



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:33 AM UTC

PDB ID : 3E1K / pdb_00003e1k
Title : Crystal structure of Kluyveromyces lactis Gal80p in complex with the acidic activation domain of Gal4p
Authors : Thoden, J.B.; Holden, H.M.
Deposited on : 2008-08-04
Resolution : 3.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

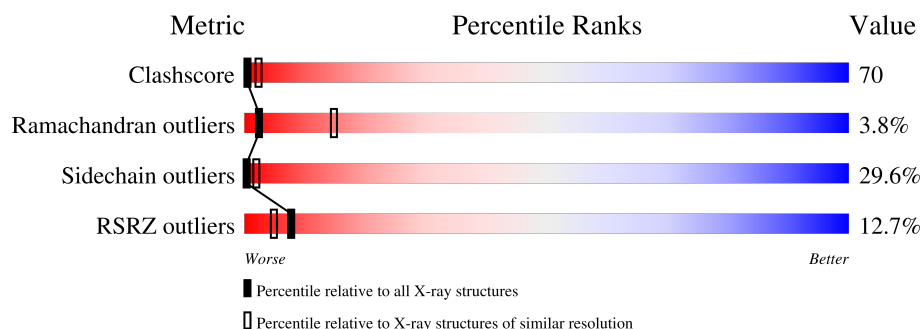
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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

Mol	Chain	Length	Quality of chain
1	A	465	14% 9% 41% 29% 6% 15%
1	C	465	7% 8% 41% 30% 5% 15%
1	E	465	16% 9% 40% 28% 7% 15%
1	G	465	5% 8% 42% 27% 8% 15%
1	I	465	13% 11% 41% 27% 6% 15%
1	K	465	8% 12% 36% 31% 5% 15%
1	M	465	12% 14% 39% 28% • 15%

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Mol	Chain	Length	Quality of chain
1	O	465	
2	B	22	
2	D	22	
2	F	22	
2	H	22	
2	J	22	
2	L	22	
2	N	22	
2	P	22	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 26057 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 Galactose/lactose metabolism regulatory protein GAL80.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			3153	2024	527	593	9			
1	C	393	Total	C	N	O	S	0	0	0
			3136	2013	525	589	9			
1	E	393	Total	C	N	O	S	0	0	0
			3136	2013	525	589	9			
1	G	393	Total	C	N	O	S	0	0	0
			3136	2013	525	589	9			
1	I	393	Total	C	N	O	S	0	0	0
			3136	2013	525	589	9			
1	K	393	Total	C	N	O	S	0	0	0
			3136	2013	525	589	9			
1	M	393	Total	C	N	O	S	0	0	0
			3136	2013	525	589	9			
1	O	393	Total	C	N	O	S	0	0	0
			3136	2013	525	589	9			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	458	LEU	-	expression tag	UNP Q06433
A	459	GLU	-	expression tag	UNP Q06433
A	460	HIS	-	expression tag	UNP Q06433
A	461	HIS	-	expression tag	UNP Q06433
A	462	HIS	-	expression tag	UNP Q06433
A	463	HIS	-	expression tag	UNP Q06433
A	464	HIS	-	expression tag	UNP Q06433
A	465	HIS	-	expression tag	UNP Q06433
C	458	LEU	-	expression tag	UNP Q06433
C	459	GLU	-	expression tag	UNP Q06433
C	460	HIS	-	expression tag	UNP Q06433
C	461	HIS	-	expression tag	UNP Q06433
C	462	HIS	-	expression tag	UNP Q06433

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Chain	Residue	Modelled	Actual	Comment	Reference
C	463	HIS	-	expression tag	UNP Q06433
C	464	HIS	-	expression tag	UNP Q06433
C	465	HIS	-	expression tag	UNP Q06433
E	458	LEU	-	expression tag	UNP Q06433
E	459	GLU	-	expression tag	UNP Q06433
E	460	HIS	-	expression tag	UNP Q06433
E	461	HIS	-	expression tag	UNP Q06433
E	462	HIS	-	expression tag	UNP Q06433
E	463	HIS	-	expression tag	UNP Q06433
E	464	HIS	-	expression tag	UNP Q06433
E	465	HIS	-	expression tag	UNP Q06433
G	458	LEU	-	expression tag	UNP Q06433
G	459	GLU	-	expression tag	UNP Q06433
G	460	HIS	-	expression tag	UNP Q06433
G	461	HIS	-	expression tag	UNP Q06433
G	462	HIS	-	expression tag	UNP Q06433
G	463	HIS	-	expression tag	UNP Q06433
G	464	HIS	-	expression tag	UNP Q06433
G	465	HIS	-	expression tag	UNP Q06433
I	458	LEU	-	expression tag	UNP Q06433
I	459	GLU	-	expression tag	UNP Q06433
I	460	HIS	-	expression tag	UNP Q06433
I	461	HIS	-	expression tag	UNP Q06433
I	462	HIS	-	expression tag	UNP Q06433
I	463	HIS	-	expression tag	UNP Q06433
I	464	HIS	-	expression tag	UNP Q06433
I	465	HIS	-	expression tag	UNP Q06433
K	458	LEU	-	expression tag	UNP Q06433
K	459	GLU	-	expression tag	UNP Q06433
K	460	HIS	-	expression tag	UNP Q06433
K	461	HIS	-	expression tag	UNP Q06433
K	462	HIS	-	expression tag	UNP Q06433
K	463	HIS	-	expression tag	UNP Q06433
K	464	HIS	-	expression tag	UNP Q06433
K	465	HIS	-	expression tag	UNP Q06433
M	458	LEU	-	expression tag	UNP Q06433
M	459	GLU	-	expression tag	UNP Q06433
M	460	HIS	-	expression tag	UNP Q06433
M	461	HIS	-	expression tag	UNP Q06433
M	462	HIS	-	expression tag	UNP Q06433
M	463	HIS	-	expression tag	UNP Q06433
M	464	HIS	-	expression tag	UNP Q06433

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Chain	Residue	Modelled	Actual	Comment	Reference
M	465	HIS	-	expression tag	UNP Q06433
O	458	LEU	-	expression tag	UNP Q06433
O	459	GLU	-	expression tag	UNP Q06433
O	460	HIS	-	expression tag	UNP Q06433
O	461	HIS	-	expression tag	UNP Q06433
O	462	HIS	-	expression tag	UNP Q06433
O	463	HIS	-	expression tag	UNP Q06433
O	464	HIS	-	expression tag	UNP Q06433
O	465	HIS	-	expression tag	UNP Q06433

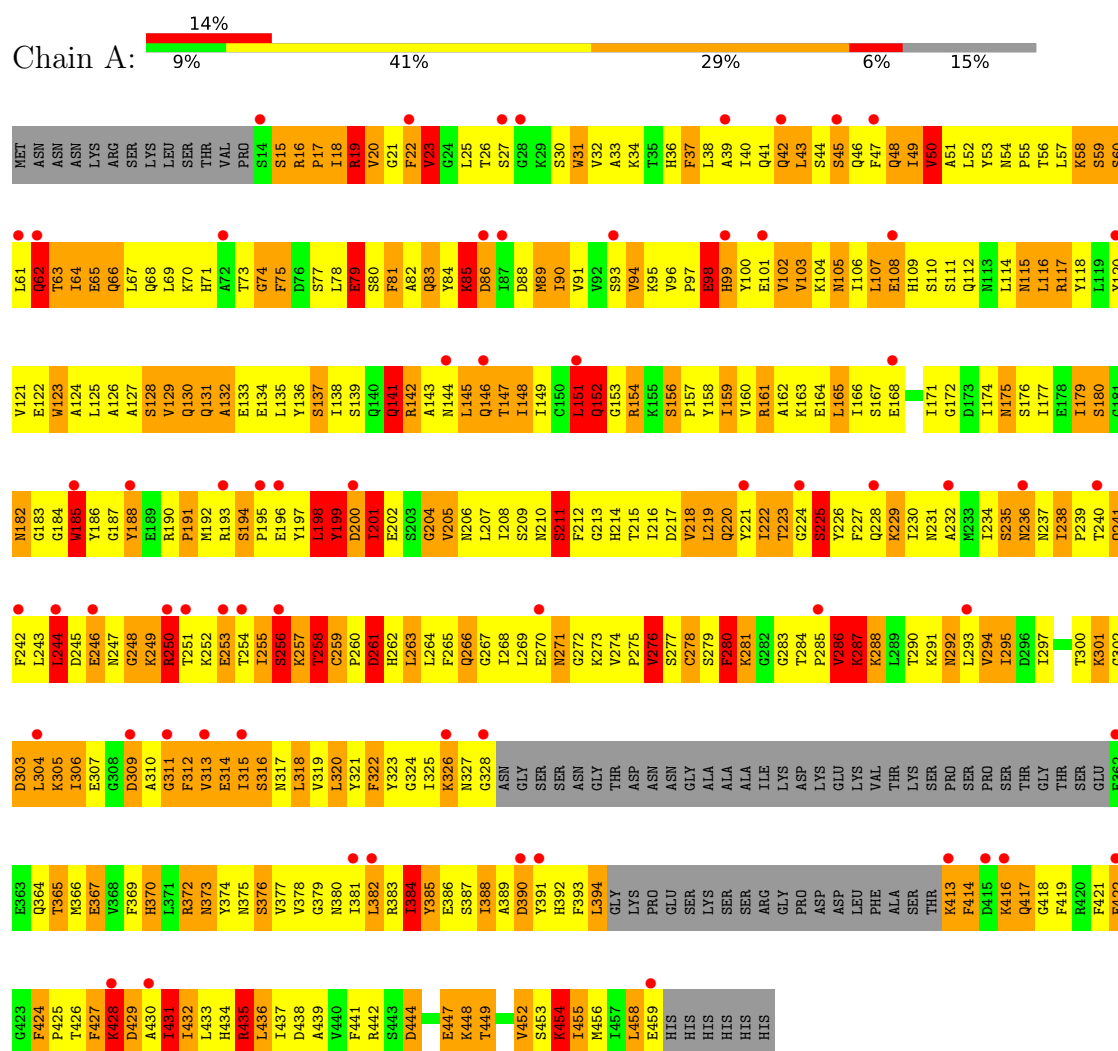
- Molecule 2 is a protein called Lactose regulatory protein LAC9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			
2	D	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			
2	F	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			
2	H	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			
2	J	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			
2	L	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			
2	N	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			
2	P	14	Total	C	N	O	S	0	0	0
			119	77	16	25	1			

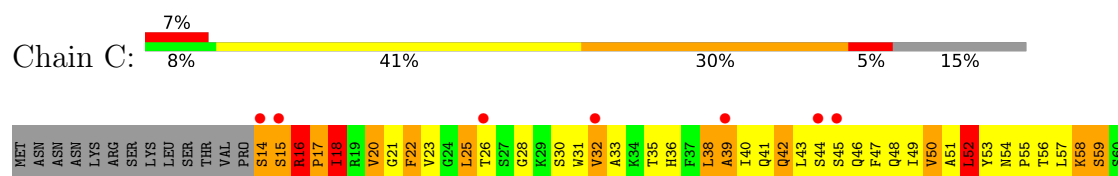
3 Residue-property plots

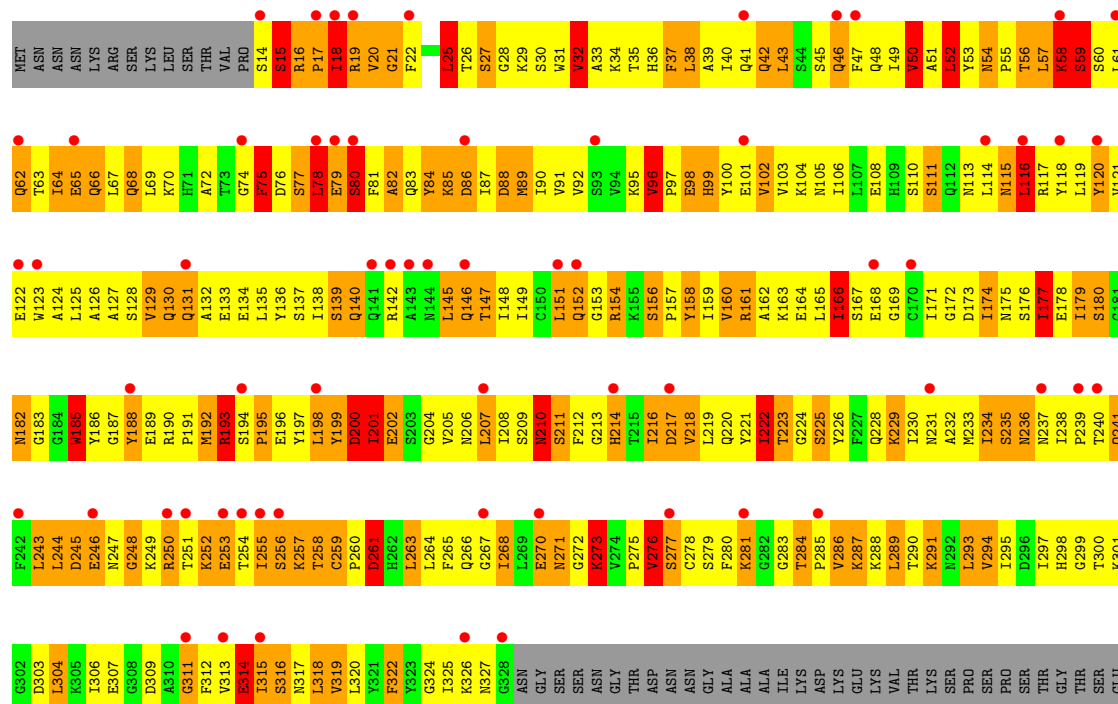
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

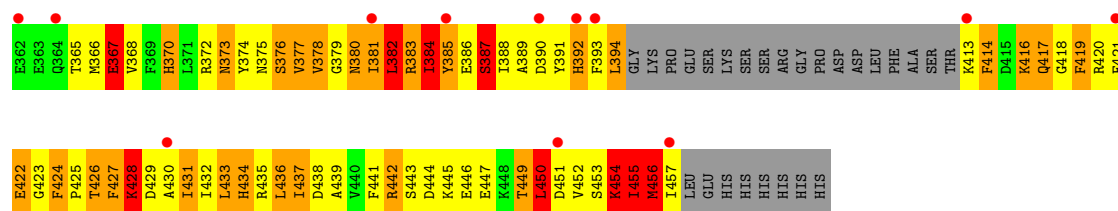
- Molecule 1: Galactose/lactose metabolism regulatory protein GAL80



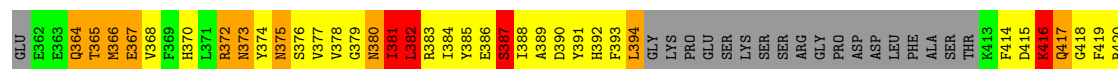
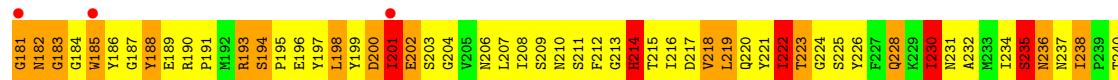
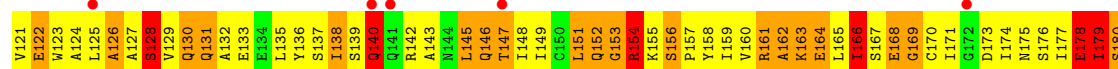
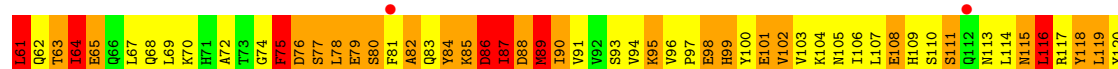
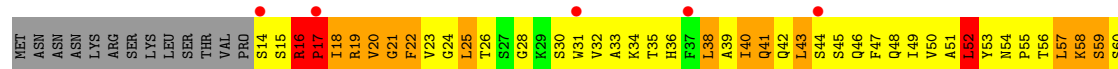
- Molecule 1: Galactose/lactose metabolism regulatory protein GAL80





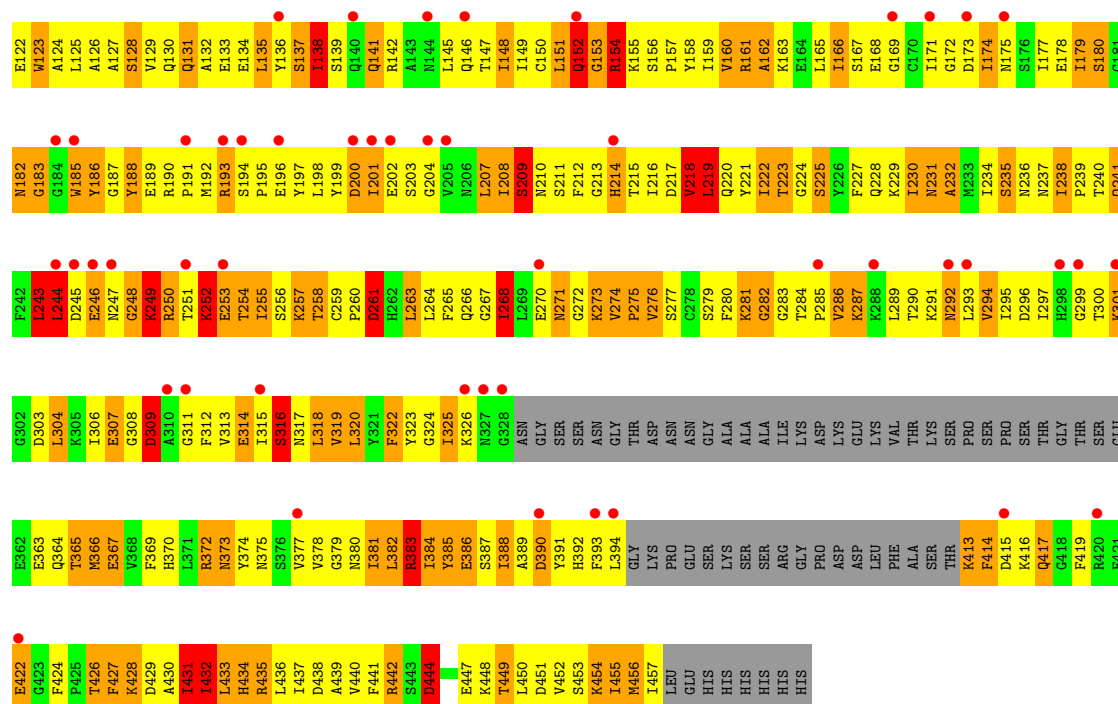


● Molecule 1: Galactose/lactose metabolism regulatory protein GAL80



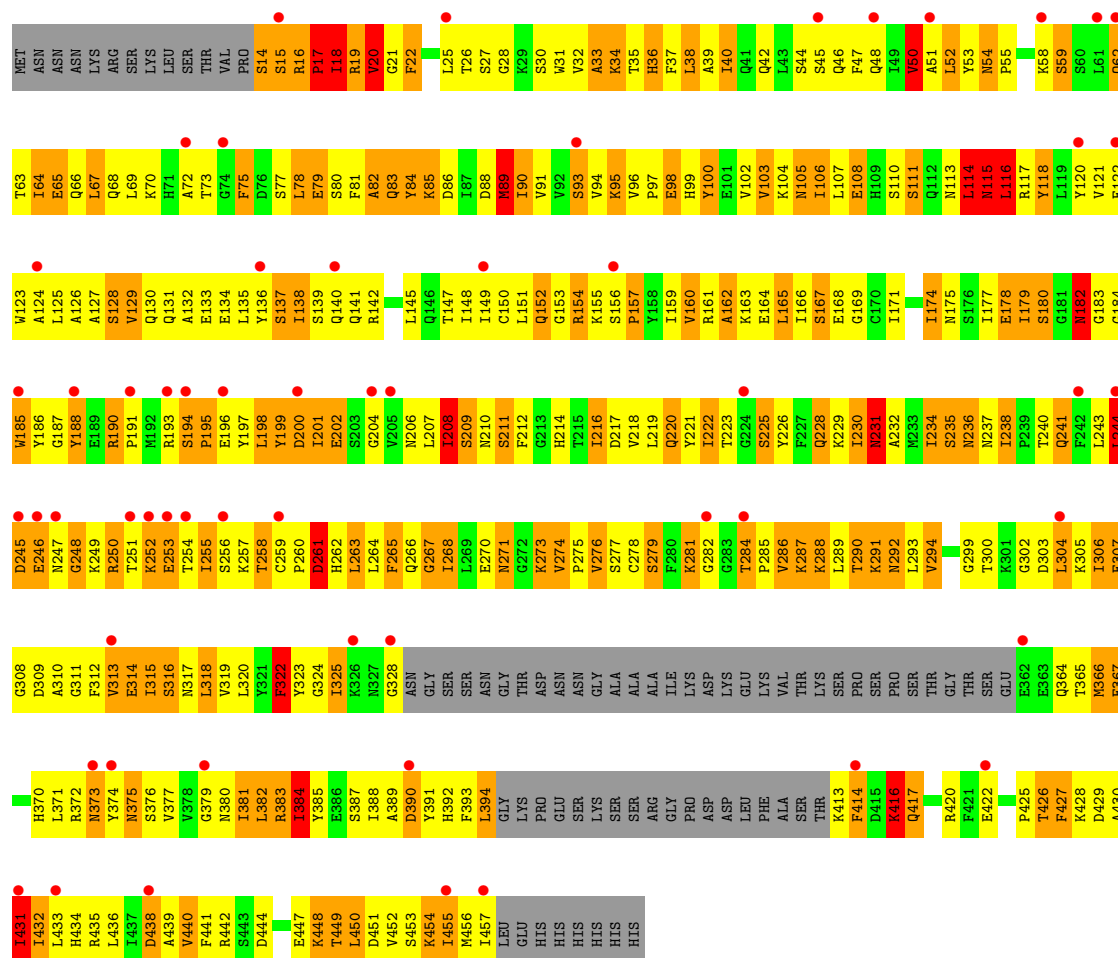
● Molecule 1: Galactose/lactose metabolism regulatory protein GAL80

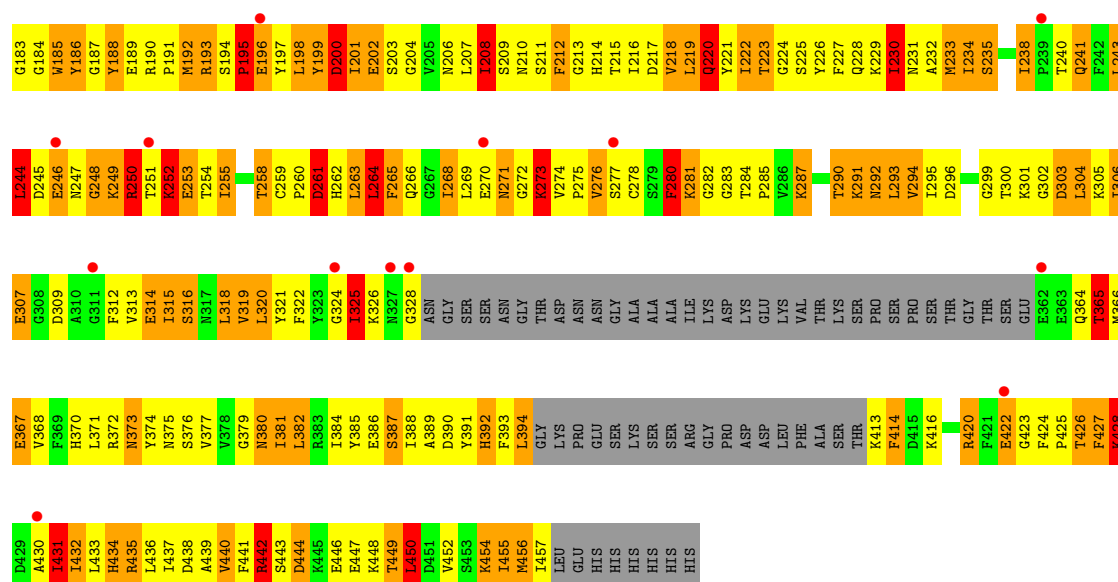






• Molecule 1: Galactose/lactose metabolism regulatory protein GAL80

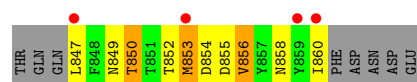




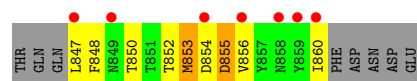
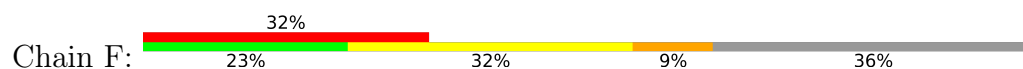
• Molecule 2: Lactose regulatory protein LAC9



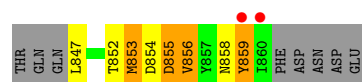
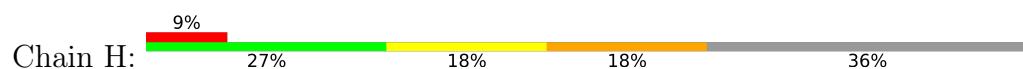
• Molecule 2: Lactose regulatory protein LAC9



• Molecule 2: Lactose regulatory protein LAC9



• Molecule 2: Lactose regulatory protein LAC9



• Molecule 2: Lactose regulatory protein LAC9

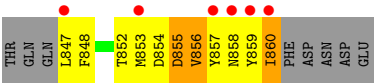




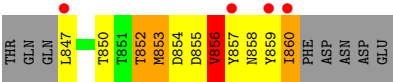
● Molecule 2: Lactose regulatory protein LAC9



● Molecule 2: Lactose regulatory protein LAC9



● Molecule 2: Lactose regulatory protein LAC9



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	101.10Å 160.50Å 132.60Å 90.00° 94.70° 90.00°	Depositor
Resolution (Å)	30.00 – 3.00 30.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	88.8 (30.00-3.00) 88.6 (30.00-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.68 (at 3.01Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.228 , 0.289 0.221 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 113.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	26057	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 19.86 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.8688e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1.32	11/3215 (0.3%)	2.08	140/4340 (3.2%)
1	C	1.18	5/3198 (0.2%)	2.11	144/4317 (3.3%)
1	E	1.36	17/3198 (0.5%)	2.07	141/4317 (3.3%)
1	G	1.30	13/3198 (0.4%)	2.09	140/4317 (3.2%)
1	I	1.33	9/3198 (0.3%)	2.13	142/4317 (3.3%)
1	K	1.30	15/3198 (0.5%)	2.10	150/4317 (3.5%)
1	M	1.29	6/3198 (0.2%)	2.06	116/4317 (2.7%)
1	O	1.18	9/3198 (0.3%)	2.09	131/4317 (3.0%)
2	B	0.93	0/121	1.81	0/165
2	D	1.05	0/121	1.54	3/165 (1.8%)
2	F	0.97	0/121	1.67	4/165 (2.4%)
2	H	0.94	0/121	1.60	1/165 (0.6%)
2	J	1.04	0/121	1.66	1/165 (0.6%)
2	L	1.16	1/121 (0.8%)	1.57	1/165 (0.6%)
2	N	1.00	0/121	1.60	1/165 (0.6%)
2	P	0.90	0/121	1.78	4/165 (2.4%)
All	All	1.28	86/26569 (0.3%)	2.08	1119/35879 (3.1%)

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

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

All (86) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	216	ILE	CA-CB	-11.77	1.41	1.54
1	K	40	ILE	CA-CB	-8.27	1.44	1.54
1	A	132	ALA	CA-CB	-8.25	1.40	1.53
1	E	200	ASP	CA-C	-8.05	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	O	151	LEU	CA-C	-7.49	1.45	1.53
1	A	258	THR	CA-CB	-7.13	1.42	1.54
1	A	74	GLY	CA-C	7.13	1.57	1.52
1	O	233	MET	SD-CE	6.92	1.96	1.79
1	M	52	LEU	C-O	-6.88	1.16	1.24
1	G	87	ILE	CA-CB	-6.66	1.45	1.53
1	C	120	TYR	C-O	-6.61	1.16	1.23
1	A	198	LEU	N-CA	-6.59	1.38	1.46
1	K	456	MET	SD-CE	6.42	1.95	1.79
1	K	73	THR	C-O	-6.29	1.16	1.23
1	I	297	ILE	CA-CB	-6.28	1.46	1.54
1	G	21	GLY	CA-C	-6.26	1.48	1.52
1	E	120	TYR	C-O	-6.21	1.16	1.23
1	I	319	VAL	CA-CB	-6.17	1.46	1.54
1	M	100	TYR	C-O	-6.12	1.17	1.24
1	I	366	MET	SD-CE	6.09	1.94	1.79
1	I	230	ILE	CA-CB	-6.07	1.49	1.55
1	G	178	GLU	CA-C	-6.06	1.44	1.52
1	A	148	ILE	CA-CB	-6.04	1.46	1.54
1	M	52	LEU	CA-C	-5.99	1.45	1.52
1	K	369	PHE	CA-C	-5.99	1.45	1.53
1	E	210	ASN	C-O	-5.95	1.16	1.24
1	K	160	VAL	CA-CB	5.95	1.62	1.54
1	I	238	ILE	CA-CB	-5.87	1.49	1.54
1	E	220	GLN	C-O	-5.82	1.16	1.24
1	G	238	ILE	CA-CB	-5.80	1.49	1.54
1	E	96	VAL	CA-CB	-5.79	1.46	1.54
1	I	219	LEU	C-O	-5.78	1.17	1.24
1	G	268	ILE	C-O	-5.75	1.17	1.24
1	E	210	ASN	CA-C	-5.74	1.45	1.52
1	A	312	PHE	CA-C	-5.72	1.46	1.53
1	G	433	LEU	C-O	-5.70	1.17	1.24
1	K	40	ILE	C-O	-5.69	1.17	1.24
1	G	382	LEU	CA-C	-5.68	1.45	1.52
1	G	382	LEU	C-O	-5.67	1.16	1.24
1	K	392	HIS	CA-C	-5.67	1.47	1.53
1	K	152	GLN	C-O	-5.65	1.16	1.24
1	I	161	ARG	C-O	-5.64	1.17	1.24
1	O	234	ILE	CA-CB	5.62	1.60	1.54
1	K	437	ILE	CG1-CD1	-5.61	1.29	1.51
1	G	18	ILE	CA-C	-5.57	1.45	1.52
1	K	279	SER	C-O	-5.57	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	89	MET	SD-CE	-5.57	1.65	1.79
1	A	175	ASN	CA-C	-5.57	1.49	1.52
1	O	168	GLU	CA-C	-5.53	1.47	1.53
1	E	383	ARG	CA-C	-5.52	1.45	1.52
1	G	84	TYR	CA-C	-5.51	1.45	1.52
1	M	222	ILE	CA-CB	-5.49	1.48	1.54
1	C	298	HIS	C-O	-5.45	1.17	1.23
1	E	314	GLU	C-O	-5.45	1.17	1.24
1	E	96	VAL	CA-C	-5.41	1.47	1.52
1	O	250	ARG	C-O	5.38	1.29	1.23
1	I	268	ILE	CA-CB	-5.36	1.47	1.53
2	L	848	PHE	C-O	-5.36	1.18	1.24
1	A	229	LYS	C-N	5.34	1.38	1.33
1	C	420	ARG	C-O	-5.34	1.17	1.23
1	K	118	TYR	C-O	-5.33	1.17	1.24
1	A	326	LYS	CE-NZ	5.31	1.65	1.49
1	E	217	ASP	C-O	-5.30	1.17	1.24
1	K	37	PHE	C-O	-5.25	1.18	1.24
1	G	435	ARG	C-O	-5.23	1.18	1.24
1	K	20	VAL	CA-CB	-5.22	1.48	1.54
1	O	168	GLU	C-O	-5.21	1.18	1.23
1	E	79	GLU	CA-C	-5.21	1.46	1.52
1	A	152	GLN	CA-C	5.20	1.60	1.52
1	E	52	LEU	C-O	-5.14	1.18	1.24
1	O	177	ILE	CA-CB	-5.14	1.47	1.54
1	G	214	HIS	C-O	-5.12	1.18	1.24
1	O	293	LEU	CA-C	-5.12	1.46	1.52
1	C	195	PRO	CA-CB	-5.12	1.46	1.53
1	E	72	ALA	CA-CB	-5.11	1.45	1.53
1	K	389	ALA	CA-CB	-5.11	1.45	1.53
1	C	184	GLY	CA-C	5.10	1.59	1.51
1	A	255	ILE	C-O	-5.07	1.19	1.24
1	I	383	ARG	C-O	-5.07	1.17	1.24
1	E	433	LEU	C-O	-5.06	1.18	1.24
1	O	293	LEU	C-O	-5.05	1.18	1.24
1	K	52	LEU	C-O	-5.04	1.17	1.24
1	E	382	LEU	C-O	-5.03	1.18	1.24
1	E	287	LYS	N-CA	-5.01	1.39	1.46
1	G	297	ILE	CA-CB	-5.01	1.48	1.54
1	E	96	VAL	N-CA	-5.00	1.40	1.46

