



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:31 PM UTC

PDB ID : 6DV5 / pdb_00006dv5
Title : Oligomeric complex of a Hsp27 24-mer at 3.6 Å resolution
Authors : Aguda, A.H.; Brayer, G.D.
Deposited on : 2018-06-22
Resolution : 3.58 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:

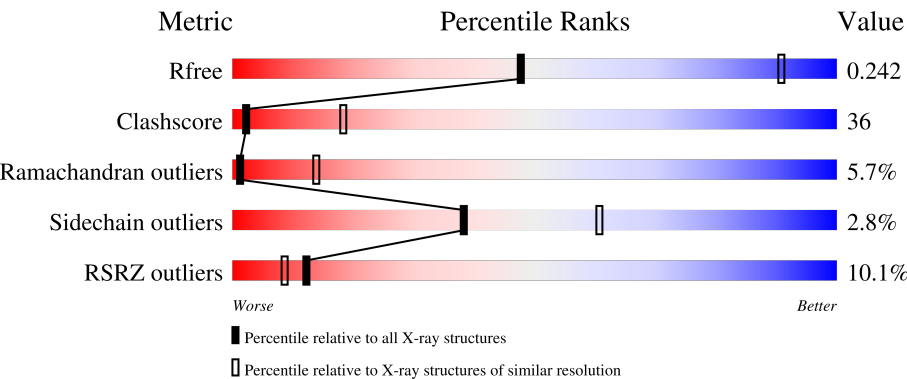
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.58 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1521 (3.66-3.50)
Clashscore	190562	1595 (3.66-3.50)
Ramachandran outliers	187476	1551 (3.66-3.50)
Sidechain outliers	187428	1551 (3.66-3.50)
RSRZ outliers	180081	1520 (3.66-3.50)

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	205	13% 43% 36% 9% 12%
1	B	205	11% 42% 31% • 24%
1	C	205	6% 43% 31% 6% • 19%
1	D	205	8% 41% 34% 6% 20%
1	E	205	7% 45% 32% 7% 16%

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Mol	Chain	Length	Quality of chain
1	F	205	
1	G	205	
1	H	205	
1	I	205	
1	J	205	
1	K	205	
1	L	205	
1	M	205	
1	N	205	
1	O	205	
1	P	205	
1	Q	205	
1	R	205	
1	S	205	
1	T	205	
1	U	205	
1	V	205	
1	W	205	
1	X	205	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 32356 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Heat shock protein beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	156	Total	C	N	O	S	0	0	0
			1256	799	219	236	2			
1	A	181	Total	C	N	O	S	0	0	0
			1442	909	256	274	3			
1	D	165	Total	C	N	O	S	0	0	0
			1335	844	240	249	2			
1	F	163	Total	C	N	O	S	0	0	0
			1307	826	233	246	2			
1	H	160	Total	C	N	O	S	0	0	0
			1292	815	232	242	3			
1	J	162	Total	C	N	O	S	0	0	0
			1307	827	232	246	2			
1	L	165	Total	C	N	O	S	0	0	0
			1321	835	232	251	3			
1	N	162	Total	C	N	O	S	0	0	0
			1302	822	232	245	3			
1	P	164	Total	C	N	O	S	0	0	0
			1316	832	233	248	3			
1	R	167	Total	C	N	O	S	0	0	0
			1339	846	237	253	3			
1	T	166	Total	C	N	O	S	0	0	0
			1331	841	236	252	2			
1	V	161	Total	C	N	O	S	0	0	0
			1295	820	229	243	3			
1	X	166	Total	C	N	O	S	0	0	0
			1334	843	236	252	3			
1	C	166	Total	C	N	O	S	0	0	0
			1335	845	236	251	3			
1	E	173	Total	C	N	O	S	0	0	0
			1378	873	241	262	2			
1	G	179	Total	C	N	O	S	0	0	0
			1427	900	254	271	2			

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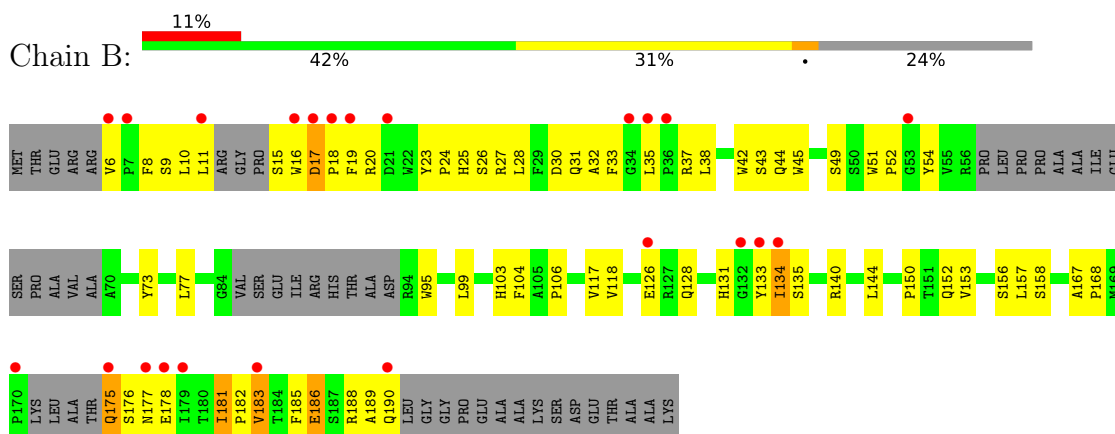
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	I	169	Total	C	N	O	S	0	0	0
			1347	855	237	253	2			
1	K	175	Total	C	N	O	S	0	0	0
			1403	884	249	267	3			
1	M	177	Total	C	N	O	S	0	0	0
			1411	891	252	266	2			
1	O	174	Total	C	N	O	S	0	0	0
			1388	878	247	260	3			
1	Q	161	Total	C	N	O	S	0	0	0
			1301	823	232	243	3			
1	S	180	Total	C	N	O	S	0	0	0
			1435	905	255	272	3			
1	U	175	Total	C	N	O	S	0	0	0
			1395	881	249	262	3			
1	W	169	Total	C	N	O	S	0	0	0
			1359	861	242	253	3			

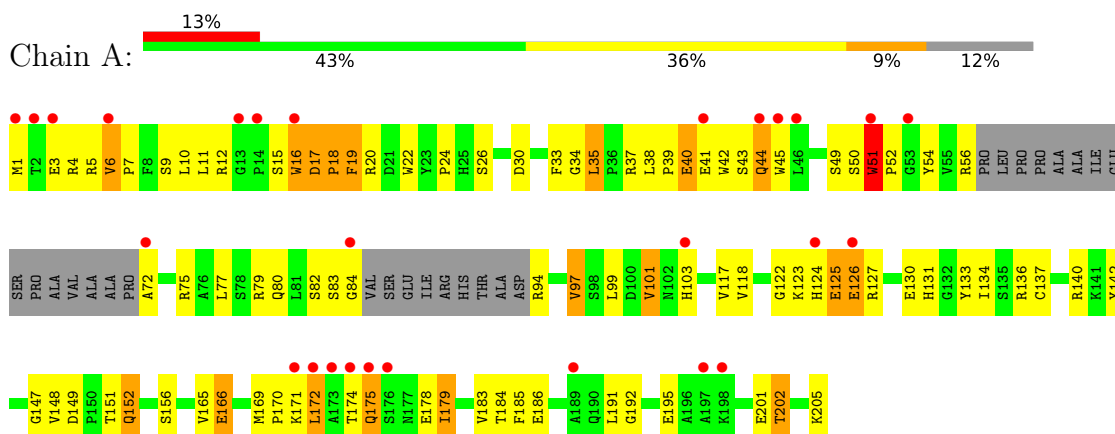
3 Residue-property plots [i](#)

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.

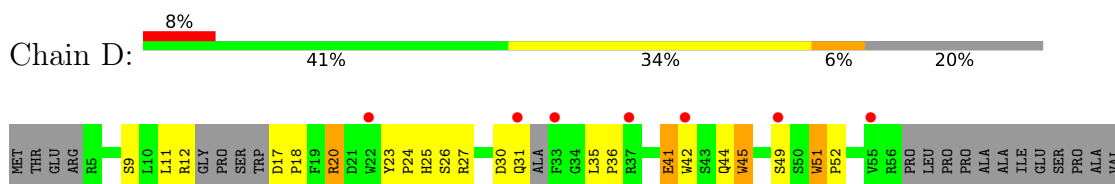
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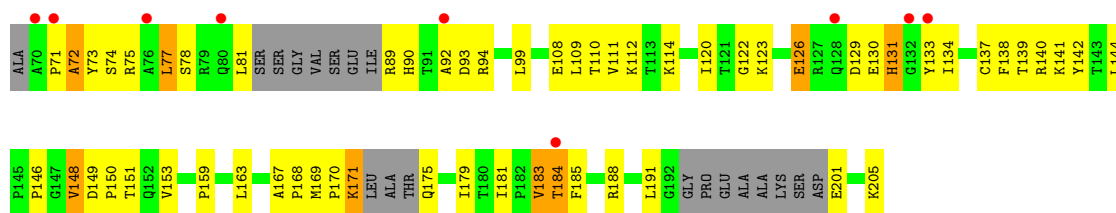


- Molecule 1: Heat shock protein beta-1

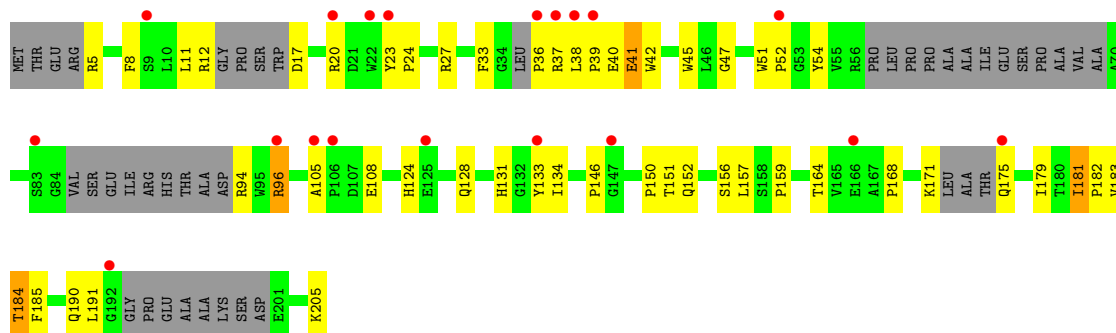


- Molecule 1: Heat shock protein beta-1

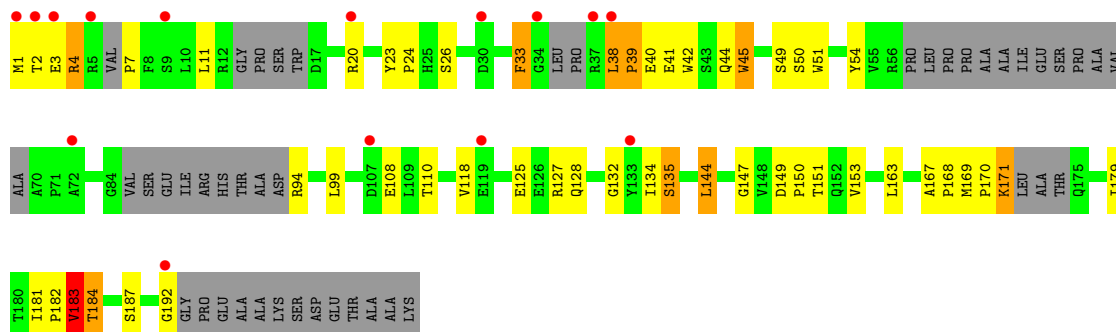




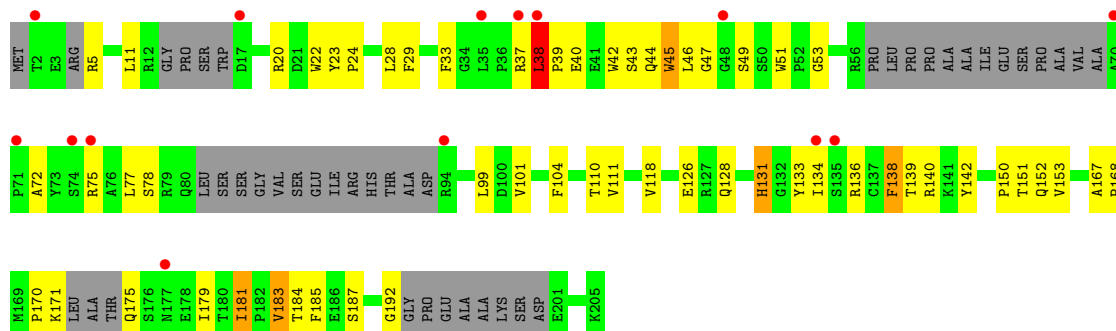
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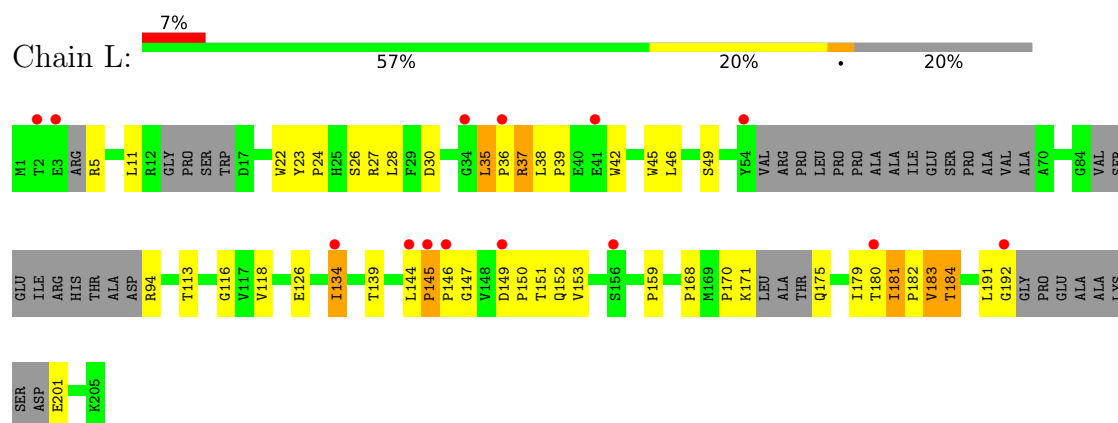
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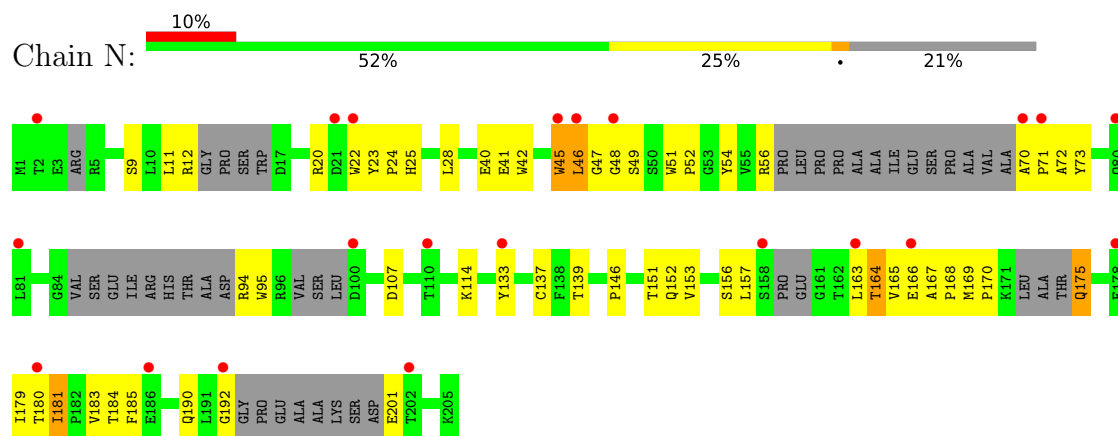
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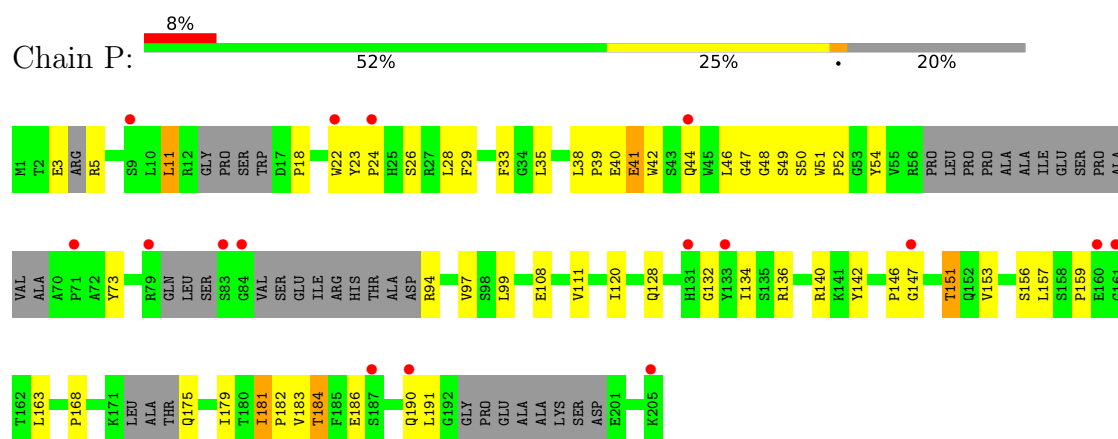
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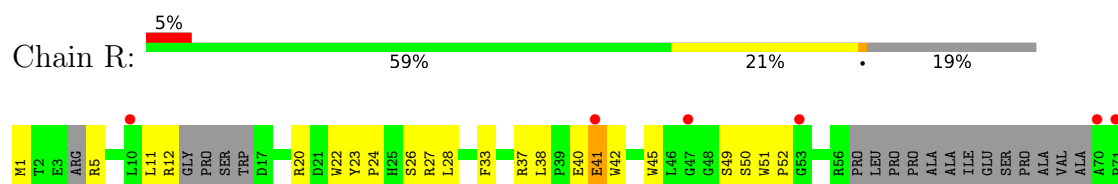
- Molecule 1: Heat shock protein beta-1



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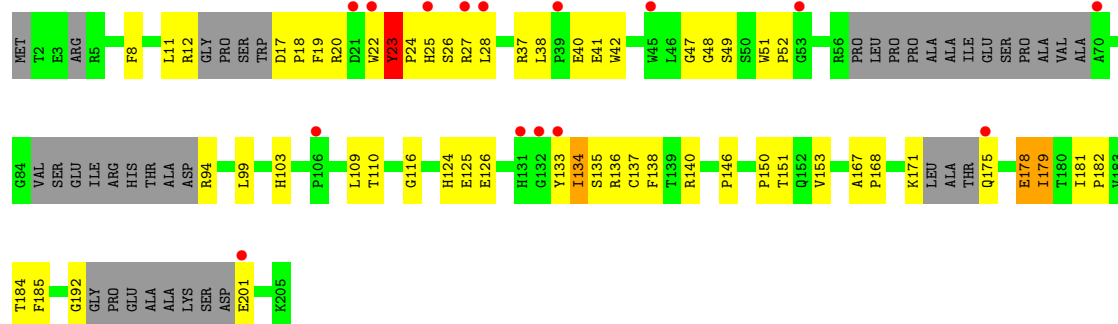


- Molecule 1: Heat shock protein beta-1

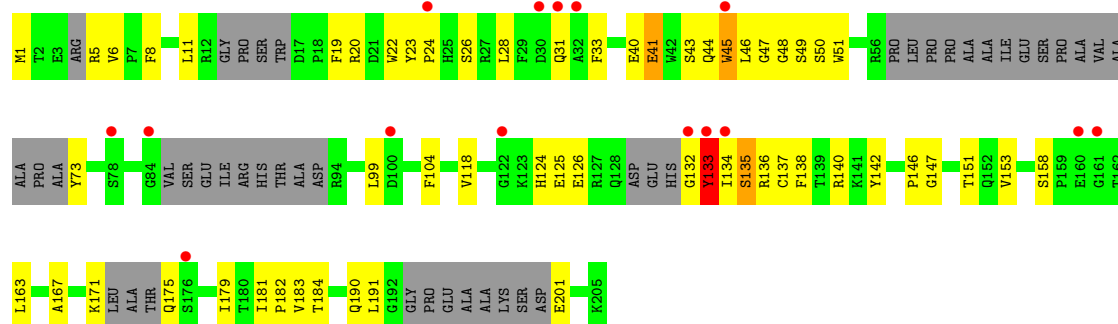




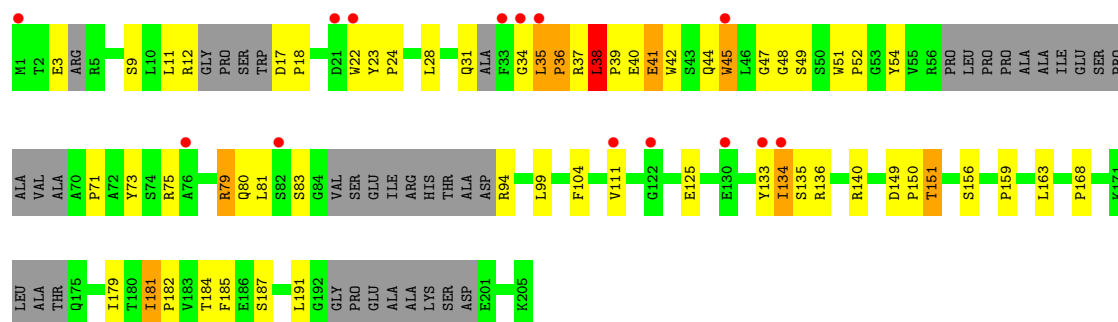
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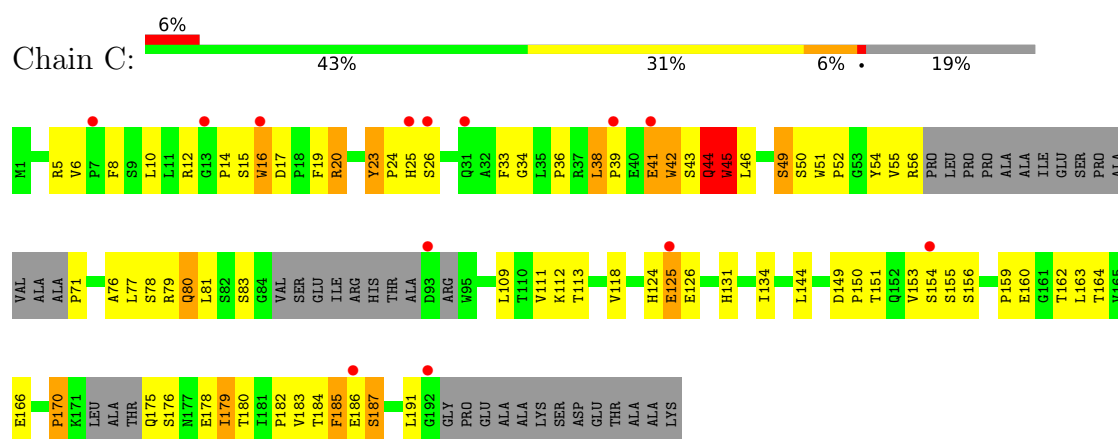
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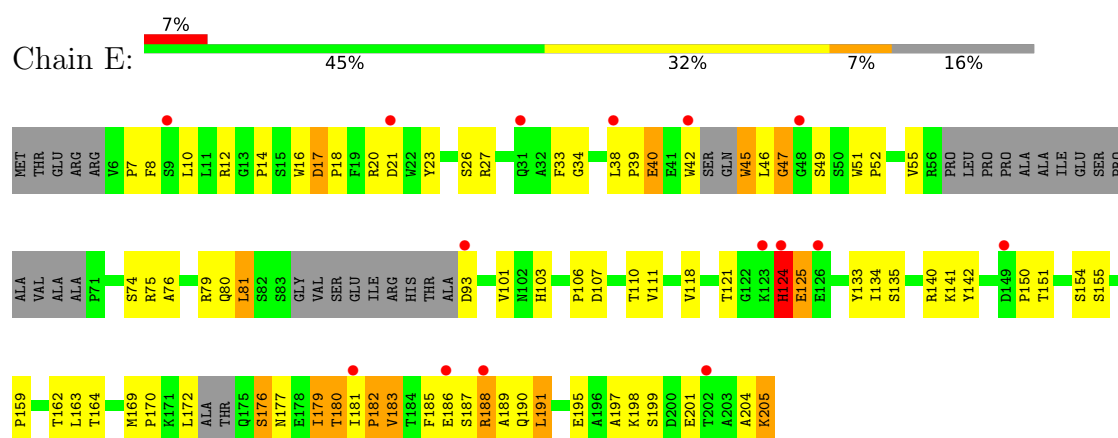
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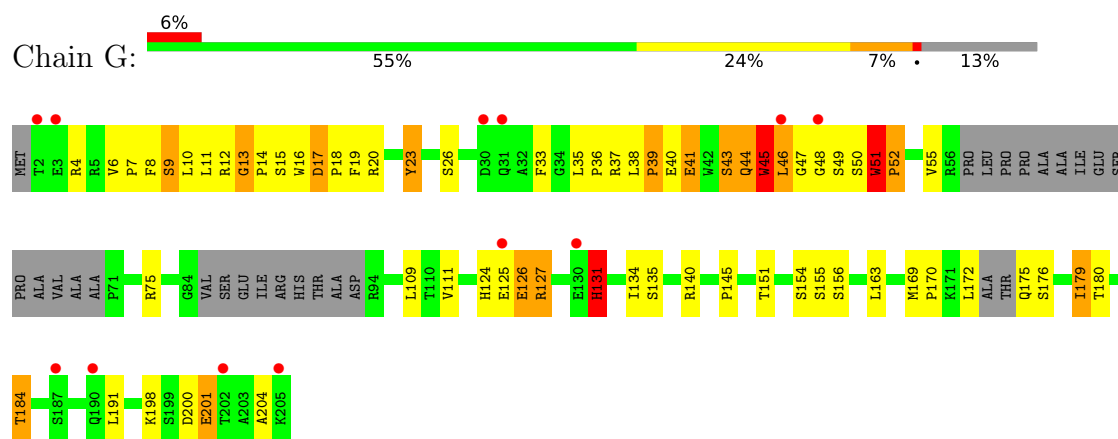
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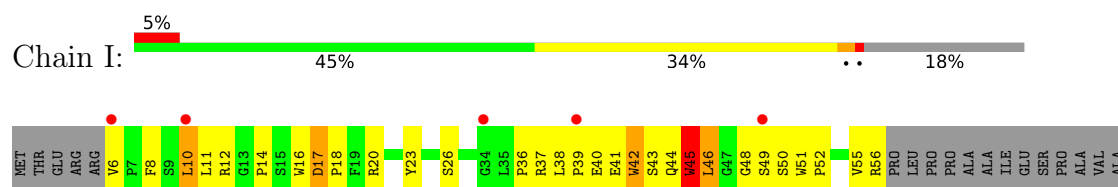
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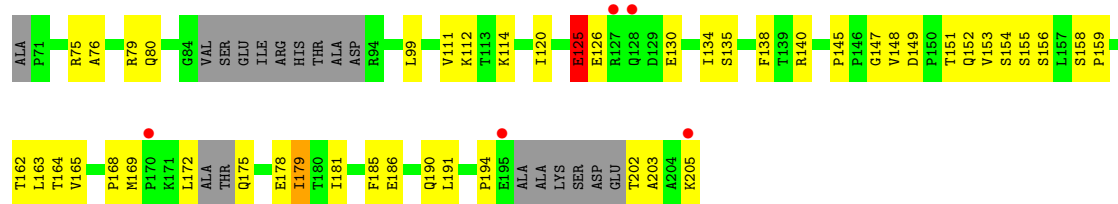


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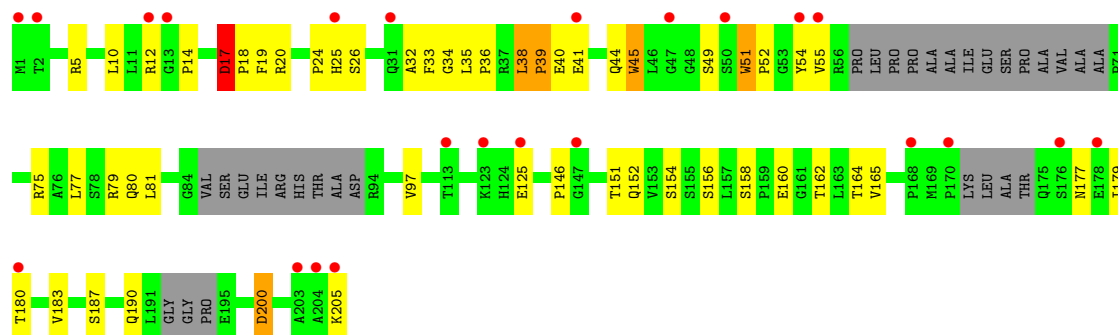


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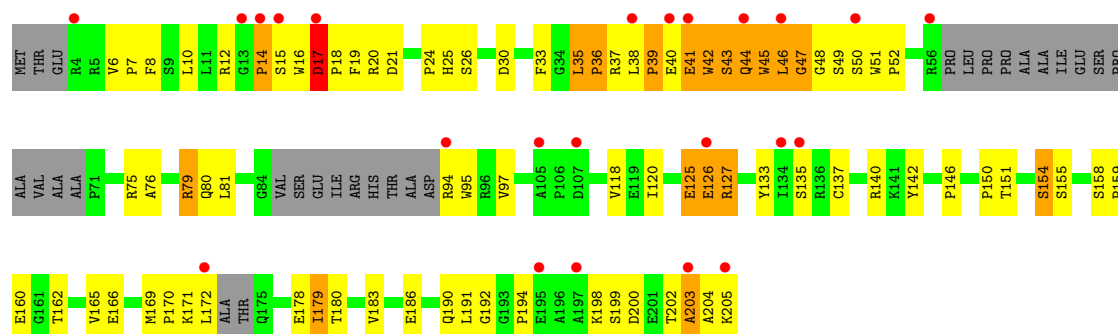




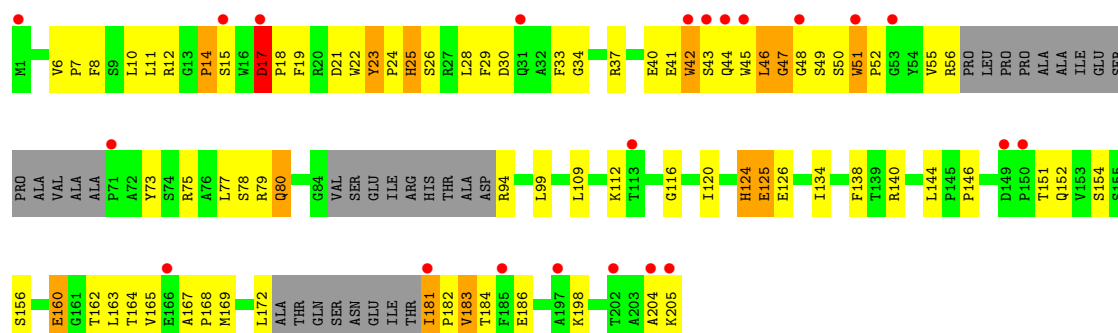
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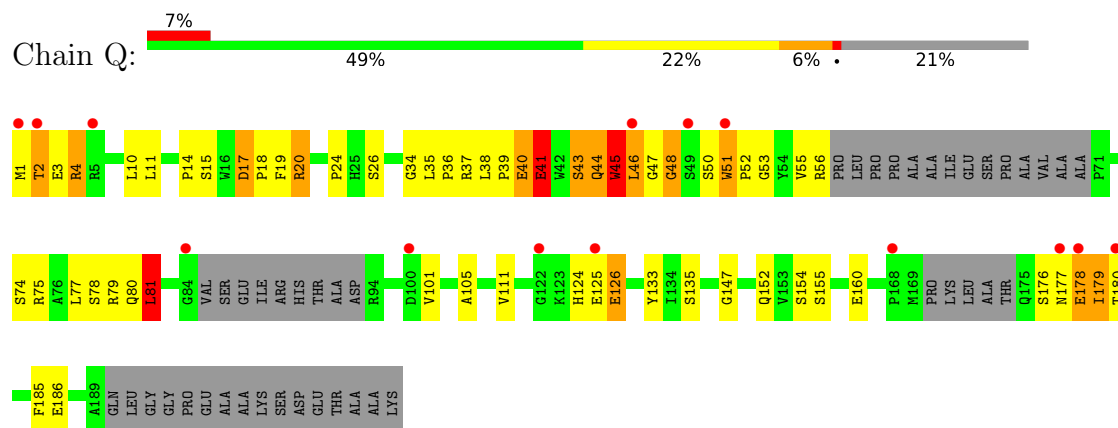
• Molecule 1: Heat shock protein beta-1



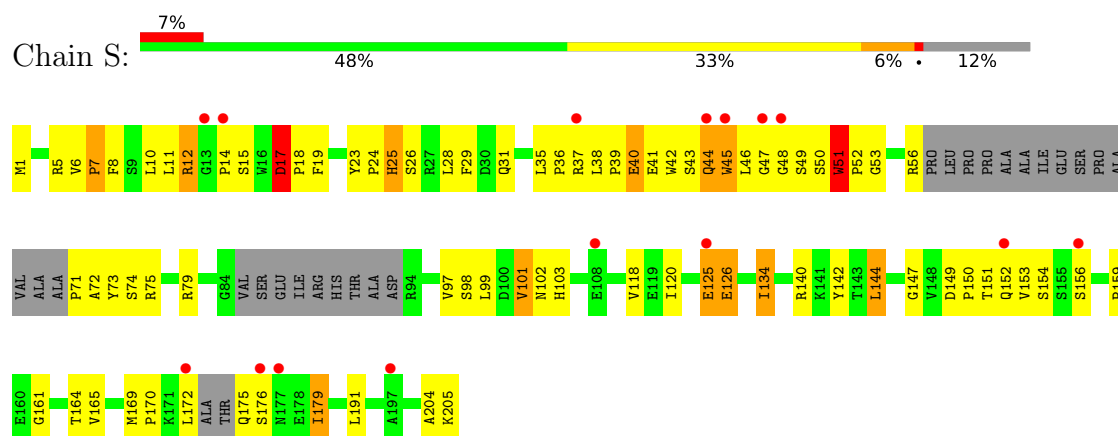
• Molecule 1: Heat shock protein beta-1



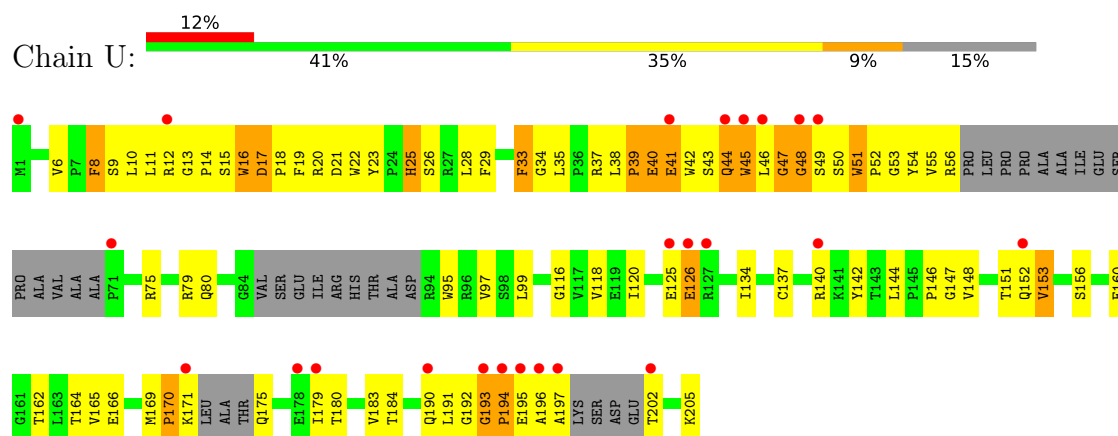
• Molecule 1: Heat shock protein beta-1



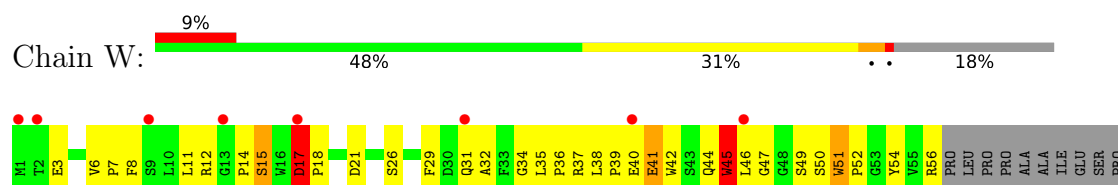
• Molecule 1: Heat shock protein beta-1

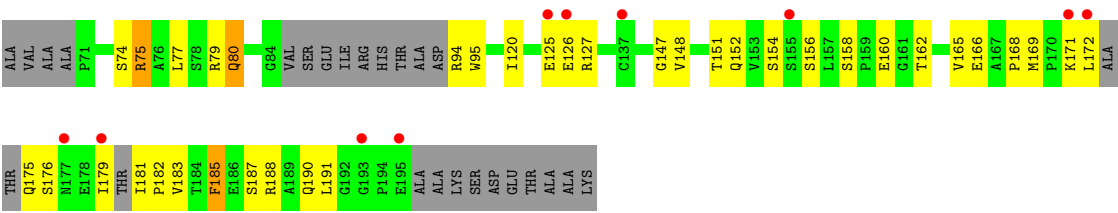


• Molecule 1: Heat shock protein beta-1



• Molecule 1: Heat shock protein beta-1





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	324.70Å 324.70Å 198.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	93.73 – 3.58 93.73 – 3.58	Depositor EDS
% Data completeness (in resolution range)	99.8 (93.73-3.58) 99.8 (93.73-3.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	18.26 (at 3.58Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.238 , 0.242 0.236 , 0.242	Depositor DCC
R_{free} test set	4645 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	48.3	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 28.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -2/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+4/3*l,-1/3*h+1/3*k+1/3*l 0.000 for -h,1/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+1/3*l 0.000 for -1/3*h+1/3*k+4/3*l,-k,2/3*h+1/3*k+1/3*l 0.000 for -h,2/3*h+1/3*k+4/3*l,1/3*h+2/3*k-1/3*l 0.000 for -1/3*h-2/3*k+4/3*l,-2/3*h-1/3*k-4/3*l,1/3*h-1/3*k-1/3*l 0.002 for 1/3*h+2/3*k-4/3*l,-k,-2/3*h-1/3*k-1/3*l 0.000 for h,-h-k,-l	Xtriage

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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.

