



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:10 AM UTC

PDB ID : 1HT2 / pdb_00001ht2
Title : Nucleotide-Dependent Conformational Changes in a Protease-Associated ATPase HslU
Authors : Wang, J.; Song, J.J.; Seong, I.S.; Franklin, M.C.; Kamtekar, S.; Eom, S.H.; Chung, C.H.
Deposited on : 2000-12-27
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

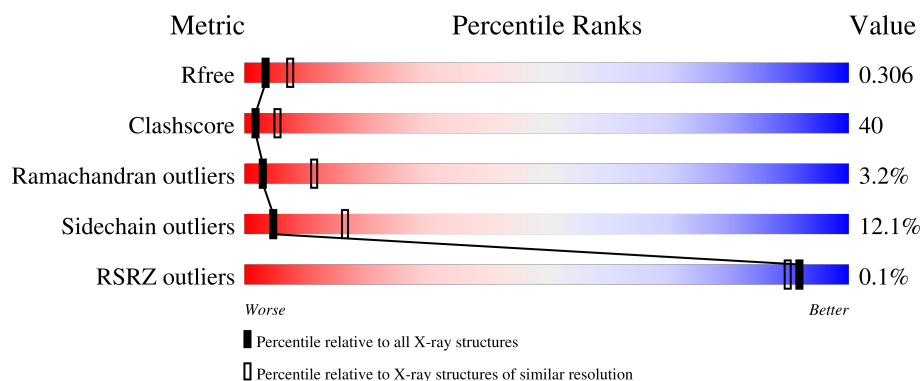
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



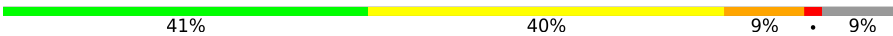
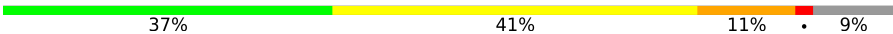
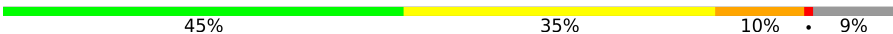
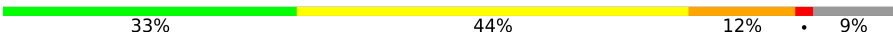
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	175	 55% 37% 6% ..
1	B	175	 40% 50% 9% ..
1	C	175	 49% 42% 9% .
1	D	175	 39% 51% 8% ..

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Mol	Chain	Length	Quality of chain
1	I	175	
1	J	175	
1	K	175	
1	L	175	
2	E	449	
2	F	449	
2	G	449	
2	H	449	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 23636 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 HEAT SHOCK LOCUS HSLV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	B	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	C	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	D	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	I	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	J	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	K	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			
1	L	174	Total	C	N	O	S	0	0	0
			1328	834	237	253	4			

- Molecule 2 is a protein called HEAT SHOCK LOCUS HSLU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	408	Total	C	N	O	S	0	0	0
			3226	2014	577	625	10			
2	F	408	Total	C	N	O	S	0	0	0
			3226	2014	577	625	10			
2	G	408	Total	C	N	O	S	0	0	0
			3226	2014	577	625	10			
2	H	408	Total	C	N	O	S	0	0	0
			3226	2014	577	625	10			

There are 28 discrepancies between the modelled and reference sequences:

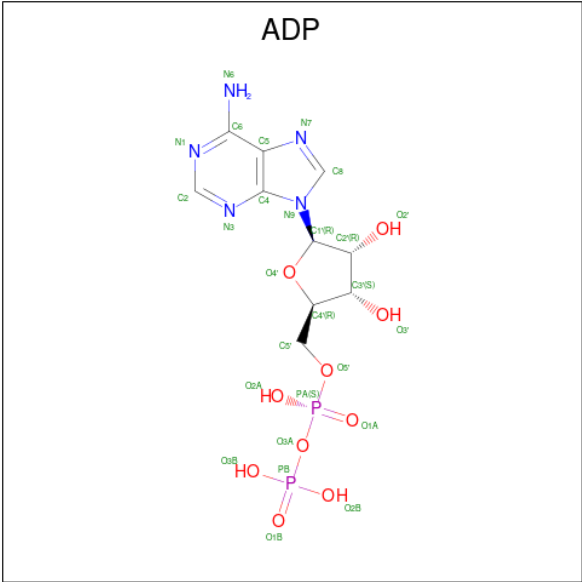
Chain	Residue	Modelled	Actual	Comment	Reference
E	-5	HIS	-	expression tag	UNP P0A6H5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	HIS	-	expression tag	UNP P0A6H5
E	-3	HIS	-	expression tag	UNP P0A6H5
E	-2	HIS	-	expression tag	UNP P0A6H5
E	-1	HIS	-	expression tag	UNP P0A6H5
E	0	HIS	-	expression tag	UNP P0A6H5
E	1	HIS	-	expression tag	UNP P0A6H5
F	-5	HIS	-	expression tag	UNP P0A6H5
F	-4	HIS	-	expression tag	UNP P0A6H5
F	-3	HIS	-	expression tag	UNP P0A6H5
F	-2	HIS	-	expression tag	UNP P0A6H5
F	-1	HIS	-	expression tag	UNP P0A6H5
F	0	HIS	-	expression tag	UNP P0A6H5
F	1	HIS	-	expression tag	UNP P0A6H5
G	-5	HIS	-	expression tag	UNP P0A6H5
G	-4	HIS	-	expression tag	UNP P0A6H5
G	-3	HIS	-	expression tag	UNP P0A6H5
G	-2	HIS	-	expression tag	UNP P0A6H5
G	-1	HIS	-	expression tag	UNP P0A6H5
G	0	HIS	-	expression tag	UNP P0A6H5
G	1	HIS	-	expression tag	UNP P0A6H5
H	-5	HIS	-	expression tag	UNP P0A6H5
H	-4	HIS	-	expression tag	UNP P0A6H5
H	-3	HIS	-	expression tag	UNP P0A6H5
H	-2	HIS	-	expression tag	UNP P0A6H5
H	-1	HIS	-	expression tag	UNP P0A6H5
H	0	HIS	-	expression tag	UNP P0A6H5
H	1	HIS	-	expression tag	UNP P0A6H5

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

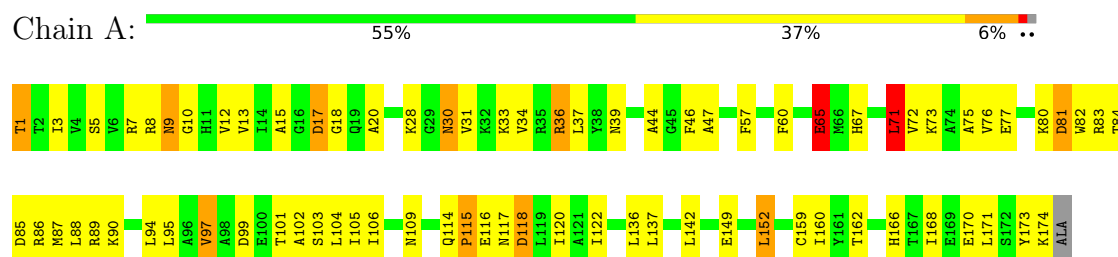


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

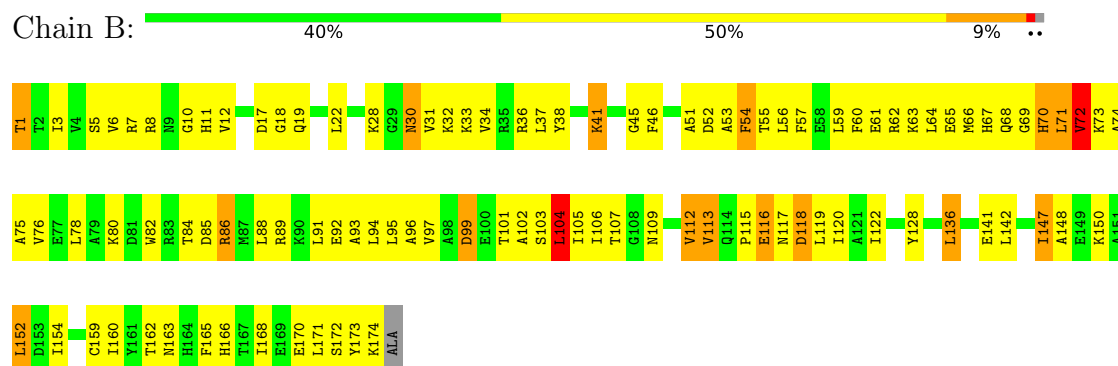
3 Residue-property plots

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.

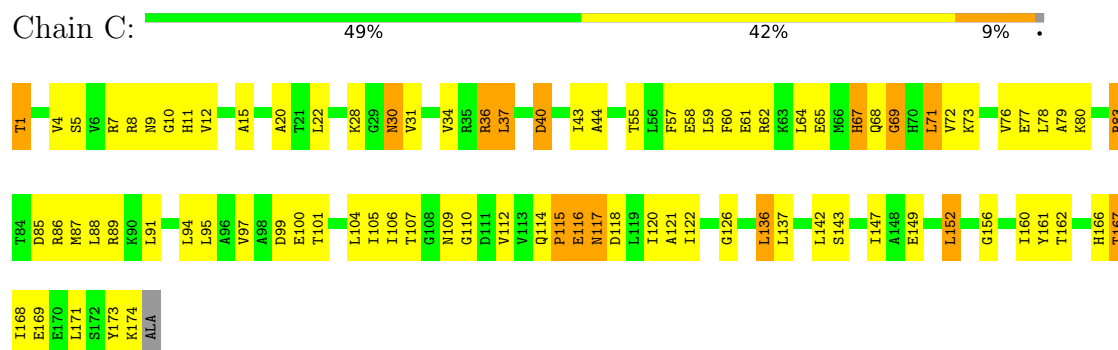
• Molecule 1: HEAT SHOCK LOCUS HSLV



• Molecule 1: HEAT SHOCK LOCUS HSLV

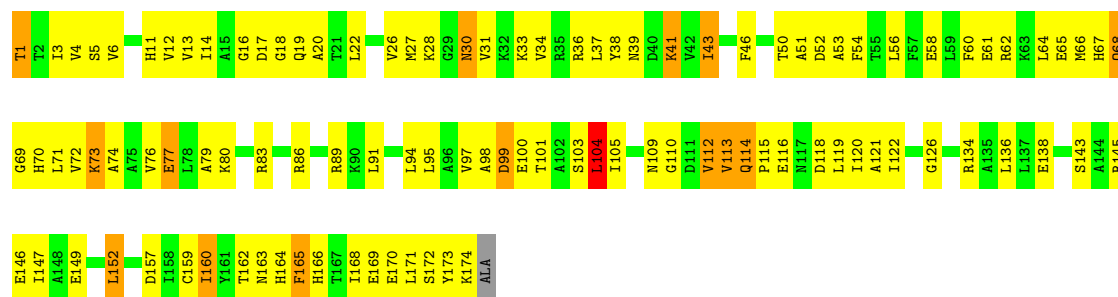


• Molecule 1: HEAT SHOCK LOCUS HSLV



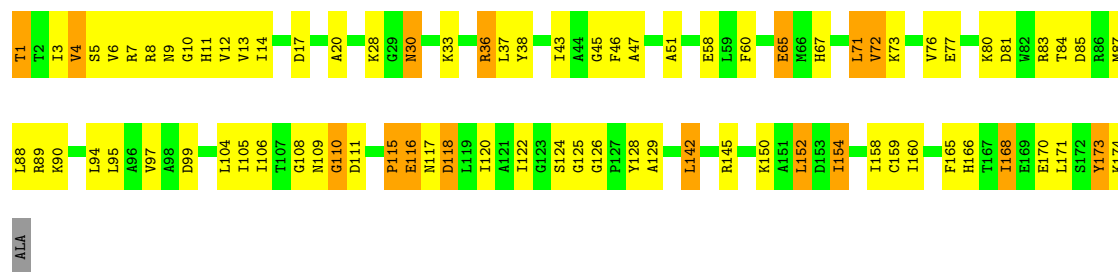
• Molecule 1: HEAT SHOCK LOCUS HSLV





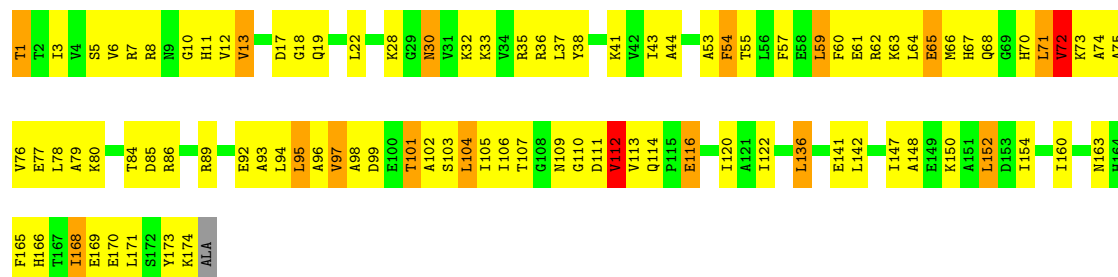
• Molecule 1: HEAT SHOCK LOCUS HSLV

Chain I: 53% 37% 9% .



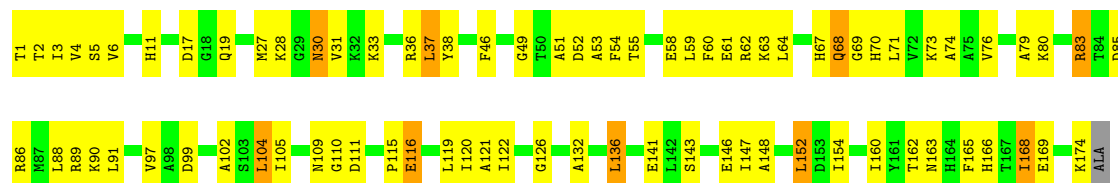
• Molecule 1: HEAT SHOCK LOCUS HSLV

Chain J: 45% 45% 9% ..



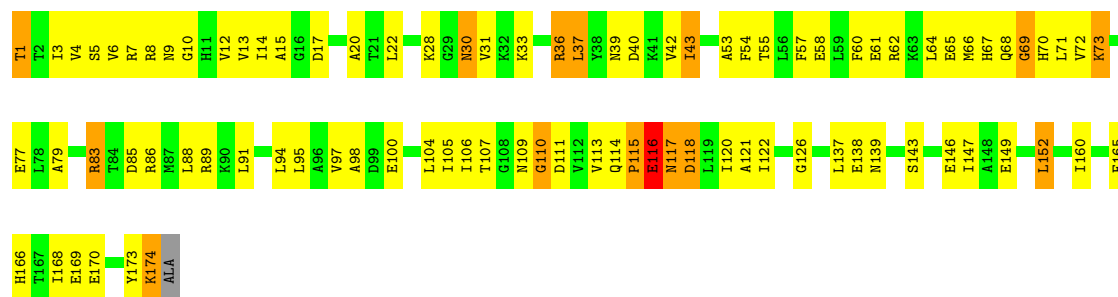
• Molecule 1: HEAT SHOCK LOCUS HSLV

Chain K: 54% 41% 5% .

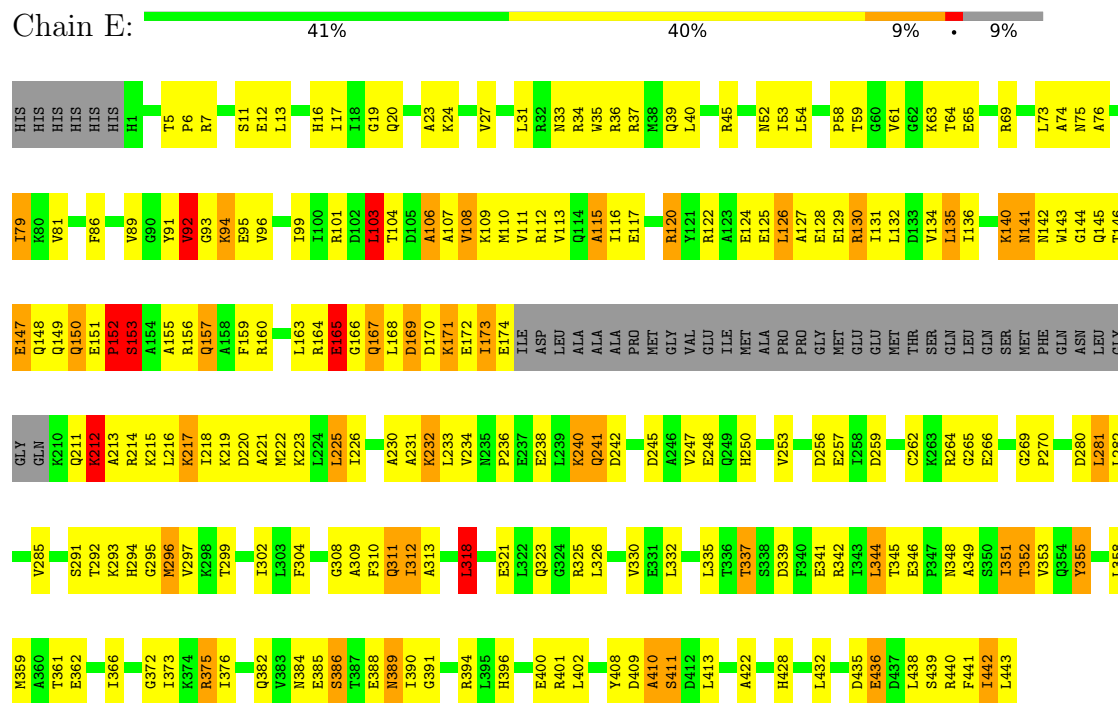


• Molecule 1: HEAT SHOCK LOCUS HSLV

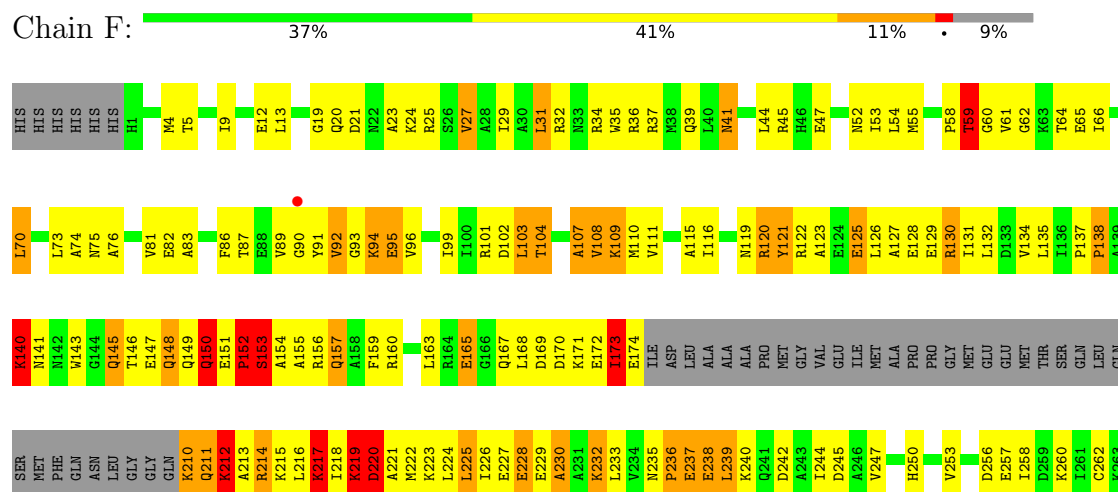
Chain L: 48% 43% 8% ..

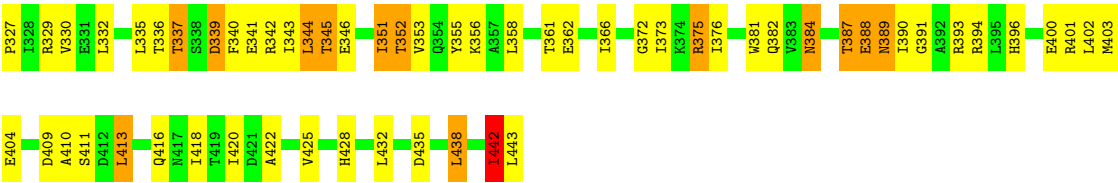


• Molecule 2: HEAT SHOCK LOCUS HSLU



• Molecule 2: HEAT SHOCK LOCUS HSLU





4 Data and refinement statistics

Property	Value	Source
Space group	P 3 1 2	Depositor
Cell constants a, b, c, α , β , γ	172.02Å 172.02Å 276.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.62 – 2.80 29.62 – 2.80	Depositor EDS
% Data completeness (in resolution range)	92.5 (29.62-2.80) 92.5 (29.62-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.49 (at 2.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.262 , 0.310 0.257 , 0.306	Depositor DCC
R_{free} test set	12111 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å ²)	67.1	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.499 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	23636	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 61.11 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3765e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	0.57	0/1345	1.06	5/1817 (0.3%)
1	B	0.50	0/1345	1.01	5/1817 (0.3%)
1	C	0.48	0/1345	0.98	2/1817 (0.1%)
1	D	0.42	0/1345	0.97	7/1817 (0.4%)
1	I	0.58	0/1345	1.06	7/1817 (0.4%)
1	J	0.51	0/1345	1.00	6/1817 (0.3%)
1	K	0.40	0/1345	0.91	3/1817 (0.2%)
1	L	0.44	0/1345	0.93	3/1817 (0.2%)
2	E	0.58	2/3266 (0.1%)	1.11	23/4400 (0.5%)
2	F	0.58	2/3266 (0.1%)	1.14	33/4400 (0.8%)
2	G	0.57	2/3266 (0.1%)	1.12	29/4400 (0.7%)
2	H	0.59	2/3266 (0.1%)	1.14	37/4400 (0.8%)
All	All	0.54	8/23824 (0.0%)	1.07	160/32136 (0.5%)

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

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

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	152	PRO	CA-C	-8.35	1.39	1.52
2	G	152	PRO	CA-C	-8.20	1.41	1.52
2	H	153	SER	N-CA	-7.60	1.36	1.46
2	G	153	SER	N-CA	-5.85	1.38	1.46
2	F	153	SER	N-CA	-5.67	1.38	1.46
2	E	153	SER	N-CA	-5.56	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	153	SER	C-N	5.41	1.41	1.33
2	F	152	PRO	C-N	-5.28	1.26	1.33

All (160) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	157	GLN	OE1-CD-NE2	-10.21	112.39	122.60
2	E	150	GLN	OE1-CD-NE2	-10.11	112.49	122.60
2	G	150	GLN	OE1-CD-NE2	-10.05	112.55	122.60
2	F	150	GLN	OE1-CD-NE2	-10.00	112.60	122.60
2	E	157	GLN	OE1-CD-NE2	-9.90	112.70	122.60
2	F	157	GLN	OE1-CD-NE2	-9.86	112.74	122.60
2	G	157	GLN	OE1-CD-NE2	-9.77	112.83	122.60
2	H	150	GLN	OE1-CD-NE2	-9.53	113.07	122.60
2	F	220	ASP	CA-CB-CG	8.78	121.38	112.60
1	A	116	GLU	N-CA-C	8.53	122.66	111.75
1	C	101	THR	N-CA-C	8.18	123.95	113.88
2	H	220	ASP	CA-CB-CG	8.06	120.66	112.60
2	E	153	SER	CA-C-N	8.03	136.87	121.54
2	E	153	SER	C-N-CA	8.03	136.87	121.54
2	F	309	ALA	N-CA-C	-7.72	103.82	113.55
2	F	155	ALA	N-CA-C	-7.62	102.91	111.14
2	G	309	ALA	N-CA-C	-7.59	103.64	113.12
1	C	72	VAL	N-CA-C	7.54	117.66	110.42
2	F	157	GLN	CG-CD-NE2	7.42	127.53	116.40
2	E	318	LEU	N-CA-C	-7.32	100.86	110.53
2	F	153	SER	CA-C-N	7.21	135.32	121.54
2	F	153	SER	C-N-CA	7.21	135.32	121.54
1	D	50	THR	N-CA-C	-7.20	104.11	114.12
2	G	152	PRO	CA-N-CD	-7.19	101.94	112.00
2	E	120	ARG	N-CA-C	-7.15	105.74	114.75
2	E	152	PRO	CA-N-CD	-7.13	102.02	112.00
2	F	150	GLN	CG-CD-NE2	7.10	127.05	116.40
2	H	107	ALA	N-CA-C	-7.10	104.61	113.20
2	G	126	LEU	N-CA-C	-7.09	104.66	113.38
2	E	126	LEU	N-CA-C	-7.08	104.51	113.72
1	I	154	ILE	N-CA-C	-7.07	103.64	110.42
2	E	150	GLN	CG-CD-NE2	7.01	126.92	116.40
2	G	220	ASP	CA-CB-CG	7.00	119.60	112.60
1	B	113	VAL	N-CA-C	6.97	117.87	108.11
2	F	115	ALA	N-CA-C	-6.92	104.51	114.12
2	F	128	GLU	N-CA-C	-6.88	104.87	113.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	128	GLU	N-CA-C	-6.87	104.90	113.28
2	E	152	PRO	CA-C-N	-6.77	108.60	121.54
2	E	152	PRO	C-N-CA	-6.77	108.60	121.54
2	H	442	ILE	N-CA-C	6.77	120.51	111.44
1	I	118	ASP	N-CA-C	-6.74	105.00	113.23
2	E	157	GLN	CG-CD-NE2	6.71	126.46	116.40
2	G	115	ALA	N-CA-C	-6.68	105.26	113.41
2	H	157	GLN	CG-CD-NE2	6.67	126.40	116.40
2	F	107	ALA	N-CA-C	-6.65	105.15	113.20
2	G	311	GLN	N-CA-C	-6.58	104.90	113.12
2	H	318	LEU	N-CA-C	-6.55	100.78	110.48
2	F	220	ASP	CB-CA-C	-6.55	97.38	110.42
2	F	219	LYS	N-CA-C	-6.53	105.03	112.87
2	G	107	ALA	N-CA-C	-6.53	105.28	113.18
2	G	152	PRO	CA-C-N	-6.51	109.10	121.54
2	G	152	PRO	C-N-CA	-6.51	109.10	121.54
2	H	150	GLN	CG-CD-NE2	6.50	126.15	116.40
2	G	157	GLN	CG-CD-NE2	6.49	126.14	116.40
2	G	135	LEU	N-CA-C	-6.47	105.96	114.31
1	B	104	LEU	N-CA-C	6.44	118.00	108.60
1	J	114	GLN	CA-C-N	6.43	126.34	119.85
1	J	114	GLN	C-N-CA	6.43	126.34	119.85
2	E	147	GLU	N-CA-C	-6.42	106.66	114.75
2	H	155	ALA	N-CA-C	-6.41	104.29	111.28
2	E	107	ALA	N-CA-C	-6.37	105.47	113.18
2	F	311	GLN	N-CA-C	-6.36	105.17	113.12
2	G	150	GLN	CG-CD-NE2	6.26	125.79	116.40
1	D	52	ASP	N-CA-C	-6.25	103.75	111.75
2	F	120	ARG	N-CA-C	-6.25	105.14	114.64
2	E	135	LEU	N-CA-C	-6.24	105.98	113.97
2	H	103	LEU	N-CA-C	-6.24	105.77	113.19
2	H	309	ALA	N-CA-C	-6.23	105.33	113.12
2	H	115	ALA	N-CA-C	-6.22	104.27	113.61
2	H	345	THR	N-CA-C	6.19	122.42	114.56
2	G	120	ARG	N-CA-C	-6.14	105.31	114.64
2	G	153	SER	CA-C-N	6.13	133.25	121.54
2	G	153	SER	C-N-CA	6.13	133.25	121.54
2	H	311	GLN	N-CA-C	-6.12	105.48	113.12
2	G	125	GLU	N-CA-C	-6.11	106.36	113.88
2	E	103	LEU	N-CA-C	-6.08	104.57	111.07
2	H	219	LYS	CA-C-N	6.05	131.64	122.56
2	H	219	LYS	C-N-CA	6.05	131.64	122.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	115	ALA	N-CA-C	-6.04	106.04	113.41
2	H	339	ASP	N-CA-C	-6.04	104.61	111.07
1	I	116	GLU	N-CA-C	6.01	123.61	110.80
2	G	147	GLU	N-CA-C	-6.00	107.19	114.75
2	F	83	ALA	N-CA-C	5.96	118.55	111.33
1	I	104	LEU	N-CA-C	5.96	117.58	108.52
1	J	104	LEU	N-CA-C	5.96	117.59	108.42
2	H	149	GLN	N-CA-C	-5.94	105.90	113.02
2	H	90	GLY	N-CA-C	-5.92	106.99	114.16
1	B	96	ALA	N-CA-C	-5.91	99.55	109.07
2	H	153	SER	CA-C-N	5.90	132.80	121.54
2	H	153	SER	C-N-CA	5.90	132.80	121.54
1	A	65	GLU	N-CA-C	-5.86	105.98	113.01
2	F	149	GLN	N-CA-C	-5.85	106.38	112.93
1	B	118	ASP	N-CA-C	-5.84	105.73	112.86
2	E	125	GLU	N-CA-C	-5.83	106.33	113.50
1	D	66	MET	N-CA-C	-5.80	105.96	113.16
2	G	155	ALA	N-CA-C	-5.79	104.88	111.14
2	G	148	GLN	N-CA-C	-5.73	105.55	112.54
1	A	118	ASP	N-CA-C	-5.72	106.25	113.23
2	E	442	ILE	N-CA-C	5.72	120.90	113.07
1	D	104	LEU	N-CA-C	5.70	116.80	108.14
2	H	152	PRO	CA-N-CD	-5.66	104.07	112.00
2	F	339	ASP	N-CA-C	-5.65	105.20	111.36
1	K	52	ASP	N-CA-C	-5.60	105.18	111.28
1	I	20	ALA	N-CA-C	-5.59	99.31	108.76
2	H	238	GLU	N-CA-C	-5.59	105.74	113.18
1	L	104	LEU	N-CA-C	5.59	117.12	109.18
1	L	20	ALA	N-CA-C	-5.58	99.33	108.76
2	F	90	GLY	N-CA-C	-5.57	108.03	115.32
2	H	273	SER	N-CA-C	-5.55	105.14	111.14
1	J	96	ALA	N-CA-C	-5.52	99.52	108.52
2	E	309	ALA	N-CA-C	-5.49	104.82	112.45
2	G	134	VAL	N-CA-C	-5.48	107.94	113.20
1	I	65	GLU	N-CA-C	-5.46	105.49	111.82
1	J	112	VAL	N-CA-C	-5.45	99.71	107.77
2	G	249	GLN	N-CA-C	5.44	120.02	112.45
2	F	153	SER	CB-CA-C	5.44	121.24	110.42
1	J	113	VAL	N-CA-C	5.44	115.69	107.75
2	E	106	ALA	N-CA-C	-5.42	106.50	113.23
2	H	387	THR	CB-CA-C	-5.41	108.65	116.54
2	H	120	ARG	N-CA-C	-5.40	106.43	114.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	152	PRO	CA-C-N	-5.39	111.24	121.54
2	F	152	PRO	C-N-CA	-5.39	111.24	121.54
2	F	350	SER	N-CA-C	-5.33	103.36	110.55
1	B	41	LYS	N-CA-C	-5.33	106.84	113.55
2	H	153	SER	CB-CA-C	5.32	121.02	110.42
2	G	220	ASP	CB-CA-C	-5.30	102.11	110.86
2	G	339	ASP	N-CA-C	-5.30	105.58	111.36
2	H	95	GLU	N-CA-C	-5.25	102.74	110.52
2	F	319	ILE	CA-C-N	5.25	124.70	119.24
2	F	319	ILE	C-N-CA	5.25	124.70	119.24
1	L	72	VAL	N-CA-C	5.25	115.46	110.42
2	F	345	THR	N-CA-C	5.23	121.94	110.80
2	H	106	ALA	N-CA-C	-5.21	107.08	113.50
1	D	20	ALA	N-CA-C	-5.21	99.95	108.76
2	G	75	ASN	N-CA-C	-5.21	103.82	111.17
2	E	436	GLU	N-CA-C	5.18	116.62	110.97
2	G	297	VAL	N-CA-C	5.18	116.43	108.71
2	G	442	ILE	N-CA-C	5.18	120.17	113.07
1	K	102	ALA	N-CA-C	5.17	117.27	109.41
2	F	405	GLU	N-CA-C	5.14	116.69	111.14
2	H	216	LEU	N-CA-C	5.14	114.62	107.73
2	H	53	ILE	N-CA-C	5.14	116.70	108.89
1	K	104	LEU	N-CA-C	5.12	116.31	108.42
2	F	152	PRO	CA-N-CD	-5.12	104.84	112.00
2	F	217	LYS	CB-CA-C	-5.11	109.70	117.07
2	E	153	SER	CB-CA-C	5.11	120.59	110.42
2	F	334	ALA	N-CA-C	-5.10	103.66	110.55
1	I	173	TYR	N-CA-C	-5.10	108.08	114.56
2	H	152	PRO	N-CA-C	-5.09	106.16	113.75
2	F	59	THR	N-CA-C	5.09	116.86	110.24
2	H	135	LEU	N-CA-C	-5.07	105.40	112.45
1	D	41	LYS	N-CA-C	-5.05	106.29	112.90
2	G	318	LEU	N-CA-C	-5.04	103.49	110.35
1	A	159	CYS	N-CA-C	5.04	116.97	109.25
1	D	165	PHE	N-CA-C	-5.04	101.09	109.46
2	H	294	HIS	N-CA-C	-5.04	106.98	114.64
2	H	152	PRO	CA-C-N	-5.03	111.93	121.54
2	H	152	PRO	C-N-CA	-5.03	111.93	121.54
1	A	17	ASP	N-CA-C	-5.01	102.09	109.86
2	F	217	LYS	CA-C-O	5.00	120.84	117.94