All (1119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	220	GLN	N-CA-C	-18.09	91.60	111.14
1	C	220	GLN	N-CA-C	-17.27	92.48	111.14
1	O	102	VAL	N-CA-C	16.79	129.76	110.62
1	K	220	GLN	N-CA-C	-15.31	94.69	111.07
1	K	18	ILE	N-CA-C	-15.25	92.98	110.21
1	I	75	PHE	N-CA-C	14.77	131.32	110.50
1	E	276	VAL	N-CA-C	13.01	126.74	107.75
1	O	222	ILE	CB-CA-C	-12.96	95.39	111.97
1	A	188	TYR	N-CA-C	-12.88	97.07	112.92
1	I	316	SER	N-CA-C	12.71	128.43	110.50
1	E	385	TYR	N-CA-C	-12.71	97.86	113.50
1	G	273	LYS	N-CA-C	-12.71	97.08	112.58
1	M	276	VAL	N-CA-C	12.59	125.73	108.11
1	G	204	GLY	N-CA-C	-12.52	96.82	115.72
1	G	276	VAL	N-CA-C	12.51	127.17	107.28
1	C	222	ILE	CB-CA-C	-12.37	95.82	112.02
1	K	276	VAL	N-CA-C	12.24	125.62	107.75
1	I	381	ILE	N-CA-C	-12.14	99.05	110.82
1	I	325	ILE	N-CA-C	12.11	126.27	107.98
1	O	204	GLY	N-CA-C	-11.91	97.73	115.72
1	I	222	ILE	CB-CA-C	-11.82	97.03	111.81
1	O	188	TYR	N-CA-C	-11.75	97.72	112.88
1	G	234	ILE	N-CA-C	11.72	124.80	107.80
1	M	188	TYR	N-CA-C	-11.72	97.60	113.30
1	M	222	ILE	CB-CA-C	-11.68	97.03	111.97
1	O	316	SER	N-CA-C	11.65	126.92	110.50
1	K	204	GLY	N-CA-C	-11.64	96.93	116.01
1	A	238	ILE	N-CA-C	-11.52	96.75	108.15
1	M	115	ASN	N-CA-C	-11.50	98.74	113.12
1	A	424	PHE	N-CA-C	-11.49	97.88	108.22
1	I	431	ILE	N-CA-C	11.45	121.41	110.42
1	C	238	ILE	N-CA-C	-11.44	96.83	108.15
1	C	276	VAL	N-CA-C	11.43	124.69	107.77
1	M	238	ILE	N-CA-C	-11.42	96.84	108.15
1	I	188	TYR	N-CA-C	-11.40	98.90	112.92
1	O	374	TYR	N-CA-C	-11.38	91.51	109.72
1	A	198	LEU	N-CA-C	-11.37	92.60	111.37
1	A	316	SER	N-CA-C	11.29	126.41	110.50
1	K	222	ILE	CB-CA-C	-11.24	97.75	111.81
1	O	102	VAL	CB-CA-C	-11.24	97.32	112.04
1	M	220	GLN	N-CA-C	-11.20	99.08	111.07
1	O	115	ASN	N-CA-C	-11.14	98.30	112.90
1	G	274	VAL	N-CA-C	-11.12	98.68	109.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	115	ASN	N-CA-C	-11.01	99.36	113.12
1	C	74	GLY	N-CA-C	10.99	128.89	111.64
1	K	381	ILE	N-CA-C	-10.96	100.19	110.82
1	E	316	SER	N-CA-C	10.94	125.92	110.50
1	C	204	GLY	N-CA-C	-10.79	99.43	115.72
1	G	222	ILE	CB-CA-C	-10.77	97.92	112.02
1	G	316	SER	N-CA-C	10.75	127.18	110.20
1	G	238	ILE	N-CA-C	-10.71	97.54	108.15
1	G	115	ASN	N-CA-C	-10.66	97.63	112.45
1	E	188	TYR	N-CA-C	-10.58	99.91	112.92
1	C	325	ILE	N-CA-C	10.51	122.72	108.84
1	K	234	ILE	N-CA-C	10.49	123.36	108.36
1	C	115	ASN	N-CA-C	-10.48	98.80	111.69
1	K	316	SER	N-CA-C	10.41	126.65	110.20
1	E	325	ILE	N-CA-C	10.39	123.67	107.98
1	K	273	LYS	N-CA-C	-10.27	100.70	113.23
1	I	204	GLY	N-CA-C	-10.14	100.84	115.64
1	I	276	VAL	N-CA-C	10.06	122.44	107.75
1	A	317	ASN	N-CA-C	-10.06	92.34	108.73
1	E	374	TYR	N-CA-C	-10.05	93.41	109.59
1	G	427	PHE	N-CA-C	-10.04	100.16	111.71
1	A	204	GLY	N-CA-C	-10.02	99.57	116.01
1	M	438	ASP	N-CA-C	-10.01	100.36	111.07
1	G	39	ALA	N-CA-C	-9.99	100.47	111.36
1	C	381	ILE	N-CA-C	-9.95	101.17	110.82
1	E	54	ASN	CA-C-N	9.91	129.67	119.56
1	E	54	ASN	C-N-CA	9.91	129.67	119.56
1	M	18	ILE	N-CA-C	-9.88	94.35	108.58
1	K	238	ILE	N-CA-C	-9.87	98.38	108.15
1	I	18	ILE	N-CA-C	-9.86	94.39	108.58
1	O	309	ASP	N-CA-C	-9.85	101.38	113.50
1	A	276	VAL	N-CA-C	9.83	122.32	107.77
1	M	234	ILE	N-CA-C	9.81	122.02	107.80
1	A	131	GLN	N-CA-C	-9.81	99.87	112.23
1	O	162	ALA	N-CA-C	-9.76	100.33	110.97
1	G	230	ILE	CB-CA-C	-9.76	102.56	111.74
1	M	230	ILE	CB-CA-C	-9.75	97.66	111.40
1	A	458	LEU	N-CA-C	9.74	120.72	108.45
1	O	381	ILE	N-CA-C	-9.72	101.39	110.53
1	G	424	PHE	N-CA-C	-9.70	99.40	108.13
1	A	384	ILE	CB-CA-C	-9.70	97.97	111.65
1	E	204	GLY	N-CA-C	-9.64	101.16	115.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	188	TYR	N-CA-C	-9.63	101.08	112.92
1	G	309	ASP	N-CA-C	-9.59	101.70	113.97
1	E	80	SER	N-CA-C	-9.56	99.36	111.02
1	K	116	LEU	N-CA-C	-9.54	95.75	109.96
1	G	417	GLN	N-CA-C	-9.54	100.41	112.90
1	I	88	ASP	N-CA-C	-9.50	100.46	112.90
1	M	235	SER	N-CA-C	9.50	125.33	109.76
1	E	309	ASP	N-CA-C	-9.49	101.82	113.97
1	K	309	ASP	N-CA-C	-9.47	101.41	113.72
1	G	98	GLU	N-CA-C	-9.47	100.67	112.88
1	M	454	LYS	N-CA-C	-9.47	101.50	113.43
1	A	309	ASP	N-CA-C	-9.43	101.91	113.50
1	E	255	ILE	N-CA-C	9.39	123.42	107.18
1	O	273	LYS	N-CA-C	-9.37	99.63	113.40
1	E	186	TYR	N-CA-C	-9.36	101.17	112.59
1	M	98	GLU	N-CA-C	-9.35	101.88	113.38
1	O	325	ILE	N-CA-C	9.35	122.38	108.54
1	A	18	ILE	N-CA-C	-9.34	95.01	108.36
1	E	424	PHE	N-CA-C	-9.33	99.73	108.13
1	M	78	LEU	N-CA-C	-9.33	100.02	111.40
1	M	204	GLY	N-CA-C	-9.33	101.64	115.72
1	C	234	ILE	N-CA-C	9.29	121.28	107.80
1	K	188	TYR	N-CA-C	-9.27	100.93	112.88
1	O	18	ILE	N-CA-C	-9.24	94.82	108.87
1	E	15	SER	N-CA-C	-9.20	92.52	108.52
1	C	316	SER	N-CA-C	9.19	124.08	110.48
1	K	454	LYS	N-CA-C	-9.19	102.64	114.04
1	A	63	THR	N-CA-C	-9.19	101.24	111.07
1	M	316	SER	N-CA-C	9.16	124.03	110.48
1	G	223	THR	N-CA-C	-9.15	101.28	111.07
1	O	238	ILE	N-CA-C	-9.14	99.10	108.15
1	G	380	ASN	N-CA-C	9.13	122.22	111.71
1	K	380	ASN	N-CA-C	9.13	122.21	111.71
1	K	32	VAL	N-CA-C	-9.13	101.31	110.62
1	I	18	ILE	CB-CA-C	-9.12	99.60	110.91
1	C	122	GLU	N-CA-C	9.11	124.26	109.59
1	C	417	GLN	N-CA-C	-9.11	100.97	112.90
1	I	49	ILE	CB-CA-C	-9.09	99.96	110.96
1	A	315	ILE	CB-CA-C	-9.09	103.06	111.06
1	G	90	ILE	CB-CA-C	-9.08	98.49	110.84
1	I	248	GLY	CA-C-N	-9.08	107.98	120.87
1	I	248	GLY	C-N-CA	-9.08	107.98	120.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	77	SER	CA-CB-OG	9.08	129.26	111.10
1	E	21	GLY	N-CA-C	-9.08	94.55	110.71
1	O	220	GLN	N-CA-C	-9.08	101.36	111.07
1	C	286	VAL	CB-CA-C	-9.06	99.13	111.63
1	M	325	ILE	N-CA-C	9.05	121.94	108.54
1	C	424	PHE	N-CA-C	-9.04	99.99	108.13
1	O	145	LEU	N-CA-C	9.04	123.66	108.20
1	K	39	ALA	N-CA-C	-9.04	101.34	111.82
1	I	454	LYS	N-CA-C	-9.03	102.05	113.43
1	G	274	VAL	CB-CA-C	-9.03	102.15	111.00
1	G	259	CYS	N-CA-C	-9.02	97.63	110.08
1	A	220	GLN	N-CA-C	-8.99	100.25	111.75
1	K	15	SER	N-CA-CB	-8.98	99.58	110.53
1	M	381	ILE	N-CA-C	-8.98	102.11	110.82
1	K	427	PHE	N-CA-C	-8.97	101.42	111.82
1	A	62	GLN	CB-CA-C	-8.96	95.63	110.85
1	I	115	ASN	N-CA-C	-8.94	101.19	112.90
1	I	380	ASN	N-CA-C	8.94	121.99	111.71
1	O	391	TYR	N-CA-CB	-8.92	97.07	110.01
1	C	90	ILE	CB-CA-C	-8.90	98.44	110.98
1	G	179	ILE	N-CA-C	8.89	120.09	108.35
1	O	276	VAL	N-CA-C	8.88	120.91	107.77
1	I	417	GLN	N-CA-C	-8.82	100.20	112.45
1	G	381	ILE	N-CA-C	-8.79	102.29	110.82
1	I	427	PHE	N-CA-C	-8.76	101.73	111.28
1	G	78	LEU	N-CA-C	-8.74	100.73	111.40
1	A	222	ILE	CB-CA-C	-8.73	100.90	111.81
1	I	238	ILE	N-CA-C	-8.72	99.51	108.15
1	A	325	ILE	N-CA-C	8.71	121.43	108.54
1	E	220	GLN	N-CA-C	-8.71	101.69	111.71
1	O	98	GLU	N-CA-C	-8.70	101.64	113.30
1	A	199	TYR	N-CA-C	8.69	122.66	112.93
1	A	98	GLU	N-CA-C	-8.68	102.25	112.92
2	P	853	MET	N-CA-C	-8.67	101.79	111.07
1	M	186	TYR	N-CA-C	-8.64	99.69	111.87
1	M	427	PHE	N-CA-C	-8.63	101.78	111.71
1	K	15	SER	CB-CA-C	8.62	125.06	112.12
1	I	21	GLY	N-CA-C	-8.61	94.85	111.12
1	I	95	LYS	CB-CA-C	-8.60	97.76	109.71
1	A	21	GLY	N-CA-C	-8.60	95.41	110.71
1	G	18	ILE	N-CA-C	-8.59	95.91	108.71
1	E	145	LEU	N-CA-C	8.57	122.70	108.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	88	ASP	N-CA-C	-8.57	101.67	112.90
1	O	427	PHE	N-CA-C	-8.57	101.85	111.71
1	E	223	THR	N-CA-C	-8.56	100.58	111.02
1	A	244	LEU	CA-C-N	-8.54	109.21	121.42
1	A	244	LEU	C-N-CA	-8.54	109.21	121.42
1	I	414	PHE	CA-C-N	8.52	131.51	120.44
1	I	414	PHE	C-N-CA	8.52	131.51	120.44
1	I	294	VAL	CB-CA-C	-8.52	99.96	111.80
1	E	391	TYR	N-CA-CB	-8.52	97.29	110.06
1	M	380	ASN	N-CA-C	8.51	121.50	111.71
1	I	27	SER	CA-CB-OG	-8.50	94.09	111.10
1	K	78	LEU	N-CA-C	-8.49	101.04	111.40
1	M	273	LYS	N-CA-C	-8.49	102.22	112.58
1	I	235	SER	N-CA-C	8.46	123.64	109.76
1	A	249	LYS	N-CA-C	-8.46	97.77	110.28
1	I	78	LEU	N-CA-C	-8.46	101.64	111.03
1	A	259	CYS	N-CA-C	-8.44	99.43	110.07
1	G	315	ILE	CB-CA-C	-8.44	101.68	110.88
2	F	855	ASP	CB-CA-C	-8.41	97.67	110.88
1	A	250	ARG	CB-CA-C	-8.41	91.86	110.19
1	I	415	ASP	N-CA-C	8.39	120.05	111.07
1	K	294	VAL	CB-CA-C	-8.39	95.89	110.65
1	M	431	ILE	N-CA-C	8.39	118.44	110.30
1	K	259	CYS	N-CA-C	-8.37	97.87	110.01
1	O	255	ILE	N-CA-C	8.36	120.81	108.45
1	I	391	TYR	N-CA-CB	-8.35	97.36	110.22
1	A	427	PHE	N-CA-C	-8.35	102.35	112.54
1	I	308	GLY	N-CA-C	-8.35	98.91	111.10
1	I	98	GLU	N-CA-C	-8.34	102.12	112.88
1	K	179	ILE	N-CA-C	8.33	121.68	108.85
1	C	18	ILE	N-CA-C	-8.32	97.90	108.89
1	I	230	ILE	CB-CA-C	-8.32	99.67	111.40
1	G	188	TYR	N-CA-C	-8.31	102.70	112.92
1	K	52	LEU	CA-C-N	-8.30	110.28	122.65
1	K	52	LEU	C-N-CA	-8.30	110.28	122.65
1	E	119	LEU	CB-CG-CD2	-8.30	85.79	110.70
1	I	244	LEU	CA-C-N	-8.29	109.83	122.09
1	I	244	LEU	C-N-CA	-8.29	109.83	122.09
1	M	223	THR	N-CA-C	-8.29	102.20	111.07
1	G	38	LEU	CA-CB-CG	-8.25	87.41	116.30
1	I	116	LEU	N-CA-C	-8.14	98.09	110.30
1	O	223	THR	CB-CA-C	-8.11	98.16	110.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	454	LYS	N-CA-C	-8.09	102.34	114.64
1	O	315	ILE	CB-CA-C	-8.08	103.95	111.06
1	O	454	LYS	N-CA-C	-8.08	104.03	114.04
1	I	50	VAL	N-CA-C	8.07	118.75	111.81
1	O	116	LEU	N-CA-C	-8.06	98.20	110.30
1	K	98	GLU	N-CA-C	-8.05	103.03	113.17
1	I	74	GLY	N-CA-C	8.04	132.24	113.18
1	E	284	THR	N-CA-C	8.04	121.39	110.29
1	A	15	SER	N-CA-C	-8.04	94.53	108.52
1	O	15	SER	N-CA-C	-8.02	97.58	109.62
1	M	116	LEU	N-CA-C	-7.99	98.81	110.64
1	C	454	LYS	N-CA-C	-7.97	104.02	114.31
1	G	374	TYR	N-CA-C	-7.97	96.24	109.07
1	C	42	GLN	N-CA-C	-7.96	103.37	113.72
1	G	88	ASP	N-CA-C	-7.96	102.68	111.36
1	O	39	ALA	N-CA-C	-7.95	101.57	111.11
1	E	222	ILE	CB-CA-C	-7.93	101.90	111.81
1	M	374	TYR	N-CA-C	-7.91	97.44	110.17
1	C	380	ASN	N-CA-C	7.90	120.80	111.71
1	C	427	PHE	N-CA-C	-7.89	102.63	111.71
1	C	78	LEU	N-CA-C	-7.89	102.62	111.14
1	O	234	ILE	N-CA-C	7.88	119.23	107.80
1	C	294	VAL	N-CA-C	7.85	118.72	108.35
1	G	64	ILE	N-CA-C	7.83	118.58	110.36
1	M	309	ASP	N-CA-C	-7.80	103.57	113.72
1	I	16	ARG	O-C-N	7.80	127.92	121.84
1	E	78	LEU	N-CA-C	-7.79	102.73	111.14
1	K	315	ILE	CB-CA-C	-7.79	104.21	111.06
1	C	166	ILE	CB-CA-C	-7.78	101.83	112.02
1	A	90	ILE	CB-CA-C	-7.77	99.00	110.81
1	A	386	GLU	CA-C-O	-7.77	112.84	121.00
1	C	193	ARG	N-CA-C	7.77	119.75	111.28
1	I	234	ILE	N-CA-C	7.77	119.07	107.80
1	I	374	TYR	N-CA-C	-7.77	97.09	109.59
1	O	21	GLY	N-CA-C	-7.76	98.83	110.71
1	A	431	ILE	N-CA-C	7.74	117.81	110.53
1	K	249	LYS	N-CA-C	-7.73	98.84	110.28
1	O	249	LYS	N-CA-C	-7.72	99.03	110.23
1	A	256	SER	N-CA-C	7.71	121.80	109.24
1	K	122	GLU	N-CA-C	7.70	122.08	110.14
1	K	162	ALA	N-CA-C	-7.68	102.59	110.97
1	I	152	GLN	N-CA-C	-7.68	103.65	112.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	248	GLY	N-CA-C	-7.68	103.94	115.00
1	A	62	GLN	N-CA-C	7.66	119.71	111.36
1	I	317	ASN	N-CA-C	-7.66	94.44	107.99
1	C	254	THR	N-CA-C	7.65	121.00	108.99
1	K	15	SER	N-CA-C	-7.64	98.16	109.62
1	I	179	ILE	N-CA-C	7.64	121.31	108.86
1	M	241	GLN	N-CA-C	7.63	121.35	109.52
1	C	162	ALA	N-CA-C	-7.62	102.66	110.97
1	A	50	VAL	N-CA-CB	-7.62	101.83	112.35
1	E	284	THR	N-CA-CB	-7.62	100.81	110.03
1	G	414	PHE	N-CA-CB	-7.62	99.47	110.36
1	I	257	LYS	N-CA-C	7.61	120.96	107.80
1	O	42	GLN	N-CA-C	-7.59	104.16	113.50
1	O	15	SER	CB-CA-C	7.59	123.51	112.12
1	O	78	LEU	N-CA-C	-7.59	102.14	111.40
1	G	365	THR	N-CA-C	7.59	120.99	109.23
1	K	115	ASN	N-CA-C	-7.58	103.83	113.23
1	G	294	VAL	N-CA-C	7.58	118.35	108.35
1	A	205	VAL	CB-CA-C	7.57	120.42	110.12
1	M	42	GLN	N-CA-C	-7.56	103.85	113.23
1	I	42	GLN	N-CA-C	-7.55	103.01	112.90
1	K	75	PHE	N-CA-C	7.54	121.76	109.85
1	O	57	LEU	N-CA-C	-7.53	103.01	111.14
1	E	317	ASN	N-CA-C	-7.52	95.34	108.20
1	G	254	THR	N-CA-C	7.51	120.79	108.99
1	A	78	LEU	N-CA-C	-7.51	104.14	113.38
1	C	71	HIS	N-CA-C	7.50	122.28	113.20
1	O	208	ILE	CB-CA-C	-7.50	98.98	111.29
1	E	417	GLN	N-CA-C	-7.50	102.78	112.23
1	I	426	THR	N-CA-C	7.50	121.81	109.96
1	E	235	SER	N-CA-C	7.50	122.24	110.32
1	O	38	LEU	CA-CB-CG	-7.50	90.07	116.30
1	A	254	THR	N-CA-C	7.49	121.56	108.75
1	A	234	ILE	N-CA-C	7.49	118.59	108.11
1	A	154	ARG	N-CA-C	7.48	121.33	111.75
1	M	440	VAL	CB-CA-C	-7.48	99.02	111.29
1	E	427	PHE	N-CA-C	-7.48	103.11	111.71
1	K	391	TYR	N-CA-CB	-7.48	97.61	110.32
1	M	250	ARG	CB-CA-C	-7.46	94.67	111.30
1	A	74	GLY	N-CA-C	7.45	124.58	111.25
1	I	255	ILE	N-CA-C	7.44	119.45	108.45
1	K	109	HIS	N-CA-C	7.42	122.36	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	162	ALA	N-CA-C	-7.42	102.79	111.03
1	G	75	PHE	N-CA-C	7.41	121.74	109.95
1	C	315	ILE	CB-CA-C	-7.41	104.54	111.06
1	M	255	ILE	N-CA-C	7.40	118.98	108.17
1	C	98	GLU	N-CA-C	-7.40	103.82	112.92
1	K	294	VAL	N-CA-C	7.39	118.40	108.27
1	M	38	LEU	CA-CB-CG	-7.39	90.43	116.30
1	C	440	VAL	CB-CA-C	-7.39	102.36	112.04
1	M	254	THR	N-CA-C	7.39	120.52	108.55
1	M	248	GLY	CA-C-N	-7.38	110.62	120.95
1	M	248	GLY	C-N-CA	-7.38	110.62	120.95
1	M	75	PHE	N-CA-C	7.36	121.48	109.85
1	I	249	LYS	N-CA-C	-7.36	99.39	110.28
1	O	254	THR	N-CA-C	7.36	120.47	108.55
1	O	16	ARG	CA-C-O	7.34	126.47	119.13
1	E	42	GLN	N-CA-C	-7.33	104.14	113.23
1	M	286	VAL	CB-CA-C	-7.33	100.76	111.68
1	I	110	SER	CB-CA-C	-7.32	99.72	111.28
1	G	193	ARG	N-CA-C	7.32	121.47	112.54
1	C	64	ILE	CB-CA-C	-7.30	102.63	111.97
1	I	17	PRO	N-CA-C	7.29	127.50	112.47
1	E	79	GLU	N-CA-C	-7.29	102.36	111.11
1	I	254	THR	N-CA-C	7.29	121.21	108.75
1	O	22	PHE	N-CA-C	7.29	120.40	108.52
1	G	145	LEU	N-CA-C	7.28	120.88	107.99
1	A	374	TYR	N-CA-C	-7.26	97.39	109.07
1	K	47	PHE	N-CA-C	7.25	121.27	109.59
1	C	150	CYS	CB-CA-C	-7.25	101.34	112.07
1	K	74	GLY	N-CA-C	7.25	124.55	113.02
1	G	325	ILE	N-CA-C	7.24	118.45	108.89
1	I	55	PRO	CB-CA-C	-7.22	99.65	111.56
1	I	183	GLY	N-CA-C	-7.22	103.70	113.37
1	A	162	ALA	N-CA-C	-7.21	103.03	111.03
1	A	414	PHE	N-CA-CB	-7.20	100.06	110.36
1	G	52	LEU	CA-C-N	-7.20	109.76	122.07
1	G	52	LEU	C-N-CA	-7.20	109.76	122.07
1	G	249	LYS	N-CA-C	-7.18	99.65	110.28
1	A	141	GLN	CA-C-N	-7.18	109.69	122.32
1	A	141	GLN	C-N-CA	-7.18	109.69	122.32
1	A	426	THR	N-CA-C	7.17	121.29	109.96
1	C	428	LYS	N-CA-C	-7.17	103.40	111.07
1	O	426	THR	N-CA-C	7.17	120.01	109.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	384	ILE	CB-CA-C	-7.16	101.89	110.84
1	E	294	VAL	CB-CA-C	-7.16	98.30	111.18
1	K	44	SER	N-CA-C	-7.15	103.49	111.71
1	A	79	GLU	N-CA-C	-7.15	102.68	111.40
1	M	414	PHE	N-CA-CB	-7.13	99.90	110.17
1	C	39	ALA	N-CA-C	-7.13	103.51	111.28
1	C	261	ASP	N-CA-C	7.13	121.80	113.18
2	L	853	MET	N-CA-C	-7.11	103.61	111.36
1	A	165	LEU	CB-CG-CD2	-7.10	89.41	110.70
1	C	223	THR	N-CA-C	-7.09	103.59	111.82
1	E	259	CYS	CA-C-N	7.06	126.98	119.85
1	E	259	CYS	C-N-CA	7.06	126.98	119.85
1	O	248	GLY	N-CA-C	-7.05	104.77	114.64
1	G	140	GLN	N-CA-C	7.03	119.54	111.11
1	G	250	ARG	CB-CA-C	-7.02	95.86	110.40
1	A	223	THR	N-CA-C	-7.02	102.69	111.11
1	I	257	LYS	CA-CB-CG	-7.02	100.06	114.10
1	C	271	ASN	N-CA-C	7.02	121.35	108.58
1	I	24	GLY	N-CA-C	-7.02	105.18	115.63
1	O	91	VAL	N-CA-CB	7.01	121.09	111.41
1	K	255	ILE	N-CA-C	7.01	118.82	108.45
1	O	380	ASN	N-CA-C	7.00	118.92	111.28
1	O	431	ILE	N-CA-C	7.00	117.09	110.30
1	C	431	ILE	N-CA-C	7.00	117.09	110.30
1	A	248	GLY	CA-C-N	-7.00	110.93	120.87
1	A	248	GLY	C-N-CA	-7.00	110.93	120.87
1	O	201	ILE	N-CA-C	7.00	123.90	109.34
1	K	325	ILE	N-CA-C	6.99	118.12	108.89
1	C	179	ILE	N-CA-C	6.99	120.13	108.81
1	G	420	ARG	N-CA-C	6.98	120.08	110.24
1	K	201	ILE	N-CA-C	6.98	123.86	109.34
1	I	274	VAL	N-CA-C	-6.97	101.29	108.96
1	E	377	VAL	N-CA-C	-6.97	102.98	110.23
1	M	313	VAL	CA-C-N	6.97	129.62	120.28
1	M	313	VAL	C-N-CA	6.97	129.62	120.28
1	M	317	ASN	N-CA-C	-6.96	97.38	108.73
1	O	294	VAL	N-CA-C	6.96	117.54	108.35
1	C	248	GLY	N-CA-C	-6.96	104.98	115.00
1	I	90	ILE	CB-CA-C	-6.96	101.17	110.98
1	K	88	ASP	N-CA-C	-6.95	103.78	111.36
1	K	427	PHE	CA-C-N	-6.94	111.42	120.44
1	K	427	PHE	C-N-CA	-6.94	111.42	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	309	ASP	N-CA-C	-6.93	104.97	113.50
1	M	417	GLN	N-CA-C	-6.93	103.49	112.23
1	C	186	TYR	N-CA-C	-6.93	103.11	112.26
1	E	75	PHE	N-CA-C	6.93	121.33	110.17
1	O	294	VAL	CB-CA-C	-6.93	98.48	111.30
1	M	391	TYR	N-CA-CB	-6.92	99.69	110.06
1	M	179	ILE	N-CA-C	6.91	120.01	108.81
1	I	286	VAL	CB-CA-C	-6.91	101.38	111.68
1	E	286	VAL	CB-CA-C	-6.91	101.39	111.68
1	O	261	ASP	N-CA-C	6.90	120.93	112.23
1	A	313	VAL	CA-C-O	6.90	127.95	120.57
1	I	85	LYS	N-CA-C	-6.90	105.28	113.21
1	K	426	THR	N-CA-C	6.87	119.85	109.95
1	K	64	ILE	CB-CA-C	-6.86	103.05	112.04
1	M	59	SER	N-CA-C	6.86	118.83	111.36
1	M	54	ASN	CA-C-N	6.86	128.41	119.84
1	M	54	ASN	C-N-CA	6.86	128.41	119.84
1	E	18	ILE	CB-CA-C	-6.85	102.25	111.15
1	A	417	GLN	N-CA-C	-6.83	103.29	111.69
1	M	426	THR	N-CA-C	6.83	120.75	109.96
1	C	15	SER	N-CA-C	6.83	125.34	110.80
1	I	38	LEU	CA-CB-CG	-6.82	92.42	116.30
1	I	259	CYS	N-CA-C	-6.82	100.67	110.08
1	K	248	GLY	N-CA-C	-6.81	105.11	114.64
1	O	88	ASP	N-CA-C	-6.79	103.96	111.36
1	A	241	GLN	N-CA-C	6.79	120.04	109.52
1	G	42	GLN	N-CA-C	-6.79	105.03	113.38
1	K	80	SER	N-CA-C	-6.75	103.84	111.07
1	M	248	GLY	N-CA-C	-6.75	105.19	114.64
1	A	211	SER	N-CA-C	6.75	125.17	110.80
1	C	444	ASP	N-CA-C	-6.74	102.79	111.02
1	E	154	ARG	NE-CZ-NH2	6.72	125.25	119.20
1	E	205	VAL	CB-CA-C	6.72	118.73	110.73
1	I	220	GLN	N-CA-C	-6.72	103.95	111.28
1	K	261	ASP	N-CA-C	6.70	121.46	113.28
1	E	18	ILE	N-CA-C	-6.70	100.05	108.89
1	I	223	THR	N-CA-C	-6.70	103.91	111.07
1	G	74	GLY	N-CA-C	6.68	124.51	112.54
1	M	244	LEU	N-CA-C	6.68	121.12	107.69
1	G	378	VAL	CB-CA-C	-6.68	105.18	111.06
1	A	75	PHE	N-CA-C	6.67	120.56	109.95
1	A	261	ASP	N-CA-C	6.67	121.25	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	315	ILE	CB-CA-C	-6.67	103.61	110.88
1	E	38	LEU	CA-CB-CG	-6.67	92.96	116.30
1	C	16	ARG	N-CA-C	6.67	120.21	110.14
1	C	391	TYR	N-CA-CB	-6.67	99.22	110.49
1	M	21	GLY	N-CA-C	-6.67	98.57	112.04
1	C	49	ILE	N-CA-CB	6.66	119.01	111.21
1	G	433	LEU	N-CA-C	-6.66	103.71	110.97
1	I	138	ILE	CB-CA-C	-6.66	103.28	111.87
1	E	414	PHE	N-CA-CB	-6.66	100.25	110.04
1	E	102	VAL	N-CA-C	6.65	123.18	109.34
1	C	44	SER	N-CA-C	-6.65	104.03	111.28
1	M	50	VAL	N-CA-CB	-6.64	104.42	112.33
1	A	380	ASN	N-CA-C	6.64	118.17	111.07
1	A	31	TRP	CB-CA-C	-6.64	99.82	110.84
1	E	50	VAL	N-CA-C	6.63	121.18	113.42
1	I	366	MET	N-CA-C	6.63	120.05	109.24
1	G	454	LYS	N-CA-C	-6.63	105.82	114.04
1	K	254	THR	N-CA-C	6.62	119.28	108.55
1	E	18	ILE	N-CA-CB	6.62	117.74	110.53
1	E	88	ASP	N-CA-C	-6.62	103.55	111.69
1	C	435	ARG	CB-CA-C	-6.61	99.44	110.68
1	E	254	THR	N-CA-C	6.61	120.06	108.75
1	I	162	ALA	N-CA-C	-6.61	103.69	111.03
1	O	154	ARG	N-CA-C	6.61	120.21	111.75
1	O	241	GLN	N-CA-C	6.60	119.91	109.81
1	O	75	PHE	N-CA-C	6.60	120.28	109.85
1	E	367	GLU	CA-C-N	-6.60	114.32	123.10
1	E	367	GLU	C-N-CA	-6.60	114.32	123.10
1	A	185	TRP	N-CA-C	6.59	121.03	112.92
1	C	271	ASN	CA-C-N	-6.59	116.31	123.30
1	C	271	ASN	C-N-CA	-6.59	116.31	123.30
1	A	259	CYS	CA-C-N	6.58	126.50	119.85
1	A	259	CYS	C-N-CA	6.58	126.50	119.85
1	E	72	ALA	N-CA-C	6.58	120.78	110.32
1	O	16	ARG	O-C-N	6.58	126.97	121.84
1	K	424	PHE	CA-C-O	6.57	126.14	119.76
1	A	235	SER	N-CA-C	6.57	120.75	110.17
1	A	73	THR	N-CA-C	-6.56	97.08	108.69
1	G	440	VAL	CB-CA-C	-6.56	103.48	111.88
1	A	274	VAL	N-CA-C	-6.55	101.82	108.96
1	G	256	SER	N-CA-C	6.53	118.73	110.24
1	E	154	ARG	N-CA-C	6.53	120.11	111.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	186	TYR	N-CA-C	-6.52	103.65	112.26
1	K	90	ILE	CB-CA-C	-6.52	101.12	110.83
1	K	368	VAL	CB-CA-C	-6.51	102.52	110.99
1	O	212	PHE	CB-CA-C	-6.51	100.66	110.88
1	O	76	ASP	N-CA-C	-6.51	105.97	114.04
1	A	315	ILE	N-CA-C	-6.51	106.45	112.96
1	O	273	LYS	CA-C-O	6.50	129.46	119.96
1	K	165	LEU	N-CA-C	6.50	118.36	111.28
1	C	317	ASN	N-CA-C	-6.49	97.10	108.20
1	I	309	ASP	N-CA-C	-6.49	105.52	113.50
1	C	145	LEU	N-CA-C	6.49	119.09	108.52
1	K	90	ILE	N-CA-C	6.49	117.25	108.17
1	C	90	ILE	N-CA-C	6.48	118.37	108.71
1	C	223	THR	CB-CA-C	-6.48	98.22	110.67
1	O	193	ARG	N-CA-C	6.47	118.33	111.28
1	A	448	LYS	N-CA-CB	-6.47	100.44	111.69
1	C	79	GLU	N-CA-C	-6.46	103.36	111.11
1	M	294	VAL	N-CA-C	6.45	116.87	108.35
1	K	47	PHE	CA-C-N	-6.45	111.49	122.33
1	K	47	PHE	C-N-CA	-6.45	111.49	122.33
1	I	273	LYS	N-CA-C	-6.44	105.37	113.23
1	M	294	VAL	CB-CA-C	-6.44	99.39	111.30
1	A	200	ASP	CA-C-N	-6.44	110.39	121.97
1	A	200	ASP	C-N-CA	-6.44	110.39	121.97
1	E	426	THR	N-CA-C	6.43	118.96	109.69
2	F	853	MET	N-CA-C	-6.43	104.19	111.07
1	M	114	LEU	N-CA-C	6.43	121.92	113.30
1	G	25	LEU	N-CA-CB	6.42	121.18	110.53
1	E	241	GLN	N-CA-C	6.42	119.64	109.50
1	G	248	GLY	N-CA-C	-6.42	105.66	114.64
1	M	194	SER	N-CA-C	6.41	117.46	109.57
1	A	391	TYR	N-CA-CB	-6.40	99.67	110.49
1	M	90	ILE	CB-CA-C	-6.40	101.30	110.83
1	A	244	LEU	N-CA-C	6.39	119.37	109.07
1	G	194	SER	N-CA-C	6.39	118.68	109.48
1	G	428	LYS	N-CA-C	-6.38	104.32	111.28
1	K	308	GLY	N-CA-C	-6.38	102.36	111.42
1	C	38	LEU	CA-CB-CG	-6.38	93.97	116.30
1	C	25	LEU	N-CA-CB	6.37	119.92	110.49
1	C	32	VAL	N-CA-C	-6.37	103.60	110.23
1	M	73	THR	N-CA-C	-6.37	97.99	108.76
1	O	259	CYS	N-CA-C	-6.36	101.00	109.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	273	LYS	N-CA-C	-6.36	105.48	113.23
1	M	33	ALA	N-CA-C	-6.34	104.06	110.97
1	E	260	PRO	N-CA-C	6.34	121.46	111.38
1	O	161	ARG	NE-CZ-NH1	-6.34	115.16	121.50
1	K	366	MET	N-CA-C	6.34	119.84	109.76
1	C	273	LYS	N-CA-C	-6.34	97.30	110.80
1	G	21	GLY	N-CA-C	-6.34	99.91	111.25
1	C	93	SER	CB-CA-C	-6.33	102.15	111.77
1	C	205	VAL	N-CA-C	6.33	117.88	106.61
1	E	17	PRO	N-CA-C	6.33	125.50	112.47
1	O	365	THR	N-CA-C	6.32	119.03	109.23
1	I	248	GLY	N-CA-C	-6.32	105.90	115.00
1	G	128	SER	N-CA-C	-6.32	99.07	108.99
1	C	52	LEU	CA-C-N	-6.31	111.28	122.07
1	C	52	LEU	C-N-CA	-6.31	111.28	122.07
1	K	267	GLY	CA-C-N	-6.30	115.37	123.19
1	K	267	GLY	C-N-CA	-6.30	115.37	123.19
1	M	375	ASN	N-CA-CB	6.30	117.41	110.35
1	C	274	VAL	N-CA-C	-6.30	102.03	108.96
1	K	16	ARG	CA-C-O	6.30	125.43	119.13
1	A	93	SER	CB-CA-C	-6.30	102.20	111.77
1	K	414	PHE	N-CA-CB	-6.29	101.11	110.17
1	C	294	VAL	CB-CA-C	-6.29	99.67	111.30
1	O	31	TRP	CA-C-O	6.28	129.50	120.51
1	K	280	PHE	N-CA-C	6.28	118.93	108.20
1	M	140	GLN	N-CA-C	6.28	118.92	111.33
1	K	304	LEU	CB-CA-C	-6.26	100.12	110.14
1	C	414	PHE	N-CA-CB	-6.26	101.41	110.36
1	G	235	SER	N-CA-C	6.26	119.79	110.52
1	C	103	VAL	CB-CA-C	-6.25	103.87	111.88
1	A	179	ILE	N-CA-C	6.25	117.93	108.80
1	K	230	ILE	CB-CA-C	-6.25	102.59	111.40
1	A	429	ASP	CA-C-O	-6.24	114.21	121.07
1	I	23	VAL	CA-C-N	-6.24	113.43	122.29
1	I	23	VAL	C-N-CA	-6.24	113.43	122.29
1	I	154	ARG	N-CA-C	6.24	124.08	110.80
1	K	42	GLN	N-CA-C	-6.24	105.50	113.23
1	K	50	VAL	N-CA-C	6.23	119.76	113.47
1	K	117	ARG	N-CA-C	-6.22	105.59	113.43
1	E	50	VAL	N-CA-CB	-6.22	103.76	112.35
1	K	183	GLY	N-CA-C	-6.22	104.81	112.77
1	M	259	CYS	N-CA-C	-6.22	101.19	109.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	241	GLN	N-CA-C	6.21	119.15	109.52
1	A	260	PRO	N-CA-C	6.20	121.24	111.38
1	K	235	SER	N-CA-C	6.20	120.15	110.17
1	M	256	SER	N-CA-C	6.20	118.98	110.24
1	E	234	ILE	N-CA-C	6.19	116.84	108.17
1	O	86	ASP	CA-C-N	-6.19	114.82	122.93
1	O	86	ASP	C-N-CA	-6.19	114.82	122.93
1	E	50	VAL	CA-C-O	6.19	124.35	118.90
1	G	22	PHE	N-CA-C	6.19	118.50	108.41
1	A	73	THR	CA-C-N	6.19	128.36	122.36
1	A	73	THR	C-N-CA	6.19	128.36	122.36
1	M	290	THR	N-CA-C	6.18	119.11	109.52
1	E	54	ASN	O-C-N	6.18	128.43	121.32
1	I	54	ASN	CA-C-N	6.18	127.56	119.84
1	I	54	ASN	C-N-CA	6.18	127.56	119.84
1	I	390	ASP	CB-CA-C	-6.18	100.58	110.84
1	K	365	THR	N-CA-C	6.17	119.30	108.75
1	G	284	THR	N-CA-C	6.17	118.80	110.29
1	A	183	GLY	N-CA-C	-6.17	104.61	113.86
1	I	427	PHE	CA-C-N	-6.16	112.22	120.54
1	I	427	PHE	C-N-CA	-6.16	112.22	120.54
1	K	154	ARG	N-CA-C	6.16	123.92	110.80
1	O	427	PHE	CA-C-N	-6.16	112.23	120.54
1	O	427	PHE	C-N-CA	-6.16	112.23	120.54
1	C	88	ASP	N-CA-C	-6.16	104.12	111.69
1	M	85	LYS	N-CA-C	-6.15	105.84	113.15
1	E	90	ILE	CB-CA-C	-6.14	102.56	110.98
1	O	109	HIS	N-CA-C	6.14	120.78	113.16
1	G	89	MET	CB-CG-SD	-6.14	94.28	112.70
1	G	309	ASP	CA-C-O	6.13	125.53	118.97
1	G	286	VAL	CB-CA-C	-6.12	102.56	111.68
1	M	44	SER	N-CA-C	-6.12	104.67	111.71
2	P	850	THR	CA-C-N	-6.12	114.28	122.72
2	P	850	THR	C-N-CA	-6.12	114.28	122.72
1	M	165	LEU	CB-CG-CD2	-6.11	92.36	110.70
1	G	90	ILE	N-CA-C	6.11	117.10	108.36
1	C	260	PRO	N-CA-C	6.11	121.76	111.32
1	E	297	ILE	N-CA-C	6.11	116.61	107.51
1	I	432	ILE	N-CA-C	-6.10	104.57	110.42
2	D	850	THR	CA-C-N	-6.09	114.31	122.72
2	D	850	THR	C-N-CA	-6.09	114.31	122.72
1	I	186	TYR	N-CA-C	-6.09	104.22	112.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	248	GLY	N-CA-C	-6.09	106.24	115.00
1	C	255	ILE	N-CA-CB	-6.08	101.48	111.45
1	C	64	ILE	N-CA-C	6.08	116.26	110.42
1	C	83	GLN	N-CA-C	6.07	120.82	113.41
1	E	261	ASP	N-CA-C	6.06	120.67	113.28
1	G	325	ILE	N-CA-CB	6.06	117.13	110.53
1	I	282	GLY	N-CA-C	6.06	122.17	114.66
1	G	16	ARG	CA-C-N	6.05	127.41	119.84
1	G	16	ARG	C-N-CA	6.05	127.41	119.84
1	A	86	ASP	CA-C-N	-6.05	114.88	123.11
1	A	86	ASP	C-N-CA	-6.05	114.88	123.11
1	A	385	TYR	N-CA-C	-6.05	104.77	111.36
1	O	15	SER	CA-CB-OG	6.05	123.20	111.10
1	A	18	ILE	CB-CA-C	-6.05	102.61	110.84
1	I	207	LEU	N-CA-C	6.04	118.36	111.11
1	E	250	ARG	CB-CA-C	-6.04	97.03	110.19
1	I	414	PHE	N-CA-C	6.04	119.51	107.62
1	K	428	LYS	N-CA-C	-6.03	104.61	111.07
1	E	151	LEU	N-CA-C	-6.03	101.21	109.71
1	C	91	VAL	N-CA-C	6.03	116.54	107.80
1	A	294	VAL	CB-CA-C	-6.02	100.34	111.18
1	K	271	ASN	N-CA-C	6.02	118.27	108.63
1	C	173	ASP	CA-C-N	-6.02	112.89	121.85
1	C	173	ASP	C-N-CA	-6.02	112.89	121.85
1	E	450	LEU	N-CA-C	6.01	119.85	110.17
1	O	186	TYR	N-CA-C	-6.01	104.33	112.26
1	A	83	GLN	N-CA-C	6.00	120.79	112.45
1	C	249	LYS	N-CA-C	-6.00	100.97	109.96
1	C	374	TYR	N-CA-C	-6.00	99.47	109.24
1	C	296	ASP	CA-C-O	5.98	126.86	120.46
1	C	368	VAL	CB-CA-C	-5.98	104.09	111.32
1	O	22	PHE	CA-C-O	5.98	126.90	120.32
1	G	79	GLU	N-CA-C	-5.98	104.10	111.33
1	C	259	CYS	CA-C-N	5.97	126.44	119.99
1	C	259	CYS	C-N-CA	5.97	126.44	119.99
1	E	25	LEU	CB-CA-C	5.97	121.71	111.68
1	M	17	PRO	N-CA-C	5.97	124.77	112.47
1	O	248	GLY	CA-C-N	-5.97	112.23	120.71
1	O	248	GLY	C-N-CA	-5.97	112.23	120.71
1	C	264	LEU	CB-CA-C	-5.97	99.41	109.50
1	A	302	GLY	N-CA-C	5.97	121.24	111.27
1	O	428	LYS	N-CA-C	-5.97	103.95	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	286	VAL	CB-CA-C	-5.97	102.79	111.68
1	I	378	VAL	N-CA-C	-5.97	107.07	111.90
1	I	257	LYS	CA-C-O	5.96	127.76	120.25
1	I	384	ILE	CB-CA-C	-5.96	104.22	112.02
1	C	50	VAL	N-CA-C	5.96	119.92	113.43
1	K	256	SER	CB-CA-C	-5.95	98.59	109.54
1	G	261	ASP	N-CA-C	5.95	120.54	113.28
1	M	261	ASP	N-CA-C	5.95	120.67	113.17
1	C	242	PHE	N-CA-C	5.94	119.21	109.76
1	E	102	VAL	CA-C-N	5.94	128.13	120.70
1	E	102	VAL	C-N-CA	5.94	128.13	120.70
1	K	50	VAL	N-CA-CB	-5.94	105.26	112.33
1	O	244	LEU	CA-C-O	5.94	127.00	120.71
1	C	21	GLY	N-CA-C	-5.93	100.63	111.25
1	K	148	ILE	N-CA-C	5.93	116.61	107.78
1	G	448	LYS	N-CA-CB	-5.93	102.02	111.62
1	A	376	SER	N-CA-CB	-5.92	101.39	110.16
1	M	22	PHE	N-CA-C	5.92	118.77	108.76
1	M	256	SER	CB-CA-C	-5.92	100.17	109.70
1	I	256	SER	N-CA-C	5.92	118.39	110.35
1	C	284	THR	N-CA-C	5.91	118.07	110.39
1	M	201	ILE	N-CA-C	5.91	121.63	109.34
1	E	43	LEU	N-CA-C	-5.91	104.46	112.26
1	K	225	SER	N-CA-C	-5.91	100.34	109.14
1	I	413	LYS	CA-C-N	5.91	131.88	123.14
1	I	413	LYS	C-N-CA	5.91	131.88	123.14
1	M	241	GLN	CB-CG-CD	-5.91	102.56	112.60
1	G	201	ILE	N-CA-C	5.90	121.62	109.34
1	K	181	GLY	N-CA-C	5.90	122.30	110.97
1	G	309	ASP	CA-C-N	-5.89	114.70	123.00
1	G	309	ASP	C-N-CA	-5.89	114.70	123.00
1	E	90	ILE	N-CA-C	5.89	116.59	107.99
1	I	173	ASP	N-CA-C	-5.89	102.60	110.55
1	C	384	ILE	CB-CA-C	-5.88	104.33	112.04
1	E	179	ILE	N-CA-C	5.88	118.65	108.95
1	A	223	THR	CB-CA-C	-5.88	101.41	110.81
1	O	90	ILE	CB-CA-C	-5.88	102.70	110.98
1	G	318	LEU	CB-CA-C	-5.87	107.06	114.40
1	E	114	LEU	N-CA-C	5.87	121.22	112.94
1	M	18	ILE	CB-CA-C	-5.87	103.63	110.91
1	G	84	TYR	N-CA-C	-5.87	101.96	110.64
1	O	307	GLU	N-CA-C	5.87	119.08	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	201	ILE	N-CA-C	5.86	121.54	109.34
1	K	207	LEU	N-CA-C	5.86	118.17	111.02
2	J	851	THR	N-CA-C	5.86	118.22	109.25
1	G	375	ASN	CB-CA-C	-5.86	102.89	112.03
1	C	448	LYS	N-CA-CB	-5.86	100.63	111.52
1	A	428	LYS	CA-C-N	-5.85	112.65	120.79
1	A	428	LYS	C-N-CA	-5.85	112.65	120.79
1	C	319	VAL	CA-C-N	-5.85	113.25	122.73
1	C	319	VAL	C-N-CA	-5.85	113.25	122.73
1	M	103	VAL	N-CA-C	5.85	116.50	110.36
1	A	301	LYS	N-CA-C	-5.85	106.12	113.72
1	A	386	GLU	N-CA-CB	5.84	118.44	109.91
1	K	374	TYR	N-CA-C	-5.83	101.05	110.32
1	C	250	ARG	CB-CA-C	-5.83	98.33	110.40
1	M	16	ARG	O-C-N	5.83	126.39	121.84
1	E	455	ILE	CB-CA-C	5.83	120.85	111.29
1	M	322	PHE	N-CA-C	-5.83	100.44	109.24
1	O	80	SER	N-CA-C	-5.83	104.83	111.07
1	M	67	LEU	N-CA-C	-5.83	106.14	113.72
1	G	161	ARG	NE-CZ-NH1	-5.83	115.67	121.50
1	G	162	ALA	N-CA-C	-5.83	104.56	111.03
1	I	73	THR	N-CA-C	-5.83	98.92	108.76
1	K	155	LYS	N-CA-C	5.82	120.37	113.16
1	G	426	THR	N-CA-C	5.81	118.32	109.95
1	K	321	TYR	CA-C-N	-5.81	113.06	122.82
1	K	321	TYR	C-N-CA	-5.81	113.06	122.82
1	M	83	GLN	N-CA-C	5.81	120.38	113.12
1	A	271	ASN	CB-CA-C	-5.80	98.88	110.42
1	G	297	ILE	N-CA-CB	-5.80	104.03	110.99
1	G	311	GLY	CA-C-N	-5.79	115.03	122.79
1	G	311	GLY	C-N-CA	-5.79	115.03	122.79
1	M	416	LYS	CA-C-O	-5.79	115.03	121.23
1	I	271	ASN	N-CA-C	5.78	118.87	108.17
1	G	122	GLU	N-CA-C	5.78	119.10	110.14
1	M	231	ASN	N-CA-C	5.78	118.92	108.69
1	M	274	VAL	N-CA-C	-5.78	102.66	108.96
1	I	259	CYS	CA-C-O	-5.78	114.40	120.70
1	A	388	ILE	CB-CG1-CD1	-5.78	101.67	113.80
1	C	325	ILE	N-CA-CB	5.78	117.23	110.82
1	E	211	SER	N-CA-C	5.77	118.32	111.33
1	I	442	ARG	CG-CD-NE	-5.77	99.30	112.00
1	G	88	ASP	CA-C-N	-5.77	112.64	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	88	ASP	C-N-CA	-5.77	112.64	122.33
1	G	416	LYS	N-CA-C	-5.76	100.18	108.60
1	E	380	ASN	N-CA-C	5.76	118.05	111.02
1	K	371	LEU	CB-CG-CD1	-5.76	93.42	110.70
1	M	25	LEU	N-CA-CB	5.76	120.09	110.53
1	K	64	ILE	N-CA-C	5.76	117.19	110.62
1	C	128	SER	N-CA-C	-5.76	100.31	109.23
1	C	126	ALA	N-CA-C	-5.75	100.81	108.34
1	C	245	ASP	CB-CA-C	5.75	119.48	109.65
1	E	256	SER	CB-CA-C	-5.74	99.00	110.42
1	G	313	VAL	CA-C-N	5.74	128.55	120.28
1	G	313	VAL	C-N-CA	5.74	128.55	120.28
1	O	74	GLY	N-CA-C	5.73	122.80	112.54
1	E	173	ASP	N-CA-C	-5.73	100.33	109.96
1	O	39	ALA	CA-C-O	-5.73	114.77	120.90
1	K	22	PHE	N-CA-C	5.73	117.75	108.41
1	O	50	VAL	N-CA-CB	-5.73	104.39	112.12
1	C	43	LEU	N-CA-C	-5.73	103.11	111.30
1	I	268	ILE	N-CA-C	5.72	115.84	107.37
1	O	440	VAL	CB-CA-C	-5.72	104.38	111.70
1	G	186	TYR	N-CA-C	-5.70	103.84	111.87
1	E	249	LYS	N-CA-C	-5.69	101.42	109.96
1	G	255	ILE	N-CA-CB	-5.69	101.61	111.63
1	G	260	PRO	N-CA-C	5.69	120.22	111.57
1	C	86	ASP	CA-C-N	-5.69	115.48	122.93
1	C	86	ASP	C-N-CA	-5.69	115.48	122.93
1	E	129	VAL	CB-CA-C	5.68	118.91	111.81
1	G	64	ILE	CB-CA-C	-5.68	104.61	111.88
1	C	293	LEU	CA-CB-CG	-5.68	96.43	116.30
1	I	444	ASP	N-CA-C	-5.68	105.01	111.14
1	K	440	VAL	CG1-CB-CG2	5.68	123.29	110.80
1	G	49	ILE	N-CA-C	-5.67	100.41	108.58
1	C	235	SER	N-CA-C	5.67	119.34	110.32
1	A	295	ILE	CB-CA-C	-5.66	104.81	111.09
1	G	153	GLY	N-CA-C	-5.66	99.78	113.18
1	G	43	LEU	CB-CG-CD1	5.64	127.64	110.70
1	C	41	GLN	CB-CA-C	-5.64	98.89	109.72
1	E	32	VAL	N-CA-CB	-5.64	101.00	110.65
1	M	302	GLY	N-CA-C	5.64	119.94	111.42
1	E	185	TRP	N-CA-C	5.64	119.15	112.72
1	C	376	SER	CA-C-O	5.63	126.45	119.97
1	G	277	SER	CB-CA-C	-5.63	100.45	109.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	435	ARG	N-CA-CB	-5.63	101.55	109.94
1	K	440	VAL	CB-CA-C	-5.63	102.06	111.29
1	O	450	LEU	N-CA-C	5.62	118.65	109.59
1	O	183	GLY	N-CA-C	-5.62	99.86	113.18
1	O	200	ASP	CA-C-O	5.62	126.95	120.60
1	O	442	ARG	CA-C-O	5.62	126.51	120.55
1	E	177	ILE	CA-CB-CG2	-5.62	100.95	110.50
1	K	57	LEU	CA-CB-CG	-5.62	96.65	116.30
1	O	115	ASN	CA-C-N	-5.62	112.33	121.26
1	O	115	ASN	C-N-CA	-5.62	112.33	121.26
1	G	17	PRO	N-CA-C	5.61	124.03	112.47
1	G	155	LYS	N-CA-C	5.61	120.12	113.16
1	E	445	LYS	CB-CA-C	-5.61	101.15	110.68
1	M	16	ARG	CA-C-O	5.61	124.74	119.13
1	K	89	MET	N-CA-C	5.60	118.61	108.69
1	M	267	GLY	O-C-N	-5.60	118.55	123.76
1	E	68	GLN	N-CA-CB	-5.60	103.40	111.91
1	O	414	PHE	N-CA-CB	-5.60	101.51	110.63
1	C	376	SER	N-CA-CB	-5.60	101.61	110.28
1	C	147	THR	CB-CA-C	-5.59	99.14	109.37
1	G	86	ASP	CA-C-N	-5.59	115.51	123.11
1	G	86	ASP	C-N-CA	-5.59	115.51	123.11
1	G	18	ILE	CB-CA-C	-5.58	103.11	110.98
1	E	319	VAL	CA-C-N	-5.58	114.15	122.74
1	E	319	VAL	C-N-CA	-5.58	114.15	122.74
1	O	264	LEU	CB-CA-C	-5.58	100.07	109.72
1	E	193	ARG	N-CA-C	5.57	119.34	112.54
1	K	307	GLU	CA-C-N	-5.57	117.21	122.17
1	K	307	GLU	C-N-CA	-5.57	117.21	122.17
1	C	254	THR	N-CA-CB	-5.57	101.16	111.52
1	I	59	SER	N-CA-C	5.57	117.43	111.36
1	O	71	HIS	N-CA-C	5.57	119.91	113.18
1	A	238	ILE	CB-CA-C	-5.56	105.79	111.08
1	G	319	VAL	O-C-N	-5.56	116.63	123.03
1	O	290	THR	N-CA-C	5.56	117.64	109.24
1	A	151	LEU	N-CA-C	-5.56	103.65	110.65
1	I	161	ARG	N-CA-C	5.55	118.09	111.71
1	I	307	GLU	CA-C-N	-5.54	115.61	121.48
1	I	307	GLU	C-N-CA	-5.54	115.61	121.48
2	H	853	MET	N-CA-C	-5.54	105.25	111.28
1	E	315	ILE	CB-CA-C	-5.53	102.22	111.29
1	E	427	PHE	CA-C-N	-5.53	113.25	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	427	PHE	C-N-CA	-5.53	113.25	120.44
2	D	853	MET	N-CA-C	-5.53	105.26	111.28
1	K	291	LYS	N-CA-C	-5.52	102.11	110.28
1	G	391	TYR	N-CA-C	-5.52	105.26	111.28
1	E	216	ILE	CB-CA-C	-5.52	104.69	112.14
1	K	301	LYS	CA-C-N	-5.52	113.30	120.91
1	K	301	LYS	C-N-CA	-5.52	113.30	120.91
1	A	159	ILE	CB-CA-C	-5.51	102.25	111.29
1	I	223	THR	CB-CA-C	-5.51	102.22	110.88
1	A	19	ARG	CA-CB-CG	-5.51	103.08	114.10
1	G	280	PHE	N-CA-C	5.51	118.54	107.41
1	M	190	ARG	NE-CZ-NH1	-5.51	115.99	121.50
1	A	179	ILE	N-CA-CB	-5.50	104.81	112.52
1	I	438	ASP	N-CA-C	-5.50	105.28	111.28
1	O	122	GLU	N-CA-C	5.50	118.67	110.14
1	A	306	ILE	CG1-CB-CG2	5.50	127.20	110.70
1	O	192	MET	N-CA-C	5.50	117.71	111.11
1	C	321	TYR	CA-C-N	-5.50	113.31	122.21
1	C	321	TYR	C-N-CA	-5.50	113.31	122.21
1	A	49	ILE	N-CA-CB	5.50	117.64	111.21
1	O	17	PRO	N-CA-C	5.49	123.78	112.47
1	O	24	GLY	N-CA-C	-5.49	107.01	116.01
1	A	154	ARG	NE-CZ-NH1	-5.49	116.02	121.50
1	E	166	ILE	N-CA-C	5.49	115.62	110.30
1	I	123	TRP	CA-C-N	5.49	131.57	121.70
1	I	123	TRP	C-N-CA	5.49	131.57	121.70
1	A	266	GLN	N-CA-C	-5.48	100.96	109.24
1	M	417	GLN	CB-CG-CD	-5.48	103.28	112.60
1	A	107	LEU	N-CA-C	5.47	117.68	111.11
1	K	140	GLN	N-CA-C	5.47	120.40	111.37
1	A	116	LEU	N-CA-C	-5.47	99.14	110.80
1	E	92	VAL	N-CA-C	5.47	114.62	106.85
1	I	225	SER	CA-CB-OG	-5.47	100.16	111.10
1	G	264	LEU	CB-CG-CD2	-5.47	94.29	110.70
1	K	223	THR	N-CA-C	-5.47	105.22	111.07
1	G	238	ILE	O-C-N	5.46	126.20	120.96
1	I	307	GLU	N-CA-C	5.46	118.36	108.69
1	G	431	ILE	N-CA-C	5.45	115.66	110.53
1	C	75	PHE	N-CA-C	5.45	118.58	110.14
1	O	179	ILE	N-CA-C	5.45	117.74	108.86
1	I	243	LEU	CB-CG-CD2	-5.45	94.37	110.70
2	N	855	ASP	N-CA-C	-5.44	105.04	110.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	271	ASN	N-CA-C	5.44	122.39	110.80
1	K	165	LEU	CA-C-N	5.44	127.36	120.72
1	K	165	LEU	C-N-CA	5.44	127.36	120.72
1	K	438	ASP	N-CA-C	-5.44	105.35	111.28
1	M	79	GLU	N-CA-C	-5.44	102.45	111.37
1	C	50	VAL	N-CA-CB	-5.44	106.23	112.21
1	K	31	TRP	CA-C-N	5.44	127.91	120.46
1	K	31	TRP	C-N-CA	5.44	127.91	120.46
1	K	250	ARG	CB-CG-CD	-5.44	98.79	111.30
1	O	150	CYS	N-CA-C	5.44	118.02	108.56
1	M	182	ASN	N-CA-C	5.43	117.20	107.80
1	O	25	LEU	CA-CB-CG	-5.43	97.29	116.30
1	C	365	THR	N-CA-C	5.43	117.64	109.23
1	G	85	LYS	N-CA-C	-5.43	106.51	113.02
1	I	201	ILE	N-CA-C	5.43	120.63	109.34
1	C	188	TYR	CA-C-O	5.42	125.91	119.56
1	I	150	CYS	N-CA-C	5.42	118.02	109.39
1	A	123	TRP	N-CA-C	-5.42	101.83	109.96
1	K	433	LEU	N-CA-C	-5.42	99.25	110.80
1	A	61	LEU	CB-CG-CD2	-5.42	94.44	110.70
1	O	155	LYS	N-CA-C	5.42	119.58	112.92
1	A	191	PRO	CB-CA-C	-5.41	101.71	110.21
1	C	256	SER	CB-CA-C	-5.41	99.93	109.62
1	O	235	SER	N-CA-C	5.41	118.64	109.76
1	G	44	SER	N-CA-C	-5.41	105.49	111.71
1	G	290	THR	N-CA-C	5.41	117.07	108.79
1	O	140	GLN	N-CA-C	5.41	120.30	111.37
1	O	52	LEU	CA-C-N	-5.41	114.16	122.87
1	O	52	LEU	C-N-CA	-5.41	114.16	122.87
1	M	313	VAL	CB-CA-C	-5.41	103.78	112.16
1	A	321	TYR	CA-C-N	-5.41	114.10	122.59
1	A	321	TYR	C-N-CA	-5.41	114.10	122.59
1	G	444	ASP	N-CA-C	-5.41	105.08	110.97
1	I	384	ILE	N-CA-CB	5.40	117.48	110.57
1	M	308	GLY	N-CA-C	-5.40	103.25	111.14
1	E	98	GLU	N-CA-C	-5.40	106.54	113.02
1	E	376	SER	N-CA-CB	-5.40	102.18	110.12
1	M	228	GLN	N-CA-C	-5.40	102.81	111.02
1	E	59	SER	N-CA-C	5.40	118.08	111.82
1	E	367	GLU	N-CA-C	5.39	117.86	108.76
1	K	59	SER	N-CA-C	5.39	117.15	111.28
1	A	23	VAL	N-CA-C	-5.39	100.63	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	88	ASP	CA-C-N	-5.38	113.28	122.33
1	C	88	ASP	C-N-CA	-5.38	113.28	122.33
1	K	145	LEU	N-CA-C	5.38	117.30	108.52
1	O	250	ARG	CB-CA-C	-5.38	101.16	113.33
1	K	245	ASP	CB-CA-C	5.38	118.61	109.84
1	I	117	ARG	N-CA-C	-5.38	106.65	113.43
1	M	20	VAL	CA-C-N	-5.38	116.57	122.38
1	M	20	VAL	C-N-CA	-5.38	116.57	122.38
1	K	118	TYR	N-CA-C	5.37	117.66	108.90
1	E	454	LYS	N-CA-C	-5.36	107.39	114.04
1	K	285	PRO	N-CD-CG	-5.36	97.37	103.80
1	K	138	ILE	CB-CA-C	-5.36	105.12	111.81
1	K	141	GLN	N-CA-C	5.35	117.86	111.71
1	M	279	SER	N-CA-CB	5.34	118.96	110.84
1	K	416	LYS	CA-C-N	-5.34	111.60	120.68
1	K	416	LYS	C-N-CA	-5.34	111.60	120.68
1	G	179	ILE	CB-CA-C	-5.34	101.42	111.30
1	A	43	LEU	N-CA-C	-5.34	105.04	112.30
1	G	313	VAL	CB-CA-C	-5.34	103.89	112.16
1	O	90	ILE	N-CA-C	5.33	116.66	108.71
1	C	55	PRO	CA-C-N	-5.33	114.67	122.19
1	C	55	PRO	C-N-CA	-5.33	114.67	122.19
1	C	102	VAL	N-CA-C	5.33	120.43	109.34
1	I	448	LYS	N-CA-CB	-5.33	102.41	111.69
1	E	156	SER	O-C-N	5.33	126.04	121.30
1	A	129	VAL	CB-CA-C	5.32	120.02	111.29
1	M	164	GLU	CB-CA-C	-5.32	101.81	110.85
1	O	161	ARG	NE-CZ-NH2	5.32	123.99	119.20
1	O	230	ILE	N-CA-C	5.32	115.30	107.75
1	E	119	LEU	CB-CA-C	-5.32	102.59	110.62
1	K	370	HIS	N-CA-C	-5.32	100.99	109.23
1	I	232	ALA	N-CA-C	5.31	117.90	109.50
1	I	372	ARG	N-CA-C	5.31	118.50	110.64
1	A	22	PHE	N-CA-C	5.31	117.07	108.41
1	E	174	ILE	CB-CA-C	-5.31	103.95	111.28
1	I	386	GLU	CA-C-O	-5.31	115.23	121.07
1	A	85	LYS	N-CA-C	-5.30	107.35	112.97
1	E	86	ASP	CA-C-N	-5.30	116.02	123.13
1	E	86	ASP	C-N-CA	-5.30	116.02	123.13
1	O	302	GLY	N-CA-C	5.30	118.27	110.80
1	C	378	VAL	N-CA-C	-5.30	107.61	111.90
1	I	16	ARG	CA-C-N	5.30	126.46	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	16	ARG	C-N-CA	5.30	126.46	119.84
1	O	365	THR	N-CA-CB	-5.30	101.68	111.53
1	K	449	THR	N-CA-C	-5.29	99.78	108.41
1	E	327	ASN	N-CA-C	5.29	122.08	110.80
1	M	417	GLN	CA-C-O	5.29	126.04	119.79
1	G	183	GLY	N-CA-C	-5.29	106.00	112.77
1	K	87	ILE	CB-CA-C	-5.29	103.83	111.19
1	E	145	LEU	CB-CG-CD2	-5.29	94.84	110.70
1	E	368	VAL	CB-CA-C	-5.29	103.27	110.77
1	E	428	LYS	N-CA-C	-5.28	105.42	111.07
1	G	166	ILE	N-CA-C	5.28	115.38	110.42
1	E	177	ILE	CB-CA-C	-5.28	101.94	110.28
1	E	56	THR	CB-CA-C	-5.28	100.15	109.70
1	K	21	GLY	N-CA-C	-5.28	100.68	113.18
1	C	267	GLY	CA-C-N	-5.27	116.27	123.12
1	C	267	GLY	C-N-CA	-5.27	116.27	123.12
1	E	58	LYS	CD-CE-NZ	5.27	128.75	111.90
1	E	27	SER	CA-CB-OG	-5.26	100.57	111.10
1	G	156	SER	N-CA-C	5.26	121.44	109.81
1	A	27	SER	CB-CA-C	-5.26	101.40	112.82
1	A	201	ILE	N-CA-C	5.26	120.28	109.34
1	C	438	ASP	CA-C-O	5.26	126.81	120.92
1	O	260	PRO	N-CA-C	5.26	119.57	111.57
1	C	116	LEU	N-CA-C	-5.26	99.60	110.80
1	G	63	THR	CA-C-N	-5.26	113.82	120.60
1	G	63	THR	C-N-CA	-5.26	113.82	120.60
1	A	370	HIS	N-CA-C	-5.26	100.12	109.06
1	G	49	ILE	N-CA-CB	5.25	116.45	110.72
1	O	319	VAL	CA-C-N	-5.25	114.65	122.74
1	O	319	VAL	C-N-CA	-5.25	114.65	122.74
1	I	39	ALA	N-CA-C	-5.25	105.56	111.28
1	C	103	VAL	O-C-N	5.25	127.19	121.94
1	M	284	THR	N-CA-C	5.24	118.47	110.50
1	C	49	ILE	CB-CA-C	-5.24	103.80	110.98
1	G	126	ALA	N-CA-C	-5.24	101.47	108.34
1	G	173	ASP	CA-C-N	-5.24	113.45	120.95
1	G	173	ASP	C-N-CA	-5.24	113.45	120.95
1	O	304	LEU	CB-CA-C	-5.24	101.75	110.14
1	I	27	SER	N-CA-CB	-5.24	103.34	111.35
1	O	440	VAL	N-CA-C	-5.24	104.78	110.23
1	E	293	LEU	N-CA-C	5.24	117.34	108.02
1	I	148	ILE	CB-CA-C	-5.24	104.44	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	384	ILE	N-CA-C	-5.24	105.74	110.82
1	I	385	TYR	N-CA-C	-5.23	105.00	111.33
1	A	128	SER	N-CA-C	-5.23	100.78	108.99
1	E	32	VAL	CA-C-O	5.23	126.17	120.57
1	C	255	ILE	N-CA-C	5.23	116.19	108.45
1	K	368	VAL	N-CA-CB	5.23	118.49	111.90
1	M	95	LYS	CB-CA-C	-5.23	100.02	110.42
1	K	41	GLN	N-CA-CB	-5.22	102.29	110.44
1	I	128	SER	N-CA-C	-5.22	101.14	109.23
1	I	135	LEU	CA-C-N	-5.22	113.53	120.63
1	I	135	LEU	C-N-CA	-5.22	113.53	120.63
1	I	271	ASN	CB-CA-C	-5.22	102.80	111.41
1	G	61	LEU	N-CA-C	5.22	119.13	112.87
1	A	122	GLU	N-CA-C	5.22	118.23	110.14
1	C	22	PHE	N-CA-C	5.22	116.91	108.41
1	E	27	SER	N-CA-CB	-5.22	103.37	111.35
1	C	76	ASP	N-CA-C	-5.21	107.58	114.04
1	G	176	SER	N-CA-C	5.21	118.22	110.14
1	E	268	ILE	N-CA-C	5.21	115.36	107.80
1	A	161	ARG	NE-CZ-NH2	5.21	123.89	119.20
1	K	302	GLY	N-CA-C	5.21	117.61	110.69
1	A	320	LEU	N-CA-C	5.20	116.88	108.41
1	I	261	ASP	N-CA-C	5.20	119.61	113.16
1	M	307	GLU	N-CA-C	5.20	117.89	108.69
1	C	308	GLY	N-CA-C	-5.20	103.56	111.14
1	G	256	SER	CB-CA-C	-5.19	100.45	109.64
1	E	16	ARG	CB-CG-CD	-5.19	99.36	111.30
1	K	248	GLY	CA-C-N	-5.19	113.50	120.87
1	K	248	GLY	C-N-CA	-5.19	113.50	120.87
1	C	369	PHE	CB-CA-C	-5.19	103.02	111.68
1	I	297	ILE	CB-CA-C	-5.18	103.88	110.98
1	G	164	GLU	CB-CA-C	-5.17	102.20	110.79
1	K	95	LYS	CB-CA-C	-5.17	100.12	110.42
1	I	218	VAL	CB-CA-C	-5.17	105.16	112.14
1	A	280	PHE	CB-CA-C	-5.17	102.33	111.22
1	E	88	ASP	CA-C-N	-5.17	113.48	122.37
1	E	88	ASP	C-N-CA	-5.17	113.48	122.37
1	E	278	CYS	CB-CA-C	-5.17	102.70	110.24
1	M	208	ILE	O-C-N	5.17	129.03	122.57
1	E	270	GLU	N-CA-C	-5.16	105.34	110.97
1	K	115	ASN	CA-C-N	-5.16	113.38	121.02
1	K	115	ASN	C-N-CA	-5.16	113.38	121.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	222	ILE	CB-CG1-CD1	-5.16	102.97	113.80
1	A	161	ARG	N-CA-C	5.16	117.57	111.33
1	O	280	PHE	N-CA-C	5.16	117.78	107.62
1	E	140	GLN	N-CA-C	5.15	121.77	110.80
1	K	17	PRO	N-CA-C	5.15	123.08	112.47
1	K	62	GLN	O-C-N	5.15	127.59	122.03
1	C	244	LEU	N-CA-C	5.15	117.36	109.07
1	E	16	ARG	NE-CZ-NH1	-5.15	116.35	121.50
1	C	185	TRP	N-CA-C	5.14	118.58	112.72
1	G	181	GLY	N-CA-C	5.14	118.78	111.12
1	O	223	THR	N-CA-C	-5.14	105.57	111.07
2	F	850	THR	CA-C-N	-5.14	115.94	122.77
2	F	850	THR	C-N-CA	-5.14	115.94	122.77
1	K	19	ARG	CG-CD-NE	-5.14	100.70	112.00
1	A	287	LYS	N-CA-C	-5.13	102.45	110.10
1	I	230	ILE	N-CA-C	5.13	115.04	107.75
1	O	320	LEU	CB-CG-CD1	-5.13	95.30	110.70
1	G	116	LEU	CA-CB-CG	-5.13	98.33	116.30
1	G	87	ILE	CB-CA-C	-5.13	104.06	111.19
1	A	242	PHE	CA-C-N	-5.13	115.01	122.65
1	A	242	PHE	C-N-CA	-5.13	115.01	122.65
1	G	255	ILE	N-CA-C	5.13	115.30	108.27
1	I	193	ARG	N-CA-C	5.13	118.69	112.23
1	G	80	SER	N-CA-C	-5.13	104.96	111.11
1	G	307	GLU	N-CA-C	5.13	116.77	108.26
1	I	319	VAL	CB-CA-C	-5.12	101.82	111.30
1	C	440	VAL	N-CA-CB	-5.12	104.07	110.47
2	P	852	THR	N-CA-C	-5.12	101.92	110.17
1	A	194	SER	N-CA-C	5.12	115.87	109.57
1	G	254	THR	N-CA-CB	-5.12	101.99	111.52
1	I	388	ILE	N-CA-C	-5.12	106.08	110.74
1	O	252	LYS	CB-CA-C	5.12	120.61	110.42
1	C	433	LEU	O-C-N	5.12	127.56	122.08
1	O	234	ILE	CG1-CB-CG2	-5.12	95.35	110.70
1	A	306	ILE	CB-CA-C	-5.12	103.06	110.63
1	M	138	ILE	CB-CA-C	-5.12	105.27	111.87
1	M	211	SER	N-CA-CB	5.12	119.14	110.49
1	C	183	GLY	N-CA-C	-5.11	106.52	113.37
1	K	317	ASN	N-CA-C	-5.11	101.42	109.25
1	O	18	ILE	N-CA-CB	5.11	117.62	110.56
1	C	140	GLN	N-CA-C	5.11	121.69	110.80
1	K	378	VAL	CB-CA-C	-5.11	106.56	111.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	250	ARG	CB-CA-C	-5.11	99.83	110.40
1	E	378	VAL	CA-C-O	5.10	126.13	120.46
1	K	31	TRP	CB-CA-C	-5.10	100.27	110.42
1	O	420	ARG	N-CA-C	5.10	117.62	110.23
1	C	102	VAL	CA-C-N	5.09	127.17	120.60
1	C	102	VAL	C-N-CA	5.09	127.17	120.60
1	K	292	ASN	CA-C-N	-5.09	114.85	122.39
1	K	292	ASN	C-N-CA	-5.09	114.85	122.39
1	A	229	LYS	CA-C-N	-5.09	116.41	122.11
1	A	229	LYS	C-N-CA	-5.09	116.41	122.11
1	I	22	PHE	N-CA-C	5.09	117.09	108.02
1	G	271	ASN	CA-C-N	-5.09	117.90	123.30
1	G	271	ASN	C-N-CA	-5.09	117.90	123.30
1	E	271	ASN	CB-CA-C	-5.09	100.29	110.42
1	E	419	PHE	O-C-N	5.09	128.61	122.35
1	E	192	MET	N-CA-C	5.08	117.22	111.02
1	K	293	LEU	CA-CB-CG	-5.08	98.51	116.30
1	A	429	ASP	OD1-CG-OD2	5.08	135.09	122.90
1	G	319	VAL	CA-C-O	5.08	126.07	120.64
1	M	36	HIS	CA-C-O	-5.07	115.17	120.55
1	I	301	LYS	N-CA-C	-5.07	106.50	113.30
1	I	111	SER	N-CA-C	-5.07	106.36	112.54
1	G	242	PHE	N-CA-C	5.07	117.81	109.76
1	K	380	ASN	CA-C-N	-5.07	113.50	120.74
1	K	380	ASN	C-N-CA	-5.07	113.50	120.74
1	A	419	PHE	CA-C-O	5.06	124.85	119.34
1	I	153	GLY	N-CA-C	-5.06	101.19	113.18
1	C	198	LEU	N-CA-C	-5.06	105.21	111.33
1	E	146	GLN	N-CA-C	-5.06	101.00	109.24
1	K	173	ASP	N-CA-C	-5.06	103.72	110.55
1	E	158	TYR	N-CA-C	5.05	117.52	111.71
1	I	239	PRO	CB-CA-C	5.05	116.11	109.89
1	O	391	TYR	N-CA-C	-5.05	105.67	111.07
1	A	225	SER	CA-CB-OG	-5.05	101.00	111.10
1	K	324	GLY	CA-C-N	-5.05	114.69	121.66
1	K	324	GLY	C-N-CA	-5.05	114.69	121.66
1	O	95	LYS	CB-CA-C	-5.05	100.37	110.42
1	O	148	ILE	CB-CA-C	-5.05	104.65	110.41
1	C	256	SER	N-CA-C	5.05	117.22	110.35
1	E	314	GLU	N-CA-C	-5.05	105.78	111.28
1	I	297	ILE	N-CA-CB	-5.04	105.31	111.21
1	O	158	TYR	N-CA-C	5.04	118.53	112.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	84	TYR	N-CA-CB	-5.04	101.97	110.49
1	E	289	LEU	CB-CA-C	5.04	118.69	110.17
1	K	91	VAL	CA-CB-CG2	-5.03	101.85	110.40
1	M	62	GLN	CB-CA-C	-5.03	103.15	110.95
1	M	93	SER	CB-CA-C	-5.03	103.42	111.17
1	A	327	ASN	N-CA-C	5.03	121.51	110.80
1	C	260	PRO	O-C-N	5.03	129.39	123.06
1	I	54	ASN	N-CA-C	-5.03	98.70	109.81
1	E	325	ILE	O-C-N	5.02	128.15	122.68
1	O	195	PRO	CB-CA-C	-5.02	106.09	111.56
1	O	265	PHE	N-CA-CB	-5.02	102.05	111.13
1	C	198	LEU	CB-CG-CD2	5.02	125.75	110.70
1	E	183	GLY	N-CA-C	-5.02	106.65	113.37
1	K	156	SER	N-CA-C	5.02	118.52	109.44
1	M	15	SER	N-CA-C	-5.02	100.11	110.80
1	K	366	MET	CA-C-N	-5.01	115.42	122.94
1	K	366	MET	C-N-CA	-5.01	115.42	122.94
1	O	22	PHE	CA-C-N	-5.01	116.61	123.12
1	O	22	PHE	C-N-CA	-5.01	116.61	123.12
1	O	244	LEU	CA-C-N	-5.01	114.25	121.42
1	O	244	LEU	C-N-CA	-5.01	114.25	121.42
1	I	141	GLN	N-CA-C	5.01	117.47	111.71
1	E	370	HIS	N-CA-C	-5.00	100.55	109.06
1	M	244	LEU	CA-C-N	-5.00	113.89	121.05
1	M	244	LEU	C-N-CA	-5.00	113.89	121.05
1	E	416	LYS	N-CA-C	-5.00	101.14	108.79

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	O	321	TYR	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3153	0	3158	502	0
1	C	3136	0	3141	483	0
1	E	3136	0	3139	488	0
1	G	3136	0	3141	496	0
1	I	3136	0	3141	443	0
1	K	3136	0	3141	411	0
1	M	3136	0	3141	388	0
1	O	3136	0	3141	454	0
2	B	119	0	107	19	0
2	D	119	0	107	9	0
2	F	119	0	107	8	0
2	H	119	0	107	10	0
2	J	119	0	107	13	0
2	L	119	0	107	12	0
2	N	119	0	107	11	0
2	P	119	0	107	11	0
All	All	26057	0	25999	3622	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 70.