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Property	Value	Source
Reported twinning fraction	0.580 for H, K, L 0.057 for K, H, -L 0.062 for -K, $-1/3H+1/3K+4/3L$, $-2/3H-1/3K-1/3L$ 0.061 for $-1/3H+1/3K+4/3L$, -K, $2/3H+1/3K+1/3L$ 0.062 for $1/3H-1/3K-4/3L$, -H, $1/3H+2/3K-1/3L$ 0.061 for -H, $1/3H-1/3K-4/3L$, $-1/3H-2/3K+1/3L$ 0.059 for $-1/3H-2/3K+4/3L$, H+K, $-1/3H+1/3K+1/3L$ 0.059 for $-2/3H-1/3K-4/3L$, H+K, $1/3H-1/3K-1/3L$	Depositor
Outliers	0 of 91924 reflections	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	32356	wwPDB-VP
Average B, all atoms ($\text{\AA}^2$)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.69% of the height of the origin peak. No significant pseudotranslation is detected.*

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	1.02	2/1483 (0.1%)	1.02	1/2014 (0.0%)
1	B	0.97	0/1294	0.91	0/1761
1	C	0.96	0/1373	1.01	3/1863 (0.2%)
1	D	0.96	0/1370	0.96	2/1855 (0.1%)
1	E	0.96	0/1417	1.02	5/1923 (0.3%)
1	F	0.97	0/1341	0.99	3/1814 (0.2%)
1	G	0.98	0/1467	1.08	9/1990 (0.5%)
1	H	0.98	1/1325 (0.1%)	0.96	0/1791
1	I	0.93	0/1386	1.05	3/1881 (0.2%)
1	J	0.95	0/1341	0.99	3/1816 (0.2%)
1	K	0.94	0/1441	1.00	4/1953 (0.2%)
1	L	0.95	1/1355 (0.1%)	0.92	1/1834 (0.1%)
1	M	0.95	1/1451 (0.1%)	1.00	6/1968 (0.3%)
1	N	0.96	0/1333	1.01	4/1799 (0.2%)
1	O	0.91	0/1428	0.97	5/1936 (0.3%)
1	P	0.91	0/1349	0.97	0/1824
1	Q	0.93	0/1339	0.99	3/1818 (0.2%)
1	R	0.95	0/1373	0.96	3/1858 (0.2%)
1	S	0.96	0/1475	1.09	9/2000 (0.5%)
1	T	0.97	2/1365 (0.1%)	0.96	1/1848 (0.1%)
1	U	0.98	0/1434	1.06	4/1944 (0.2%)
1	V	0.95	1/1326 (0.1%)	1.00	3/1791 (0.2%)
1	W	1.00	2/1398 (0.1%)	1.05	8/1896 (0.4%)
1	X	0.96	0/1367	0.97	2/1848 (0.1%)
All	All	0.96	10/33231 (0.0%)	1.00	82/45025 (0.2%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	T	23	TYR	CA-C	-6.51	1.44	1.52
1	A	35	LEU	CA-C	-6.38	1.47	1.52
1	T	23	TYR	C-O	-6.34	1.16	1.24
1	W	183	VAL	C-O	-6.13	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	V	133	TYR	N-CA	6.09	1.54	1.46
1	L	153	VAL	C-O	-5.64	1.18	1.24
1	M	154	SER	C-O	-5.47	1.16	1.23
1	H	183	VAL	C-O	-5.30	1.17	1.24
1	W	42	TRP	CA-C	5.24	1.55	1.52
1	A	166	GLU	C-O	-5.19	1.17	1.24

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	51	TRP	CA-C-N	-9.17	111.41	120.21
1	G	51	TRP	C-N-CA	-9.17	111.41	120.21
1	W	14	PRO	N-CA-CB	8.77	111.65	103.41
1	E	14	PRO	N-CA-CB	8.55	111.45	103.41
1	Q	14	PRO	N-CA-CB	8.54	111.71	103.51
1	K	14	PRO	N-CA-CB	8.40	111.31	103.41
1	M	14	PRO	N-CA-CB	8.21	111.12	103.41
1	J	20	ARG	N-CA-C	7.79	120.76	111.33
1	I	14	PRO	N-CA-CB	7.76	110.71	103.41
1	O	14	PRO	N-CA-CB	7.65	111.29	103.25
1	W	3	GLU	N-CA-C	7.37	120.30	109.69
1	S	102	ASN	N-CA-C	7.18	119.78	111.02
1	C	14	PRO	N-CA-CB	7.04	109.57	102.17
1	E	38	LEU	CA-C-N	-6.92	111.19	119.84
1	E	38	LEU	C-N-CA	-6.92	111.19	119.84
1	I	145	PRO	O-C-N	6.90	124.39	121.15
1	V	158	SER	CA-C-N	6.88	126.58	119.56
1	V	158	SER	C-N-CA	6.88	126.58	119.56
1	S	14	PRO	N-CA-CB	6.81	110.40	103.25
1	F	181	ILE	CA-C-N	-6.58	112.73	119.83
1	F	181	ILE	C-N-CA	-6.58	112.73	119.83
1	G	44	GLN	N-CA-C	6.57	121.25	113.23
1	U	14	PRO	N-CA-CB	6.53	110.24	102.60
1	I	50	SER	N-CA-C	6.50	114.99	108.75
1	S	17	ASP	CA-C-N	-6.50	111.72	119.84
1	S	17	ASP	C-N-CA	-6.50	111.72	119.84
1	W	185	PHE	N-CA-C	6.46	118.86	111.11
1	D	77	LEU	N-CA-C	-6.32	103.69	111.40
1	Q	51	TRP	CA-C-N	-6.28	113.22	119.93
1	Q	51	TRP	C-N-CA	-6.28	113.22	119.93
1	W	17	ASP	CA-C-N	-6.16	113.28	120.12
1	W	17	ASP	C-N-CA	-6.16	113.28	120.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	133	TYR	N-CA-C	6.15	123.90	110.80
1	X	184	THR	N-CA-C	6.15	119.39	110.42
1	K	51	TRP	N-CA-C	-6.12	103.09	110.13
1	C	126	GLU	N-CA-C	6.10	119.10	109.96
1	E	124	HIS	N-CA-C	6.07	123.73	110.80
1	T	184	THR	N-CA-C	6.07	119.16	110.24
1	M	35	LEU	CA-C-N	6.06	127.42	119.84
1	M	35	LEU	C-N-CA	6.06	127.42	119.84
1	E	176	SER	N-CA-C	6.04	117.67	110.19
1	V	184	THR	N-CA-C	6.03	118.79	110.35
1	D	20	ARG	N-CA-C	5.83	120.40	112.88
1	S	51	TRP	CA-C-N	-5.76	113.61	119.83
1	S	51	TRP	C-N-CA	-5.76	113.61	119.83
1	N	181	ILE	CA-C-N	-5.70	113.92	119.90
1	N	181	ILE	C-N-CA	-5.70	113.92	119.90
1	U	40	GLU	N-CA-C	-5.68	106.01	113.17
1	O	47	GLY	N-CA-C	5.65	118.13	111.35
1	S	126	GLU	N-CA-C	5.64	117.84	108.20
1	L	145	PRO	O-C-N	5.60	123.89	121.31
1	K	17	ASP	CA-C-N	-5.57	113.93	120.12
1	K	17	ASP	C-N-CA	-5.57	113.93	120.12
1	R	184	THR	N-CA-C	5.51	118.46	110.42
1	O	17	ASP	CA-C-N	-5.50	114.02	120.12
1	O	17	ASP	C-N-CA	-5.50	114.02	120.12
1	W	176	SER	N-CA-C	5.49	116.98	109.18
1	R	132	GLY	N-CA-C	5.48	117.77	111.36
1	J	181	ILE	CA-C-N	-5.48	113.92	119.83
1	J	181	ILE	C-N-CA	-5.48	113.92	119.83
1	N	184	THR	N-CA-C	5.47	118.29	110.24
1	U	193	GLY	CA-C-N	5.38	126.56	119.84
1	U	193	GLY	C-N-CA	5.38	126.56	119.84
1	W	125	GLU	N-CA-C	5.32	122.13	110.80
1	M	37	ARG	N-CA-C	-5.31	103.01	110.50
1	S	45	TRP	N-CA-C	5.30	122.10	110.80
1	A	3	GLU	N-CA-C	5.30	117.64	111.02
1	G	13	GLY	CA-C-N	5.25	126.40	119.84
1	G	13	GLY	C-N-CA	5.25	126.40	119.84
1	X	38	LEU	N-CA-C	5.24	121.40	109.81
1	S	125	GLU	N-CA-C	5.24	115.31	108.07
1	M	17	ASP	CA-C-N	-5.23	114.31	120.12
1	M	17	ASP	C-N-CA	-5.23	114.31	120.12
1	W	126	GLU	N-CA-C	5.23	121.94	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	181	ILE	N-CA-C	5.20	120.11	108.88
1	O	126	GLU	N-CA-C	5.19	117.69	109.96
1	G	52	PRO	N-CA-C	5.09	118.35	111.22
1	C	42	TRP	N-CA-C	5.08	119.02	112.41
1	G	184	THR	N-CA-C	5.07	117.70	111.82
1	F	184	THR	N-CA-C	5.07	117.69	110.24
1	G	50	SER	N-CA-C	5.03	114.98	107.88
1	G	131	HIS	N-CA-CB	5.01	117.55	110.13

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1442	0	1393	202	0
1	B	1256	0	1195	135	0
1	C	1335	0	1277	147	0
1	D	1335	0	1285	195	0
1	E	1378	0	1318	158	0
1	F	1307	0	1257	115	0
1	G	1427	0	1370	106	0
1	H	1292	0	1243	88	0
1	I	1347	0	1292	122	0
1	J	1307	0	1256	78	0
1	K	1403	0	1344	87	0
1	L	1321	0	1270	74	0
1	M	1411	0	1357	156	0
1	N	1302	0	1252	119	0
1	O	1388	0	1339	183	0
1	P	1316	0	1267	74	0
1	Q	1301	0	1245	116	0
1	R	1339	0	1292	91	0
1	S	1435	0	1382	173	0
1	T	1331	0	1280	98	0
1	U	1395	0	1342	150	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V	1295	0	1257	111	0
1	W	1359	0	1306	130	0
1	X	1334	0	1286	85	0
All	All	32356	0	31105	2300	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 36.

