:C:225:ASN:ND2	2.16	0.60
1:D:297:PHE:HE2	1:D:308:MET:HE3	1.65	0.60
1:F:202:MET:SD	1:F:203:LEU:CA	2.88	0.60
1:A:285:ILE:HA	1:A:288:LEU:HD11	1.82	0.60
1:C:192:ALA:HB1	1:D:151:VAL:CG1	2.31	0.60
1:C:239:VAL:HG12	1:C:373:PRO:HB3	1.84	0.60
1:C:275:ILE:HG22	1:C:277:LEU:HD11	1.83	0.60
1:E:131:ARG:NH1	1:E:316:THR:HA	2.16	0.60
1:E:335:VAL:HG22	1:E:368:LEU:HD13	1.83	0.60
1:C:130:ARG:CB	1:D:271:SER:OG	2.50	0.60
1:D:184:LYS:NZ	1:D:231:ASP:HA	2.17	0.60
1:G:197:MET:HE3	1:G:358:LEU:CD2	2.22	0.60
1:A:158:ASN:H	1:A:158:ASN:ND2	2.00	0.60
1:A:206:TYR:O	1:A:210:ARG:HB3	2.01	0.60
1:A:297:PHE:CE2	1:A:309:TRP:CZ2	2.89	0.60
1:B:201:PRO:CA	1:B:204:GLN:HB2	2.32	0.60
1:F:203:LEU:HD22	1:F:204:GLN:HA	1.83	0.60
1:A:124:ILE:O	1:A:126:MET:SD	2.59	0.60
1:B:125:ILE:HG12	1:B:127:PRO:HG3	1.84	0.60
1:B:134:ILE:HD12	1:B:134:ILE:N	2.16	0.60
1:D:130:ARG:CZ	1:D:131:ARG:HB2	2.31	0.60
1:E:202:MET:HE1	1:E:203:LEU:HB2	1.84	0.60
1:E:204:GLN:O	1:E:208:ASN:HB2	2.01	0.60
1:A:125:ILE:O	1:A:126:MET:HE3	2.02	0.60
1:A:146:ASN:ND2	1:G:145:SER:HB2	2.17	0.60
1:B:126:MET:HE3	1:B:212:MET:HG3	1.82	0.60
1:B:129:LEU:C	1:B:129:LEU:CD2	2.74	0.60
1:C:190:VAL:HG22	1:D:176:PHE:CE1	2.36	0.60
1:D:303:PHE:N	1:D:303:PHE:HD1	1.99	0.60
1:E:194:ARG:HH11	1:E:347:ARG:CZ	2.15	0.60
1:F:327:GLY:O	1:F:329:PHE:CE1	2.53	0.60
1:F:346:SER:HB3	1:F:348:GLU:HG3	1.84	0.60
1:G:376:ILE:HD12	1:G:376:ILE:N	2.16	0.60
1:C:130:ARG:CG	1:D:271:SER:CB	2.69	0.60
1:C:224:LEU:HD13	1:C:237:ASN:ND2	2.16	0.60
1:E:155:VAL:CG1	1:E:374:THR:HB	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:TRP:HB3	1:A:361:LEU:HD13	1.84	0.59
1:C:155:VAL:CG2	1:C:174:ILE:HG22	2.31	0.59
1:C:247:LEU:HB3	1:C:260:HIS:HD2	1.66	0.59
1:D:261:ALA:O	1:D:265:VAL:HG23	2.02	0.59
1:C:129:LEU:HD22	1:C:129:LEU:N	2.15	0.59
1:D:201:PRO:O	1:D:204:GLN:N	2.34	0.59
1:F:292:GLU:O	1:F:294:ARG:HG2	2.02	0.59
1:G:174:ILE:H	1:G:174:ILE:CD1	2.12	0.59
1:A:285:ILE:O	1:A:288:LEU:CG	2.49	0.59
1:B:148:LEU:C	1:B:180:THR:HG23	2.28	0.59
1:B:194:ARG:HA	1:B:358:LEU:CD1	2.32	0.59
1:D:155:VAL:HG11	1:D:374:THR:HB	1.83	0.59
1:F:376:ILE:C	1:F:377:ILE:HD12	2.27	0.59
1:G:196:VAL:C	1:G:198:ASP:N	2.58	0.59
1:G:280:ARG:C	1:G:282:TRP:N	2.56	0.59
1:A:280:ARG:HG3	1:A:281:ASP:N	2.07	0.59
1:A:287:LEU:C	1:A:288:LEU:HD22	2.24	0.59
1:B:236:LEU:HD23	1:B:370:HIS:HE1	1.66	0.59
1:B:341:ALA:HB1	1:B:362:CYS:SG	2.43	0.59
1:G:345:VAL:HG22	1:G:360:ILE:HG22	1.84	0.59
1:A:176:PHE:CE1	1:F:190:VAL:HG13	2.37	0.59
1:A:191:GLN:HE21	1:A:191:GLN:N	1.98	0.59
1:C:187:ALA:HB2	1:C:363:GLU:CA	2.23	0.59
1:C:200:ALA:C	1:C:202:MET:N	2.58	0.59
1:C:203:LEU:O	1:C:206:TYR:CA	2.50	0.59
1:D:155:VAL:CG1	1:D:374:THR:HG21	2.32	0.59
1:D:289:LYS:N	1:D:289:LYS:HD2	2.17	0.59
1:E:194:ARG:HA	1:E:358:LEU:HD11	1.82	0.59
1:E:300:PRO:HB2	1:F:309:TRP:CE2	2.37	0.59
1:F:206:TYR:O	1:F:207:ILE:C	2.45	0.59
1:C:330:ASP:OD1	1:C:331:MET:N	2.35	0.59
1:D:241:THR:O	1:D:377:ILE:HA	2.03	0.59
1:E:182:ASN:HB2	1:E:184:LYS:NZ	2.17	0.59
1:E:199:ASP:CB	1:E:202:MET:HE2	2.32	0.59
1:F:254:ARG:HG2	1:F:381:PHE:CD2	2.38	0.59
1:G:291:ASN:C	1:G:293:GLY:H	2.09	0.59
1:A:155:VAL:CG1	1:A:374:THR:HG21	2.32	0.59
1:A:277:LEU:O	1:A:315:PRO:HA	2.03	0.59
1:B:158:ASN:ND2	1:B:158:ASN:N	2.48	0.59
1:B:180:THR:HG22	1:B:181:ALA:N	2.18	0.59
1:B:194:ARG:CZ	1:B:347:ARG:NH2	2.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:ILE:HD12	1:D:186:ILE:N	2.17	0.59
1:F:142:ARG:HG3	1:F:337:ASP:CB	2.11	0.59
1:F:207:ILE:HD12	1:F:207:ILE:C	2.28	0.59
1:F:227:ASP:O	1:F:232:ASN:HB2	2.03	0.59
1:F:327:GLY:CA	1:F:329:PHE:CE1	2.85	0.59
1:G:351:ASP:O	1:G:355:LYS:CG	2.48	0.59
1:B:262:ILE:H	1:B:262:ILE:HD12	1.66	0.59
1:E:227:ASP:C	1:E:229:THR:HG23	2.28	0.59
1:E:382:SER:O	1:E:383:SER:CB	2.49	0.59
1:A:155:VAL:CG1	1:A:374:THR:OG1	2.50	0.59
1:B:142:ARG:HG3	1:B:337:ASP:HB2	1.85	0.59
1:B:329:PHE:O	1:B:330:ASP:C	2.45	0.59
1:B:368:LEU:HD23	1:B:368:LEU:C	2.28	0.59
1:D:132:LEU:HD23	1:D:132:LEU:N	2.16	0.59
1:E:218:LYS:HG3	1:E:218:LYS:O	2.03	0.59
1:F:175:THR:HG22	1:F:176:PHE:H	1.67	0.59
1:G:155:VAL:HG23	1:G:174:ILE:HG22	1.83	0.59
1:A:224:LEU:HD12	1:A:225:ASN:ND2	2.17	0.59
1:A:265:VAL:HG11	1:A:327:GLY:HA2	1.85	0.59
1:C:347:ARG:O	1:C:352:ASN:HB2	2.02	0.59
1:E:202:MET:SD	1:E:203:LEU:N	2.76	0.59
1:G:189:TRP:HB3	1:G:361:LEU:HD13	1.84	0.59
1:G:355:LYS:O	1:G:356:ASN:C	2.46	0.59
1:A:183:VAL:HG22	1:A:367:ALA:HB2	1.83	0.58
1:A:187:ALA:HB1	1:A:361:LEU:HD11	1.85	0.58
1:A:237:ASN:ND2	1:A:325:THR:HG21	2.18	0.58
1:A:343:VAL:HG12	1:A:362:CYS:CB	2.31	0.58
1:D:207:ILE:HD12	1:D:207:ILE:N	2.18	0.58
1:E:200:ALA:HB3	1:E:201:PRO:CD	2.33	0.58
1:F:202:MET:O	1:F:205:SER:CB	2.51	0.58
1:B:161:GLY:O	1:B:162:ASP:C	2.45	0.58
1:B:358:LEU:N	1:B:358:LEU:CD1	2.66	0.58
1:C:133:THR:HG22	1:C:135:ARG:H	1.68	0.58
1:C:227:ASP:O	1:C:232:ASN:CB	2.51	0.58
1:C:376:ILE:N	1:C:376:ILE:HD12	2.18	0.58
1:D:358:LEU:N	1:D:358:LEU:HD12	2.18	0.58
1:E:335:VAL:HG22	1:E:368:LEU:CD1	2.33	0.58
1:B:368:LEU:HD23	1:B:369:ALA:N	2.18	0.58
1:C:194:ARG:O	1:C:196:VAL:CB	2.52	0.58
1:C:244:ASP:H	1:C:264:GLN:NE2	2.01	0.58
1:F:210:ARG:HH11	1:F:210:ARG:CG	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ASP:OD2	1:A:246:SER:HB3	2.02	0.58
1:A:345:VAL:HG13	1:A:359:THR:O	2.04	0.58
1:D:244:ASP:O	1:D:247:LEU:HB3	2.03	0.58
1:D:290:ASP:OD2	1:D:294:ARG:HB3	2.03	0.58
1:E:194:ARG:NH1	1:E:347:ARG:CZ	2.67	0.58
1:F:210:ARG:NH1	1:F:210:ARG:CG	2.65	0.58
1:G:150:TYR:HE2	1:G:181:ALA:HB2	1.67	0.58
1:G:285:ILE:HA	1:G:288:LEU:CG	2.34	0.58
1:A:224:LEU:HD21	1:A:276:VAL:HG11	1.84	0.58
1:C:344:GLU:H	1:C:361:LEU:HD12	1.69	0.58
1:F:199:ASP:O	1:F:200:ALA:C	2.47	0.58
1:C:285:ILE:HG21	1:C:308:MET:HE1	1.83	0.58
1:F:155:VAL:HG13	1:F:155:VAL:O	2.03	0.58
1:F:195:GLN:OE1	1:F:195:GLN:CA	2.50	0.58
1:G:226:GLY:H	1:G:235:GLY:HA3	1.68	0.58
1:G:278:ASN:O	1:G:279:PRO:C	2.46	0.58
1:C:201:PRO:O	1:C:204:GLN:CA	2.51	0.58
1:C:207:ILE:H	1:C:207:ILE:HD13	1.68	0.58
1:E:193:SER:O	1:E:195:GLN:N	2.36	0.58
1:E:210:ARG:NH2	1:F:153:GLU:OE2	2.35	0.58
1:E:215:LEU:HD23	1:E:215:LEU:C	2.28	0.58
1:F:175:THR:HG22	1:F:176:PHE:N	2.19	0.58
1:G:199:ASP:HB3	1:G:202:MET:CB	2.31	0.58
1:A:190:VAL:HG21	1:A:210:ARG:NH1	2.19	0.58
1:C:138:LEU:HD23	1:C:329:PHE:HB3	1.84	0.58
1:D:301:GLN:O	1:D:302:ALA:C	2.47	0.58
1:E:220:GLU:OE2	1:E:316:THR:OG1	2.22	0.58
1:F:331:MET:O	1:F:331:MET:HG2	2.04	0.58
1:G:175:THR:HG22	1:G:176:PHE:N	2.18	0.58
1:A:366:LEU:C	1:A:366:LEU:CD1	2.76	0.58
1:B:202:MET:O	1:B:203:LEU:C	2.47	0.58
1:C:190:VAL:N	1:C:360:ILE:O	2.31	0.58
1:C:227:ASP:C	1:C:229:THR:N	2.61	0.58
1:C:244:ASP:OD2	1:C:247:LEU:HG	2.04	0.58
1:C:306:ASN:HB3	1:C:313:VAL:HB	1.85	0.58
1:G:354:VAL:O	1:G:356:ASN:N	2.37	0.58
1:A:345:VAL:HA	1:A:359:THR:O	2.05	0.57
1:B:149:GLU:HG2	1:B:180:THR:OG1	2.04	0.57
1:A:155:VAL:HG23	1:A:174:ILE:CG2	2.30	0.57
1:C:200:ALA:HB1	1:C:201:PRO:HD2	1.86	0.57
1:F:282:TRP:CZ3	1:F:308:MET:CE	2.74	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:281:ASP:O	1:G:285:ILE:CD1	2.52	0.57
1:B:148:LEU:O	1:B:180:THR:HG23	2.04	0.57
1:C:155:VAL:HA	1:C:174:ILE:HA	1.86	0.57
1:E:158:ASN:N	1:E:158:ASN:ND2	2.50	0.57
1:E:206:TYR:C	1:E:206:TYR:HD2	2.11	0.57
1:C:184:LYS:HB2	1:C:233:LEU:HD21	1.86	0.57
1:D:239:VAL:HG12	1:D:373:PRO:HB3	1.86	0.57
1:D:356:ASN:CG	1:E:178:LYS:NZ	2.62	0.57
1:E:148:LEU:N	1:E:148:LEU:HD23	2.20	0.57
1:E:253:THR:HB	1:E:256:ASP:OD1	2.04	0.57
1:A:174:ILE:H	1:A:174:ILE:CD1	2.11	0.57
1:B:279:PRO:HD3	1:B:316:THR:O	2.04	0.57
1:D:155:VAL:O	1:D:155:VAL:HG13	2.03	0.57
1:D:356:ASN:ND2	1:E:178:LYS:NZ	2.53	0.57
1:E:185:THR:HG22	1:E:365:ARG:HG2	1.87	0.57
1:E:207:ILE:CG1	1:E:208:ASN:H	2.12	0.57
1:E:339:MET:HE2	1:E:365:ARG:CD	2.35	0.57
1:C:152:ARG:HB3	1:C:177:SER:HB2	1.86	0.57
1:D:158:ASN:ND2	1:D:158:ASN:N	2.48	0.57
1:E:155:VAL:HG23	1:E:174:ILE:CG2	2.32	0.57
1:E:185:THR:O	1:E:186:ILE:HD13	2.03	0.57
1:F:143:THR:OG1	1:F:144:SER:N	2.37	0.57
1:F:206:TYR:C	1:F:208:ASN:H	2.10	0.57
1:A:191:GLN:N	1:A:191:GLN:NE2	2.53	0.57
1:A:339:MET:HB3	1:A:365:ARG:HB2	1.87	0.57
1:C:184:LYS:HG3	1:C:233:LEU:CD2	2.35	0.57
1:D:125:ILE:HD13	1:D:208:ASN:OD1	1.97	0.57
1:E:273:SER:H	1:E:328:GLY:HA2	1.70	0.57
1:G:175:THR:HG22	1:G:176:PHE:H	1.69	0.57
1:A:183:VAL:HA	1:A:367:ALA:HB2	1.87	0.57
1:B:129:LEU:C	1:B:131:ARG:H	2.12	0.57
1:C:150:TYR:CE1	1:C:179:GLN:HB2	2.40	0.57
1:C:292:GLU:HG2	1:C:294:ARG:HE	1.66	0.57
1:D:346:SER:O	1:D:347:ARG:HB3	2.05	0.57
1:F:327:GLY:C	1:F:329:PHE:CD1	2.83	0.57
1:B:134:ILE:HD13	1:B:220:GLU:CG	2.35	0.57
1:B:202:MET:C	1:B:204:GLN:N	2.50	0.57
1:B:253:THR:HG22	1:B:254:ARG:N	2.19	0.57
1:B:342:THR:O	1:B:362:CYS:CA	2.49	0.57
1:B:342:THR:OG1	1:B:363:GLU:HB2	2.05	0.57
1:D:127:PRO:HB3	1:D:212:MET:HB3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:174:ILE:HD13	1:F:174:ILE:N	2.14	0.57