All (3622) 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:C:452:VAL:HG13	1:C:455:ILE:CD1	1.46	1.43
1:C:452:VAL:CG1	1:C:455:ILE:HD12	1.47	1.43
1:E:198:LEU:HD13	1:E:199:TYR:CE1	1.57	1.38
1:E:194:SER:HB3	1:E:199:TYR:OH	1.20	1.27
1:I:281:LYS:HD2	1:I:282:GLY:N	1.51	1.23
1:G:392:HIS:CD2	1:G:393:PHE:CE2	2.25	1.23
1:I:228:GLN:NE2	1:I:273:LYS:HE3	1.53	1.21
1:I:390:ASP:O	1:I:394:LEU:HB2	1.41	1.20
1:G:392:HIS:CD2	1:G:393:PHE:CD2	2.32	1.17
1:M:390:ASP:O	1:M:394:LEU:HB2	1.44	1.16
1:E:433:LEU:O	1:E:437:ILE:HD12	1.45	1.15
1:O:68:GLN:HE21	1:O:68:GLN:HA	1.02	1.14
1:E:198:LEU:HD12	1:E:198:LEU:H	1.09	1.14
1:O:390:ASP:O	1:O:394:LEU:HB2	1.49	1.11
1:E:198:LEU:HD13	1:E:199:TYR:CD1	1.84	1.11
1:G:281:LYS:NZ	1:G:285:PRO:O	1.84	1.11
1:G:123:TRP:CD1	1:G:214:HIS:CD2	2.39	1.11
1:I:281:LYS:HD2	1:I:282:GLY:H	1.01	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:LEU:HD12	1:A:250:ARG:HA	1.34	1.09
1:G:392:HIS:NE2	1:G:393:PHE:CE2	2.21	1.09
1:K:238:ILE:HD12	1:K:261:ASP:HB2	1.35	1.09
1:E:387:SER:OG	1:E:423:GLY:O	1.71	1.08
1:I:252:LYS:H	1:I:252:LYS:HD2	0.99	1.08
1:I:192:MET:HE2	1:I:243:LEU:HD22	1.34	1.08
1:M:244:LEU:HD23	1:M:248:GLY:HA2	1.30	1.08
1:G:219:LEU:HA	1:G:222:ILE:HD12	1.30	1.08
1:O:244:LEU:HD12	1:O:250:ARG:HA	1.36	1.08
1:O:68:GLN:HE21	1:O:68:GLN:CA	1.61	1.08
1:A:168:GLU:O	1:A:328:GLY:O	1.70	1.07
1:E:192:MET:HE1	1:O:15:SER:HB3	1.36	1.07
1:I:53:TYR:C	1:I:53:TYR:CD2	2.30	1.07
1:O:208:ILE:HG22	1:O:209:SER:N	1.35	1.06
1:E:390:ASP:O	1:E:394:LEU:HB2	1.55	1.06
1:G:123:TRP:CD1	1:G:214:HIS:HD2	1.74	1.06
1:G:177:ILE:C	1:G:178:GLU:HG3	1.79	1.06
1:K:452:VAL:HG13	1:K:455:ILE:HG13	1.35	1.06
1:E:102:VAL:O	1:E:106:ILE:CD1	2.03	1.06
1:O:208:ILE:CG2	1:O:209:SER:N	2.12	1.06
1:A:145:LEU:O	1:A:413:LYS:HD3	1.55	1.05
1:I:192:MET:CE	1:I:243:LEU:HD22	1.86	1.05
1:A:458:LEU:HG	1:A:459:GLU:H	1.19	1.05
1:O:57:LEU:CD2	1:O:61:LEU:HD11	1.86	1.04
1:E:194:SER:CB	1:E:199:TYR:OH	2.05	1.04
1:G:433:LEU:HG	1:G:437:ILE:HD11	1.35	1.04
1:I:117:ARG:O	1:I:145:LEU:HD12	1.57	1.04
1:I:289:LEU:HD12	1:K:303:ASP:HB3	1.10	1.04
1:E:379:GLY:O	1:E:382:LEU:HB3	1.57	1.04
1:M:289:LEU:HD12	1:O:303:ASP:HB3	1.39	1.04
1:A:266:GLN:HB2	1:C:264:LEU:HD22	1.08	1.03
1:E:384:ILE:O	1:E:388:ILE:HD12	1.56	1.03
1:I:270:GLU:OE1	1:I:456:MET:HE3	1.58	1.03
1:A:266:GLN:NE2	1:C:231:ASN:HD22	1.56	1.03
1:C:96:VAL:O	1:C:99:HIS:HB2	1.58	1.03
1:K:390:ASP:O	1:K:394:LEU:HB2	1.57	1.03
1:A:65:GLU:HG3	1:A:66:GLN:N	1.72	1.03
1:G:212:PHE:HD1	1:G:280:PHE:CE1	1.76	1.02
1:I:228:GLN:HE22	1:I:273:LYS:CE	1.72	1.01
1:M:194:SER:HB3	1:M:199:TYR:OH	1.59	1.01
1:C:238:ILE:HD12	1:C:261:ASP:HB2	1.41	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:89:MET:HB2	1:E:118:TYR:HB2	1.43	1.01
1:I:53:TYR:CD2	1:I:54:ASN:N	2.27	1.01
1:O:385:TYR:HA	1:O:388:ILE:HD12	1.41	1.01
1:M:197:TYR:CE1	1:M:198:LEU:CD1	2.43	1.00
1:O:68:GLN:HA	1:O:68:GLN:NE2	1.57	1.00
1:A:244:LEU:HD11	1:A:250:ARG:HG3	1.43	1.00
1:G:238:ILE:HD12	1:G:261:ASP:HB2	1.41	1.00
1:I:228:GLN:NE2	1:I:273:LYS:CE	2.23	1.00
1:E:382:LEU:HD12	1:E:382:LEU:C	1.87	0.99
1:G:87:ILE:O	1:G:87:ILE:HG22	1.58	0.99
1:A:304:LEU:HD23	1:A:322:PHE:HB2	1.44	0.99
1:I:57:LEU:CD2	1:I:74:GLY:O	2.11	0.99
1:A:42:GLN:O	1:A:43:LEU:HD23	1.61	0.99
1:O:57:LEU:HD23	1:O:61:LEU:CD1	1.93	0.99
1:G:392:HIS:NE2	1:G:393:PHE:HE2	1.59	0.98
1:C:244:LEU:HD12	1:C:250:ARG:HA	1.44	0.98
1:M:152:GLN:HE21	1:M:152:GLN:N	1.60	0.98
1:I:289:LEU:CD1	1:K:303:ASP:HB3	1.94	0.97
1:C:160:VAL:O	1:C:164:GLU:HG3	1.62	0.97
1:A:192:MET:HE1	1:K:15:SER:HB3	1.47	0.97
1:A:266:GLN:HE21	1:C:231:ASN:ND2	1.64	0.96
1:E:198:LEU:CD1	1:E:199:TYR:CE1	2.48	0.96
1:I:183:GLY:CA	1:I:207:LEU:CD1	2.43	0.96
1:A:56:THR:OG1	1:A:59:SER:OG	1.84	0.95
1:C:304:LEU:HD23	1:C:322:PHE:HB2	1.46	0.95
1:E:198:LEU:HD12	1:E:198:LEU:N	1.72	0.95
1:G:52:LEU:HD21	1:G:63:THR:HG21	1.47	0.95
1:I:244:LEU:HD12	1:I:250:ARG:HA	1.48	0.95
1:A:266:GLN:CB	1:C:264:LEU:HD22	1.95	0.95
1:E:152:GLN:N	1:E:152:GLN:HE21	1.65	0.95
1:E:156:SER:HB3	1:E:159:ILE:HG12	1.45	0.95
1:K:452:VAL:CG1	1:K:455:ILE:HG13	1.96	0.95
1:G:304:LEU:HD22	1:G:320:LEU:HD11	1.48	0.95
1:E:67:LEU:HD12	1:E:69:LEU:HD11	1.49	0.95
1:K:85:LYS:O	1:K:115:ASN:ND2	2.00	0.95
1:E:102:VAL:O	1:E:106:ILE:HD12	1.67	0.95
1:C:306:ILE:HG12	1:C:320:LEU:HD12	1.48	0.94
1:E:381:ILE:H	1:E:381:ILE:HD13	1.32	0.94
1:A:148:ILE:HD13	1:A:388:ILE:HD11	1.46	0.94
1:I:192:MET:HE2	1:I:243:LEU:CD2	1.96	0.94
1:K:385:TYR:HA	1:K:388:ILE:HD12	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:LEU:O	1:A:413:LYS:CD	2.14	0.94
1:A:126:ALA:HB3	1:A:132:ALA:HB2	1.48	0.94
1:A:194:SER:HB3	1:A:199:TYR:OH	1.67	0.94
1:I:252:LYS:HD2	1:I:252:LYS:N	1.82	0.94
1:I:289:LEU:HD12	1:K:303:ASP:CB	1.97	0.94
1:E:381:ILE:H	1:E:381:ILE:CD1	1.79	0.94
1:E:382:LEU:HD12	1:E:382:LEU:O	1.67	0.94
1:A:208:ILE:HD13	1:A:441:PHE:CZ	2.03	0.94
1:A:65:GLU:CG	1:A:66:GLN:N	2.29	0.93
1:I:183:GLY:HA3	1:I:207:LEU:HD13	1.48	0.93
1:O:432:ILE:HG22	1:O:455:ILE:HD12	1.51	0.93
1:A:266:GLN:HE21	1:C:231:ASN:HD22	1.09	0.93
1:G:453:SER:HA	1:G:456:MET:HE1	1.50	0.93
1:M:152:GLN:H	1:M:152:GLN:NE2	1.64	0.93
1:G:117:ARG:HB3	1:G:118:TYR:CD1	2.04	0.92
1:I:57:LEU:HD21	1:I:74:GLY:O	1.69	0.92
1:C:90:ILE:CD1	1:C:116:LEU:HD13	2.00	0.92
1:G:91:VAL:HG22	1:G:120:TYR:HB3	1.49	0.92
1:I:147:THR:HB	1:I:427:PHE:CD1	2.04	0.92
1:I:312:PHE:HB3	1:I:315:ILE:HD12	1.49	0.92
1:O:67:LEU:O	1:O:68:GLN:CB	2.17	0.92
1:G:123:TRP:HD1	1:G:214:HIS:CD2	1.85	0.92
1:G:117:ARG:HB3	1:G:118:TYR:CE1	2.05	0.91
1:M:244:LEU:CD2	1:M:248:GLY:HA2	1.98	0.91
1:C:238:ILE:HD12	1:C:261:ASP:CB	2.01	0.91
1:I:195:PRO:HB2	1:I:198:LEU:HG	1.53	0.91
1:C:453:SER:HA	1:C:456:MET:HE1	1.50	0.91
1:C:52:LEU:HD11	1:C:63:THR:HG21	1.53	0.91
1:A:303:ASP:HB3	1:C:289:LEU:HD12	1.51	0.91
1:C:39:ALA:HA	1:C:382:LEU:HD12	1.53	0.91
1:E:229:LYS:NZ	1:G:447:GLU:OE2	2.03	0.91
1:E:453:SER:HA	1:E:456:MET:HE1	1.51	0.91
1:O:69:LEU:HD23	1:O:72:ALA:CB	2.01	0.91
1:E:322:PHE:HD2	1:E:367:GLU:HB3	1.34	0.90
1:I:228:GLN:HE22	1:I:273:LYS:HE3	1.31	0.90
1:A:266:GLN:HB2	1:C:264:LEU:CD2	1.99	0.90
1:O:67:LEU:O	1:O:68:GLN:HB2	1.71	0.90
1:I:53:TYR:C	1:I:53:TYR:HD2	1.75	0.90
1:O:432:ILE:CG2	1:O:455:ILE:HD12	2.01	0.90
1:C:312:PHE:HB3	1:C:315:ILE:HD12	1.52	0.90
1:K:40:ILE:O	1:K:40:ILE:HG22	1.70	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:118:TYR:HH	1:C:392:HIS:HD1	1.05	0.90
1:E:238:ILE:O	1:E:257:LYS:NZ	2.04	0.90
1:A:130:GLN:HA	1:A:133:GLU:HB2	1.53	0.90
1:E:152:GLN:HE21	1:E:152:GLN:H	1.19	0.90
1:A:192:MET:HE1	1:K:15:SER:CB	2.02	0.89
1:I:25:LEU:HD13	1:I:52:LEU:HD11	1.54	0.89
1:A:458:LEU:HG	1:A:459:GLU:N	1.88	0.89
1:E:218:VAL:HG13	1:E:222:ILE:CD1	2.02	0.89
1:G:244:LEU:HD23	1:G:250:ARG:HA	1.54	0.89
1:I:372:ARG:O	1:I:373:ASN:ND2	2.05	0.89
1:K:89:MET:HB2	1:K:118:TYR:HB2	1.55	0.89
1:M:156:SER:HB3	1:M:159:ILE:HG12	1.53	0.89
1:G:392:HIS:HE2	1:G:393:PHE:HE2	1.15	0.88
1:E:381:ILE:CD1	1:E:381:ILE:N	2.30	0.88
1:G:214:HIS:ND1	1:G:314:GLU:HG2	1.87	0.88
1:G:433:LEU:C	1:G:437:ILE:HD12	1.97	0.88
1:O:208:ILE:HG22	1:O:209:SER:H	1.36	0.88
1:O:244:LEU:CD1	1:O:250:ARG:HA	2.01	0.88
1:E:28:GLY:HA2	1:E:67:LEU:HD21	1.54	0.88
1:G:238:ILE:HD12	1:G:261:ASP:CB	2.04	0.88
1:A:77:SER:HB3	1:A:80:SER:CB	2.03	0.88
1:G:238:ILE:O	1:G:257:LYS:NZ	2.05	0.88
1:K:238:ILE:HD12	1:K:261:ASP:CB	2.03	0.88
1:E:198:LEU:HD13	1:E:199:TYR:HE1	1.20	0.88
1:M:168:GLU:O	1:M:328:GLY:O	1.91	0.88
1:O:171:ILE:HD12	1:O:299:GLY:CA	2.03	0.88
1:O:57:LEU:CD2	1:O:61:LEU:CD1	2.50	0.88
1:C:77:SER:HB3	1:C:80:SER:HB2	1.54	0.88
1:C:304:LEU:CD2	1:C:322:PHE:HB2	2.03	0.88
1:I:281:LYS:CD	1:I:282:GLY:H	1.85	0.87
1:A:229:LYS:HE3	1:C:233:MET:HE2	1.56	0.87
1:M:312:PHE:HB3	1:M:315:ILE:HD12	1.56	0.87
1:E:62:GLN:HG2	1:E:66:GLN:HE21	1.38	0.87
1:I:383:ARG:HH11	1:I:383:ARG:HG3	1.36	0.87
1:E:136:TYR:HB2	1:E:431:ILE:HD11	1.55	0.87
1:E:304:LEU:HD23	1:E:322:PHE:HB2	1.55	0.87
1:O:171:ILE:HD12	1:O:299:GLY:HA3	1.57	0.87
1:A:272:GLY:O	1:A:273:LYS:HB2	1.74	0.87
1:E:381:ILE:N	1:E:381:ILE:HD12	1.87	0.87
1:K:77:SER:HB3	1:K:80:SER:CB	2.04	0.87
1:A:128:SER:OG	1:A:131:GLN:HB2	1.73	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:183:GLY:HA3	1:I:207:LEU:CD1	2.03	0.86
1:K:57:LEU:O	1:K:61:LEU:HD13	1.76	0.86
1:C:77:SER:HB3	1:C:80:SER:CB	2.05	0.86
1:O:158:TYR:CD1	1:O:318:LEU:HD12	2.09	0.86
1:E:177:ILE:HD13	1:E:219:LEU:HD11	1.58	0.86
1:G:19:ARG:HB3	1:G:50:VAL:HG21	1.58	0.86
1:A:89:MET:HB2	1:A:118:TYR:HB2	1.57	0.86
1:E:195:PRO:CB	1:E:198:LEU:HD11	2.04	0.86
1:I:102:VAL:HG12	1:I:106:ILE:HD11	1.56	0.86
1:E:218:VAL:HG13	1:E:222:ILE:HD12	1.58	0.85
1:E:152:GLN:H	1:E:152:GLN:NE2	1.73	0.85
1:G:219:LEU:HA	1:G:222:ILE:CD1	2.06	0.85
1:I:102:VAL:HG12	1:I:106:ILE:CD1	2.06	0.85
1:I:118:TYR:HH	1:I:392:HIS:HD1	0.88	0.85
1:E:238:ILE:HD12	1:E:261:ASP:CB	2.06	0.85
1:M:225:SER:HB2	1:M:271:ASN:HB2	1.58	0.85
1:A:16:ARG:O	1:A:17:PRO:O	1.94	0.85
1:C:89:MET:HB2	1:C:118:TYR:HB2	1.57	0.85
1:K:88:ASP:HA	1:K:115:ASN:O	1.75	0.85
1:M:161:ARG:O	1:M:161:ARG:HD2	1.77	0.85
1:A:147:THR:HB	1:A:427:PHE:CD1	2.11	0.85
1:A:200:ASP:O	1:A:201:ILE:C	2.14	0.85
1:K:126:ALA:HB3	1:K:132:ALA:HB2	1.57	0.85
1:O:57:LEU:HD23	1:O:61:LEU:HD13	1.59	0.85
1:E:102:VAL:CG1	1:E:106:ILE:HD11	2.06	0.85
1:K:208:ILE:HD13	1:K:441:PHE:CZ	2.12	0.85
1:O:100:TYR:HB2	1:O:131:GLN:OE1	1.76	0.84
1:I:28:GLY:HA2	1:I:67:LEU:HD21	1.57	0.84
1:A:304:LEU:CD2	1:A:322:PHE:HB2	2.07	0.84
1:O:142:ARG:HB3	1:O:142:ARG:HH11	1.43	0.84
1:G:225:SER:HB2	1:G:271:ASN:HB2	1.60	0.84
1:K:149:ILE:HD13	1:K:430:ALA:HB2	1.58	0.84
1:K:192:MET:HG2	1:K:244:LEU:O	1.77	0.84
1:A:77:SER:HB3	1:A:80:SER:HB2	1.60	0.84
1:A:199:TYR:N	1:A:199:TYR:CD1	2.40	0.84
2:H:852:THR:HG22	2:H:854:ASP:H	1.43	0.84
1:A:148:ILE:CD1	1:A:388:ILE:HD11	2.07	0.83
1:C:90:ILE:HD12	1:C:116:LEU:HD13	1.58	0.83
1:K:77:SER:HB3	1:K:80:SER:HB2	1.59	0.83
1:K:149:ILE:HD13	1:K:430:ALA:CB	2.07	0.83
1:G:212:PHE:HD1	1:G:280:PHE:HE1	1.24	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:433:LEU:HG	1:C:437:ILE:HD11	1.58	0.83
1:M:452:VAL:HG13	1:M:455:ILE:HD12	1.60	0.83
1:O:154:ARG:HD2	1:O:425:PRO:HG3	1.60	0.83
1:A:244:LEU:CD1	1:A:250:ARG:HA	2.08	0.83
1:O:287:LYS:HG2	1:O:290:THR:HB	1.60	0.83
1:E:255:ILE:HG23	1:E:255:ILE:O	1.77	0.83
1:E:384:ILE:O	1:E:388:ILE:CD1	2.25	0.83
1:C:100:TYR:CD1	1:C:135:LEU:HD21	2.14	0.82
1:E:238:ILE:HD12	1:E:261:ASP:HB2	1.60	0.82
1:G:32:VAL:HG13	1:G:36:HIS:HB2	1.61	0.82
1:G:416:LYS:HD2	1:G:418:GLY:CA	2.08	0.82
1:C:416:LYS:HD2	1:C:418:GLY:CA	2.08	0.82
1:E:266:GLN:HB2	1:G:264:LEU:HD22	1.61	0.82
1:K:165:LEU:O	1:K:170:CYS:HB2	1.80	0.82
1:M:117:ARG:HB3	1:M:118:TYR:CD1	2.14	0.82
1:O:100:TYR:CD1	1:O:135:LEU:HD21	2.14	0.82
1:C:79:GLU:HG2	1:C:109:HIS:CD2	2.14	0.82
1:C:175:ASN:O	1:C:274:VAL:HG13	1.80	0.82
1:I:453:SER:HA	1:I:456:MET:HE1	1.62	0.82
1:O:84:TYR:CE1	1:O:86:ASP:HB2	2.15	0.82
1:E:436:LEU:HB2	1:E:455:ILE:HD11	1.60	0.82
1:C:225:SER:HB2	1:C:271:ASN:HB2	1.62	0.81
1:E:102:VAL:HG12	1:E:106:ILE:HD11	1.61	0.81
1:M:315:ILE:CG2	1:M:377:VAL:HG22	2.09	0.81
1:E:198:LEU:CD1	1:E:199:TYR:HE1	1.87	0.81
1:A:62:GLN:O	1:A:66:GLN:HG3	1.79	0.81
1:M:89:MET:HB2	1:M:118:TYR:HB2	1.62	0.81
1:C:219:LEU:HA	1:C:222:ILE:HD12	1.63	0.81
1:E:136:TYR:HB2	1:E:431:ILE:CD1	2.10	0.81
1:O:51:ALA:C	1:O:52:LEU:HD12	2.06	0.81
1:E:195:PRO:O	1:E:199:TYR:CE1	2.32	0.81
1:G:116:LEU:HD21	1:G:145:LEU:HD13	1.63	0.81
1:I:252:LYS:H	1:I:252:LYS:CD	1.83	0.81
1:G:212:PHE:CD1	1:G:280:PHE:CE1	2.67	0.80
1:I:228:GLN:HE22	1:I:273:LYS:HE2	1.46	0.80
1:O:52:LEU:HD12	1:O:52:LEU:N	1.92	0.80
1:E:263:LEU:HD12	1:E:264:LEU:N	1.96	0.80
1:G:100:TYR:CD1	1:G:135:LEU:HD21	2.15	0.80
1:I:244:LEU:HD11	1:I:250:ARG:HB2	1.62	0.80
1:E:384:ILE:O	1:E:384:ILE:CG2	2.30	0.80
1:I:225:SER:HB2	1:I:271:ASN:HB2	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:135:LEU:HA	1:K:138:ILE:HD12	1.63	0.80
1:O:69:LEU:HD23	1:O:72:ALA:HB2	1.64	0.80
1:A:191:PRO:HG2	1:A:194:SER:OG	1.81	0.80
1:E:194:SER:HB3	1:E:199:TYR:HH	1.41	0.80
1:G:177:ILE:C	1:G:178:GLU:CG	2.53	0.80
1:M:53:TYR:O	1:M:54:ASN:ND2	2.15	0.80
1:E:60:SER:O	1:E:64:ILE:HD12	1.82	0.80
1:G:19:ARG:HB3	1:G:50:VAL:CG2	2.12	0.80
1:I:136:TYR:HB2	1:I:431:ILE:CD1	2.11	0.80
1:E:273:LYS:HD3	1:E:273:LYS:N	1.95	0.80
1:M:117:ARG:HB3	1:M:118:TYR:CE1	2.17	0.80
1:M:147:THR:HB	1:M:427:PHE:CD1	2.17	0.80
1:G:154:ARG:HD2	1:G:425:PRO:HG3	1.64	0.79
1:A:185:TRP:HZ3	1:A:186:TYR:HH	1.28	0.79
1:A:312:PHE:HB3	1:A:315:ILE:HD12	1.62	0.79
1:K:40:ILE:O	1:K:40:ILE:CG2	2.30	0.79
1:I:100:TYR:HB2	1:I:131:GLN:OE1	1.80	0.79
1:C:319:VAL:HG22	1:C:370:HIS:CD2	2.17	0.79
1:M:115:ASN:O	1:M:116:LEU:C	2.23	0.79
1:A:118:TYR:HH	1:A:392:HIS:HD1	1.28	0.79
1:G:175:ASN:O	1:G:274:VAL:HG13	1.80	0.79
1:E:433:LEU:O	1:E:437:ILE:CD1	2.29	0.79
1:I:214:HIS:CD2	1:I:314:GLU:HG2	2.17	0.79
1:A:281:LYS:HD2	1:C:298:HIS:CD2	2.18	0.79
1:C:115:ASN:O	1:C:117:ARG:HG2	1.83	0.79
1:G:136:TYR:HB2	1:G:431:ILE:HD13	1.63	0.79
1:E:103:VAL:HA	1:E:106:ILE:HD12	1.64	0.79
1:E:281:LYS:HE2	1:G:175:ASN:OD1	1.81	0.79
1:G:96:VAL:O	1:G:99:HIS:HB2	1.83	0.79
1:K:104:LYS:O	1:K:107:LEU:HB2	1.82	0.79
1:K:147:THR:HB	1:K:427:PHE:CD1	2.18	0.79
1:K:312:PHE:HB3	1:K:315:ILE:HD12	1.63	0.79
1:K:84:TYR:CE1	1:K:86:ASP:HB2	2.18	0.79
1:A:199:TYR:HD1	1:A:199:TYR:H	1.30	0.78
1:G:147:THR:HB	1:G:427:PHE:CD1	2.18	0.78
1:A:195:PRO:O	1:A:199:TYR:CE1	2.35	0.78
1:G:453:SER:CA	1:G:456:MET:HE1	2.13	0.78
1:O:136:TYR:HB2	1:O:431:ILE:HD13	1.65	0.78
1:A:136:TYR:HB2	1:A:431:ILE:CD1	2.14	0.78
1:E:195:PRO:HB2	1:E:198:LEU:HD11	1.66	0.78
1:E:208:ILE:HD13	1:E:441:PHE:CZ	2.18	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:115:ASN:O	1:G:116:LEU:C	2.25	0.78
1:I:294:VAL:HG22	1:I:307:GLU:HG2	1.66	0.78
1:A:452:VAL:HG12	1:A:455:ILE:HG12	1.63	0.78
1:C:244:LEU:HD11	1:C:250:ARG:HG3	1.65	0.78
1:G:433:LEU:O	1:G:437:ILE:HD12	1.82	0.78
1:K:215:THR:O	1:K:218:VAL:HG12	1.84	0.78
1:M:228:GLN:OE1	1:M:229:LYS:HE3	1.82	0.78
1:A:263:LEU:HD12	1:A:264:LEU:N	1.99	0.78
1:M:197:TYR:CZ	1:M:198:LEU:HD11	2.19	0.78
1:G:416:LYS:HG3	1:G:418:GLY:N	1.98	0.78
1:M:197:TYR:CE1	1:M:198:LEU:HD11	2.15	0.78
1:I:96:VAL:O	1:I:99:HIS:HB2	1.83	0.78
1:O:123:TRP:CD2	1:O:124:ALA:HA	2.19	0.78
1:C:452:VAL:HG13	1:C:455:ILE:HD12	0.80	0.78
1:A:156:SER:HB3	1:A:159:ILE:HG12	1.66	0.78
1:A:435:ARG:NH1	1:A:455:ILE:O	2.16	0.78
1:A:41:GLN:O	1:A:43:LEU:N	2.17	0.77
1:G:152:GLN:O	1:G:153:GLY:C	2.23	0.77
1:I:136:TYR:HB2	1:I:431:ILE:HD13	1.66	0.77
1:I:377:VAL:HG11	2:J:859:TYR:CD2	2.18	0.77
1:C:182:ASN:ND2	1:C:283:GLY:HA2	1.99	0.77
1:C:452:VAL:HG13	1:C:455:ILE:HD11	1.61	0.77
2:D:852:THR:HG22	2:D:854:ASP:N	2.00	0.77
1:E:433:LEU:C	1:E:437:ILE:HD12	2.09	0.77
1:O:57:LEU:O	1:O:58:LYS:C	2.26	0.77
1:O:96:VAL:O	1:O:99:HIS:HB2	1.85	0.77
1:C:115:ASN:O	1:C:116:LEU:C	2.27	0.77
2:D:852:THR:HG22	2:D:854:ASP:H	1.47	0.77
1:C:452:VAL:CG1	1:C:455:ILE:CD1	2.29	0.77
1:G:64:ILE:HG22	1:G:65:GLU:N	1.99	0.77
1:I:183:GLY:CA	1:I:207:LEU:HD11	2.13	0.77
1:K:225:SER:HB2	1:K:271:ASN:HB2	1.66	0.77
1:M:129:VAL:HG13	1:M:130:GLN:H	1.48	0.77
1:E:322:PHE:CD2	1:E:367:GLU:HB3	2.20	0.77
2:H:852:THR:HG22	2:H:854:ASP:N	1.98	0.77
1:A:184:GLY:HA2	2:B:853:MET:HE3	1.66	0.77
1:M:187:GLY:HA3	1:M:284:THR:H	1.50	0.77
1:E:96:VAL:CG1	1:E:96:VAL:O	2.33	0.77
1:M:212:PHE:O	1:M:216:ILE:HG22	1.85	0.77
1:M:436:LEU:O	1:M:439:ALA:HB3	1.85	0.77
1:G:315:ILE:CG2	1:G:377:VAL:HG22	2.14	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:376:SER:O	1:G:380:ASN:HB2	1.84	0.77
1:A:255:ILE:HG13	1:A:256:SER:N	1.99	0.76
1:G:26:THR:HB	1:G:30:SER:HB3	1.67	0.76
1:K:123:TRP:CD2	1:K:124:ALA:HA	2.21	0.76
1:M:416:LYS:HB3	1:M:428:LYS:HD2	1.65	0.76
1:C:154:ARG:HD2	1:C:425:PRO:HG3	1.66	0.76
1:C:416:LYS:HD2	1:C:418:GLY:HA3	1.67	0.76
1:G:125:LEU:HD13	1:G:430:ALA:CB	2.16	0.76
1:I:287:LYS:HG2	1:I:290:THR:HB	1.66	0.76
1:C:147:THR:HB	1:C:427:PHE:CD1	2.19	0.76
1:I:453:SER:CA	1:I:456:MET:HE1	2.15	0.76
1:K:96:VAL:O	1:K:99:HIS:HB2	1.85	0.76
1:K:180:SER:O	1:K:293:LEU:HD12	1.84	0.76
1:K:454:LYS:HA	1:K:457:ILE:HD12	1.66	0.76
1:E:384:ILE:O	1:E:384:ILE:HG22	1.84	0.76
1:I:377:VAL:HG11	2:J:859:TYR:CE2	2.21	0.76
1:O:180:SER:O	1:O:293:LEU:HD12	1.86	0.76
1:E:64:ILE:HA	1:E:69:LEU:HD12	1.65	0.76
1:I:187:GLY:HA3	1:I:284:THR:H	1.51	0.76
1:E:103:VAL:CA	1:E:106:ILE:HD12	2.16	0.76
1:A:19:ARG:HB3	1:A:50:VAL:HG21	1.68	0.76
1:C:62:GLN:O	1:C:63:THR:C	2.26	0.76
1:A:105:ASN:HD22	1:A:105:ASN:N	1.82	0.76
1:I:182:ASN:HA	1:I:281:LYS:O	1.85	0.76
1:K:61:LEU:CD1	1:K:61:LEU:H	1.99	0.76
1:A:312:PHE:HE1	2:B:853:MET:HE1	1.51	0.75
1:C:179:ILE:HB	1:C:278:CYS:HB2	1.68	0.75
1:E:177:ILE:CD1	1:E:219:LEU:HD11	2.17	0.75
1:G:179:ILE:HD12	1:G:278:CYS:HB2	1.65	0.75
1:G:212:PHE:O	1:G:216:ILE:HG22	1.87	0.75
1:I:89:MET:HB2	1:I:118:TYR:HB2	1.67	0.75
1:O:52:LEU:N	1:O:52:LEU:CD1	2.50	0.75
1:C:136:TYR:HB2	1:C:431:ILE:CD1	2.16	0.75
1:G:322:PHE:HD2	1:G:367:GLU:HB3	1.51	0.75
1:K:136:TYR:HB2	1:K:431:ILE:CD1	2.16	0.75
1:O:142:ARG:HH11	1:O:142:ARG:CB	1.99	0.75
1:I:100:TYR:HB2	1:I:131:GLN:CD	2.12	0.75
1:A:96:VAL:HB	1:A:97:PRO:HD3	1.69	0.75
1:C:67:LEU:HD12	1:C:69:LEU:HD11	1.65	0.75
1:E:195:PRO:O	1:E:199:TYR:CD1	2.39	0.75
1:E:304:LEU:CD2	1:E:322:PHE:HB2	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:96:VAL:HB	1:G:97:PRO:HD3	1.67	0.75
1:E:272:GLY:O	1:E:273:LYS:HB2	1.85	0.74
1:K:96:VAL:HA	1:K:99:HIS:CG	2.22	0.74
1:C:123:TRP:CD2	1:C:124:ALA:HA	2.22	0.74
1:M:289:LEU:CD1	1:O:303:ASP:HB3	2.16	0.74
1:A:197:TYR:O	1:A:198:LEU:C	2.25	0.74
1:G:156:SER:O	1:G:157:PRO:C	2.27	0.74
1:K:433:LEU:O	1:K:436:LEU:HB3	1.87	0.74
1:O:84:TYR:CD1	1:O:86:ASP:HB2	2.22	0.74
1:E:306:ILE:HG12	1:E:320:LEU:HD12	1.68	0.74
1:K:177:ILE:C	1:K:178:GLU:HG3	2.12	0.74
1:M:123:TRP:CD2	1:M:124:ALA:HA	2.21	0.74
1:G:304:LEU:HD23	1:G:322:PHE:HB2	1.70	0.74
1:I:212:PHE:O	1:I:216:ILE:HG22	1.88	0.74
1:M:136:TYR:HB2	1:M:431:ILE:CD1	2.17	0.74
1:M:231:ASN:C	1:M:231:ASN:OD1	2.30	0.74
1:O:225:SER:HB2	1:O:271:ASN:HB2	1.70	0.74
1:E:385:TYR:HA	1:E:388:ILE:HD12	1.68	0.74
1:O:149:ILE:HG23	1:O:151:LEU:HD12	1.70	0.74
1:E:62:GLN:HG2	1:E:66:GLN:NE2	2.03	0.74
1:A:26:THR:HB	1:A:30:SER:HB3	1.69	0.73
1:A:416:LYS:HD2	1:A:418:GLY:CA	2.18	0.73
1:C:390:ASP:O	1:C:394:LEU:HB2	1.87	0.73
1:M:194:SER:CB	1:M:199:TYR:OH	2.36	0.73
1:A:286:VAL:O	1:A:288:LYS:HE3	1.88	0.73
1:C:225:SER:CB	1:C:271:ASN:HB2	2.16	0.73
1:E:102:VAL:C	1:E:106:ILE:HD12	2.13	0.73
1:M:319:VAL:HG22	1:M:370:HIS:CD2	2.22	0.73
1:O:25:LEU:HD23	1:O:63:THR:CG2	2.18	0.73
1:A:105:ASN:O	1:A:106:ILE:C	2.29	0.73
1:I:383:ARG:HH11	1:I:383:ARG:CG	1.96	0.73
1:G:104:LYS:HA	1:G:107:LEU:HD12	1.69	0.73
1:I:19:ARG:HA	1:I:48:GLN:O	1.89	0.73
1:M:77:SER:HB3	1:M:80:SER:CB	2.18	0.73
1:G:142:ARG:HB3	1:G:145:LEU:CB	2.18	0.73
1:C:215:THR:O	1:C:218:VAL:HG12	1.87	0.73
1:O:68:GLN:CA	1:O:68:GLN:NE2	2.30	0.73
1:E:428:LYS:O	1:E:432:ILE:HG13	1.89	0.73
1:G:219:LEU:CA	1:G:222:ILE:HD12	2.14	0.73
1:K:212:PHE:CZ	1:K:216:ILE:HD13	2.22	0.73
1:A:84:TYR:CE1	1:A:86:ASP:HB2	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:LEU:HA	1:A:222:ILE:HD12	1.70	0.73
1:A:306:ILE:HG12	1:A:320:LEU:HD12	1.71	0.73
1:E:225:SER:HB2	1:E:271:ASN:HB2	1.69	0.73
1:K:182:ASN:ND2	1:K:283:GLY:HA2	2.03	0.73
1:M:208:ILE:HD13	1:M:441:PHE:CZ	2.24	0.73
1:O:142:ARG:O	1:O:145:LEU:N	2.18	0.73
1:E:115:ASN:O	1:E:117:ARG:N	2.22	0.72
1:E:200:ASP:C	1:E:200:ASP:OD1	2.29	0.72
1:I:393:PHE:O	1:I:394:LEU:HD12	1.89	0.72
1:O:20:VAL:HA	1:O:89:MET:O	1.89	0.72
1:C:322:PHE:HD2	1:C:367:GLU:HB3	1.52	0.72
1:E:452:VAL:CG1	1:E:455:ILE:HD13	2.19	0.72
1:G:91:VAL:HG22	1:G:120:TYR:CB	2.18	0.72
1:M:77:SER:HB3	1:M:80:SER:HB2	1.70	0.72
1:C:64:ILE:HG12	1:C:72:ALA:HB3	1.71	0.72
1:G:67:LEU:HD12	1:G:69:LEU:HD11	1.69	0.72
1:I:121:VAL:HG12	1:I:122:GLU:H	1.54	0.72
1:I:77:SER:HB3	1:I:80:SER:CB	2.19	0.72
1:K:156:SER:O	1:K:157:PRO:C	2.31	0.72
1:M:216:ILE:HG23	1:M:217:ASP:N	2.03	0.72
1:C:136:TYR:HB2	1:C:431:ILE:HD13	1.69	0.72
1:I:372:ARG:O	1:I:373:ASN:CG	2.33	0.72
1:O:147:THR:HB	1:O:427:PHE:CD1	2.24	0.72
1:A:40:ILE:HG23	1:A:47:PHE:HB2	1.70	0.72
1:C:452:VAL:HG12	1:C:455:ILE:HD12	1.62	0.72
1:C:453:SER:CA	1:C:456:MET:HE1	2.17	0.72
1:O:89:MET:HB2	1:O:118:TYR:HB2	1.70	0.72
1:E:147:THR:HB	1:E:427:PHE:CD1	2.24	0.72
1:G:306:ILE:HG12	1:G:320:LEU:HD12	1.70	0.72
1:I:201:ILE:HB	1:I:258:THR:HB	1.70	0.72
1:A:41:GLN:O	1:A:44:SER:N	2.21	0.72
1:A:123:TRP:CH2	1:A:433:LEU:HD23	2.24	0.72
1:A:195:PRO:O	1:A:198:LEU:HB2	1.89	0.72
1:A:257:LYS:HD2	1:A:259:CYS:O	1.90	0.72
1:C:212:PHE:O	1:C:216:ILE:HG22	1.89	0.72
1:E:298:HIS:HD2	1:G:281:LYS:HD2	1.54	0.72
1:C:208:ILE:HG13	1:C:263:LEU:HD22	1.71	0.72
1:E:102:VAL:HG12	1:E:106:ILE:CD1	2.20	0.72
1:E:375:ASN:O	1:E:379:GLY:N	2.22	0.72
1:K:96:VAL:HB	1:K:97:PRO:HD3	1.71	0.72
1:A:89:MET:CB	1:A:118:TYR:HB2	2.18	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:201:ILE:HB	1:K:258:THR:HB	1.71	0.72
1:C:319:VAL:HG13	1:C:370:HIS:HB2	1.71	0.71
1:M:26:THR:HB	1:M:30:SER:CB	2.20	0.71
1:O:96:VAL:HA	1:O:99:HIS:CG	2.25	0.71
1:O:452:VAL:HG12	1:O:455:ILE:HG12	1.71	0.71
1:G:125:LEU:HB2	1:G:430:ALA:HB1	1.71	0.71
1:G:163:LYS:NZ	1:G:419:PHE:O	2.21	0.71
1:I:304:LEU:CD2	1:I:320:LEU:HD11	2.20	0.71
1:I:322:PHE:HD2	1:I:367:GLU:HB3	1.55	0.71
1:O:120:TYR:CD2	1:O:148:ILE:HG21	2.26	0.71
1:E:96:VAL:O	1:E:96:VAL:HG12	1.89	0.71
1:G:214:HIS:ND1	1:G:314:GLU:CG	2.52	0.71
1:A:195:PRO:O	1:A:199:TYR:HE1	1.74	0.71
1:A:231:ASN:HB2	1:A:449:THR:OG1	1.91	0.71
1:A:416:LYS:HD2	1:A:418:GLY:HA2	1.72	0.71
1:O:88:ASP:OD1	1:O:115:ASN:HB3	1.91	0.71
1:A:281:LYS:HD2	1:C:298:HIS:NE2	2.06	0.71
1:E:436:LEU:HB2	1:E:455:ILE:CD1	2.21	0.71
1:G:123:TRP:HB3	1:G:214:HIS:HE2	1.55	0.71
1:I:231:ASN:ND2	1:K:266:GLN:HE21	1.88	0.71
1:I:245:ASP:O	1:I:247:ASN:N	2.23	0.71
1:O:212:PHE:HD1	1:O:280:PHE:CE1	2.09	0.71
2:P:853:MET:O	2:P:856:VAL:HB	1.91	0.71
1:A:190:ARG:HG3	1:A:191:PRO:HD2	1.71	0.71
1:A:285:PRO:HG3	1:C:300:THR:O	1.90	0.71
1:A:372:ARG:NH2	2:B:847:LEU:HD23	2.06	0.71
1:A:390:ASP:O	1:A:394:LEU:HB2	1.91	0.71
1:I:244:LEU:CD1	1:I:250:ARG:HB2	2.21	0.71
1:K:57:LEU:HD23	1:K:61:LEU:HD11	1.72	0.71
1:A:447:GLU:OE2	1:C:229:LYS:NZ	2.19	0.71
1:C:96:VAL:HA	1:C:99:HIS:CG	2.27	0.70
1:G:113:ASN:O	1:G:114:LEU:HD23	1.92	0.70
1:K:182:ASN:HA	1:K:281:LYS:O	1.91	0.70
1:O:244:LEU:HD11	1:O:250:ARG:HG3	1.73	0.70
1:I:156:SER:HB3	1:I:159:ILE:HG12	1.71	0.70
1:O:136:TYR:HB2	1:O:431:ILE:CD1	2.21	0.70
1:O:432:ILE:HG22	1:O:455:ILE:CD1	2.21	0.70
1:O:433:LEU:HG	1:O:437:ILE:HD11	1.73	0.70
1:A:136:TYR:HB2	1:A:431:ILE:HD11	1.71	0.70
1:C:112:GLN:O	1:C:114:LEU:HD12	1.92	0.70
1:K:231:ASN:HB2	1:K:449:THR:OG1	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:281:LYS:HE2	1:O:175:ASN:OD1	1.91	0.70
1:C:30:SER:O	1:C:33:ALA:HB3	1.91	0.70
1:C:115:ASN:O	1:C:117:ARG:N	2.24	0.70
1:G:436:LEU:HB2	1:G:455:ILE:CD1	2.21	0.70
1:K:195:PRO:HB2	1:K:198:LEU:HD13	1.73	0.70
1:M:201:ILE:HG23	1:M:202:GLU:N	2.05	0.70
1:O:77:SER:HB3	1:O:80:SER:HB2	1.73	0.70
1:E:175:ASN:O	1:E:275:PRO:HD2	1.92	0.70
1:E:436:LEU:O	1:E:439:ALA:HB3	1.91	0.70
1:O:195:PRO:O	1:O:198:LEU:HB2	1.91	0.70
1:E:386:GLU:O	1:E:387:SER:C	2.30	0.70
1:I:155:LYS:HB3	1:I:383:ARG:HD3	1.72	0.70
1:O:77:SER:HB3	1:O:80:SER:CB	2.20	0.70
1:A:126:ALA:CB	1:A:132:ALA:HB2	2.20	0.70
1:C:286:VAL:O	1:C:288:LYS:HD2	1.92	0.70
1:G:83:GLN:O	1:G:84:TYR:C	2.35	0.70
1:I:102:VAL:CG1	1:I:106:ILE:HD11	2.21	0.70
1:O:208:ILE:HG22	1:O:209:SER:CA	2.22	0.70
1:G:65:GLU:O	1:G:68:GLN:NE2	2.25	0.69
1:G:89:MET:HG3	1:G:89:MET:O	1.90	0.69
1:G:381:ILE:O	1:G:382:LEU:C	2.32	0.69
1:M:126:ALA:HB3	1:M:132:ALA:HB2	1.74	0.69
1:E:158:TYR:HB2	1:E:318:LEU:HD12	1.72	0.69
1:G:206:ASN:C	1:G:206:ASN:OD1	2.34	0.69
1:O:105:ASN:O	1:O:106:ILE:C	2.36	0.69
1:M:201:ILE:HB	1:M:258:THR:HB	1.73	0.69
1:C:290:THR:HG22	1:C:291:LYS:O	1.93	0.69
1:E:146:GLN:HA	1:E:146:GLN:NE2	2.06	0.69
1:E:159:ILE:HD13	1:E:159:ILE:N	2.04	0.69
1:E:244:LEU:HD12	1:E:250:ARG:HA	1.74	0.69
1:K:416:LYS:HA	1:K:426:THR:OG1	1.93	0.69
1:E:442:ARG:O	1:E:446:GLU:HG3	1.92	0.69
1:G:118:TYR:CD1	1:G:118:TYR:N	2.60	0.69
1:G:200:ASP:OD1	1:G:200:ASP:C	2.34	0.69
1:G:375:ASN:O	1:G:379:GLY:N	2.25	0.69
1:K:435:ARG:NH1	1:K:455:ILE:O	2.25	0.69
1:A:64:ILE:HA	1:A:69:LEU:HD12	1.75	0.69
1:E:102:VAL:O	1:E:106:ILE:HD11	1.90	0.69
1:E:284:THR:HA	1:E:285:PRO:C	2.15	0.69
1:G:96:VAL:HA	1:G:99:HIS:CG	2.26	0.69
1:I:30:SER:O	1:I:34:LYS:HG3	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:183:GLY:HA2	1:I:207:LEU:CD1	2.21	0.69
1:K:156:SER:HB3	1:K:159:ILE:HG12	1.75	0.69
1:E:19:ARG:HB3	1:E:50:VAL:HG21	1.74	0.69
1:G:52:LEU:HD21	1:G:63:THR:CG2	2.20	0.69
1:G:142:ARG:CB	1:G:145:LEU:HB3	2.23	0.69
1:E:208:ILE:O	1:E:212:PHE:HB3	1.93	0.69
1:I:231:ASN:HB2	1:I:449:THR:OG1	1.92	0.69
1:C:20:VAL:HG23	1:C:48:GLN:O	1.92	0.69
1:C:304:LEU:HD21	1:C:320:LEU:HD21	1.75	0.69
1:G:195:PRO:O	1:G:198:LEU:HB2	1.93	0.69
1:I:102:VAL:C	1:I:106:ILE:HD12	2.17	0.69
1:K:290:THR:HG22	1:K:291:LYS:O	1.93	0.69
1:O:385:TYR:CA	1:O:388:ILE:HD12	2.20	0.69
1:A:284:THR:HA	1:A:285:PRO:C	2.18	0.68
1:I:115:ASN:O	1:I:116:LEU:C	2.36	0.68
1:I:152:GLN:NE2	1:I:152:GLN:H	1.91	0.68
1:I:270:GLU:OE1	1:I:456:MET:CE	2.39	0.68
1:M:53:TYR:CG	1:M:54:ASN:N	2.61	0.68
1:O:375:ASN:O	1:O:379:GLY:N	2.24	0.68
1:C:132:ALA:O	1:C:133:GLU:C	2.35	0.68
1:G:22:PHE:O	1:G:53:TYR:N	2.26	0.68
1:K:75:PHE:HD2	1:K:80:SER:HB3	1.57	0.68
1:M:197:TYR:CE1	1:M:198:LEU:HD12	2.29	0.68
1:O:100:TYR:HB2	1:O:131:GLN:CD	2.17	0.68
1:C:431:ILE:HG23	1:C:435:ARG:HD2	1.75	0.68
1:C:433:LEU:HG	1:C:437:ILE:CD1	2.22	0.68
1:M:197:TYR:CZ	1:M:198:LEU:CD1	2.75	0.68
1:O:187:GLY:HA3	1:O:284:THR:H	1.58	0.68
1:A:238:ILE:HD12	1:A:261:ASP:CB	2.23	0.68
1:C:142:ARG:HB3	1:C:145:LEU:HB3	1.75	0.68
1:E:19:ARG:HA	1:E:48:GLN:O	1.92	0.68
1:G:52:LEU:CD2	1:G:63:THR:HG21	2.22	0.68
1:M:19:ARG:HA	1:M:48:GLN:O	1.93	0.68
1:A:375:ASN:O	1:A:379:GLY:N	2.26	0.68
1:C:152:GLN:O	1:C:153:GLY:C	2.32	0.68
1:E:298:HIS:CD2	1:G:281:LYS:HD2	2.28	0.68
1:I:67:LEU:HD12	1:I:69:LEU:HD11	1.74	0.68
1:K:435:ARG:HB3	1:K:455:ILE:HG23	1.74	0.68
1:M:197:TYR:CD1	1:M:198:LEU:CD1	2.76	0.68
1:O:156:SER:O	1:O:157:PRO:C	2.36	0.68
1:A:67:LEU:HD12	1:A:69:LEU:HD11	1.73	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:228:GLN:O	1:C:452:VAL:N	2.27	0.68
1:E:198:LEU:CD1	1:E:198:LEU:N	2.44	0.68
1:G:30:SER:O	1:G:34:LYS:HG3	1.93	0.68
1:K:212:PHE:O	1:K:213:GLY:C	2.35	0.68
1:A:319:VAL:HG22	1:A:370:HIS:CD2	2.29	0.68
1:E:233:MET:HE1	1:G:266:GLN:O	1.92	0.68
1:K:102:VAL:HG12	1:K:106:ILE:CD1	2.23	0.68
1:K:104:LYS:O	1:K:107:LEU:CB	2.42	0.68
1:M:177:ILE:HB	1:M:276:VAL:HG22	1.76	0.68
1:A:436:LEU:O	1:A:439:ALA:HB3	1.94	0.68
1:E:142:ARG:HB3	1:E:145:LEU:CB	2.24	0.68
1:M:136:TYR:HB2	1:M:431:ILE:HD11	1.75	0.68
1:M:324:GLY:O	1:M:365:THR:N	2.26	0.68
1:O:26:THR:HB	1:O:30:SER:HB3	1.76	0.68
1:O:146:GLN:HA	1:O:146:GLN:NE2	2.08	0.68
1:E:25:LEU:HD23	1:E:63:THR:HG21	1.76	0.68
1:E:195:PRO:HB2	1:E:198:LEU:CD1	2.23	0.68
1:G:312:PHE:O	1:G:316:SER:N	2.27	0.68
1:I:96:VAL:HA	1:I:99:HIS:CG	2.29	0.68
1:I:130:GLN:O	1:I:131:GLN:C	2.37	0.68
1:I:312:PHE:O	1:I:316:SER:N	2.27	0.68
1:I:385:TYR:HA	1:I:388:ILE:HD12	1.74	0.68
1:M:225:SER:CB	1:M:271:ASN:HB2	2.24	0.68
1:C:90:ILE:HD12	1:C:116:LEU:CD1	2.24	0.67
1:E:96:VAL:HG12	1:E:127:ALA:HB2	1.75	0.67
1:E:125:LEU:HB2	1:E:430:ALA:HB1	1.76	0.67
1:O:155:LYS:HE2	1:O:384:ILE:HD13	1.76	0.67
1:O:208:ILE:CG2	1:O:209:SER:H	1.95	0.67
1:C:159:ILE:HD12	1:C:218:VAL:HG22	1.76	0.67
1:G:30:SER:O	1:G:33:ALA:HB3	1.94	0.67
1:I:26:THR:HB	1:I:30:SER:HB3	1.76	0.67
1:I:107:LEU:HD13	1:I:138:ILE:CG2	2.25	0.67
1:I:284:THR:HA	1:I:285:PRO:C	2.18	0.67
1:C:206:ASN:C	1:C:206:ASN:OD1	2.36	0.67
1:C:293:LEU:HB2	1:C:311:GLY:HA2	1.76	0.67
1:E:43:LEU:HB3	1:E:46:GLN:HG3	1.75	0.67
1:G:182:ASN:ND2	1:G:283:GLY:HA2	2.09	0.67
1:G:452:VAL:HG13	1:G:455:ILE:HG21	1.75	0.67
1:I:216:ILE:HG23	1:I:217:ASP:N	2.09	0.67
1:M:312:PHE:O	1:M:316:SER:N	2.27	0.67
1:A:433:LEU:HG	1:A:437:ILE:HD11	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:26:THR:HB	1:I:30:SER:CB	2.24	0.67
1:C:100:TYR:HB2	1:C:131:GLN:OE1	1.93	0.67
1:E:142:ARG:HB3	1:E:145:LEU:HB3	1.77	0.67
1:A:62:GLN:HG3	1:O:252:LYS:HD2	1.77	0.67
1:E:291:LYS:HG3	1:E:307:GLU:HB3	1.75	0.67
1:E:370:HIS:CD2	2:F:848:PHE:HD2	2.11	0.67
1:K:136:TYR:HB2	1:K:431:ILE:HD13	1.76	0.67
1:C:177:ILE:HD13	1:C:219:LEU:HD11	1.75	0.67
1:I:142:ARG:HB3	1:I:145:LEU:HB2	1.76	0.67
1:G:84:TYR:CE1	1:G:86:ASP:HB2	2.29	0.67
1:K:251:THR:O	1:K:253:GLU:N	2.27	0.67
1:M:195:PRO:O	1:M:199:TYR:CE1	2.48	0.67
1:A:172:GLY:CA	1:A:301:LYS:HD2	2.25	0.67
1:K:125:LEU:HB2	1:K:430:ALA:HB1	1.76	0.67
1:K:384:ILE:HG22	1:K:388:ILE:HD11	1.77	0.67
1:O:443:SER:HB2	1:O:450:LEU:HD12	1.77	0.67
1:C:304:LEU:HD22	1:C:320:LEU:HD11	1.76	0.67
1:E:89:MET:CB	1:E:118:TYR:HB2	2.22	0.67
1:G:89:MET:HB2	1:G:118:TYR:HB2	1.76	0.67
1:M:152:GLN:HE21	1:M:152:GLN:H	0.79	0.67
1:O:166:ILE:HG22	1:O:167:SER:N	2.10	0.67
1:A:216:ILE:HG23	1:A:217:ASP:N	2.10	0.66
1:E:78:LEU:O	1:E:81:PHE:HB3	1.95	0.66
1:I:231:ASN:HD22	1:K:266:GLN:NE2	1.92	0.66
1:K:195:PRO:O	1:K:198:LEU:HB2	1.94	0.66
1:M:130:GLN:O	1:M:131:GLN:C	2.37	0.66
1:E:199:TYR:CD1	1:E:199:TYR:N	2.62	0.66
1:G:392:HIS:HD2	1:G:393:PHE:CE2	2.07	0.66
1:M:26:THR:HB	1:M:30:SER:HB3	1.78	0.66
1:M:315:ILE:HG23	1:M:377:VAL:HG22	1.78	0.66
1:O:61:LEU:CD1	1:O:61:LEU:N	2.58	0.66
1:C:85:LYS:O	1:C:115:ASN:ND2	2.28	0.66
1:E:100:TYR:OH	1:E:104:LYS:NZ	2.28	0.66
1:E:293:LEU:O	1:E:307:GLU:HA	1.94	0.66
1:G:212:PHE:CD1	1:G:280:PHE:HE1	2.10	0.66
1:I:121:VAL:HG12	1:I:122:GLU:N	2.11	0.66
1:K:65:GLU:O	1:K:68:GLN:NE2	2.28	0.66
1:K:196:GLU:HG2	1:O:56:THR:CG2	2.25	0.66
1:M:104:LYS:O	1:M:107:LEU:HB2	1.96	0.66
1:O:69:LEU:HB3	1:O:72:ALA:HB3	1.76	0.66
1:I:75:PHE:N	1:I:75:PHE:CD1	2.63	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:16:ARG:HB2	1:K:17:PRO:HD3	1.78	0.66
1:K:129:VAL:HG13	1:K:130:GLN:H	1.60	0.66
1:O:432:ILE:HD13	1:O:456:MET:HA	1.75	0.66
1:C:251:THR:O	1:C:253:GLU:N	2.29	0.66
1:O:149:ILE:CG2	1:O:151:LEU:HD12	2.26	0.66
1:O:312:PHE:O	1:O:316:SER:OG	2.10	0.66
1:K:322:PHE:HD2	1:K:367:GLU:HB3	1.60	0.66
1:A:134:GLU:HA	1:A:137:SER:OG	1.95	0.66
1:K:61:LEU:CD1	1:K:61:LEU:N	2.59	0.66
1:M:142:ARG:HB3	1:M:145:LEU:CB	2.26	0.66
1:O:125:LEU:HB2	1:O:430:ALA:HB1	1.77	0.66
1:A:177:ILE:HD13	1:A:219:LEU:HD11	1.76	0.66
1:A:187:GLY:HA3	1:A:284:THR:H	1.60	0.66
1:E:206:ASN:C	1:E:206:ASN:OD1	2.38	0.66
1:G:103:VAL:HG12	1:G:107:LEU:HD11	1.77	0.66
1:I:96:VAL:N	1:I:97:PRO:HD2	2.10	0.66
1:K:151:LEU:O	1:K:153:GLY:N	2.29	0.66
1:A:195:PRO:HB2	1:A:198:LEU:HD22	1.77	0.66
1:C:263:LEU:HG	1:C:263:LEU:O	1.95	0.66
1:G:436:LEU:CD1	1:G:452:VAL:HG11	2.26	0.66
1:I:427:PHE:O	1:I:428:LYS:C	2.33	0.66
1:K:83:GLN:O	1:K:84:TYR:C	2.39	0.66
1:K:177:ILE:HB	1:K:276:VAL:HG22	1.77	0.66
1:M:432:ILE:HD13	1:M:456:MET:HA	1.77	0.66
1:A:77:SER:HB3	1:A:80:SER:OG	1.96	0.66
1:G:25:LEU:O	1:G:54:ASN:ND2	2.29	0.66
1:O:115:ASN:O	1:O:116:LEU:C	2.35	0.66
1:A:16:ARG:O	1:A:17:PRO:C	2.37	0.65
1:A:206:ASN:C	1:A:206:ASN:OD1	2.38	0.65
1:A:263:LEU:HD12	1:A:264:LEU:C	2.21	0.65
1:G:446:GLU:OE1	1:G:448:LYS:NZ	2.29	0.65
1:I:229:LYS:HE3	1:I:449:THR:HG21	1.78	0.65
1:M:84:TYR:CE1	1:M:86:ASP:HB2	2.30	0.65
1:A:281:LYS:HE2	1:C:298:HIS:CD2	2.31	0.65
1:C:81:PHE:O	1:C:83:GLN:N	2.29	0.65
1:K:375:ASN:O	1:K:379:GLY:N	2.26	0.65
1:M:322:PHE:HD2	1:M:367:GLU:HB3	1.61	0.65
1:A:102:VAL:HG12	1:A:106:ILE:CD1	2.26	0.65
1:G:81:PHE:O	1:G:83:GLN:N	2.30	0.65
1:K:116:LEU:HD23	1:K:116:LEU:O	1.97	0.65
1:M:67:LEU:HD12	1:M:69:LEU:HD11	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:61:LEU:CD1	1:O:61:LEU:H	2.09	0.65
1:C:129:VAL:HG13	1:C:130:GLN:H	1.60	0.65
1:A:117:ARG:NH2	1:A:392:HIS:HE1	1.94	0.65
1:A:322:PHE:CD2	1:A:367:GLU:HG2	2.31	0.65
1:I:77:SER:HB3	1:I:80:SER:HB2	1.78	0.65
1:K:123:TRP:CE3	1:K:124:ALA:HA	2.31	0.65
1:O:22:PHE:CE2	1:O:91:VAL:HB	2.32	0.65
1:C:65:GLU:O	1:C:68:GLN:NE2	2.29	0.65
2:D:855:ASP:O	2:D:858:ASN:N	2.27	0.65
1:I:375:ASN:O	1:I:379:GLY:N	2.20	0.65
1:K:166:ILE:HG22	1:K:167:SER:N	2.12	0.65
1:M:218:VAL:O	1:M:222:ILE:N	2.28	0.65
1:M:372:ARG:O	1:M:373:ASN:ND2	2.29	0.65
1:C:216:ILE:HG23	1:C:217:ASP:N	2.11	0.65
1:E:162:ALA:O	1:E:166:ILE:HD12	1.97	0.65
1:G:19:ARG:HA	1:G:48:GLN:O	1.96	0.65
1:I:103:VAL:HA	1:I:106:ILE:CD1	2.26	0.65
1:O:381:ILE:O	1:O:382:LEU:C	2.38	0.65
1:C:123:TRP:CZ2	1:C:433:LEU:HD23	2.32	0.65
1:E:40:ILE:HG23	1:E:47:PHE:HB2	1.79	0.65
1:E:102:VAL:HG13	1:E:106:ILE:HD11	1.79	0.65
1:E:266:GLN:CB	1:G:264:LEU:HD22	2.26	0.65
1:G:156:SER:O	1:G:158:TYR:N	2.29	0.65
1:G:416:LYS:HD2	1:G:418:GLY:HA2	1.77	0.65
1:I:20:VAL:HG23	1:I:48:GLN:O	1.97	0.65
1:M:125:LEU:HB2	1:M:149:ILE:HD13	1.79	0.65
1:M:182:ASN:HA	1:M:281:LYS:O	1.96	0.65
1:M:251:THR:O	1:M:253:GLU:N	2.29	0.65
1:K:228:GLN:O	1:K:452:VAL:N	2.30	0.65
1:O:39:ALA:HA	1:O:382:LEU:HD12	1.78	0.65
1:C:14:SER:O	1:C:16:ARG:N	2.30	0.65
1:E:18:ILE:HD11	1:E:392:HIS:CD2	2.32	0.65
1:E:159:ILE:O	1:E:160:VAL:C	2.39	0.65
1:G:218:VAL:O	1:G:222:ILE:N	2.29	0.65
1:K:26:THR:HB	1:K:30:SER:HB3	1.79	0.65
1:K:187:GLY:HA3	1:K:284:THR:H	1.61	0.65
1:A:195:PRO:O	1:A:199:TYR:CD1	2.50	0.64
1:A:197:TYR:C	1:A:199:TYR:N	2.44	0.64
1:E:201:ILE:HG23	1:E:202:GLU:H	1.62	0.64
1:G:64:ILE:HG12	1:G:72:ALA:HB3	1.79	0.64
1:M:100:TYR:HB2	1:M:131:GLN:NE2	2.12	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:20:VAL:HA	1:G:89:MET:O	1.98	0.64
1:G:129:VAL:O	1:G:133:GLU:N	2.28	0.64
1:G:136:TYR:HB2	1:G:431:ILE:CD1	2.26	0.64
1:I:228:GLN:O	1:I:451:ASP:OD2	2.15	0.64
1:M:27:SER:HA	1:M:63:THR:HG23	1.78	0.64
1:M:230:ILE:HA	1:M:267:GLY:HA2	1.80	0.64
1:O:452:VAL:CG1	1:O:455:ILE:HG12	2.28	0.64
1:A:287:LYS:HG2	1:A:290:THR:HB	1.78	0.64
1:A:459:GLU:O	1:A:459:GLU:HG3	1.98	0.64
1:E:192:MET:HG2	1:E:244:LEU:O	1.97	0.64
1:G:102:VAL:HG12	1:G:106:ILE:CD1	2.26	0.64
1:K:385:TYR:CA	1:K:388:ILE:HD12	2.23	0.64
1:O:61:LEU:N	1:O:61:LEU:HD12	2.11	0.64
1:E:238:ILE:HD12	1:E:261:ASP:HB3	1.79	0.64
1:E:436:LEU:O	1:E:436:LEU:HG	1.88	0.64
1:G:115:ASN:O	1:G:117:ARG:N	2.30	0.64
1:G:389:ALA:O	1:G:392:HIS:HB3	1.98	0.64
1:K:17:PRO:HA	1:K:46:GLN:O	1.97	0.64
1:K:312:PHE:O	1:K:316:SER:N	2.26	0.64
1:M:28:GLY:HA2	1:M:67:LEU:HD21	1.80	0.64
1:C:201:ILE:HG23	1:C:202:GLU:H	1.62	0.64
1:C:293:LEU:O	1:C:307:GLU:HA	1.98	0.64
1:C:389:ALA:O	1:C:393:PHE:N	2.30	0.64
1:E:115:ASN:O	1:E:116:LEU:C	2.39	0.64
1:E:312:PHE:O	1:E:316:SER:N	2.28	0.64
1:I:142:ARG:HB3	1:I:145:LEU:CB	2.28	0.64
2:J:853:MET:O	2:J:854:ASP:C	2.36	0.64
1:O:319:VAL:HG22	1:O:370:HIS:CG	2.32	0.64
1:A:281:LYS:CD	1:C:298:HIS:CD2	2.80	0.64
1:A:216:ILE:HD11	1:A:227:PHE:HE1	1.61	0.64
1:E:26:THR:HB	1:E:30:SER:HB3	1.79	0.64
1:E:312:PHE:HB3	1:E:315:ILE:HD12	1.80	0.64
1:G:99:HIS:O	1:G:103:VAL:HG23	1.98	0.64
1:G:111:SER:N	1:G:142:ARG:HH22	1.95	0.64
1:G:450:LEU:N	1:G:450:LEU:HD23	2.13	0.64
1:I:281:LYS:HD2	1:I:281:LYS:C	2.13	0.64
1:K:102:VAL:HG12	1:K:106:ILE:HD11	1.79	0.64
1:K:323:TYR:OH	1:K:364:GLN:HB2	1.98	0.64
2:L:852:THR:HG22	2:L:854:ASP:H	1.61	0.64
1:C:64:ILE:HD11	1:C:72:ALA:HB1	1.79	0.64
1:C:89:MET:HG3	1:C:89:MET:O	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:287:LYS:HG2	1:C:290:THR:HB	1.78	0.64
1:E:452:VAL:HG13	1:E:455:ILE:HD13	1.78	0.64
1:K:100:TYR:CD1	1:K:135:LEU:HD21	2.32	0.64
1:C:416:LYS:HA	1:C:426:THR:OG1	1.98	0.64
1:E:198:LEU:CD1	1:E:199:TYR:CD1	2.75	0.64
1:G:142:ARG:HB3	1:G:145:LEU:HB3	1.77	0.64
1:I:62:GLN:O	1:I:63:THR:C	2.40	0.64
1:I:236:ASN:ND2	1:I:260:PRO:HA	2.13	0.64
1:A:36:HIS:O	1:A:39:ALA:N	2.30	0.64
1:E:195:PRO:O	1:E:199:TYR:HE1	1.77	0.64
1:G:105:ASN:O	1:G:106:ILE:C	2.40	0.64
1:I:92:VAL:O	1:I:92:VAL:HG12	1.98	0.64
1:K:25:LEU:HB3	1:K:52:LEU:HD21	1.81	0.64
1:K:78:LEU:O	1:K:81:PHE:HB3	1.97	0.64
1:K:192:MET:CG	1:K:244:LEU:O	2.45	0.64
1:O:123:TRP:CE3	1:O:124:ALA:HA	2.32	0.64
1:I:64:ILE:HG22	1:I:65:GLU:N	2.11	0.63
1:K:142:ARG:HB2	1:K:145:LEU:HB3	1.80	0.63
1:O:64:ILE:HG22	1:O:65:GLU:N	2.13	0.63
1:O:319:VAL:HG22	1:O:370:HIS:CD2	2.33	0.63
1:C:20:VAL:HA	1:C:89:MET:O	1.98	0.63
1:C:446:GLU:OE1	1:C:448:LYS:NZ	2.30	0.63
1:G:251:THR:O	1:G:253:GLU:N	2.30	0.63
1:G:324:GLY:O	1:G:365:THR:N	2.30	0.63
1:M:375:ASN:O	1:M:379:GLY:N	2.22	0.63
1:O:182:ASN:ND2	1:O:283:GLY:HA2	2.13	0.63
1:C:96:VAL:N	1:C:97:PRO:CD	2.62	0.63
1:G:263:LEU:HG	1:G:263:LEU:O	1.98	0.63
1:I:251:THR:O	1:I:253:GLU:N	2.32	0.63
1:M:115:ASN:O	1:M:117:ARG:N	2.31	0.63
1:A:58:LYS:HG2	1:O:252:LYS:O	1.98	0.63
1:A:201:ILE:HB	1:A:258:THR:HB	1.80	0.63
1:A:225:SER:HB2	1:A:271:ASN:HB2	1.81	0.63
1:C:102:VAL:HG12	1:C:106:ILE:CD1	2.28	0.63
1:C:103:VAL:O	1:C:107:LEU:HG	1.98	0.63
1:C:179:ILE:HD12	1:C:278:CYS:HB2	1.79	0.63
1:C:201:ILE:HB	1:C:258:THR:HB	1.80	0.63
1:E:214:HIS:ND1	1:E:314:GLU:HG2	2.13	0.63
1:M:150:CYS:O	1:M:152:GLN:NE2	2.32	0.63
1:M:284:THR:HA	1:M:285:PRO:C	2.22	0.63
1:E:146:GLN:OE1	1:E:413:LYS:HB2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:165:LEU:O	1:G:170:CYS:HB2	1.97	0.63
1:K:213:GLY:O	1:K:216:ILE:HG22	1.99	0.63
1:M:200:ASP:C	1:M:200:ASP:OD1	2.39	0.63
1:O:156:SER:HB3	1:O:159:ILE:HG12	1.80	0.63
1:A:177:ILE:HB	1:A:276:VAL:HG13	1.80	0.63
2:B:852:THR:HG22	2:B:854:ASP:H	1.64	0.63
1:C:375:ASN:O	1:C:379:GLY:N	2.30	0.63
1:E:22:PHE:O	1:E:53:TYR:N	2.24	0.63
1:E:62:GLN:O	1:E:63:THR:C	2.42	0.63
1:G:129:VAL:HG13	1:G:130:GLN:H	1.64	0.63
1:G:228:GLN:O	1:G:451:ASP:OD2	2.16	0.63
1:K:212:PHE:HD1	1:K:280:PHE:CE1	2.16	0.63
1:M:115:ASN:N	1:M:115:ASN:OD1	2.31	0.63
1:G:216:ILE:HG23	1:G:217:ASP:N	2.13	0.63
1:K:105:ASN:HD22	1:K:105:ASN:N	1.97	0.63
1:M:142:ARG:HG3	1:M:145:LEU:HD23	1.80	0.63
1:A:20:VAL:HG23	1:A:48:GLN:O	1.98	0.63
1:A:125:LEU:HB2	1:A:430:ALA:HB1	1.80	0.63
1:C:110:SER:O	1:C:113:ASN:N	2.32	0.63
1:E:218:VAL:O	1:E:221:TYR:HB3	1.98	0.63
1:I:172:GLY:CA	1:I:301:LYS:HD2	2.29	0.63
1:M:33:ALA:O	1:M:37:PHE:HB3	1.99	0.63
1:M:263:LEU:HD12	1:M:264:LEU:N	2.14	0.63
1:C:148:ILE:HG12	1:C:424:PHE:CE1	2.34	0.63
1:E:231:ASN:HB2	1:E:449:THR:OG1	1.98	0.63
1:E:442:ARG:HD2	1:E:446:GLU:OE2	1.99	0.63
1:G:416:LYS:HD2	1:G:418:GLY:HA3	1.80	0.63
1:G:436:LEU:HD13	1:G:452:VAL:HG11	1.81	0.63
1:I:107:LEU:HD13	1:I:138:ILE:HG21	1.79	0.63
1:K:432:ILE:O	1:K:433:LEU:C	2.41	0.63
1:E:18:ILE:HD11	1:E:392:HIS:CG	2.34	0.62
1:E:142:ARG:CB	1:E:145:LEU:HB3	2.29	0.62
1:E:225:SER:HB2	1:E:271:ASN:CG	2.23	0.62
1:G:416:LYS:HA	1:G:426:THR:OG1	1.99	0.62
1:A:60:SER:O	1:A:64:ILE:HD12	1.99	0.62
1:E:62:GLN:O	1:E:65:GLU:N	2.32	0.62
1:E:130:GLN:O	1:E:131:GLN:C	2.42	0.62
1:E:285:PRO:HG3	1:G:300:THR:O	1.99	0.62
1:G:181:GLY:HA3	1:G:280:PHE:CE2	2.34	0.62
1:G:319:VAL:HG22	1:G:370:HIS:ND1	2.14	0.62
1:I:79:GLU:O	1:I:80:SER:C	2.41	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:293:LEU:O	1:K:307:GLU:HA	1.99	0.62
1:K:368:VAL:O	1:K:368:VAL:HG12	1.97	0.62
1:G:226:TYR:O	1:G:270:GLU:HB2	1.99	0.62
1:G:313:VAL:HG13	1:G:314:GLU:N	2.14	0.62
1:I:18:ILE:HB	1:I:47:PHE:CD2	2.34	0.62
1:K:129:VAL:O	1:K:133:GLU:N	2.26	0.62
1:O:228:GLN:O	1:O:452:VAL:N	2.32	0.62
1:A:118:TYR:OH	1:A:392:HIS:ND1	2.22	0.62
1:A:182:ASN:ND2	1:A:283:GLY:HA2	2.14	0.62
1:C:324:GLY:O	1:C:365:THR:N	2.31	0.62
1:C:431:ILE:HG22	1:C:432:ILE:N	2.13	0.62
1:E:218:VAL:HG13	1:E:222:ILE:HD11	1.82	0.62
1:G:26:THR:HB	1:G:30:SER:CB	2.29	0.62
1:I:238:ILE:O	1:I:257:LYS:NZ	2.31	0.62
1:K:57:LEU:CD2	1:K:61:LEU:HD11	2.29	0.62
1:M:195:PRO:HB2	1:M:198:LEU:HD22	1.80	0.62
1:M:263:LEU:O	1:M:263:LEU:HG	1.97	0.62
1:A:293:LEU:O	1:A:307:GLU:HA	1.99	0.62
1:G:126:ALA:HB3	1:G:132:ALA:HB2	1.81	0.62
1:G:201:ILE:HB	1:G:258:THR:HB	1.81	0.62
1:G:218:VAL:O	1:G:221:TYR:HB3	1.98	0.62
1:M:134:GLU:HA	1:M:137:SER:OG	1.98	0.62
1:M:318:LEU:O	1:M:370:HIS:HD2	1.83	0.62
1:O:89:MET:O	1:O:89:MET:HG3	1.99	0.62
1:O:201:ILE:HB	1:O:258:THR:HB	1.82	0.62
1:C:22:PHE:O	1:C:53:TYR:N	2.29	0.62
1:C:26:THR:HB	1:C:30:SER:HB3	1.80	0.62
1:C:115:ASN:OD1	1:C:115:ASN:N	2.31	0.62
1:C:138:ILE:O	1:C:139:SER:C	2.42	0.62
1:C:159:ILE:O	1:C:160:VAL:C	2.43	0.62
1:C:312:PHE:O	1:C:316:SER:N	2.33	0.62
1:K:91:VAL:HG22	1:K:120:TYR:HB3	1.81	0.62
1:K:134:GLU:HG2	1:K:138:ILE:HD11	1.81	0.62
1:O:26:THR:HB	1:O:30:SER:CB	2.29	0.62
1:C:123:TRP:CE3	1:C:124:ALA:HA	2.34	0.62
1:C:431:ILE:HG23	1:C:435:ARG:CD	2.30	0.62
1:G:28:GLY:HA2	1:G:67:LEU:HD21	1.81	0.62
1:G:148:ILE:HG12	1:G:424:PHE:CE1	2.35	0.62
1:K:306:ILE:HG12	1:K:320:LEU:HD12	1.82	0.62
1:E:154:ARG:NH1	1:E:417:GLN:OE1	2.29	0.62
1:I:134:GLU:HA	1:I:137:SER:OG	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:177:ILE:HD13	1:I:219:LEU:HD11	1.80	0.62
1:K:61:LEU:HD13	1:K:61:LEU:H	1.63	0.62
1:M:231:ASN:HB2	1:M:449:THR:OG1	1.99	0.62
1:A:102:VAL:C	1:A:106:ILE:HD12	2.24	0.62
1:A:132:ALA:O	1:A:133:GLU:C	2.39	0.62
1:A:146:GLN:HA	1:A:146:GLN:NE2	2.14	0.62
1:A:447:GLU:HG3	1:C:449:THR:CG2	2.30	0.62
1:C:450:LEU:N	1:C:450:LEU:HD23	2.15	0.62
1:E:134:GLU:HA	1:E:137:SER:OG	1.99	0.62
2:H:855:ASP:O	2:H:858:ASN:N	2.29	0.62
1:I:50:VAL:O	1:I:72:ALA:HA	2.00	0.62
1:I:231:ASN:HD22	1:K:266:GLN:HE21	1.47	0.62
1:M:148:ILE:HD13	1:M:388:ILE:CD1	2.29	0.62
2:P:855:ASP:O	2:P:858:ASN:N	2.32	0.62
1:A:294:VAL:HA	1:A:306:ILE:O	2.00	0.62
1:C:273:LYS:HD3	1:C:273:LYS:N	2.14	0.62
1:C:393:PHE:O	1:C:394:LEU:HD12	1.99	0.62
1:E:96:VAL:HA	1:E:99:HIS:CG	2.35	0.62
1:I:208:ILE:HA	1:I:212:PHE:HB3	1.82	0.62
1:M:14:SER:OG	1:M:15:SER:N	2.30	0.62
1:O:324:GLY:O	1:O:365:THR:N	2.29	0.62
1:C:126:ALA:HB3	1:C:132:ALA:HB2	1.82	0.61
1:C:129:VAL:HG13	1:C:130:GLN:N	2.15	0.61
1:I:188:TYR:N	1:I:284:THR:O	2.32	0.61
1:K:320:LEU:HB3	1:K:369:PHE:HB3	1.81	0.61
1:M:125:LEU:HB2	1:M:430:ALA:HB1	1.81	0.61
1:O:134:GLU:O	1:O:135:LEU:C	2.43	0.61
1:O:142:ARG:HH11	1:O:142:ARG:CG	2.12	0.61
1:A:266:GLN:NE2	1:C:231:ASN:ND2	2.31	0.61
1:C:123:TRP:HD1	1:C:214:HIS:CD2	2.18	0.61
1:C:148:ILE:HD13	1:C:388:ILE:CD1	2.30	0.61
1:E:96:VAL:HG22	1:E:99:HIS:CE1	2.34	0.61
1:E:129:VAL:O	1:E:133:GLU:N	2.25	0.61
1:E:225:SER:HB2	1:E:271:ASN:CB	2.30	0.61
1:G:284:THR:HA	1:G:285:PRO:C	2.24	0.61
1:K:304:LEU:HD23	1:K:322:PHE:HB2	1.82	0.61
1:K:306:ILE:HG12	1:K:320:LEU:CD1	2.31	0.61
1:M:319:VAL:HG22	1:M:370:HIS:CG	2.35	0.61
1:A:161:ARG:NH2	1:A:367:GLU:OE2	2.32	0.61
1:C:79:GLU:HG2	1:C:109:HIS:CG	2.35	0.61
1:C:91:VAL:HG22	1:C:120:TYR:HB3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:452:VAL:O	1:I:452:VAL:HG12	2.00	0.61
1:M:210:ASN:O	1:M:211:SER:C	2.36	0.61
1:O:96:VAL:HB	1:O:97:PRO:HD3	1.81	0.61
1:A:20:VAL:HA	1:A:89:MET:O	2.00	0.61
1:A:255:ILE:HG13	1:A:256:SER:H	1.66	0.61
1:C:244:LEU:CD1	1:C:250:ARG:HA	2.26	0.61
1:I:279:SER:HB2	1:K:277:SER:HB2	1.81	0.61
1:K:416:LYS:HG3	1:K:418:GLY:N	2.15	0.61
1:O:96:VAL:HG12	1:O:127:ALA:HB2	1.80	0.61
1:A:123:TRP:CD2	1:A:124:ALA:HA	2.34	0.61
1:A:129:VAL:O	1:A:133:GLU:N	2.25	0.61
1:A:251:THR:O	1:A:253:GLU:N	2.34	0.61
1:A:459:GLU:O	1:A:459:GLU:CG	2.48	0.61
1:E:25:LEU:O	1:E:54:ASN:ND2	2.33	0.61
1:O:146:GLN:OE1	1:O:414:PHE:CB	2.48	0.61
1:A:290:THR:HG22	1:A:291:LYS:O	2.00	0.61
1:C:148:ILE:HD13	1:C:388:ILE:HD13	1.83	0.61
1:E:218:VAL:O	1:E:222:ILE:HD12	1.99	0.61
1:E:313:VAL:HG23	1:E:318:LEU:HD11	1.82	0.61
1:G:14:SER:OG	1:G:15:SER:N	2.32	0.61
1:G:208:ILE:CG1	1:G:263:LEU:HD22	2.30	0.61
1:G:372:ARG:O	1:G:373:ASN:ND2	2.33	0.61
1:I:166:ILE:HG22	1:I:167:SER:N	2.16	0.61
1:I:237:ASN:N	1:I:261:ASP:OD2	2.29	0.61
1:M:188:TYR:N	1:M:284:THR:O	2.32	0.61
1:A:305:LYS:NZ	1:A:307:GLU:OE2	2.23	0.61
2:B:855:ASP:O	2:B:858:ASN:N	2.33	0.61
1:E:290:THR:HG22	1:E:291:LYS:O	2.00	0.61
1:G:57:LEU:HD22	1:G:61:LEU:HD21	1.83	0.61
1:G:125:LEU:HD23	1:G:132:ALA:HB1	1.83	0.61
1:G:132:ALA:O	1:G:133:GLU:C	2.43	0.61
1:G:142:ARG:HB3	1:G:145:LEU:HB2	1.82	0.61
1:I:125:LEU:HB2	1:I:430:ALA:HB1	1.82	0.61
1:I:428:LYS:O	1:I:432:ILE:HG13	2.00	0.61
1:O:105:ASN:HD22	1:O:105:ASN:N	1.97	0.61
1:A:238:ILE:HD12	1:A:261:ASP:HB2	1.81	0.61
2:F:853:MET:O	2:F:856:VAL:HB	2.01	0.61
1:O:129:VAL:O	1:O:133:GLU:N	2.29	0.61
1:I:156:SER:O	1:I:157:PRO:C	2.42	0.61
1:K:324:GLY:O	1:K:365:THR:N	2.33	0.61
1:M:129:VAL:HG13	1:M:130:GLN:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:GLN:HE22	1:A:214:HIS:HE1	1.48	0.61
1:E:218:VAL:O	1:E:222:ILE:N	2.28	0.61
1:G:166:ILE:HG22	1:G:167:SER:N	2.13	0.61
1:I:57:LEU:HD23	1:I:74:GLY:O	2.00	0.61
1:I:78:LEU:O	1:I:81:PHE:HB3	2.00	0.61
1:I:232:ALA:O	1:I:444:ASP:HA	2.01	0.61
1:M:136:TYR:HB2	1:M:431:ILE:HD13	1.83	0.61
1:M:228:GLN:O	1:M:452:VAL:N	2.31	0.61
1:O:68:GLN:O	1:O:69:LEU:C	2.43	0.61
1:O:215:THR:O	1:O:218:VAL:HG12	2.00	0.61
1:A:22:PHE:O	1:A:53:TYR:N	2.29	0.60
1:C:134:GLU:HA	1:C:137:SER:OG	2.00	0.60
1:C:208:ILE:H	1:C:208:ILE:HD12	1.66	0.60
1:C:225:SER:HB2	1:C:271:ASN:CB	2.31	0.60
1:G:286:VAL:O	1:G:288:LYS:HE3	2.01	0.60
1:I:185:TRP:HZ3	1:I:186:TYR:HH	1.48	0.60
1:M:208:ILE:HA	1:M:212:PHE:HB3	1.83	0.60
1:E:26:THR:HB	1:E:30:SER:CB	2.32	0.60
1:E:266:GLN:HA	1:E:276:VAL:O	2.01	0.60
1:E:431:ILE:HG22	1:E:432:ILE:N	2.16	0.60
1:G:85:LYS:O	1:G:115:ASN:ND2	2.34	0.60
1:I:185:TRP:CE3	1:I:186:TYR:CE1	2.89	0.60
1:I:244:LEU:HD11	1:I:250:ARG:CB	2.30	0.60
1:K:20:VAL:HA	1:K:89:MET:O	2.01	0.60
1:M:34:LYS:O	1:M:35:THR:HG22	2.01	0.60
1:M:230:ILE:HG22	1:M:267:GLY:HA3	1.82	0.60
1:O:177:ILE:HB	1:O:276:VAL:HG22	1.83	0.60
1:A:123:TRP:HD1	1:A:214:HIS:CD2	2.20	0.60
1:A:172:GLY:HA3	1:A:301:LYS:HD2	1.82	0.60
1:C:89:MET:CB	1:C:118:TYR:HB2	2.30	0.60
1:E:142:ARG:HG3	1:E:145:LEU:HD23	1.83	0.60
1:E:177:ILE:HB	1:E:276:VAL:HG22	1.82	0.60
1:E:201:ILE:HB	1:E:258:THR:HB	1.82	0.60
1:G:306:ILE:HG12	1:G:320:LEU:CD1	2.32	0.60
1:I:171:ILE:O	1:I:300:THR:N	2.33	0.60
2:L:852:THR:HG22	2:L:853:MET:N	2.15	0.60
1:M:128:SER:O	1:M:129:VAL:C	2.43	0.60
1:I:319:VAL:HG22	1:I:370:HIS:ND1	2.16	0.60
1:K:54:ASN:HB3	1:K:55:PRO:HD2	1.82	0.60
1:M:96:VAL:HG12	1:M:127:ALA:HB2	1.84	0.60
1:O:225:SER:CB	1:O:271:ASN:HB2	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:THR:HB	1:C:30:SER:CB	2.32	0.60
1:E:147:THR:O	1:E:426:THR:HG22	2.01	0.60
1:E:158:TYR:CB	1:E:318:LEU:HD12	2.31	0.60
1:G:161:ARG:HA	1:G:164:GLU:OE1	2.01	0.60
1:I:136:TYR:HB2	1:I:431:ILE:HD11	1.82	0.60
1:I:177:ILE:HB	1:I:276:VAL:HG22	1.84	0.60
1:M:159:ILE:O	1:M:160:VAL:C	2.44	0.60
1:M:166:ILE:HG22	1:M:167:SER:N	2.14	0.60
1:M:389:ALA:O	1:M:393:PHE:N	2.33	0.60
1:M:435:ARG:HB3	1:M:455:ILE:CG2	2.31	0.60
1:E:123:TRP:CD2	1:E:124:ALA:HA	2.36	0.60
1:E:212:PHE:O	1:E:216:ILE:HG22	2.00	0.60
1:E:251:THR:C	1:E:253:GLU:H	2.10	0.60
1:K:159:ILE:O	1:K:160:VAL:C	2.45	0.60
1:K:222:ILE:HG22	1:K:223:THR:N	2.12	0.60
1:O:115:ASN:O	1:O:117:ARG:N	2.34	0.60
1:A:62:GLN:HG3	1:O:252:LYS:CD	2.31	0.60
1:C:125:LEU:HB2	1:C:430:ALA:HB1	1.84	0.60
1:C:142:ARG:CB	1:C:145:LEU:HB3	2.32	0.60
1:E:230:ILE:C	1:E:230:ILE:HD12	2.27	0.60
1:E:251:THR:O	1:E:253:GLU:N	2.35	0.60
1:G:84:TYR:CZ	1:G:86:ASP:HB2	2.36	0.60
1:G:107:LEU:O	1:G:142:ARG:NH2	2.35	0.60
1:I:33:ALA:O	1:I:37:PHE:HB3	2.00	0.60
1:O:293:LEU:HG	1:O:294:VAL:N	2.16	0.60
1:A:26:THR:HB	1:A:30:SER:CB	2.31	0.60
1:A:136:TYR:HB2	1:A:431:ILE:HD13	1.82	0.60
1:A:201:ILE:HG23	1:A:202:GLU:H	1.67	0.60
1:A:229:LYS:NZ	1:C:447:GLU:OE2	2.30	0.60
1:G:263:LEU:HD12	1:G:264:LEU:O	2.01	0.60
1:G:322:PHE:CD2	1:G:367:GLU:HB3	2.36	0.60
1:I:291:LYS:HG3	1:I:307:GLU:HB3	1.84	0.60
1:O:152:GLN:O	1:O:153:GLY:C	2.44	0.60
1:C:64:ILE:HA	1:C:69:LEU:HD12	1.84	0.60
1:E:77:SER:CB	1:E:80:SER:HB2	2.32	0.60
1:I:199:TYR:N	1:I:199:TYR:CD1	2.70	0.60
1:I:245:ASP:OD1	1:I:249:LYS:HB3	2.02	0.60
1:K:61:LEU:N	1:K:61:LEU:HD12	2.17	0.60
1:A:312:PHE:CE1	2:B:853:MET:HE1	2.36	0.60
1:C:25:LEU:O	1:C:54:ASN:ND2	2.35	0.60
1:C:171:ILE:O	1:C:300:THR:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:452:VAL:HG13	1:E:455:ILE:HG21	1.83	0.60
1:G:225:SER:CB	1:G:271:ASN:HB2	2.31	0.60
1:I:105:ASN:N	1:I:105:ASN:HD22	2.00	0.60
1:I:236:ASN:HA	1:I:261:ASP:OD1	2.01	0.60
1:K:158:TYR:CD1	1:K:318:LEU:HD12	2.37	0.60
1:M:64:ILE:O	1:M:68:GLN:N	2.35	0.60
1:M:124:ALA:O	1:M:125:LEU:C	2.41	0.60
1:M:199:TYR:CD1	1:M:199:TYR:N	2.70	0.60
1:A:19:ARG:HA	1:A:48:GLN:O	2.02	0.59
1:A:433:LEU:HG	1:A:437:ILE:CD1	2.32	0.59
1:C:320:LEU:HG	1:C:321:TYR:N	2.16	0.59
1:E:172:GLY:CA	1:E:301:LYS:HD2	2.32	0.59
1:G:315:ILE:HG23	1:G:377:VAL:HG22	1.84	0.59
1:I:53:TYR:O	1:I:54:ASN:ND2	2.35	0.59
1:I:89:MET:CB	1:I:118:TYR:HB2	2.31	0.59
1:I:225:SER:CB	1:I:271:ASN:HB2	2.31	0.59
1:K:30:SER:O	1:K:34:LYS:HG3	2.01	0.59
1:K:393:PHE:O	1:K:394:LEU:HD12	2.01	0.59
1:M:263:LEU:HD12	1:M:264:LEU:C	2.27	0.59
1:O:229:LYS:HE2	1:O:268:ILE:HG13	1.83	0.59
1:O:318:LEU:O	1:O:370:HIS:HD2	1.85	0.59
1:C:195:PRO:HB3	1:C:197:TYR:CD2	2.36	0.59
1:E:225:SER:CB	1:E:271:ASN:HB2	2.31	0.59
1:G:67:LEU:HB2	1:G:69:LEU:HG	1.83	0.59
1:G:103:VAL:O	1:G:107:LEU:HG	2.02	0.59
1:I:431:ILE:O	1:I:435:ARG:HB2	2.02	0.59
1:K:244:LEU:HD12	1:K:250:ARG:HA	1.84	0.59
1:G:123:TRP:CD2	1:G:124:ALA:HA	2.36	0.59
1:G:209:SER:OG	1:G:210:ASN:N	2.36	0.59
1:I:53:TYR:CG	1:I:54:ASN:N	2.70	0.59
1:I:117:ARG:O	1:I:145:LEU:CD1	2.43	0.59
1:I:129:VAL:O	1:I:133:GLU:N	2.31	0.59
1:K:287:LYS:HG2	1:K:290:THR:HB	1.84	0.59
1:K:431:ILE:HG22	1:K:432:ILE:N	2.17	0.59
1:M:19:ARG:HB3	1:M:50:VAL:HG21	1.85	0.59
1:O:32:VAL:HG13	1:O:36:HIS:HB2	1.83	0.59
1:O:161:ARG:HA	1:O:164:GLU:OE1	2.02	0.59
1:C:304:LEU:HD23	1:C:322:PHE:CB	2.27	0.59
1:G:188:TYR:N	1:G:284:THR:O	2.31	0.59
1:I:290:THR:HG22	1:I:291:LYS:O	2.01	0.59
1:O:227:PHE:CD2	1:O:269:LEU:HD23	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:VAL:HG12	1:C:106:ILE:HD12	1.84	0.59
1:C:110:SER:OG	1:C:142:ARG:NH2	2.36	0.59
1:C:392:HIS:C	1:C:394:LEU:H	2.10	0.59
1:E:454:LYS:HA	1:E:457:ILE:HD12	1.83	0.59
1:K:62:GLN:O	1:K:65:GLU:N	2.35	0.59
1:K:284:THR:HA	1:K:285:PRO:C	2.27	0.59
1:O:20:VAL:HG21	1:O:40:ILE:HD13	1.85	0.59
1:O:436:LEU:O	1:O:436:LEU:HG	2.01	0.59
2:P:852:THR:HG22	2:P:854:ASP:H	1.66	0.59
1:C:158:TYR:HB2	1:C:318:LEU:HD12	1.83	0.59
1:E:96:VAL:HG22	1:E:99:HIS:ND1	2.18	0.59
1:E:157:PRO:HG3	1:E:383:ARG:HH22	1.67	0.59
1:M:96:VAL:HB	1:M:97:PRO:HD3	1.84	0.59
1:M:264:LEU:HD13	1:O:266:GLN:HB2	1.83	0.59
1:C:183:GLY:HA3	1:C:207:LEU:HD13	1.84	0.59
1:G:290:THR:HG22	1:G:291:LYS:O	2.02	0.59
1:I:177:ILE:CD1	1:I:219:LEU:HD11	2.32	0.59
1:M:381:ILE:O	1:M:382:LEU:C	2.45	0.59
1:O:209:SER:OG	1:O:210:ASN:N	2.34	0.59
1:A:281:LYS:CE	1:C:298:HIS:CD2	2.86	0.59
1:C:177:ILE:CD1	1:C:219:LEU:HD11	2.31	0.59
1:E:99:HIS:O	1:E:103:VAL:HG23	2.01	0.59
1:E:294:VAL:HA	1:E:306:ILE:O	2.03	0.59
1:I:31:TRP:O	1:I:35:THR:HG23	2.01	0.59
1:K:84:TYR:CD1	1:K:86:ASP:HB2	2.37	0.59
1:K:384:ILE:O	1:K:385:TYR:C	2.44	0.59
1:O:126:ALA:HB3	1:O:132:ALA:HB2	1.84	0.59
1:O:427:PHE:O	1:O:428:LYS:C	2.41	0.59
1:A:455:ILE:N	1:A:455:ILE:CD1	2.65	0.59
1:C:32:VAL:HG13	1:C:36:HIS:HB2	1.85	0.59
1:E:198:LEU:H	1:E:198:LEU:CD1	1.80	0.59
1:G:169:GLY:O	1:G:328:GLY:HA3	2.02	0.59
1:G:177:ILE:HG22	1:G:178:GLU:N	2.18	0.59
1:G:179:ILE:CD1	1:G:278:CYS:HB2	2.32	0.59
1:G:208:ILE:HG13	1:G:263:LEU:HD22	1.84	0.59
1:I:306:ILE:HG12	1:I:320:LEU:HD12	1.85	0.59
1:K:154:ARG:NH1	1:K:425:PRO:HB3	2.17	0.59
1:M:123:TRP:CH2	1:M:433:LEU:HD23	2.37	0.59
1:O:25:LEU:HD23	1:O:63:THR:HG21	1.83	0.59
1:O:178:GLU:C	1:O:179:ILE:HG13	2.26	0.59
1:O:215:THR:O	1:O:216:ILE:C	2.42	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:219:LEU:O	1:O:219:LEU:HG	2.03	0.59
1:C:88:ASP:OD1	1:C:115:ASN:HB3	2.03	0.59
1:C:129:VAL:O	1:C:133:GLU:N	2.26	0.59
1:C:147:THR:O	1:C:426:THR:HG22	2.02	0.59
2:F:852:THR:HG22	2:F:854:ASP:H	1.68	0.59
1:I:83:GLN:O	1:I:84:TYR:C	2.46	0.59
1:I:103:VAL:HA	1:I:106:ILE:HD12	1.84	0.59
1:K:142:ARG:CB	1:K:145:LEU:HB3	2.32	0.59
1:K:218:VAL:O	1:K:222:ILE:N	2.34	0.59
1:O:132:ALA:O	1:O:133:GLU:C	2.46	0.59
1:O:192:MET:HG2	1:O:244:LEU:O	2.03	0.59
1:A:102:VAL:CG1	1:A:106:ILE:HD11	2.32	0.58
1:G:177:ILE:HB	1:G:276:VAL:HG13	1.85	0.58
1:I:89:MET:HB2	1:I:118:TYR:O	2.03	0.58
1:I:115:ASN:O	1:I:117:ARG:N	2.36	0.58
1:K:436:LEU:O	1:K:440:VAL:HG23	2.02	0.58
1:M:152:GLN:O	1:M:153:GLY:C	2.45	0.58
1:O:436:LEU:CD1	1:O:452:VAL:HG11	2.32	0.58
1:C:123:TRP:CH2	1:C:433:LEU:HD23	2.38	0.58
1:G:428:LYS:O	1:G:432:ILE:HG13	2.02	0.58
1:I:124:ALA:O	1:I:125:LEU:C	2.42	0.58
1:I:138:ILE:O	1:I:139:SER:C	2.44	0.58
1:I:381:ILE:O	1:I:384:ILE:N	2.35	0.58
1:I:390:ASP:O	1:I:394:LEU:CB	2.35	0.58
1:M:454:LYS:HA	1:M:457:ILE:HD12	1.85	0.58
1:O:178:GLU:HB2	1:O:296:ASP:HB3	1.84	0.58
1:A:129:VAL:O	1:A:132:ALA:N	2.34	0.58
1:A:156:SER:O	1:A:157:PRO:C	2.46	0.58
1:A:238:ILE:O	1:A:257:LYS:NZ	2.34	0.58
1:G:62:GLN:O	1:G:63:THR:C	2.46	0.58
1:G:88:ASP:OD1	1:G:115:ASN:HB3	2.04	0.58
1:G:304:LEU:HD21	1:G:320:LEU:HD21	1.85	0.58
1:K:131:GLN:O	1:K:135:LEU:HG	2.03	0.58
1:K:208:ILE:HG22	1:K:209:SER:N	2.17	0.58
1:M:85:LYS:O	1:M:115:ASN:ND2	2.36	0.58