All (2300) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:PHE:CE1	1:A:35:LEU:HG	1.31	1.62
1:O:94:ARG:HB2	1:O:169:MET:CG	1.39	1.52
1:O:45:TRP:HB2	1:O:50:SER:CB	1.37	1.50
1:A:35:LEU:HB3	1:Q:46:LEU:CD2	1.42	1.45
1:A:15:SER:HB2	1:A:16:TRP:CE3	1.52	1.40
1:M:41:GLU:CD	1:M:42:TRP:H	1.28	1.40
1:D:11:LEU:HD11	1:D:171:LYS:NZ	1.32	1.39
1:T:19:PHE:HA	1:T:28:LEU:CD2	1.52	1.38
1:N:152:GLN:HB3	1:N:168:PRO:CD	1.51	1.37
1:Q:37:ARG:CB	1:Q:40:GLU:HG3	1.52	1.35
1:N:163:LEU:HD12	1:N:164:THR:N	1.39	1.34
1:N:45:TRP:CD1	1:N:48:GLY:HA3	1.61	1.34
1:T:178:GLU:O	1:T:179:ILE:HG12	1.24	1.34
1:O:45:TRP:CB	1:O:50:SER:HB2	1.58	1.33
1:L:36:PRO:O	1:L:37:ARG:HG3	1.22	1.33
1:S:175:GLN:HG3	1:S:191:LEU:CD1	1.59	1.33
1:B:18:PRO:HG3	1:B:77:LEU:CD2	1.59	1.32
1:M:202:THR:HG21	1:M:205:LYS:NZ	1.42	1.31
1:V:44:GLN:HB2	1:V:45:TRP:CZ3	1.64	1.31
1:Q:38:LEU:CD1	1:Q:39:PRO:HD3	1.59	1.30
1:N:45:TRP:HD1	1:N:48:GLY:CA	1.41	1.30
1:Q:37:ARG:HB2	1:Q:40:GLU:CG	1.59	1.30
1:D:146:PRO:HD2	1:D:175:GLN:NE2	1.44	1.29
1:Q:37:ARG:HD2	1:Q:40:GLU:CD	1.58	1.28
1:N:152:GLN:CB	1:N:168:PRO:HD2	1.63	1.28
1:O:94:ARG:CB	1:O:169:MET:HG2	1.61	1.27
1:M:42:TRP:HB3	1:U:41:GLU:OE1	1.32	1.27
1:L:182:PRO:O	1:L:183:VAL:HG13	1.35	1.26
1:P:38:LEU:HD22	1:P:44:GLN:NE2	1.50	1.26
1:T:18:PRO:O	1:T:28:LEU:HD23	1.36	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:THR:CA	1:C:191:LEU:HD23	1.67	1.25
1:Q:38:LEU:HD12	1:Q:39:PRO:CD	1.66	1.24
1:M:172:LEU:HD22	1:M:204:ALA:CB	1.70	1.22
1:S:29:PHE:CB	1:S:45:TRP:HZ2	1.52	1.22
1:D:159:PRO:CA	1:C:186:GLU:HG2	1.71	1.21
1:J:104:PHE:CE2	1:J:138:PHE:CE1	2.27	1.21
1:A:174:THR:O	1:A:191:LEU:HD13	1.41	1.20
1:S:10:LEU:O	1:S:10:LEU:HD12	1.39	1.20
1:X:133:TYR:CE1	1:X:134:ILE:HD11	1.76	1.19
1:B:17:ASP:HB3	1:B:18:PRO:CD	1.72	1.19
1:S:45:TRP:HD1	1:S:51:TRP:CH2	1.61	1.18
1:L:181:ILE:H	1:L:182:PRO:CD	1.49	1.18
1:V:133:TYR:CD1	1:U:142:TYR:HE1	1.60	1.18
1:D:159:PRO:CB	1:C:186:GLU:HG2	1.73	1.18
1:M:146:PRO:HG2	1:M:205:LYS:HD2	1.25	1.18
1:A:33:PHE:CE1	1:A:35:LEU:CG	2.26	1.17
1:Q:38:LEU:CG	1:Q:39:PRO:HD3	1.75	1.17
1:S:45:TRP:CD1	1:S:51:TRP:CH2	2.31	1.17
1:B:19:PHE:CA	1:B:28:LEU:HG	1.75	1.16
1:L:146:PRO:HB2	1:L:175:GLN:N	1.57	1.16
1:V:44:GLN:HB2	1:V:45:TRP:CE3	1.78	1.16
1:W:35:LEU:HD23	1:W:37:ARG:NH1	1.60	1.16
1:U:184:THR:HA	1:U:191:LEU:HD11	1.27	1.16
1:I:42:TRP:H	1:I:44:GLN:NE2	1.43	1.16
1:C:184:THR:HB	1:C:191:LEU:CD2	1.73	1.16
1:Q:38:LEU:HD12	1:Q:39:PRO:N	1.60	1.16
1:R:151:THR:HG21	1:S:154:SER:HB3	1.25	1.16
1:J:110:THR:HG22	1:K:180:THR:HG21	1.28	1.15
1:B:15:SER:O	1:B:20:ARG:HG3	1.46	1.15
1:L:151:THR:CG2	1:M:154:SER:HB3	1.76	1.14
1:M:12:ARG:HH12	1:M:21:ASP:HB3	1.09	1.14
1:W:35:LEU:HD23	1:W:37:ARG:HH12	1.04	1.14
1:D:81:LEU:HD13	1:D:92:ALA:CB	1.76	1.14
1:M:26:SER:HB3	1:U:40:GLU:OE1	1.47	1.14
1:C:44:GLN:HB3	1:W:44:GLN:HG3	1.30	1.14
1:C:184:THR:CB	1:C:191:LEU:HD23	1.77	1.14
1:B:17:ASP:HB3	1:B:18:PRO:HD3	1.26	1.14
1:I:181:ILE:HG22	1:I:190:GLN:NE2	1.61	1.14
1:J:104:PHE:CD2	1:J:138:PHE:CE1	2.37	1.13
1:L:149:ASP:OD1	1:L:152:GLN:HG2	1.49	1.13
1:V:44:GLN:CB	1:V:45:TRP:CZ3	2.30	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:37:ARG:HB2	1:O:40:GLU:OE1	1.46	1.13
1:W:37:ARG:HB2	1:W:40:GLU:HG2	1.31	1.13
1:I:45:TRP:CE3	1:I:46:LEU:CD1	2.31	1.12
1:T:19:PHE:CA	1:T:28:LEU:HD22	1.80	1.12
1:N:45:TRP:CD1	1:N:48:GLY:CA	2.27	1.11
1:N:45:TRP:HZ3	1:R:51:TRP:CD1	1.69	1.11
1:O:41:GLU:HB3	1:S:44:GLN:OE1	1.47	1.11
1:B:18:PRO:HG3	1:B:77:LEU:HD23	1.22	1.11
1:C:81:LEU:HD12	1:C:83:SER:N	1.64	1.11
1:M:172:LEU:HD22	1:M:204:ALA:HB1	1.19	1.11
1:A:12:ARG:NH1	1:A:16:TRP:H	1.48	1.10
1:V:44:GLN:CB	1:V:45:TRP:CE3	2.33	1.10
1:S:175:GLN:HG3	1:S:191:LEU:HD12	1.32	1.10
1:O:146:PRO:HG2	1:O:205:LYS:HD2	1.33	1.10
1:N:107:ASP:O	1:O:181:ILE:HD13	1.49	1.10
1:X:35:LEU:HB3	1:X:36:PRO:CD	1.81	1.10
1:H:1:MET:HG2	1:H:7:PRO:HD3	1.27	1.10
1:P:49:SER:HA	1:Q:52:PRO:HG3	1.27	1.09
1:T:23:TYR:HB2	1:T:24:PRO:CD	1.81	1.09
1:C:81:LEU:HD12	1:C:83:SER:H	0.95	1.09
1:A:45:TRP:HH2	1:Q:51:TRP:CD1	1.71	1.09
1:B:19:PHE:HA	1:B:28:LEU:HG	1.24	1.09
1:O:12:ARG:HH12	1:O:21:ASP:HB3	1.03	1.09
1:H:20:ARG:HH12	1:W:15:SER:HA	1.17	1.09
1:S:175:GLN:HG3	1:S:191:LEU:HD11	1.29	1.08
1:A:35:LEU:CB	1:Q:46:LEU:CD2	2.31	1.08
1:O:33:PHE:CE2	1:O:42:TRP:HA	1.89	1.08
1:I:45:TRP:CE3	1:I:46:LEU:HD12	1.88	1.08
1:B:17:ASP:CB	1:B:18:PRO:CD	2.29	1.07
1:A:124:HIS:HB2	1:A:136:ARG:HG2	1.35	1.07
1:D:146:PRO:HG2	1:D:175:GLN:HG3	1.15	1.07
1:A:45:TRP:CD1	1:A:49:SER:HG	1.71	1.07
1:P:38:LEU:CD2	1:P:44:GLN:HE21	1.66	1.07
1:U:12:ARG:HH12	1:U:21:ASP:HB3	1.19	1.07
1:R:52:PRO:HB2	1:S:10:LEU:HD13	1.30	1.07
1:C:184:THR:N	1:C:191:LEU:HD23	1.70	1.06
1:M:178:GLU:O	1:M:179:ILE:HG22	1.55	1.06
1:F:108:GLU:HB2	1:E:180:THR:HG21	1.33	1.06
1:A:12:ARG:HD3	1:X:12:ARG:HH22	1.13	1.06
1:V:19:PHE:HA	1:V:28:LEU:HD12	1.11	1.06
1:M:6:VAL:HG12	1:M:8:PHE:CZ	1.91	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:16:TRP:HE1	1:Q:15:SER:CB	1.67	1.06
1:N:152:GLN:HB3	1:N:168:PRO:CG	1.86	1.06
1:Q:38:LEU:CD1	1:Q:39:PRO:CD	2.27	1.06
1:S:29:PHE:HB3	1:S:45:TRP:HZ2	1.17	1.06
1:J:104:PHE:CE2	1:J:138:PHE:HE1	1.71	1.06
1:A:12:ARG:HH12	1:A:16:TRP:N	1.53	1.05
1:C:184:THR:HB	1:C:191:LEU:HD23	1.34	1.05
1:M:41:GLU:CD	1:M:42:TRP:N	2.14	1.05
1:X:111:VAL:HG13	1:I:151:THR:CG2	1.85	1.05
1:M:6:VAL:CG1	1:M:8:PHE:CZ	2.38	1.05
1:B:133:TYR:HB3	1:E:140:ARG:CD	1.87	1.05
1:A:126:GLU:HG2	1:A:127:ARG:H	1.21	1.05
1:D:81:LEU:HD13	1:D:92:ALA:HB2	1.34	1.05
1:Q:75:ARG:HD2	1:Q:79:ARG:HD2	1.38	1.05
1:U:183:VAL:HG11	1:U:190:GLN:HE21	1.13	1.05
1:Q:37:ARG:HD2	1:Q:40:GLU:OE2	1.54	1.05
1:O:30:ASP:OD1	1:O:42:TRP:HB3	1.57	1.05
1:K:38:LEU:HB3	1:K:39:PRO:HD2	1.33	1.04
1:G:40:GLU:CG	1:W:46:LEU:HD11	1.87	1.04
1:T:19:PHE:HA	1:T:28:LEU:HD22	1.07	1.04
1:I:99:LEU:CD1	1:I:140:ARG:HD3	1.86	1.04
1:B:18:PRO:CG	1:B:77:LEU:HD23	1.87	1.04
1:F:159:PRO:HG3	1:E:186:GLU:HB2	1.12	1.04
1:X:133:TYR:HD1	1:X:134:ILE:HG13	1.17	1.04
1:K:41:GLU:HB3	1:O:44:GLN:HG3	1.40	1.04
1:O:51:TRP:HB2	1:O:52:PRO:HD2	1.38	1.04
1:C:33:PHE:HE1	1:G:46:LEU:HD21	1.17	1.04
1:I:42:TRP:N	1:I:44:GLN:HE22	1.56	1.04
1:D:159:PRO:HA	1:C:186:GLU:HG2	1.36	1.03
1:V:147:GLY:HA2	1:V:181:ILE:CG2	1.87	1.03
1:M:26:SER:HB2	1:M:45:TRP:CZ3	1.93	1.03
1:C:34:GLY:HA3	1:G:46:LEU:HG	1.40	1.03
1:L:181:ILE:H	1:L:182:PRO:HD2	1.22	1.02
1:B:18:PRO:HG3	1:B:77:LEU:HD21	1.39	1.02
1:A:10:LEU:HG	1:A:77:LEU:CD1	1.89	1.02
1:B:18:PRO:CG	1:B:77:LEU:CD2	2.37	1.02
1:T:52:PRO:HA	1:U:55:VAL:HG12	1.36	1.02
1:C:23:TYR:HB3	1:C:25:HIS:HD2	1.22	1.02
1:A:35:LEU:CB	1:Q:46:LEU:HD23	1.87	1.02
1:D:146:PRO:HG2	1:D:175:GLN:CG	1.88	1.02
1:F:156:SER:HB3	1:E:185:PHE:CZ	1.95	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:99:LEU:HD11	1:I:140:ARG:HD3	1.41	1.02
1:S:29:PHE:CB	1:S:45:TRP:CZ2	2.41	1.02
1:R:52:PRO:HG2	1:S:11:LEU:HD23	1.41	1.02
1:N:45:TRP:CZ2	1:S:52:PRO:HA	1.95	1.01
1:R:52:PRO:HB2	1:S:10:LEU:CD1	1.89	1.01
1:T:52:PRO:HA	1:U:55:VAL:CG1	1.90	1.01
1:Q:38:LEU:HG	1:Q:39:PRO:HD3	1.39	1.01
1:I:45:TRP:CZ3	1:I:46:LEU:CD1	2.43	1.01
1:A:45:TRP:CH2	1:Q:51:TRP:HD1	1.77	1.00
1:L:151:THR:HG21	1:M:154:SER:HB3	1.02	1.00
1:X:133:TYR:CD1	1:X:134:ILE:HG13	1.96	1.00
1:O:94:ARG:HG3	1:O:169:MET:HB2	1.41	1.00
1:D:99:LEU:HD12	1:D:163:LEU:HD23	1.43	1.00
1:H:1:MET:HE2	1:H:192:GLY:C	1.85	1.00
1:M:202:THR:HG21	1:M:205:LYS:HZ1	1.20	1.00
1:U:183:VAL:HG11	1:U:190:GLN:NE2	1.77	1.00
1:A:10:LEU:HG	1:A:77:LEU:HD13	1.41	0.99
1:D:159:PRO:HB3	1:C:186:GLU:HG2	1.42	0.99
1:N:163:LEU:CD1	1:N:164:THR:H	1.75	0.99
1:X:111:VAL:HG13	1:I:151:THR:HG23	1.40	0.99
1:B:126:GLU:CD	1:B:134:ILE:HD13	1.86	0.99
1:K:38:LEU:HB3	1:K:39:PRO:CD	1.93	0.99
1:T:178:GLU:O	1:T:179:ILE:CG1	2.10	0.99
1:C:184:THR:N	1:C:191:LEU:CD2	2.25	0.99
1:E:42:TRP:HB2	1:U:44:GLN:OE1	1.60	0.99
1:B:126:GLU:OE1	1:B:134:ILE:HD13	1.59	0.99
1:L:181:ILE:N	1:L:182:PRO:HD2	1.76	0.99
1:F:157:LEU:O	1:E:185:PHE:HD2	1.44	0.99
1:H:149:ASP:HB2	1:H:184:THR:HG22	1.45	0.99
1:T:19:PHE:HA	1:T:28:LEU:HD23	1.44	0.99
1:O:94:ARG:CB	1:O:169:MET:CG	2.28	0.98
1:V:49:SER:N	1:W:52:PRO:HG3	1.78	0.98
1:V:147:GLY:HA2	1:V:181:ILE:HG22	1.41	0.98
1:I:181:ILE:HG22	1:I:190:GLN:CD	1.88	0.98
1:A:45:TRP:CH2	1:Q:51:TRP:CD1	2.50	0.98
1:L:36:PRO:O	1:L:37:ARG:CG	2.11	0.98
1:R:45:TRP:HD1	1:R:49:SER:HG	1.12	0.98
1:D:11:LEU:CD1	1:D:171:LYS:NZ	2.26	0.98
1:T:19:PHE:CA	1:T:28:LEU:CD2	2.40	0.98
1:D:146:PRO:CG	1:D:175:GLN:HG3	1.93	0.98
1:B:133:TYR:HB3	1:E:140:ARG:NE	1.78	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:163:LEU:CD1	1:N:164:THR:N	2.26	0.97
1:N:45:TRP:CZ3	1:R:51:TRP:CD1	2.51	0.97
1:P:38:LEU:HD22	1:P:44:GLN:HE21	0.82	0.97
1:A:5:ARG:O	1:A:6:VAL:HB	1.64	0.97
1:D:146:PRO:CD	1:D:175:GLN:NE2	2.27	0.97
1:B:17:ASP:CB	1:B:18:PRO:HD2	1.94	0.97
1:T:17:ASP:N	1:T:20:ARG:HH21	1.63	0.97
1:V:44:GLN:O	1:V:45:TRP:HE3	1.46	0.97
1:U:184:THR:HG22	1:U:191:LEU:HD13	1.45	0.97
1:N:163:LEU:HD12	1:N:164:THR:CA	1.95	0.97
1:V:133:TYR:CD1	1:U:142:TYR:CE1	2.52	0.97
1:S:45:TRP:CE3	1:S:46:LEU:N	2.33	0.97
1:W:80:GLN:NE2	1:W:160:GLU:HG3	1.79	0.97
1:N:45:TRP:HD1	1:N:48:GLY:N	1.62	0.97
1:H:149:ASP:CB	1:H:184:THR:HG22	1.94	0.96
1:T:23:TYR:HB2	1:T:24:PRO:HD2	1.44	0.96
1:I:169:MET:SD	1:I:172:LEU:HD12	2.06	0.96
1:A:142:TYR:CD1	1:D:133:TYR:HE1	1.82	0.96
1:E:93:ASP:OD2	1:E:169:MET:HG3	1.66	0.96
1:E:172:LEU:HD22	1:E:204:ALA:HA	1.46	0.96
1:D:11:LEU:HD11	1:D:171:LYS:HZ3	1.13	0.96
1:A:142:TYR:HD1	1:D:133:TYR:HE1	1.11	0.95
1:D:11:LEU:HD21	1:D:201:GLU:OE2	1.65	0.95
1:D:168:PRO:HB3	1:D:188:ARG:NH2	1.82	0.95
1:T:20:ARG:HG2	1:T:25:HIS:ND1	1.81	0.95
1:H:11:LEU:HD11	1:H:171:LYS:HE3	1.46	0.95
1:G:45:TRP:O	1:G:46:LEU:HB2	1.66	0.94
1:P:190:GLN:OE1	1:Q:74:SER:HB3	1.67	0.94
1:M:172:LEU:CD2	1:M:204:ALA:CB	2.46	0.94
1:V:126:GLU:HG3	1:V:134:ILE:HG21	1.49	0.94
1:N:151:THR:CG2	1:O:154:SER:HB3	1.97	0.94
1:O:45:TRP:CB	1:O:50:SER:CB	2.29	0.94
1:A:15:SER:CB	1:A:16:TRP:CE3	2.49	0.94
1:F:12:ARG:CZ	1:F:20:ARG:HD3	1.98	0.94
1:S:97:VAL:HG11	1:S:142:TYR:HE2	1.33	0.94
1:R:151:THR:CG2	1:S:154:SER:HB3	1.98	0.94
1:C:33:PHE:CE1	1:G:46:LEU:CD2	2.51	0.94
1:A:35:LEU:HD12	1:A:35:LEU:O	1.68	0.94
1:A:50:SER:O	1:A:51:TRP:HB2	1.64	0.94
1:V:19:PHE:CA	1:V:28:LEU:HD12	1.97	0.94
1:A:33:PHE:HE1	1:A:35:LEU:HG	1.16	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:41:GLU:HB3	1:I:44:GLN:NE2	1.82	0.93
1:M:30:ASP:HB2	1:M:45:TRP:HZ2	1.33	0.93
1:A:15:SER:HB2	1:A:16:TRP:CZ3	2.03	0.93
1:A:33:PHE:CD1	1:A:35:LEU:HG	2.03	0.93
1:M:202:THR:HG21	1:M:205:LYS:HZ2	1.32	0.93
1:M:202:THR:CG2	1:M:205:LYS:NZ	2.31	0.93
1:N:45:TRP:HZ2	1:S:52:PRO:HA	1.29	0.93
1:B:17:ASP:HB2	1:B:18:PRO:HD2	1.50	0.93
1:A:1:MET:SD	1:A:9:SER:OG	2.25	0.93
1:A:12:ARG:HD3	1:X:12:ARG:NH2	1.83	0.93
1:V:44:GLN:HB2	1:V:45:TRP:HZ3	1.30	0.93
1:O:12:ARG:NH1	1:O:21:ASP:HB3	1.82	0.93
1:C:183:VAL:HG12	1:C:187:SER:CB	1.99	0.92
1:D:99:LEU:HD23	1:D:140:ARG:NH1	1.83	0.92
1:L:181:ILE:N	1:L:182:PRO:CD	2.23	0.92
1:O:80:GLN:OE1	1:O:160:GLU:HG2	1.69	0.92
1:U:191:LEU:O	1:U:191:LEU:HD12	1.70	0.92
1:D:159:PRO:HA	1:C:186:GLU:CG	1.98	0.92
1:U:40:GLU:O	1:U:41:GLU:HG2	1.70	0.92
1:N:152:GLN:HB3	1:N:168:PRO:HD2	0.94	0.92
1:T:23:TYR:CB	1:T:24:PRO:CD	2.43	0.92
1:X:133:TYR:CE1	1:X:134:ILE:CD1	2.52	0.92
1:I:45:TRP:CZ3	1:I:46:LEU:HD11	2.04	0.92
1:A:123:LYS:HA	1:A:136:ARG:O	1.69	0.92
1:F:159:PRO:CG	1:E:186:GLU:HB2	1.99	0.92
1:W:35:LEU:CD2	1:W:37:ARG:HH12	1.82	0.92
1:D:81:LEU:CD1	1:D:92:ALA:HB1	1.99	0.92
1:F:159:PRO:HG3	1:E:186:GLU:CB	1.99	0.92
1:C:184:THR:CB	1:C:191:LEU:CD2	2.43	0.92
1:V:44:GLN:C	1:V:45:TRP:HE3	1.78	0.92
1:B:133:TYR:CZ	1:E:142:TYR:CD1	2.58	0.92
1:D:146:PRO:CD	1:D:175:GLN:HE21	1.82	0.92
1:X:133:TYR:HE1	1:X:134:ILE:HD11	1.29	0.91
1:O:45:TRP:CE3	1:O:46:LEU:N	2.39	0.91
1:B:19:PHE:HA	1:B:28:LEU:CG	2.00	0.91
1:B:128:GLN:HB2	1:B:131:HIS:O	1.68	0.91
1:B:16:TRP:HE1	1:Q:15:SER:HB2	1.32	0.91
1:L:146:PRO:CB	1:L:175:GLN:N	2.33	0.91
1:U:183:VAL:CG1	1:U:190:GLN:HE21	1.83	0.91
1:L:182:PRO:O	1:L:183:VAL:CG1	2.18	0.91
1:U:184:THR:HG22	1:U:191:LEU:CD1	1.99	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:44:GLN:HG2	1:Q:44:GLN:HE21	1.33	0.91
1:O:94:ARG:CG	1:O:169:MET:HB2	1.99	0.91
1:R:45:TRP:CD1	1:R:49:SER:HG	1.89	0.91
1:L:151:THR:HG21	1:M:154:SER:CB	1.98	0.91
1:F:191:LEU:HD11	1:E:75:ARG:CZ	2.00	0.91
1:O:55:VAL:HG23	1:O:56:ARG:H	1.34	0.91
1:D:11:LEU:CD1	1:D:171:LYS:HZ3	1.82	0.90
1:P:49:SER:CA	1:Q:52:PRO:HG3	2.01	0.90
1:C:23:TYR:HB3	1:C:25:HIS:CD2	2.06	0.90
1:B:15:SER:HA	1:B:20:ARG:NH2	1.86	0.90
1:F:37:ARG:O	1:F:42:TRP:CD1	2.24	0.90
1:N:133:TYR:CD1	1:M:140:ARG:NH2	2.39	0.90
1:R:33:PHE:CG	1:S:7:PRO:HG2	2.06	0.90
1:G:184:THR:CG2	1:G:191:LEU:HD23	2.00	0.90
1:D:183:VAL:HG13	1:C:156:SER:HB3	1.53	0.90
1:C:33:PHE:HE1	1:G:46:LEU:CD2	1.84	0.90
1:M:41:GLU:OE2	1:M:42:TRP:HB2	1.72	0.90
1:X:34:GLY:C	1:X:35:LEU:HD12	1.96	0.90
1:W:80:GLN:HE22	1:W:160:GLU:HG3	1.34	0.90
1:D:44:GLN:O	1:D:45:TRP:CD1	2.25	0.90
1:F:156:SER:HB3	1:E:185:PHE:HZ	1.33	0.90
1:N:163:LEU:HD12	1:N:164:THR:H	1.10	0.90
1:C:33:PHE:CE1	1:G:46:LEU:HD21	2.05	0.89
1:D:81:LEU:CD1	1:D:92:ALA:CB	2.50	0.89
1:V:44:GLN:C	1:V:45:TRP:CE3	2.50	0.89
1:O:51:TRP:CB	1:O:52:PRO:HD2	2.01	0.89
1:A:45:TRP:HH2	1:Q:51:TRP:HD1	0.91	0.89
1:M:172:LEU:HD21	1:M:204:ALA:HA	1.53	0.89
1:O:30:ASP:O	1:O:33:PHE:CE2	2.25	0.89
1:A:35:LEU:HB3	1:Q:46:LEU:HD23	0.92	0.89
1:C:183:VAL:HG12	1:C:187:SER:HB2	1.53	0.89
1:O:21:ASP:OD2	1:O:73:TYR:CE1	2.25	0.89
1:M:95:TRP:HZ3	1:M:165:VAL:HG12	1.34	0.89
1:M:12:ARG:NH1	1:M:21:ASP:HB3	1.86	0.89
1:S:29:PHE:HB3	1:S:45:TRP:CZ2	2.06	0.89
1:S:97:VAL:HG11	1:S:142:TYR:CE2	2.08	0.89
1:I:181:ILE:HG22	1:I:190:GLN:HE22	1.38	0.89
1:O:51:TRP:HB2	1:O:52:PRO:CD	2.01	0.89
1:W:12:ARG:HH12	1:W:21:ASP:HB3	1.35	0.89
1:G:40:GLU:HG3	1:W:46:LEU:HD11	1.52	0.88
1:O:30:ASP:OD1	1:O:42:TRP:CB	2.21	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:29:PHE:CD2	1:S:45:TRP:HH2	1.92	0.88
1:L:149:ASP:OD2	1:L:184:THR:HB	1.72	0.88
1:O:30:ASP:OD1	1:O:33:PHE:HE2	1.56	0.88
1:B:10:LEU:O	1:B:15:SER:HB3	1.72	0.88
1:D:11:LEU:HD11	1:D:171:LYS:HZ2	1.05	0.88
1:C:81:LEU:CD1	1:C:83:SER:HA	2.03	0.88
1:X:111:VAL:CG1	1:I:151:THR:CG2	2.52	0.88
1:A:33:PHE:CD2	1:A:42:TRP:O	2.27	0.87
1:J:104:PHE:CE2	1:J:138:PHE:CD1	2.62	0.87
1:T:110:THR:HA	1:U:180:THR:HG21	1.53	0.87
1:A:133:TYR:CD1	1:D:141:LYS:O	2.27	0.87
1:L:181:ILE:H	1:L:182:PRO:HD3	1.38	0.87
1:L:149:ASP:OD1	1:L:152:GLN:CG	2.23	0.87
1:M:6:VAL:HG11	1:M:8:PHE:CZ	2.07	0.87
1:A:124:HIS:HB2	1:A:136:ARG:CG	2.04	0.87
1:J:43:SER:HA	1:R:45:TRP:HH2	1.39	0.87
1:I:181:ILE:CG2	1:I:190:GLN:OE1	2.23	0.87
1:V:49:SER:CA	1:W:52:PRO:HG3	2.05	0.86
1:R:33:PHE:CD2	1:S:7:PRO:HG2	2.09	0.86
1:T:133:TYR:HB3	1:S:140:ARG:HE	1.38	0.86
1:J:38:LEU:HB3	1:J:39:PRO:HD3	1.55	0.86
1:C:49:SER:HA	1:W:51:TRP:CE2	2.11	0.86
1:V:48:GLY:C	1:W:52:PRO:HG3	2.00	0.86
1:X:35:LEU:HB3	1:X:36:PRO:HD2	1.55	0.86
1:E:183:VAL:HG22	1:E:187:SER:HB2	1.58	0.86
1:V:49:SER:HA	1:W:52:PRO:HG3	1.57	0.86
1:A:12:ARG:HD2	1:A:18:PRO:HA	1.57	0.86
1:A:174:THR:HG22	1:A:192:GLY:N	1.90	0.86
1:D:45:TRP:CZ3	1:H:51:TRP:CD2	2.64	0.86
1:Q:37:ARG:CD	1:Q:40:GLU:CD	2.47	0.86
1:U:45:TRP:CZ3	1:U:46:LEU:HG	2.11	0.86
1:W:80:GLN:CD	1:W:160:GLU:HG3	2.01	0.86
1:K:25:HIS:CE1	1:S:37:ARG:NE	2.45	0.85
1:N:151:THR:HG23	1:O:154:SER:N	1.91	0.85
1:P:49:SER:HA	1:Q:52:PRO:CG	2.07	0.85
1:Q:37:ARG:CD	1:Q:40:GLU:OE2	2.24	0.85
1:D:146:PRO:HD2	1:D:175:GLN:HE21	1.06	0.85
1:M:172:LEU:CD2	1:M:204:ALA:HA	2.05	0.85
1:F:41:GLU:HG3	1:L:26:SER:HB2	1.57	0.85
1:F:20:ARG:CZ	1:U:15:SER:HA	2.05	0.85
1:T:17:ASP:N	1:T:18:PRO:HD2	1.92	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:33:PHE:HD1	1:O:34:GLY:N	1.74	0.85
1:V:44:GLN:O	1:V:45:TRP:CE3	2.29	0.85
1:O:41:GLU:CB	1:S:44:GLN:OE1	2.23	0.85
1:D:81:LEU:HD13	1:D:92:ALA:HB1	1.54	0.85
1:P:23:TYR:HB2	1:P:24:PRO:HD3	1.57	0.85
1:E:75:ARG:HD2	1:E:79:ARG:HD2	1.58	0.85
1:B:140:ARG:HH11	1:E:134:ILE:HG12	1.41	0.84
1:O:172:LEU:HD21	1:O:204:ALA:HA	1.59	0.84
1:S:45:TRP:CD1	1:S:51:TRP:CZ2	2.65	0.84
1:D:51:TRP:CE2	1:V:45:TRP:CD1	2.66	0.84
1:D:81:LEU:CD2	1:D:92:ALA:HA	2.08	0.84
1:H:149:ASP:CB	1:H:184:THR:CG2	2.56	0.84
1:O:43:SER:HB3	1:O:45:TRP:CD1	2.13	0.84
1:D:45:TRP:HH2	1:H:51:TRP:N	1.74	0.84
1:R:190:GLN:HB2	1:S:74:SER:HB2	1.60	0.84
1:A:10:LEU:HD11	1:A:77:LEU:HD21	1.58	0.83
1:A:51:TRP:HB2	1:A:52:PRO:HD3	1.59	0.83
1:O:42:TRP:NE1	1:O:44:GLN:NE2	2.26	0.83
1:A:142:TYR:CD1	1:D:133:TYR:CE1	2.65	0.83
1:S:10:LEU:O	1:S:10:LEU:CD1	2.23	0.83
1:O:40:GLU:HG3	1:S:26:SER:HB3	1.59	0.83
1:N:151:THR:HG21	1:O:154:SER:HB3	1.58	0.83
1:M:202:THR:CG2	1:M:205:LYS:HZ1	1.90	0.83
1:O:77:LEU:HD12	1:O:78:SER:N	1.93	0.83
1:S:45:TRP:HD1	1:S:51:TRP:HH2	1.17	0.83
1:A:10:LEU:HD21	1:A:77:LEU:HD22	1.59	0.83
1:M:30:ASP:HB2	1:M:45:TRP:CZ2	2.14	0.83
1:T:20:ARG:NH1	1:M:15:SER:HA	1.94	0.83
1:O:37:ARG:CB	1:O:40:GLU:OE1	2.27	0.83
1:D:51:TRP:CZ2	1:V:45:TRP:CD1	2.67	0.82
1:N:45:TRP:CD1	1:N:48:GLY:N	2.45	0.82
1:O:146:PRO:CG	1:O:205:LYS:HD2	2.09	0.82
1:D:31:GLN:O	1:D:73:TYR:HE2	1.61	0.82
1:D:99:LEU:CD2	1:D:140:ARG:NH1	2.42	0.82
1:C:184:THR:HB	1:C:191:LEU:HD21	1.59	0.82
1:O:29:PHE:CD2	1:O:45:TRP:HZ2	1.97	0.82
1:B:10:LEU:O	1:B:15:SER:CB	2.28	0.82
1:G:40:GLU:HG2	1:W:46:LEU:HD11	1.61	0.82
1:R:52:PRO:CB	1:S:10:LEU:HD13	2.10	0.82
1:G:184:THR:HG22	1:G:191:LEU:HD23	1.61	0.82
1:H:20:ARG:HH12	1:W:15:SER:CA	1.93	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:20:ARG:NH1	1:G:23:TYR:H	1.76	0.82
1:I:41:GLU:HB3	1:I:44:GLN:HE22	1.44	0.82
1:C:33:PHE:CD1	1:G:46:LEU:HD23	2.15	0.82
1:B:133:TYR:HB3	1:E:140:ARG:CG	2.09	0.82
1:H:20:ARG:NH1	1:W:15:SER:HA	1.95	0.82
1:R:52:PRO:HG2	1:S:11:LEU:CD2	2.08	0.82
1:O:30:ASP:O	1:O:33:PHE:CD2	2.33	0.82
1:B:99:LEU:CD1	1:B:140:ARG:HD3	2.10	0.81
1:T:19:PHE:HD1	1:T:28:LEU:CB	1.93	0.81
1:M:146:PRO:HG2	1:M:205:LYS:CD	2.08	0.81
1:O:33:PHE:CD1	1:O:34:GLY:N	2.47	0.81
1:B:16:TRP:HE1	1:Q:15:SER:HB3	1.44	0.81
1:P:184:THR:HA	1:Q:75:ARG:HH21	1.43	0.81
1:C:44:GLN:HB2	1:G:44:GLN:HG2	1.63	0.81
1:O:94:ARG:HB2	1:O:169:MET:HG3	1.57	0.81
1:B:133:TYR:CZ	1:E:142:TYR:HD1	1.98	0.81
1:A:10:LEU:CG	1:A:77:LEU:HD22	2.10	0.81
1:K:40:GLU:C	1:K:41:GLU:OE2	2.23	0.81
1:M:6:VAL:HG12	1:M:8:PHE:CE1	2.15	0.81
1:M:80:GLN:HG3	1:M:160:GLU:HG3	1.62	0.81
1:M:94:ARG:HB2	1:M:169:MET:HG2	1.62	0.81
1:S:45:TRP:HB2	1:S:50:SER:CB	2.11	0.81
1:D:131:HIS:CD2	1:D:133:TYR:OH	2.34	0.81
1:M:46:LEU:HD12	1:M:46:LEU:H	1.46	0.81
1:P:190:GLN:NE2	1:Q:55:VAL:HG13	1.95	0.81
1:A:149:ASP:HA	1:A:175:GLN:HE22	1.46	0.81
1:R:52:PRO:CG	1:S:11:LEU:HD23	2.10	0.80
1:U:40:GLU:C	1:U:41:GLU:HG2	2.06	0.80
1:A:126:GLU:HG2	1:A:127:ARG:N	1.94	0.80
1:D:81:LEU:HD22	1:D:92:ALA:HA	1.62	0.80
1:A:12:ARG:CD	1:X:12:ARG:NH2	2.44	0.80
1:I:181:ILE:CG2	1:I:190:GLN:CD	2.53	0.80
1:O:45:TRP:HE3	1:O:47:GLY:H	1.30	0.80
1:A:10:LEU:HD11	1:A:77:LEU:CD2	2.12	0.80
1:N:45:TRP:CH2	1:R:50:SER:N	2.50	0.80
1:K:177:ASN:HD21	1:K:200:ASP:HA	1.44	0.80
1:D:99:LEU:HD21	1:D:142:TYR:OH	1.81	0.80
1:M:42:TRP:CB	1:U:41:GLU:OE1	2.26	0.80
1:D:44:GLN:O	1:D:45:TRP:HD1	1.63	0.80
1:Q:38:LEU:CG	1:Q:39:PRO:CD	2.57	0.80
1:B:15:SER:O	1:B:20:ARG:CG	2.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:1:MET:CE	1:H:192:GLY:C	2.55	0.80
1:O:12:ARG:HH12	1:O:21:ASP:CB	1.92	0.79
1:F:179:ILE:O	1:F:181:ILE:HD12	1.83	0.79
1:U:40:GLU:O	1:U:41:GLU:CG	2.29	0.79
1:I:202:THR:HB	1:I:205:LYS:NZ	1.97	0.79
1:D:131:HIS:CD2	1:D:133:TYR:CZ	2.71	0.79
1:T:23:TYR:CB	1:T:24:PRO:HD3	2.11	0.79
1:V:11:LEU:HD13	1:W:56:ARG:HD2	1.64	0.79
1:I:169:MET:SD	1:I:172:LEU:CD1	2.70	0.79
1:T:19:PHE:CD1	1:T:28:LEU:HB3	2.17	0.79
1:B:18:PRO:CD	1:B:77:LEU:HD23	2.11	0.79
1:K:12:ARG:HG3	1:K:19:PHE:HD1	1.48	0.79
1:S:118:VAL:HG23	1:S:144:LEU:HD21	1.63	0.79
1:A:5:ARG:O	1:A:6:VAL:CB	2.25	0.78
1:A:51:TRP:CB	1:A:52:PRO:HD3	2.13	0.78
1:O:12:ARG:HG2	1:O:19:PHE:HA	1.65	0.78
1:B:26:SER:HB2	1:P:41:GLU:HG3	1.62	0.78
1:J:37:ARG:O	1:J:39:PRO:HD2	1.84	0.78
1:C:34:GLY:HA3	1:G:46:LEU:CG	2.13	0.78
1:S:29:PHE:HB2	1:S:45:TRP:HZ2	1.48	0.78
1:D:184:THR:HG22	1:D:191:LEU:HD13	1.66	0.78
1:L:175:GLN:N	1:L:181:ILE:CD1	2.46	0.78
1:A:44:GLN:OE1	1:I:44:GLN:CB	2.31	0.78
1:D:45:TRP:CH2	1:H:51:TRP:CG	2.70	0.78
1:O:33:PHE:CE2	1:O:42:TRP:CA	2.64	0.78
1:N:95:TRP:HE3	1:N:167:ALA:HB3	1.48	0.78
1:W:80:GLN:OE1	1:W:160:GLU:HG3	1.83	0.78
1:A:35:LEU:HB3	1:Q:46:LEU:HD21	1.59	0.78
1:L:151:THR:CG2	1:M:154:SER:CB	2.59	0.78
1:T:18:PRO:O	1:T:28:LEU:CD2	2.26	0.78
1:X:133:TYR:CD1	1:X:134:ILE:CG1	2.66	0.78
1:U:12:ARG:NH1	1:U:21:ASP:HB3	1.98	0.78
1:B:140:ARG:HH11	1:E:134:ILE:CG1	1.97	0.77
1:T:18:PRO:C	1:T:28:LEU:HD23	2.08	0.77
1:K:40:GLU:HB3	1:O:46:LEU:HD21	1.65	0.77
1:U:184:THR:CA	1:U:191:LEU:HD11	2.12	0.77
1:D:45:TRP:CH2	1:H:51:TRP:N	2.51	0.77
1:X:35:LEU:HB3	1:X:36:PRO:HD3	1.65	0.77
1:I:75:ARG:HD2	1:I:79:ARG:HD2	1.66	0.77
1:O:42:TRP:CD1	1:O:44:GLN:NE2	2.52	0.77
1:E:42:TRP:C	1:U:44:GLN:HE22	1.92	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:46:LEU:HD12	1:M:46:LEU:N	1.98	0.77
1:W:147:GLY:HA2	1:W:175:GLN:HA	1.65	0.77
1:B:133:TYR:CB	1:E:140:ARG:NE	2.47	0.77
1:A:51:TRP:CD1	1:Q:50:SER:O	2.37	0.77
1:V:44:GLN:HB3	1:V:45:TRP:CE3	2.19	0.77
1:V:133:TYR:HD1	1:U:142:TYR:HE1	1.26	0.77
1:B:19:PHE:O	1:B:28:LEU:HD23	1.84	0.77
1:A:12:ARG:CD	1:X:12:ARG:HH22	1.96	0.77
1:G:10:LEU:O	1:G:10:LEU:HD23	1.85	0.77
1:D:99:LEU:CD2	1:D:140:ARG:HD3	2.15	0.77
1:N:45:TRP:CD1	1:N:48:GLY:H	2.00	0.77
1:A:10:LEU:CD2	1:A:77:LEU:HD22	2.14	0.77
1:L:116:GLY:O	1:L:144:LEU:HG	1.85	0.77
1:C:184:THR:H	1:C:191:LEU:CD2	1.96	0.77
1:M:14:PRO:O	1:M:15:SER:OG	2.03	0.77
1:O:169:MET:HE3	1:O:172:LEU:HD12	1.67	0.77
1:K:41:GLU:CB	1:O:44:GLN:HG3	2.13	0.77
1:S:29:PHE:CD2	1:S:45:TRP:CH2	2.73	0.77
1:S:169:MET:HE3	1:S:172:LEU:HD11	1.64	0.77
1:F:20:ARG:NH2	1:U:15:SER:HA	2.00	0.77
1:D:45:TRP:CZ3	1:H:51:TRP:CG	2.73	0.76
1:B:16:TRP:NE1	1:Q:15:SER:HB2	2.00	0.76
1:Q:41:GLU:N	1:Q:41:GLU:OE1	2.18	0.76
1:M:16:TRP:O	1:M:17:ASP:O	2.03	0.76
1:D:49:SER:HA	1:C:52:PRO:HG3	1.65	0.76
1:U:40:GLU:O	1:U:41:GLU:CB	2.31	0.76
1:A:44:GLN:HG3	1:A:45:TRP:CE3	2.19	0.76
1:F:157:LEU:O	1:E:185:PHE:CD2	2.35	0.76
1:J:51:TRP:NE1	1:R:45:TRP:CZ3	2.54	0.76
1:R:151:THR:HG23	1:S:154:SER:CA	2.16	0.76
1:V:44:GLN:HB3	1:V:45:TRP:CZ3	2.19	0.76
1:M:38:LEU:HB2	1:M:39:PRO:HD3	1.68	0.76
1:U:169:MET:HB3	1:U:170:PRO:HD2	1.68	0.76
1:J:185:PHE:CE2	1:K:156:SER:OG	2.38	0.76
1:T:19:PHE:C	1:T:28:LEU:HD22	2.10	0.76
1:T:48:GLY:HA2	1:M:50:SER:O	1.85	0.76
1:K:38:LEU:CB	1:K:39:PRO:CD	2.60	0.76
1:O:33:PHE:CD2	1:O:42:TRP:HA	2.21	0.76
1:S:29:PHE:HB2	1:S:45:TRP:CZ2	2.21	0.76
1:T:17:ASP:N	1:T:18:PRO:CD	2.47	0.76
1:T:23:TYR:HB2	1:T:24:PRO:HD3	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:37:ARG:HB2	1:W:40:GLU:CG	2.13	0.76
1:N:151:THR:HG23	1:O:154:SER:HB3	1.68	0.76
1:B:133:TYR:CE2	1:E:142:TYR:HE1	2.03	0.76
1:T:133:TYR:HB3	1:S:140:ARG:NE	2.01	0.76
1:X:133:TYR:CD1	1:X:134:ILE:CD1	2.68	0.75
1:B:133:TYR:CE1	1:E:142:TYR:CD1	2.75	0.75
1:X:37:ARG:O	1:X:42:TRP:CD1	2.39	0.75
1:S:175:GLN:CG	1:S:191:LEU:HD12	2.13	0.75
1:C:77:LEU:HD12	1:C:78:SER:N	2.01	0.75
1:M:172:LEU:CD2	1:M:204:ALA:CA	2.64	0.75
1:O:51:TRP:CD1	1:O:52:PRO:HD2	2.21	0.75
1:B:133:TYR:CE2	1:E:142:TYR:CE1	2.74	0.75
1:M:46:LEU:HB3	1:U:33:PHE:O	1.86	0.75
1:M:81:LEU:HA	1:M:162:THR:HG21	1.69	0.75
1:O:30:ASP:OD1	1:O:33:PHE:CE2	2.40	0.75
1:A:10:LEU:CD1	1:A:77:LEU:HD21	2.17	0.74
1:N:151:THR:HG23	1:O:154:SER:CA	2.16	0.74
1:S:29:PHE:CG	1:S:45:TRP:CZ2	2.74	0.74
1:O:45:TRP:HB2	1:O:50:SER:OG	1.87	0.74
1:A:126:GLU:CG	1:A:127:ARG:H	1.97	0.74
1:H:40:GLU:HB2	1:G:8:PHE:CE2	2.21	0.74
1:I:42:TRP:H	1:I:44:GLN:HE22	0.77	0.74
1:D:159:PRO:HB3	1:C:186:GLU:CG	2.16	0.74
1:C:183:VAL:HG12	1:C:187:SER:HB3	1.69	0.74
1:M:171:LYS:HD2	1:M:192:GLY:O	1.86	0.74
1:V:147:GLY:CA	1:V:181:ILE:CG2	2.66	0.74
1:N:45:TRP:CZ3	1:R:51:TRP:NE1	2.55	0.74
1:J:37:ARG:HG2	1:J:40:GLU:CD	2.12	0.74
1:A:44:GLN:HG3	1:A:45:TRP:CD2	2.23	0.74
1:K:44:GLN:CD	1:S:41:GLU:HB3	2.13	0.74
1:U:194:PRO:O	1:U:195:GLU:CD	2.30	0.74
1:B:133:TYR:HB3	1:E:140:ARG:HG3	1.70	0.73
1:A:50:SER:O	1:A:51:TRP:CB	2.32	0.73
1:T:151:THR:N	1:U:152:GLN:O	2.21	0.73
1:O:45:TRP:CB	1:O:50:SER:OG	2.37	0.73
1:S:45:TRP:CE3	1:S:46:LEU:CA	2.71	0.73
1:S:172:LEU:HD22	1:S:204:ALA:HA	1.69	0.73
1:G:19:PHE:CZ	1:G:55:VAL:HG13	2.24	0.73
1:T:8:PHE:HE1	1:U:56:ARG:HH12	1.34	0.73
1:Q:38:LEU:HG	1:Q:39:PRO:CD	2.16	0.73
1:J:77:LEU:HD12	1:J:78:SER:N	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:107:ASP:O	1:O:181:ILE:CD1	2.35	0.73
1:M:16:TRP:HD1	1:M:20:ARG:HD2	1.54	0.73
1:M:30:ASP:CB	1:M:45:TRP:HZ2	2.01	0.73
1:F:157:LEU:N	1:E:185:PHE:HE2	1.86	0.73
1:F:191:LEU:CD1	1:E:75:ARG:NH2	2.52	0.73
1:J:38:LEU:HB3	1:J:39:PRO:CD	2.14	0.72
1:T:20:ARG:HG2	1:T:25:HIS:CE1	2.23	0.72
1:X:44:GLN:O	1:X:49:SER:HB3	1.88	0.72
1:K:10:LEU:CD1	1:K:77:LEU:HD13	2.19	0.72
1:M:16:TRP:CD1	1:M:20:ARG:HD2	2.23	0.72
1:M:41:GLU:CG	1:M:42:TRP:H	2.01	0.72
1:O:94:ARG:N	1:O:168:PRO:HA	2.04	0.72
1:D:11:LEU:HD23	1:C:56:ARG:HG2	1.70	0.72
1:T:49:SER:HA	1:U:52:PRO:HG2	1.70	0.72
1:U:196:ALA:O	1:U:197:ALA:CB	2.36	0.72
1:D:169:MET:HB3	1:D:170:PRO:HD2	1.69	0.72
1:T:25:HIS:C	1:T:27:ARG:H	1.97	0.72
1:G:37:ARG:HB2	1:G:40:GLU:HB2	1.70	0.72
1:L:183:VAL:HG23	1:L:184:THR:N	2.04	0.72
1:C:51:TRP:HB2	1:C:52:PRO:HD2	1.70	0.72
1:T:25:HIS:O	1:T:27:ARG:N	2.22	0.72
1:C:33:PHE:CD1	1:G:46:LEU:CD2	2.72	0.72
1:M:43:SER:O	1:M:44:GLN:HB2	1.87	0.72
1:U:47:GLY:O	1:U:49:SER:N	2.22	0.72
1:D:12:ARG:NH1	1:D:20:ARG:HD3	2.05	0.72
1:B:54:TYR:CD2	1:A:7:PRO:HG3	2.25	0.72
1:N:49:SER:HA	1:O:52:PRO:HG3	1.69	0.72
1:V:126:GLU:CG	1:V:134:ILE:HG21	2.20	0.72
1:I:202:THR:HB	1:I:205:LYS:HZ1	1.54	0.72
1:V:8:PHE:HE2	1:W:34:GLY:HA2	1.53	0.71
1:O:45:TRP:CE3	1:O:46:LEU:CA	2.72	0.71
1:F:108:GLU:HB2	1:E:180:THR:CG2	2.15	0.71
1:U:16:TRP:HB2	1:U:20:ARG:HD2	1.73	0.71
1:H:149:ASP:HB2	1:H:184:THR:CG2	2.19	0.71
1:F:12:ARG:NH2	1:F:20:ARG:HD3	2.05	0.71
1:F:128:GLN:OE1	1:F:133:TYR:CE1	2.44	0.71
1:R:5:ARG:HE	1:S:36:PRO:HG3	1.55	0.71
1:K:25:HIS:CE1	1:S:37:ARG:HE	2.06	0.71
1:U:51:TRP:HB2	1:U:52:PRO:CD	2.21	0.71
1:X:35:LEU:CB	1:X:36:PRO:CD	2.63	0.71
1:S:45:TRP:HB3	1:S:51:TRP:CZ3	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:LEU:HG	1:A:77:LEU:CD2	2.21	0.71
1:D:99:LEU:CD2	1:D:140:ARG:CZ	2.69	0.71
1:L:37:ARG:O	1:L:42:TRP:CD1	2.44	0.71
1:L:149:ASP:CG	1:L:152:GLN:HG2	2.14	0.71
1:I:45:TRP:CE3	1:I:46:LEU:HD13	2.25	0.71
1:A:12:ARG:HB3	1:A:19:PHE:HA	1.71	0.71
1:H:3:GLU:O	1:H:4:ARG:CB	2.39	0.71
1:O:29:PHE:CD2	1:O:45:TRP:CZ2	2.79	0.71
1:A:12:ARG:NE	1:A:17:ASP:O	2.23	0.71
1:D:110:THR:OG1	1:C:180:THR:HG23	1.91	0.71
1:V:147:GLY:CA	1:V:181:ILE:HG21	2.20	0.71
1:B:16:TRP:NE1	1:Q:15:SER:CB	2.49	0.71
1:B:99:LEU:HD12	1:B:140:ARG:HD3	1.72	0.71
1:F:184:THR:HA	1:E:75:ARG:HH21	1.54	0.71
1:O:29:PHE:CG	1:O:45:TRP:HZ2	2.09	0.71
1:J:104:PHE:CD2	1:J:138:PHE:HE1	1.91	0.70
1:C:81:LEU:CD1	1:C:83:SER:CA	2.67	0.70
1:H:1:MET:HG2	1:H:7:PRO:CD	2.17	0.70
1:M:146:PRO:CG	1:M:205:LYS:HD2	2.15	0.70
1:A:33:PHE:CZ	1:A:35:LEU:HG	2.18	0.70
1:D:99:LEU:HD22	1:D:140:ARG:HD3	1.73	0.70
1:R:33:PHE:CZ	1:S:7:PRO:HB2	2.26	0.70
1:B:18:PRO:CG	1:B:77:LEU:HD21	2.12	0.70
1:A:142:TYR:HD1	1:D:133:TYR:CE1	2.02	0.70
1:D:159:PRO:CB	1:C:186:GLU:CG	2.63	0.70
1:N:45:TRP:HZ2	1:S:52:PRO:CA	2.04	0.70
1:S:99:LEU:HD11	1:S:140:ARG:HD3	1.72	0.70
1:R:33:PHE:CD1	1:S:7:PRO:HG2	2.26	0.70
1:V:44:GLN:O	1:V:49:SER:HB3	1.90	0.70
1:C:81:LEU:CD1	1:C:83:SER:H	1.90	0.70
1:R:192:GLY:HA3	1:R:201:GLU:HA	1.74	0.70
1:V:151:THR:CG2	1:W:154:SER:HB3	2.21	0.70
1:I:49:SER:O	1:Q:51:TRP:CE2	2.45	0.70
1:M:26:SER:HB3	1:U:40:GLU:CD	2.16	0.70
1:D:129:ASP:OD1	1:D:130:GLU:N	2.23	0.70
1:N:45:TRP:O	1:N:46:LEU:HB2	1.90	0.70
1:I:120:ILE:HG21	1:I:163:LEU:HD21	1.71	0.70
1:W:12:ARG:NH1	1:W:21:ASP:HB3	2.05	0.70
1:J:139:THR:O	1:I:135:SER:HB2	1.92	0.70
1:G:40:GLU:HG2	1:W:46:LEU:CD1	2.22	0.70
1:O:33:PHE:CZ	1:O:42:TRP:HA	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:5:ARG:NH1	1:P:175:GLN:OE1	2.25	0.69
1:K:45:TRP:CZ3	1:S:41:GLU:OE1	2.44	0.69
1:Q:37:ARG:CB	1:Q:40:GLU:CG	2.41	0.69
1:S:175:GLN:CG	1:S:191:LEU:HD11	2.17	0.69
1:H:3:GLU:O	1:H:4:ARG:HB2	1.92	0.69
1:V:1:MET:H2	1:W:31:GLN:NE2	1.88	0.69
1:M:81:LEU:HD23	1:M:162:THR:HG21	1.74	0.69
1:A:10:LEU:CG	1:A:77:LEU:CD2	2.71	0.69
1:V:133:TYR:CE1	1:U:142:TYR:HE1	2.08	0.69
1:E:176:SER:HB2	1:E:181:ILE:HG13	1.72	0.69
1:A:142:TYR:CE1	1:D:133:TYR:CE1	2.81	0.69
1:D:11:LEU:CD2	1:D:201:GLU:OE2	2.39	0.69
1:F:37:ARG:HG3	1:F:37:ARG:HH11	1.56	0.69
1:B:19:PHE:N	1:B:28:LEU:HG	2.08	0.69
1:A:44:GLN:OE1	1:I:44:GLN:HB2	1.93	0.69
1:P:38:LEU:HD11	1:X:39:PRO:HB3	1.74	0.69
1:T:20:ARG:HH12	1:M:15:SER:C	2.01	0.69
1:X:159:PRO:HG3	1:I:186:GLU:HB2	1.74	0.69
1:D:45:TRP:CH2	1:H:51:TRP:CD1	2.80	0.69
1:V:8:PHE:CE1	1:W:56:ARG:NH2	2.61	0.69
1:E:12:ARG:HH12	1:E:21:ASP:HB3	1.57	0.69
1:D:81:LEU:HD11	1:D:92:ALA:HB1	1.73	0.69
1:D:150:PRO:HD2	1:C:154:SER:HB2	1.74	0.69
1:T:49:SER:HA	1:U:52:PRO:CG	2.23	0.69
1:V:134:ILE:HA	1:U:140:ARG:NH1	2.07	0.69
1:S:45:TRP:HB2	1:S:50:SER:HB2	1.73	0.69
1:A:131:HIS:HB3	1:A:134:ILE:HD12	1.74	0.69
1:H:1:MET:CG	1:H:7:PRO:HD3	2.14	0.69
1:V:147:GLY:HA2	1:V:181:ILE:HG21	1.70	0.69
1:I:99:LEU:HD12	1:I:140:ARG:HD3	1.73	0.69
1:O:94:ARG:N	1:O:167:ALA:O	2.26	0.69
1:Q:17:ASP:HB3	1:Q:47:GLY:HA3	1.75	0.69
1:Q:35:LEU:CD2	1:Q:37:ARG:HG3	2.22	0.69
1:W:51:TRP:HB2	1:W:52:PRO:HD2	1.74	0.69
1:W:171:LYS:NZ	1:W:188:ARG:NH1	2.41	0.69
1:D:99:LEU:CD2	1:D:142:TYR:OH	2.41	0.69
1:N:146:PRO:HB3	1:N:181:ILE:CD1	2.23	0.69
1:V:44:GLN:O	1:V:45:TRP:HB2	1.92	0.69
1:S:175:GLN:C	1:S:191:LEU:HD11	2.18	0.69
1:A:41:GLU:HB3	1:Q:44:GLN:HA	1.75	0.68
1:A:12:ARG:HH12	1:A:16:TRP:H	0.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:157:LEU:HD22	1:E:182:PRO:HB3	1.74	0.68
1:M:125:GLU:HG2	1:M:126:GLU:H	1.59	0.68
1:O:45:TRP:CG	1:O:46:LEU:H	2.06	0.68
1:D:184:THR:HG22	1:D:191:LEU:CD1	2.22	0.68
1:J:185:PHE:CE2	1:K:156:SER:CB	2.76	0.68
1:C:183:VAL:CG1	1:C:187:SER:CB	2.70	0.68
1:G:45:TRP:O	1:G:46:LEU:CB	2.40	0.68
1:T:126:GLU:CD	1:T:134:ILE:HD12	2.18	0.68
1:M:45:TRP:CZ3	1:U:41:GLU:HG2	2.28	0.68
1:N:163:LEU:CG	1:N:164:THR:H	2.06	0.68
1:A:44:GLN:OE1	1:I:44:GLN:HB3	1.92	0.68
1:D:23:TYR:HB2	1:D:24:PRO:HD3	1.74	0.68
1:D:150:PRO:HB2	1:C:153:VAL:O	1.94	0.68
1:C:81:LEU:HD12	1:C:83:SER:CA	2.24	0.68
1:Q:46:LEU:H	1:Q:50:SER:HB2	1.58	0.68
1:U:29:PHE:CD1	1:U:45:TRP:CZ3	2.82	0.68
1:J:23:TYR:HB2	1:J:24:PRO:HD3	1.75	0.68
1:N:23:TYR:HB2	1:N:24:PRO:HD3	1.75	0.68
1:U:12:ARG:HG3	1:U:19:PHE:CD1	2.29	0.68
1:A:18:PRO:HG3	1:X:47:GLY:HA3	1.74	0.68
1:N:192:GLY:HA3	1:N:201:GLU:HA	1.76	0.68
1:S:37:ARG:HB2	1:S:40:GLU:HG2	1.74	0.68
1:H:1:MET:SD	1:H:192:GLY:C	2.77	0.68
1:M:41:GLU:OE1	1:M:42:TRP:N	2.23	0.68
1:A:136:ARG:HA	1:D:138:PHE:HA	1.75	0.67
1:A:184:THR:HA	1:A:191:LEU:HD11	1.75	0.67
1:G:184:THR:HG23	1:G:191:LEU:HD23	1.75	0.67
1:K:12:ARG:HG3	1:K:19:PHE:CD1	2.29	0.67
1:F:5:ARG:HD3	1:F:205:LYS:O	1.95	0.67
1:N:152:GLN:CG	1:N:168:PRO:HG2	2.25	0.67
1:P:146:PRO:HB3	1:P:181:ILE:HD11	1.76	0.67
1:X:111:VAL:CG1	1:I:151:THR:HG23	2.18	0.67
1:B:23:TYR:HB2	1:B:24:PRO:HD3	1.76	0.67
1:A:45:TRP:HB2	1:A:50:SER:CA	2.24	0.67
1:C:184:THR:N	1:C:191:LEU:HD22	2.07	0.67
1:K:10:LEU:CD1	1:K:77:LEU:CD1	2.72	0.67
1:O:45:TRP:O	1:O:46:LEU:HB2	1.95	0.67
1:A:75:ARG:O	1:A:79:ARG:HB3	1.95	0.67
1:P:50:SER:H	1:Q:52:PRO:CG	2.07	0.67
1:C:10:LEU:CD2	1:C:77:LEU:HD22	2.24	0.67
1:S:23:TYR:O	1:S:25:HIS:N	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:20:ARG:HG2	1:D:25:HIS:ND1	2.10	0.67
1:N:45:TRP:CZ3	1:R:49:SER:HB2	2.29	0.67
1:V:19:PHE:HA	1:V:28:LEU:CD1	2.06	0.67
1:O:94:ARG:CG	1:O:169:MET:CB	2.70	0.67
1:S:29:PHE:CG	1:S:45:TRP:CH2	2.82	0.67
1:B:157:LEU:HB3	1:A:183:VAL:HG22	1.76	0.67
1:F:5:ARG:CZ	1:F:205:LYS:O	2.43	0.67
1:C:46:LEU:HD13	1:W:40:GLU:OE1	1.94	0.67
1:J:111:VAL:CG1	1:K:151:THR:HG21	2.25	0.67
1:C:33:PHE:HD1	1:G:46:LEU:HD23	1.58	0.67
1:M:172:LEU:HD22	1:M:204:ALA:CA	2.25	0.67
1:U:40:GLU:O	1:U:41:GLU:HB2	1.94	0.67
1:D:12:ARG:CZ	1:D:20:ARG:HD3	2.25	0.67
1:D:35:LEU:HB3	1:D:36:PRO:HD2	1.77	0.67
1:L:183:VAL:HG23	1:L:184:THR:H	1.60	0.67
1:R:151:THR:CG2	1:S:154:SER:CB	2.72	0.67
1:O:51:TRP:CH2	1:S:49:SER:HB3	2.29	0.67
1:W:75:ARG:HD3	1:W:79:ARG:HB2	1.77	0.67
1:A:51:TRP:CB	1:A:52:PRO:CD	2.73	0.66
1:F:191:LEU:HD11	1:E:75:ARG:NH2	2.10	0.66
1:V:23:TYR:HB2	1:V:24:PRO:HD3	1.76	0.66
1:O:51:TRP:CG	1:O:52:PRO:HD2	2.30	0.66
1:A:10:LEU:CD1	1:A:77:LEU:CD2	2.72	0.66
1:A:35:LEU:HD22	1:A:40:GLU:HB3	1.77	0.66
1:A:51:TRP:HB2	1:A:52:PRO:CD	2.25	0.66
1:N:151:THR:HG23	1:O:154:SER:CB	2.23	0.66
1:N:152:GLN:HB3	1:N:168:PRO:HG2	1.74	0.66
1:P:175:GLN:N	1:P:181:ILE:HD13	2.09	0.66
1:V:132:GLY:O	1:V:134:ILE:N	2.28	0.66
1:B:140:ARG:NH1	1:E:134:ILE:CG1	2.58	0.66
1:E:187:SER:C	1:E:189:ALA:H	2.02	0.66
1:M:26:SER:CB	1:M:45:TRP:CZ3	2.76	0.66
1:Q:3:GLU:O	1:Q:4:ARG:HB2	1.93	0.66
1:F:39:PRO:HD3	1:L:38:LEU:HD11	1.76	0.66
1:O:45:TRP:HB2	1:O:50:SER:HB2	0.67	0.66
1:L:118:VAL:HG23	1:L:144:LEU:HD23	1.78	0.66
1:O:43:SER:HB3	1:O:45:TRP:HD1	1.57	0.66
1:D:45:TRP:CE2	1:H:49:SER:HB3	2.31	0.66
1:R:151:THR:HG21	1:S:154:SER:CB	2.16	0.66
1:U:41:GLU:C	1:U:42:TRP:CD1	2.74	0.66
1:D:151:THR:HG21	1:C:166:GLU:HG3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:104:PHE:CZ	1:J:138:PHE:CD1	2.84	0.66
1:R:23:TYR:HB2	1:R:24:PRO:HD3	1.77	0.66
1:N:152:GLN:HE21	1:N:168:PRO:CG	2.09	0.66
1:E:176:SER:HB2	1:E:181:ILE:CG1	2.26	0.66