1:F:347:ARG:O	1:F:352:ASN:HB2	2.04	0.57
1:G:295:TYR:HB2	1:G:298:GLY:O	2.05	0.57
1:B:205:SER:O	1:B:206:TYR:C	2.46	0.56
1:E:194:ARG:CZ	1:E:347:ARG:NH2	2.68	0.56
1:F:212:MET:HA	1:F:212:MET:CE	2.34	0.56
1:B:162:ASP:HB3	1:B:173:ASP:HB2	1.86	0.56
1:B:288:LEU:C	1:B:296:ILE:HD11	2.30	0.56
1:C:131:ARG:HB2	1:C:131:ARG:HH11	1.70	0.56
1:C:266:THR:HA	1:C:270:PHE:O	2.05	0.56
1:D:302:ALA:O	1:D:304:THR:N	2.38	0.56
1:D:309:TRP:HE3	1:D:309:TRP:H	1.53	0.56
1:E:199:ASP:O	1:E:202:MET:CE	2.53	0.56
1:A:190:VAL:CG1	1:A:211:LEU:HD21	2.35	0.56
1:A:368:LEU:HD21	1:A:370:HIS:CD2	2.36	0.56
1:A:368:LEU:CD2	1:A:370:HIS:CD2	2.89	0.56
1:B:158:ASN:CG	1:B:172:SER:C	2.74	0.56
1:B:217:LEU:HD12	1:B:218:LYS:N	2.20	0.56
1:B:251:GLY:O	1:B:252:ASP:CG	2.49	0.56
1:B:252:ASP:HB3	1:B:256:ASP:HB2	1.87	0.56
1:C:288:LEU:HD23	1:C:289:LYS:O	2.04	0.56
1:E:151:VAL:HG23	1:E:151:VAL:O	2.06	0.56
1:E:222:GLN:OE1	1:E:232:ASN:HA	2.05	0.56
1:E:261:ALA:O	1:E:265:VAL:HG23	2.06	0.56
1:G:128:GLY:C	1:G:130:ARG:N	2.60	0.56
1:G:304:THR:HG22	1:G:305:SER:N	2.14	0.56
1:B:126:MET:CE	1:B:212:MET:HG3	2.36	0.56
1:B:134:ILE:H	1:B:134:ILE:CD1	2.19	0.56
1:C:177:SER:O	1:C:179:GLN:HG2	2.05	0.56
1:D:254:ARG:O	1:D:258:ILE:HD13	2.06	0.56
1:E:134:ILE:HD12	1:E:134:ILE:N	2.21	0.56
1:E:203:LEU:HD12	1:E:206:TYR:HB3	1.87	0.56
1:F:142:ARG:HA	1:F:337:ASP:H	1.71	0.56
1:F:327:GLY:C	1:F:329:PHE:HE1	2.12	0.56
1:D:343:VAL:HG12	1:D:362:CYS:SG	2.45	0.56
1:D:358:LEU:H	1:D:358:LEU:CD1	2.19	0.56
1:E:157:THR:CG2	1:E:267:GLU:CG	2.78	0.56
1:E:190:VAL:HG12	1:F:176:PHE:CZ	2.40	0.56
1:E:224:LEU:HD12	1:E:225:ASN:OD1	2.05	0.56
1:F:277:LEU:N	1:F:277:LEU:HD12	2.21	0.56
1:G:311:LEU:HD22	1:G:311:LEU:N	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:366:LEU:CD1	1:G:367:ALA:N	2.68	0.56
1:A:240:ALA:CB	1:A:376:ILE:HG22	2.36	0.56
1:A:276:VAL:HB	1:A:325:THR:OG1	2.06	0.56
1:C:276:VAL:HG22	1:C:314:VAL:CG2	2.36	0.56
1:E:193:SER:C	1:E:195:GLN:H	2.12	0.56
1:F:249:ALA:C	1:F:250:THR:O	2.41	0.56
1:G:376:ILE:C	1:G:377:ILE:HD12	2.30	0.56
1:A:129:LEU:N	1:A:129:LEU:CD2	2.69	0.56
1:A:184:LYS:HE3	1:A:230:GLY:O	2.05	0.56
1:A:185:THR:HG22	1:A:365:ARG:HG2	1.88	0.56
1:A:207:ILE:HG23	1:A:211:LEU:HD12	1.86	0.56
1:B:155:VAL:HG13	1:B:374:THR:CB	2.35	0.56
1:B:261:ALA:O	1:B:265:VAL:HG23	2.06	0.56
1:D:377:ILE:HD12	1:D:377:ILE:N	2.21	0.56
1:E:155:VAL:HG13	1:E:155:VAL:O	2.06	0.56
1:E:193:SER:O	1:E:196:VAL:HG23	2.06	0.56
1:E:225:ASN:HA	1:E:235:GLY:HA3	1.88	0.56
1:C:213:TYR:CD2	1:C:217:LEU:CD1	2.89	0.56
1:C:296:ILE:C	1:C:297:PHE:HD2	2.13	0.56
1:D:209:ASN:O	1:D:213:TYR:HB3	2.06	0.56
1:G:377:ILE:HD12	1:G:377:ILE:N	2.21	0.56
1:A:275:ILE:CD1	1:A:308:MET:SD	2.94	0.56
1:A:287:LEU:N	1:A:288:LEU:CD2	2.69	0.56
1:B:255:ALA:HA	1:B:258:ILE:HD13	1.88	0.56
1:B:289:LYS:HD2	1:B:293:GLY:C	2.30	0.56
1:C:196:VAL:CG1	1:C:203:LEU:HD13	2.32	0.56
1:C:207:ILE:HG22	1:C:211:LEU:HD13	1.87	0.56
1:D:290:ASP:CG	1:D:294:ARG:HB3	2.30	0.56
1:E:127:PRO:HG2	1:E:129:LEU:CD1	2.35	0.56
1:E:224:LEU:HD11	1:E:319:GLN:CD	2.31	0.56
1:E:200:ALA:N	1:E:201:PRO:HD2	2.20	0.56
1:F:254:ARG:HB3	1:F:285:ILE:CD1	2.37	0.56
1:A:349:ASP:OD1	1:A:350:ARG:CG	2.55	0.55
1:B:194:ARG:O	1:B:195:GLN:HB2	2.06	0.55
1:B:209:ASN:C	1:C:331:MET:CE	2.79	0.55
1:B:354:VAL:C	1:B:356:ASN:N	2.63	0.55
1:D:190:VAL:HG11	1:D:211:LEU:HD21	1.84	0.55
1:E:354:VAL:O	1:E:356:ASN:N	2.40	0.55
1:F:212:MET:HA	1:F:212:MET:HE3	1.87	0.55
1:G:196:VAL:O	1:G:198:ASP:N	2.39	0.55
1:D:127:PRO:CD	1:D:212:MET:HE2	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:154:GLU:HB3	1:D:175:THR:HB	1.87	0.55
1:E:135:ARG:NH2	1:E:337:ASP:OD2	2.34	0.55
1:G:152:ARG:HG3	1:G:371:TYR:O	2.06	0.55
1:D:244:ASP:HB2	1:D:264:GLN:NE2	2.21	0.55
1:E:128:GLY:O	1:E:129:LEU:HB2	2.05	0.55
1:E:305:SER:HB2	1:E:307:ILE:HG12	1.87	0.55
1:F:377:ILE:HD12	1:F:377:ILE:N	2.21	0.55
1:B:125:ILE:CD1	1:B:127:PRO:HG3	2.37	0.55
1:B:132:LEU:HD23	1:B:132:LEU:N	2.18	0.55
1:C:202:MET:CE	1:C:203:LEU:HD23	2.35	0.55
1:C:224:LEU:HD13	1:C:225:ASN:CG	2.31	0.55
1:C:284:ASN:O	1:C:288:LEU:HB2	2.07	0.55
1:D:349:ASP:OD1	1:D:349:ASP:C	2.49	0.55
1:E:236:LEU:HD23	1:E:370:HIS:CE1	2.41	0.55
1:F:192:ALA:O	1:F:357:MET:HA	2.05	0.55
1:F:339:MET:HE2	1:F:365:ARG:HG3	1.87	0.55
1:C:268:SER:O	1:C:269:GLU:HB2	2.06	0.55
1:A:297:PHE:HD2	1:A:297:PHE:N	2.04	0.55
1:B:250:THR:HG22	1:B:251:GLY:N	2.18	0.55
1:C:225:ASN:N	1:C:225:ASN:HD22	2.02	0.55
1:D:257:ILE:HA	1:D:260:HIS:HD2	1.71	0.55
1:D:295:TYR:CE1	1:D:300:PRO:HD3	2.41	0.55
1:E:227:ASP:O	1:E:229:THR:HG22	2.07	0.55
1:F:203:LEU:HD23	1:F:206:TYR:HB3	1.89	0.55
1:F:376:ILE:HD12	1:F:376:ILE:N	2.22	0.55
1:A:175:THR:HG22	1:A:176:PHE:N	2.22	0.55
1:D:356:ASN:HD21	1:E:178:LYS:NZ	2.04	0.55
1:D:376:ILE:C	1:D:377:ILE:HD12	2.32	0.55
1:E:132:LEU:H	1:E:132:LEU:CD2	2.17	0.55
1:E:297:PHE:CD2	1:E:298:GLY:N	2.75	0.55
1:G:278:ASN:O	1:G:281:ASP:N	2.40	0.55
1:G:327:GLY:C	1:G:329:PHE:CD2	2.85	0.55
1:C:357:MET:SD	1:D:178:LYS:HD3	2.47	0.55
1:D:356:ASN:ND2	1:E:178:LYS:HZ1	2.04	0.55
1:E:194:ARG:HH11	1:E:347:ARG:NH1	2.04	0.55
1:E:296:ILE:HG22	1:E:298:GLY:H	1.71	0.55
1:E:360:ILE:HD12	1:E:360:ILE:C	2.32	0.55
1:F:260:HIS:O	1:F:263:TYR:HB3	2.07	0.55
1:G:335:VAL:HG12	1:G:368:LEU:HB3	1.89	0.55
1:G:372:ARG:NH1	1:G:372:ARG:HG2	2.22	0.55
1:G:372:ARG:HG2	1:G:372:ARG:HH11	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:ILE:O	1:B:296:ILE:HG12	2.06	0.55
1:C:194:ARG:HB2	1:C:358:LEU:HG	1.88	0.55
1:B:144:SER:HA	1:B:338:ARG:NH1	2.22	0.55
1:C:366:LEU:CD1	1:C:366:LEU:C	2.75	0.55
1:E:359:THR:O	1:E:359:THR:HG22	2.07	0.55
1:G:196:VAL:CG2	1:G:202:MET:HE2	2.29	0.55
1:G:282:TRP:CZ3	1:G:313:VAL:HG21	2.41	0.55
1:B:194:ARG:HD2	1:B:358:LEU:HD12	1.89	0.54
1:C:146:ASN:HD21	1:C:365:ARG:HH22	1.54	0.54
1:C:278:ASN:HD21	1:C:280:ARG:HB3	1.70	0.54
1:E:197:MET:HE1	1:E:345:VAL:HG11	1.89	0.54
1:F:194:ARG:NH1	1:F:347:ARG:CZ	2.69	0.54
1:G:270:PHE:HE1	1:G:372:ARG:CZ	2.19	0.54
1:C:196:VAL:HG11	1:C:203:LEU:CD1	2.29	0.54
1:C:276:VAL:C	1:C:277:LEU:HD12	2.32	0.54
1:D:129:LEU:CD1	1:D:131:ARG:N	2.67	0.54
1:E:215:LEU:O	1:E:218:LYS:CA	2.55	0.54
1:E:262:ILE:N	1:E:262:ILE:HD12	2.22	0.54
1:A:286:ALA:C	1:A:288:LEU:CD2	2.79	0.54
1:B:158:ASN:CG	1:B:172:SER:O	2.50	0.54
1:B:289:LYS:HD2	1:B:293:GLY:CA	2.37	0.54
1:D:343:VAL:HA	1:D:361:LEU:O	2.06	0.54
1:G:244:ASP:CG	1:G:246:SER:HB3	2.33	0.54
1:B:153:GLU:HB2	1:B:371:TYR:O	2.08	0.54
1:B:258:ILE:H	1:B:258:ILE:CD1	2.20	0.54
1:C:132:LEU:CD2	1:C:136:ASP:HB2	2.38	0.54
1:C:275:ILE:HG13	1:C:326:VAL:HG12	1.89	0.54
1:D:244:ASP:HB2	1:D:264:GLN:HE22	1.72	0.54
1:D:290:ASP:C	1:D:292:GLU:H	2.15	0.54
1:D:343:VAL:HG12	1:D:362:CYS:HB2	1.89	0.54
1:E:202:MET:CE	1:E:203:LEU:H	1.97	0.54
1:A:202:MET:CG	1:A:203:LEU:N	2.71	0.54
1:A:377:ILE:HD12	1:A:377:ILE:N	2.22	0.54
1:D:191:GLN:HB2	1:E:151:VAL:HG21	1.88	0.54
1:E:296:ILE:O	1:E:297:PHE:C	2.49	0.54
1:G:316:THR:HG22	1:G:318:ALA:N	2.17	0.54
1:B:144:SER:HA	1:B:338:ARG:HH11	1.71	0.54
1:B:161:GLY:O	1:B:172:SER:N	2.41	0.54
1:B:344:GLU:N	1:B:361:LEU:O	2.38	0.54
1:F:344:GLU:H	1:F:361:LEU:CD1	2.21	0.54
1:A:121:ILE:HG23	1:A:343:VAL:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:ALA:C	1:A:288:LEU:HD21	2.33	0.54
1:A:297:PHE:CD2	1:A:297:PHE:N	2.74	0.54
1:A:308:MET:C	1:A:310:GLY:H	2.14	0.54
1:B:210:ARG:HH22	1:C:153:GLU:CG	2.18	0.54
1:B:280:ARG:O	1:B:281:ASP:C	2.51	0.54
1:F:281:ASP:O	1:F:285:ILE:HG12	2.08	0.54
1:G:197:MET:C	1:G:198:ASP:OD1	2.51	0.54
1:B:278:ASN:HB3	1:B:281:ASP:OD2	2.08	0.54
1:E:191:GLN:HE21	1:E:191:GLN:C	2.15	0.54
1:E:191:GLN:HB3	1:E:359:THR:HA	1.90	0.54
1:F:158:ASN:N	1:F:158:ASN:HD22	2.04	0.54
1:F:225:ASN:HA	1:F:235:GLY:HA3	1.88	0.54
1:G:131:ARG:O	1:G:133:THR:N	2.33	0.54
1:C:215:LEU:HD23	1:C:215:LEU:C	2.32	0.54
1:D:129:LEU:HD13	1:D:129:LEU:C	2.33	0.54
1:E:141:GLY:C	1:E:336:PHE:HA	2.32	0.54
1:E:277:LEU:N	1:E:277:LEU:HD23	2.23	0.54
1:F:206:TYR:CD2	1:F:206:TYR:C	2.86	0.54
1:F:211:LEU:CD2	1:F:362:CYS:SG	2.93	0.54
1:G:128:GLY:O	1:G:130:ARG:HG2	2.08	0.54
1:A:201:PRO:O	1:A:202:MET:C	2.49	0.54
1:E:155:VAL:CG1	1:E:374:THR:CB	2.85	0.54
1:E:287:LEU:HD12	1:E:295:TYR:HE1	1.73	0.54
1:F:358:LEU:HD23	1:F:358:LEU:C	2.32	0.54
1:B:195:GLN:CA	1:B:197:MET:HG2	2.38	0.53
1:B:344:GLU:O	1:B:361:LEU:N	2.42	0.53
1:C:281:ASP:O	1:C:285:ILE:HG12	2.08	0.53
1:D:138:LEU:HD12	1:D:138:LEU:N	2.22	0.53
1:D:148:LEU:HD12	1:D:148:LEU:O	2.06	0.53
1:D:174:ILE:H	1:D:174:ILE:HD13	1.72	0.53
1:G:285:ILE:CA	1:G:288:LEU:HG	2.37	0.53
1:C:366:LEU:HD13	1:C:367:ALA:N	2.22	0.53
1:D:174:ILE:O	1:D:174:ILE:CG1	2.56	0.53
1:E:217:LEU:HD11	1:F:269:GLU:HB3	1.89	0.53
1:A:158:ASN:ND2	1:A:158:ASN:N	2.54	0.53
1:C:345:VAL:HG13	1:C:360:ILE:HD13	1.91	0.53
1:E:199:ASP:O	1:E:202:MET:HE3	2.08	0.53
1:G:158:ASN:CG	1:G:172:SER:HA	2.31	0.53
1:G:281:ASP:O	1:G:285:ILE:HD12	2.07	0.53
