Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:51 AM GMT

PDB ID	:	2EIV
Title	:	Crystal Structure of the arginase from Thermus thermophilus
Authors	:	Kumarevel, T.S.; Karthe, P.; Kuramitsu, S.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2007-03-13
Resolution	:	2.91 Å(reported)

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

The following versions of software and data (see references (1)) were used in the production of this report:

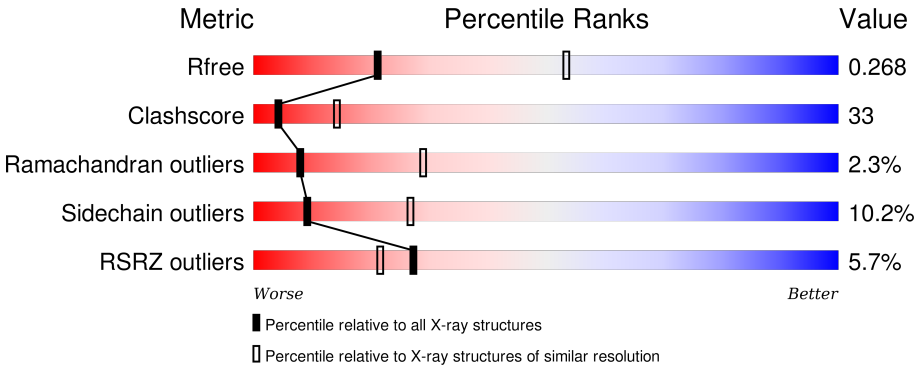
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1643 (2.94-2.90)
Clashscore	102246	1871 (2.94-2.90)
Ramachandran outliers	100387	1824 (2.94-2.90)
Sidechain outliers	100360	1826 (2.94-2.90)
RSRZ outliers	91569	1650 (2.94-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	291	% 53% 37% • 6%
1	C	291	% 57% 33% • 6%
1	D	291	3% 55% 35% • 6%
1	E	291	3% 52% 36% 6% 6%
1	F	291	% 55% 33% 5% 6%

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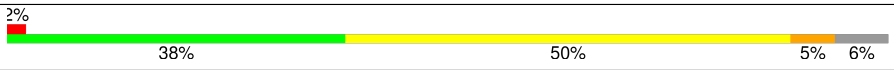
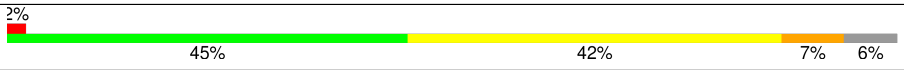
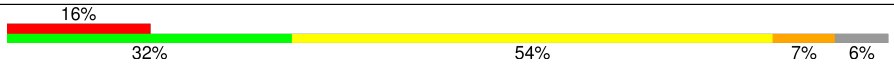
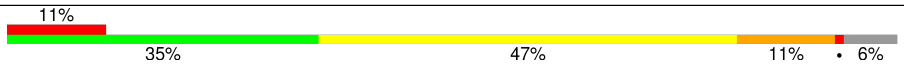
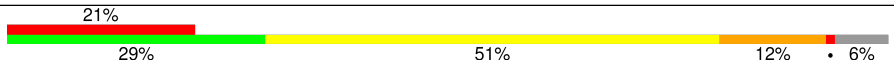
Mol	Chain	Length	Quality of chain
1	G	291	
1	H	291	
1	I	291	
1	J	291	
1	K	291	
1	L	291	
1	M	291	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 24799 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 Arginase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	C	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	D	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	E	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	F	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	G	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	H	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	I	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	J	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	K	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	L	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			
1	M	273	Total	C	N	O	S	0	0	0
			2052	1300	363	382	7			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	26	Total	O	0	0
			26	26		
2	C	12	Total	O	0	0
			12	12		

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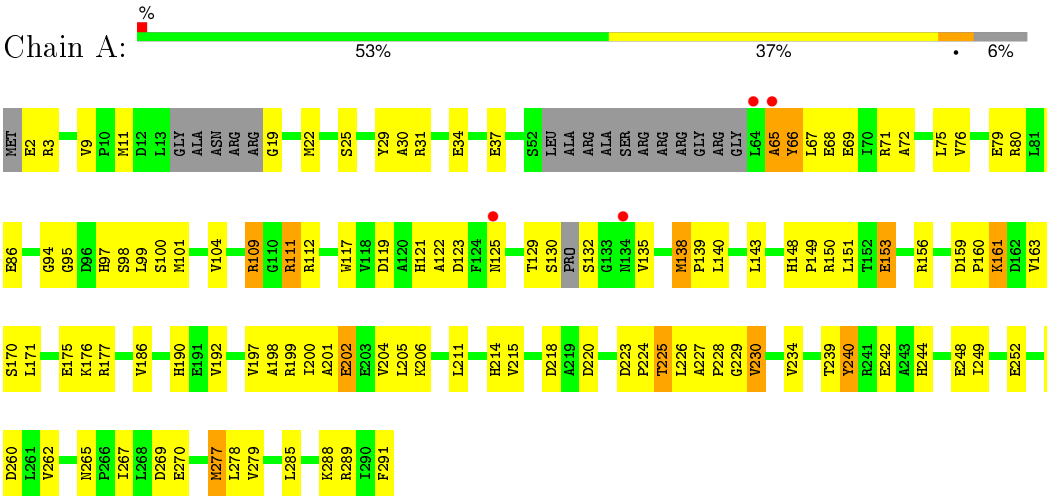
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	9	Total O 9 9	0	0
2	E	18	Total O 18 18	0	0
2	F	17	Total O 17 17	0	0
2	G	10	Total O 10 10	0	0
2	H	19	Total O 19 19	0	0
2	I	14	Total O 14 14	0	0
2	J	17	Total O 17 17	0	0
2	K	5	Total O 5 5	0	0
2	L	17	Total O 17 17	0	0
2	M	11	Total O 11 11	0	0

3 Residue-property plots (i)

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

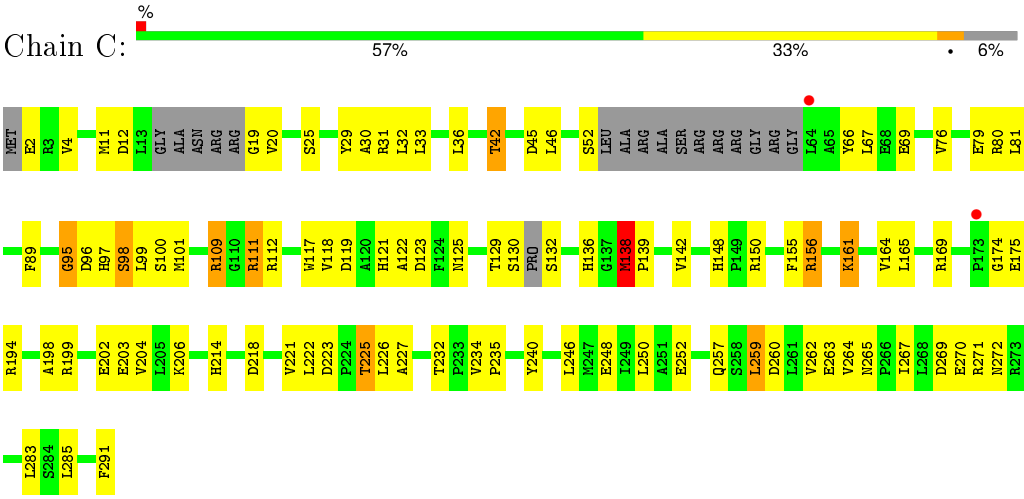
- Molecule 1: Arginase

Chain A:



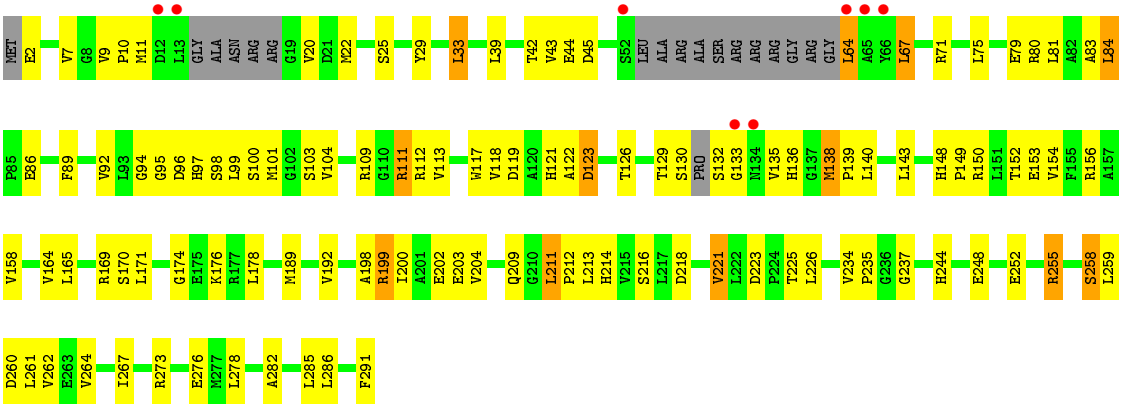
- Molecule 1: Arginase

Chain C:



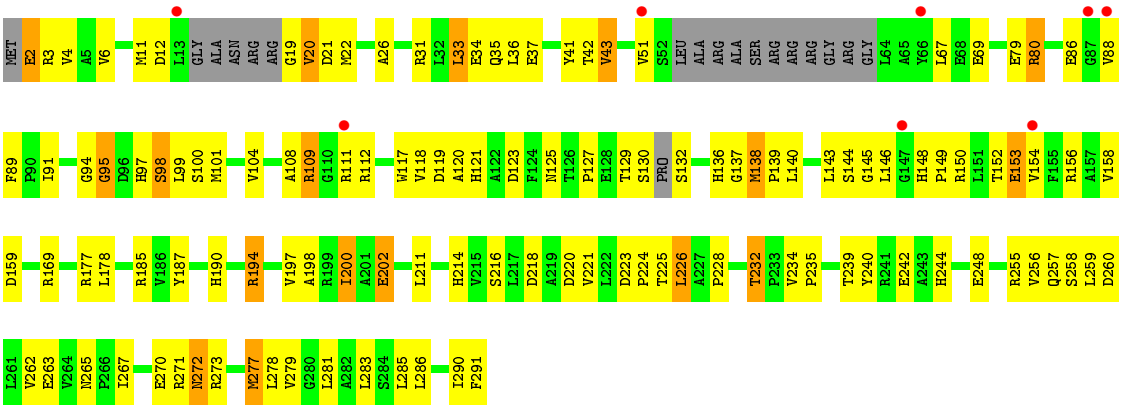
- Molecule 1: Arginase

Chain D:



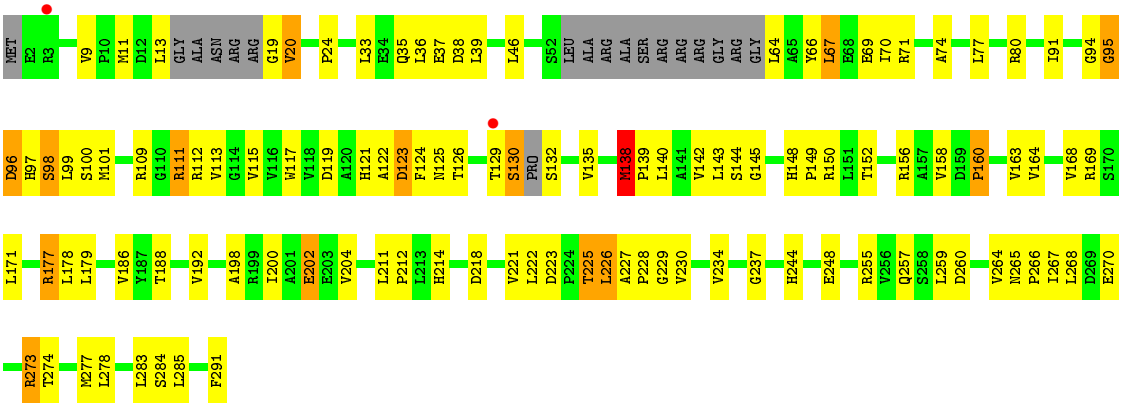
• Molecule 1: Arginase

Chain E:



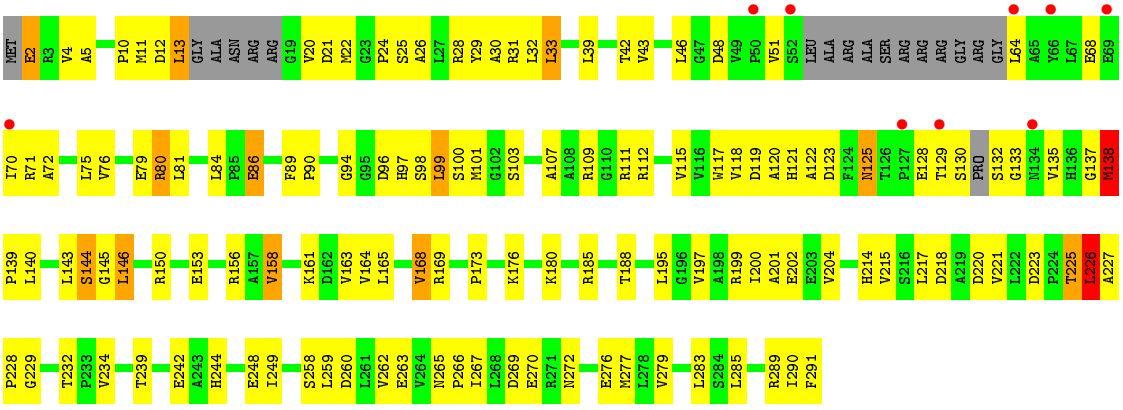
• Molecule 1: Arginase

Chain F:



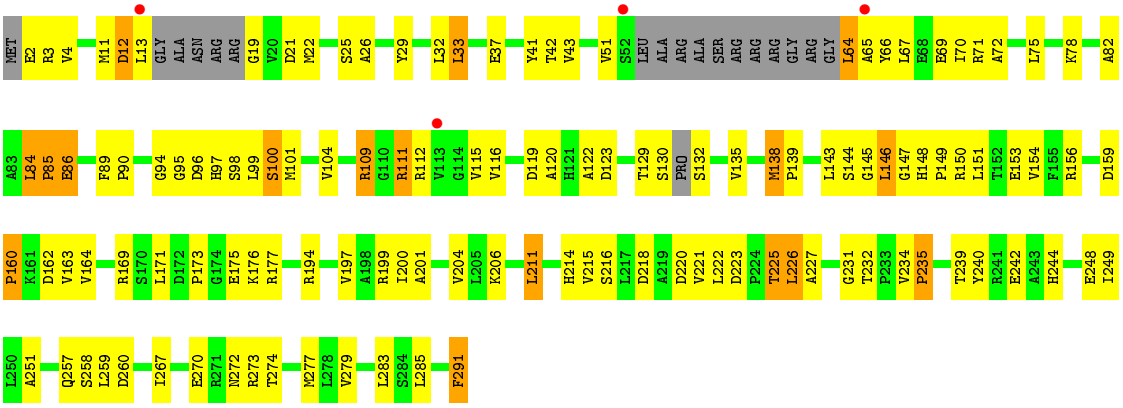
• Molecule 1: Arginase

Chain G:



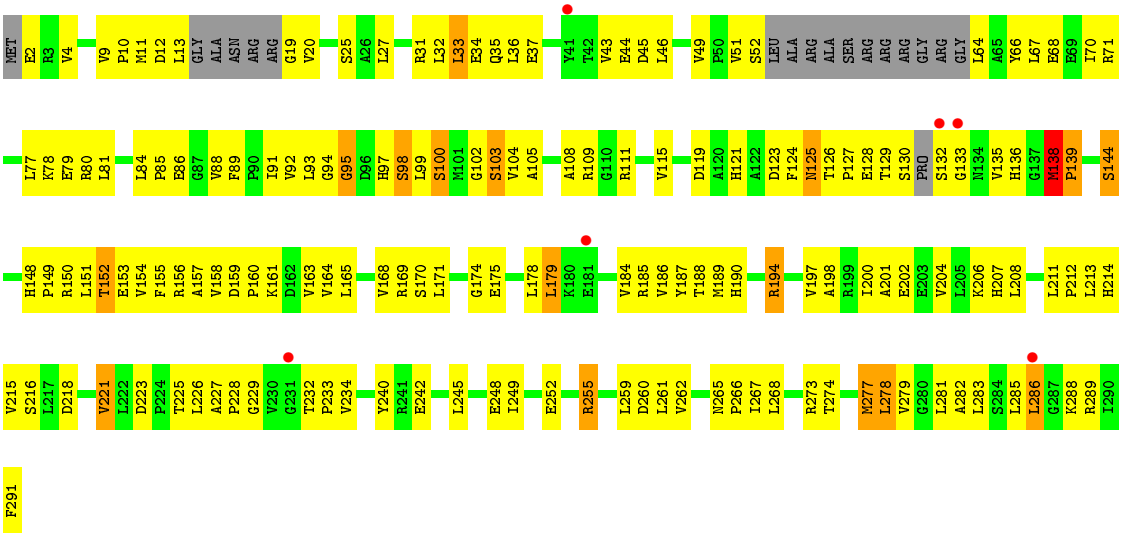
• Molecule 1: Arginase

Chain H:



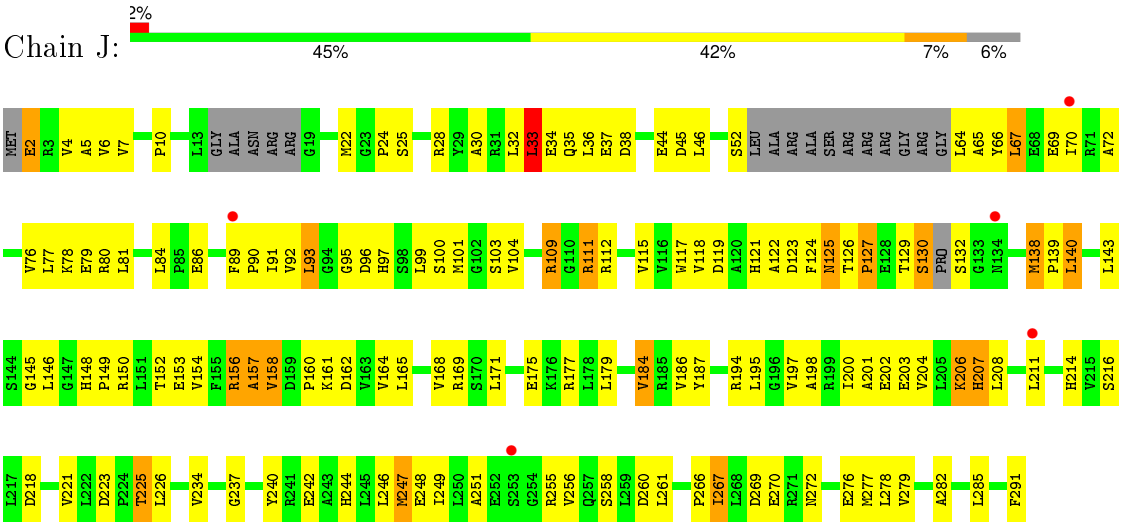
• Molecule 1: Arginase

Chain I:



• Molecule 1: Arginase

Chain J:

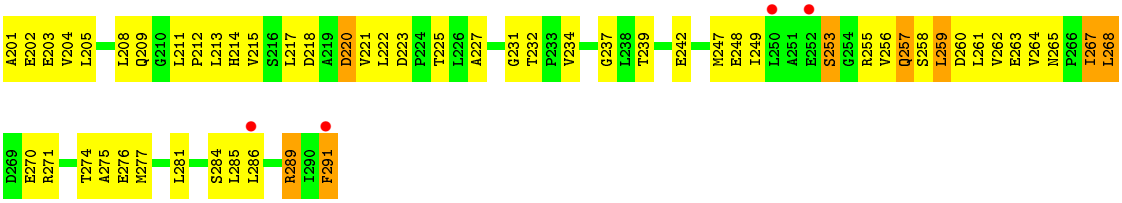


• Molecule 1: Arginase

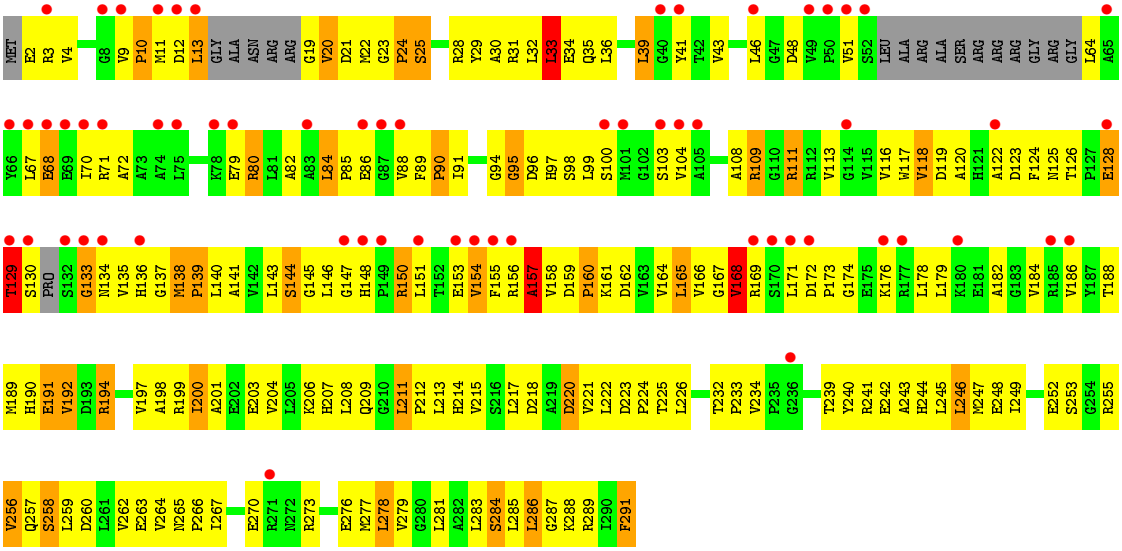
Chain K:

• Molecule 1: Arginase

Chain L:



- Molecule 1: Arginase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	159.98Å 139.89Å 84.37Å 90.00° 90.26° 90.00°	Depositor
Resolution (Å)	20.00 – 2.91 39.99 – 2.91	Depositor EDS
% Data completeness (in resolution range)	98.9 (20.00-2.91) 99.0 (39.99-2.91)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 2.90Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.232 , 0.269 0.231 , 0.268	Depositor DCC
R_{free} test set	4069 reflections (5.05%)	DCC
Wilson B-factor (Å^2)	60.3	Xtriage
Anisotropy	0.511	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 67.5	EDS
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	1 of 80760 reflections (0.001%)	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	24799	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.52	0/2083	0.83	2/2828 (0.1%)
1	C	0.53	0/2083	0.81	2/2828 (0.1%)
1	D	0.53	0/2083	0.82	2/2828 (0.1%)
1	E	0.51	0/2083	0.80	1/2828 (0.0%)
1	F	0.50	0/2083	0.81	1/2828 (0.0%)
1	G	0.49	0/2083	0.83	2/2828 (0.1%)
1	H	0.48	0/2083	0.83	2/2828 (0.1%)
1	I	0.49	0/2083	0.83	2/2828 (0.1%)
1	J	0.46	0/2083	0.80	1/2828 (0.0%)
1	K	0.45	0/2083	0.83	2/2828 (0.1%)
1	L	0.45	0/2083	0.83	0/2828
1	M	0.49	0/2083	0.89	5/2828 (0.2%)
All	All	0.49	0/24996	0.83	22/33936 (0.1%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	133	GLY	N-CA-C	9.38	136.55	113.10
1	J	95	GLY	N-CA-C	-8.96	90.71	113.10
1	M	157	ALA	CB-CA-C	8.88	123.42	110.10
1	M	95	GLY	N-CA-C	-7.86	93.46	113.10
1	I	95	GLY	N-CA-C	-7.57	94.17	113.10
1	M	133	GLY	N-CA-C	7.33	131.43	113.10
1	A	95	GLY	N-CA-C	-7.12	95.29	113.10
1	E	95	GLY	N-CA-C	-6.53	96.79	113.10
1	F	95	GLY	N-CA-C	-6.51	96.83	113.10
1	H	95	GLY	N-CA-C	-6.38	97.15	113.10
1	M	158	VAL	N-CA-CB	-6.22	97.81	111.50
1	G	64	LEU	CA-CB-CG	6.19	129.54	115.30
1	D	42	THR	N-CA-C	-5.90	95.07	111.00
1	D	133	GLY	N-CA-C	5.81	127.63	113.10
1	C	42	THR	N-CA-C	-5.76	95.44	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	66	TYR	N-CA-C	5.64	126.24	111.00
1	C	95	GLY	N-CA-C	-5.62	99.05	113.10
1	H	226	LEU	CA-CB-CG	5.60	128.18	115.30
1	K	94	GLY	N-CA-C	5.47	126.78	113.10
1	K	95	GLY	N-CA-C	-5.39	99.61	113.10
1	M	165	LEU	CA-CB-CG	-5.28	103.16	115.30
1	G	226	LEU	CA-CB-CG	5.20	127.25	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2052	0	2101	129	0
1	C	2052	0	2101	119	0
1	D	2052	0	2101	127	0
1	E	2052	0	2101	112	0
1	F	2052	0	2101	104	0
1	G	2052	0	2101	111	0
1	H	2052	0	2101	138	0
1	I	2052	0	2101	147	0
1	J	2052	0	2101	151	0
1	K	2052	0	2101	178	0
1	L	2052	0	2101	179	0
1	M	2052	0	2101	234	0
2	A	26	0	0	1	0
2	C	12	0	0	2	0
2	D	9	0	0	2	0
2	E	18	0	0	4	0
2	F	17	0	0	2	0
2	G	10	0	0	2	0
2	H	19	0	0	2	0
2	I	14	0	0	1	0
2	J	17	0	0	3	0
2	K	5	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	17	0	0	5	0
2	M	11	0	0	6	0
All	All	24799	0	25212	1655	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 33.