1:S:45:TRP:HE3	1:S:47:GLY:H	1.41	0.66
1:H:20:ARG:HH22	1:W:15:SER:HB2	1.60	0.66
1:B:185:PHE:O	1:A:94:ARG:NH1	2.29	0.66
1:N:11:LEU:HD22	1:O:56:ARG:HB2	1.77	0.66
1:P:186:GLU:OE2	1:P:186:GLU:HA	1.96	0.66
1:O:94:ARG:HB2	1:O:169:MET:HG2	0.68	0.66
1:Q:125:GLU:CD	1:Q:135:SER:OG	2.39	0.66
1:A:45:TRP:CE3	1:A:50:SER:HA	2.31	0.65
1:A:49:SER:O	1:A:51:TRP:CE3	2.49	0.65
1:P:48:GLY:O	1:Q:52:PRO:HD3	1.95	0.65
1:V:147:GLY:N	1:V:181:ILE:HG21	2.12	0.65
1:C:183:VAL:CG1	1:C:187:SER:HB2	2.25	0.65
1:S:45:TRP:CE3	1:S:46:LEU:HA	2.30	0.65
1:C:81:LEU:CD1	1:C:83:SER:N	2.51	0.65
1:H:149:ASP:HB3	1:H:184:THR:CG2	2.26	0.65
1:G:169:MET:HB3	1:G:172:LEU:HD12	1.77	0.65
1:I:181:ILE:HG21	1:I:190:GLN:OE1	1.95	0.65
1:K:40:GLU:HB3	1:O:46:LEU:CD2	2.25	0.65
1:I:190:GLN:HG3	1:I:191:LEU:HD12	1.78	0.65
1:A:44:GLN:HG2	1:A:45:TRP:CZ3	2.31	0.65
1:A:124:HIS:HB3	1:A:134:ILE:O	1.97	0.65
1:A:191:LEU:HD12	1:A:191:LEU:O	1.97	0.65
1:C:10:LEU:HD21	1:C:77:LEU:HD22	1.78	0.65
1:A:142:TYR:CE1	1:D:133:TYR:CD1	2.85	0.65
1:D:170:PRO:O	1:D:171:LYS:HB3	1.95	0.65
1:F:156:SER:CB	1:E:185:PHE:HZ	2.10	0.65
1:A:124:HIS:CB	1:A:136:ARG:HG2	2.19	0.65
1:A:134:ILE:HG12	1:D:140:ARG:HD2	1.79	0.65
1:S:17:ASP:HB3	1:S:47:GLY:HA3	1.79	0.65
1:A:16:TRP:CD1	1:A:17:ASP:OD1	2.49	0.65
1:V:151:THR:HB	1:W:154:SER:HB3	1.77	0.65
1:X:111:VAL:CG1	1:I:151:THR:HG21	2.26	0.65
1:E:33:PHE:O	1:U:47:GLY:CA	2.44	0.65
1:B:185:PHE:O	1:B:186:GLU:CB	2.44	0.65
1:F:181:ILE:O	1:F:183:VAL:HG23	1.96	0.64
1:E:172:LEU:CD2	1:E:204:ALA:HA	2.24	0.64
1:E:33:PHE:O	1:U:47:GLY:HA2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:33:PHE:CD2	1:O:42:TRP:CA	2.79	0.64
1:S:99:LEU:CD1	1:S:140:ARG:HD3	2.28	0.64
1:W:29:PHE:HB2	1:W:45:TRP:CZ2	2.31	0.64
1:R:154:SER:HB3	1:S:152:GLN:HE21	1.62	0.64
1:V:1:MET:N	1:W:31:GLN:HE22	1.94	0.64
1:O:45:TRP:CE3	1:O:46:LEU:HA	2.33	0.64
1:X:111:VAL:HG11	1:I:151:THR:HG21	1.80	0.64
1:E:46:LEU:HD22	1:M:40:GLU:HB2	1.80	0.64
1:M:125:GLU:O	1:M:126:GLU:HB2	1.97	0.64
1:B:19:PHE:O	1:B:28:LEU:CD2	2.46	0.64
1:A:51:TRP:HH2	1:I:51:TRP:HA	1.62	0.64
1:T:19:PHE:HD1	1:T:28:LEU:HB2	1.63	0.64
1:M:190:GLN:HG3	1:M:191:LEU:HD12	1.78	0.64
1:O:44:GLN:NE2	1:S:44:GLN:OE1	2.31	0.64
1:W:47:GLY:HA2	1:W:50:SER:OG	1.98	0.64
1:A:26:SER:HB3	1:I:41:GLU:OE1	1.97	0.64
1:A:52:PRO:O	1:A:54:TYR:CD2	2.51	0.64
1:D:45:TRP:NE1	1:H:49:SER:HB3	2.13	0.64
1:F:185:PHE:HE2	1:E:79:ARG:HE	1.43	0.64
1:N:152:GLN:HG3	1:N:168:PRO:HG2	1.79	0.64
1:N:157:LEU:HD21	1:O:182:PRO:O	1.97	0.64
1:P:140:ARG:NE	1:O:134:ILE:HD12	2.12	0.64
1:R:33:PHE:CE2	1:S:7:PRO:HG2	2.32	0.64
1:T:19:PHE:HD1	1:T:28:LEU:HB3	1.53	0.64
1:F:23:TYR:HB2	1:F:24:PRO:HD3	1.78	0.64
1:U:195:GLU:O	1:U:202:THR:N	2.30	0.64
1:B:15:SER:HA	1:B:20:ARG:CZ	2.28	0.64
1:B:133:TYR:CZ	1:E:142:TYR:CE1	2.86	0.64
1:D:11:LEU:CD1	1:D:171:LYS:HZ2	1.96	0.64
1:J:38:LEU:CB	1:J:39:PRO:CD	2.76	0.64
1:X:71:PRO:O	1:X:75:ARG:HG3	1.97	0.63
1:O:45:TRP:CD2	1:O:46:LEU:N	2.56	0.63
1:S:149:ASP:OD1	1:S:150:PRO:HD2	1.98	0.63
1:A:15:SER:CB	1:A:16:TRP:CZ3	2.78	0.63
1:D:45:TRP:HH2	1:H:50:SER:C	2.05	0.63
1:C:38:LEU:HB3	1:C:39:PRO:HD3	1.80	0.63
1:M:202:THR:CG2	1:M:205:LYS:HZ2	2.05	0.63
1:U:26:SER:O	1:U:45:TRP:CZ2	2.51	0.63
1:E:181:ILE:HG21	1:E:191:LEU:HG	1.81	0.63
1:O:94:ARG:HG3	1:O:169:MET:CB	2.24	0.63
1:A:44:GLN:CG	1:A:45:TRP:CE3	2.82	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:45:TRP:CH2	1:Q:41:GLU:OE2	2.52	0.63
1:Q:45:TRP:O	1:Q:46:LEU:HB2	1.96	0.63
1:A:45:TRP:HB2	1:A:50:SER:HA	1.80	0.63
1:H:183:VAL:HG13	1:G:156:SER:HB3	1.79	0.63
1:N:133:TYR:HD1	1:M:140:ARG:NH2	1.93	0.63
1:A:35:LEU:HD21	1:A:41:GLU:O	1.99	0.63
1:D:131:HIS:HD2	1:D:133:TYR:OH	1.82	0.63
1:F:156:SER:HB3	1:E:185:PHE:CE2	2.33	0.63
1:J:38:LEU:CB	1:J:39:PRO:HD3	2.28	0.63
1:O:55:VAL:HG23	1:O:56:ARG:N	2.12	0.63
1:U:16:TRP:CD1	1:U:20:ARG:HD2	2.33	0.63
1:I:120:ILE:HG21	1:I:163:LEU:CD2	2.28	0.63
1:K:146:PRO:HG2	1:K:205:LYS:HE3	1.80	0.63
1:D:99:LEU:HD23	1:D:140:ARG:CZ	2.27	0.63
1:A:137:CYS:O	1:D:137:CYS:HB3	1.99	0.63
1:A:147:GLY:HA2	1:A:175:GLN:HB2	1.79	0.63
1:A:171:LYS:O	1:A:172:LEU:HB2	1.98	0.63
1:D:184:THR:CG2	1:D:191:LEU:HD13	2.29	0.63
1:W:171:LYS:HZ1	1:W:188:ARG:NH1	1.96	0.63
1:I:26:SER:HB2	1:I:45:TRP:CH2	2.33	0.62
1:D:81:LEU:HD21	1:D:92:ALA:HA	1.81	0.62
1:D:26:SER:HB3	1:H:41:GLU:HG2	1.81	0.62
1:T:19:PHE:CD1	1:T:28:LEU:CB	2.76	0.62
1:F:12:ARG:NE	1:F:20:ARG:HH11	1.97	0.62
1:L:182:PRO:C	1:L:183:VAL:HG13	2.20	0.62
1:P:108:GLU:OE1	1:Q:180:THR:CG2	2.48	0.62
1:E:39:PRO:O	1:E:40:GLU:HG3	1.98	0.62
1:O:33:PHE:CE2	1:O:42:TRP:HB3	2.35	0.62
1:O:37:ARG:HB2	1:O:40:GLU:CD	2.22	0.62
1:A:43:SER:O	1:A:44:GLN:HB3	2.00	0.62
1:F:157:LEU:CD2	1:E:182:PRO:HB3	2.30	0.62
1:H:1:MET:CE	1:H:192:GLY:O	2.48	0.62
1:P:50:SER:N	1:Q:52:PRO:HG3	2.14	0.62
1:X:23:TYR:HB2	1:X:24:PRO:HD3	1.80	0.62
1:E:12:ARG:NH1	1:E:21:ASP:HB3	2.14	0.62
1:I:45:TRP:HE3	1:I:46:LEU:CD1	2.10	0.62
1:Q:38:LEU:CD1	1:Q:39:PRO:N	2.50	0.62
1:Q:45:TRP:C	1:Q:45:TRP:HE3	2.07	0.62
1:U:192:GLY:N	1:U:195:GLU:OE2	2.31	0.62
1:W:45:TRP:HB2	1:W:50:SER:HA	1.82	0.62
1:W:80:GLN:HE22	1:W:160:GLU:CG	2.11	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:40:GLU:HA	1:O:26:SER:HB3	1.81	0.62
1:D:159:PRO:CA	1:C:186:GLU:CG	2.58	0.62
1:H:40:GLU:HB2	1:G:8:PHE:HE2	1.61	0.62
1:C:12:ARG:HH22	1:C:77:LEU:HD23	1.65	0.62
1:E:49:SER:HB2	1:M:33:PHE:O	1.98	0.62
1:Q:35:LEU:HD23	1:Q:37:ARG:HG3	1.82	0.62
1:S:51:TRP:HB2	1:S:52:PRO:HD2	1.82	0.62
1:A:130:GLU:O	1:D:140:ARG:NH2	2.31	0.62
1:D:111:VAL:O	1:C:150:PRO:HB2	1.99	0.62
1:M:46:LEU:HD23	1:U:33:PHE:HB2	1.82	0.62
1:P:50:SER:H	1:Q:52:PRO:HG3	1.64	0.62
1:R:151:THR:HG23	1:S:154:SER:HA	1.81	0.62
1:T:185:PHE:CZ	1:U:164:THR:OG1	2.52	0.62
1:K:10:LEU:HD13	1:K:77:LEU:CD1	2.30	0.62
1:V:124:HIS:HB3	1:V:136:ARG:HG3	1.81	0.61
1:B:175:GLN:OE1	1:B:176:SER:N	2.31	0.61
1:A:51:TRP:CZ2	1:P:48:GLY:O	2.53	0.61
1:D:17:ASP:HB3	1:D:89:ARG:HB3	1.81	0.61
1:N:41:GLU:OE2	1:O:11:LEU:HD13	2.00	0.61
1:N:45:TRP:HH2	1:R:50:SER:H	1.48	0.61
1:V:8:PHE:HE1	1:W:56:ARG:NH2	1.98	0.61
1:M:95:TRP:CZ3	1:M:165:VAL:HG12	2.26	0.61
1:O:21:ASP:OD1	1:O:22:TRP:N	2.32	0.61
1:P:3:GLU:C	1:Q:36:PRO:HB3	2.24	0.61
1:P:184:THR:H	1:P:191:LEU:HD13	1.64	0.61
1:T:52:PRO:HA	1:U:55:VAL:HG11	1.77	0.61
1:M:44:GLN:HG3	1:U:44:GLN:HB2	1.82	0.61
1:A:12:ARG:CZ	1:A:16:TRP:O	2.49	0.61
1:D:146:PRO:CB	1:D:175:GLN:HG3	2.29	0.61
1:L:5:ARG:HE	1:M:36:PRO:HG3	1.65	0.61
1:P:184:THR:HB	1:P:191:LEU:HD13	1.81	0.61
1:A:10:LEU:HG	1:A:77:LEU:HD22	1.79	0.61
1:T:41:GLU:HB3	1:U:11:LEU:HD22	1.83	0.61
1:C:45:TRP:HE3	1:C:45:TRP:H	1.46	0.61
1:S:75:ARG:HB3	1:S:79:ARG:HD2	1.82	0.61
1:A:22:TRP:CD1	1:A:72:ALA:HB1	2.36	0.61
1:H:23:TYR:HB2	1:H:24:PRO:HD3	1.81	0.61
1:N:152:GLN:CB	1:N:168:PRO:CG	2.72	0.61
1:P:159:PRO:HA	1:Q:186:GLU:CD	2.25	0.61
1:R:190:GLN:HB2	1:S:74:SER:CB	2.29	0.61
1:X:40:GLU:HB2	1:I:8:PHE:CZ	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:51:TRP:CD1	1:U:49:SER:HB2	2.36	0.61
1:Q:45:TRP:O	1:Q:46:LEU:CB	2.48	0.61
1:B:133:TYR:CD2	1:E:140:ARG:NH2	2.69	0.61
1:A:33:PHE:CE1	1:A:35:LEU:CD1	2.84	0.61
1:I:99:LEU:CD1	1:I:140:ARG:CD	2.73	0.61
1:G:17:ASP:HB3	1:G:18:PRO:HD2	1.83	0.61
1:O:94:ARG:HG2	1:O:169:MET:H	1.64	0.61
1:D:99:LEU:HD21	1:D:140:ARG:HD3	1.82	0.61
1:F:179:ILE:O	1:F:181:ILE:CD1	2.49	0.61
1:N:45:TRP:HH2	1:R:50:SER:N	1.97	0.61
1:P:190:GLN:NE2	1:Q:55:VAL:CG1	2.62	0.61
1:R:151:THR:CG2	1:S:154:SER:N	2.64	0.61
1:I:42:TRP:N	1:I:44:GLN:NE2	2.28	0.61
1:B:19:PHE:HA	1:B:28:LEU:CB	2.30	0.61
1:A:51:TRP:HZ2	1:P:48:GLY:O	1.84	0.61
1:F:134:ILE:HG23	1:F:134:ILE:O	2.00	0.61
1:H:33:PHE:HB3	1:H:42:TRP:CH2	2.36	0.61
1:H:183:VAL:HG13	1:G:156:SER:CB	2.29	0.61
1:N:190:GLN:NE2	1:O:55:VAL:HG21	2.16	0.61
1:P:97:VAL:HG21	1:P:142:TYR:CE2	2.36	0.61
1:A:49:SER:O	1:A:51:TRP:CZ3	2.54	0.60
1:N:25:HIS:N	1:R:41:GLU:OE2	2.34	0.60
1:C:118:VAL:HG23	1:C:144:LEU:HD11	1.81	0.60
1:O:23:TYR:O	1:O:25:HIS:N	2.33	0.60
1:U:191:LEU:HA	1:U:195:GLU:OE1	2.01	0.60
1:M:49:SER:HB2	1:U:56:ARG:NH2	2.16	0.60
1:U:29:PHE:HB2	1:U:45:TRP:CE2	2.36	0.60
1:E:49:SER:OG	1:M:33:PHE:HB2	2.02	0.60
1:W:17:ASP:HB3	1:W:47:GLY:HA3	1.83	0.60
1:L:23:TYR:HB2	1:L:24:PRO:HD3	1.82	0.60
1:O:94:ARG:CB	1:O:169:MET:HG3	2.24	0.60
1:B:43:SER:HA	1:X:45:TRP:HH2	1.66	0.60
1:D:27:ARG:NH1	1:D:30:ASP:OD2	2.33	0.60
1:F:128:GLN:OE1	1:F:133:TYR:CZ	2.54	0.60
1:V:133:TYR:HD1	1:U:142:TYR:CE1	2.08	0.60
1:C:44:GLN:CB	1:W:44:GLN:HG3	2.20	0.60
1:E:183:VAL:O	1:E:187:SER:CB	2.50	0.60
1:G:51:TRP:HB2	1:G:52:PRO:HD2	1.81	0.60
1:D:77:LEU:HD12	1:D:89:ARG:HE	1.66	0.60
1:D:183:VAL:CG1	1:C:156:SER:HB3	2.29	0.60
1:K:10:LEU:HG	1:K:10:LEU:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:35:LEU:HG	1:S:36:PRO:HD2	1.84	0.60
1:U:99:LEU:HD11	1:U:140:ARG:HD2	1.84	0.60
1:B:33:PHE:HB3	1:B:42:TRP:CH2	2.36	0.60
1:A:133:TYR:CE1	1:D:142:TYR:HA	2.36	0.60
1:J:38:LEU:HD23	1:R:38:LEU:HD13	1.84	0.60
1:I:43:SER:N	1:I:44:GLN:OE1	2.34	0.60
1:O:33:PHE:CE2	1:O:42:TRP:CB	2.85	0.60
1:G:20:ARG:HG3	1:G:20:ARG:O	2.01	0.60
1:O:183:VAL:HG23	1:O:184:THR:H	1.67	0.60
1:S:45:TRP:CZ3	1:S:46:LEU:HA	2.36	0.60
1:A:17:ASP:HB2	1:A:18:PRO:HD2	1.83	0.60
1:D:75:ARG:C	1:D:77:LEU:H	2.10	0.60
1:N:146:PRO:HB2	1:N:175:GLN:HG2	1.83	0.60
1:E:81:LEU:HD23	1:E:162:THR:HG21	1.84	0.60
1:D:51:TRP:NE1	1:V:45:TRP:NE1	2.49	0.59
1:J:185:PHE:CZ	1:K:156:SER:HB2	2.36	0.59
1:V:48:GLY:C	1:W:52:PRO:CG	2.73	0.59
1:Q:35:LEU:HD22	1:Q:37:ARG:NE	2.17	0.59
1:U:192:GLY:H	1:U:195:GLU:CD	2.09	0.59
1:A:97:VAL:HG22	1:A:165:VAL:HB	1.84	0.59
1:C:77:LEU:HD12	1:C:78:SER:HB2	1.83	0.59
1:K:44:GLN:CD	1:S:44:GLN:HE21	2.10	0.59
1:D:78:SER:OG	1:D:81:LEU:HD23	2.02	0.59
1:J:51:TRP:CD1	1:R:45:TRP:CZ3	2.90	0.59
1:N:52:PRO:HA	1:O:55:VAL:HG13	1.84	0.59
1:R:191:LEU:HD23	1:S:71:PRO:O	2.01	0.59
1:T:140:ARG:HD2	1:S:134:ILE:HG23	1.83	0.59
1:Q:50:SER:OG	1:Q:51:TRP:N	2.34	0.59
1:S:45:TRP:HE3	1:S:46:LEU:N	1.96	0.59
1:E:150:PRO:HG3	1:E:179:ILE:HG21	1.84	0.59
1:F:175:GLN:OE1	1:F:205:LYS:OXT	2.20	0.59
1:L:183:VAL:HA	1:M:155:SER:O	2.02	0.59
1:V:151:THR:HG21	1:W:154:SER:HB3	1.85	0.59
1:W:175:GLN:CD	1:W:191:LEU:O	2.45	0.59
1:B:133:TYR:O	1:B:135:SER:N	2.35	0.59
1:N:163:LEU:HD12	1:N:164:THR:HA	1.83	0.59
1:T:12:ARG:NH2	1:T:20:ARG:HH11	2.00	0.59
1:S:12:ARG:HG2	1:S:18:PRO:HA	1.85	0.59
1:A:43:SER:O	1:A:44:GLN:CB	2.51	0.59
1:N:165:VAL:O	1:N:165:VAL:HG12	2.03	0.59
1:R:52:PRO:CB	1:S:10:LEU:CD1	2.74	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:99:LEU:HG	1:I:140:ARG:NH1	2.17	0.59
1:K:97:VAL:HG23	1:K:165:VAL:HG22	1.85	0.59
1:M:45:TRP:O	1:M:45:TRP:HE3	1.86	0.59
1:P:94:ARG:HG2	1:P:168:PRO:HA	1.85	0.59
1:K:38:LEU:HG	1:K:39:PRO:HD3	1.83	0.59
1:O:33:PHE:CD2	1:O:42:TRP:C	2.81	0.59
1:O:181:ILE:O	1:O:181:ILE:HG23	2.02	0.59
1:N:47:GLY:HA2	1:S:48:GLY:HA2	1.85	0.59
1:U:37:ARG:HB2	1:U:40:GLU:CG	2.33	0.59
1:D:168:PRO:CB	1:D:188:ARG:NH2	2.60	0.59
1:N:152:GLN:HB2	1:N:168:PRO:HD2	1.74	0.59
1:V:1:MET:H2	1:W:31:GLN:HE22	1.48	0.59
1:I:42:TRP:C	1:I:44:GLN:OE1	2.46	0.59
1:A:35:LEU:CB	1:Q:46:LEU:HD21	2.25	0.58
1:N:45:TRP:HH2	1:R:51:TRP:H	1.49	0.58
1:V:183:VAL:O	1:W:156:SER:OG	2.20	0.58
1:S:5:ARG:O	1:S:6:VAL:HG13	2.03	0.58
1:B:140:ARG:NH1	1:E:134:ILE:HG13	2.17	0.58
1:J:133:TYR:O	1:I:140:ARG:NE	2.36	0.58
1:K:26:SER:HA	1:K:45:TRP:HH2	1.68	0.58
1:O:21:ASP:OD2	1:O:73:TYR:CD1	2.56	0.58
1:U:29:PHE:HD1	1:U:45:TRP:CH2	2.20	0.58
1:U:196:ALA:O	1:U:197:ALA:HB3	2.03	0.58
1:F:12:ARG:HB3	1:F:20:ARG:HH12	1.68	0.58
1:N:153:VAL:HA	1:N:166:GLU:O	2.04	0.58
1:N:157:LEU:HD11	1:O:183:VAL:HG12	1.84	0.58
1:E:118:VAL:HB	1:E:142:TYR:HB2	1.85	0.58
1:B:19:PHE:C	1:B:28:LEU:HG	2.28	0.58
1:V:153:VAL:O	1:W:151:THR:O	2.22	0.58
1:I:99:LEU:HD12	1:I:140:ARG:CD	2.34	0.58
1:B:16:TRP:CD1	1:B:20:ARG:NH1	2.71	0.58
1:D:20:ARG:HG2	1:D:25:HIS:HB3	1.83	0.58
1:D:81:LEU:HD22	1:D:92:ALA:CA	2.34	0.58
1:F:12:ARG:NH1	1:F:20:ARG:HD3	2.17	0.58
1:V:153:VAL:HA	1:V:167:ALA:HB2	1.84	0.58
1:W:35:LEU:HG	1:W:36:PRO:HD2	1.85	0.58
1:A:12:ARG:NH1	1:A:16:TRP:N	2.28	0.58
1:A:174:THR:HG21	1:A:202:THR:O	2.04	0.58
1:C:26:SER:HB3	1:C:45:TRP:CZ3	2.38	0.58
1:Q:38:LEU:HD11	1:Q:39:PRO:HD3	1.75	0.58
1:A:35:LEU:HD13	1:A:37:ARG:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:3:GLU:O	1:H:4:ARG:CG	2.52	0.58
1:R:185:PHE:HZ	1:S:164:THR:HB	1.68	0.58
1:T:23:TYR:HB3	1:T:24:PRO:HD3	1.85	0.58
1:G:45:TRP:CD1	1:G:51:TRP:CH2	2.92	0.58
1:U:51:TRP:HB2	1:U:52:PRO:HD2	1.85	0.58
1:B:16:TRP:NE1	1:Q:15:SER:HB3	2.16	0.58
1:D:81:LEU:HD21	1:D:188:ARG:NH1	2.18	0.58
1:A:20:ARG:HG3	1:A:24:PRO:HD3	1.86	0.58
1:D:77:LEU:O	1:D:89:ARG:HG2	2.03	0.58
1:A:15:SER:HB2	1:A:16:TRP:HE3	1.51	0.58
1:A:131:HIS:HB3	1:A:134:ILE:CD1	2.34	0.58
1:E:189:ALA:O	1:E:201:GLU:CD	2.47	0.58
1:K:177:ASN:ND2	1:K:200:ASP:HA	2.17	0.58
1:N:25:HIS:CD2	1:S:11:LEU:HB2	2.39	0.57
1:N:45:TRP:HH2	1:R:51:TRP:N	2.01	0.57
1:P:47:GLY:HA2	1:I:48:GLY:HA2	1.85	0.57
1:M:16:TRP:C	1:M:17:ASP:O	2.44	0.57
1:A:30:ASP:O	1:A:33:PHE:CE2	2.57	0.57
1:H:184:THR:HG23	1:H:184:THR:O	2.03	0.57
1:B:99:LEU:HD11	1:B:140:ARG:HD3	1.85	0.57
1:J:29:PHE:HB2	1:J:46:LEU:HD21	1.85	0.57
1:N:152:GLN:CB	1:N:168:PRO:HG2	2.34	0.57
1:E:79:ARG:O	1:E:81:LEU:N	2.33	0.57
1:A:12:ARG:NH1	1:A:15:SER:OG	2.37	0.57
1:D:150:PRO:O	1:C:151:THR:O	2.23	0.57
1:L:175:GLN:N	1:L:181:ILE:HD13	2.20	0.57
1:N:48:GLY:O	1:O:52:PRO:HD3	2.05	0.57
1:M:162:THR:O	1:M:162:THR:HG22	2.05	0.57
1:F:157:LEU:N	1:E:185:PHE:CE2	2.71	0.57
1:V:8:PHE:CE2	1:W:34:GLY:HA2	2.39	0.57
1:X:35:LEU:HD12	1:X:35:LEU:N	2.19	0.57
1:E:183:VAL:HG22	1:E:187:SER:CB	2.32	0.57
1:I:44:GLN:CG	1:Q:44:GLN:HE21	2.12	0.57
1:O:33:PHE:CG	1:O:42:TRP:O	2.58	0.57
1:B:118:VAL:HG23	1:B:144:LEU:HD11	1.85	0.57
1:I:148:VAL:HG22	1:I:169:MET:HG2	1.85	0.57
1:Q:45:TRP:O	1:Q:45:TRP:HE3	1.87	0.57
1:W:51:TRP:CZ2	1:W:54:TYR:HE2	2.22	0.57
1:C:49:SER:HA	1:W:51:TRP:CZ2	2.39	0.57
1:K:146:PRO:CG	1:K:205:LYS:HE3	2.34	0.57
1:M:94:ARG:HB2	1:M:169:MET:CG	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:94:ARG:CG	1:O:169:MET:CG	2.82	0.57
1:U:45:TRP:HB3	1:U:51:TRP:CZ2	2.40	0.57
1:D:52:PRO:HG2	1:C:10:LEU:O	2.04	0.57
1:L:144:LEU:O	1:L:144:LEU:HD12	2.05	0.57
1:X:191:LEU:HD11	1:I:75:ARG:HH21	1.70	0.57
1:C:39:PRO:O	1:G:26:SER:OG	2.22	0.57
1:G:45:TRP:O	1:G:46:LEU:HD23	2.04	0.57
1:K:26:SER:HA	1:K:45:TRP:CH2	2.39	0.57
1:U:26:SER:O	1:U:45:TRP:HZ2	1.88	0.57
1:B:128:GLN:CB	1:B:131:HIS:O	2.48	0.57
1:H:151:THR:HG23	1:G:154:SER:HB3	1.86	0.57
1:N:157:LEU:HD12	1:N:157:LEU:O	2.04	0.57
1:R:128:GLN:HB2	1:R:132:GLY:CA	2.34	0.57
1:R:151:THR:HG23	1:S:154:SER:N	2.19	0.57
1:T:12:ARG:CZ	1:T:20:ARG:HD3	2.34	0.57
1:V:49:SER:HA	1:W:52:PRO:CG	2.31	0.57
1:M:160:GLU:OE1	1:M:160:GLU:HA	2.05	0.57
1:X:104:PHE:CE1	1:X:136:ARG:HG3	2.39	0.57
1:I:49:SER:HB3	1:Q:51:TRP:CZ3	2.39	0.57
1:O:30:ASP:CG	1:O:42:TRP:CB	2.76	0.57
1:D:25:HIS:HB2	1:H:41:GLU:OE1	2.05	0.56
1:R:151:THR:CG2	1:S:154:SER:CA	2.83	0.56
1:T:25:HIS:C	1:T:27:ARG:N	2.63	0.56
1:V:8:PHE:HE1	1:W:56:ARG:CZ	2.18	0.56
1:K:183:VAL:O	1:K:187:SER:OG	2.23	0.56
1:D:111:VAL:HG23	1:D:120:ILE:HG12	1.86	0.56
1:L:192:GLY:HA3	1:L:201:GLU:HA	1.86	0.56
1:N:45:TRP:O	1:N:46:LEU:CB	2.51	0.56
1:V:133:TYR:CE1	1:U:142:TYR:CE1	2.90	0.56
1:X:44:GLN:O	1:X:45:TRP:HB2	2.04	0.56
1:C:184:THR:HA	1:C:191:LEU:HD23	1.76	0.56
1:Q:38:LEU:HD12	1:Q:39:PRO:CA	2.35	0.56
1:S:28:LEU:HD21	1:S:73:TYR:OH	2.05	0.56
1:D:149:ASP:OD2	1:D:183:VAL:O	2.23	0.56
1:F:156:SER:C	1:E:185:PHE:HE2	2.11	0.56
1:F:191:LEU:CD1	1:E:75:ARG:CZ	2.78	0.56
1:L:150:PRO:O	1:M:151:THR:O	2.23	0.56
1:T:23:TYR:N	1:T:23:TYR:CD1	2.73	0.56
1:E:46:LEU:O	1:E:46:LEU:HG	2.05	0.56
1:K:44:GLN:HG3	1:O:44:GLN:CB	2.36	0.56
1:M:80:GLN:CG	1:M:160:GLU:HG3	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:16:TRP:HD1	1:U:20:ARG:HD2	1.69	0.56
1:B:133:TYR:CB	1:E:140:ARG:HG3	2.34	0.56
1:D:94:ARG:HG2	1:D:168:PRO:HA	1.88	0.56
1:H:45:TRP:CE3	1:H:45:TRP:HA	2.40	0.56
1:J:175:GLN:N	1:J:181:ILE:HD12	2.20	0.56
1:M:16:TRP:HB2	1:M:20:ARG:HD2	1.86	0.56
1:B:158:SER:HA	1:A:186:GLU:HG2	1.86	0.56
1:R:33:PHE:CZ	1:S:7:PRO:CB	2.89	0.56
1:D:71:PRO:O	1:D:72:ALA:HB2	2.04	0.56
1:N:152:GLN:HE21	1:N:168:PRO:HG3	1.70	0.56
1:Q:38:LEU:HD12	1:Q:39:PRO:CG	2.34	0.56
1:B:37:ARG:NH2	1:A:4:ARG:HD2	2.21	0.56
1:D:146:PRO:HB2	1:D:175:GLN:CD	2.31	0.56
1:V:5:ARG:HE	1:W:36:PRO:HG3	1.71	0.56
1:O:152:GLN:O	1:O:167:ALA:HB1	2.06	0.56
1:A:97:VAL:HG21	1:A:142:TYR:CE2	2.41	0.56
1:J:111:VAL:HG12	1:K:151:THR:HG21	1.88	0.56
1:J:140:ARG:CZ	1:I:134:ILE:HG12	2.36	0.56
1:N:49:SER:CA	1:O:52:PRO:HG3	2.35	0.56
1:T:20:ARG:NH1	1:M:15:SER:CA	2.68	0.56
1:C:51:TRP:HE1	1:C:54:TYR:HE2	1.53	0.56
1:K:97:VAL:HG23	1:K:165:VAL:CG2	2.36	0.56
1:A:35:LEU:HD12	1:A:35:LEU:C	2.31	0.56
1:J:185:PHE:CE1	1:K:164:THR:O	2.59	0.56
1:L:171:LYS:HG3	1:L:192:GLY:HA2	1.88	0.56
1:N:146:PRO:HB3	1:N:181:ILE:HD11	1.88	0.56
1:C:46:LEU:HD23	1:W:34:GLY:HA3	1.88	0.56
1:W:7:PRO:O	1:W:11:LEU:HD13	2.06	0.56
1:D:20:ARG:CG	1:D:25:HIS:ND1	2.69	0.56
1:D:45:TRP:CE3	1:H:51:TRP:CE2	2.94	0.56
1:H:3:GLU:O	1:H:4:ARG:HG2	2.05	0.56
1:H:149:ASP:CG	1:H:184:THR:HG22	2.31	0.56
1:L:11:LEU:HD11	1:L:171:LYS:NZ	2.20	0.56
1:N:45:TRP:CE3	1:R:51:TRP:NE1	2.74	0.56
1:N:45:TRP:HB3	1:N:49:SER:N	2.20	0.56
1:T:133:TYR:O	1:T:135:SER:N	2.39	0.56
1:V:104:PHE:HE1	1:V:136:ARG:HG3	1.71	0.56
1:U:12:ARG:HG3	1:U:19:PHE:HD1	1.68	0.56
1:W:26:SER:HA	1:W:45:TRP:HH2	1.71	0.56
1:R:201:GLU:OE2	1:S:56:ARG:HB2	2.06	0.55
1:V:40:GLU:O	1:V:41:GLU:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:17:ASP:HB3	1:G:18:PRO:CD	2.36	0.55
1:K:146:PRO:HG2	1:K:205:LYS:CE	2.35	0.55
1:A:16:TRP:CD1	1:A:17:ASP:H	2.24	0.55
1:L:180:THR:C	1:L:181:ILE:HG13	2.31	0.55
1:N:153:VAL:O	1:O:151:THR:O	2.24	0.55
1:T:94:ARG:HG2	1:T:168:PRO:HA	1.88	0.55
1:V:50:SER:H	1:W:52:PRO:HB3	1.71	0.55
1:X:36:PRO:O	1:X:38:LEU:HD22	2.06	0.55
1:X:51:TRP:CZ3	1:I:11:LEU:HD22	2.41	0.55
1:X:151:THR:HG23	1:I:154:SER:CB	2.36	0.55
1:O:51:TRP:CE2	1:S:49:SER:HA	2.40	0.55
1:N:152:GLN:CB	1:N:168:PRO:CD	2.43	0.55
1:A:134:ILE:O	1:A:134:ILE:HG22	2.05	0.55
1:E:188:ARG:HG3	1:E:188:ARG:O	2.07	0.55
1:Q:37:ARG:HD2	1:Q:40:GLU:OE1	2.04	0.55
1:B:11:LEU:C	1:B:11:LEU:HD12	2.32	0.55
1:B:49:SER:HB2	1:X:45:TRP:CH2	2.42	0.55
1:A:45:TRP:HB2	1:A:50:SER:HB3	1.87	0.55
1:D:146:PRO:CG	1:D:175:GLN:NE2	2.70	0.55
1:T:40:GLU:OE1	1:U:6:VAL:HG13	2.06	0.55
1:V:99:LEU:HB3	1:V:163:LEU:HB3	1.89	0.55
1:V:151:THR:CB	1:W:154:SER:HB3	2.36	0.55
1:L:94:ARG:HG2	1:L:168:PRO:HA	1.88	0.55
1:N:12:ARG:NH1	1:S:12:ARG:HB3	2.22	0.55
1:T:116:GLY:HA3	1:T:181:ILE:HD11	1.87	0.55
1:V:51:TRP:CE3	1:W:11:LEU:HG	2.42	0.55
1:C:45:TRP:N	1:C:45:TRP:CE3	2.75	0.55
1:T:51:TRP:CE3	1:U:11:LEU:HD23	2.41	0.55
1:C:175:GLN:HB2	1:C:191:LEU:HD11	1.89	0.55
1:I:49:SER:O	1:Q:51:TRP:CD2	2.59	0.55
1:B:51:TRP:CD1	1:X:45:TRP:CZ2	2.94	0.55
1:F:5:ARG:NH1	1:F:205:LYS:O	2.40	0.55
1:J:49:SER:HA	1:K:52:PRO:HG3	1.88	0.55
1:K:97:VAL:CG2	1:K:165:VAL:CG2	2.85	0.55
1:U:194:PRO:O	1:U:195:GLU:CG	2.55	0.55
1:A:16:TRP:CD1	1:A:17:ASP:CG	2.85	0.55
1:D:183:VAL:HG13	1:C:156:SER:CB	2.32	0.55
1:P:99:LEU:HB3	1:P:163:LEU:HB3	1.89	0.55
1:B:16:TRP:NE1	1:B:20:ARG:NH1	2.54	0.55
1:D:146:PRO:CG	1:D:175:GLN:CG	2.70	0.55
1:F:191:LEU:HD12	1:E:75:ARG:NH2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:150:PRO:O	1:G:151:THR:O	2.25	0.55
1:N:45:TRP:CE3	1:R:49:SER:HB2	2.41	0.55
1:N:183:VAL:O	1:O:156:SER:OG	2.22	0.55
1:T:133:TYR:CE1	1:S:142:TYR:CD2	2.94	0.55
1:M:178:GLU:O	1:M:179:ILE:CG2	2.44	0.55
1:W:45:TRP:CG	1:W:46:LEU:H	2.25	0.55
1:A:1:MET:CG	1:A:9:SER:OG	2.54	0.54
1:V:51:TRP:HE3	1:W:11:LEU:HG	1.73	0.54
1:C:51:TRP:CE2	1:G:49:SER:HB2	2.42	0.54
1:E:107:ASP:H	1:E:124:HIS:HB3	1.72	0.54
1:K:10:LEU:HD11	1:K:77:LEU:HD13	1.88	0.54
1:S:6:VAL:HG23	1:S:6:VAL:O	2.06	0.54
1:B:133:TYR:OH	1:E:142:TYR:HD1	1.88	0.54
1:T:20:ARG:HH12	1:M:15:SER:CA	2.20	0.54
1:E:183:VAL:HG11	1:E:190:GLN:HE21	1.72	0.54
1:G:55:VAL:HG23	1:G:55:VAL:O	2.07	0.54
1:K:38:LEU:CG	1:K:39:PRO:HD3	2.37	0.54
1:B:133:TYR:CE1	1:E:141:LYS:O	2.61	0.54
1:L:149:ASP:CG	1:L:184:THR:HB	2.31	0.54
1:G:19:PHE:HZ	1:G:55:VAL:HG13	1.71	0.54
1:O:12:ARG:CG	1:O:19:PHE:HA	2.37	0.54
1:X:150:PRO:HB2	1:I:153:VAL:O	2.07	0.54
1:E:51:TRP:HB2	1:E:52:PRO:HD2	1.89	0.54
1:U:41:GLU:C	1:U:42:TRP:HD1	2.15	0.54
1:A:12:ARG:NH2	1:X:12:ARG:NH2	2.55	0.54
1:F:156:SER:CB	1:E:185:PHE:CZ	2.81	0.54
1:M:49:SER:HB2	1:U:56:ARG:HH22	1.72	0.54
1:W:171:LYS:HZ3	1:W:188:ARG:CZ	2.19	0.54
1:D:31:GLN:O	1:D:73:TYR:CE2	2.52	0.54
1:N:12:ARG:HH12	1:S:12:ARG:HB3	1.72	0.54
1:N:114:LYS:HD2	1:O:112:LYS:HD2	1.90	0.54
1:O:30:ASP:OD1	1:O:42:TRP:HB2	2.07	0.54
1:U:169:MET:HB3	1:U:170:PRO:CD	2.38	0.54
1:B:95:TRP:CZ2	1:B:144:LEU:HD23	2.43	0.54
1:D:75:ARG:C	1:D:77:LEU:N	2.63	0.54
1:N:22:TRP:HB2	1:N:28:LEU:HD11	1.89	0.54
1:N:40:GLU:OE1	1:O:6:VAL:HG21	2.07	0.54
1:N:41:GLU:CD	1:O:11:LEU:HD13	2.33	0.54
1:T:135:SER:HB2	1:S:140:ARG:HA	1.89	0.54
1:E:42:TRP:C	1:U:44:GLN:NE2	2.65	0.54
1:A:44:GLN:CG	1:A:45:TRP:CZ3	2.91	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:171:LYS:HG3	1:M:171:LYS:O	2.07	0.54
1:U:95:TRP:HB2	1:U:169:MET:HE3	1.89	0.54
1:D:44:GLN:O	1:D:49:SER:HB2	2.07	0.54
1:D:99:LEU:CD2	1:D:140:ARG:CD	2.86	0.54
1:H:50:SER:H	1:G:52:PRO:HB3	1.72	0.54
1:N:45:TRP:CE2	1:S:52:PRO:HA	2.42	0.54
1:N:152:GLN:HE21	1:N:168:PRO:HG2	1.71	0.54
1:N:180:THR:HG21	1:O:109:LEU:H	1.73	0.54
1:V:201:GLU:OE2	1:W:56:ARG:HG3	2.08	0.54
1:O:45:TRP:CG	1:O:50:SER:HG	2.25	0.54
1:U:29:PHE:HD1	1:U:45:TRP:CZ3	2.26	0.54
1:A:51:TRP:CH2	1:I:51:TRP:HA	2.42	0.54
1:D:108:GLU:HB2	1:C:180:THR:HG22	1.90	0.54
1:D:111:VAL:HG22	1:C:151:THR:CG2	2.38	0.54
1:J:150:PRO:O	1:K:151:THR:O	2.25	0.54
1:R:37:ARG:HB2	1:R:40:GLU:OE2	2.08	0.54
1:F:36:PRO:O	1:F:37:ARG:HB2	2.08	0.53
1:L:146:PRO:HG2	1:L:175:GLN:HG2	1.89	0.53
1:M:80:GLN:O	1:M:162:THR:HB	2.09	0.53
1:M:172:LEU:CD2	1:M:204:ALA:HB2	2.36	0.53
1:A:122:GLY:O	1:A:137:CYS:HA	2.09	0.53
1:F:5:ARG:CD	1:F:205:LYS:O	2.56	0.53
1:F:133:TYR:O	1:F:134:ILE:HG22	2.07	0.53
1:V:140:ARG:CZ	1:U:134:ILE:HD13	2.38	0.53
1:G:169:MET:CB	1:G:172:LEU:HD12	2.38	0.53
1:I:42:TRP:CE3	1:I:44:GLN:NE2	2.76	0.53
1:K:39:PRO:C	1:K:41:GLU:H	2.16	0.53
1:O:42:TRP:CD1	1:O:44:GLN:CD	2.86	0.53
1:A:30:ASP:HA	1:A:43:SER:HB2	1.91	0.53
1:F:8:PHE:HZ	1:E:33:PHE:O	1.90	0.53
1:J:185:PHE:CE2	1:K:156:SER:HB2	2.43	0.53
1:G:6:VAL:N	1:G:7:PRO:HD3	2.23	0.53
1:O:30:ASP:CG	1:O:42:TRP:HB2	2.32	0.53
1:B:156:SER:OG	1:A:185:PHE:HB2	2.08	0.53
1:L:35:LEU:HB3	1:L:36:PRO:CD	2.38	0.53
1:T:20:ARG:HH12	1:M:15:SER:HA	1.70	0.53
1:X:185:PHE:CZ	1:I:156:SER:HB3	2.44	0.53
1:E:172:LEU:HD22	1:E:204:ALA:CA	2.31	0.53
1:E:187:SER:O	1:E:189:ALA:N	2.38	0.53
1:G:8:PHE:O	1:G:9:SER:CB	2.57	0.53
1:D:99:LEU:HD11	1:D:120:ILE:CD1	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:45:TRP:CE3	1:O:47:GLY:N	2.73	0.53
1:W:154:SER:OG	1:W:166:GLU:HG2	2.08	0.53
1:W:175:GLN:NE2	1:W:191:LEU:O	2.41	0.53
1:F:39:PRO:HB3	1:L:38:LEU:HD21	1.90	0.53
1:H:1:MET:HE2	1:H:192:GLY:O	2.07	0.53
1:H:33:PHE:HE1	1:H:54:TYR:HB3	1.73	0.53
1:N:185:PHE:HZ	1:O:164:THR:HB	1.74	0.53
1:T:109:LEU:O	1:U:180:THR:HG22	2.09	0.53
1:K:45:TRP:HZ3	1:S:41:GLU:OE1	1.90	0.53
1:O:21:ASP:CG	1:O:73:TYR:CE1	2.85	0.53
1:O:33:PHE:HE2	1:O:42:TRP:HB3	1.73	0.53
1:J:37:ARG:O	1:J:39:PRO:CD	2.56	0.53
1:O:183:VAL:HG23	1:O:184:THR:N	2.24	0.53
1:Q:38:LEU:HD12	1:Q:39:PRO:CB	2.38	0.53
1:J:170:PRO:HB2	1:J:192:GLY:HA3	1.91	0.53
1:V:19:PHE:HD1	1:V:28:LEU:HB2	1.73	0.53
1:K:40:GLU:O	1:K:41:GLU:OE2	2.26	0.53
1:M:16:TRP:HB2	1:M:20:ARG:HB2	1.91	0.53
1:F:37:ARG:HG3	1:F:37:ARG:NH1	2.23	0.53
1:V:44:GLN:CA	1:V:45:TRP:CE3	2.92	0.53
1:G:45:TRP:N	1:G:45:TRP:CE3	2.77	0.53
1:M:38:LEU:CB	1:M:39:PRO:HD3	2.38	0.53
1:M:120:ILE:HD11	1:M:165:VAL:HG21	1.91	0.53
1:B:126:GLU:OE2	1:B:134:ILE:HD13	2.08	0.53
1:F:24:PRO:HG2	1:F:27:ARG:HB3	1.91	0.53
1:E:39:PRO:O	1:E:40:GLU:CG	2.57	0.53
1:U:17:ASP:HB3	1:U:18:PRO:HD2	1.90	0.53
1:D:109:LEU:HD23	1:D:122:GLY:HA3	1.92	0.52
1:V:44:GLN:O	1:V:45:TRP:CB	2.56	0.52
1:S:19:PHE:CD2	1:S:45:TRP:CZ3	2.96	0.52
1:L:126:GLU:HG3	1:L:134:ILE:HD11	1.91	0.52
1:E:111:VAL:HG21	1:E:155:SER:HB3	1.90	0.52
1:I:202:THR:CB	1:I:205:LYS:NZ	2.72	0.52
1:O:33:PHE:HA	1:S:49:SER:OG	2.10	0.52
1:B:54:TYR:CE2	1:A:7:PRO:HG3	2.44	0.52
1:B:176:SER:O	1:B:178:GLU:N	2.43	0.52
1:H:149:ASP:CG	1:H:183:VAL:O	2.52	0.52
1:L:170:PRO:HB2	1:L:192:GLY:C	2.35	0.52
1:V:44:GLN:HB2	1:V:45:TRP:HE3	1.60	0.52
1:Q:35:LEU:HD22	1:Q:37:ARG:HG3	1.92	0.52
1:S:37:ARG:HB2	1:S:40:GLU:CG	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:184:THR:H	1:C:191:LEU:HD22	1.68	0.52
1:I:45:TRP:HE3	1:I:46:LEU:HD13	1.73	0.52
1:O:10:LEU:HD22	1:O:77:LEU:HD22	1.91	0.52
1:W:51:TRP:CD1	1:W:52:PRO:HD2	2.44	0.52
1:A:12:ARG:CZ	1:X:12:ARG:HH21	2.22	0.52
1:L:151:THR:CG2	1:M:154:SER:CA	2.87	0.52
1:R:183:VAL:HA	1:S:156:SER:HA	1.92	0.52
1:C:26:SER:OG	1:W:40:GLU:OE1	2.25	0.52
1:E:17:ASP:HB3	1:E:47:GLY:HA3	1.92	0.52
1:F:157:LEU:CD2	1:E:182:PRO:CB	2.88	0.52
1:J:37:ARG:O	1:J:38:LEU:HB2	2.09	0.52
1:N:153:VAL:HG22	1:N:167:ALA:HB2	1.92	0.52
1:W:6:VAL:CG2	1:W:8:PHE:CE2	2.93	0.52
1:D:72:ALA:HB1	1:D:75:ARG:HB3	1.92	0.52
1:F:12:ARG:HB3	1:F:20:ARG:NH1	2.25	0.52
1:F:94:ARG:HE	1:F:96:ARG:NH2	2.07	0.52
1:H:94:ARG:HG2	1:H:168:PRO:HA	1.90	0.52
1:G:41:GLU:HB3	1:W:44:GLN:CD	2.35	0.52
1:F:40:GLU:O	1:F:41:GLU:HB2	2.10	0.52
1:P:153:VAL:O	1:Q:152:GLN:HG2	2.10	0.52
1:C:41:GLU:HB3	1:G:44:GLN:CD	2.35	0.52
1:K:51:TRP:HB2	1:K:52:PRO:HD2	1.91	0.52
1:O:77:LEU:HD12	1:O:78:SER:HB2	1.91	0.52
1:F:51:TRP:HB3	1:F:52:PRO:HD2	1.92	0.52
1:F:151:THR:N	1:E:154:SER:HB3	2.25	0.52
1:H:169:MET:HG3	1:H:170:PRO:HD2	1.92	0.52
1:E:176:SER:CB	1:E:181:ILE:CG1	2.87	0.52
1:W:51:TRP:CB	1:W:52:PRO:HD2	2.39	0.52
1:A:33:PHE:HE1	1:A:35:LEU:CG	1.93	0.52
1:G:40:GLU:CG	1:W:46:LEU:CD1	2.73	0.52
1:A:175:GLN:CD	1:A:179:ILE:O	2.53	0.51
1:H:3:GLU:C	1:H:4:ARG:HG2	2.35	0.51
1:J:53:GLY:H	1:K:55:VAL:HG12	1.75	0.51
1:N:24:PRO:HB3	1:R:41:GLU:OE1	2.11	0.51
1:R:171:LYS:HZ2	1:R:190:GLN:H	1.56	0.51
1:X:187:SER:HB3	1:I:75:ARG:HH22	1.75	0.51
1:I:38:LEU:HD12	1:I:39:PRO:HD3	1.92	0.51
1:K:154:SER:O	1:K:165:VAL:HA	2.10	0.51
1:S:45:TRP:O	1:S:46:LEU:C	2.53	0.51
1:U:17:ASP:HB3	1:U:18:PRO:CD	2.40	0.51
1:U:43:SER:OG	1:U:45:TRP:NE1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:TYR:HE1	1:D:133:TYR:CD1	2.27	0.51
1:L:49:SER:HA	1:M:52:PRO:HG3	1.93	0.51
1:N:156:SER:O	1:N:164:THR:HB	2.09	0.51
1:O:51:TRP:CZ3	1:S:49:SER:O	2.63	0.51
1:P:40:GLU:O	1:P:41:GLU:HB2	2.10	0.51
1:R:24:PRO:HG2	1:R:27:ARG:HB3	1.91	0.51
1:V:140:ARG:NH1	1:U:134:ILE:HD13	2.25	0.51
1:A:12:ARG:CB	1:A:19:PHE:HA	2.38	0.51
1:H:45:TRP:HA	1:H:45:TRP:HE3	1.73	0.51
1:H:45:TRP:NE1	1:V:49:SER:OG	2.42	0.51
1:J:185:PHE:C	1:J:187:SER:H	2.19	0.51
1:P:38:LEU:CD2	1:P:44:GLN:NE2	2.41	0.51
1:V:125:GLU:HG2	1:V:135:SER:HB3	1.91	0.51
1:V:137:CYS:O	1:U:137:CYS:O	2.29	0.51
1:E:39:PRO:HB2	1:E:42:TRP:HE1	1.75	0.51
1:E:110:THR:HB	1:E:121:THR:OG1	2.10	0.51
1:G:6:VAL:HG23	1:G:6:VAL:O	2.09	0.51
1:W:190:GLN:HG3	1:W:191:LEU:HD12	1.91	0.51
1:B:18:PRO:HD3	1:B:77:LEU:HD23	1.89	0.51
1:B:35:LEU:O	1:B:42:TRP:CH2	2.63	0.51
1:D:74:SER:O	1:D:75:ARG:NH1	2.44	0.51
1:L:151:THR:HG23	1:M:154:SER:CA	2.40	0.51
1:C:46:LEU:HD21	1:W:35:LEU:H	1.75	0.51
1:B:133:TYR:HD2	1:E:140:ARG:NH2	2.09	0.51
1:D:11:LEU:HD23	1:C:56:ARG:CG	2.40	0.51
1:D:149:ASP:CG	1:D:183:VAL:O	2.53	0.51
1:T:19:PHE:CA	1:T:28:LEU:HD23	2.23	0.51
1:T:40:GLU:OE1	1:U:6:VAL:CG1	2.59	0.51
1:X:71:PRO:O	1:X:75:ARG:CG	2.59	0.51
1:X:133:TYR:CD1	1:G:140:ARG:NH2	2.78	0.51
1:Q:3:GLU:O	1:Q:4:ARG:CB	2.58	0.51
1:Q:125:GLU:HG3	1:Q:135:SER:OG	2.11	0.51
1:D:112:LYS:HG3	1:C:113:THR:O	2.11	0.51
1:J:72:ALA:HB1	1:J:75:ARG:HB2	1.93	0.51
1:V:50:SER:N	1:W:52:PRO:HB3	2.25	0.51
1:S:19:PHE:CZ	1:S:53:GLY:HA2	2.46	0.51
1:D:89:ARG:HG2	1:D:90:HIS:CD2	2.45	0.51
1:P:50:SER:H	1:Q:52:PRO:CB	2.23	0.51
1:G:12:ARG:HD2	1:G:19:PHE:CD1	2.46	0.51
1:M:6:VAL:HG11	1:M:8:PHE:HZ	1.66	0.51
1:A:12:ARG:CZ	1:X:12:ARG:NH2	2.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:30:ASP:HA	1:D:42:TRP:HZ3	1.75	0.51
1:H:45:TRP:CE3	1:V:51:TRP:CZ2	2.98	0.51
1:J:104:PHE:CZ	1:J:138:PHE:HD1	2.28	0.51
1:N:12:ARG:HD3	1:S:18:PRO:HD3	1.92	0.51
1:G:47:GLY:O	1:G:48:GLY:C	2.54	0.51
1:O:51:TRP:CE3	1:S:49:SER:O	2.64	0.51
1:Q:46:LEU:HG	1:Q:46:LEU:O	2.09	0.51
1:S:51:TRP:HB2	1:S:52:PRO:CD	2.40	0.51
1:A:10:LEU:HG	1:A:77:LEU:HD11	1.88	0.50
1:A:40:GLU:HA	1:Q:26:SER:HB3	1.92	0.50
1:H:26:SER:HB2	1:V:41:GLU:HG3	1.94	0.50
1:L:36:PRO:C	1:L:37:ARG:HG3	2.22	0.50
1:C:183:VAL:CG1	1:C:187:SER:HB3	2.38	0.50
1:E:45:TRP:HD1	1:E:51:TRP:CH2	2.30	0.50
1:I:41:GLU:CB	1:I:44:GLN:HE22	2.21	0.50
1:O:17:ASP:HB3	1:O:18:PRO:HD2	1.93	0.50
1:D:191:LEU:HD23	1:C:71:PRO:O	2.11	0.50
1:J:51:TRP:NE1	1:R:45:TRP:CE3	2.79	0.50
1:R:126:GLU:OE1	1:R:128:GLN:OE1	2.30	0.50
1:T:146:PRO:HB2	1:T:175:GLN:HG3	1.93	0.50
1:C:175:GLN:HB2	1:C:191:LEU:CD1	2.41	0.50
1:M:44:GLN:O	1:M:51:TRP:HZ3	1.94	0.50
1:W:187:SER:OG	1:W:190:GLN:HG2	2.10	0.50
1:D:27:ARG:HD2	1:D:30:ASP:HB3	1.92	0.50
1:T:22:TRP:O	1:T:23:TYR:O	2.29	0.50
1:X:9:SER:O	1:X:17:ASP:N	2.45	0.50
1:E:140:ARG:CZ	1:E:142:TYR:OH	2.60	0.50
1:O:40:GLU:HG3	1:S:26:SER:CB	2.37	0.50
1:S:72:ALA:HB1	1:S:159:PRO:HD3	1.92	0.50
1:A:39:PRO:C	1:A:41:GLU:H	2.19	0.50
1:L:144:LEU:HD12	1:L:144:LEU:C	2.36	0.50
1:N:11:LEU:HD22	1:O:56:ARG:CB	2.41	0.50
1:I:6:VAL:HB	1:I:8:PHE:CE2	2.46	0.50
1:M:16:TRP:O	1:M:17:ASP:C	2.54	0.50
1:O:51:TRP:HD1	1:O:52:PRO:HD2	1.75	0.50
1:O:51:TRP:CZ2	1:S:49:SER:HB3	2.45	0.50
1:Q:52:PRO:O	1:Q:53:GLY:C	2.53	0.50
1:W:148:VAL:O	1:W:179:ILE:HD11	2.12	0.50
1:T:37:ARG:HB2	1:U:6:VAL:HG21	1.93	0.50
1:C:45:TRP:HB2	1:C:50:SER:HB2	1.93	0.50
1:I:42:TRP:O	1:I:44:GLN:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:30:ASP:HA	1:M:45:TRP:HE1	1.77	0.50
1:A:99:LEU:HG	1:A:140:ARG:HH11	1.76	0.50
1:P:136:ARG:HA	1:O:138:PHE:HB2	1.92	0.50
1:R:24:PRO:HG2	1:R:27:ARG:CB	2.41	0.50
1:R:154:SER:HB3	1:S:152:GLN:NE2	2.25	0.50
1:T:11:LEU:HD21	1:T:171:LYS:NZ	2.27	0.50
1:M:35:LEU:O	1:M:40:GLU:OE1	2.30	0.50
1:M:146:PRO:CG	1:M:205:LYS:CD	2.84	0.50
1:B:6:VAL:HB	1:A:34:GLY:HA2	1.94	0.50
1:B:133:TYR:CG	1:E:140:ARG:NE	2.80	0.50
1:D:151:THR:HG23	1:C:154:SER:OG	2.12	0.50
1:Q:147:GLY:HA2	1:Q:176:SER:H	1.76	0.50
1:U:37:ARG:HB2	1:U:40:GLU:HG2	1.94	0.50
1:W:80:GLN:OE1	1:W:160:GLU:CG	2.57	0.50
1:X:22:TRP:HB2	1:X:28:LEU:HD11	1.93	0.50
1:G:38:LEU:HB3	1:G:39:PRO:HD3	1.92	0.50
1:I:112:LYS:HD3	1:I:114:LYS:HB2	1.94	0.50
1:K:44:GLN:HG3	1:S:44:GLN:HG3	1.93	0.50
1:K:44:GLN:OE1	1:S:41:GLU:HB3	2.12	0.50
1:M:81:LEU:HA	1:M:162:THR:CG2	2.40	0.50
1:S:45:TRP:HE3	1:S:46:LEU:CA	2.24	0.50
1:A:45:TRP:HB2	1:A:50:SER:CB	2.42	0.50
1:F:175:GLN:CD	1:F:205:LYS:OXT	2.55	0.50
1:K:20:ARG:HG3	1:K:24:PRO:HG3	1.93	0.50
1:M:49:SER:OG	1:U:54:TYR:CE2	2.65	0.50
1:U:175:GLN:NE2	1:U:192:GLY:O	2.45	0.50
1:A:52:PRO:O	1:A:54:TYR:HD2	1.95	0.49
1:D:12:ARG:CZ	1:G:18:PRO:HA	2.42	0.49
1:F:151:THR:HG23	1:E:154:SER:CB	2.42	0.49
1:N:52:PRO:HA	1:O:55:VAL:CG1	2.41	0.49
1:R:33:PHE:CE1	1:S:7:PRO:HG2	2.47	0.49
1:I:147:GLY:HA3	1:I:175:GLN:N	2.27	0.49
1:O:152:GLN:O	1:O:167:ALA:CB	2.60	0.49
1:U:75:ARG:HG3	1:U:79:ARG:HD2	1.94	0.49
1:U:184:THR:HG22	1:U:191:LEU:HD11	1.90	0.49
1:A:202:THR:CG2	1:A:205:LYS:HE3	2.41	0.49
1:F:20:ARG:HD2	1:U:13:GLY:HA2	1.94	0.49
1:J:45:TRP:HH2	1:N:42:TRP:C	2.21	0.49
1:J:51:TRP:CD1	1:R:45:TRP:HZ3	2.30	0.49
1:V:191:LEU:HD11	1:W:75:ARG:NH1	2.26	0.49
1:I:37:ARG:HB3	1:I:39:PRO:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:41:GLU:HB2	1:O:44:GLN:HA	1.94	0.49
1:M:14:PRO:C	1:M:15:SER:HG	2.13	0.49
1:Q:77:LEU:HD12	1:Q:78:SER:OG	2.11	0.49
1:B:185:PHE:O	1:B:186:GLU:HB3	2.11	0.49
1:R:111:VAL:HG13	1:R:120:ILE:HD13	1.93	0.49
1:E:17:ASP:HB3	1:E:18:PRO:HD2	1.94	0.49
1:M:51:TRP:HB2	1:M:52:PRO:HD2	1.95	0.49
1:O:42:TRP:NE1	1:O:44:GLN:HE22	2.09	0.49
1:H:118:VAL:HG23	1:H:144:LEU:HD11	1.93	0.49
1:J:43:SER:HA	1:R:45:TRP:CH2	2.32	0.49
1:E:39:PRO:HG2	1:E:42:TRP:HZ2	1.77	0.49
1:S:176:SER:HB2	1:S:179:ILE:HA	1.94	0.49
1:A:33:PHE:CZ	1:A:35:LEU:CD1	2.96	0.49
1:D:89:ARG:HG2	1:D:90:HIS:HD2	1.77	0.49
1:L:146:PRO:HB2	1:L:175:GLN:HG3	1.94	0.49
1:R:190:GLN:CB	1:S:74:SER:HB2	2.36	0.49
1:V:47:GLY:O	1:W:52:PRO:HG2	2.13	0.49
1:K:10:LEU:HD11	1:K:77:LEU:CD1	2.43	0.49
1:B:45:TRP:CZ3	1:P:51:TRP:CD2	3.01	0.49
1:B:51:TRP:CD1	1:X:45:TRP:CH2	3.00	0.49
1:F:51:TRP:CD1	1:L:45:TRP:CZ2	3.00	0.49
1:H:128:GLN:HB2	1:H:132:GLY:HA2	1.95	0.49
1:M:40:GLU:O	1:M:41:GLU:HB3	2.12	0.49
1:O:45:TRP:HE3	1:O:47:GLY:N	2.03	0.49
1:D:51:TRP:CZ2	1:V:45:TRP:HD1	2.25	0.49
1:F:181:ILE:N	1:F:182:PRO:HD2	2.27	0.49
1:T:103:HIS:CE1	1:S:103:HIS:CE1	3.00	0.49
1:T:125:GLU:HA	1:T:134:ILE:O	2.13	0.49
1:T:185:PHE:HZ	1:U:164:THR:OG1	1.93	0.49
1:X:133:TYR:HD1	1:X:134:ILE:CG1	2.00	0.49
1:S:1:MET:SD	1:S:1:MET:N	2.74	0.49
1:B:188:ARG:O	1:B:190:GLN:N	2.45	0.49
1:A:44:GLN:NE2	1:Q:44:GLN:O	2.45	0.49
1:F:181:ILE:O	1:F:181:ILE:HG22	2.12	0.49
1:F:185:PHE:HZ	1:E:164:THR:HB	1.78	0.49
1:S:45:TRP:HE3	1:S:47:GLY:N	2.10	0.49
1:U:46:LEU:O	1:U:48:GLY:N	2.46	0.49
1:F:94:ARG:NE	1:F:96:ARG:NH2	2.61	0.49
1:J:111:VAL:HG12	1:K:151:THR:CG2	2.42	0.49
1:R:23:TYR:HB2	1:R:24:PRO:CD	2.43	0.49
1:K:97:VAL:HG22	1:K:165:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:149:ASP:OD2	1:H:183:VAL:O	2.29	0.49
1:T:12:ARG:NH2	1:T:20:ARG:NH1	2.60	0.49
1:V:99:LEU:HD11	1:V:138:PHE:HE2	1.78	0.49
1:I:45:TRP:O	1:I:46:LEU:HB2	2.12	0.49