1:O:136:TYR:O	1:O:137:SER:C	2.46	0.58
1:O:226:TYR:O	1:O:270:GLU:HB2	2.02	0.58
1:A:177:ILE:CG2	1:A:276:VAL:HG13	2.34	0.58
1:C:218:VAL:O	1:C:222:ILE:N	2.35	0.58
1:E:431:ILE:O	1:E:432:ILE:C	2.47	0.58
1:G:375:ASN:C	1:G:375:ASN:OD1	2.43	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:194:SER:HB3	1:I:199:TYR:OH	2.04	0.58
1:M:20:VAL:HA	1:M:89:MET:O	2.03	0.58
1:O:88:ASP:HA	1:O:115:ASN:O	2.03	0.58
1:E:78:LEU:O	1:E:82:ALA:N	2.33	0.58
1:E:105:ASN:O	1:E:106:ILE:C	2.45	0.58
1:E:152:GLN:N	1:E:152:GLN:NE2	2.39	0.58
1:E:189:GLU:HB2	1:E:284:THR:OG1	2.03	0.58
1:G:431:ILE:HG22	1:G:432:ILE:N	2.17	0.58
1:I:96:VAL:HG12	1:I:127:ALA:HB2	1.86	0.58
1:A:158:TYR:HB2	1:A:318:LEU:HD12	1.85	0.58
1:G:130:GLN:O	1:G:131:GLN:C	2.46	0.58
2:N:852:THR:HG22	2:N:854:ASP:H	1.69	0.58
1:A:104:LYS:HA	1:A:107:LEU:HD12	1.85	0.58
1:A:257:LYS:NZ	1:A:261:ASP:OD1	2.37	0.58
1:C:386:GLU:O	1:C:387:SER:C	2.46	0.58
1:I:198:LEU:HB2	1:I:199:TYR:CE1	2.39	0.58
1:M:96:VAL:N	1:M:97:PRO:HD2	2.19	0.58
1:M:161:ARG:O	1:M:161:ARG:CD	2.49	0.58
1:M:211:SER:O	1:M:214:HIS:HB2	2.04	0.58
2:N:853:MET:O	2:N:854:ASP:C	2.47	0.58
1:O:150:CYS:O	1:O:152:GLN:NE2	2.36	0.58
1:O:263:LEU:HG	1:O:263:LEU:O	1.95	0.58
1:A:156:SER:CB	1:A:159:ILE:HG12	2.34	0.58
1:I:429:ASP:O	1:I:430:ALA:C	2.47	0.58
1:K:102:VAL:CG1	1:K:106:ILE:HD11	2.34	0.58
1:M:105:ASN:HD22	1:M:105:ASN:N	2.00	0.58
1:O:146:GLN:OE1	1:O:414:PHE:HB3	2.04	0.58
1:A:200:ASP:O	1:A:202:GLU:N	2.37	0.58
1:A:312:PHE:O	1:A:316:SER:N	2.30	0.58
1:E:142:ARG:HG3	1:E:145:LEU:CD2	2.34	0.58
1:E:177:ILE:CG2	1:E:276:VAL:HG13	2.34	0.58
1:G:156:SER:HB3	1:G:159:ILE:HG12	1.86	0.58
1:I:244:LEU:HD12	1:I:250:ARG:CA	2.26	0.58
1:K:22:PHE:CE2	1:K:91:VAL:HB	2.39	0.58
1:M:90:ILE:HD12	1:M:116:LEU:CD1	2.33	0.58
1:M:94:VAL:O	1:M:99:HIS:CD2	2.57	0.58
1:M:232:ALA:O	1:M:444:ASP:HA	2.03	0.58
1:O:389:ALA:O	1:O:393:PHE:N	2.35	0.58
1:A:38:LEU:O	1:A:39:ALA:C	2.47	0.58
1:C:197:TYR:HA	1:C:200:ASP:HB3	1.85	0.58
1:K:216:ILE:HG23	1:K:217:ASP:N	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:435:ARG:NH1	1:O:455:ILE:O	2.37	0.58
1:A:96:VAL:N	1:A:97:PRO:HD2	2.18	0.57
1:G:236:ASN:HA	1:G:261:ASP:OD1	2.04	0.57
1:I:105:ASN:O	1:I:106:ILE:C	2.46	0.57
1:I:126:ALA:HB3	1:I:132:ALA:HB2	1.86	0.57
1:K:129:VAL:HG13	1:K:130:GLN:N	2.18	0.57
1:M:142:ARG:CB	1:M:145:LEU:HB3	2.34	0.57
1:M:273:LYS:HD3	1:M:273:LYS:N	2.19	0.57
1:O:179:ILE:HG22	1:O:180:SER:N	2.18	0.57
1:A:41:GLN:C	1:A:43:LEU:H	2.11	0.57
1:A:272:GLY:O	1:A:273:LYS:CB	2.48	0.57
1:E:190:ARG:HG3	1:E:191:PRO:HD2	1.86	0.57
1:G:16:ARG:HG2	1:G:16:ARG:O	2.05	0.57
1:M:129:VAL:O	1:M:132:ALA:N	2.37	0.57
1:C:142:ARG:HB3	1:C:145:LEU:CB	2.34	0.57
1:E:148:ILE:HD13	1:E:388:ILE:HG12	1.86	0.57
1:E:230:ILE:HD12	1:E:230:ILE:O	2.04	0.57
1:E:237:ASN:O	1:E:239:PRO:HD3	2.04	0.57
1:G:20:VAL:HG21	1:G:40:ILE:CD1	2.34	0.57
1:G:89:MET:HB2	1:G:118:TYR:O	2.04	0.57
1:G:436:LEU:O	1:G:439:ALA:HB3	2.03	0.57
1:M:30:SER:O	1:M:34:LYS:HG3	2.04	0.57
1:M:34:LYS:O	1:M:35:THR:CG2	2.52	0.57
1:M:64:ILE:HG12	1:M:72:ALA:HB3	1.84	0.57
1:M:68:GLN:NE2	1:M:68:GLN:HA	2.19	0.57
1:M:129:VAL:O	1:M:130:GLN:C	2.47	0.57
1:M:198:LEU:CD1	1:M:198:LEU:N	2.67	0.57
1:M:294:VAL:HA	1:M:306:ILE:O	2.04	0.57
1:O:85:LYS:O	1:O:115:ASN:ND2	2.37	0.57
1:O:89:MET:HB2	1:O:118:TYR:O	2.04	0.57
1:O:158:TYR:CG	1:O:318:LEU:HD12	2.39	0.57
1:C:222:ILE:HG22	1:C:223:THR:N	2.12	0.57
1:C:389:ALA:O	1:C:390:ASP:C	2.48	0.57
1:E:19:ARG:HB3	1:E:50:VAL:CG2	2.35	0.57
1:E:96:VAL:N	1:E:97:PRO:CD	2.66	0.57
1:G:121:VAL:HG12	1:G:122:GLU:N	2.18	0.57
1:K:177:ILE:O	1:K:178:GLU:HG3	2.02	0.57
1:E:102:VAL:O	1:E:106:ILE:CG1	2.52	0.57
1:E:452:VAL:HG13	1:E:455:ILE:CG2	2.34	0.57
1:I:85:LYS:O	1:I:115:ASN:ND2	2.38	0.57
1:I:147:THR:HB	1:I:427:PHE:CE1	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:852:THR:HG22	2:J:854:ASP:H	1.68	0.57
1:M:142:ARG:HB3	1:M:145:LEU:HB3	1.86	0.57
1:O:89:MET:SD	1:O:118:TYR:HB2	2.44	0.57
1:O:192:MET:SD	1:O:243:LEU:HD22	2.43	0.57
1:O:195:PRO:HB2	1:O:198:LEU:HD13	1.86	0.57
1:C:16:ARG:O	1:C:17:PRO:O	2.22	0.57
1:E:294:VAL:HG22	1:E:307:GLU:HG2	1.85	0.57
1:K:218:VAL:O	1:K:221:TYR:HB3	2.05	0.57
1:M:136:TYR:O	1:M:137:SER:C	2.47	0.57
1:O:40:ILE:O	1:O:40:ILE:HG22	2.05	0.57
1:C:100:TYR:HB2	1:C:131:GLN:CD	2.29	0.57
1:C:187:GLY:HA3	1:C:284:THR:H	1.70	0.57
1:G:96:VAL:N	1:G:97:PRO:HD2	2.19	0.57
1:I:78:LEU:O	1:I:79:GLU:C	2.47	0.57
1:M:156:SER:O	1:M:157:PRO:C	2.43	0.57
1:A:153:GLY:O	1:A:159:ILE:HG13	2.05	0.57
1:A:175:ASN:O	1:A:275:PRO:HD2	2.05	0.57
1:C:56:THR:O	1:C:59:SER:OG	2.22	0.57
1:C:154:ARG:NH1	1:C:417:GLN:OE1	2.32	0.57
1:C:208:ILE:HD11	1:C:234:ILE:HD13	1.86	0.57
1:E:75:PHE:CZ	1:E:84:TYR:CD2	2.93	0.57
1:G:161:ARG:HG3	1:G:161:ARG:O	2.03	0.57
1:I:75:PHE:HD1	1:I:75:PHE:H	1.53	0.57
1:K:115:ASN:O	1:K:116:LEU:C	2.42	0.57
1:K:151:LEU:C	1:K:153:GLY:N	2.63	0.57
1:C:84:TYR:CE1	1:C:86:ASP:HB2	2.39	0.57
1:C:208:ILE:HA	1:C:212:PHE:HB3	1.87	0.57
1:E:95:LYS:HB3	1:E:97:PRO:HD2	1.86	0.57
1:G:106:ILE:HG21	1:G:119:LEU:HD11	1.86	0.57
1:G:129:VAL:O	1:G:132:ALA:N	2.37	0.57
1:G:156:SER:O	1:G:159:ILE:N	2.35	0.57
1:G:244:LEU:HD22	1:G:248:GLY:O	2.05	0.57
1:K:57:LEU:HD23	1:K:61:LEU:CD1	2.34	0.57
1:K:315:ILE:CG2	1:K:377:VAL:HG22	2.35	0.57
1:O:57:LEU:O	1:O:59:SER:N	2.37	0.57
1:O:152:GLN:NE2	1:O:152:GLN:H	2.03	0.57
1:A:138:ILE:O	1:A:141:GLN:HG2	2.05	0.57
1:A:182:ASN:HA	1:A:281:LYS:O	2.05	0.57
1:A:238:ILE:HD12	1:A:261:ASP:HB3	1.87	0.57
1:C:96:VAL:N	1:C:97:PRO:HD2	2.20	0.57
1:C:200:ASP:C	1:C:200:ASP:OD1	2.48	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:20:VAL:HA	1:I:89:MET:O	2.05	0.57
1:I:115:ASN:OD1	1:I:115:ASN:N	2.34	0.57
1:I:324:GLY:O	1:I:365:THR:N	2.32	0.57
1:M:22:PHE:O	1:M:53:TYR:N	2.37	0.57
1:M:225:SER:HB2	1:M:271:ASN:CB	2.32	0.57
1:O:431:ILE:HG22	1:O:432:ILE:N	2.20	0.57
1:A:19:ARG:HB3	1:A:50:VAL:CG2	2.34	0.56
1:A:25:LEU:O	1:A:54:ASN:ND2	2.38	0.56
1:A:217:ASP:HB2	1:A:433:LEU:HD13	1.87	0.56
1:E:36:HIS:O	1:E:39:ALA:N	2.37	0.56
1:E:126:ALA:HB1	1:E:131:GLN:OE1	2.05	0.56
1:G:64:ILE:O	1:G:68:GLN:N	2.38	0.56
1:I:422:GLU:OE1	1:I:422:GLU:N	2.37	0.56
1:M:304:LEU:CD2	1:M:320:LEU:HD11	2.35	0.56
1:O:313:VAL:HG13	1:O:314:GLU:N	2.20	0.56
1:A:88:ASP:HA	1:A:115:ASN:O	2.06	0.56
1:A:96:VAL:HG12	1:A:127:ALA:HB2	1.86	0.56
1:A:276:VAL:C	1:C:264:LEU:HD21	2.29	0.56
1:C:16:ARG:HB2	1:C:17:PRO:CD	2.35	0.56
1:M:142:ARG:HB3	1:M:145:LEU:HB2	1.85	0.56
1:O:121:VAL:HG12	1:O:122:GLU:N	2.19	0.56
1:O:142:ARG:O	1:O:144:ASN:N	2.38	0.56
1:O:384:ILE:HG22	1:O:388:ILE:HD11	1.87	0.56
1:A:40:ILE:HG23	1:A:47:PHE:CB	2.35	0.56
1:A:142:ARG:HB2	1:A:145:LEU:HB2	1.87	0.56
1:A:192:MET:HG2	1:A:244:LEU:O	2.05	0.56
1:A:218:VAL:O	1:A:222:ILE:HD12	2.05	0.56
1:C:188:TYR:N	1:C:284:THR:O	2.35	0.56
1:E:287:LYS:HE3	1:E:290:THR:HB	1.87	0.56
1:G:88:ASP:O	1:G:116:LEU:HA	2.05	0.56
1:G:295:ILE:HD13	1:G:306:ILE:HD12	1.85	0.56
1:I:152:GLN:O	1:I:153:GLY:C	2.48	0.56
1:I:230:ILE:O	1:I:230:ILE:HG13	2.04	0.56
1:K:67:LEU:O	1:K:68:GLN:HB2	2.05	0.56
1:K:154:ARG:NH1	1:K:417:GLN:OE1	2.38	0.56
2:L:853:MET:O	2:L:856:VAL:HB	2.05	0.56
1:M:89:MET:HB2	1:M:118:TYR:O	2.06	0.56
1:M:102:VAL:HG12	1:M:106:ILE:HD12	1.86	0.56
1:M:182:ASN:O	1:M:183:GLY:C	2.46	0.56
1:M:195:PRO:O	1:M:199:TYR:HE1	1.87	0.56
1:O:216:ILE:HG23	1:O:217:ASP:N	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:PHE:CE2	1:A:91:VAL:HB	2.41	0.56
1:A:138:ILE:O	1:A:139:SER:C	2.49	0.56
1:C:53:TYR:HB2	1:C:81:PHE:CD1	2.40	0.56
1:E:188:TYR:N	1:E:284:THR:O	2.36	0.56
1:G:129:VAL:CG1	1:G:130:GLN:OE1	2.53	0.56
1:C:452:VAL:HG12	1:C:452:VAL:O	2.05	0.56
1:E:96:VAL:O	1:E:127:ALA:HB2	2.06	0.56
1:E:255:ILE:O	1:E:255:ILE:CG2	2.47	0.56
1:G:312:PHE:HB3	1:G:315:ILE:HD12	1.88	0.56
1:G:390:ASP:O	1:G:394:LEU:CB	2.53	0.56
1:I:19:ARG:NE	1:I:86:ASP:O	2.37	0.56
1:I:375:ASN:C	1:I:375:ASN:OD1	2.48	0.56
1:M:245:ASP:O	1:M:247:ASN:N	2.39	0.56
1:O:171:ILE:O	1:O:300:THR:N	2.38	0.56
1:A:185:TRP:CE3	1:A:186:TYR:CE1	2.93	0.56
1:C:216:ILE:HG23	1:C:217:ASP:H	1.69	0.56
1:E:85:LYS:O	1:E:115:ASN:ND2	2.38	0.56
1:I:174:ILE:HB	1:I:274:VAL:HG21	1.88	0.56
1:I:322:PHE:CG	1:I:323:TYR:N	2.72	0.56
1:I:383:ARG:CG	1:I:383:ARG:NH1	2.59	0.56
1:M:94:VAL:O	1:M:99:HIS:NE2	2.38	0.56
1:M:293:LEU:HB2	1:M:311:GLY:HA2	1.87	0.56
1:O:436:LEU:HD12	1:O:452:VAL:HG11	1.86	0.56
1:A:89:MET:HB2	1:A:118:TYR:O	2.05	0.56
1:C:304:LEU:CD2	1:C:320:LEU:HD21	2.35	0.56
1:E:245:ASP:O	1:E:248:GLY:N	2.28	0.56
1:E:431:ILE:CG2	1:E:432:ILE:N	2.69	0.56
1:E:443:SER:HA	1:E:450:LEU:HD21	1.87	0.56
1:G:171:ILE:O	1:G:300:THR:N	2.39	0.56
1:G:177:ILE:CG2	1:G:178:GLU:N	2.68	0.56
1:I:183:GLY:N	1:I:207:LEU:HD11	2.19	0.56
1:I:197:TYR:CE1	1:I:198:LEU:HD23	2.40	0.56
1:K:416:LYS:HD2	1:K:418:GLY:CA	2.35	0.56
1:O:120:TYR:CE2	1:O:148:ILE:HG21	2.40	0.56
1:O:251:THR:O	1:O:253:GLU:N	2.39	0.56
1:G:138:ILE:O	1:G:139:SER:C	2.46	0.56
1:I:222:ILE:HG22	1:I:223:THR:N	2.13	0.56
1:K:179:ILE:HG22	1:K:180:SER:N	2.21	0.56
1:K:375:ASN:C	1:K:375:ASN:OD1	2.45	0.56
1:E:195:PRO:HB2	1:E:198:LEU:CG	2.36	0.56
1:E:209:SER:OG	1:E:210:ASN:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:183:GLY:N	1:G:282:GLY:O	2.39	0.56
1:G:453:SER:C	1:G:456:MET:HE1	2.31	0.56
1:I:110:SER:C	1:I:142:ARG:HH22	2.14	0.56
1:I:218:VAL:HG12	1:I:219:LEU:N	2.20	0.56
1:K:436:LEU:O	1:K:436:LEU:HG	2.03	0.56
1:M:216:ILE:HG23	1:M:217:ASP:H	1.70	0.56
1:O:62:GLN:O	1:O:63:THR:C	2.49	0.56
1:O:223:THR:OG1	1:O:224:GLY:N	2.37	0.56
1:A:105:ASN:N	1:A:105:ASN:ND2	2.54	0.56
1:A:120:TYR:C	1:A:121:VAL:HG23	2.31	0.56
1:C:166:ILE:HG22	1:C:167:SER:N	2.18	0.56
1:C:322:PHE:CD2	1:C:367:GLU:HB3	2.37	0.56
1:E:89:MET:HB2	1:E:118:TYR:O	2.06	0.56
1:E:176:SER:HB2	1:G:262:HIS:CE1	2.41	0.56
1:G:16:ARG:O	1:G:16:ARG:CG	2.54	0.56
1:G:304:LEU:CD2	1:G:322:PHE:HB2	2.36	0.56
1:I:25:LEU:CD1	1:I:52:LEU:HD11	2.31	0.56
1:K:149:ILE:HD13	1:K:430:ALA:HB1	1.87	0.56
1:K:177:ILE:HG22	1:K:178:GLU:N	2.21	0.56
1:K:182:ASN:HD21	1:K:283:GLY:HA2	1.70	0.56
1:K:228:GLN:NE2	1:K:273:LYS:HE3	2.21	0.56
1:E:77:SER:HB3	1:E:80:SER:H	1.71	0.55
1:G:187:GLY:HA3	1:G:284:THR:H	1.71	0.55
1:G:390:ASP:O	1:G:394:LEU:HB3	2.05	0.55
1:G:454:LYS:HA	1:G:457:ILE:HD12	1.88	0.55
1:I:245:ASP:O	1:I:246:GLU:C	2.49	0.55
1:I:392:HIS:C	1:I:394:LEU:H	2.14	0.55
1:K:226:TYR:O	1:K:270:GLU:HB2	2.06	0.55
1:A:102:VAL:HG12	1:A:103:VAL:N	2.21	0.55
1:A:306:ILE:HG12	1:A:320:LEU:CD1	2.36	0.55
1:C:89:MET:HB2	1:C:118:TYR:O	2.06	0.55
1:C:124:ALA:HB1	1:C:434:HIS:HE1	1.71	0.55
1:E:208:ILE:HA	1:E:212:PHE:HB3	1.87	0.55
1:G:452:VAL:HG12	1:G:452:VAL:O	2.06	0.55
1:I:431:ILE:HG22	1:I:432:ILE:N	2.20	0.55
1:O:186:TYR:OH	1:O:206:ASN:HA	2.06	0.55
1:O:218:VAL:O	1:O:222:ILE:N	2.34	0.55
1:A:281:LYS:HE2	1:C:175:ASN:OD1	2.06	0.55
1:E:105:ASN:HD22	1:E:105:ASN:N	2.04	0.55
1:E:233:MET:HE3	1:G:231:ASN:HB3	1.88	0.55
1:I:218:VAL:O	1:I:221:TYR:HB3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:197:TYR:HA	1:K:200:ASP:HB3	1.88	0.55
2:L:855:ASP:O	2:L:858:ASN:N	2.37	0.55
1:M:175:ASN:O	1:M:275:PRO:HD2	2.06	0.55
1:M:195:PRO:O	1:M:198:LEU:HB2	2.06	0.55
1:A:384:ILE:O	1:A:384:ILE:HG22	2.06	0.55
1:C:454:LYS:HA	1:C:457:ILE:HD12	1.88	0.55
1:E:102:VAL:C	1:E:106:ILE:CD1	2.73	0.55
1:I:216:ILE:HD11	1:I:227:PHE:HE1	1.71	0.55
1:I:322:PHE:CD1	1:I:323:TYR:N	2.74	0.55
1:O:130:GLN:O	1:O:131:GLN:C	2.47	0.55
1:O:177:ILE:HG22	1:O:178:GLU:N	2.20	0.55
1:O:208:ILE:HG13	1:O:263:LEU:HD22	1.88	0.55
1:O:373:ASN:O	1:O:373:ASN:ND2	2.26	0.55
1:I:207:LEU:O	1:I:208:ILE:O	2.25	0.55
1:M:431:ILE:HG22	1:M:432:ILE:N	2.20	0.55
1:O:120:TYR:CD2	1:O:148:ILE:CG2	2.89	0.55
1:O:142:ARG:O	1:O:143:ALA:C	2.50	0.55
1:C:384:ILE:O	1:C:385:TYR:C	2.49	0.55
1:C:386:GLU:O	1:C:388:ILE:N	2.39	0.55
1:E:21:GLY:HA3	1:E:87:ILE:HD13	1.88	0.55
1:E:195:PRO:HD2	1:E:198:LEU:HD21	1.89	0.55
1:G:245:ASP:O	1:G:248:GLY:N	2.26	0.55
1:G:313:VAL:HG13	1:G:314:GLU:HG3	1.89	0.55
1:I:389:ALA:O	1:I:393:PHE:N	2.39	0.55
1:O:61:LEU:HD13	1:O:61:LEU:H	1.72	0.55
1:O:290:THR:HG22	1:O:291:LYS:N	2.21	0.55
1:O:452:VAL:HG12	1:O:452:VAL:O	2.06	0.55
1:A:322:PHE:HD2	1:A:367:GLU:HG2	1.71	0.55
1:A:435:ARG:HH22	1:A:458:LEU:HD13	1.71	0.55
1:C:195:PRO:CB	1:C:197:TYR:CE2	2.90	0.55
1:E:100:TYR:HB2	1:E:131:GLN:CD	2.31	0.55
1:E:324:GLY:O	1:E:365:THR:N	2.33	0.55
1:G:64:ILE:HD11	1:G:72:ALA:HB1	1.89	0.55
1:G:216:ILE:HG23	1:G:217:ASP:H	1.71	0.55
1:I:103:VAL:CA	1:I:106:ILE:HD12	2.37	0.55
1:I:452:VAL:HG12	1:I:455:ILE:HG12	1.88	0.55
1:M:83:GLN:O	1:M:84:TYR:C	2.49	0.55
1:M:304:LEU:HD22	1:M:320:LEU:HD11	1.89	0.55
1:O:188:TYR:N	1:O:284:THR:O	2.38	0.55
1:A:142:ARG:O	1:A:143:ALA:C	2.46	0.55
1:A:318:LEU:O	1:A:370:HIS:HD2	1.90	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:225:SER:CB	1:K:271:ASN:HB2	2.33	0.55
1:K:436:LEU:HD13	1:K:452:VAL:HG11	1.88	0.55
1:M:123:TRP:CE3	1:M:124:ALA:HA	2.42	0.55
1:M:187:GLY:HA3	1:M:284:THR:N	2.20	0.55
1:M:217:ASP:HB2	1:M:433:LEU:HD13	1.87	0.55
1:M:279:SER:HB2	1:O:277:SER:HB2	1.89	0.55
1:O:171:ILE:HD12	1:O:299:GLY:HA2	1.86	0.55
1:A:212:PHE:O	1:A:213:GLY:C	2.50	0.55
1:A:257:LYS:CD	1:A:259:CYS:O	2.55	0.55
1:C:152:GLN:NE2	1:C:152:GLN:H	2.04	0.55
1:C:436:LEU:O	1:C:440:VAL:HG23	2.06	0.55
1:E:375:ASN:C	1:E:375:ASN:OD1	2.50	0.55
1:G:304:LEU:CD2	1:G:320:LEU:HD11	2.31	0.55
1:K:62:GLN:O	1:K:63:THR:C	2.49	0.55
1:K:100:TYR:HB2	1:K:131:GLN:CD	2.32	0.55
1:M:75:PHE:HD2	1:M:80:SER:HB3	1.72	0.55
1:M:265:PHE:C	1:M:265:PHE:CD2	2.85	0.55
1:M:293:LEU:O	1:M:307:GLU:HA	2.06	0.55
1:O:41:GLN:HG2	1:O:41:GLN:O	2.05	0.55
1:O:52:LEU:C	1:O:81:PHE:CE1	2.85	0.55
1:O:199:TYR:N	1:O:199:TYR:CD1	2.75	0.55
1:A:49:ILE:HD12	1:A:69:LEU:HD22	1.89	0.55
1:A:123:TRP:CZ2	1:A:433:LEU:HD23	2.42	0.55
1:A:257:LYS:HG2	1:A:259:CYS:O	2.07	0.55
1:A:262:HIS:CE1	1:C:176:SER:HB2	2.43	0.55
1:C:57:LEU:O	1:C:58:LYS:C	2.50	0.55
1:E:161:ARG:HA	1:E:164:GLU:OE1	2.07	0.55
1:E:201:ILE:HG23	1:E:202:GLU:N	2.21	0.55
1:E:378:VAL:O	1:E:379:GLY:C	2.46	0.55
1:G:102:VAL:HG12	1:G:106:ILE:HD11	1.89	0.55
1:G:237:ASN:H	1:G:261:ASP:CG	2.14	0.55
1:I:200:ASP:C	1:I:200:ASP:OD1	2.50	0.55
1:K:208:ILE:O	1:K:209:SER:C	2.50	0.55
1:K:416:LYS:HD2	1:K:418:GLY:HA2	1.89	0.55
1:M:26:THR:HB	1:M:30:SER:HB2	1.89	0.55
1:A:30:SER:OG	1:A:33:ALA:HB2	2.06	0.54
1:A:152:GLN:NE2	1:A:214:HIS:HE1	2.05	0.54
1:C:167:SER:OG	1:C:168:GLU:N	2.38	0.54
1:C:199:TYR:N	1:C:199:TYR:CD1	2.74	0.54
1:E:22:PHE:CE2	1:E:91:VAL:HB	2.42	0.54
1:E:78:LEU:O	1:E:79:GLU:C	2.49	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:194:SER:HB3	1:E:199:TYR:CZ	2.32	0.54
1:K:158:TYR:HB2	1:K:318:LEU:HD12	1.89	0.54
1:K:453:SER:HA	1:K:456:MET:HE1	1.88	0.54
1:M:78:LEU:O	1:M:79:GLU:C	2.50	0.54
1:M:149:ILE:HG23	1:M:151:LEU:HD12	1.88	0.54
2:H:852:THR:HG22	2:H:853:MET:N	2.21	0.54
1:K:136:TYR:O	1:K:137:SER:C	2.50	0.54
1:K:215:THR:O	1:K:216:ILE:C	2.48	0.54
1:A:229:LYS:C	1:A:230:ILE:HG23	2.32	0.54
1:G:215:THR:O	1:G:216:ILE:C	2.50	0.54
1:I:416:LYS:HB3	1:I:428:LYS:HG2	1.89	0.54
1:O:312:PHE:O	1:O:316:SER:N	2.40	0.54
1:A:455:ILE:H	1:A:455:ILE:HD13	1.73	0.54
1:C:126:ALA:HB1	1:C:131:GLN:OE1	2.05	0.54
1:C:212:PHE:HD1	1:C:280:PHE:CE1	2.26	0.54
1:E:218:VAL:C	1:E:222:ILE:HD12	2.32	0.54
1:G:125:LEU:HD13	1:G:430:ALA:HB1	1.89	0.54
1:I:65:GLU:O	1:I:68:GLN:NE2	2.40	0.54
1:I:229:LYS:HE3	1:I:449:THR:CG2	2.37	0.54
1:K:232:ALA:O	1:K:444:ASP:HA	2.08	0.54
1:A:81:PHE:O	1:A:83:GLN:N	2.40	0.54
1:A:188:TYR:N	1:A:284:THR:O	2.34	0.54
1:C:77:SER:HB3	1:C:80:SER:OG	2.07	0.54
1:C:129:VAL:CG1	1:C:130:GLN:H	2.20	0.54
1:E:111:SER:N	1:E:142:ARG:HH22	2.06	0.54
1:E:443:SER:O	1:E:444:ASP:C	2.50	0.54
1:I:107:LEU:O	1:I:142:ARG:NH2	2.38	0.54
1:I:293:LEU:HG	1:I:294:VAL:N	2.18	0.54
1:O:129:VAL:HG13	1:O:130:GLN:H	1.73	0.54
1:A:83:GLN:O	1:A:84:TYR:C	2.50	0.54
1:E:138:ILE:O	1:E:139:SER:C	2.50	0.54
1:G:40:ILE:O	1:G:40:ILE:HG22	2.08	0.54
1:G:128:SER:O	1:G:129:VAL:C	2.50	0.54
1:G:151:LEU:C	1:G:153:GLY:N	2.64	0.54
1:K:149:ILE:CD1	1:K:430:ALA:HB2	2.36	0.54
1:M:245:ASP:C	1:M:245:ASP:OD1	2.48	0.54
1:M:435:ARG:CB	1:M:455:ILE:HG23	2.38	0.54
1:O:128:SER:O	1:O:129:VAL:C	2.50	0.54
1:A:25:LEU:HB3	1:A:52:LEU:HD21	1.90	0.54
1:A:177:ILE:CB	1:A:276:VAL:HG13	2.38	0.54
1:C:159:ILE:HD12	1:C:218:VAL:CG2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:195:PRO:CB	1:C:197:TYR:CD2	2.91	0.54
1:C:232:ALA:O	1:C:444:ASP:HA	2.08	0.54
1:I:393:PHE:C	1:I:394:LEU:HD12	2.33	0.54
1:K:190:ARG:HG3	1:K:199:TYR:CZ	2.42	0.54
1:K:196:GLU:HG2	1:O:56:THR:HG21	1.87	0.54
1:K:245:ASP:O	1:K:247:ASN:N	2.40	0.54
1:O:64:ILE:HG12	1:O:72:ALA:HB3	1.89	0.54
1:O:83:GLN:O	1:O:84:TYR:C	2.49	0.54
1:O:373:ASN:HD22	1:O:373:ASN:C	2.12	0.54
1:A:96:VAL:O	1:A:99:HIS:HB2	2.08	0.54
1:C:106:ILE:HG21	1:C:119:LEU:HD11	1.90	0.54
1:E:38:LEU:O	1:E:39:ALA:C	2.51	0.54
1:I:201:ILE:HB	1:I:258:THR:CB	2.37	0.54
1:K:179:ILE:HD11	1:K:219:LEU:HD13	1.90	0.54
1:M:171:ILE:O	1:M:300:THR:N	2.41	0.54
1:A:208:ILE:HA	1:A:212:PHE:HB3	1.90	0.54
1:A:229:LYS:O	1:A:230:ILE:CG2	2.55	0.54
1:C:195:PRO:O	1:C:198:LEU:HB2	2.08	0.54
1:C:389:ALA:O	1:C:390:ASP:O	2.25	0.54
1:E:382:LEU:C	1:E:384:ILE:H	2.15	0.54
1:G:129:VAL:O	1:G:132:ALA:HB3	2.08	0.54
1:G:379:GLY:O	1:G:382:LEU:HB3	2.07	0.54
1:I:134:GLU:O	1:I:135:LEU:C	2.49	0.54
1:O:56:THR:HG1	1:O:59:SER:HG	1.55	0.54
1:O:96:VAL:N	1:O:97:PRO:HD2	2.23	0.54
1:C:105:ASN:O	1:C:106:ILE:C	2.49	0.54
1:C:432:ILE:HG23	1:C:455:ILE:HG22	1.90	0.54
1:E:452:VAL:O	1:E:452:VAL:HG12	2.08	0.54
1:G:202:GLU:O	1:G:203:SER:C	2.50	0.54
1:G:214:HIS:ND1	1:G:314:GLU:CD	2.66	0.54
1:K:31:TRP:O	1:K:35:THR:HG23	2.08	0.54
1:K:56:THR:O	1:K:59:SER:OG	2.25	0.54
1:K:322:PHE:CG	1:K:323:TYR:N	2.76	0.54
1:M:39:ALA:HA	1:M:382:LEU:HD12	1.90	0.54
1:M:84:TYR:CD1	1:M:86:ASP:HB2	2.42	0.54
1:M:313:VAL:HG23	1:M:318:LEU:HD11	1.90	0.54
1:O:123:TRP:HD1	1:O:214:HIS:CD2	2.26	0.54
1:O:129:VAL:O	1:O:132:ALA:N	2.41	0.54
1:O:312:PHE:O	1:O:316:SER:CB	2.55	0.54
1:A:105:ASN:HA	1:A:108:GLU:HG3	1.90	0.53
1:C:52:LEU:HD11	1:C:63:THR:CG2	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:263:LEU:HD12	1:C:264:LEU:O	2.07	0.53
1:E:191:PRO:HG2	1:E:194:SER:OG	2.07	0.53
1:E:233:MET:HE3	1:G:266:GLN:HG3	1.89	0.53
1:G:102:VAL:C	1:G:106:ILE:HD12	2.33	0.53
1:G:104:LYS:O	1:G:107:LEU:HB2	2.08	0.53
1:G:115:ASN:O	1:G:117:ARG:HB2	2.07	0.53
1:I:381:ILE:HG22	1:I:385:TYR:CE1	2.44	0.53
1:K:313:VAL:HG13	1:K:314:GLU:N	2.23	0.53
1:O:208:ILE:HG21	1:O:441:PHE:CE1	2.44	0.53
1:A:48:GLN:OE1	1:A:71:HIS:CD2	2.62	0.53
1:A:216:ILE:HG23	1:A:217:ASP:H	1.72	0.53
1:A:232:ALA:O	1:A:444:ASP:HA	2.07	0.53
1:C:208:ILE:O	1:C:209:SER:C	2.52	0.53
1:I:279:SER:HB2	1:K:277:SER:CB	2.38	0.53
1:I:381:ILE:CG2	1:I:385:TYR:HE1	2.20	0.53
1:K:436:LEU:CD1	1:K:452:VAL:HG11	2.39	0.53
1:M:129:VAL:O	1:M:133:GLU:N	2.33	0.53
1:C:78:LEU:O	1:C:82:ALA:N	2.38	0.53
1:C:178:GLU:C	1:C:179:ILE:HG13	2.31	0.53
1:E:171:ILE:HD12	1:E:299:GLY:HA3	1.90	0.53
1:G:212:PHE:O	1:G:213:GLY:C	2.51	0.53
1:G:435:ARG:NH1	1:G:455:ILE:O	2.40	0.53
1:I:218:VAL:O	1:I:222:ILE:N	2.34	0.53
1:I:436:LEU:O	1:I:440:VAL:HG23	2.08	0.53
1:K:89:MET:CB	1:K:118:TYR:HB2	2.32	0.53
1:K:134:GLU:O	1:K:138:ILE:HG13	2.08	0.53
1:M:177:ILE:HG22	1:M:178:GLU:N	2.22	0.53
1:O:372:ARG:O	1:O:373:ASN:C	2.51	0.53
1:A:152:GLN:O	1:A:153:GLY:C	2.52	0.53
1:A:228:GLN:HE22	1:A:273:LYS:CE	2.22	0.53
1:A:262:HIS:CD2	1:A:263:LEU:N	2.77	0.53
1:C:107:LEU:O	1:C:142:ARG:NH2	2.41	0.53
1:C:180:SER:O	1:C:293:LEU:HD12	2.09	0.53
1:C:435:ARG:NH1	1:C:455:ILE:O	2.41	0.53
2:D:856:VAL:O	2:D:860:ILE:HG22	2.08	0.53
1:E:129:VAL:O	1:E:132:ALA:HB3	2.08	0.53
1:E:195:PRO:O	1:E:199:TYR:HD1	1.91	0.53
1:E:237:ASN:H	1:E:261:ASP:CG	2.15	0.53
1:G:178:GLU:HA	1:G:277:SER:O	2.09	0.53
1:M:134:GLU:O	1:M:135:LEU:C	2.51	0.53
1:A:149:ILE:CG2	1:A:151:LEU:HD12	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:TYR:CB	1:A:318:LEU:HD12	2.38	0.53
1:C:61:LEU:N	1:C:61:LEU:CD1	2.72	0.53
1:E:14:SER:OG	1:E:15:SER:N	2.42	0.53
1:G:251:THR:C	1:G:253:GLU:H	2.15	0.53
1:O:159:ILE:O	1:O:160:VAL:C	2.50	0.53
1:E:30:SER:O	1:E:34:LYS:HG3	2.08	0.53
1:E:166:ILE:HG22	1:E:167:SER:N	2.23	0.53
1:I:159:ILE:HD13	1:I:159:ILE:N	2.24	0.53
1:K:53:TYR:C	1:K:53:TYR:CD2	2.86	0.53
1:K:100:TYR:HB2	1:K:131:GLN:OE1	2.09	0.53
1:K:266:GLN:HA	1:K:276:VAL:O	2.08	0.53
1:M:428:LYS:O	1:M:432:ILE:HG13	2.09	0.53
1:C:284:THR:HA	1:C:285:PRO:C	2.32	0.53
1:E:40:ILE:HG23	1:E:47:PHE:CB	2.39	0.53
1:I:96:VAL:HB	1:I:97:PRO:HD3	1.91	0.53
1:M:313:VAL:HG13	1:M:314:GLU:N	2.22	0.53
1:M:452:VAL:O	1:M:452:VAL:HG12	2.07	0.53
1:O:79:GLU:HG2	1:O:109:HIS:CD2	2.44	0.53
1:O:138:ILE:O	1:O:139:SER:C	2.51	0.53
1:O:189:GLU:HB2	1:O:284:THR:OG1	2.09	0.53
1:O:248:GLY:O	1:O:249:LYS:C	2.46	0.53
1:O:322:PHE:HD2	1:O:367:GLU:HB3	1.73	0.53
1:A:38:LEU:HD23	1:A:41:GLN:OE1	2.09	0.53
1:A:266:GLN:HA	1:A:276:VAL:O	2.09	0.53
1:I:208:ILE:HD13	1:I:441:PHE:CZ	2.44	0.53
1:M:91:VAL:HG22	1:M:120:TYR:HB3	1.89	0.53
1:M:177:ILE:HD13	1:M:219:LEU:HD11	1.90	0.53
1:M:244:LEU:O	1:M:245:ASP:C	2.51	0.53
1:O:177:ILE:HD13	1:O:219:LEU:HD11	1.91	0.53
1:A:39:ALA:HA	1:A:382:LEU:HD12	1.90	0.53
1:A:84:TYR:C	1:A:86:ASP:H	2.17	0.53
1:A:190:ARG:HG3	1:A:191:PRO:CD	2.38	0.53
1:A:428:LYS:O	1:A:429:ASP:C	2.49	0.53
1:C:179:ILE:HG22	1:C:180:SER:N	2.23	0.53
1:E:370:HIS:CD2	2:F:848:PHE:CD2	2.95	0.53
1:G:245:ASP:O	1:G:247:ASN:N	2.41	0.53
1:I:28:GLY:HA2	1:I:67:LEU:CD2	2.34	0.53
1:K:125:LEU:HB2	1:K:149:ILE:HD13	1.91	0.53
1:K:313:VAL:HG13	1:K:314:GLU:H	1.73	0.53
1:K:453:SER:CA	1:K:456:MET:HE1	2.39	0.53
1:M:64:ILE:HG22	1:M:65:GLU:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:65:GLU:O	1:M:68:GLN:NE2	2.42	0.53
1:M:206:ASN:C	1:M:206:ASN:OD1	2.51	0.53
1:C:263:LEU:HD12	1:C:264:LEU:N	2.24	0.53
1:G:158:TYR:HB2	1:G:318:LEU:HD12	1.91	0.53
1:G:427:PHE:HA	1:G:430:ALA:HB3	1.91	0.53
1:M:105:ASN:HA	1:M:108:GLU:HG3	1.89	0.53
1:M:128:SER:O	1:M:131:GLN:HB2	2.08	0.53
1:O:231:ASN:HB2	1:O:449:THR:OG1	2.08	0.53
1:A:226:TYR:O	1:A:270:GLU:HB2	2.08	0.52
1:A:427:PHE:O	1:A:431:ILE:HB	2.09	0.52
1:C:75:PHE:N	1:C:75:PHE:CD1	2.77	0.52
1:C:147:THR:HB	1:C:427:PHE:CE1	2.43	0.52
1:C:245:ASP:O	1:C:246:GLU:C	2.52	0.52
2:D:852:THR:O	2:D:856:VAL:HG23	2.09	0.52
1:E:293:LEU:HB2	1:E:311:GLY:HA2	1.91	0.52
1:E:389:ALA:O	1:E:392:HIS:HB3	2.09	0.52
1:G:148:ILE:HD13	1:G:388:ILE:HD11	1.91	0.52
1:G:174:ILE:HG22	1:G:175:ASN:N	2.23	0.52
1:G:222:ILE:HG22	1:G:223:THR:N	2.23	0.52
1:O:40:ILE:HG23	1:O:47:PHE:HB2	1.91	0.52
1:A:265:PHE:C	1:C:266:GLN:HE22	2.17	0.52
1:K:105:ASN:O	1:K:106:ILE:C	2.52	0.52
1:M:218:VAL:O	1:M:221:TYR:HB3	2.09	0.52
1:O:129:VAL:HA	1:O:434:HIS:HD2	1.74	0.52
1:A:89:MET:O	1:A:89:MET:HG3	2.09	0.52
1:A:201:ILE:HG23	1:A:202:GLU:N	2.24	0.52
1:A:281:LYS:CE	1:C:298:HIS:NE2	2.72	0.52
1:A:291:LYS:HG3	1:A:307:GLU:HB3	1.91	0.52
1:E:57:LEU:HD21	1:E:74:GLY:O	2.09	0.52
1:G:218:VAL:O	1:G:222:ILE:HD12	2.09	0.52
1:I:454:LYS:HA	1:I:457:ILE:HD12	1.91	0.52
1:O:52:LEU:C	1:O:81:PHE:HE1	2.16	0.52
1:O:422:GLU:H	1:O:422:GLU:CD	2.17	0.52
1:A:208:ILE:HD13	1:A:441:PHE:HZ	1.67	0.52
1:C:226:TYR:O	1:C:270:GLU:HB2	2.09	0.52
1:E:232:ALA:O	1:E:444:ASP:HA	2.10	0.52
1:G:75:PHE:N	1:G:75:PHE:CD1	2.78	0.52
1:G:384:ILE:O	1:G:385:TYR:C	2.51	0.52
1:M:120:TYR:HE2	1:M:150:CYS:HB2	1.74	0.52
1:M:201:ILE:HG23	1:M:202:GLU:H	1.74	0.52
1:M:226:TYR:O	1:M:270:GLU:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:251:THR:C	1:O:253:GLU:H	2.18	0.52
1:A:96:VAL:HA	1:A:99:HIS:CG	2.44	0.52
1:A:123:TRP:CE3	1:A:124:ALA:HA	2.45	0.52
1:E:142:ARG:HB3	1:E:145:LEU:HB2	1.91	0.52
1:E:233:MET:CE	1:G:266:GLN:HG3	2.40	0.52
1:G:78:LEU:O	1:G:82:ALA:N	2.38	0.52
1:K:251:THR:C	1:K:253:GLU:H	2.16	0.52
1:M:64:ILE:HA	1:M:69:LEU:HD12	1.91	0.52
1:M:197:TYR:CD1	1:M:198:LEU:HD12	2.43	0.52
1:M:219:LEU:O	1:M:220:GLN:C	2.50	0.52
1:A:30:SER:O	1:A:34:LYS:HG3	2.10	0.52
1:A:147:THR:C	1:A:148:ILE:HG13	2.33	0.52
1:A:455:ILE:N	1:A:455:ILE:HD13	2.25	0.52
1:E:49:ILE:HD13	1:E:69:LEU:CD2	2.40	0.52
1:E:103:VAL:HA	1:E:106:ILE:CD1	2.38	0.52
1:E:263:LEU:HD12	1:E:263:LEU:C	2.34	0.52
1:G:223:THR:OG1	1:G:224:GLY:N	2.40	0.52
1:I:128:SER:OG	1:I:131:GLN:HB2	2.10	0.52
1:I:218:VAL:CG1	1:I:219:LEU:N	2.70	0.52
1:K:77:SER:CB	1:K:80:SER:HB2	2.38	0.52
1:M:244:LEU:CD2	1:M:248:GLY:CA	2.81	0.52
1:O:168:GLU:O	1:O:170:CYS:N	2.42	0.52
1:A:238:ILE:O	1:A:257:LYS:CE	2.58	0.52
1:A:290:THR:HG22	1:A:291:LYS:N	2.24	0.52
1:I:84:TYR:C	1:I:86:ASP:H	2.15	0.52
1:I:154:ARG:NH1	1:I:417:GLN:OE1	2.37	0.52
1:K:123:TRP:HD1	1:K:214:HIS:CD2	2.27	0.52
1:K:389:ALA:O	1:K:393:PHE:N	2.42	0.52
1:K:431:ILE:HG23	1:K:435:ARG:HD2	1.92	0.52
1:M:313:VAL:CG1	1:M:314:GLU:N	2.72	0.52
1:O:81:PHE:O	1:O:83:GLN:N	2.43	0.52
1:C:189:GLU:HB2	1:C:284:THR:OG1	2.10	0.52
1:E:75:PHE:HZ	1:E:84:TYR:CD2	2.28	0.52
1:E:142:ARG:O	1:E:413:LYS:NZ	2.34	0.52
1:G:100:TYR:HB2	1:G:131:GLN:CD	2.35	0.52
1:I:136:TYR:O	1:I:137:SER:C	2.51	0.52
1:K:426:THR:O	1:K:429:ASP:N	2.43	0.52
1:O:88:ASP:O	1:O:117:ARG:N	2.34	0.52
1:A:146:GLN:OE1	1:A:413:LYS:HB2	2.09	0.52
1:A:263:LEU:HD12	1:A:263:LEU:C	2.35	0.52
1:A:288:LYS:HD2	1:C:323:TYR:CE2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:SER:OG	1:C:210:ASN:N	2.38	0.52
1:E:192:MET:CE	1:O:15:SER:HB3	2.25	0.52
1:E:392:HIS:CD2	1:E:393:PHE:CD2	2.97	0.52
1:I:372:ARG:HH21	2:J:847:LEU:HB3	1.74	0.52
1:K:136:TYR:HB2	1:K:431:ILE:HD11	1.91	0.52
1:K:187:GLY:HA3	1:K:284:THR:N	2.25	0.52
1:M:251:THR:C	1:M:253:GLU:H	2.18	0.52
1:E:77:SER:HB3	1:E:80:SER:HB2	1.92	0.52
1:E:124:ALA:O	1:E:125:LEU:C	2.51	0.52
1:E:128:SER:OG	1:E:131:GLN:HB2	2.10	0.52
1:E:177:ILE:HG22	1:E:276:VAL:HG13	1.91	0.52
1:G:152:GLN:O	1:G:153:GLY:O	2.27	0.52
1:I:312:PHE:CB	1:I:315:ILE:HD12	2.31	0.52
1:M:121:VAL:HG21	1:M:427:PHE:HZ	1.75	0.52
1:M:198:LEU:HB2	1:M:199:TYR:CE1	2.45	0.52
1:O:23:VAL:HG22	1:O:53:TYR:HB3	1.92	0.52
1:A:25:LEU:HD23	1:A:63:THR:CG2	2.39	0.51
1:A:42:GLN:C	1:A:43:LEU:HD23	2.31	0.51
1:A:209:SER:OG	1:A:210:ASN:N	2.42	0.51
1:A:313:VAL:HG13	1:A:314:GLU:N	2.25	0.51
1:C:90:ILE:HB	1:C:119:LEU:HD12	1.91	0.51
1:G:105:ASN:N	1:G:105:ASN:HD22	2.08	0.51
1:G:136:TYR:O	1:G:137:SER:C	2.53	0.51
1:G:147:THR:O	1:G:426:THR:HG22	2.10	0.51
1:G:187:GLY:HA3	1:G:284:THR:N	2.25	0.51
1:G:434:HIS:N	1:G:437:ILE:HD12	2.25	0.51
1:G:456:MET:N	1:G:456:MET:SD	2.83	0.51
1:I:103:VAL:HA	1:I:106:ILE:HD13	1.92	0.51
1:I:166:ILE:O	1:I:167:SER:C	2.52	0.51
1:K:208:ILE:O	1:K:212:PHE:HB3	2.10	0.51
1:K:422:GLU:CD	1:K:422:GLU:H	2.17	0.51
1:K:454:LYS:CA	1:K:457:ILE:HD12	2.38	0.51
1:M:201:ILE:CG2	1:M:202:GLU:N	2.73	0.51
1:M:286:VAL:HG23	1:M:288:LYS:HE3	1.91	0.51
1:O:427:PHE:O	1:O:431:ILE:HB	2.10	0.51
1:A:372:ARG:O	1:A:373:ASN:C	2.52	0.51
1:C:64:ILE:HG12	1:C:69:LEU:HB2	1.92	0.51
1:C:318:LEU:O	1:C:370:HIS:HD2	1.93	0.51
1:C:372:ARG:O	1:C:373:ASN:C	2.53	0.51
1:E:64:ILE:O	1:E:68:GLN:N	2.43	0.51
1:E:195:PRO:HB2	1:E:198:LEU:HG	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:266:GLN:NE2	1:G:231:ASN:OD1	2.42	0.51
1:E:451:ASP:OD1	1:E:451:ASP:O	2.28	0.51
1:G:142:ARG:HB2	1:G:145:LEU:HB3	1.91	0.51
1:G:201:ILE:HG23	1:G:202:GLU:H	1.74	0.51
1:I:40:ILE:O	1:I:40:ILE:HG22	2.10	0.51
1:I:53:TYR:CD2	1:I:54:ASN:CA	2.93	0.51
1:I:225:SER:HB2	1:I:271:ASN:CB	2.38	0.51
1:K:181:GLY:O	1:K:281:LYS:N	2.41	0.51
1:K:182:ASN:HD21	1:K:283:GLY:CA	2.22	0.51
1:K:272:GLY:O	1:K:273:LYS:HB2	2.10	0.51
1:M:107:LEU:O	1:M:142:ARG:NH2	2.41	0.51
1:O:64:ILE:O	1:O:68:GLN:N	2.42	0.51
1:O:188:TYR:CZ	1:O:238:ILE:HG12	2.46	0.51
1:O:381:ILE:O	1:O:384:ILE:N	2.39	0.51
1:A:84:TYR:CD1	1:A:86:ASP:HB2	2.46	0.51
1:A:237:ASN:O	1:A:239:PRO:HD3	2.10	0.51
1:C:123:TRP:CD1	1:C:214:HIS:CD2	2.98	0.51
1:E:100:TYR:HA	1:E:135:LEU:HD11	1.92	0.51
1:E:182:ASN:HA	1:E:281:LYS:O	2.10	0.51
1:E:233:MET:HE1	1:G:231:ASN:N	2.25	0.51
1:E:385:TYR:CA	1:E:388:ILE:HD12	2.40	0.51
1:K:134:GLU:HA	1:K:137:SER:OG	2.10	0.51
1:M:198:LEU:N	1:M:198:LEU:HD13	2.25	0.51
1:O:273:LYS:N	1:O:273:LYS:HD3	2.25	0.51
1:O:284:THR:HA	1:O:285:PRO:C	2.35	0.51
1:A:103:VAL:HG11	1:A:135:LEU:HD13	1.92	0.51
1:A:161:ARG:HA	1:A:164:GLU:OE1	2.11	0.51
1:A:392:HIS:C	1:A:394:LEU:H	2.18	0.51
1:C:272:GLY:O	1:C:273:LYS:HB2	2.09	0.51
1:E:132:ALA:O	1:E:133:GLU:C	2.52	0.51
1:E:417:GLN:HB2	1:E:424:PHE:C	2.35	0.51
1:G:105:ASN:HA	1:G:108:GLU:HG3	1.93	0.51
1:G:199:TYR:CD1	1:G:199:TYR:N	2.78	0.51
1:I:207:LEU:O	1:I:208:ILE:C	2.53	0.51
1:I:211:SER:O	1:I:215:THR:OG1	2.25	0.51
1:I:250:ARG:O	1:I:250:ARG:HG2	2.05	0.51
1:I:266:GLN:NE2	1:K:231:ASN:OD1	2.43	0.51
1:M:19:ARG:HB3	1:M:50:VAL:CG2	2.40	0.51
1:M:121:VAL:CG2	1:M:427:PHE:HZ	2.23	0.51
1:O:190:ARG:HH22	1:O:196:GLU:HA	1.76	0.51
1:A:41:GLN:C	1:A:43:LEU:N	2.66	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:ARG:O	1:C:17:PRO:C	2.53	0.51
1:E:25:LEU:HD23	1:E:63:THR:CG2	2.41	0.51
1:E:51:ALA:HB3	1:E:87:ILE:HD11	1.92	0.51
1:E:111:SER:HA	1:E:142:ARG:NH2	2.25	0.51
1:G:185:TRP:O	1:G:199:TYR:HE2	1.94	0.51
1:I:185:TRP:CE3	1:I:186:TYR:CZ	2.98	0.51
1:I:185:TRP:CZ3	1:I:186:TYR:OH	2.63	0.51
1:I:244:LEU:CD1	1:I:250:ARG:CB	2.87	0.51
1:I:266:GLN:HA	1:I:276:VAL:O	2.10	0.51
1:K:152:GLN:O	1:K:153:GLY:C	2.54	0.51
1:K:292:ASN:H	1:K:292:ASN:HD22	1.57	0.51
1:M:30:SER:O	1:M:33:ALA:HB3	2.11	0.51
1:O:53:TYR:CD2	1:O:54:ASN:N	2.78	0.51
1:A:217:ASP:O	1:A:221:TYR:N	2.44	0.51
1:A:245:ASP:OD1	1:A:249:LYS:HB3	2.10	0.51
1:A:315:ILE:CG2	1:A:377:VAL:HG22	2.41	0.51
1:C:372:ARG:O	1:C:373:ASN:ND2	2.43	0.51
2:L:853:MET:O	2:L:854:ASP:C	2.50	0.51
1:M:322:PHE:CG	1:M:323:TYR:N	2.76	0.51
1:O:77:SER:CB	1:O:80:SER:HB2	2.39	0.51
1:O:301:LYS:HD3	1:O:325:ILE:HD11	1.92	0.51
1:E:200:ASP:O	1:E:201:ILE:C	2.51	0.51
1:E:233:MET:CE	1:G:231:ASN:HB3	2.41	0.51
1:G:32:VAL:CG1	1:G:36:HIS:HB2	2.38	0.51
1:G:436:LEU:HB2	1:G:455:ILE:HD11	1.93	0.51
1:I:197:TYR:CE1	1:I:198:LEU:CD2	2.94	0.51
1:M:179:ILE:HG22	1:M:180:SER:N	2.25	0.51
1:O:104:LYS:O	1:O:107:LEU:HB2	2.10	0.51
1:A:48:GLN:OE1	1:A:71:HIS:CG	2.64	0.51
1:A:62:GLN:CG	1:O:252:LYS:HD2	2.41	0.51
1:A:287:LYS:HZ3	1:A:290:THR:HB	1.75	0.51
1:A:319:VAL:HG22	1:A:370:HIS:CG	2.46	0.51
1:C:218:VAL:O	1:C:221:TYR:HB3	2.10	0.51
1:C:436:LEU:O	1:C:436:LEU:HG	2.08	0.51
1:E:79:GLU:O	1:E:80:SER:C	2.53	0.51
1:E:245:ASP:O	1:E:247:ASN:N	2.44	0.51
1:E:281:LYS:HD2	1:G:298:HIS:CD2	2.46	0.51
1:G:218:VAL:HG13	1:G:222:ILE:HD11	1.92	0.51
1:I:64:ILE:O	1:I:68:GLN:N	2.43	0.51
1:I:84:TYR:CE1	1:I:86:ASP:HB2	2.45	0.51
1:K:179:ILE:HB	1:K:278:CYS:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:452:VAL:HG12	1:K:455:ILE:HG13	1.90	0.51
1:M:216:ILE:CG2	1:M:217:ASP:N	2.72	0.51
1:M:377:VAL:HG11	2:N:859:TYR:CD2	2.46	0.51
1:O:146:GLN:HA	1:O:146:GLN:HE21	1.74	0.51
1:O:292:ASN:HD22	1:O:292:ASN:H	1.59	0.51
1:A:100:TYR:HA	1:A:135:LEU:HD11	1.91	0.51
1:A:158:TYR:CD1	1:A:318:LEU:HD12	2.46	0.51
1:A:245:ASP:N	1:A:249:LYS:O	2.39	0.51
1:C:145:LEU:O	1:C:413:LYS:HD2	2.10	0.51
1:E:54:ASN:O	1:E:75:PHE:O	2.29	0.51
1:G:116:LEU:HD21	1:G:145:LEU:CD1	2.37	0.51
1:G:189:GLU:HB2	1:G:284:THR:OG1	2.11	0.51
1:G:368:VAL:O	1:G:368:VAL:HG12	2.10	0.51
2:H:855:ASP:O	2:H:856:VAL:C	2.53	0.51
1:I:98:GLU:O	1:I:102:VAL:HG23	2.11	0.51
2:L:855:ASP:O	2:L:856:VAL:C	2.53	0.51
1:M:89:MET:CB	1:M:118:TYR:HB2	2.37	0.51
1:A:65:GLU:O	1:A:66:GLN:C	2.53	0.51
1:A:94:VAL:O	1:A:95:LYS:C	2.50	0.51
1:A:110:SER:OG	1:A:142:ARG:NH2	2.43	0.51
1:C:94:VAL:O	1:C:95:LYS:C	2.54	0.51
1:C:136:TYR:O	1:C:137:SER:C	2.54	0.51
1:C:437:ILE:O	1:C:438:ASP:C	2.54	0.51
1:E:375:ASN:OD1	1:E:377:VAL:HB	2.10	0.51
1:E:416:LYS:HA	1:E:426:THR:OG1	2.10	0.51
1:G:56:THR:OG1	1:G:59:SER:OG	2.28	0.51
1:G:102:VAL:CG1	1:G:106:ILE:HD11	2.41	0.51
1:G:151:LEU:C	1:G:153:GLY:H	2.19	0.51
1:I:54:ASN:O	1:I:75:PHE:O	2.29	0.51
1:I:266:GLN:CB	1:K:264:LEU:HD22	2.41	0.51
1:K:19:ARG:HA	1:K:48:GLN:O	2.11	0.51
1:K:431:ILE:CG2	1:K:432:ILE:N	2.74	0.51
1:O:227:PHE:CE2	1:O:269:LEU:HD23	2.46	0.51
1:A:58:LYS:HA	1:O:252:LYS:O	2.10	0.50
1:A:304:LEU:HD23	1:A:322:PHE:CB	2.29	0.50
1:A:431:ILE:HG22	1:A:432:ILE:N	2.26	0.50
1:C:52:LEU:CD1	1:C:63:THR:HG21	2.35	0.50
1:C:177:ILE:HA	1:C:296:ASP:O	2.11	0.50
1:E:20:VAL:HA	1:E:89:MET:O	2.11	0.50
1:E:65:GLU:O	1:E:68:GLN:NE2	2.28	0.50
1:E:206:ASN:OD1	1:E:206:ASN:O	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:386:GLU:O	1:E:388:ILE:N	2.44	0.50
1:G:168:GLU:O	1:G:169:GLY:C	2.54	0.50
1:G:389:ALA:O	1:G:393:PHE:N	2.35	0.50
1:I:146:GLN:OE1	1:I:414:PHE:HB3	2.10	0.50
1:I:384:ILE:HG22	1:I:388:ILE:HD11	1.92	0.50
1:K:427:PHE:O	1:K:428:LYS:C	2.51	0.50
1:O:103:VAL:HA	1:O:106:ILE:HD12	1.94	0.50
1:O:238:ILE:H	1:O:261:ASP:CG	2.20	0.50
1:O:384:ILE:O	1:O:385:TYR:C	2.54	0.50
1:A:230:ILE:HG22	1:A:267:GLY:HA3	1.93	0.50
1:C:64:ILE:O	1:C:68:GLN:N	2.44	0.50
1:E:212:PHE:O	1:E:213:GLY:C	2.54	0.50
1:G:123:TRP:CE3	1:G:124:ALA:HA	2.46	0.50
1:K:103:VAL:HA	1:K:106:ILE:HD12	1.93	0.50
1:M:40:ILE:HG22	1:M:40:ILE:O	2.11	0.50
1:M:174:ILE:HB	1:M:274:VAL:HG21	1.92	0.50
1:M:195:PRO:O	1:M:199:TYR:CD1	2.64	0.50
1:O:196:GLU:O	1:O:199:TYR:N	2.44	0.50
1:E:40:ILE:HG22	1:E:40:ILE:O	2.10	0.50
1:G:307:GLU:OE1	1:G:321:TYR:HE1	1.93	0.50
1:I:53:TYR:CD1	1:I:78:LEU:HD12	2.46	0.50
1:I:185:TRP:HZ3	1:I:186:TYR:OH	1.93	0.50
1:C:25:LEU:HB3	1:C:52:LEU:CD1	2.42	0.50
1:C:53:TYR:N	1:C:81:PHE:CE1	2.79	0.50
1:C:162:ALA:HA	1:C:304:LEU:HD11	1.93	0.50
1:C:177:ILE:HB	1:C:276:VAL:HG22	1.92	0.50
1:C:181:GLY:O	1:C:281:LYS:N	2.44	0.50
1:E:195:PRO:HB3	1:E:197:TYR:CD2	2.47	0.50
1:E:273:LYS:HD3	1:E:273:LYS:H	1.74	0.50
1:G:182:ASN:HD21	1:G:283:GLY:HA2	1.76	0.50
1:G:293:LEU:HB2	1:G:311:GLY:HA2	1.94	0.50
1:I:102:VAL:O	1:I:106:ILE:HD12	2.12	0.50
1:K:77:SER:HB3	1:K:80:SER:OG	2.10	0.50
1:M:111:SER:N	1:M:142:ARG:HH22	2.10	0.50
1:M:390:ASP:O	1:M:394:LEU:CB	2.38	0.50
1:A:22:PHE:HB2	1:A:52:LEU:HD12	1.94	0.50
1:A:185:TRP:CD1	2:B:857:TYR:HE1	2.29	0.50
1:A:198:LEU:HB2	1:A:199:TYR:CE1	2.46	0.50
1:C:67:LEU:N	1:C:67:LEU:HD23	2.26	0.50
1:E:53:TYR:C	1:E:53:TYR:CD2	2.89	0.50
1:E:236:ASN:HA	1:E:261:ASP:OD1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:319:VAL:HG12	1:E:320:LEU:N	2.25	0.50
1:G:85:LYS:HB3	1:G:85:LYS:NZ	2.26	0.50
1:G:136:TYR:CB	1:G:431:ILE:HD13	2.39	0.50
1:G:244:LEU:HD23	1:G:250:ARG:CA	2.33	0.50
1:K:22:PHE:N	1:K:51:ALA:O	2.28	0.50
1:K:253:GLU:HG2	1:O:61:LEU:HB3	1.91	0.50
1:O:216:ILE:CG2	1:O:217:ASP:N	2.73	0.50
1:A:96:VAL:HB	1:A:97:PRO:CD	2.40	0.50
1:A:142:ARG:O	1:A:144:ASN:N	2.45	0.50
1:C:59:SER:O	1:C:63:THR:OG1	2.24	0.50
1:G:208:ILE:HA	1:G:212:PHE:HB3	1.92	0.50
1:G:431:ILE:CG2	1:G:432:ILE:N	2.75	0.50
2:H:855:ASP:OD2	2:H:855:ASP:N	2.43	0.50
1:I:55:PRO:O	1:I:76:ASP:OD1	2.29	0.50
1:K:88:ASP:HA	1:K:115:ASN:C	2.35	0.50
1:K:273:LYS:HD3	1:K:273:LYS:N	2.27	0.50
1:M:257:LYS:O	1:M:257:LYS:HG3	2.12	0.50
1:O:67:LEU:O	1:O:68:GLN:HB3	2.09	0.50
1:O:77:SER:HB3	1:O:80:SER:H	1.76	0.50
1:O:290:THR:CG2	1:O:291:LYS:N	2.75	0.50
1:A:102:VAL:HG13	1:A:106:ILE:HD11	1.93	0.50
1:A:158:TYR:CG	1:A:318:LEU:HD12	2.47	0.50
1:C:251:THR:C	1:C:253:GLU:H	2.18	0.50
1:E:134:GLU:O	1:E:135:LEU:C	2.52	0.50
1:G:387:SER:OG	1:G:423:GLY:O	2.26	0.50
1:I:64:ILE:HG12	1:I:72:ALA:HB3	1.93	0.50
1:I:77:SER:O	1:I:80:SER:HB2	2.12	0.50
1:I:161:ARG:O	1:I:161:ARG:HG3	2.11	0.50
1:I:185:TRP:CD1	2:J:857:TYR:HE1	2.30	0.50
1:I:216:ILE:HG23	1:I:217:ASP:H	1.75	0.50
1:K:263:LEU:O	1:K:263:LEU:HG	2.04	0.50
1:M:162:ALA:O	1:M:163:LYS:C	2.54	0.50
1:M:310:ALA:C	1:M:312:PHE:H	2.19	0.50
1:O:222:ILE:HG22	1:O:223:THR:N	2.19	0.50
1:O:319:VAL:HG22	1:O:370:HIS:HB2	1.94	0.50
1:O:416:LYS:HB3	1:O:428:LYS:HG2	1.94	0.50
1:A:102:VAL:O	1:A:106:ILE:HD12	2.12	0.50
1:A:216:ILE:CG2	1:A:217:ASP:N	2.75	0.50
1:A:290:THR:CG2	1:A:291:LYS:N	2.74	0.50
1:C:177:ILE:HG22	1:C:178:GLU:N	2.25	0.50
1:E:102:VAL:O	1:E:106:ILE:HG13	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:118:TYR:N	1:E:118:TYR:CD1	2.80	0.50
1:I:231:ASN:ND2	1:K:266:GLN:NE2	2.55	0.50
2:L:852:THR:HG22	2:L:854:ASP:N	2.27	0.50
1:M:90:ILE:O	1:M:90:ILE:HG22	2.05	0.50
1:M:435:ARG:HD3	1:M:455:ILE:HG23	1.92	0.50
1:M:448:LYS:HB3	1:M:450:LEU:HD23	1.94	0.50
1:O:105:ASN:HA	1:O:108:GLU:HG3	1.94	0.50
1:O:443:SER:O	1:O:444:ASP:C	2.52	0.50
2:P:852:THR:HG22	2:P:854:ASP:N	2.27	0.50
1:A:453:SER:HA	1:A:456:MET:HE1	1.94	0.50
1:C:136:TYR:HB2	1:C:431:ILE:HD11	1.90	0.50
1:E:115:ASN:N	1:E:115:ASN:OD1	2.44	0.50
1:G:19:ARG:CB	1:G:50:VAL:HG21	2.36	0.50
1:I:294:VAL:HG12	1:I:295:ILE:N	2.27	0.50
1:O:136:TYR:CB	1:O:431:ILE:HD13	2.36	0.50
1:A:159:ILE:O	1:A:160:VAL:C	2.55	0.49
1:C:31:TRP:CH2	1:C:35:THR:HG21	2.47	0.49
1:E:25:LEU:HD23	1:E:52:LEU:HD21	1.94	0.49
1:E:165:LEU:HD13	1:E:322:PHE:CD1	2.47	0.49
1:G:208:ILE:O	1:G:209:SER:C	2.54	0.49
1:G:216:ILE:O	1:G:217:ASP:C	2.54	0.49
1:G:217:ASP:HB2	1:G:433:LEU:HD13	1.94	0.49
1:K:293:LEU:HB2	1:K:311:GLY:HA2	1.93	0.49
1:K:315:ILE:HG23	1:K:377:VAL:HG22	1.93	0.49
1:K:392:HIS:C	1:K:394:LEU:H	2.19	0.49
1:K:431:ILE:HG23	1:K:435:ARG:CD	2.42	0.49
1:O:40:ILE:HG23	1:O:47:PHE:CB	2.43	0.49
1:O:272:GLY:O	1:O:273:LYS:HB2	2.12	0.49
1:A:179:ILE:CG2	1:A:180:SER:N	2.74	0.49
1:C:100:TYR:CE1	1:C:135:LEU:HD21	2.46	0.49
1:E:223:THR:OG1	1:E:224:GLY:N	2.45	0.49
1:G:126:ALA:HB1	1:G:131:GLN:OE1	2.11	0.49
1:G:148:ILE:HD13	1:G:388:ILE:CD1	2.42	0.49
1:I:136:TYR:HD1	1:I:139:SER:OG	1.95	0.49
1:I:313:VAL:CG1	1:I:314:GLU:N	2.74	0.49
1:I:386:GLU:O	1:I:389:ALA:HB3	2.11	0.49
1:K:16:ARG:HB2	1:K:17:PRO:CD	2.42	0.49
1:K:454:LYS:O	1:K:455:ILE:C	2.54	0.49
1:O:142:ARG:CG	1:O:142:ARG:NH1	2.68	0.49
1:O:433:LEU:O	1:O:436:LEU:HB3	2.11	0.49
1:A:195:PRO:HB3	1:A:197:TYR:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:ASN:HA	1:A:261:ASP:OD1	2.12	0.49
1:G:68:GLN:NE2	1:G:68:GLN:HA	2.25	0.49
1:G:263:LEU:HD12	1:G:264:LEU:N	2.28	0.49
1:I:208:ILE:O	1:I:209:SER:C	2.55	0.49
1:I:287:LYS:N	1:I:292:ASN:OD1	2.45	0.49
1:K:32:VAL:HG13	1:K:36:HIS:HB2	1.93	0.49
1:K:422:GLU:OE1	1:K:422:GLU:N	2.42	0.49
1:M:197:TYR:CD1	1:M:198:LEU:HD13	2.47	0.49
1:O:123:TRP:CD1	1:O:214:HIS:CD2	3.00	0.49
1:O:273:LYS:N	1:O:273:LYS:CD	2.74	0.49
1:A:142:ARG:C	1:A:144:ASN:N	2.70	0.49
1:C:245:ASP:O	1:C:247:ASN:N	2.45	0.49
1:C:258:THR:O	1:C:259:CYS:C	2.53	0.49
1:E:64:ILE:HG22	1:E:65:GLU:N	2.26	0.49
1:E:84:TYR:CD1	1:E:86:ASP:HB2	2.48	0.49
1:E:290:THR:HG22	1:E:291:LYS:N	2.28	0.49
1:G:96:VAL:HG12	1:G:127:ALA:HB2	1.93	0.49
1:G:182:ASN:HA	1:G:281:LYS:O	2.11	0.49
1:I:103:VAL:N	1:I:106:ILE:HD12	2.27	0.49
1:I:142:ARG:CB	1:I:145:LEU:HB3	2.42	0.49
1:I:304:LEU:HD22	1:I:320:LEU:HD11	1.95	0.49
1:K:142:ARG:HB3	1:K:142:ARG:HH11	1.78	0.49
1:M:435:ARG:HB3	1:M:455:ILE:HG23	1.93	0.49
1:O:182:ASN:HA	1:O:281:LYS:O	2.13	0.49
1:O:223:THR:HG21	1:O:269:LEU:HD11	1.94	0.49
1:O:245:ASP:O	1:O:247:ASN:N	2.45	0.49
1:A:208:ILE:O	1:A:212:PHE:HB3	2.13	0.49
1:A:453:SER:O	1:A:454:LYS:HD3	2.12	0.49
1:C:385:TYR:O	1:C:386:GLU:C	2.55	0.49
1:E:171:ILE:O	1:E:300:THR:N	2.46	0.49
1:K:14:SER:OG	1:K:15:SER:N	2.42	0.49
1:K:147:THR:C	1:K:148:ILE:HG13	2.36	0.49
1:K:149:ILE:HG23	1:K:151:LEU:HD12	1.94	0.49
1:K:188:TYR:N	1:K:284:THR:O	2.46	0.49
1:K:216:ILE:CG2	1:K:217:ASP:N	2.74	0.49
1:K:236:ASN:HA	1:K:261:ASP:OD1	2.12	0.49
1:M:245:ASP:O	1:M:245:ASP:OD1	2.30	0.49
1:O:216:ILE:O	1:O:217:ASP:C	2.55	0.49
1:O:375:ASN:C	1:O:375:ASN:OD1	2.53	0.49
1:A:79:GLU:O	1:A:80:SER:C	2.55	0.49
1:A:103:VAL:HA	1:A:106:ILE:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:67:LEU:O	1:C:68:GLN:HB2	2.11	0.49
1:C:172:GLY:CA	1:C:301:LYS:HD3	2.42	0.49
1:C:216:ILE:CG2	1:C:217:ASP:N	2.75	0.49
1:G:50:VAL:HG12	1:G:84:TYR:HE2	1.75	0.49
1:G:96:VAL:HB	1:G:97:PRO:CD	2.40	0.49
1:G:125:LEU:HD11	1:G:427:PHE:CG	2.48	0.49
1:G:146:GLN:HA	1:G:146:GLN:NE2	2.27	0.49
1:K:103:VAL:O	1:K:104:LYS:C	2.55	0.49
1:K:200:ASP:C	1:K:200:ASP:OD1	2.55	0.49
1:M:273:LYS:N	1:M:273:LYS:CD	2.75	0.49
1:M:436:LEU:O	1:M:440:VAL:HG23	2.13	0.49
1:M:438:ASP:O	1:M:441:PHE:N	2.45	0.49
1:O:161:ARG:O	1:O:165:LEU:HG	2.12	0.49
1:O:208:ILE:HG21	1:O:441:PHE:HE1	1.77	0.49
1:A:43:LEU:O	1:A:44:SER:C	2.55	0.49
1:A:64:ILE:O	1:A:68:GLN:N	2.45	0.49
1:I:123:TRP:CD2	1:I:124:ALA:HA	2.47	0.49
1:K:25:LEU:HB3	1:K:52:LEU:CD2	2.41	0.49
1:K:171:ILE:O	1:K:300:THR:N	2.46	0.49
1:M:149:ILE:CG2	1:M:151:LEU:HD12	2.42	0.49
1:M:262:HIS:CD2	1:M:263:LEU:N	2.81	0.49
1:M:287:LYS:HG2	1:M:290:THR:HB	1.94	0.49
1:O:169:GLY:O	1:O:328:GLY:HA3	2.13	0.49
1:O:212:PHE:HA	1:O:280:PHE:CE1	2.48	0.49
1:E:22:PHE:N	1:E:51:ALA:O	2.39	0.49
1:G:178:GLU:C	1:G:179:ILE:HG13	2.37	0.49
1:I:111:SER:HA	1:I:142:ARG:CZ	2.42	0.49
1:K:381:ILE:O	1:K:382:LEU:C	2.54	0.49
1:M:89:MET:O	1:M:89:MET:HG3	2.12	0.49
1:M:228:GLN:HB3	1:M:268:ILE:O	2.12	0.49
1:M:266:GLN:OE1	1:O:264:LEU:HD22	2.13	0.49
1:O:14:SER:OG	1:O:15:SER:N	2.41	0.49
1:O:156:SER:HB2	1:O:380:ASN:HD21	1.78	0.49
1:A:287:LYS:N	1:A:292:ASN:OD1	2.41	0.49
1:C:179:ILE:HB	1:C:278:CYS:CB	2.41	0.49
1:C:223:THR:OG1	1:C:224:GLY:N	2.46	0.49
1:E:136:TYR:HB2	1:E:431:ILE:HD13	1.94	0.49
1:K:53:TYR:CD2	1:K:54:ASN:N	2.81	0.49
1:M:245:ASP:O	1:M:246:GLU:C	2.55	0.49
1:A:210:ASN:OD1	1:A:211:SER:N	2.45	0.49
1:A:218:VAL:HG13	1:A:222:ILE:CD1	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:ASN:O	1:C:117:ARG:CG	2.59	0.49
1:C:390:ASP:O	1:C:391:TYR:C	2.56	0.49
1:C:431:ILE:CG2	1:C:432:ILE:N	2.73	0.49
1:E:84:TYR:CE1	1:E:86:ASP:HB2	2.48	0.49
1:G:163:LYS:HD3	1:G:421:PHE:CZ	2.48	0.49
1:I:192:MET:HG2	1:I:244:LEU:O	2.12	0.49
1:I:231:ASN:HB3	1:K:233:MET:HE3	1.93	0.49
1:I:319:VAL:HG22	1:I:370:HIS:HB2	1.94	0.49
1:M:22:PHE:N	1:M:51:ALA:O	2.33	0.49
1:M:132:ALA:O	1:M:133:GLU:C	2.55	0.49
1:M:384:ILE:O	1:M:385:TYR:C	2.56	0.49
1:A:281:LYS:CD	1:C:298:HIS:NE2	2.75	0.48
1:C:25:LEU:HB3	1:C:52:LEU:HD13	1.94	0.48
1:C:322:PHE:CG	1:C:323:TYR:N	2.79	0.48
1:E:33:ALA:O	1:E:37:PHE:HB3	2.12	0.48
1:E:54:ASN:HB3	1:E:55:PRO:HD2	1.94	0.48
1:E:179:ILE:HG22	1:E:180:SER:N	2.26	0.48
1:G:115:ASN:N	1:G:115:ASN:OD1	2.43	0.48
1:G:154:ARG:NH1	1:G:417:GLN:OE1	2.34	0.48
1:G:322:PHE:CG	1:G:323:TYR:N	2.80	0.48
1:I:56:THR:OG1	1:I:59:SER:OG	2.31	0.48
1:K:249:LYS:HE2	1:K:250:ARG:O	2.13	0.48
1:M:325:ILE:O	1:M:325:ILE:HG13	2.12	0.48
1:O:57:LEU:HD22	1:O:61:LEU:HD11	1.87	0.48
1:A:263:LEU:HD11	1:A:265:PHE:HB2	1.95	0.48
1:A:438:ASP:O	1:A:439:ALA:C	2.56	0.48
1:A:458:LEU:CG	1:A:459:GLU:H	2.00	0.48
1:C:150:CYS:O	1:C:152:GLN:NE2	2.47	0.48
1:E:56:THR:O	1:E:56:THR:OG1	2.30	0.48
1:G:53:TYR:HB2	1:G:81:PHE:CD1	2.48	0.48
1:G:432:ILE:O	1:G:455:ILE:HD12	2.13	0.48
1:I:187:GLY:HA3	1:I:284:THR:N	2.22	0.48
1:M:237:ASN:H	1:M:261:ASP:CG	2.21	0.48
1:A:105:ASN:HD22	1:A:105:ASN:H	1.59	0.48
1:A:431:ILE:O	1:A:435:ARG:HB2	2.13	0.48
2:B:855:ASP:O	2:B:856:VAL:C	2.57	0.48
1:C:123:TRP:CE3	1:C:123:TRP:HA	2.48	0.48
1:C:136:TYR:HD1	1:C:139:SER:OG	1.96	0.48
1:C:268:ILE:CG2	1:C:273:LYS:HA	2.43	0.48
1:E:179:ILE:CG2	1:E:180:SER:N	2.75	0.48
1:E:290:THR:CG2	1:E:291:LYS:N	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:90:ILE:O	1:G:90:ILE:HG22	2.10	0.48
1:G:110:SER:O	1:G:113:ASN:N	2.46	0.48
2:H:852:THR:CG2	2:H:853:MET:N	2.75	0.48
1:I:118:TYR:N	1:I:118:TYR:CD1	2.81	0.48
1:M:100:TYR:CD1	1:M:135:LEU:HD21	2.48	0.48
1:M:148:ILE:HD13	1:M:388:ILE:HD13	1.94	0.48
1:O:432:ILE:HG23	1:O:455:ILE:HD12	1.91	0.48
1:A:145:LEU:O	1:A:413:LYS:HD2	2.06	0.48
1:A:377:VAL:HG11	2:B:859:TYR:CD2	2.48	0.48
1:C:105:ASN:HB3	1:C:109:HIS:CE1	2.48	0.48
1:C:118:TYR:OH	1:C:392:HIS:ND1	2.24	0.48
1:C:133:GLU:HA	1:C:133:GLU:OE1	2.13	0.48
1:E:20:VAL:HG21	1:E:40:ILE:CD1	2.43	0.48
1:E:30:SER:O	1:E:31:TRP:C	2.56	0.48
1:E:214:HIS:CG	1:E:314:GLU:HG2	2.48	0.48
1:G:55:PRO:O	1:G:76:ASP:OD1	2.31	0.48
1:G:60:SER:O	1:G:63:THR:HB	2.12	0.48
1:G:77:SER:HB3	1:G:80:SER:H	1.78	0.48
1:M:129:VAL:CG1	1:M:130:GLN:H	2.24	0.48
1:M:185:TRP:CD1	2:N:857:TYR:HE1	2.32	0.48
1:A:176:SER:OG	1:A:177:ILE:N	2.44	0.48
1:A:324:GLY:O	1:A:365:THR:N	2.32	0.48
1:E:389:ALA:O	1:E:393:PHE:N	2.45	0.48
1:G:179:ILE:HG22	1:G:180:SER:N	2.28	0.48
1:I:309:ASP:N	1:I:309:ASP:OD1	2.45	0.48
1:K:115:ASN:O	1:K:117:ARG:N	2.47	0.48
1:K:129:VAL:O	1:K:132:ALA:N	2.46	0.48
1:K:132:ALA:O	1:K:133:GLU:C	2.55	0.48
1:M:78:LEU:O	1:M:82:ALA:N	2.42	0.48
1:M:138:ILE:O	1:M:139:SER:C	2.55	0.48
1:O:23:VAL:HG12	1:O:94:VAL:CG1	2.44	0.48
1:O:133:GLU:O	1:O:136:TYR:HB3	2.13	0.48
1:A:104:LYS:O	1:A:107:LEU:HB2	2.14	0.48
1:C:61:LEU:CD1	1:C:61:LEU:H	2.27	0.48
1:E:25:LEU:HB3	1:E:52:LEU:HG	1.94	0.48
1:G:53:TYR:CD2	1:G:54:ASN:N	2.82	0.48
1:G:84:TYR:CD1	1:G:86:ASP:HB2	2.49	0.48
1:G:113:ASN:O	1:G:114:LEU:CD2	2.61	0.48
1:G:232:ALA:O	1:G:444:ASP:HA	2.13	0.48
1:K:89:MET:O	1:K:89:MET:HG3	2.13	0.48
1:K:179:ILE:CG2	1:K:180:SER:N	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:182:ASN:ND2	1:K:283:GLY:CA	2.76	0.48
1:K:230:ILE:HA	1:K:267:GLY:HA2	1.96	0.48
1:K:452:VAL:HG12	1:K:452:VAL:O	2.13	0.48
1:M:38:LEU:O	1:M:39:ALA:C	2.56	0.48
1:M:78:LEU:O	1:M:81:PHE:HB3	2.13	0.48
1:M:113:ASN:OD1	1:M:114:LEU:N	2.47	0.48
1:O:18:ILE:HD11	1:O:392:HIS:CD2	2.48	0.48
2:P:855:ASP:O	2:P:856:VAL:C	2.55	0.48
1:A:79:GLU:HG2	1:A:109:HIS:ND1	2.29	0.48
1:A:388:ILE:HG22	1:A:389:ALA:N	2.29	0.48
1:E:417:GLN:HB2	1:E:424:PHE:O	2.13	0.48
1:G:62:GLN:O	1:G:65:GLU:N	2.47	0.48
1:K:77:SER:O	1:K:80:SER:HB2	2.13	0.48
1:M:155:LYS:HB3	1:M:383:ARG:HB3	1.95	0.48
1:M:174:ILE:HG22	1:M:175:ASN:N	2.29	0.48
1:M:201:ILE:HB	1:M:258:THR:CB	2.43	0.48
1:M:427:PHE:O	1:M:428:LYS:C	2.53	0.48
1:O:263:LEU:HD12	1:O:264:LEU:N	2.28	0.48
1:O:295:ILE:HD12	1:O:306:ILE:HB	1.96	0.48
1:O:436:LEU:O	1:O:440:VAL:HG23	2.12	0.48
2:B:853:MET:O	2:B:856:VAL:HB	2.13	0.48
1:C:22:PHE:CE2	1:C:91:VAL:HB	2.48	0.48
1:G:16:ARG:O	1:G:17:PRO:O	2.32	0.48
1:G:31:TRP:CH2	1:G:35:THR:HG21	2.49	0.48
1:I:209:SER:OG	1:I:210:ASN:N	2.43	0.48
1:I:251:THR:C	1:I:253:GLU:H	2.22	0.48
1:K:141:GLN:OE1	1:K:141:GLN:N	2.47	0.48
1:M:263:LEU:HD12	1:M:264:LEU:O	2.13	0.48
1:A:229:LYS:O	1:A:230:ILE:HG23	2.13	0.48
1:C:133:GLU:O	1:C:136:TYR:HB3	2.13	0.48
1:C:433:LEU:O	1:C:436:LEU:HB3	2.13	0.48
1:C:436:LEU:O	1:C:439:ALA:HB3	2.13	0.48
1:E:84:TYR:C	1:E:86:ASP:H	2.21	0.48
1:E:233:MET:CE	1:G:231:ASN:CB	2.92	0.48
1:E:372:ARG:O	1:E:373:ASN:ND2	2.47	0.48
1:E:427:PHE:O	1:E:428:LYS:C	2.56	0.48
1:G:197:TYR:HA	1:G:200:ASP:HB3	1.95	0.48
1:I:177:ILE:HG22	1:I:178:GLU:N	2.29	0.48
1:I:201:ILE:HB	1:I:258:THR:CG2	2.42	0.48
1:O:384:ILE:HG23	1:O:384:ILE:HD12	1.48	0.48
1:C:120:TYR:C	1:C:121:VAL:HG23	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:449:THR:O	1:E:449:THR:HG22	2.14	0.48
1:G:219:LEU:HG	1:G:219:LEU:O	2.14	0.48
1:G:231:ASN:HB2	1:G:449:THR:OG1	2.14	0.48
1:I:294:VAL:CG1	1:I:295:ILE:N	2.77	0.48
1:M:79:GLU:O	1:M:80:SER:C	2.57	0.48
1:M:188:TYR:HB2	1:M:284:THR:O	2.14	0.48
1:M:236:ASN:OD1	1:M:260:PRO:HA	2.13	0.48
1:M:392:HIS:CD2	1:M:393:PHE:CD2	3.01	0.48
1:O:84:TYR:CE1	1:O:86:ASP:CB	2.91	0.48
1:O:208:ILE:O	1:O:212:PHE:HB3	2.13	0.48
1:O:213:GLY:O	1:O:216:ILE:HG22	2.13	0.48
1:A:154:ARG:NH1	1:A:417:GLN:OE1	2.39	0.47
1:A:312:PHE:CB	1:A:315:ILE:HD12	2.39	0.47
1:C:325:ILE:O	1:C:326:LYS:C	2.56	0.47
1:E:117:ARG:HB3	1:E:118:TYR:CE1	2.49	0.47
1:E:121:VAL:HG12	1:E:122:GLU:N	2.29	0.47
1:G:96:VAL:N	1:G:97:PRO:CD	2.77	0.47
1:G:151:LEU:O	1:G:153:GLY:N	2.47	0.47
1:I:216:ILE:CG2	1:I:217:ASP:N	2.77	0.47
1:K:151:LEU:C	1:K:153:GLY:H	2.22	0.47
1:A:147:THR:HB	1:A:427:PHE:CE1	2.48	0.47
1:A:216:ILE:HD12	1:A:219:LEU:HD23	1.96	0.47
1:A:228:GLN:NE2	1:A:273:LYS:HE3	2.28	0.47
1:A:231:ASN:ND2	1:C:266:GLN:OE1	2.44	0.47
1:A:425:PRO:HA	1:A:429:ASP:OD2	2.15	0.47
1:A:447:GLU:HG3	1:C:449:THR:HG21	1.96	0.47
1:C:152:GLN:NE2	1:C:214:HIS:HE1	2.12	0.47
1:C:266:GLN:HA	1:C:276:VAL:O	2.15	0.47
2:D:855:ASP:O	2:D:856:VAL:C	2.56	0.47
1:E:185:TRP:CD1	1:E:185:TRP:N	2.75	0.47
1:E:224:GLY:HA2	1:E:419:PHE:CD2	2.49	0.47
1:E:298:HIS:NE2	1:G:281:LYS:NZ	2.62	0.47
1:E:382:LEU:O	1:E:384:ILE:N	2.47	0.47
1:G:208:ILE:HG12	1:G:263:LEU:HD22	1.96	0.47
1:I:105:ASN:HA	1:I:108:GLU:HG3	1.96	0.47
1:K:150:CYS:O	1:K:152:GLN:NE2	2.47	0.47
1:K:290:THR:CG2	1:K:291:LYS:N	2.77	0.47
1:K:323:TYR:CZ	1:K:364:GLN:HB2	2.49	0.47
1:M:179:ILE:HB	1:M:278:CYS:HB2	1.97	0.47
1:O:115:ASN:N	1:O:115:ASN:OD1	2.45	0.47
1:O:389:ALA:O	1:O:392:HIS:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:GLN:HB2	1:A:424:PHE:C	2.39	0.47
1:E:30:SER:O	1:E:33:ALA:N	2.46	0.47
1:G:67:LEU:O	1:G:68:GLN:HB2	2.14	0.47
1:I:287:LYS:NZ	1:I:287:LYS:CB	2.77	0.47
1:K:147:THR:O	1:K:426:THR:HG22	2.15	0.47
1:M:81:PHE:O	1:M:83:GLN:N	2.47	0.47
1:O:325:ILE:O	1:O:326:LYS:C	2.57	0.47
1:O:387:SER:OG	1:O:423:GLY:O	2.28	0.47
1:A:276:VAL:O	1:C:264:LEU:HD21	2.15	0.47
1:A:294:VAL:HG22	1:A:307:GLU:HG2	1.96	0.47
1:C:56:THR:OG1	1:C:59:SER:OG	2.29	0.47
1:C:118:TYR:N	1:C:118:TYR:CD1	2.83	0.47
1:C:431:ILE:O	1:C:432:ILE:C	2.57	0.47
1:E:20:VAL:HG21	1:E:40:ILE:HD13	1.97	0.47
1:E:208:ILE:HB	1:E:209:SER:H	1.56	0.47
1:G:94:VAL:O	1:G:95:LYS:C	2.57	0.47
1:G:293:LEU:O	1:G:307:GLU:HA	2.14	0.47
1:G:372:ARG:O	1:G:373:ASN:C	2.57	0.47
1:I:78:LEU:O	1:I:82:ALA:N	2.40	0.47
1:K:78:LEU:O	1:K:82:ALA:N	2.40	0.47
1:K:88:ASP:OD1	1:K:115:ASN:HB2	2.15	0.47
1:M:32:VAL:CG1	1:M:36:HIS:HB2	2.45	0.47
1:M:287:LYS:N	1:M:292:ASN:OD1	2.46	0.47
1:A:22:PHE:N	1:A:51:ALA:O	2.42	0.47
1:A:251:THR:C	1:A:253:GLU:H	2.22	0.47
1:A:375:ASN:OD1	1:A:377:VAL:HB	2.14	0.47
1:C:77:SER:CB	1:C:80:SER:HB2	2.35	0.47
1:C:156:SER:O	1:C:157:PRO:C	2.55	0.47
1:C:161:ARG:NH2	1:C:367:GLU:OE1	2.47	0.47
1:E:136:TYR:HD1	1:E:139:SER:OG	1.98	0.47
1:E:136:TYR:CB	1:E:431:ILE:HD11	2.38	0.47
1:E:234:ILE:HG12	1:E:263:LEU:HB2	1.95	0.47
1:I:379:GLY:O	1:I:382:LEU:HB3	2.14	0.47
1:K:130:GLN:O	1:K:131:GLN:C	2.57	0.47
1:K:208:ILE:CG2	1:K:209:SER:N	2.75	0.47
1:K:376:SER:OG	1:K:377:VAL:N	2.47	0.47
1:M:63:THR:O	1:M:67:LEU:HG	2.14	0.47
1:M:287:LYS:NZ	1:M:287:LYS:CB	2.77	0.47
1:O:100:TYR:CE1	1:O:135:LEU:HD21	2.48	0.47
1:O:273:LYS:O	1:O:274:VAL:C	2.53	0.47
1:A:133:GLU:O	1:A:136:TYR:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:149:ILE:HD13	1:G:430:ALA:CB	2.45	0.47
1:G:177:ILE:O	1:G:178:GLU:CG	2.63	0.47
1:G:315:ILE:O	1:G:315:ILE:HG22	2.13	0.47
1:I:179:ILE:CG2	1:I:180:SER:N	2.77	0.47
1:M:94:VAL:O	1:M:95:LYS:C	2.56	0.47
1:M:96:VAL:N	1:M:97:PRO:CD	2.77	0.47
1:M:133:GLU:O	1:M:136:TYR:HB3	2.14	0.47
1:M:136:TYR:HD1	1:M:139:SER:OG	1.98	0.47
1:O:78:LEU:O	1:O:82:ALA:N	2.42	0.47
1:O:313:VAL:CG1	1:O:314:GLU:N	2.77	0.47
1:A:65:GLU:CG	1:A:66:GLN:H	2.24	0.47
1:A:96:VAL:N	1:A:97:PRO:CD	2.77	0.47
1:A:177:ILE:HG22	1:A:276:VAL:HG13	1.96	0.47
1:A:228:GLN:HB3	1:A:268:ILE:O	2.13	0.47
1:A:432:ILE:HD13	1:A:456:MET:HA	1.96	0.47
1:C:95:LYS:HB3	1:C:97:PRO:HD2	1.96	0.47
1:C:188:TYR:O	1:C:242:PHE:HB2	2.15	0.47
1:C:195:PRO:HB3	1:C:197:TYR:CE2	2.49	0.47
1:C:276:VAL:HG12	1:C:277:SER:N	2.29	0.47
1:C:389:ALA:O	1:C:392:HIS:HB3	2.15	0.47
1:E:75:PHE:N	1:E:75:PHE:CD1	2.83	0.47
1:E:88:ASP:O	1:E:116:LEU:HA	2.14	0.47
1:E:182:ASN:ND2	1:E:283:GLY:HA2	2.30	0.47
1:E:192:MET:CE	1:E:243:LEU:HD22	2.45	0.47
1:E:387:SER:O	1:E:390:ASP:HB2	2.15	0.47
1:E:422:GLU:OE1	1:E:422:GLU:N	2.48	0.47
1:G:21:GLY:HA3	1:G:87:ILE:CD1	2.45	0.47
1:I:16:ARG:HB2	1:I:17:PRO:HD2	1.96	0.47
1:I:104:LYS:O	1:I:107:LEU:HB2	2.15	0.47
1:I:129:VAL:O	1:I:132:ALA:N	2.48	0.47
1:I:129:VAL:HA	1:I:434:HIS:HD2	1.80	0.47
1:I:245:ASP:O	1:I:248:GLY:N	2.26	0.47
1:K:129:VAL:HA	1:K:434:HIS:HD2	1.80	0.47
1:K:146:GLN:NE2	1:K:146:GLN:HA	2.29	0.47
1:K:245:ASP:O	1:K:246:GLU:C	2.58	0.47
1:M:30:SER:OG	1:M:33:ALA:HB2	2.15	0.47
1:M:110:SER:O	1:M:113:ASN:N	2.47	0.47
1:M:236:ASN:HA	1:M:261:ASP:OD1	2.15	0.47
1:O:172:GLY:CA	1:O:301:LYS:HD2	2.44	0.47
1:O:211:SER:O	1:O:214:HIS:HB2	2.14	0.47
2:P:853:MET:O	2:P:854:ASP:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:TRP:HD1	1:A:32:VAL:HG22	1.80	0.47
1:A:103:VAL:CA	1:A:106:ILE:HD12	2.44	0.47
1:C:104:LYS:O	1:C:107:LEU:HB2	2.15	0.47
1:C:120:TYR:O	1:C:121:VAL:HG23	2.14	0.47
1:C:187:GLY:HA3	1:C:284:THR:N	2.30	0.47
2:D:853:MET:HA	2:D:856:VAL:CG2	2.44	0.47
1:G:22:PHE:N	1:G:51:ALA:O	2.34	0.47
1:G:53:TYR:CG	1:G:54:ASN:N	2.82	0.47
1:G:386:GLU:O	1:G:388:ILE:N	2.48	0.47
1:I:104:LYS:O	1:I:105:ASN:C	2.58	0.47
1:I:185:TRP:HD1	2:J:857:TYR:HE1	1.62	0.47
1:I:320:LEU:HB3	1:I:369:PHE:HB3	1.96	0.47
1:K:42:GLN:CD	1:K:382:LEU:HD11	2.40	0.47
1:M:456:MET:HE3	1:M:456:MET:HB3	1.82	0.47
1:O:75:PHE:N	1:O:75:PHE:CD1	2.83	0.47
1:O:129:VAL:O	1:O:130:GLN:C	2.58	0.47
1:O:171:ILE:HB	1:O:299:GLY:HA3	1.97	0.47
1:O:171:ILE:CD1	1:O:299:GLY:HA3	2.37	0.47
1:O:187:GLY:HA3	1:O:284:THR:N	2.25	0.47
1:A:134:GLU:O	1:A:137:SER:OG	2.29	0.47
1:E:83:GLN:O	1:E:84:TYR:C	2.57	0.47
1:G:123:TRP:CE3	1:G:123:TRP:HA	2.49	0.47
1:I:18:ILE:HD12	1:I:18:ILE:HG21	1.71	0.47
1:O:188:TYR:CE1	1:O:238:ILE:HD11	2.50	0.47
1:C:134:GLU:HG2	1:C:138:ILE:HD11	1.96	0.47
1:C:368:VAL:O	1:C:368:VAL:HG12	2.15	0.47