All (1655) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ARG:NH2	1:D:79:GLU:HA	1.57	1.19
1:F:111:ARG:HD3	1:F:112:ARG:N	1.62	1.14
1:F:111:ARG:HD3	1:F:112:ARG:H	0.97	1.11
1:H:109:ARG:HG2	1:H:109:ARG:HH11	1.05	1.11
1:A:79:GLU:HB3	1:D:111:ARG:HH22	1.16	1.10
1:J:109:ARG:HH11	1:J:109:ARG:HB3	1.11	1.10
1:C:109:ARG:HH11	1:C:109:ARG:HG2	0.92	1.09
1:H:111:ARG:HD3	1:H:112:ARG:H	1.17	1.08
1:F:130:SER:HG	1:F:132:SER:N	1.52	1.08
1:J:130:SER:HG	1:J:132:SER:N	1.52	1.07
1:L:111:ARG:HD3	1:L:112:ARG:H	1.14	1.06
1:M:138:MET:H	1:M:139:PRO:HD2	1.17	1.04
1:M:129:THR:HB	1:M:174:GLY:HA3	1.38	1.03
1:G:145:GLY:HA2	1:G:156:ARG:HD3	1.39	1.01
1:K:113:VAL:HG12	1:K:212:PRO:HG2	1.41	1.01
1:K:130:SER:HG	1:K:132:SER:N	1.59	0.98
1:L:109:ARG:HH11	1:L:109:ARG:HG2	1.26	0.98
1:H:111:ARG:CD	1:H:112:ARG:H	1.77	0.97
1:C:109:ARG:HG2	1:C:109:ARG:NH1	1.72	0.96
1:I:130:SER:HG	1:I:132:SER:N	1.64	0.94
1:J:72:ALA:O	1:J:76:VAL:HG23	1.66	0.94
1:L:138:MET:H	1:L:139:PRO:HD2	1.32	0.94
1:M:113:VAL:HA	2:M:296:HOH:O	1.68	0.93
1:A:111:ARG:HH21	1:D:79:GLU:HA	1.13	0.93
1:M:145:GLY:HA3	1:M:156:ARG:HH11	1.32	0.93
1:M:140:LEU:HA	1:M:143:LEU:HD12	1.50	0.93
1:M:199:ARG:O	1:M:203:GLU:HG3	1.69	0.92
1:C:86:GLU:HG2	1:C:109:ARG:HE	1.35	0.92
1:K:111:ARG:HD3	1:K:112:ARG:H	1.34	0.92
1:C:271:ARG:NH2	1:K:228:PRO:HB2	1.84	0.92
1:H:111:ARG:HE	1:H:111:ARG:HA	1.34	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:111:ARG:HD3	1:H:112:ARG:N	1.85	0.91
1:M:80:ARG:HG2	1:M:80:ARG:HH11	1.36	0.91
1:M:138:MET:N	1:M:139:PRO:HD2	1.85	0.91
1:E:138:MET:N	1:E:139:PRO:HD2	1.86	0.91
1:G:101:MET:HA	1:G:143:LEU:HD21	1.53	0.91
1:K:123:ASP:HB3	1:K:139:PRO:HD2	1.52	0.90
1:K:227:ALA:HB1	1:K:274:THR:HG23	1.53	0.90
1:H:109:ARG:NH1	1:H:109:ARG:HG2	1.85	0.90
1:A:79:GLU:CB	1:D:111:ARG:HH22	1.85	0.90
1:H:223:ASP:OD2	1:H:225:THR:HB	1.72	0.90
1:J:216:SER:HA	1:J:260:ASP:HB2	1.51	0.90
1:G:117:TRP:HB3	1:G:165:LEU:HD23	1.52	0.89
1:K:259:LEU:HD22	1:K:285:LEU:HD23	1.55	0.89
1:H:4:VAL:HG22	1:H:89:PHE:HB3	1.53	0.89
1:A:111:ARG:NH2	1:D:79:GLU:CA	2.34	0.88
1:H:111:ARG:HA	1:H:111:ARG:NE	1.84	0.88
1:C:83:ALA:C	1:H:111:ARG:HH12	1.77	0.88
1:J:109:ARG:NH1	1:J:109:ARG:HB3	1.89	0.88
1:E:138:MET:H	1:E:139:PRO:HD2	1.38	0.88
1:M:153:GLU:HG3	1:M:154:VAL:H	1.39	0.88
1:C:79:GLU:HB2	1:H:86:GLU:OE1	1.73	0.87
1:I:197:VAL:HG21	1:I:242:GLU:HB3	1.57	0.87
1:L:33:LEU:HD23	1:L:43:VAL:HB	1.56	0.87
1:H:197:VAL:HG21	1:H:242:GLU:HG2	1.55	0.87
1:D:111:ARG:HE	1:D:112:ARG:H	1.23	0.87
1:I:227:ALA:HB1	1:I:274:THR:HG23	1.56	0.87
1:K:164:VAL:HG23	1:K:208:LEU:HD11	1.56	0.86
1:K:129:THR:O	1:K:130:SER:HB2	1.75	0.85
1:J:164:VAL:HG11	1:J:204:VAL:HG22	1.58	0.85
1:M:111:ARG:HA	1:M:111:ARG:HE	1.41	0.85
1:L:111:ARG:HD3	1:L:112:ARG:N	1.92	0.85
1:C:148:HIS:HD2	1:C:150:ARG:H	1.25	0.85
1:A:111:ARG:HD3	1:A:112:ARG:H	1.42	0.85
1:J:125:ASN:ND2	1:J:175:GLU:HG3	1.92	0.85
1:L:223:ASP:HB3	1:L:225:THR:HG22	1.58	0.85
1:M:82:ALA:HA	1:M:109:ARG:HH12	1.42	0.85
1:C:83:ALA:HB1	1:H:111:ARG:CZ	2.07	0.84
1:I:36:LEU:HD21	1:I:286:LEU:HD23	1.59	0.84
1:G:125:ASN:O	1:G:138:MET:HB3	1.78	0.84
1:A:111:ARG:HH12	1:D:83:ALA:HB2	1.42	0.84
1:L:25:SER:O	1:L:29:TYR:HD2	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:197:VAL:HG21	1:E:242:GLU:HG2	1.58	0.84
1:F:111:ARG:CD	1:F:112:ARG:H	1.88	0.83
1:H:109:ARG:HH11	1:H:109:ARG:CG	1.91	0.83
1:H:239:THR:OG1	1:H:242:GLU:HB2	1.78	0.83
1:I:4:VAL:HG22	1:I:89:PHE:HB3	1.60	0.83
1:J:156:ARG:HH11	1:J:156:ARG:HG2	1.42	0.83
1:F:244:HIS:O	1:F:248:GLU:HG3	1.79	0.83
1:J:195:LEU:HD12	1:J:200:ILE:HD11	1.60	0.83
1:L:4:VAL:HG22	1:L:89:PHE:HB3	1.58	0.83
1:F:148:HIS:HD2	1:F:150:ARG:H	1.27	0.83
1:J:109:ARG:HH11	1:J:109:ARG:CB	1.89	0.83
1:J:66:TYR:O	1:J:70:ILE:HD13	1.79	0.82
1:M:226:LEU:HD21	1:M:240:TYR:HB2	1.59	0.82
1:H:82:ALA:HA	1:H:109:ARG:HH12	1.44	0.82
1:C:83:ALA:O	1:H:111:ARG:NH1	2.13	0.81
1:L:138:MET:N	1:L:139:PRO:HD2	1.95	0.81
1:K:200:ILE:O	1:K:204:VAL:HG23	1.79	0.81
1:L:215:VAL:HG21	1:L:285:LEU:HD21	1.61	0.81
1:L:138:MET:H	1:L:139:PRO:CD	1.92	0.81
1:I:138:MET:N	1:I:139:PRO:HD2	1.94	0.81
1:M:34:GLU:H	1:M:34:GLU:CD	1.85	0.81
1:L:138:MET:HA	2:L:301:HOH:O	1.80	0.81
1:L:190:HIS:HE1	1:L:194:ARG:HE	1.27	0.81
1:A:138:MET:N	1:A:139:PRO:HD2	1.96	0.81
1:M:36:LEU:HD21	1:M:286:LEU:HD23	1.62	0.80
1:A:79:GLU:HB3	1:D:111:ARG:NH2	1.96	0.80
1:F:227:ALA:HB1	1:F:274:THR:HG23	1.63	0.80
1:M:13:LEU:HD12	1:M:70:ILE:HG12	1.61	0.80
1:L:165:LEU:HD12	1:L:186:VAL:CG2	2.11	0.80
1:J:138:MET:N	1:J:139:PRO:HD2	1.96	0.80
1:E:119:ASP:HA	1:E:218:ASP:HB3	1.64	0.80
1:F:119:ASP:OD2	1:F:123:ASP:OD2	2.00	0.80
1:I:67:LEU:C	1:I:67:LEU:HD23	2.02	0.80
1:M:113:VAL:HG12	1:M:212:PRO:HG2	1.61	0.80
1:E:130:SER:HG	1:E:132:SER:N	1.80	0.80
1:E:37:GLU:HG2	1:E:43:VAL:HG23	1.64	0.79
1:H:216:SER:HA	1:H:260:ASP:HB2	1.64	0.79
1:A:130:SER:HG	1:A:132:SER:N	1.80	0.79
1:C:109:ARG:HH11	1:C:109:ARG:CG	1.85	0.79
1:G:197:VAL:HG21	1:G:242:GLU:HB3	1.63	0.79
1:M:211:LEU:HB3	2:M:296:HOH:O	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:193:ASP:HB3	1:M:245:LEU:HD22	1.65	0.78
1:E:153:GLU:HG3	1:E:154:VAL:HG13	1.65	0.78
1:M:208:LEU:O	1:M:211:LEU:HG	1.83	0.78
1:C:218:ASP:OD2	2:C:292:HOH:O	1.99	0.78
1:K:144:SER:HB3	1:K:160:PRO:HG3	1.66	0.78
1:F:259:LEU:HD13	1:F:285:LEU:HD23	1.65	0.78
1:E:120:ALA:HB2	1:E:220:ASP:O	1.82	0.78
1:M:218:ASP:HA	1:M:262:VAL:HG23	1.65	0.78
1:A:111:ARG:HD3	1:A:112:ARG:N	1.98	0.78
1:H:259:LEU:HD13	1:H:285:LEU:HD23	1.66	0.78
1:I:164:VAL:HG22	1:I:185:ARG:HB3	1.66	0.78
1:M:12:ASP:HB2	1:M:21:ASP:HB3	1.66	0.78
1:G:138:MET:N	1:G:139:PRO:HD2	1.99	0.77
1:M:168:VAL:HG12	1:M:188:THR:HA	1.67	0.77
1:E:145:GLY:O	1:E:146:LEU:HD23	1.84	0.77
1:G:109:ARG:HG2	1:G:109:ARG:HH11	1.50	0.77
1:G:12:ASP:O	1:G:13:LEU:HD23	1.85	0.77
1:G:272:ASN:O	1:G:276:GLU:HG3	1.84	0.77
1:M:109:ARG:HH11	1:M:109:ARG:HG2	1.49	0.77
1:C:84:LEU:O	1:C:109:ARG:NH2	2.19	0.76
1:C:97:HIS:ND1	1:C:123:ASP:OD2	2.18	0.76
1:L:122:ALA:HB3	1:L:175:GLU:OE2	1.84	0.76
1:C:164:VAL:HG11	1:C:204:VAL:HG22	1.66	0.76
1:K:109:ARG:HB3	1:K:109:ARG:HH11	1.50	0.76
1:A:149:PRO:O	1:A:153:GLU:HB3	1.85	0.76
1:I:109:ARG:HH11	1:I:109:ARG:HG2	1.48	0.76
1:K:19:GLY:HA3	1:K:265:ASN:ND2	2.01	0.76
1:M:111:ARG:HA	1:M:111:ARG:NE	1.99	0.76
1:K:12:ASP:HB2	1:K:21:ASP:HB3	1.68	0.76
1:M:146:LEU:HD13	1:M:178:LEU:HD22	1.67	0.76
1:F:101:MET:HA	1:F:143:LEU:HD21	1.67	0.75
1:C:19:GLY:N	1:C:265:ASN:HD21	1.84	0.75
1:G:4:VAL:HG22	1:G:89:PHE:HB3	1.68	0.75
1:M:138:MET:H	1:M:139:PRO:CD	1.97	0.75
1:K:165:LEU:HD12	1:K:186:VAL:HG22	1.69	0.75
1:J:100:SER:HA	1:J:103:SER:OG	1.86	0.75
1:D:11:MET:CE	1:D:98:SER:HB2	2.15	0.75
1:J:168:VAL:HG11	1:J:171:LEU:HD21	1.69	0.75
1:M:145:GLY:HA2	1:M:156:ARG:CG	2.17	0.75
1:H:11:MET:CE	1:H:98:SER:HB2	2.17	0.75
1:M:168:VAL:HG21	1:M:171:LEU:HD21	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:115:VAL:HG23	1:G:158:VAL:HG21	1.69	0.75
1:M:97:HIS:ND1	1:M:123:ASP:OD2	2.20	0.74
1:J:272:ASN:O	1:J:276:GLU:HG3	1.87	0.74
1:F:130:SER:OG	1:F:132:SER:N	2.20	0.74
1:M:126:THR:HG22	1:M:147:GLY:HA2	1.69	0.74
1:L:109:ARG:HH11	1:L:109:ARG:CG	1.99	0.74
1:I:169:ARG:NH1	1:I:234:VAL:O	2.20	0.74
1:M:36:LEU:CD2	1:M:286:LEU:HD23	2.16	0.74
1:L:198:ALA:O	1:L:202:GLU:HG2	1.86	0.74
1:L:208:LEU:O	1:L:255:ARG:NH1	2.19	0.74
1:A:159:ASP:OD1	1:A:161:LYS:HD3	1.87	0.73
1:C:156:ARG:HH11	1:C:156:ARG:HG2	1.53	0.73
1:G:84:LEU:O	1:G:109:ARG:NH2	2.21	0.73
1:M:145:GLY:CA	1:M:156:ARG:HH11	2.00	0.73
1:H:25:SER:O	1:H:29:TYR:HD2	1.71	0.73
1:G:130:SER:HG	1:G:132:SER:N	1.85	0.73
1:F:145:GLY:HA3	1:F:156:ARG:HD3	1.70	0.73
1:L:33:LEU:O	1:L:37:GLU:HG3	1.88	0.73
1:K:70:ILE:HD13	1:K:135:VAL:HG11	1.70	0.73
1:D:244:HIS:O	1:D:248:GLU:HG3	1.89	0.73
1:H:97:HIS:ND1	1:H:123:ASP:OD2	2.21	0.73
1:I:278:LEU:HD12	1:I:281:LEU:HD12	1.71	0.73
1:C:227:ALA:HB1	1:C:274:THR:HG23	1.69	0.73
1:J:97:HIS:ND1	1:J:123:ASP:OD2	2.22	0.73
1:G:146:LEU:HD23	1:G:146:LEU:N	2.04	0.73
1:F:200:ILE:O	1:F:204:VAL:HG23	1.89	0.73
1:F:125:ASN:O	1:F:138:MET:HB3	1.88	0.72
1:E:149:PRO:O	1:E:153:GLU:HG2	1.89	0.72
1:M:117:TRP:CD1	1:M:165:LEU:HD21	2.24	0.72
1:C:83:ALA:CA	1:H:111:ARG:HH12	2.02	0.72
1:H:129:THR:O	1:H:130:SER:HB2	1.89	0.72
1:C:83:ALA:CA	1:H:111:ARG:NH1	2.52	0.72
1:M:153:GLU:HG3	1:M:154:VAL:HG13	1.70	0.72
1:D:273:ARG:HA	1:D:276:GLU:HG3	1.72	0.72
1:M:84:LEU:HD13	1:M:88:VAL:HG11	1.71	0.72
1:F:148:HIS:CD2	1:F:150:ARG:H	2.08	0.72
1:D:104:VAL:HG22	1:D:214:HIS:CE1	2.25	0.71
1:A:111:ARG:HH22	1:D:79:GLU:C	1.92	0.71
1:M:80:ARG:CG	1:M:80:ARG:HH11	2.02	0.71
1:H:11:MET:HE3	1:H:98:SER:HB2	1.73	0.71
1:I:184:VAL:O	1:I:186:VAL:HG23	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:172:ASP:HB3	2:M:293:HOH:O	1.90	0.71
1:J:99:LEU:C	1:J:99:LEU:HD12	2.11	0.71
1:D:9:VAL:O	1:D:11:MET:N	2.23	0.71
1:M:36:LEU:HD21	1:M:286:LEU:CD2	2.20	0.71
1:H:66:TYR:O	1:H:70:ILE:HD13	1.91	0.71
1:D:119:ASP:HB3	1:D:121:HIS:O	1.90	0.71
1:J:201:ALA:HB1	1:J:249:ILE:HG21	1.73	0.71
1:G:115:VAL:HB	1:G:163:VAL:HG22	1.71	0.71
1:A:223:ASP:OD2	1:A:225:THR:HB	1.92	0.70
1:K:164:VAL:CG2	1:K:208:LEU:HD11	2.21	0.70
1:G:109:ARG:NH1	1:G:109:ARG:HG2	2.03	0.70
1:D:214:HIS:CD2	1:D:258:SER:HB2	2.26	0.70
1:H:101:MET:HA	1:H:143:LEU:HD21	1.73	0.70
1:A:84:LEU:O	1:A:109:ARG:NH2	2.23	0.70
1:K:214:HIS:HE1	1:K:260:ASP:OD2	1.73	0.70
1:D:99:LEU:HD21	1:D:262:VAL:HG12	1.74	0.70
1:C:119:ASP:OD2	1:C:123:ASP:OD2	2.10	0.70
1:J:30:ALA:HB3	1:J:279:VAL:HG21	1.73	0.70
1:K:118:VAL:HG23	1:K:216:SER:O	1.92	0.70
1:I:119:ASP:OD2	1:I:123:ASP:OD2	2.10	0.70
1:L:97:HIS:ND1	1:L:123:ASP:OD2	2.25	0.70
1:G:111:ARG:HD3	1:G:112:ARG:H	1.56	0.70
1:H:130:SER:HG	1:H:132:SER:N	1.89	0.70
1:I:11:MET:CE	1:I:98:SER:HB2	2.22	0.69
1:A:119:ASP:OD2	1:A:218:ASP:OD2	2.09	0.69
1:D:129:THR:O	1:D:130:SER:HB2	1.91	0.69
1:C:148:HIS:CD2	1:C:150:ARG:H	2.07	0.69
1:F:169:ARG:HG3	1:F:234:VAL:HG11	1.74	0.69
1:G:97:HIS:ND1	1:G:123:ASP:OD2	2.26	0.69
1:A:220:ASP:OD2	2:A:293:HOH:O	2.10	0.69
1:A:117:TRP:CE3	1:A:140:LEU:HD13	2.27	0.69
1:M:190:HIS:HE1	1:M:194:ARG:HG3	1.57	0.69
1:K:19:GLY:HA3	1:K:265:ASN:HD21	1.57	0.69
1:I:12:ASP:OD2	1:I:19:GLY:HA2	1.92	0.69
1:A:198:ALA:O	1:A:202:GLU:HG2	1.93	0.69
1:A:79:GLU:CB	1:D:111:ARG:NH2	2.56	0.69
1:M:80:ARG:HD2	1:M:80:ARG:O	1.93	0.69
1:J:6:VAL:HG13	1:J:93:LEU:HD21	1.74	0.69
1:J:119:ASP:OD2	1:J:123:ASP:OD2	2.11	0.69
1:M:125:ASN:HB2	1:M:137:GLY:O	1.92	0.68
1:L:149:PRO:O	1:L:153:GLU:HB3	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ARG:HH11	1:A:109:ARG:HG2	1.56	0.68
1:L:156:ARG:HG2	1:L:156:ARG:HH11	1.57	0.68
1:E:239:THR:OG1	1:E:242:GLU:HB2	1.93	0.68
1:J:66:TYR:HB3	1:J:70:ILE:CD1	2.23	0.68
1:E:99:LEU:HD12	1:E:100:SER:N	2.08	0.68
1:M:11:MET:HG2	1:M:96:ASP:HB2	1.75	0.68
1:G:195:LEU:HD22	1:G:199:ARG:NH1	2.09	0.68
1:J:66:TYR:HB3	1:J:70:ILE:HD11	1.74	0.68
1:M:190:HIS:CE1	1:M:194:ARG:HG3	2.29	0.68
1:K:78:LYS:HA	1:K:102:GLY:O	1.93	0.68
1:J:211:LEU:O	1:J:255:ARG:NH1	2.25	0.68
1:M:244:HIS:O	1:M:248:GLU:HG3	1.94	0.68
1:J:125:ASN:HD21	1:J:175:GLU:HG3	1.58	0.68
1:I:259:LEU:HD13	1:I:285:LEU:HD23	1.76	0.68
1:L:119:ASP:OD1	1:L:121:HIS:ND1	2.27	0.67
1:D:86:GLU:HG2	1:D:109:ARG:HH21	1.58	0.67
1:I:179:LEU:HD22	1:I:186:VAL:HG21	1.77	0.67
1:G:218:ASP:OD1	1:G:263:GLU:HG3	1.93	0.67
1:J:164:VAL:HG11	1:J:204:VAL:CG2	2.25	0.67
1:I:119:ASP:OD2	1:I:218:ASP:OD2	2.13	0.67
1:M:124:PHE:HE2	1:M:178:LEU:HB3	1.60	0.67
1:D:101:MET:HA	1:D:143:LEU:HD21	1.76	0.67
1:F:223:ASP:OD2	1:F:225:THR:HB	1.93	0.67
1:M:120:ALA:O	1:M:168:VAL:HA	1.95	0.67
1:A:156:ARG:NH2	1:D:156:ARG:NH2	2.42	0.67
1:H:84:LEU:O	1:H:85:PRO:O	2.12	0.67
1:H:111:ARG:NE	1:H:112:ARG:H	1.92	0.67
1:K:119:ASP:OD2	1:K:123:ASP:OD2	2.13	0.67
1:J:148:HIS:HD2	1:J:150:ARG:HB2	1.59	0.67
1:I:148:HIS:HD2	1:I:149:PRO:HD2	1.60	0.67
1:E:240:TYR:HB3	2:E:306:HOH:O	1.95	0.67
1:M:153:GLU:HG3	1:M:154:VAL:N	2.08	0.67
1:J:177:ARG:HH11	1:J:177:ARG:HB3	1.59	0.67
1:J:86:GLU:HG2	1:J:109:ARG:HE	1.60	0.67
1:L:130:SER:OG	1:L:132:SER:N	2.27	0.67
1:M:128:GLU:O	1:M:130:SER:N	2.27	0.66
1:M:109:ARG:NH1	1:M:109:ARG:HG2	2.08	0.66
1:A:119:ASP:OD2	1:A:123:ASP:OD2	2.13	0.66
1:K:117:TRP:HB3	1:K:165:LEU:HD23	1.75	0.66
1:K:41:TYR:OH	1:K:286:LEU:O	2.12	0.66
1:D:43:VAL:HG12	1:D:44:GLU:N	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:125:ASN:ND2	1:M:129:THR:OG1	2.28	0.66
1:L:140:LEU:HD21	1:L:163:VAL:HG11	1.77	0.66
1:M:12:ASP:OD2	1:M:19:GLY:HA2	1.95	0.66
1:K:9:VAL:HB	1:K:99:LEU:HD22	1.77	0.66
1:C:117:TRP:HB3	1:C:165:LEU:HD23	1.78	0.66
1:L:96:ASP:HB3	1:L:98:SER:OG	1.94	0.66
1:I:25:SER:HB3	1:M:22:MET:CE	2.26	0.66
1:H:111:ARG:NE	1:H:111:ARG:CA	2.58	0.66
1:M:117:TRP:HD1	1:M:165:LEU:HD21	1.61	0.66
1:K:211:LEU:O	1:K:255:ARG:HD2	1.96	0.66
1:K:214:HIS:CE1	1:K:260:ASP:OD2	2.49	0.66
1:G:11:MET:CE	1:G:98:SER:HB2	2.24	0.66
1:L:189:MET:HA	1:L:192:VAL:HG23	1.77	0.66
1:D:138:MET:H	1:D:139:PRO:HD3	1.60	0.66
1:F:259:LEU:HD13	1:F:285:LEU:CD2	2.25	0.66
1:L:129:THR:O	1:L:130:SER:HB3	1.96	0.66
1:M:165:LEU:HB2	1:M:186:VAL:HG22	1.77	0.66
1:I:97:HIS:CD2	1:I:262:VAL:HG21	2.31	0.66
1:D:119:ASP:OD2	1:D:123:ASP:OD2	2.13	0.66
1:L:239:THR:OG1	1:L:242:GLU:HG3	1.96	0.66
1:M:29:TYR:C	1:M:31:ARG:H	1.98	0.66
1:E:4:VAL:HG11	1:E:36:LEU:HD13	1.77	0.66
1:I:81:LEU:HA	1:I:84:LEU:HD12	1.77	0.66
1:H:22:MET:SD	1:H:267:ILE:HD13	2.35	0.66
1:H:33:LEU:HG	1:H:43:VAL:HG11	1.78	0.66
1:E:138:MET:H	1:E:139:PRO:CD	2.10	0.65
1:I:169:ARG:NH2	1:I:221:VAL:O	2.28	0.65
1:K:72:ALA:O	1:K:76:VAL:HG23	1.96	0.65
1:A:11:MET:CE	1:A:98:SER:HB2	2.26	0.65
1:L:169:ARG:HD2	1:L:234:VAL:HB	1.77	0.65
1:A:130:SER:OG	1:A:132:SER:N	2.29	0.65
1:G:11:MET:HE1	1:G:98:SER:HB2	1.77	0.65
1:C:86:GLU:HG2	1:C:109:ARG:NE	2.11	0.65
1:J:129:THR:O	1:J:130:SER:HB2	1.96	0.65
1:H:129:THR:O	1:H:130:SER:CB	2.44	0.65
1:A:169:ARG:HG3	1:A:234:VAL:HG11	1.79	0.65
1:L:97:HIS:CD2	1:L:262:VAL:HG21	2.32	0.65
1:L:3:ARG:NH2	1:L:88:VAL:N	2.44	0.65
1:L:201:ALA:HB1	1:L:249:ILE:HG21	1.78	0.65
1:F:149:PRO:HA	1:F:152:THR:OG1	1.97	0.65
1:I:109:ARG:HG2	1:I:109:ARG:NH1	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:244:HIS:O	1:G:248:GLU:HG3	1.97	0.65
1:K:239:THR:OG1	1:K:242:GLU:HG3	1.96	0.65
1:M:31:ARG:O	1:M:35:GLN:HG3	1.96	0.65
1:E:290:ILE:HD12	1:E:290:ILE:H	1.62	0.65
1:D:11:MET:HE1	1:D:98:SER:HB2	1.76	0.65
1:M:35:GLN:HB3	1:M:283:LEU:HD11	1.79	0.65
1:K:71:ARG:NH2	1:K:153:GLU:OE2	2.30	0.64
1:J:138:MET:N	1:J:139:PRO:CD	2.60	0.64
1:H:222:LEU:HD13	1:H:277:MET:HE2	1.78	0.64
1:A:256:VAL:HG21	1:A:285:LEU:HD11	1.79	0.64
1:A:111:ARG:HH22	1:D:79:GLU:CA	2.10	0.64
1:M:145:GLY:HA3	1:M:156:ARG:NH1	2.08	0.64