1:A:285:ILE:C	1:A:288:LEU:CD2	2.62	0.53
1:A:308:MET:C	1:A:310:GLY:N	2.66	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:304:THR:HG21	1:C:309:TRP:O	2.07	0.53
1:D:174:ILE:HG12	1:D:174:ILE:O	2.07	0.53
1:D:247:LEU:HD21	1:D:260:HIS:CB	2.32	0.53
1:F:211:LEU:CD2	1:F:212:MET:HE3	2.37	0.53
1:F:275:ILE:HG23	1:F:326:VAL:CG1	2.38	0.53
1:G:239:VAL:HG12	1:G:373:PRO:HB3	1.91	0.53
1:G:366:LEU:C	1:G:366:LEU:CD1	2.74	0.53
1:A:366:LEU:HD12	1:A:366:LEU:O	2.08	0.53
1:B:149:GLU:HA	1:B:180:THR:HA	1.91	0.53
1:B:175:THR:HG22	1:B:176:PHE:H	1.73	0.53
1:C:132:LEU:HD23	1:C:136:ASP:OD2	2.09	0.53
1:C:243:TYR:OH	1:C:260:HIS:HB2	2.08	0.53
1:D:307:ILE:HB	1:D:311:LEU:O	2.09	0.53
1:F:204:GLN:HA	1:F:207:ILE:HG13	1.90	0.53
1:G:210:ARG:O	1:G:211:LEU:C	2.49	0.53
1:A:331:MET:HE1	1:F:209:ASN:O	2.09	0.53
1:C:287:LEU:HD23	1:C:300:PRO:HA	1.89	0.53
1:E:187:ALA:HB2	1:E:363:GLU:HA	1.90	0.53
1:E:191:GLN:C	1:E:191:GLN:NE2	2.66	0.53
1:E:307:ILE:HG22	1:E:312:PRO:HA	1.91	0.53
1:G:200:ALA:O	1:G:204:GLN:CA	2.57	0.53
1:A:125:ILE:CG2	1:A:204:GLN:HE21	2.09	0.53
1:D:202:MET:O	1:D:203:LEU:C	2.51	0.53
1:E:157:THR:CG2	1:E:267:GLU:HG2	2.38	0.53
1:F:253:THR:O	1:F:256:ASP:N	2.42	0.53
1:G:175:THR:C	1:G:176:PHE:HD2	2.16	0.53
1:B:153:GLU:OE1	1:B:371:TYR:O	2.27	0.53
1:B:158:ASN:ND2	1:B:172:SER:CB	2.72	0.53
1:C:152:ARG:O	1:C:176:PHE:HA	2.09	0.53
1:D:309:TRP:N	1:D:309:TRP:CE3	2.77	0.53
1:E:252:ASP:HB3	1:E:256:ASP:HB2	1.90	0.53
1:E:282:TRP:HA	1:E:282:TRP:CE3	2.44	0.53
1:F:314:VAL:HG23	1:F:314:VAL:O	2.08	0.53
1:B:194:ARG:HG2	1:B:356:ASN:O	2.08	0.53
1:C:194:ARG:HA	1:C:358:LEU:CD1	2.39	0.53
1:C:210:ARG:HH21	1:D:153:GLU:CD	1.77	0.53
1:D:158:ASN:N	1:D:158:ASN:HD22	2.05	0.53
1:D:245:THR:C	1:D:247:LEU:H	2.17	0.53
1:E:158:ASN:N	1:E:158:ASN:HD22	2.06	0.53
1:E:196:VAL:O	1:E:196:VAL:HG12	2.09	0.53
1:E:207:ILE:O	1:E:211:LEU:N	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:203:LEU:C	1:G:205:SER:N	2.57	0.53
1:A:289:LYS:HD2	1:A:289:LYS:N	2.23	0.53
1:A:303:PHE:C	1:A:303:PHE:CD2	2.87	0.53
1:B:150:TYR:HE2	1:B:181:ALA:HB2	1.73	0.53
1:E:220:GLU:CG	1:E:316:THR:HG21	2.39	0.53
1:F:155:VAL:HG23	1:F:174:ILE:CG2	2.33	0.53
1:F:268:SER:O	1:F:269:GLU:HB2	2.09	0.53
1:G:278:ASN:HD22	1:G:321:ALA:CA	2.22	0.53
1:B:148:LEU:CD2	1:B:181:ALA:HB3	2.40	0.52
1:C:155:VAL:CB	1:C:174:ILE:HG22	2.39	0.52
1:D:224:LEU:C	1:D:224:LEU:HD13	2.33	0.52
1:E:282:TRP:HA	1:E:282:TRP:HE3	1.74	0.52
1:F:292:GLU:O	1:F:294:ARG:N	2.42	0.52
1:G:137:LEU:HD11	1:G:314:VAL:HG21	1.91	0.52
1:A:240:ALA:HB2	1:A:376:ILE:HG21	1.89	0.52
1:B:155:VAL:HG13	1:B:155:VAL:O	2.09	0.52
1:B:249:ALA:HB3	1:B:252:ASP:CG	2.33	0.52
1:C:190:VAL:HG22	1:D:176:PHE:CZ	2.44	0.52
1:C:213:TYR:O	1:C:217:LEU:HD13	2.08	0.52
1:E:224:LEU:HD13	1:E:224:LEU:C	2.33	0.52
1:E:287:LEU:N	1:E:287:LEU:HD22	2.24	0.52
1:F:342:THR:O	1:F:363:GLU:N	2.42	0.52
1:A:194:ARG:HG2	1:A:195:GLN:N	2.23	0.52
1:B:148:LEU:CD2	1:B:148:LEU:N	2.72	0.52
1:C:349:ASP:O	1:C:352:ASN:OD1	2.27	0.52
1:D:210:ARG:NH1	1:E:371:TYR:CE2	2.77	0.52
1:F:156:PHE:HD2	1:F:158:ASN:CA	2.22	0.52
1:B:206:TYR:HD2	1:B:210:ARG:HB2	1.74	0.52
1:D:184:LYS:HA	1:D:184:LYS:NZ	2.25	0.52
1:G:189:TRP:HZ3	1:G:350:ARG:HH22	1.55	0.52
1:A:340:ASP:O	1:A:342:THR:HG23	2.09	0.52
1:B:158:ASN:CG	1:B:172:SER:HB2	2.35	0.52
1:E:207:ILE:CA	1:E:211:LEU:HB2	2.38	0.52
1:E:262:ILE:HD12	1:E:262:ILE:H	1.73	0.52
1:F:158:ASN:ND2	1:F:172:SER:HA	2.25	0.52
1:G:268:SER:O	1:G:269:GLU:CB	2.58	0.52
1:G:268:SER:O	1:G:269:GLU:HB3	2.10	0.52
1:G:280:ARG:O	1:G:283:HIS:N	2.42	0.52
1:G:356:ASN:C	1:G:356:ASN:ND2	2.67	0.52
1:A:266:THR:C	1:A:268:SER:H	2.18	0.52
1:B:175:THR:HG22	1:B:176:PHE:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:130:ARG:HB3	1:D:271:SER:OG	2.10	0.52
1:C:287:LEU:HD21	1:C:300:PRO:CB	2.36	0.52
1:C:347:ARG:O	1:C:348:GLU:C	2.51	0.52
1:E:156:PHE:HD2	1:E:158:ASN:CA	2.22	0.52
1:E:203:LEU:C	1:E:206:TYR:H	2.09	0.52
1:F:153:GLU:OE2	1:F:372:ARG:NH2	2.42	0.52
1:F:276:VAL:HG22	1:F:314:VAL:CG2	2.40	0.52
1:F:343:VAL:HA	1:F:362:CYS:HA	1.91	0.52
1:G:156:PHE:O	1:G:158:ASN:OD1	2.28	0.52
1:A:304:THR:O	1:A:306:ASN:N	2.43	0.52
1:B:158:ASN:CG	1:B:172:SER:CA	2.83	0.52
1:B:206:TYR:HE2	1:B:210:ARG:HE	1.58	0.52
1:D:155:VAL:CG1	1:D:374:THR:HB	2.38	0.52
1:D:303:PHE:O	1:D:306:ASN:HB3	2.10	0.52
1:G:280:ARG:C	1:G:282:TRP:H	2.16	0.52
1:B:329:PHE:HA	1:B:332:ALA:HB3	1.91	0.52
1:B:354:VAL:C	1:B:356:ASN:H	2.18	0.52
1:C:130:ARG:HB3	1:D:271:SER:CB	2.40	0.52
1:C:287:LEU:HD21	1:C:300:PRO:HB2	1.92	0.52
1:E:193:SER:C	1:E:195:GLN:N	2.68	0.52
1:E:216:ALA:O	1:E:217:LEU:C	2.53	0.52
1:E:249:ALA:O	1:E:250:THR:C	2.51	0.52
1:F:188:HIS:O	1:F:361:LEU:HA	2.10	0.52
1:C:275:ILE:HG23	1:C:326:VAL:HG12	1.91	0.52
1:D:284:ASN:O	1:D:287:LEU:HD12	2.10	0.52
1:E:135:ARG:HD2	1:E:219:GLU:OE1	2.10	0.52
1:F:202:MET:O	1:F:205:SER:CA	2.57	0.52
1:F:301:GLN:O	1:F:302:ALA:C	2.53	0.52
1:F:361:LEU:C	1:F:361:LEU:CD1	2.83	0.52
1:B:156:PHE:HB3	1:B:158:ASN:CG	2.34	0.52
1:B:156:PHE:HD2	1:B:158:ASN:CA	2.23	0.52
1:C:330:ASP:OD1	1:C:330:ASP:C	2.52	0.52
1:F:195:GLN:C	1:F:197:MET:N	2.65	0.52
1:G:155:VAL:HA	1:G:174:ILE:HG22	1.90	0.52
1:G:324:PHE:CZ	1:G:379:GLY:HA3	2.45	0.52
1:B:208:ASN:HD22	1:B:208:ASN:N	2.07	0.51
1:B:307:ILE:HG22	1:B:312:PRO:HA	1.91	0.51
1:C:212:MET:HA	1:C:212:MET:HE3	1.90	0.51
1:C:277:LEU:HD12	1:C:277:LEU:N	2.25	0.51
1:D:156:PHE:HD2	1:D:158:ASN:CA	2.23	0.51
1:D:282:TRP:CD1	1:D:304:THR:HG1	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:127:PRO:HB2	1:E:213:TYR:CE1	2.25	0.51
1:F:145:SER:O	1:F:338:ARG:HD3	2.09	0.51
1:F:158:ASN:ND2	1:F:158:ASN:N	2.49	0.51
1:F:212:MET:HE3	1:F:212:MET:CA	2.40	0.51
1:G:299:GLY:O	1:G:300:PRO:C	2.52	0.51
1:D:194:ARG:O	1:D:195:GLN:C	2.54	0.51
1:G:132:LEU:HG	1:G:136:ASP:CG	2.35	0.51
1:A:155:VAL:HG13	1:A:155:VAL:O	2.10	0.51
1:D:224:LEU:O	1:D:237:ASN:OD1	2.29	0.51
1:D:301:GLN:C	1:D:303:PHE:N	2.66	0.51
1:F:138:LEU:CD2	1:F:329:PHE:HB3	2.39	0.51
1:G:150:TYR:CE2	1:G:369:ALA:HB1	2.45	0.51
1:A:202:MET:CG	1:A:203:LEU:H	2.23	0.51
1:B:317:LYS:HG2	1:B:317:LYS:O	2.11	0.51
1:D:124:ILE:CG2	1:D:125:ILE:N	2.72	0.51
1:E:329:PHE:H	1:E:329:PHE:HD1	1.57	0.51
1:G:216:ALA:HA	1:G:219:GLU:HG2	1.91	0.51
1:A:240:ALA:HB2	1:A:376:ILE:CG2	2.40	0.51
1:B:161:GLY:C	1:B:172:SER:N	2.68	0.51
1:B:299:GLY:O	1:B:302:ALA:N	2.44	0.51
1:D:155:VAL:CG1	1:D:374:THR:CG2	2.89	0.51
1:D:293:GLY:H	1:F:294:ARG:HB2	1.75	0.51
1:D:300:PRO:HG2	1:E:301:GLN:NE2	2.25	0.51
1:E:134:ILE:H	1:E:134:ILE:CD1	2.24	0.51
1:B:308:MET:HG3	1:B:309:TRP:HD1	1.75	0.51
1:C:195:GLN:O	1:C:197:MET:N	2.43	0.51
1:D:210:ARG:NH1	1:E:371:TYR:CD2	2.79	0.51
1:F:193:SER:HA	1:F:357:MET:HA	1.92	0.51
1:G:155:VAL:HG22	1:G:156:PHE:H	1.74	0.51
1:G:158:ASN:OD1	1:G:172:SER:CA	2.44	0.51
1:G:343:VAL:HG22	1:G:362:CYS:SG	2.50	0.51
1:A:156:PHE:C	1:A:158:ASN:N	2.64	0.51
1:B:137:LEU:CD2	1:B:329:PHE:HB2	2.40	0.51
1:D:349:ASP:O	1:D:350:ARG:C	2.54	0.51
1:E:150:TYR:CE1	1:E:179:GLN:HB2	2.45	0.51
1:E:199:ASP:HB3	1:E:202:MET:HB3	1.92	0.51
1:G:237:ASN:HD21	1:G:319:GLN:HE22	1.57	0.51
1:A:153:GLU:OE2	1:A:372:ARG:NH2	2.43	0.51
1:A:203:LEU:HD12	1:A:207:ILE:HD11	1.92	0.51
1:A:358:LEU:C	1:A:358:LEU:HD12	2.36	0.51
1:C:227:ASP:C	1:C:229:THR:H	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:146:ASN:O	1:D:147:ALA:HB2	2.10	0.51
1:D:175:THR:HG22	1:D:176:PHE:N	2.25	0.51
1:A:254:ARG:O	1:A:258:ILE:HD13	2.11	0.51
1:C:201:PRO:O	1:C:202:MET:C	2.54	0.51
1:F:198:ASP:O	1:F:199:ASP:C	2.54	0.51
1:F:202:MET:O	1:F:203:LEU:C	2.53	0.51
1:G:343:VAL:HG13	1:G:361:LEU:O	2.10	0.51
1:A:138:LEU:HD12	1:A:138:LEU:N	2.26	0.51
1:C:132:LEU:HD21	1:C:136:ASP:CB	2.40	0.51
1:C:211:LEU:HD23	1:C:211:LEU:C	2.35	0.51
1:D:201:PRO:O	1:D:202:MET:C	2.52	0.51
1:E:158:ASN:ND2	1:E:172:SER:HA	2.26	0.51
1:E:190:VAL:HG12	1:F:176:PHE:CE1	2.46	0.51
1:E:281:ASP:O	1:E:285:ILE:HG13	2.11	0.51
1:E:349:ASP:O	1:E:352:ASN:OD1	2.29	0.51
1:F:138:LEU:HD23	1:F:329:PHE:HB3	1.93	0.51
1:F:162:ASP:OD1	1:F:173:ASP:CG	2.54	0.51
1:F:193:SER:O	1:F:196:VAL:HG13	2.11	0.51
1:G:131:ARG:HD3	1:G:306:ASN:HD21	1.76	0.51
1:G:371:TYR:O	1:G:373:PRO:HD3	2.10	0.51
1:B:162:ASP:O	1:B:173:ASP:N	2.44	0.50
1:C:129:LEU:CD1	1:D:331:MET:CE	2.69	0.50
1:D:224:LEU:HD12	1:D:225:ASN:CG	2.36	0.50
1:E:236:LEU:HD13	1:E:329:PHE:HE2	1.75	0.50
1:F:184:LYS:HB2	1:F:233:LEU:HD21	1.92	0.50
1:G:211:LEU:HD21	1:G:362:CYS:HB2	1.93	0.50
1:G:302:ALA:O	1:G:303:PHE:HB2	2.11	0.50
1:B:158:ASN:CB	1:B:172:SER:HB2	2.41	0.50
1:B:212:MET:O	1:B:214:GLY:N	2.45	0.50
1:C:207:ILE:HD13	1:C:207:ILE:N	2.25	0.50
1:D:358:LEU:N	1:D:358:LEU:CD1	2.74	0.50
1:G:200:ALA:O	1:G:201:PRO:C	2.53	0.50
1:G:301:GLN:CG	1:G:302:ALA:H	2.11	0.50
1:B:204:GLN:OE1	1:B:204:GLN:HA	2.09	0.50
1:B:216:ALA:O	1:B:217:LEU:O	2.29	0.50
1:B:289:LYS:HD2	1:B:294:ARG:N	2.26	0.50