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	128	TYR	Sidechain

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	1328	0	1348	95	0
1	B	1328	0	1348	113	0
1	C	1328	0	1348	83	0
1	D	1328	0	1348	110	1
1	I	1328	0	1348	82	0
1	J	1328	0	1348	106	0
1	K	1328	0	1348	75	1
1	L	1328	0	1348	97	0
2	E	3226	0	3293	274	1
2	F	3226	0	3293	297	1
2	G	3226	0	3293	311	0
2	H	3226	0	3293	358	0
3	E	27	0	12	2	0
3	F	27	0	12	3	0
3	G	27	0	12	2	0
3	H	27	0	12	4	0
All	All	23636	0	24004	1887	3

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 40.

All (1887) 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)
2:G:152:PRO:O	2:G:154:ALA:CA	1.76	1.33
2:G:152:PRO:O	2:G:153:SER:C	1.74	1.27
2:G:152:PRO:C	2:G:154:ALA:N	1.72	1.27
2:E:174:GLU:HB3	2:E:211:GLN:HG3	1.30	1.10
2:G:109:LYS:HB2	2:H:296:MET:HG2	1.32	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:216:LEU:HG	2:H:221:ALA:HB2	1.32	1.09
1:I:80:LYS:HA	1:I:83:ARG:HH12	1.12	1.09
2:G:174:GLU:HB3	2:G:211:GLN:HG3	1.34	1.08
2:G:109:LYS:HD3	2:H:296:MET:HB3	1.31	1.08
1:L:83:ARG:NH1	1:L:83:ARG:HB3	1.66	1.08
2:G:168:LEU:HG	2:G:219:LYS:HD3	1.30	1.07
2:G:152:PRO:HB2	2:G:156:ARG:HB2	1.37	1.06
1:C:83:ARG:HB3	1:C:83:ARG:NH1	1.72	1.05
1:L:83:ARG:HB3	1:L:83:ARG:HH11	1.12	1.03
2:E:212:LYS:HD3	2:E:216:LEU:HD21	1.41	1.03
2:G:130:ARG:HD2	2:G:225:LEU:HD11	1.38	1.03
1:A:13:VAL:HG12	1:A:170:GLU:HG3	1.41	1.01
2:H:150:GLN:O	2:H:153:SER:HB2	1.61	1.00
1:K:105:ILE:HD11	1:K:120:ILE:HG23	1.41	1.00
2:E:312:ILE:H	2:E:312:ILE:HD13	1.27	1.00
2:F:122:ARG:HH11	2:F:126:LEU:HD23	1.27	1.00
2:E:152:PRO:HB2	2:E:156:ARG:HB2	1.43	0.99
2:H:351:ILE:HD13	2:H:351:ILE:H	1.27	0.98
2:G:220:ASP:HA	2:G:223:LYS:HD2	1.43	0.98
1:B:65:GLU:HG2	2:F:143:TRP:CD1	1.97	0.97
2:G:92:VAL:HG21	2:H:92:VAL:HG13	1.42	0.97
2:G:88:GLU:HB3	2:H:90:GLY:HA2	1.44	0.96
2:H:123:ALA:HA	2:H:127:ALA:HB3	1.46	0.96
2:G:170:ASP:HA	2:G:217:LYS:HA	1.44	0.96
2:F:132:LEU:HD11	2:F:160:ARG:HG3	1.47	0.96
2:G:92:VAL:HG21	2:H:92:VAL:CG1	1.94	0.96
1:I:80:LYS:HA	1:I:83:ARG:NH1	1.81	0.95
1:A:80:LYS:HA	1:A:83:ARG:NH1	1.81	0.95
2:G:94:LYS:HA	2:G:94:LYS:HE2	1.49	0.95
2:H:312:ILE:HD13	2:H:312:ILE:H	1.31	0.95
1:B:65:GLU:HB3	2:F:143:TRP:HA	1.47	0.95
2:H:135:LEU:HD23	2:H:171:LYS:HE2	1.46	0.95
2:G:103:LEU:HD22	2:G:247:VAL:HG22	1.48	0.94
1:A:80:LYS:HA	1:A:83:ARG:HH12	1.29	0.94
2:F:94:LYS:HE2	2:F:94:LYS:HA	1.48	0.93
2:H:172:GLU:HB3	2:H:215:LYS:HD2	1.51	0.93
2:H:132:LEU:HD11	2:H:160:ARG:HG3	1.50	0.91
1:D:83:ARG:NH1	1:D:83:ARG:HB3	1.86	0.91
1:J:71:LEU:HB2	1:J:99:ASP:OD2	1.71	0.91
2:F:351:ILE:H	2:F:351:ILE:HD13	1.35	0.91
2:G:130:ARG:NH2	2:G:130:ARG:HB2	1.85	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:59:THR:HG22	2:F:393:ARG:NH2	1.84	0.90
2:G:359:MET:HE1	2:H:36:ARG:NH1	1.85	0.90
1:B:65:GLU:OE1	2:F:143:TRP:CD1	2.25	0.90
2:H:122:ARG:HH11	2:H:126:LEU:HD23	1.34	0.90
1:I:85:ASP:O	1:I:89:ARG:HB2	1.70	0.90
1:D:83:ARG:HB3	1:D:83:ARG:HH11	1.37	0.89
2:E:94:LYS:HE2	2:E:94:LYS:HA	1.52	0.89
2:H:94:LYS:HE2	2:H:94:LYS:HA	1.53	0.88
1:D:105:ILE:HD11	1:D:120:ILE:HG21	1.54	0.88
2:E:299:THR:HA	2:E:302:ILE:HD13	1.55	0.87
2:G:344:LEU:O	2:G:352:THR:HB	1.73	0.87
1:I:10:GLY:HA3	1:I:174:LYS:HA	1.55	0.87
2:G:64:THR:HB	3:G:2450:ADP:O2A	1.74	0.87
1:I:87:MET:HE1	1:J:84:THR:HG23	1.54	0.87
2:H:216:LEU:CG	2:H:221:ALA:HB2	2.05	0.87
1:B:104:LEU:HD12	1:B:112:VAL:HG12	1.57	0.86
2:E:344:LEU:O	2:E:352:THR:HB	1.75	0.86
1:K:105:ILE:HD11	1:K:120:ILE:CG2	2.05	0.86
1:L:174:LYS:HA	1:L:174:LYS:NZ	1.90	0.86
2:E:217:LYS:HG3	2:E:219:LYS:HZ3	1.38	0.86
2:H:312:ILE:H	2:H:312:ILE:CD1	1.89	0.86
2:G:397:THR:HG22	2:H:327:PRO:HA	1.58	0.85
1:B:65:GLU:OE1	2:F:143:TRP:CG	2.29	0.85
2:E:132:LEU:HD11	2:E:160:ARG:HG3	1.58	0.85
1:D:152:LEU:HD13	1:D:166:HIS:ND1	1.91	0.84
1:I:47:ALA:HB3	1:I:94:LEU:HB2	1.58	0.84
2:G:312:ILE:H	2:G:312:ILE:HD13	1.40	0.84
1:A:85:ASP:O	1:A:89:ARG:HB2	1.76	0.84
1:B:17:ASP:HA	1:B:165:PHE:O	1.78	0.84
2:F:91:TYR:O	2:F:92:VAL:HG13	1.78	0.84
1:C:83:ARG:HB3	1:C:83:ARG:HH11	1.34	0.84
2:H:132:LEU:HA	2:H:135:LEU:HD12	1.58	0.84
1:B:65:GLU:CG	2:F:143:TRP:CD1	2.60	0.84
2:F:59:THR:HG22	2:F:393:ARG:HH21	1.42	0.84
2:E:130:ARG:HB2	2:E:130:ARG:NH2	1.92	0.84
2:E:214:ARG:HD3	2:E:216:LEU:HD22	1.59	0.83
2:H:174:GLU:HA	2:H:213:ALA:H	1.43	0.83
1:B:72:VAL:O	1:B:76:VAL:HG23	1.78	0.83
2:E:389:ASN:HD22	2:E:389:ASN:C	1.83	0.83
2:E:64:THR:HB	3:E:450:ADP:O2A	1.78	0.83
2:F:123:ALA:HA	2:F:127:ALA:HB3	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:362:GLU:OE2	2:H:32:ARG:NH2	2.08	0.83
2:E:131:ILE:HD11	2:E:218:ILE:HG12	1.61	0.83
2:G:91:TYR:HB2	2:H:90:GLY:O	1.78	0.82
2:F:103:LEU:HD13	2:F:247:VAL:HG22	1.61	0.82
1:J:72:VAL:O	1:J:76:VAL:HG23	1.79	0.82
2:G:220:ASP:O	2:G:223:LYS:N	2.10	0.82
2:E:145:GLN:HB2	2:E:148:GLN:HB2	1.62	0.82
2:G:361:THR:HG22	2:H:35:TRP:CZ3	2.15	0.82
1:A:10:GLY:HA2	1:A:173:TYR:CE1	2.15	0.82
2:F:173:ILE:HG12	2:F:212:LYS:HD2	1.59	0.82
2:F:171:LYS:NZ	2:F:218:ILE:HD11	1.94	0.81
2:G:359:MET:HE1	2:H:36:ARG:HH12	1.43	0.81
2:E:312:ILE:H	2:E:312:ILE:CD1	1.93	0.81
2:F:312:ILE:HD13	2:F:312:ILE:H	1.46	0.81
2:H:173:ILE:HG12	2:H:212:LYS:HD2	1.63	0.81
1:D:71:LEU:HD21	1:D:97:VAL:HG11	1.62	0.80
1:K:152:LEU:HD13	1:K:166:HIS:ND1	1.96	0.80
1:D:43:ILE:HD13	1:D:43:ILE:H	1.46	0.80
2:H:171:LYS:NZ	2:H:218:ILE:HD11	1.96	0.80
2:F:64:THR:HB	3:F:1450:ADP:O2A	1.82	0.80
2:H:131:ILE:HD11	2:H:218:ILE:HD13	1.64	0.80
2:E:150:GLN:O	2:E:153:SER:HB2	1.82	0.79
2:F:27:VAL:HG13	2:F:70:LEU:HG	1.62	0.79
2:E:173:ILE:HG12	2:E:212:LYS:HD2	1.64	0.79
2:E:389:ASN:ND2	2:E:391:GLY:H	1.80	0.79
1:I:10:GLY:HA2	1:I:173:TYR:CE1	2.18	0.79
2:G:92:VAL:HG11	2:H:92:VAL:CG1	2.12	0.79
2:G:211:GLN:HG2	2:G:212:LYS:H	1.47	0.79
1:L:62:ARG:O	1:L:66:MET:HB2	1.82	0.79
2:H:345:THR:CG2	2:H:373:ILE:HD13	2.13	0.79
2:E:152:PRO:HB3	2:E:156:ARG:H	1.48	0.79
1:D:105:ILE:HD11	1:D:120:ILE:CG2	2.13	0.79
2:H:384:ASN:ND2	2:H:394:ARG:HE	1.80	0.79
2:H:389:ASN:ND2	2:H:391:GLY:H	1.81	0.79
2:F:224:LEU:O	2:F:228:GLU:HB2	1.83	0.78
1:L:13:VAL:HG12	1:L:170:GLU:HG3	1.64	0.78
1:J:57:PHE:O	1:J:61:GLU:HG3	1.83	0.78
1:L:138:GLU:C	1:L:139:ASN:HD22	1.90	0.78
2:G:147:GLU:HA	2:G:150:GLN:HG3	1.66	0.78
2:F:172:GLU:HB3	2:F:215:LYS:HD2	1.64	0.78
2:H:91:TYR:O	2:H:92:VAL:HG13	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:65:GLU:HG2	2:F:143:TRP:HD1	1.46	0.77
2:F:223:LYS:HA	2:F:226:ILE:HG12	1.64	0.77
2:G:131:ILE:HG21	2:G:222:MET:HE1	1.66	0.77
2:H:132:LEU:HD23	2:H:135:LEU:HD12	1.66	0.77
2:E:211:GLN:HG2	2:E:212:LYS:H	1.49	0.76
1:A:10:GLY:HA3	1:A:174:LYS:HA	1.65	0.76
2:G:389:ASN:HD22	2:G:389:ASN:C	1.92	0.76
1:B:105:ILE:HD11	1:B:120:ILE:HG23	1.68	0.76
2:G:109:LYS:CD	2:H:296:MET:HB3	2.13	0.76
2:F:257:GLU:HB2	2:F:260:LYS:HG3	1.68	0.76
2:F:148:GLN:OE1	2:F:151:GLU:HG3	1.85	0.76
2:G:291:SER:HA	2:G:296:MET:HE2	1.66	0.76
2:H:103:LEU:HD13	2:H:247:VAL:HG22	1.68	0.76
1:J:1:THR:HB	1:J:33:LYS:HZ2	1.50	0.75
1:B:170:GLU:HG2	1:B:171:LEU:H	1.51	0.75
2:G:92:VAL:CG2	2:H:91:TYR:C	2.59	0.75
2:G:142:ASN:HB2	2:G:149:GLN:HE22	1.51	0.75
2:H:217:LYS:HB2	2:H:217:LYS:NZ	2.01	0.75
1:L:30:ASN:H	1:L:30:ASN:HD22	1.31	0.75
1:D:54:PHE:O	1:D:58:GLU:HB2	1.86	0.75
2:H:64:THR:HB	3:H:3450:ADP:O2A	1.85	0.75
1:L:105:ILE:HD11	1:L:120:ILE:HG23	1.68	0.75
2:E:130:ARG:HD2	2:E:225:LEU:HD11	1.67	0.75
1:J:104:LEU:HD12	1:J:112:VAL:HG12	1.68	0.75
1:B:1:THR:HB	1:B:33:LYS:NZ	2.01	0.75
2:G:152:PRO:CB	2:G:156:ARG:HB2	2.16	0.74
2:E:384:ASN:ND2	2:E:394:ARG:HE	1.85	0.74
1:J:1:THR:HB	1:J:33:LYS:NZ	2.03	0.74
2:E:174:GLU:HA	2:E:213:ALA:H	1.51	0.74
2:G:136:ILE:O	2:G:136:ILE:HG22	1.88	0.74
1:I:83:ARG:HG2	1:I:83:ARG:HH11	1.52	0.74
2:G:152:PRO:O	2:G:154:ALA:N	0.59	0.74
2:H:130:ARG:HH21	2:H:229:GLU:HG3	1.50	0.74
1:B:60:PHE:CD1	1:B:78:LEU:HD22	2.23	0.74
2:E:104:THR:HG21	2:E:292:THR:HG21	1.69	0.74
1:L:64:LEU:HB3	1:L:69:GLY:HA2	1.69	0.74
2:F:384:ASN:ND2	2:F:394:ARG:HE	1.85	0.74
1:B:57:PHE:O	1:B:61:GLU:HG3	1.88	0.73
2:G:168:LEU:HA	2:G:219:LYS:HB3	1.68	0.73
2:H:108:VAL:HA	2:H:111:VAL:HG22	1.68	0.73
2:G:145:GLN:HB2	2:G:148:GLN:HB2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:130:ARG:HG2	2:H:225:LEU:HD11	1.70	0.73
1:B:28:LYS:HZ2	1:B:30:ASN:HD21	1.36	0.73
1:B:63:LYS:HA	1:B:66:MET:HE3	1.70	0.73
1:B:65:GLU:CD	2:F:143:TRP:CD1	2.65	0.73
2:F:122:ARG:NH1	2:F:126:LEU:HD23	2.02	0.73
1:C:85:ASP:HB3	1:C:88:LEU:HB2	1.69	0.73
2:H:356:LYS:HG3	2:H:366:ILE:HG22	1.71	0.73
2:G:389:ASN:ND2	2:G:391:GLY:H	1.86	0.73
2:E:167:GLN:NE2	2:E:168:LEU:HG	2.04	0.73
1:J:19:GLN:HB2	1:J:163:ASN:ND2	2.03	0.73
2:H:147:GLU:O	2:H:151:GLU:HG2	1.89	0.73
1:L:1:THR:HB	1:L:33:LYS:HZ3	1.54	0.73
1:D:3:ILE:HB	1:D:122:ILE:HG12	1.71	0.72
1:L:115:PRO:HG3	1:L:120:ILE:HG12	1.68	0.72
1:B:36:ARG:O	1:B:37:LEU:HD23	1.88	0.72
2:F:108:VAL:C	2:F:110:MET:H	1.96	0.72
1:C:136:LEU:HB3	1:C:147:ILE:HD12	1.72	0.72
2:H:219:LYS:HA	2:H:219:LYS:HE3	1.71	0.72
1:B:86:ARG:HA	1:B:89:ARG:NE	2.03	0.72
2:F:356:LYS:HG3	2:F:366:ILE:HG22	1.70	0.72
2:G:312:ILE:H	2:G:312:ILE:CD1	2.02	0.72
2:H:232:LYS:H	2:H:232:LYS:HD2	1.54	0.72
2:H:220:ASP:O	2:H:224:LEU:HD23	1.88	0.72
1:A:28:LYS:HZ1	1:A:30:ASN:ND2	1.87	0.72
2:G:91:TYR:HD1	2:H:91:TYR:CD2	2.06	0.72
1:K:71:LEU:HG	1:K:99:ASP:OD1	1.88	0.72
1:L:152:LEU:HD13	1:L:166:HIS:CE1	2.24	0.72
2:E:124:GLU:HA	2:E:127:ALA:HB3	1.72	0.72
2:E:167:GLN:HE22	2:E:168:LEU:HG	1.54	0.72
1:D:71:LEU:HD21	1:D:97:VAL:CG1	2.19	0.72
1:D:79:ALA:HB1	1:D:110:GLY:HA2	1.69	0.72
1:J:152:LEU:HD13	1:J:166:HIS:ND1	2.05	0.72
2:E:91:TYR:O	2:E:92:VAL:HG13	1.89	0.72
1:I:1:THR:HB	1:I:33:LYS:NZ	2.05	0.72
2:F:81:VAL:HG11	2:F:99:ILE:HG12	1.72	0.72
2:G:362:GLU:HG2	2:G:410:ALA:HB1	1.72	0.72
2:E:171:LYS:HG3	2:E:218:ILE:HD11	1.72	0.71
2:H:242:ASP:HA	2:H:245:ASP:OD1	1.90	0.71
2:E:140:LYS:O	2:E:141:ASN:HB2	1.90	0.71
1:D:115:PRO:HG3	1:D:120:ILE:HG12	1.71	0.71
1:A:65:GLU:CD	2:E:141:ASN:HB3	2.15	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:5:SER:HB3	1:J:120:ILE:HD13	1.72	0.71
2:G:361:THR:CG2	2:H:35:TRP:CZ3	2.74	0.71
2:G:124:GLU:HA	2:G:127:ALA:HB3	1.73	0.71
2:G:153:SER:O	2:G:157:GLN:NE2	2.23	0.71
1:L:174:LYS:HA	1:L:174:LYS:HZ3	1.53	0.71
1:L:30:ASN:H	1:L:30:ASN:ND2	1.87	0.71
1:B:28:LYS:NZ	1:B:30:ASN:HD21	1.88	0.70
2:F:108:VAL:HG21	2:F:294:HIS:HD2	1.56	0.70
1:J:105:ILE:HD11	1:J:120:ILE:HG23	1.73	0.70
1:K:64:LEU:HD23	1:K:74:ALA:CB	2.20	0.70
2:F:242:ASP:HA	2:F:245:ASP:OD1	1.90	0.70
2:G:130:ARG:HB2	2:G:130:ARG:HH21	1.54	0.70
2:H:344:LEU:O	2:H:352:THR:HB	1.90	0.70
2:F:312:ILE:H	2:F:312:ILE:CD1	2.04	0.70
1:D:14:ILE:HD13	1:D:43:ILE:CG1	2.22	0.70
2:E:291:SER:HA	2:E:296:MET:HE2	1.74	0.70
2:F:174:GLU:HA	2:F:213:ALA:H	1.56	0.70
1:L:43:ILE:HD13	1:L:43:ILE:H	1.57	0.70
2:G:91:TYR:HD1	2:H:91:TYR:CE2	2.09	0.70
2:G:92:VAL:HG21	2:H:91:TYR:C	2.15	0.70
2:E:165:GLU:HG2	2:E:166:GLY:H	1.55	0.69
2:F:344:LEU:O	2:F:352:THR:HB	1.92	0.69
1:D:6:VAL:HG21	1:D:147:ILE:HG22	1.74	0.69
2:G:91:TYR:O	2:G:92:VAL:HG13	1.91	0.69
2:H:217:LYS:O	2:H:221:ALA:N	2.13	0.69
2:G:174:GLU:HA	2:G:212:LYS:HB3	1.73	0.69
2:F:217:LYS:HB2	2:F:217:LYS:NZ	2.07	0.69
2:H:174:GLU:HB3	2:H:211:GLN:HB2	1.74	0.69
2:E:293:LYS:HG3	2:E:294:HIS:CD2	2.28	0.69
1:J:104:LEU:CD1	1:J:112:VAL:HG12	2.22	0.69
2:H:108:VAL:C	2:H:110:MET:H	1.98	0.69
1:A:71:LEU:HD23	1:A:99:ASP:OD2	1.92	0.69
1:I:1:THR:HB	1:I:33:LYS:HZ2	1.57	0.69
2:H:27:VAL:HG13	2:H:70:LEU:HG	1.75	0.69
2:H:148:GLN:HA	2:H:151:GLU:HG3	1.72	0.69
1:B:86:ARG:HA	1:B:89:ARG:CZ	2.23	0.69
1:I:8:ARG:HG2	1:I:9:ASN:ND2	2.08	0.69
1:J:86:ARG:HA	1:J:89:ARG:CZ	2.23	0.69
2:H:389:ASN:C	2:H:389:ASN:HD22	2.01	0.69
1:K:86:ARG:HA	1:K:89:ARG:NH1	2.06	0.69
2:E:170:ASP:HA	2:E:217:LYS:HA	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:141:GLU:HA	1:J:141:GLU:OE2	1.93	0.69
2:E:312:ILE:HG12	2:E:313:ALA:H	1.58	0.69
2:G:91:TYR:CD1	2:H:91:TYR:CE2	2.81	0.69
1:B:104:LEU:CD1	1:B:112:VAL:HG12	2.22	0.69
2:E:359:MET:HG3	2:E:366:ILE:HG13	1.75	0.69
2:G:359:MET:HG3	2:G:366:ILE:HG13	1.74	0.69
2:E:337:THR:O	2:E:341:GLU:HG3	1.92	0.68
2:G:345:THR:HG21	2:G:373:ILE:HD13	1.74	0.68
2:H:236:PRO:HG2	2:H:237:GLU:H	1.58	0.68
2:H:389:ASN:HD22	2:H:391:GLY:H	1.41	0.68
2:E:214:ARG:HG2	2:E:215:LYS:N	2.08	0.68
1:I:77:GLU:O	1:I:80:LYS:HB2	1.93	0.68
2:H:223:LYS:HA	2:H:226:ILE:HG12	1.76	0.68
2:F:264:ARG:NE	2:F:265:GLY:H	1.91	0.68
2:F:375:ARG:CZ	2:F:422:ALA:HB1	2.23	0.68
2:H:235:ASN:HB2	2:H:236:PRO:HD2	1.73	0.68
1:I:10:GLY:HA2	1:I:173:TYR:CZ	2.29	0.68
2:E:122:ARG:CZ	2:E:126:LEU:HD21	2.24	0.68
2:H:375:ARG:CZ	2:H:422:ALA:HB1	2.23	0.68
2:F:41:ASN:HD22	2:F:41:ASN:C	2.02	0.68
2:G:152:PRO:HB2	2:G:156:ARG:CB	2.21	0.68
1:D:28:LYS:HD3	1:D:31:VAL:HG22	1.74	0.68
2:H:135:LEU:HB3	2:H:159:PHE:CD2	2.28	0.68
1:K:73:LYS:HA	1:K:76:VAL:HG12	1.76	0.68
2:E:174:GLU:CB	2:E:211:GLN:HG3	2.18	0.67
2:G:173:ILE:HD13	2:G:173:ILE:N	2.09	0.67
2:H:96:VAL:HG11	2:H:281:LEU:HD12	1.75	0.67
2:G:147:GLU:HG3	2:G:150:GLN:NE2	2.10	0.67
1:A:65:GLU:CD	2:E:141:ASN:CB	2.68	0.67
2:F:291:SER:HA	2:F:296:MET:HE2	1.75	0.67
1:C:11:HIS:NE2	1:C:174:LYS:HE2	2.08	0.67
1:J:86:ARG:HA	1:J:89:ARG:NE	2.09	0.67
1:B:152:LEU:HD13	1:B:166:HIS:ND1	2.10	0.67
2:E:216:LEU:HD23	2:E:216:LEU:H	1.60	0.67
2:F:163:LEU:HD11	2:F:222:MET:CE	2.24	0.67
2:F:82:GLU:HB3	2:F:257:GLU:OE2	1.93	0.67
2:G:153:SER:HA	2:G:157:GLN:HG3	1.75	0.67
2:F:216:LEU:HD11	2:F:221:ALA:HA	1.76	0.67
2:G:130:ARG:CD	2:G:225:LEU:HD11	2.20	0.67
2:G:384:ASN:ND2	2:G:394:ARG:HE	1.92	0.67
2:F:152:PRO:HB2	2:F:156:ARG:HB2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:LEU:HD13	1:C:166:HIS:CE1	2.29	0.67
1:D:73:LYS:NZ	1:D:77:GLU:HG2	2.09	0.67
1:J:85:ASP:O	1:J:89:ARG:HG3	1.95	0.66
2:G:89:VAL:HG12	2:G:93:GLY:HA3	1.77	0.66
2:G:231:ALA:C	2:G:233:LEU:H	2.03	0.66
1:C:10:GLY:HA2	1:C:173:TYR:CE1	2.30	0.66
2:F:223:LYS:HD2	2:F:223:LYS:N	2.09	0.66
2:G:140:LYS:O	2:G:141:ASN:HB2	1.95	0.66
1:B:19:GLN:HB2	1:B:163:ASN:ND2	2.11	0.66
2:E:136:ILE:HG22	2:E:136:ILE:O	1.95	0.66
1:C:79:ALA:HB1	1:C:110:GLY:HA2	1.78	0.66
2:F:135:LEU:CD2	2:F:171:LYS:HE2	2.25	0.66
2:E:217:LYS:CG	2:E:219:LYS:HZ3	2.08	0.66
2:F:130:ARG:HD2	2:F:225:LEU:HD11	1.77	0.66
2:F:389:ASN:ND2	2:F:391:GLY:H	1.93	0.66
1:J:8:ARG:NH1	1:J:142:LEU:O	2.26	0.66
1:K:27:MET:SD	1:L:113:VAL:HG21	2.35	0.66
2:E:211:GLN:HG2	2:E:212:LYS:N	2.11	0.66
2:F:174:GLU:HA	2:F:212:LYS:HB3	1.76	0.66
2:G:173:ILE:HG12	2:G:212:LYS:HD2	1.76	0.66
2:H:130:ARG:HG2	2:H:225:LEU:CD1	2.26	0.66
2:H:130:ARG:NH2	2:H:229:GLU:HG3	2.10	0.66
1:A:65:GLU:OE1	2:E:141:ASN:CB	2.44	0.66
2:E:103:LEU:HD22	2:E:247:VAL:HG22	1.78	0.66
2:E:122:ARG:O	2:E:126:LEU:HD23	1.96	0.66
2:F:211:GLN:HE21	2:F:212:LYS:H	1.43	0.66
2:F:362:GLU:HG2	2:F:410:ALA:CB	2.25	0.66
1:A:28:LYS:NZ	1:A:30:ASN:ND2	2.43	0.66
2:F:151:GLU:HB2	2:F:152:PRO:CD	2.26	0.66
1:J:36:ARG:O	1:J:37:LEU:HD23	1.95	0.66
1:B:62:ARG:HA	1:B:65:GLU:HG3	1.77	0.65
2:G:174:GLU:HB3	2:G:211:GLN:CG	2.20	0.65
2:E:52:ASN:HB2	2:E:325:ARG:O	1.97	0.65
1:C:73:LYS:HA	1:C:76:VAL:HG12	1.78	0.65
2:G:293:LYS:HG3	2:G:294:HIS:CD2	2.31	0.65
2:G:359:MET:CE	2:H:36:ARG:NH1	2.57	0.65
2:H:55:MET:HE2	2:H:332:LEU:HD11	1.78	0.65
2:E:345:THR:CG2	2:E:373:ILE:HD13	2.27	0.65
1:J:28:LYS:NZ	1:J:30:ASN:HD21	1.94	0.65
2:H:223:LYS:HA	2:H:226:ILE:CG1	2.27	0.65
1:J:28:LYS:HZ2	1:J:30:ASN:HD21	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1:THR:HB	1:B:33:LYS:HZ2	1.60	0.65
1:B:28:LYS:NZ	1:B:30:ASN:ND2	2.44	0.65
2:G:92:VAL:HG11	2:H:92:VAL:HG12	1.76	0.65
2:F:89:VAL:HG11	2:F:94:LYS:O	1.97	0.65
2:F:130:ARG:CD	2:F:225:LEU:HD11	2.27	0.65
2:H:168:LEU:O	2:H:217:LYS:HD2	1.97	0.65
2:H:148:GLN:OE1	2:H:151:GLU:HG3	1.97	0.65
2:H:219:LYS:O	2:H:223:LYS:HD3	1.96	0.65
2:H:229:GLU:HA	2:H:232:LYS:HD3	1.78	0.65
1:K:168:ILE:N	1:K:168:ILE:HD12	2.12	0.65
2:F:145:GLN:HB2	2:F:148:GLN:HG2	1.78	0.64
2:F:210:LYS:HD3	2:F:210:LYS:N	2.12	0.64
1:D:30:ASN:H	1:D:30:ASN:HD22	1.45	0.64
2:G:174:GLU:C	2:G:211:GLN:HB2	2.22	0.64
1:J:168:ILE:H	1:J:168:ILE:HD12	1.63	0.64
2:G:92:VAL:CG2	2:H:92:VAL:HG13	2.23	0.64
2:G:361:THR:HG21	2:H:36:ARG:HA	1.79	0.64
1:K:115:PRO:HG3	1:K:120:ILE:HG12	1.80	0.64
1:A:1:THR:HB	1:A:33:LYS:NZ	2.11	0.64
1:J:17:ASP:HA	1:J:165:PHE:O	1.98	0.64
2:G:152:PRO:HB3	2:G:156:ARG:H	1.63	0.64
1:L:91:LEU:HD12	1:L:91:LEU:O	1.98	0.64
1:I:152:LEU:HD13	1:I:166:HIS:CE1	2.32	0.64
2:G:142:ASN:CB	2:G:149:GLN:HE22	2.10	0.64
2:E:147:GLU:HA	2:E:150:GLN:HG3	1.80	0.64
2:E:173:ILE:HD13	2:E:173:ILE:N	2.12	0.64
2:E:174:GLU:HB3	2:E:211:GLN:CG	2.19	0.64
1:D:17:ASP:HA	1:D:165:PHE:O	1.97	0.64
1:D:30:ASN:HD22	1:D:30:ASN:N	1.95	0.64
2:G:112:ARG:HG3	2:G:112:ARG:HH11	1.62	0.64
1:I:168:ILE:N	1:I:168:ILE:HD12	2.13	0.64
2:H:145:GLN:HB2	2:H:148:GLN:HG2	1.80	0.64
2:H:214:ARG:HE	2:H:216:LEU:HB3	1.61	0.64
2:F:127:ALA:HA	2:F:130:ARG:NH2	2.13	0.64
2:F:132:LEU:HA	2:F:135:LEU:HD12	1.80	0.64
1:C:30:ASN:HD22	1:C:30:ASN:H	1.43	0.64
1:D:19:GLN:HB2	1:D:163:ASN:ND2	2.12	0.64
2:H:232:LYS:HD2	2:H:232:LYS:N	2.11	0.64
1:K:168:ILE:HD12	1:K:168:ILE:H	1.63	0.64
1:L:79:ALA:HB1	1:L:110:GLY:HA2	1.80	0.64
2:F:123:ALA:HA	2:F:127:ALA:CB	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:152:PRO:O	2:G:154:ALA:C	2.41	0.64
2:E:116:ILE:O	2:E:120:ARG:HB2	1.98	0.64
1:D:34:VAL:HG12	1:D:169:GLU:HG3	1.80	0.64
2:G:122:ARG:CZ	2:G:126:LEU:HD21	2.28	0.64
2:H:167:GLN:O	2:H:168:LEU:HB3	1.98	0.64
1:A:7:ARG:HB2	1:A:12:VAL:HG23	1.80	0.63
1:A:84:THR:HG23	1:A:85:ASP:H	1.63	0.63
1:A:88:LEU:H	1:A:88:LEU:HD12	1.63	0.63
1:C:28:LYS:HD2	1:D:113:VAL:HG13	1.79	0.63
1:I:67:HIS:CD2	1:I:73:LYS:HD2	2.33	0.63
2:G:408:TYR:HB2	2:H:29:ILE:HD11	1.80	0.63
2:E:152:PRO:HB2	2:E:156:ARG:CB	2.25	0.63
2:E:311:GLN:CA	2:E:311:GLN:HE21	2.11	0.63
2:E:375:ARG:CZ	2:E:422:ALA:HB1	2.27	0.63
2:F:147:GLU:O	2:F:151:GLU:HG2	1.99	0.63
2:F:236:PRO:HG2	2:F:237:GLU:H	1.64	0.63
2:F:132:LEU:HD11	2:F:160:ARG:CG	2.27	0.63
2:F:218:ILE:C	2:F:220:ASP:H	2.06	0.63
2:F:235:ASN:HB2	2:F:236:PRO:HD2	1.81	0.63
1:C:83:ARG:HB3	1:C:83:ARG:CZ	2.29	0.63
2:H:174:GLU:HA	2:H:212:LYS:HB3	1.81	0.63
1:K:83:ARG:HH11	1:K:83:ARG:HG3	1.63	0.63
1:J:28:LYS:NZ	1:J:30:ASN:ND2	2.47	0.63
1:K:36:ARG:O	1:K:37:LEU:HD23	1.98	0.63
1:A:67:HIS:HD2	1:A:73:LYS:HD2	1.62	0.63
2:F:96:VAL:HG11	2:F:281:LEU:HD12	1.80	0.63
1:I:8:ARG:O	1:I:11:HIS:HB2	1.99	0.63
2:H:312:ILE:HD13	2:H:312:ILE:N	2.08	0.63
2:F:132:LEU:HD23	2:F:135:LEU:HD12	1.80	0.63
2:H:315:PRO:O	2:H:318:LEU:HB2	1.99	0.63
1:L:6:VAL:HG21	1:L:147:ILE:HG22	1.79	0.63
2:G:88:GLU:CB	2:H:90:GLY:HA2	2.25	0.63
2:G:375:ARG:CZ	2:G:422:ALA:HB1	2.29	0.63
2:F:27:VAL:CG1	2:F:70:LEU:HG	2.30	0.62
1:I:36:ARG:HB3	1:I:36:ARG:HH11	1.63	0.62
2:F:147:GLU:CG	2:F:150:GLN:NE2	2.62	0.62
2:F:211:GLN:NE2	2:F:212:LYS:H	1.97	0.62
2:F:31:LEU:HD11	2:F:74:ALA:HB2	1.81	0.62
2:F:101:ARG:O	2:F:104:THR:HB	1.99	0.62
2:F:389:ASN:C	2:F:389:ASN:HD22	2.06	0.62
1:D:37:LEU:HD11	1:D:60:PHE:HD2	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:95:LEU:HB2	1:L:106:ILE:HB	1.81	0.62
1:D:28:LYS:HZ2	1:D:30:ASN:ND2	1.96	0.62
2:F:401:ARG:NH2	2:F:442:ILE:HG13	2.15	0.62
2:H:123:ALA:HA	2:H:127:ALA:CB	2.24	0.62
1:B:28:LYS:HD3	1:B:31:VAL:HG22	1.82	0.62
2:F:108:VAL:HG21	2:F:294:HIS:CD2	2.34	0.62
2:F:163:LEU:HD11	2:F:222:MET:HE1	1.82	0.62
1:J:86:ARG:HA	1:J:89:ARG:NH1	2.14	0.62
2:G:145:GLN:C	2:G:147:GLU:H	2.05	0.62
2:G:170:ASP:HB3	2:G:217:LYS:HD3	1.81	0.62
1:K:28:LYS:HE2	1:K:30:ASN:ND2	2.15	0.62
1:L:152:LEU:HD13	1:L:166:HIS:ND1	2.13	0.62
2:E:130:ARG:HB2	2:E:130:ARG:CZ	2.30	0.62
2:E:389:ASN:HD22	2:E:391:GLY:H	1.46	0.62
1:A:65:GLU:OE1	2:E:141:ASN:HB3	2.00	0.62
2:E:312:ILE:HD13	2:E:312:ILE:N	2.09	0.62
2:E:312:ILE:HG12	2:E:313:ALA:N	2.14	0.62
2:F:108:VAL:C	2:F:110:MET:N	2.58	0.62
2:F:219:LYS:O	2:F:223:LYS:HD3	2.00	0.62
2:G:362:GLU:HG2	2:G:410:ALA:CB	2.30	0.62
2:H:239:LEU:HD23	2:H:240:LYS:N	2.14	0.62
1:B:46:PHE:CE2	1:B:53:ALA:HB2	2.35	0.61
2:F:129:GLU:HB2	2:F:130:ARG:NH1	2.15	0.61
2:F:218:ILE:C	2:F:220:ASP:N	2.57	0.61
2:E:140:LYS:H	2:E:140:LYS:HD3	1.66	0.61
1:I:87:MET:HE1	1:J:84:THR:HA	1.82	0.61
1:I:87:MET:CE	1:J:84:THR:HA	2.30	0.61
2:H:221:ALA:O	2:H:225:LEU:HD23	2.00	0.61
1:L:55:THR:O	1:L:58:GLU:HB3	2.00	0.61
2:H:81:VAL:HG11	2:H:99:ILE:HG12	1.82	0.61
2:F:362:GLU:HG2	2:F:410:ALA:HB1	1.80	0.61
2:G:140:LYS:HD3	2:G:140:LYS:H	1.65	0.61
2:H:19:GLY:O	2:H:24:LYS:HE3	2.00	0.61
2:H:20:GLN:O	2:H:24:LYS:HG3	2.00	0.61
1:D:38:TYR:HE1	1:D:65:GLU:HB3	1.64	0.61
1:D:86:ARG:HA	1:D:89:ARG:CZ	2.30	0.61
1:B:168:ILE:HD12	1:B:168:ILE:N	2.15	0.61
2:E:293:LYS:HG3	2:E:294:HIS:HD2	1.65	0.61
2:G:108:VAL:HG21	2:G:294:HIS:ND1	2.16	0.61
2:G:148:GLN:HA	2:G:151:GLU:HG2	1.82	0.61
2:H:393:ARG:HG2	2:H:393:ARG:HH11	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ARG:NH1	1:A:142:LEU:O	2.23	0.61