1:K:218:ASP:HA	1:K:262:VAL:HG23	1.78	0.64
1:E:149:PRO:HA	1:E:152:THR:OG1	1.97	0.64
1:L:218:ASP:OD1	1:L:220:ASP:OD2	2.15	0.64
1:E:31:ARG:NH2	1:E:34:GLU:HG2	2.12	0.64
1:C:83:ALA:HA	1:H:111:ARG:NH1	2.12	0.64
1:K:94:GLY:HA2	1:K:99:LEU:HD21	1.80	0.64
1:I:164:VAL:HG11	1:I:204:VAL:HG22	1.79	0.64
1:C:248:GLU:OE1	1:I:190:HIS:HD2	1.81	0.64
1:H:130:SER:OG	1:H:132:SER:N	2.31	0.64
1:I:85:PRO:O	1:I:88:VAL:HG23	1.97	0.64
1:G:169:ARG:NH2	1:G:221:VAL:O	2.31	0.64
1:J:101:MET:HA	1:J:143:LEU:HD21	1.79	0.64
1:F:98:SER:HA	1:F:139:PRO:HG3	1.79	0.64
1:D:214:HIS:HD2	1:D:258:SER:HB2	1.62	0.64
1:K:205:LEU:O	1:K:209:GLN:N	2.30	0.64
1:J:7:VAL:CG1	1:J:92:VAL:HG22	2.28	0.64
1:D:111:ARG:HE	1:D:112:ARG:N	1.96	0.64
1:E:197:VAL:HG21	1:E:242:GLU:CG	2.27	0.64
1:E:101:MET:HA	1:E:143:LEU:HD21	1.80	0.64
1:I:67:LEU:C	1:I:67:LEU:CD2	2.66	0.64
1:J:156:ARG:HH11	1:J:156:ARG:CG	2.10	0.64
1:A:156:ARG:NH2	1:D:156:ARG:HH21	1.95	0.64
1:D:71:ARG:O	1:D:75:LEU:HB2	1.98	0.64
1:H:171:LEU:HB2	1:H:176:LYS:HE2	1.80	0.64
1:E:80:ARG:HD3	2:E:293:HOH:O	1.97	0.64
1:E:138:MET:N	1:E:139:PRO:CD	2.61	0.63
1:E:6:VAL:HG22	1:E:91:ILE:HB	1.80	0.63
1:I:31:ARG:HD2	2:I:294:HOH:O	1.97	0.63
1:J:169:ARG:NH1	1:J:234:VAL:O	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:226:LEU:HD21	1:K:240:TYR:N	2.13	0.63
1:L:112:ARG:NH1	1:L:211:LEU:HD21	2.12	0.63
1:L:108:ALA:C	1:L:109:ARG:HG3	2.19	0.63
1:L:130:SER:HG	1:L:132:SER:N	1.94	0.63
1:L:164:VAL:HG13	1:L:185:ARG:HB3	1.79	0.63
1:E:156:ARG:HH11	1:E:156:ARG:HG2	1.63	0.63
1:M:126:THR:OG1	1:M:129:THR:HG23	1.98	0.63
1:C:271:ARG:HH21	1:K:228:PRO:HB2	1.61	0.63
1:G:138:MET:N	1:G:139:PRO:CD	2.61	0.63
1:K:243:ALA:HB1	1:K:281:LEU:HD11	1.79	0.63
1:A:109:ARG:NH1	1:A:109:ARG:HG2	2.11	0.63
1:A:226:LEU:HD21	1:A:240:TYR:HB2	1.80	0.63
1:K:159:ASP:O	1:K:161:LYS:N	2.32	0.63
1:A:71:ARG:O	1:A:75:LEU:HB2	1.97	0.63
1:M:20:VAL:HG12	1:M:264:VAL:O	1.99	0.63
1:C:119:ASP:HB3	1:C:121:HIS:O	1.98	0.63
1:D:259:LEU:HD13	1:D:285:LEU:HD23	1.79	0.63
1:F:115:VAL:HG23	1:F:158:VAL:HG21	1.81	0.63
1:L:93:LEU:CD2	1:L:261:LEU:HD12	2.29	0.63
1:L:27:LEU:HD21	1:L:264:VAL:HG21	1.81	0.63
1:K:192:VAL:HA	1:K:200:ILE:HD11	1.80	0.63
1:G:119:ASP:OD2	1:G:218:ASP:OD2	2.17	0.62
1:M:259:LEU:HD13	1:M:285:LEU:CD2	2.28	0.62
1:H:244:HIS:O	1:H:248:GLU:HG3	1.99	0.62
1:M:138:MET:N	1:M:139:PRO:CD	2.60	0.62
1:I:216:SER:HA	1:I:260:ASP:HB2	1.80	0.62
1:E:51:VAL:O	1:E:51:VAL:HG12	1.99	0.62
1:L:247:MET:HG3	1:L:281:LEU:O	1.99	0.62
1:F:99:LEU:HD12	1:F:100:SER:N	2.14	0.62
1:A:104:VAL:HG22	1:A:214:HIS:CE1	2.33	0.62
1:E:119:ASP:HB3	1:E:121:HIS:O	1.99	0.62
1:I:49:VAL:HG21	1:I:77:LEU:HD13	1.81	0.62
1:D:117:TRP:CE3	1:D:140:LEU:HD13	2.35	0.62
1:J:104:VAL:HB	1:J:143:LEU:HD22	1.81	0.62
1:A:67:LEU:HD11	1:A:148:HIS:CD2	2.35	0.62
1:J:148:HIS:CD2	1:J:150:ARG:HB2	2.34	0.62
1:A:119:ASP:HA	1:A:218:ASP:HB3	1.82	0.62
1:E:256:VAL:HG11	1:E:285:LEU:HD11	1.80	0.62
1:A:69:GLU:OE1	1:A:69:GLU:N	2.31	0.62
1:K:176:LYS:HB3	1:M:291:PHE:HE2	1.64	0.62
1:K:165:LEU:HD12	1:K:186:VAL:CG2	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:SER:O	1:A:29:TYR:HD2	1.81	0.62
1:A:164:VAL:HG11	1:A:204:VAL:HG22	1.81	0.62
1:I:126:THR:HG23	1:I:178:LEU:HD13	1.81	0.62
1:J:46:LEU:HD22	1:J:80:ARG:NH2	2.15	0.62
1:F:13:LEU:HB2	1:F:70:ILE:HD11	1.82	0.62
1:D:138:MET:N	1:D:139:PRO:CD	2.62	0.62
1:L:12:ASP:HA	1:L:96:ASP:OD1	1.99	0.62
1:M:164:VAL:HG11	1:M:204:VAL:CG2	2.30	0.61
1:I:198:ALA:O	1:I:202:GLU:HG2	1.99	0.61
1:K:100:SER:HA	1:K:103:SER:OG	2.00	0.61
1:D:223:ASP:OD2	1:D:225:THR:HG22	2.00	0.61
1:L:119:ASP:HA	1:L:218:ASP:HB3	1.81	0.61
1:L:169:ARG:HG3	1:L:234:VAL:HG11	1.83	0.61
1:H:94:GLY:HA3	1:H:99:LEU:CD2	2.30	0.61
1:F:179:LEU:HD13	1:F:186:VAL:HG21	1.82	0.61
1:M:30:ALA:HB3	1:M:279:VAL:HG21	1.83	0.61
1:A:138:MET:N	1:A:139:PRO:CD	2.63	0.61
1:A:169:ARG:HA	1:E:290:ILE:HG21	1.82	0.61
1:C:130:SER:HG	1:C:132:SER:N	1.98	0.61
1:K:101:MET:HA	1:K:143:LEU:HD21	1.83	0.61
1:G:12:ASP:C	1:G:13:LEU:HD23	2.19	0.61
1:M:4:VAL:HG23	1:M:41:TYR:HD1	1.65	0.61
1:E:129:THR:O	1:E:130:SER:CB	2.49	0.61
1:D:94:GLY:HA3	1:D:99:LEU:CD2	2.30	0.61
1:G:195:LEU:HD22	1:G:199:ARG:HH11	1.66	0.61
1:H:201:ALA:HB1	1:H:249:ILE:HG21	1.83	0.61
1:I:248:GLU:O	1:I:252:GLU:HG3	2.00	0.61
1:I:123:ASP:HB3	1:I:139:PRO:HG2	1.81	0.61
1:M:244:HIS:CE1	1:M:281:LEU:HD23	2.35	0.61
1:A:79:GLU:HG2	1:D:111:ARG:NH2	2.15	0.61
1:C:80:ARG:O	1:C:83:ALA:HB3	2.00	0.61
1:F:71:ARG:HD3	2:F:299:HOH:O	2.00	0.61
1:J:119:ASP:HA	1:J:218:ASP:HB3	1.83	0.61
1:A:94:GLY:HA3	1:A:99:LEU:CD2	2.31	0.61
1:M:12:ASP:C	1:M:13:LEU:HD23	2.22	0.60
1:K:113:VAL:CG1	1:K:212:PRO:HG2	2.25	0.60
1:M:84:LEU:CD1	1:M:88:VAL:HG11	2.29	0.60
1:F:138:MET:H	1:F:139:PRO:HD3	1.64	0.60
1:M:31:ARG:HB2	1:M:31:ARG:HH11	1.66	0.60
1:D:81:LEU:O	1:D:84:LEU:HD12	2.01	0.60
1:G:2:GLU:HB2	2:G:294:HOH:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:84:LEU:O	1:H:109:ARG:NH2	2.33	0.60
1:E:130:SER:OG	1:E:132:SER:N	2.34	0.60
1:L:11:MET:HG3	1:L:12:ASP:N	2.16	0.60
1:K:124:PHE:HD1	1:K:140:LEU:HB3	1.66	0.60
1:E:148:HIS:CD2	1:E:150:ARG:HB2	2.36	0.60
1:H:111:ARG:CD	1:H:112:ARG:N	2.51	0.60
1:L:112:ARG:HD3	1:L:211:LEU:CD2	2.31	0.60
1:D:129:THR:O	1:D:130:SER:CB	2.49	0.60
1:A:97:HIS:CE1	1:A:117:TRP:CZ2	2.89	0.60
1:K:169:ARG:NH1	1:K:234:VAL:O	2.34	0.60
1:C:25:SER:O	1:C:29:TYR:HD2	1.84	0.60
1:D:22:MET:HE3	1:J:25:SER:HB2	1.82	0.60
1:G:138:MET:H	1:G:139:PRO:CD	2.14	0.60
1:G:119:ASP:HB3	1:G:121:HIS:O	2.02	0.60
1:H:138:MET:N	1:H:139:PRO:HD2	2.16	0.60
1:L:119:ASP:OD2	1:L:123:ASP:OD2	2.19	0.60
1:I:149:PRO:HA	1:I:152:THR:OG1	2.02	0.60
1:J:35:GLN:HA	1:J:38:ASP:OD2	2.01	0.60
1:L:209:GLN:HA	1:L:255:ARG:HH22	1.65	0.60
1:L:3:ARG:NH2	1:L:87:GLY:C	2.54	0.60
1:K:124:PHE:HD2	1:K:179:LEU:HG	1.67	0.60
1:C:225:THR:CG2	1:C:226:LEU:N	2.63	0.60
1:J:269:ASP:OD1	1:J:270:GLU:N	2.30	0.60
1:M:117:TRP:CE3	1:M:140:LEU:HD13	2.37	0.60
1:J:122:ALA:O	1:J:123:ASP:C	2.39	0.60
1:A:68:GLU:CD	1:A:150:ARG:HH21	2.05	0.60
1:I:37:GLU:HG2	1:I:43:VAL:HG23	1.83	0.60
1:G:262:VAL:O	1:G:263:GLU:HB2	2.01	0.60
1:L:4:VAL:HG13	1:L:91:ILE:HD11	1.84	0.60
1:F:99:LEU:C	1:F:99:LEU:HD12	2.22	0.60
1:H:169:ARG:NH2	1:H:221:VAL:O	2.35	0.60
1:H:111:ARG:HE	1:H:111:ARG:CA	2.10	0.60
1:K:111:ARG:HD3	1:K:112:ARG:N	2.12	0.60
1:L:165:LEU:HB2	1:L:186:VAL:HG22	1.83	0.60
1:C:218:ASP:O	1:C:221:VAL:HG12	2.02	0.60
1:C:125:ASN:ND2	1:C:175:GLU:HG3	2.16	0.60
1:C:32:LEU:O	1:C:36:LEU:HD12	2.02	0.60
1:C:119:ASP:OD2	1:C:218:ASP:OD2	2.20	0.59
1:A:153:GLU:HA	1:D:156:ARG:CZ	2.31	0.59
1:H:71:ARG:NH2	1:H:154:VAL:HG11	2.17	0.59
1:J:81:LEU:HD23	1:J:84:LEU:HD11	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:25:SER:O	1:K:29:TYR:HD2	1.85	0.59
1:F:112:ARG:CZ	1:F:211:LEU:HD21	2.32	0.59
1:J:261:LEU:HD11	1:J:282:ALA:HB2	1.84	0.59
1:L:33:LEU:CD2	1:L:43:VAL:HB	2.30	0.59
1:E:33:LEU:HD23	1:E:43:VAL:HB	1.84	0.59
1:D:92:VAL:HG11	1:D:99:LEU:HD13	1.84	0.59
1:J:30:ALA:CB	1:J:279:VAL:HG21	2.33	0.59
1:M:194:ARG:HG2	1:M:194:ARG:HH11	1.67	0.59
1:C:99:LEU:C	1:C:99:LEU:HD12	2.23	0.59
1:C:12:ASP:OD2	1:C:19:GLY:HA2	2.02	0.59
1:J:22:MET:SD	1:J:267:ILE:HD12	2.43	0.59
1:C:223:ASP:OD2	1:C:225:THR:HB	2.02	0.59
1:C:225:THR:HG22	1:C:226:LEU:N	2.18	0.59
1:A:239:THR:OG1	1:A:242:GLU:HG3	2.03	0.59
1:D:97:HIS:CE1	1:D:119:ASP:OD2	2.56	0.59
1:J:177:ARG:NH1	1:J:177:ARG:HB3	2.17	0.59
1:I:99:LEU:HD12	1:I:99:LEU:C	2.22	0.59
1:K:67:LEU:HD23	1:K:67:LEU:C	2.23	0.59
1:H:149:PRO:O	1:H:153:GLU:HG2	2.03	0.59
1:M:11:MET:SD	1:M:70:ILE:HD13	2.42	0.59
1:L:37:GLU:HG2	1:L:43:VAL:CG2	2.32	0.59
1:A:138:MET:H	1:A:139:PRO:HD2	1.66	0.59
1:L:156:ARG:HG2	1:L:156:ARG:NH1	2.16	0.59
1:E:119:ASP:OD2	1:E:218:ASP:OD2	2.21	0.59
1:K:49:VAL:O	1:K:51:VAL:HG23	2.02	0.59
1:L:91:ILE:HD13	1:L:91:ILE:N	2.18	0.59
1:D:153:GLU:HG3	1:D:154:VAL:HG13	1.84	0.59
1:K:104:VAL:HG22	1:K:214:HIS:CE1	2.38	0.58
1:E:97:HIS:CD2	1:E:262:VAL:HG21	2.38	0.58
1:G:129:THR:O	1:G:130:SER:HB3	2.03	0.58
1:D:97:HIS:CD2	1:D:262:VAL:HG21	2.38	0.58
1:E:148:HIS:HD2	1:E:150:ARG:H	1.51	0.58
1:C:96:ASP:HA	1:C:263:GLU:OE2	2.03	0.58
1:L:138:MET:N	1:L:139:PRO:CD	2.60	0.58
1:I:125:ASN:O	1:I:138:MET:HG2	2.03	0.58
1:M:31:ARG:CB	1:M:31:ARG:HH11	2.15	0.58
1:G:223:ASP:OD2	1:G:225:THR:HB	2.02	0.58
1:K:119:ASP:HB3	1:K:121:HIS:O	2.04	0.58
1:E:145:GLY:C	1:E:146:LEU:HD23	2.23	0.58
1:D:138:MET:N	1:D:139:PRO:HD3	2.17	0.58
1:I:259:LEU:HG	1:I:260:ASP:N	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:129:THR:O	1:L:130:SER:CB	2.51	0.58
1:L:129:THR:CG2	1:L:174:GLY:HA3	2.34	0.58
1:I:94:GLY:HA3	1:I:99:LEU:HD21	1.86	0.58
1:A:161:LYS:H	1:A:161:LYS:HD3	1.67	0.58
1:F:214:HIS:HE1	1:F:260:ASP:OD2	1.86	0.58
1:L:104:VAL:HB	1:L:143:LEU:HD21	1.84	0.58
1:M:156:ARG:O	1:M:157:ALA:HB2	2.04	0.58
1:L:165:LEU:HD12	1:L:186:VAL:HG22	1.85	0.58
1:E:119:ASP:OD2	1:E:123:ASP:OD2	2.20	0.58
1:M:31:ARG:CB	1:M:31:ARG:NH1	2.66	0.58
1:M:253:SER:O	1:M:255:ARG:HG3	2.02	0.58
1:J:34:GLU:N	1:J:34:GLU:OE1	2.36	0.58
1:F:13:LEU:HD22	1:F:66:TYR:CG	2.38	0.58
1:H:94:GLY:HA3	1:H:99:LEU:HD21	1.84	0.58
1:M:164:VAL:HG11	1:M:204:VAL:HG22	1.84	0.58
1:K:169:ARG:HG3	1:K:234:VAL:HG11	1.85	0.58
1:M:145:GLY:HA2	1:M:156:ARG:HG2	1.86	0.58
1:A:82:ALA:HA	1:A:109:ARG:NH1	2.19	0.58
1:E:99:LEU:HD12	1:E:99:LEU:C	2.23	0.58
1:K:159:ASP:HB3	1:K:162:ASP:OD1	2.03	0.58
1:H:270:GLU:O	1:H:273:ARG:HG2	2.03	0.58
1:M:2:GLU:OE2	1:M:3:ARG:HG3	2.04	0.58
1:I:232:THR:O	1:I:234:VAL:HG23	2.04	0.58
1:M:124:PHE:HA	1:M:141:ALA:HB2	1.86	0.58
1:L:220:ASP:O	1:L:220:ASP:OD1	2.22	0.58
1:A:215:VAL:O	1:A:259:LEU:HD12	2.04	0.58
1:H:144:SER:HB3	1:H:160:PRO:HG3	1.86	0.58
1:D:164:VAL:HG11	1:D:204:VAL:HG22	1.85	0.58
1:C:30:ALA:HB3	1:C:279:VAL:HG21	1.85	0.58
1:C:161:LYS:HD3	2:C:296:HOH:O	2.04	0.58
1:C:214:HIS:HE1	1:C:260:ASP:OD2	1.87	0.58
1:E:69:GLU:N	1:E:69:GLU:OE1	2.37	0.58
1:M:22:MET:HB2	1:M:266:PRO:HG3	1.84	0.57
1:K:169:ARG:NH2	1:K:237:GLY:HA3	2.19	0.57
1:H:145:GLY:C	1:H:146:LEU:HD23	2.25	0.57
1:L:118:VAL:HB	1:L:217:LEU:CD1	2.34	0.57
1:H:12:ASP:O	1:H:12:ASP:OD1	2.21	0.57
1:D:169:ARG:NH1	1:D:234:VAL:O	2.37	0.57
1:I:36:LEU:CD2	1:I:286:LEU:HD23	2.32	0.57
1:L:153:GLU:HG2	1:L:154:VAL:CG1	2.34	0.57
1:G:10:PRO:HG3	1:G:48:ASP:OD2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:24:PRO:HD3	1:F:94:GLY:O	2.04	0.57
1:K:192:VAL:HA	1:K:200:ILE:CD1	2.35	0.57
1:G:68:GLU:OE1	1:G:150:ARG:NH2	2.26	0.57
1:L:148:HIS:HD2	1:L:150:ARG:HB2	1.69	0.57
1:G:239:THR:OG1	1:G:242:GLU:HG3	2.04	0.57
1:C:156:ARG:HG2	1:C:156:ARG:NH1	2.18	0.57
1:L:153:GLU:HG2	1:L:154:VAL:HG13	1.85	0.57
1:E:273:ARG:O	1:E:277:MET:HG3	2.04	0.57
1:I:31:ARG:O	1:I:35:GLN:HG3	2.04	0.57
1:K:159:ASP:C	1:K:161:LYS:H	2.06	0.57
1:C:198:ALA:O	1:C:202:GLU:HG2	2.05	0.57
1:F:111:ARG:HH22	1:G:249:ILE:HG23	1.70	0.57
1:M:108:ALA:HB2	1:M:113:VAL:HG21	1.86	0.57
1:L:89:PHE:HZ	1:L:256:VAL:HG12	1.69	0.57
1:D:118:VAL:HG12	1:D:221:VAL:HG11	1.87	0.57
1:H:156:ARG:HH11	1:H:156:ARG:HG2	1.69	0.57
1:M:71:ARG:HG3	1:M:155:PHE:HE2	1.68	0.57
1:E:190:HIS:O	1:E:194:ARG:HB2	2.05	0.57
1:E:244:HIS:O	1:E:248:GLU:HG3	2.05	0.57
1:M:129:THR:O	1:M:130:SER:CB	2.53	0.57
1:E:2:GLU:O	1:E:42:THR:HG23	2.05	0.57
1:G:24:PRO:O	1:G:28:ARG:HG3	2.04	0.57
1:M:270:GLU:O	1:M:273:ARG:HG2	2.04	0.57
1:K:74:ALA:O	1:K:77:LEU:HB3	2.05	0.56
1:I:187:TYR:CD1	1:I:200:ILE:HD12	2.39	0.56
1:G:25:SER:O	1:G:29:TYR:HD2	1.88	0.56
1:G:138:MET:H	1:G:139:PRO:HD2	1.68	0.56
1:I:104:VAL:HG22	1:I:214:HIS:ND1	2.20	0.56
1:I:190:HIS:CE1	1:I:194:ARG:HE	2.24	0.56
1:E:177:ARG:HH11	1:E:177:ARG:HB3	1.69	0.56
1:I:67:LEU:HD23	1:I:67:LEU:O	2.04	0.56
1:M:97:HIS:CE1	1:M:119:ASP:OD2	2.57	0.56
1:G:109:ARG:HH11	1:G:109:ARG:CG	2.16	0.56
1:J:52:SER:O	1:J:69:GLU:HB3	2.06	0.56
1:G:81:LEU:HD13	1:G:107:ALA:HB2	1.86	0.56
1:M:211:LEU:CB	2:M:296:HOH:O	2.47	0.56
1:H:119:ASP:OD2	1:H:218:ASP:OD2	2.24	0.56
1:A:94:GLY:HA3	1:A:99:LEU:HD21	1.88	0.56
1:E:177:ARG:HB3	1:E:177:ARG:NH1	2.21	0.56
1:M:239:THR:OG1	1:M:242:GLU:HG3	2.05	0.56
1:C:83:ALA:C	1:H:111:ARG:NH1	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:283:LEU:HD23	1:M:283:LEU:N	2.21	0.56
1:A:148:HIS:HD2	1:A:150:ARG:HB2	1.71	0.56
1:C:83:ALA:HA	1:H:111:ARG:HH12	1.69	0.56
1:L:112:ARG:HH11	1:L:211:LEU:HD21	1.69	0.56
1:J:169:ARG:HG3	1:J:234:VAL:HG11	1.87	0.56
1:K:245:LEU:O	1:K:249:ILE:HG12	2.05	0.56
1:K:253:SER:C	1:K:255:ARG:H	2.09	0.56
1:A:214:HIS:HD2	1:A:258:SER:OG	1.88	0.56
1:C:125:ASN:O	1:C:138:MET:HB3	2.06	0.56
1:J:161:LYS:HG3	2:J:293:HOH:O	2.06	0.56
1:J:37:GLU:HB2	2:J:298:HOH:O	2.05	0.56
1:M:188:THR:O	1:M:191:GLU:HB2	2.05	0.56
1:M:244:HIS:O	1:M:248:GLU:CG	2.54	0.56
1:K:124:PHE:CD2	1:K:179:LEU:HG	2.41	0.56
1:A:244:HIS:O	1:A:248:GLU:HG3	2.06	0.56
1:G:122:ALA:O	1:G:123:ASP:C	2.44	0.55
1:A:156:ARG:NH1	1:D:153:GLU:O	2.39	0.55
1:F:265:ASN:HD22	1:F:268:LEU:HD12	1.71	0.55
1:I:169:ARG:HD2	1:I:234:VAL:HG12	1.89	0.55
1:L:97:HIS:HE1	1:L:119:ASP:HB2	1.70	0.55
1:M:31:ARG:NH1	1:M:31:ARG:HB3	2.20	0.55
1:A:169:ARG:HA	1:E:290:ILE:CG2	2.36	0.55
1:J:7:VAL:HG13	1:J:92:VAL:HG22	1.88	0.55
1:C:129:THR:O	1:C:130:SER:CB	2.53	0.55
1:L:214:HIS:HD2	1:L:258:SER:OG	1.88	0.55
1:F:169:ARG:NH1	1:F:234:VAL:O	2.40	0.55
1:L:124:PHE:HD1	1:L:140:LEU:HD23	1.71	0.55
1:C:199:ARG:O	1:C:203:GLU:HG3	2.05	0.55
1:L:13:LEU:HB2	1:L:70:ILE:HD11	1.88	0.55
1:I:25:SER:HB3	1:M:22:MET:HE3	1.87	0.55
1:M:259:LEU:HD13	1:M:285:LEU:HD23	1.87	0.55
1:G:128:GLU:N	1:G:128:GLU:OE1	2.29	0.55
1:K:290:ILE:H	1:K:290:ILE:HD12	1.71	0.55
1:F:91:ILE:HG23	1:F:259:LEU:HD23	1.89	0.55
1:J:117:TRP:CD2	1:J:140:LEU:HD22	2.42	0.55
1:K:124:PHE:CD1	1:K:140:LEU:HG	2.42	0.55
1:I:228:PRO:HD3	1:I:273:ARG:HH21	1.71	0.55
1:K:244:HIS:O	1:K:248:GLU:HG3	2.07	0.55
1:M:125:ASN:O	1:M:138:MET:HG2	2.06	0.55
1:M:225:THR:HG23	1:M:226:LEU:N	2.21	0.55
1:I:119:ASP:HB3	1:I:121:HIS:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:169:ARG:NH2	1:D:221:VAL:O	2.40	0.55
1:D:169:ARG:NH2	1:D:237:GLY:HA3	2.22	0.55
1:G:145:GLY:HA2	1:G:156:ARG:CD	2.25	0.55
1:G:145:GLY:CA	1:G:156:ARG:HD3	2.24	0.55
1:C:169:ARG:HD2	1:C:234:VAL:O	2.06	0.55
1:C:169:ARG:HH22	1:C:221:VAL:C	2.09	0.55
1:M:197:VAL:HG21	1:M:242:GLU:HB3	1.89	0.55
1:L:248:GLU:HA	2:L:294:HOH:O	2.06	0.55
1:D:112:ARG:NH1	1:D:211:LEU:HD21	2.21	0.55
1:I:98:SER:OG	1:I:136:HIS:HB3	2.07	0.55
1:A:11:MET:HE3	1:A:98:SER:HB2	1.89	0.55
1:L:66:TYR:O	1:L:68:GLU:N	2.40	0.55
1:I:127:PRO:HD2	1:I:128:GLU:OE1	2.06	0.55
1:G:94:GLY:HA3	1:G:99:LEU:HD21	1.88	0.55
1:M:13:LEU:N	1:M:96:ASP:OD2	2.36	0.55
1:L:188:THR:O	1:L:192:VAL:HG23	2.07	0.55
1:K:159:ASP:O	1:K:162:ASP:N	2.40	0.55
1:K:124:PHE:CD1	1:K:141:ALA:N	2.75	0.55