1:E:151:LEU:HD12	1:E:151:LEU:N	2.29	0.47
1:G:177:ILE:CG2	1:G:276:VAL:HG13	2.45	0.47
1:G:195:PRO:HB3	1:G:197:TYR:CD2	2.50	0.47
1:G:385:TYR:O	1:G:386:GLU:C	2.57	0.47
1:I:53:TYR:CE1	1:I:78:LEU:HD12	2.50	0.47
1:K:88:ASP:O	1:K:116:LEU:HA	2.15	0.47
1:K:96:VAL:N	1:K:97:PRO:HD2	2.30	0.47
1:K:381:ILE:O	1:K:384:ILE:N	2.48	0.47
1:M:100:TYR:HB2	1:M:131:GLN:CD	2.39	0.47
1:M:100:TYR:HD1	1:M:135:LEU:HD21	1.80	0.47
1:O:129:VAL:O	1:O:132:ALA:HB3	2.15	0.47
1:A:165:LEU:HD12	1:A:304:LEU:HD21	1.96	0.46
1:A:223:THR:OG1	1:A:224:GLY:N	2.47	0.46
1:A:228:GLN:HE22	1:A:273:LYS:HE2	1.80	0.46
1:C:180:SER:HA	1:C:279:SER:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:182:ASN:HA	1:C:281:LYS:O	2.14	0.46
1:C:216:ILE:CG2	1:C:217:ASP:H	2.29	0.46
1:C:291:LYS:HA	1:C:291:LYS:HD2	1.52	0.46
1:C:321:TYR:HD2	1:C:368:VAL:HG22	1.79	0.46
2:D:853:MET:O	2:D:856:VAL:HB	2.15	0.46
1:E:26:THR:HG22	1:E:27:SER:OG	2.14	0.46
1:E:281:LYS:CE	1:G:298:HIS:HD2	2.28	0.46
1:E:437:ILE:O	1:E:438:ASP:C	2.56	0.46
1:G:310:ALA:C	1:G:312:PHE:H	2.24	0.46
1:I:103:VAL:O	1:I:104:LYS:C	2.57	0.46
1:I:454:LYS:O	1:I:455:ILE:C	2.57	0.46
1:K:313:VAL:CG1	1:K:314:GLU:H	2.28	0.46
1:M:67:LEU:O	1:M:68:GLN:HB2	2.14	0.46
1:M:185:TRP:HD1	2:N:857:TYR:CE1	2.33	0.46
1:M:231:ASN:OD1	1:M:231:ASN:O	2.33	0.46
1:O:431:ILE:HG23	1:O:435:ARG:HD2	1.97	0.46
1:A:68:GLN:HA	1:A:68:GLN:NE2	2.30	0.46
1:A:230:ILE:HA	1:A:267:GLY:HA2	1.97	0.46
1:A:293:LEU:HB2	1:A:311:GLY:HA2	1.96	0.46
1:C:84:TYR:HB3	1:C:87:ILE:HD12	1.97	0.46
1:C:101:GLU:OE1	1:C:101:GLU:HA	2.12	0.46
1:C:201:ILE:HB	1:C:258:THR:CG2	2.45	0.46
1:E:197:TYR:C	1:E:199:TYR:N	2.72	0.46
1:E:426:THR:O	1:E:429:ASP:N	2.49	0.46
1:G:269:LEU:HB2	1:G:274:VAL:O	2.15	0.46
1:G:416:LYS:HG3	1:G:417:GLN:N	2.28	0.46
1:G:434:HIS:CA	1:G:437:ILE:HD12	2.45	0.46
1:I:88:ASP:OD1	1:I:115:ASN:HB3	2.16	0.46
1:I:178:GLU:HB2	1:I:296:ASP:HB3	1.96	0.46
1:I:187:GLY:O	1:I:238:ILE:HD13	2.15	0.46
1:M:190:ARG:HD2	1:M:199:TYR:CE2	2.51	0.46
1:O:115:ASN:O	1:O:117:ARG:HB2	2.15	0.46
1:O:179:ILE:CG2	1:O:180:SER:N	2.78	0.46
1:O:210:ASN:O	1:O:211:SER:C	2.57	0.46
1:O:218:VAL:O	1:O:221:TYR:HB3	2.15	0.46
1:O:232:ALA:O	1:O:444:ASP:HA	2.14	0.46
1:A:42:GLN:HB2	1:A:382:LEU:HD11	1.97	0.46
1:A:166:ILE:HG22	1:A:167:SER:N	2.30	0.46
1:A:185:TRP:HD1	2:B:857:TYR:CE1	2.32	0.46
1:A:458:LEU:HD12	1:A:458:LEU:HA	1.69	0.46
1:C:88:ASP:O	1:C:116:LEU:HA	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:125:LEU:HD11	1:C:427:PHE:CE2	2.50	0.46
1:C:128:SER:OG	1:C:130:GLN:NE2	2.49	0.46
1:C:158:TYR:CB	1:C:318:LEU:HD12	2.45	0.46
1:C:234:ILE:HG12	1:C:263:LEU:HB2	1.97	0.46
1:E:230:ILE:HA	1:E:267:GLY:HA2	1.97	0.46
1:G:212:PHE:CD1	1:G:280:PHE:CD1	3.03	0.46
1:G:434:HIS:HA	1:G:437:ILE:HD12	1.97	0.46
1:I:257:LYS:HG3	1:I:257:LYS:O	2.03	0.46
1:K:374:TYR:OH	1:K:380:ASN:OD1	2.17	0.46
1:M:312:PHE:HA	1:M:314:GLU:OE2	2.15	0.46
1:O:20:VAL:HG23	1:O:48:GLN:O	2.15	0.46
1:O:315:ILE:HG23	1:O:377:VAL:HG22	1.96	0.46
1:O:368:VAL:O	1:O:368:VAL:HG12	2.16	0.46
1:A:118:TYR:N	1:A:118:TYR:CD1	2.84	0.46
1:A:245:ASP:O	1:A:246:GLU:C	2.59	0.46
1:A:309:ASP:OD2	2:B:850:THR:OG1	2.31	0.46
2:B:853:MET:O	2:B:854:ASP:C	2.56	0.46
1:C:62:GLN:O	1:C:65:GLU:N	2.48	0.46
1:C:151:LEU:C	1:C:153:GLY:N	2.69	0.46
1:C:294:VAL:HG22	1:C:307:GLU:HG2	1.96	0.46
1:E:91:VAL:HG13	1:E:120:TYR:HB3	1.97	0.46
1:E:208:ILE:O	1:E:213:GLY:N	2.34	0.46
1:E:289:LEU:HD12	1:G:303:ASP:HB3	1.96	0.46
1:E:304:LEU:HD23	1:E:322:PHE:CB	2.38	0.46
1:G:121:VAL:CG1	1:G:122:GLU:N	2.78	0.46
1:G:129:VAL:HG13	1:G:130:GLN:N	2.28	0.46
1:I:26:THR:HB	1:I:30:SER:HB2	1.98	0.46
1:I:294:VAL:HA	1:I:306:ILE:O	2.14	0.46
1:K:208:ILE:HA	1:K:212:PHE:HB3	1.97	0.46
2:L:852:THR:CG2	2:L:853:MET:N	2.78	0.46
1:M:121:VAL:HG21	1:M:427:PHE:CZ	2.50	0.46
1:M:290:THR:CG2	1:M:291:LYS:N	2.78	0.46
1:O:146:GLN:OE1	1:O:414:PHE:N	2.40	0.46
1:C:22:PHE:N	1:C:51:ALA:O	2.35	0.46
1:C:105:ASN:HA	1:C:108:GLU:HG3	1.98	0.46
1:C:125:LEU:HD11	1:C:427:PHE:CD2	2.50	0.46
1:C:312:PHE:HB3	1:C:315:ILE:CD1	2.35	0.46
1:E:53:TYR:O	1:E:54:ASN:ND2	2.49	0.46
1:G:198:LEU:HD12	1:G:198:LEU:HA	1.56	0.46
1:I:14:SER:O	1:I:16:ARG:N	2.45	0.46
1:K:22:PHE:O	1:K:53:TYR:N	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:136:TYR:HD1	1:K:139:SER:OG	1.98	0.46
1:K:156:SER:O	1:K:158:TYR:N	2.48	0.46
1:M:54:ASN:HB3	1:M:55:PRO:HD2	1.96	0.46
1:M:190:ARG:HA	1:M:191:PRO:HD3	1.63	0.46
1:O:95:LYS:HE2	1:O:197:TYR:CE2	2.51	0.46
1:O:100:TYR:CG	1:O:131:GLN:HG2	2.51	0.46
1:O:168:GLU:O	1:O:169:GLY:C	2.57	0.46
1:O:184:GLY:N	1:O:282:GLY:O	2.48	0.46
1:O:244:LEU:HD12	1:O:244:LEU:HA	1.43	0.46
1:A:23:VAL:HG12	1:A:94:VAL:CG1	2.45	0.46
1:A:36:HIS:O	1:A:38:LEU:N	2.48	0.46
1:A:40:ILE:O	1:A:40:ILE:HG22	2.15	0.46
1:A:40:ILE:HG21	1:A:40:ILE:HD13	1.63	0.46
1:A:57:LEU:HD21	1:A:74:GLY:O	2.14	0.46
1:A:123:TRP:CE3	1:A:123:TRP:HA	2.50	0.46
1:A:163:LYS:HE3	1:A:421:PHE:CE1	2.51	0.46
1:A:429:ASP:O	1:A:430:ALA:C	2.57	0.46
1:C:134:GLU:O	1:C:138:ILE:HG13	2.16	0.46
1:C:146:GLN:NE2	1:C:146:GLN:HA	2.30	0.46
1:C:179:ILE:CG2	1:C:180:SER:N	2.78	0.46
1:C:313:VAL:CG1	1:C:314:GLU:N	2.79	0.46
1:E:78:LEU:O	1:E:81:PHE:CB	2.63	0.46
1:G:53:TYR:CD2	1:G:53:TYR:C	2.93	0.46
1:G:123:TRP:CD1	1:G:214:HIS:NE2	2.82	0.46
1:G:152:GLN:NE2	1:G:152:GLN:H	2.13	0.46
1:I:188:TYR:HB2	1:I:284:THR:O	2.16	0.46
1:K:81:PHE:O	1:K:83:GLN:N	2.49	0.46
1:K:182:ASN:HD21	1:K:283:GLY:C	2.23	0.46
1:M:14:SER:O	1:M:16:ARG:N	2.45	0.46
1:M:201:ILE:HB	1:M:258:THR:CG2	2.46	0.46
1:M:431:ILE:CG2	1:M:432:ILE:N	2.79	0.46
1:O:202:GLU:O	1:O:203:SER:C	2.58	0.46
1:A:102:VAL:CG1	1:A:106:ILE:CD1	2.92	0.46
1:A:458:LEU:CG	1:A:459:GLU:N	2.63	0.46
1:C:304:LEU:HD21	1:C:322:PHE:HB2	1.90	0.46
1:E:100:TYR:HB2	1:E:131:GLN:OE1	2.16	0.46
1:E:238:ILE:O	1:E:257:LYS:CE	2.63	0.46
1:G:79:GLU:HG2	1:G:109:HIS:CD2	2.50	0.46
1:G:136:TYR:HD1	1:G:139:SER:OG	1.99	0.46
1:G:427:PHE:O	1:G:428:LYS:C	2.56	0.46
1:I:51:ALA:HB1	1:I:75:PHE:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:231:ASN:ND2	1:I:231:ASN:C	2.74	0.46
1:K:185:TRP:HD1	2:L:857:TYR:CE1	2.33	0.46
1:M:78:LEU:O	1:M:81:PHE:N	2.49	0.46
1:O:245:ASP:C	1:O:245:ASP:OD1	2.59	0.46
1:A:120:TYR:O	1:A:121:VAL:CG2	2.63	0.46
1:A:147:THR:HG21	1:A:427:PHE:CD2	2.51	0.46
1:A:185:TRP:HD1	2:B:857:TYR:HE1	1.64	0.46
1:A:278:CYS:O	1:A:278:CYS:SG	2.73	0.46
1:C:32:VAL:CG1	1:C:36:HIS:HB2	2.44	0.46
1:C:190:ARG:HA	1:C:191:PRO:HD3	1.74	0.46
1:C:432:ILE:O	1:C:433:LEU:C	2.57	0.46
1:E:165:LEU:HA	1:E:165:LEU:HD23	1.44	0.46
2:F:853:MET:O	2:F:854:ASP:C	2.59	0.46
1:I:77:SER:HB3	1:I:80:SER:H	1.80	0.46
1:I:134:GLU:HA	1:I:137:SER:HG	1.81	0.46
1:I:175:ASN:O	1:I:275:PRO:HD2	2.14	0.46
1:I:252:LYS:N	1:I:252:LYS:CD	2.59	0.46
1:K:68:GLN:NE2	1:K:68:GLN:HA	2.30	0.46
1:K:105:ASN:HA	1:K:108:GLU:HG3	1.97	0.46
1:K:119:LEU:HB2	1:K:145:LEU:HD11	1.97	0.46
1:K:136:TYR:CB	1:K:431:ILE:HD13	2.43	0.46
1:M:38:LEU:H	1:M:38:LEU:HG	1.36	0.46
1:M:118:TYR:CD1	1:M:118:TYR:N	2.83	0.46
1:M:454:LYS:O	1:M:455:ILE:C	2.57	0.46
1:O:57:LEU:O	1:O:60:SER:N	2.48	0.46
1:O:142:ARG:NH1	1:O:142:ARG:HG3	2.31	0.46
1:O:273:LYS:HA	1:O:273:LYS:HD2	1.74	0.46
1:O:443:SER:HB2	1:O:450:LEU:CD1	2.45	0.46
1:O:454:LYS:O	1:O:455:ILE:C	2.59	0.46
1:A:30:SER:O	1:A:33:ALA:HB3	2.15	0.46
1:A:100:TYR:O	1:A:101:GLU:C	2.57	0.46
1:C:61:LEU:H	1:C:61:LEU:HD13	1.81	0.46
1:E:208:ILE:HA	1:E:212:PHE:CB	2.46	0.46
1:G:111:SER:HA	1:G:142:ARG:NH2	2.31	0.46
1:G:422:GLU:OE1	1:G:422:GLU:N	2.44	0.46
1:I:172:GLY:HA2	1:I:301:LYS:HD2	1.98	0.46
1:M:65:GLU:HG3	1:M:66:GLN:N	2.30	0.46
1:M:187:GLY:O	1:M:238:ILE:HD12	2.16	0.46
1:M:188:TYR:CD1	1:M:238:ILE:HD11	2.50	0.46
1:M:291:LYS:HD2	1:M:291:LYS:HA	1.48	0.46
2:N:852:THR:HG22	2:N:854:ASP:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:19:ARG:HA	1:O:48:GLN:O	2.14	0.46
1:O:121:VAL:CG1	1:O:122:GLU:N	2.79	0.46
1:O:245:ASP:N	1:O:249:LYS:O	2.44	0.46
1:O:389:ALA:HA	1:O:392:HIS:HB3	1.97	0.46
1:C:218:VAL:O	1:C:222:ILE:HD12	2.15	0.46
1:C:219:LEU:HA	1:C:222:ILE:CD1	2.41	0.46
1:C:375:ASN:OD1	1:C:377:VAL:HB	2.16	0.46
1:E:433:LEU:HA	1:E:433:LEU:HD12	1.54	0.46
1:E:454:LYS:O	1:E:455:ILE:C	2.59	0.46
1:G:19:ARG:HB3	1:G:50:VAL:HG23	1.93	0.46
1:G:179:ILE:CG2	1:G:180:SER:N	2.78	0.46
1:I:244:LEU:HD12	1:I:244:LEU:HA	1.57	0.46
1:I:266:GLN:HB2	1:K:264:LEU:HD22	1.98	0.46
1:I:290:THR:CG2	1:I:291:LYS:N	2.79	0.46
1:K:133:GLU:O	1:K:136:TYR:HB3	2.16	0.46
1:K:184:GLY:N	1:K:282:GLY:O	2.48	0.46
1:K:208:ILE:CD1	1:K:441:PHE:CZ	2.94	0.46
1:M:179:ILE:CG2	1:M:180:SER:N	2.77	0.46
1:A:25:LEU:HD12	1:A:25:LEU:HA	1.76	0.45
1:C:131:GLN:O	1:C:135:LEU:HG	2.16	0.45
1:C:290:THR:CG2	1:C:291:LYS:N	2.79	0.45
1:E:152:GLN:O	1:E:153:GLY:C	2.57	0.45
1:E:392:HIS:C	1:E:394:LEU:H	2.24	0.45
1:G:43:LEU:HA	1:G:43:LEU:HD23	1.55	0.45
1:G:216:ILE:CG2	1:G:217:ASP:N	2.78	0.45
1:G:386:GLU:O	1:G:389:ALA:N	2.49	0.45
1:G:437:ILE:O	1:G:438:ASP:C	2.55	0.45
1:I:43:LEU:C	1:I:45:SER:N	2.73	0.45
1:I:51:ALA:HB2	1:I:84:TYR:CE2	2.51	0.45
1:I:90:ILE:HD12	1:I:116:LEU:CD1	2.46	0.45
1:I:228:GLN:HE21	1:I:273:LYS:HE3	1.63	0.45
1:I:244:LEU:CD1	1:I:250:ARG:HA	2.34	0.45
1:I:381:ILE:O	1:I:382:LEU:C	2.58	0.45
1:K:30:SER:O	1:K:31:TRP:C	2.58	0.45
1:K:189:GLU:HB2	1:K:284:THR:OG1	2.16	0.45
1:K:190:ARG:HG2	1:K:191:PRO:N	2.30	0.45
1:K:201:ILE:HB	1:K:258:THR:CB	2.43	0.45
1:M:31:TRP:O	1:M:35:THR:HG23	2.16	0.45
1:M:197:TYR:CE1	1:M:198:LEU:HD13	2.46	0.45
1:M:208:ILE:O	1:M:209:SER:C	2.59	0.45
1:M:381:ILE:O	1:M:384:ILE:N	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:315:ILE:O	1:O:376:SER:OG	2.28	0.45
1:A:134:GLU:C	1:A:136:TYR:N	2.74	0.45
1:A:194:SER:CB	1:A:199:TYR:OH	2.52	0.45
1:C:18:ILE:HG23	1:C:18:ILE:HD13	1.47	0.45
1:C:28:GLY:HA2	1:C:67:LEU:HD21	1.98	0.45
1:C:321:TYR:CD2	1:C:368:VAL:HG22	2.51	0.45
1:E:59:SER:O	1:E:63:THR:OG1	2.28	0.45
1:E:162:ALA:HB1	1:E:304:LEU:CD1	2.46	0.45
1:E:257:LYS:HD2	1:E:259:CYS:O	2.16	0.45
1:E:386:GLU:O	1:E:389:ALA:N	2.49	0.45
1:G:100:TYR:O	1:G:101:GLU:C	2.59	0.45
1:G:230:ILE:HG22	1:G:267:GLY:HA3	1.97	0.45
1:G:314:GLU:HG3	1:G:314:GLU:H	1.49	0.45
1:I:186:TYR:HB2	1:I:282:GLY:O	2.16	0.45
1:I:456:MET:SD	1:I:456:MET:N	2.88	0.45
1:K:177:ILE:CG2	1:K:178:GLU:N	2.79	0.45
1:K:383:ARG:HA	1:K:386:GLU:HG3	1.99	0.45
1:M:171:ILE:HB	1:M:299:GLY:HA3	1.97	0.45
1:M:231:ASN:HB3	1:O:233:MET:CE	2.46	0.45
1:M:427:PHE:HA	1:M:430:ALA:HB3	1.98	0.45
1:O:148:ILE:O	1:O:148:ILE:HG22	2.16	0.45
1:O:244:LEU:HG	1:O:248:GLY:O	2.16	0.45
1:O:244:LEU:HD13	1:O:244:LEU:N	2.31	0.45
2:B:854:ASP:O	2:B:857:TYR:HB2	2.16	0.45
1:E:89:MET:HA	1:E:118:TYR:O	2.16	0.45
1:E:217:ASP:O	1:E:221:TYR:N	2.49	0.45
1:E:245:ASP:C	1:E:245:ASP:OD1	2.59	0.45
1:G:129:VAL:HG12	1:G:130:GLN:OE1	2.15	0.45
1:G:272:GLY:O	1:G:273:LYS:HB2	2.16	0.45
1:I:264:LEU:HD22	1:K:266:GLN:HB2	1.97	0.45
1:M:319:VAL:CG2	1:M:370:HIS:CD2	2.97	0.45
1:O:100:TYR:CB	1:O:131:GLN:CD	2.88	0.45
1:O:177:ILE:CG2	1:O:178:GLU:N	2.79	0.45
1:A:322:PHE:CD2	1:A:322:PHE:C	2.94	0.45
1:A:417:GLN:HB2	1:A:424:PHE:O	2.16	0.45
1:E:103:VAL:N	1:E:106:ILE:HD12	2.31	0.45
1:E:133:GLU:O	1:E:136:TYR:HB3	2.17	0.45
1:E:294:VAL:HG12	1:E:295:ILE:N	2.32	0.45
1:E:382:LEU:C	1:E:384:ILE:N	2.72	0.45
1:G:81:PHE:C	1:G:83:GLN:H	2.25	0.45
1:G:291:LYS:HD2	1:G:291:LYS:HA	1.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:381:ILE:HG22	1:G:385:TYR:CE1	2.52	0.45
2:J:852:THR:HG22	2:J:854:ASP:N	2.30	0.45
1:M:16:ARG:HA	1:M:17:PRO:HD3	1.74	0.45
1:M:147:THR:HB	1:M:427:PHE:CE1	2.51	0.45
1:O:294:VAL:HA	1:O:306:ILE:O	2.16	0.45
1:O:319:VAL:CG2	1:O:370:HIS:CD2	2.99	0.45
1:A:136:TYR:O	1:A:139:SER:OG	2.22	0.45
1:C:40:ILE:HG23	1:C:47:PHE:HB2	1.98	0.45
1:E:54:ASN:CB	1:E:55:PRO:HD2	2.47	0.45
1:E:61:LEU:HD21	1:K:242:PHE:HZ	1.82	0.45
1:E:83:GLN:O	1:E:85:LYS:N	2.50	0.45
1:G:230:ILE:HA	1:G:267:GLY:HA2	1.98	0.45
1:I:38:LEU:H	1:I:38:LEU:HG	1.41	0.45
1:I:121:VAL:CG1	1:I:122:GLU:H	2.26	0.45
1:I:167:SER:OG	1:I:168:GLU:N	2.49	0.45
1:K:123:TRP:CD1	1:K:214:HIS:CD2	3.05	0.45
1:K:322:PHE:CD2	1:K:367:GLU:HB3	2.46	0.45
1:O:102:VAL:O	1:O:106:ILE:HD12	2.17	0.45
1:O:185:TRP:HD1	2:P:857:TYR:CE1	2.35	0.45
1:A:25:LEU:HD23	1:A:63:THR:HG21	1.99	0.45
1:A:225:SER:HB2	1:A:271:ASN:CG	2.42	0.45
1:A:323:TYR:HA	1:A:365:THR:O	2.16	0.45
1:E:163:LYS:HE3	1:E:421:PHE:CE1	2.52	0.45
1:E:226:TYR:O	1:E:270:GLU:HB2	2.17	0.45
1:E:231:ASN:OD1	1:G:266:GLN:NE2	2.49	0.45
1:G:235:SER:O	1:G:260:PRO:HB3	2.17	0.45
1:G:266:GLN:HA	1:G:276:VAL:O	2.16	0.45
1:G:436:LEU:O	1:G:436:LEU:HG	2.10	0.45
1:I:34:LYS:HG3	1:I:34:LYS:H	1.56	0.45
1:I:53:TYR:HD2	1:I:53:TYR:O	1.97	0.45
1:I:237:ASN:H	1:I:261:ASP:CG	2.20	0.45
1:K:53:TYR:CG	1:K:54:ASN:N	2.83	0.45
1:K:138:ILE:O	1:K:139:SER:C	2.59	0.45
1:K:161:ARG:O	1:K:161:ARG:HG3	2.17	0.45
1:O:88:ASP:O	1:O:116:LEU:HA	2.17	0.45
1:O:266:GLN:HA	1:O:276:VAL:O	2.16	0.45
1:A:372:ARG:HH21	2:B:847:LEU:HD23	1.80	0.45
1:E:129:VAL:HA	1:E:434:HIS:HD2	1.82	0.45
1:E:171:ILE:HD12	1:E:299:GLY:CA	2.46	0.45
1:E:187:GLY:HA3	1:E:284:THR:N	2.32	0.45
1:G:87:ILE:HG21	1:G:90:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:120:TYR:C	1:G:121:VAL:HG23	2.40	0.45
1:I:63:THR:O	1:I:67:LEU:HG	2.17	0.45
1:I:117:ARG:C	1:I:145:LEU:HD12	2.37	0.45
1:I:138:ILE:HG21	1:I:138:ILE:HD12	1.76	0.45
1:I:381:ILE:CG2	1:I:385:TYR:CE1	2.98	0.45
1:M:47:PHE:HE2	1:M:89:MET:HE2	1.82	0.45
1:M:150:CYS:SG	1:M:152:GLN:NE2	2.90	0.45
1:M:263:LEU:HD12	1:M:263:LEU:C	2.42	0.45
1:O:438:ASP:O	1:O:439:ALA:C	2.60	0.45
1:A:123:TRP:CD1	1:A:214:HIS:CD2	3.02	0.45
1:A:149:ILE:HG21	1:A:151:LEU:HD12	1.97	0.45
1:A:269:LEU:HD23	1:A:269:LEU:HA	1.86	0.45
1:C:381:ILE:HG22	1:C:385:TYR:CE1	2.52	0.45
1:C:390:ASP:C	1:C:392:HIS:N	2.71	0.45
1:E:120:TYR:HD2	1:E:121:VAL:N	2.15	0.45
1:E:304:LEU:HD23	1:E:304:LEU:HA	1.77	0.45
1:K:149:ILE:CG2	1:K:151:LEU:HD12	2.46	0.45
1:M:373:ASN:C	1:M:373:ASN:HD22	2.24	0.45
1:O:262:HIS:CD2	1:O:263:LEU:N	2.84	0.45
1:A:123:TRP:CZ2	1:A:433:LEU:CD2	2.99	0.45
1:A:171:ILE:O	1:A:300:THR:N	2.49	0.45
1:A:315:ILE:HG23	1:A:377:VAL:HG22	1.98	0.45
1:A:431:ILE:CG2	1:A:432:ILE:N	2.79	0.45
1:C:91:VAL:HG22	1:C:120:TYR:CB	2.47	0.45
1:C:171:ILE:HG22	1:C:302:GLY:C	2.42	0.45
1:C:215:THR:O	1:C:216:ILE:C	2.59	0.45
1:E:85:LYS:HA	1:E:113:ASN:OD1	2.16	0.45
1:I:187:GLY:CA	1:I:283:GLY:HA3	2.47	0.45
1:I:290:THR:HG22	1:I:291:LYS:N	2.31	0.45
1:K:292:ASN:N	1:K:292:ASN:ND2	2.65	0.45
1:K:438:ASP:O	1:K:439:ALA:C	2.60	0.45
1:M:62:GLN:O	1:M:63:THR:C	2.58	0.45
1:O:151:LEU:C	1:O:153:GLY:N	2.74	0.45
1:O:228:GLN:HB3	1:O:268:ILE:O	2.17	0.45
1:A:16:ARG:HE	1:A:16:ARG:HB2	1.45	0.45
1:C:130:GLN:O	1:C:131:GLN:C	2.60	0.45
1:C:151:LEU:C	1:C:153:GLY:H	2.25	0.45
1:C:201:ILE:HG23	1:C:202:GLU:N	2.31	0.45
1:C:245:ASP:OD1	1:C:249:LYS:HB3	2.16	0.45
1:C:454:LYS:HB2	1:C:454:LYS:HE2	1.71	0.45
1:E:32:VAL:H	1:E:32:VAL:HG23	1.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:78:LEU:O	1:E:81:PHE:N	2.50	0.45
1:G:215:THR:O	1:G:218:VAL:HG12	2.16	0.45
1:G:269:LEU:HD23	1:G:269:LEU:HA	1.69	0.45
1:I:121:VAL:CG1	1:I:122:GLU:N	2.80	0.45
2:J:854:ASP:O	2:J:857:TYR:HB2	2.17	0.45
1:M:77:SER:HB3	1:M:80:SER:H	1.82	0.45
1:M:183:GLY:O	1:M:312:PHE:CZ	2.70	0.45
1:O:31:TRP:O	1:O:34:LYS:N	2.49	0.45
1:O:117:ARG:O	1:O:145:LEU:HD12	2.17	0.45
1:A:77:SER:CB	1:A:80:SER:HB2	2.40	0.44
1:A:136:TYR:O	1:A:137:SER:C	2.60	0.44
1:C:129:VAL:HG12	1:C:130:GLN:OE1	2.17	0.44
1:C:136:TYR:CB	1:C:431:ILE:HD13	2.44	0.44
1:C:310:ALA:C	1:C:312:PHE:H	2.25	0.44
1:E:134:GLU:O	1:E:137:SER:OG	2.29	0.44
1:E:291:LYS:HD2	1:E:291:LYS:HA	1.64	0.44
1:E:381:ILE:O	1:E:384:ILE:HB	2.17	0.44
1:G:166:ILE:HD11	1:G:304:LEU:HD12	1.99	0.44
1:G:194:SER:HB3	1:G:199:TYR:OH	2.17	0.44
1:I:162:ALA:O	1:I:165:LEU:N	2.50	0.44
1:I:313:VAL:HG13	1:I:314:GLU:N	2.30	0.44
1:K:26:THR:HB	1:K:30:SER:CB	2.46	0.44
1:K:104:LYS:O	1:K:107:LEU:N	2.50	0.44
1:K:384:ILE:O	1:K:387:SER:N	2.50	0.44
1:K:393:PHE:C	1:K:394:LEU:HD12	2.41	0.44
1:O:175:ASN:O	1:O:275:PRO:HD2	2.17	0.44
1:A:77:SER:O	1:A:80:SER:HB2	2.17	0.44
1:A:177:ILE:CD1	1:A:219:LEU:HD11	2.44	0.44
1:A:219:LEU:O	1:A:220:GLN:C	2.60	0.44
1:C:231:ASN:HB2	1:C:449:THR:OG1	2.15	0.44
1:G:138:ILE:O	1:G:140:GLN:N	2.51	0.44
1:G:265:PHE:C	1:G:265:PHE:CD2	2.95	0.44
1:G:436:LEU:HB2	1:G:455:ILE:HD13	1.97	0.44
1:I:185:TRP:HD1	2:J:857:TYR:CE1	2.35	0.44
1:I:190:ARG:HA	1:I:191:PRO:HD3	1.57	0.44
1:I:452:VAL:CG1	1:I:455:ILE:HG12	2.47	0.44
1:K:102:VAL:C	1:K:106:ILE:HD12	2.43	0.44
1:K:129:VAL:O	1:K:130:GLN:C	2.59	0.44
1:K:215:THR:HB	1:K:216:ILE:H	1.64	0.44
1:K:372:ARG:O	1:K:373:ASN:ND2	2.50	0.44
1:M:161:ARG:CD	1:M:161:ARG:C	2.84	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:382:LEU:O	1:O:386:GLU:HG3	2.17	0.44
1:O:424:PHE:C	1:O:424:PHE:CD1	2.95	0.44
1:A:192:MET:SD	1:K:15:SER:O	2.76	0.44
1:A:257:LYS:HE3	1:A:257:LYS:HB3	1.67	0.44
1:A:319:VAL:CG2	1:A:370:HIS:CD2	3.00	0.44
1:C:16:ARG:HB2	1:C:17:PRO:HD3	1.97	0.44
1:C:373:ASN:C	1:C:373:ASN:HD22	2.23	0.44
1:C:433:LEU:C	1:C:437:ILE:HD12	2.42	0.44
1:E:154:ARG:HD2	1:E:425:PRO:HG3	2.00	0.44
1:E:251:THR:C	1:E:253:GLU:N	2.70	0.44
1:G:111:SER:CA	1:G:142:ARG:NH2	2.81	0.44
1:I:16:ARG:HA	1:I:17:PRO:HD3	1.69	0.44
1:I:251:THR:C	1:I:253:GLU:N	2.75	0.44
1:I:422:GLU:H	1:I:422:GLU:CD	2.24	0.44
1:K:125:LEU:HB2	1:K:149:ILE:CD1	2.47	0.44
1:K:187:GLY:O	1:K:238:ILE:HG21	2.16	0.44
1:K:251:THR:C	1:K:253:GLU:N	2.73	0.44
1:K:433:LEU:HG	1:K:437:ILE:HD11	1.98	0.44
1:K:456:MET:SD	1:K:456:MET:N	2.87	0.44
1:M:438:ASP:O	1:M:439:ALA:C	2.60	0.44
2:N:855:ASP:O	2:N:858:ASN:N	2.46	0.44
1:O:53:TYR:HB2	1:O:81:PHE:CD1	2.52	0.44
1:O:96:VAL:N	1:O:97:PRO:CD	2.79	0.44
1:A:54:ASN:HA	1:A:55:PRO:HD3	1.82	0.44
1:A:98:GLU:O	1:A:102:VAL:HG23	2.17	0.44
1:A:212:PHE:HA	1:A:280:PHE:CZ	2.52	0.44
1:C:245:ASP:O	1:C:248:GLY:N	2.30	0.44
1:E:456:MET:N	1:E:456:MET:SD	2.89	0.44
1:G:218:VAL:C	1:G:222:ILE:HD12	2.42	0.44
1:G:313:VAL:CG1	1:G:314:GLU:HG3	2.47	0.44
1:G:319:VAL:HG22	1:G:370:HIS:CG	2.52	0.44
1:I:30:SER:O	1:I:33:ALA:HB3	2.17	0.44
1:I:319:VAL:HG22	1:I:370:HIS:CG	2.52	0.44
1:I:388:ILE:O	1:I:389:ALA:C	2.60	0.44
1:K:25:LEU:CB	1:K:52:LEU:HD21	2.46	0.44
1:K:35:THR:HA	1:K:378:VAL:HG22	2.00	0.44
1:K:123:TRP:CE3	1:K:123:TRP:HA	2.52	0.44
1:M:100:TYR:CB	1:M:131:GLN:NE2	2.78	0.44
1:M:134:GLU:O	1:M:137:SER:OG	2.28	0.44
1:M:214:HIS:O	1:M:218:VAL:HG23	2.17	0.44
1:O:201:ILE:HB	1:O:258:THR:CB	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:287:LYS:N	1:O:292:ASN:OD1	2.51	0.44
1:A:314:GLU:H	1:A:314:GLU:HG3	1.33	0.44
1:E:268:ILE:CG2	1:E:273:LYS:HA	2.48	0.44
1:E:417:GLN:O	1:E:420:ARG:HB2	2.18	0.44
1:E:424:PHE:C	1:E:424:PHE:CD1	2.95	0.44
1:G:142:ARG:O	1:G:143:ALA:C	2.61	0.44
1:G:156:SER:C	1:G:158:TYR:N	2.75	0.44
1:I:200:ASP:O	1:I:203:SER:OG	2.24	0.44
2:J:855:ASP:O	2:J:858:ASN:N	2.45	0.44
1:K:455:ILE:H	1:K:455:ILE:HG12	1.45	0.44
1:M:266:GLN:CB	1:O:264:LEU:HD22	2.47	0.44
1:O:62:GLN:O	1:O:65:GLU:N	2.50	0.44
1:A:212:PHE:O	1:A:216:ILE:HG22	2.17	0.44
1:A:287:LYS:CB	1:A:287:LYS:NZ	2.79	0.44
1:A:389:ALA:O	1:A:390:ASP:C	2.60	0.44
2:B:852:THR:HG22	2:B:854:ASP:N	2.30	0.44
1:C:142:ARG:O	1:C:143:ALA:C	2.58	0.44
1:C:178:GLU:HB2	1:C:296:ASP:HB3	1.99	0.44
1:E:281:LYS:HE2	1:G:175:ASN:CG	2.42	0.44
1:G:124:ALA:O	1:G:125:LEU:C	2.60	0.44
1:I:61:LEU:N	1:I:61:LEU:CD1	2.80	0.44
1:I:100:TYR:CB	1:I:131:GLN:CD	2.89	0.44
1:K:185:TRP:CD1	2:L:857:TYR:HE1	2.36	0.44
1:K:432:ILE:HG23	1:K:432:ILE:HD13	1.73	0.44
2:N:856:VAL:O	2:N:860:ILE:HG22	2.18	0.44
1:O:75:PHE:HD2	1:O:80:SER:HB3	1.82	0.44
1:O:154:ARG:CD	1:O:425:PRO:HG3	2.41	0.44
1:A:218:VAL:HG13	1:A:222:ILE:HD11	1.99	0.44
1:A:292:ASN:H	1:A:292:ASN:HD22	1.66	0.44
1:E:128:SER:O	1:E:129:VAL:C	2.57	0.44
1:G:180:SER:O	1:G:293:LEU:HD12	2.18	0.44
1:G:189:GLU:HB3	1:G:244:LEU:HD11	2.00	0.44
1:G:201:ILE:HG23	1:G:202:GLU:N	2.32	0.44
1:G:432:ILE:HD13	1:G:456:MET:HA	2.00	0.44
1:I:77:SER:HB3	1:I:80:SER:OG	2.17	0.44
1:I:146:GLN:NE2	1:I:146:GLN:HA	2.33	0.44
2:J:853:MET:O	2:J:856:VAL:N	2.51	0.44
1:K:244:LEU:N	1:K:244:LEU:CD1	2.81	0.44
1:K:391:TYR:C	1:K:391:TYR:CD2	2.95	0.44
1:M:14:SER:C	1:M:16:ARG:N	2.75	0.44
1:M:34:LYS:C	1:M:35:THR:CG2	2.91	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:102:VAL:HG12	1:M:106:ILE:CD1	2.48	0.44
1:M:147:THR:HB	1:M:427:PHE:CG	2.52	0.44
1:O:91:VAL:HG13	1:O:120:TYR:HD1	1.83	0.44
1:O:129:VAL:HG13	1:O:130:GLN:N	2.33	0.44
1:O:142:ARG:HB2	1:O:145:LEU:HB3	2.00	0.44
1:A:141:GLN:HG2	1:A:141:GLN:H	1.37	0.44
1:A:378:VAL:O	1:A:379:GLY:C	2.59	0.44
1:A:381:ILE:O	1:A:384:ILE:N	2.43	0.44
1:C:389:ALA:O	1:C:392:HIS:N	2.51	0.44
1:C:448:LYS:O	1:C:450:LEU:CD2	2.66	0.44
1:E:263:LEU:HD12	1:E:264:LEU:C	2.43	0.44
1:E:426:THR:O	1:E:429:ASP:HB2	2.18	0.44
2:F:852:THR:O	2:F:855:ASP:HB2	2.18	0.44
1:I:151:LEU:HD23	1:I:217:ASP:OD2	2.18	0.44
1:I:188:TYR:CZ	1:I:238:ILE:HG12	2.52	0.44
1:I:244:LEU:CD1	1:I:250:ARG:CA	2.96	0.44
1:M:188:TYR:CD1	1:M:238:ILE:CD1	3.01	0.44
1:O:152:GLN:NE2	1:O:152:GLN:N	2.65	0.44
1:O:292:ASN:N	1:O:292:ASN:ND2	2.66	0.44
1:O:381:ILE:HG22	1:O:385:TYR:CE1	2.53	0.44
1:A:53:TYR:C	1:A:53:TYR:CD2	2.96	0.44
1:A:67:LEU:O	1:A:68:GLN:HB2	2.17	0.44
1:A:251:THR:C	1:A:253:GLU:N	2.76	0.44
1:A:422:GLU:OE1	1:A:422:GLU:N	2.49	0.44
1:C:262:HIS:CD2	1:C:263:LEU:N	2.86	0.44
1:E:322:PHE:CD2	1:E:322:PHE:C	2.96	0.44
1:G:126:ALA:HB2	1:G:135:LEU:HD12	1.99	0.44
1:G:313:VAL:CG1	1:G:314:GLU:N	2.80	0.44
1:G:452:VAL:HG13	1:G:455:ILE:CG2	2.45	0.44
1:I:55:PRO:HB2	1:I:56:THR:H	1.37	0.44
1:I:158:TYR:HB2	1:I:318:LEU:HD12	1.99	0.44
1:I:314:GLU:H	1:I:314:GLU:HG3	1.06	0.44
1:K:126:ALA:CB	1:K:132:ALA:HB2	2.40	0.44
1:K:293:LEU:HD12	1:K:293:LEU:HA	1.75	0.44
1:O:20:VAL:HG21	1:O:40:ILE:CD1	2.48	0.44
1:O:198:LEU:HB2	1:O:199:TYR:CE1	2.53	0.44
1:O:265:PHE:CD2	1:O:265:PHE:C	2.95	0.44
1:A:454:LYS:O	1:A:455:ILE:C	2.60	0.43
1:C:40:ILE:O	1:C:40:ILE:HG22	2.17	0.43
1:C:84:TYR:CD1	1:C:86:ASP:HB2	2.53	0.43
1:E:15:SER:O	1:E:16:ARG:HB3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:218:VAL:HG12	1:E:219:LEU:N	2.33	0.43
1:I:38:LEU:HD23	1:I:38:LEU:HA	1.60	0.43
1:I:183:GLY:HA2	1:I:207:LEU:HD12	1.99	0.43
1:I:230:ILE:HA	1:I:267:GLY:HA2	2.00	0.43
1:I:437:ILE:HA	1:I:440:VAL:HG23	2.00	0.43
1:K:156:SER:O	1:K:159:ILE:N	2.45	0.43
1:K:192:MET:O	1:O:58:LYS:HD3	2.18	0.43
1:K:199:TYR:CD1	1:K:199:TYR:N	2.85	0.43
1:K:422:GLU:CD	1:K:422:GLU:N	2.76	0.43
1:M:96:VAL:O	1:M:99:HIS:HB2	2.18	0.43
1:M:208:ILE:O	1:M:212:PHE:HB3	2.17	0.43
1:M:290:THR:HG22	1:M:291:LYS:O	2.18	0.43
1:O:31:TRP:O	1:O:32:VAL:C	2.61	0.43
1:O:135:LEU:O	1:O:138:ILE:HB	2.18	0.43
1:O:371:LEU:O	1:O:372:ARG:C	2.61	0.43
1:A:65:GLU:HG2	1:A:66:GLN:N	2.26	0.43
1:A:129:VAL:C	1:A:131:GLN:H	2.26	0.43
1:A:268:ILE:CG2	1:A:273:LYS:HA	2.49	0.43
1:C:195:PRO:HB2	1:C:197:TYR:CE2	2.54	0.43
1:C:313:VAL:HG12	1:C:314:GLU:HG3	2.01	0.43
1:E:63:THR:O	1:E:64:ILE:C	2.60	0.43
1:E:85:LYS:HE2	1:E:113:ASN:HA	1.99	0.43
1:G:432:ILE:CG2	1:G:455:ILE:HG13	2.48	0.43
1:I:152:GLN:H	1:I:152:GLN:HE21	1.62	0.43
1:I:155:LYS:O	1:I:383:ARG:HD3	2.18	0.43
1:I:248:GLY:O	1:I:249:LYS:C	2.52	0.43
1:I:436:LEU:O	1:I:439:ALA:HB3	2.18	0.43
1:K:134:GLU:O	1:K:137:SER:OG	2.24	0.43
1:K:319:VAL:HG22	1:K:370:HIS:CG	2.53	0.43
1:M:293:LEU:HD23	1:M:318:LEU:HD22	2.00	0.43
1:M:315:ILE:O	1:M:376:SER:HB2	2.18	0.43
1:O:100:TYR:HA	1:O:135:LEU:HD11	2.00	0.43
1:O:156:SER:HB3	1:O:159:ILE:CG1	2.46	0.43
1:O:377:VAL:HG11	2:P:859:TYR:CD2	2.53	0.43
1:O:424:PHE:CD1	1:O:424:PHE:O	2.71	0.43
1:A:36:HIS:O	1:A:37:PHE:C	2.61	0.43
1:A:53:TYR:CD2	1:A:54:ASN:N	2.87	0.43
1:A:120:TYR:O	1:A:121:VAL:HG23	2.18	0.43
1:C:195:PRO:HB3	1:C:197:TYR:HD2	1.80	0.43
1:E:129:VAL:O	1:E:132:ALA:N	2.51	0.43
1:E:172:GLY:HA3	1:E:301:LYS:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:178:GLU:C	1:E:179:ILE:HG13	2.41	0.43
1:E:193:ARG:O	1:E:194:SER:C	2.62	0.43
1:E:375:ASN:HD21	1:E:378:VAL:HG23	1.83	0.43
1:G:118:TYR:N	1:G:118:TYR:HD1	2.16	0.43
1:G:177:ILE:CB	1:G:276:VAL:HG13	2.48	0.43
1:I:107:LEU:HD13	1:I:138:ILE:HG22	1.98	0.43
1:K:146:GLN:OE1	1:K:424:PHE:CZ	2.71	0.43
1:K:432:ILE:O	1:K:433:LEU:O	2.36	0.43
1:K:443:SER:O	1:K:444:ASP:C	2.61	0.43
1:M:161:ARG:HA	1:M:161:ARG:HD3	1.73	0.43
1:O:54:ASN:HA	1:O:55:PRO:HD3	1.70	0.43
1:A:124:ALA:O	1:A:125:LEU:C	2.60	0.43
1:C:64:ILE:HD11	1:C:72:ALA:CB	2.48	0.43
1:C:428:LYS:O	1:C:432:ILE:HG13	2.18	0.43
1:E:62:GLN:CG	1:E:66:GLN:NE2	2.78	0.43
1:E:77:SER:O	1:E:80:SER:HB2	2.18	0.43
1:E:252:LYS:H	1:E:252:LYS:HG3	1.19	0.43
1:E:376:SER:O	1:E:377:VAL:C	2.59	0.43
1:G:197:TYR:CE1	1:G:198:LEU:HD13	2.54	0.43
1:G:365:THR:CG2	1:G:366:MET:N	2.80	0.43
1:G:381:ILE:O	1:G:384:ILE:N	2.48	0.43
1:G:381:ILE:CG2	1:G:385:TYR:CE1	3.01	0.43
1:G:422:GLU:H	1:G:422:GLU:CD	2.26	0.43
1:I:67:LEU:HB2	1:I:69:LEU:HG	2.00	0.43
1:K:77:SER:HB3	1:K:80:SER:H	1.82	0.43
1:K:136:TYR:CD2	1:K:431:ILE:HD13	2.53	0.43
1:M:20:VAL:H	1:M:20:VAL:HG23	1.51	0.43
1:M:322:PHE:CD1	1:M:323:TYR:N	2.86	0.43
1:O:442:ARG:O	1:O:446:GLU:HB2	2.17	0.43
1:A:287:LYS:HG2	1:A:287:LYS:HZ3	1.49	0.43
1:A:313:VAL:CG1	1:A:314:GLU:N	2.81	0.43
1:A:389:ALA:O	1:A:393:PHE:N	2.50	0.43
1:C:81:PHE:C	1:C:83:GLN:H	2.26	0.43
1:C:152:GLN:HG3	1:C:314:GLU:O	2.17	0.43
1:C:174:ILE:HG22	1:C:175:ASN:N	2.34	0.43
1:C:230:ILE:HA	1:C:267:GLY:HA2	2.01	0.43
1:E:110:SER:C	1:E:142:ARG:HH22	2.27	0.43
1:G:104:LYS:CA	1:G:107:LEU:HD12	2.45	0.43
1:I:69:LEU:HA	1:I:69:LEU:HD23	1.74	0.43
1:I:436:LEU:HB2	1:I:455:ILE:HD13	2.01	0.43
1:K:158:TYR:CB	1:K:318:LEU:HD12	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:304:LEU:HD21	1:K:320:LEU:HD21	2.00	0.43
1:M:179:ILE:HD11	1:M:219:LEU:HD22	2.00	0.43
1:O:68:GLN:HE21	1:O:68:GLN:N	2.13	0.43
1:O:269:LEU:HD23	1:O:269:LEU:HA	1.77	0.43
1:O:293:LEU:O	1:O:307:GLU:HA	2.18	0.43
1:A:165:LEU:HD13	1:A:322:PHE:CD1	2.53	0.43
1:A:204:GLY:C	1:A:205:VAL:HG23	2.44	0.43
1:A:437:ILE:O	1:A:438:ASP:C	2.56	0.43
1:C:443:SER:O	1:C:444:ASP:C	2.59	0.43
1:E:42:GLN:C	1:E:43:LEU:HD23	2.44	0.43
1:E:58:LYS:HG2	1:K:252:LYS:O	2.18	0.43
1:E:136:TYR:CD1	1:E:136:TYR:C	2.92	0.43
1:E:187:GLY:HA3	1:E:284:THR:H	1.84	0.43
1:G:433:LEU:C	1:G:437:ILE:CD1	2.81	0.43
1:I:51:ALA:HB2	1:I:84:TYR:HE2	1.83	0.43
1:I:286:VAL:O	1:I:286:VAL:HG23	2.17	0.43
1:M:150:CYS:O	1:M:150:CYS:SG	2.76	0.43
1:M:154:ARG:NH1	1:M:417:GLN:OE1	2.44	0.43
1:O:59:SER:O	1:O:63:THR:OG1	2.26	0.43
1:O:197:TYR:HA	1:O:200:ASP:HB3	2.01	0.43
1:A:185:TRP:HZ3	1:A:186:TYR:OH	1.94	0.43
1:A:192:MET:HE1	1:K:15:SER:OG	2.18	0.43
1:A:245:ASP:O	1:A:247:ASN:N	2.51	0.43
1:A:248:GLY:O	1:A:249:LYS:C	2.60	0.43
1:C:25:LEU:HD12	1:C:25:LEU:HA	1.61	0.43
1:C:194:SER:HB3	1:C:199:TYR:OH	2.18	0.43
1:C:432:ILE:HD13	1:C:432:ILE:HG21	1.53	0.43
1:E:53:TYR:CG	1:E:54:ASN:N	2.86	0.43
1:E:111:SER:N	1:E:142:ARG:NH2	2.67	0.43
1:E:431:ILE:HG22	1:E:432:ILE:H	1.83	0.43
1:G:208:ILE:HG13	1:G:263:LEU:CD2	2.48	0.43
1:G:251:THR:C	1:G:253:GLU:N	2.76	0.43
1:G:252:LYS:H	1:G:252:LYS:HG3	1.23	0.43
1:G:436:LEU:HD12	1:G:452:VAL:HG11	2.00	0.43
1:I:129:VAL:O	1:I:132:ALA:HB3	2.19	0.43
1:I:416:LYS:HA	1:I:426:THR:OG1	2.19	0.43
1:K:23:VAL:HG12	1:K:94:VAL:CG1	2.49	0.43
1:O:57:LEU:HD21	1:O:61:LEU:HD11	1.89	0.43
1:O:79:GLU:O	1:O:83:GLN:HG3	2.18	0.43
1:O:91:VAL:HG22	1:O:120:TYR:HB3	2.01	0.43
1:O:220:GLN:HE21	1:O:220:GLN:HB2	1.55	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:251:THR:C	1:O:253:GLU:N	2.76	0.43
1:A:190:ARG:HA	1:A:191:PRO:HD3	1.73	0.43
1:A:200:ASP:OD1	1:A:200:ASP:C	2.60	0.43
1:A:273:LYS:HA	1:A:273:LYS:HD3	1.64	0.43
1:C:61:LEU:N	1:C:61:LEU:HD12	2.34	0.43
1:C:79:GLU:O	1:C:80:SER:C	2.61	0.43
1:C:388:ILE:O	1:C:389:ALA:C	2.56	0.43
1:E:38:LEU:HA	1:E:38:LEU:HD23	1.73	0.43
1:G:159:ILE:O	1:G:162:ALA:N	2.51	0.43
1:G:197:TYR:CD1	1:G:197:TYR:C	2.97	0.43
1:I:40:ILE:HG23	1:I:47:PHE:CB	2.48	0.43
1:I:135:LEU:O	1:I:138:ILE:HB	2.19	0.43
1:I:171:ILE:HB	1:I:299:GLY:HA3	2.01	0.43
1:I:315:ILE:CG2	1:I:377:VAL:HG22	2.48	0.43
1:K:35:THR:OG1	1:K:36:HIS:N	2.50	0.43
1:K:129:VAL:CG1	1:K:130:GLN:H	2.29	0.43
1:K:133:GLU:OE2	1:K:133:GLU:HA	2.19	0.43
2:L:854:ASP:O	2:L:857:TYR:HB2	2.19	0.43
1:M:134:GLU:C	1:M:136:TYR:N	2.75	0.43
1:M:149:ILE:HB	1:M:430:ALA:HB2	2.01	0.43
1:M:436:LEU:HD12	1:M:452:VAL:HG11	2.00	0.43
1:A:95:LYS:HE2	1:A:197:TYR:CE2	2.54	0.43
1:A:262:HIS:HE1	1:C:176:SER:OG	2.02	0.43
1:A:295:ILE:O	1:A:295:ILE:HG22	2.19	0.43
1:C:121:VAL:HG12	1:C:122:GLU:N	2.34	0.43
1:C:183:GLY:CA	1:C:207:LEU:HD13	2.48	0.43
1:C:216:ILE:O	1:C:217:ASP:C	2.61	0.43
1:C:292:ASN:N	1:C:292:ASN:HD22	2.17	0.43
1:C:455:ILE:HD13	1:C:455:ILE:HG21	1.77	0.43
1:E:138:ILE:O	1:E:140:GLN:N	2.52	0.43
1:E:284:THR:H	1:E:284:THR:HG23	1.48	0.43
1:G:168:GLU:O	1:G:170:CYS:N	2.52	0.43
1:I:105:ASN:N	1:I:105:ASN:ND2	2.66	0.43
1:I:188:TYR:C	1:I:189:GLU:CG	2.92	0.43
1:K:57:LEU:O	1:K:58:LYS:C	2.61	0.43
1:K:89:MET:HB2	1:K:118:TYR:O	2.18	0.43
1:K:245:ASP:O	1:K:248:GLY:N	2.27	0.43
1:M:381:ILE:HG22	1:M:385:TYR:CE1	2.53	0.43
1:O:124:ALA:O	1:O:125:LEU:C	2.61	0.43
1:O:245:ASP:O	1:O:246:GLU:C	2.61	0.43
1:O:255:ILE:O	1:O:255:ILE:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:313:VAL:HG12	1:O:314:GLU:HG3	2.01	0.43
1:A:88:ASP:O	1:A:117:ARG:N	2.50	0.43
1:A:195:PRO:CB	1:A:198:LEU:HD22	2.48	0.43
1:A:219:LEU:C	1:A:221:TYR:N	2.71	0.43
1:C:159:ILE:HG21	1:C:218:VAL:HG22	2.01	0.43
1:C:201:ILE:HB	1:C:258:THR:CB	2.47	0.43
1:C:236:ASN:HA	1:C:261:ASP:OD1	2.19	0.43
1:C:386:GLU:C	1:C:388:ILE:N	2.77	0.43
1:E:35:THR:O	1:E:36:HIS:C	2.59	0.43
1:E:384:ILE:C	1:E:388:ILE:HD12	2.36	0.43
1:G:57:LEU:O	1:G:58:LYS:C	2.61	0.43
1:G:444:ASP:O	1:G:445:LYS:C	2.62	0.43
1:I:372:ARG:C	1:I:373:ASN:CG	2.87	0.43
1:M:365:THR:CG2	1:M:366:MET:N	2.82	0.43
1:M:451:ASP:OD1	1:M:453:SER:OG	2.35	0.43
1:O:22:PHE:N	1:O:51:ALA:O	2.35	0.43
1:O:25:LEU:O	1:O:54:ASN:ND2	2.50	0.43
1:O:51:ALA:O	1:O:52:LEU:HD12	2.17	0.43
1:O:212:PHE:O	1:O:213:GLY:C	2.61	0.43
1:A:187:GLY:O	1:A:238:ILE:HG21	2.19	0.42
1:A:229:LYS:C	1:A:230:ILE:CG2	2.92	0.42
1:A:310:ALA:C	1:A:312:PHE:H	2.26	0.42
1:A:376:SER:O	1:A:377:VAL:C	2.62	0.42
1:C:39:ALA:HB1	1:C:382:LEU:HA	2.01	0.42
1:C:84:TYR:C	1:C:86:ASP:H	2.27	0.42
1:C:168:GLU:O	1:C:328:GLY:O	2.37	0.42
1:C:424:PHE:CD1	1:C:424:PHE:C	2.97	0.42
1:E:312:PHE:CE1	2:F:853:MET:HE1	2.53	0.42
2:F:855:ASP:O	2:F:856:VAL:C	2.62	0.42
1:G:23:VAL:HG12	1:G:94:VAL:CG1	2.50	0.42
1:G:291:LYS:HG3	1:G:307:GLU:HB3	2.01	0.42
1:G:424:PHE:C	1:G:424:PHE:CD1	2.97	0.42
1:I:94:VAL:O	1:I:95:LYS:C	2.62	0.42
1:I:147:THR:HG21	1:I:427:PHE:CD2	2.54	0.42
1:I:286:VAL:O	1:I:287:LYS:C	2.62	0.42
1:K:39:ALA:HB1	1:K:382:LEU:HA	2.01	0.42
1:K:57:LEU:HD23	1:K:61:LEU:HD21	2.01	0.42
1:K:228:GLN:HE22	1:K:273:LYS:HE3	1.83	0.42
1:K:292:ASN:HD22	1:K:292:ASN:N	2.17	0.42
1:M:115:ASN:O	1:M:117:ARG:HB2	2.19	0.42
1:M:142:ARG:HG3	1:M:145:LEU:CD2	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:166:ILE:C	1:M:168:GLU:N	2.76	0.42
1:M:281:LYS:HE2	1:O:175:ASN:CG	2.43	0.42
1:O:38:LEU:HA	1:O:38:LEU:HD23	1.30	0.42
1:O:195:PRO:HB2	1:O:198:LEU:HD22	2.01	0.42
1:O:208:ILE:HA	1:O:212:PHE:HB3	2.01	0.42
1:O:216:ILE:HA	1:O:216:ILE:HD12	1.75	0.42
1:A:43:LEU:C	1:A:45:SER:N	2.77	0.42
1:A:211:SER:O	1:A:215:THR:OG1	2.33	0.42
1:A:212:PHE:CZ	1:A:216:ILE:HB	2.54	0.42
1:A:218:VAL:O	1:A:222:ILE:N	2.37	0.42
1:A:225:SER:HB2	1:A:271:ASN:CB	2.47	0.42
1:A:297:ILE:HG21	1:A:297:ILE:HD13	1.61	0.42
1:A:300:THR:O	1:A:300:THR:HG22	2.19	0.42
1:A:424:PHE:C	1:A:424:PHE:CD1	2.98	0.42
1:C:198:LEU:HD12	1:C:198:LEU:HA	1.46	0.42
1:E:152:GLN:NE2	1:E:214:HIS:HE1	2.17	0.42
1:E:161:ARG:O	1:E:161:ARG:HG3	2.18	0.42
1:G:190:ARG:HA	1:G:191:PRO:HD3	1.79	0.42
1:G:301:LYS:O	1:G:364:GLN:NE2	2.51	0.42
1:G:417:GLN:HB2	1:G:424:PHE:C	2.45	0.42
1:G:427:PHE:HA	1:G:430:ALA:CB	2.48	0.42
1:I:174:ILE:HG22	1:I:175:ASN:N	2.34	0.42
1:K:174:ILE:HB	1:K:274:VAL:HG21	2.01	0.42
1:K:244:LEU:HD12	1:K:244:LEU:HA	1.83	0.42
1:M:30:SER:O	1:M:31:TRP:C	2.63	0.42
1:M:77:SER:CB	1:M:80:SER:HB2	2.43	0.42
1:O:133:GLU:HA	1:O:133:GLU:OE2	2.18	0.42
1:O:165:LEU:O	1:O:170:CYS:SG	2.78	0.42
1:A:30:SER:H	1:A:33:ALA:HB3	1.84	0.42
1:A:228:GLN:O	1:A:452:VAL:N	2.47	0.42
1:A:262:HIS:ND1	1:C:176:SER:HB2	2.34	0.42
1:C:314:GLU:HG3	1:C:314:GLU:H	1.19	0.42
1:C:386:GLU:O	1:C:389:ALA:N	2.52	0.42
1:C:426:THR:O	1:C:429:ASP:N	2.52	0.42
1:E:84:TYR:C	1:E:86:ASP:N	2.74	0.42
1:E:149:ILE:HD12	1:E:149:ILE:HA	1.87	0.42
1:E:200:ASP:OD1	1:E:201:ILE:N	2.51	0.42
1:E:228:GLN:O	1:E:452:VAL:N	2.52	0.42
1:E:416:LYS:HD2	1:E:418:GLY:CA	2.49	0.42
1:I:84:TYR:C	1:I:86:ASP:N	2.78	0.42
1:I:91:VAL:HG22	1:I:120:TYR:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:93:SER:C	1:I:94:VAL:HG13	2.44	0.42
1:M:375:ASN:C	1:M:375:ASN:OD1	2.62	0.42
1:M:435:ARG:HB3	1:M:455:ILE:HG21	2.00	0.42
1:O:50:VAL:HG13	1:O:84:TYR:CE2	2.55	0.42
1:O:416:LYS:HA	1:O:426:THR:OG1	2.20	0.42
1:O:455:ILE:C	1:O:457:ILE:H	2.26	0.42
2:P:853:MET:HB2	2:P:853:MET:HE2	1.86	0.42
1:A:149:ILE:HG23	1:A:151:LEU:HD12	2.01	0.42
1:A:208:ILE:O	1:A:209:SER:C	2.62	0.42
1:C:79:GLU:HG2	1:C:109:HIS:NE2	2.34	0.42
1:C:92:VAL:HB	1:C:121:VAL:HG22	2.01	0.42
1:C:110:SER:O	1:C:111:SER:C	2.61	0.42
1:C:134:GLU:O	1:C:135:LEU:C	2.62	0.42
1:C:177:ILE:CG2	1:C:178:GLU:N	2.81	0.42
1:C:211:SER:O	1:C:215:THR:OG1	2.33	0.42
1:C:217:ASP:HB2	1:C:433:LEU:HD13	2.01	0.42
1:C:251:THR:C	1:C:253:GLU:N	2.77	0.42
1:C:323:TYR:HA	1:C:365:THR:O	2.20	0.42
1:C:392:HIS:C	1:C:394:LEU:N	2.74	0.42
1:E:386:GLU:C	1:E:388:ILE:N	2.75	0.42
1:G:16:ARG:HA	1:G:17:PRO:HD3	1.90	0.42
1:G:64:ILE:CG1	1:G:72:ALA:HB3	2.46	0.42
1:I:67:LEU:O	1:I:68:GLN:HB2	2.18	0.42
1:I:111:SER:HA	1:I:142:ARG:NH2	2.35	0.42
1:K:25:LEU:O	1:K:54:ASN:ND2	2.51	0.42
1:K:103:VAL:CA	1:K:106:ILE:HD12	2.49	0.42
1:K:136:TYR:CG	1:K:431:ILE:HD13	2.54	0.42
1:K:152:GLN:HE21	1:K:152:GLN:H	1.66	0.42
1:K:231:ASN:CG	1:K:232:ALA:N	2.77	0.42
1:K:273:LYS:N	1:K:273:LYS:CD	2.82	0.42
1:O:165:LEU:HD23	1:O:165:LEU:HA	1.87	0.42
1:O:212:PHE:HA	1:O:280:PHE:CZ	2.54	0.42
1:O:304:LEU:HD23	1:O:322:PHE:HB2	2.01	0.42
1:A:53:TYR:CG	1:A:54:ASN:N	2.87	0.42
1:A:103:VAL:HA	1:A:106:ILE:CD1	2.50	0.42
1:A:154:ARG:HH11	1:A:154:ARG:HD3	1.60	0.42
1:A:381:ILE:CG2	1:A:385:TYR:CE1	3.03	0.42
1:C:178:GLU:OE2	1:C:296:ASP:HB3	2.20	0.42
1:C:319:VAL:HG12	1:C:320:LEU:N	2.34	0.42
1:E:28:GLY:HA2	1:E:67:LEU:CD2	2.39	0.42
1:E:110:SER:HB2	1:E:116:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:286:VAL:O	1:E:286:VAL:HG23	2.19	0.42
1:G:160:VAL:O	1:G:160:VAL:HG12	2.19	0.42
1:G:216:ILE:CG2	1:G:217:ASP:H	2.32	0.42
1:G:294:VAL:HA	1:G:306:ILE:O	2.19	0.42
1:G:294:VAL:HG22	1:G:307:GLU:HG2	2.00	0.42
1:G:377:VAL:HG11	2:H:859:TYR:CD2	2.55	0.42
1:G:392:HIS:HD2	1:G:393:PHE:CD2	2.17	0.42
2:H:853:MET:O	2:H:854:ASP:C	2.62	0.42
1:K:128:SER:O	1:K:129:VAL:C	2.62	0.42
1:K:201:ILE:HG21	1:K:258:THR:HG21	2.00	0.42
1:K:244:LEU:HD11	1:K:250:ARG:HG3	2.02	0.42
1:M:84:TYR:C	1:M:86:ASP:H	2.28	0.42
1:O:69:LEU:HB3	1:O:72:ALA:CB	2.46	0.42
1:O:215:THR:HB	1:O:216:ILE:H	1.66	0.42
1:O:230:ILE:O	1:O:230:ILE:HG13	2.19	0.42
1:O:381:ILE:CG2	1:O:385:TYR:HE1	2.33	0.42
1:A:161:ARG:HH11	1:A:161:ARG:HD2	1.66	0.42
1:A:292:ASN:N	1:A:292:ASN:ND2	2.68	0.42
1:C:53:TYR:CD2	1:C:53:TYR:C	2.98	0.42
1:C:134:GLU:O	1:C:137:SER:OG	2.26	0.42
1:E:30:SER:OG	1:E:33:ALA:HB2	2.18	0.42
1:E:88:ASP:O	1:E:117:ARG:N	2.47	0.42
1:E:422:GLU:N	1:E:422:GLU:CD	2.78	0.42
1:G:24:GLY:HA3	1:G:93:SER:O	2.19	0.42
2:H:853:MET:O	2:H:856:VAL:HB	2.17	0.42
1:I:18:ILE:HG23	1:I:18:ILE:HD13	1.71	0.42
1:I:136:TYR:C	1:I:138:ILE:N	2.75	0.42
1:I:185:TRP:CZ3	1:I:186:TYR:CE1	3.08	0.42
1:I:325:ILE:O	1:I:326:LYS:C	2.62	0.42
1:I:375:ASN:O	1:I:375:ASN:OD1	2.38	0.42
1:M:231:ASN:OD1	1:O:266:GLN:NE2	2.52	0.42
1:M:389:ALA:O	1:M:392:HIS:HB3	2.18	0.42
1:M:436:LEU:O	1:M:439:ALA:CB	2.63	0.42
1:O:30:SER:O	1:O:31:TRP:C	2.61	0.42
1:O:77:SER:O	1:O:80:SER:HB2	2.19	0.42
1:O:185:TRP:CD1	2:P:857:TYR:HE1	2.38	0.42
1:O:313:VAL:CG1	1:O:314:GLU:HG3	2.49	0.42
1:O:431:ILE:O	1:O:432:ILE:C	2.61	0.42
1:A:33:ALA:O	1:A:37:PHE:HB3	2.20	0.42
1:A:96:VAL:HG12	1:A:96:VAL:O	2.19	0.42
1:E:30:SER:O	1:E:33:ALA:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:266:GLN:CD	1:G:266:GLN:HG2	2.45	0.42
1:E:315:ILE:O	1:E:315:ILE:HG22	2.19	0.42
1:G:111:SER:N	1:G:142:ARG:NH2	2.66	0.42
1:G:290:THR:CG2	1:G:291:LYS:N	2.82	0.42
1:G:386:GLU:O	1:G:387:SER:C	2.62	0.42
1:I:436:LEU:O	1:I:436:LEU:HG	2.07	0.42
1:K:209:SER:OG	1:K:210:ASN:N	2.53	0.42
1:M:251:THR:C	1:M:253:GLU:N	2.76	0.42
1:M:371:LEU:O	1:M:372:ARG:C	2.63	0.42
1:O:220:GLN:HG2	1:O:226:TYR:HA	2.01	0.42
1:O:306:ILE:HG12	1:O:320:LEU:HD12	2.01	0.42
1:A:53:TYR:O	1:A:54:ASN:ND2	2.52	0.42
1:A:185:TRP:CD1	1:A:185:TRP:N	2.82	0.42
1:A:244:LEU:CD1	1:A:250:ARG:HG3	2.30	0.42
1:C:23:VAL:HG12	1:C:94:VAL:HG11	2.00	0.42
1:C:174:ILE:HB	1:C:274:VAL:HG21	2.02	0.42
1:C:263:LEU:HD12	1:C:263:LEU:C	2.44	0.42
1:C:290:THR:HG22	1:C:291:LYS:N	2.34	0.42
1:E:31:TRP:CH2	1:E:35:THR:HG21	2.55	0.42
1:E:125:LEU:HD11	1:E:427:PHE:CE2	2.55	0.42
1:E:231:ASN:O	1:E:265:PHE:HA	2.20	0.42
1:G:184:GLY:N	1:G:282:GLY:O	2.50	0.42
1:I:62:GLN:O	1:I:65:GLU:N	2.53	0.42
1:I:197:TYR:CZ	1:I:198:LEU:HD21	2.55	0.42
1:I:293:LEU:HB2	1:I:311:GLY:HA2	2.02	0.42
1:I:424:PHE:O	1:I:424:PHE:CD1	2.73	0.42
1:O:376:SER:O	1:O:377:VAL:C	2.63	0.42
1:O:384:ILE:HD13	1:O:384:ILE:HA	1.84	0.42
1:O:432:ILE:O	1:O:433:LEU:C	2.63	0.42
1:A:179:ILE:HG22	1:A:180:SER:N	2.34	0.42
1:A:195:PRO:HB3	1:A:197:TYR:CD2	2.55	0.42
1:A:257:LYS:CG	1:A:259:CYS:O	2.68	0.42
1:C:75:PHE:HB2	1:C:81:PHE:HD1	1.84	0.42
1:C:96:VAL:HB	1:C:97:PRO:HD3	2.02	0.42
1:E:149:ILE:HG23	1:E:151:LEU:HD13	2.01	0.42
1:E:430:ALA:O	1:E:434:HIS:HB2	2.19	0.42
1:G:20:VAL:HG21	1:G:40:ILE:HD12	2.01	0.42
1:G:136:TYR:C	1:G:138:ILE:N	2.77	0.42
1:G:251:THR:HG22	1:G:252:LYS:N	2.35	0.42
1:I:134:GLU:C	1:I:136:TYR:N	2.76	0.42
1:I:159:ILE:O	1:I:160:VAL:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:122:GLU:HA	1:M:150:CYS:HB3	2.01	0.42
1:M:166:ILE:O	1:M:168:GLU:N	2.52	0.42
1:M:313:VAL:HG12	1:M:314:GLU:HG3	2.02	0.42
1:O:422:GLU:CD	1:O:422:GLU:N	2.77	0.42
1:A:99:HIS:O	1:A:103:VAL:HG23	2.19	0.42
1:A:185:TRP:CZ3	1:A:186:TYR:OH	2.68	0.42
1:A:188:TYR:CZ	1:A:238:ILE:HG12	2.55	0.42
1:A:216:ILE:CG2	1:A:217:ASP:H	2.32	0.42
1:A:447:GLU:HG3	1:C:449:THR:HG22	2.00	0.42
1:C:111:SER:N	1:C:142:ARG:HH22	2.17	0.42
1:C:128:SER:O	1:C:129:VAL:C	2.60	0.42
1:C:136:TYR:O	1:C:138:ILE:N	2.53	0.42
1:C:292:ASN:HD22	1:C:292:ASN:H	1.67	0.42
1:E:134:GLU:C	1:E:136:TYR:N	2.76	0.42
1:E:281:LYS:CE	1:G:298:HIS:CD2	3.02	0.42
1:G:147:THR:HB	1:G:427:PHE:CE1	2.54	0.42
1:G:159:ILE:O	1:G:160:VAL:C	2.62	0.42
1:G:213:GLY:O	1:G:216:ILE:HG22	2.19	0.42
1:I:111:SER:N	1:I:142:ARG:HH22	2.18	0.42
1:I:224:GLY:HA2	1:I:419:PHE:CD2	2.54	0.42
1:I:263:LEU:O	1:I:263:LEU:HG	2.11	0.42
1:K:219:LEU:O	1:K:223:THR:OG1	2.34	0.42
1:M:138:ILE:HG21	1:M:138:ILE:HD13	1.52	0.42
1:M:325:ILE:HD11	1:M:328:GLY:HA2	2.02	0.42
1:M:425:PRO:HA	1:M:429:ASP:OD2	2.20	0.42
1:O:381:ILE:CG2	1:O:385:TYR:CE1	3.03	0.42
1:A:218:VAL:HA	1:A:221:TYR:HB3	2.01	0.41
1:A:320:LEU:HB3	1:A:369:PHE:HB3	2.02	0.41
1:C:171:ILE:HG22	1:C:302:GLY:CA	2.50	0.41
1:E:384:ILE:O	1:E:384:ILE:HG23	2.15	0.41
1:G:151:LEU:O	1:G:154:ARG:HG3	2.20	0.41
1:I:132:ALA:O	1:I:133:GLU:C	2.63	0.41
1:I:162:ALA:O	1:I:163:LYS:C	2.62	0.41
1:I:426:THR:O	1:I:429:ASP:N	2.53	0.41
1:K:56:THR:HG21	1:O:196:GLU:HG2	2.02	0.41
1:K:96:VAL:N	1:K:97:PRO:CD	2.83	0.41
1:K:146:GLN:OE1	1:K:424:PHE:HZ	2.03	0.41
1:K:152:GLN:HE21	1:K:152:GLN:N	2.17	0.41
1:K:176:SER:OG	1:K:177:ILE:N	2.52	0.41
1:M:18:ILE:HD12	1:M:47:PHE:CE2	2.55	0.41
1:M:120:TYR:HD2	1:M:121:VAL:N	2.17	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:266:GLN:HB2	1:O:264:LEU:HD22	2.02	0.41
1:O:54:ASN:HB3	1:O:55:PRO:HD2	2.02	0.41
1:O:219:LEU:O	1:O:223:THR:HG23	2.20	0.41
1:A:372:ARG:HH21	2:B:847:LEU:HB3	1.85	0.41
1:C:436:LEU:CD1	1:C:452:VAL:HG11	2.50	0.41
1:E:238:ILE:H	1:E:261:ASP:CG	2.27	0.41
1:E:245:ASP:O	1:E:246:GLU:C	2.63	0.41
1:G:34:LYS:HG3	1:G:34:LYS:H	1.60	0.41
1:G:216:ILE:O	1:G:219:LEU:N	2.51	0.41
1:I:147:THR:C	1:I:148:ILE:HG13	2.45	0.41
1:I:208:ILE:HB	1:I:209:SER:H	1.46	0.41
1:I:229:LYS:C	1:I:230:ILE:HG23	2.45	0.41
1:I:266:GLN:HB3	1:K:264:LEU:HD22	2.01	0.41
1:I:392:HIS:C	1:I:394:LEU:N	2.79	0.41
1:K:53:TYR:HB2	1:K:81:PHE:CD1	2.55	0.41
1:K:151:LEU:O	1:K:152:GLN:C	2.62	0.41
1:K:158:TYR:CG	1:K:318:LEU:HD12	2.54	0.41
1:M:314:GLU:HG3	1:M:314:GLU:H	1.28	0.41
1:C:136:TYR:C	1:C:138:ILE:N	2.78	0.41
1:C:149:ILE:HD12	1:C:149:ILE:HA	1.88	0.41
1:C:287:LYS:N	1:C:292:ASN:OD1	2.53	0.41
1:E:372:ARG:O	1:E:373:ASN:C	2.62	0.41
1:G:386:GLU:C	1:G:388:ILE:N	2.79	0.41
1:I:79:GLU:HB3	1:I:80:SER:H	1.65	0.41
1:I:165:LEU:HA	1:I:165:LEU:HD23	1.39	0.41
1:I:213:GLY:O	1:I:214:HIS:C	2.62	0.41
1:I:265:PHE:CD2	1:I:265:PHE:C	2.98	0.41
1:K:201:ILE:CG2	1:K:258:THR:HG21	2.50	0.41
1:K:268:ILE:HG23	1:K:273:LYS:O	2.20	0.41
1:K:310:ALA:C	1:K:312:PHE:H	2.29	0.41
1:K:424:PHE:CD1	1:K:424:PHE:C	2.98	0.41
1:O:136:TYR:HD1	1:O:139:SER:OG	2.03	0.41
1:A:198:LEU:HA	1:A:198:LEU:HD12	1.48	0.41
1:A:198:LEU:CB	1:A:199:TYR:CE1	3.03	0.41
1:A:322:PHE:CG	1:A:323:TYR:N	2.87	0.41
1:C:82:ALA:CB	1:C:109:HIS:HB2	2.50	0.41
1:C:265:PHE:CD2	1:C:265:PHE:C	2.98	0.41
1:E:176:SER:OG	1:E:177:ILE:N	2.53	0.41
1:G:135:LEU:H	1:G:135:LEU:HG	1.60	0.41
1:G:293:LEU:C	1:G:294:VAL:HG23	2.44	0.41
1:G:415:ASP:O	1:G:426:THR:OG1	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:437:ILE:O	1:G:440:VAL:HG23	2.20	0.41
1:I:189:GLU:HG3	1:I:284:THR:OG1	2.21	0.41
1:K:84:TYR:CZ	1:K:86:ASP:HB2	2.54	0.41
1:K:113:ASN:OD1	1:K:114:LEU:N	2.54	0.41
1:K:147:THR:HB	1:K:427:PHE:CE1	2.55	0.41
1:K:216:ILE:O	1:K:219:LEU:HB3	2.20	0.41
1:K:230:ILE:O	1:K:230:ILE:HG13	2.21	0.41
1:K:313:VAL:CG1	1:K:314:GLU:N	2.84	0.41
1:K:370:HIS:CD2	2:L:848:PHE:HD2	2.38	0.41
1:K:424:PHE:CD1	1:K:424:PHE:O	2.74	0.41
1:O:25:LEU:HD12	1:O:32:VAL:HG11	2.02	0.41
1:O:113:ASN:OD1	1:O:114:LEU:N	2.53	0.41
1:O:138:ILE:HD13	1:O:138:ILE:HG21	1.73	0.41
1:O:190:ARG:HG3	1:O:199:TYR:OH	2.20	0.41
1:O:197:TYR:CD1	1:O:197:TYR:C	2.99	0.41
1:C:100:TYR:O	1:C:104:LYS:HB2	2.20	0.41
1:C:259:CYS:HA	1:C:260:PRO:HD2	1.91	0.41
1:C:273:LYS:HA	1:C:273:LYS:HD2	1.78	0.41
1:E:42:GLN:O	1:E:43:LEU:HD23	2.20	0.41
1:E:208:ILE:CA	1:E:212:PHE:HB3	2.51	0.41
1:E:279:SER:HB2	1:G:277:SER:CB	2.50	0.41
1:E:318:LEU:H	1:E:318:LEU:HG	1.57	0.41
1:G:85:LYS:HE2	1:G:113:ASN:HA	2.02	0.41
1:G:133:GLU:O	1:G:136:TYR:HB3	2.21	0.41
1:G:136:TYR:C	1:G:136:TYR:CD1	2.96	0.41
1:G:422:GLU:N	1:G:422:GLU:CD	2.78	0.41
1:I:272:GLY:O	1:I:273:LYS:HB2	2.20	0.41
1:I:322:PHE:CD2	1:I:367:GLU:HB3	2.45	0.41
1:I:384:ILE:O	1:I:388:ILE:HG13	2.21	0.41
1:M:54:ASN:O	1:M:75:PHE:O	2.38	0.41
1:M:184:GLY:N	1:M:282:GLY:O	2.46	0.41
1:M:393:PHE:O	1:M:394:LEU:HD12	2.20	0.41
1:O:123:TRP:CE3	1:O:123:TRP:HA	2.54	0.41
1:O:315:ILE:CG2	1:O:377:VAL:HG22	2.51	0.41
1:A:147:THR:O	1:A:148:ILE:HG13	2.21	0.41
1:A:381:ILE:O	1:A:382:LEU:C	2.63	0.41
1:C:69:LEU:HB3	1:C:72:ALA:HB2	2.01	0.41
1:C:129:VAL:HA	1:C:434:HIS:HD2	1.85	0.41
1:C:301:LYS:N	1:C:301:LYS:HD2	2.36	0.41
1:C:429:ASP:O	1:C:430:ALA:C	2.63	0.41
1:E:319:VAL:HG13	1:E:370:HIS:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:79:GLU:O	1:G:83:GLN:HG3	2.20	0.41
1:G:129:VAL:HA	1:G:434:HIS:HD2	1.86	0.41
1:G:216:ILE:HA	1:G:216:ILE:HD12	1.86	0.41
1:G:432:ILE:HG22	1:G:455:ILE:HG13	2.02	0.41
1:I:54:ASN:HB3	1:I:55:PRO:HD2	2.01	0.41
1:K:136:TYR:C	1:K:136:TYR:CD1	2.97	0.41
1:K:169:GLY:O	1:K:328:GLY:HA3	2.20	0.41
1:K:291:LYS:HA	1:K:291:LYS:HD2	1.51	0.41
1:M:148:ILE:HD13	1:M:388:ILE:HD11	2.01	0.41
1:M:273:LYS:HA	1:M:273:LYS:HD2	1.84	0.41
1:O:18:ILE:HB	1:O:47:PHE:CD2	2.55	0.41
1:O:455:ILE:O	1:O:457:ILE:N	2.53	0.41
1:A:54:ASN:O	1:A:75:PHE:O	2.39	0.41
1:A:90:ILE:HD12	1:A:116:LEU:CD1	2.50	0.41
1:A:422:GLU:N	1:A:422:GLU:CD	2.79	0.41
1:C:161:ARG:O	1:C:161:ARG:HG3	2.19	0.41
1:C:252:LYS:H	1:C:252:LYS:HG3	1.41	0.41
1:C:427:PHE:HA	1:C:430:ALA:HB3	2.01	0.41
1:E:230:ILE:C	1:E:230:ILE:CD1	2.90	0.41
1:E:380:ASN:O	1:E:381:ILE:C	2.62	0.41
1:G:51:ALA:HB3	1:G:87:ILE:HD11	2.03	0.41
1:G:79:GLU:O	1:G:80:SER:C	2.64	0.41
1:G:138:ILE:C	1:G:140:GLN:N	2.78	0.41
1:G:274:VAL:HA	1:G:275:PRO:HD3	1.81	0.41
1:I:147:THR:HB	1:I:427:PHE:CG	2.51	0.41
1:I:153:GLY:O	1:I:154:ARG:C	2.63	0.41
1:K:105:ASN:N	1:K:105:ASN:ND2	2.65	0.41
1:K:177:ILE:HG21	1:K:219:LEU:HD11	2.03	0.41
1:M:194:SER:HA	1:M:195:PRO:HD3	1.93	0.41
1:M:279:SER:HB2	1:O:277:SER:CB	2.50	0.41
1:M:310:ALA:C	1:M:312:PHE:N	2.79	0.41
1:O:166:ILE:O	1:O:167:SER:C	2.64	0.41
1:O:375:ASN:OD1	1:O:377:VAL:HB	2.20	0.41
1:C:18:ILE:HD11	1:C:392:HIS:CD2	2.55	0.41
1:C:117:ARG:HB2	1:C:118:TYR:CE1	2.56	0.41
1:C:320:LEU:O	1:C:369:PHE:N	2.46	0.41
1:E:217:ASP:HB2	1:E:433:LEU:HD22	2.03	0.41
1:E:276:VAL:HG12	1:E:277:SER:N	2.36	0.41
1:E:427:PHE:O	1:E:431:ILE:HB	2.20	0.41
1:G:40:ILE:HG23	1:G:47:PHE:HB2	2.02	0.41
1:G:53:TYR:N	1:G:81:PHE:CE1	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:245:ASP:O	1:G:246:GLU:C	2.63	0.41
1:I:197:TYR:CD1	1:I:197:TYR:C	2.98	0.41
1:I:238:ILE:H	1:I:261:ASP:CG	2.29	0.41
1:K:162:ALA:O	1:K:166:ILE:HD12	2.21	0.41
1:K:208:ILE:HG13	1:K:263:LEU:HD22	2.03	0.41
1:K:371:LEU:O	1:K:372:ARG:C	2.64	0.41
1:M:166:ILE:O	1:M:169:GLY:N	2.54	0.41
1:M:208:ILE:HB	1:M:209:SER:H	1.62	0.41
1:M:268:ILE:CG2	1:M:273:LYS:O	2.68	0.41
1:M:322:PHE:CD2	1:M:367:GLU:HB3	2.49	0.41
2:P:857:TYR:HA	2:P:860:ILE:HG22	2.03	0.41
1:A:25:LEU:CB	1:A:52:LEU:HD11	2.51	0.41
1:A:32:VAL:H	1:A:32:VAL:HG23	1.48	0.41
1:A:64:ILE:HG22	1:A:65:GLU:N	2.36	0.41
1:A:103:VAL:O	1:A:106:ILE:HB	2.20	0.41
1:A:130:GLN:HA	1:A:133:GLU:CB	2.35	0.41
1:A:182:ASN:HD21	1:A:283:GLY:C	2.29	0.41
1:C:105:ASN:N	1:C:105:ASN:ND2	2.69	0.41
1:C:152:GLN:HE22	1:C:214:HIS:HE1	1.69	0.41
1:C:315:ILE:CG2	1:C:377:VAL:HG22	2.51	0.41
1:C:432:ILE:CG2	1:C:455:ILE:HG22	2.51	0.41
1:E:136:TYR:O	1:E:137:SER:C	2.63	0.41
1:E:216:ILE:HG23	1:E:217:ASP:N	2.35	0.41
1:E:263:LEU:HD11	1:E:265:PHE:HB2	2.03	0.41
1:E:381:ILE:O	1:E:382:LEU:C	2.64	0.41
1:E:450:LEU:HD23	1:E:450:LEU:N	2.36	0.41
1:G:25:LEU:HD12	1:G:25:LEU:HA	1.60	0.41
1:G:41:GLN:HE21	1:G:41:GLN:HB3	1.73	0.41
1:G:104:LYS:O	1:G:107:LEU:N	2.54	0.41
1:G:159:ILE:HD12	1:G:159:ILE:HG23	1.86	0.41
1:G:179:ILE:HB	1:G:278:CYS:HB2	2.03	0.41
1:G:217:ASP:O	1:G:218:VAL:C	2.64	0.41
1:G:230:ILE:O	1:G:230:ILE:HG13	2.20	0.41
1:G:322:PHE:CD2	1:G:322:PHE:C	2.94	0.41
1:G:389:ALA:O	1:G:392:HIS:N	2.54	0.41
1:I:88:ASP:HA	1:I:115:ASN:O	2.20	0.41
1:I:96:VAL:HB	1:I:97:PRO:CD	2.50	0.41
1:I:142:ARG:HB2	1:I:145:LEU:HB3	2.02	0.41
1:I:228:GLN:HB3	1:I:268:ILE:O	2.21	0.41
1:I:453:SER:C	1:I:456:MET:HE1	2.46	0.41
1:K:23:VAL:HG12	1:K:23:VAL:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:79:GLU:O	1:K:83:GLN:HG3	2.21	0.41
1:K:171:ILE:HD12	1:K:299:GLY:HA3	2.03	0.41
1:K:190:ARG:HG3	1:K:199:TYR:CE2	2.55	0.41
1:K:216:ILE:CG2	1:K:217:ASP:H	2.34	0.41
1:M:103:VAL:O	1:M:104:LYS:C	2.63	0.41
1:M:198:LEU:HD12	1:M:198:LEU:HA	1.67	0.41
1:M:248:GLY:O	1:M:249:LYS:C	2.60	0.41
1:M:456:MET:SD	1:M:456:MET:N	2.92	0.41
2:N:853:MET:O	2:N:856:VAL:N	2.54	0.41
1:O:53:TYR:CD2	1:O:53:TYR:C	2.99	0.41
1:O:195:PRO:O	1:O:196:GLU:C	2.63	0.41
1:O:195:PRO:HB3	1:O:197:TYR:CD2	2.56	0.41
1:O:216:ILE:O	1:O:219:LEU:N	2.50	0.41
1:O:234:ILE:HG12	1:O:263:LEU:HB2	2.03	0.41
1:O:314:GLU:HG3	1:O:314:GLU:H	1.21	0.41
1:O:319:VAL:HG22	1:O:370:HIS:CB	2.50	0.41
1:A:90:ILE:HD12	1:A:116:LEU:HD11	2.03	0.41
1:A:134:GLU:O	1:A:135:LEU:C	2.64	0.41
1:C:16:ARG:CB	1:C:17:PRO:CD	2.98	0.41
1:C:85:LYS:HA	1:C:113:ASN:CG	2.46	0.41
1:C:124:ALA:HB1	1:C:434:HIS:CE1	2.53	0.41
1:E:88:ASP:OD1	1:E:115:ASN:HB3	2.21	0.41
1:E:105:ASN:N	1:E:105:ASN:ND2	2.69	0.41
1:E:197:TYR:C	1:E:199:TYR:H	2.29	0.41
1:G:63:THR:O	1:G:64:ILE:C	2.63	0.41
1:G:102:VAL:O	1:G:106:ILE:HD12	2.21	0.41
1:G:245:ASP:C	1:G:245:ASP:OD1	2.63	0.41
1:G:245:ASP:N	1:G:249:LYS:O	2.54	0.41
1:I:230:ILE:HG22	1:I:267:GLY:HA3	2.02	0.41
1:I:320:LEU:N	1:I:369:PHE:O	2.29	0.41
1:M:69:LEU:HB3	1:M:72:ALA:HB2	2.03	0.41
1:M:245:ASP:N	1:M:249:LYS:O	2.53	0.41
2:N:848:PHE:CD1	2:N:848:PHE:N	2.89	0.41
1:O:84:TYR:CZ	1:O:86:ASP:HB2	2.54	0.41
1:A:392:HIS:C	1:A:394:LEU:N	2.77	0.40
1:C:182:ASN:ND2	1:C:283:GLY:CA	2.79	0.40
1:C:208:ILE:H	1:C:208:ILE:CD1	2.32	0.40
1:C:309:ASP:OD2	2:D:850:THR:OG1	2.32	0.40
1:E:111:SER:CA	1:E:142:ARG:NH2	2.85	0.40
1:E:208:ILE:C	1:E:212:PHE:HB3	2.45	0.40
1:G:436:LEU:O	1:G:440:VAL:HG23	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:149:ILE:HB	1:I:430:ALA:HB2	2.03	0.40
2:J:855:ASP:O	2:J:856:VAL:C	2.62	0.40
1:K:237:ASN:H	1:K:261:ASP:CG	2.28	0.40
1:K:315:ILE:O	1:K:376:SER:OG	2.25	0.40
1:O:187:GLY:O	1:O:238:ILE:HG21	2.22	0.40
1:A:85:LYS:HD2	1:A:112:GLN:HE22	1.85	0.40
1:A:120:TYR:C	1:A:121:VAL:CG2	2.93	0.40
1:A:151:LEU:C	1:A:153:GLY:N	2.79	0.40
1:A:291:LYS:HD2	1:A:291:LYS:HA	1.75	0.40
1:C:32:VAL:O	1:C:33:ALA:C	2.64	0.40
1:C:38:LEU:HA	1:C:38:LEU:HD23	1.11	0.40
1:C:53:TYR:CD2	1:C:54:ASN:N	2.90	0.40
1:C:57:LEU:HD22	1:C:61:LEU:CD1	2.51	0.40
1:C:113:ASN:O	1:C:114:LEU:HG	2.21	0.40
1:C:136:TYR:O	1:C:139:SER:N	2.54	0.40
1:C:159:ILE:O	1:C:161:ARG:N	2.55	0.40
1:C:238:ILE:HD12	1:C:261:ASP:HB3	1.97	0.40
1:E:61:LEU:HD21	1:K:242:PHE:CZ	2.56	0.40
1:E:435:ARG:NH1	1:E:455:ILE:O	2.54	0.40
1:G:38:LEU:HA	1:G:38:LEU:HD23	1.07	0.40
1:I:96:VAL:N	1:I:97:PRO:CD	2.75	0.40
1:I:216:ILE:HD11	1:I:227:PHE:CE1	2.54	0.40
1:I:274:VAL:HA	1:I:275:PRO:HD3	1.77	0.40
1:I:385:TYR:O	1:I:386:GLU:C	2.62	0.40
1:K:90:ILE:HD13	1:K:90:ILE:HG21	1.91	0.40
1:K:245:ASP:N	1:K:249:LYS:O	2.46	0.40
1:K:433:LEU:O	1:K:436:LEU:N	2.54	0.40
1:M:183:GLY:O	1:M:312:PHE:HZ	2.04	0.40
1:M:389:ALA:HA	1:M:392:HIS:HB3	2.02	0.40
1:O:201:ILE:CG2	1:O:258:THR:HG21	2.51	0.40
1:O:290:THR:HG22	1:O:291:LYS:O	2.21	0.40
1:O:385:TYR:O	1:O:388:ILE:HB	2.20	0.40
1:A:215:THR:O	1:A:216:ILE:C	2.63	0.40
1:A:263:LEU:HD12	1:A:264:LEU:CA	2.51	0.40
1:E:149:ILE:HD13	1:E:430:ALA:HB2	2.02	0.40
1:E:162:ALA:HB1	1:E:304:LEU:HD11	2.03	0.40
1:E:442:ARG:O	1:E:443:SER:C	2.64	0.40
1:G:78:LEU:O	1:G:79:GLU:C	2.64	0.40
1:G:195:PRO:HB3	1:G:197:TYR:CE2	2.57	0.40
1:I:123:TRP:CE3	1:I:123:TRP:HA	2.57	0.40
1:K:113:ASN:O	1:K:114:LEU:HG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:31:TRP:CH2	1:M:35:THR:HG21	2.57	0.40
1:M:117:ARG:O	1:M:145:LEU:HD12	2.21	0.40
1:M:426:THR:N	1:M:429:ASP:OD2	2.47	0.40
1:O:23:VAL:HG12	1:O:94:VAL:HG13	2.02	0.40
1:O:147:THR:HB	1:O:427:PHE:CE1	2.56	0.40
1:A:195:PRO:CB	1:A:197:TYR:CE2	3.04	0.40
1:A:262:HIS:CE1	1:C:176:SER:CB	3.04	0.40
1:A:372:ARG:HH22	2:B:847:LEU:HD23	1.80	0.40
1:C:244:LEU:HD12	1:C:244:LEU:HA	1.82	0.40
1:C:269:LEU:HD23	1:C:269:LEU:HA	1.94	0.40
1:C:392:HIS:O	1:C:394:LEU:N	2.52	0.40
1:G:162:ALA:O	1:G:166:ILE:HD12	2.22	0.40
1:G:166:ILE:O	1:G:169:GLY:N	2.54	0.40
1:G:426:THR:O	1:G:429:ASP:N	2.54	0.40
1:G:454:LYS:O	1:G:455:ILE:C	2.64	0.40
1:I:433:LEU:HB3	1:I:434:HIS:H	1.78	0.40
1:K:78:LEU:O	1:K:81:PHE:CB	2.67	0.40
1:K:177:ILE:HA	1:K:296:ASP:O	2.21	0.40
1:K:186:TYR:OH	1:K:206:ASN:HA	2.22	0.40
1:K:454:LYS:O	1:K:457:ILE:HB	2.22	0.40
1:O:74:GLY:C	1:O:75:PHE:CD1	3.00	0.40
1:O:103:VAL:O	1:O:104:LYS:C	2.65	0.40
1:C:62:GLN:C	1:C:64:ILE:N	2.77	0.40
1:C:77:SER:O	1:C:80:SER:HB2	2.21	0.40
1:C:87:ILE:HG21	1:C:90:ILE:HG13	2.03	0.40
1:C:320:LEU:HB3	1:C:369:PHE:HB3	2.03	0.40
1:C:365:THR:CG2	1:C:366:MET:N	2.80	0.40
1:I:121:VAL:CG2	1:I:427:PHE:HZ	2.34	0.40
1:K:56:THR:CG2	1:O:196:GLU:HG2	2.52	0.40
1:K:201:ILE:HB	1:K:258:THR:CG2	2.51	0.40
1:K:304:LEU:CD2	1:K:320:LEU:HD21	2.52	0.40
1:M:134:GLU:O	1:M:136:TYR:N	2.55	0.40
1:M:165:LEU:HA	1:M:165:LEU:HD23	1.17	0.40
2:N:852:THR:HG22	2:N:853:MET:N	2.36	0.40
1:O:68:GLN:O	1:O:70:LYS:N	2.55	0.40
1:O:190:ARG:HA	1:O:191:PRO:HD3	1.59	0.40
1:O:454:LYS:O	1:O:457:ILE:HB	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	389/465 (84%)	301 (77%)	73 (19%)	15 (4%)	2	14
1	C	387/465 (83%)	299 (77%)	71 (18%)	17 (4%)	2	12
1	E	387/465 (83%)	300 (78%)	67 (17%)	20 (5%)	1	9
1	G	387/465 (83%)	301 (78%)	75 (19%)	11 (3%)	4	21
1	I	387/465 (83%)	303 (78%)	70 (18%)	14 (4%)	2	16
1	K	387/465 (83%)	305 (79%)	66 (17%)	16 (4%)	2	13
1	M	387/465 (83%)	308 (80%)	68 (18%)	11 (3%)	4	21
1	O	387/465 (83%)	309 (80%)	67 (17%)	11 (3%)	4	21
2	B	12/22 (54%)	9 (75%)	2 (17%)	1 (8%)	0	3
2	D	12/22 (54%)	10 (83%)	1 (8%)	1 (8%)	0	3
2	F	12/22 (54%)	10 (83%)	2 (17%)	0	100	100
2	H	12/22 (54%)	10 (83%)	1 (8%)	1 (8%)	0	3
2	J	12/22 (54%)	11 (92%)	1 (8%)	0	100	100
2	L	12/22 (54%)	10 (83%)	1 (8%)	1 (8%)	0	3
2	N	12/22 (54%)	11 (92%)	1 (8%)	0	100	100
2	P	12/22 (54%)	9 (75%)	2 (17%)	1 (8%)	0	3
All	All	3194/3896 (82%)	2506 (78%)	568 (18%)	120 (4%)	2	15