1:L:1:THR:HB	1:L:33:LYS:NZ	2.16	0.61
1:A:88:LEU:H	1:A:88:LEU:CD1	2.13	0.61
2:E:152:PRO:CB	2:E:156:ARG:H	2.13	0.61
2:F:116:ILE:O	2:F:120:ARG:HB2	2.01	0.61
2:F:170:ASP:HA	2:F:217:LYS:HA	1.81	0.61
2:G:345:THR:HG22	2:G:352:THR:HG21	1.82	0.61
2:H:123:ALA:CA	2:H:127:ALA:HB3	2.25	0.61
1:C:95:LEU:HB2	1:C:106:ILE:HB	1.83	0.60
2:G:88:GLU:CD	2:H:90:GLY:HA3	2.26	0.60
1:A:105:ILE:CD1	1:A:120:ILE:HG23	2.30	0.60
1:B:65:GLU:OE1	2:F:143:TRP:CD2	2.55	0.60
1:D:13:VAL:HG12	1:D:170:GLU:HA	1.82	0.60
1:D:86:ARG:HA	1:D:89:ARG:NH1	2.15	0.60
2:H:262:CYS:SG	2:H:318:LEU:HD13	2.41	0.60
1:J:168:ILE:HD12	1:J:168:ILE:N	2.16	0.60
2:G:109:LYS:HB2	2:H:296:MET:CG	2.21	0.60
2:G:214:ARG:NH2	2:H:233:LEU:HD13	2.16	0.60
2:G:242:ASP:HA	2:G:245:ASP:OD1	2.02	0.60
2:H:127:ALA:HA	2:H:130:ARG:NH2	2.15	0.60
1:J:19:GLN:HB2	1:J:163:ASN:HD22	1.65	0.60
2:H:63:LYS:HE2	2:H:307:SER:OG	2.01	0.60
2:F:312:ILE:HG12	2:F:313:ALA:N	2.15	0.60
2:H:108:VAL:HG21	2:H:294:HIS:HD2	1.67	0.60
2:H:375:ARG:HB3	2:H:425:VAL:HG11	1.83	0.60
1:B:70:HIS:HE1	1:B:72:VAL:HB	1.67	0.60
1:C:55:THR:O	1:C:58:GLU:HB3	2.02	0.60
1:D:14:ILE:HD13	1:D:43:ILE:HG13	1.83	0.60
2:H:25:ARG:O	2:H:29:ILE:HG12	2.02	0.60
2:H:132:LEU:HD23	2:H:135:LEU:CD1	2.31	0.60
2:H:211:GLN:NE2	2:H:212:LYS:H	2.00	0.60
2:F:212:LYS:NZ	2:F:212:LYS:HB2	2.17	0.60
2:G:389:ASN:HD22	2:G:391:GLY:H	1.49	0.60
2:E:168:LEU:HA	2:E:219:LYS:HB3	1.84	0.60
2:F:19:GLY:O	2:F:24:LYS:HE3	2.02	0.60
2:F:130:ARG:CG	2:F:225:LEU:HD11	2.32	0.60
1:C:94:LEU:CD2	1:C:107:THR:HG22	2.31	0.60
1:D:14:ILE:HD13	1:D:43:ILE:HG12	1.83	0.60
2:G:219:LYS:O	2:G:223:LYS:HE3	2.01	0.60
1:K:136:LEU:HB3	1:K:147:ILE:HD12	1.82	0.60
1:L:109:ASN:O	1:L:110:GLY:C	2.45	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:LYS:HZ2	1:B:89:ARG:NH2	1.98	0.60
2:E:33:ASN:ND2	2:E:36:ARG:HD2	2.17	0.60
2:E:168:LEU:HD23	2:E:219:LYS:HB3	1.82	0.60
2:F:86:PHE:O	2:F:89:VAL:HG22	2.02	0.60
1:I:14:ILE:HD12	1:I:43:ILE:HG13	1.84	0.60
2:H:311:GLN:NE2	2:H:311:GLN:HA	2.17	0.60
1:L:174:LYS:HA	1:L:174:LYS:HZ2	1.65	0.60
1:A:77:GLU:O	1:A:80:LYS:HB2	2.01	0.60
2:F:147:GLU:HG2	2:F:150:GLN:NE2	2.16	0.60
2:F:229:GLU:OE2	2:F:232:LYS:HD2	2.02	0.60
2:G:88:GLU:HB3	2:H:90:GLY:CA	2.25	0.60
2:G:131:ILE:HD11	2:G:218:ILE:HG12	1.83	0.60
2:H:337:THR:O	2:H:341:GLU:HG3	2.02	0.60
2:E:108:VAL:C	2:E:110:MET:H	2.09	0.59
2:E:131:ILE:HD11	2:E:218:ILE:CG1	2.30	0.59
2:E:432:LEU:H	2:E:432:LEU:HD12	1.67	0.59
2:F:12:GLU:HG2	2:F:73:LEU:CD1	2.32	0.59
2:F:163:LEU:HD21	2:F:222:MET:HE1	1.84	0.59
1:I:105:ILE:CD1	1:I:120:ILE:HG23	2.31	0.59
2:G:142:ASN:HB2	2:G:149:GLN:NE2	2.15	0.59
2:G:174:GLU:HA	2:G:213:ALA:H	1.67	0.59
2:H:218:ILE:O	2:H:222:MET:HB3	2.02	0.59
2:H:291:SER:HA	2:H:296:MET:HE2	1.84	0.59
2:E:33:ASN:HD22	2:E:36:ARG:HD2	1.66	0.59
2:E:130:ARG:CD	2:E:225:LEU:HD11	2.33	0.59
2:F:59:THR:CG2	2:F:393:ARG:HH21	2.13	0.59
1:I:83:ARG:NH1	1:I:83:ARG:HG2	2.17	0.59
2:G:153:SER:CA	2:G:157:GLN:HG3	2.32	0.59
2:H:212:LYS:HB2	2:H:212:LYS:NZ	2.18	0.59
1:L:30:ASN:HD22	1:L:30:ASN:N	1.96	0.59
2:F:219:LYS:C	2:F:223:LYS:HD3	2.27	0.59
2:H:311:GLN:CA	2:H:311:GLN:HE21	2.15	0.59
2:F:55:MET:HE3	2:F:305:ILE:HG21	1.83	0.59
2:H:108:VAL:HG21	2:H:294:HIS:CD2	2.36	0.59
2:H:264:ARG:NE	2:H:265:GLY:H	1.99	0.59
2:H:169:ASP:O	2:H:218:ILE:HG13	2.02	0.59
1:A:39:ASN:OD1	2:E:143:TRP:CZ2	2.55	0.59
2:F:340:PHE:O	2:F:344:LEU:HD22	2.03	0.59
2:F:389:ASN:HD22	2:F:391:GLY:H	1.51	0.59
1:J:38:TYR:HB2	1:J:64:LEU:CD1	2.33	0.59
2:G:311:GLN:CA	2:G:311:GLN:HE21	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:312:ILE:HG12	2:G:313:ALA:N	2.18	0.59
2:F:351:ILE:HD13	2:F:351:ILE:N	2.13	0.59
1:J:6:VAL:HG12	1:J:7:ARG:N	2.17	0.59
2:H:41:ASN:HD22	2:H:41:ASN:C	2.10	0.59
1:J:63:LYS:HA	1:J:66:MET:HE3	1.85	0.59
2:H:335:LEU:HD22	2:H:339:ASP:HB3	1.84	0.59
1:L:10:GLY:HA2	1:L:173:TYR:CZ	2.38	0.59
2:E:174:GLU:HA	2:E:212:LYS:HB3	1.83	0.59
2:F:65:GLU:HG3	3:F:1450:ADP:H2'	1.84	0.59
1:I:17:ASP:HA	1:I:165:PHE:O	2.03	0.59
1:J:62:ARG:HA	1:J:65:GLU:HG3	1.83	0.59
2:H:12:GLU:HG2	2:H:73:LEU:HD11	1.84	0.59
1:J:98:ALA:CB	1:J:103:SER:HB3	2.33	0.59
1:K:54:PHE:O	1:K:58:GLU:HB2	2.02	0.59
2:E:89:VAL:HG12	2:E:93:GLY:HA3	1.84	0.58
2:E:96:VAL:HG11	2:E:281:LEU:HD12	1.85	0.58
2:F:130:ARG:HH21	2:F:229:GLU:HG3	1.67	0.58
1:L:8:ARG:NH2	1:L:137:LEU:HD12	2.18	0.58
1:L:83:ARG:HH11	1:L:83:ARG:CB	2.01	0.58
2:F:366:ILE:HD12	2:F:418:ILE:HB	1.84	0.58
1:C:100:GLU:OE2	1:C:173:TYR:HB2	2.04	0.58
1:D:14:ILE:HD11	1:D:98:ALA:HB3	1.84	0.58
1:I:87:MET:HE1	1:J:84:THR:CG2	2.28	0.58
1:J:63:LYS:HD3	1:J:66:MET:HE3	1.85	0.58
1:L:57:PHE:O	1:L:61:GLU:HG2	2.02	0.58
1:B:86:ARG:HA	1:B:89:ARG:NH1	2.18	0.58
2:E:124:GLU:HA	2:E:127:ALA:CB	2.33	0.58
2:E:142:ASN:HB2	2:E:149:GLN:HE22	1.67	0.58
2:E:362:GLU:HG2	2:E:410:ALA:HB1	1.84	0.58
2:F:131:ILE:HD11	2:F:218:ILE:HD13	1.83	0.58
1:C:149:GLU:CD	1:C:168:ILE:HD11	2.27	0.58
1:J:53:ALA:C	1:J:55:THR:H	2.11	0.58
2:H:23:ALA:HB1	2:H:55:MET:HE3	1.84	0.58
1:B:63:LYS:HD3	1:B:66:MET:HE3	1.85	0.58
2:H:401:ARG:NH2	2:H:442:ILE:HG13	2.18	0.58
1:A:90:LYS:NZ	1:B:89:ARG:NH2	2.51	0.58
2:G:58:PRO:HG2	2:G:61:VAL:HG11	1.84	0.58
2:G:116:ILE:O	2:G:120:ARG:HB2	2.03	0.58
2:E:89:VAL:HA	2:E:93:GLY:N	2.17	0.58
2:E:382:GLN:O	2:E:386:SER:HB3	2.03	0.58
2:F:174:GLU:C	2:F:211:GLN:HB2	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:109:ASN:O	1:I:110:GLY:C	2.46	0.58
1:L:143:SER:OG	1:L:146:GLU:HG3	2.03	0.58
1:B:115:PRO:HG3	1:B:120:ILE:HG12	1.85	0.58
1:D:159:CYS:HB3	1:D:162:THR:HB	1.84	0.58
1:L:14:ILE:HD12	1:L:43:ILE:HG12	1.85	0.58
2:G:389:ASN:HD22	2:G:390:ILE:N	2.02	0.58
1:L:15:ALA:HB1	1:L:152:LEU:HD12	1.86	0.58
1:A:149:GLU:HG2	1:A:168:ILE:HD11	1.85	0.58
2:E:132:LEU:HD11	2:E:160:ARG:CG	2.32	0.58
1:C:30:ASN:H	1:C:30:ASN:ND2	2.01	0.58
1:D:73:LYS:HA	1:D:76:VAL:HG12	1.85	0.58
2:G:217:LYS:HG3	2:G:219:LYS:HZ1	1.69	0.58
2:H:345:THR:HG21	2:H:373:ILE:HD13	1.85	0.58
1:K:59:LEU:HD11	1:K:63:LYS:HE2	1.86	0.58
1:B:141:GLU:HA	1:B:141:GLU:OE2	2.04	0.58
1:D:67:HIS:CD2	1:D:73:LYS:HE2	2.38	0.58
1:I:117:ASN:O	1:I:118:ASP:HB2	2.03	0.58
2:E:222:MET:O	2:E:226:ILE:HG12	2.04	0.57
2:F:76:ALA:HB1	2:F:250:HIS:O	2.03	0.57
2:F:123:ALA:CA	2:F:127:ALA:HB3	2.33	0.57
2:H:52:ASN:HB2	2:H:325:ARG:O	2.04	0.57
2:H:351:ILE:H	2:H:351:ILE:CD1	2.07	0.57
1:L:64:LEU:O	1:L:69:GLY:N	2.36	0.57
1:A:67:HIS:CD2	1:A:73:LYS:HD2	2.38	0.57
2:F:311:GLN:HE21	2:F:311:GLN:CA	2.17	0.57
2:F:413:LEU:O	2:F:416:GLN:HG3	2.03	0.57
1:D:170:GLU:HG2	1:D:171:LEU:H	1.69	0.57
2:G:31:LEU:HD12	2:G:70:LEU:CD2	2.34	0.57
2:G:92:VAL:HG21	2:H:92:VAL:CA	2.34	0.57
2:E:172:GLU:HG3	2:E:214:ARG:O	2.05	0.57
2:G:131:ILE:O	2:G:134:VAL:HG12	2.04	0.57
1:A:10:GLY:HA3	1:A:174:LYS:CA	2.33	0.57
1:A:12:VAL:HG12	1:A:171:LEU:HB3	1.86	0.57
1:B:159:CYS:HB3	1:B:162:THR:HB	1.87	0.57
1:J:38:TYR:CD2	1:J:41:LYS:HD2	2.39	0.57
1:J:60:PHE:CD1	1:J:78:LEU:HD22	2.39	0.57
2:G:170:ASP:CB	2:G:217:LYS:HD3	2.34	0.57
1:A:37:LEU:HD21	1:A:57:PHE:HB3	1.86	0.57
2:E:131:ILE:CD1	2:E:218:ILE:HG12	2.31	0.57
2:F:140:LYS:O	2:F:141:ASN:HB3	2.05	0.57
2:F:151:GLU:CB	2:F:152:PRO:CD	2.82	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:122:ARG:NH1	2:G:126:LEU:HD21	2.20	0.57
1:B:60:PHE:HD1	1:B:78:LEU:HD22	1.69	0.57
1:C:71:LEU:HD12	1:C:104:LEU:HD21	1.86	0.57
2:F:223:LYS:HA	2:F:226:ILE:CG1	2.31	0.57
2:F:258:ILE:HG22	2:F:307:SER:O	2.05	0.57
2:G:257:GLU:HG3	2:G:257:GLU:O	2.05	0.57
2:H:211:GLN:HE21	2:H:212:LYS:H	1.52	0.57
1:D:36:ARG:C	1:D:37:LEU:HD23	2.30	0.57
2:G:89:VAL:HG12	2:G:93:GLY:C	2.29	0.57
2:G:130:ARG:HB2	2:G:130:ARG:CZ	2.35	0.57
2:G:145:GLN:HG3	2:G:148:GLN:HG3	1.87	0.57
2:G:240:LYS:HE3	2:G:294:HIS:O	2.04	0.57
2:H:145:GLN:CA	2:H:145:GLN:HE21	2.17	0.57
2:H:432:LEU:HD12	2:H:432:LEU:N	2.18	0.57
1:A:86:ARG:HA	1:A:89:ARG:NH2	2.20	0.57
1:C:10:GLY:HA2	1:C:173:TYR:CZ	2.39	0.57
1:D:28:LYS:NZ	1:D:30:ASN:ND2	2.52	0.57
2:G:293:LYS:HG3	2:G:294:HIS:HD2	1.68	0.57
2:H:103:LEU:O	2:H:107:ALA:HB2	2.04	0.57
2:E:145:GLN:HG3	2:E:148:GLN:HG3	1.86	0.57
2:F:145:GLN:HB2	2:F:148:GLN:CG	2.35	0.57
1:C:7:ARG:HB2	1:C:12:VAL:HG23	1.87	0.57
1:D:46:PHE:CE2	1:D:53:ALA:HB2	2.39	0.57
1:I:4:VAL:HG11	1:I:129:ALA:HB1	1.86	0.57
2:G:312:ILE:HG12	2:G:313:ALA:H	1.69	0.57
2:G:441:PHE:HA	2:H:315:PRO:HG2	1.87	0.57
2:H:108:VAL:C	2:H:110:MET:N	2.58	0.57
2:H:168:LEU:HD12	2:H:217:LYS:HD2	1.87	0.57
1:A:65:GLU:OE1	2:E:141:ASN:HB2	2.05	0.56
2:F:52:ASN:HB2	2:F:325:ARG:O	2.05	0.56
1:C:105:ILE:HD11	1:C:120:ILE:HG23	1.87	0.56
1:B:8:ARG:NH1	1:B:142:LEU:O	2.39	0.56
2:E:170:ASP:HB3	2:E:217:LYS:HD3	1.87	0.56
2:F:89:VAL:HA	2:F:92:VAL:O	2.05	0.56
1:I:88:LEU:CD1	1:I:88:LEU:H	2.18	0.56
2:G:27:VAL:HG13	2:G:70:LEU:HG	1.88	0.56
2:G:174:GLU:CB	2:G:211:GLN:HG3	2.21	0.56
2:G:269:GLY:N	2:G:270:PRO:HD2	2.21	0.56
1:L:28:LYS:HD3	1:L:31:VAL:HG22	1.88	0.56
1:A:88:LEU:HD12	1:A:88:LEU:N	2.21	0.56
1:B:152:LEU:HD13	1:B:166:HIS:CE1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:89:VAL:HA	2:F:92:VAL:C	2.30	0.56
2:F:355:TYR:CD1	2:F:403:MET:HE2	2.40	0.56
2:G:122:ARG:NE	2:G:126:LEU:HD21	2.21	0.56
2:H:145:GLN:C	2:H:147:GLU:H	2.12	0.56
1:K:71:LEU:C	1:K:71:LEU:HD13	2.31	0.56
2:F:168:LEU:O	2:F:217:LYS:HD2	2.04	0.56
1:D:68:GLN:O	1:D:70:HIS:N	2.38	0.56
2:G:147:GLU:HA	2:G:150:GLN:CG	2.34	0.56
2:H:171:LYS:HZ2	2:H:218:ILE:HD11	1.68	0.56
2:E:148:GLN:HA	2:E:151:GLU:HG2	1.87	0.56
2:F:211:GLN:HE21	2:F:212:LYS:N	2.03	0.56
2:G:86:PHE:O	2:G:89:VAL:HG22	2.06	0.56
2:G:89:VAL:HG12	2:G:93:GLY:CA	2.35	0.56
2:G:211:GLN:HG2	2:G:212:LYS:N	2.18	0.56
2:H:228:GLU:O	2:H:232:LYS:HE2	2.05	0.56
2:H:351:ILE:HD13	2:H:351:ILE:N	2.10	0.56
2:E:257:GLU:HG3	2:E:257:GLU:O	2.06	0.56
1:D:18:GLY:C	1:D:163:ASN:HD21	2.12	0.56
1:I:150:LYS:O	1:I:154:ILE:HG12	2.04	0.56
1:J:59:LEU:HG	1:J:78:LEU:HD13	1.88	0.56
1:K:86:ARG:HA	1:K:89:ARG:HH12	1.69	0.56
2:E:86:PHE:O	2:E:89:VAL:HG22	2.05	0.56
2:E:131:ILE:HD11	2:E:218:ILE:CD1	2.35	0.56
1:C:136:LEU:HB3	1:C:147:ILE:CD1	2.35	0.56
1:J:120:ILE:HD12	1:J:120:ILE:N	2.21	0.56
2:H:95:GLU:H	2:H:95:GLU:CD	2.14	0.56
2:F:292:THR:C	2:F:294:HIS:H	2.14	0.56
1:J:98:ALA:HB2	1:J:103:SER:HB3	1.87	0.56
2:G:312:ILE:HD13	2:G:312:ILE:N	2.18	0.56
2:H:163:LEU:HD21	2:H:222:MET:HE1	1.88	0.56
2:H:244:ILE:HD11	2:H:294:HIS:O	2.06	0.56
2:E:311:GLN:NE2	2:E:311:GLN:HA	2.21	0.55
2:G:91:TYR:C	2:G:92:VAL:HG22	2.31	0.55
2:H:389:ASN:HD22	2:H:390:ILE:N	2.03	0.55
2:F:32:ARG:O	2:F:36:ARG:HG3	2.06	0.55
2:G:60:GLY:N	2:G:393:ARG:NH2	2.54	0.55
1:L:36:ARG:HH12	1:L:40:ASP:C	2.14	0.55
2:E:108:VAL:HG21	2:E:294:HIS:ND1	2.22	0.55
2:F:130:ARG:HG2	2:F:225:LEU:HD11	1.88	0.55
2:G:37:ARG:HB3	2:G:37:ARG:HH11	1.72	0.55
2:G:89:VAL:HA	2:G:93:GLY:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:92:VAL:HG21	2:H:92:VAL:N	2.20	0.55
2:H:312:ILE:HG12	2:H:313:ALA:N	2.21	0.55
2:F:151:GLU:HB2	2:F:152:PRO:HD2	1.88	0.55
1:I:33:LYS:HA	1:I:46:PHE:CE1	2.41	0.55
2:G:52:ASN:HB2	2:G:325:ARG:O	2.06	0.55
2:E:130:ARG:CG	2:E:225:LEU:HD11	2.36	0.55
2:E:160:ARG:HH12	2:E:164:ARG:HH22	1.52	0.55
2:G:147:GLU:HG3	2:G:150:GLN:CD	2.32	0.55
1:A:149:GLU:OE1	1:A:168:ILE:HD11	2.06	0.55
1:B:150:LYS:O	1:B:154:ILE:HG12	2.07	0.55
2:E:211:GLN:O	2:E:212:LYS:HB2	2.06	0.55
2:E:242:ASP:HA	2:E:245:ASP:OD1	2.06	0.55
1:D:13:VAL:C	1:D:14:ILE:HD12	2.32	0.55
2:H:64:THR:HG21	2:H:68:ARG:NH1	2.21	0.55
2:E:109:LYS:HG3	2:E:109:LYS:O	2.05	0.55
2:E:212:LYS:CD	2:E:216:LEU:HD21	2.27	0.55
2:F:217:LYS:HB2	2:F:217:LYS:HZ3	1.71	0.55
1:I:105:ILE:HD11	1:I:120:ILE:HG23	1.89	0.55
1:L:8:ARG:HG2	1:L:9:ASN:ND2	2.22	0.55
2:E:441:PHE:CZ	2:F:314:LYS:HG2	2.42	0.55
1:L:83:ARG:HB3	1:L:83:ARG:CZ	2.36	0.55
1:A:33:LYS:HA	1:A:46:PHE:CE1	2.42	0.55
2:E:151:GLU:CB	2:E:152:PRO:CD	2.84	0.55
2:G:4:MET:HE1	2:G:73:LEU:HD11	1.89	0.55
2:G:412:ASP:CG	2:H:7:ARG:HE	2.14	0.55
1:K:51:ALA:HB3	1:L:110:GLY:O	2.07	0.55
1:B:72:VAL:O	1:B:75:ALA:HB3	2.07	0.54
2:F:95:GLU:CD	2:F:95:GLU:H	2.15	0.54
2:H:151:GLU:HB2	2:H:152:PRO:CD	2.37	0.54
1:K:86:ARG:HG3	1:K:89:ARG:HH22	1.71	0.54
2:E:91:TYR:C	2:E:92:VAL:HG22	2.32	0.54
1:J:59:LEU:HD12	1:J:59:LEU:O	2.06	0.54
2:H:211:GLN:HE21	2:H:212:LYS:N	2.05	0.54
2:E:134:VAL:HG13	2:E:171:LYS:HD3	1.88	0.54
2:E:152:PRO:CB	2:E:156:ARG:HB2	2.29	0.54
2:E:165:GLU:HG2	2:E:166:GLY:N	2.23	0.54
2:F:390:ILE:O	2:F:393:ARG:HB2	2.07	0.54
1:D:86:ARG:HA	1:D:89:ARG:NH2	2.22	0.54
2:G:131:ILE:CD1	2:G:218:ILE:HG12	2.37	0.54
2:E:103:LEU:HD13	2:E:247:VAL:HG13	1.90	0.54
2:F:389:ASN:HD22	2:F:390:ILE:N	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:442:ILE:O	2:G:442:ILE:HG22	2.07	0.54
2:H:217:LYS:HB2	2:H:217:LYS:HZ3	1.72	0.54
2:H:362:GLU:HG3	2:H:411:SER:HA	1.88	0.54
1:L:37:LEU:HB2	1:L:61:GLU:OE1	2.07	0.54
1:D:143:SER:OG	1:D:146:GLU:HG3	2.06	0.54
1:J:71:LEU:HD11	1:J:104:LEU:HD21	1.90	0.54
2:H:174:GLU:CA	2:H:212:LYS:HB3	2.38	0.54
2:E:108:VAL:C	2:E:110:MET:N	2.63	0.54
2:E:147:GLU:HA	2:E:150:GLN:CG	2.36	0.54
2:E:212:LYS:HB2	2:E:212:LYS:NZ	2.21	0.54
2:G:147:GLU:CA	2:G:150:GLN:HG3	2.37	0.54
2:G:264:ARG:CZ	2:G:265:GLY:H	2.20	0.54
2:H:122:ARG:NH1	2:H:126:LEU:HD23	2.12	0.54
2:E:89:VAL:HG12	2:E:93:GLY:C	2.32	0.54
2:F:74:ALA:O	2:F:75:ASN:C	2.51	0.54
2:G:108:VAL:C	2:G:110:MET:H	2.16	0.54
2:G:132:LEU:HB3	2:G:156:ARG:NH1	2.23	0.54
2:G:145:GLN:O	2:G:147:GLU:N	2.41	0.54
2:H:89:VAL:HG11	2:H:94:LYS:O	2.07	0.54
2:H:135:LEU:CD2	2:H:171:LYS:HE2	2.29	0.54
1:K:5:SER:HB3	1:K:120:ILE:HB	1.89	0.54
2:F:135:LEU:HD23	2:F:171:LYS:HE2	1.89	0.54
1:C:43:ILE:O	1:C:43:ILE:HG13	2.08	0.54
1:J:13:VAL:HG12	1:J:170:GLU:HG3	1.90	0.54
2:G:127:ALA:HA	2:G:130:ARG:HH22	1.73	0.54
2:G:168:LEU:HD12	2:G:219:LYS:HB3	1.89	0.54
2:H:12:GLU:HG2	2:H:73:LEU:CD1	2.38	0.54
2:H:167:GLN:NE2	2:H:219:LYS:NZ	2.56	0.54
2:H:413:LEU:O	2:H:416:GLN:HG3	2.08	0.54
2:H:435:ASP:CG	2:H:438:LEU:HB2	2.32	0.54
1:B:3:ILE:HB	1:B:122:ILE:HG12	1.90	0.54
2:F:345:THR:HG22	2:F:352:THR:HG21	1.89	0.54
2:F:432:LEU:N	2:F:432:LEU:HD12	2.22	0.54
1:C:91:LEU:HD12	1:C:91:LEU:O	2.07	0.54
1:D:70:HIS:CE1	1:D:72:VAL:HB	2.43	0.54
2:H:96:VAL:HG21	2:H:280:ASP:HB3	1.90	0.54
2:H:210:LYS:N	2:H:210:LYS:HD3	2.23	0.54
2:H:292:THR:C	2:H:294:HIS:H	2.16	0.54
1:K:64:LEU:HD23	1:K:74:ALA:HB3	1.89	0.54
1:A:28:LYS:HZ1	1:A:30:ASN:HD21	1.54	0.53
2:E:335:LEU:HD22	2:E:339:ASP:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:167:GLN:O	2:F:168:LEU:HB3	2.07	0.53
1:D:30:ASN:N	1:D:30:ASN:ND2	2.55	0.53
2:G:134:VAL:CG1	2:G:171:LYS:HD3	2.38	0.53
2:G:212:LYS:C	2:G:214:ARG:H	2.15	0.53
2:H:340:PHE:O	2:H:344:LEU:HD22	2.07	0.53
1:L:30:ASN:ND2	1:L:30:ASN:N	2.50	0.53
1:L:73:LYS:HZ2	1:L:77:GLU:HG2	1.73	0.53
1:B:10:GLY:HA2	1:B:173:TYR:CZ	2.43	0.53
2:E:134:VAL:CG1	2:E:171:LYS:HD3	2.39	0.53
2:F:239:LEU:HD23	2:F:240:LYS:N	2.23	0.53
1:D:43:ILE:HD12	1:D:171:LEU:HD22	1.91	0.53
1:D:73:LYS:HZ2	1:D:77:GLU:HG2	1.71	0.53
1:D:99:ASP:OD1	1:D:101:THR:N	2.40	0.53
1:I:10:GLY:HA3	1:I:174:LYS:CA	2.34	0.53
1:J:3:ILE:HB	1:J:122:ILE:HG12	1.91	0.53
1:J:70:HIS:HE1	1:J:72:VAL:HB	1.73	0.53
2:G:95:GLU:H	2:G:95:GLU:CD	2.15	0.53
1:B:86:ARG:HA	1:B:89:ARG:HE	1.72	0.53
2:E:441:PHE:CE2	2:F:314:LYS:HG2	2.44	0.53
1:I:87:MET:HE1	1:J:84:THR:CA	2.39	0.53
2:G:145:GLN:C	2:G:147:GLU:N	2.66	0.53
2:G:268:SER:HA	2:G:271:ASP:OD2	2.09	0.53
2:H:33:ASN:ND2	2:H:36:ARG:HD2	2.24	0.53
2:H:119:ASN:ND2	2:H:233:LEU:HD23	2.24	0.53
2:H:420:ILE:N	2:H:420:ILE:HD12	2.24	0.53
1:L:68:GLN:O	1:L:70:HIS:N	2.41	0.53
2:E:34:ARG:CZ	2:E:250:HIS:HA	2.38	0.53
2:F:173:ILE:HD13	2:F:173:ILE:N	2.23	0.53
1:C:64:LEU:HB3	1:C:69:GLY:HA2	1.90	0.53
1:I:125:GLY:HA2	1:I:128:TYR:CD2	2.43	0.53
1:K:115:PRO:HB2	1:K:119:LEU:O	2.08	0.53
1:A:1:THR:HB	1:A:33:LYS:HZ2	1.72	0.53
1:A:13:VAL:CG1	1:A:170:GLU:HG3	2.29	0.53
2:E:58:PRO:HG2	2:E:61:VAL:HG11	1.91	0.53
2:F:269:GLY:N	2:F:270:PRO:HD2	2.22	0.53
2:F:315:PRO:O	2:F:318:LEU:HB2	2.08	0.53
2:H:167:GLN:CD	2:H:219:LYS:HZ1	2.16	0.53
2:H:223:LYS:N	2:H:223:LYS:HD2	2.23	0.53
1:K:148:ALA:O	1:K:152:LEU:HB2	2.09	0.53
2:E:145:GLN:C	2:E:147:GLU:H	2.16	0.53
1:I:80:LYS:O	1:I:84:THR:HG22	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:71:LEU:CD1	1:J:104:LEU:HD21	2.37	0.53
2:G:231:ALA:C	2:G:233:LEU:N	2.67	0.53
2:G:349:ALA:CB	2:H:44:LEU:HD23	2.39	0.53
2:H:91:TYR:O	2:H:92:VAL:HG22	2.08	0.53
2:H:255:ILE:HD11	2:H:304:PHE:HD2	1.74	0.53
1:K:17:ASP:HA	1:K:165:PHE:O	2.09	0.53
1:K:91:LEU:HD12	1:K:91:LEU:O	2.09	0.53
1:A:10:GLY:HA2	1:A:173:TYR:CD1	2.42	0.53
1:B:104:LEU:HD23	1:B:104:LEU:N	2.23	0.53
2:F:103:LEU:CD1	2:F:247:VAL:HG13	2.38	0.53
2:G:432:LEU:HD12	2:G:432:LEU:N	2.23	0.53
1:K:83:ARG:HG3	1:K:109:ASN:O	2.09	0.53
1:L:6:VAL:HG21	1:L:147:ILE:CG2	2.38	0.53
1:L:10:GLY:HA2	1:L:173:TYR:CE1	2.43	0.53
2:E:81:VAL:HG11	2:E:99:ILE:HG12	1.90	0.53
2:E:361:THR:HG21	2:F:36:ARG:HA	1.90	0.53
2:E:432:LEU:HD12	2:E:432:LEU:N	2.22	0.53
2:F:41:ASN:HD21	2:F:44:LEU:H	1.57	0.53
1:J:95:LEU:H	1:J:95:LEU:HD12	1.74	0.53
2:G:94:LYS:HA	2:G:94:LYS:CE	2.30	0.53
2:H:5:THR:O	2:H:9:ILE:HG12	2.09	0.53
2:H:358:LEU:O	2:H:361:THR:HB	2.08	0.53
1:L:58:GLU:O	1:L:61:GLU:HB2	2.09	0.53
1:C:152:LEU:HD13	1:C:166:HIS:ND1	2.24	0.53
1:D:56:LEU:HD13	1:D:95:LEU:HD11	1.91	0.53
1:D:83:ARG:HD3	1:D:109:ASN:O	2.09	0.53
1:D:115:PRO:HG3	1:D:120:ILE:CG1	2.39	0.53
2:G:104:THR:HG21	2:G:292:THR:HG21	1.91	0.53
1:K:30:ASN:HD22	1:K:30:ASN:H	1.57	0.53
1:B:136:LEU:HB3	1:B:147:ILE:CD1	2.39	0.53
2:F:54:LEU:HD12	2:F:306:ALA:HB3	1.90	0.53
2:F:103:LEU:O	2:F:107:ALA:HB2	2.09	0.53
2:F:375:ARG:HB3	2:F:425:VAL:HG11	1.91	0.53
1:D:71:LEU:HD13	1:D:71:LEU:C	2.34	0.53
1:D:115:PRO:HB2	1:D:119:LEU:O	2.09	0.53
1:J:30:ASN:C	1:J:30:ASN:HD22	2.17	0.53
1:L:36:ARG:HB3	1:L:36:ARG:HH11	1.74	0.53
1:I:88:LEU:H	1:I:88:LEU:HD12	1.74	0.52
2:G:132:LEU:HD11	2:G:160:ARG:CG	2.39	0.52
2:H:21:ASP:O	2:H:24:LYS:HB2	2.08	0.52
2:H:89:VAL:HA	2:H:92:VAL:C	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:122:ARG:HA	2:H:122:ARG:NE	2.25	0.52
1:L:54:PHE:O	1:L:58:GLU:HB2	2.09	0.52
1:A:99:ASP:C	1:A:99:ASP:OD1	2.52	0.52
2:E:372:GLY:O	2:E:376:ILE:HG13	2.09	0.52
2:F:5:THR:O	2:F:9:ILE:HG12	2.08	0.52
2:F:147:GLU:HG3	2:F:150:GLN:NE2	2.24	0.52
1:I:67:HIS:HD2	1:I:73:LYS:HD2	1.71	0.52
1:J:10:GLY:HA2	1:J:173:TYR:CZ	2.43	0.52
2:G:150:GLN:O	2:G:153:SER:HB2	2.09	0.52
2:G:168:LEU:HA	2:G:219:LYS:CB	2.39	0.52
2:H:160:ARG:HG2	2:H:160:ARG:HH11	1.74	0.52
2:F:73:LEU:HG	2:F:73:LEU:O	2.10	0.52
1:I:28:LYS:NZ	1:I:30:ASN:ND2	2.58	0.52
2:G:92:VAL:HG21	2:H:91:TYR:O	2.09	0.52
2:G:127:ALA:HA	2:G:130:ARG:NH2	2.24	0.52
1:L:28:LYS:NZ	1:L:30:ASN:ND2	2.57	0.52
2:E:131:ILE:HG21	2:E:222:MET:HE1	1.92	0.52
2:F:12:GLU:HG2	2:F:73:LEU:HD13	1.92	0.52
1:I:90:LYS:NZ	1:J:89:ARG:NH2	2.58	0.52
2:F:256:ASP:O	2:F:257:GLU:HG2	2.10	0.52
1:D:64:LEU:HD23	1:D:74:ALA:CB	2.40	0.52
1:I:5:SER:HB2	1:I:14:ILE:HG12	1.92	0.52
2:G:147:GLU:CG	2:G:150:GLN:NE2	2.73	0.52
1:A:152:LEU:HD13	1:A:166:HIS:CE1	2.45	0.52
2:H:152:PRO:HB2	2:H:156:ARG:HB2	1.90	0.52
1:A:80:LYS:O	1:A:81:ASP:C	2.52	0.52
1:K:3:ILE:HD11	1:K:46:PHE:O	2.10	0.52
1:K:28:LYS:HD3	1:K:31:VAL:HG22	1.92	0.52
1:B:38:TYR:HB2	1:B:64:LEU:HD12	1.92	0.52
2:E:269:GLY:N	2:E:270:PRO:HD2	2.25	0.52
2:F:119:ASN:ND2	2:F:233:LEU:HD23	2.24	0.52
2:H:396:HIS:O	2:H:400:GLU:HB2	2.10	0.52
1:K:83:ARG:HB3	1:K:83:ARG:CZ	2.40	0.52
2:E:311:GLN:CA	2:E:311:GLN:NE2	2.73	0.52
2:E:401:ARG:HG2	2:E:443:LEU:HD21	1.91	0.52
2:F:153:SER:HA	2:F:157:GLN:H	1.74	0.52
2:G:108:VAL:C	2:G:110:MET:N	2.67	0.52
2:H:173:ILE:N	2:H:173:ILE:HD13	2.25	0.52
2:H:269:GLY:N	2:H:270:PRO:HD2	2.23	0.52
2:H:366:ILE:HD11	2:H:420:ILE:HD11	1.92	0.52
1:K:19:GLN:HB2	1:K:163:ASN:ND2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:91:LEU:HB3	1:L:83:ARG:HE	1.74	0.52
2:F:108:VAL:HA	2:F:111:VAL:HG22	1.91	0.52
2:F:435:ASP:CG	2:F:438:LEU:HB2	2.35	0.52
1:C:8:ARG:HG2	1:C:9:ASN:ND2	2.25	0.52
2:G:34:ARG:CZ	2:G:250:HIS:HA	2.39	0.52
1:A:37:LEU:CD2	1:A:57:PHE:HB3	2.40	0.51
1:B:51:ALA:O	1:B:52:ASP:C	2.52	0.51
2:E:214:ARG:HG2	2:E:215:LYS:H	1.76	0.51
2:F:262:CYS:SG	2:F:318:LEU:HD13	2.50	0.51
2:G:74:ALA:O	2:G:75:ASN:C	2.53	0.51
2:G:212:LYS:HB2	2:G:212:LYS:NZ	2.25	0.51
2:G:389:ASN:C	2:G:389:ASN:ND2	2.64	0.51
2:F:312:ILE:HG12	2:F:313:ALA:H	1.75	0.51
1:I:115:PRO:HG3	1:I:120:ILE:HG12	1.92	0.51
2:E:94:LYS:HA	2:E:94:LYS:CE	2.32	0.51
1:D:94:LEU:HD13	1:D:122:ILE:HB	1.93	0.51
1:J:72:VAL:O	1:J:75:ALA:HB3	2.10	0.51
1:L:73:LYS:NZ	1:L:77:GLU:HG2	2.24	0.51
1:B:1:THR:HB	1:B:33:LYS:HZ3	1.73	0.51
2:E:153:SER:O	2:E:157:GLN:NE2	2.43	0.51
1:D:43:ILE:HD13	1:D:98:ALA:O	2.10	0.51
1:D:100:GLU:OE2	1:D:173:TYR:HB2	2.11	0.51
1:D:170:GLU:HG2	1:D:171:LEU:N	2.25	0.51
2:G:401:ARG:NH2	2:H:329:ARG:O	2.42	0.51
2:H:35:TRP:O	2:H:39:GLN:HG2	2.10	0.51
2:H:255:ILE:N	2:H:255:ILE:HD12	2.26	0.51
1:L:62:ARG:HA	1:L:65:GLU:CG	2.41	0.51