1:C:191:GLN:OE1	1:C:191:GLN:O	2.30	0.50
1:C:204:GLN:O	1:C:207:ILE:HD13	2.11	0.50
1:E:361:LEU:HG	1:E:362:CYS:N	2.26	0.50
1:F:142:ARG:HG2	1:F:337:ASP:HB2	1.81	0.50
1:A:131:ARG:HH21	1:A:316:THR:HB	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:SER:H	1:A:338:ARG:HD3	1.77	0.50
1:A:290:ASP:C	1:A:292:GLU:N	2.69	0.50
1:B:299:GLY:O	1:B:300:PRO:C	2.55	0.50
1:A:151:VAL:HG22	1:A:152:ARG:N	2.27	0.50
1:A:266:THR:C	1:A:268:SER:N	2.67	0.50
1:A:321:ALA:C	1:A:323:THR:H	2.18	0.50
1:B:129:LEU:O	1:B:131:ARG:N	2.44	0.50
1:B:158:ASN:OD1	1:B:172:SER:C	2.55	0.50
1:B:258:ILE:HD11	1:B:381:PHE:CZ	2.46	0.50
1:B:282:TRP:HA	1:B:282:TRP:HE3	1.76	0.50
1:C:130:ARG:HB2	1:D:271:SER:OG	2.12	0.50
1:D:303:PHE:CA	1:D:306:ASN:HB3	2.38	0.50
1:E:215:LEU:C	1:E:218:LYS:H	2.17	0.50
1:E:264:GLN:O	1:E:267:GLU:HB2	2.12	0.50
1:B:188:HIS:O	1:B:361:LEU:HD12	2.12	0.50
1:B:199:ASP:O	1:B:200:ALA:CB	2.59	0.50
1:C:206:TYR:O	1:C:210:ARG:N	2.36	0.50
1:C:296:ILE:C	1:C:297:PHE:CD2	2.90	0.50
1:C:361:LEU:HD12	1:C:361:LEU:C	2.36	0.50
1:D:129:LEU:CD1	1:D:131:ARG:HD3	2.42	0.50
1:E:214:GLY:O	1:E:217:LEU:HB3	2.11	0.50
1:E:226:GLY:N	1:E:235:GLY:HA3	2.27	0.50
1:F:129:LEU:HD12	1:F:129:LEU:N	2.22	0.50
1:F:290:ASP:CG	1:F:291:ASN:H	2.20	0.50
1:A:348:GLU:O	1:A:348:GLU:CG	2.60	0.50
1:B:137:LEU:HD22	1:B:329:PHE:HB2	1.93	0.50
1:B:282:TRP:HA	1:B:282:TRP:CE3	2.47	0.50
1:E:137:LEU:HD22	1:E:329:PHE:CB	2.36	0.50
1:F:291:ASN:CG	1:F:292:GLU:H	2.20	0.50
1:G:134:ILE:CG1	1:G:220:GLU:HG3	2.42	0.50
1:G:352:ASN:O	1:G:355:LYS:O	2.29	0.50
1:A:296:ILE:C	1:A:297:PHE:CD2	2.90	0.50
1:C:157:THR:OG1	1:C:158:ASN:N	2.38	0.50
1:C:184:LYS:HB3	1:C:231:ASP:O	2.12	0.50
1:D:152:ARG:HB3	1:D:177:SER:HB2	1.94	0.50
1:D:266:THR:HA	1:D:270:PHE:O	2.11	0.50
1:E:199:ASP:HB3	1:E:202:MET:HE2	1.94	0.50
1:F:327:GLY:O	1:F:329:PHE:HE1	1.95	0.50
1:B:148:LEU:N	1:B:148:LEU:HD22	2.26	0.49
1:B:158:ASN:OD1	1:B:172:SER:O	2.29	0.49
1:B:319:GLN:HE22	1:B:324:PHE:HA	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:368:LEU:HD21	1:B:370:HIS:CE1	2.46	0.49
1:C:195:GLN:NE2	1:C:198:ASP:O	2.45	0.49
1:C:202:MET:O	1:C:205:SER:CA	2.60	0.49
1:D:162:ASP:C	1:D:173:ASP:N	2.70	0.49
1:D:296:ILE:C	1:D:298:GLY:N	2.70	0.49
1:E:307:ILE:HG13	1:E:307:ILE:O	2.12	0.49
1:A:190:VAL:HG21	1:A:210:ARG:HH12	1.77	0.49
1:A:296:ILE:O	1:A:297:PHE:HB2	2.12	0.49
1:A:309:TRP:HA	1:A:309:TRP:CE3	2.47	0.49
1:D:349:ASP:OD1	1:D:350:ARG:CG	2.58	0.49
1:E:206:TYR:HD2	1:E:210:ARG:HB2	1.77	0.49
1:E:347:ARG:C	1:E:349:ASP:H	2.20	0.49
1:F:129:LEU:O	1:F:130:ARG:HB2	2.11	0.49
1:F:132:LEU:CD2	1:F:136:ASP:CB	2.90	0.49
1:D:197:MET:CE	1:D:203:LEU:HA	2.42	0.49
1:D:277:LEU:HD13	1:D:324:PHE:HB3	1.93	0.49
1:G:192:ALA:O	1:G:357:MET:SD	2.70	0.49
1:B:268:SER:HB3	1:B:374:THR:HG22	1.93	0.49
1:B:280:ARG:O	1:B:283:HIS:N	2.45	0.49
1:D:155:VAL:HG13	1:D:374:THR:HG21	1.94	0.49
1:F:200:ALA:O	1:F:203:LEU:N	2.44	0.49
1:F:258:ILE:CD1	1:F:275:ILE:HG21	2.42	0.49
1:F:280:ARG:O	1:F:283:HIS:HB3	2.12	0.49
1:G:129:LEU:C	1:G:131:ARG:N	2.69	0.49
1:G:329:PHE:O	1:G:330:ASP:C	2.56	0.49
1:A:197:MET:C	1:A:199:ASP:N	2.70	0.49
1:A:267:GLU:OE1	1:F:317:LYS:NZ	2.41	0.49
1:C:343:VAL:HA	1:C:362:CYS:HA	1.95	0.49
1:D:131:ARG:HG2	1:D:132:LEU:O	2.12	0.49
1:D:201:PRO:C	1:D:203:LEU:N	2.68	0.49
1:E:182:ASN:HB2	1:E:184:LYS:HZ2	1.77	0.49
1:E:273:SER:HB2	1:E:330:ASP:OD1	2.12	0.49
1:E:279:PRO:HG3	1:E:315:PRO:O	2.12	0.49
1:E:287:LEU:HD12	1:E:295:TYR:CE1	2.48	0.49
1:G:273:SER:O	1:G:311:LEU:HD12	2.13	0.49
1:E:300:PRO:HG2	1:F:309:TRP:NE1	2.27	0.49
1:F:142:ARG:NH2	1:F:340:ASP:CG	2.71	0.49
1:F:212:MET:O	1:F:215:LEU:N	2.46	0.49
1:A:374:THR:C	1:A:376:ILE:H	2.21	0.49
1:C:217:LEU:HD23	1:D:269:GLU:HB3	1.95	0.49
1:D:162:ASP:OD1	1:D:173:ASP:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:184:LYS:HG3	1:E:232:ASN:O	2.12	0.49
1:E:227:ASP:C	1:E:229:THR:CG2	2.85	0.49
1:F:226:GLY:N	1:F:235:GLY:HA3	2.25	0.49
1:F:327:GLY:O	1:F:329:PHE:CD1	2.66	0.49
1:G:303:PHE:CD2	1:G:304:THR:O	2.66	0.49
1:A:174:ILE:O	1:A:174:ILE:HG12	2.13	0.49
1:A:263:TYR:CZ	1:A:267:GLU:OE2	2.66	0.49
1:E:125:ILE:CG1	1:E:126:MET:N	2.73	0.49
1:C:155:VAL:HB	1:C:174:ILE:HG22	1.94	0.49
1:C:305:SER:O	1:C:307:ILE:HG23	2.13	0.49
1:D:290:ASP:O	1:D:291:ASN:HB2	2.11	0.49
1:D:343:VAL:HG12	1:D:362:CYS:CB	2.43	0.49
1:G:174:ILE:O	1:G:174:ILE:HG12	2.12	0.49
1:A:254:ARG:HA	1:A:257:ILE:HD12	1.95	0.49
1:A:263:TYR:OH	1:F:280:ARG:NE	2.25	0.49
1:C:148:LEU:HB2	1:C:181:ALA:HB3	1.94	0.49
1:E:194:ARG:NH1	1:E:347:ARG:NH1	2.61	0.49
1:E:199:ASP:HB2	1:E:202:MET:HE2	1.95	0.49
1:F:192:ALA:O	1:F:357:MET:CA	2.60	0.49
1:F:285:ILE:HG21	1:F:308:MET:HE1	1.94	0.49
1:A:266:THR:HG21	1:F:279:PRO:CB	2.39	0.48
1:B:135:ARG:HH11	1:B:135:ARG:HG3	1.77	0.48
1:B:153:GLU:OE1	1:B:371:TYR:HB3	2.12	0.48
1:B:224:LEU:HD13	1:B:224:LEU:C	2.38	0.48
1:D:199:ASP:OD1	1:D:200:ALA:N	2.46	0.48
1:D:206:TYR:OH	1:E:371:TYR:HE2	1.96	0.48
1:E:155:VAL:HG11	1:E:374:THR:HB	1.95	0.48
1:E:290:ASP:C	1:E:292:GLU:H	2.21	0.48
1:E:295:TYR:HH	1:F:256:ASP:CG	2.09	0.48
1:A:121:ILE:C	1:A:123:GLY:H	2.20	0.48
1:A:308:MET:O	1:A:310:GLY:N	2.45	0.48
1:B:151:VAL:HG13	1:B:151:VAL:O	2.12	0.48
1:B:155:VAL:HG12	1:B:374:THR:CB	2.39	0.48
1:B:244:ASP:OD1	1:B:247:LEU:HG	2.12	0.48
1:C:131:ARG:HH21	1:C:316:THR:HB	1.78	0.48
1:C:258:ILE:CD1	1:C:275:ILE:HG21	2.42	0.48
1:C:343:VAL:HA	1:C:361:LEU:O	2.13	0.48
1:D:131:ARG:HH21	1:D:133:THR:HG22	1.78	0.48
1:E:134:ILE:HD12	1:E:314:VAL:HG11	1.95	0.48
1:F:146:ASN:N	1:F:146:ASN:OD1	2.46	0.48
1:F:194:ARG:HH22	1:G:363:GLU:CD	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:198:ASP:OD2	1:F:198:ASP:O	2.30	0.48
1:F:204:GLN:O	1:F:206:TYR:N	2.45	0.48
1:F:257:ILE:C	1:F:259:ALA:N	2.69	0.48
1:A:202:MET:HG3	1:A:203:LEU:N	2.28	0.48
1:A:217:LEU:C	1:A:217:LEU:HD23	2.38	0.48
1:A:302:ALA:HA	1:A:306:ASN:HD22	1.77	0.48
1:A:307:ILE:C	1:A:307:ILE:CD1	2.82	0.48
1:B:249:ALA:N	1:B:252:ASP:OD2	2.46	0.48
1:B:360:ILE:CG2	1:B:361:LEU:N	2.75	0.48
1:C:342:THR:O	1:C:363:GLU:N	2.43	0.48
1:D:161:GLY:O	1:D:162:ASP:C	2.56	0.48
1:E:220:GLU:CD	1:E:316:THR:HG21	2.35	0.48
1:G:132:LEU:HG	1:G:136:ASP:OD1	2.13	0.48
1:G:142:ARG:HG2	1:G:142:ARG:HH11	1.78	0.48
1:G:199:ASP:O	1:G:203:LEU:N	2.45	0.48
1:A:137:LEU:HD22	1:A:329:PHE:CB	2.40	0.48
1:A:309:TRP:HA	1:A:309:TRP:HE3	1.78	0.48
1:C:245:THR:HA	1:C:248:ASN:ND2	2.28	0.48
1:D:158:ASN:H	1:D:158:ASN:HD22	1.58	0.48
1:E:126:MET:HE1	1:E:129:LEU:HD21	1.93	0.48
1:E:189:TRP:HA	1:E:360:ILE:HD12	1.95	0.48
1:E:216:ALA:O	1:E:218:LYS:N	2.46	0.48
1:F:131:ARG:HH21	1:F:220:GLU:CD	2.20	0.48
1:A:258:ILE:N	1:A:258:ILE:HD12	2.29	0.48
1:A:292:GLU:C	1:A:294:ARG:H	2.22	0.48
1:A:303:PHE:CD2	1:A:304:THR:N	2.82	0.48
1:B:146:ASN:N	1:B:146:ASN:ND2	2.62	0.48
1:B:349:ASP:O	1:B:352:ASN:HB2	2.13	0.48
1:D:194:ARG:HA	1:D:358:LEU:HD22	1.94	0.48
1:D:302:ALA:O	1:D:305:SER:N	2.46	0.48
1:E:296:ILE:O	1:E:298:GLY:O	2.31	0.48
1:F:195:GLN:O	1:F:197:MET:N	2.47	0.48
1:F:249:ALA:N	1:F:252:ASP:OD2	2.44	0.48
1:B:155:VAL:HG13	1:B:374:THR:OG1	2.13	0.48
1:E:280:ARG:HG2	1:E:280:ARG:HH11	1.79	0.48
1:C:345:VAL:HA	1:C:359:THR:O	2.12	0.48
1:D:303:PHE:HA	1:D:306:ASN:CB	2.39	0.48
1:E:154:GLU:OE2	1:E:177:SER:OG	2.23	0.48
1:E:195:GLN:OE1	1:E:195:GLN:HA	2.14	0.48
1:G:343:VAL:HA	1:G:361:LEU:O	2.13	0.48
1:B:262:ILE:HD12	1:B:262:ILE:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:ARG:HA	1:C:358:LEU:HD12	1.96	0.48
1:C:339:MET:HG2	1:C:340:ASP:N	2.28	0.48
1:D:125:ILE:CG1	1:D:208:ASN:HD21	2.26	0.48
1:D:290:ASP:C	1:D:292:GLU:N	2.70	0.48
1:E:130:ARG:CB	1:F:271:SER:OG	2.59	0.48
1:F:215:LEU:C	1:F:215:LEU:HD23	2.38	0.48
1:G:156:PHE:CZ	1:G:158:ASN:HB3	2.49	0.48
1:G:239:VAL:HG12	1:G:239:VAL:O	2.13	0.48
1:A:285:ILE:O	1:A:288:LEU:HD11	2.14	0.48
1:A:300:PRO:CA	1:A:303:PHE:HB3	2.39	0.48
1:B:262:ILE:H	1:B:262:ILE:CD1	2.27	0.48
1:C:296:ILE:HG13	1:C:297:PHE:CE2	2.48	0.48
1:D:155:VAL:HG11	1:D:374:THR:HG21	1.95	0.48
1:D:302:ALA:HB3	1:D:305:SER:OG	2.13	0.48
1:E:309:TRP:HA	1:E:309:TRP:HE3	1.79	0.48
1:F:222:GLN:HE22	1:F:232:ASN:HB3	1.79	0.48
1:G:148:LEU:HB2	1:G:181:ALA:HB3	1.95	0.48
1:A:224:LEU:HD12	1:A:225:ASN:CG	2.38	0.48
1:A:283:HIS:HA	1:A:303:PHE:HE1	1.79	0.48
1:C:275:ILE:CG2	1:C:277:LEU:HD11	2.43	0.48
1:D:158:ASN:CG	1:D:172:SER:CA	2.80	0.48
1:D:239:VAL:HB	1:D:370:HIS:HD1	1.79	0.48
1:E:309:TRP:HA	1:E:309:TRP:CE3	2.49	0.48
1:F:225:ASN:N	1:F:225:ASN:ND2	2.60	0.48
1:F:265:VAL:HG22	1:F:377:ILE:HD13	1.94	0.48
1:F:361:LEU:O	1:F:361:LEU:CD1	2.55	0.48
1:A:132:LEU:O	1:A:314:VAL:HG13	2.13	0.47
1:A:179:GLN:HG3	1:A:180:THR:N	2.29	0.47
1:B:354:VAL:O	1:B:356:ASN:N	2.47	0.47
1:F:142:ARG:CG	1:F:337:ASP:CB	2.72	0.47
1:B:125:ILE:CG1	1:B:127:PRO:HG3	2.44	0.47
1:B:253:THR:HB	1:B:256:ASP:OD1	2.13	0.47
1:B:288:LEU:C	1:B:288:LEU:HD23	2.39	0.47