All (120) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	PRO
1	A	37	PHE
1	A	42	GLN
1	A	82	ALA
1	A	201	ILE
1	A	246	GLU

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Mol	Chain	Res	Type
1	A	252	LYS
1	A	390	ASP
1	C	15	SER
1	C	17	PRO
1	C	82	ALA
1	C	246	GLU
1	C	252	LYS
1	C	390	ASP
1	E	246	GLU
1	E	252	LYS
1	E	326	LYS
1	G	17	PRO
1	G	82	ALA
1	G	102	VAL
1	G	246	GLU
1	G	252	LYS
1	I	17	PRO
1	I	102	VAL
1	I	208	ILE
1	I	246	GLU
1	K	82	ALA
1	K	152	GLN
1	K	208	ILE
1	K	246	GLU
1	K	252	LYS
1	M	17	PRO
1	M	82	ALA
1	M	208	ILE
1	M	246	GLU
1	M	252	LYS
1	O	82	ALA
1	O	246	GLU
1	O	252	LYS
1	A	102	VAL
1	C	102	VAL
1	C	201	ILE
2	D	856	VAL
1	E	17	PRO
1	E	37	PHE
1	E	82	ALA
1	E	84	TYR
1	E	169	GLY

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Mol	Chain	Res	Type
1	E	201	ILE
1	G	154	ARG
1	G	169	GLY
2	H	856	VAL
1	I	82	ALA
1	I	154	ARG
1	I	169	GLY
1	I	209	SER
1	K	102	VAL
1	K	169	GLY
1	K	191	PRO
1	K	455	ILE
1	M	167	SER
1	O	17	PRO
1	O	143	ALA
1	O	169	GLY
1	O	456	MET
1	C	84	TYR
1	C	101	GLU
1	C	387	SER
1	E	207	LEU
1	E	256	SER
1	E	392	HIS
1	E	456	MET
1	G	387	SER
1	I	55	PRO
1	I	252	LYS
2	L	856	VAL
1	O	58	LYS
1	O	208	ILE
1	O	392	HIS
1	A	81	PHE
1	A	326	LYS
1	C	81	PHE
1	C	95	LYS
1	C	391	TYR
1	K	17	PRO
1	K	81	PHE
1	K	209	SER
1	K	433	LEU
2	P	856	VAL
1	A	207	LEU