2:G:86:PHE:HA	2:G:89:VAL:HG13	1.93	0.51
2:G:117:GLU:OE2	2:G:120:ARG:NH2	2.41	0.51
2:G:220:ASP:O	2:G:221:ALA:C	2.53	0.51
2:H:311:GLN:NE2	2:H:311:GLN:CA	2.74	0.51
1:A:28:LYS:HD2	1:B:113:VAL:CG1	2.40	0.51
2:E:76:ALA:HB1	2:E:250:HIS:O	2.11	0.51
2:E:362:GLU:HG2	2:E:410:ALA:CB	2.40	0.51
2:F:54:LEU:CD1	2:F:306:ALA:HB3	2.41	0.51
2:F:174:GLU:HB3	2:F:211:GLN:HB2	1.90	0.51
1:J:95:LEU:HD12	1:J:95:LEU:N	2.25	0.51
2:G:349:ALA:HB1	2:H:44:LEU:HD23	1.91	0.51
2:G:358:LEU:HD22	2:H:36:ARG:HB2	1.93	0.51
2:H:167:GLN:CD	2:H:219:LYS:NZ	2.68	0.51
2:E:409:ASP:O	2:E:410:ALA:C	2.54	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:102:ASP:C	2:F:104:THR:H	2.18	0.51
2:F:174:GLU:CA	2:F:212:LYS:HB3	2.40	0.51
2:G:122:ARG:O	2:G:126:LEU:HD23	2.11	0.51
2:G:124:GLU:HA	2:G:127:ALA:CB	2.41	0.51
2:H:150:GLN:O	2:H:153:SER:CB	2.48	0.51
2:H:339:ASP:O	2:H:343:ILE:HG13	2.10	0.51
1:B:59:LEU:HD12	1:B:59:LEU:O	2.11	0.51
2:E:130:ARG:HB2	2:E:130:ARG:HH21	1.71	0.51
1:I:36:ARG:O	1:I:37:LEU:HD23	2.11	0.51
1:J:18:GLY:HA2	1:J:33:LYS:HE3	1.91	0.51
2:G:358:LEU:HD23	2:H:36:ARG:HB3	1.92	0.51
1:K:85:ASP:O	1:K:89:ARG:HB2	2.11	0.51
2:F:280:ASP:O	2:F:283:PRO:HD2	2.09	0.51
2:G:112:ARG:HG3	2:G:112:ARG:NH1	2.26	0.51
2:H:31:LEU:HD11	2:H:74:ALA:HB2	1.93	0.51
2:H:217:LYS:O	2:H:220:ASP:HB2	2.11	0.51
1:A:86:ARG:HA	1:A:89:ARG:CZ	2.41	0.51
2:E:23:ALA:HA	2:E:330:VAL:HG21	1.92	0.51
2:E:171:LYS:HB2	2:E:218:ILE:HG13	1.93	0.51
2:E:401:ARG:HD2	2:E:432:LEU:CD2	2.41	0.51
2:F:20:GLN:O	2:F:24:LYS:HG3	2.10	0.51
1:C:22:LEU:HD23	1:C:22:LEU:C	2.36	0.51
1:C:36:ARG:HD3	1:C:40:ASP:OD1	2.10	0.51
1:I:81:ASP:HA	1:I:84:THR:CG2	2.41	0.51
1:J:170:GLU:HG2	1:J:171:LEU:H	1.76	0.51
1:K:80:LYS:HD2	1:K:80:LYS:C	2.36	0.51
1:A:36:ARG:HB3	1:A:36:ARG:HH11	1.76	0.50
1:B:60:PHE:CE2	1:B:97:VAL:HG21	2.46	0.50
2:F:312:ILE:HD13	2:F:312:ILE:N	2.21	0.50
2:G:355:TYR:CE2	2:G:400:GLU:OE2	2.64	0.50
1:A:39:ASN:OD1	2:E:143:TRP:CH2	2.65	0.50
1:A:65:GLU:CG	2:E:141:ASN:HB3	2.41	0.50
2:E:128:GLU:O	2:E:131:ILE:HG22	2.11	0.50
2:E:408:TYR:HA	2:F:29:ILE:CD1	2.40	0.50
1:C:36:ARG:HH12	1:C:40:ASP:C	2.19	0.50
1:D:28:LYS:HG2	1:D:30:ASN:ND2	2.26	0.50
2:G:357:ALA:HB1	2:H:40:LEU:HD22	1.93	0.50
2:H:217:LYS:HB2	2:H:217:LYS:HZ2	1.76	0.50
2:H:345:THR:HG21	2:H:373:ILE:CD1	2.41	0.50
1:K:83:ARG:HH11	1:K:83:ARG:CG	2.21	0.50
2:E:89:VAL:HG12	2:E:93:GLY:CA	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:122:ARG:NE	2:E:126:LEU:HD21	2.27	0.50
2:E:230:ALA:O	2:E:233:LEU:HB3	2.10	0.50
2:F:34:ARG:CZ	2:F:250:HIS:HA	2.41	0.50
2:F:351:ILE:H	2:F:351:ILE:CD1	2.14	0.50
2:G:442:ILE:O	2:G:442:ILE:CG2	2.59	0.50
1:B:92:GLU:O	1:B:93:ALA:HB2	2.11	0.50
2:G:151:GLU:CB	2:G:152:PRO:CD	2.89	0.50
2:H:211:GLN:O	2:H:212:LYS:HB2	2.11	0.50
2:H:216:LEU:CD2	2:H:221:ALA:HB2	2.41	0.50
2:F:346:GLU:HB2	2:F:347:PRO:HD3	1.94	0.50
2:G:92:VAL:CG2	2:H:92:VAL:N	2.74	0.50
2:H:145:GLN:HE21	2:H:145:GLN:HA	1.77	0.50
2:F:148:GLN:HA	2:F:151:GLU:CG	2.42	0.50
2:F:362:GLU:HG2	2:F:410:ALA:C	2.36	0.50
1:C:77:GLU:O	1:C:80:LYS:HB3	2.11	0.50
1:C:105:ILE:CD1	1:C:120:ILE:HG23	2.42	0.50
2:H:76:ALA:HB1	2:H:250:HIS:O	2.11	0.50
1:K:58:GLU:HG3	1:K:62:ARG:NH2	2.27	0.50
1:A:5:SER:HB3	1:A:120:ILE:HB	1.92	0.50
1:A:84:THR:HG23	1:A:85:ASP:N	2.26	0.50
2:E:95:GLU:H	2:E:95:GLU:CD	2.20	0.50
2:F:135:LEU:HD22	2:F:159:PHE:CD2	2.47	0.50
1:C:143:SER:O	1:C:147:ILE:HG12	2.11	0.50
2:H:23:ALA:HA	2:H:330:VAL:HG21	1.93	0.50
2:H:101:ARG:O	2:H:104:THR:HB	2.11	0.50
2:H:235:ASN:HB2	2:H:236:PRO:CD	2.42	0.50
1:L:86:ARG:HA	1:L:89:ARG:HH12	1.76	0.50
1:L:117:ASN:O	1:L:118:ASP:HB2	2.10	0.50
1:A:28:LYS:HE3	1:B:113:VAL:HG13	1.93	0.50
1:A:87:MET:HE1	1:B:84:THR:HG23	1.93	0.50
1:B:38:TYR:HB2	1:B:64:LEU:CD1	2.40	0.50
1:J:71:LEU:HD13	1:J:71:LEU:C	2.37	0.50
2:H:41:ASN:ND2	2:H:44:LEU:HB2	2.27	0.50
2:F:221:ALA:O	2:F:225:LEU:HD23	2.12	0.50
1:C:8:ARG:NH1	1:C:142:LEU:O	2.45	0.50
1:C:10:GLY:HA3	1:C:174:LYS:HA	1.93	0.50
1:D:91:LEU:HD12	1:D:91:LEU:O	2.12	0.50
1:D:145:ARG:NH1	1:D:168:ILE:HD12	2.27	0.50
2:G:88:GLU:CD	2:H:90:GLY:CA	2.85	0.50
2:G:109:LYS:HD3	2:H:296:MET:O	2.12	0.50
1:A:103:SER:OG	1:A:118:ASP:HB3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:235:ASN:OD1	2:F:238:GLU:HB2	2.12	0.49
1:D:73:LYS:HZ1	1:D:77:GLU:HG2	1.76	0.49
2:H:94:LYS:NZ	2:H:101:ARG:HH12	2.10	0.49
1:L:85:ASP:HB3	1:L:88:LEU:HB2	1.93	0.49
2:E:152:PRO:HB3	2:E:155:ALA:HB3	1.94	0.49
1:I:88:LEU:HD12	1:I:88:LEU:N	2.26	0.49
1:J:6:VAL:HG12	1:J:7:ARG:H	1.75	0.49
1:J:10:GLY:HA2	1:J:173:TYR:CE1	2.46	0.49
2:G:23:ALA:HB1	2:G:55:MET:HE2	1.93	0.49
2:G:77:PRO:HB2	2:G:103:LEU:HD21	1.94	0.49
2:H:151:GLU:CB	2:H:152:PRO:CD	2.91	0.49
1:K:105:ILE:HD12	1:K:122:ILE:HG21	1.94	0.49
1:B:53:ALA:O	1:B:55:THR:N	2.45	0.49
2:E:167:GLN:OE1	2:E:168:LEU:N	2.46	0.49
2:E:318:LEU:O	2:E:323:GLN:NE2	2.44	0.49
2:F:108:VAL:O	2:F:110:MET:N	2.45	0.49
1:I:4:VAL:CG1	1:I:129:ALA:HB1	2.42	0.49
1:I:30:ASN:ND2	1:I:30:ASN:H	2.11	0.49
1:I:84:THR:HG23	1:I:85:ASP:H	1.76	0.49
2:G:382:GLN:O	2:G:386:SER:HB3	2.12	0.49
2:H:270:PRO:O	2:H:274:ARG:HD2	2.11	0.49
1:L:37:LEU:HD13	1:L:57:PHE:HB3	1.93	0.49
1:A:18:GLY:HA2	1:A:33:LYS:HE3	1.94	0.49
2:E:95:GLU:OE1	2:E:101:ARG:NH1	2.43	0.49
2:E:382:GLN:HA	2:E:382:GLN:NE2	2.27	0.49
2:F:25:ARG:O	2:F:29:ILE:HG12	2.13	0.49
1:C:12:VAL:HG12	1:C:171:LEU:HB3	1.95	0.49
1:C:28:LYS:HG2	1:C:30:ASN:ND2	2.27	0.49
1:J:28:LYS:HZ1	1:J:30:ASN:ND2	2.10	0.49
2:H:352:THR:HG22	2:H:353:VAL:N	2.27	0.49
1:B:71:LEU:HB2	1:B:99:ASP:OD1	2.12	0.49
2:F:384:ASN:HD21	2:F:390:ILE:HG12	1.77	0.49
1:I:8:ARG:HG2	1:I:9:ASN:CG	2.38	0.49
1:J:136:LEU:HB3	1:J:147:ILE:CD1	2.42	0.49
2:G:103:LEU:HD13	2:G:247:VAL:HG13	1.93	0.49
2:G:362:GLU:HG3	2:G:411:SER:HA	1.95	0.49
2:H:135:LEU:HD13	2:H:159:PHE:HB3	1.94	0.49
2:H:345:THR:CG2	2:H:373:ILE:CD1	2.88	0.49
2:H:393:ARG:HG2	2:H:393:ARG:NH1	2.27	0.49
1:A:30:ASN:HD22	1:A:30:ASN:C	2.20	0.49
1:B:65:GLU:OE1	2:F:143:TRP:CE2	2.65	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:163:LEU:O	2:E:163:LEU:HG	2.12	0.49
2:E:151:GLU:HB2	2:E:152:PRO:HD2	1.95	0.49
2:F:140:LYS:HD3	2:F:140:LYS:H	1.78	0.49
2:F:345:THR:CG2	2:F:373:ILE:HD13	2.43	0.49
1:C:116:GLU:C	1:C:118:ASP:H	2.21	0.49
1:D:36:ARG:O	1:D:37:LEU:HB3	2.13	0.49
1:J:66:MET:C	1:J:67:HIS:ND1	2.70	0.49
2:H:147:GLU:CG	2:H:150:GLN:NE2	2.75	0.49
2:H:432:LEU:HD12	2:H:432:LEU:H	1.77	0.49
1:L:86:ARG:HA	1:L:89:ARG:NH1	2.28	0.49
1:A:65:GLU:HG3	2:E:141:ASN:HB3	1.94	0.49
1:A:103:SER:O	1:A:104:LEU:HB3	2.13	0.49
2:E:282:LEU:HD11	2:E:321:GLU:HB3	1.94	0.49
2:F:171:LYS:HZ2	2:F:218:ILE:HD11	1.72	0.49
1:D:12:VAL:O	1:D:12:VAL:HG13	2.13	0.49
2:G:31:LEU:HD12	2:G:70:LEU:HD22	1.95	0.49
2:G:131:ILE:HD11	2:G:218:ILE:CD1	2.43	0.49
2:G:136:ILE:O	2:G:136:ILE:CG2	2.60	0.49
2:G:248:GLU:HG2	2:G:297:VAL:HG13	1.95	0.49
2:H:257:GLU:HB2	2:H:260:LYS:HG3	1.95	0.49
2:E:355:TYR:HE2	2:E:400:GLU:OE2	1.94	0.49
2:F:132:LEU:HD23	2:F:135:LEU:CD1	2.41	0.49
2:F:232:LYS:HZ2	2:F:232:LYS:HB2	1.77	0.49
1:D:3:ILE:HB	1:D:122:ILE:CG1	2.41	0.49
1:I:5:SER:HB3	1:I:120:ILE:HB	1.94	0.49
1:I:85:ASP:CG	1:I:88:LEU:HD13	2.37	0.49
1:J:53:ALA:O	1:J:55:THR:N	2.46	0.49
2:G:153:SER:C	2:G:157:GLN:HG3	2.37	0.49
2:H:212:LYS:HB2	2:H:212:LYS:HZ2	1.76	0.49
2:H:384:ASN:HD21	2:H:390:ILE:HG12	1.77	0.49
1:B:64:LEU:HD23	1:B:74:ALA:CB	2.43	0.49
1:B:65:GLU:CD	2:F:143:TRP:NE1	2.71	0.49
1:J:35:ARG:O	1:J:169:GLU:HG3	2.13	0.49
2:H:108:VAL:HA	2:H:111:VAL:CG2	2.41	0.49
2:H:164:ARG:O	2:H:165:GLU:HB3	2.13	0.49
1:A:104:LEU:HD12	1:A:104:LEU:O	2.13	0.48
1:I:109:ASN:HD22	1:I:109:ASN:N	2.09	0.48
2:H:64:THR:CG2	2:H:68:ARG:NH1	2.76	0.48
1:A:47:ALA:HB3	1:A:94:LEU:HB2	1.95	0.48
2:E:147:GLU:O	2:E:150:GLN:HG3	2.13	0.48
2:E:171:LYS:HE3	2:E:172:GLU:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:362:GLU:OE1	2:F:36:ARG:NE	2.46	0.48
1:C:5:SER:HB3	1:C:120:ILE:HB	1.95	0.48
1:C:83:ARG:HH11	1:C:83:ARG:CB	2.17	0.48
2:G:132:LEU:HD11	2:G:160:ARG:HG2	1.96	0.48
2:G:168:LEU:HG	2:G:219:LYS:CD	2.21	0.48
2:H:167:GLN:NE2	2:H:219:LYS:HZ2	2.11	0.48
2:H:170:ASP:HB3	2:H:217:LYS:HD3	1.95	0.48
2:E:256:ASP:O	2:E:257:GLU:HG2	2.12	0.48
2:F:132:LEU:CD1	2:F:160:ARG:HG3	2.31	0.48
1:C:60:PHE:CZ	1:C:97:VAL:HG11	2.48	0.48
2:H:102:ASP:C	2:H:104:THR:H	2.21	0.48
1:L:5:SER:HB3	1:L:120:ILE:HB	1.94	0.48
2:E:311:GLN:HE21	2:E:311:GLN:HA	1.77	0.48
2:E:362:GLU:HG3	2:E:411:SER:HA	1.95	0.48
2:G:355:TYR:HE2	2:G:400:GLU:OE2	1.96	0.48
1:A:105:ILE:HD11	1:A:120:ILE:HG23	1.95	0.48
2:F:153:SER:HB3	2:F:157:GLN:HG3	1.95	0.48
1:C:64:LEU:O	1:C:69:GLY:N	2.39	0.48
1:C:71:LEU:HD11	1:C:97:VAL:HG12	1.94	0.48
1:J:12:VAL:HG12	1:J:171:LEU:HB3	1.95	0.48
2:G:211:GLN:O	2:G:212:LYS:HB2	2.13	0.48
1:A:117:ASN:O	1:A:118:ASP:HB2	2.13	0.48
1:B:70:HIS:CE1	1:B:72:VAL:HB	2.48	0.48
2:E:74:ALA:O	2:E:75:ASN:C	2.56	0.48
2:F:86:PHE:HB2	2:F:277:VAL:HG13	1.94	0.48
2:F:240:LYS:O	2:F:244:ILE:HD13	2.14	0.48
2:F:279:ARG:O	2:F:283:PRO:HD3	2.14	0.48
1:J:44:ALA:HB2	1:J:97:VAL:HG23	1.96	0.48
2:G:408:TYR:CB	2:H:29:ILE:HD11	2.43	0.48
2:H:34:ARG:CZ	2:H:250:HIS:HA	2.44	0.48
2:H:140:LYS:O	2:H:141:ASN:HB3	2.14	0.48
2:H:318:LEU:O	2:H:323:GLN:NE2	2.45	0.48
1:K:49:GLY:HA2	1:L:111:ASP:OD1	2.14	0.48
1:A:20:ALA:HB2	1:A:31:VAL:HG21	1.94	0.48
2:E:299:THR:HA	2:E:302:ILE:CD1	2.38	0.48
2:F:236:PRO:C	2:F:238:GLU:H	2.22	0.48
2:F:311:GLN:NE2	2:F:311:GLN:HA	2.29	0.48
2:G:361:THR:HG22	2:H:35:TRP:HZ3	1.74	0.48
2:G:361:THR:HG23	2:H:39:GLN:HG3	1.96	0.48
2:H:103:LEU:HD13	2:H:247:VAL:CG2	2.42	0.48
1:K:85:ASP:HB3	1:K:88:LEU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:71:LEU:HD21	1:L:97:VAL:CG1	2.44	0.48
1:L:94:LEU:CD2	1:L:107:THR:HG22	2.44	0.48
2:E:174:GLU:C	2:E:211:GLN:HB2	2.39	0.48
2:E:442:ILE:O	2:E:442:ILE:CG2	2.62	0.48
2:F:219:LYS:HA	2:F:223:LYS:HZ3	1.79	0.48
2:F:366:ILE:HD11	2:F:406:ILE:HD13	1.95	0.48
1:C:30:ASN:HD22	1:C:30:ASN:N	2.04	0.48
1:C:83:ARG:O	1:C:83:ARG:HG2	2.13	0.48
1:D:17:ASP:O	1:D:33:LYS:HD2	2.14	0.48
1:I:95:LEU:HB2	1:I:106:ILE:HB	1.95	0.48
1:I:109:ASN:N	1:I:109:ASN:ND2	2.62	0.48
2:G:355:TYR:HH	2:G:400:GLU:CD	2.22	0.48
2:E:240:LYS:HE3	2:E:294:HIS:O	2.13	0.48
1:J:3:ILE:HB	1:J:122:ILE:CG1	2.43	0.48
2:G:31:LEU:HD12	2:G:70:LEU:HD21	1.96	0.48
2:H:267:SER:O	2:H:271:ASP:OD2	2.32	0.48
1:A:87:MET:HE1	1:B:84:THR:HA	1.96	0.48
1:B:59:LEU:HG	1:B:78:LEU:CD1	2.44	0.48
1:B:174:LYS:N	1:B:174:LYS:HD2	2.29	0.48
2:E:112:ARG:HH11	2:E:112:ARG:HG3	1.78	0.48
2:E:345:THR:HG21	2:E:373:ILE:HD13	1.95	0.48
2:F:125:GLU:C	2:F:127:ALA:H	2.22	0.48
2:F:152:PRO:CB	2:F:156:ARG:HB2	2.43	0.48
2:F:227:GLU:O	2:F:228:GLU:C	2.56	0.48
2:H:223:LYS:C	2:H:225:LEU:H	2.21	0.48
1:B:5:SER:HB3	1:B:120:ILE:HB	1.95	0.47
2:E:130:ARG:HG2	2:E:225:LEU:HD11	1.95	0.47
1:I:60:PHE:CE2	1:I:97:VAL:HG21	2.49	0.47
2:G:221:ALA:O	2:G:225:LEU:HD23	2.14	0.47
2:G:222:MET:O	2:G:226:ILE:HG12	2.14	0.47
2:H:122:ARG:HA	2:H:122:ARG:CZ	2.43	0.47
2:H:236:PRO:C	2:H:238:GLU:H	2.22	0.47
1:K:17:ASP:O	1:K:33:LYS:HD2	2.14	0.47
1:L:116:GLU:C	1:L:118:ASP:H	2.22	0.47
1:B:65:GLU:OE1	2:F:143:TRP:NE1	2.47	0.47
2:E:170:ASP:CB	2:E:217:LYS:HD3	2.45	0.47
2:F:23:ALA:HA	2:F:330:VAL:HG21	1.97	0.47
1:I:77:GLU:HA	1:I:80:LYS:HD2	1.97	0.47
2:G:407:SER:OG	2:H:29:ILE:HG23	2.13	0.47
2:H:272:VAL:HA	2:H:275:GLU:HB2	1.96	0.47
1:K:136:LEU:HB3	1:K:147:ILE:CD1	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:PRO:HG3	1:A:120:ILE:HG12	1.96	0.47
1:B:38:TYR:CD2	1:B:41:LYS:HD2	2.49	0.47
1:B:105:ILE:HG22	1:B:106:ILE:N	2.29	0.47
1:B:170:GLU:CG	1:B:171:LEU:H	2.22	0.47
2:E:142:ASN:CB	2:E:149:GLN:HE22	2.27	0.47
1:D:94:LEU:HB3	1:D:122:ILE:HD12	1.96	0.47
2:G:89:VAL:HA	2:G:92:VAL:C	2.40	0.47
2:G:116:ILE:O	2:G:116:ILE:HG22	2.14	0.47
2:H:103:LEU:CD1	2:H:247:VAL:HG13	2.44	0.47
1:L:43:ILE:HG12	1:L:43:ILE:O	2.13	0.47
1:L:105:ILE:CD1	1:L:120:ILE:HG23	2.41	0.47
2:E:401:ARG:HD2	2:E:432:LEU:HD21	1.96	0.47
2:F:102:ASP:C	2:F:104:THR:N	2.71	0.47
2:F:134:VAL:HG21	2:F:172:GLU:O	2.15	0.47
1:D:36:ARG:NH1	1:D:43:ILE:HG22	2.29	0.47
1:D:99:ASP:HA	1:D:171:LEU:CD2	2.45	0.47
1:J:98:ALA:HB2	1:J:103:SER:CB	2.45	0.47
1:K:11:HIS:HE1	1:K:174:LYS:NZ	2.11	0.47
2:F:235:ASN:ND2	2:F:238:GLU:OE1	2.47	0.47
2:G:408:TYR:CA	2:H:29:ILE:HD11	2.45	0.47
2:H:27:VAL:CG1	2:H:70:LEU:HG	2.43	0.47
2:H:86:PHE:HB2	2:H:277:VAL:HG13	1.95	0.47
2:E:389:ASN:C	2:E:389:ASN:ND2	2.56	0.47
2:F:216:LEU:HG	2:F:221:ALA:HB2	1.96	0.47
2:F:219:LYS:HA	2:F:219:LYS:HE3	1.95	0.47
2:F:365:ASN:ND2	2:F:417:ASN:OD1	2.47	0.47
1:C:149:GLU:OE1	1:C:166:HIS:CD2	2.67	0.47
2:H:133:ASP:O	2:H:137:PRO:HA	2.13	0.47
1:A:83:ARG:HG2	1:A:83:ARG:HH11	1.80	0.47
2:E:131:ILE:O	2:E:134:VAL:HG12	2.14	0.47
2:E:348:ASN:O	2:E:349:ALA:HB3	2.15	0.47
2:F:41:ASN:ND2	2:F:44:LEU:HB2	2.30	0.47
2:F:62:GLY:O	2:F:66:ILE:HG13	2.15	0.47
1:C:1:THR:N	1:C:161:TYR:O	2.47	0.47
1:C:67:HIS:N	1:C:67:HIS:ND1	2.62	0.47
1:C:67:HIS:O	1:C:68:GLN:C	2.57	0.47
1:I:8:ARG:NH1	1:I:142:LEU:O	2.48	0.47
2:G:76:ALA:HB1	2:G:250:HIS:O	2.15	0.47
2:G:214:ARG:HG2	2:G:215:LYS:N	2.28	0.47
2:G:217:LYS:HB3	2:G:219:LYS:HZ3	1.80	0.47
2:G:358:LEU:CD2	2:H:36:ARG:HB3	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:94:LYS:NZ	2:H:98:SER:HB3	2.29	0.47
2:H:147:GLU:HG3	2:H:150:GLN:NE2	2.30	0.47
2:H:356:LYS:CG	2:H:366:ILE:HG22	2.42	0.47
2:H:393:ARG:NH2	3:H:3450:ADP:O1B	2.47	0.47
1:K:67:HIS:O	1:K:68:GLN:C	2.57	0.47
1:K:68:GLN:O	1:K:70:HIS:N	2.48	0.47
1:K:132:ALA:HB2	1:K:154:ILE:HG21	1.97	0.47
1:L:8:ARG:HH21	1:L:137:LEU:HD12	1.80	0.47
2:E:432:LEU:H	2:E:432:LEU:CD1	2.27	0.47
1:I:33:LYS:O	1:I:45:GLY:HA2	2.15	0.47
2:G:382:GLN:HA	2:G:382:GLN:NE2	2.30	0.47
2:H:65:GLU:HG3	3:H:3450:ADP:H2'	1.97	0.47
1:K:6:VAL:HG21	1:K:147:ILE:HG22	1.96	0.47
1:K:36:ARG:NE	1:K:169:GLU:OE1	2.47	0.47
1:L:36:ARG:HB3	1:L:36:ARG:NH1	2.30	0.47
1:B:12:VAL:HG12	1:B:171:LEU:HB3	1.97	0.47
2:E:132:LEU:HB3	2:E:156:ARG:NH1	2.29	0.47
2:E:171:LYS:HB3	2:E:172:GLU:H	1.53	0.47
2:E:173:ILE:HG12	2:E:212:LYS:CD	2.42	0.47
2:E:259:ASP:HB3	2:E:310:PHE:CZ	2.50	0.47
2:F:96:VAL:CG1	2:F:281:LEU:HD12	2.45	0.47
1:D:28:LYS:CD	1:D:31:VAL:HG22	2.45	0.47
1:I:90:LYS:HZ1	1:J:89:ARG:NH2	2.13	0.47
2:G:165:GLU:HG2	2:G:166:GLY:N	2.29	0.47
2:G:293:LYS:C	2:G:294:HIS:HD2	2.23	0.47
2:G:345:THR:CG2	2:G:373:ILE:HD13	2.43	0.47
1:K:121:ALA:HB1	1:K:126:GLY:O	2.15	0.47
2:E:153:SER:HA	2:E:157:GLN:HG3	1.97	0.47
2:F:60:GLY:H	2:F:393:ARG:NH2	2.12	0.47
2:F:358:LEU:O	2:F:361:THR:HB	2.14	0.47
1:I:3:ILE:HB	1:I:122:ILE:HG12	1.97	0.47
2:G:217:LYS:HG3	2:G:219:LYS:NZ	2.30	0.47
2:H:84:THR:C	2:H:86:PHE:H	2.22	0.47
2:H:145:GLN:HA	2:H:145:GLN:NE2	2.30	0.47
1:K:55:THR:O	1:K:58:GLU:HB3	2.15	0.47
1:L:37:LEU:N	1:L:37:LEU:HD23	2.30	0.46
2:E:151:GLU:C	2:E:153:SER:N	2.71	0.46
2:F:135:LEU:HD13	2:F:159:PHE:HD2	1.79	0.46
1:D:5:SER:HB3	1:D:120:ILE:HB	1.96	0.46
1:J:60:PHE:CE2	1:J:97:VAL:HG21	2.50	0.46
2:H:131:ILE:HG23	2:H:132:LEU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:135:LEU:HD13	2:H:159:PHE:HD2	1.80	0.46
2:H:236:PRO:O	2:H:238:GLU:N	2.47	0.46
1:L:12:VAL:O	1:L:12:VAL:HG13	2.15	0.46
1:A:149:GLU:CG	1:A:168:ILE:HD11	2.46	0.46
2:F:148:GLN:HA	2:F:151:GLU:HG3	1.96	0.46
1:D:3:ILE:O	1:D:121:ALA:HA	2.15	0.46
2:G:311:GLN:HE21	2:G:311:GLN:HA	1.80	0.46
2:H:172:GLU:O	2:H:173:ILE:HG23	2.15	0.46
1:L:168:ILE:HG22	1:L:169:GLU:N	2.29	0.46
2:G:60:GLY:H	2:G:393:ARG:HH22	1.62	0.46
2:G:109:LYS:O	2:G:113:VAL:HG23	2.15	0.46
2:G:171:LYS:HA	2:G:171:LYS:NZ	2.30	0.46
2:H:74:ALA:O	2:H:75:ASN:C	2.58	0.46
2:H:366:ILE:HG13	2:H:420:ILE:HD13	1.97	0.46
1:K:71:LEU:HD21	1:K:97:VAL:CG1	2.45	0.46
1:A:80:LYS:O	1:A:82:TRP:N	2.49	0.46
1:A:149:GLU:HG2	1:A:168:ILE:CD1	2.46	0.46
2:E:240:LYS:HD3	2:E:241:GLN:N	2.29	0.46
2:F:130:ARG:NH2	2:F:229:GLU:HG3	2.31	0.46
1:J:59:LEU:HD12	1:J:59:LEU:C	2.40	0.46
1:J:99:ASP:OD1	1:J:101:THR:HB	2.16	0.46
1:K:73:LYS:HA	1:K:76:VAL:CG1	2.44	0.46
1:C:117:ASN:O	1:C:118:ASP:HB2	2.15	0.46
1:D:46:PHE:HA	1:D:94:LEU:O	2.16	0.46
2:G:91:TYR:O	2:G:92:VAL:HG22	2.14	0.46
2:G:358:LEU:CD2	2:H:36:ARG:CB	2.93	0.46
2:H:163:LEU:HD11	2:H:222:MET:CE	2.45	0.46
1:B:3:ILE:HB	1:B:122:ILE:CG1	2.45	0.46
2:E:221:ALA:O	2:E:225:LEU:HD23	2.15	0.46
2:E:231:ALA:C	2:E:233:LEU:H	2.22	0.46
2:E:389:ASN:HD22	2:E:390:ILE:N	2.12	0.46
2:H:174:GLU:C	2:H:212:LYS:HB3	2.40	0.46
1:A:80:LYS:O	1:A:84:THR:HG22	2.15	0.46
1:A:173:TYR:O	1:A:174:LYS:C	2.58	0.46
1:B:85:ASP:O	1:B:86:ARG:C	2.59	0.46
2:E:234:VAL:O	2:E:236:PRO:HD3	2.15	0.46
2:E:442:ILE:O	2:E:442:ILE:HG22	2.15	0.46
2:F:147:GLU:HG2	2:F:150:GLN:HE21	1.79	0.46
2:F:217:LYS:HG3	2:F:218:ILE:H	1.81	0.46
2:F:403:MET:O	2:F:404:GLU:C	2.59	0.46
1:C:28:LYS:HE2	1:D:114:GLN:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:83:ARG:HH11	1:D:83:ARG:CB	2.17	0.46
2:G:113:VAL:C	2:G:115:ALA:H	2.23	0.46
2:H:86:PHE:O	2:H:89:VAL:HG22	2.16	0.46
2:F:53:ILE:HG12	2:F:328:ILE:HB	1.97	0.46
2:F:145:GLN:C	2:F:147:GLU:H	2.23	0.46
2:F:145:GLN:CA	2:F:145:GLN:HE21	2.28	0.46
2:F:223:LYS:N	2:F:223:LYS:CD	2.79	0.46
2:G:92:VAL:CG2	2:H:92:VAL:CG1	2.80	0.46
2:H:312:ILE:HG12	2:H:313:ALA:H	1.81	0.46
2:H:372:GLY:O	2:H:376:ILE:HG13	2.16	0.46
1:A:17:ASP:CB	1:A:162:THR:HG23	2.46	0.46
2:E:212:LYS:HB2	2:E:212:LYS:HZ2	1.80	0.46
2:E:231:ALA:C	2:E:233:LEU:N	2.73	0.46
2:E:352:THR:HG22	2:E:353:VAL:N	2.31	0.46
2:G:95:GLU:OE1	2:G:101:ARG:NH1	2.47	0.46
1:A:1:THR:HB	1:A:33:LYS:HZ3	1.80	0.45
1:A:17:ASP:HB3	1:A:162:THR:HG23	1.98	0.45
2:E:436:GLU:O	2:E:439:SER:HB2	2.16	0.45
2:F:169:ASP:O	2:F:218:ILE:HG13	2.15	0.45
1:D:62:ARG:O	1:D:65:GLU:HG2	2.16	0.45
1:D:105:ILE:HD12	1:D:122:ILE:HG21	1.98	0.45
2:H:17:ILE:HD12	2:H:17:ILE:N	2.31	0.45
2:H:145:GLN:C	2:H:147:GLU:N	2.74	0.45
1:K:86:ARG:HA	1:K:89:ARG:CZ	2.47	0.45
1:L:28:LYS:HZ2	1:L:30:ASN:ND2	2.13	0.45
1:B:95:LEU:HD12	1:B:95:LEU:N	2.31	0.45
2:E:147:GLU:CA	2:E:150:GLN:HG3	2.46	0.45
2:E:308:GLY:HA3	2:E:310:PHE:CE2	2.51	0.45
2:F:236:PRO:O	2:F:238:GLU:N	2.49	0.45
1:D:149:GLU:CD	1:D:168:ILE:HD11	2.41	0.45
2:G:262:CYS:SG	2:G:318:LEU:HD13	2.55	0.45
2:F:61:VAL:C	3:F:1450:ADP:N7	2.74	0.45
2:F:122:ARG:CZ	2:F:122:ARG:HA	2.46	0.45
2:F:212:LYS:HB2	2:F:212:LYS:HZ2	1.81	0.45
1:J:53:ALA:C	1:J:55:THR:N	2.75	0.45
2:H:220:ASP:C	2:H:224:LEU:HD23	2.42	0.45
1:K:90:LYS:NZ	1:L:89:ARG:CZ	2.80	0.45
1:L:89:ARG:NH1	1:L:89:ARG:HB3	2.31	0.45
1:L:100:GLU:OE2	1:L:173:TYR:HB2	2.16	0.45
2:E:292:THR:C	2:E:294:HIS:H	2.24	0.45
2:F:398:VAL:HG13	2:F:429:LEU:HD13	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:148:ALA:O	1:J:152:LEU:HB2	2.15	0.45
2:H:135:LEU:O	2:H:136:ILE:HD13	2.17	0.45
2:E:149:GLN:C	2:E:151:GLU:H	2.25	0.45
2:E:240:LYS:HD3	2:E:240:LYS:C	2.41	0.45
2:F:233:LEU:HD12	2:F:233:LEU:O	2.17	0.45
1:C:109:ASN:O	1:C:110:GLY:C	2.60	0.45
1:I:30:ASN:HD22	1:I:30:ASN:C	2.25	0.45
1:I:51:ALA:CB	1:J:111:ASP:OD2	2.65	0.45
1:J:86:ARG:HA	1:J:89:ARG:HE	1.82	0.45
2:G:311:GLN:HA	2:G:311:GLN:NE2	2.31	0.45
1:K:73:LYS:O	1:K:76:VAL:HG12	2.16	0.45
1:A:10:GLY:HA2	1:A:173:TYR:CZ	2.51	0.45
1:A:95:LEU:HB2	1:A:106:ILE:HB	1.99	0.45
2:E:86:PHE:HA	2:E:89:VAL:HG13	1.98	0.45
2:E:128:GLU:O	2:E:129:GLU:C	2.60	0.45
2:E:169:ASP:O	2:E:218:ILE:CG1	2.65	0.45
2:E:220:ASP:O	2:E:221:ALA:C	2.59	0.45
2:E:312:ILE:CG1	2:E:313:ALA:H	2.27	0.45
2:F:41:ASN:ND2	2:F:44:LEU:H	2.14	0.45
2:F:96:VAL:HG12	2:F:284:LEU:HD11	1.97	0.45
2:F:119:ASN:HD21	2:F:233:LEU:HD23	1.81	0.45
2:F:121:TYR:O	2:F:125:GLU:HB2	2.17	0.45
2:F:160:ARG:HG2	2:F:160:ARG:HH11	1.82	0.45
1:J:136:LEU:HB3	1:J:147:ILE:HD12	1.97	0.45
2:G:54:LEU:HD12	2:G:306:ALA:HB3	1.98	0.45
2:G:173:ILE:HD11	2:G:221:ALA:HB1	1.98	0.45
2:G:358:LEU:HD22	2:H:36:ARG:CB	2.46	0.45
1:K:58:GLU:O	1:K:61:GLU:HB2	2.16	0.45
1:L:62:ARG:HA	1:L:65:GLU:HG2	1.98	0.45
1:B:38:TYR:CE2	1:B:41:LYS:HD2	2.52	0.45
1:B:71:LEU:O	1:B:72:VAL:C	2.60	0.45
2:E:214:ARG:CG	2:E:215:LYS:N	2.79	0.45
2:E:264:ARG:NE	2:E:265:GLY:H	2.15	0.45
2:E:402:LEU:HD12	2:E:428:HIS:HB2	1.98	0.45
1:J:94:LEU:HB3	1:J:122:ILE:HD12	1.98	0.45
2:G:153:SER:N	2:G:156:ARG:HB3	2.32	0.45
2:G:227:GLU:O	2:G:230:ALA:N	2.49	0.45
2:G:230:ALA:O	2:G:233:LEU:HB3	2.17	0.45
1:L:64:LEU:CB	1:L:69:GLY:HA2	2.43	0.45
1:B:66:MET:C	1:B:67:HIS:ND1	2.75	0.45
2:E:145:GLN:C	2:E:147:GLU:N	2.75	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:311:GLN:CA	2:F:311:GLN:NE2	2.80	0.45
2:F:312:ILE:CG1	2:F:313:ALA:N	2.78	0.45
1:C:7:ARG:O	1:C:8:ARG:HB2	2.17	0.45
1:C:11:HIS:CE1	1:C:174:LYS:HE2	2.52	0.45
1:I:85:ASP:OD1	1:I:88:LEU:HD13	2.17	0.45
1:J:60:PHE:HB2	1:J:78:LEU:HD22	1.97	0.45
1:J:70:HIS:CE1	1:J:72:VAL:HB	2.51	0.45
2:G:216:LEU:CD1	2:G:221:ALA:HB2	2.47	0.45
2:H:308:GLY:HA3	2:H:310:PHE:CE2	2.52	0.45
1:K:58:GLU:HG3	1:K:62:ARG:HH21	1.82	0.45
2:E:126:LEU:O	2:E:130:ARG:NH2	2.45	0.45
2:E:134:VAL:HG22	2:E:134:VAL:O	2.17	0.45