1:K:176:LYS:HB3	1:M:291:PHE:CE2	2.41	0.55
1:G:201:ALA:HB1	1:G:249:ILE:HG21	1.89	0.55
1:M:150:ARG:HD3	1:M:150:ARG:O	2.07	0.55
1:M:109:ARG:CG	1:M:109:ARG:HH11	2.19	0.55
1:M:29:TYR:C	1:M:31:ARG:N	2.60	0.55
1:I:144:SER:HA	1:I:158:VAL:O	2.07	0.55
1:J:129:THR:O	1:J:130:SER:CB	2.54	0.54
1:G:169:ARG:HH22	1:G:221:VAL:C	2.10	0.54
1:D:96:ASP:HB3	1:D:136:HIS:HB3	1.89	0.54
1:H:97:HIS:O	1:H:100:SER:HB2	2.07	0.54
1:M:159:ASP:O	1:M:162:ASP:HB2	2.07	0.54
1:G:156:ARG:HG2	1:G:156:ARG:HH11	1.72	0.54
1:G:26:ALA:HB1	1:G:272:ASN:OD1	2.07	0.54
1:D:143:LEU:O	1:D:158:VAL:HG12	2.07	0.54
1:H:173:PRO:HA	1:H:176:LYS:HG3	1.89	0.54
1:D:189:MET:HA	1:D:189:MET:HE3	1.90	0.54
1:K:109:ARG:C	1:K:111:ARG:H	2.10	0.54
1:D:192:VAL:HA	1:D:200:ILE:HD11	1.90	0.54
1:H:112:ARG:HD3	1:H:211:LEU:HD22	1.90	0.54
1:C:148:HIS:HD2	1:C:150:ARG:N	2.01	0.54
1:L:3:ARG:CZ	1:L:88:VAL:HG23	2.38	0.54
1:I:138:MET:N	1:I:139:PRO:CD	2.68	0.54
1:H:119:ASP:OD2	1:H:123:ASP:OD2	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:148:HIS:CD2	1:I:149:PRO:HD2	2.42	0.54
1:M:4:VAL:CG2	1:M:41:TYR:HD1	2.20	0.54
1:M:82:ALA:C	1:M:84:LEU:H	2.09	0.54
1:I:91:ILE:HD11	1:I:286:LEU:HD21	1.89	0.54
1:L:205:LEU:HD13	1:L:253:SER:HB3	1.89	0.54
1:C:30:ALA:CB	1:C:279:VAL:HG21	2.36	0.54
1:J:187:TYR:CD1	1:J:200:ILE:HD12	2.43	0.54
1:M:247:MET:HB2	1:M:284:SER:HB3	1.90	0.54
1:A:99:LEU:C	1:A:99:LEU:HD12	2.28	0.54
1:K:112:ARG:HD3	1:K:211:LEU:HD21	1.90	0.54
1:J:125:ASN:ND2	1:J:175:GLU:CG	2.67	0.54
1:H:11:MET:HE1	1:H:98:SER:HB2	1.89	0.54
1:L:126:THR:HG23	1:L:178:LEU:HD13	1.90	0.54
1:A:79:GLU:CG	1:D:111:ARG:NH2	2.70	0.54
1:J:86:GLU:HG2	1:J:109:ARG:NE	2.21	0.54
1:I:261:LEU:HD11	1:I:282:ALA:HB2	1.90	0.54
1:L:12:ASP:HB2	1:L:20:VAL:HG23	1.90	0.54
1:M:22:MET:HB2	1:M:266:PRO:CG	2.38	0.54
1:F:123:ASP:HB3	1:F:139:PRO:HD2	1.88	0.54
1:M:22:MET:SD	1:M:267:ILE:HD13	2.48	0.54
1:D:117:TRP:HB3	1:D:165:LEU:HD23	1.91	0.54
1:D:113:VAL:HG12	1:D:212:PRO:HG2	1.90	0.54
1:A:125:ASN:ND2	1:A:175:GLU:HG3	2.23	0.54
1:M:129:THR:HB	1:M:174:GLY:CA	2.25	0.53
1:A:153:GLU:HA	1:D:156:ARG:NH2	2.23	0.53
1:M:124:PHE:CE2	1:M:178:LEU:HB3	2.41	0.53
1:L:265:ASN:ND2	1:L:268:LEU:HD13	2.23	0.53
1:G:279:VAL:O	1:G:283:LEU:HG	2.08	0.53
1:M:117:TRP:O	1:M:165:LEU:HD23	2.08	0.53
1:M:122:ALA:HB2	1:M:171:LEU:CD2	2.38	0.53
1:L:196:GLY:O	1:L:200:ILE:HG13	2.08	0.53
1:K:215:VAL:O	1:K:259:LEU:HD12	2.07	0.53
1:K:215:VAL:HB	1:K:259:LEU:HD13	1.89	0.53
1:M:226:LEU:HD21	1:M:240:TYR:CB	2.33	0.53
1:D:11:MET:HG2	1:D:96:ASP:OD2	2.08	0.53
1:L:100:SER:HA	1:L:103:SER:OG	2.08	0.53
1:L:189:MET:HA	1:L:192:VAL:CG2	2.38	0.53
1:I:25:SER:HB3	1:M:22:MET:HE2	1.90	0.53
1:I:35:GLN:OE1	1:I:283:LEU:HD11	2.08	0.53
1:F:270:GLU:O	1:F:273:ARG:HG2	2.08	0.53
1:E:216:SER:HA	1:E:260:ASP:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:97:HIS:ND1	1:K:119:ASP:OD2	2.42	0.53
1:M:124:PHE:O	1:M:124:PHE:CD2	2.62	0.53
1:J:122:ALA:O	1:J:124:PHE:HB2	2.09	0.53
1:L:145:GLY:HA3	1:L:156:ARG:CD	2.38	0.53
1:J:4:VAL:HG22	1:J:89:PHE:HB3	1.90	0.53
1:F:177:ARG:HG2	1:F:177:ARG:HH11	1.74	0.53
1:C:81:LEU:C	1:C:83:ALA:H	2.12	0.53
1:L:33:LEU:HD23	1:L:43:VAL:CB	2.36	0.53
1:F:140:LEU:HD11	1:F:163:VAL:HG11	1.89	0.53
1:M:148:HIS:HD2	1:M:150:ARG:H	1.57	0.53
1:M:94:GLY:HA2	1:M:99:LEU:CD2	2.39	0.53
1:H:97:HIS:CE1	1:H:218:ASP:HB2	2.43	0.53
1:A:228:PRO:HG2	1:A:269:ASP:OD1	2.09	0.53
1:L:64:LEU:HD13	1:L:65:ALA:N	2.24	0.53
1:K:277:MET:HA	1:K:277:MET:CE	2.39	0.53
1:L:37:GLU:O	1:L:40:GLY:N	2.35	0.53
1:I:11:MET:HE2	1:I:98:SER:HB2	1.88	0.53
1:I:32:LEU:HD12	1:I:279:VAL:HG13	1.90	0.53
1:L:81:LEU:HD13	1:L:107:ALA:HB2	1.90	0.53
1:J:117:TRP:HB3	1:J:165:LEU:HD23	1.90	0.53
1:I:165:LEU:HD12	1:I:186:VAL:HG22	1.90	0.53
1:L:97:HIS:ND1	1:L:218:ASP:OD2	2.42	0.53
1:A:31:ARG:HA	1:A:34:GLU:OE1	2.09	0.53
1:M:41:TYR:O	1:M:43:VAL:HG23	2.09	0.53
1:D:169:ARG:HG3	1:D:234:VAL:HG11	1.90	0.53
1:K:270:GLU:HB2	1:K:273:ARG:HD3	1.89	0.53
1:K:272:ASN:O	1:K:276:GLU:HG3	2.09	0.53
1:J:111:ARG:HD3	1:J:112:ARG:H	1.74	0.53
1:H:51:VAL:O	1:H:51:VAL:HG12	2.09	0.53
1:A:138:MET:H	1:A:139:PRO:CD	2.21	0.53
1:H:156:ARG:HG2	1:H:156:ARG:NH1	2.23	0.53
1:D:169:ARG:HD3	1:D:235:PRO:O	2.09	0.53
1:M:144:SER:OG	1:M:160:PRO:HG3	2.09	0.53
1:M:287:GLY:O	1:M:289:ARG:HD3	2.08	0.53
1:K:91:ILE:HA	1:K:259:LEU:O	2.09	0.52
1:J:149:PRO:HA	1:J:152:THR:OG1	2.08	0.52
1:C:138:MET:N	1:C:139:PRO:CD	2.72	0.52
1:G:75:LEU:O	1:G:79:GLU:HG3	2.09	0.52
1:F:198:ALA:O	1:F:202:GLU:HG2	2.08	0.52
1:I:20:VAL:HG12	1:I:265:ASN:HB2	1.91	0.52
1:M:126:THR:C	1:M:128:GLU:N	2.61	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:97:HIS:ND1	1:K:123:ASP:OD2	2.42	0.52
1:D:156:ARG:HH11	1:D:156:ARG:HG2	1.73	0.52
1:I:179:LEU:HD23	1:I:184:VAL:HB	1.91	0.52
1:D:119:ASP:OD2	1:D:218:ASP:OD2	2.26	0.52
1:M:225:THR:CG2	1:M:226:LEU:N	2.72	0.52
1:K:243:ALA:O	1:K:247:MET:HG2	2.10	0.52
1:M:213:LEU:O	1:M:257:GLN:N	2.43	0.52
1:G:12:ASP:HB2	1:G:21:ASP:HB3	1.92	0.52
1:M:29:TYR:O	1:M:31:ARG:HG3	2.09	0.52
1:J:169:ARG:NH2	1:J:237:GLY:HA3	2.25	0.52
1:K:8:GLY:O	1:K:48:ASP:HA	2.09	0.52
1:A:111:ARG:CD	1:A:112:ARG:H	2.18	0.52
1:J:204:VAL:C	1:J:206:LYS:N	2.62	0.52
1:I:13:LEU:HD22	1:I:66:TYR:CD1	2.45	0.52
1:K:237:GLY:O	1:M:241:ARG:NH1	2.42	0.52
1:E:221:VAL:O	1:E:221:VAL:HG22	2.08	0.52
1:E:19:GLY:N	1:E:265:ASN:HD21	2.08	0.52
1:H:109:ARG:NH1	1:H:109:ARG:CG	2.61	0.52
1:M:153:GLU:CG	1:M:154:VAL:H	2.18	0.52
1:F:11:MET:CE	1:F:98:SER:HB2	2.39	0.52
1:H:13:LEU:HB2	1:H:70:ILE:HD11	1.91	0.52
1:F:214:HIS:CE1	1:F:260:ASP:OD2	2.62	0.52
1:C:83:ALA:HB1	1:H:111:ARG:NH1	2.23	0.52
1:I:130:SER:OG	1:I:132:SER:N	2.36	0.52
1:A:109:ARG:CG	1:A:109:ARG:HH11	2.21	0.52
1:L:124:PHE:CD1	1:L:140:LEU:HD23	2.44	0.52
1:K:159:ASP:C	1:K:161:LYS:N	2.63	0.52
1:I:13:LEU:HD13	1:I:70:ILE:HG13	1.92	0.52
1:F:94:GLY:HA3	1:F:99:LEU:HD21	1.92	0.52
1:E:259:LEU:HD22	1:E:285:LEU:HD23	1.91	0.52
1:M:118:VAL:HG13	1:M:166:VAL:HB	1.91	0.52
1:C:81:LEU:C	1:C:83:ALA:N	2.61	0.52
1:I:170:SER:O	1:I:171:LEU:HD23	2.10	0.52
1:L:190:HIS:HE1	1:L:194:ARG:NE	2.03	0.52
1:M:125:ASN:C	1:M:138:MET:HG2	2.30	0.51
1:K:109:ARG:O	1:K:111:ARG:N	2.41	0.51
1:M:80:ARG:HD2	1:M:80:ARG:C	2.29	0.51
1:E:271:ARG:HH22	1:F:228:PRO:HB3	1.75	0.51
1:M:169:ARG:NH1	1:M:234:VAL:O	2.42	0.51
1:F:20:VAL:HB	1:F:95:GLY:HA2	1.92	0.51
1:D:129:THR:HB	1:D:174:GLY:HA3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:130:SER:OG	1:J:132:SER:N	2.33	0.51
1:M:20:VAL:O	1:M:95:GLY:HA2	2.11	0.51
1:A:156:ARG:CZ	1:D:156:ARG:NH2	2.74	0.51
1:D:122:ALA:O	1:D:123:ASP:C	2.48	0.51
1:D:22:MET:CE	1:J:22:MET:HB3	2.40	0.51
1:K:277:MET:HA	1:K:277:MET:HE3	1.92	0.51
1:G:120:ALA:HB2	1:G:220:ASP:O	2.11	0.51
1:C:97:HIS:CE1	1:C:119:ASP:OD2	2.64	0.51
1:J:119:ASP:OD2	1:J:218:ASP:OD2	2.29	0.51
1:D:216:SER:HA	1:D:260:ASP:HB2	1.92	0.51
1:J:118:VAL:HG12	1:J:221:VAL:HG21	1.93	0.51
1:M:13:LEU:N	1:M:13:LEU:HD23	2.25	0.51
1:H:97:HIS:ND1	1:H:218:ASP:OD2	2.44	0.51
1:I:20:VAL:HB	1:I:95:GLY:HA2	1.92	0.51
1:E:118:VAL:HG12	1:E:221:VAL:HG21	1.92	0.51
1:E:26:ALA:HB1	1:E:272:ASN:OD1	2.11	0.51
1:I:44:GLU:HG2	1:I:46:LEU:HD23	1.92	0.51
1:G:117:TRP:HB3	1:G:165:LEU:CD2	2.35	0.51
1:H:119:ASP:HA	1:H:218:ASP:HB3	1.93	0.51
1:I:259:LEU:HD21	1:I:261:LEU:HD21	1.91	0.51
1:L:169:ARG:NH2	1:L:237:GLY:HA2	2.25	0.51
1:I:94:GLY:HA3	1:I:99:LEU:CD2	2.40	0.51
1:M:128:GLU:C	1:M:130:SER:H	2.13	0.51
1:M:223:ASP:OD2	1:M:225:THR:HG22	2.11	0.51
1:A:129:THR:O	1:A:130:SER:CB	2.59	0.51
1:K:243:ALA:C	1:K:281:LEU:HD21	2.31	0.51
1:E:98:SER:OG	1:E:136:HIS:HB3	2.11	0.51
1:A:248:GLU:O	1:A:252:GLU:HG3	2.11	0.51
1:I:68:GLU:OE2	1:I:150:ARG:NE	2.44	0.51
1:C:4:VAL:HG22	1:C:89:PHE:HB3	1.92	0.51
1:A:65:ALA:O	1:A:66:TYR:HB2	2.09	0.51
1:M:168:VAL:CG1	1:M:168:VAL:O	2.58	0.51
1:K:190:HIS:HD2	1:M:248:GLU:OE1	1.94	0.51
1:A:148:HIS:CD2	1:A:150:ARG:HB2	2.46	0.51
1:I:126:THR:HG23	1:I:178:LEU:CD1	2.41	0.51
1:G:226:LEU:HD11	1:G:277:MET:SD	2.50	0.51
1:M:203:GLU:O	1:M:206:LYS:HB3	2.11	0.51
1:G:22:MET:SD	1:G:267:ILE:HD11	2.50	0.51
1:E:4:VAL:HG12	1:E:43:VAL:HG13	1.91	0.50
1:C:169:ARG:NH2	1:C:221:VAL:O	2.44	0.50
1:I:109:ARG:HH11	1:I:109:ARG:CG	2.22	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:169:ARG:HB3	1:M:189:MET:HG2	1.93	0.50
1:E:11:MET:HE1	1:E:98:SER:HB2	1.92	0.50
1:C:111:ARG:CD	1:C:112:ARG:H	2.23	0.50
1:C:83:ALA:HB1	1:H:111:ARG:NH2	2.25	0.50
1:K:97:HIS:CD2	1:K:262:VAL:HG21	2.45	0.50
1:D:43:VAL:CG1	1:D:44:GLU:N	2.73	0.50
1:A:72:ALA:O	1:A:76:VAL:HG23	2.11	0.50
1:M:129:THR:O	1:M:130:SER:HB2	2.12	0.50
1:F:122:ALA:O	1:F:123:ASP:C	2.49	0.50
1:A:97:HIS:ND1	1:A:123:ASP:OD2	2.44	0.50
1:E:104:VAL:O	1:E:108:ALA:HB2	2.12	0.50
1:H:26:ALA:HB1	1:H:272:ASN:OD1	2.12	0.50
1:G:33:LEU:HG	1:G:43:VAL:HG11	1.94	0.50
1:E:158:VAL:HG22	1:E:159:ASP:N	2.27	0.50
1:H:32:LEU:HA	1:H:279:VAL:HG13	1.93	0.50
1:J:187:TYR:OH	1:J:203:GLU:HG2	2.11	0.50
1:C:11:MET:CE	1:C:98:SER:HB2	2.42	0.50
1:L:118:VAL:HB	1:L:217:LEU:HD12	1.93	0.50
1:M:249:ILE:O	1:M:252:GLU:HB2	2.11	0.50
1:H:90:PRO:HD2	1:H:257:GLN:O	2.10	0.50
1:A:79:GLU:CG	1:D:111:ARG:HH22	2.24	0.50
1:E:97:HIS:ND1	1:E:119:ASP:OD2	2.44	0.50
1:M:122:ALA:HB2	1:M:171:LEU:HD21	1.93	0.50
1:F:142:VAL:O	1:F:145:GLY:N	2.42	0.50
1:H:99:LEU:HD12	1:H:100:SER:N	2.27	0.50
1:F:169:ARG:NH2	1:F:221:VAL:O	2.44	0.50
1:L:98:SER:OG	1:L:136:HIS:HB3	2.11	0.50
1:M:30:ALA:HB1	1:M:276:GLU:HA	1.92	0.50
1:L:148:HIS:CD2	1:L:150:ARG:HB2	2.45	0.50
1:K:115:VAL:HB	1:K:163:VAL:HG22	1.94	0.50
1:I:212:PRO:HA	1:I:255:ARG:O	2.12	0.50
1:C:118:VAL:HG12	1:C:221:VAL:HG21	1.94	0.50
1:M:188:THR:O	1:M:192:VAL:HG23	2.11	0.50
1:H:111:ARG:NE	1:H:112:ARG:N	2.59	0.50
1:L:177:ARG:O	1:L:179:LEU:N	2.44	0.50
1:H:153:GLU:HG3	1:H:154:VAL:HG13	1.92	0.50
1:E:169:ARG:NH1	1:E:234:VAL:O	2.45	0.50
1:H:115:VAL:HB	1:H:163:VAL:HG22	1.94	0.50
1:H:82:ALA:HA	1:H:109:ARG:NH1	2.20	0.50
1:I:89:PHE:CE2	1:I:286:LEU:HD11	2.46	0.50
1:D:97:HIS:ND1	1:D:119:ASP:OD2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:228:PRO:HG3	1:E:270:GLU:HG3	1.93	0.50
1:I:27:LEU:HD13	1:I:93:LEU:HD22	1.93	0.50
1:F:144:SER:HB3	1:F:160:PRO:HG3	1.94	0.50
1:M:173:PRO:HG2	2:M:293:HOH:O	2.11	0.50
1:I:100:SER:HA	1:I:103:SER:OG	2.12	0.50
1:I:168:VAL:O	1:I:188:THR:HA	2.12	0.50
1:G:97:HIS:NE2	1:G:117:TRP:CZ2	2.80	0.49
1:J:143:LEU:O	1:J:158:VAL:HG12	2.11	0.49
1:C:221:VAL:HG22	1:C:221:VAL:O	2.12	0.49
1:M:97:HIS:ND1	1:M:119:ASP:OD2	2.45	0.49
1:A:22:MET:CE	1:H:25:SER:HB2	2.42	0.49
1:D:259:LEU:HD13	1:D:285:LEU:CD2	2.41	0.49
1:K:124:PHE:CE1	1:K:140:LEU:HG	2.47	0.49
1:C:11:MET:HE1	1:C:98:SER:HB2	1.94	0.49
1:E:12:ASP:HB2	1:E:21:ASP:HB3	1.93	0.49
1:L:109:ARG:NH1	1:L:109:ARG:CG	2.65	0.49
1:F:138:MET:N	1:F:139:PRO:HD3	2.26	0.49
1:H:119:ASP:OD1	1:H:120:ALA:N	2.44	0.49
1:I:32:LEU:CD1	1:I:279:VAL:HG13	2.42	0.49
1:J:89:PHE:HD2	1:J:91:ILE:HD12	1.78	0.49
1:I:213:LEU:HD11	1:I:255:ARG:NH1	2.26	0.49
1:K:128:GLU:CD	1:K:128:GLU:H	2.15	0.49
1:D:33:LEU:HD11	1:D:45:ASP:HB2	1.94	0.49
1:I:51:VAL:CG1	1:I:52:SER:N	2.75	0.49
1:F:122:ALA:O	1:F:124:PHE:HB2	2.11	0.49
1:J:124:PHE:HD1	1:J:140:LEU:HB3	1.78	0.49
1:H:135:VAL:O	1:H:139:PRO:HD3	2.12	0.49
1:I:11:MET:HE3	1:I:70:ILE:HG12	1.93	0.49
1:G:195:LEU:HB2	1:G:200:ILE:HD11	1.94	0.49
1:G:99:LEU:HD12	1:G:100:SER:N	2.26	0.49
1:E:169:ARG:HH11	1:E:234:VAL:HB	1.76	0.49
1:F:19:GLY:N	2:F:302:HOH:O	2.45	0.49
1:F:188:THR:HG21	1:H:291:PHE:HB2	1.94	0.49
1:A:111:ARG:NH1	1:D:83:ALA:HB2	2.19	0.49
1:E:127:PRO:N	1:E:138:MET:HE1	2.27	0.49
1:G:119:ASP:HA	1:G:218:ASP:HB3	1.93	0.49
1:G:130:SER:OG	1:G:132:SER:N	2.46	0.49
1:F:192:VAL:HA	1:F:200:ILE:HD12	1.95	0.49
1:I:11:MET:HE1	1:I:98:SER:HB2	1.91	0.49
1:M:41:TYR:CD2	1:M:41:TYR:N	2.79	0.49
1:E:198:ALA:O	1:E:202:GLU:HG2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:112:ARG:HD3	1:E:211:LEU:HD21	1.93	0.49
1:L:112:ARG:HD3	1:L:211:LEU:HD22	1.94	0.49
1:J:152:THR:O	1:J:156:ARG:HB2	2.11	0.49
1:F:138:MET:N	1:F:139:PRO:CD	2.75	0.49
1:L:186:VAL:O	1:L:186:VAL:HG12	2.11	0.49
1:E:79:GLU:HB3	2:E:303:HOH:O	2.13	0.49
1:J:207:HIS:O	1:J:207:HIS:CD2	2.66	0.49
1:C:83:ALA:CB	1:H:111:ARG:NH1	2.76	0.49
1:D:43:VAL:HG12	1:D:44:GLU:H	1.77	0.49
1:J:169:ARG:NH2	1:J:221:VAL:O	2.46	0.49
1:G:100:SER:HA	1:G:103:SER:OG	2.13	0.49
1:E:88:VAL:HG12	1:E:88:VAL:O	2.12	0.49
1:C:86:GLU:OE2	1:C:109:ARG:HD3	2.12	0.49
1:J:99:LEU:HD12	1:J:100:SER:N	2.27	0.49
1:D:223:ASP:OD2	1:D:225:THR:CG2	2.61	0.49
1:C:11:MET:HG2	1:C:96:ASP:OD2	2.12	0.49
1:K:279:VAL:O	1:K:283:LEU:HG	2.12	0.49
1:E:156:ARG:HG2	1:E:156:ARG:NH1	2.28	0.49
1:K:158:VAL:HG22	1:K:159:ASP:N	2.27	0.49
1:G:173:PRO:HA	1:G:176:LYS:HG3	1.95	0.49
1:F:66:TYR:HB3	1:F:69:GLU:HB2	1.95	0.49
1:C:169:ARG:HD2	1:C:234:VAL:HB	1.93	0.49
1:L:201:ALA:CB	1:L:249:ILE:HG21	2.42	0.49
1:F:115:VAL:CG2	1:F:158:VAL:HG21	2.42	0.49
1:L:200:ILE:HA	1:L:203:GLU:HB2	1.95	0.49
1:K:270:GLU:O	1:K:273:ARG:HG2	2.13	0.49
1:J:226:LEU:HD21	1:J:240:TYR:HB2	1.94	0.49
1:K:75:LEU:O	1:K:79:GLU:HB2	2.13	0.49
1:K:137:GLY:HA3	2:K:293:HOH:O	2.13	0.49
1:M:19:GLY:N	1:M:265:ASN:HD21	2.11	0.48
1:L:117:TRP:HB3	1:L:165:LEU:HD23	1.95	0.48
1:K:124:PHE:CE1	1:K:141:ALA:HA	2.48	0.48
1:K:264:VAL:CG2	1:K:278:LEU:HD22	2.43	0.48
1:K:4:VAL:HG12	1:K:43:VAL:HG13	1.95	0.48
1:D:199:ARG:O	1:D:203:GLU:HG3	2.13	0.48
1:E:67:LEU:HD23	1:E:67:LEU:C	2.33	0.48
1:M:135:VAL:O	1:M:139:PRO:HD3	2.14	0.48
1:L:25:SER:O	1:L:29:TYR:CD2	2.52	0.48
1:C:226:LEU:HD21	1:C:240:TYR:HB2	1.95	0.48
1:I:33:LEU:HD11	1:I:45:ASP:HB2	1.95	0.48
1:A:171:LEU:HB2	1:A:176:LYS:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:164:VAL:HG22	1:G:185:ARG:HB3	1.95	0.48
1:J:260:ASP:O	1:J:261:LEU:HD23	2.13	0.48
1:C:169:ARG:HG3	1:C:234:VAL:HG11	1.94	0.48
1:D:97:HIS:ND1	1:D:123:ASP:OD2	2.46	0.48
1:E:34:GLU:CD	1:E:34:GLU:H	2.16	0.48
1:K:175:GLU:O	1:K:176:LYS:C	2.52	0.48
1:K:169:ARG:NH2	1:K:221:VAL:O	2.46	0.48
1:H:214:HIS:CD2	1:H:258:SER:OG	2.66	0.48
1:A:30:ALA:HB3	1:A:279:VAL:HG21	1.95	0.48
1:D:198:ALA:O	1:D:202:GLU:HG2	2.13	0.48
1:F:112:ARG:NE	1:F:211:LEU:HD21	2.28	0.48
1:K:119:ASP:OD2	1:K:218:ASP:OD2	2.30	0.48
1:G:119:ASP:OD2	1:G:123:ASP:OD2	2.32	0.48
1:M:222:LEU:HD13	1:M:277:MET:HE2	1.95	0.48
1:D:100:SER:HA	1:D:103:SER:OG	2.12	0.48
1:K:148:HIS:CD2	1:K:150:ARG:HB2	2.48	0.48
1:K:159:ASP:HB3	1:K:162:ASP:CG	2.33	0.48
1:A:214:HIS:HE1	1:A:260:ASP:OD2	1.96	0.48
1:K:185:ARG:CZ	1:K:207:HIS:ND1	2.76	0.48
1:L:213:LEU:O	1:L:257:GLN:HG3	2.13	0.48
1:C:33:LEU:HD21	1:C:45:ASP:HB2	1.95	0.48
1:A:97:HIS:NE2	1:A:117:TRP:CZ2	2.81	0.48
1:C:97:HIS:CD2	1:C:262:VAL:HG21	2.48	0.48
1:A:86:GLU:OE1	1:D:86:GLU:N	2.47	0.48