1:B:308:MET:HE3	1:B:309:TRP:HE1	1.79	0.47
1:G:345:VAL:CG2	1:G:360:ILE:HG22	2.43	0.47
1:A:264:GLN:OE1	1:A:377:ILE:HG21	2.14	0.47
1:A:287:LEU:N	1:A:288:LEU:HD23	2.29	0.47
1:B:158:ASN:H	1:B:158:ASN:HD22	1.56	0.47
1:B:307:ILE:HA	1:B:313:VAL:HG23	1.96	0.47
1:C:132:LEU:HD21	1:C:136:ASP:HB2	1.95	0.47
1:C:174:ILE:HD13	1:C:174:ILE:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:192:ALA:C	1:F:357:MET:SD	2.97	0.47
1:G:156:PHE:CE2	1:G:158:ASN:CB	2.94	0.47
1:G:329:PHE:HA	1:G:332:ALA:HB2	1.90	0.47
1:A:184:LYS:HD2	1:A:231:ASP:HA	1.97	0.47
1:A:263:TYR:O	1:A:266:THR:HB	2.14	0.47
1:A:331:MET:HE3	1:F:213:TYR:HB2	1.96	0.47
1:B:194:ARG:NH1	1:B:347:ARG:NH2	2.62	0.47
1:B:204:GLN:O	1:B:207:ILE:HB	2.15	0.47
1:B:212:MET:O	1:B:215:LEU:CA	2.59	0.47
1:B:236:LEU:HD13	1:B:329:PHE:HE2	1.80	0.47
1:C:274:GLY:C	1:C:275:ILE:HD12	2.40	0.47
1:D:155:VAL:HG12	1:D:374:THR:CB	2.39	0.47
1:D:307:ILE:HD13	1:D:310:GLY:O	2.15	0.47
1:E:162:ASP:OD1	1:E:173:ASP:HB2	2.15	0.47
1:B:128:GLY:O	1:B:213:TYR:OH	2.30	0.47
1:B:140:GLN:OE1	1:B:140:GLN:N	2.47	0.47
1:C:189:TRP:HB3	1:C:361:LEU:HB3	1.96	0.47
1:C:195:GLN:C	1:C:197:MET:N	2.71	0.47
1:C:197:MET:HE3	1:C:197:MET:CA	2.42	0.47
1:C:258:ILE:HD12	1:C:275:ILE:HG21	1.97	0.47
1:D:129:LEU:CD2	1:D:130:ARG:H	2.07	0.47
1:E:190:VAL:HG22	1:E:211:LEU:HD11	1.95	0.47
1:G:138:LEU:HD21	1:G:329:PHE:HB3	1.94	0.47
1:G:342:THR:O	1:G:363:GLU:N	2.47	0.47
1:A:224:LEU:HD13	1:A:237:ASN:OD1	2.14	0.47
1:B:125:ILE:CD1	1:B:127:PRO:CG	2.93	0.47
1:B:158:ASN:HD22	1:B:172:SER:HB2	1.77	0.47
1:D:142:ARG:HA	1:D:337:ASP:H	1.79	0.47
1:F:304:THR:HG22	1:F:305:SER:N	2.30	0.47
1:A:245:THR:HG23	1:A:248:ASN:HD21	1.80	0.47
1:A:265:VAL:O	1:A:265:VAL:HG12	2.14	0.47
1:B:190:VAL:HG23	1:B:190:VAL:O	2.15	0.47
1:B:194:ARG:CD	1:B:357:MET:HA	2.43	0.47
1:C:191:GLN:HA	1:C:358:LEU:O	2.15	0.47
1:C:195:GLN:OE1	1:C:195:GLN:HA	2.15	0.47
1:C:335:VAL:HG13	1:C:366:LEU:CD2	2.45	0.47
1:D:155:VAL:HG11	1:D:374:THR:CG2	2.45	0.47
1:E:131:ARG:HH12	1:E:316:THR:HA	1.78	0.47
1:E:201:PRO:HG2	1:E:202:MET:H	1.79	0.47
1:E:296:ILE:CG2	1:E:297:PHE:CD1	2.97	0.47
1:E:296:ILE:C	1:E:298:GLY:N	2.70	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:301:GLN:OE1	1:E:304:THR:HB	2.14	0.47
1:F:189:TRP:HA	1:F:360:ILE:O	2.15	0.47
1:G:174:ILE:HD13	1:G:174:ILE:N	2.14	0.47
1:G:194:ARG:O	1:G:195:GLN:C	2.55	0.47
1:A:150:TYR:HE1	1:A:181:ALA:HB2	1.79	0.47
1:A:179:GLN:HA	1:A:179:GLN:NE2	2.30	0.47
1:A:331:MET:CE	1:F:209:ASN:O	2.63	0.47
1:B:159:ALA:HB1	1:B:160:PRO:CD	2.39	0.47
1:E:130:ARG:HG2	1:F:271:SER:OG	2.15	0.47
1:E:155:VAL:CG2	1:E:174:ILE:HG22	2.35	0.47
1:G:200:ALA:N	1:G:201:PRO:HD3	2.29	0.47
1:G:360:ILE:HG13	1:G:360:ILE:O	2.14	0.47
1:A:349:ASP:OD1	1:A:349:ASP:C	2.57	0.47
1:B:156:PHE:CD2	1:B:158:ASN:HB3	2.50	0.47
1:C:146:ASN:ND2	1:C:365:ARG:HH21	2.11	0.47
1:C:225:ASN:ND2	1:C:225:ASN:N	2.62	0.47
1:E:186:ILE:HD11	1:E:222:GLN:HG3	1.96	0.47
1:E:301:GLN:O	1:E:302:ALA:C	2.58	0.47
1:E:329:PHE:CD1	1:E:329:PHE:N	2.82	0.47
1:A:155:VAL:CG1	1:A:374:THR:CG2	2.92	0.47
1:C:206:TYR:CE2	1:C:210:ARG:HD3	2.50	0.47
1:C:275:ILE:HG22	1:C:277:LEU:CD1	2.45	0.47
1:C:297:PHE:CD2	1:C:297:PHE:N	2.83	0.47
1:C:376:ILE:C	1:C:377:ILE:HD12	2.39	0.47
1:D:124:ILE:O	1:D:125:ILE:HG22	2.15	0.47
1:D:217:LEU:O	1:D:217:LEU:HD23	2.15	0.47
1:E:295:TYR:O	1:E:296:ILE:O	2.33	0.47
1:E:352:ASN:O	1:E:355:LYS:O	2.32	0.47
1:F:322:GLY:O	1:F:380:THR:HG22	2.14	0.47
1:G:211:LEU:C	1:G:211:LEU:HD23	2.40	0.47
1:A:158:ASN:N	1:A:158:ASN:HD22	2.12	0.46
1:B:306:ASN:HD22	1:B:315:PRO:HG2	1.80	0.46
1:C:198:ASP:O	1:C:198:ASP:CG	2.57	0.46
1:E:209:ASN:O	1:F:331:MET:HE2	2.15	0.46
1:E:220:GLU:OE2	1:E:316:THR:HG23	2.13	0.46
1:F:195:GLN:O	1:F:196:VAL:C	2.58	0.46
1:F:227:ASP:C	1:F:229:THR:H	2.23	0.46
1:A:202:MET:HB2	1:B:336:PHE:CE2	2.41	0.46
1:A:240:ALA:CB	1:A:376:ILE:CG2	2.93	0.46
1:B:211:LEU:HD13	1:B:211:LEU:HA	1.64	0.46
1:B:217:LEU:O	1:B:218:LYS:C	2.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:THR:HA	1:C:220:GLU:OE2	2.14	0.46
1:C:200:ALA:O	1:C:202:MET:N	2.48	0.46
1:C:288:LEU:HD23	1:C:288:LEU:C	2.40	0.46
1:C:342:THR:O	1:C:362:CYS:HA	2.16	0.46
1:C:377:ILE:HD12	1:C:377:ILE:N	2.31	0.46
1:D:185:THR:C	1:D:186:ILE:HD12	2.40	0.46
1:E:325:THR:HG22	1:E:329:PHE:HZ	1.79	0.46
1:E:356:ASN:O	1:E:357:MET:HB3	2.16	0.46
1:F:137:LEU:O	1:F:137:LEU:HD23	2.15	0.46
1:G:280:ARG:C	1:G:283:HIS:H	2.23	0.46
1:G:352:ASN:O	1:G:353:PHE:C	2.56	0.46
1:A:207:ILE:O	1:A:211:LEU:HB2	2.16	0.46
1:B:244:ASP:CG	1:B:247:LEU:HG	2.40	0.46
1:C:227:ASP:O	1:C:228:GLY:C	2.59	0.46
1:D:174:ILE:H	1:D:174:ILE:CD1	2.27	0.46
1:E:301:GLN:O	1:E:304:THR:N	2.48	0.46
1:A:196:VAL:O	1:A:199:ASP:HB2	2.16	0.46
1:B:209:ASN:HB3	1:C:331:MET:CE	2.45	0.46
1:D:346:SER:O	1:D:348:GLU:HG3	2.16	0.46
1:E:128:GLY:N	1:E:213:TYR:CD1	2.81	0.46
1:E:302:ALA:HA	1:E:305:SER:OG	2.16	0.46
1:E:358:LEU:HD12	1:E:358:LEU:N	2.30	0.46
1:F:295:TYR:CE2	1:F:300:PRO:HG3	2.51	0.46
1:B:148:LEU:HD21	1:B:181:ALA:HB3	1.97	0.46
1:D:122:PRO:CB	1:D:343:VAL:HG23	2.45	0.46
1:D:150:TYR:OH	1:D:152:ARG:NH2	2.49	0.46
1:F:257:ILE:O	1:F:258:ILE:C	2.59	0.46
1:F:342:THR:O	1:F:362:CYS:CA	2.62	0.46
1:G:155:VAL:CG2	1:G:156:PHE:N	2.78	0.46
1:G:156:PHE:CG	1:G:158:ASN:HB3	2.49	0.46
1:D:149:GLU:HA	1:D:180:THR:HA	1.98	0.46
1:E:145:SER:C	1:E:147:ALA:H	2.23	0.46
1:F:227:ASP:C	1:F:229:THR:N	2.73	0.46
1:G:153:GLU:OE1	1:G:372:ARG:NE	2.48	0.46
1:G:199:ASP:O	1:G:200:ALA:C	2.59	0.46
1:G:217:LEU:HD12	1:G:217:LEU:N	2.31	0.46
1:G:273:SER:H	1:G:328:GLY:HA2	1.81	0.46
1:A:196:VAL:O	1:A:199:ASP:N	2.47	0.46
1:A:256:ASP:O	1:A:259:ALA:HB3	2.16	0.46
1:A:290:ASP:C	1:A:292:GLU:H	2.23	0.46
1:A:309:TRP:CH2	1:F:301:GLN:HB3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:190:VAL:HG12	1:C:176:PHE:HZ	1.79	0.46
1:B:209:ASN:O	1:C:331:MET:CE	2.63	0.46
1:C:184:LYS:CB	1:C:233:LEU:HD21	2.46	0.46
1:C:296:ILE:O	1:C:297:PHE:HD2	1.98	0.46
1:E:300:PRO:HG2	1:F:309:TRP:HE1	1.81	0.46
1:E:302:ALA:HA	1:E:305:SER:HG	1.80	0.46
1:F:151:VAL:O	1:F:151:VAL:HG13	2.16	0.46
1:F:208:ASN:OD1	1:F:208:ASN:C	2.58	0.46
1:F:292:GLU:HB2	1:F:294:ARG:HD3	1.96	0.46
1:G:152:ARG:HH21	1:G:370:HIS:HB2	1.79	0.46
1:G:197:MET:SD	1:G:197:MET:O	2.73	0.46
1:A:158:ASN:ND2	1:A:172:SER:CA	2.79	0.46
1:A:206:TYR:HB3	1:A:207:ILE:HD12	1.98	0.46
1:A:343:VAL:HA	1:A:361:LEU:O	2.16	0.46
1:B:266:THR:HA	1:B:270:PHE:O	2.16	0.46
1:C:207:ILE:H	1:C:207:ILE:CD1	2.28	0.46
1:D:217:LEU:HD23	1:D:217:LEU:C	2.40	0.46
1:E:126:MET:HE3	1:E:129:LEU:CD2	2.44	0.46
1:G:217:LEU:HD12	1:G:217:LEU:H	1.80	0.46
1:G:366:LEU:HD12	1:G:367:ALA:CA	2.46	0.46
1:A:155:VAL:CG2	1:A:174:ILE:HG22	2.37	0.46
1:A:183:VAL:HG13	1:A:366:LEU:C	2.41	0.46
1:A:289:LYS:HD2	1:A:289:LYS:H	1.80	0.46
1:D:174:ILE:HD13	1:D:174:ILE:O	2.16	0.46
1:D:299:GLY:O	1:D:301:GLN:HG2	2.16	0.46
1:E:174:ILE:O	1:E:174:ILE:HG12	2.15	0.46
1:F:224:LEU:CD1	1:F:237:ASN:HD21	2.29	0.46
1:G:128:GLY:C	1:G:130:ARG:H	2.24	0.46
1:G:327:GLY:N	1:G:329:PHE:CE2	2.74	0.46
1:A:149:GLU:OE1	1:F:195:GLN:CG	2.64	0.46
1:B:174:ILE:HD13	1:B:174:ILE:O	2.15	0.46
1:D:190:VAL:HG11	1:D:211:LEU:CD2	2.41	0.46
1:F:254:ARG:HG2	1:F:381:PHE:HD2	1.81	0.46
1:G:202:MET:HG2	1:G:203:LEU:N	2.31	0.46
1:A:131:ARG:HH21	1:A:316:THR:CB	2.29	0.45
1:C:217:LEU:CD2	1:D:269:GLU:HB3	2.46	0.45
1:C:339:MET:HE3	1:C:342:THR:OG1	2.15	0.45
1:D:153:GLU:O	1:D:155:VAL:N	2.49	0.45
1:F:189:TRP:CD1	1:F:189:TRP:H	2.33	0.45
1:A:263:TYR:CE2	1:F:280:ARG:NE	2.84	0.45
1:E:328:GLY:C	1:E:330:ASP:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:134:ILE:O	1:G:137:LEU:HB2	2.15	0.45
1:B:180:THR:CG2	1:B:181:ALA:N	2.80	0.45
1:C:186:ILE:CD1	1:C:222:GLN:HG3	2.41	0.45
1:C:283:HIS:HE1	1:D:260:HIS:HA	1.81	0.45
1:C:290:ASP:C	1:C:292:GLU:N	2.74	0.45
1:E:141:GLY:O	1:E:336:PHE:HA	2.17	0.45
1:E:157:THR:HB	1:E:267:GLU:OE1	2.15	0.45
1:E:203:LEU:C	1:E:205:SER:H	2.19	0.45
1:E:280:ARG:O	1:E:283:HIS:HB3	2.17	0.45
1:A:194:ARG:O	1:A:198:ASP:N	2.44	0.45
1:A:282:TRP:HA	1:A:282:TRP:CE3	2.51	0.45
1:A:286:ALA:CB	1:A:303:PHE:HD1	2.29	0.45
1:B:326:VAL:HG12	1:B:327:GLY:N	2.32	0.45
1:C:130:ARG:O	1:C:131:ARG:O	2.34	0.45
1:B:158:ASN:N	1:B:158:ASN:HD22	2.13	0.45
1:C:227:ASP:O	1:C:232:ASN:ND2	2.50	0.45
1:D:156:PHE:CD2	1:D:158:ASN:N	2.78	0.45
1:F:153:GLU:O	1:F:155:VAL:N	2.50	0.45
1:A:139:ALA:O	1:A:335:VAL:HG12	2.16	0.45
1:B:158:ASN:C	1:B:172:SER:HB2	2.42	0.45
1:B:323:THR:HG22	1:B:324:PHE:N	2.32	0.45
1:D:223:LEU:N	1:D:223:LEU:HD12	2.32	0.45
1:E:218:LYS:O	1:E:219:GLU:C	2.59	0.45
1:E:258:ILE:H	1:E:258:ILE:CD1	2.30	0.45
1:F:192:ALA:O	1:F:357:MET:CB	2.64	0.45
1:F:236:LEU:O	1:F:240:ALA:N	2.50	0.45
1:F:253:THR:O	1:F:255:ALA:N	2.48	0.45
1:F:322:GLY:O	1:F:380:THR:HB	2.17	0.45
1:G:327:GLY:C	1:G:329:PHE:HD2	2.21	0.45
1:A:155:VAL:HA	1:A:174:ILE:HG22	1.99	0.45