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Mol	Chain	Res	Type
1	C	215	THR
1	C	393	PHE
1	E	101	GLU
1	E	116	LEU
1	E	160	VAL
1	E	311	GLY
1	E	387	SER
1	G	95	LYS
1	K	84	TYR
1	K	160	VAL
1	M	271	ASN
1	O	271	ASN
1	A	103	VAL
1	A	311	GLY
1	A	372	ARG
1	E	139	SER
1	G	101	GLU
1	I	84	TYR
1	K	393	PHE
1	M	390	ASP
2	B	856	VAL
1	I	160	VAL
1	M	129	VAL
1	M	455	ILE
1	G	201	ILE
1	I	275	PRO
1	I	455	ILE
1	C	208	ILE
1	E	96	VAL
1	M	160	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	350/411 (85%)	240 (69%)	110 (31%)	0 1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	348/411 (85%)	248 (71%)	100 (29%)	0	2
1	E	348/411 (85%)	243 (70%)	105 (30%)	0	1
1	G	348/411 (85%)	238 (68%)	110 (32%)	0	1
1	I	348/411 (85%)	243 (70%)	105 (30%)	0	1
1	K	348/411 (85%)	248 (71%)	100 (29%)	0	2
1	M	348/411 (85%)	248 (71%)	100 (29%)	0	2
1	O	348/411 (85%)	244 (70%)	104 (30%)	0	2
2	B	14/22 (64%)	11 (79%)	3 (21%)	1	6
2	D	14/22 (64%)	12 (86%)	2 (14%)	3	16
2	F	14/22 (64%)	12 (86%)	2 (14%)	3	16
2	H	14/22 (64%)	11 (79%)	3 (21%)	1	6
2	J	14/22 (64%)	8 (57%)	6 (43%)	0	0
2	L	14/22 (64%)	12 (86%)	2 (14%)	3	16
2	N	14/22 (64%)	11 (79%)	3 (21%)	1	6
2	P	14/22 (64%)	11 (79%)	3 (21%)	1	6
All	All	2898/3464 (84%)	2040 (70%)	858 (30%)	0	2