1:E:271:ARG:NH2	1:F:228:PRO:HB3	2.28	0.48
1:F:264:VAL:CG2	1:F:278:LEU:HD22	2.43	0.48
1:F:119:ASP:HB3	1:F:121:HIS:O	2.13	0.48
1:D:71:ARG:HD3	2:D:295:HOH:O	2.12	0.48
1:G:99:LEU:HD12	1:G:99:LEU:C	2.34	0.48
1:M:46:LEU:N	1:M:46:LEU:HD23	2.28	0.48
1:J:246:LEU:HG	1:J:247:MET:HE1	1.96	0.48
1:C:97:HIS:ND1	1:C:119:ASP:OD2	2.46	0.48
1:M:167:GLY:O	1:M:168:VAL:C	2.51	0.48
1:I:115:VAL:HB	1:I:163:VAL:HG22	1.95	0.48
1:A:169:ARG:HG3	1:A:234:VAL:CG1	2.44	0.48
1:J:81:LEU:O	1:J:84:LEU:HD12	2.13	0.48
1:E:279:VAL:O	1:E:283:LEU:HG	2.13	0.48
1:L:222:LEU:HD13	1:L:277:MET:HG2	1.95	0.48
1:E:214:HIS:CD2	1:E:258:SER:OG	2.66	0.48
1:K:84:LEU:O	1:K:109:ARG:NH2	2.47	0.48
1:K:97:HIS:CE1	1:K:119:ASP:OD2	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:225:THR:O	1:D:273:ARG:NH2	2.46	0.48
1:D:130:SER:HG	1:D:132:SER:N	2.11	0.48
1:F:221:VAL:HG22	1:F:221:VAL:O	2.14	0.48
1:K:161:LYS:HA	2:K:294:HOH:O	2.14	0.48
1:K:29:TYR:C	1:K:31:ARG:H	2.17	0.48
1:J:33:LEU:HD11	1:J:45:ASP:HB2	1.96	0.48
1:C:275:ALA:O	1:C:279:VAL:HG23	2.13	0.48
1:L:116:VAL:CG1	1:L:204:VAL:HG11	2.44	0.48
1:E:117:TRP:CE3	1:E:140:LEU:HD13	2.48	0.48
1:M:70:ILE:HG21	1:M:135:VAL:HG11	1.95	0.48
1:J:32:LEU:HA	1:J:279:VAL:HG13	1.95	0.48
1:H:169:ARG:HH22	1:H:221:VAL:C	2.16	0.48
1:K:32:LEU:CD1	1:K:279:VAL:HG13	2.43	0.48
1:H:177:ARG:NH1	2:H:304:HOH:O	2.44	0.48
1:I:78:LYS:O	1:I:78:LYS:HG2	2.13	0.48
1:I:119:ASP:C	1:I:221:VAL:HG23	2.34	0.48
1:J:138:MET:H	1:J:139:PRO:CD	2.26	0.48
1:M:100:SER:HA	1:M:103:SER:OG	2.14	0.48
1:H:11:MET:HE2	1:H:96:ASP:HB2	1.95	0.48
1:D:214:HIS:HD2	1:D:258:SER:CB	2.26	0.48
1:E:109:ARG:HH11	1:E:109:ARG:CG	2.27	0.48
1:A:156:ARG:CZ	1:D:153:GLU:HA	2.44	0.47
1:L:153:GLU:HG2	1:L:154:VAL:N	2.29	0.47
1:I:215:VAL:O	1:I:259:LEU:HD12	2.14	0.47
1:A:200:ILE:O	1:A:204:VAL:HG23	2.14	0.47
1:M:151:LEU:HD22	1:M:155:PHE:CD2	2.49	0.47
1:K:8:GLY:HA2	1:K:93:LEU:HB2	1.95	0.47
1:J:198:ALA:O	1:J:202:GLU:HG2	2.14	0.47
1:G:51:VAL:O	1:G:51:VAL:HG12	2.12	0.47
1:L:112:ARG:HD3	1:L:211:LEU:HD21	1.97	0.47
1:L:125:ASN:N	2:L:301:HOH:O	2.47	0.47
1:I:97:HIS:ND1	1:I:123:ASP:OD2	2.47	0.47
1:D:214:HIS:HE1	1:D:260:ASP:OD2	1.97	0.47
1:K:221:VAL:HG22	1:K:238:LEU:HD12	1.96	0.47
1:K:30:ALA:C	1:K:31:ARG:HG2	2.34	0.47
1:K:259:LEU:HD12	1:K:260:ASP:H	1.79	0.47
1:J:149:PRO:O	1:J:153:GLU:HB3	2.13	0.47
1:F:20:VAL:HB	1:F:95:GLY:CA	2.45	0.47
1:J:66:TYR:C	1:J:70:ILE:HD13	2.34	0.47
1:L:145:GLY:N	1:L:156:ARG:HG3	2.30	0.47
1:I:214:HIS:CE1	1:I:260:ASP:OD2	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:92:VAL:HG21	1:I:103:SER:HB3	1.97	0.47
1:K:152:THR:O	1:K:156:ARG:HB3	2.15	0.47
1:G:146:LEU:CD2	1:G:146:LEU:N	2.70	0.47
1:L:149:PRO:O	1:L:153:GLU:CB	2.62	0.47
1:A:11:MET:HE1	1:A:98:SER:HB2	1.96	0.47
1:I:92:VAL:HG11	1:I:99:LEU:HD13	1.95	0.47
1:L:13:LEU:HD23	1:L:66:TYR:CD1	2.49	0.47
1:C:20:VAL:HB	1:C:95:GLY:HA2	1.96	0.47
1:M:116:VAL:HB	1:M:215:VAL:HG22	1.96	0.47
1:M:97:HIS:CD2	1:M:262:VAL:HG21	2.50	0.47
1:D:11:MET:HE3	1:D:98:SER:HB2	1.94	0.47
1:D:225:THR:CG2	1:D:226:LEU:N	2.78	0.47
1:K:78:LYS:O	1:K:106:GLY:HA3	2.14	0.47
1:F:228:PRO:O	1:F:230:VAL:N	2.41	0.47
1:I:229:GLY:O	1:I:274:THR:HG21	2.14	0.47
1:I:67:LEU:HD21	1:I:151:LEU:HD21	1.96	0.47
1:G:86:GLU:OE2	1:G:109:ARG:HD3	2.14	0.47
1:K:265:ASN:C	1:K:265:ASN:OD1	2.53	0.47
1:I:9:VAL:HG21	1:I:77:LEU:HD22	1.97	0.47
1:K:33:LEU:HD23	1:K:43:VAL:CG1	2.44	0.47
1:J:2:GLU:HG2	2:J:303:HOH:O	2.15	0.47
1:L:125:ASN:HA	1:L:125:ASN:HD22	1.53	0.47
1:J:156:ARG:CG	1:J:156:ARG:NH1	2.73	0.47
1:L:214:HIS:CD2	1:L:258:SER:OG	2.68	0.47
1:K:201:ALA:O	1:K:204:VAL:HB	2.14	0.47
1:A:140:LEU:HD21	1:A:163:VAL:HG11	1.95	0.47
1:E:36:LEU:HD22	1:E:286:LEU:HD23	1.97	0.47
1:H:259:LEU:HD13	1:H:285:LEU:CD2	2.40	0.47
1:J:124:PHE:HD2	1:J:124:PHE:O	1.97	0.47
1:F:222:LEU:O	1:F:223:ASP:C	2.53	0.47
1:D:169:ARG:HH22	1:D:221:VAL:C	2.18	0.47
1:H:226:LEU:HD21	1:H:240:TYR:HB2	1.97	0.47
1:J:214:HIS:HD2	1:J:258:SER:OG	1.98	0.47
1:E:20:VAL:HG11	1:E:263:GLU:HA	1.97	0.47
1:L:227:ALA:HB1	1:L:274:THR:HG23	1.97	0.47
1:E:31:ARG:O	1:E:35:GLN:HG3	2.15	0.47
1:M:32:LEU:HB2	1:M:279:VAL:HG22	1.97	0.47
1:G:42:THR:HG23	2:G:294:HOH:O	2.13	0.47
1:G:214:HIS:HE1	1:G:260:ASP:OD2	1.97	0.47
1:K:92:VAL:HG23	1:K:260:ASP:HA	1.97	0.47
1:M:22:MET:O	1:M:23:GLY:C	2.52	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:LEU:HD13	1:A:285:LEU:CD2	2.44	0.47
1:K:290:ILE:N	1:K:290:ILE:HD12	2.30	0.47
1:A:170:SER:O	1:A:171:LEU:HD23	2.14	0.47
1:D:2:GLU:HB2	2:D:293:HOH:O	2.14	0.47
1:C:76:VAL:HA	1:H:86:GLU:HG3	1.96	0.47
1:I:77:LEU:C	1:I:79:GLU:N	2.68	0.47
1:M:169:ARG:HD2	1:M:234:VAL:HB	1.97	0.47
1:M:9:VAL:O	1:M:11:MET:N	2.47	0.46
1:M:145:GLY:HA2	1:M:156:ARG:CD	2.45	0.46
1:G:218:ASP:CG	1:G:263:GLU:HG3	2.35	0.46
1:J:187:TYR:CE1	1:J:200:ILE:HD12	2.50	0.46
1:E:4:VAL:HG22	1:E:89:PHE:HB3	1.96	0.46
1:I:179:LEU:CD2	1:I:186:VAL:HG21	2.44	0.46
1:K:78:LYS:CA	1:K:102:GLY:O	2.63	0.46
1:A:214:HIS:CD2	1:A:258:SER:OG	2.67	0.46
1:K:181:GLU:C	1:K:183:GLY:H	2.18	0.46
1:K:257:GLN:HG3	1:K:258:SER:N	2.29	0.46
1:F:111:ARG:CD	1:F:112:ARG:N	2.54	0.46
1:M:79:GLU:HA	1:M:82:ALA:HB3	1.96	0.46
1:I:138:MET:H	1:I:139:PRO:HD2	1.73	0.46
1:J:124:PHE:O	1:J:124:PHE:CD2	2.68	0.46
1:D:97:HIS:O	1:D:100:SER:HB2	2.15	0.46
1:M:246:LEU:HB3	1:M:247:MET:HE3	1.98	0.46
1:L:129:THR:HG21	1:L:174:GLY:HA3	1.97	0.46
1:K:176:LYS:HD3	1:M:291:PHE:CD2	2.50	0.46
1:L:13:LEU:HD23	1:L:66:TYR:CE1	2.50	0.46
1:D:209:GLN:HA	1:D:255:ARG:NH2	2.30	0.46
1:M:12:ASP:OD1	1:M:20:VAL:HG23	2.15	0.46
1:M:145:GLY:HA2	1:M:156:ARG:HD2	1.97	0.46
1:I:135:VAL:HA	1:I:138:MET:SD	2.55	0.46
1:K:77:LEU:O	1:K:78:LYS:C	2.53	0.46
1:L:201:ALA:HB1	1:L:249:ILE:CG2	2.44	0.46
1:J:4:VAL:HG13	1:J:91:ILE:HD13	1.96	0.46
1:E:214:HIS:HD2	1:E:258:SER:OG	1.98	0.46
1:H:75:LEU:HA	1:H:75:LEU:HD12	1.78	0.46
1:F:69:GLU:N	1:F:69:GLU:OE1	2.41	0.46
1:E:129:THR:O	1:E:130:SER:HB2	2.15	0.46
1:G:115:VAL:CG2	1:G:158:VAL:HG21	2.44	0.46
1:L:163:VAL:HG12	1:L:184:VAL:CG1	2.46	0.46
1:I:279:VAL:O	1:I:283:LEU:HG	2.16	0.46
1:M:160:PRO:HB2	1:M:182:ALA:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:46:LEU:HD13	1:G:80:ARG:CZ	2.45	0.46
1:C:76:VAL:HG22	1:H:86:GLU:HG3	1.98	0.46
1:A:122:ALA:O	1:A:123:ASP:C	2.54	0.46
1:C:97:HIS:O	1:C:100:SER:HB2	2.15	0.46
1:K:144:SER:CB	1:K:160:PRO:HG3	2.41	0.46
1:H:11:MET:CE	1:H:96:ASP:HB2	2.45	0.46
1:D:213:LEU:N	1:D:255:ARG:O	2.36	0.46
1:H:64:LEU:HB3	1:H:65:ALA:H	1.51	0.46
1:H:138:MET:N	1:H:139:PRO:CD	2.77	0.46
1:C:214:HIS:CE1	1:C:260:ASP:OD2	2.68	0.46
1:K:32:LEU:HD13	1:K:279:VAL:HG13	1.97	0.46
1:C:83:ALA:C	1:H:111:ARG:HH22	2.19	0.46
1:K:92:VAL:CG2	1:K:260:ASP:OD1	2.64	0.46
1:M:278:LEU:O	1:M:279:VAL:C	2.54	0.46
1:H:145:GLY:HA3	1:H:156:ARG:HD2	1.97	0.46
1:C:109:ARG:CG	1:C:109:ARG:NH1	2.55	0.46
1:C:46:LEU:HD22	1:C:80:ARG:NH2	2.30	0.46
1:I:274:THR:O	1:I:277:MET:HB2	2.16	0.46
1:D:248:GLU:O	1:D:252:GLU:HG3	2.15	0.46
1:C:225:THR:HG22	1:C:226:LEU:H	1.81	0.46
1:M:68:GLU:O	1:M:72:ALA:HB2	2.16	0.46
1:C:272:ASN:HB2	1:K:267:ILE:HA	1.98	0.46
1:J:150:ARG:O	1:J:153:GLU:HG2	2.14	0.46
1:K:70:ILE:CD1	1:K:135:VAL:HG21	2.46	0.46
1:M:33:LEU:O	1:M:34:GLU:C	2.55	0.46
1:J:124:PHE:CD1	1:J:140:LEU:HB3	2.51	0.46
1:I:214:HIS:HE1	1:I:260:ASP:OD2	1.99	0.46
1:C:29:TYR:C	1:C:31:ARG:H	2.19	0.46
1:M:169:ARG:HH22	1:M:221:VAL:C	2.19	0.46
1:A:101:MET:HA	1:A:143:LEU:HD21	1.98	0.46
1:L:42:THR:HA	2:L:299:HOH:O	2.15	0.46
1:D:149:PRO:HA	1:D:152:THR:OG1	2.16	0.46
1:K:94:GLY:HA3	1:K:262:VAL:HG12	1.97	0.45
1:I:97:HIS:CG	1:I:262:VAL:HG21	2.51	0.45
1:K:157:ALA:O	1:K:158:VAL:HB	2.16	0.45
1:K:122:ALA:C	1:K:124:PHE:N	2.67	0.45
1:J:33:LEU:O	1:J:34:GLU:C	2.54	0.45
1:G:259:LEU:HD22	1:G:285:LEU:HD23	1.98	0.45
1:A:99:LEU:HD12	1:A:100:SER:N	2.30	0.45
1:J:22:MET:SD	1:J:267:ILE:CD1	3.04	0.45
1:C:279:VAL:O	1:C:283:LEU:HG	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:HIS:HD2	1:E:248:GLU:OE1	1.99	0.45
1:I:105:ALA:O	1:I:108:ALA:HB3	2.16	0.45
1:A:135:VAL:HA	1:A:138:MET:SD	2.57	0.45
1:M:245:LEU:HA	1:M:245:LEU:HD12	1.78	0.45
1:L:142:VAL:O	1:L:145:GLY:N	2.49	0.45
1:A:67:LEU:HD21	1:A:151:LEU:HG	1.98	0.45
1:H:169:ARG:NH1	1:H:234:VAL:O	2.48	0.45
1:K:35:GLN:HB2	1:K:283:LEU:HD21	1.98	0.45
1:D:126:THR:HG23	1:D:178:LEU:CD1	2.46	0.45
1:H:148:HIS:HD2	1:H:150:ARG:H	1.63	0.45
1:C:52:SER:O	1:C:69:GLU:HG2	2.17	0.45
1:C:150:ARG:HD2	1:C:150:ARG:HA	1.79	0.45
1:L:189:MET:O	1:L:190:HIS:C	2.55	0.45
1:A:119:ASP:HB3	1:A:121:HIS:O	2.16	0.45
1:M:120:ALA:HB2	1:M:220:ASP:O	2.17	0.45
1:D:135:VAL:O	1:D:139:PRO:HD3	2.17	0.45
1:H:25:SER:O	1:H:29:TYR:CD2	2.61	0.45
1:K:81:LEU:HD12	1:K:103:SER:HA	1.97	0.45
1:J:33:LEU:O	1:J:36:LEU:N	2.48	0.45
1:C:138:MET:O	1:C:142:VAL:HG23	2.17	0.45
1:C:222:LEU:O	1:C:223:ASP:C	2.54	0.45
1:K:128:GLU:CD	1:K:128:GLU:N	2.70	0.45
1:L:270:GLU:O	1:L:271:ARG:HB2	2.17	0.45
1:K:11:MET:CE	1:K:96:ASP:HB2	2.47	0.45
1:L:84:LEU:HA	1:L:85:PRO:HD2	1.87	0.45
1:M:179:LEU:HD13	1:M:186:VAL:HG21	1.98	0.45
1:F:66:TYR:HA	1:F:69:GLU:OE1	2.17	0.45
1:F:97:HIS:ND1	1:F:123:ASP:OD2	2.50	0.45
1:A:97:HIS:CE1	1:A:117:TRP:CE2	3.04	0.45
1:H:120:ALA:HB2	1:H:220:ASP:O	2.17	0.45
1:E:94:GLY:HA3	1:E:99:LEU:HD21	1.98	0.45
1:A:29:TYR:C	1:A:31:ARG:H	2.19	0.45
1:E:169:ARG:HH22	1:E:221:VAL:C	2.20	0.45
1:E:86:GLU:HA	1:E:109:ARG:HH21	1.81	0.45
1:I:201:ALA:HB1	1:I:249:ILE:HG21	1.98	0.45
1:K:70:ILE:O	1:K:73:ALA:N	2.50	0.45
1:E:277:MET:HE2	1:E:277:MET:HB3	1.89	0.45
1:K:8:GLY:HA3	1:K:48:ASP:OD1	2.16	0.45
1:L:39:LEU:O	1:L:39:LEU:HG	2.17	0.45
1:L:291:PHE:C	1:L:291:PHE:CD2	2.90	0.45
1:G:169:ARG:HG3	1:G:234:VAL:HG11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:138:MET:O	1:I:139:PRO:C	2.55	0.45
1:I:175:GLU:O	1:I:179:LEU:HB2	2.17	0.45
1:H:231:GLY:N	2:H:299:HOH:O	2.30	0.45
1:F:80:ARG:HA	1:F:80:ARG:HD2	1.60	0.45
1:A:205:LEU:HD23	1:A:205:LEU:HA	1.75	0.45
1:H:197:VAL:CG2	1:H:242:GLU:HG2	2.38	0.45
1:M:223:ASP:OD2	1:M:225:THR:CG2	2.64	0.45
1:I:125:ASN:ND2	1:I:129:THR:OG1	2.50	0.45
1:L:189:MET:O	1:L:192:VAL:N	2.49	0.45
1:K:149:PRO:O	1:K:153:GLU:HG2	2.17	0.45
1:K:150:ARG:HA	1:K:153:GLU:HG2	1.99	0.45
1:J:77:LEU:O	1:J:79:GLU:N	2.50	0.45
1:I:99:LEU:HD12	1:I:100:SER:N	2.32	0.45
1:J:223:ASP:OD2	1:J:225:THR:HB	2.16	0.45
1:G:215:VAL:O	1:G:259:LEU:HA	2.16	0.45
1:F:113:VAL:HG12	1:F:212:PRO:HG2	1.99	0.45
1:L:67:LEU:C	1:L:67:LEU:HD23	2.38	0.45
1:K:174:GLY:C	1:K:178:LEU:HD12	2.37	0.45
1:A:79:GLU:HG2	1:D:111:ARG:HH21	1.80	0.45
1:F:119:ASP:HA	1:F:218:ASP:HB3	1.99	0.45
1:J:104:VAL:HB	1:J:143:LEU:CD2	2.46	0.45
1:C:122:ALA:O	1:C:123:ASP:C	2.55	0.45
1:F:169:ARG:HD2	1:F:234:VAL:CG1	2.47	0.45
1:A:19:GLY:HA3	1:A:267:ILE:HD12	1.98	0.45
1:L:82:ALA:HA	1:L:109:ARG:HH12	1.82	0.44
1:L:125:ASN:HB2	1:L:137:GLY:O	2.17	0.44
1:I:169:ARG:HH22	1:I:221:VAL:C	2.20	0.44
1:M:34:GLU:N	1:M:34:GLU:CD	2.61	0.44
1:K:169:ARG:HB3	1:K:189:MET:HG2	1.99	0.44
1:I:265:ASN:HA	1:I:266:PRO:HD2	1.76	0.44
1:L:159:ASP:OD1	1:L:160:PRO:HD2	2.17	0.44
1:M:82:ALA:C	1:M:84:LEU:N	2.71	0.44
1:I:169:ARG:HB3	1:I:189:MET:HG2	1.99	0.44
1:C:97:HIS:CE1	1:C:117:TRP:CZ2	3.06	0.44
1:C:19:GLY:N	1:C:265:ASN:ND2	2.61	0.44
1:I:9:VAL:O	1:I:11:MET:N	2.47	0.44
1:L:22:MET:SD	1:L:267:ILE:HD13	2.57	0.44
1:E:20:VAL:O	1:E:95:GLY:HA2	2.17	0.44
1:I:155:PHE:O	1:I:156:ARG:C	2.55	0.44
1:M:126:THR:C	1:M:128:GLU:H	2.18	0.44
1:L:82:ALA:HB2	1:L:106:GLY:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:238:LEU:HA	1:M:241:ARG:HH12	1.83	0.44
1:M:24:PRO:HB2	2:M:294:HOH:O	2.17	0.44
1:E:178:LEU:HA	1:E:178:LEU:HD23	1.80	0.44
1:L:69:GLU:N	1:L:69:GLU:OE1	2.47	0.44
1:G:140:LEU:O	1:G:144:SER:OG	2.36	0.44
1:D:225:THR:HG23	1:D:226:LEU:N	2.33	0.44
1:K:124:PHE:CD1	1:K:140:LEU:HB3	2.51	0.44
1:E:278:LEU:O	1:E:281:LEU:N	2.49	0.44
1:I:226:LEU:HD21	1:I:240:TYR:HB2	1.99	0.44
1:G:229:GLY:HA3	1:G:269:ASP:HB2	1.99	0.44
1:J:66:TYR:HB3	1:J:70:ILE:HD13	1.99	0.44
1:A:165:LEU:HD12	1:A:186:VAL:HG22	1.99	0.44
1:A:223:ASP:HA	1:A:224:PRO:HD3	1.92	0.44
1:L:145:GLY:HA3	1:L:156:ARG:HD3	1.99	0.44
1:J:79:GLU:O	1:J:81:LEU:N	2.51	0.44
1:D:192:VAL:HA	1:D:200:ILE:CD1	2.48	0.44
1:J:244:HIS:O	1:J:248:GLU:HG3	2.16	0.44
1:L:289:ARG:HH11	1:L:289:ARG:HB2	1.82	0.44
1:H:84:LEU:C	1:H:85:PRO:O	2.56	0.44
1:F:119:ASP:OD2	1:F:218:ASP:OD2	2.35	0.44
1:F:66:TYR:O	1:F:67:LEU:C	2.56	0.44
1:I:129:THR:HB	1:I:174:GLY:HA3	1.99	0.44
1:H:122:ALA:O	1:H:123:ASP:C	2.56	0.44
1:D:214:HIS:CE1	1:D:260:ASP:OD2	2.71	0.44
1:J:177:ARG:NH1	1:J:177:ARG:CB	2.80	0.44
1:E:2:GLU:HB2	2:E:300:HOH:O	2.17	0.44
1:I:223:ASP:OD2	1:I:225:THR:HG22	2.17	0.44
1:M:10:PRO:CD	1:M:48:ASP:OD2	2.65	0.44
1:K:251:ALA:O	1:K:254:GLY:N	2.40	0.44
1:D:80:ARG:HD2	1:D:80:ARG:HA	1.63	0.44
1:J:197:VAL:HG21	1:J:242:GLU:HB3	1.99	0.44
1:H:84:LEU:O	1:H:85:PRO:C	2.55	0.44
1:M:96:ASP:C	1:M:98:SER:H	2.20	0.44
1:K:9:VAL:HB	1:K:99:LEU:CD2	2.48	0.44
1:G:169:ARG:NH1	1:G:234:VAL:O	2.49	0.44
1:C:99:LEU:HD21	1:C:262:VAL:HG12	1.98	0.44
1:I:278:LEU:HD12	1:I:281:LEU:CD1	2.44	0.44
1:F:164:VAL:HG11	1:F:204:VAL:HG22	2.00	0.44
1:L:9:VAL:O	1:L:11:MET:N	2.50	0.44
1:L:169:ARG:HG3	1:L:234:VAL:CG1	2.46	0.44
1:C:32:LEU:HD11	1:C:36:LEU:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:223:ASP:O	1:J:226:LEU:N	2.51	0.44
1:F:37:GLU:O	1:F:38:ASP:C	2.54	0.44
1:M:161:LYS:HG2	1:M:161:LYS:H	1.60	0.44
1:A:277:MET:HE2	1:A:277:MET:HB3	1.85	0.44
1:F:111:ARG:HH11	1:F:111:ARG:HG2	1.81	0.44
1:F:97:HIS:CE1	1:F:117:TRP:CZ2	3.05	0.44
1:M:226:LEU:HD21	1:M:240:TYR:CA	2.48	0.44
1:M:4:VAL:HA	1:M:89:PHE:O	2.18	0.44
1:I:213:LEU:HD11	1:I:255:ARG:HH12	1.82	0.44
1:H:147:GLY:O	1:H:148:HIS:C	2.56	0.44
1:L:144:SER:HB3	1:L:160:PRO:HG3	1.99	0.44
1:G:290:ILE:N	1:G:290:ILE:HD12	2.32	0.44
1:C:234:VAL:HA	1:C:235:PRO:HD2	1.80	0.44
1:L:71:ARG:NH2	1:L:154:VAL:HG11	2.33	0.44
1:D:22:MET:CE	1:J:25:SER:HB2	2.48	0.44
1:I:46:LEU:N	1:I:46:LEU:HD23	2.33	0.44
1:M:104:VAL:HG22	1:M:214:HIS:CE1	2.52	0.44
1:K:112:ARG:HD3	1:K:211:LEU:CD2	2.48	0.43
1:M:119:ASP:OD2	1:M:123:ASP:OD2	2.36	0.43
1:M:32:LEU:HA	1:M:279:VAL:HG13	2.00	0.43
1:G:29:TYR:C	1:G:31:ARG:H	2.20	0.43
1:J:126:THR:O	1:J:127:PRO:C	2.56	0.43
1:C:264:VAL:CG2	1:C:278:LEU:HD22	2.48	0.43
1:C:188:THR:O	1:C:192:VAL:HG23	2.18	0.43
1:M:224:PRO:CG	1:M:233:PRO:HB2	2.48	0.43
1:G:97:HIS:ND1	1:G:119:ASP:OD2	2.51	0.43
1:J:148:HIS:HA	1:J:149:PRO:HD3	1.82	0.43
1:H:13:LEU:CB	1:H:70:ILE:HD11	2.47	0.43
1:A:199:ARG:HA	1:A:202:GLU:HG3	1.99	0.43
1:K:124:PHE:O	1:K:175:GLU:HG2	2.18	0.43
1:D:169:ARG:HB3	1:D:189:MET:HG2	1.99	0.43
1:D:169:ARG:NH2	1:D:237:GLY:CA	2.80	0.43
1:I:153:GLU:HG3	1:I:154:VAL:HG13	2.01	0.43
1:G:97:HIS:CE1	1:G:119:ASP:OD2	2.71	0.43