1:A:267:GLU:OE1	1:F:317:LYS:CE	2.65	0.45
1:B:227:ASP:O	1:B:229:THR:HG23	2.17	0.45
1:D:194:ARG:HG3	1:D:358:LEU:HD21	1.98	0.45
1:G:129:LEU:O	1:G:130:ARG:HB2	2.17	0.45
1:A:123:GLY:O	1:A:124:ILE:CG2	2.59	0.45
1:C:224:LEU:HD13	1:C:224:LEU:C	2.42	0.45
1:D:158:ASN:ND2	1:D:172:SER:HA	2.29	0.45
1:F:275:ILE:HG22	1:F:276:VAL:N	2.32	0.45
1:G:187:ALA:HB1	1:G:362:CYS:O	2.17	0.45
1:A:290:ASP:OD1	1:A:294:ARG:HB3	2.17	0.45
1:D:309:TRP:C	1:D:311:LEU:H	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:132:LEU:HG	1:E:132:LEU:O	2.15	0.45
1:E:341:ALA:HA	1:E:363:GLU:O	2.16	0.45
1:F:142:ARG:HH22	1:F:340:ASP:CG	2.25	0.45
1:G:236:LEU:N	1:G:236:LEU:HD12	2.32	0.45
1:A:207:ILE:HG22	1:A:212:MET:HG2	1.98	0.45
1:A:219:GLU:O	1:A:223:LEU:HD13	2.17	0.45
1:A:282:TRP:HA	1:A:282:TRP:HE3	1.82	0.45
1:A:361:LEU:HD12	1:A:362:CYS:H	1.82	0.45
1:B:209:ASN:O	1:C:331:MET:HE1	2.16	0.45
1:B:266:THR:C	1:B:268:SER:H	2.24	0.45
1:E:194:ARG:HE	1:E:356:ASN:ND2	2.15	0.45
1:E:202:MET:CE	1:E:203:LEU:HB2	2.47	0.45
1:F:244:ASP:OD2	1:F:246:SER:HB3	2.17	0.45
1:G:270:PHE:CE1	1:G:372:ARG:NE	2.85	0.45
1:G:356:ASN:O	1:G:356:ASN:CG	2.60	0.45
1:A:179:GLN:HA	1:A:179:GLN:HE21	1.82	0.44
1:A:197:MET:SD	1:A:198:ASP:N	2.90	0.44
1:B:289:LYS:HA	1:B:296:ILE:CD1	2.47	0.44
1:D:224:LEU:HD13	1:D:237:ASN:OD1	2.17	0.44
1:D:305:SER:O	1:D:307:ILE:N	2.45	0.44
1:E:156:PHE:O	1:E:158:ASN:ND2	2.50	0.44
1:E:191:GLN:HB2	1:E:358:LEU:O	2.17	0.44
1:E:203:LEU:HD12	1:E:206:TYR:CB	2.47	0.44
1:E:206:TYR:O	1:E:206:TYR:HD2	2.00	0.44
1:E:262:ILE:H	1:E:262:ILE:CD1	2.30	0.44
1:E:301:GLN:OE1	1:E:301:GLN:O	2.35	0.44
1:F:264:GLN:HA	1:F:267:GLU:HG2	1.98	0.44
1:F:323:THR:HA	1:F:380:THR:HG22	1.98	0.44
1:G:150:TYR:CE1	1:G:179:GLN:HB3	2.52	0.44
1:A:239:VAL:HG21	1:A:370:HIS:HD1	1.82	0.44
1:A:273:SER:O	1:A:312:PRO:HD2	2.17	0.44
1:B:279:PRO:HG3	1:B:315:PRO:C	2.42	0.44
1:B:329:PHE:CD1	1:B:329:PHE:N	2.81	0.44
1:B:333:SER:HB2	1:B:369:ALA:O	2.17	0.44
1:B:349:ASP:O	1:B:350:ARG:C	2.60	0.44
1:C:245:THR:HG23	1:C:248:ASN:HD22	1.81	0.44
1:C:247:LEU:HB3	1:C:260:HIS:CD2	2.51	0.44
1:E:125:ILE:HG23	1:E:126:MET:H	1.82	0.44
1:E:194:ARG:NH1	1:E:347:ARG:HH22	2.12	0.44
1:F:174:ILE:H	1:F:174:ILE:CD1	2.17	0.44
1:G:327:GLY:C	1:G:329:PHE:CE2	2.95	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:LEU:HD23	1:A:370:HIS:CE1	2.53	0.44
1:B:173:ASP:OD1	1:B:174:ILE:N	2.50	0.44
1:C:196:VAL:O	1:C:197:MET:C	2.60	0.44
1:C:359:THR:O	1:C:359:THR:HG23	2.18	0.44
1:D:124:ILE:C	1:D:125:ILE:CG2	2.90	0.44
1:E:211:LEU:HG	1:E:362:CYS:SG	2.56	0.44
1:F:275:ILE:CG2	1:F:277:LEU:HD11	2.47	0.44
1:F:347:ARG:O	1:F:349:ASP:N	2.50	0.44
1:G:249:ALA:O	1:G:250:THR:C	2.60	0.44
1:C:142:ARG:CB	1:C:337:ASP:O	2.66	0.44
1:C:156:PHE:HD2	1:C:156:PHE:HA	1.72	0.44
1:D:202:MET:CA	1:D:205:SER:OG	2.61	0.44
1:D:247:LEU:HD21	1:D:260:HIS:CG	2.53	0.44
1:D:303:PHE:C	1:D:306:ASN:HB3	2.42	0.44
1:F:211:LEU:HD22	1:F:212:MET:HE3	1.98	0.44
1:F:288:LEU:HD23	1:F:289:LYS:O	2.18	0.44
1:A:188:HIS:O	1:A:361:LEU:HD12	2.17	0.44
1:A:295:TYR:HD2	1:A:295:TYR:HA	1.69	0.44
1:B:129:LEU:HD23	1:B:129:LEU:O	2.17	0.44
1:D:258:ILE:O	1:D:261:ALA:HB3	2.17	0.44
1:A:200:ALA:C	1:A:202:MET:H	2.25	0.44
1:C:185:THR:HA	1:C:365:ARG:HA	1.99	0.44
1:C:203:LEU:O	1:C:206:TYR:HB2	2.16	0.44
1:C:234:GLU:O	1:C:368:LEU:HD23	2.18	0.44
1:D:191:GLN:NE2	1:E:176:PHE:CD2	2.85	0.44
1:D:239:VAL:CB	1:D:370:HIS:HD1	2.30	0.44
1:D:297:PHE:CD2	1:D:308:MET:HB2	2.52	0.44
1:G:254:ARG:HD3	1:G:381:PHE:CE1	2.52	0.44
1:G:290:ASP:O	1:G:292:GLU:N	2.50	0.44
1:A:194:ARG:O	1:A:198:ASP:CG	2.60	0.44
1:A:241:THR:O	1:A:377:ILE:HA	2.17	0.44
1:A:269:GLU:CB	1:F:217:LEU:HD21	2.16	0.44
1:B:194:ARG:NH2	1:B:347:ARG:CZ	2.80	0.44
1:B:237:ASN:HD22	1:B:237:ASN:N	2.15	0.44
1:D:141:GLY:C	1:D:142:ARG:HG2	2.42	0.44
1:D:280:ARG:HG3	1:E:309:TRP:HB3	2.00	0.44
1:F:290:ASP:CG	1:F:291:ASN:N	2.76	0.44
1:F:349:ASP:O	1:F:352:ASN:OD1	2.35	0.44
1:F:356:ASN:O	1:F:357:MET:HG2	2.18	0.44
1:G:155:VAL:HG11	1:G:374:THR:CG2	2.47	0.44
1:G:162:ASP:OD1	1:G:173:ASP:CG	2.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ASP:C	1:A:246:SER:H	2.25	0.44
1:A:330:ASP:OD2	1:F:130:ARG:NH2	2.43	0.44
1:E:156:PHE:CD2	1:E:158:ASN:N	2.77	0.44
1:G:327:GLY:H	1:G:329:PHE:HE2	1.63	0.44
1:G:355:LYS:O	1:G:357:MET:HB2	2.17	0.44
1:A:154:GLU:OE2	1:A:177:SER:HB2	2.18	0.44
1:A:223:LEU:N	1:A:223:LEU:HD12	2.32	0.44
1:B:142:ARG:HG2	1:B:337:ASP:O	2.18	0.44
1:B:200:ALA:HB1	1:B:201:PRO:HD2	1.98	0.44
1:B:210:ARG:HH22	1:C:153:GLU:CD	2.26	0.44
1:D:194:ARG:HB2	1:D:358:LEU:CD1	2.48	0.44
1:D:194:ARG:HB2	1:D:358:LEU:HD13	1.99	0.44
1:E:219:GLU:HG2	1:E:223:LEU:HD11	1.99	0.44
1:E:254:ARG:CG	1:E:381:PHE:CE2	2.98	0.44
1:A:263:TYR:HB2	1:F:303:PHE:CE2	2.53	0.43
1:A:345:VAL:HG22	1:A:360:ILE:HG23	2.00	0.43
1:B:142:ARG:HA	1:B:337:ASP:H	1.83	0.43
1:B:156:PHE:CD2	1:B:157:THR:C	2.96	0.43
1:C:227:ASP:HB3	1:C:229:THR:HG1	1.83	0.43
1:C:300:PRO:O	1:C:301:GLN:C	2.61	0.43
1:C:301:GLN:HG2	1:C:302:ALA:N	2.32	0.43
1:E:190:VAL:CG2	1:E:360:ILE:HD11	2.48	0.43
1:E:290:ASP:C	1:E:292:GLU:N	2.74	0.43
1:E:366:LEU:HD12	1:E:367:ALA:N	2.32	0.43
1:F:324:PHE:HD2	1:F:381:PHE:HE1	0.86	0.43
1:F:358:LEU:HD23	1:F:359:THR:C	2.43	0.43
1:G:175:THR:C	1:G:176:PHE:CD2	2.96	0.43
1:A:194:ARG:CA	1:A:198:ASP:OD2	2.66	0.43
1:B:273:SER:HB2	1:B:330:ASP:H	1.82	0.43
1:C:335:VAL:HG13	1:C:366:LEU:HD21	2.00	0.43
1:D:355:LYS:O	1:E:178:LYS:NZ	2.45	0.43
1:E:254:ARG:HG3	1:E:381:PHE:HE2	1.83	0.43
1:F:127:PRO:O	1:F:128:GLY:C	2.60	0.43
1:F:204:GLN:O	1:F:208:ASN:HB2	2.18	0.43
1:F:213:TYR:O	1:F:217:LEU:HB2	2.17	0.43
1:G:184:LYS:HD2	1:G:231:ASP:HA	1.98	0.43
1:B:208:ASN:N	1:B:208:ASN:ND2	2.66	0.43
1:C:283:HIS:CE1	1:D:260:HIS:HA	2.53	0.43
1:D:195:GLN:OE1	1:D:195:GLN:HA	2.18	0.43
1:D:224:LEU:C	1:D:224:LEU:CD1	2.91	0.43
1:E:288:LEU:O	1:E:295:TYR:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:345:VAL:HG13	1:E:359:THR:O	2.18	0.43
1:G:155:VAL:CG1	1:G:374:THR:OG1	2.58	0.43
1:G:212:MET:HE1	1:G:341:ALA:HB3	2.01	0.43
1:G:288:LEU:HD12	1:G:296:ILE:HD12	2.00	0.43
1:A:329:PHE:HA	1:A:332:ALA:HB3	2.01	0.43
1:B:155:VAL:HG13	1:B:374:THR:HG21	2.00	0.43
1:B:158:ASN:CB	1:B:172:SER:CA	2.86	0.43
1:B:206:TYR:O	1:B:210:ARG:HB2	2.19	0.43
1:D:148:LEU:HD12	1:D:148:LEU:C	2.43	0.43
1:D:355:LYS:HE2	1:D:357:MET:HE2	2.00	0.43
1:E:186:ILE:CD1	1:E:222:GLN:HG3	2.48	0.43
1:E:258:ILE:O	1:E:261:ALA:HB3	2.18	0.43
1:E:296:ILE:HD13	1:E:296:ILE:HA	1.88	0.43
1:E:311:LEU:HA	1:E:312:PRO:HD3	1.92	0.43
1:A:148:LEU:O	1:A:180:THR:HG23	2.19	0.43
1:B:129:LEU:O	1:B:130:ARG:C	2.62	0.43
1:B:194:ARG:HH11	1:B:356:ASN:HD21	1.66	0.43
1:C:345:VAL:HG12	1:C:346:SER:N	2.33	0.43
1:E:191:GLN:CB	1:E:359:THR:HA	2.47	0.43
1:F:174:ILE:O	1:F:174:ILE:HG12	2.18	0.43
1:F:343:VAL:CA	1:F:361:LEU:O	2.66	0.43
1:G:158:ASN:ND2	1:G:172:SER:OG	2.46	0.43
1:G:335:VAL:HA	1:G:368:LEU:HA	2.00	0.43
1:A:202:MET:CB	1:B:336:PHE:HE2	2.25	0.43
1:D:197:MET:C	1:D:199:ASP:H	2.27	0.43
1:D:328:GLY:C	1:D:330:ASP:N	2.74	0.43
1:E:202:MET:SD	1:E:202:MET:C	3.02	0.43
1:F:270:PHE:HE1	1:F:372:ARG:NH1	2.15	0.43
1:F:322:GLY:O	1:F:380:THR:CG2	2.67	0.43
1:G:347:ARG:C	1:G:349:ASP:H	2.27	0.43
1:A:236:LEU:HD23	1:A:370:HIS:NE2	2.34	0.43
1:B:156:PHE:HD2	1:B:157:THR:C	2.27	0.43
1:B:182:ASN:HB2	1:B:184:LYS:NZ	2.33	0.43
1:B:287:LEU:HD22	1:B:287:LEU:N	2.33	0.43
1:C:229:THR:O	1:C:232:ASN:HB2	2.19	0.43
1:D:243:TYR:HE2	1:D:248:ASN:HD21	1.67	0.43
1:F:148:LEU:O	1:F:181:ALA:N	2.46	0.43
1:F:156:PHE:O	1:F:158:ASN:ND2	2.52	0.43
1:G:202:MET:O	1:G:205:SER:N	2.52	0.43
1:C:185:THR:OG1	1:C:365:ARG:HG2	2.18	0.43
1:C:254:ARG:HB3	1:C:381:PHE:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:ALA:O	1:C:303:PHE:C	2.62	0.43
1:C:314:VAL:HG23	1:C:314:VAL:O	2.19	0.43
1:C:325:THR:HA	1:C:377:ILE:O	2.18	0.43
1:D:130:ARG:CD	1:D:131:ARG:N	2.82	0.43
1:D:208:ASN:N	1:D:208:ASN:HD22	2.15	0.43
1:D:278:ASN:HB3	1:D:281:ASP:OD2	2.19	0.43
1:D:307:ILE:HD13	1:D:310:GLY:C	2.44	0.43
1:E:156:PHE:C	1:E:158:ASN:H	2.26	0.43
1:E:162:ASP:C	1:E:173:ASP:H	2.27	0.43
1:E:218:LYS:C	1:E:220:GLU:N	2.76	0.43
1:E:279:PRO:HD3	1:E:316:THR:O	2.19	0.43
1:E:295:TYR:OH	1:F:256:ASP:CG	2.60	0.43
1:F:222:GLN:HA	1:F:222:GLN:HE21	1.84	0.43
1:F:263:TYR:C	1:F:265:VAL:N	2.75	0.43
1:A:296:ILE:O	1:A:297:PHE:CB	2.67	0.43
1:A:343:VAL:HA	1:A:362:CYS:HA	2.01	0.43
1:B:238:LYS:HD2	1:B:238:LYS:HA	1.73	0.43
1:B:253:THR:HG22	1:B:254:ARG:H	1.83	0.43
1:C:347:ARG:HG2	1:C:348:GLU:N	2.34	0.43
1:F:329:PHE:O	1:F:330:ASP:C	2.60	0.43
1:G:349:ASP:OD2	1:G:350:ARG:HG3	2.18	0.43
1:D:174:ILE:CG1	1:D:176:PHE:HE2	2.28	0.43
1:D:236:LEU:HD23	1:D:370:HIS:CE1	2.54	0.43
1:E:333:SER:HA	1:E:371:TYR:CD1	2.53	0.43
1:F:211:LEU:CD2	1:F:212:MET:CE	2.97	0.43
1:F:306:ASN:HB3	1:F:313:VAL:HB	2.00	0.43
1:F:344:GLU:O	1:F:361:LEU:HD12	2.19	0.43