All (858) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	SER
1	A	16	ARG
1	A	18	ILE
1	A	19	ARG
1	A	20	VAL
1	A	23	VAL
1	A	45	SER
1	A	46	GLN
1	A	48	GLN
1	A	50	VAL
1	A	58	LYS
1	A	59	SER
1	A	60	SER
1	A	62	GLN
1	A	64	ILE
1	A	65	GLU
1	A	66	GLN

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Mol	Chain	Res	Type
1	A	70	LYS
1	A	79	GLU
1	A	85	LYS
1	A	89	MET
1	A	94	VAL
1	A	98	GLU
1	A	99	HIS
1	A	105	ASN
1	A	108	GLU
1	A	111	SER
1	A	114	LEU
1	A	115	ASN
1	A	117	ARG
1	A	130	GLN
1	A	137	SER
1	A	141	GLN
1	A	142	ARG
1	A	145	LEU
1	A	146	GLN
1	A	147	THR
1	A	151	LEU
1	A	152	GLN
1	A	156	SER
1	A	174	ILE
1	A	180	SER
1	A	182	ASN
1	A	185	TRP
1	A	193	ARG
1	A	196	GLU
1	A	198	LEU
1	A	199	TYR
1	A	201	ILE
1	A	211	SER
1	A	218	VAL
1	A	219	LEU
1	A	225	SER
1	A	235	SER
1	A	236	ASN
1	A	240	THR
1	A	241	GLN
1	A	243	LEU
1	A	244	LEU

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Mol	Chain	Res	Type
1	A	250	ARG
1	A	253	GLU
1	A	256	SER
1	A	257	LYS
1	A	258	THR
1	A	261	ASP
1	A	263	LEU
1	A	276	VAL
1	A	277	SER
1	A	278	CYS
1	A	279	SER
1	A	280	PHE
1	A	281	LYS
1	A	286	VAL
1	A	287	LYS
1	A	288	LYS
1	A	292	ASN
1	A	303	ASP
1	A	304	LEU
1	A	305	LYS
1	A	314	GLU
1	A	318	LEU
1	A	322	PHE
1	A	364	GLN
1	A	365	THR
1	A	366	MET
1	A	367	GLU
1	A	373	ASN
1	A	382	LEU
1	A	383	ARG
1	A	384	ILE
1	A	387	SER
1	A	394	LEU
1	A	413	LYS
1	A	414	PHE
1	A	416	LYS
1	A	422	GLU
1	A	428	LYS
1	A	431	ILE
1	A	432	ILE
1	A	434	HIS
1	A	435	ARG

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Mol	Chain	Res	Type
1	A	436	LEU
1	A	442	ARG
1	A	444	ASP
1	A	447	GLU
1	A	448	LYS
1	A	449	THR
1	A	452	VAL
1	A	454	LYS
1	A	455	ILE
2	B	855	ASP
2	B	857	TYR
2	B	860	ILE
1	C	14	SER
1	C	16	ARG
1	C	18	ILE
1	C	20	VAL
1	C	42	GLN
1	C	45	SER
1	C	46	GLN
1	C	50	VAL
1	C	52	LEU
1	C	58	LYS
1	C	59	SER
1	C	61	LEU
1	C	64	ILE
1	C	65	GLU
1	C	70	LYS
1	C	76	ASP
1	C	89	MET
1	C	99	HIS
1	C	108	GLU
1	C	111	SER
1	C	114	LEU
1	C	115	ASN
1	C	116	LEU
1	C	118	TYR
1	C	128	SER
1	C	130	GLN
1	C	131	GLN
1	C	133	GLU
1	C	137	SER
1	C	140	GLN

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Mol	Chain	Res	Type
1	C	141	GLN
1	C	151	LEU
1	C	152	GLN
1	C	166	ILE
1	C	168	GLU
1	C	174	ILE
1	C	177	ILE
1	C	180	SER
1	C	182	ASN
1	C	185	TRP
1	C	193	ARG
1	C	196	GLU
1	C	198	LEU
1	C	199	TYR
1	C	200	ASP
1	C	201	ILE
1	C	202	GLU
1	C	207	LEU
1	C	218	VAL
1	C	219	LEU
1	C	222	ILE
1	C	230	ILE
1	C	240	THR
1	C	241	GLN
1	C	243	LEU
1	C	244	LEU
1	C	249	LYS
1	C	250	ARG
1	C	253	GLU
1	C	257	LYS
1	C	258	THR
1	C	263	LEU
1	C	277	SER
1	C	278	CYS
1	C	280	PHE
1	C	281	LYS
1	C	287	LYS
1	C	288	LYS
1	C	292	ASN
1	C	303	ASP
1	C	304	LEU
1	C	305	LYS

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Mol	Chain	Res	Type
1	C	306	ILE
1	C	314	GLU
1	C	318	LEU
1	C	320	LEU
1	C	322	PHE
1	C	364	GLN
1	C	366	MET
1	C	367	GLU
1	C	373	ASN
1	C	381	ILE
1	C	382	LEU
1	C	383	ARG
1	C	387	SER
1	C	394	LEU
1	C	413	LYS
1	C	414	PHE
1	C	416	LYS
1	C	428	LYS
1	C	431	ILE
1	C	434	HIS
1	C	435	ARG
1	C	442	ARG
1	C	444	ASP
1	C	447	GLU
1	C	448	LYS
1	C	449	THR
1	C	450	LEU
1	C	456	MET
2	D	847	LEU
2	D	849	ASN
1	E	15	SER
1	E	18	ILE
1	E	19	ARG
1	E	20	VAL
1	E	25	LEU
1	E	29	LYS
1	E	32	VAL
1	E	41	GLN
1	E	45	SER
1	E	46	GLN
1	E	50	VAL
1	E	52	LEU

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Mol	Chain	Res	Type
1	E	57	LEU
1	E	58	LYS
1	E	59	SER
1	E	62	GLN
1	E	64	ILE
1	E	65	GLU
1	E	66	GLN
1	E	70	LYS
1	E	75	PHE
1	E	76	ASP
1	E	77	SER
1	E	78	LEU
1	E	80	SER
1	E	85	LYS
1	E	89	MET
1	E	98	GLU
1	E	99	HIS
1	E	108	GLU
1	E	111	SER
1	E	116	LEU
1	E	130	GLN
1	E	131	GLN
1	E	147	THR
1	E	152	GLN
1	E	161	ARG
1	E	166	ILE
1	E	168	GLU
1	E	174	ILE
1	E	177	ILE
1	E	180	SER
1	E	182	ASN
1	E	185	TRP
1	E	193	ARG
1	E	195	PRO
1	E	196	GLU
1	E	198	LEU
1	E	199	TYR
1	E	200	ASP
1	E	202	GLU
1	E	207	LEU
1	E	210	ASN
1	E	211	SER

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Mol	Chain	Res	Type
1	E	214	HIS
1	E	218	VAL
1	E	222	ILE
1	E	225	SER
1	E	229	LYS
1	E	235	SER
1	E	236	ASN
1	E	240	THR
1	E	241	GLN
1	E	243	LEU
1	E	244	LEU
1	E	245	ASP
1	E	253	GLU
1	E	257	LYS
1	E	258	THR
1	E	261	ASP
1	E	263	LEU
1	E	273	LYS
1	E	276	VAL
1	E	277	SER
1	E	280	PHE
1	E	281	LYS
1	E	288	LYS
1	E	291	LYS
1	E	303	ASP
1	E	304	LEU
1	E	314	GLU
1	E	318	LEU
1	E	322	PHE
1	E	366	MET
1	E	367	GLU
1	E	373	ASN
1	E	381	ILE
1	E	382	LEU
1	E	384	ILE
1	E	387	SER
1	E	394	LEU
1	E	414	PHE
1	E	422	GLU
1	E	428	LYS
1	E	431	ILE
1	E	434	HIS

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Mol	Chain	Res	Type
1	E	436	LEU
1	E	437	ILE
1	E	442	ARG
1	E	447	GLU
1	E	449	THR
1	E	450	LEU
1	E	454	LYS
1	E	455	ILE
1	E	456	MET
2	F	847	LEU
2	F	860	ILE
1	G	16	ARG
1	G	18	ILE
1	G	19	ARG
1	G	20	VAL
1	G	40	ILE
1	G	41	GLN
1	G	45	SER
1	G	46	GLN
1	G	52	LEU
1	G	57	LEU
1	G	58	LYS
1	G	59	SER
1	G	61	LEU
1	G	64	ILE
1	G	65	GLU
1	G	70	LYS
1	G	75	PHE
1	G	76	ASP
1	G	77	SER
1	G	86	ASP
1	G	87	ILE
1	G	89	MET
1	G	98	GLU
1	G	99	HIS
1	G	108	GLU
1	G	111	SER
1	G	116	LEU
1	G	118	TYR
1	G	119	LEU
1	G	128	SER
1	G	130	GLN

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Mol	Chain	Res	Type
1	G	131	GLN
1	G	138	ILE
1	G	140	GLN
1	G	146	GLN
1	G	147	THR
1	G	151	LEU
1	G	152	GLN
1	G	154	ARG
1	G	163	LYS
1	G	166	ILE
1	G	168	GLU
1	G	178	GLU
1	G	179	ILE
1	G	180	SER
1	G	182	ASN
1	G	185	TRP
1	G	193	ARG
1	G	196	GLU
1	G	198	LEU
1	G	200	ASP
1	G	201	ILE
1	G	202	GLU
1	G	207	LEU
1	G	211	SER
1	G	214	HIS
1	G	218	VAL
1	G	219	LEU
1	G	222	ILE
1	G	228	GLN
1	G	230	ILE
1	G	235	SER
1	G	236	ASN
1	G	240	THR
1	G	241	GLN
1	G	250	ARG
1	G	253	GLU
1	G	257	LYS
1	G	258	THR
1	G	263	LEU
1	G	268	ILE
1	G	276	VAL
1	G	277	SER

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Mol	Chain	Res	Type
1	G	278	CYS
1	G	281	LYS
1	G	286	VAL
1	G	287	LYS
1	G	288	LYS
1	G	291	LYS
1	G	303	ASP
1	G	304	LEU
1	G	305	LYS
1	G	314	GLU
1	G	318	LEU
1	G	322	PHE
1	G	364	GLN
1	G	366	MET
1	G	367	GLU
1	G	372	ARG
1	G	373	ASN
1	G	381	ILE
1	G	382	LEU
1	G	383	ARG
1	G	387	SER
1	G	394	LEU
1	G	416	LYS
1	G	422	GLU
1	G	428	LYS
1	G	431	ILE
1	G	432	ILE
1	G	434	HIS
1	G	435	ARG
1	G	442	ARG
1	G	447	GLU
1	G	448	LYS
1	G	449	THR
1	G	450	LEU
1	G	454	LYS
1	G	455	ILE
1	G	456	MET
2	H	847	LEU
2	H	855	ASP
2	H	859	TYR
1	I	15	SER
1	I	18	ILE

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Mol	Chain	Res	Type
1	I	19	ARG
1	I	20	VAL
1	I	22	PHE
1	I	25	LEU
1	I	34	LYS
1	I	40	ILE
1	I	41	GLN
1	I	45	SER
1	I	46	GLN
1	I	48	GLN
1	I	50	VAL
1	I	52	LEU
1	I	53	TYR
1	I	58	LYS
1	I	59	SER
1	I	61	LEU
1	I	64	ILE
1	I	65	GLU
1	I	70	LYS
1	I	75	PHE
1	I	79	GLU
1	I	89	MET
1	I	93	SER
1	I	98	GLU
1	I	99	HIS
1	I	108	GLU
1	I	111	SER
1	I	115	ASN
1	I	116	LEU
1	I	117	ARG
1	I	118	TYR
1	I	119	LEU
1	I	131	GLN
1	I	137	SER
1	I	138	ILE
1	I	141	GLN
1	I	151	LEU
1	I	152	GLN
1	I	166	ILE
1	I	174	ILE
1	I	180	SER
1	I	182	ASN

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Mol	Chain	Res	Type
1	I	185	TRP
1	I	193	ARG
1	I	196	GLU
1	I	200	ASP
1	I	202	GLU
1	I	209	SER
1	I	214	HIS
1	I	218	VAL
1	I	219	LEU
1	I	231	ASN
1	I	235	SER
1	I	240	THR
1	I	241	GLN
1	I	243	LEU
1	I	244	LEU
1	I	249	LYS
1	I	250	ARG
1	I	252	LYS
1	I	253	GLU
1	I	254	THR
1	I	255	ILE
1	I	258	THR
1	I	261	ASP
1	I	263	LEU
1	I	268	ILE
1	I	277	SER
1	I	280	PHE
1	I	281	LYS
1	I	287	LYS
1	I	292	ASN
1	I	303	ASP
1	I	304	LEU
1	I	309	ASP
1	I	314	GLU
1	I	316	SER
1	I	318	LEU
1	I	320	LEU
1	I	322	PHE
1	I	363	GLU
1	I	364	GLN
1	I	365	THR
1	I	366	MET

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Mol	Chain	Res	Type
1	I	367	GLU
1	I	373	ASN
1	I	382	LEU
1	I	383	ARG
1	I	387	SER
1	I	413	LYS
1	I	422	GLU
1	I	428	LYS
1	I	431	ILE
1	I	432	ILE
1	I	433	LEU
1	I	434	HIS
1	I	435	ARG
1	I	442	ARG
1	I	444	ASP
1	I	447	GLU
1	I	449	THR
1	I	450	LEU
1	I	456	MET
2	J	847	LEU
2	J	855	ASP
2	J	856	VAL
2	J	857	TYR
2	J	859	TYR
2	J	860	ILE
1	K	18	ILE
1	K	19	ARG
1	K	20	VAL
1	K	34	LYS
1	K	38	LEU
1	K	40	ILE
1	K	44	SER
1	K	45	SER
1	K	46	GLN
1	K	50	VAL
1	K	57	LEU
1	K	58	LYS
1	K	59	SER
1	K	61	LEU
1	K	64	ILE
1	K	65	GLU
1	K	67	LEU

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Mol	Chain	Res	Type
1	K	70	LYS
1	K	73	THR
1	K	76	ASP
1	K	80	SER
1	K	89	MET
1	K	98	GLU
1	K	99	HIS
1	K	107	LEU
1	K	108	GLU
1	K	111	SER
1	K	114	LEU
1	K	115	ASN
1	K	116	LEU
1	K	130	GLN
1	K	141	GLN
1	K	142	ARG
1	K	147	THR
1	K	152	GLN
1	K	166	ILE
1	K	168	GLU
1	K	174	ILE
1	K	178	GLU
1	K	180	SER
1	K	182	ASN
1	K	185	TRP
1	K	193	ARG
1	K	196	GLU
1	K	198	LEU
1	K	199	TYR
1	K	200	ASP
1	K	207	LEU
1	K	211	SER
1	K	216	ILE
1	K	218	VAL
1	K	219	LEU
1	K	235	SER
1	K	236	ASN
1	K	240	THR
1	K	241	GLN
1	K	244	LEU
1	K	253	GLU
1	K	258	THR

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Mol	Chain	Res	Type
1	K	263	LEU
1	K	264	LEU
1	K	273	LYS
1	K	281	LYS
1	K	287	LYS
1	K	291	LYS
1	K	292	ASN
1	K	303	ASP
1	K	305	LYS
1	K	309	ASP
1	K	314	GLU
1	K	318	LEU
1	K	320	LEU
1	K	322	PHE
1	K	364	GLN
1	K	366	MET
1	K	367	GLU
1	K	373	ASN
1	K	381	ILE
1	K	382	LEU
1	K	383	ARG
1	K	384	ILE
1	K	386	GLU
1	K	387	SER
1	K	394	LEU
1	K	413	LYS
1	K	414	PHE
1	K	416	LYS
1	K	422	GLU
1	K	428	LYS
1	K	431	ILE
1	K	432	ILE
1	K	434	HIS
1	K	435	ARG
1	K	442	ARG
1	K	444	ASP
1	K	447	GLU
1	K	448	LYS
1	K	449	THR
1	K	450	LEU
1	K	456	MET
2	L	847	LEU

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Mol	Chain	Res	Type
2	L	859	TYR
1	M	14	SER
1	M	18	ILE
1	M	19	ARG
1	M	20	VAL
1	M	34	LYS
1	M	40	ILE
1	M	45	SER
1	M	46	GLN
1	M	50	VAL
1	M	52	LEU
1	M	58	LYS
1	M	59	SER
1	M	64	ILE
1	M	65	GLU
1	M	70	LYS
1	M	89	MET
1	M	93	SER
1	M	98	GLU
1	M	105	ASN
1	M	106	ILE
1	M	108	GLU
1	M	111	SER
1	M	114	LEU
1	M	115	ASN
1	M	116	LEU
1	M	118	TYR
1	M	128	SER
1	M	137	SER
1	M	141	GLN
1	M	152	GLN
1	M	154	ARG
1	M	157	PRO
1	M	174	ILE
1	M	178	GLU
1	M	180	SER
1	M	182	ASN
1	M	185	TRP
1	M	193	ARG
1	M	195	PRO
1	M	196	GLU
1	M	198	LEU

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Mol	Chain	Res	Type
1	M	199	TYR
1	M	200	ASP
1	M	202	GLU
1	M	207	LEU
1	M	209	SER
1	M	225	SER
1	M	231	ASN
1	M	234	ILE
1	M	235	SER
1	M	236	ASN
1	M	240	THR
1	M	241	GLN
1	M	243	LEU
1	M	244	LEU
1	M	245	ASP
1	M	250	ARG
1	M	252	LYS
1	M	253	GLU
1	M	255	ILE
1	M	258	THR
1	M	261	ASP
1	M	263	LEU
1	M	265	PHE
1	M	268	ILE
1	M	277	SER
1	M	281	LYS
1	M	287	LYS
1	M	288	LYS
1	M	291	LYS
1	M	292	ASN
1	M	303	ASP
1	M	304	LEU
1	M	305	LYS
1	M	306	ILE
1	M	314	GLU
1	M	318	LEU
1	M	322	PHE
1	M	364	GLN
1	M	366	MET
1	M	367	GLU
1	M	373	ASN
1	M	382	LEU

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Mol	Chain	Res	Type
1	M	383	ARG
1	M	384	ILE
1	M	387	SER
1	M	394	LEU
1	M	413	LYS
1	M	414	PHE
1	M	416	LYS
1	M	420	ARG
1	M	422	GLU
1	M	431	ILE
1	M	432	ILE
1	M	434	HIS
1	M	442	ARG
1	M	447	GLU
1	M	448	LYS
1	M	449	THR
1	M	450	LEU
2	N	847	LEU
2	N	856	VAL
2	N	860	ILE
1	O	14	SER
1	O	18	ILE
1	O	19	ARG
1	O	20	VAL
1	O	23	VAL
1	O	25	LEU
1	O	45	SER
1	O	46	GLN
1	O	50	VAL
1	O	57	LEU
1	O	58	LYS
1	O	59	SER
1	O	61	LEU
1	O	64	ILE
1	O	65	GLU
1	O	68	GLN
1	O	70	LYS
1	O	76	ASP
1	O	80	SER
1	O	89	MET
1	O	98	GLU
1	O	99	HIS

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Mol	Chain	Res	Type
1	O	101	GLU
1	O	108	GLU
1	O	111	SER
1	O	114	LEU
1	O	116	LEU
1	O	128	SER
1	O	130	GLN
1	O	131	GLN
1	O	140	GLN
1	O	141	GLN
1	O	142	ARG
1	O	147	THR
1	O	152	GLN
1	O	157	PRO
1	O	166	ILE
1	O	174	ILE
1	O	180	SER
1	O	182	ASN
1	O	185	TRP
1	O	193	ARG
1	O	194	SER
1	O	195	PRO
1	O	196	GLU
1	O	198	LEU
1	O	199	TYR
1	O	200	ASP
1	O	202	GLU
1	O	207	LEU
1	O	208	ILE
1	O	218	VAL
1	O	219	LEU
1	O	220	GLN
1	O	230	ILE
1	O	235	SER
1	O	240	THR
1	O	241	GLN
1	O	243	LEU
1	O	244	LEU
1	O	250	ARG
1	O	252	LYS
1	O	253	GLU
1	O	258	THR

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Mol	Chain	Res	Type
1	O	261	ASP
1	O	263	LEU
1	O	264	LEU
1	O	268	ILE
1	O	273	LYS
1	O	278	CYS
1	O	280	PHE
1	O	281	LYS
1	O	287	LYS
1	O	291	LYS
1	O	292	ASN
1	O	303	ASP
1	O	305	LYS
1	O	306	ILE
1	O	314	GLU
1	O	318	LEU
1	O	325	ILE
1	O	364	GLN
1	O	365	THR
1	O	366	MET
1	O	367	GLU
1	O	373	ASN
1	O	382	LEU
1	O	387	SER
1	O	394	LEU
1	O	413	LYS
1	O	420	ARG
1	O	422	GLU
1	O	428	LYS
1	O	431	ILE
1	O	432	ILE
1	O	434	HIS
1	O	435	ARG
1	O	442	ARG
1	O	444	ASP
1	O	447	GLU
1	O	448	LYS
1	O	449	THR
1	O	450	LEU
1	O	455	ILE
2	P	847	LEU
2	P	856	VAL

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Mol	Chain	Res	Type
2	P	860	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	A	62	GLN
1	A	66	GLN
1	A	68	GLN
1	A	71	HIS
1	A	105	ASN
1	A	152	GLN
1	A	182	ASN
1	A	214	HIS
1	A	220	GLN
1	A	228	GLN
1	A	231	ASN
1	A	236	ASN
1	A	262	HIS
1	A	370	HIS
1	C	42	GLN
1	C	62	GLN
1	C	66	GLN
1	C	105	ASN
1	C	130	GLN
1	C	152	GLN
1	C	182	ASN
1	C	214	HIS
1	C	220	GLN
1	C	231	ASN
1	C	262	HIS
1	C	266	GLN
1	C	370	HIS
1	E	41	GLN
1	E	62	GLN
1	E	66	GLN
1	E	105	ASN
1	E	152	GLN
1	E	175	ASN
1	E	214	HIS
1	E	220	GLN
1	E	228	GLN

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Mol	Chain	Res	Type
1	E	236	ASN
2	F	849	ASN
1	G	41	GLN
1	G	62	GLN
1	G	105	ASN
1	G	152	GLN
1	G	182	ASN
1	G	220	GLN
1	G	241	GLN
1	G	262	HIS
1	G	392	HIS
1	G	434	HIS
1	I	41	GLN
1	I	54	ASN
1	I	62	GLN
1	I	71	HIS
1	I	105	ASN
1	I	112	GLN
1	I	152	GLN
1	I	220	GLN
1	I	228	GLN
1	I	231	ASN
1	I	236	ASN
1	I	241	GLN
1	I	434	HIS
1	K	41	GLN
1	K	62	GLN
1	K	105	ASN
1	K	115	ASN
1	K	130	GLN
1	K	152	GLN
1	K	182	ASN
1	K	228	GLN
1	K	262	HIS
1	M	62	GLN
1	M	105	ASN
1	M	152	GLN
1	M	220	GLN
1	M	241	GLN
1	M	262	HIS
1	M	370	HIS
1	M	373	ASN

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Mol	Chain	Res	Type
2	N	858	ASN
1	O	62	GLN
1	O	68	GLN
1	O	105	ASN
1	O	130	GLN
1	O	152	GLN
1	O	182	ASN
1	O	220	GLN
1	O	228	GLN
1	O	241	GLN
1	O	262	HIS
1	O	370	HIS
1	O	434	HIS
2	P	849	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	395/465 (84%)	1.05	64 (16%) 4 3	5, 40, 76, 100	0
1	C	393/465 (84%)	0.78	31 (7%) 18 10	2, 34, 76, 100	0
1	E	393/465 (84%)	1.19	75 (19%) 3 2	2, 42, 78, 100	0
1	G	393/465 (84%)	0.58	23 (5%) 28 14	4, 35, 72, 100	0
1	I	393/465 (84%)	1.02	61 (15%) 5 3	4, 41, 76, 100	0
1	K	393/465 (84%)	0.82	38 (9%) 13 7	1, 39, 74, 100	0
1	M	393/465 (84%)	1.04	57 (14%) 6 3	5, 41, 76, 100	0
1	O	393/465 (84%)	0.75	30 (7%) 20 10	4, 39, 78, 93	0
2	B	14/22 (63%)	1.91	4 (28%) 1 1	42, 59, 84, 85	0
2	D	14/22 (63%)	1.22	4 (28%) 1 1	21, 55, 77, 80	0
2	F	14/22 (63%)	2.03	7 (50%) 0 0	29, 59, 77, 91	0
2	H	14/22 (63%)	0.86	2 (14%) 6 3	25, 42, 75, 78	0
2	J	14/22 (63%)	1.90	5 (35%) 1 1	13, 54, 74, 90	0
2	L	14/22 (63%)	1.40	3 (21%) 2 1	23, 59, 88, 100	0
2	N	14/22 (63%)	1.82	6 (42%) 0 1	15, 53, 70, 81	0
2	P	14/22 (63%)	1.43	4 (28%) 1 1	19, 50, 86, 98	0
All	All	3258/3896 (83%)	0.93	414 (12%) 8 5	1, 39, 77, 100	0

All (414) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	328	GLY	7.5
1	K	328	GLY	6.9
1	M	251	THR	6.7
2	F	860	ILE	6.6
1	C	328	GLY	6.5

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Mol	Chain	Res	Type	RSRZ
1	E	194	SER	5.6
2	B	860	ILE	5.4
2	N	860	ILE	5.2
1	C	14	SER	5.2
1	E	413	LYS	5.0
2	J	860	ILE	5.0
1	E	251	THR	4.6
1	M	253	GLU	4.5
1	A	251	THR	4.5
1	E	144	ASN	4.5
1	I	61	LEU	4.5
1	G	181	GLY	4.4
1	I	251	THR	4.4
1	K	48	GLN	4.3
1	E	250	ARG	4.1
2	B	847	LEU	4.1
1	M	61	LEU	4.0
1	M	455	ILE	4.0
1	M	254	THR	4.0
1	E	61	LEU	3.9
1	I	193	ARG	3.9
2	J	847	LEU	3.9
1	E	256	SER	3.9
2	L	860	ILE	3.8
1	K	14	SER	3.8
1	A	146	GLN	3.8
1	M	200	ASP	3.8
2	F	847	LEU	3.7
1	A	246	GLU	3.7
1	I	136	TYR	3.7
1	O	26	THR	3.6
1	C	140	GLN	3.6
1	E	143	ALA	3.6
2	N	859	TYR	3.6
1	E	285	PRO	3.6
1	A	101	GLU	3.6
1	M	244	LEU	3.6
1	E	242	PHE	3.5
1	I	194	SER	3.5
1	O	251	THR	3.5
1	E	451	ASP	3.5
1	I	244	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	413	LYS	3.5
1	O	112	GLN	3.5
1	O	43	LEU	3.4
1	M	252	LYS	3.4
1	O	328	GLY	3.4
1	E	17	PRO	3.4
1	E	14	SER	3.4
1	M	282	GLY	3.4
1	A	228	GLN	3.4
1	K	69	LEU	3.4
1	A	315	ILE	3.4
1	A	242	PHE	3.3
1	O	14	SER	3.3
1	E	214	HIS	3.3
1	A	28	GLY	3.3
1	A	188	TYR	3.3
1	C	311	GLY	3.3
1	A	93	SER	3.3
1	I	311	GLY	3.3
1	K	323	TYR	3.3
1	I	191	PRO	3.3
1	M	326	LYS	3.3
1	E	101	GLU	3.3
1	A	61	LEU	3.3
1	K	311	GLY	3.2
1	E	254	THR	3.2
1	A	430	ALA	3.2
1	E	392	HIS	3.2
2	J	858	ASN	3.2
2	P	847	LEU	3.2
1	A	195	PRO	3.2
1	A	328	GLY	3.2
1	A	244	LEU	3.2
1	A	459	GLU	3.2
1	C	15	SER	3.2
1	G	14	SER	3.2
1	C	327	ASN	3.1
2	F	859	TYR	3.1
1	M	457	ILE	3.1
1	O	324	GLY	3.1
1	A	86	ASP	3.1
1	I	326	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	I	422	GLU	3.1
1	M	247	ASN	3.1
1	E	146	GLN	3.1
1	E	74	GLY	3.1
1	E	19	ARG	3.1
1	C	44	SER	3.1
1	O	17	PRO	3.1
2	N	847	LEU	3.0
1	E	58	LYS	3.0
1	O	15	SER	3.0
1	E	18	ILE	3.0
1	M	328	GLY	3.0
1	E	93	SER	3.0
1	K	277	SER	3.0
1	O	327	ASN	3.0
1	K	393	PHE	3.0
1	A	270	GLU	3.0
1	C	246	GLU	3.0
2	H	860	ILE	3.0
1	A	362	GLU	3.0
1	E	270	GLU	3.0
1	C	39	ALA	3.0
2	D	859	TYR	3.0
1	A	99	HIS	3.0
1	E	328	GLY	3.0
1	I	310	ALA	2.9
1	K	143	ALA	2.9
1	M	373	ASN	2.9
1	I	285	PRO	2.9
1	M	422	GLU	2.9
1	I	415	ASP	2.9
1	G	326	LYS	2.9
1	K	32	VAL	2.9
1	G	172	GLY	2.9
1	M	15	SER	2.9
1	M	224	GLY	2.9
1	M	193	ARG	2.9
1	C	249	LYS	2.9
1	A	254	THR	2.9
1	M	191	PRO	2.9
1	C	178	GLU	2.9
1	E	385	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	I	393	PHE	2.9
1	M	204	GLY	2.9
1	E	246	GLU	2.8
1	M	246	GLU	2.8
1	I	39	ALA	2.8
1	I	390	ASP	2.8
1	I	315	ILE	2.8
1	O	37	PHE	2.8
1	E	62	GLN	2.8
1	I	58	LYS	2.8
1	M	242	PHE	2.8
1	I	214	HIS	2.8
1	O	143	ALA	2.8
1	A	196	GLU	2.8
1	E	393	PHE	2.8
1	E	142	ARG	2.8
1	I	301	LYS	2.8
1	A	256	SER	2.8
1	E	253	GLU	2.8
1	E	313	VAL	2.7
1	I	146	GLN	2.7
1	O	270	GLU	2.7
1	E	315	ILE	2.7
1	O	196	GLU	2.7
1	G	31	TRP	2.7
1	I	120	TYR	2.7
1	G	327	ASN	2.7
1	M	140	GLN	2.7
1	C	414	PHE	2.7
2	D	860	ILE	2.7
1	A	232	ALA	2.7
2	P	860	ILE	2.7
1	A	108	GLU	2.7
1	E	170	CYS	2.7
1	K	365	THR	2.7
1	M	93	SER	2.7
1	A	151	LEU	2.7
1	K	114	LEU	2.7
1	M	25	LEU	2.7
1	M	62	GLN	2.6
1	M	185	TRP	2.6
1	M	72	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	62	GLN	2.6
1	A	14	SER	2.6
1	O	277	SER	2.6
1	M	136	TYR	2.6
1	E	47	PHE	2.6
1	A	193	ARG	2.6
1	I	288	LYS	2.6
2	B	859	TYR	2.6
2	P	857	TYR	2.6
2	N	853	MET	2.6
1	I	152	GLN	2.6
1	E	231	ASN	2.6
1	A	293	LEU	2.6
1	E	114	LEU	2.6
1	I	205	VAL	2.6
1	M	259	CYS	2.6
1	M	156	SER	2.6
1	O	140	GLN	2.6
1	A	309	ASP	2.6
1	M	74	GLY	2.6
1	O	311	GLY	2.6
1	I	175	ASN	2.6
1	E	277	SER	2.5
1	M	45	SER	2.5
1	G	140	GLN	2.5
1	K	379	GLY	2.5
1	E	207	LEU	2.5
1	A	253	GLU	2.5
1	A	313	VAL	2.5
1	I	200	ASP	2.5
1	K	144	ASN	2.5
1	O	72	ALA	2.5
2	H	859	TYR	2.5
2	F	858	ASN	2.5
1	E	78	LEU	2.5
1	I	328	GLY	2.5
1	M	194	SER	2.5
1	O	27	SER	2.5
1	E	122	GLU	2.5
1	I	247	ASN	2.5
1	A	382	LEU	2.5
1	I	169	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	M	431	ILE	2.5
1	A	390	ASP	2.5
1	G	37	PHE	2.5
1	M	414	PHE	2.5
1	O	144	ASN	2.5
1	O	239	PRO	2.5
1	A	120	TYR	2.5
1	C	391	TYR	2.5
1	M	374	TYR	2.5
1	O	74	GLY	2.5
1	C	32	VAL	2.5
1	C	112	GLN	2.5
1	I	62	GLN	2.5
1	O	430	ALA	2.4
1	I	15	SER	2.4
2	J	853	MET	2.4
1	C	88	ASP	2.4
1	C	326	LYS	2.4
1	O	175	ASN	2.4
1	I	185	TRP	2.4
1	A	285	PRO	2.4
2	N	857	TYR	2.4
1	G	311	GLY	2.4
1	G	423	GLY	2.4
1	I	299	GLY	2.4
1	M	379	GLY	2.4
1	K	455	ILE	2.4
1	A	27	SER	2.4
1	C	277	SER	2.4
1	I	253	GLU	2.4
1	A	22	PHE	2.4
1	E	151	LEU	2.4
1	K	390	ASP	2.4
1	C	310	ALA	2.4
1	G	141	GLN	2.4
1	I	270	GLU	2.4
1	A	304	LEU	2.4
1	I	57	LEU	2.4
1	I	377	VAL	2.4
1	I	74	GLY	2.4
1	O	84	TYR	2.4
2	P	859	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	I	171	ILE	2.4
1	M	58	LYS	2.4
1	G	125	LEU	2.4
1	I	196	GLU	2.4
1	I	202	GLU	2.4
1	A	236	ASN	2.4
2	J	849	ASN	2.4
1	K	303	ASP	2.4
1	E	255	ILE	2.4
2	L	859	TYR	2.4
1	E	80	SER	2.4
1	K	324	GLY	2.3
1	A	144	ASN	2.3
1	M	51	ALA	2.3
2	N	858	ASN	2.3
1	E	86	ASP	2.3
1	E	120	TYR	2.3
1	K	78	LEU	2.3
1	K	140	GLN	2.3
1	O	69	LEU	2.3
2	D	847	LEU	2.3
1	K	249	LYS	2.3
1	A	87	ILE	2.3
2	D	853	MET	2.3
1	K	415	ASP	2.3
1	K	43	LEU	2.3
2	L	847	LEU	2.3
1	E	381	ILE	2.3
1	C	26	THR	2.3
1	A	221	TYR	2.3
1	K	120	TYR	2.3
2	B	857	TYR	2.3
1	C	292	ASN	2.3
1	C	242	PHE	2.3
1	E	41	GLN	2.3
1	A	422	GLU	2.3
1	O	362	GLU	2.3
1	A	39	ALA	2.3
1	A	72	ALA	2.3
1	I	72	ALA	2.3
1	C	120	TYR	2.3
1	E	118	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	I	327	ASN	2.3
1	I	48	GLN	2.3
1	I	140	GLN	2.3
1	I	114	LEU	2.3
1	C	137	SER	2.3
1	E	421	PHE	2.3
1	A	415	ASP	2.3
1	E	217	ASP	2.3
1	E	390	ASP	2.3
1	E	168	GLU	2.2
1	M	196	GLU	2.2
1	E	239	PRO	2.2
1	I	204	GLY	2.2
1	A	185	TRP	2.2
1	E	240	THR	2.2
1	G	81	PHE	2.2
1	E	326	LYS	2.2
1	E	131	GLN	2.2
1	C	101	GLU	2.2
1	C	270	GLU	2.2
1	E	65	GLU	2.2
1	E	362	GLU	2.2
1	M	362	GLU	2.2
1	M	390	ASP	2.2
1	E	457	ILE	2.2
1	E	311	GLY	2.2
1	I	293	LEU	2.2
1	K	224	GLY	2.2
1	A	428	LYS	2.2
1	C	45	SER	2.2
1	E	237	ASN	2.2
1	I	173	ASP	2.2
1	I	394	LEU	2.2
1	M	245	ASP	2.2
1	E	123	TRP	2.2
1	E	141	GLN	2.2
1	E	152	GLN	2.2
1	E	364	GLN	2.2
1	O	171	ILE	2.2
1	M	122	GLU	2.2
1	G	454	LYS	2.2
2	F	854	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	47	PHE	2.2
2	F	856	VAL	2.2
1	E	116	LEU	2.2
1	K	246	GLU	2.2
2	F	849	ASN	2.2
1	A	311	GLY	2.2
1	I	28	GLY	2.2
1	C	303	ASP	2.2
1	I	298	HIS	2.2
1	A	240	THR	2.1
1	C	251	THR	2.1
1	K	313	VAL	2.1
1	K	378	VAL	2.1
1	M	120	TYR	2.1
1	I	201	ILE	2.1
1	E	198	LEU	2.1
1	A	168	GLU	2.1
1	K	270	GLU	2.1
1	I	144	ASN	2.1
1	K	327	ASN	2.1
1	C	300	THR	2.1
1	G	112	GLN	2.1
1	M	48	GLN	2.1
1	G	310	ALA	2.1
1	I	292	ASN	2.1
1	G	185	TRP	2.1
1	M	438	ASP	2.1
1	I	420	ARG	2.1
1	E	46	GLN	2.1
1	M	124	ALA	2.1
1	A	224	GLY	2.1
1	O	246	GLU	2.1
1	M	256	SER	2.1
1	M	205	VAL	2.1
1	E	281	LYS	2.1
1	A	381	ILE	2.1
1	E	188	TYR	2.1
1	K	385	TYR	2.1
1	M	188	TYR	2.1
1	A	45	SER	2.1
1	A	250	ARG	2.1
1	I	245	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	K	132	ALA	2.1
1	K	310	ALA	2.1
1	K	228	GLN	2.1
1	G	17	PRO	2.1
1	G	273	LYS	2.0
1	G	44	SER	2.0
1	I	77	SER	2.0
1	G	201	ILE	2.0
1	C	390	ASP	2.0
1	G	147	THR	2.0
1	M	284	THR	2.0
1	A	416	LYS	2.0
1	E	79	GLU	2.0
1	E	430	ALA	2.0
1	A	391	TYR	2.0
1	A	200	ASP	2.0
1	E	22	PHE	2.0
1	E	267	GLY	2.0
1	I	184	GLY	2.0
1	K	74	GLY	2.0
1	K	169	GLY	2.0
1	A	42	GLN	2.0
1	A	326	LYS	2.0
1	K	41	GLN	2.0
1	I	246	GLU	2.0
1	M	313	VAL	2.0
1	O	422	GLU	2.0
1	K	190	ARG	2.0
1	M	304	LEU	2.0
1	M	433	LEU	2.0
1	M	149	ILE	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.