1:K:25:HIS:CE1	1:S:37:ARG:CD	2.96	0.49
1:F:159:PRO:HB3	1:E:186:GLU:CB	2.42	0.48
1:N:45:TRP:CH2	1:R:49:SER:HA	2.48	0.48
1:X:35:LEU:N	1:X:35:LEU:CD1	2.76	0.48
1:X:99:LEU:HB3	1:X:163:LEU:HB3	1.95	0.48
1:Q:45:TRP:C	1:Q:45:TRP:CE3	2.88	0.48
1:W:45:TRP:O	1:W:49:SER:HB2	2.13	0.48
1:D:18:PRO:HA	1:D:89:ARG:CD	2.43	0.48
1:M:198:LYS:O	1:M:200:ASP:N	2.45	0.48
1:O:45:TRP:CA	1:O:50:SER:HB2	2.36	0.48
1:W:120:ILE:HD11	1:W:165:VAL:HG21	1.94	0.48
1:V:1:MET:N	1:W:31:GLN:NE2	2.53	0.48
1:E:81:LEU:CD2	1:E:162:THR:HG21	2.43	0.48
1:O:51:TRP:HB3	1:S:50:SER:O	2.13	0.48
1:F:51:TRP:NE1	1:L:45:TRP:CD2	2.82	0.48
1:F:131:HIS:O	1:F:133:TYR:CE1	2.66	0.48
1:H:151:THR:HG23	1:G:154:SER:CB	2.43	0.48
1:N:9:SER:HA	1:N:20:ARG:HH22	1.78	0.48
1:G:16:TRP:HB2	1:G:20:ARG:HB2	1.95	0.48
1:G:47:GLY:C	1:G:49:SER:N	2.70	0.48
1:Q:178:GLU:C	1:Q:179:ILE:HD12	2.38	0.48
1:W:51:TRP:HB2	1:W:52:PRO:CD	2.41	0.48
1:A:133:TYR:O	1:D:140:ARG:HG3	2.14	0.48
1:D:153:VAL:HA	1:D:167:ALA:HB2	1.94	0.48
1:D:185:PHE:HZ	1:C:164:THR:HB	1.78	0.48
1:F:151:THR:HG23	1:E:154:SER:OG	2.14	0.48
1:P:23:TYR:HB2	1:P:24:PRO:CD	2.38	0.48
1:R:133:TYR:O	1:R:135:SER:N	2.47	0.48
1:E:39:PRO:O	1:E:40:GLU:CB	2.61	0.48
1:B:16:TRP:NE1	1:B:20:ARG:HH11	2.12	0.48
1:D:159:PRO:HB3	1:C:186:GLU:CD	2.38	0.48
1:H:51:TRP:CZ3	1:G:11:LEU:HD22	2.47	0.48
1:V:8:PHE:HE1	1:W:56:ARG:NE	2.10	0.48
1:C:33:PHE:CE1	1:G:46:LEU:HD23	2.33	0.48
1:G:131:HIS:HB2	1:G:134:ILE:CD1	2.43	0.48
1:O:109:LEU:HD13	1:O:163:LEU:HD13	1.95	0.48
1:B:133:TYR:CD1	1:E:141:LYS:O	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:99:LEU:HD11	1:D:120:ILE:HD13	1.95	0.48
1:F:159:PRO:HB3	1:E:186:GLU:HG2	1.94	0.48
1:R:153:VAL:HA	1:R:167:ALA:HB2	1.95	0.48
1:V:147:GLY:CA	1:V:181:ILE:HG22	2.29	0.48
1:X:35:LEU:CB	1:X:36:PRO:HD3	2.40	0.48
1:X:40:GLU:O	1:X:41:GLU:HB2	2.13	0.48
1:X:48:GLY:C	1:I:52:PRO:HG3	2.38	0.48
1:I:120:ILE:HD11	1:I:165:VAL:HG21	1.96	0.48
1:M:194:PRO:HB3	1:M:203:ALA:HB2	1.95	0.48
1:O:79:ARG:NH1	1:O:162:THR:O	2.45	0.48
1:D:111:VAL:HG13	1:C:151:THR:HG23	1.95	0.48
1:F:24:PRO:HG2	1:F:27:ARG:CB	2.43	0.48
1:N:70:ALA:N	1:N:71:PRO:CD	2.77	0.48
1:K:49:SER:HA	1:S:51:TRP:CE2	2.49	0.48
1:M:39:PRO:C	1:M:41:GLU:N	2.69	0.48
1:Q:37:ARG:HB2	1:Q:40:GLU:HG3	0.64	0.48
1:S:45:TRP:CD2	1:S:46:LEU:N	2.77	0.48
1:F:157:LEU:C	1:E:185:PHE:HD2	2.18	0.48
1:H:45:TRP:HE1	1:V:49:SER:CB	2.26	0.48
1:V:11:LEU:HD21	1:V:171:LYS:NZ	2.29	0.48
1:O:45:TRP:CB	1:O:50:SER:HG	2.26	0.48
1:Q:80:GLN:HG2	1:Q:160:GLU:HG3	1.96	0.48
1:B:18:PRO:O	1:B:19:PHE:CG	2.67	0.48
1:F:51:TRP:CE2	1:L:45:TRP:CE3	3.02	0.48
1:L:180:THR:O	1:L:181:ILE:HG13	2.13	0.48
1:N:49:SER:HA	1:O:52:PRO:CG	2.40	0.48
1:P:181:ILE:N	1:P:182:PRO:CD	2.77	0.48
1:V:140:ARG:NH1	1:U:134:ILE:CD1	2.77	0.48
1:C:124:HIS:O	1:C:125:GLU:HB2	2.14	0.48
1:I:51:TRP:HB2	1:I:52:PRO:HD2	1.95	0.48
1:M:38:LEU:HB2	1:M:39:PRO:CD	2.40	0.48
1:S:97:VAL:HG12	1:S:98:SER:N	2.29	0.48
1:D:108:GLU:HB2	1:C:180:THR:O	2.14	0.47
1:H:40:GLU:C	1:H:41:GLU:HG3	2.37	0.47
1:J:101:VAL:HG23	1:J:138:PHE:CZ	2.49	0.47
1:P:48:GLY:O	1:Q:52:PRO:CD	2.62	0.47
1:G:33:PHE:HB2	1:W:49:SER:OG	2.14	0.47
1:K:45:TRP:HD1	1:K:51:TRP:CZ2	2.32	0.47
1:W:171:LYS:NZ	1:W:188:ARG:CZ	2.77	0.47
1:A:33:PHE:CZ	1:A:35:LEU:CG	2.91	0.47
1:H:33:PHE:CE1	1:H:54:TYR:HB3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:43:SER:CA	1:R:45:TRP:HH2	2.20	0.47
1:X:151:THR:HG23	1:I:154:SER:HB3	1.95	0.47
1:C:77:LEU:HD12	1:C:78:SER:CB	2.44	0.47
1:E:47:GLY:C	1:E:49:SER:H	2.22	0.47
1:G:155:SER:HB2	1:G:163:LEU:HD11	1.96	0.47
1:M:6:VAL:CG1	1:M:8:PHE:CE2	2.94	0.47
1:B:44:GLN:HA	1:P:39:PRO:HA	1.97	0.47
1:A:195:GLU:HB2	1:A:201:GLU:HB2	1.96	0.47
1:N:28:LEU:HD23	1:N:73:TYR:HE1	1.79	0.47
1:P:33:PHE:HB3	1:P:42:TRP:CH2	2.50	0.47
1:V:6:VAL:CG2	1:W:32:ALA:HA	2.44	0.47
1:C:49:SER:CB	1:W:51:TRP:CZ2	2.97	0.47
1:G:169:MET:HB3	1:G:172:LEU:CD1	2.44	0.47
1:O:17:ASP:HB3	1:O:18:PRO:CD	2.44	0.47
1:B:140:ARG:NH1	1:E:134:ILE:HG12	2.20	0.47
1:H:42:TRP:CD1	1:G:8:PHE:HZ	2.32	0.47
1:N:54:TYR:HE1	1:N:56:ARG:HB2	1.79	0.47
1:P:151:THR:OG1	1:Q:154:SER:N	2.47	0.47
1:C:20:ARG:HG3	1:C:24:PRO:HB3	1.96	0.47
1:C:33:PHE:CD1	1:G:46:LEU:HG	2.49	0.47
1:O:186:GLU:HG3	1:O:186:GLU:O	2.13	0.47
1:S:19:PHE:HD2	1:S:45:TRP:CZ3	2.32	0.47
1:A:183:VAL:O	1:A:191:LEU:HD11	2.15	0.47
1:R:52:PRO:CG	1:S:11:LEU:CD2	2.81	0.47
1:E:180:THR:O	1:E:181:ILE:HD13	2.14	0.47
1:K:33:PHE:CG	1:K:34:GLY:N	2.81	0.47
1:W:17:ASP:HB3	1:W:18:PRO:HD2	1.95	0.47
1:B:15:SER:O	1:B:20:ARG:NE	2.47	0.47
1:D:99:LEU:HD21	1:D:140:ARG:CD	2.42	0.47
1:T:17:ASP:N	1:T:20:ARG:NH2	2.47	0.47
1:E:45:TRP:HE3	1:E:46:LEU:N	2.12	0.47
1:G:200:ASP:O	1:G:201:GLU:HG2	2.13	0.47
1:I:202:THR:CB	1:I:205:LYS:HZ1	2.23	0.47
1:M:18:PRO:HD3	1:M:48:GLY:CA	2.44	0.47
1:O:45:TRP:CZ3	1:O:46:LEU:HA	2.49	0.47
1:U:6:VAL:HG13	1:U:6:VAL:O	2.15	0.47
1:U:120:ILE:HD11	1:U:165:VAL:HG21	1.96	0.47
1:B:45:TRP:CZ3	1:P:41:GLU:HB3	2.49	0.47
1:B:153:VAL:HA	1:B:167:ALA:HB2	1.96	0.47
1:A:33:PHE:CD1	1:A:34:GLY:N	2.83	0.47
1:D:18:PRO:HA	1:D:89:ARG:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:52:PRO:HB3	1:C:55:VAL:HG21	1.97	0.47
1:D:99:LEU:CD1	1:D:120:ILE:HD13	2.44	0.47
1:D:120:ILE:O	1:D:139:THR:HA	2.15	0.47
1:F:5:ARG:NE	1:F:205:LYS:O	2.47	0.47
1:H:38:LEU:HA	1:H:42:TRP:CD1	2.49	0.47
1:P:183:VAL:HG12	1:P:184:THR:N	2.30	0.47
1:T:18:PRO:C	1:T:28:LEU:CD2	2.85	0.47
1:V:190:GLN:HB2	1:W:74:SER:HB2	1.97	0.47
1:X:191:LEU:HD11	1:I:75:ARG:NH2	2.29	0.47
1:E:76:ALA:HB2	1:E:159:PRO:HG2	1.97	0.47
1:I:194:PRO:HB3	1:I:203:ALA:HB2	1.97	0.47
1:K:51:TRP:CE2	1:O:49:SER:HA	2.49	0.47
1:S:11:LEU:O	1:S:12:ARG:O	2.32	0.47
1:B:52:PRO:HG3	1:A:11:LEU:HA	1.97	0.47
1:J:11:LEU:HD21	1:J:171:LYS:NZ	2.30	0.47
1:P:147:GLY:N	1:P:181:ILE:HD12	2.29	0.47
1:V:134:ILE:HA	1:U:140:ARG:HH11	1.75	0.47
1:J:131:HIS:HB3	1:J:133:TYR:CE1	2.50	0.47
1:T:181:ILE:N	1:T:182:PRO:CD	2.78	0.47
1:X:79:ARG:HB2	1:X:81:LEU:HG	1.97	0.47
1:E:181:ILE:HG21	1:E:191:LEU:CG	2.44	0.47
1:I:17:ASP:HB3	1:I:18:PRO:CD	2.45	0.47
1:Q:177:ASN:O	1:Q:178:GLU:HB2	2.15	0.47
1:W:171:LYS:HZ3	1:W:188:ARG:NH1	2.13	0.47
1:B:133:TYR:CD2	1:E:142:TYR:CE1	3.03	0.47
1:A:12:ARG:NH1	1:A:16:TRP:C	2.72	0.47
1:F:146:PRO:HB2	1:F:175:GLN:HG3	1.96	0.47
1:L:113:THR:HG22	1:L:118:VAL:HG22	1.96	0.47
1:V:22:TRP:HB2	1:V:28:LEU:HD21	1.96	0.47
1:C:44:GLN:HB3	1:W:44:GLN:CG	2.22	0.47
1:E:176:SER:OG	1:E:177:ASN:N	2.47	0.47
1:E:195:GLU:HB2	1:E:201:GLU:HB2	1.96	0.47
1:B:35:LEU:O	1:B:42:TRP:CZ2	2.68	0.46
1:B:38:LEU:HD22	1:B:44:GLN:HE21	1.80	0.46
1:A:10:LEU:CD1	1:A:77:LEU:HD22	2.44	0.46
1:A:15:SER:HB3	1:A:20:ARG:HH11	1.80	0.46
1:J:140:ARG:NH1	1:I:134:ILE:HG12	2.31	0.46
1:R:191:LEU:HD11	1:S:75:ARG:HG3	1.97	0.46
1:C:23:TYR:O	1:C:25:HIS:N	2.48	0.46
1:F:157:LEU:HD22	1:E:182:PRO:CB	2.45	0.46
1:C:81:LEU:HD11	1:C:83:SER:HA	1.92	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:46:LEU:HD23	1:U:33:PHE:CB	2.44	0.46
1:S:10:LEU:O	1:S:11:LEU:HG	2.16	0.46
1:W:6:VAL:HG23	1:W:8:PHE:CE2	2.51	0.46
1:B:175:GLN:CD	1:B:176:SER:N	2.73	0.46
1:D:99:LEU:HB2	1:D:163:LEU:HB3	1.98	0.46
1:R:33:PHE:CZ	1:S:7:PRO:HG2	2.51	0.46
1:E:33:PHE:CG	1:E:34:GLY:N	2.82	0.46
1:G:45:TRP:O	1:G:46:LEU:CD2	2.63	0.46
1:B:11:LEU:HD22	1:B:77:LEU:HD13	1.98	0.46
1:N:139:THR:O	1:M:135:SER:OG	2.34	0.46
1:E:45:TRP:HD1	1:E:51:TRP:HH2	1.63	0.46
1:E:106:PRO:HA	1:E:124:HIS:HB3	1.95	0.46
1:E:172:LEU:HD22	1:E:205:LYS:H	1.81	0.46
1:U:147:GLY:O	1:U:170:PRO:HG3	2.14	0.46
1:B:15:SER:O	1:B:20:ARG:CD	2.63	0.46
1:D:159:PRO:HA	1:C:186:GLU:CB	2.45	0.46
1:F:33:PHE:HB3	1:F:42:TRP:CH2	2.49	0.46
1:V:44:GLN:CA	1:V:45:TRP:HE3	2.29	0.46
1:V:134:ILE:HG13	1:V:135:SER:N	2.31	0.46
1:C:109:LEU:HD13	1:C:163:LEU:HD13	1.98	0.46
1:C:184:THR:OG1	1:C:185:PHE:N	2.48	0.46
1:D:81:LEU:CD2	1:D:188:ARG:NH1	2.78	0.46
1:F:159:PRO:CG	1:E:186:GLU:CB	2.79	0.46
1:H:45:TRP:HZ2	1:V:43:SER:HA	1.80	0.46
1:J:37:ARG:HG2	1:J:40:GLU:OE1	2.15	0.46
1:J:153:VAL:HA	1:J:167:ALA:HB2	1.97	0.46
1:J:175:GLN:N	1:J:181:ILE:CD1	2.79	0.46
1:T:185:PHE:HD1	1:U:166:GLU:HG2	1.80	0.46
1:I:42:TRP:C	1:I:44:GLN:CD	2.83	0.46
1:O:42:TRP:CD1	1:O:44:GLN:HE22	2.30	0.46
1:J:5:ARG:HG3	1:K:36:PRO:HG3	1.98	0.46
1:M:41:GLU:CG	1:M:42:TRP:N	2.68	0.46
1:O:44:GLN:HB2	1:S:44:GLN:HG3	1.98	0.46
1:U:194:PRO:C	1:U:195:GLU:CD	2.83	0.46
1:B:133:TYR:HB3	1:E:140:ARG:HD2	1.88	0.46
1:D:41:GLU:HG3	1:V:26:SER:HB3	1.97	0.46
1:N:25:HIS:CD2	1:S:11:LEU:HD12	2.51	0.46
1:T:124:HIS:HB3	1:T:136:ARG:HG3	1.97	0.46
1:X:181:ILE:HD12	1:X:182:PRO:HD3	1.97	0.46
1:M:16:TRP:HD1	1:M:20:ARG:CD	2.27	0.46
1:Q:20:ARG:HG3	1:Q:24:PRO:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:43:SER:HB3	1:Q:45:TRP:NE1	2.30	0.46
1:D:99:LEU:HD21	1:D:140:ARG:NE	2.30	0.46
1:F:131:HIS:O	1:F:133:TYR:CD1	2.69	0.46
1:F:156:SER:HB2	1:F:164:THR:HG23	1.98	0.46
1:J:44:GLN:O	1:J:49:SER:HB3	2.15	0.46
1:T:151:THR:CA	1:U:152:GLN:O	2.64	0.46
1:V:134:ILE:O	1:V:135:SER:CB	2.64	0.46
1:E:17:ASP:HB3	1:E:18:PRO:CD	2.45	0.46
1:M:44:GLN:NE2	1:M:44:GLN:HA	2.30	0.46
1:B:32:ALA:HB2	1:B:73:TYR:CD2	2.51	0.46
1:J:136:ARG:HA	1:I:138:PHE:HB2	1.98	0.46
1:V:146:PRO:HB2	1:V:175:GLN:HG3	1.98	0.46
1:C:178:GLU:O	1:C:179:ILE:HG22	2.16	0.46
1:G:35:LEU:HD23	1:G:37:ARG:HG2	1.98	0.46
1:K:187:SER:HB2	1:K:190:GLN:OE1	2.16	0.46
1:M:46:LEU:H	1:M:46:LEU:CD1	2.23	0.46
1:S:45:TRP:HB2	1:S:50:SER:CA	2.45	0.46
1:U:16:TRP:HB2	1:U:20:ARG:HB2	1.98	0.46
1:W:51:TRP:CB	1:W:52:PRO:CD	2.94	0.46
1:C:184:THR:CB	1:C:191:LEU:HD21	2.31	0.45
1:K:38:LEU:CB	1:K:39:PRO:HD3	2.44	0.45
1:M:45:TRP:CZ3	1:U:41:GLU:CG	2.96	0.45
1:W:79:ARG:HD3	1:W:158:SER:HB3	1.98	0.45
1:B:150:PRO:HD2	1:B:182:PRO:HB3	1.97	0.45
1:D:93:ASP:HB3	1:D:169:MET:HB2	1.99	0.45
1:F:150:PRO:O	1:E:151:THR:O	2.34	0.45
1:H:110:THR:HB	1:G:180:THR:HG23	1.96	0.45
1:J:152:GLN:HB3	1:J:168:PRO:HD2	1.98	0.45
1:J:185:PHE:HE1	1:K:164:THR:O	1.97	0.45
1:L:144:LEU:HD12	1:L:145:PRO:O	2.16	0.45
1:L:183:VAL:HG23	1:L:191:LEU:HD13	1.98	0.45
1:R:22:TRP:HB2	1:R:28:LEU:HD11	1.98	0.45
1:T:153:VAL:HA	1:T:167:ALA:HB2	1.99	0.45
1:X:156:SER:HA	1:I:185:PHE:CE2	2.51	0.45
1:I:125:GLU:OE2	1:I:135:SER:HA	2.15	0.45
1:K:17:ASP:HB3	1:K:18:PRO:CD	2.46	0.45
1:M:42:TRP:O	1:M:44:GLN:N	2.50	0.45
1:O:30:ASP:OD1	1:O:30:ASP:O	2.34	0.45
1:W:26:SER:HA	1:W:45:TRP:CH2	2.50	0.45
1:D:151:THR:H	1:C:154:SER:HB3	1.82	0.45
1:F:157:LEU:C	1:E:185:PHE:CD2	2.94	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:51:TRP:NE1	1:R:45:TRP:HZ3	2.12	0.45
1:M:79:ARG:HD3	1:M:158:SER:HB3	1.98	0.45
1:A:33:PHE:CZ	1:A:35:LEU:HD11	2.52	0.45
1:F:45:TRP:HH2	1:T:42:TRP:C	2.24	0.45
1:J:126:GLU:C	1:J:128:GLN:H	2.24	0.45
1:N:40:GLU:HB3	1:O:8:PHE:CE1	2.52	0.45
1:E:181:ILE:CG2	1:E:191:LEU:HG	2.46	0.45
1:G:19:PHE:CZ	1:G:55:VAL:CG1	2.95	0.45
1:M:169:MET:HE3	1:M:172:LEU:CD1	2.46	0.45
1:M:183:VAL:HG11	1:M:190:GLN:HE21	1.82	0.45
1:O:22:TRP:O	1:O:23:TYR:O	2.34	0.45
1:U:38:LEU:HB3	1:U:39:PRO:HD3	1.99	0.45
1:H:2:THR:O	1:H:3:GLU:HB2	2.17	0.45
1:R:45:TRP:HB2	1:R:49:SER:OG	2.17	0.45
1:K:97:VAL:CG2	1:K:165:VAL:HG23	2.46	0.45
1:F:156:SER:O	1:F:164:THR:HG22	2.16	0.45
1:L:35:LEU:HB3	1:L:36:PRO:HD2	1.98	0.45
1:N:12:ARG:CD	1:S:18:PRO:N	2.80	0.45
1:R:45:TRP:HB2	1:R:49:SER:N	2.32	0.45
1:R:185:PHE:CZ	1:S:164:THR:HB	2.50	0.45
1:T:19:PHE:CD1	1:T:28:LEU:HB2	2.47	0.45
1:C:49:SER:HA	1:W:51:TRP:NE1	2.31	0.45
1:B:10:LEU:O	1:B:15:SER:HB2	2.13	0.45
1:A:97:VAL:HG21	1:A:142:TYR:CZ	2.51	0.45
1:A:124:HIS:O	1:A:125:GLU:HB3	2.15	0.45
1:H:108:GLU:HB2	1:G:180:THR:HG22	1.99	0.45
1:J:151:THR:HA	1:K:152:GLN:C	2.42	0.45
1:N:185:PHE:CZ	1:O:164:THR:HB	2.51	0.45
1:K:75:ARG:HD2	1:K:79:ARG:HB2	1.98	0.45
1:S:18:PRO:HD2	1:S:47:GLY:HA3	1.98	0.45
1:V:201:GLU:CD	1:W:56:ARG:HG3	2.42	0.45
1:C:51:TRP:HB2	1:C:52:PRO:CD	2.44	0.45
1:K:32:ALA:HB3	1:K:54:TYR:OH	2.16	0.45
1:U:196:ALA:O	1:U:197:ALA:HB2	2.17	0.45
1:D:11:LEU:CG	1:D:171:LYS:HZ3	2.28	0.45
1:H:187:SER:HB2	1:G:75:ARG:HH22	1.82	0.45
1:J:49:SER:HA	1:K:52:PRO:CG	2.47	0.45
1:P:22:TRP:HB2	1:P:28:LEU:HD13	1.99	0.45
1:P:151:THR:OG1	1:Q:154:SER:OG	2.28	0.45
1:T:12:ARG:NH1	1:T:20:ARG:HD3	2.32	0.45
1:G:51:TRP:HB2	1:G:52:PRO:CD	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:81:LEU:HA	1:K:162:THR:HB	1.98	0.45
1:O:45:TRP:CG	1:O:46:LEU:N	2.75	0.45
1:D:45:TRP:CZ3	1:H:51:TRP:CE2	3.05	0.45
1:D:52:PRO:HA	1:C:55:VAL:HG23	1.98	0.45
1:D:111:VAL:CG2	1:D:120:ILE:HG12	2.46	0.45
1:H:1:MET:SD	1:H:192:GLY:O	2.74	0.45
1:J:185:PHE:CZ	1:K:156:SER:CB	2.99	0.45
1:L:35:LEU:CB	1:L:36:PRO:CD	2.95	0.45
1:C:41:GLU:HB3	1:G:44:GLN:HG3	1.99	0.45
1:E:140:ARG:NE	1:E:142:TYR:OH	2.50	0.45
1:O:184:THR:O	1:O:186:GLU:N	2.45	0.45
1:U:194:PRO:O	1:U:195:GLU:HG3	2.17	0.45
1:W:17:ASP:HB3	1:W:18:PRO:CD	2.47	0.45
1:F:51:TRP:NE1	1:E:52:PRO:HB2	2.32	0.44
1:H:33:PHE:HB3	1:H:42:TRP:HH2	1.82	0.44
1:R:12:ARG:HB3	1:R:20:ARG:HH21	1.82	0.44
1:T:47:GLY:HA2	1:M:48:GLY:HA2	1.99	0.44
1:X:149:ASP:OD2	1:I:154:SER:HB2	2.17	0.44
1:G:41:GLU:HB3	1:W:44:GLN:OE1	2.17	0.44
1:G:111:VAL:HG21	1:G:155:SER:HB3	1.99	0.44
1:M:40:GLU:O	1:M:41:GLU:CB	2.65	0.44
1:Q:125:GLU:HG2	1:Q:126:GLU:H	1.81	0.44
1:U:170:PRO:HB2	1:U:171:LYS:H	1.68	0.44
1:B:9:SER:O	1:B:16:TRP:HD1	1.99	0.44
1:B:126:GLU:CD	1:B:134:ILE:CD1	2.75	0.44
1:B:183:VAL:CG1	1:A:75:ARG:HG3	2.48	0.44
1:D:99:LEU:HD21	1:D:140:ARG:CZ	2.47	0.44
1:D:168:PRO:CB	1:D:188:ARG:HH21	2.30	0.44
1:J:187:SER:HB2	1:K:75:ARG:HH22	1.82	0.44
1:P:26:SER:H	1:X:41:GLU:CD	2.26	0.44
1:V:118:VAL:HB	1:V:142:TYR:HB2	1.99	0.44
1:X:3:GLU:C	1:I:36:PRO:HB3	2.43	0.44
1:C:33:PHE:CG	1:C:43:SER:HB3	2.52	0.44
1:E:183:VAL:O	1:E:183:VAL:HG13	2.18	0.44
1:I:202:THR:CG2	1:I:205:LYS:HZ1	2.31	0.44
1:M:126:GLU:O	1:M:127:ARG:HB2	2.16	0.44
1:S:35:LEU:HG	1:S:36:PRO:CD	2.47	0.44
1:A:5:ARG:C	1:A:6:VAL:HG23	2.42	0.44
1:A:118:VAL:HB	1:A:142:TYR:HB2	1.99	0.44
1:X:150:PRO:O	1:I:151:THR:O	2.35	0.44
1:C:183:VAL:HG12	1:C:183:VAL:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:46:LEU:CD2	1:M:35:LEU:H	2.31	0.44
1:O:56:ARG:HH22	1:S:48:GLY:C	2.25	0.44
1:U:125:GLU:HG2	1:U:126:GLU:H	1.82	0.44
1:W:51:TRP:CD1	1:W:52:PRO:CD	3.00	0.44
1:A:12:ARG:HD2	1:A:18:PRO:CA	2.40	0.44
1:A:174:THR:HG22	1:A:192:GLY:CA	2.48	0.44
1:D:45:TRP:HA	1:H:51:TRP:CZ2	2.52	0.44
1:D:184:THR:HG22	1:D:191:LEU:CB	2.48	0.44
1:V:151:THR:HA	1:W:152:GLN:C	2.42	0.44
1:X:17:ASP:N	1:X:18:PRO:CD	2.81	0.44
1:G:172:LEU:CD2	1:G:204:ALA:HA	2.47	0.44
1:O:44:GLN:NE2	1:S:44:GLN:CD	2.76	0.44
1:W:95:TRP:HB2	1:W:169:MET:HE3	1.99	0.44
1:A:12:ARG:NE	1:X:12:ARG:NH2	2.65	0.44
1:A:79:ARG:NH2	1:A:156:SER:O	2.50	0.44
1:D:175:GLN:NE2	1:D:205:LYS:OXT	2.51	0.44
1:F:47:GLY:O	1:U:48:GLY:O	2.36	0.44
1:N:45:TRP:CZ2	1:S:52:PRO:CA	2.82	0.44
1:P:111:VAL:HG22	1:P:120:ILE:HG23	1.99	0.44
1:X:34:GLY:O	1:X:35:LEU:HD12	2.14	0.44
1:X:51:TRP:CE3	1:I:11:LEU:HD22	2.53	0.44
1:C:44:GLN:CB	1:G:44:GLN:HG2	2.41	0.44
1:M:80:GLN:CD	1:M:160:GLU:HG3	2.43	0.44
1:H:38:LEU:N	1:H:39:PRO:CD	2.81	0.44
1:R:37:ARG:O	1:R:42:TRP:CD1	2.71	0.44
1:M:25:HIS:CE1	1:U:37:ARG:NE	2.85	0.44
1:Q:39:PRO:O	1:Q:41:GLU:OE1	2.35	0.44
1:U:23:TYR:O	1:U:25:HIS:N	2.51	0.44
1:U:153:VAL:HG13	1:U:165:VAL:HG13	2.00	0.44
1:A:202:THR:HG23	1:A:205:LYS:HE3	2.00	0.44
1:R:128:GLN:C	1:R:132:GLY:H	2.25	0.44
1:T:137:CYS:SG	1:T:138:PHE:N	2.91	0.44
1:T:150:PRO:C	1:U:152:GLN:O	2.60	0.44
1:X:151:THR:HG23	1:I:154:SER:N	2.33	0.44
1:G:126:GLU:O	1:G:127:ARG:HB2	2.18	0.44
1:D:99:LEU:CD2	1:D:140:ARG:HH11	2.25	0.44
1:F:12:ARG:C	1:F:20:ARG:NH1	2.76	0.44
1:P:49:SER:C	1:Q:52:PRO:HG3	2.42	0.44
1:X:149:ASP:OD1	1:X:182:PRO:HB2	2.17	0.44
1:G:45:TRP:CD1	1:G:51:TRP:CZ2	3.06	0.44
1:G:175:GLN:HG3	1:G:191:LEU:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:152:GLN:OE1	1:I:168:PRO:HG2	2.17	0.44
1:Q:17:ASP:HB3	1:Q:18:PRO:HD2	2.00	0.44
1:Q:111:VAL:HG21	1:Q:155:SER:HB3	2.00	0.44
1:S:17:ASP:C	1:S:19:PHE:H	2.26	0.44
1:U:8:PHE:O	1:U:9:SER:HB3	2.17	0.44
1:B:8:PHE:CZ	1:Q:48:GLY:HA3	2.53	0.44
1:B:31:GLN:HB3	1:B:73:TYR:OH	2.18	0.44
1:F:54:TYR:HD1	1:E:10:LEU:HD12	1.82	0.44
1:N:137:CYS:O	1:M:137:CYS:O	2.36	0.44
1:C:77:LEU:HD12	1:C:78:SER:CA	2.48	0.44
1:C:80:GLN:OE1	1:C:160:GLU:HG3	2.18	0.44
1:G:175:GLN:HG2	1:G:191:LEU:HG	2.00	0.44
1:I:6:VAL:O	1:I:6:VAL:HG23	2.18	0.44
1:M:16:TRP:CB	1:M:20:ARG:HB2	2.48	0.44
1:Q:125:GLU:CG	1:Q:135:SER:OG	2.66	0.44
1:W:47:GLY:CA	1:W:50:SER:OG	2.64	0.44
1:B:27:ARG:O	1:B:30:ASP:N	2.51	0.43
1:L:159:PRO:HG3	1:M:186:GLU:HB2	2.00	0.43
1:K:34:GLY:C	1:K:35:LEU:HD12	2.43	0.43
1:B:181:ILE:HD12	1:B:182:PRO:HD3	2.00	0.43
1:A:44:GLN:OE1	1:I:44:GLN:O	2.35	0.43
1:C:44:GLN:HG2	1:W:44:GLN:CG	2.49	0.43
1:C:76:ALA:HB2	1:C:159:PRO:HG2	2.01	0.43
1:E:39:PRO:HB2	1:E:42:TRP:NE1	2.34	0.43
1:F:185:PHE:CZ	1:E:164:THR:HB	2.52	0.43
1:T:109:LEU:O	1:U:180:THR:CG2	2.67	0.43
1:G:8:PHE:O	1:G:9:SER:OG	2.32	0.43
1:U:116:GLY:HA2	1:U:144:LEU:HD12	2.00	0.43
1:U:146:PRO:HG2	1:U:205:LYS:HE2	2.01	0.43
1:W:154:SER:O	1:W:165:VAL:HA	2.18	0.43
1:W:181:ILE:HG21	1:W:191:LEU:HD11	1.99	0.43
1:D:126:GLU:HG3	1:D:133:TYR:O	2.19	0.43
1:F:12:ARG:CZ	1:F:20:ARG:HH11	2.31	0.43
1:F:38:LEU:HA	1:F:42:TRP:HB2	2.00	0.43
1:F:45:TRP:HZ3	1:T:41:GLU:HA	1.84	0.43
1:V:20:ARG:NH2	1:C:15:SER:O	2.51	0.43
1:C:79:ARG:NH1	1:C:162:THR:O	2.43	0.43
1:E:176:SER:HB2	1:E:181:ILE:CD1	2.48	0.43
1:G:109:LEU:HD13	1:G:163:LEU:HD13	2.00	0.43
1:G:125:GLU:OE2	1:G:135:SER:HA	2.18	0.43
1:K:79:ARG:HD3	1:K:158:SER:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:169:MET:CE	1:O:172:LEU:HD12	2.43	0.43
1:D:111:VAL:HG22	1:C:151:THR:HG23	2.00	0.43
1:F:190:GLN:HB2	1:E:74:SER:HB2	2.01	0.43
1:C:5:ARG:O	1:C:6:VAL:C	2.61	0.43
1:C:46:LEU:HD22	1:W:40:GLU:HB3	2.00	0.43
1:C:124:HIS:O	1:C:125:GLU:CB	2.66	0.43
1:E:125:GLU:HB3	1:E:135:SER:HA	2.00	0.43
1:S:38:LEU:HB2	1:S:39:PRO:HD3	2.01	0.43
1:U:50:SER:OG	1:U:51:TRP:N	2.50	0.43
1:B:49:SER:HB2	1:X:45:TRP:CZ2	2.54	0.43
1:F:23:TYR:HB2	1:F:24:PRO:CD	2.46	0.43
1:J:33:PHE:HB3	1:J:42:TRP:CH2	2.54	0.43
1:X:52:PRO:HB2	1:I:10:LEU:HG	2.01	0.43
1:I:55:VAL:O	1:I:55:VAL:HG13	2.19	0.43
1:W:12:ARG:HH21	1:W:77:LEU:HD23	1.82	0.43
1:A:12:ARG:NH1	1:A:16:TRP:O	2.52	0.43
1:A:125:GLU:C	1:A:126:GLU:OE1	2.61	0.43
1:J:151:THR:HB	1:K:154:SER:HB3	2.01	0.43
1:N:180:THR:CG2	1:O:109:LEU:O	2.66	0.43
1:R:151:THR:HG23	1:S:154:SER:CB	2.46	0.43
1:T:192:GLY:HA3	1:T:201:GLU:HA	2.00	0.43
1:C:186:GLU:OE1	1:C:186:GLU:HA	2.18	0.43
1:K:44:GLN:CD	1:S:44:GLN:NE2	2.75	0.43
1:M:26:SER:HG	1:M:45:TRP:HH2	1.56	0.43
1:M:80:GLN:HG3	1:M:160:GLU:CG	2.39	0.43
1:W:79:ARG:NH1	1:W:162:THR:O	2.51	0.43
1:H:51:TRP:CE3	1:G:11:LEU:HD22	2.53	0.43
1:J:181:ILE:O	1:J:183:VAL:HG23	2.19	0.43
1:N:54:TYR:CE1	1:N:56:ARG:HB2	2.54	0.43
1:P:128:GLN:HB2	1:P:132:GLY:HA2	2.00	0.43
1:I:75:ARG:HD2	1:I:79:ARG:CD	2.44	0.43
1:S:12:ARG:HD3	1:S:18:PRO:C	2.44	0.43
1:S:18:PRO:HD2	1:S:47:GLY:CA	2.47	0.43
1:U:194:PRO:C	1:U:195:GLU:OE1	2.62	0.43
1:B:44:GLN:OE1	1:P:44:GLN:NE2	2.52	0.43
1:D:151:THR:N	1:C:154:SER:HB3	2.33	0.43
1:D:185:PHE:CZ	1:C:164:THR:HB	2.54	0.43
1:H:153:VAL:HA	1:H:167:ALA:HB2	2.01	0.43
1:J:49:SER:CA	1:K:52:PRO:HG3	2.49	0.43
1:P:51:TRP:HB3	1:P:52:PRO:HD2	2.01	0.43
1:P:146:PRO:HB2	1:P:175:GLN:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:197:ALA:O	1:E:199:SER:N	2.52	0.43
1:K:44:GLN:HG3	1:O:44:GLN:HB3	2.01	0.43
1:S:38:LEU:HB2	1:S:39:PRO:CD	2.48	0.43
1:A:33:PHE:HE1	1:A:35:LEU:O	2.01	0.43
1:D:146:PRO:CG	1:D:175:GLN:CD	2.92	0.43
1:F:159:PRO:CB	1:E:186:GLU:CB	2.97	0.43
1:H:20:ARG:HH12	1:W:15:SER:CB	2.31	0.43
1:L:22:TRP:HB2	1:L:28:LEU:HD11	2.01	0.43
1:E:39:PRO:HG2	1:E:42:TRP:CZ2	2.54	0.43
1:I:120:ILE:CG2	1:I:163:LEU:HD21	2.46	0.43
1:S:147:GLY:O	1:S:170:PRO:HG3	2.18	0.43
1:U:45:TRP:CE3	1:U:46:LEU:HG	2.52	0.43
1:A:133:TYR:CG	1:D:141:LYS:O	2.71	0.42
1:D:44:GLN:O	1:D:45:TRP:CG	2.69	0.42
1:F:157:LEU:HD23	1:E:182:PRO:C	2.43	0.42
1:L:151:THR:OG1	1:L:152:GLN:NE2	2.50	0.42
1:L:152:GLN:HB3	1:L:168:PRO:HD2	2.00	0.42
1:V:49:SER:HA	1:W:52:PRO:CB	2.48	0.42
1:V:181:ILE:N	1:V:182:PRO:CD	2.82	0.42
1:G:43:SER:HB2	1:G:51:TRP:HH2	1.83	0.42
1:I:26:SER:HB2	1:I:45:TRP:HH2	1.80	0.42
1:A:54:TYR:HB2	1:A:56:ARG:HG2	2.01	0.42
1:P:146:PRO:CB	1:P:181:ILE:HD11	2.48	0.42
1:R:99:LEU:HD11	1:R:138:PHE:HE2	1.84	0.42
1:C:26:SER:OG	1:W:40:GLU:HA	2.19	0.42
1:C:44:GLN:HG2	1:W:44:GLN:HE21	1.82	0.42
1:K:40:GLU:HA	1:O:26:SER:CB	2.49	0.42
1:O:94:ARG:HG2	1:O:169:MET:HB2	1.95	0.42
1:S:149:ASP:OD1	1:S:150:PRO:CD	2.67	0.42
1:B:27:ARG:O	1:B:28:LEU:C	2.62	0.42
1:L:151:THR:HG23	1:M:154:SER:HA	2.01	0.42
1:N:151:THR:CG2	1:O:154:SER:CB	2.79	0.42
1:V:31:GLN:HG2	1:V:73:TYR:OH	2.20	0.42
1:X:125:GLU:HG2	1:X:135:SER:HB2	2.01	0.42
1:C:77:LEU:CD1	1:C:78:SER:HB2	2.49	0.42
1:G:4:ARG:O	1:G:4:ARG:HG3	2.20	0.42
1:G:13:GLY:O	1:G:15:SER:N	2.51	0.42
1:G:35:LEU:HG	1:G:36:PRO:HD2	2.01	0.42
1:Q:1:MET:O	1:Q:2:THR:OG1	2.32	0.42
1:A:99:LEU:HD22	1:A:101:VAL:HG23	2.02	0.42
1:A:149:ASP:C	1:A:151:THR:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:89:ARG:HD3	1:D:90:HIS:NE2	2.34	0.42
1:D:144:LEU:HD22	1:D:148:VAL:HG11	2.02	0.42
1:L:183:VAL:CG2	1:L:184:THR:H	2.25	0.42
1:T:151:THR:HA	1:U:152:GLN:HG3	2.00	0.42
1:C:56:ARG:NH2	1:G:48:GLY:O	2.52	0.42
1:G:38:LEU:CB	1:G:39:PRO:HD3	2.50	0.42
1:I:76:ALA:HA	1:I:159:PRO:HD2	2.02	0.42
1:M:16:TRP:HB2	1:M:20:ARG:CB	2.49	0.42
1:O:99:LEU:HG	1:O:140:ARG:HH11	1.85	0.42
1:W:38:LEU:HB2	1:W:39:PRO:HD3	2.00	0.42
1:A:26:SER:HB2	1:I:40:GLU:HA	2.00	0.42
1:D:17:ASP:N	1:D:20:ARG:NH2	2.67	0.42
1:F:181:ILE:N	1:F:182:PRO:CD	2.82	0.42
1:H:181:ILE:O	1:H:183:VAL:HG23	2.19	0.42
1:J:39:PRO:O	1:R:26:SER:HB3	2.19	0.42
1:N:169:MET:O	1:N:170:PRO:C	2.61	0.42
1:P:108:GLU:OE1	1:Q:180:THR:HG21	2.16	0.42
1:P:183:VAL:HG11	1:Q:75:ARG:HG3	2.01	0.42
1:X:11:LEU:CD2	1:I:56:ARG:HD2	2.50	0.42
1:X:99:LEU:HD13	1:X:140:ARG:HD3	2.01	0.42
1:E:176:SER:HB2	1:E:181:ILE:HD11	2.02	0.42
1:G:124:HIS:CG	1:G:125:GLU:H	2.38	0.42
1:S:101:VAL:HB	1:S:161:GLY:C	2.44	0.42
1:A:75:ARG:O	1:A:79:ARG:CB	2.67	0.42
1:A:75:ARG:HA	1:A:75:ARG:HD3	1.92	0.42
1:D:35:LEU:HB3	1:D:36:PRO:CD	2.46	0.42
1:F:36:PRO:HB2	1:F:37:ARG:H	1.69	0.42
1:N:133:TYR:HD1	1:M:140:ARG:CZ	2.32	0.42
1:R:128:GLN:HB2	1:R:132:GLY:N	2.34	0.42
1:T:11:LEU:HD21	1:T:171:LYS:HZ1	1.85	0.42
1:C:33:PHE:CD1	1:G:46:LEU:CG	3.02	0.42
1:C:131:HIS:HB3	1:C:134:ILE:HD12	2.00	0.42
1:E:189:ALA:O	1:E:201:GLU:HG2	2.20	0.42
1:G:145:PRO:HG2	1:G:169:MET:HE1	2.01	0.42
1:K:25:HIS:HE1	1:S:37:ARG:CD	2.32	0.42
1:S:6:VAL:O	1:S:8:PHE:N	2.52	0.42
1:B:15:SER:C	1:B:20:ARG:NE	2.76	0.42
1:A:126:GLU:OE1	1:A:126:GLU:N	2.52	0.42
1:J:22:TRP:HB2	1:J:28:LEU:HD11	2.02	0.42
1:J:42:TRP:O	1:R:45:TRP:CH2	2.72	0.42
1:P:184:THR:HB	1:P:191:LEU:CD1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:10:LEU:HG	1:I:10:LEU:O	2.20	0.42
1:I:149:ASP:OD1	1:I:151:THR:OG1	2.35	0.42
1:M:75:ARG:HB3	1:M:79:ARG:HD2	2.02	0.42
1:H:125:GLU:HG2	1:H:135:SER:HB3	2.02	0.42
1:H:147:GLY:HA2	1:H:181:ILE:CG2	2.50	0.42
1:V:134:ILE:HG13	1:V:135:SER:H	1.84	0.42
1:G:40:GLU:OE2	1:W:46:LEU:HD21	2.20	0.42
1:M:26:SER:CB	1:M:45:TRP:CH2	3.02	0.42
1:M:33:PHE:CZ	1:M:40:GLU:CD	2.98	0.42
1:M:194:PRO:HB3	1:M:203:ALA:CB	2.50	0.42
1:O:51:TRP:CZ2	1:S:49:SER:CB	3.03	0.42
1:O:116:GLY:HA2	1:O:144:LEU:HD12	2.01	0.42
1:O:198:LYS:HE2	1:O:198:LYS:HA	2.02	0.42
1:D:20:ARG:HB3	1:D:25:HIS:ND1	2.35	0.42
1:D:181:ILE:O	1:D:183:VAL:HG23	2.20	0.42
1:F:54:TYR:CD1	1:E:10:LEU:HD12	2.53	0.42
1:F:183:VAL:HG12	1:E:75:ARG:HE	1.85	0.42
1:C:149:ASP:HB2	1:C:170:PRO:HG3	2.02	0.42
1:E:16:TRP:HB2	1:E:20:ARG:HB2	2.02	0.42
1:M:95:TRP:O	1:M:166:GLU:HA	2.19	0.42
1:O:77:LEU:HD12	1:O:78:SER:CA	2.49	0.42
1:Q:79:ARG:C	1:Q:81:LEU:H	2.27	0.42
1:B:168:PRO:HB3	1:B:188:ARG:HH21	1.85	0.42
1:A:148:VAL:O	1:A:175:GLN:OE1	2.38	0.42
1:T:22:TRP:HB3	1:T:23:TYR:H	1.73	0.42
1:T:150:PRO:O	1:U:152:GLN:HA	2.20	0.42
1:C:44:GLN:HA	1:W:41:GLU:HB3	2.02	0.42
1:C:51:TRP:NE1	1:G:49:SER:HB2	2.35	0.42
1:O:22:TRP:O	1:O:28:LEU:HD22	2.20	0.42
1:O:184:THR:C	1:O:186:GLU:H	2.27	0.42
1:S:125:GLU:HB3	1:S:126:GLU:H	1.73	0.42
1:B:45:TRP:CE3	1:P:51:TRP:CE2	3.08	0.41
1:B:133:TYR:HE1	1:E:142:TYR:HA	1.84	0.41
1:B:150:PRO:O	1:A:152:GLN:HA	2.19	0.41
1:A:1:MET:CE	1:A:9:SER:OG	2.67	0.41
1:A:175:GLN:HA	1:A:191:LEU:HD22	2.01	0.41
1:F:40:GLU:O	1:E:8:PHE:CZ	2.73	0.41
1:L:23:TYR:HB2	1:L:24:PRO:CD	2.48	0.41
1:L:175:GLN:N	1:L:181:ILE:HD11	2.31	0.41
1:P:140:ARG:CD	1:O:134:ILE:HD12	2.50	0.41
1:X:185:PHE:HZ	1:I:164:THR:HB	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:178:GLU:O	1:I:179:ILE:HG22	2.19	0.41
1:O:33:PHE:CB	1:O:42:TRP:O	2.68	0.41
1:D:12:ARG:NH2	1:G:12:ARG:O	2.45	0.41
1:D:49:SER:CA	1:C:52:PRO:HG3	2.42	0.41
1:J:185:PHE:C	1:J:187:SER:N	2.78	0.41
1:G:43:SER:N	1:W:44:GLN:OE1	2.53	0.41
1:I:79:ARG:HD3	1:I:158:SER:HB3	2.02	0.41
1:K:44:GLN:OE1	1:S:42:TRP:N	2.46	0.41
1:M:17:ASP:HB3	1:M:47:GLY:C	2.45	0.41
1:M:20:ARG:HG3	1:M:24:PRO:HG3	2.03	0.41
1:U:22:TRP:O	1:U:28:LEU:HD21	2.20	0.41
1:U:33:PHE:CG	1:U:34:GLY:N	2.88	0.41
1:A:12:ARG:NH2	1:X:12:ARG:HH21	2.18	0.41
1:A:54:TYR:CD2	1:A:56:ARG:NH2	2.88	0.41
1:F:151:THR:H	1:E:154:SER:HB3	1.85	0.41
1:J:47:GLY:O	1:O:48:GLY:HA2	2.21	0.41
1:X:94:ARG:HG2	1:X:168:PRO:HA	2.02	0.41
1:G:13:GLY:C	1:G:15:SER:H	2.29	0.41
1:M:46:LEU:HD11	1:U:51:TRP:CH2	2.55	0.41
1:M:95:TRP:CH2	1:M:97:VAL:HG22	2.55	0.41
1:M:150:PRO:HG3	1:M:179:ILE:HD11	2.02	0.41
1:S:10:LEU:C	1:S:11:LEU:HG	2.46	0.41
1:U:79:ARG:NH1	1:U:162:THR:O	2.53	0.41
1:W:38:LEU:HB2	1:W:39:PRO:CD	2.50	0.41
1:B:103:HIS:NE2	1:E:103:HIS:CE1	2.89	0.41
1:D:146:PRO:CG	1:D:175:GLN:HE21	2.32	0.41
1:T:12:ARG:NH2	1:M:17:ASP:O	2.53	0.41
1:V:133:TYR:HE1	1:U:97:VAL:CG1	2.33	0.41
1:C:111:VAL:HG21	1:C:155:SER:HB3	2.01	0.41
1:U:79:ARG:NH2	1:U:156:SER:HB2	2.35	0.41
1:B:185:PHE:O	1:B:186:GLU:HB2	2.19	0.41
1:A:38:LEU:HB3	1:A:39:PRO:HD3	2.01	0.41
1:D:44:GLN:O	1:D:45:TRP:CB	2.68	0.41
1:D:111:VAL:HG23	1:D:120:ILE:CG1	2.51	0.41
1:D:114:LYS:HD2	1:C:112:LYS:HD3	2.01	0.41
1:H:44:GLN:O	1:H:49:SER:HB2	2.21	0.41
1:L:39:PRO:N	1:T:38:LEU:HD11	2.35	0.41
1:P:11:LEU:HD23	1:Q:56:ARG:HD2	2.01	0.41
1:R:201:GLU:CD	1:S:56:ARG:HB2	2.45	0.41
1:X:37:ARG:HD2	1:I:6:VAL:HG11	2.02	0.41
1:X:80:GLN:HG2	1:X:80:GLN:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:TRP:HA	1:C:16:TRP:CE3	2.55	0.41
1:E:46:LEU:HD23	1:M:35:LEU:H	1.85	0.41
1:I:169:MET:SD	1:I:172:LEU:HD11	2.58	0.41
1:M:6:VAL:HG12	1:M:8:PHE:CE2	2.50	0.41
1:U:35:LEU:HD22	1:U:37:ARG:HH12	1.85	0.41
1:U:193:GLY:HA3	1:U:194:PRO:HD3	1.85	0.41
1:D:114:LYS:HD2	1:C:112:LYS:CD	2.50	0.41
1:F:51:TRP:NE1	1:E:52:PRO:CB	2.84	0.41
1:F:175:GLN:NE2	1:F:205:LYS:OXT	2.54	0.41
1:H:44:GLN:O	1:H:45:TRP:HB2	2.20	0.41
1:L:39:PRO:CA	1:T:38:LEU:HD11	2.50	0.41
1:V:134:ILE:CG1	1:V:135:SER:N	2.84	0.41
1:E:26:SER:OG	1:E:27:ARG:N	2.53	0.41
1:E:183:VAL:O	1:E:187:SER:HB3	2.21	0.41
1:I:111:VAL:HG21	1:I:155:SER:CB	2.50	0.41
1:S:120:ILE:HD11	1:S:165:VAL:HG21	2.01	0.41
1:A:51:TRP:CE3	1:A:51:TRP:HA	2.56	0.41
1:H:45:TRP:CE3	1:V:51:TRP:CE2	3.08	0.41
1:J:138:PHE:CD1	1:J:138:PHE:N	2.89	0.41
1:L:30:ASP:HA	1:L:42:TRP:HZ3	1.86	0.41
1:P:18:PRO:O	1:P:28:LEU:HD23	2.21	0.41
1:P:157:LEU:O	1:Q:185:PHE:HB2	2.21	0.41
1:C:42:TRP:O	1:C:43:SER:OG	2.39	0.41
1:G:39:PRO:C	1:G:41:GLU:H	2.29	0.41
1:G:47:GLY:O	1:G:49:SER:N	2.53	0.41
1:K:165:VAL:HG23	1:K:165:VAL:O	2.20	0.41
1:O:55:VAL:CG2	1:O:56:ARG:H	2.14	0.41
1:S:99:LEU:HD22	1:S:120:ILE:HD13	2.01	0.41
1:S:149:ASP:OD2	1:S:151:THR:OG1	2.36	0.41
1:W:39:PRO:C	1:W:41:GLU:H	2.29	0.41
1:B:25:HIS:HB2	1:P:41:GLU:OE2	2.21	0.41
1:B:103:HIS:O	1:B:103:HIS:CG	2.74	0.41
1:B:104:PHE:CE2	1:B:106:PRO:HB3	2.56	0.41
1:A:171:LYS:O	1:A:171:LYS:HG3	2.21	0.41
1:D:20:ARG:CB	1:D:25:HIS:ND1	2.83	0.41
1:F:41:GLU:HB3	1:L:45:TRP:CZ3	2.55	0.41
1:J:134:ILE:HG13	1:I:140:ARG:CZ	2.51	0.41
1:N:45:TRP:CH2	1:R:51:TRP:N	2.85	0.41
1:P:51:TRP:CE3	1:Q:11:LEU:HD22	2.55	0.41
1:P:97:VAL:HG21	1:P:142:TYR:CZ	2.56	0.41
1:T:126:GLU:CG	1:T:134:ILE:HD12	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:28:LEU:HG	1:X:73:TYR:HE2	1.86	0.41
1:C:10:LEU:HD23	1:C:77:LEU:HD22	2.01	0.41
1:E:172:LEU:HD22	1:E:205:LYS:N	2.35	0.41
1:M:76:ALA:HA	1:M:159:PRO:HD2	2.02	0.41
1:O:33:PHE:CD1	1:O:33:PHE:C	2.99	0.41
1:S:45:TRP:HB2	1:S:50:SER:HA	2.01	0.41
1:B:9:SER:O	1:B:16:TRP:HB2	2.21	0.41
1:B:133:TYR:CB	1:E:140:ARG:CZ	2.98	0.41
1:B:133:TYR:CA	1:E:140:ARG:HG3	2.50	0.41
1:A:169:MET:O	1:A:170:PRO:C	2.62	0.41
1:D:9:SER:HA	1:G:15:SER:O	2.21	0.41
1:D:12:ARG:CZ	1:D:20:ARG:CD	2.98	0.41
1:D:41:GLU:O	1:C:8:PHE:CZ	2.74	0.41
1:F:11:LEU:HD21	1:F:171:LYS:NZ	2.36	0.41
1:F:152:GLN:HB3	1:F:168:PRO:HD2	2.03	0.41
1:H:99:LEU:HB3	1:H:163:LEU:HB3	2.03	0.41
1:L:24:PRO:HG2	1:L:27:ARG:CB	2.50	0.41
1:N:12:ARG:NE	1:S:17:ASP:C	2.79	0.41
1:T:151:THR:HA	1:U:152:GLN:O	2.21	0.41
1:C:155:SER:HB2	1:C:163:LEU:HD11	2.03	0.41
1:E:39:PRO:O	1:E:40:GLU:HB2	2.20	0.41
1:G:45:TRP:C	1:G:46:LEU:CD2	2.94	0.41
1:I:16:TRP:HB2	1:I:20:ARG:HD2	2.03	0.41
1:I:46:LEU:HD23	1:Q:34:GLY:HA3	2.03	0.41
1:K:79:ARG:NH1	1:K:162:THR:O	2.46	0.41
1:Q:41:GLU:N	1:Q:41:GLU:CD	2.77	0.41
1:S:118:VAL:CG2	1:S:144:LEU:HD21	2.43	0.41
1:U:40:GLU:C	1:U:41:GLU:CG	2.73	0.41
1:W:51:TRP:HD1	1:W:52:PRO:HD2	1.84	0.41
1:W:94:ARG:HG2	1:W:168:PRO:HA	2.02	0.41
1:B:9:SER:O	1:B:16:TRP:CD1	2.74	0.41
1:F:40:GLU:HB3	1:E:8:PHE:CE2	2.56	0.41
1:J:45:TRP:HZ3	1:N:41:GLU:HA	1.86	0.41
1:J:118:VAL:HB	1:J:142:TYR:HB2	2.03	0.41
1:N:153:VAL:HA	1:N:167:ALA:HB2	2.03	0.41
1:P:54:TYR:HD1	1:Q:10:LEU:HD12	1.86	0.41
1:T:150:PRO:HA	1:T:153:VAL:HG23	2.03	0.41
1:E:55:VAL:O	1:E:55:VAL:HG13	2.21	0.41
1:I:79:ARG:NH1	1:I:162:THR:O	2.43	0.41
1:M:118:VAL:HB	1:M:142:TYR:HB2	2.03	0.41
1:Q:105:ALA:O	1:Q:124:HIS:ND1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:41:GLU:O	1:U:42:TRP:CD1	2.74	0.41
1:W:51:TRP:HD1	1:W:52:PRO:CD	2.34	0.41
1:B:35:LEU:HD11	1:A:4:ARG:HB3	2.02	0.40
1:F:105:ALA:O	1:F:124:HIS:ND1	2.54	0.40
1:P:28:LEU:HG	1:P:73:TYR:OH	2.21	0.40
1:T:150:PRO:O	1:U:151:THR:O	2.38	0.40
1:E:155:SER:HB2	1:E:163:LEU:HD11	2.03	0.40
1:O:45:TRP:O	1:O:49:SER:OG	2.39	0.40
1:W:169:MET:HB3	1:W:172:LEU:HD23	2.03	0.40
1:A:35:LEU:O	1:A:35:LEU:CD1	2.53	0.40
1:A:124:HIS:HB3	1:A:125:GLU:H	1.59	0.40
1:F:156:SER:CA	1:E:185:PHE:HE2	2.34	0.40
1:N:22:TRP:CD1	1:N:28:LEU:HD21	2.56	0.40
1:P:46:LEU:HD23	1:P:50:SER:HA	2.03	0.40
1:I:45:TRP:HB3	1:I:51:TRP:HZ3	1.86	0.40
1:B:152:GLN:HB3	1:B:168:PRO:HD2	2.02	0.40
1:A:1:MET:HG2	1:A:9:SER:OG	2.22	0.40
1:A:82:SER:C	1:A:84:GLY:H	2.29	0.40
1:H:181:ILE:N	1:H:182:PRO:CD	2.84	0.40
1:J:153:VAL:HG22	1:J:167:ALA:HB2	2.03	0.40
1:N:94:ARG:HG2	1:N:167:ALA:O	2.22	0.40
1:R:151:THR:HG23	1:S:153:VAL:C	2.46	0.40
1:X:40:GLU:O	1:I:8:PHE:CD1	2.74	0.40
1:X:54:TYR:HB2	1:I:10:LEU:CD2	2.51	0.40
1:G:176:SER:HB2	1:G:179:ILE:HA	2.03	0.40
1:M:35:LEU:O	1:M:40:GLU:CD	2.64	0.40
1:O:51:TRP:O	1:O:52:PRO:C	2.64	0.40
1:O:124:HIS:O	1:O:125:GLU:HB2	2.21	0.40
1:U:29:PHE:CD1	1:U:45:TRP:CH2	3.04	0.40
1:U:148:VAL:HA	1:U:170:PRO:HD3	2.03	0.40
1:U:148:VAL:HG22	1:U:169:MET:HG2	2.04	0.40
1:U:184:THR:CG2	1:U:191:LEU:HD11	2.52	0.40
1:H:11:LEU:CD1	1:H:171:LYS:HE3	2.31	0.40
1:L:139:THR:O	1:Q:135:SER:HB2	2.21	0.40
1:N:51:TRP:HE3	1:N:52:PRO:HD2	1.86	0.40
1:P:29:PHE:HB2	1:P:46:LEU:HD11	2.03	0.40
1:P:156:SER:HB3	1:Q:185:PHE:CD1	2.57	0.40
1:R:1:MET:N	1:R:175:GLN:O	2.55	0.40
1:R:11:LEU:HD21	1:R:171:LYS:NZ	2.36	0.40
1:V:8:PHE:HE2	1:W:34:GLY:CA	2.28	0.40
1:Q:40:GLU:O	1:Q:41:GLU:O	2.39	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:43:SER:C	1:S:44:GLN:HG2	2.45	0.40
1:U:8:PHE:C	1:U:10:LEU:H	2.30	0.40
1:U:118:VAL:HB	1:U:142:TYR:HB2	2.03	0.40
1:U:191:LEU:HA	1:U:195:GLU:CD	2.47	0.40
1:D:45:TRP:CZ2	1:H:49:SER:HB3	2.57	0.40
1:F:17:ASP:N	1:F:20:ARG:NH2	2.69	0.40
1:F:47:GLY:O	1:U:49:SER:HA	2.22	0.40
1:F:190:GLN:OE1	1:E:74:SER:HB2	2.21	0.40
1:N:12:ARG:HD3	1:S:18:PRO:CD	2.50	0.40
1:R:133:TYR:CD1	1:R:133:TYR:N	2.88	0.40
1:G:43:SER:HB2	1:G:51:TRP:CH2	2.57	0.40
1:M:12:ARG:HG3	1:M:19:PHE:CD2	2.57	0.40
1:M:14:PRO:C	1:M:16:TRP:H	2.30	0.40
1:O:120:ILE:HD11	1:O:165:VAL:HG21	2.03	0.40
1:Q:43:SER:HB3	1:Q:45:TRP:HE1	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	175/205 (85%)	124 (71%)	37 (21%)	14 (8%)	1	8
1	B	146/205 (71%)	112 (77%)	28 (19%)	6 (4%)	2	19
1	C	157/205 (77%)	107 (68%)	36 (23%)	14 (9%)	0	7
1	D	151/205 (74%)	129 (85%)	15 (10%)	7 (5%)	2	17
1	E	163/205 (80%)	120 (74%)	29 (18%)	14 (9%)	0	7
1	F	149/205 (73%)	125 (84%)	22 (15%)	2 (1%)	9	39
1	G	171/205 (83%)	125 (73%)	31 (18%)	15 (9%)	0	7
1	H	146/205 (71%)	122 (84%)	14 (10%)	10 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	159/205 (78%)	119 (75%)	30 (19%)	10 (6%)	1	12
1	J	148/205 (72%)	126 (85%)	17 (12%)	5 (3%)	3	23
1	K	165/205 (80%)	124 (75%)	35 (21%)	6 (4%)	2	22
1	L	151/205 (74%)	129 (85%)	15 (10%)	7 (5%)	2	17
1	M	169/205 (82%)	123 (73%)	29 (17%)	17 (10%)	0	6
1	N	144/205 (70%)	117 (81%)	22 (15%)	5 (4%)	3	23
1	O	166/205 (81%)	119 (72%)	36 (22%)	11 (7%)	1	12
1	P	148/205 (72%)	125 (84%)	18 (12%)	5 (3%)	3	23
1	Q	153/205 (75%)	113 (74%)	26 (17%)	14 (9%)	0	6
1	R	153/205 (75%)	131 (86%)	19 (12%)	3 (2%)	6	32
1	S	172/205 (84%)	129 (75%)	34 (20%)	9 (5%)	1	15
1	T	152/205 (74%)	125 (82%)	22 (14%)	5 (3%)	3	23
1	U	165/205 (80%)	111 (67%)	39 (24%)	15 (9%)	0	7
1	V	145/205 (71%)	124 (86%)	15 (10%)	6 (4%)	2	19
1	W	159/205 (78%)	120 (76%)	33 (21%)	6 (4%)	2	21
1	X	150/205 (73%)	127 (85%)	14 (9%)	9 (6%)	1	13
All	All	3757/4920 (76%)	2926 (78%)	616 (16%)	215 (6%)	1	14