1:G:158:ASN:HD22	1:G:158:ASN:C	2.22	0.43
1:G:282:TRP:CH2	1:G:313:VAL:HG21	2.54	0.43
1:B:126:MET:N	1:B:126:MET:HE3	2.34	0.42
1:B:194:ARG:HD2	1:B:358:LEU:CD1	2.49	0.42
1:B:215:LEU:HD22	1:B:216:ALA:CA	2.49	0.42
1:B:215:LEU:HD22	1:B:216:ALA:HA	2.00	0.42
1:E:194:ARG:NE	1:E:356:ASN:OD1	2.52	0.42
1:G:285:ILE:HA	1:G:288:LEU:CD1	2.49	0.42
1:G:309:TRP:HA	1:G:309:TRP:CE3	2.54	0.42
1:A:137:LEU:HB3	1:A:138:LEU:HD12	2.01	0.42
1:A:203:LEU:CD1	1:A:207:ILE:HD11	2.49	0.42
1:A:345:VAL:HG22	1:A:360:ILE:HG12	2.00	0.42
1:B:296:ILE:O	1:B:297:PHE:C	2.62	0.42
1:C:207:ILE:CA	1:C:211:LEU:HB3	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:300:PRO:C	1:C:302:ALA:N	2.74	0.42
1:D:280:ARG:HG3	1:E:309:TRP:O	2.19	0.42
1:D:284:ASN:HD22	1:D:284:ASN:C	2.27	0.42
1:E:194:ARG:HE	1:E:356:ASN:CG	2.27	0.42
1:E:194:ARG:H	1:E:357:MET:HA	1.84	0.42
1:F:142:ARG:HG2	1:F:337:ASP:C	2.43	0.42
1:G:233:LEU:HD13	1:G:368:LEU:HD22	2.00	0.42
1:A:127:PRO:HD3	1:A:212:MET:CE	2.38	0.42
1:A:203:LEU:O	1:A:206:TYR:N	2.52	0.42
1:A:277:LEU:HD23	1:A:277:LEU:HA	1.52	0.42
1:D:195:GLN:HG3	1:D:196:VAL:N	2.34	0.42
1:D:277:LEU:CD1	1:D:324:PHE:HB3	2.49	0.42
1:F:344:GLU:H	1:F:361:LEU:HD13	1.84	0.42
1:G:244:ASP:OD2	1:G:247:LEU:HG	2.20	0.42
1:G:355:LYS:HB3	1:G:355:LYS:HE2	1.61	0.42
1:A:132:LEU:N	1:A:132:LEU:HD12	2.33	0.42
1:C:183:VAL:CA	1:C:367:ALA:HB2	2.35	0.42
1:C:256:ASP:O	1:C:259:ALA:HB3	2.20	0.42
1:C:280:ARG:O	1:C:283:HIS:HB3	2.20	0.42
1:D:156:PHE:CD2	1:D:157:THR:C	2.98	0.42
1:D:236:LEU:HA	1:D:370:HIS:CE1	2.54	0.42
1:D:258:ILE:N	1:D:258:ILE:HD12	2.34	0.42
1:D:354:VAL:C	1:D:356:ASN:H	2.28	0.42
1:E:127:PRO:HA	1:E:213:TYR:HB2	2.01	0.42
1:E:253:THR:HG22	1:E:255:ALA:H	1.84	0.42
1:A:194:ARG:HA	1:A:198:ASP:OD2	2.20	0.42
1:A:200:ALA:C	1:A:202:MET:N	2.77	0.42
1:B:158:ASN:CG	1:B:172:SER:CB	2.91	0.42
1:B:206:TYR:CD2	1:B:210:ARG:HB2	2.55	0.42
1:C:202:MET:O	1:C:205:SER:HB3	2.19	0.42
1:D:268:SER:HB3	1:D:374:THR:HG22	2.01	0.42
1:E:158:ASN:H	1:E:158:ASN:HD22	1.61	0.42
1:E:236:LEU:HD13	1:E:329:PHE:CE2	2.54	0.42
1:F:129:LEU:O	1:F:130:ARG:CB	2.66	0.42
1:G:333:SER:HB3	1:G:369:ALA:O	2.18	0.42
1:A:195:GLN:HG3	1:A:196:VAL:CG2	2.35	0.42
1:A:208:ASN:N	1:A:208:ASN:HD22	2.17	0.42
1:B:156:PHE:C	1:B:158:ASN:N	2.77	0.42
1:B:217:LEU:O	1:B:220:GLU:N	2.53	0.42
1:C:224:LEU:HD13	1:C:237:ASN:HD21	1.82	0.42
1:E:339:MET:HE2	1:E:365:ARG:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:GLU:O	1:A:155:VAL:N	2.52	0.42
1:C:263:TYR:C	1:C:265:VAL:N	2.75	0.42
1:C:282:TRP:CZ3	1:C:308:MET:HE3	2.53	0.42
1:E:275:ILE:HG22	1:E:326:VAL:HG13	2.02	0.42
1:E:358:LEU:HB3	1:E:359:THR:H	1.61	0.42
1:F:345:VAL:HG13	1:F:358:LEU:HD11	2.02	0.42
1:G:133:THR:HB	1:G:220:GLU:OE2	2.19	0.42
1:A:244:ASP:C	1:A:246:SER:N	2.78	0.42
1:B:125:ILE:HD11	1:B:127:PRO:HG3	2.02	0.42
1:B:152:ARG:O	1:B:154:GLU:N	2.53	0.42
1:B:289:LYS:HG2	1:B:294:ARG:C	2.44	0.42
1:C:190:VAL:HG22	1:D:176:PHE:HE1	1.84	0.42
1:D:173:ASP:OD1	1:D:174:ILE:HD13	2.20	0.42
1:F:222:GLN:HA	1:F:222:GLN:NE2	2.35	0.42
1:G:299:GLY:O	1:G:303:PHE:HB2	2.20	0.42
1:A:148:LEU:C	1:A:148:LEU:HD12	2.45	0.42
1:A:175:THR:HG22	1:A:176:PHE:H	1.84	0.42
1:A:297:PHE:CE1	1:A:308:MET:HE2	2.54	0.42
1:B:186:ILE:HG22	1:B:187:ALA:N	2.34	0.42
1:B:342:THR:O	1:B:362:CYS:SG	2.77	0.42
1:C:132:LEU:CD2	1:C:132:LEU:C	2.93	0.42
1:C:152:ARG:HG3	1:C:371:TYR:O	2.19	0.42
1:C:224:LEU:CD1	1:C:237:ASN:HD21	2.33	0.42
1:D:292:GLU:O	1:D:294:ARG:N	2.53	0.42
1:D:343:VAL:CG1	1:D:362:CYS:SG	3.08	0.42
1:E:125:ILE:HG13	1:E:212:MET:CG	2.49	0.42
1:E:156:PHE:C	1:E:158:ASN:N	2.78	0.42
1:F:187:ALA:HB2	1:F:363:GLU:HA	2.02	0.42
1:F:225:ASN:ND2	1:F:225:ASN:O	2.53	0.42
1:G:128:GLY:O	1:G:129:LEU:C	2.63	0.42
1:A:152:ARG:HB3	1:A:177:SER:HB3	2.02	0.42
1:B:156:PHE:CD2	1:B:158:ASN:CA	3.01	0.42
1:C:128:GLY:C	1:C:129:LEU:HD13	2.44	0.42
1:C:258:ILE:O	1:C:261:ALA:HB3	2.20	0.42
1:C:278:ASN:HB3	1:C:319:GLN:O	2.20	0.42
1:C:322:GLY:O	1:C:380:THR:HA	2.20	0.42
1:C:328:GLY:O	1:C:331:MET:N	2.45	0.42
1:D:207:ILE:HG13	1:D:211:LEU:CD1	2.41	0.42
1:E:139:ALA:HB3	1:E:334:GLN:HB3	2.00	0.42
1:E:189:TRP:O	1:E:191:GLN:N	2.53	0.42
1:E:227:ASP:O	1:E:229:THR:CG2	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:254:ARG:HA	1:E:257:ILE:CD1	2.49	0.42
1:A:203:LEU:O	1:A:207:ILE:HD13	2.20	0.41
1:A:210:ARG:HG2	1:A:210:ARG:HH11	1.85	0.41
1:A:329:PHE:H	1:A:329:PHE:HD1	1.66	0.41
1:B:127:PRO:C	1:B:129:LEU:HD22	2.42	0.41
1:B:137:LEU:HD23	1:B:137:LEU:O	2.20	0.41
1:B:191:GLN:HA	1:B:359:THR:HA	2.02	0.41
1:B:252:ASP:HB3	1:B:256:ASP:CB	2.49	0.41
1:B:279:PRO:HD3	1:B:316:THR:C	2.44	0.41
1:B:299:GLY:C	1:B:301:GLN:N	2.74	0.41
1:B:321:ALA:C	1:B:323:THR:H	2.28	0.41
1:B:349:ASP:O	1:B:352:ASN:CB	2.67	0.41
1:B:351:ASP:HB3	1:B:355:LYS:HE3	2.02	0.41
1:D:125:ILE:CG1	1:D:208:ASN:ND2	2.80	0.41
1:D:173:ASP:OD1	1:D:174:ILE:CD1	2.68	0.41
1:E:125:ILE:HD11	1:E:127:PRO:CD	2.42	0.41
1:E:158:ASN:CG	1:E:172:SER:CA	2.80	0.41
1:E:245:THR:C	1:E:247:LEU:H	2.27	0.41
1:A:131:ARG:HB3	1:A:131:ARG:HH11	1.85	0.41
1:A:331:MET:SD	1:F:209:ASN:O	2.78	0.41
1:B:153:GLU:O	1:B:155:VAL:N	2.54	0.41
1:B:187:ALA:HB1	1:B:362:CYS:O	2.20	0.41
1:D:149:GLU:HG2	1:D:180:THR:HG23	2.03	0.41
1:D:187:ALA:HB1	1:D:361:LEU:HD11	2.00	0.41
1:E:295:TYR:C	1:E:296:ILE:O	2.63	0.41
1:B:296:ILE:O	1:B:297:PHE:CG	2.73	0.41
1:D:206:TYR:O	1:D:210:ARG:HB3	2.20	0.41
1:D:305:SER:C	1:D:307:ILE:N	2.78	0.41
1:E:156:PHE:CD2	1:E:158:ASN:CA	3.04	0.41
1:E:190:VAL:HG23	1:E:190:VAL:O	2.20	0.41
1:F:338:ARG:HH11	1:F:338:ARG:HG3	1.84	0.41
1:B:216:ALA:O	1:B:219:GLU:HB3	2.20	0.41
1:B:295:TYR:HB3	1:B:298:GLY:C	2.44	0.41
1:C:357:MET:CE	1:D:178:LYS:HD3	2.51	0.41
1:D:225:ASN:ND2	1:D:318:ALA:O	2.54	0.41
1:E:190:VAL:N	1:E:360:ILE:CD1	2.78	0.41
1:E:268:SER:O	1:E:269:GLU:C	2.64	0.41
1:F:184:LYS:HD2	1:F:231:ASP:HA	2.02	0.41
1:G:132:LEU:CB	1:G:136:ASP:CG	2.89	0.41
1:A:134:ILE:O	1:A:138:LEU:HD13	2.20	0.41
1:A:202:MET:O	1:A:203:LEU:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:THR:O	1:A:245:THR:HG22	2.21	0.41
1:B:128:GLY:C	1:B:130:ARG:H	2.28	0.41
1:C:268:SER:HB2	1:C:372:ARG:HD3	2.02	0.41
1:D:221:GLY:O	1:D:225:ASN:N	2.47	0.41
1:E:235:GLY:O	1:E:238:LYS:HB3	2.20	0.41
1:E:300:PRO:CG	1:F:309:TRP:NE1	2.83	0.41
1:F:151:VAL:CG2	1:F:176:PHE:HB3	2.50	0.41
1:F:348:GLU:H	1:F:348:GLU:HG2	1.55	0.41
1:A:186:ILE:N	1:A:186:ILE:CD1	2.83	0.41
1:A:345:VAL:CG2	1:A:360:ILE:HG12	2.51	0.41
1:D:206:TYR:OH	1:D:210:ARG:NH1	2.53	0.41
1:D:207:ILE:CD1	1:D:207:ILE:N	2.84	0.41
1:F:223:LEU:O	1:F:224:LEU:C	2.64	0.41
1:G:211:LEU:O	1:G:212:MET:C	2.64	0.41
1:G:282:TRP:CE3	1:G:313:VAL:HG11	2.55	0.41
1:A:149:GLU:OE1	1:F:195:GLN:HG2	2.21	0.41
1:A:193:SER:OG	1:A:195:GLN:HG2	2.20	0.41
1:A:266:THR:O	1:A:268:SER:N	2.53	0.41
1:A:316:THR:HG23	1:A:319:GLN:H	1.85	0.41
1:B:125:ILE:CG1	1:B:127:PRO:CG	2.96	0.41
1:D:124:ILE:HG23	1:D:125:ILE:N	2.34	0.41
1:D:195:GLN:O	1:D:196:VAL:C	2.64	0.41
1:D:233:LEU:HD11	1:D:366:LEU:HD11	2.03	0.41
1:D:268:SER:O	1:D:270:PHE:HD1	2.04	0.41
1:E:237:ASN:N	1:E:237:ASN:HD22	2.18	0.41
1:E:325:THR:HA	1:E:377:ILE:O	2.21	0.41
1:E:328:GLY:C	1:E:330:ASP:N	2.78	0.41
1:E:347:ARG:O	1:E:352:ASN:HB2	2.21	0.41
1:F:274:GLY:C	1:F:275:ILE:HD12	2.45	0.41
1:F:288:LEU:O	1:F:295:TYR:HA	2.21	0.41
1:F:320:ALA:O	1:F:323:THR:HB	2.20	0.41
1:G:162:ASP:C	1:G:173:ASP:H	2.28	0.41
1:G:335:VAL:HG12	1:G:368:LEU:CB	2.51	0.41
1:A:125:ILE:N	1:A:125:ILE:CD1	2.74	0.41
1:B:143:THR:OG1	1:B:144:SER:N	2.54	0.41
1:C:207:ILE:CG2	1:C:211:LEU:HD13	2.50	0.41
1:C:212:MET:HE2	1:C:215:LEU:HD13	2.02	0.41
1:C:277:LEU:HA	1:C:319:GLN:HG2	2.03	0.41
1:D:256:ASP:O	1:D:259:ALA:HB3	2.19	0.41
1:E:220:GLU:C	1:E:222:GLN:N	2.79	0.41
1:F:152:ARG:O	1:F:154:GLU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:156:PHE:C	1:F:158:ASN:H	2.29	0.41
1:F:192:ALA:C	1:F:357:MET:CE	2.94	0.41
1:F:211:LEU:HD23	1:F:212:MET:HE3	2.02	0.41
1:G:207:ILE:O	1:G:211:LEU:HB3	2.21	0.41
1:G:236:LEU:O	1:G:240:ALA:N	2.54	0.41
1:G:345:VAL:CG1	1:G:358:LEU:HD11	2.48	0.41
1:A:333:SER:HB3	1:A:369:ALA:O	2.21	0.41
1:B:324:PHE:N	1:B:324:PHE:CD1	2.89	0.41
1:C:204:GLN:C	1:C:206:TYR:N	2.79	0.41
1:D:196:VAL:HA	1:D:199:ASP:OD1	2.21	0.41
1:D:208:ASN:ND2	1:D:208:ASN:N	2.69	0.41
1:D:309:TRP:HE3	1:D:309:TRP:N	2.17	0.41
1:E:154:GLU:OE2	1:E:177:SER:CB	2.69	0.41
1:E:189:TRP:HE3	1:E:189:TRP:C	2.28	0.41
1:E:203:LEU:C	1:E:203:LEU:HD12	2.45	0.41
1:E:296:ILE:O	1:E:298:GLY:N	2.53	0.41
1:F:178:LYS:HE3	1:F:178:LYS:HB2	1.80	0.41
1:F:193:SER:O	1:F:196:VAL:CG1	2.69	0.41
1:F:194:ARG:NH2	1:G:363:GLU:CD	2.78	0.41
1:F:224:LEU:HD13	1:F:224:LEU:C	2.46	0.41
1:F:253:THR:C	1:F:255:ALA:N	2.74	0.41
1:F:275:ILE:HG22	1:F:277:LEU:HD11	2.02	0.41
1:F:331:MET:O	1:F:331:MET:CG	2.69	0.41
1:G:306:ASN:OD1	1:G:306:ASN:O	2.39	0.41