1:J:100:SER:O	1:J:101:MET:C	2.57	0.43
1:L:172:ASP:O	1:L:175:GLU:HB2	2.18	0.43
1:D:104:VAL:CG2	1:D:214:HIS:CE1	2.99	0.43
1:G:32:LEU:HD12	1:G:279:VAL:HG13	2.00	0.43
1:H:279:VAL:O	1:H:283:LEU:HG	2.18	0.43
1:H:227:ALA:HB1	1:H:274:THR:HG23	2.00	0.43
1:L:113:VAL:HB	1:L:212:PRO:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:109:ARG:NH1	1:F:109:ARG:HG2	2.32	0.43
1:M:80:ARG:CG	1:M:80:ARG:NH1	2.69	0.43
1:L:247:MET:SD	1:L:285:LEU:HD22	2.58	0.43
1:G:129:THR:O	1:G:130:SER:CB	2.66	0.43
1:J:165:LEU:HD12	1:J:186:VAL:HG22	2.00	0.43
1:J:77:LEU:C	1:J:79:GLU:N	2.71	0.43
1:M:3:ARG:HH12	1:M:85:PRO:HB2	1.84	0.43
1:A:229:GLY:HA3	1:A:269:ASP:HB2	2.00	0.43
1:G:118:VAL:HB	1:G:217:LEU:HD12	1.99	0.43
1:F:13:LEU:N	1:F:96:ASP:OD2	2.43	0.43
1:K:69:GLU:O	1:K:72:ALA:HB3	2.18	0.43
1:I:78:LYS:HE3	1:I:105:ALA:HB1	2.00	0.43
1:E:187:TYR:CD1	1:E:200:ILE:HG12	2.54	0.43
1:D:264:VAL:CG2	1:D:278:LEU:HD22	2.48	0.43
1:A:123:ASP:HB3	1:A:139:PRO:HG2	2.01	0.43
1:L:262:VAL:O	1:L:263:GLU:HB2	2.18	0.43
1:F:169:ARG:CZ	1:F:237:GLY:HA2	2.48	0.43
1:D:43:VAL:CG1	1:D:44:GLU:H	2.32	0.43
1:E:290:ILE:N	1:E:290:ILE:HD12	2.33	0.43
1:K:124:PHE:HD1	1:K:140:LEU:CB	2.30	0.43
1:C:98:SER:O	1:C:101:MET:HG3	2.18	0.43
1:E:169:ARG:NH2	1:E:221:VAL:O	2.51	0.43
1:J:225:THR:HG22	1:J:226:LEU:N	2.33	0.43
1:K:222:LEU:O	1:K:223:ASP:C	2.56	0.43
1:J:145:GLY:HA2	1:J:156:ARG:HG3	2.00	0.43
1:F:122:ALA:O	1:F:124:PHE:N	2.52	0.43
1:J:70:ILE:N	1:J:70:ILE:HD12	2.34	0.43
1:J:214:HIS:CD2	1:J:258:SER:OG	2.72	0.43
1:K:96:ASP:C	1:K:98:SER:H	2.21	0.43
1:L:173:PRO:O	1:L:176:LYS:HB2	2.19	0.43
1:C:269:ASP:OD1	1:C:270:GLU:N	2.46	0.43
1:L:190:HIS:CE1	1:L:194:ARG:HE	2.19	0.43
1:L:186:VAL:O	1:L:186:VAL:CG1	2.67	0.43
1:F:169:ARG:HD2	1:F:234:VAL:HG12	2.01	0.43
1:C:246:LEU:O	1:C:250:LEU:HG	2.19	0.43
1:K:253:SER:C	1:K:255:ARG:N	2.72	0.43
1:K:12:ASP:O	1:K:13:LEU:HD23	2.19	0.43
1:I:278:LEU:HA	1:I:281:LEU:HD12	2.00	0.43
1:M:172:ASP:O	1:M:176:LYS:HG3	2.19	0.43
1:E:226:LEU:HD11	1:E:240:TYR:HB2	2.01	0.43
1:A:256:VAL:HG21	1:A:285:LEU:CD1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:243:ALA:HB1	1:K:281:LEU:CD1	2.47	0.43
1:E:11:MET:CE	1:E:98:SER:HB2	2.49	0.43
1:G:164:VAL:HG11	1:G:204:VAL:HG22	2.00	0.43
1:E:119:ASP:OD1	1:E:220:ASP:OD2	2.36	0.43
1:C:129:THR:O	1:C:130:SER:HB3	2.18	0.43
1:J:251:ALA:HB2	1:J:285:LEU:HA	2.01	0.43
1:A:201:ALA:HB1	1:A:249:ILE:HG21	2.01	0.43
1:A:177:ARG:HH11	1:A:177:ARG:HG2	1.83	0.43
1:L:6:VAL:O	1:L:6:VAL:HG12	2.18	0.43
1:J:24:PRO:O	1:J:28:ARG:HG3	2.19	0.43
1:M:80:ARG:HG2	1:M:80:ARG:NH1	2.17	0.42
1:L:247:MET:HA	1:L:285:LEU:HD13	2.00	0.42
1:M:124:PHE:CA	1:M:141:ALA:HB2	2.49	0.42
1:M:146:LEU:CD1	1:M:178:LEU:HD22	2.43	0.42
1:A:197:VAL:HG21	1:A:242:GLU:HB3	2.00	0.42
1:C:199:ARG:HA	1:C:202:GLU:HG3	2.01	0.42
1:M:201:ALA:CB	1:M:249:ILE:HG21	2.50	0.42
1:E:3:ARG:HB3	1:E:88:VAL:HG22	2.01	0.42
1:E:185:ARG:HG2	1:E:185:ARG:NH1	2.34	0.42
1:J:5:ALA:HA	1:J:44:GLU:O	2.19	0.42
1:G:218:ASP:O	1:G:221:VAL:HG12	2.18	0.42
1:M:84:LEU:O	1:M:109:ARG:NH2	2.52	0.42
1:L:215:VAL:O	1:L:259:LEU:HA	2.19	0.42
1:D:95:GLY:O	1:D:96:ASP:C	2.58	0.42
1:M:3:ARG:NH1	1:M:85:PRO:HB2	2.35	0.42
1:L:291:PHE:OXT	1:L:291:PHE:HD2	2.02	0.42
1:I:207:HIS:O	1:I:207:HIS:CG	2.72	0.42
1:K:165:LEU:HB2	1:K:186:VAL:HG22	2.00	0.42
1:J:204:VAL:C	1:J:206:LYS:H	2.22	0.42
1:L:124:PHE:CD2	1:L:179:LEU:HG	2.54	0.42
1:A:25:SER:HB2	1:H:22:MET:CE	2.49	0.42
1:H:148:HIS:CD2	1:H:150:ARG:HB2	2.55	0.42
1:L:275:ALA:O	1:L:276:GLU:C	2.58	0.42
1:M:25:SER:O	1:M:28:ARG:HB2	2.19	0.42
1:I:245:LEU:O	1:I:245:LEU:HG	2.15	0.42
1:M:148:HIS:CD2	1:M:150:ARG:H	2.36	0.42
1:H:251:ALA:HB2	1:H:285:LEU:HA	2.01	0.42
1:L:177:ARG:C	1:L:179:LEU:H	2.21	0.42
1:J:169:ARG:HG3	1:J:234:VAL:CG1	2.49	0.42
1:J:22:MET:HB2	1:J:266:PRO:HG2	2.01	0.42
1:J:89:PHE:HA	1:J:90:PRO:HD3	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:168:VAL:CG1	1:I:171:LEU:HD21	2.49	0.42
1:D:25:SER:O	1:D:29:TYR:HD2	2.03	0.42
1:M:165:LEU:CB	1:M:186:VAL:HG22	2.49	0.42
1:L:90:PRO:HG2	1:L:258:SER:HB3	2.02	0.42
1:M:240:TYR:HD1	1:M:277:MET:SD	2.42	0.42
1:L:126:THR:C	1:L:128:GLU:N	2.73	0.42
1:I:20:VAL:CG1	1:I:265:ASN:HB2	2.48	0.42
1:E:108:ALA:O	1:E:109:ARG:HB2	2.19	0.42
1:H:164:VAL:HG11	1:H:204:VAL:HG22	2.01	0.42
1:A:278:LEU:O	1:A:279:VAL:C	2.58	0.42
1:G:70:ILE:O	1:G:71:ARG:C	2.56	0.42
1:H:111:ARG:HE	1:H:112:ARG:N	2.17	0.42
1:M:11:MET:O	1:M:96:ASP:N	2.50	0.42
1:J:145:GLY:C	1:J:146:LEU:HD23	2.39	0.42
1:C:155:PHE:O	1:C:156:ARG:C	2.55	0.42
1:H:101:MET:HG3	1:H:139:PRO:HB3	2.02	0.42
1:K:221:VAL:HG22	1:K:221:VAL:O	2.20	0.42
1:H:149:PRO:C	1:H:151:LEU:N	2.73	0.42
1:F:74:ALA:O	1:F:77:LEU:HB3	2.19	0.42
1:G:39:LEU:HD12	1:G:39:LEU:HA	1.75	0.42
1:E:22:MET:SD	1:E:267:ILE:CD1	3.08	0.42
1:M:220:ASP:OD1	1:M:220:ASP:C	2.58	0.42
1:L:120:ALA:HB2	1:L:220:ASP:O	2.19	0.42
1:L:118:VAL:HG13	1:L:166:VAL:HB	2.01	0.42
1:L:126:THR:CG2	1:L:178:LEU:HD13	2.49	0.42
1:D:64:LEU:O	1:D:67:LEU:HB2	2.20	0.42
1:L:36:LEU:HD22	1:L:286:LEU:HD23	2.02	0.42
1:F:35:GLN:HB3	1:F:283:LEU:HD11	2.02	0.42
1:G:5:ALA:O	1:G:90:PRO:HA	2.19	0.42
1:J:179:LEU:HD23	1:J:184:VAL:HG21	2.02	0.42
1:A:111:ARG:NE	1:A:111:ARG:HA	2.35	0.42
1:M:211:LEU:HD23	1:M:211:LEU:N	2.35	0.42
1:F:95:GLY:O	1:F:96:ASP:O	2.38	0.42
1:M:218:ASP:CG	1:M:263:GLU:HG3	2.40	0.42
1:J:249:ILE:HD13	1:J:249:ILE:HA	1.75	0.42
1:F:169:ARG:HH11	1:F:234:VAL:HB	1.85	0.42
1:A:9:VAL:O	1:A:11:MET:N	2.52	0.42
1:A:192:VAL:HA	1:A:200:ILE:CD1	2.49	0.42
1:K:219:ALA:C	1:K:221:VAL:H	2.22	0.42
1:A:269:ASP:CG	1:A:270:GLU:H	2.23	0.42
1:H:32:LEU:HA	1:H:279:VAL:CG1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:202:GLU:HG2	1:E:202:GLU:H	1.66	0.42
1:H:104:VAL:HG22	1:H:214:HIS:CE1	2.55	0.42
1:H:82:ALA:CA	1:H:109:ARG:HH12	2.24	0.42
1:L:37:GLU:HG2	1:L:43:VAL:HG23	2.01	0.42
1:I:278:LEU:HA	1:I:278:LEU:HD12	1.75	0.42
1:A:202:GLU:H	1:A:202:GLU:HG2	1.63	0.42
1:L:163:VAL:HB	1:L:184:VAL:HG13	2.01	0.42
1:L:177:ARG:O	1:L:181:GLU:HB2	2.20	0.42
1:M:256:VAL:HG11	1:M:285:LEU:HD21	2.01	0.42
1:C:125:ASN:ND2	1:C:129:THR:OG1	2.52	0.42
1:H:69:GLU:O	1:H:72:ALA:HB3	2.19	0.42
1:F:126:THR:HG23	1:F:178:LEU:HD13	2.00	0.42
1:I:34:GLU:H	1:I:34:GLU:CD	2.22	0.42
1:J:206:LYS:C	1:J:208:LEU:H	2.23	0.42
1:M:99:LEU:HD12	1:M:100:SER:N	2.34	0.42
1:C:129:THR:HB	1:C:174:GLY:HA3	2.02	0.42
1:E:177:ARG:CB	1:E:177:ARG:NH1	2.81	0.42
1:J:89:PHE:HE1	1:J:256:VAL:O	2.03	0.42
1:K:275:ALA:O	1:K:276:GLU:C	2.58	0.42
1:H:163:VAL:CG1	1:H:164:VAL:N	2.83	0.42
1:F:36:LEU:O	1:F:39:LEU:N	2.53	0.42
1:G:201:ALA:CB	1:G:249:ILE:HG21	2.49	0.41
1:M:140:LEU:HD23	1:M:165:LEU:HD11	2.01	0.41
1:C:271:ARG:CZ	1:K:268:LEU:O	2.68	0.41
1:K:94:GLY:N	1:K:261:LEU:O	2.44	0.41
1:I:119:ASP:HA	1:I:218:ASP:HB3	2.02	0.41
1:J:115:VAL:CG2	1:J:158:VAL:HG21	2.50	0.41
1:K:226:LEU:HD21	1:K:240:TYR:CA	2.49	0.41
1:H:234:VAL:HA	1:H:235:PRO:HD2	1.81	0.41
1:F:113:VAL:HG11	1:F:257:GLN:NE2	2.35	0.41
1:M:214:HIS:CD2	1:M:258:SER:HB2	2.55	0.41
1:G:71:ARG:NH2	1:G:153:GLU:OE2	2.51	0.41
1:D:261:LEU:HD11	1:D:282:ALA:HB2	2.01	0.41
1:H:116:VAL:HB	1:H:215:VAL:HG22	2.01	0.41
1:K:119:ASP:HA	1:K:218:ASP:HB3	2.01	0.41
1:E:121:HIS:HE1	1:E:232:THR:HB	1.85	0.41
1:J:6:VAL:CG1	1:J:93:LEU:HD21	2.47	0.41
1:M:91:ILE:HG23	1:M:259:LEU:HD23	2.01	0.41
1:C:111:ARG:CD	1:C:112:ARG:N	2.82	0.41
1:D:39:LEU:HD12	1:D:39:LEU:HA	1.84	0.41
1:G:227:ALA:N	1:G:228:PRO:HD3	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:138:MET:C	2:L:301:HOH:O	2.58	0.41
1:M:119:ASP:OD2	1:M:218:ASP:OD2	2.38	0.41
1:M:99:LEU:C	1:M:99:LEU:HD12	2.41	0.41
1:H:12:ASP:O	1:H:13:LEU:HD23	2.21	0.41
1:L:20:VAL:C	1:L:22:MET:H	2.23	0.41
1:C:252:GLU:OE2	1:I:194:ARG:NH2	2.53	0.41
1:K:277:MET:CE	1:K:277:MET:CA	2.98	0.41
1:K:22:MET:SD	1:K:267:ILE:CD1	3.09	0.41
1:G:168:VAL:HG12	1:G:188:THR:HG22	2.02	0.41
1:D:148:HIS:CD2	1:D:150:ARG:H	2.38	0.41
1:J:160:PRO:C	1:J:162:ASP:H	2.24	0.41
1:L:99:LEU:HD12	1:L:99:LEU:C	2.40	0.41
1:I:124:PHE:O	1:I:124:PHE:CD2	2.73	0.41
1:M:39:LEU:HA	1:M:39:LEU:HD12	1.75	0.41
1:L:89:PHE:CZ	1:L:256:VAL:HG12	2.52	0.41
1:J:139:PRO:O	1:J:143:LEU:HD12	2.20	0.41
1:J:119:ASP:HB3	1:J:121:HIS:O	2.19	0.41
1:F:265:ASN:HA	1:F:266:PRO:HD2	1.93	0.41
1:I:265:ASN:ND2	1:I:268:LEU:HG	2.36	0.41
1:K:35:GLN:OE1	1:K:283:LEU:HD11	2.19	0.41
1:J:247:MET:SD	1:J:285:LEU:HD13	2.61	0.41
1:H:3:ARG:HB2	1:H:3:ARG:HE	1.59	0.41
1:C:84:LEU:O	1:C:85:PRO:C	2.58	0.41
1:G:139:PRO:O	1:G:143:LEU:HG	2.20	0.41
1:F:9:VAL:O	1:F:11:MET:N	2.53	0.41
1:A:97:HIS:CD2	1:A:262:VAL:HG21	2.56	0.41
1:K:193:ASP:HB2	1:M:245:LEU:HD13	2.01	0.41
1:E:153:GLU:HG3	1:E:154:VAL:N	2.35	0.41
1:K:148:HIS:HA	1:K:149:PRO:HD3	1.85	0.41
1:E:34:GLU:OE1	1:E:34:GLU:N	2.34	0.41
1:L:93:LEU:HD22	1:L:261:LEU:HD12	2.03	0.41
1:D:234:VAL:HA	1:D:235:PRO:HD3	1.91	0.41
1:G:32:LEU:CD1	1:G:279:VAL:HG13	2.50	0.41
1:L:277:MET:CE	1:L:277:MET:HA	2.51	0.41
1:I:288:LYS:O	1:I:289:ARG:HG3	2.21	0.41
1:F:168:VAL:HG11	1:F:171:LEU:HD21	2.02	0.41
1:H:199:ARG:O	1:H:200:ILE:C	2.57	0.41
1:M:13:LEU:HD12	1:M:70:ILE:CG1	2.42	0.41
1:C:148:HIS:CD2	1:C:150:ARG:HB2	2.56	0.41
1:C:67:LEU:HD21	1:C:150:ARG:HB2	2.02	0.41
1:E:37:GLU:HG2	1:E:43:VAL:CG2	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:MET:HE1	1:H:25:SER:HB2	2.03	0.41
1:K:190:HIS:O	1:K:194:ARG:HB2	2.21	0.41
1:M:243:ALA:HB1	1:M:281:LEU:CD1	2.50	0.41
1:G:11:MET:O	1:G:96:ASP:OD2	2.39	0.41
1:C:248:GLU:OE1	1:I:190:HIS:CD2	2.68	0.41
1:H:146:LEU:HD23	1:H:146:LEU:N	2.36	0.41
1:G:94:GLY:HA3	1:G:99:LEU:CD2	2.50	0.41
1:G:22:MET:CB	1:G:266:PRO:HG2	2.51	0.41
1:D:171:LEU:HB2	1:D:176:LYS:HE2	2.03	0.41
1:M:150:ARG:CD	1:M:150:ARG:O	2.67	0.41
1:A:117:TRP:HB3	1:A:165:LEU:HD23	2.03	0.41
1:M:286:LEU:CD1	1:M:286:LEU:N	2.83	0.41
1:M:172:ASP:HB3	1:M:173:PRO:HD2	2.03	0.41
1:I:225:THR:O	1:I:273:ARG:NH2	2.54	0.41
1:L:64:LEU:HD13	1:L:65:ALA:H	1.84	0.41
1:G:265:ASN:OD1	1:G:267:ILE:HB	2.20	0.41
1:F:46:LEU:HD13	1:F:80:ARG:NH2	2.35	0.41
1:I:159:ASP:C	1:I:159:ASP:OD1	2.59	0.41
1:M:150:ARG:O	1:M:153:GLU:OE2	2.38	0.41
1:M:243:ALA:O	1:M:247:MET:HG2	2.21	0.41
1:A:67:LEU:HD11	1:A:148:HIS:CG	2.55	0.41
1:E:109:ARG:C	1:E:111:ARG:H	2.24	0.41
1:C:259:LEU:HD13	1:C:285:LEU:HD22	2.03	0.41
1:M:217:LEU:HA	1:M:217:LEU:HD12	1.85	0.41
1:J:208:LEU:HD23	1:J:208:LEU:HA	1.91	0.41
1:J:145:GLY:CA	1:J:156:ARG:HD2	2.51	0.41
1:F:67:LEU:O	1:F:71:ARG:HB2	2.21	0.41
1:J:100:SER:C	1:J:103:SER:HG	2.23	0.41
1:J:99:LEU:C	1:J:99:LEU:CD1	2.82	0.41
1:E:37:GLU:HA	1:E:41:TYR:O	2.20	0.41
1:M:218:ASP:OD1	1:M:263:GLU:HB2	2.21	0.41
1:M:99:LEU:HD21	1:M:262:VAL:HG12	2.03	0.41
1:J:168:VAL:CG1	1:J:171:LEU:HD21	2.45	0.41
1:J:140:LEU:HD23	1:J:165:LEU:HD21	2.03	0.41
1:I:163:VAL:HG12	1:I:184:VAL:HG13	2.03	0.41
1:H:12:ASP:HB3	1:H:21:ASP:HB3	2.03	0.41
1:D:99:LEU:HD21	1:D:262:VAL:CG1	2.47	0.41
1:L:97:HIS:ND1	1:L:119:ASP:OD2	2.53	0.41
1:G:11:MET:O	1:G:96:ASP:CG	2.59	0.41
1:K:176:LYS:HD3	1:M:291:PHE:HD2	1.85	0.41
1:C:96:ASP:HB3	1:C:136:HIS:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:168:VAL:HG11	1:I:171:LEU:HD21	2.03	0.41
1:K:75:LEU:HG	1:K:79:GLU:HG3	2.03	0.41
1:K:4:VAL:HG22	1:K:89:PHE:HB3	2.03	0.41
1:K:185:ARG:NH1	1:K:207:HIS:ND1	2.69	0.41
1:I:153:GLU:CG	1:I:154:VAL:HG13	2.51	0.41
1:L:10:PRO:O	1:L:51:VAL:HG21	2.20	0.41
1:H:159:ASP:O	1:H:162:ASP:N	2.47	0.41
1:G:72:ALA:O	1:G:76:VAL:HG23	2.20	0.41
1:F:277:MET:HB3	1:F:277:MET:HE2	2.00	0.41
1:M:128:GLU:C	1:M:130:SER:N	2.74	0.41
1:J:138:MET:H	1:J:139:PRO:HD2	1.76	0.41
1:H:135:VAL:O	1:H:138:MET:N	2.46	0.41
1:M:194:ARG:CG	1:M:194:ARG:HH11	2.33	0.41
1:K:169:ARG:CZ	1:K:237:GLY:HA3	2.51	0.41
1:J:79:GLU:C	1:J:81:LEU:N	2.74	0.41
1:J:278:LEU:HD12	1:J:278:LEU:HA	1.84	0.41
1:F:111:ARG:NH2	1:G:249:ILE:O	2.54	0.40
1:F:211:LEU:H	1:F:255:ARG:NH1	2.19	0.40
1:C:84:LEU:HG	1:C:84:LEU:H	1.67	0.40
1:M:82:ALA:O	1:M:84:LEU:N	2.48	0.40
1:F:67:LEU:HD21	1:F:150:ARG:HB2	2.03	0.40
1:I:232:THR:O	1:I:233:PRO:C	2.60	0.40
1:L:202:GLU:OE1	1:L:202:GLU:HA	2.21	0.40
1:L:205:LEU:O	1:L:255:ARG:NH2	2.54	0.40
1:F:145:GLY:CA	1:F:156:ARG:HD3	2.47	0.40
1:L:81:LEU:HD12	1:L:103:SER:HA	2.02	0.40
1:D:89:PHE:CZ	1:D:286:LEU:HD11	2.56	0.40
1:E:223:ASP:HA	1:E:224:PRO:HD3	1.96	0.40
1:E:125:ASN:HB2	1:E:137:GLY:O	2.21	0.40
1:K:39:LEU:HA	1:K:39:LEU:HD12	1.60	0.40
1:J:153:GLU:HG3	1:J:154:VAL:HG13	2.02	0.40
1:J:156:ARG:O	1:J:157:ALA:HB2	2.21	0.40
1:F:11:MET:HE1	1:F:70:ILE:HG23	2.04	0.40
1:L:285:LEU:HA	1:L:285:LEU:HD12	1.84	0.40
1:H:12:ASP:CB	1:H:21:ASP:HB3	2.51	0.40
1:A:29:TYR:CE1	1:H:19:GLY:HA2	2.57	0.40
1:I:71:ARG:CZ	1:I:150:ARG:NH1	2.84	0.40
1:A:19:GLY:N	1:A:265:ASN:HD21	2.20	0.40
1:I:206:LYS:C	1:I:208:LEU:H	2.25	0.40
1:A:288:LYS:O	1:A:289:ARG:HG3	2.20	0.40
1:G:135:VAL:C	1:G:137:GLY:H	2.24	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:145:GLY:HA2	1:J:156:ARG:CG	2.52	0.40
1:K:67:LEU:HA	1:K:70:ILE:HD12	2.03	0.40
1:H:138:MET:H	1:H:139:PRO:HD2	1.86	0.40
1:A:86:GLU:HB2	1:D:86:GLU:HG3	2.02	0.40
1:E:112:ARG:CZ	1:E:211:LEU:HD21	2.51	0.40
1:M:214:HIS:CD2	1:M:258:SER:OG	2.74	0.40
1:A:227:ALA:O	1:A:230:VAL:HG13	2.21	0.40
1:D:112:ARG:HH11	1:D:211:LEU:HD21	1.84	0.40
1:K:97:HIS:CE1	1:K:117:TRP:CZ2	3.10	0.40
1:D:204:VAL:HG12	1:D:204:VAL:O	2.20	0.40
1:G:30:ALA:HB3	1:G:279:VAL:HG21	2.04	0.40
1:L:79:GLU:O	1:L:81:LEU:N	2.54	0.40
1:H:37:GLU:HA	1:H:41:TYR:O	2.21	0.40
1:A:111:ARG:NH2	1:D:79:GLU:O	2.28	0.40
1:F:129:THR:O	1:F:130:SER:CB	2.69	0.40
1:L:90:PRO:C	1:L:91:ILE:HD13	2.42	0.40
1:D:98:SER:HA	1:D:139:PRO:HG3	2.04	0.40
1:F:225:THR:HG22	1:F:226:LEU:N	2.35	0.40
1:M:283:LEU:O	1:M:288:LYS:CB	2.69	0.40
1:L:104:VAL:HG21	1:L:143:LEU:CD1	2.52	0.40
1:M:209:GLN:HA	1:M:255:ARG:NH2	2.37	0.40
1:L:79:GLU:O	1:L:80:ARG:C	2.60	0.40
1:J:225:THR:CG2	1:J:226:LEU:N	2.82	0.40
1:J:202:GLU:HG2	1:J:202:GLU:H	1.67	0.40
1:M:198:ALA:C	1:M:200:ILE:H	2.25	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	265/291 (91%)	246 (93%)	17 (6%)	2 (1%)	24 58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	265/291 (91%)	245 (92%)	18 (7%)	2 (1%)	24 58
1	D	265/291 (91%)	248 (94%)	14 (5%)	3 (1%)	17 50
1	E	265/291 (91%)	236 (89%)	25 (9%)	4 (2%)	13 41
1	F	265/291 (91%)	242 (91%)	19 (7%)	4 (2%)	13 41
1	G	265/291 (91%)	231 (87%)	32 (12%)	2 (1%)	24 58
1	H	265/291 (91%)	240 (91%)	21 (8%)	4 (2%)	13 41
1	I	265/291 (91%)	225 (85%)	34 (13%)	6 (2%)	8 29
1	J	265/291 (91%)	217 (82%)	37 (14%)	11 (4%)	3 12
1	K	265/291 (91%)	206 (78%)	50 (19%)	9 (3%)	5 18
1	L	265/291 (91%)	220 (83%)	34 (13%)	11 (4%)	3 12
1	M	265/291 (91%)	217 (82%)	33 (12%)	15 (6%)	2 6
All	All	3180/3492 (91%)	2773 (87%)	334 (10%)	73 (2%)	8 29