All (215) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	17	ASP
1	B	134	ILE
1	B	177	ASN
1	B	189	ALA
1	A	44	GLN
1	A	51	TRP
1	A	179	ILE
1	D	72	ALA
1	D	184	THR
1	H	45	TRP
1	H	184	THR
1	J	38	LEU
1	J	184	THR
1	L	37	ARG
1	L	181	ILE

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Mol	Chain	Res	Type
1	L	183	VAL
1	P	184	THR
1	T	23	TYR
1	T	26	SER
1	T	134	ILE
1	T	178	GLU
1	T	179	ILE
1	V	133	TYR
1	V	135	SER
1	X	41	GLU
1	X	79	ARG
1	X	83	SER
1	C	38	LEU
1	C	125	GLU
1	C	179	ILE
1	E	40	GLU
1	E	198	LYS
1	G	9	SER
1	G	14	PRO
1	G	45	TRP
1	G	51	TRP
1	G	126	GLU
1	I	46	LEU
1	I	125	GLU
1	K	38	LEU
1	K	179	ILE
1	K	200	ASP
1	M	17	ASP
1	M	41	GLU
1	M	127	ARG
1	M	179	ILE
1	O	125	GLU
1	Q	4	ARG
1	Q	41	GLU
1	Q	46	LEU
1	Q	178	GLU
1	S	7	PRO
1	S	12	ARG
1	S	24	PRO
1	S	40	GLU
1	S	51	TRP
1	S	179	ILE