2:E:167:GLN:CD	2:E:168:LEU:N	2.75	0.45
2:E:293:LYS:C	2:E:294:HIS:HD2	2.25	0.45
1:D:73:LYS:O	1:D:76:VAL:HG12	2.17	0.45
1:J:104:LEU:HD23	1:J:104:LEU:N	2.31	0.45
2:G:171:LYS:HG3	2:G:218:ILE:HD11	1.98	0.45
2:E:53:ILE:HG22	2:E:54:LEU:N	2.32	0.45
2:E:65:GLU:O	2:E:69:ARG:HG2	2.17	0.45
2:E:96:VAL:HG21	2:E:280:ASP:HB3	1.99	0.45
2:E:384:ASN:HD21	2:E:390:ILE:HG12	1.82	0.45
1:C:8:ARG:O	1:C:11:HIS:HB2	2.16	0.45
1:I:17:ASP:O	1:I:33:LYS:HD2	2.17	0.45
2:G:140:LYS:O	2:G:141:ASN:CB	2.63	0.45
1:L:89:ARG:NH1	1:L:89:ARG:CB	2.80	0.45
1:A:34:VAL:HG13	1:A:44:ALA:O	2.17	0.44
1:A:71:LEU:O	1:A:75:ALA:N	2.49	0.44
2:E:89:VAL:HA	2:E:93:GLY:HA3	1.99	0.44
2:F:211:GLN:O	2:F:212:LYS:HB2	2.17	0.44
1:I:72:VAL:O	1:I:76:VAL:HG23	2.18	0.44
2:G:23:ALA:HA	2:G:330:VAL:HG21	1.99	0.44
2:G:109:LYS:O	2:G:109:LYS:HG3	2.17	0.44
2:G:130:ARG:HD2	2:G:225:LEU:CD1	2.27	0.44
2:E:262:CYS:SG	2:E:318:LEU:HD13	2.57	0.44
2:F:135:LEU:HB3	2:F:159:PHE:CD2	2.52	0.44
2:F:345:THR:CG2	2:F:373:ILE:CD1	2.95	0.44
1:C:156:GLY:HA2	1:C:162:THR:HG22	1.99	0.44
2:G:152:PRO:O	2:G:154:ALA:CB	2.58	0.44
1:L:22:LEU:C	1:L:22:LEU:HD23	2.42	0.44
1:B:30:ASN:C	1:B:30:ASN:HD22	2.24	0.44
2:E:19:GLY:O	2:E:24:LYS:HE3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:147:GLU:HG3	2:E:150:GLN:CD	2.42	0.44
1:C:20:ALA:HB2	1:C:31:VAL:HG21	1.98	0.44
1:D:98:ALA:HA	1:D:103:SER:HA	2.00	0.44
1:D:99:ASP:HA	1:D:171:LEU:HD23	1.99	0.44
1:D:100:GLU:CD	1:D:173:TYR:HB2	2.42	0.44
2:H:255:ILE:HD12	2:H:255:ILE:H	1.80	0.44
1:K:73:LYS:CA	1:K:76:VAL:HG12	2.47	0.44
1:L:67:HIS:O	1:L:68:GLN:C	2.60	0.44
1:A:28:LYS:NZ	1:A:30:ASN:HD21	2.12	0.44
2:E:89:VAL:HA	2:E:93:GLY:CA	2.48	0.44
2:E:216:LEU:HD23	2:E:216:LEU:N	2.31	0.44
2:E:248:GLU:HG2	2:E:297:VAL:HG13	1.99	0.44
2:E:264:ARG:CZ	2:E:265:GLY:H	2.30	0.44
2:E:408:TYR:HD1	2:F:29:ILE:HD11	1.82	0.44
2:F:362:GLU:HG3	2:F:411:SER:HA	2.00	0.44
1:D:41:LYS:O	1:D:171:LEU:HD21	2.16	0.44
1:D:73:LYS:HD2	1:D:76:VAL:CG1	2.47	0.44
2:G:165:GLU:HG2	2:G:166:GLY:H	1.82	0.44
2:H:158:ALA:HB1	2:H:162:LYS:NZ	2.33	0.44
2:H:223:LYS:C	2:H:225:LEU:N	2.74	0.44
2:E:35:TRP:O	2:E:39:GLN:HG2	2.17	0.44
2:F:21:ASP:O	2:F:24:LYS:HB2	2.17	0.44
2:F:150:GLN:O	2:F:153:SER:HB2	2.18	0.44
1:C:121:ALA:HB1	1:C:126:GLY:O	2.18	0.44
1:D:70:HIS:HE1	1:D:72:VAL:HB	1.83	0.44
1:D:168:ILE:HG22	1:D:169:GLU:N	2.32	0.44
2:G:362:GLU:HB3	2:G:364:VAL:HG23	2.00	0.44
2:G:408:TYR:CE1	2:H:10:VAL:HG21	2.52	0.44
2:H:119:ASN:OD1	2:H:234:VAL:HG23	2.16	0.44
2:H:121:TYR:O	2:H:125:GLU:HB2	2.18	0.44
1:B:59:LEU:HG	1:B:78:LEU:HD13	1.99	0.44
1:B:65:GLU:O	2:F:143:TRP:O	2.35	0.44
2:E:145:GLN:HB2	2:E:148:GLN:CB	2.39	0.44
2:E:220:ASP:HA	2:E:223:LYS:HD2	1.98	0.44
2:E:342:ARG:NH2	2:E:346:GLU:OE2	2.40	0.44
2:F:172:GLU:O	2:F:173:ILE:HG23	2.18	0.44
1:D:11:HIS:HA	1:D:171:LEU:O	2.17	0.44
1:J:62:ARG:O	1:J:66:MET:HG3	2.18	0.44
2:H:102:ASP:C	2:H:104:THR:N	2.75	0.44
2:H:145:GLN:HB2	2:H:148:GLN:CG	2.46	0.44
2:H:214:ARG:NE	2:H:216:LEU:HB3	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:282:LEU:HD12	2:H:282:LEU:HA	1.76	0.44
2:H:299:THR:O	2:H:302:ILE:HG12	2.18	0.44
2:H:356:LYS:HG3	2:H:366:ILE:CG2	2.46	0.44
2:F:41:ASN:O	2:F:45:ARG:HG3	2.17	0.44
2:F:145:GLN:C	2:F:147:GLU:N	2.75	0.44
2:F:171:LYS:O	2:F:172:GLU:HB3	2.17	0.44
2:F:268:SER:HA	2:F:271:ASP:OD2	2.16	0.44
2:F:345:THR:HG21	2:F:373:ILE:CD1	2.47	0.44
2:G:34:ARG:NH2	2:G:250:HIS:HA	2.32	0.44
2:H:16:HIS:HB2	2:H:17:ILE:HD12	1.99	0.44
2:H:151:GLU:HB2	2:H:152:PRO:HD2	1.99	0.44
1:A:60:PHE:CE2	1:A:97:VAL:HG21	2.53	0.44
2:E:113:VAL:C	2:E:115:ALA:H	2.26	0.44
2:E:219:LYS:O	2:E:223:LYS:HG3	2.18	0.44
2:F:174:GLU:HB3	2:F:211:GLN:NE2	2.33	0.44
1:C:34:VAL:HB	1:C:167:THR:HG22	1.99	0.44
1:I:84:THR:HG23	1:I:85:ASP:N	2.32	0.44
1:J:92:GLU:O	1:J:93:ALA:HB2	2.17	0.44
2:H:96:VAL:HG12	2:H:284:LEU:HD11	2.00	0.44
2:H:167:GLN:OE1	2:H:168:LEU:N	2.51	0.44
1:K:79:ALA:HB1	1:K:110:GLY:HA2	2.00	0.44
1:K:115:PRO:HG3	1:K:120:ILE:CG1	2.47	0.44
1:L:60:PHE:CZ	1:L:97:VAL:HG11	2.53	0.44
1:A:1:THR:HA	1:A:17:ASP:OD1	2.18	0.44
1:A:15:ALA:HB1	1:A:152:LEU:HD12	2.00	0.44
1:A:72:VAL:O	1:A:76:VAL:HG23	2.18	0.44
1:I:108:GLY:C	1:I:109:ASN:HD22	2.26	0.44
1:J:37:LEU:HD11	1:J:57:PHE:CD1	2.53	0.44
1:J:38:TYR:HB2	1:J:64:LEU:HD12	1.99	0.44
2:G:171:LYS:HB3	2:G:172:GLU:H	1.48	0.44
2:G:255:ILE:HD13	2:G:281:LEU:HD21	2.00	0.44
2:G:436:GLU:O	2:G:439:SER:HB2	2.17	0.44
2:H:127:ALA:HB1	2:H:229:GLU:HB3	1.99	0.44
2:H:167:GLN:CG	2:H:219:LYS:HZ1	2.31	0.44
1:K:91:LEU:HB3	1:L:83:ARG:NE	2.32	0.44
1:K:143:SER:OG	1:K:146:GLU:HG3	2.18	0.44
1:L:149:GLU:OE1	1:L:166:HIS:CD2	2.71	0.44
2:E:212:LYS:C	2:E:214:ARG:H	2.26	0.43
2:F:47:GLU:OE1	2:F:47:GLU:HA	2.18	0.43
1:D:157:ASP:OD2	1:D:164:HIS:NE2	2.37	0.43
2:G:47:GLU:OE1	2:G:47:GLU:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:53:ILE:HA	2:G:328:ILE:HB	2.00	0.43
2:G:126:LEU:N	2:G:126:LEU:HD22	2.33	0.43
2:G:311:GLN:CA	2:G:311:GLN:NE2	2.81	0.43
2:H:432:LEU:H	2:H:432:LEU:CD1	2.30	0.43
1:L:89:ARG:CB	1:L:89:ARG:HH11	2.31	0.43
1:A:88:LEU:CD1	1:A:88:LEU:N	2.80	0.43
2:E:91:TYR:O	2:E:92:VAL:HG22	2.18	0.43
2:E:122:ARG:NH1	2:E:126:LEU:HD21	2.33	0.43
2:E:169:ASP:O	2:E:218:ILE:HG13	2.18	0.43
2:E:401:ARG:CZ	2:E:442:ILE:HG23	2.48	0.43
1:I:99:ASP:OD1	1:I:99:ASP:C	2.61	0.43
2:H:103:LEU:O	2:H:103:LEU:HD22	2.18	0.43
2:H:218:ILE:C	2:H:220:ASP:N	2.73	0.43
1:K:2:THR:OG1	1:K:162:THR:OG1	2.29	0.43
1:K:60:PHE:CZ	1:K:97:VAL:HG11	2.53	0.43
1:L:37:LEU:HD23	1:L:37:LEU:H	1.83	0.43
1:B:7:ARG:NE	1:B:118:ASP:OD2	2.48	0.43
2:E:12:GLU:HG2	2:E:73:LEU:HD11	2.00	0.43
2:F:58:PRO:HG2	2:F:61:VAL:HG11	2.00	0.43
2:F:170:ASP:HB3	2:F:217:LYS:HD3	2.00	0.43
1:D:115:PRO:HG2	1:D:118:ASP:HA	2.00	0.43
1:I:28:LYS:HZ1	1:I:30:ASN:ND2	2.16	0.43
2:H:220:ASP:O	2:H:224:LEU:N	2.44	0.43
1:L:17:ASP:HA	1:L:165:PHE:O	2.18	0.43
1:B:107:THR:C	1:B:109:ASN:N	2.75	0.43
1:B:148:ALA:O	1:B:152:LEU:HB2	2.19	0.43
2:E:358:LEU:O	2:E:361:THR:HB	2.17	0.43
2:F:60:GLY:N	2:F:393:ARG:NH2	2.66	0.43
2:F:214:ARG:O	2:F:214:ARG:HD3	2.19	0.43
1:C:15:ALA:HB1	1:C:152:LEU:HD12	2.00	0.43
1:D:11:HIS:HE1	1:D:172:SER:OG	2.01	0.43
1:D:104:LEU:HD22	1:D:112:VAL:HG12	2.00	0.43
1:J:64:LEU:HD23	1:J:74:ALA:CB	2.48	0.43
2:G:106:ALA:O	2:G:110:MET:HB2	2.18	0.43
2:G:257:GLU:O	2:G:257:GLU:CG	2.65	0.43
2:G:273:SER:O	2:G:277:VAL:HG23	2.18	0.43
2:H:65:GLU:O	2:H:69:ARG:HG2	2.18	0.43
1:B:71:LEU:HD13	1:B:71:LEU:C	2.44	0.43
2:E:63:LYS:HG2	2:E:332:LEU:HD13	2.00	0.43
2:E:79:ILE:CG2	2:E:103:LEU:HG	2.48	0.43
2:F:129:GLU:HB2	2:F:130:ARG:HH11	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:VAL:HG12	1:C:112:VAL:O	2.18	0.43
1:I:12:VAL:HG12	1:I:171:LEU:HB3	2.00	0.43
1:I:125:GLY:O	1:I:126:GLY:C	2.61	0.43
2:H:96:VAL:CG1	2:H:281:LEU:HD12	2.45	0.43
2:H:140:LYS:H	2:H:140:LYS:HD3	1.83	0.43
2:H:141:ASN:O	2:H:142:ASN:C	2.61	0.43
2:H:296:MET:HA	2:H:296:MET:CE	2.48	0.43
1:K:28:LYS:CE	1:K:30:ASN:ND2	2.81	0.43
1:K:83:ARG:CG	1:K:83:ARG:NH1	2.80	0.43
2:E:20:GLN:O	2:E:24:LYS:HG3	2.18	0.43
2:E:292:THR:HB	2:E:295:GLY:O	2.18	0.43
2:F:91:TYR:O	2:F:92:VAL:HG22	2.19	0.43
2:F:322:LEU:HD12	2:F:322:LEU:HA	1.77	0.43
2:F:341:GLU:O	2:F:344:LEU:HB2	2.19	0.43
1:D:13:VAL:HG11	1:D:145:ARG:HB2	1.99	0.43
1:I:109:ASN:O	1:I:111:ASP:N	2.51	0.43
1:J:65:GLU:HB3	2:H:143:TRP:HA	2.00	0.43
2:G:134:VAL:HG13	2:G:171:LYS:HD3	1.99	0.43
2:G:173:ILE:HG12	2:G:212:LYS:CD	2.45	0.43
2:G:282:LEU:HD11	2:G:321:GLU:HB3	2.00	0.43
2:G:384:ASN:HD21	2:G:390:ILE:HG12	1.84	0.43
2:H:94:LYS:HA	2:H:94:LYS:CE	2.35	0.43
1:B:99:ASP:OD1	1:B:101:THR:HB	2.18	0.43
1:B:99:ASP:OD2	1:B:101:THR:N	2.29	0.43
2:F:159:PHE:O	2:F:163:LEU:HB2	2.18	0.43
2:F:267:SER:O	2:F:271:ASP:OD2	2.35	0.43
2:F:312:ILE:CG1	2:F:313:ALA:H	2.31	0.43
2:F:388:GLU:N	2:F:388:GLU:OE2	2.52	0.43
1:C:28:LYS:NZ	1:C:30:ASN:ND2	2.67	0.43
2:G:96:VAL:HG11	2:G:281:LEU:HD12	2.00	0.43
2:G:212:LYS:HB2	2:G:212:LYS:HZ2	1.84	0.43
2:G:231:ALA:O	2:G:233:LEU:N	2.51	0.43
2:G:292:THR:HG22	2:G:293:LYS:N	2.34	0.43
2:G:342:ARG:NH2	2:G:346:GLU:OE2	2.37	0.43
2:G:384:ASN:HD22	2:G:384:ASN:HA	1.61	0.43
2:H:122:ARG:HH21	2:H:122:ARG:HG2	1.84	0.43
1:K:3:ILE:HB	1:K:122:ILE:CG1	2.49	0.43
1:K:46:PHE:CD2	1:K:53:ALA:HB2	2.54	0.43
1:L:68:GLN:O	1:L:69:GLY:C	2.61	0.43
1:A:101:THR:O	1:A:102:ALA:HB2	2.18	0.43
1:B:117:ASN:C	1:B:119:LEU:N	2.76	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:140:LYS:O	2:E:141:ASN:CB	2.65	0.43
1:C:86:ARG:HA	1:C:89:ARG:NH2	2.34	0.43
2:G:108:VAL:O	2:G:110:MET:N	2.52	0.43
2:G:165:GLU:O	2:G:167:GLN:HG3	2.18	0.43
2:H:224:LEU:O	2:H:228:GLU:HB2	2.19	0.43
2:F:35:TRP:O	2:F:39:GLN:HG2	2.19	0.43
2:F:41:ASN:C	2:F:41:ASN:ND2	2.72	0.43
2:F:123:ALA:HB2	2:F:229:GLU:O	2.19	0.43
2:F:214:ARG:HE	2:F:216:LEU:HB3	1.84	0.43
1:I:145:ARG:NE	1:I:170:GLU:OE1	2.44	0.43
1:J:60:PHE:HD1	1:J:78:LEU:HD22	1.81	0.43
2:G:174:GLU:HG3	2:G:213:ALA:HA	2.01	0.43
2:H:111:VAL:HG21	2:H:243:ALA:HB2	2.01	0.43
2:H:136:ILE:HD11	2:H:159:PHE:CZ	2.54	0.43
2:H:366:ILE:HD12	2:H:418:ILE:HB	2.00	0.43
1:A:102:ALA:HB1	1:A:114:GLN:OE1	2.19	0.43
2:E:16:HIS:HB2	2:E:17:ILE:HD12	2.00	0.43
2:F:403:MET:SD	2:F:420:ILE:HD13	2.59	0.43
1:C:36:ARG:NH1	1:C:40:ASP:CA	2.82	0.43
1:D:28:LYS:HG2	1:D:30:ASN:HD22	1.82	0.43
1:D:37:LEU:HB2	1:D:61:GLU:OE1	2.19	0.43
2:G:54:LEU:HB3	2:G:329:ARG:HD3	2.01	0.43
2:G:337:THR:O	2:G:341:GLU:HG3	2.19	0.43
2:H:108:VAL:O	2:H:110:MET:N	2.51	0.43
1:K:86:ARG:HG3	1:K:89:ARG:NH2	2.34	0.43
1:C:36:ARG:NH1	1:C:40:ASP:HB3	2.34	0.42
1:C:85:ASP:CB	1:C:88:LEU:HD12	2.49	0.42
1:D:16:GLY:C	1:D:152:LEU:HD11	2.44	0.42
1:J:67:HIS:CD2	1:J:73:LYS:HD2	2.54	0.42
2:G:164:ARG:HA	2:G:164:ARG:HH11	1.83	0.42
2:H:79:ILE:HG21	2:H:103:LEU:HB2	2.00	0.42
2:F:264:ARG:HE	2:F:265:GLY:H	1.64	0.42
1:C:168:ILE:HG22	1:C:169:GLU:N	2.34	0.42
1:D:152:LEU:HB3	1:D:166:HIS:CE1	2.54	0.42
1:J:78:LEU:C	1:J:80:LYS:N	2.75	0.42
2:G:65:GLU:OE2	2:G:65:GLU:HA	2.19	0.42
2:G:145:GLN:HB2	2:G:148:GLN:CB	2.44	0.42
2:G:151:GLU:HB2	2:G:152:PRO:HD2	2.01	0.42
1:A:109:ASN:N	1:A:109:ASN:HD22	2.16	0.42
2:E:116:ILE:O	2:E:116:ILE:HG22	2.18	0.42
2:E:435:ASP:OD1	2:E:438:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:135:LEU:HD22	2:F:159:PHE:CE2	2.54	0.42
1:C:37:LEU:HB3	1:C:61:GLU:OE1	2.19	0.42
1:D:121:ALA:HB1	1:D:126:GLY:O	2.18	0.42
2:G:132:LEU:C	2:G:134:VAL:H	2.28	0.42
2:G:170:ASP:HB3	2:G:217:LYS:CD	2.47	0.42
2:G:358:LEU:O	2:G:361:THR:HB	2.18	0.42
2:G:392:ALA:HB3	3:G:2450:ADP:C8	2.55	0.42
1:K:30:ASN:ND2	1:K:30:ASN:H	2.17	0.42
1:L:14:ILE:HD12	1:L:43:ILE:O	2.19	0.42
2:E:217:LYS:O	2:E:221:ALA:N	2.36	0.42
2:E:351:ILE:HD13	2:E:396:HIS:ND1	2.34	0.42
1:D:43:ILE:H	1:D:43:ILE:CD1	2.24	0.42
2:G:140:LYS:HD3	2:G:140:LYS:N	2.33	0.42
1:K:36:ARG:C	1:K:37:LEU:HD23	2.43	0.42
2:E:108:VAL:HA	2:E:111:VAL:HG22	2.01	0.42
2:F:171:LYS:HZ3	2:F:218:ILE:HD11	1.82	0.42
1:D:22:LEU:HD12	1:D:27:MET:CE	2.49	0.42
1:J:70:HIS:ND1	1:J:73:LYS:HB2	2.34	0.42
2:G:163:LEU:HG	2:G:163:LEU:O	2.19	0.42
2:H:61:VAL:C	3:H:3450:ADP:N7	2.78	0.42
2:H:94:LYS:HZ1	2:H:101:ARG:HH12	1.68	0.42
2:H:220:ASP:C	2:H:222:MET:H	2.26	0.42
2:H:312:ILE:CG1	2:H:313:ALA:N	2.82	0.42
1:K:38:TYR:HB2	1:K:64:LEU:CD1	2.50	0.42
2:E:232:LYS:NZ	2:E:232:LYS:HB3	2.33	0.42
1:J:32:LYS:HE3	1:J:32:LYS:HB2	1.78	0.42
1:J:59:LEU:HD11	1:J:63:LYS:HE2	2.02	0.42
1:J:150:LYS:O	1:J:154:ILE:HG12	2.18	0.42
2:G:33:ASN:ND2	2:G:36:ARG:HD2	2.35	0.42
1:B:11:HIS:CE1	1:B:172:SER:OG	2.73	0.42
1:B:32:LYS:HE3	1:B:32:LYS:HB2	1.78	0.42
2:F:264:ARG:CZ	2:F:265:GLY:H	2.31	0.42
1:D:134:ARG:HD2	1:D:138:GLU:OE1	2.19	0.42
1:I:80:LYS:O	1:I:81:ASP:C	2.62	0.42
2:G:216:LEU:HD12	2:G:216:LEU:O	2.19	0.42
2:G:349:ALA:HB1	2:H:44:LEU:CD2	2.50	0.42
2:H:96:VAL:CG1	2:H:99:ILE:HD12	2.49	0.42
2:H:147:GLU:HG2	2:H:150:GLN:NE2	2.35	0.42
2:H:432:LEU:N	2:H:432:LEU:CD1	2.83	0.42
1:K:141:GLU:OE2	1:K:141:GLU:HA	2.20	0.42
1:A:28:LYS:HD2	1:B:113:VAL:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:ARG:HG2	1:A:89:ARG:HH22	1.85	0.42
1:B:104:LEU:HB2	1:B:113:VAL:O	2.19	0.42
1:B:117:ASN:O	1:B:118:ASP:HB2	2.19	0.42
2:E:40:LEU:O	2:E:45:ARG:NH1	2.53	0.42
2:F:55:MET:HE3	2:F:305:ILE:CG2	2.49	0.42
2:F:403:MET:HE1	2:F:420:ILE:HD11	2.01	0.42
1:I:94:LEU:C	1:I:95:LEU:HD12	2.44	0.42
1:J:8:ARG:O	1:J:11:HIS:HB2	2.20	0.42
2:H:84:THR:C	2:H:86:PHE:N	2.77	0.42
1:B:53:ALA:O	1:B:56:LEU:N	2.53	0.42
2:E:167:GLN:CD	2:E:168:LEU:HG	2.44	0.42
1:I:6:VAL:HG12	1:I:7:ARG:N	2.35	0.42
1:I:173:TYR:O	1:I:174:LYS:C	2.62	0.42
2:G:366:ILE:HD13	2:G:366:ILE:HA	1.92	0.42
1:L:89:ARG:HH11	1:L:89:ARG:HB2	1.84	0.42
1:B:6:VAL:HG12	1:B:7:ARG:N	2.34	0.42
2:E:299:THR:CA	2:E:302:ILE:HD13	2.38	0.42
2:F:151:GLU:CB	2:F:152:PRO:HD3	2.50	0.42
1:D:1:THR:HB	1:D:33:LYS:NZ	2.35	0.42
1:J:63:LYS:HD2	1:J:77:GLU:HB3	2.01	0.42
1:J:79:ALA:HB1	1:J:110:GLY:C	2.45	0.42
2:G:214:ARG:HD3	2:G:216:LEU:HD23	2.02	0.42
2:H:32:ARG:O	2:H:36:ARG:HG3	2.20	0.42
2:H:40:LEU:O	2:H:45:ARG:NH1	2.52	0.42
2:H:342:ARG:O	2:H:346:GLU:HB2	2.20	0.42
1:A:99:ASP:OD1	1:A:101:THR:N	2.36	0.41
2:E:89:VAL:HA	2:E:92:VAL:C	2.45	0.41
2:E:173:ILE:N	2:E:173:ILE:CD1	2.82	0.41
1:C:95:LEU:N	1:C:95:LEU:HD12	2.35	0.41
1:C:114:GLN:O	1:C:115:PRO:O	2.38	0.41
2:G:92:VAL:CG1	2:H:92:VAL:CG1	2.93	0.41
2:G:128:GLU:C	2:G:130:ARG:N	2.76	0.41
2:G:161:LYS:O	2:G:164:ARG:HB2	2.19	0.41
2:G:174:GLU:OE2	2:G:213:ALA:HA	2.19	0.41
2:G:349:ALA:CB	2:H:44:LEU:CD2	2.98	0.41
2:H:257:GLU:HB2	2:H:260:LYS:CG	2.50	0.41
2:E:257:GLU:O	2:E:257:GLU:CG	2.63	0.41
2:E:408:TYR:CB	2:F:29:ILE:HD11	2.50	0.41
1:C:44:ALA:HB1	1:C:57:PHE:CE1	2.55	0.41
1:D:43:ILE:HD13	1:D:43:ILE:N	2.25	0.41
1:D:160:ILE:HD13	1:D:160:ILE:HA	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:131:ILE:HD11	2:G:218:ILE:CG1	2.49	0.41
2:H:80:LYS:HG3	2:H:254:PHE:HD1	1.85	0.41
2:H:135:LEU:HB3	2:H:159:PHE:HD2	1.80	0.41
2:H:285:VAL:HG12	2:H:304:PHE:CD1	2.55	0.41
2:H:289:THR:CG2	2:H:296:MET:HG3	2.50	0.41
1:B:103:SER:C	1:B:104:LEU:HD23	2.45	0.41
2:E:106:ALA:O	2:E:110:MET:HB2	2.20	0.41
2:E:214:ARG:CD	2:E:216:LEU:HD22	2.41	0.41
2:F:220:ASP:O	2:F:221:ALA:C	2.62	0.41
1:C:73:LYS:HD2	1:C:76:VAL:HG11	2.02	0.41
2:G:89:VAL:HA	2:G:93:GLY:HA3	2.02	0.41
2:G:400:GLU:HG3	2:H:327:PRO:HB2	2.02	0.41
2:H:148:GLN:HA	2:H:151:GLU:CG	2.44	0.41
2:F:168:LEU:HD12	2:F:217:LYS:HG2	2.02	0.41
2:F:212:LYS:O	2:F:213:ALA:HB3	2.20	0.41
2:F:311:GLN:HE21	2:F:311:GLN:HA	1.83	0.41
1:C:8:ARG:NH2	1:C:137:LEU:HD12	2.35	0.41
1:C:73:LYS:HA	1:C:73:LYS:HD2	1.92	0.41
1:D:51:ALA:C	1:D:53:ALA:N	2.76	0.41
1:I:38:TYR:HE1	1:I:65:GLU:HG2	1.85	0.41
2:G:91:TYR:CE1	2:H:91:TYR:CE2	3.09	0.41
2:H:41:ASN:HD21	2:H:44:LEU:HB2	1.84	0.41
2:H:89:VAL:HA	2:H:92:VAL:O	2.20	0.41
2:H:218:ILE:C	2:H:220:ASP:H	2.28	0.41
2:H:269:GLY:N	2:H:270:PRO:CD	2.84	0.41
1:L:42:VAL:HG13	1:L:98:ALA:O	2.21	0.41
2:F:109:LYS:HG3	2:F:109:LYS:O	2.19	0.41
2:F:167:GLN:OE1	2:F:168:LEU:N	2.53	0.41
2:F:223:LYS:HD2	2:F:223:LYS:H	1.84	0.41
1:J:101:THR:HG22	1:J:102:ALA:N	2.34	0.41
2:G:408:TYR:HE1	2:H:10:VAL:HG21	1.85	0.41
2:H:387:THR:OG1	2:H:388:GLU:N	2.53	0.41
1:L:3:ILE:HB	1:L:122:ILE:HG12	2.02	0.41
1:L:53:ALA:O	1:L:54:PHE:C	2.63	0.41
1:L:121:ALA:HB1	1:L:126:GLY:O	2.20	0.41
1:B:28:LYS:HZ1	1:B:30:ASN:ND2	2.17	0.41
1:B:73:LYS:HA	1:B:76:VAL:HG23	2.03	0.41
2:E:296:MET:HA	2:E:296:MET:CE	2.50	0.41
2:E:312:ILE:CG1	2:E:313:ALA:N	2.81	0.41
2:F:89:VAL:HG12	2:F:93:GLY:HA3	2.02	0.41
2:F:103:LEU:HD13	2:F:247:VAL:CG2	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:LEU:HD22	1:C:166:HIS:CE1	2.56	0.41
2:G:12:GLU:HG2	2:G:73:LEU:CD1	2.51	0.41
2:G:147:GLU:O	2:G:150:GLN:HG3	2.21	0.41
1:K:71:LEU:HD21	1:K:97:VAL:HG12	2.02	0.41
1:B:17:ASP:HB2	1:B:163:ASN:OD1	2.20	0.41
1:B:88:LEU:HD12	1:B:91:LEU:HD11	2.03	0.41
1:B:170:GLU:HG2	1:B:171:LEU:N	2.27	0.41
2:E:5:THR:O	2:E:6:PRO:C	2.62	0.41
2:F:94:LYS:HA	2:F:94:LYS:CE	2.29	0.41
2:F:375:ARG:HA	2:F:378:GLU:HB2	2.02	0.41
2:F:384:ASN:HD21	2:F:394:ARG:HE	1.62	0.41
1:C:99:ASP:HA	1:C:171:LEU:HD22	2.01	0.41
2:H:219:LYS:HA	2:H:223:LYS:HZ3	1.86	0.41
2:H:236:PRO:CG	2:H:237:GLU:H	2.32	0.41
2:H:247:VAL:O	2:H:302:ILE:HD13	2.21	0.41
2:H:268:SER:HA	2:H:271:ASP:OD2	2.20	0.41
2:H:409:ASP:O	2:H:410:ALA:C	2.62	0.41
1:L:6:VAL:HG12	1:L:7:ARG:N	2.36	0.41
1:B:18:GLY:C	1:B:163:ASN:HD21	2.29	0.41
1:B:101:THR:HG22	1:B:102:ALA:N	2.35	0.41
2:E:352:THR:CG2	2:E:353:VAL:N	2.84	0.41
2:F:4:MET:HE1	2:F:73:LEU:HD11	2.01	0.41
2:F:96:VAL:HG21	2:F:280:ASP:HB3	2.03	0.41
2:F:217:LYS:CG	2:F:218:ILE:H	2.31	0.41
2:F:432:LEU:N	2:F:432:LEU:CD1	2.83	0.41
1:J:99:ASP:OD1	1:J:101:THR:N	2.53	0.41
1:J:174:LYS:HD2	1:J:174:LYS:N	2.36	0.41
2:G:107:ALA:O	2:G:111:VAL:HG22	2.20	0.41
2:G:148:GLN:OE1	2:G:151:GLU:HG3	2.21	0.41
2:G:173:ILE:N	2:G:173:ILE:CD1	2.79	0.41
2:G:212:LYS:HD3	2:G:216:LEU:HD11	2.02	0.41
2:H:355:TYR:CD1	2:H:403:MET:HE2	2.56	0.41
2:H:443:LEU:HD23	2:H:443:LEU:HA	1.94	0.41
1:A:3:ILE:HB	1:A:122:ILE:HG12	2.03	0.41
1:A:71:LEU:HD11	1:A:97:VAL:HG13	2.02	0.41
1:B:6:VAL:HG21	1:B:147:ILE:HG22	2.02	0.41
2:E:135:LEU:HB3	2:E:159:PHE:CD2	2.55	0.41
2:E:168:LEU:HD22	2:E:219:LYS:HD3	2.02	0.41
2:E:174:GLU:CA	2:E:212:LYS:HB3	2.51	0.41
2:E:285:VAL:HG12	2:E:304:PHE:CD1	2.56	0.41
2:E:408:TYR:CD1	2:F:29:ILE:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:152:LEU:HD22	1:C:166:HIS:HE1	1.86	0.41
1:D:64:LEU:HA	1:D:74:ALA:HB2	2.03	0.41
1:J:38:TYR:HB2	1:J:64:LEU:HD13	2.03	0.41
1:J:105:ILE:HG22	1:J:106:ILE:N	2.35	0.41
2:G:27:VAL:CG1	2:G:70:LEU:HG	2.51	0.41
2:G:226:ILE:O	2:G:230:ALA:HB2	2.20	0.41
2:G:240:LYS:HD3	2:G:240:LYS:C	2.46	0.41
2:H:145:GLN:H	2:H:148:GLN:HB2	1.86	0.41
2:H:228:GLU:C	2:H:232:LYS:HE2	2.46	0.41
2:H:402:LEU:HD12	2:H:428:HIS:HB2	2.03	0.41
1:A:82:TRP:CH2	1:A:95:LEU:HD13	2.56	0.41
1:C:59:LEU:HD23	1:C:78:LEU:HD12	2.03	0.41
1:D:80:LYS:HD2	1:D:80:LYS:C	2.46	0.41
1:D:80:LYS:HD2	1:D:80:LYS:O	2.21	0.41
1:I:88:LEU:CD1	1:I:88:LEU:N	2.82	0.41
1:J:12:VAL:CG1	1:J:171:LEU:HB3	2.50	0.41
2:H:145:GLN:CA	2:H:145:GLN:NE2	2.84	0.41
2:H:174:GLU:HB3	2:H:211:GLN:NE2	2.36	0.41
2:H:292:THR:OG1	2:H:295:GLY:O	2.36	0.41
2:H:293:LYS:HG3	2:H:294:HIS:CE1	2.56	0.41
1:L:28:LYS:HG2	1:L:30:ASN:ND2	2.36	0.41
2:E:65:GLU:HG3	3:E:450:ADP:H2'	2.02	0.40
2:E:440:ARG:HB3	2:F:316:SER:OG	2.20	0.40
2:F:384:ASN:ND2	2:F:390:ILE:H	2.19	0.40
1:C:28:LYS:HG2	1:C:30:ASN:HD22	1.86	0.40
1:C:68:GLN:O	1:C:69:GLY:C	2.64	0.40
1:D:67:HIS:O	1:D:68:GLN:C	2.64	0.40
2:G:167:GLN:OE1	2:G:168:LEU:N	2.53	0.40
2:G:312:ILE:CG1	2:G:313:ALA:N	2.84	0.40
2:H:235:ASN:OD1	2:H:238:GLU:HB2	2.20	0.40
2:H:270:PRO:O	2:H:273:SER:HB3	2.21	0.40
2:H:336:THR:H	2:H:339:ASP:HB2	1.86	0.40
2:H:381:TRP:CD1	2:H:381:TRP:C	2.99	0.40
1:A:83:ARG:NH1	1:A:83:ARG:HG2	2.36	0.40
1:B:34:VAL:HA	1:B:45:GLY:HA2	2.03	0.40
1:B:78:LEU:C	1:B:80:LYS:N	2.79	0.40
2:E:151:GLU:HB2	2:E:152:PRO:CD	2.51	0.40
2:E:215:LYS:HG3	2:E:215:LYS:O	2.21	0.40
2:E:253:VAL:HB	2:E:304:PHE:CD2	2.56	0.40
2:F:108:VAL:HG12	2:F:109:LYS:N	2.35	0.40
2:F:122:ARG:HA	2:F:122:ARG:NE	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:PHE:CZ	1:D:97:VAL:HG11	2.56	0.40
1:I:171:LEU:HD12	1:I:171:LEU:HA	1.93	0.40
2:H:384:ASN:HD22	2:H:384:ASN:HA	1.60	0.40
1:L:85:ASP:CB	1:L:88:LEU:HD12	2.52	0.40
1:L:114:GLN:O	1:L:115:PRO:O	2.39	0.40
1:B:66:MET:O	1:B:67:HIS:ND1	2.54	0.40
2:F:253:VAL:HB	2:F:304:PHE:CD2	2.57	0.40
1:C:62:ARG:HA	1:C:65:GLU:OE2	2.21	0.40
1:C:105:ILE:HD12	1:C:122:ILE:CG2	2.52	0.40
2:G:339:ASP:O	2:G:343:ILE:HG13	2.22	0.40
2:G:408:TYR:CE1	2:H:25:ARG:HG2	2.55	0.40
2:H:22:ASN:HD22	2:H:22:ASN:HA	1.66	0.40
2:H:160:ARG:HG2	2:H:160:ARG:NH1	2.36	0.40
2:H:168:LEU:HD12	2:H:217:LYS:CD	2.49	0.40
2:H:366:ILE:HG13	2:H:420:ILE:CD1	2.51	0.40
1:A:80:LYS:C	1:A:82:TRP:N	2.78	0.40
1:B:94:LEU:HB3	1:B:122:ILE:HD12	2.03	0.40
1:B:168:ILE:N	1:B:168:ILE:CD1	2.84	0.40
2:E:108:VAL:O	2:E:110:MET:N	2.55	0.40
2:E:355:TYR:CE2	2:E:400:GLU:OE2	2.73	0.40
2:F:168:LEU:O	2:F:168:LEU:HG	2.21	0.40
1:D:26:VAL:HG12	1:D:28:LYS:O	2.22	0.40
1:I:13:VAL:HG12	1:I:170:GLU:HG3	2.03	0.40
1:I:124:SER:HB3	1:I:159:CYS:SG	2.62	0.40
1:J:6:VAL:CG1	1:J:7:ARG:N	2.83	0.40
1:J:43:ILE:HG12	1:J:98:ALA:O	2.21	0.40
1:J:107:THR:C	1:J:109:ASN:N	2.79	0.40
2:G:145:GLN:HG3	2:G:148:GLN:CG	2.50	0.40
2:G:234:VAL:O	2:G:236:PRO:HD3	2.22	0.40
1:A:137:LEU:HD23	1:A:137:LEU:O	2.22	0.40
1:B:53:ALA:C	1:B:55:THR:H	2.29	0.40
1:B:107:THR:O	1:B:109:ASN:N	2.54	0.40
2:F:12:GLU:HG2	2:F:73:LEU:HD11	2.02	0.40
2:F:229:GLU:O	2:F:230:ALA:HB2	2.22	0.40
2:G:432:LEU:HD12	2:G:432:LEU:H	1.87	0.40
1:L:88:LEU:O	1:L:91:LEU:HG	2.22	0.40
1:L:95:LEU:HD12	1:L:95:LEU:N	2.36	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:7:ARG:NH2	2:F:409:ASP:OD2[2_665]	2.01	0.19
1:K:160:ILE:CG2	1:K:160:ILE:CG2[4_666]	2.04	0.16
1:D:160:ILE:CG2	1:D:160:ILE:CG2[6_577]	2.19	0.01