1:A:244:ASP:CG	1:A:246:SER:HB3	2.45	0.41
1:C:131:ARG:HB2	1:C:131:ARG:NH1	2.34	0.41
1:C:189:TRP:CD2	1:C:189:TRP:O	2.74	0.41
1:C:196:VAL:HG11	1:C:203:LEU:HD13	1.98	0.41
1:C:236:LEU:O	1:C:240:ALA:HB2	2.21	0.41
1:D:236:LEU:HD23	1:D:370:HIS:NE2	2.35	0.41
1:E:194:ARG:HE	1:E:356:ASN:HD21	1.69	0.41
1:E:200:ALA:C	1:E:202:MET:N	2.78	0.41
1:E:211:LEU:HD12	1:E:211:LEU:HA	1.65	0.41
1:F:290:ASP:OD1	1:F:291:ASN:N	2.49	0.41
1:G:142:ARG:HG2	1:G:142:ARG:NH1	2.35	0.41
1:G:381:PHE:C	1:G:383:SER:H	2.30	0.41
1:A:152:ARG:O	1:A:154:GLU:N	2.55	0.40
1:B:148:LEU:HD23	1:B:181:ALA:HB3	2.04	0.40
1:B:253:THR:C	1:B:255:ALA:H	2.29	0.40
1:D:131:ARG:NH2	1:D:133:THR:HG22	2.36	0.40
1:D:184:LYS:HD3	1:D:231:ASP:C	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:292:GLU:O	1:E:294:ARG:N	2.50	0.40
1:F:263:TYR:C	1:F:265:VAL:H	2.29	0.40
1:G:188:HIS:N	1:G:215:LEU:HD13	2.37	0.40
1:G:199:ASP:O	1:G:202:MET:CB	2.67	0.40
1:G:346:SER:O	1:G:358:LEU:HD12	2.20	0.40
1:A:195:GLN:O	1:A:199:ASP:OD2	2.39	0.40
1:A:258:ILE:O	1:A:262:ILE:HG13	2.21	0.40
1:A:329:PHE:O	1:A:330:ASP:C	2.61	0.40
1:B:196:VAL:HG23	1:B:196:VAL:H	1.68	0.40
1:B:342:THR:O	1:B:363:GLU:N	2.54	0.40
1:C:202:MET:O	1:C:203:LEU:O	2.39	0.40
1:D:127:PRO:HB3	1:D:212:MET:CB	2.49	0.40
1:D:355:LYS:O	1:D:356:ASN:CG	2.63	0.40
1:E:120:GLN:O	1:E:122:PRO:HD3	2.22	0.40
1:F:143:THR:HG22	1:F:336:PHE:HB3	2.03	0.40
1:G:204:GLN:HG2	1:G:204:GLN:O	2.21	0.40
1:G:211:LEU:HD12	1:G:360:ILE:HD12	2.03	0.40
1:A:297:PHE:HE1	1:A:308:MET:CE	2.34	0.40
1:A:304:THR:O	1:A:306:ASN:CG	2.65	0.40
1:B:253:THR:CG2	1:B:254:ARG:N	2.83	0.40
1:C:204:GLN:HA	1:C:207:ILE:CD1	2.51	0.40
1:E:156:PHE:CD2	1:E:157:THR:C	3.00	0.40
1:E:289:LYS:HA	1:E:294:ARG:O	2.21	0.40
1:F:282:TRP:CE3	1:F:282:TRP:HA	2.57	0.40
1:F:303:PHE:CD1	1:F:303:PHE:C	2.99	0.40
1:F:374:THR:C	1:F:376:ILE:H	2.28	0.40
1:G:155:VAL:CG2	1:G:156:PHE:H	2.35	0.40
1:G:202:MET:C	1:G:205:SER:HG	2.02	0.40
1:G:248:ASN:N	1:G:248:ASN:HD22	2.19	0.40
1:A:260:HIS:O	1:A:263:TYR:HB3	2.21	0.40
1:A:285:ILE:HA	1:A:288:LEU:CD1	2.47	0.40
1:B:253:THR:C	1:B:255:ALA:N	2.79	0.40
1:C:184:LYS:HE3	1:C:230:GLY:O	2.22	0.40
1:D:260:HIS:O	1:D:263:TYR:HB3	2.21	0.40
1:D:347:ARG:O	1:D:347:ARG:CG	2.69	0.40
1:E:134:ILE:HD13	1:E:220:GLU:HG3	2.02	0.40
1:E:194:ARG:HD2	1:E:347:ARG:NE	2.36	0.40
1:F:211:LEU:HD23	1:F:212:MET:N	2.37	0.40
1:F:291:ASN:CG	1:F:292:GLU:N	2.79	0.40
1:F:308:MET:C	1:F:310:GLY:N	2.79	0.40
1:G:197:MET:HE1	1:G:345:VAL:HG11	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:ASP:OD2	1:A:292:GLU:O	2.39	0.40
1:B:156:PHE:CD2	1:B:158:ASN:CB	3.05	0.40
1:B:213:TYR:O	1:B:214:GLY:C	2.62	0.40
1:B:288:LEU:HD23	1:B:289:LYS:N	2.36	0.40
1:C:194:ARG:HA	1:C:358:LEU:HG	2.02	0.40
1:C:224:LEU:O	1:C:237:ASN:ND2	2.55	0.40
1:C:244:ASP:OD2	1:C:246:SER:HB3	2.22	0.40
1:D:296:ILE:HG22	1:D:297:PHE:CD1	2.57	0.40
1:E:253:THR:C	1:E:255:ALA:N	2.79	0.40
1:F:252:ASP:HB3	1:F:256:ASP:HB2	2.04	0.40
1:F:282:TRP:HA	1:F:282:TRP:HE3	1.86	0.40
1:G:188:HIS:O	1:G:361:LEU:HD12	2.22	0.40
1:G:189:TRP:CD1	1:G:189:TRP:H	2.40	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	254/273 (93%)	195 (77%)	49 (19%)	10 (4%)	2	18
1	B	248/273 (91%)	189 (76%)	48 (19%)	11 (4%)	2	16
1	C	246/273 (90%)	188 (76%)	47 (19%)	11 (4%)	2	15
1	D	252/273 (92%)	209 (83%)	34 (14%)	9 (4%)	2	19
1	E	253/273 (93%)	190 (75%)	49 (19%)	14 (6%)	1	13
1	F	246/273 (90%)	192 (78%)	40 (16%)	14 (6%)	1	12
1	G	245/273 (90%)	199 (81%)	36 (15%)	10 (4%)	2	17
All	All	1744/1911 (91%)	1362 (78%)	303 (17%)	79 (4%)	2	15

All (79) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	ILE
1	A	208	ASN
1	B	200	ALA
1	B	297	PHE
1	C	131	ARG
1	C	195	GLN
1	C	306	ASN
1	D	194	ARG
1	D	195	GLN
1	D	303	PHE
1	E	296	ILE
1	F	200	ALA
1	F	201	PRO
1	G	199	ASP
1	G	204	GLN
1	G	279	PRO
1	A	304	THR
1	B	129	LEU
1	B	350	ARG
1	C	157	THR
1	C	196	VAL
1	C	228	GLY
1	C	229	THR
1	D	154	GLU
1	D	293	GLY
1	F	128	GLY
1	F	293	GLY
1	F	348	GLU
1	G	132	LEU
1	G	296	ILE
1	G	354	VAL
1	A	154	GLU
1	A	358	LEU
1	B	153	GLU
1	C	200	ALA
1	D	127	PRO
1	D	173	ASP
1	E	161	GLY
1	E	200	ALA
1	E	348	GLU
1	F	153	GLU
1	F	154	GLU
1	F	161	GLY

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Mol	Chain	Res	Type
1	F	382	SER
1	A	309	TRP
1	C	348	GLU
1	D	160	PRO
1	E	194	ARG
1	E	213	TYR
1	E	354	VAL
1	G	197	MET
1	A	160	PRO
1	B	172	SER
1	B	354	VAL
1	B	355	LYS
1	D	382	SER
1	E	125	ILE
1	E	190	VAL
1	E	357	MET
1	F	199	ASP
1	F	207	ILE
1	F	283	HIS
1	G	160	PRO
1	G	348	GLU
1	A	198	ASP
1	A	305	SER
1	B	162	ASP
1	C	230	GLY
1	E	154	GLU
1	E	201	PRO
1	F	160	PRO
1	G	161	GLY
1	A	161	GLY
1	E	160	PRO
1	B	207	ILE
1	C	298	GLY
1	B	159	ALA
1	F	196	VAL
1	E	251	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	211/223 (95%)	188 (89%)	23 (11%)	6	25
1	B	206/223 (92%)	186 (90%)	20 (10%)	8	29
1	C	204/223 (92%)	184 (90%)	20 (10%)	7	29
1	D	209/223 (94%)	192 (92%)	17 (8%)	11	34
1	E	210/223 (94%)	188 (90%)	22 (10%)	6	27
1	F	204/223 (92%)	169 (83%)	35 (17%)	2	12
1	G	203/223 (91%)	188 (93%)	15 (7%)	13	37
All	All	1447/1561 (93%)	1295 (90%)	152 (10%)	6	27

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	MET
1	A	121	ILE
1	A	124	ILE
1	A	125	ILE
1	A	129	LEU
1	A	131	ARG
1	A	137	LEU
1	A	157	THR
1	A	158	ASN
1	A	174	ILE
1	A	191	GLN
1	A	193	SER
1	A	194	ARG
1	A	207	ILE
1	A	209	ASN
1	A	266	THR
1	A	280	ARG
1	A	282	TRP
1	A	288	LEU
1	A	289	LYS
1	A	295	TYR
1	A	297	PHE
1	A	366	LEU
1	B	126	MET
1	B	129	LEU
1	B	132	LEU

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Mol	Chain	Res	Type
1	B	134	ILE
1	B	140	GLN
1	B	146	ASN
1	B	148	LEU
1	B	158	ASN
1	B	174	ILE
1	B	178	LYS
1	B	199	ASP
1	B	211	LEU
1	B	215	LEU
1	B	217	LEU
1	B	270	PHE
1	B	271	SER
1	B	277	LEU
1	B	282	TRP
1	B	296	ILE
1	B	358	LEU
1	C	129	LEU
1	C	132	LEU
1	C	156	PHE
1	C	174	ILE
1	C	190	VAL
1	C	191	GLN
1	C	193	SER
1	C	194	ARG
1	C	195	GLN
1	C	197	MET
1	C	202	MET
1	C	207	ILE
1	C	225	ASN
1	C	233	LEU
1	C	282	TRP
1	C	301	GLN
1	C	331	MET
1	C	347	ARG
1	C	356	ASN
1	C	366	LEU
1	D	121	ILE
1	D	124	ILE
1	D	127	PRO
1	D	129	LEU
1	D	130	ARG

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Mol	Chain	Res	Type
1	D	131	ARG
1	D	132	LEU
1	D	158	ASN
1	D	174	ILE
1	D	184	LYS
1	D	190	VAL
1	D	247	LEU
1	D	282	TRP
1	D	287	LEU
1	D	303	PHE
1	D	309	TRP
1	D	348	GLU
1	E	121	ILE
1	E	125	ILE
1	E	129	LEU
1	E	140	GLN
1	E	158	ASN
1	E	174	ILE
1	E	189	TRP
1	E	191	GLN
1	E	199	ASP
1	E	202	MET
1	E	205	SER
1	E	217	LEU
1	E	219	GLU
1	E	220	GLU
1	E	229	THR
1	E	282	TRP
1	E	296	ILE
1	E	301	GLN
1	E	305	SER
1	E	309	TRP
1	E	359	THR
1	E	382	SER
1	F	129	LEU
1	F	132	LEU
1	F	133	THR
1	F	143	THR
1	F	145	SER
1	F	154	GLU
1	F	158	ASN
1	F	174	ILE

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Mol	Chain	Res	Type
1	F	178	LYS
1	F	193	SER
1	F	194	ARG
1	F	195	GLN
1	F	196	VAL
1	F	197	MET
1	F	198	ASP
1	F	202	MET
1	F	203	LEU
1	F	210	ARG
1	F	212	MET
1	F	217	LEU
1	F	225	ASN
1	F	247	LEU
1	F	253	THR
1	F	254	ARG
1	F	257	ILE
1	F	277	LEU
1	F	282	TRP
1	F	287	LEU
1	F	289	LYS
1	F	307	ILE
1	F	329	PHE
1	F	348	GLU
1	F	361	LEU
1	F	363	GLU
1	F	378	LYS
1	G	130	ARG
1	G	132	LEU
1	G	158	ASN
1	G	174	ILE
1	G	193	SER
1	G	229	THR
1	G	245	THR
1	G	269	GLU
1	G	296	ILE
1	G	329	PHE
1	G	338	ARG
1	G	355	LYS
1	G	356	ASN
1	G	357	MET
1	G	372	ARG

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

Mol	Chain	Res	Type
1	A	146	ASN
1	A	158	ASN
1	A	179	GLN
1	A	204	GLN
1	A	208	ASN
1	A	306	ASN
1	A	334	GLN
1	B	146	ASN
1	B	158	ASN
1	B	208	ASN
1	B	209	ASN
1	B	284	ASN
1	B	319	GLN
1	B	334	GLN
1	B	356	ASN
1	B	370	HIS
1	C	140	GLN
1	C	146	ASN
1	C	191	GLN
1	C	195	GLN
1	C	204	GLN
1	C	222	GLN
1	C	225	ASN
1	C	232	ASN
1	C	237	ASN
1	C	248	ASN
1	C	264	GLN
1	C	283	HIS
1	C	284	ASN
1	C	301	GLN
1	C	356	ASN
1	D	158	ASN
1	D	179	GLN
1	D	182	ASN
1	D	222	GLN
1	D	225	ASN
1	D	334	GLN
1	E	146	ASN
1	E	158	ASN
1	E	179	GLN
1	E	191	GLN

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Mol	Chain	Res	Type
1	E	232	ASN
1	E	237	ASN
1	F	140	GLN
1	F	158	ASN
1	F	179	GLN
1	F	222	GLN
1	F	225	ASN
1	F	237	ASN
1	F	306	ASN
1	G	140	GLN
1	G	158	ASN
1	G	209	ASN
1	G	248	ASN
1	G	260	HIS
1	G	283	HIS
1	G	291	ASN
1	G	356	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	256/273 (93%)	-1.40	0 100 100	1, 28, 53, 72	0
1	B	250/273 (91%)	-1.40	0 100 100	1, 31, 59, 78	0
1	C	248/273 (90%)	-1.34	0 100 100	7, 33, 59, 69	0
1	D	254/273 (93%)	-1.38	0 100 100	1, 32, 54, 79	0
1	E	255/273 (93%)	-1.39	0 100 100	5, 34, 57, 90	0
1	F	248/273 (90%)	-1.42	0 100 100	1, 31, 54, 75	0
1	G	247/273 (90%)	-1.37	0 100 100	3, 31, 57, 87	0
All	All	1758/1911 (91%)	-1.39	0 100 100	1, 31, 57, 90	0

There are no RSRZ outliers to report.

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 oligosaccharides 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.