All (73) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	67	LEU
1	L	67	LEU
1	L	138	MET
1	M	129	THR
1	M	133	GLY
1	C	66	TYR
1	F	96	ASP
1	F	229	GLY
1	H	85	PRO
1	J	33	LEU
1	J	111	ARG
1	J	157	ALA
1	K	168	VAL
1	L	66	TYR
1	L	80	ARG
1	L	253	SER
1	M	33	LEU
1	M	139	PRO
1	M	168	VAL
1	H	235	PRO
1	J	65	ALA
1	J	78	LYS

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Mol	Chain	Res	Type
1	J	207	HIS
1	K	157	ALA
1	K	160	PRO
1	K	182	ALA
1	L	178	LEU
1	L	231	GLY
1	M	157	ALA
1	M	184	VAL
1	M	246	LEU
1	D	10	PRO
1	D	123	ASP
1	E	153	GLU
1	E	235	PRO
1	F	123	ASP
1	G	138	MET
1	I	103	SER
1	J	96	ASP
1	K	177	ARG
1	L	12	ASP
1	L	79	GLU
1	L	86	GLU
1	M	90	PRO
1	M	128	GLU
1	M	136	HIS
1	M	207	HIS
1	M	220	ASP
1	A	65	ALA
1	E	272	ASN
1	F	138	MET
1	G	133	GLY
1	I	157	ALA
1	J	67	LEU
1	K	110	GLY
1	M	10	PRO
1	M	138	MET
1	E	138	MET
1	I	10	PRO
1	I	139	PRO
1	J	127	PRO
1	K	267	ILE
1	A	138	MET
1	K	90	PRO