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	172/175 (98%)	152 (88%)	16 (9%)	4 (2%)	5	18
1	B	172/175 (98%)	137 (80%)	25 (14%)	10 (6%)	1	4
1	C	172/175 (98%)	150 (87%)	17 (10%)	5 (3%)	3	13
1	D	172/175 (98%)	145 (84%)	23 (13%)	4 (2%)	5	18
1	I	172/175 (98%)	147 (86%)	20 (12%)	5 (3%)	3	13
1	J	172/175 (98%)	140 (81%)	26 (15%)	6 (4%)	3	10
1	K	172/175 (98%)	146 (85%)	23 (13%)	3 (2%)	7	25
1	L	172/175 (98%)	149 (87%)	18 (10%)	5 (3%)	3	13
2	E	404/449 (90%)	348 (86%)	47 (12%)	9 (2%)	5	19
2	F	404/449 (90%)	344 (85%)	43 (11%)	17 (4%)	2	7
2	G	404/449 (90%)	344 (85%)	48 (12%)	12 (3%)	3	12
2	H	404/449 (90%)	343 (85%)	45 (11%)	16 (4%)	2	8
All	All	2992/3196 (94%)	2545 (85%)	351 (12%)	96 (3%)	3	11

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	71	LEU
1	B	72	VAL
1	B	116	GLU
2	E	92	VAL
2	E	144	GLY