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Mol	Chain	Res	Type
1	U	41	GLU
1	U	48	GLY
1	W	51	TRP
1	B	186	GLU
1	A	126	GLU
1	A	172	LEU
1	D	45	TRP
1	F	96	ARG
1	H	4	ARG
1	H	127	ARG
1	J	45	TRP
1	N	46	LEU
1	V	41	GLU
1	V	45	TRP
1	X	35	LEU
1	X	45	TRP
1	C	49	SER
1	C	176	SER
1	C	182	PRO
1	E	125	GLU
1	E	180	THR
1	G	17	ASP
1	G	43	SER
1	G	46	LEU
1	G	179	ILE
1	I	179	ILE
1	M	47	GLY
1	M	199	SER
1	M	203	ALA
1	O	46	LEU
1	O	183	VAL
1	Q	40	GLU
1	Q	81	LEU
1	U	45	TRP
1	U	47	GLY
1	U	170	PRO
1	B	183	VAL
1	A	40	GLU
1	A	80	GLN
1	N	72	ALA
1	R	133	TYR
1	X	36	PRO

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Mol	Chain	Res	Type
1	C	44	GLN
1	C	80	GLN
1	E	188	ARG
1	G	39	PRO
1	I	10	LEU
1	I	12	ARG
1	I	17	ASP
1	I	23	TYR
1	I	126	GLU
1	K	17	ASP
1	M	36	PRO
1	M	44	GLN
1	M	125	GLU
1	M	180	THR
1	O	15	SER
1	O	80	GLN
1	Q	2	THR
1	S	15	SER
1	U	16	TRP
1	U	39	PRO
1	U	126	GLU
1	U	179	ILE
1	U	194	PRO
1	W	15	SER
1	W	45	TRP
1	W	80	GLN
1	W	182	PRO
1	A	6	VAL
1	A	16	TRP
1	A	83	SER
1	A	152	GLN
1	D	183	VAL
1	F	41	GLU
1	L	46	LEU
1	N	45	TRP
1	P	41	GLU
1	R	41	GLU
1	C	45	TRP
1	E	17	ASP
1	E	80	GLN
1	G	201	GLU
1	I	45	TRP