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Mol	Chain	Res	Type
1	I	102	GLY
1	J	10	PRO
1	C	138	MET
1	J	138	MET
1	L	85	PRO
1	D	138	MET
1	H	84	LEU
1	H	138	MET
1	I	138	MET

5.3.2 Protein sidechains (i)

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	218/232 (94%)	200 (92%)	18 (8%)	14 38
1	C	218/232 (94%)	202 (93%)	16 (7%)	17 45
1	D	218/232 (94%)	203 (93%)	15 (7%)	19 48
1	E	218/232 (94%)	200 (92%)	18 (8%)	14 38
1	F	218/232 (94%)	200 (92%)	18 (8%)	14 38
1	G	218/232 (94%)	195 (89%)	23 (11%)	8 24
1	H	218/232 (94%)	198 (91%)	20 (9%)	11 32
1	I	218/232 (94%)	194 (89%)	24 (11%)	8 23
1	J	218/232 (94%)	199 (91%)	19 (9%)	13 35
1	K	218/232 (94%)	192 (88%)	26 (12%)	6 18
1	L	218/232 (94%)	185 (85%)	33 (15%)	3 10
1	M	218/232 (94%)	181 (83%)	37 (17%)	2 7
All	All	2616/2784 (94%)	2349 (90%)	267 (10%)	9 27

All (267) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU

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Mol	Chain	Res	Type
1	A	3	ARG
1	A	37	GLU
1	A	80	ARG
1	A	109	ARG
1	A	111	ARG
1	A	153	GLU
1	A	160	PRO
1	A	161	LYS
1	A	202	GLU
1	A	206	LYS
1	A	211	LEU
1	A	225	THR
1	A	230	VAL
1	A	240	TYR
1	A	257	GLN
1	A	277	MET
1	A	291	PHE
1	C	2	GLU
1	C	42	THR
1	C	98	SER
1	C	109	ARG
1	C	111	ARG
1	C	138	MET
1	C	156	ARG
1	C	161	LYS
1	C	194	ARG
1	C	206	LYS
1	C	225	THR
1	C	232	THR
1	C	257	GLN
1	C	259	LEU
1	C	267	ILE
1	C	291	PHE
1	D	7	VAL
1	D	20	VAL
1	D	33	LEU
1	D	64	LEU
1	D	67	LEU
1	D	84	LEU
1	D	111	ARG
1	D	170	SER
1	D	199	ARG

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Mol	Chain	Res	Type
1	D	211	LEU
1	D	221	VAL
1	D	255	ARG
1	D	258	SER
1	D	267	ILE
1	D	291	PHE
1	E	2	GLU
1	E	20	VAL
1	E	33	LEU
1	E	43	VAL
1	E	80	ARG
1	E	98	SER
1	E	109	ARG
1	E	144	SER
1	E	194	ARG
1	E	200	ILE
1	E	202	GLU
1	E	225	THR
1	E	226	LEU
1	E	232	THR
1	E	255	ARG
1	E	257	GLN
1	E	277	MET
1	E	291	PHE
1	F	20	VAL
1	F	33	LEU
1	F	64	LEU
1	F	67	LEU
1	F	98	SER
1	F	111	ARG
1	F	130	SER
1	F	135	VAL
1	F	138	MET
1	F	160	PRO
1	F	177	ARG
1	F	202	GLU
1	F	225	THR
1	F	226	LEU
1	F	267	ILE
1	F	273	ARG
1	F	284	SER
1	F	291	PHE

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Mol	Chain	Res	Type
1	G	2	GLU
1	G	13	LEU
1	G	20	VAL
1	G	33	LEU
1	G	80	ARG
1	G	86	GLU
1	G	99	LEU
1	G	125	ASN
1	G	138	MET
1	G	144	SER
1	G	146	LEU
1	G	158	VAL
1	G	161	LYS
1	G	168	VAL
1	G	180	LYS
1	G	202	GLU
1	G	225	THR
1	G	226	LEU
1	G	232	THR
1	G	258	SER
1	G	270	GLU
1	G	289	ARG
1	G	291	PHE
1	H	2	GLU
1	H	12	ASP
1	H	33	LEU
1	H	42	THR
1	H	64	LEU
1	H	67	LEU
1	H	78	LYS
1	H	86	GLU
1	H	100	SER
1	H	109	ARG
1	H	111	ARG
1	H	146	LEU
1	H	160	PRO
1	H	175	GLU
1	H	194	ARG
1	H	206	LYS
1	H	211	LEU
1	H	225	THR
1	H	232	THR

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Mol	Chain	Res	Type
1	H	291	PHE
1	I	2	GLU
1	I	33	LEU
1	I	64	LEU
1	I	80	ARG
1	I	86	GLU
1	I	98	SER
1	I	100	SER
1	I	111	ARG
1	I	125	ASN
1	I	138	MET
1	I	144	SER
1	I	152	THR
1	I	160	PRO
1	I	161	LYS
1	I	179	LEU
1	I	194	ARG
1	I	211	LEU
1	I	221	VAL
1	I	255	ARG
1	I	267	ILE
1	I	277	MET
1	I	278	LEU
1	I	286	LEU
1	I	291	PHE
1	J	2	GLU
1	J	33	LEU
1	J	64	LEU
1	J	67	LEU
1	J	93	LEU
1	J	109	ARG
1	J	125	ASN
1	J	130	SER
1	J	140	LEU
1	J	156	ARG
1	J	158	VAL
1	J	184	VAL
1	J	194	ARG
1	J	206	LYS
1	J	225	THR
1	J	247	MET
1	J	267	ILE

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Mol	Chain	Res	Type
1	J	277	MET
1	J	291	PHE
1	K	2	GLU
1	K	31	ARG
1	K	33	LEU
1	K	44	GLU
1	K	64	LEU
1	K	68	GLU
1	K	90	PRO
1	K	92	VAL
1	K	98	SER
1	K	109	ARG
1	K	113	VAL
1	K	118	VAL
1	K	126	THR
1	K	130	SER
1	K	156	ARG
1	K	160	PRO
1	K	162	ASP
1	K	194	ARG
1	K	208	LEU
1	K	216	SER
1	K	225	THR
1	K	226	LEU
1	K	230	VAL
1	K	277	MET
1	K	289	ARG
1	K	291	PHE
1	L	2	GLU
1	L	6	VAL
1	L	11	MET
1	L	33	LEU
1	L	43	VAL
1	L	51	VAL
1	L	80	ARG
1	L	85	PRO
1	L	86	GLU
1	L	88	VAL
1	L	91	ILE
1	L	98	SER
1	L	109	ARG
1	L	111	ARG

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Mol	Chain	Res	Type
1	L	118	VAL
1	L	125	ASN
1	L	127	PRO
1	L	164	VAL
1	L	166	VAL
1	L	173	PRO
1	L	194	ARG
1	L	199	ARG
1	L	220	ASP
1	L	221	VAL
1	L	232	THR
1	L	257	GLN
1	L	259	LEU
1	L	260	ASP
1	L	267	ILE
1	L	268	LEU
1	L	284	SER
1	L	289	ARG
1	L	291	PHE
1	M	13	LEU
1	M	20	VAL
1	M	24	PRO
1	M	25	SER
1	M	33	LEU
1	M	39	LEU
1	M	51	VAL
1	M	64	LEU
1	M	67	LEU
1	M	68	GLU
1	M	80	ARG
1	M	84	LEU
1	M	86	GLU
1	M	90	PRO
1	M	109	ARG
1	M	111	ARG
1	M	118	VAL
1	M	129	THR
1	M	134	ASN
1	M	144	SER
1	M	150	ARG
1	M	154	VAL
1	M	160	PRO

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Mol	Chain	Res	Type
1	M	168	VAL
1	M	191	GLU
1	M	192	VAL
1	M	194	ARG
1	M	200	ILE
1	M	211	LEU
1	M	232	THR
1	M	256	VAL
1	M	258	SER
1	M	260	ASP
1	M	278	LEU
1	M	284	SER
1	M	286	LEU
1	M	291	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	HIS
1	A	190	HIS
1	A	214	HIS
1	C	35	GLN
1	C	125	ASN
1	C	134	ASN
1	C	148	HIS
1	C	214	HIS
1	D	125	ASN
1	D	134	ASN
1	D	136	HIS
1	D	148	HIS
1	D	214	HIS
1	E	125	ASN
1	E	134	ASN
1	E	148	HIS
1	E	190	HIS
1	E	214	HIS
1	F	125	ASN
1	F	134	ASN
1	F	148	HIS
1	F	214	HIS
1	F	257	GLN
1	G	125	ASN

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Mol	Chain	Res	Type
1	G	134	ASN
1	G	148	HIS
1	G	209	GLN
1	G	214	HIS
1	H	136	HIS
1	H	148	HIS
1	H	214	HIS
1	I	125	ASN
1	I	134	ASN
1	I	148	HIS
1	I	190	HIS
1	I	214	HIS
1	J	125	ASN
1	J	134	ASN
1	J	148	HIS
1	J	214	HIS
1	K	125	ASN
1	K	134	ASN
1	K	148	HIS
1	K	190	HIS
1	K	209	GLN
1	K	214	HIS
1	L	35	GLN
1	L	125	ASN
1	L	148	HIS
1	L	190	HIS
1	L	214	HIS
1	M	125	ASN
1	M	148	HIS
1	M	190	HIS
1	M	207	HIS
1	M	214	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	273/291 (93%)	-0.11	4 (1%) 76 74	26, 42, 57, 68	0
1	C	273/291 (93%)	-0.09	2 (0%) 89 88	28, 48, 60, 72	0
1	D	273/291 (93%)	-0.01	8 (2%) 55 49	31, 45, 60, 70	0
1	E	273/291 (93%)	0.06	8 (2%) 55 49	28, 48, 62, 72	0
1	F	273/291 (93%)	0.03	2 (0%) 89 88	34, 47, 61, 68	0
1	G	273/291 (93%)	0.12	9 (3%) 50 43	27, 53, 70, 79	0
1	H	273/291 (93%)	0.03	4 (1%) 76 74	35, 55, 68, 74	0
1	I	273/291 (93%)	0.01	6 (2%) 65 61	37, 56, 69, 72	0
1	J	273/291 (93%)	0.11	5 (1%) 71 68	42, 60, 74, 79	0
1	K	273/291 (93%)	0.68	48 (17%) 2 1	50, 68, 78, 81	0
1	L	273/291 (93%)	0.63	31 (11%) 7 4	52, 67, 76, 84	0
1	M	273/291 (93%)	0.99	61 (22%) 1 1	54, 73, 82, 88	0
All	All	3276/3492 (93%)	0.20	188 (5%) 27 22	26, 55, 75, 88	0

All (188) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	67	LEU	8.9
1	M	70	ILE	6.9
1	M	88	VAL	6.9
1	M	101	MET	6.5
1	L	129	THR	6.0
1	M	79	GLU	5.7
1	M	49	VAL	5.4
1	M	75	LEU	5.4
1	K	145	GLY	5.4
1	M	66	TYR	5.3
1	M	171	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
1	M	40	GLY	5.1
1	M	105	ALA	5.0
1	M	87	GLY	4.9
1	L	173	PRO	4.8
1	K	291	PHE	4.8
1	M	149	PRO	4.7
1	M	74	ALA	4.5
1	M	104	VAL	4.4
1	H	52	SER	4.4
1	M	68	GLU	4.4
1	L	128	GLU	4.3
1	D	64	LEU	4.3
1	D	52	SER	4.3
1	H	113	VAL	4.3
1	M	186	VAL	4.2
1	M	52	SER	4.2
1	M	41	TYR	4.2
1	M	147	GLY	4.1
1	M	50	PRO	4.0
1	M	13	LEU	4.0
1	M	148	HIS	4.0
1	K	171	LEU	3.9
1	F	129	THR	3.8
1	M	100	SER	3.8
1	L	130	SER	3.8
1	M	128	GLU	3.8
1	L	50	PRO	3.8
1	G	134	ASN	3.7
1	A	64	LEU	3.7
1	G	66	TYR	3.7
1	L	127	PRO	3.7
1	M	154	VAL	3.6
1	M	129	THR	3.5
1	M	78	LYS	3.5
1	A	65	ALA	3.5
1	M	153	GLU	3.5
1	K	144	SER	3.5
1	G	69	GLU	3.4
1	M	71	ARG	3.4
1	K	127	PRO	3.4
1	L	125	ASN	3.4
1	M	65	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	L	291	PHE	3.3
1	M	8	GLY	3.3
1	K	173	PRO	3.3
1	M	151	LEU	3.2
1	K	149	PRO	3.2
1	K	91	ILE	3.2
1	K	132	SER	3.2
1	L	250	LEU	3.2
1	K	87	GLY	3.1
1	K	170	SER	3.1
1	D	13	LEU	3.1
1	K	5	ALA	3.1
1	K	178	LEU	3.0
1	L	46	LEU	3.0
1	K	3	ARG	3.0
1	E	111	ARG	3.0
1	I	41	TYR	3.0
1	J	253	SER	3.0
1	G	127	PRO	3.0
1	I	286	LEU	3.0
1	K	85	PRO	3.0
1	M	9	VAL	3.0
1	E	66	TYR	3.0
1	D	133	GLY	3.0
1	L	181	GLU	3.0
1	M	170	SER	3.0
1	L	148	HIS	2.9
1	J	211	LEU	2.9
1	K	154	VAL	2.9
1	L	111	ARG	2.9
1	M	176	LYS	2.9
1	K	4	VAL	2.9
1	K	184	VAL	2.9
1	G	52	SER	2.9
1	A	125	ASN	2.9
1	K	172	ASP	2.8
1	L	183	GLY	2.8
1	M	122	ALA	2.8
1	K	66	TYR	2.8
1	G	70	ILE	2.8
1	L	126	THR	2.8
1	D	134	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	I	133	GLY	2.8
1	M	236	GLY	2.8
1	E	147	GLY	2.8
1	G	64	LEU	2.8
1	M	51	VAL	2.8
1	J	89	PHE	2.7
1	M	156	ARG	2.7
1	K	86	GLU	2.7
1	L	108	ALA	2.7
1	M	132	SER	2.7
1	D	66	TYR	2.7
1	K	147	GLY	2.7
1	M	185	ARG	2.7
1	K	148	HIS	2.7
1	M	114	GLY	2.7
1	L	252	GLU	2.6
1	K	88	VAL	2.6
1	G	129	THR	2.6
1	M	155	PHE	2.6
1	K	43	VAL	2.6
1	E	51	VAL	2.6
1	M	3	ARG	2.6
1	E	88	VAL	2.6
1	A	134	ASN	2.6
1	M	11	MET	2.6
1	C	64	LEU	2.6
1	K	125	ASN	2.6
1	L	186	VAL	2.6
1	K	65	ALA	2.5
1	M	271	ARG	2.5
1	M	130	SER	2.5
1	J	134	ASN	2.5
1	L	158	VAL	2.5
1	E	87	GLY	2.5
1	L	180	LYS	2.5
1	K	6	VAL	2.5
1	K	129	THR	2.5
1	D	65	ALA	2.5
1	K	44	GLU	2.5
1	K	126	THR	2.5
1	I	181	GLU	2.5
1	K	169	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	M	69	GLU	2.4
1	K	231	GLY	2.4
1	L	52	SER	2.4
1	F	3	ARG	2.4
1	M	103	SER	2.4
1	H	65	ALA	2.4
1	L	134	ASN	2.4
1	K	134	ASN	2.4
1	M	180	LYS	2.3
1	M	46	LEU	2.3
1	K	2	GLU	2.3
1	L	286	LEU	2.3
1	M	12	ASP	2.3
1	M	136	HIS	2.3
1	I	231	GLY	2.3
1	E	154	VAL	2.3
1	E	13	LEU	2.3
1	L	176	LYS	2.3
1	M	83	ALA	2.2
1	K	128	GLU	2.2
1	K	92	VAL	2.2
1	M	172	ASP	2.2
1	M	133	GLY	2.2
1	H	13	LEU	2.2
1	K	42	THR	2.2
1	L	124	PHE	2.2
1	D	12	ASP	2.2
1	M	86	GLU	2.2
1	M	134	ASN	2.2
1	K	84	LEU	2.2
1	K	93	LEU	2.2
1	L	179	LEU	2.2
1	L	174	GLY	2.1
1	K	180	LYS	2.1
1	K	67	LEU	2.1
1	M	177	ARG	2.1
1	K	40	GLY	2.1
1	G	50	PRO	2.1
1	L	138	MET	2.1
1	M	169	ARG	2.1
1	K	111	ARG	2.1
1	C	173	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	L	2	GLU	2.1
1	J	70	ILE	2.1
1	L	147	GLY	2.0
1	K	232	THR	2.0
1	K	258	SER	2.0
1	K	146	LEU	2.0
1	L	115	VAL	2.0
1	I	132	SER	2.0
1	K	82	ALA	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.