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Mol	Chain	Res	Type
2	E	153	SER
2	E	212	LYS
2	F	92	VAL
2	F	153	SER
2	F	165	GLU
2	F	212	LYS
2	F	237	GLU
1	C	116	GLU
1	D	69	GLY
1	J	116	GLU
2	G	92	VAL
2	G	144	GLY
2	G	146	THR
2	G	153	SER
2	G	212	LYS
2	H	92	VAL
2	H	153	SER
2	H	165	GLU
2	H	212	LYS
2	H	236	PRO
2	H	237	GLU
1	L	116	GLU
1	A	9	ASN
1	B	54	PHE
2	E	165	GLU
2	E	410	ALA
2	F	230	ALA
2	F	236	PRO
2	F	300	ASP
1	D	68	GLN
1	D	113	VAL
1	J	54	PHE
2	G	165	GLU
2	G	170	ASP
2	H	138	PRO
2	H	154	ALA
2	H	228	GLU
2	H	230	ALA
2	H	300	ASP
1	K	68	GLN
1	K	69	GLY
1	K	116	GLU

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Mol	Chain	Res	Type
1	L	69	GLY
1	A	115	PRO
1	B	68	GLN
2	E	141	ASN
2	E	146	THR
2	F	138	PRO
1	C	115	PRO
1	C	117	ASN
1	I	71	LEU
1	I	115	PRO
1	J	71	LEU
1	J	101	THR
2	G	141	ASN
2	G	227	GLU
2	G	232	LYS
2	H	143	TRP
2	H	146	THR
1	L	115	PRO
1	A	71	LEU
1	A	81	ASP
1	B	70	HIS
2	E	217	LYS
2	F	109	LYS
2	F	125	GLU
2	F	137	PRO
1	I	110	GLY
1	I	142	LEU
1	J	68	GLN
2	G	44	LEU
2	G	172	GLU
2	H	125	GLU
1	L	117	ASN
2	F	140	LYS
2	F	228	GLU
1	D	99	ASP
2	H	137	PRO
1	B	69	GLY
1	B	82	TRP
1	B	86	ARG
2	F	146	THR
2	F	154	ALA
1	C	40	ASP

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Mol	Chain	Res	Type
1	L	110	GLY
1	C	69	GLY
2	H	144	GLY
2	F	173	ILE
1	J	72	VAL
1	B	147	ILE
1	I	72	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	136/136 (100%)	126 (93%)	10 (7%)	13	37
1	B	136/136 (100%)	124 (91%)	12 (9%)	9	29
1	C	136/136 (100%)	123 (90%)	13 (10%)	8	26
1	D	136/136 (100%)	121 (89%)	15 (11%)	6	20
1	I	136/136 (100%)	125 (92%)	11 (8%)	11	33
1	J	136/136 (100%)	120 (88%)	16 (12%)	5	17
1	K	136/136 (100%)	125 (92%)	11 (8%)	11	33
1	L	136/136 (100%)	122 (90%)	14 (10%)	7	23
2	E	350/383 (91%)	305 (87%)	45 (13%)	4	14
2	F	350/383 (91%)	291 (83%)	59 (17%)	2	7
2	G	350/383 (91%)	306 (87%)	44 (13%)	4	15
2	H	350/383 (91%)	298 (85%)	52 (15%)	3	10
All	All	2488/2620 (95%)	2186 (88%)	302 (12%)	5	16

All (302) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	THR
1	A	9	ASN
1	A	30	ASN

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Mol	Chain	Res	Type
1	A	36	ARG
1	A	65	GLU
1	A	71	LEU
1	A	97	VAL
1	A	136	LEU
1	A	152	LEU
1	A	160	ILE
1	B	1	THR
1	B	22	LEU
1	B	30	ASN
1	B	54	PHE
1	B	72	VAL
1	B	99	ASP
1	B	104	LEU
1	B	112	VAL
1	B	116	GLU
1	B	136	LEU
1	B	152	LEU
1	B	160	ILE
2	E	11	SER
2	E	13	LEU
2	E	27	VAL
2	E	31	LEU
2	E	37	ARG
2	E	59	THR
2	E	79	ILE
2	E	92	VAL
2	E	94	LYS
2	E	103	LEU
2	E	108	VAL
2	E	117	GLU
2	E	130	ARG
2	E	140	LYS
2	E	152	PRO
2	E	165	GLU
2	E	167	GLN
2	E	169	ASP
2	E	171	LYS
2	E	173	ILE
2	E	212	LYS
2	E	225	LEU
2	E	232	LYS

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Mol	Chain	Res	Type
2	E	238	GLU
2	E	240	LYS
2	E	241	GLN
2	E	266	GLU
2	E	281	LEU
2	E	296	MET
2	E	311	GLN
2	E	312	ILE
2	E	318	LEU
2	E	326	LEU
2	E	337	THR
2	E	344	LEU
2	E	351	ILE
2	E	352	THR
2	E	355	TYR
2	E	375	ARG
2	E	385	GLU
2	E	386	SER
2	E	388	GLU
2	E	389	ASN
2	E	411	SER
2	E	413	LEU
2	F	13	LEU
2	F	27	VAL
2	F	31	LEU
2	F	37	ARG
2	F	41	ASN
2	F	59	THR
2	F	70	LEU
2	F	87	THR
2	F	94	LYS
2	F	95	GLU
2	F	103	LEU
2	F	104	THR
2	F	108	VAL
2	F	121	TYR
2	F	130	ARG
2	F	138	PRO
2	F	140	LYS
2	F	145	GLN
2	F	148	GLN
2	F	150	GLN

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Mol	Chain	Res	Type
2	F	152	PRO
2	F	165	GLU
2	F	173	ILE
2	F	210	LYS
2	F	211	GLN
2	F	212	LYS
2	F	214	ARG
2	F	217	LYS
2	F	219	LYS
2	F	220	ASP
2	F	225	LEU
2	F	232	LYS
2	F	238	GLU
2	F	239	LEU
2	F	266	GLU
2	F	281	LEU
2	F	296	MET
2	F	302	ILE
2	F	311	GLN
2	F	312	ILE
2	F	318	LEU
2	F	326	LEU
2	F	337	THR
2	F	344	LEU
2	F	351	ILE
2	F	352	THR
2	F	353	VAL
2	F	355	TYR
2	F	366	ILE
2	F	367	GLU
2	F	375	ARG
2	F	382	GLN
2	F	384	ASN
2	F	385	GLU
2	F	389	ASN
2	F	404	GLU
2	F	413	LEU
2	F	438	LEU
2	F	442	ILE
1	C	1	THR
1	C	4	VAL
1	C	30	ASN

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Mol	Chain	Res	Type
1	C	36	ARG
1	C	37	LEU
1	C	67	HIS
1	C	71	LEU
1	C	83	ARG
1	C	87	MET
1	C	136	LEU
1	C	152	LEU
1	C	160	ILE
1	C	167	THR
1	D	1	THR
1	D	4	VAL
1	D	30	ASN
1	D	39	ASN
1	D	43	ILE
1	D	73	LYS
1	D	77	GLU
1	D	104	LEU
1	D	112	VAL
1	D	114	GLN
1	D	116	GLU
1	D	136	LEU
1	D	152	LEU
1	D	160	ILE
1	D	174	LYS
1	I	1	THR
1	I	4	VAL
1	I	30	ASN
1	I	36	ARG
1	I	58	GLU
1	I	71	LEU
1	I	116	GLU
1	I	152	LEU
1	I	158	ILE
1	I	160	ILE
1	I	168	ILE
1	J	1	THR
1	J	13	VAL
1	J	22	LEU
1	J	30	ASN
1	J	54	PHE
1	J	59	LEU

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Mol	Chain	Res	Type
1	J	65	GLU
1	J	72	VAL
1	J	95	LEU
1	J	97	VAL
1	J	112	VAL
1	J	116	GLU
1	J	136	LEU
1	J	152	LEU
1	J	160	ILE
1	J	168	ILE
2	G	13	LEU
2	G	27	VAL
2	G	31	LEU
2	G	34	ARG
2	G	37	ARG
2	G	49	THR
2	G	70	LEU
2	G	92	VAL
2	G	94	LYS
2	G	103	LEU
2	G	108	VAL
2	G	117	GLU
2	G	130	ARG
2	G	140	LYS
2	G	152	PRO
2	G	164	ARG
2	G	168	LEU
2	G	169	ASP
2	G	171	LYS
2	G	173	ILE
2	G	212	LYS
2	G	225	LEU
2	G	238	GLU
2	G	240	LYS
2	G	241	GLN
2	G	266	GLU
2	G	296	MET
2	G	311	GLN
2	G	312	ILE
2	G	318	LEU
2	G	326	LEU
2	G	337	THR

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Mol	Chain	Res	Type
2	G	344	LEU
2	G	352	THR
2	G	353	VAL
2	G	355	TYR
2	G	370	ASP
2	G	375	ARG
2	G	378	GLU
2	G	385	GLU
2	G	386	SER
2	G	388	GLU
2	G	413	LEU
2	G	438	LEU
2	H	13	LEU
2	H	27	VAL
2	H	31	LEU
2	H	37	ARG
2	H	41	ASN
2	H	59	THR
2	H	70	LEU
2	H	79	ILE
2	H	87	THR
2	H	94	LYS
2	H	95	GLU
2	H	103	LEU
2	H	104	THR
2	H	108	VAL
2	H	121	TYR
2	H	130	ARG
2	H	138	PRO
2	H	140	LYS
2	H	145	GLN
2	H	148	GLN
2	H	150	GLN
2	H	152	PRO
2	H	160	ARG
2	H	169	ASP
2	H	173	ILE
2	H	210	LYS
2	H	211	GLN
2	H	212	LYS
2	H	217	LYS
2	H	219	LYS

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Mol	Chain	Res	Type
2	H	229	GLU
2	H	238	GLU
2	H	239	LEU
2	H	266	GLU
2	H	296	MET
2	H	311	GLN
2	H	312	ILE
2	H	318	LEU
2	H	326	LEU
2	H	337	THR
2	H	344	LEU
2	H	351	ILE
2	H	352	THR
2	H	375	ARG
2	H	382	GLN
2	H	384	ASN
2	H	388	GLU
2	H	389	ASN
2	H	404	GLU
2	H	413	LEU
2	H	438	LEU
2	H	442	ILE
1	K	1	THR
1	K	4	VAL
1	K	30	ASN
1	K	37	LEU
1	K	83	ARG
1	K	104	LEU
1	K	111	ASP
1	K	116	GLU
1	K	136	LEU
1	K	152	LEU
1	K	168	ILE
1	L	1	THR
1	L	4	VAL
1	L	30	ASN
1	L	36	ARG
1	L	37	LEU
1	L	39	ASN
1	L	43	ILE
1	L	73	LYS
1	L	83	ARG