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Mol	Chain	Res	Type
1	K	39	PRO
1	M	43	SER
1	O	14	PRO
1	O	17	ASP
1	O	23	TYR
1	Q	44	GLN
1	Q	126	GLU
1	S	44	GLN
1	U	44	GLN
1	W	17	ASP
1	A	125	GLU
1	H	39	PRO
1	H	144	LEU
1	H	183	VAL
1	N	164	THR
1	C	20	ARG
1	C	23	TYR
1	E	7	PRO
1	E	124	HIS
1	E	182	PRO
1	G	127	ARG
1	M	79	ARG
1	M	126	GLU
1	Q	20	ARG
1	Q	45	TRP
1	U	17	ASP
1	U	53	GLY
1	D	41	GLU
1	J	183	VAL
1	L	184	THR
1	P	134	ILE
1	R	134	ILE
1	V	46	LEU
1	X	38	LEU
1	C	170	PRO
1	E	47	GLY
1	G	41	GLU
1	G	170	PRO
1	I	80	GLN
1	K	80	GLN
1	M	39	PRO
1	O	51	TRP

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Mol	Chain	Res	Type
1	Q	17	ASP
1	D	134	ILE
1	J	179	ILE
1	P	179	ILE
1	X	134	ILE
1	C	36	PRO
1	E	170	PRO
1	E	179	ILE
1	G	23	TYR
1	M	170	PRO
1	Q	48	GLY
1	A	18	PRO
1	H	38	LEU
1	L	147	GLY
1	L	179	ILE
1	V	179	ILE
1	X	179	ILE
1	N	179	ILE
1	C	17	ASP
1	O	7	PRO
1	S	17	ASP
1	U	153	VAL
1	A	17	ASP
1	D	179	ILE
1	H	179	ILE
1	E	183	VAL
1	M	7	PRO
1	O	24	PRO
1	Q	179	ILE
1	H	134	ILE
1	P	181	ILE
1	U	51	TRP

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	157/175 (90%)	147 (94%)	10 (6%)	16	43
1	B	139/175 (79%)	136 (98%)	3 (2%)	45	65
1	C	147/175 (84%)	140 (95%)	7 (5%)	23	49
1	D	146/175 (83%)	140 (96%)	6 (4%)	27	53
1	E	150/175 (86%)	143 (95%)	7 (5%)	23	50
1	F	143/175 (82%)	143 (100%)	0	100	100
1	G	155/175 (89%)	152 (98%)	3 (2%)	50	67
1	H	142/175 (81%)	139 (98%)	3 (2%)	47	65
1	I	147/175 (84%)	143 (97%)	4 (3%)	39	61
1	J	143/175 (82%)	139 (97%)	4 (3%)	38	61
1	K	153/175 (87%)	149 (97%)	4 (3%)	40	62
1	L	145/175 (83%)	143 (99%)	2 (1%)	59	71
1	M	153/175 (87%)	148 (97%)	5 (3%)	33	58
1	N	142/175 (81%)	141 (99%)	1 (1%)	76	78
1	O	150/175 (86%)	144 (96%)	6 (4%)	28	53
1	P	144/175 (82%)	141 (98%)	3 (2%)	47	65
1	Q	143/175 (82%)	136 (95%)	7 (5%)	22	49
1	R	147/175 (84%)	143 (97%)	4 (3%)	39	61
1	S	156/175 (89%)	150 (96%)	6 (4%)	29	55
1	T	146/175 (83%)	145 (99%)	1 (1%)	76	78
1	U	151/175 (86%)	146 (97%)	5 (3%)	33	58
1	V	143/175 (82%)	142 (99%)	1 (1%)	76	78
1	W	149/175 (85%)	144 (97%)	5 (3%)	32	57
1	X	147/175 (84%)	144 (98%)	3 (2%)	48	66
All	All	3538/4200 (84%)	3438 (97%)	100 (3%)	38	61

All (100) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	117	VAL
1	B	175	GLN
1	B	181	ILE
1	A	19	PHE
1	A	51	TRP
1	A	97	VAL

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Mol	Chain	Res	Type
1	A	101	VAL
1	A	103	HIS
1	A	117	VAL
1	A	166	GLU
1	A	175	GLN
1	A	178	GLU
1	A	202	THR
1	D	51	TRP
1	D	123	LYS
1	D	126	GLU
1	D	131	HIS
1	D	148	VAL
1	D	171	LYS
1	H	33	PHE
1	H	135	SER
1	H	171	LYS
1	J	38	LEU
1	J	99	LEU
1	J	131	HIS
1	J	138	PHE
1	L	35	LEU
1	L	134	ILE
1	N	175	GLN
1	P	11	LEU
1	P	35	LEU
1	P	151	THR
1	R	120	ILE
1	R	127	ARG
1	R	133	TYR
1	R	181	ILE
1	T	99	LEU
1	V	33	PHE
1	X	31	GLN
1	X	151	THR
1	X	181	ILE
1	C	16	TRP
1	C	19	PHE
1	C	41	GLU
1	C	44	GLN
1	C	45	TRP
1	C	185	PHE
1	C	187	SER

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Mol	Chain	Res	Type
1	E	23	TYR
1	E	45	TRP
1	E	81	LEU
1	E	101	VAL
1	E	133	TYR
1	E	191	LEU
1	E	205	LYS
1	G	45	TRP
1	G	131	HIS
1	G	198	LYS
1	I	42	TRP
1	I	45	TRP
1	I	125	GLU
1	I	130	GLU
1	K	5	ARG
1	K	45	TRP
1	K	125	GLU
1	K	160	GLU
1	M	10	LEU
1	M	42	TRP
1	M	45	TRP
1	M	46	LEU
1	M	133	TYR
1	O	25	HIS
1	O	42	TRP
1	O	75	ARG
1	O	124	HIS
1	O	160	GLU
1	O	181	ILE
1	Q	19	PHE
1	Q	41	GLU
1	Q	43	SER
1	Q	45	TRP
1	Q	81	LEU
1	Q	101	VAL
1	Q	133	TYR
1	S	25	HIS
1	S	31	GLN
1	S	101	VAL
1	S	134	ILE
1	S	144	LEU
1	S	205	LYS

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Mol	Chain	Res	Type
1	U	8	PHE
1	U	25	HIS
1	U	33	PHE
1	U	80	GLN
1	U	160	GLU
1	W	41	GLU
1	W	45	TRP
1	W	75	ARG
1	W	127	ARG
1	W	185	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (57) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	131	HIS
1	A	102	ASN
1	A	124	HIS
1	A	175	GLN
1	D	44	GLN
1	D	90	HIS
1	D	131	HIS
1	D	152	GLN
1	F	131	HIS
1	F	175	GLN
1	H	152	GLN
1	J	103	HIS
1	L	152	GLN
1	N	31	GLN
1	N	103	HIS
1	N	152	GLN
1	N	190	GLN
1	P	31	GLN
1	P	44	GLN
1	R	124	HIS
1	R	152	GLN
1	R	175	GLN
1	T	103	HIS
1	T	152	GLN
1	T	175	GLN
1	V	44	GLN
1	V	128	GLN
1	X	103	HIS

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Mol	Chain	Res	Type
1	C	25	HIS
1	C	152	GLN
1	C	175	GLN
1	C	190	GLN
1	E	124	HIS
1	E	190	GLN
1	G	103	HIS
1	I	44	GLN
1	I	80	GLN
1	I	175	GLN
1	K	25	HIS
1	K	31	GLN
1	K	80	GLN
1	K	131	HIS
1	M	25	HIS
1	M	80	GLN
1	M	103	HIS
1	M	190	GLN
1	O	31	GLN
1	Q	44	GLN
1	S	25	HIS
1	S	102	ASN
1	S	103	HIS
1	S	152	GLN
1	S	177	ASN
1	U	190	GLN
1	W	31	GLN
1	W	131	HIS
1	W	175	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	181/205 (88%)	0.98	27 (14%) 5 5	27, 61, 113, 195	0
1	B	156/205 (76%)	0.99	23 (14%) 6 5	47, 60, 112, 161	0
1	C	166/205 (80%)	0.73	13 (7%) 19 12	28, 60, 95, 158	0
1	D	165/205 (80%)	0.85	16 (9%) 13 9	13, 65, 104, 165	0
1	E	173/205 (84%)	0.80	15 (8%) 16 10	24, 65, 99, 131	0
1	F	163/205 (79%)	0.88	19 (11%) 9 7	27, 65, 112, 138	0
1	G	179/205 (87%)	0.76	12 (6%) 24 14	16, 64, 105, 133	0
1	H	160/205 (78%)	0.83	15 (9%) 14 9	24, 66, 100, 166	0
1	I	169/205 (82%)	0.72	10 (5%) 28 16	18, 61, 99, 152	0
1	J	162/205 (79%)	0.76	14 (8%) 16 11	26, 65, 101, 136	0
1	K	175/205 (85%)	0.90	23 (13%) 7 6	19, 68, 100, 135	0
1	L	165/205 (80%)	0.72	14 (8%) 16 11	16, 61, 95, 177	0
1	M	177/205 (86%)	0.89	23 (12%) 7 6	29, 65, 123, 159	0
1	N	162/205 (79%)	0.90	21 (12%) 7 6	31, 67, 112, 156	0
1	O	174/205 (84%)	0.88	22 (12%) 8 6	27, 66, 107, 146	0
1	P	164/205 (80%)	0.79	16 (9%) 13 9	25, 65, 108, 137	0
1	Q	161/205 (78%)	0.78	14 (8%) 16 10	27, 63, 102, 175	0
1	R	167/205 (81%)	0.68	11 (6%) 24 14	20, 64, 97, 138	0
1	S	180/205 (87%)	0.87	15 (8%) 17 11	28, 67, 106, 141	0
1	T	166/205 (80%)	0.83	15 (9%) 15 10	23, 67, 97, 151	0
1	U	175/205 (85%)	0.90	24 (13%) 6 6	26, 64, 108, 246	0
1	V	161/205 (78%)	0.79	15 (9%) 14 9	29, 63, 106, 156	0
1	W	169/205 (82%)	0.74	18 (10%) 11 8	24, 65, 114, 159	0
1	X	166/205 (80%)	0.81	14 (8%) 17 11	32, 63, 98, 177	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	4036/4920 (82%)	0.83	409 (10%) 12 8	13, 64, 107, 246	0

All (409) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	33	PHE	6.3
1	V	132	GLY	6.3
1	D	76	ALA	5.9
1	A	172	LEU	5.5
1	P	84	GLY	5.4
1	I	195	GLU	5.2
1	X	33	PHE	5.2
1	A	84	GLY	5.0
1	O	42	TRP	5.0
1	U	48	GLY	4.8
1	O	150	PRO	4.7
1	B	16	TRP	4.7
1	F	147	GLY	4.7
1	K	41	GLU	4.5
1	S	45	TRP	4.5
1	A	44	GLN	4.4
1	Q	51	TRP	4.4
1	A	2	THR	4.3
1	O	43	SER	4.3
1	U	1	MET	4.2
1	B	190	GLN	4.2
1	B	11	LEU	4.2
1	L	36	PRO	4.2
1	B	133	TYR	4.2
1	W	31	GLN	4.1
1	F	106	PRO	4.1
1	M	40	GLU	4.0
1	G	125	GLU	4.0
1	K	1	MET	4.0
1	T	21	ASP	3.9
1	R	71	PRO	3.9
1	W	1	MET	3.9
1	B	18	PRO	3.8
1	B	17	ASP	3.8
1	I	34	GLY	3.8
1	M	38	LEU	3.8
1	J	94	ARG	3.8

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Mol	Chain	Res	Type	RSRZ
1	G	205	LYS	3.7
1	B	134	ILE	3.7
1	H	34	GLY	3.7
1	P	44	GLN	3.6
1	V	133	TYR	3.6
1	T	25	HIS	3.6
1	H	1	MET	3.6
1	U	193	GLY	3.6
1	E	123	LYS	3.5
1	H	133	TYR	3.5
1	S	125	GLU	3.5
1	F	36	PRO	3.5
1	N	70	ALA	3.5
1	C	125	GLU	3.5
1	U	197	ALA	3.5
1	T	22	TRP	3.5
1	H	30	ASP	3.4
1	L	149	ASP	3.4
1	V	100	ASP	3.4
1	E	124	HIS	3.4
1	N	22	TRP	3.4
1	A	189	ALA	3.4
1	M	126	GLU	3.3
1	T	70	ALA	3.3
1	S	156	SER	3.3
1	U	44	GLN	3.3
1	E	48	GLY	3.3
1	P	79	ARG	3.2
1	L	144	LEU	3.2
1	K	147	GLY	3.2
1	J	38	LEU	3.2
1	V	84	GLY	3.2
1	R	70	ALA	3.2
1	A	1	MET	3.2
1	L	192	GLY	3.2
1	V	134	ILE	3.2
1	S	48	GLY	3.2
1	A	197	ALA	3.2
1	O	185	PHE	3.1
1	N	192	GLY	3.1
1	D	22	TRP	3.1
1	Q	1	MET	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	178	GLU	3.1
1	A	41	GLU	3.1
1	M	203	ALA	3.1
1	X	34	GLY	3.1
1	S	47	GLY	3.1
1	C	93	ASP	3.1
1	M	13	GLY	3.1
1	W	177	ASN	3.1
1	A	171	LYS	3.1
1	N	100	ASP	3.1
1	R	47	GLY	3.1
1	N	133	TYR	3.0
1	Q	46	LEU	3.0
1	B	53	GLY	3.0
1	I	205	LYS	3.0
1	A	175	GLN	3.0
1	J	37	ARG	3.0
1	C	41	GLU	3.0
1	I	170	PRO	3.0
1	U	190	GLN	3.0
1	M	197	ALA	3.0
1	J	75	ARG	3.0
1	K	170	PRO	3.0
1	A	14	PRO	3.0
1	X	82	SER	3.0
1	U	196	ALA	3.0
1	C	39	PRO	2.9
1	W	195	GLU	2.9
1	H	5	ARG	2.9
1	M	135	SER	2.9
1	T	133	TYR	2.9
1	V	160	GLU	2.9
1	C	186	GLU	2.9
1	J	70	ALA	2.9
1	O	45	TRP	2.9
1	D	133	TYR	2.9
1	M	41	GLU	2.9
1	P	161	GLY	2.9
1	Q	84	GLY	2.9
1	S	13	GLY	2.9
1	C	25	HIS	2.8
1	C	13	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	L	134	ILE	2.8
1	G	46	LEU	2.8
1	B	19	PHE	2.8
1	P	205	LYS	2.8
1	U	171	LYS	2.8
1	F	175	GLN	2.8
1	J	48	GLY	2.8
1	G	202	THR	2.8
1	O	204	ALA	2.8
1	Q	180	THR	2.8
1	V	78	SER	2.8
1	B	177	ASN	2.8
1	R	53	GLY	2.8
1	N	21	ASP	2.8
1	O	17	ASP	2.8
1	B	170	PRO	2.8
1	P	9	SER	2.8
1	F	133	TYR	2.8
1	K	178	GLU	2.8
1	O	48	GLY	2.8
1	O	113	THR	2.8
1	W	46	LEU	2.7
1	U	71	PRO	2.7
1	H	192	GLY	2.7
1	W	2	THR	2.7
1	W	126	GLU	2.7
1	X	21	ASP	2.7
1	Q	100	ASP	2.7
1	S	172	LEU	2.7
1	U	127	ARG	2.7
1	M	205	LYS	2.7
1	M	17	ASP	2.7
1	W	172	LEU	2.7
1	K	113	THR	2.7
1	J	71	PRO	2.7
1	D	31	GLN	2.7
1	M	107	ASP	2.7
1	H	72	ALA	2.7
1	K	204	ALA	2.7
1	K	125	GLU	2.7
1	U	41	GLU	2.7
1	V	176	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	K	50	SER	2.7
1	P	24	PRO	2.6
1	A	16	TRP	2.6
1	S	44	GLN	2.6
1	V	122	GLY	2.6
1	E	93	ASP	2.6
1	K	176	SER	2.6
1	N	180	THR	2.6
1	T	201	GLU	2.6
1	Q	125	GLU	2.6
1	H	38	LEU	2.6
1	B	6	VAL	2.6
1	S	37	ARG	2.6
1	R	131	HIS	2.6
1	M	105	ALA	2.6
1	P	160	GLU	2.6
1	U	140	ARG	2.6
1	A	72	ALA	2.6
1	B	132	GLY	2.6
1	N	163	LEU	2.6
1	O	53	GLY	2.6
1	A	126	GLU	2.6
1	W	125	GLU	2.6
1	J	134	ILE	2.6
1	W	155	SER	2.6
1	K	13	GLY	2.6
1	J	2	THR	2.6
1	O	166	GLU	2.6
1	I	6	VAL	2.6
1	D	70	ALA	2.6
1	X	76	ALA	2.6
1	O	44	GLN	2.6
1	X	22	TRP	2.5
1	S	176	SER	2.5
1	Q	168	PRO	2.5
1	A	53	GLY	2.5
1	X	133	TYR	2.5
1	V	45	TRP	2.5
1	R	10	LEU	2.5
1	J	177	ASN	2.5
1	D	80	GLN	2.5
1	R	128	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	T	175	GLN	2.5
1	B	35	LEU	2.5
1	A	45	TRP	2.5
1	H	3	GLU	2.5
1	T	45	TRP	2.5
1	B	7	PRO	2.5
1	S	152	GLN	2.5
1	A	174	THR	2.5
1	J	35	LEU	2.5
1	A	198	LYS	2.5
1	N	71	PRO	2.5
1	O	149	ASP	2.5
1	L	34	GLY	2.5
1	L	156	SER	2.5
1	K	203	ALA	2.5
1	X	35	LEU	2.5
1	M	14	PRO	2.4
1	A	13	GLY	2.4
1	V	161	GLY	2.4
1	J	135	SER	2.4
1	B	183	VAL	2.4
1	E	38	LEU	2.4
1	O	51	TRP	2.4
1	T	106	PRO	2.4
1	U	194	PRO	2.4
1	N	48	GLY	2.4
1	E	126	GLU	2.4
1	Q	178	GLU	2.4
1	F	96	ARG	2.4
1	C	31	GLN	2.4
1	U	45	TRP	2.4
1	I	39	PRO	2.4
1	I	49	SER	2.4
1	K	180	THR	2.4
1	W	179	ILE	2.4
1	E	188	ARG	2.4
1	N	80	GLN	2.4
1	A	176	SER	2.4
1	O	205	LYS	2.4
1	D	184	THR	2.4
1	M	134	ILE	2.4
1	W	40	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	192	GLY	2.4
1	F	20	ARG	2.4
1	H	37	ARG	2.4
1	J	17	ASP	2.4
1	P	190	GLN	2.3
1	L	145	PRO	2.3
1	C	26	SER	2.3
1	U	46	LEU	2.3
1	D	49	SER	2.3
1	P	83	SER	2.3
1	P	187	SER	2.3
1	E	9	SER	2.3
1	I	127	ARG	2.3
1	Q	5	ARG	2.3
1	K	54	TYR	2.3
1	F	52	PRO	2.3
1	L	2	THR	2.3
1	S	197	ALA	2.3
1	D	128	GLN	2.3
1	E	31	GLN	2.3
1	G	3	GLU	2.3
1	K	31	GLN	2.3
1	G	30	ASP	2.3
1	G	2	THR	2.3
1	Q	2	THR	2.3
1	M	4	ARG	2.3
1	L	54	TYR	2.3
1	U	179	ILE	2.3
1	U	152	GLN	2.3
1	B	34	GLY	2.3
1	B	36	PRO	2.3
1	A	6	VAL	2.3
1	T	132	GLY	2.3
1	W	13	GLY	2.3
1	F	37	ARG	2.3
1	P	131	HIS	2.3
1	B	175	GLN	2.3
1	O	31	GLN	2.3
1	U	126	GLU	2.3
1	P	71	PRO	2.3
1	T	27	ARG	2.3
1	W	17	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	R	113	THR	2.2
1	I	10	LEU	2.2
1	O	197	ALA	2.2
1	N	166	GLU	2.2
1	X	130	GLU	2.2
1	V	24	PRO	2.2
1	X	122	GLY	2.2
1	E	181	ILE	2.2
1	A	173	ALA	2.2
1	U	49	SER	2.2
1	M	195	GLU	2.2
1	U	125	GLU	2.2
1	D	71	PRO	2.2
1	N	110	THR	2.2
1	V	30	ASP	2.2
1	D	55	VAL	2.2
1	D	132	GLY	2.2
1	G	130	GLU	2.2
1	E	202	THR	2.2
1	K	205	LYS	2.2
1	V	32	ALA	2.2
1	R	82	SER	2.2
1	X	45	TRP	2.2
1	Q	49	SER	2.2
1	F	125	GLU	2.2
1	P	147	GLY	2.2
1	R	41	GLU	2.2
1	T	53	GLY	2.2
1	X	134	ILE	2.2
1	K	47	GLY	2.2
1	W	193	GLY	2.2
1	H	2	THR	2.2
1	O	202	THR	2.2
1	X	1	MET	2.2
1	M	46	LEU	2.2
1	B	21	ASP	2.1
1	U	12	ARG	2.1
1	W	9	SER	2.1
1	A	51	TRP	2.1
1	E	42	TRP	2.1
1	S	108	GLU	2.1
1	H	20	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	83	SER	2.1
1	J	74	SER	2.1
1	C	154	SER	2.1
1	A	103	HIS	2.1
1	D	42	TRP	2.1
1	X	111	VAL	2.1
1	P	133	TYR	2.1
1	F	39	PRO	2.1
1	N	158	SER	2.1
1	I	128	GLN	2.1
1	K	55	VAL	2.1
1	F	22	TRP	2.1
1	C	16	TRP	2.1
1	W	137	CYS	2.1
1	F	38	LEU	2.1
1	F	166	GLU	2.1
1	L	3	GLU	2.1
1	N	186	GLU	2.1
1	U	195	GLU	2.1
1	O	1	MET	2.1
1	D	92	ALA	2.1
1	M	15	SER	2.1
1	O	15	SER	2.1
1	S	177	ASN	2.1
1	V	31	GLN	2.1
1	G	31	GLN	2.1
1	G	190	GLN	2.1
1	M	44	GLN	2.1
1	E	21	ASP	2.1
1	E	149	ASP	2.1
1	F	192	GLY	2.1
1	H	119	GLU	2.1
1	L	41	GLU	2.1
1	N	178	GLU	2.1
1	N	202	THR	2.1
1	U	178	GLU	2.1
1	D	37	ARG	2.1
1	K	12	ARG	2.1
1	M	56	ARG	2.1
1	O	181	ILE	2.1
1	H	9	SER	2.1
1	M	50	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	46	LEU	2.1
1	K	25	HIS	2.1
1	H	107	ASP	2.1
1	W	171	LYS	2.1
1	Q	177	ASN	2.1
1	N	81	LEU	2.1
1	M	172	LEU	2.1
1	F	23	TYR	2.0
1	N	45	TRP	2.0
1	P	22	TRP	2.0
1	L	180	THR	2.0
1	N	2	THR	2.0
1	F	105	ALA	2.0
1	T	28	LEU	2.0
1	Q	122	GLY	2.0
1	L	146	PRO	2.0
1	C	7	PRO	2.0
1	M	94	ARG	2.0
1	S	14	PRO	2.0
1	U	202	THR	2.0
1	B	126	GLU	2.0
1	A	3	GLU	2.0
1	E	186	GLU	2.0
1	F	9	SER	2.0
1	G	187	SER	2.0
1	B	179	ILE	2.0
1	R	94	ARG	2.0
1	G	48	GLY	2.0
1	K	123	LYS	2.0
1	T	39	PRO	2.0
1	K	168	PRO	2.0
1	O	71	PRO	2.0
1	A	124	HIS	2.0
1	T	131	HIS	2.0
1	K	2	THR	2.0
1	N	46	LEU	2.0

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

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.