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Mol	Chain	Res	Type
1	L	116	GLU
1	L	118	ASP
1	L	152	LEU
1	L	160	ILE
1	L	174	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (103) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	HIS
1	A	30	ASN
1	A	39	ASN
1	A	68	GLN
1	A	109	ASN
1	A	114	GLN
1	A	166	HIS
1	B	9	ASN
1	B	11	HIS
1	B	30	ASN
1	B	109	ASN
1	B	130	GLN
2	E	22	ASN
2	E	33	ASN
2	E	75	ASN
2	E	114	GLN
2	E	141	ASN
2	E	149	GLN
2	E	241	GLN
2	E	250	HIS
2	E	294	HIS
2	E	311	GLN
2	E	348	ASN
2	E	382	GLN
2	E	384	ASN
2	E	389	ASN
2	E	416	GLN
2	E	428	HIS
2	F	22	ASN
2	F	41	ASN
2	F	75	ASN
2	F	114	GLN
2	F	119	ASN

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Mol	Chain	Res	Type
2	F	141	ASN
2	F	142	ASN
2	F	145	GLN
2	F	149	GLN
2	F	150	GLN
2	F	211	GLN
2	F	241	GLN
2	F	311	GLN
2	F	348	ASN
2	F	384	ASN
2	F	389	ASN
2	F	416	GLN
1	C	9	ASN
1	C	30	ASN
1	C	166	HIS
1	D	11	HIS
1	D	19	GLN
1	D	30	ASN
1	D	114	GLN
1	I	9	ASN
1	I	11	HIS
1	I	30	ASN
1	I	39	ASN
1	I	67	HIS
1	I	109	ASN
1	I	114	GLN
1	J	30	ASN
1	J	109	ASN
1	J	130	GLN
2	G	22	ASN
2	G	33	ASN
2	G	75	ASN
2	G	114	GLN
2	G	149	GLN
2	G	150	GLN
2	G	241	GLN
2	G	250	HIS
2	G	294	HIS
2	G	301	HIS
2	G	311	GLN
2	G	348	ASN
2	G	382	GLN

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Mol	Chain	Res	Type
2	G	384	ASN
2	G	389	ASN
2	G	416	GLN
2	H	22	ASN
2	H	33	ASN
2	H	41	ASN
2	H	114	GLN
2	H	142	ASN
2	H	145	GLN
2	H	149	GLN
2	H	150	GLN
2	H	167	GLN
2	H	211	GLN
2	H	241	GLN
2	H	311	GLN
2	H	348	ASN
2	H	384	ASN
2	H	389	ASN
2	H	416	GLN
1	K	11	HIS
1	K	30	ASN
1	K	39	ASN
1	K	114	GLN
1	L	9	ASN
1	L	11	HIS
1	L	30	ASN
1	L	114	GLN
1	L	139	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ADP	G	2450	-	28,29,29	1.54	7 (25%)	43,45,45	1.30	7 (16%)
3	ADP	H	3450	-	28,29,29	1.58	6 (21%)	43,45,45	1.30	5 (11%)
3	ADP	F	1450	-	28,29,29	1.55	6 (21%)	43,45,45	1.28	5 (11%)
3	ADP	E	450	-	28,29,29	1.51	5 (17%)	43,45,45	1.33	6 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	G	2450	-	-	3/16/32/32	0/3/3/3
3	ADP	H	3450	-	-	3/16/32/32	0/3/3/3
3	ADP	F	1450	-	-	3/16/32/32	0/3/3/3
3	ADP	E	450	-	-	3/16/32/32	0/3/3/3

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1450	ADP	C1'-N9	3.68	1.56	1.46
3	H	3450	ADP	PA-O3A	3.52	1.63	1.59
3	H	3450	ADP	C1'-N9	3.46	1.55	1.46
3	G	2450	ADP	C1'-N9	3.37	1.55	1.46
3	E	450	ADP	C1'-N9	3.33	1.55	1.46
3	F	1450	ADP	PA-O3A	3.28	1.63	1.59
3	G	2450	ADP	PA-O3A	2.74	1.62	1.59
3	H	3450	ADP	C4-N3	2.70	1.39	1.34
3	G	2450	ADP	C4-N3	2.55	1.39	1.34
3	E	450	ADP	C4-N3	2.51	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1450	ADP	C4-N3	2.48	1.39	1.34
3	E	450	ADP	C8-N7	-2.42	1.27	1.31
3	H	3450	ADP	C8-N7	-2.38	1.27	1.31
3	E	450	ADP	PA-O1A	-2.37	1.42	1.50
3	F	1450	ADP	C8-N9	-2.28	1.33	1.37
3	G	2450	ADP	C8-N7	-2.25	1.27	1.31
3	F	1450	ADP	C8-N7	-2.16	1.27	1.31
3	H	3450	ADP	C8-N9	-2.14	1.33	1.37
3	G	2450	ADP	C8-N9	-2.12	1.33	1.37
3	H	3450	ADP	PA-O1A	-2.09	1.43	1.50
3	E	450	ADP	PA-O2A	-2.09	1.45	1.55
3	G	2450	ADP	PA-O2A	-2.05	1.45	1.55
3	F	1450	ADP	PB-O3B	-2.03	1.47	1.54
3	G	2450	ADP	PB-O3B	-2.00	1.47	1.54

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	2450	ADP	C4'-O4'-C1'	3.54	117.28	109.47
3	H	3450	ADP	C4'-O4'-C1'	3.48	117.15	109.47
3	F	1450	ADP	C4'-O4'-C1'	3.47	117.13	109.47
3	E	450	ADP	C4'-O4'-C1'	3.44	117.05	109.47
3	G	2450	ADP	C2'-C3'-C4'	3.25	108.88	102.61
3	H	3450	ADP	C2'-C3'-C4'	3.23	108.86	102.61
3	E	450	ADP	C2'-C3'-C4'	3.15	108.70	102.61
3	F	1450	ADP	C2'-C3'-C4'	3.11	108.61	102.61
3	E	450	ADP	C2'-C1'-N9	-2.93	106.03	113.30
3	H	3450	ADP	N3-C2-N1	-2.46	124.86	128.58
3	F	1450	ADP	N3-C2-N1	-2.37	125.00	128.58
3	G	2450	ADP	N3-C2-N1	-2.31	125.08	128.58
3	E	450	ADP	O2A-PA-O1A	2.31	123.19	112.44
3	E	450	ADP	C3'-C2'-C1'	2.26	105.74	101.46
3	H	3450	ADP	O2A-PA-O1A	2.24	122.86	112.44
3	E	450	ADP	N3-C2-N1	-2.23	125.20	128.58
3	G	2450	ADP	C2'-C1'-N9	-2.22	107.79	113.30
3	H	3450	ADP	C3'-C2'-C1'	2.21	105.64	101.46
3	F	1450	ADP	C3'-C2'-C1'	2.16	105.54	101.46
3	G	2450	ADP	O2A-PA-O1A	2.13	122.37	112.44
3	G	2450	ADP	O3B-PB-O3A	2.09	111.64	104.64
3	F	1450	ADP	O2A-PA-O1A	2.05	121.96	112.44
3	G	2450	ADP	C3'-C2'-C1'	2.02	105.28	101.46

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	1450	ADP	O4'-C4'-C5'-O5'
3	G	2450	ADP	O4'-C4'-C5'-O5'
3	H	3450	ADP	O4'-C4'-C5'-O5'
3	E	450	ADP	O4'-C4'-C5'-O5'
3	H	3450	ADP	C3'-C4'-C5'-O5'
3	F	1450	ADP	C3'-C4'-C5'-O5'
3	G	2450	ADP	C3'-C4'-C5'-O5'
3	H	3450	ADP	C4'-C5'-O5'-PA
3	E	450	ADP	C4'-C5'-O5'-PA
3	G	2450	ADP	C4'-C5'-O5'-PA
3	F	1450	ADP	C4'-C5'-O5'-PA
3	E	450	ADP	C3'-C4'-C5'-O5'

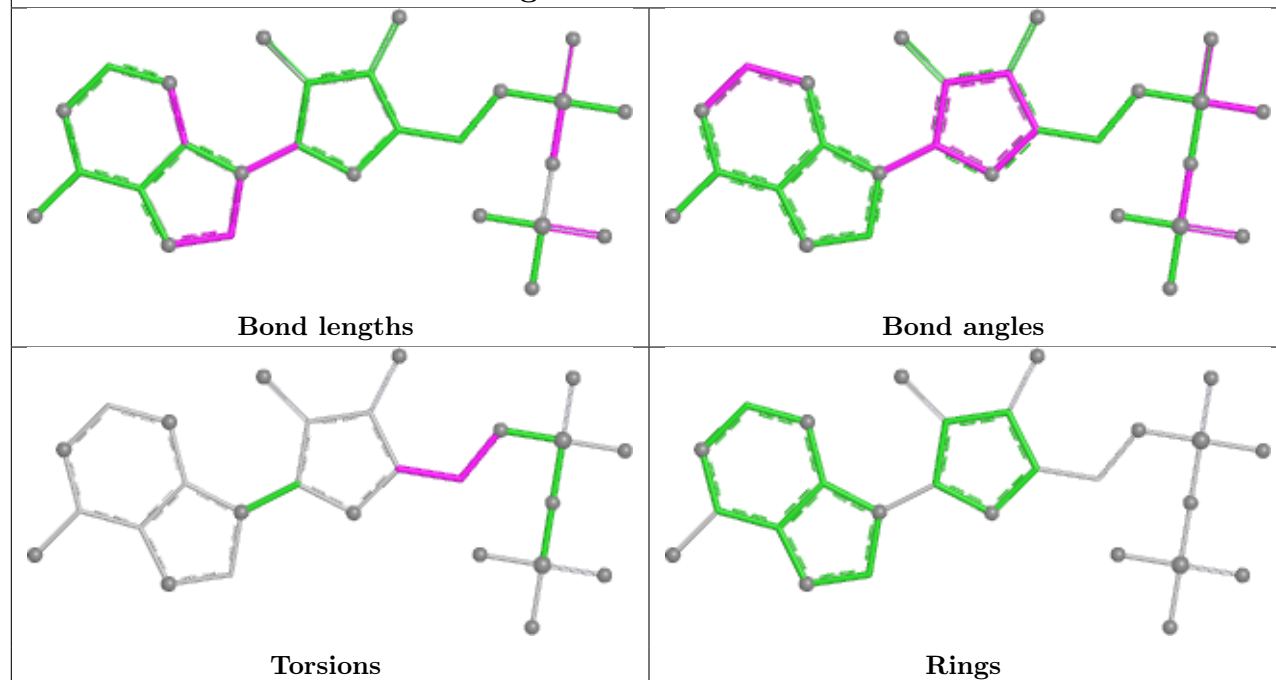
There are no ring outliers.

4 monomers are involved in 11 short contacts:

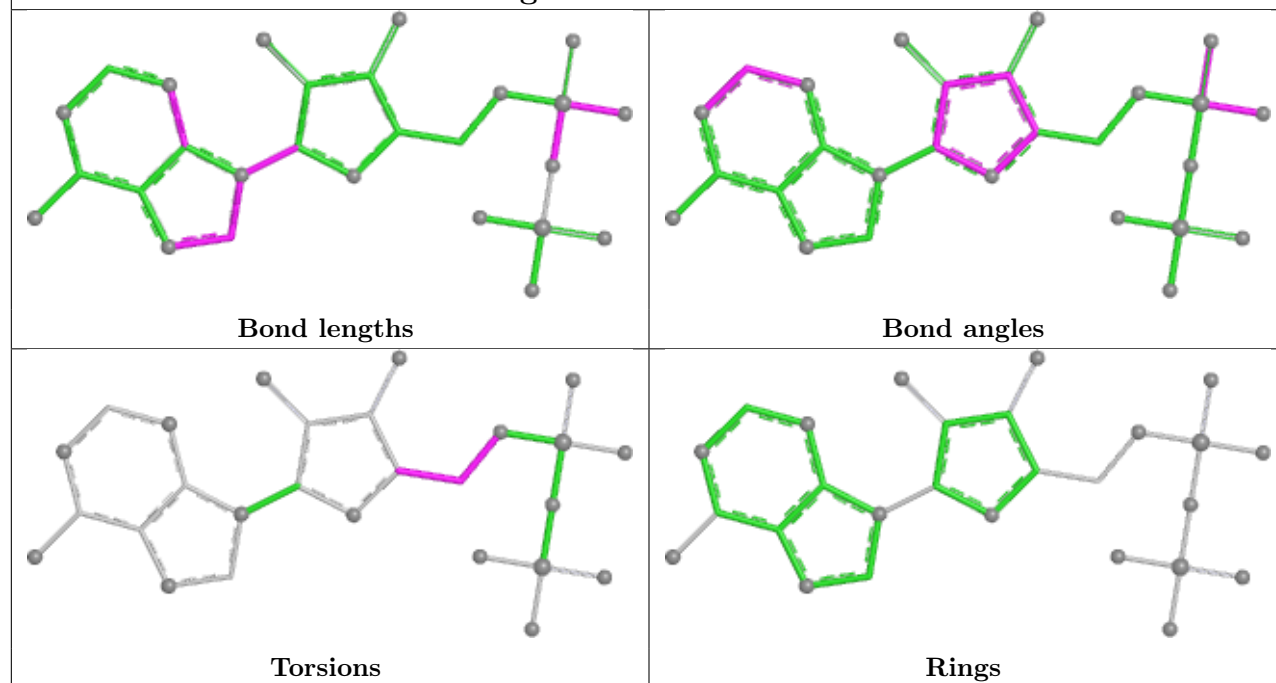
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	2450	ADP	2	0
3	H	3450	ADP	4	0
3	F	1450	ADP	3	0
3	E	450	ADP	2	0

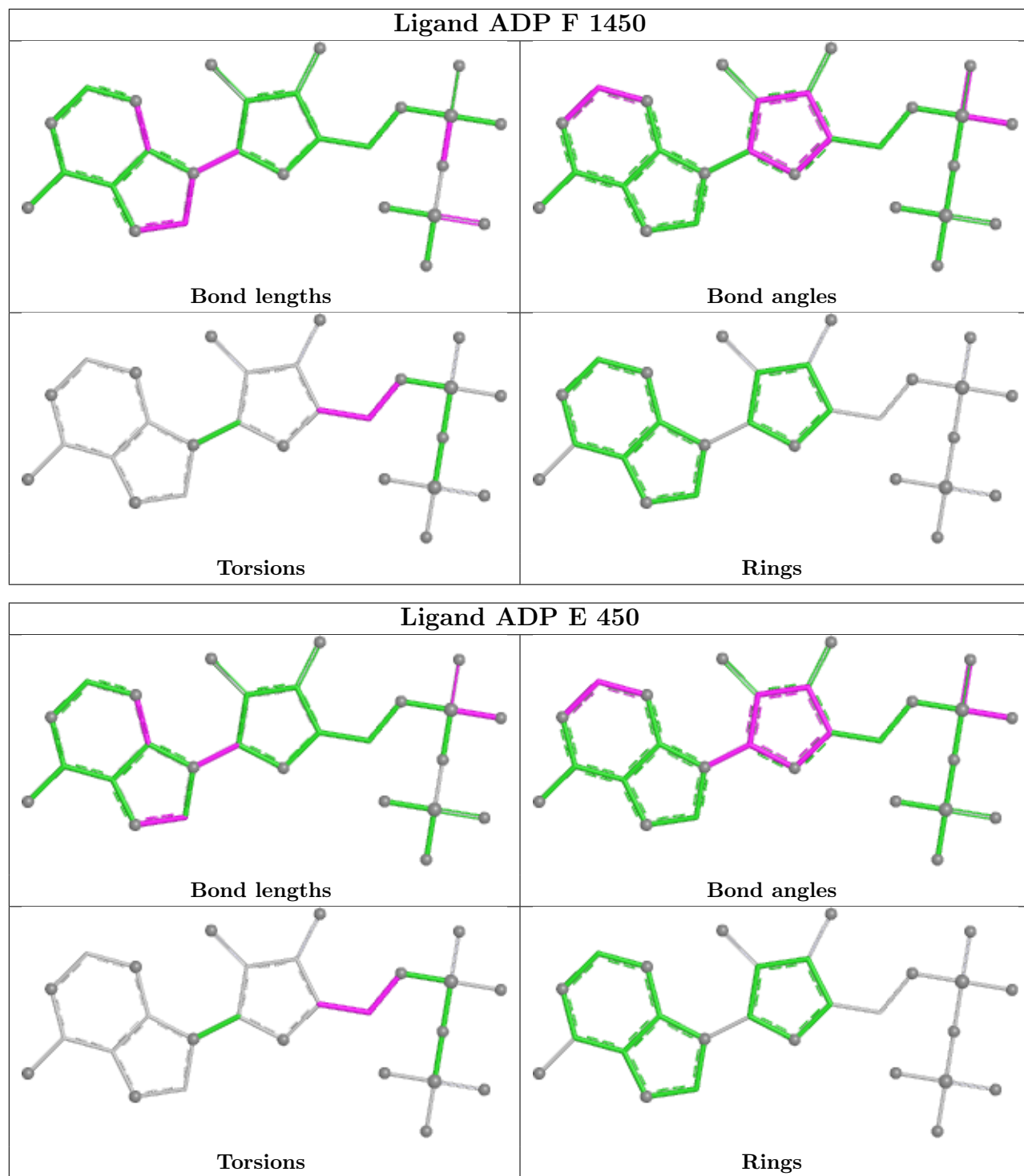
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ADP G 2450



Ligand ADP H 3450





5.7 Other polymers ⓘ

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	174/175 (99%)	-1.46	0	100	100	33, 58, 91, 99	0
1	B	174/175 (99%)	-1.34	0	100	100	38, 70, 101, 102	0
1	C	174/175 (99%)	-1.34	0	100	100	51, 68, 98, 101	0
1	D	174/175 (99%)	-1.15	0	100	100	54, 87, 101, 102	0
1	I	174/175 (99%)	-1.42	0	100	100	29, 56, 89, 97	0
1	J	174/175 (99%)	-1.32	0	100	100	36, 70, 100, 102	0
1	K	174/175 (99%)	-1.07	0	100	100	62, 95, 102, 102	0
1	L	174/175 (99%)	-1.26	0	100	100	57, 80, 102, 102	0
2	E	408/449 (90%)	-1.36	0	100	100	32, 59, 102, 102	0
2	F	408/449 (90%)	-1.35	1 (0%)	91	88	35, 61, 102, 102	0
2	G	408/449 (90%)	-1.35	1 (0%)	91	88	35, 62, 102, 102	0
2	H	408/449 (90%)	-1.36	0	100	100	35, 63, 102, 102	0
All	All	3024/3196 (94%)	-1.33	2 (0%)	92	90	29, 66, 102, 102	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	90	GLY	3.8
2	G	90	GLY	3.6

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](#)

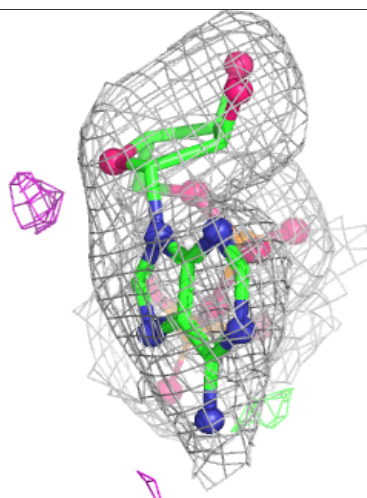
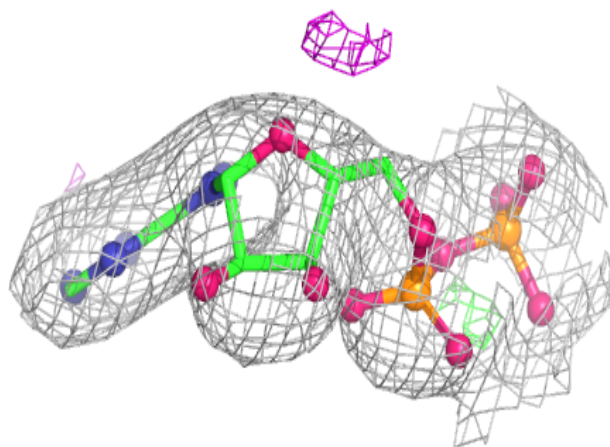
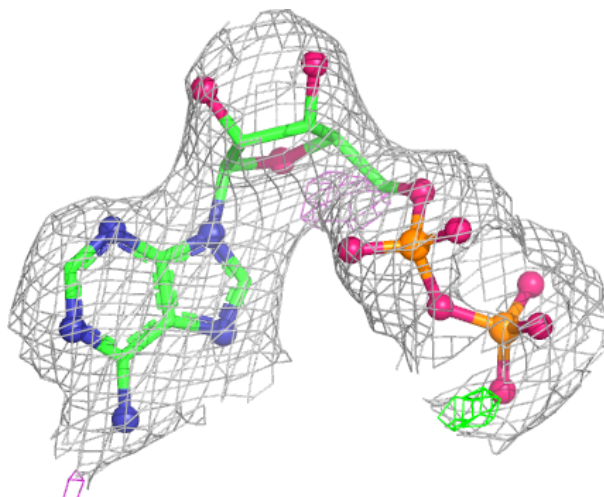
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ADP	E	450	27/27	0.99	0.04	46,50,60,62	0
3	ADP	F	1450	27/27	0.99	0.03	45,50,57,59	0
3	ADP	G	2450	27/27	0.99	0.04	43,51,61,61	0
3	ADP	H	3450	27/27	1.00	0.03	53,55,58,61	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

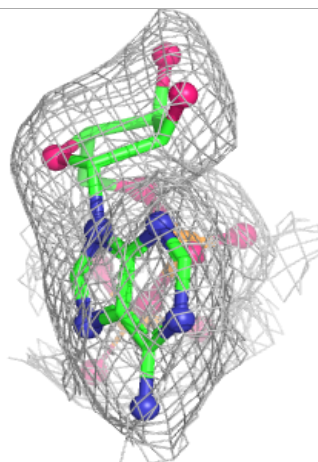
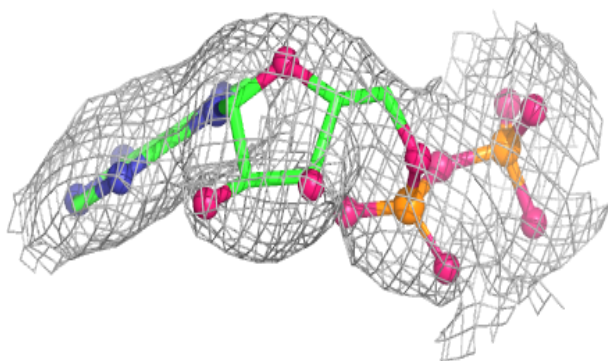
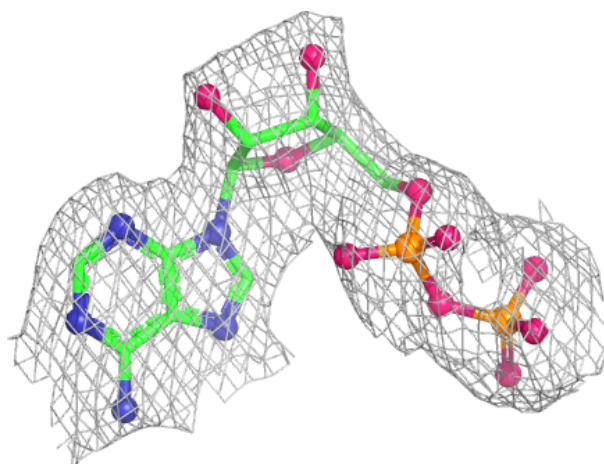
Electron density around ADP E 450:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



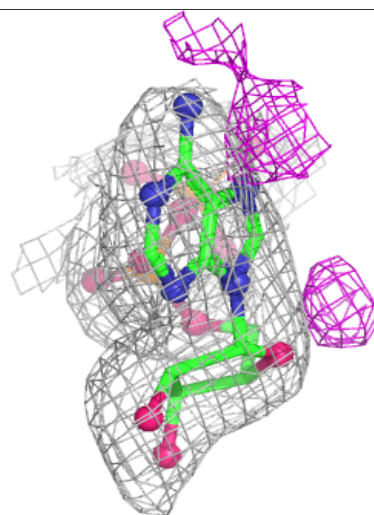
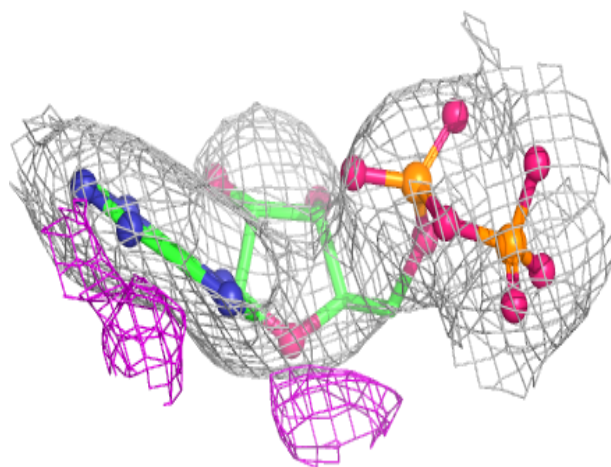
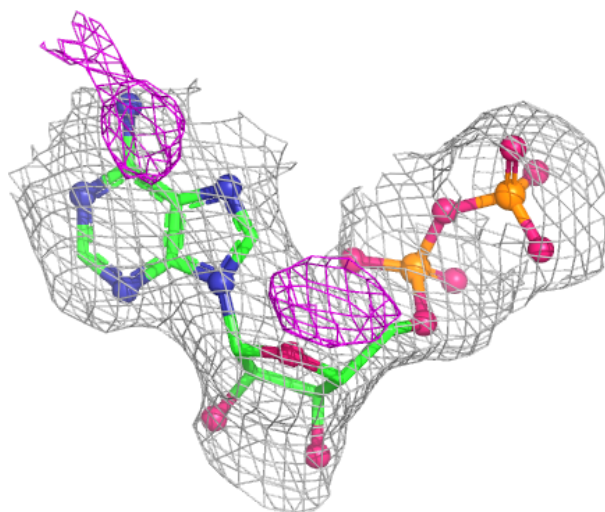
Electron density around ADP F 1450:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



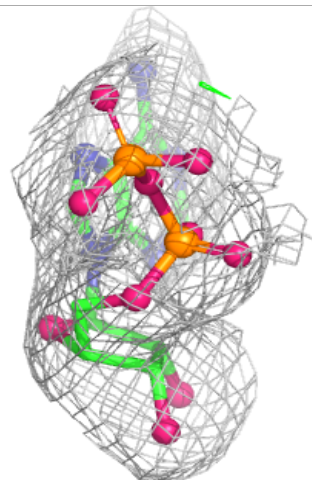
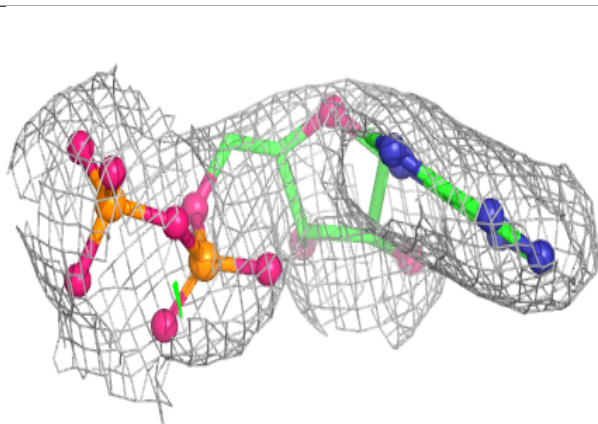
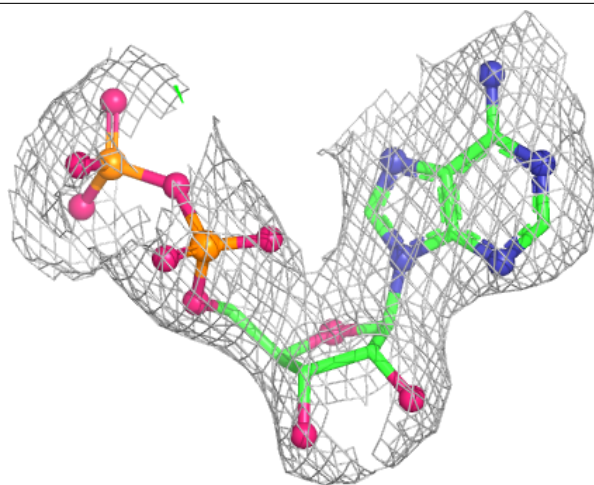
Electron density around ADP G 2450:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ADP H 3450:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.